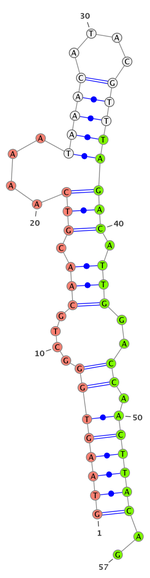
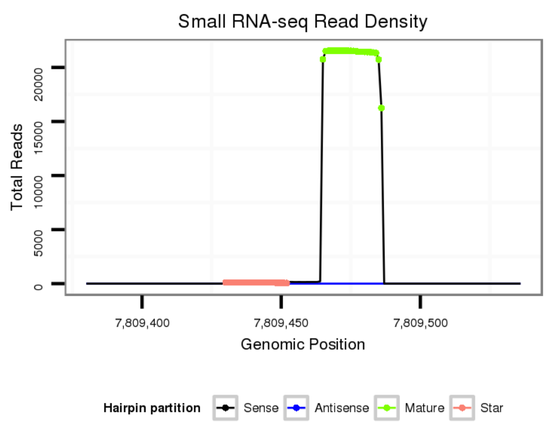
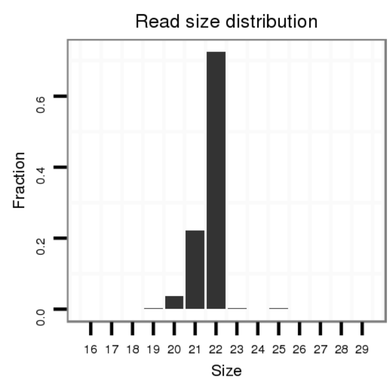
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dps_7	**3:7809430-7809486 +**	**confident**	**Mirtron**	**intron**	[View on UCSC Genome Browser (Cornell Mirror)]

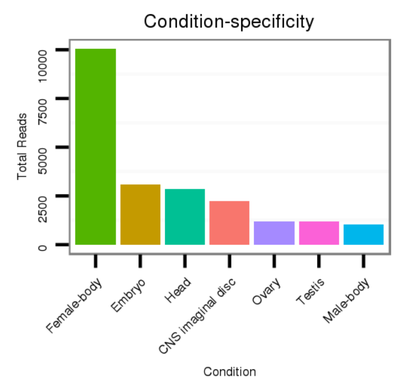
Legend: mature star mismatch in alignment mismatch in read

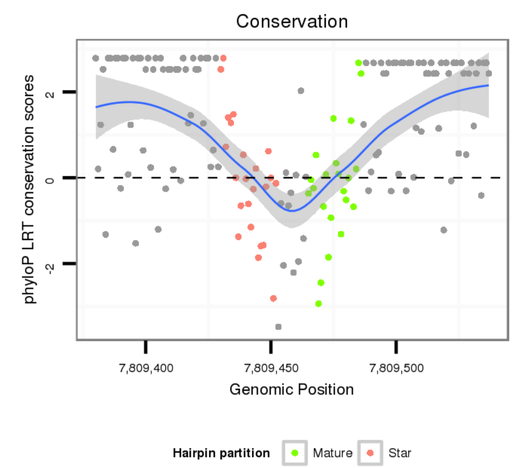
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dpse\GA21273-in]; CDS [Dpse\GA21273-cds]; CDS [Dpse\GA21273-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

AGCGCAATATCAAGCTGAAGGAGCTCACTGGGGGCAGCATGGACAAGCTGGTAAGTGGGCTGCAACGTCAAAATAAACATACGTTTAGACATTGGACCAACTTACAGGTGCTGCTGGAGAAAATCAATAACTGGTGGCTCTCGTTCTGCCAGCAGAT ********** (((((((.... (((. (((.... (((((....))))))))) .))) ..)).)))))) .. **********	Read size	# Mismatch	Hit Count	Total Norm	Total	M040 female body	M059 embryo	SRR902012 CNS imaginal disc	GSM444067 head	GSM343916 embryo	SRR902010 ovaries	SRR902011 testis	M062 head	V112 male body	M022 male body
.....TAGACATTGGACCAACTTACAG.....	22	0	1	15645.00	15645	6551	1597	1941	1291	808	1064	1029	534	617	213
.....TAGACATTGGACCAACTTACA.....	21	0	1	4251.00	4251	2248	222	250	565	340	110	141	213	133	29
.....TAGACATTGGACCAACTTACAGT.....	23	1	1	1364.00	1364	405	216	178	86	131	50	89	49	119	41
.....TAGACATTGGACCAACTTAC.....	20	0	1	590.00	590	291	29	7	137	12	2	4	75	29	4
.....AGACATTGGACCAACTTACAG.....	21	0	1	542.00	542	525	1	4	1	2	2	5	2	0	0
.....TAGACATTGGACCAACTTACAC.....	22	1	1	379.00	379	174	106	13	7	10	33	2	24	3	7
.....AGACATTGGACCAACTTACA.....	20	0	1	191.00	191	190	0	0	1	0	0	0	0	0	0
.....TAGACATTGGACCAACTTACAGA.....	23	1	1	178.00	178	80	19	35	6	5	21	10	2	0	0
.....TAGACATTGGACCAACTTACAA.....	22	1	1	107.00	107	73	15	1	1	7	7	0	1	1	1
.....TAGACATTGGACCAACTTACAGC.....	23	1	1	85.00	85	0	65	1	1	0	1	0	16	0	1
.....TAGACATTGGACCAACTTA.....	19	0	1	46.00	46	32	3	1	4	3	0	0	2	0	1
.....TAAACATACGTTTAGACATTGGACC.....	25	0	1	42.00	42	10	5	9	0	0	0	3	15	0	0
.....AGACATTGGACCAACTTACAGT.....	22	1	1	38.00	38	33	1	1	1	2	0	0	0	0	0
.....GACATTGGACCAACTTACAG.....	20	0	1	31.00	31	26	0	0	1	0	2	0	1	1	0
.....GTAAGTGGGCTGCAACGTCAAAA.....	23	0	1	30.00	30	5	3	8	5	9	0	0	0	0	0
.....TTAGACATTGGACCAACTTACA.....	22	0	1	28.00	28	18	0	2	0	3	4	0	0	1	0
.....TAAACATACGTTTAGACATTGGACCAACT.....	29	0	1	27.00	27	11	6	0	0	0	0	0	9	0	1
.....TAAACATACGTTTAGACATTGGAC.....	24	0	1	26.00	26	10	4	0	0	1	0	2	9	0	0
.....TAGACATTGGACCAACTTACAT.....	22	1	1	25.00	25	10	3	0	4	3	0	5	0	0	0
.....GTAAGTGGGCTGCAACGTCAAA.....	22	0	1	17.00	17	6	0	0	0	9	0	0	0	2	0
.....GTAAGTGGGCTGCAACGT.....	18	0	1	16.00	16	14	1	0	0	1	0	0	0	0	0
.....TTAGACATTGGACCAACTTACAG.....	23	0	1	15.00	15	8	0	1	0	0	2	3	0	1	0
.....AGACATTGGACCAACTTACAC.....	21	1	1	14.00	14	13	1	0	0	0	0	0	0	0	0
.....AGACATTGGACCAACTTAC.....	19	0	1	13.00	13	12	0	0	1	0	0	0	0	0	0
.....TAAACATACGTTTAGACATTGGACCA.....	26	0	1	13.00	13	7	2	1	0	0	0	0	3	0	0
.....TAAACATACGTTTAGACATTGG.....	22	0	1	12.00	12	11	1	0	0	0	0	0	0	0	0
.....TAAACATACGTTTAGACATTGGA.....	23	0	1	10.00	10	6	1	1	0	1	0	0	0	0	1
.....GTAAGTGGGCTGCAACGTCAAAAT.....	24	0	1	10.00	10	3	0	0	0	0	1	0	0	5	1
.....AGACATTGGACCAACTTACAGA.....	22	1	1	10.00	10	9	0	0	0	0	1	0	0	0	0
.....TAGACATTGGACCAACTTACAGAA.....	24	2	1	9.00	9	8	1	0	0	0	0	0	0	0	0
.....GACATTGGACCAACTTACA.....	19	0	1	9.00	9	9	0	0	0	0	0	0	0	0	0
.....GTAAGTGGGCTGCAACGTCAA.....	21	0	1	9.00	9	5	0	0	0	2	0	0	0	2	0
.....GTAAGTGGGCTGCAACGTC.....	19	0	1	8.00	8	7	0	0	0	0	0	0	0	1	0
.....AGACATTGGACCAACTTACAA.....	21	1	1	8.00	8	8	0	0	0	0	0	0	0	0	0
.....TAGACATTGGACCAACTTACG.....	21	1	1	7.00	7	2	3	0	1	0	0	0	1	0	0
.....TAAACATACGTTTAGACATTGGACCAAC.....	28	0	1	7.00	7	1	3	1	0	0	0	0	2	0	0
.....TTTAGACATTGGACCAACTTACA.....	23	0	1	7.00	7	7	0	0	0	0	0	0	0	0	0
.....TAGACATTGGACCAACTT.....	18	0	1	7.00	7	4	0	0	0	0	2	0	0	0	1
.....GTAAGTGGGCTGCAACGTCA.....	20	0	1	6.00	6	3	0	0	0	2	0	0	0	1	0
.....TAGACATTGGACCAACTTACAGG.....	23	0	1	6.00	6	5	0	0	0	0	0	0	0	0	1
.....TAGACATTGGACCAACTTTT.....	19	1	1	6.00	6	6	0	0	0	0	0	0	0	0	0
.....TAGACATTGGACCAACTTACACC.....	23	2	1	6.00	6	1	2	0	1	2	0	0	0	0	0
.....TAAACATACGTTTAGACATTG.....	21	0	1	6.00	6	5	0	0	1	0	0	0	0	0	0
.....GTAAGTGGGCTGCAACGTCAAAATA.....	25	0	1	6.00	6	2	0	0	0	0	0	0	0	4	0
.....TTAGACATTGGACCAACTTACAGT.....	24	1	1	5.00	5	0	0	0	0	0	5	0	0	0	0
.....TAGACATTGGACCAACTTACAGTA.....	24	2	1	5.00	5	3	0	0	1	0	1	0	0	0	0
.....TAGACATTGGACCAACTTACACT.....	23	2	1	5.00	5	2	3	0	0	0	0	0	0	0	0
.....TAGACATTGGACCAACTTACACA.....	23	2	1	5.00	5	2	2	0	0	1	0	0	0	0	0
.....TAGACATTGGACCAACTTACT.....	21	1	1	4.00	4	1	1	0	1	0	0	0	1	0	0
.....TAGACATTGGACCAACTTACAGTAA.....	25	3	1	4.00	4	4	0	0	0	0	0	0	0	0	0
.....TAGACATTGGACCAACTTACAAAA.....	24	3	1	4.00	4	3	1	0	0	0	0	0	0	0	0
.....TAGACATTGGACCAACTTACAGCA.....	24	2	1	4.00	4	0	0	0	0	0	4	0	0	0	0
.....TTAGACATTGGACCAACTTAC.....	21	0	1	4.00	4	3	0	0	0	0	0	0	0	1	0
.....TTGGACCAACTTACAG.....	16	0	1	4.00	4	0	0	2	0	0	1	1	0	0	0
.....AGACATTGGACCAACTTA.....	18	0	1	4.00	4	4	0	0	0	0	0	0	0	0	0
.....CATTGGACCAACTTACAG.....	18	0	1	3.00	3	3	0	0	0	0	0	0	0	0	0
.....TACGTTTAGACATTGGACCAACTTACAG.....	28	0	1	3.00	3	3	0	0	0	0	0	0	0	0	0
.....TAGACATTGGACCAACTTACAGAAA.....	25	3	1	3.00	3	3	0	0	0	0	0	0	0	0	0
.....TAGACATTGGACCAACTTACAGGA.....	24	1	1	3.00	3	0	0	3	0	0	0	0	0	0	0
.....AAACATACGTTTAGACATTGGACC.....	24	0	1	3.00	3	3	0	0	0	0	0	0	0	0	0
.....TAGACATTGGACCAACTTACACAA.....	24	3	1	3.00	3	3	0	0	0	0	0	0	0	0	0
.....AGACATTGGACCAACTTTT.....	18	1	1	3.00	3	3	0	0	0	0	0	0	0	0	0
.....GTAAGTGGGCTGCAACGTCAAAATAAAC.....	28	0	1	2.00	2	0	1	0	0	0	0	0	0	1	0
.....TTAGACATTGGACCAACTT.....	19	0	1	2.00	2	2	0	0	0	0	0	0	0	0	0
.....TTAGACATTGGACCAACTTACAC.....	23	1	1	2.00	2	2	0	0	0	0	0	0	0	0	0
.....GACATTGGACCAACTTACAGA.....	21	1	1	2.00	2	0	0	1	0	0	1	0	0	0	0
.....ATAAACATACGTTTAGACATTGGACC.....	26	0	1	2.00	2	0	1	0	0	0	0	0	1	0	0
.....TAGACATTGGACCAACTTACACTG.....	24	3	1	2.00	2	0	0	0	0	0	0	2	0	0	0
.....TAGACATTGGACCAACT.....	17	0	1	2.00	2	0	0	2	0	0	0	0	0	0	0
.....TAGACATTGGACCAACTTACC.....	21	1	1	2.00	2	2	0	0	0	0	0	0	0	0	0
.....AGCTGAAGGAGCTCACTGGGGGCAGCA.....	27	0	1	2.00	2	0	0	0	0	0	0	2	0	0	0
.....ACATTGGACCAACTTACAG.....	19	0	1	2.00	2	2	0	0	0	0	0	0	0	0	0
.....ACATACGTTTAGACATTGGACCAACT.....	26	0	1	2.00	2	1	1	0	0	0	0	0	0	0	0
.....TAGACATTGGACCAACTTACATT.....	23	2	1	2.00	2	0	0	0	0	0	0	2	0	0	0
.....GACATTGGACCAACTTACAGT.....	21	1	1	2.00	2	2	0	0	0	0	0	0	0	0	0
.....TTAGACATTGGACCAACTTACAA.....	23	1	1	2.00	2	2	0	0	0	0	0	0	0	0	0
.....AGACATTGGACCAACTTACAT.....	21	1	1	2.00	2	2	0	0	0	0	0	0	0	0	0
.....AGACATTGGACCAACTTACAGC.....	22	1	1	2.00	2	0	0	0	1	0	0	0	1	0	0
.....AAATCAATAACTGGTGGCTCT.....	21	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....TAGACATTGGACCAACTTAAG.....	21	2	1	1.00	1	0	0	1	0	0	0	0	0	0	0
.....TAGACATTGGACCAACTTACAGGC.....	24	1	1	1.00	1	0	0	1	0	0	0	0	0	0	0
.....CATACGTTTAGACATTGGACCAACTT.....	26	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....GTAAGTGGGCTGCAACGTCAAAATAA.....	26	0	1	1.00	1	0	0	0	0	0	0	0	0	1	0
.....TAAGTGGGCTGCAACGTCAAAA.....	22	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....AGACATTGGACCAACTTACACT.....	22	2	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....TAGACATTGGACCAACTTACAGAC.....	24	2	1	1.00	1	0	0	1	0	0	0	0	0	0	0
.....AAGTGGGCTGCAACGTCAAAATAAA.....	25	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....GTTTAGACATTGGACCAACTTACA.....	24	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....ATTGGACCAACTTACAGT.....	18	1	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....AGACATTGGACCAACTTACAAA.....	22	2	1	1.00	1	1	0	0	0	0	0	0	0	0	0

Anti-sense strand reads

TCGCGTTATAGTTCGACTTCCTCGAGTGACCCCCGTCGTACCTGTTCGACCATTCACCCGACGTTGCAGTTTTATTTGTATGCAAATCTGTAACCTGGTTGAATGTCCACGACGACCTCTTTTAGTTATTGACCACCGAGAGCAAGACGGTCGTCTA ********** (((((((.... (((. (((.... (((((....))))))))) .))) ..)).)))))) .. **********	Read size	# Mismatch	Hit Count	Total Norm	Total	M040 female body
.....CGAGAGCAAGACGGTCGTCTA	21	0	1	1.00	1	1

Show Alignment With Reads

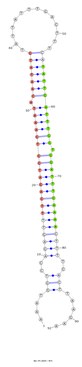
Re-alignment of all predicted orthologs

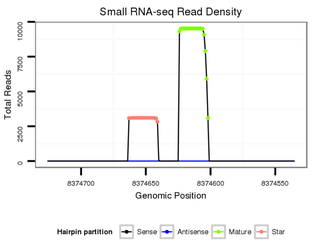
Species	Coordinate	ID	Alignment
dp5	3:7809380-7809537 +	dps_7	AGCGCAATATCAAGCTGAAGGAGCTCACTGGGGGCAGCATGGACAAGCTGGTAAGTGGGCTG-----CAA----------CGTC-AAAAT--AAACAT-------ACGTTT-----A----------G----------ACATTG----------GACCAACTTACAGGTGCTGCTGGAGAAAATCAATAACTGGTGGCTCTCGTTCTGCCAGCAGATG
droPer2	scaffold_4:1720063-1720220 +	dpe_22	AACGCAATATCAAGCTGAAGGAGCTCACTGGGGGCAGCATGGACAAGCTGGTAAGTGGGCTG-----CAA----------CGTC-AAAAT--AAACAT-------ACGTTT-----A----------G----------ACATTG----------GACCAACTTACAGGTGCTGCTGGAGAAAATCAATAACTGGTGGCTCTCGTTCTGCCAGCAGATG
droWil2	scf2_1100000004954:2253224-2253384 +		AAGGAACATCAAACTAAAGAACTCACTGGCGGCAGCATGGACAAATGGTAAGTGACTTT----C-G----------T--TAAATGTATGTATAC--ATTTT----CGTATAA----------T----------ACGTTG----------A-GA-TCTTTAGGTACTTCTGGAGAAAATAATAACTGGTGGCTCTCATTCTGCCAGCAAATG
droVir3	scaffold_12875:14890753-14890810 -		AAGGAACATCAAGCTAAGGAACTAACTGGCGGCAGCATGGACAAGCTAGTAAGTGG----------------------

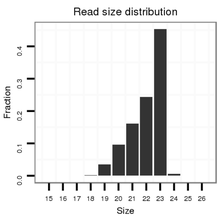
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dps_245	**XL_group1e:8374585-8374676 -**	**confident**	**Testes-restricted**	**intergenic**	[View on UCSC Genome Browser [Cornell Mirror]]

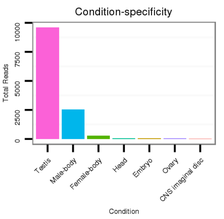
Legend: nomatch mm mismatch in alignment mismatch in seed

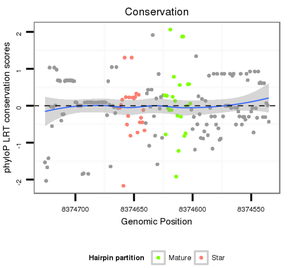
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

mature	star
1. dps_245 XL_group1e:8374602-8374624 - 2. dps-mir-2517a-2 XL_group1e:8378049-8378071 - 3. dps-mir-2517a-3 XL_group1e:8380453-8380473 - 4. dps-mir-2517a-1 Unknown_singleton_1920:1654-1676 +	1. dps_245 XL_group1e:8374641-8374663 - 2. Unknown_singleton_1920:859-881 +

Sense Strand Reads

hide 3p reads show mid mismatch reads

TATCTAGTTCGTTGGGCGAATAAACGAGTGCGACCGAGTAACCGGGTCAAATGGTCCAGAGTTTTCAGATCCTCAAATACAATATGTATTATTTGACTTTCATATTGATTTGGTGGATTTGAAAACTTTTCACTTAAGAACACTTGATACAAGTCTCTATCTCAACGAATATTTTTCGTTGTTCTCCCTACC	Read size	# Mismatch	Hit Count	Total Norm	Total	SRR902011 testis	V112 male body	M040 female body	M022 male body	GSM444067 head	SRR902010 ovaries	GSM343916 embryo	M062 head	SRR902012 CNS imaginal disc	M059 embryo
....((((.(((((((((((((((((((.((((((((.....)))))))))))))).))))))))))))))).))))).....	23	0	4	3010.50	12042	10432	1357	82	3	23	56	41	4	38	6
.....TATTGATTTGGTGGATTTGAAAA.....	22	0	4	2760.00	11040	7784	2885	154	19	53	49	55	13	17	11
.....TTCAGATCCTCAAATACAATATG.....	23	0	2	2721.00	5442	4885	107	94	269	17	18	4	19	10	19
.....TATTGATTTGGTGGATTTGAA.....	21	0	4	1943.50	7774	4929	2571	129	11	42	33	30	10	11	8
.....TATTGATTTGGTGGATTTGA.....	20	0	4	1152.00	4608	2396	1838	230	4	39	29	46	5	16	5
.....TATTGATTTGGTGGATTTGAAAAG.....	24	1	4	592.75	2371	2152	199	9	1	4	1	1	1	3	0
.....TATTGATTTGGTGGATTTG.....	19	0	4	417.00	1668	1226	327	68	11	22	6	3	2	3	0
.....TTCAGATCCTCAAATACAATAT.....	22	0	2	235.50	471	369	31	53	1	3	0	0	12	0	2
.....TTCAGATCCTCAAATACAATATG.....	24	1	2	160.00	320	313	1	1	2	0	3	0	0	0	0
.....TATTGATTTGGTGGATTTGAAAAAA.....	25	2	4	134.00	536	498	33	2	0	1	1	0	0	1	1
.....TTCAGATCCTCAAATACAATATGT.....	24	0	2	76.50	153	99	42	6	0	4	0	0	1	0	1
.....ATTGATTTGGTGGATTTGAAAA.....	22	0	4	70.25	281	230	36	10	0	1	0	2	1	1	0
.....ATTGATTTGGTGGATTTGAAAA.....	22	0	4	55.75	223	145	61	11	1	2	3	0	0	0	0
.....TATTGATTTGGTGGATTTGAAA.....	22	1	4	46.25	185	130	53	2	0	0	0	0	0	0	0
.....TATTGATTTGGTGGATTTG.....	19	1	4	43.75	175	135	27	8	0	5	0	0	0	0	0
.....ATTGATTTGGTGGATTTGAA.....	20	0	4	38.00	152	90	49	12	0	0	0	0	1	0	0
.....TTCAGATCCTCAAATACAATA.....	21	0	2	32.50	65	59	3	2	0	0	0	0	1	0	0
.....ATTGATTTGGTGGATTTGA.....	19	0	4	28.00	112	45	44	23	0	0	0	0	0	0	0
.....TATTGATTTGGTGGATTTGAAAAAAA.....	26	3	4	26.50	106	98	7	1	0	0	0	0	0	0	0
.....TATTGATTTGGTGGATTTGAAAAA.....	23	1	4	24.50	98	91	5	0	0	0	2	0	0	0	0
.....TATTGATTTGGTGGATTTGAAA.....	23	1	4	23.75	95	73	18	2	0	1	0	0	0	1	0
.....TTCAGATCCTCAAATACAATATGT.....	25	1	2	22.00	44	33	7	0	0	1	0	0	3	0	0
.....ATTGATTTGGTGGATTTA.....	18	0	4	20.75	83	79	0	1	1	2	0	0	0	0	0
.....TCAGATCCTCAAATACAATATG.....	22	0	2	20.00	40	24	0	12	3	0	0	0	1	0	0
.....TATTGATTTGGTGGATTTGAAAAG.....	24	1	4	19.75	79	69	7	1	0	0	0	0	2	0	0
.....TATTGATTTGGTGGATTTG.....	20	1	4	18.00	72	26	38	5	1	2	0	0	0	0	0
.....TATTGATTTGGTGGATTTG.....	20	2	10	15.50	159	113	41	3	1	1	0	0	0	0	0
.....TTCAGATCCTCAAATACAAT.....	20	0	2	12.00	24	18	0	5	0	0	0	0	1	0	0
.....TTCAGATCCTCAAATACAATATG.....	23	1	2	11.50	23	19	2	1	0	1	0	0	0	0	0
.....TTCAGATCCTCAAATACAATATG.....	23	1	2	10.50	21	19	0	0	1	0	0	0	1	0	0
.....TTGATTTGGTGGATTTGAAAA.....	21	0	4	10.00	40	32	6	2	0	0	0	0	0	0	0
.....TATTGATTTGGTGGATTTGAAAAG.....	21	2	4	9.50	38	23	14	0	0	1	0	0	0	0	0
.....TTGATTTGGTGGATTTGAAA.....	20	0	4	9.50	38	26	8	3	0	0	0	1	0	0	0
.....TATTGATTTGGTGGATTTG.....	19	1	4	8.25	33	26	4	2	0	1	0	0	0	0	0
.....TTCAGATCCTCAAATACAATA.....	22	1	2	8.00	16	12	2	1	0	1	0	0	0	0	0
.....ATTGATTTGGTGGATTTGAAAAG.....	23	1	4	7.75	31	22	7	2	0	0	0	0	0	0	0
.....TATTGATTTGGTGGATTTGAA.....	22	1	4	7.75	31	21	9	1	0	0	0	0	0	0	0
.....TTCAGATCCTCAAATACAATATGTCCC.....	27	3	2	6.50	13	12	1	0	0	0	0	0	0	0	0
.....TATTGATTTGGTGGATTTGAA.....	21	2	4	6.25	25	14	11	0	0	0	0	0	0	0	0
.....TATTGATTTGGTGGATTTGA.....	21	1	4	5.75	23	14	9	0	0	0	0	0	0	0	0
.....TTCAGATCCTCAAATACAATATGT.....	25	1	2	5.50	11	9	2	0	0	0	0	0	0	0	0
.....TTCAGATCCTCAAATACAATAT.....	23	1	2	5.50	11	8	1	0	0	1	0	0	1	0	0
.....TATTGATTTGGTGGATTTGAA.....	22	1	4	5.50	22	13	9	0	0	0	0	0	0	0	0
.....TATTGATTTGGTGGATT.....	17	0	4	5.00	20	19	0	0	0	0	1	0	0	0	0
.....ATTGATTTGGTGGATTTG.....	19	1	5	4.80	24	17	7	0	0	0	0	0	0	0	0
.....ATTGATTTGGTGGATTTGAAAA.....	23	2	4	4.50	18	13	2	0	0	0	3	0	0	0	0
.....TATTGATTTGGTGGATTTGCG.....	20	2	5	4.20	21	9	12	0	0	0	0	0	0	0	0
.....TATTGATTTGGTGGATTTGAA.....	21	1	4	3.75	15	10	1	0	1	0	0	0	3	0	0
.....TATTGATTTGGTGGATTTGAA.....	21	1	4	3.75	15	7	7	1	0	0	0	0	0	0	0
.....TATTGATTTGGTGGATTTCG.....	20	2	8	3.63	29	18	11	0	0	0	0	0	0	0	0
.....TTCAGATCCTCAAATACAATATGTCC.....	26	2	2	3.50	7	4	3	0	0	0	0	0	0	0	0
.....ATTGATTTGGTGGATTTGCCC.....	22	3	4	3.50	14	10	4	0	0	0	0	0	0	0	0
.....TCAGATCCTCAAATACAATAT.....	21	0	2	3.00	6	1	0	5	0	0	0	0	0	0	0
.....TTCAGATCCTCAAATACAATAAAA.....	24	3	2	3.00	6	6	0	0	0	0	0	0	0	0	0
.....TATTGATTTGGTGGATTTGAAAA.....	23	1	4	2.75	11	9	2	0	0	0	0	0	0	0	0
.....TATTGATTTGGTGGATTTGAAAAA.....	24	0	4	2.75	11	10	1	0	0	0	0	0	0	0	0
.....TATTGATTTGGTGGATTTGAAA.....	23	2	4	2.75	11	10	0	0	0	1	0	0	0	0	0
.....TTCAGATCCTCAAATACAA.....	19	0	2	2.50	5	5	0	0	0	0	0	0	0	0	0
.....TTCAGATCCTCAAATACAATATG.....	24	1	2	2.50	5	3	0	0	0	0	0	0	2	0	0
.....ATTGATTTGGTGGATTTGAAAG.....	22	1	4	2.50	10	8	2	0	0	0	0	0	0	0	0
.....TATTGATTTGGTGGATTTGAAAG.....	24	1	4	2.50	10	10	0	0	0	0	0	0	0	0	0
.....TATTGATTTGGTGGATTTG.....	20	1	4	2.25	9	5	4	0	0	0	0	0	0	0	0
.....TTCAGATCCTCAAATACAATTCC.....	22	2	4	2.00	4	2	1	0	0	0	0	0	1	0	0
.....TATTGATTTGGTGGATTTGATC.....	22	2	4	2.00	8	4	4	0	0	0	0	0	0	0	0
.....TATTGATTTGGTGGATTTGAAAACC.....	24	2	4	2.00	8	6	2	0	0	0	0	0	0	0	0
.....TATTGATTTGGTGGATTTGAAATC.....	24	2	4	2.00	8	8	0	0	0	0	0	0	0	0	0
.....ATTGATTTGGTGGATTTGCG.....	19	1	4	1.75	7	2	4	1	0	0	0	0	0	0	0
.....TTGATTTGGTGGATTTGAAAAG.....	22	0	4	1.75	7	6	0	0	0	0	0	0	0	0	1
.....TTGATTTGGTGGATTTGAAAAG.....	22	1	4	1.75	7	6	1	0	0	0	0	0	0	0	0
.....TATTGATTTGGTGGATTTCG.....	20	2	5	1.60	8	5	3	0	0	0	0	0	0	0	0
.....TTCAGATCCTCAAATACAATATGTAAA.....	27	2	2	1.50	3	3	0	0	0	0	0	0	0	0	0
.....AGATCCTCAAATACAATATGTC.....	21	0	2	1.50	3	3	0	0	0	0	0	0	0	0	0
.....TTTCAGATCCTCAAATACAATATGCC.....	25	3	2	1.50	3	3	0	0	0	0	0	0	0	0	0
.....TTCAGATCCTCAAATACAATATGTAT.....	26	0	2	1.50	3	3	0	0	0	0	0	0	0	0	0
.....ATTGATTTGGTGGATTTGAAAAAA.....	24	2	4	1.50	6	5	1	0	0	0	0	0	0	0	0
.....TATTGATTTGGTGGATTTG.....	15	0	4	1.50	6	6	0	0	0	0	0	0	0	0	0
.....TATTGATTTGGTGGATTTGCG.....	22	2	4	1.50	6	4	2	0	0	0	0	0	0	0	0
.....TATTGATTTGGTGGATTTGAAAAA.....	25	3	4	1.50	6	5	1	0	0	0	0	0	0	0	0
.....TTGATTTGGTGGATTTGA.....	18	0	4	1.50	6	4	0	2	0	0	0	0	0	0	0
.....ATATTGATTTGGTGGATTTG.....	23	0	4	1.50	6	6	0	0	0	0	0	0	0	0	0
.....TATTGATTTGGTGGATTTGCCCC.....	22	3	14	1.50	21	12	7	0	1	1	0	0	0	0	0
.....TATTGATTTGGTGGATTTCCC.....	21	2	4	1.25	5	3	2	0	0	0	0	0	0	0	0
.....TATTGATTTGGTGGATTTCG.....	25	2	4	1.25	5	5	0	0	0	0	0	0	0	0	0
.....TGATTTGGTGGATTTGAAAA.....	20	0	4	1.25	5	5	0	0	0	0	0	0	0	0	0
.....ATTGATTTGGTGGATTTGAA.....	21	1	4	1.25	5	4	1	0	0	0	0	0	0	0	0
.....TTGATTTGGTGGATTTGAA.....	19	0	4	1.25	5	4	0	1	0	0	0	0	0	0	0
.....TATTGATTTGGTGGATTTGAAAAAA.....	25	2	4	1.25	5	5	0	0	0	0	0	0	0	0	0
.....TATTGATTTGGTGGATTTG.....	20	1	4	1.25	5	3	2	0	0	0	0	0	0	0	0
.....TATTGATTTGGTGGATTTGAAACA.....	24	2	4	1.25	5	5	0	0	0	0	0	0	0	0	0
.....TTCAGATCCTCAAATACAATA.....	21	0	2	1.00	2	2	0	0	0	0	0	0	0	0	0
.....AGATCCTCAAATACAATATG.....	20	0	2	1.00	2	2	0	0	0	0	0	0	0	0	0
.....TTCAGATCCTCAAATACAATATGTCA.....	26	2	2	1.00	2	1	1	0	0	0	0	0	0	0	0
.....TTTCAGATCCTCAAATACAATAT.....	21	0	2	1.00	2	2	0	0	0	0	0	0	0	0	0
.....TCAGATCCTCAAATACAATATGT.....	23	0	2	1.00	2	2	0	0	0	0	0	0	0	0	0
.....ATTGATTTGGTGGATTTGAAAT.....	22	1	4	1.00	4	3	1	0	0	0	0	0	0	0	0
.....TATTGATTTGGTGGATTTGCG.....	22	2	4	1.00	4	4	0	0	0	0	0	0	0	0	0
.....TATTTGACTTTCATATTGATTTGG.....	26	0	4	1.00	4	4	0	0	0	0	0	0	0	0	0
.....TATTGATTTGGTGGATTTGAAAACG.....	25	1	4	1.00	4	4	0	0	0	0	0	0	0	0	0
.....TATTTGACTTTCATATTGATTTGG.....	24	0	4	1.00	4	4	0	0	0	0	0	0	0	0	0
.....TATTGATTTGGTGGATTTCG.....	20	2	4	1.00	4	2	1	0	0	0	0	0	1	0	0
.....TATTGATTTGGTGGATTTGAAAAG.....	25	2	4	1.00	4	4	0	0	0	0	0	0	0	0	0
.....TATTGATTTGGTGGATTTCCC.....	22	3	5	1.00	5	3	1	0	1	0	0	0	0	0	0
.....TATTGATTTGGTGGATTTCCCC.....	23	3	4	0.75	3	3	0	0	0	0	0	0	0	0	0
.....TATTGATTTGGTGGATTTGAAATC.....	24	3	4	0.75	3	3	0	0	0	0	0	0	0	0	0
.....TATTGATTTGGTGGATTTGAAATCC.....	24	3	4	0.75	3	2	1	0	0	0	0	0	0	0	0
.....ATTGATTTGGTGGATTTGAAAAG.....	23	1	4	0.75	3	3	0	0	0	0	0	0	0	0	0
.....TATTGATTTGGTGGATTTGAAAG.....	23	2	4	0.75	3	2	1	0	0	0	0	0	0	0	0
.....TATTGATTTGGTGGATTTGAAAAAG.....	25	2	4	0.75	3	3	0	0	0	0	0	0	0	0	0
.....TATTGATTTGGTGGATTTGAAAAAAA.....	26	3	4	0.75	3	3	0	0	0	0	0	0	0	0	0
.....TATTGATTTGGTGGATTTGAAA.....	23	1	4	0.75	3	3	0	0	0	0	0	0	0	0	0
.....TATTGATTTGGTGGATTTCG.....	20	2	6	0.67	4	4	0	0	0	0	0	0	0	0	0
.....ATTGATTTGGTGGATTTGT.....	18	1	5	0.60	3	3	0	0	0	0	0	0	0	0	0
.....TATTGATTTGGTGGATTTGCCC.....	23	3	5	0.60	3	3	0	0	0	0	0	0	0	0	0
.....TATTGATTTGGTGGATTTCC.....	19	2	9	0.56	5	3	2	0	0	0	0	0	0	0	0
.....TATTGATTTGGTGGATTTCCC.....	21	3	9	0.56	5	4	0	0	0	1	0	0	0	0	0
.....TTCAGATCCTCAAATACAATATGTCA.....	26	2	2	0.50	1	0	1	0	0	0	0	0	0	0	0
.....TTCAGATCCTCAAATACAATATGA.....	24	2	2	0.50	1	1	0	0	0	0	0	0	0	0	0
.....CAGATCCTCAAATACAATATG.....	21	0	2	0.50	1	1	0	0	0	0	0	0	0	0	0
.....TTCAGATCCTCAAATACAATATAA.....	24	2	2	0.50	1	1	0	0	0	0	0	0	0	0	0
.....AGATCCTCAAATACAATAT.....	20	1	2	0.50	1	0	1	0	0	0	0	0	0	0	0
.....TATTGATTTGGTGGATTTGAAAATAA.....	25	3	4	0.50	2	2	0	0	0	0	0	0	0	0	0
.....ATATTGATTTGGTGGATTTGA.....	21	0	4	0.50	2	1	1	0	0	0	0	0	0	0	0
.....TATTGATTTGGTGGATTTGAAACCC.....	24	3	4	0.50	2	1	1	0	0	0	0	0	0	0	0
.....TTGATTTGGTGGATTTGAAAG.....	21	1	4	0.50	2	2	0	0	0	0	0	0	0	0	0

Anti-sense strand reads

ATAGATCAAGCAACCCGCTTATTTGCTCACGCTGGCTCATTGGCCCAGTTTACCAGGTCTCAAAAGTCTAGGAGTTTATGTTATACATAATAAACTGAAAGTATAACTAAACCACCTAAACTTTTGAAAAGTGAATTCTTGTGAACTATGTTCAGAGATAGAGTTGCTTATAAAAAGCAACAAGAGGGATGG	Read size	# Mismatch	Hit Count	Total Norm	M040 female body	SRR902011 testis	GSM343916 embryo
....((((.(((((((((((((((((((.((((((((.....)))))))))))))).))))))))))))))).))))).....	26	0	1	1.00	1	1	0
.....GCTCACGCTGGCTCATTGGCCCAGTT.....	23	0	6	0.50	3	0	3
.....TACCAGGTCTCAAAAGTCTAGGA.....	24	0	4	0.25	1	0	0
.....AACTGAAAGTATAACTAAACCACC.....							

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
dp5	XL_group1e:8374535-8374726 -	dps_245	TATCTAGTTCGTTGGGCGAATAAACGAGTGCGACCGAGTAACCGGGTCAAATGGTCCAGAGTTTTCAGATCCTCAAATACAATATGTATTATTTGACTTTCATATTGATTTGGTGGATTTGAAAACTTTTCACTTAAGAACACTTGATACAAGTCTCTATCTCAACGAATATTTTTCGTTGTTCTCCCTAGC
droPer2	scaffold_13:187524-187652 +	dps_55	TATCTAGTTCGTTGGGCGAATAAACGAGTCGATAACCGGGTCAAATGGTCAGAGTTTTCATACCCTCAAATACCATATGTATTATTCGATTTCATATTGATTTGATGGATTTGAAAACTTTTCAC
droWil2	scf2_1100000004590:2157842-2157891 +		TAT
droVir3	scaffold_12954:1915840-1915865 +		AATATTATTTGTTTCATAATAAACC
droMoj3	scaffold_6500:19217358-19217431 +		TGG TTTGAATTTTTTTATTATATATATAAA
droKik1	scf7180000303244:1745808-1745850 +		CGAG
droFic1	scf7180000453841:240436-240486 -		GT
droEle1	scf7180000490583:9115-9173 +		AAA
droRho1	scf7180000706602:13-75 +		TGA
droBia1	scf7180000302168:136112-136122 -		ATCTGTA
droTak1	scf7180000415379:251441-251548 -		A
droEug1	scf7180000409218:8049-8142 +		CAG
droYak3	v2_chr2b_random_026:267953-268001 -		TA

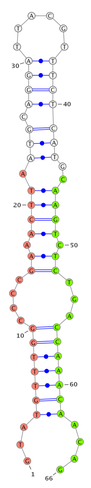
Generated: 09/08/2015 at 08:41 PM

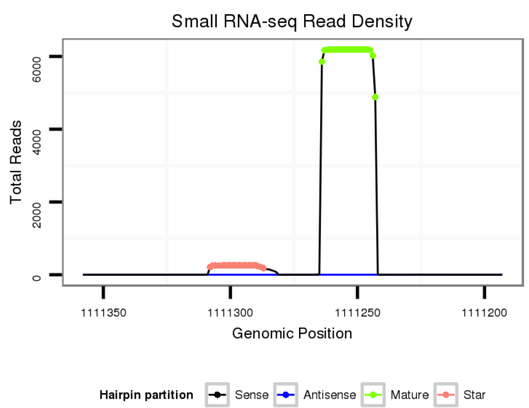
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.mismatch	1
crit.top3	1
crit.blnp3	0
crit.uri	0
crit.back	0
rescue.precursor	0
rescue.dominant	0
rescue.known	0
rescue.confident	4
rescue.candidate	0

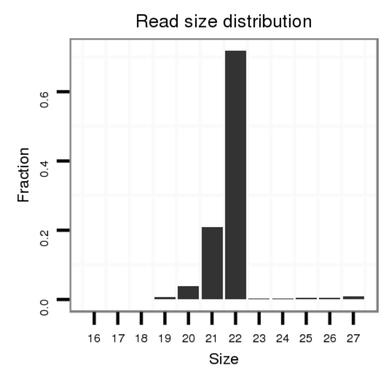
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dps_2613	**XL_group1e:1111243-1111308 -**	**confident**	**Mirtron**	**intron**	[View on UCSC Genome Browser [Cornell Mirror]]

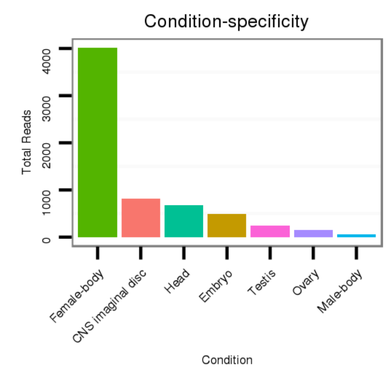
Legend: mature star mismatch in alignment mismatch in read

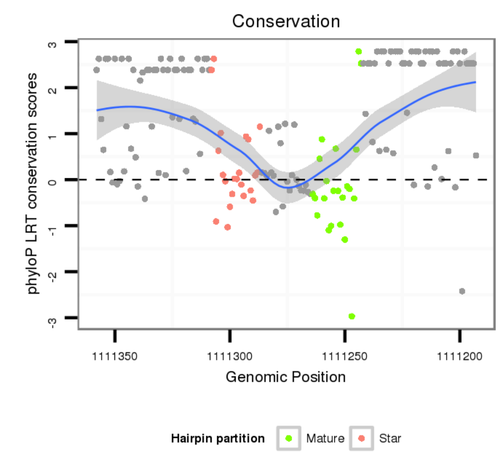
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dpse\GA27402-in]; CDS [Dpse\GA27402-cds]; CDS [Dpse\GA27402-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

GAGCTACAATGATGACGTGGGCCCGCCAAGTCATCGGAGACGTTTGGATGGTATGTTTGGCCCCGAAACTTAATGCAGGATTACGTTTCTCATGCAAGTCTCTGACCAAACAACAGGTCGACATAACGAGAATGCTGATATGGATATTAGCGGAGATTCGACGCCC **********...(((((((....((.((((.(((.((((.....)))))))..))))).))...)))))))....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M040 female body	SRR902012 CNS imaginal disc	M062 head	M059 embryo	SRR902011 testis	GSM444067 head	SRR902010 ovaries	GSM343916 embryo	M022 male body	V112 male body
.....CAAGTCTCTGACCAAACAACAG.....	22	0	1	4608.00	4608	2772	767	192	272	203	118	133	104	37	10
.....CAAGTCTCTGACCAAACAACA.....	21	0	1	1074.00	1074	664	34	218	54	32	36	14	10	10	2
.....AAGTCTCTGACCAAACAACAG.....	21	0	1	245.00	245	233	4	2	3	1	1	0	1	0	0
.....CAAGTCTCTGACCAAACAAC.....	20	0	1	149.00	149	73	1	57	9	1	3	1	0	4	0
.....CAAGTCTCTGACCAAACAACAGT.....	23	1	1	95.00	95	32	4	23	24	0	4	2	6	0	0
.....GTATGTTTGGCCCCGAAACTTAATGCA.....	27	0	1	66.00	66	35	2	17	11	0	0	0	1	0	0
.....AAGTCTCTGACCAAACAACA.....	20	0	1	62.00	62	60	0	1	0	0	0	0	1	0	0
.....CAAGTCTCTGACCAAACAACAGA.....	23	1	1	47.00	47	22	9	3	5	1	2	2	2	1	0
.....GTATGTTTGGCCCCGAAACTT.....	21	0	1	30.00	30	22	0	3	0	0	5	0	0	0	0
.....GTATGTTTGGCCCCGAAAC.....	19	0	1	28.00	28	22	0	3	1	0	1	0	1	0	0
.....GTATGTTTGGCCCCGAAACTTA.....	22	0	1	20.00	20	18	0	0	2	0	0	0	0	0	0
.....GTATGTTTGGCCCCGAAACTTAATGC.....	26	0	1	19.00	19	15	1	0	3	0	0	0	0	0	0
.....GTATGTTTGGCCCCGAAACT.....	20	0	1	18.00	18	13	0	0	0	0	5	0	0	0	0
.....CAAGTCTCTGACCAAACAACAGC.....	23	1	1	18.00	18	1	4	4	9	0	0	0	0	0	0
.....GTATGTTTGGCCCCGAAACTTAATG.....	25	0	1	17.00	17	16	0	0	0	0	0	0	1	0	0
.....CAAGTCTCTGACCAAACAACAG.....	22	1	1	14.00	14	2	0	4	8	0	0	0	0	0	0
.....TATGTTTGGCCCCGAAACTTAAT.....	23	0	1	12.00	12	5	0	3	3	0	1	0	0	0	0
.....CAAGTCTCTGACCAAACAA.....	19	0	1	11.00	11	7	0	2	1	1	0	0	0	0	0
.....AGTCTCTGACCAAACAACAG.....	20	0	1	10.00	10	10	0	0	0	0	0	0	0	0	0
.....GTATGTTTGGCCCCGAAACTTAAT.....	24	0	1	10.00	10	7	0	2	1	0	0	0	0	0	0
.....CAAGTCTCTGACCAAACAACAA.....	22	1	1	9.00	9	6	0	1	1	0	0	0	1	0	0
.....TATGTTTGGCCCCGAAACTTAATGC.....	25	0	1	8.00	8	3	0	3	2	0	0	0	0	0	0
.....TATGTTTGGCCCCGAAACTTAATGCA.....	26	0	1	8.00	8	8	0	0	0	0	0	0	0	0	0
.....CAAGTCTCTGACCAAACAACG.....	21	1	1	6.00	6	0	0	5	1	0	0	0	0	0	0
.....TATGTTTGGCCCCGAAACTTAATG.....	24	0	1	6.00	6	3	1	0	2	0	0	0	0	0	0
.....AAGTCTCTGACCAAACAAC.....	19	0	1	5.00	5	5	0	0	0	0	0	0	0	0	0
.....GTCTCTGACCAAACAACAG.....	19	0	1	5.00	5	5	0	0	0	0	0	0	0	0	0
.....TGCAAGTCTCTGACCAAACAACAG.....	24	0	1	5.00	5	0	0	0	1	0	0	4	0	0	0
.....CAAGTCTCTGACCAAACAACT.....	21	1	1	4.00	4	2	0	1	0	0	0	0	0	1	0
.....TATGTTTGGCCCCGAAACTTA.....	21	0	1	4.00	4	4	0	0	0	0	0	0	0	0	0
.....GCAAGTCTCTGACCAAACAACAG.....	23	0	1	3.00	3	2	0	0	0	0	0	0	1	0	0
.....CAAGTCTCTGACCAAACAACAGG.....	23	0	1	3.00	3	3	0	0	0	0	0	0	0	0	0
.....TATGTTTGGCCCCGAAACTT.....	20	0	1	3.00	3	2	0	1	0	0	0	0	0	0	0
.....CAAGTCTCTGACCAAACAACAT.....	22	1	1	2.00	2	1	0	0	1	0	0	0	0	0	0
.....TTTGGCCCCGAAACTTAATGCA.....	22	0	1	2.00	2	1	0	0	0	0	1	0	0	0	0
.....AGTCTCTGACCAAACAACA.....	19	0	1	2.00	2	2	0	0	0	0	0	0	0	0	0
.....AAGTCTCTGACCAAACAACAGT.....	22	1	1	2.00	2	2	0	0	0	0	0	0	0	0	0
.....AAGTCTCTGACCAAACAACAGA.....	22	1	1	2.00	2	2	0	0	0	0	0	0	0	0	0
.....ATGCAAGTCTCTGACCAAACAACAG.....	25	0	1	2.00	2	0	0	0	0	0	0	2	0	0	0
.....GTATGTTTGGCCCCGAAACTTAA.....	23	0	1	2.00	2	2	0	0	0	0	0	0	0	0	0
.....CAAGTCTCTGACCAAACAACAGTG.....	24	2	1	1.00	1	0	0	0	1	0	0	0	0	0	0
.....CGGAGACGTTTGGATGGT.....	18	0	1	1.00	1	0	1	0	0	0	0	0	0	0	0
.....CAAGTCTCTGACCAAACAAA.....	20	1	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....TGCAAGTCTCTGACCAAACAACA.....	23	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....AGTCTCTGACCAAACAACAGG.....	21	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....GTCATCGGAGACGTTTGGATGGTCG.....	25	2	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....ATGTTTGGCCCCGAAACTTAATGCA.....	25	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....CGGAGACGTTTGGATGGTAT.....	20	0	1	1.00	1	0	1	0	0	0	0	0	0	0	0
.....TATGTTTGGCCCCGAAACTTAA.....	22	0	1	1.00	1	0	0	1	0	0	0	0	0	0	0
.....CAAGTCTCTGACCAAACA.....	18	0	1	1.00	1	0	0	0	0	0	0	1	0	0	0
.....CTCTGACCAAACAACAG.....	17	0	1	1.00	1	0	0	0	0	0	0	1	0	0	0
.....GTATGTTTGGCCCCGAAACTTAATGT.....	26	1	1	1.00	1	0	0	1	0	0	0	0	0	0	0
.....CAAGTCTCTGACCAAACAACAGAAA.....	25	3	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....GAGAATGCTGATATGGAT.....	18	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....TCTCTGACCAAACAACAG.....	18	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....CAAGTCTCTGACCAAACAACC.....	21	1	1	1.00	1	0	0	1	0	0	0	0	0	0	0
.....TCTGACCAAACAACAG.....	16	0	1	1.00	1	0	1	0	0	0	0	0	0	0	0
.....TTTGGCCCCGAAACTTAATG.....	20	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....TATGTTTGGCCCCGAAAA.....	18	1	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....AAGTCTCTGACCAAACAA.....	18	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....TATGTTTGGCCCCGAAACTTAATGCT.....	26	1	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....CAAGTCTCTGACCAAACAACTC.....	22	2	1	1.00	1	0	0	1	0	0	0	0	0	0	0
.....CATAACGAGAATGCTGATATGGA.....	23	0	1	1.00	1	0	0	0	0	0	0	0	1	0	0
.....ATGTTTGGCCCCGAAACTTAATGC.....	24	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....TATGTTTGGCCCCGAAACT.....	19	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....AAGTCTCTGACCAAACAACAA.....	21	1	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....GTATGTTTGGCCCCGAAACTTAATT.....	25	1	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....CGGAGACGTTTGGATGGTCGA.....	21	3	2	0.50	1	1	0	0	0	0	0	0	0	0	0
.....GTATGTTTGGCCCCGATT.....	18	2	7	0.14	1	1	0	0	0	0	0	0	0	0	0

Anti-sense strand reads

CTCGATGTTACTACTGCACCCGGGCGGTTCAGTAGCCTCTGCAAACCTACCATACAAACCGGGGCTTTGAATTACGTCCTAATGCAAAGAGTACGTTCAGAGACTGGTTTGTTGTCCAGCTGTATTGCTCTTACGACTATACCTATAATCGCCTCTAAGCTGCGGG **********...(((((((....((.((((.(((.((((.....)))))))..))))).))...)))))))....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M040 female body

Show Alignment With Reads

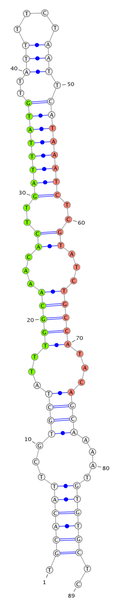
Re-alignment of all predicted orthologs

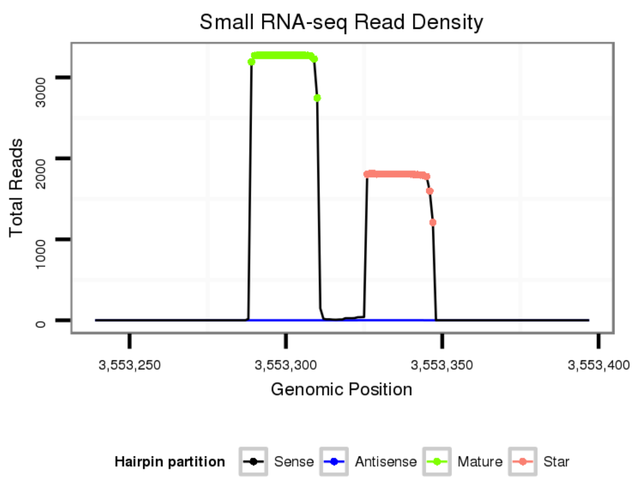
Species	Coordinate	ID	Alignment
dp5	XL_grouple:1111193-1111358 -	dps_2613	GAGCTACAATGATGACGTGGGCCCGCCAAGTCATCGGAGACGTTTGGATGGTATGTTTGG---CCCCG----------A--------AA----------CTTAATGC-AGGA-TTACGTTTCTCATG-CAAGTC----------T----------CTGAC----------C-----AAACAACAGGTCGACATAACGAGAATGCTGATATGGATATTAGCGGAGATTCGACGCCC
droPer2	scaffold_30:84744-84909 +	dpe_66	GAGCTACAATGATGACGTGGGCCCGCCAAGTCATCGGAGACGTTTGGATGGTATGTTTGG---CCCCG----------A--------AA----------CTTAATGC-AGGA-TTACGTTTCTCATG-CAAGTC----------T----------CTGAC----------C-----AAACAACAGGTCGACATAACGAGAATGCTGATATGGATATTAGCGGAGATTCGACGCCC
droWil2	scf2_1100000004909:3951869-3952034 +		GAATTATAATGATGATGGTGGTCCGCCTAGTCATCGAAGCGGTGTAGATGGTAACTAAGATGA-----TTACATTTGGGCTACA--------**----------TTTATGCTA----------**----**----------**------ATTGT-----ATT----------C----CGTTC----T-TGTTTCCTGTTAGGTCGACATAACGATAATGCAGATATGGATATCAGTGCGGATTCCACGCCC
droVir3	scaffold_12970:9692047-9692208 -		GAATTATGACAACGATGCGGTCCGCCAGCCATCGAAGCGTTTGGATGGTAAGTAGCA----T---CTGCAG--------**--------**----------C----A----------CGTCT--AACA----------**----**----------**------GTTGA-----TCTACCATACTCAA----TAATT----**-----CTTATGCAGGTCGACATAACGATAATGCTGATATGGACATCAGCGGCGACTCAACGCCC
droMoj3	scaffold_6473:11876601-11876774 +		GAACTAGGAAATGATGCGGCCGGCCGCCAGCCATCGAAGCGGATTGGATGGTGAGTGGCA----T---TGAAGGAT----T----------**----------GCTGTCGA----ATTGCTCGATTGATCGT----------**----**----TAAT----------**------AT----ATG----------T----TGTTT----**-GATTTGTCTGCAGGTCGACATAACGATAATGCTGATATGGACATTAGTGGCGACTCGACGCCC
droGri2	scaffold_14853:346387-346569 +		GAATTAGACAACGATGGTGGCCGGCCGCCAGCCATCGAAGCGTTTGGATGGTGAGCAACAGCA----G---CGACAAGC----A----------**----------GCAGCAGC----ACCATTTAATTAATTGT----------**----**----TCATCA-----T--**---G----AGCTAATGTTTT------**-----GAA---TTG----ATTGCGCAGGTCGACATAACGATAATGCTGATATGGATATCAGCGGCGACTCAACGCCC
droAna3	scaffold_13334:780666-780821 +		GAATTAGACAACGATGGC---CCGCCCAGCCATCGAAGCGTTTGGATGGTCTGTACTT----TCCCT----------**----------TAAATACTACAAGACT----------**----**----T---------T---**---A-----AGCTAATCCTGG------**-----GTA-----T-----ATCCTACAGGACGACACAATGACAATGCTGACATGGACATAAGCGGCGACTCGACGCCC
droBip1	scf7180000396733:412644-412804 +		GAATTACAACGACGATG---GCCCGCCCAGCCATCGAAGCGTTTGGATGGTGAGTTCTTTGG-TGG---CCGTAGGTGCTT---ATCCT----------**----------TGGTG----**----**----**----------**------GCTAA-----TTT---------G----AAATA----TT----TCCCTCAGGTCGACACAATGACAATGCTGACATGGACATAAGCGGCGATTCGACGCCC
droKik1	scf7180000302610:1225933-1226096 -		GAATTATGAAACGATGCGGACCGCCAGCCATCGAAGCGTTTGGATGGTAAGAAAAACAC---TA----------**----------TAAATC----------AAT-TAAAACAAGA-TTATATT-------**---C----**----------TAT----------TA----AAACC----T----TCCCCCCAGGTCGACACAATGACAATGCTGATATGGATATAAGCGGCGATTCCACGCCC
droFic1	scf7180000454077:1214357-1214552 +		GAATTAGACAACGATGCGGTCCACCGCAGCCATCGAAGACGTTTGGATGGTAAGAAAATTGA-----T----------**-CGATTGA--TTGATAGTCAGTCAATTGCAACATCGGAATGATACCATTTGATACC----------**----**----**----------**-----ATTTGATCTAATATT----------**-----**-----GATA-T-----TATTCGCAGGTCGACACAACGACAATGCTGATATGGACATAAGCGGCGACTCGACGCCC
droEle1	scf7180000490546:445981-446033 +		----------**----**----------**----------**----**----**----------**----**----**----------**----**----

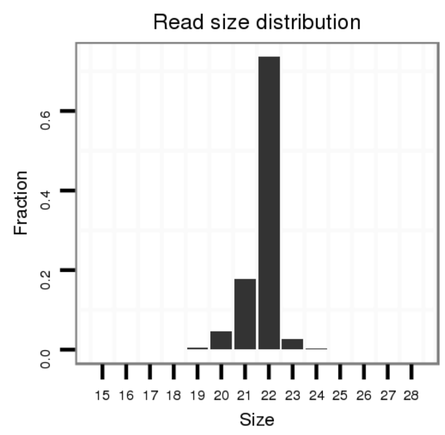
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dps_14	**4_group4:3553289-3553347 +**	**confident**	**Testes-restricted**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

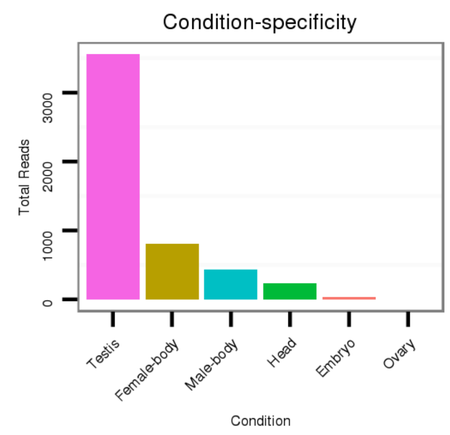
Legend: mature star mismatch in alignment mismatch in read

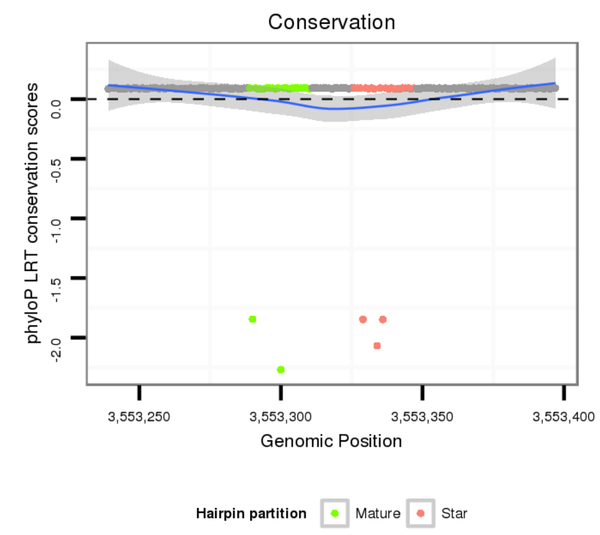
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

GTAACCGTGTTGAGGAAAGTGTTTCCCCCACCAAATGCACATTCGTGCTATTTGGCAAACACTTGATTTATGTTATTTTCTAATTCATAAATCTCGTATCTGCCATACAGCAAAATGTGTGCTCTATCCTGATGCATCCTATGCTGGCTTAGATCAGAA ********** .((((((... ((((... (((((... ((.((((((((.(((....))) .)))))))) ..)) ...))))) ...)))) ....)))))) .. **********	Read size	# Mismatch	Hit Count	Total Norm	Total	SRR902011 testis	M040 female body	V112 male body	M062 head	GSM444067 head	M059 embryo	M022 male body	GSM343916 embryo	SRR902010 ovaries
.....TTTGGCAAACACTTGATTTATG.....	22	0	1	2529.00	2529	1479	605	219	110	60	24	24	5	3
.....TAAATCTCGTATCTGCCATACA.....	22	0	1	1200.00	1200	1144	34	13	3	5	0	0	1	0
.....TTTGGCAAACACTTGATTTAT.....	21	0	1	459.00	459	302	72	53	15	13	2	2	0	0
.....TAAATCTCGTATCTGCCATAC.....	21	0	1	380.00	380	318	12	35	7	6	2	0	0	0
.....TAAATCTCGTATCTGCCATA.....	20	0	1	171.00	171	144	4	19	2	2	0	0	0	0
.....TTTGGCAAACACTTGATTTATGT.....	23	0	1	131.00	131	51	20	54	1	3	1	1	0	0
.....TTTGGCAAACACTTGATTTATGA.....	23	1	1	89.00	89	69	11	7	0	2	0	0	0	0
.....TTGGCAAACACTTGATTTATG.....	21	0	1	56.00	56	20	35	0	0	1	0	0	0	0
.....TTTGGCAAACACTTGATTTA.....	20	0	1	36.00	36	21	6	5	2	2	0	0	0	0
.....TTTGGCAAACACTTGATTTATT.....	22	1	1	36.00	36	24	6	2	3	1	0	0	0	0
.....TAAATCTCGTATCTGCCATACAA.....	23	1	1	23.00	23	21	2	0	0	0	0	0	0	0
.....TTTGGCAAACACTTGATTTATGTC.....	24	1	1	23.00	23	8	1	12	1	1	0	0	0	0
.....TAAATCTCGTATCTGCCATACC.....	22	1	1	21.00	21	17	1	1	2	0	0	0	0	0
.....TAAATCTCGTATCTGCCATAA.....	21	1	1	19.00	19	17	0	0	0	2	0	0	0	0
.....TTGGCAAACACTTGATTTAT.....	20	0	1	17.00	17	7	9	1	0	0	0	0	0	0
.....TTTGGCAAACACTTGATTTATC.....	22	1	1	16.00	16	9	1	2	3	1	0	0	0	0
.....TTTGGCAAACACTTGATTTAA.....	21	1	1	12.00	12	7	3	2	0	0	0	0	0	0
.....ATTTGGCAAACACTTGATTTATG.....	23	0	1	12.00	12	11	0	0	0	0	0	1	0	0
.....TTTGGCAAACACTTGATTTATGAA.....	24	2	1	9.00	9	8	0	1	0	0	0	0	0	0
.....TAAATCTCGTATCTGCCAT.....	19	0	1	9.00	9	9	0	0	0	0	0	0	0	0
.....TTTGGCAAACACTTGATTTATGC.....	23	1	1	8.00	8	5	0	0	2	0	1	0	0	0
.....TTTGGCAAACACTTGATTTATGTT.....	24	0	1	7.00	7	1	2	2	2	0	0	0	0	0
.....TTTGGCAAACACTTGATTTATA.....	22	1	1	7.00	7	5	0	2	0	0	0	0	0	0
.....TAAATCTCGTATCTGCCATT.....	20	1	1	7.00	7	6	1	0	0	0	0	0	0	0
.....TTTGGCAAACACTTGATTTATGTCG.....	25	2	1	6.00	6	2	2	1	0	1	0	0	0	0
.....TAAATCTCGTATCTGCCATAT.....	21	1	1	6.00	6	6	0	0	0	0	0	0	0	0
.....TAAATCTCGTATCTGCCATACTAA.....	24	3	1	6.00	6	6	0	0	0	0	0	0	0	0
.....TTTGGCAAACACTTGATTT.....	19	0	1	6.00	6	4	1	0	0	1	0	0	0	0
.....TATTTTCTAATTCATAA.....	17	0	2	5.50	11	11	0	0	0	0	0	0	0	0
.....TAATTCATAAATCTCGTATCTGCCAT.....	26	0	1	5.00	5	5	0	0	0	0	0	0	0	0
.....TTTGGCAAACACTTGATTTATGTG.....	24	1	1	5.00	5	5	0	0	0	0	0	0	0	0
.....ATTTGGCAAACACTTGATTTAT.....	22	0	1	5.00	5	5	0	0	0	0	0	0	0	0
.....TTTGGCAAACACTTGATTTATGTCC.....	25	2	1	5.00	5	2	1	0	2	0	0	0	0	0
.....TAAATCTCGTATCTGCCATACT.....	22	1	1	5.00	5	5	0	0	0	0	0	0	0	0
.....TTTGGCAAACACTTGATTTATGTTTGG.....	27	3	1	4.00	4	4	0	0	0	0	0	0	0	0
.....TCATAAATCTCGTATCTGCCATAC.....	24	0	1	4.00	4	4	0	0	0	0	0	0	0	0
.....TCATAAATCTCGTATCTGCCATACC.....	25	1	1	4.00	4	4	0	0	0	0	0	0	0	0
.....TTTGGCAAACACTTGATTTATGTTAA.....	26	1	1	3.00	3	3	0	0	0	0	0	0	0	0
.....TTTGGCAAACACTTGATTTATGTCCC.....	26	3	1	3.00	3	2	0	0	1	0	0	0	0	0
.....TAATTCATAAATCTCGTATCTGCCATA.....	27	0	1	3.00	3	1	0	1	1	0	0	0	0	0
.....AAATCTCGTATCTGCCATACA.....	21	0	1	3.00	3	1	2	0	0	0	0	0	0	0
.....TTTGGCAAACACTTGATTTATGTCT.....	25	2	1	2.00	2	0	1	1	0	0	0	0	0	0
.....TCATAAATCTCGTATCTGCC.....	20	0	1	2.00	2	1	1	0	0	0	0	0	0	0
.....TAATTCATAAATCTCGTATCTGT.....	23	1	1	2.00	2	2	0	0	0	0	0	0	0	0
.....TTTGGCAAACACTTGATTTATGTTAT.....	26	0	1	2.00	2	0	2	0	0	0	0	0	0	0
.....TTGGCAAACACTTGATTTATGT.....	22	0	1	2.00	2	1	1	0	0	0	0	0	0	0
.....AAATCTCGTATCTGCCATAC.....	20	0	1	2.00	2	2	0	0	0	0	0	0	0	0
.....TCATAAATCTCGTATCTGCCATACAAA.....	27	2	1	2.00	2	2	0	0	0	0	0	0	0	0
.....TTTGGCAAACACTTGATTTATTC.....	23	2	1	2.00	2	1	0	1	0	0	0	0	0	0
.....TTTGGCAAACACTTGATTTATCG.....	23	2	1	2.00	2	2	0	0	0	0	0	0	0	0
.....TAATTCATAAATCTCGTATCTGCCATAC.....	28	0	1	2.00	2	2	0	0	0	0	0	0	0	0
.....AAATCTCGTATCTGCCATA.....	19	0	1	2.00	2	2	0	0	0	0	0	0	0	0
.....TAAATCTCGTATCTGCCA.....	18	0	1	2.00	2	1	0	0	1	0	0	0	0	0
.....TCATAAATCTCGTATCTGCCATACAA.....	26	1	1	2.00	2	2	0	0	0	0	0	0	0	0
.....TTTGGCAAACACTTGATTTATGTA.....	24	1	1	2.00	2	1	0	1	0	0	0	0	0	0
.....TTTGGCAAACACTTGATTTT.....	20	1	1	2.00	2	2	0	0	0	0	0	0	0	0
.....TCTAATTCATAAATCTCGTATCTG.....	24	0	1	2.00	2	2	0	0	0	0	0	0	0	0
.....TTCATAAATCTCGTATCTGCCATA.....	24	0	1	2.00	2	2	0	0	0	0	0	0	0	0
.....TTGGCAAACACTTGATTTATGA.....	22	1	1	2.00	2	1	1	0	0	0	0	0	0	0
.....TAAATCTCGTATCTGCCATC.....	20	1	1	2.00	2	2	0	0	0	0	0	0	0	0
.....TCATAAATCTCGTATCTGCCAT.....	22	0	1	2.00	2	2	0	0	0	0	0	0	0	0
.....TCATAAATCTCGTATCTGCCATACA.....	25	0	1	2.00	2	2	0	0	0	0	0	0	0	0
.....TAATTCATAAATCTCGTATCTG.....	22	0	1	2.00	2	2	0	0	0	0	0	0	0	0
.....TTTGGCAAACACTTGATTTATGTTATT.....	27	0	1	2.00	2	2	0	0	0	0	0	0	0	0
.....TTTGGCAAACACTTGATTTATTA.....	23	2	2	2.00	4	4	0	0	0	0	0	0	0	0
.....TTTTCTAATTCATAA.....	15	0	3	1.33	4	4	0	0	0	0	0	0	0	0
.....TTTGGCAAACACTTGATTTATGTCCG.....	26	3	1	1.00	1	0	1	0	0	0	0	0	0	0
.....TGGCAAACACTTGATTTATG.....	20	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....TTTGGCAAACACTTGATTTATGTAG.....	25	2	1	1.00	1	1	0	0	0	0	0	0	0	0
.....CATAAATCTCGTATCTGCCATACA.....	24	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....GGCAAACACTTGATTTATGTCG.....	22	2	1	1.00	1	0	0	1	0	0	0	0	0	0
.....ATTTGGCAAACACTTGAT.....	18	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....AATCTCGTATCTGCCATA.....	18	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....TGGCAAACACTTGATTTATGT.....	21	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....TAAATCTCGTATCTGCCATATT.....	22	2	1	1.00	1	1	0	0	0	0	0	0	0	0
.....TAAATCTCGTATCTGCCATACATTC.....	25	3	1	1.00	1	1	0	0	0	0	0	0	0	0
.....TAATTCATAAATCTCGTATCTGC.....	23	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....TTTGGCAAACACTTGATTTATCA.....	23	2	1	1.00	1	1	0	0	0	0	0	0	0	0
.....TTTGGCAAACACTTGATTTATGTTA.....	25	0	1	1.00	1	0	1	0	0	0	0	0	0	0
.....ATTTGGCAAACACTTGATTTATGTA.....	25	1	1	1.00	1	1	0	0	0	0	0	0	0	0
.....TAATTCATAAATCTCGTATCTGCCA.....	25	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....TTTGGCAAACACTTGATT.....	18	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....TTGGCAAACACTTGATTTATGTTAT.....	25	0	1	1.00	1	0	1	0	0	0	0	0	0	0
.....TTGGCAAACACTTGATTTA.....	19	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....TGGCAAACACTTGATTTAT.....	19	0	1	1.00	1	0	1	0	0	0	0	0	0	0
.....TAAATCTCGTATCTGCCATACTC.....	23	2	1	1.00	1	0	1	0	0	0	0	0	0	0
.....TTTGGCAAACACTTGATTTATAA.....	23	2	1	1.00	1	1	0	0	0	0	0	0	0	0
.....ATTTGGCAAACACTTGATTTATT.....	23	1	1	1.00	1	1	0	0	0	0	0	0	0	0
.....TAATTCATAAATCTCGTATCTGCCC.....	25	1	1	1.00	1	1	0	0	0	0	0	0	0	0
.....GCAAACACTTGATTTATGTTTG.....	22	2	1	1.00	1	1	0	0	0	0	0	0	0	0
.....TAATTCATAAATCTCGTATCTGCC.....	24	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....CTCGTATCTGCCATACA.....	17	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....TTGGCAAACACTTGATT.....	17	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....TAAATCTCGTATCTG.....	15	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....TTGGCAAACACTTGATTTATC.....	21	1	1	1.00	1	0	1	0	0	0	0	0	0	0
.....TAAATCTCGTATCTGCCATACCA.....	23	2	1	1.00	1	1	0	0	0	0	0	0	0	0
.....TCTAATTCATAAATCTCGTATCTGCC.....	26	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....TTTGGCAAACACTTGATTTATGG.....	23	1	1	1.00	1	1	0	0	0	0	0	0	0	0
.....TTTGGCAAACACTTGATTTATCCC.....	24	3	1	1.00	1	1	0	0	0	0	0	0	0	0
.....GGCAAACACTTGATTTATG.....	19	0	1	1.00	1	0	1	0	0	0	0	0	0	0
.....TTTGGCAAACACTTGATTTATGTTATTT.....	28	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....ATAAATCTCGTATCTGCCATAC.....	22	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....TAATTCATAAATCTCGTAT.....	19	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....TAAATCTCGTATCTGCCATAG.....	21	1	1	1.00	1	1	0	0	0	0	0	0	0	0
.....TCATAAATCTCGTATCTGCCATACCA.....	26	2	1	1.00	1	1	0	0	0	0	0	0	0	0
.....TCTAATTCATAAATCTCGTATCTGC.....	25	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....ATTTGGCAAACACTTGATTTATAAA.....	25	3	1	1.00	1	1	0	0	0	0	0	0	0	0
.....TTTGGCAAACACTTGATTTATAG.....	23	2	1	1.00	1	1	0	0	0	0	0	0	0	0
.....ATAAATCTCGTATCTGCCATACA.....	23	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....TTTGGCAAACACTTGATTTATGTTCC.....	26	2	1	1.00	1	1	0	0	0	0	0	0	0	0
.....TAAATCTCGTATCTGCCATAAC.....	22	2	1	1.00	1	1	0	0	0	0	0	0	0	0
.....TTTGGCAAACACTTGAT.....	17	0	2	0.50	1	1	0	0	0	0	0	0	0	0
.....AACACTTGATTTATG.....	15	0	3	0.33	1	1	0	0	0	0	0	0	0	0
.....TTTGGCAAACACTTGATTATT.....	20	2	5	0.20	1	1	0	0	0	0	0	0	0	0
.....ATTTGGCAAACACTT.....	15	0	5	0.20	1	1	0	0	0	0	0	0	0	0
.....TTTGGCAAACACTTGATTATG.....	21	3	13	0.08	1	1	0	0	0	0	0	0	0	0

Anti-sense strand reads

CATTGGCACAACTCCTTTCACAAAGGGGGTGGTTTACGTGTAAGCACGATAAACCGTTTGTGAACTAAATACAATAAAAGATTAAGTATTTAGAGCATAGACGGTATGTCGTTTTACACACGAGATAGGACTACGTAGGATACGACCGAATCTAGTCTT ********** .((((((... ((((... (((((... ((.((((((((.(((....))) .)))))))) ..)) ...))))) ...)))) ....)))))) .. **********	Read size	# Mismatch	Hit Count	Total Norm	Total	M040 female body	SRR902012 CNS imaginal disc	V112 male body	GSM343916 embryo
.....AGTATTTAGAGCATAGACGGTA.....	22	0	1	1.00	1	0	1	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
dp5	4_group4:3553239-3553397 +	dps_14	GTAACCGTGTTGAGGAAAGTGTTTCCCCCACCAAATGCACATTCGTGCTATTTGGCAAACACTTGATTTATGTTATTTTCTAATTCATAAATCTCGTATCTGCCATACAGCAAAATGTGTGCTCTATCCTGATGCATCCTATGCTGGCTTAGATCAGAA
droPer2	scaffold_7821:1029-1187 +	dpe_88	GTAACCGTGTTGAGGAAAGTGTTTCCCCCACCAAATGCACATTCGTGCTATATGGCAAACACTTGATTTATGTTATTTTCTAATTCATAAGTCTCTTGTCTGCCATACAGCAAAATGTGTGCTCTATCCTGATGCATCCTATGCTGGCTTAGATCAGAA

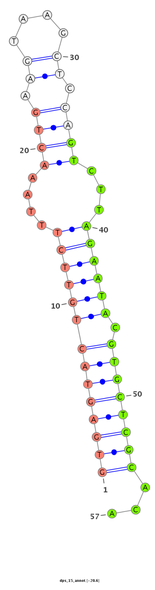
Generated: 09/08/2015 at 08:35 PM

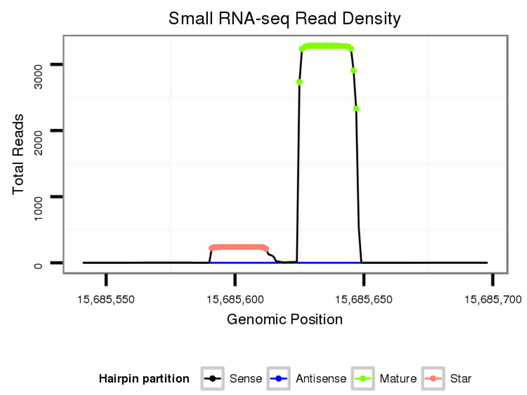
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	2
rescue.candidate	0

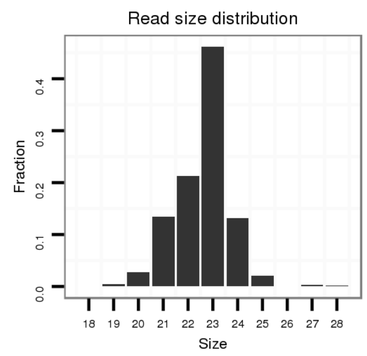
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dps_15	**3:15685591-15685648 +**	**confident**	**Mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

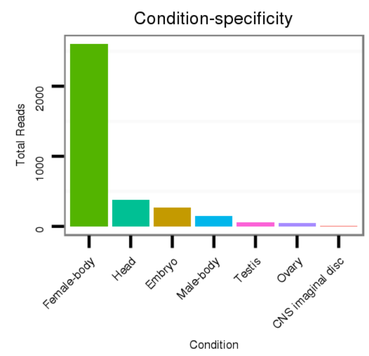
Legend: mature star mismatch in alignment mismatch in read

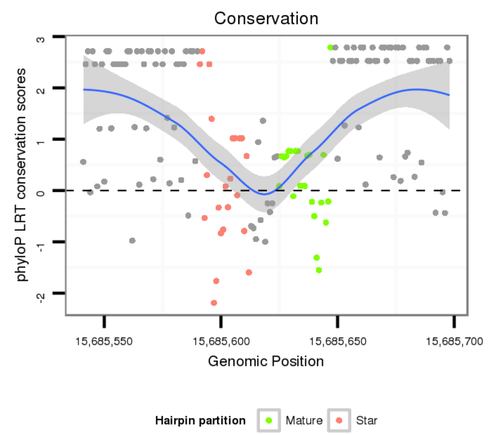
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dpse\GA25012-in]; CDS [Dpse\GA25012-cds]; CDS [Dpse\GA25012-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

CGATACCTCCAAGCCGGCCATCGTCACCTATCATGATCTGGGCCTAAACTGTGAGTACTGTTCTTTAAACTGAAGTAAGCTCCAGTCTTAGAATACGTGCTCGCACAGATGCCACCAGCTTCGCTGGCTTCTTCAACTTCCCAGTGATGCGGGGCCTG **********((((((((((((((....((((.((....)).))))...)))))))).))))))))...**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M040 female body	M062 head	M059 embryo	GSM444067 head	GSM343916 embryo	V112 male body	M022 male body	SRR902011 testis	SRR902010 ovaries	SRR902012 CNS imaginal disc
.....GTCTTAGAATACGTGCTCGCACA.....	23	0	1	1524.00	1524	1125	92	92	92	47	28	36	4	8	0
.....GTCTTAGAATACGTGCTCGCACAG.....	24	0	1	440.00	440	339	13	16	40	24	3	0	0	4	1
.....GTCTTAGAATACGTGCTCGCAC.....	22	0	1	425.00	425	366	31	16	10	0	0	2	0	0	0
.....GTCTTAGAATACGTGCTCGCA.....	21	0	1	288.00	288	217	10	2	22	2	20	13	2	0	0
.....TCTTAGAATACGTGCTCGCACA.....	22	0	1	239.00	239	172	16	13	17	5	13	3	0	0	0
.....TCTTAGAATACGTGCTCGCAC.....	21	0	1	138.00	138	109	4	17	2	1	4	1	0	0	0
.....TCTTAGAATACGTGCTCGCACAG.....	23	0	1	84.00	84	67	2	2	7	3	3	0	0	0	0
.....GTGAGTACTGTTCTTTAAACTG.....	22	0	1	78.00	78	33	0	2	6	17	7	0	3	0	10
.....GTGAGTACTGTTCTTTAAACTGAAG.....	25	0	1	70.00	70	8	0	0	0	0	0	0	31	31	0
.....TCTTAGAATACGTGCTCGCA.....	20	0	1	38.00	38	29	0	1	3	0	5	0	0	0	0
.....GTCTTAGAATACGTGCTCGCACAA.....	24	1	1	34.00	34	31	0	3	0	0	0	0	0	0	0
.....GTCTTAGAATACGTGCTCGC.....	20	0	1	30.00	30	27	0	0	1	0	2	0	0	0	0
.....GTCTTAGAATACGTGCTCGCAA.....	22	1	1	25.00	25	22	0	1	1	1	0	0	0	0	0
.....GTCTTAGAATACGTGCTCGCACC.....	23	1	1	23.00	23	14	1	2	5	0	0	1	0	0	0
.....GTGAGTACTGTTCTTTAAACTGAA.....	24	0	1	22.00	22	15	0	1	0	0	0	5	1	0	0
.....GTCTTAGAATACGTGCTCGCACAGT.....	25	1	1	20.00	20	18	0	1	1	0	0	0	0	0	0
.....GTGAGTACTGTTCTTTAAACT.....	21	0	1	18.00	18	10	0	0	1	3	1	1	0	1	1
.....GTCTTAGAATACGTGCTCGCACT.....	23	1	1	17.00	17	13	0	1	1	1	0	1	0	0	0
.....CTTAGAATACGTGCTCGCACA.....	21	0	1	16.00	16	16	0	0	0	0	0	0	0	0	0
.....GTGAGTACTGTTCTTTAAACTGA.....	23	0	1	13.00	13	11	0	0	0	0	1	0	1	0	0
.....TTAGAATACGTGCTCGCACA.....	20	0	1	13.00	13	2	8	1	1	1	0	0	0	0	0
.....GTGAGTACTGTTCTTTAAACTGAAGTA.....	27	0	1	10.00	10	1	0	0	0	0	0	0	9	0	0
.....TCTTAGAATACGTGCTCGCACAA.....	23	1	1	8.00	8	7	1	0	0	0	0	0	0	0	0
.....GTCTTAGAATACGTGCTCG.....	19	0	1	7.00	7	7	0	0	0	0	0	0	0	0	0
.....TGAGTACTGTTCTTTAAACTG.....	21	0	1	7.00	7	7	0	0	0	0	0	0	0	0	0
.....TCTTAGAATACGTGCTCGCAA.....	21	1	1	6.00	6	6	0	0	0	0	0	0	0	0	0
.....TCTTAGAATACGTGCTCGCACT.....	22	1	1	6.00	6	5	0	0	0	0	1	0	0	0	0
.....GTGAGTACTGTTCTTTAAAC.....	20	0	1	5.00	5	1	0	1	0	2	0	1	0	0	0
.....GTCTTAGAATACGTGCTCGCACTT.....	24	2	1	5.00	5	4	0	0	0	0	1	0	0	0	0
.....CTTAGAATACGTGCTCGCAC.....	20	0	1	5.00	5	5	0	0	0	0	0	0	0	0	0
.....TCTTAGAATACGTGCTCGCACAGT.....	24	1	1	5.00	5	4	0	0	0	1	0	0	0	0	0
.....GTGAGTACTGTTCTTTAAACTGAAGTAA.....	28	0	1	4.00	4	2	0	0	0	0	0	0	2	0	0
.....CTTAGAATACGTGCTCGCACAG.....	22	0	1	4.00	4	4	0	0	0	0	0	0	0	0	0
.....GTCTTAGAATACGTGCTCGCACAC.....	24	1	1	4.00	4	3	0	1	0	0	0	0	0	0	0
.....TCTTAGAATACGTGCTCGCACC.....	22	1	1	4.00	4	2	1	0	0	0	0	1	0	0	0
.....TTAGAATACGTGCTCGCACAG.....	21	0	1	4.00	4	4	0	0	0	0	0	0	0	0	0
.....GTCTTAGAATACGTGCTCGT.....	20	1	1	3.00	3	2	0	0	1	0	0	0	0	0	0
.....TAGAATACGTGCTCGCACA.....	19	0	1	3.00	3	2	1	0	0	0	0	0	0	0	0
.....TGAGTACTGTTCTTTAAACT.....	20	0	1	3.00	3	3	0	0	0	0	0	0	0	0	0
.....AGTCTTAGAATACGTGCTCGCAC.....	23	0	1	3.00	3	3	0	0	0	0	0	0	0	0	0
.....GTCTTAGAATACGTGCTCGCACAGA.....	25	0	1	3.00	3	2	0	0	1	0	0	0	0	0	0
.....TCTTAGAATACGTGCTCGCACCA.....	23	2	1	2.00	2	2	0	0	0	0	0	0	0	0	0
.....TCTTAGAATACGTGCTCGCACAT.....	23	1	1	2.00	2	2	0	0	0	0	0	0	0	0	0
.....TGAGTACTGTTCTTTAAAC.....	19	0	1	2.00	2	2	0	0	0	0	0	0	0	0	0
.....GTCTTAGAATACGTGCTCGCACAT.....	24	1	1	2.00	2	2	0	0	0	0	0	0	0	0	0
.....GTCTTAGAATACGTGCTCGCACCA.....	24	2	1	2.00	2	1	0	0	0	1	0	0	0	0	0
.....AGTAAGCTCCAGTCTTAGAATACGTGCT.....	28	0	1	2.00	2	1	0	0	0	0	1	0	0	0	0
.....GTCTTAGAATACGTGCTCGCAT.....	22	1	1	2.00	2	2	0	0	0	0	0	0	0	0	0
.....TAGAATACGTGCTCGCAC.....	18	0	1	2.00	2	1	1	0	0	0	0	0	0	0	0
.....TCTTAGAATACGTGCTCGC.....	19	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....TCTTAGAATACGTGCTCGCACCT.....	23	2	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....GTTCTTTAAACTGAAGTAAGCTCC.....	24	0	1	1.00	1	0	1	0	0	0	0	0	0	0	0
.....TCTTAGAATACGTGCTCGCATT.....	22	2	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....GTGAGTACTGTTCTTTAAACTGA.....	23	1	1	1.00	1	0	0	0	0	0	1	0	0	0	0
.....AGTCTTAGAATACGTGCTCGCACAG.....	25	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....AGAATACGTGCTCGCACAT.....	19	1	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....TCCAGTCTTAGAATACGTGCTCGCA.....	25	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....CTTAGAATACGTGCTCGCACC.....	21	1	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....TTAGAATACGTGCTCGCAC.....	19	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....ATCGTCACCTATCATGATCTGGGCC.....	25	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....CAACTTCCCAGTGATGCGGGGC...	22	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....CTCCAGTCTTAGAATACGTGCTCGC.....	25	0	1	1.00	1	0	1	0	0	0	0	0	0	0	0
.....TCCAGTCTTAGAATACGTGCTCGCACAG.....	28	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....GTAAGCTCCAGTCTTAGAATACGTGC.....	26	0	1	1.00	1	0	0	1	0	0	0	0	0	0	0
.....CTTAGAATACGTGCTCGCA.....	19	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....TTAGAATACGTGCTCGCACC.....	20	1	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....CCAGTCTTAGAATACGTGCTCG.....	22	0	1	1.00	1	0	0	0	0	0	0	0	1	0	0
.....CTTAGAATACGTGCTCGCACAA.....	22	1	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....CTCCAGTCTTAGAATACGTGC.....	21	0	1	1.00	1	0	0	1	0	0	0	0	0	0	0
.....GTACTGTTCTTTAAACTGAA.....	20	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....GTCTTAGAATACGTGCTCGCACAGC.....	25	1	1	1.00	1	0	0	1	0	0	0	0	0	0	0
.....GTGAGTACTGTTCTTTAAACTGAAGTAAA.....	29	1	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....TGAGTACTGTTCTTTAAACTA.....	21	1	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....AGTAAGCTCCAGTCTTAGA.....	19	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....GTCTTAGAATACGTGCTCGCATT.....	23	2	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....TTCTTCAACTTCCCAGTGATGCGGGGC...	27	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....CATCGTCACCTATCATGATCTGGGC.....	25	0	1	1.00	1	0	0	0	0	1	0	0	0	0	0
.....TGAGTACTGTTCTTTAAACTGAAG.....	24	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....GTCACCTATCATGATCTGGGCCT.....	23	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....CTTAGAATACGTGCTCGCACAT.....	22	1	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....GAGTACTGTTCTTTAAACTGAA.....	22	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....TGAGTACTGTTCTTTAAACTGAA.....	23	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....GTCTTAGAATACGTGCTCGTTT.....	21	2	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....GTGAGTACTGTTCTTTAAACTGAAGT.....	26	0	1	1.00	1	0	0	0	1	0	0	0	0	0	0
.....CACCTATCATGATCTGGGC.....	19	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....TCTTAGAATACGTGCTCGCACAGA.....	24	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....GTCTTAGAATACGTGCTCGCAG.....	22	1	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....AGCTCCAGTCTTAGAATACGT.....	21	0	1	1.00	1	0	0	0	0	0	1	0	0	0	0
.....GAAGTAAGCTCCAGTCTTAGA.....	21	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....TAGAATACGTGCTCGCACAG.....	20	0	1	1.00	1	0	0	0	1	0	0	0	0	0	0
.....AGTCTTAGAATACGTGCTCGCA.....	22	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....AGTCTTAGAATACGTGCTCGCACC.....	24	1	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....GTACTGTTCTTTAAACTGA.....	19	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....GTGAGTACTGTTCTTTAAA.....	19	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....GTCTTAGAATACGTGCTCGCACCT.....	24	2	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....CTTAGAATACGTGCTCGCACAGT.....	23	1	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....GTCTTAGAATACGTGCTTT.....	19	2	2	0.50	1	1	0	0	0	0	0	0	0	0	0

Anti-sense strand reads

GCTATGGAGGTTCGGCCGGTAGCAGTGGATAGTACTAGACCCGGATTTGACACTCATGACAAGAAATTTGACTTCATTCGAGGTCAGAATCTTATGCACGAGCGTGTCTACGGTGGTCGAAGCGACCGAAGAAGTTGAAGGGTCACTACGCCCCGGAC **********((((((((((((((....((((.((....)).))))...)))))))).))))))))...**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M040 female body	V112 male body

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
dp5	3:15685541-15685698 +	dps_15	CGATACCTCCAAGCCGGCCATCGTCACCTATCATGATCTGGGCCTAAACTGTGAGTACT-----TGTT----CT----------TTAAACTGA----------A---GTAAGCTCCAGTCTTAGAATACGTGC----------TCGCACAGATGCCACCAGCTTCGCTGGCTTCTTCAACTTCCCAGTGATGCGGGGCCTG
droPer2	scaffold_4:3367476-3367633 -	dpe_68	CGATACCTCCAAGCCGGCCATCGTCACCTATCATGATCTGGGCCTAAACTGTGAGTAC-----TGTT----CT----------TTAAACTGA----------A---GTAAGCTCCAGTCTTAGAATACGTGC----------TCGCACAGATGCCACCAGCTTCGCTGGCTTCTTCAACTTCCCAGTGATGCGGGGCCTG
droWil2	scf2_1100000004510:1737920-1738088 +		TGATACATCGAACCGGCCATTGTCACCTATCATGATTTGGGTCTGAATTGTAAGTCC-----TTT--CT-AG---------------TCTTA-T----------AATAA----------ACTGTATCCTAACTAAT--------TCTCCTTTTTCTCTGGG----------ATAAACAGATGGTACCAGCTTTGCTGGCTTCTTTAATTATCGCGTGATGCGTGGCCTG
droVir3	scaffold_12875:17803634-17803811 -		CGACACCTCAAAGCCGGCCATAGTCACCTACCACGATCTGGGACTCAACTGTGAGTTG-----TCAC----AA----------TTGACG-CCACGAG--------|---|----------|---CATCTGAGCCA----------ACGCATATTT---CATTTTCAT----------TTTCATTTTGACTCAAACAGATGCCACCAGTTTCGCTGGCTTCTTCAATTATCCAGTCATGCGCGGTTG
droMoj3	scaffold_6496:11427625-11427821 -		CGACACCTCAAAGCCGGCCATAGTCAGTTATCACGATTTGGGACTCAACTGTAAGCAA-----GC----CTGCCTG------------------|---|----------|----------CCACCTGCCACCCACACCTGAACTAATACAGATATATATATATATATTTATATGTATTTCATGTTGT-----ATA--AAAACAGATGCCACCAGTTTCGCTGGCTTCTTCAATTTATCCAGTCATGCGCGGATTG
droGri2	scaffold_15245:13887642-13887814 +		CGACACCTCAAAGCCGGCCATAGTCACCTACCACGATCTGGGACTCAACTGTAAGTC-----AAAC----ATTTCTACTATTTTTGAAATCATCA-T----------|CAACA----------AT--GCAA---CA----------ATGCATTCTT---CA----------CTCTCATCAGATGCCACCAGTTTTGCTGGCTTCTTCAACTTTCCCGTGTTATGCGCGGCCTG
droAna3	scaffold_13266:5227364-5227521 +		CGATACGGCCAAGCCGGCCATTGTCACCTACCACGATCTGGGCCTCAATTGTAAGTGT-----TTT-----|----------TTGAACTTACTACCC----------A---GAGAGTGTCATCTTAAAA------|----------G--------TG----------TT--TTTTTTAGATGCCACCAGCTTTGCTGGCTTCTTCAACTTCCCAGTGATGCGGGGCTTG
droBip1	scf7180000395751:1014686-1014839 +		CGATACGGCCAAGCCGGCCATCGTCACCTACCACGATCTGGGCCTCAACTGTAAGTCC-----AGTC----CA----------|-----G-ATAG-CCAGAGGAGTCTGTT---|----------TAAAA------|----------TGTG----------TA----------TTTTTCAGATGCCACCAGCTTCGCTGGCTTCTTCAACTTCCGGTGATGCGGGGATCTG
droKik1	scf7180000302411:668605-668767 +		CGATACGGCCAAGCCGGCCATTGTTACCTACCACGATTTGGGCCTCAACTGTGAGTAGATACTCCTT-T--AG-T----------|-----TCCCCA-T----------|-AAAAA----------AT--AAACAAACCCTT--------T----------TGGTTTTTA--TCTTTTAGATGCCACCAGCTTTGCTGGCTTCTTCAACTTTCCAGTGATGCGAGGGTTG
droFic1	scf7180000453201:159232-159396 -		CGACACGGCCAAGCCGGCCATTGTCACCTACCACGATTTGGGCCTCAACTGTTACGTAC-----TTG--CA-TACTCC-----|----------|----------TCA--AAAAA----------AGATATCCTTATTCAT--------CAT----------CCTAATCTTAT--CATTACAGATGCCACCAGCTTTGCTGGCTTCTTCAACTTTCCAGTGATGCGAGGTTTG
droEle1	scf7180000491201:1725996-1726156 -		CGATACGGCTAAGCCGGCCATCGTCACCTACCACGATTTGGGCCTAAACTGTACGTAG-----TTT--AA-TACCTT-----|----------|----------ACA--AAAAT----------AG---TTTCACATAT--------TAT----------TGTAAAATATT--CTTTTACAGACGCCACCAGCTTTGCTGGCTTCTTCAACTTTCCAGTGATGCGAGGTTTG
droRho1	scf7180000780066:367631-367787 +		CGACACGGCCAAGCCGGCCATTGTCACCTACCACGATTTGGGCCTAAACTGTAGGTTG-----CTC--AT-T----------|-----TCCTCA-CCAAAAA--------|---|----------|---TATCCCTACTAAT--------TGC----------TATT----TT--TCTTTACAGACGCCACCAGCTTTGCTGGCTTCTTTAACTTTCCAGTGATGCGAGGTTTG
droBia1	scf7180000302143:976929-977088 -		CGATACGGCCAAGCCGGCCATCGTCACCTACCACGATTTGGGACTCAACTGTGAGTGG-----TTT--AG-TAACCC-----|----------|----------GAC--CAGAT----------ATACATACTTATTCAT--------TCC----------TCATTT--CTCTGCCAGACGCCACCAGCTTTGCTGGATTCTTTAACTTTCCAGTGATGCGAGGTTTG
droTak1	scf7180000415722:337982-338039 +		|----------|-----|----|----|--|----------|----------|----------|---|----------|----------TCTTGCCAGACGCCACCAGCTTTGCTGGCTTCTTCAACTTTCCAGTGATGCGGGGTCTG
droEug1	scf7180000409474:534046-534205 -		CGACACGGCCAAGCCGGCCATCGTCACCTACCACGATTTGGGCCTGAACTGTGAGTGG-----TTC--AA-TATTCT-----|----------|----------AGT--CAAAG----------ATATATCTTAATCAAC--------TGA----------TCTATC--CCCTTTAGATGCCACCAGCTTGCTGGTTCTTCAACTTTCCAGTGATGCGCGGTTTG
[illegible]	[illegible]	[illegible]	[illegible]
droSim2	[illegible]	[illegible]	CGATACGGCCAAGCCGGCCATATCACCTACCACGATTTGGGCCTCAACTGTGAGTGG-----TCC-AAAA-TACCTG-----|----------|----------TTC--AAT----------TCGGATT--------CATGCTAATCAG----------TATTTTCCTCC--CATTGTAGACGCCACCAGCTTTGCTGGCTTCTTCAATTTTCCAGTGATGCGAGGTCTG
droSec2	scaffold_9:728153-728316 +	dse_1620	CGATACGGCCAAGCCGGCCATCATCACCTACCACGATTTGGGCCTCAACTGTGAGTGG-----TCA-AAAA-TACCTG-----|----------|----------TTA--AAT----------TTGGATT--------CTTACTAATCGG----------TATTGCTCTTC--CATTGCAGACGCCACCAGCTTTGCTGGCTTCTTCAATTTTCCAGTGATGCGAGGTCTG
droYak3	2R:11781101-11781263 -		CGATACGGCCAAGCCGGCCATCATCACCTACCACGATTTGGGCCTCAACTGTTGAGTAA-----TTA---A-TACTAG-----|----------|----------TACTA|----------G---TTTTGCCA--ATTACTAATCCG----------TATAACTCTTC--AATTACAGACGCCACCAGCTTTGCTGGCTTCTTCAACTTTCCAGTGATGCGAGGTCTG
droEre2	scaffold_4845:11543597-11543762 +		CGATACCGCCAAGCCGGCCATGATCACCTACCACGATTTAGGCCTAAACTGTGAGTGT-----TCA--AC-TACTTG-----|----------|----------TGCAG|----------GTATCCGCCCT--------CTTACTAATCCG----------TATATTTATCC--AATTACAGACGCCACCAGCTTTGCTGGCTTCTTCAACTTTCCAGTGATGCGAGGTCTG

Generated: 09/08/2015 at 07:00 PM

	PASS/FAIL
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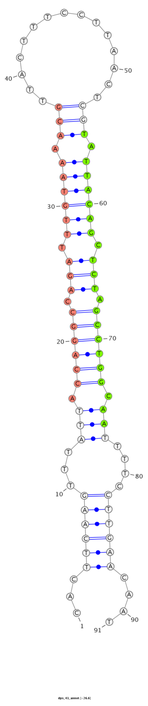
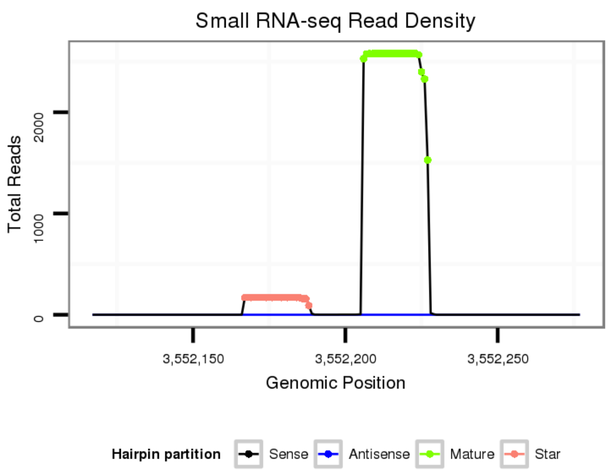
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	2
rescue.candidate	1

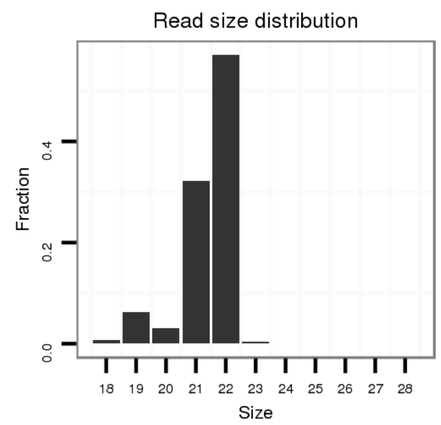
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dps_41	**4_group4:3552167-3552227 +**	**confident**	**Testes-restricted**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

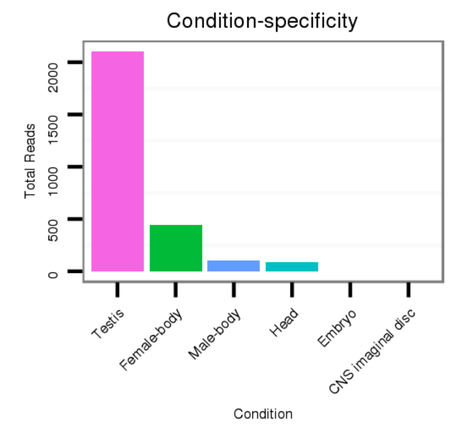
Legend: mature star mismatch in alignment mismatch in read

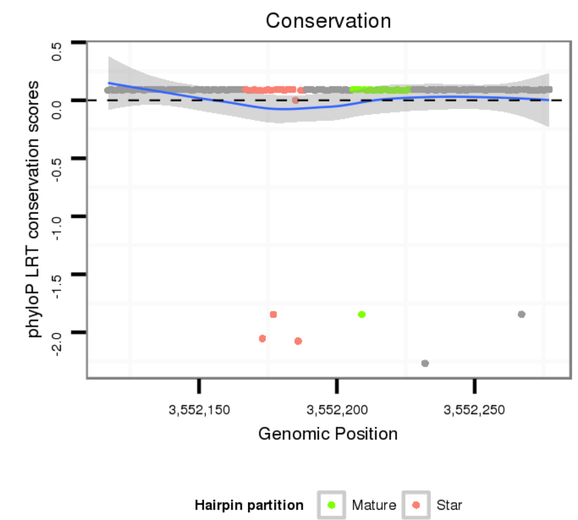
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

CTCCACAAAGAATGATTAAATGAAAATTAAGCAAACACTTCAAGTTTATTACCAGGCCAGATTTGTAAAACGTTACTTTCCTTAACTCGTATTACAGCTCTAGCCTGGCAATTTTCCTTGAACAATACCTCTTTTTAGAAAATTTCGAGATAAGCGCACAA **********...((((((...(((.((((((.(((.(((((((.(((.....))).)))))).))).)))))).))).....)))))))....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	SRR902011 testis	M040 female body	M062 head	M022 male body	V112 male body	GSM444067 head	M059 embryo	SRR902012 CNS imaginal disc	GSM343916 embryo	SRR902010 ovaries
.....TATTACAGCTCTAGCCTGGCAA.....	22	0	1	1478.00	1478	1185	210	40	16	13	14	0	0	0	0
.....TATTACAGCTCTAGCCTGGCA.....	21	0	1	786.00	786	614	121	14	26	7	2	1	0	1	0
.....TATTACAGCTCTAGCCTGG.....	19	0	1	164.00	164	86	64	5	6	2	1	0	0	0	0
.....ACCAGGCCAGATTTGTAAAACG.....	22	0	1	80.00	80	69	1	0	2	8	0	0	0	0	0
.....TATTACAGCTCTAGCCTGGCAAA.....	23	1	1	80.00	80	76	3	0	0	1	0	0	0	0	0
.....TATTACAGCTCTAGCCTGGCAT.....	22	1	1	79.00	79	65	7	2	0	4	1	0	0	0	0
.....TATTACAGCTCTAGCCTGGC.....	20	0	1	68.00	68	53	9	4	0	1	1	0	0	0	0
.....ACCAGGCCAGATTTGTAAAAC.....	21	0	1	65.00	65	63	0	0	0	1	0	0	1	0	0
.....ATTACAGCTCTAGCCTGGCAA.....	21	0	1	31.00	31	12	19	0	0	0	0	0	0	0	0
.....TATTACAGCTCTAGCCTGGCAAAA.....	24	2	1	16.00	16	16	0	0	0	0	0	0	0	0	0
.....TATTACAGCTCTAGCCTGGCC.....	21	1	1	12.00	12	10	2	0	0	0	0	0	0	0	0
.....TATTACAGCTCTAGCCTG.....	18	0	1	12.00	12	1	0	1	10	0	0	0	0	0	0
.....ATTACAGCTCTAGCCTGGCA.....	20	0	1	11.00	11	2	9	0	0	0	0	0	0	0	0
.....ACCAGGCCAGATTTGTAAAACGT.....	23	0	1	10.00	10	2	0	0	0	8	0	0	0	0	0
.....TATTACAGCTCTAGCCTGGCT.....	21	1	1	10.00	10	5	2	2	0	1	0	0	0	0	0
.....TATTACAGCTCTAGCCTGGCAAT.....	23	0	1	10.00	10	8	2	0	0	0	0	0	0	0	0
.....TATTACAGCTCTAGCCTGGT.....	20	1	1	9.00	9	7	0	0	0	0	2	0	0	0	0
.....ACCAGGCCAGATTTGTAAA.....	19	0	1	8.00	8	5	0	0	0	2	1	0	0	0	0
.....TATTACAGCTCTAGCCTGGCAATT.....	24	0	1	6.00	6	6	0	0	0	0	0	0	0	0	0
.....ATTACAGCTCTAGCCTGG.....	18	0	1	5.00	5	0	5	0	0	0	0	0	0	0	0
.....TATTACAGCTCTAGCCTGGCAAAAA.....	25	3	2	3.50	7	6	0	0	0	0	0	0	0	0	1
.....TATTACAGCTCTAGCCTGGCCG.....	22	2	1	3.00	3	2	0	0	1	0	0	0	0	0	0
.....ACCAGGCCAGATTTGTAAAA.....	20	0	1	3.00	3	2	1	0	0	0	0	0	0	0	0
.....TATTACAGCTCTAGCCTGGA.....	20	1	1	3.00	3	0	2	1	0	0	0	0	0	0	0
.....ACCAGGCCAGATTTGTAAAACT.....	22	1	1	3.00	3	2	0	0	1	0	0	0	0	0	0
.....TATTACAGCTCTAGCCTGGCATC.....	23	2	1	3.00	3	3	0	0	0	0	0	0	0	0	0
.....TATTACAGCTCTAGCCTGT.....	19	1	1	3.00	3	0	0	0	1	0	2	0	0	0	0
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.....GTATTACAGCTCTAGCCTGGCA.....	22	0	1	2.00	2	2	0	0	0	0	0	0	0	0	0
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.....TATTACAGCTCTAGCCTGGCAGA.....	23	2	1	2.00	2	2	0	0	0	0	0	0	0	0	0
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.....TATTACAGCTCTAGCCTGGCAG.....	22	1	1	2.00	2	1	1	0	0	0	0	0	0	0	0
.....TATTACAGCTCTAGCCTGGCAATC.....	24	1	1	2.00	2	1	0	0	1	0	0	0	0	0	0
.....TATTACAGCTCTAGCCTGGCG.....	21	1	1	2.00	2	1	0	0	1	0	0	0	0	0	0
.....ACAGCTCTAGCCTGGCAA.....	18	0	2	2.00	4	1	1	2	0	0	0	0	0	0	0
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.....ACCAGGCCAGATTTGTAAAACGTC.....	24	1	1	1.00	1	0	0	0	0	1	0	0	0	0	0
.....ACCAGGCCAGATTTGTAAAACGTTA.....	25	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....TTAACTCGTATTACAGCTCTAGCCTGGC.....	28	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....TATTACAGCTCTAGCCTGGCAATTTGG.....	27	2	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....ATTACAGCTCTAGCCTGGCAAT.....	22	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....TATTACAGCTCTAGCCTT.....	18	1	1	1.00	1	0	0	0	1	0	0	0	0	0	0
.....TTACAGCTCTAGCCTGGCAA.....	20	0	1	1.00	1	0	1	0	0	0	0	0	0	0	0
.....TATTACAGCTCTAGCCTGGCAAAG.....	24	2	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....TATTACAGCTCTAGCCTGGCAAC.....	23	1	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....ACCAGGCCAGATTTGTAAAACGC.....	23	1	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....TATTACAGCTCTAGCCTGGCATA.....	23	2	1	1.00	1	0	0	0	1	0	0	0	0	0	0
.....TACAGCTCTAGCCTGGCAAA.....	20	1	1	1.00	1	0	1	0	0	0	0	0	0	0	0
.....TATTACAGCTCTAGCCTGGCAACC.....	24	2	1	1.00	1	0	1	0	0	0	0	0	0	0	0
.....ACCAGGCCAGATTTGTAAAAA.....	21	1	1	1.00	1	0	1	0	0	0	0	0	0	0	0
.....TATTACAGCTCTAGCCTGGTT.....	21	2	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....TACTTTCCTTAACTCGTATTACAGC.....	25	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....TATTACAGCTCTAGCCTGGTTC.....	22	3	1	1.00	1	0	1	0	0	0	0	0	0	0	0
.....TTACAGCTCTAGCCTGGCA.....	19	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....TATTACAGCTCTAGCCTGGCATCC.....	24	3	1	1.00	1	0	0	0	1	0	0	0	0	0	0
.....ATTACAGCTCTAGCCTGGCAC.....	21	1	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....CGTATTACAGCTCTAGCCTGGC.....	22	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....TATTACAGCTCTAGCCTGGCCCC.....	23	3	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....TATTACAGCTCTAGCCTTT.....	19	2	2	1.00	2	2	0	0	0	0	0	0	0	0	0
.....CAGCTCTAGCCTGGCAAC.....	18	1	3	0.33	1	0	0	1	0	0	0	0	0	0	0

Anti-sense strand reads

GAGGTGTTTCTTACTAATTTACTTTTAATTCGTTTGTGAAGTTCAAATAATGGTCCGGTCTAAACATTTTGCAATGAAAGGAATTGAGCATAATGTCGAGATCGGACCGTTAAAAGGAACTTGTTATGGAGAAAAATCTTTTAAAGCTCTATTCGCGTGTT **********...((((((...(((.((((((.(((.(((((((.(((.....))).)))))).))).)))))).))).....)))))))....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M040 female body	GSM343916 embryo

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
dp5	4_group4:3552117-3552277 +	dps_41	CTCCACAAAGAATGATTAAATGAAAATTAAGCAAACACTTCAAGTTTATTACCAGGCCAGATTTGTAAAACGTTACTTTCCTTAACTCGTATTACAGCTCTAGCCTGGCAATTTTCCTTGAACAATACCTCTTTTTAGAAAATTTCGAGATAAGCGCACAA
droPer2	scaffold_10:2579966-2580125 +	dpe_2484	CTCCACAAAGAATGATTAAATGAAAATTAAGCAAACACTTCAAGTTTATTACCAGGACAGGTTTGTAA-CCGTTACTTTCCTTAACTCGTATCACAGCTCTAGCCTGGCAATTTTGCTTGAACAATACCTCTTTTTAGAAAATTTCGAGAAAAGCGCACAA

Generated: 09/08/2015 at 08:36 PM

	PASS/FAIL
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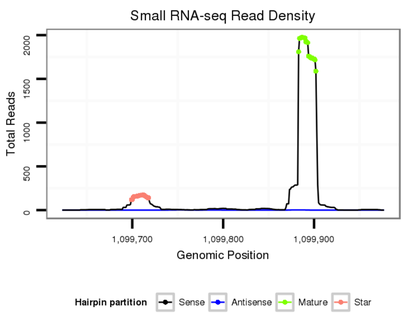
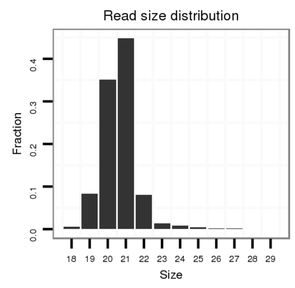
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	1

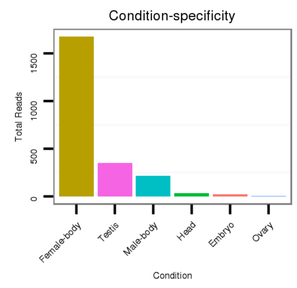
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dps_3602	**XR_group3a:1099673-1099927 +**	**confident**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser [Cornell Mirror]]

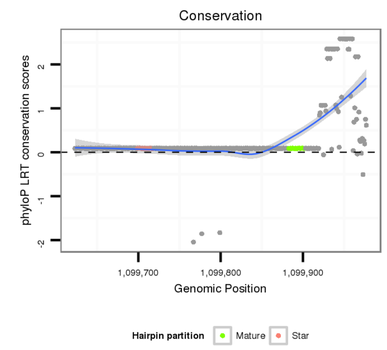
Legend: mature star mismatch in alignment mismatch in read

Predicted structure









Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

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GCTTAAGCTTATGGAGTGTATCTCGTCGTATCACGTAACCTTCCCCTGGAAGTTTTACCATCTTCCAATTGAAACGAATATGTCGTCGGGCTTGTCAAGTTGATCGAGACATGCGTAGTCATCATTTCAACAGATCATCACAAACATTTTCTGCCCCAGACAAGAAAGCAGCTGTTACACTGTTAGCCATGTCTCTTTTCAGAGAATTTTTGTGAGAATCTCCGTTGGTATGGTAAGTCGATATCTCGCGGCCAACATGACGAGATCGACGATACATTCGTACCAGTTGGAGGATGCCAAAACTTGTGTTGAGTTTATTACTATAAATAAATGCAATTTCTAGGAAACGTTAAAG
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```

Read size	# Mismatch	Hit Count	Total Norm	Total	M040 female body	SRR902011 testis	V112 male body	M022 male body	GSM444067 head	M062 head	M059 embryo	GSM343916 embryo	SRR902010 ovaries
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21	0	1	151.00	151	139	1	11	0	0	0	0	0	0
19	0	1	127.00	127	49	61	1	14	1	1	0	0	0
22	0	1	113.00	113	105	4	2	1	0	0	1	0	0
21	0	1	93.00	93	93	0	0	0	0	0	0	0	0
22	1	1	72.00	72	54	0	16	1	1	0	0	0	0
22	1	1	46.00	46	26	8	8	0	4	0	0	0	0
20	0	1	38.00	38	18	13	5	2	0	0	0	0	0
20	0	1	31.00	31	31	0	0	0	0	0	0	0	0
21	0	1	27.00	27	22	0	5	0	0	0	0	0	0
19	0	1	23.00	23	17	5	1	0	0	0	0	0	0
22	1	1	20.00	20	1	15	4	0	0	0	0	0	0
22	0	1	17.00	17	14	0	3	0	0	0	0	0	0
21	0	1	16.00	16	12	4	0	0	0	0	0	0	0
20	0	1	15.00	15	6	0	8	0	1	0	0	0	0
21	0	1	13.00	13	8	5	0	0	0	0	0	0	0
21	0	1	12.00	12	12	0	0	0	0	0	0	0	0
21	0	1	12.00	12	7	2	3	0	0	0	0	0	0
21	0	1	12.00	12	12	0	0	0	0	0	0	0	0
23	2	1	12.00	12	10	0	1	1	0	0	0	0	0
23	2	1	10.00	10	2	4	4	0	0	0	0	0	0
20	0	1	10.00	10	8	0	2	0	0	0	0	0	0
19	1	1	10.00	10	1	7	0	1	0	1	0	0	0
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22	0	1	9.00	9	4	0	5	0	0	0	0	0	0
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19	0	1	2.00	2	2	0	0	0	0	0	0	0	0
18	0	1	2.00	2	0	1	0	0	1	0	0	0	0
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23	0	1	2.00	2	1	0	1	0	0	0	0	0	0
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21	0	1	2.00	2	0	0	2	0	0	0	0	0	0
24	0	1	2.00	2	0	0	1	0	0	0	1	0	0
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22	0	1	2.00	2	2	0	0	0	0	0	0	0	0
22	0	1	2.00	2	1	0	1	0	0	0	0	0	0
20	0	1	2.00	2	2	0	0	0	0	0	0	0	0
20	1	1	2.00	2	0	2	0	0	0	0	0	0	0
19	0	1	2.00	2	2	0	0	0	0	0	0	0	0
19	0	1	2.00	2	2	0	0	0	0	0	0	0	0
24	0	1	2.00	2	0	0	2	0	0	0	0	0	0
18	0	1	2.00	2	2	0	0	0	0	0	0	0	0
24	0	1	2.00	2	1	0	0	0	0	0	1	0	0
19	0	1	2.00	2	1	0	0	0	1	0	0	0	0
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21	3	2	1.50	3	2	0	1	0	0	0	0	0	0
19	0	1	1.00	1	1	0	0	0	0	0	0	0	0
23	0	1	1.00	1	1	0	0	0	0	0	0	0	0
18	0	1	1.00	1	1	0	0	0	0	0	0	0	0
25	3	1	1.00	1	0	1	0	0	0	0	0	0	0
19	1	1	1.00	1	0	0	0	1	0	0	0	0	0
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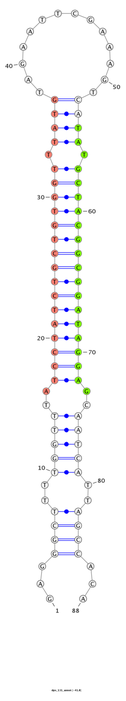
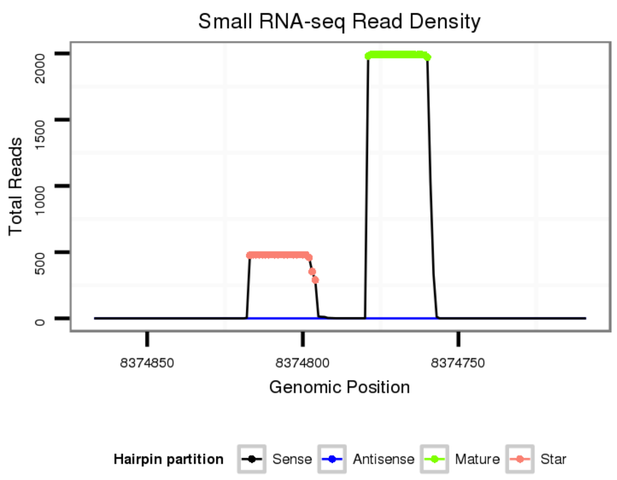
22	0	1	1.00	1	1	0	0	0	0	0	0	0	0
20	0	1	1.00	1	1	0	0	0	0	0	0	0	0
20	0	1	1.00	1	1	0	0	0	0	0	0	0	0
27	0	1	1.00	1	1	0	0	0	0	0	0	0	0
20	0	1	1.00	1	1	0	0	0	0	0	0	0	0
20	0	1	1.00	1	1	0	0	0	0	0	0	0	0
21

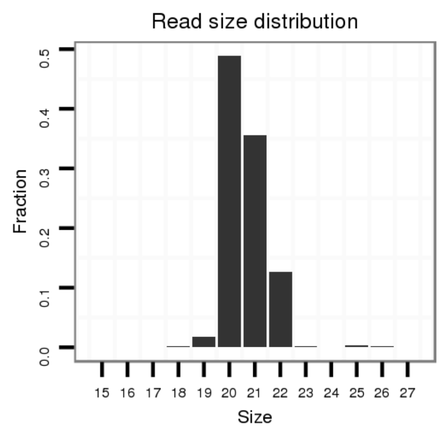
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dps_131	**XL_group1e:8374759-8374817 -**	**confident**	**Testes-restricted**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

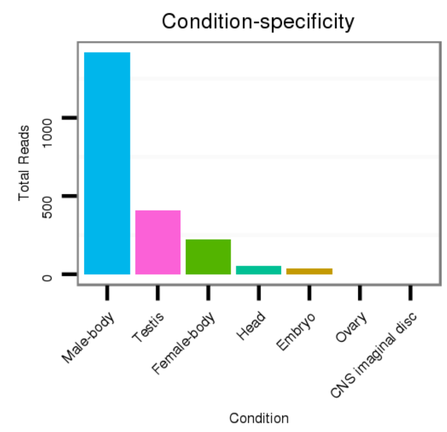
Legend: mature star mismatch in alignment mismatch in read

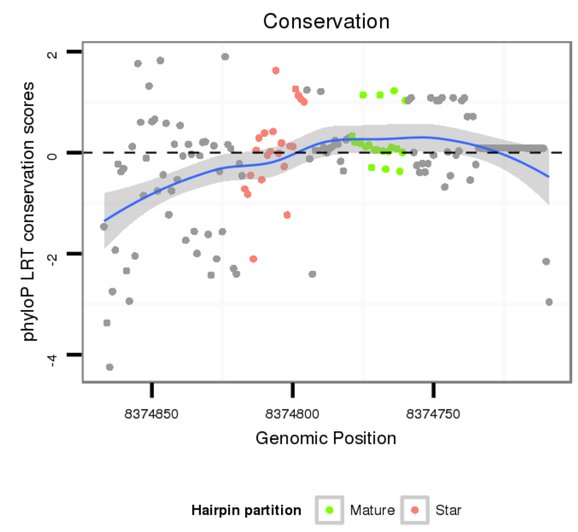
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

mature	star
	1. dps-mir-2543a-2 XL_group1e:8374048-8374069 - 2. dps_131 XL_group1e:8374796-8374817 - 3. dps-mir-2543a-1 Unknown_singleton_1920:1461-1482 +

Sense Strand Reads

hide 3p reads show mid mismatch reads

AACCTTTATCTCAAAATTTCTGCAAACCTGCCAGAGAGGGCTTTTGGTTTATCCTATCTGCTGTGGTTTATGTAGAATTCGAAAGTCATATGCTACGGCGGATAGGAGCAATCATTAGCCACAAAGCCAACTATCCGTGGATATCTAGTTCGTTGGGCG **********...((((..(((((..((((((((((((((((.((((.....))))).))))))))))))))..)))))..))))...**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V112 male body	SRR902011 testis	M040 female body	GSM444067 head	GSM343916 embryo	M022 male body	M062 head	M059 embryo	SRR902010 ovaries	SRR902012 CNS imaginal disc
.....TATGCTACGGCGGATAGGAG.....	20	0	1	937.00	937	820	9	95	11	1	0	1	0	0	0
.....TATGCTACGGCGGATAGGAGC.....	21	0	1	696.00	696	531	2	91	14	25	7	17	9	0	0
.....TATGCTACGGCGGATAGGAGCA.....	22	0	1	318.00	318	209	2	67	12	12	7	2	7	0	0
.....ATCCTATCTGCTGTGGTTTATG.....	22	0	3	271.67	815	64	699	32	4	8	1	2	0	4	1
.....ATCCTATCTGCTGTGGTTTA.....	20	0	3	106.00	318	37	260	16	2	0	1	1	0	1	0
.....ATCCTATCTGCTGTGGTTTAT.....	21	0	3	64.67	194	40	142	11	0	0	0	0	0	0	1
.....TATGCTACGGCGGATAGGAGCC.....	22	1	1	60.00	60	46	0	3	5	0	5	1	0	0	0
.....TATGCTACGGCGGATAGGAGT.....	21	1	1	41.00	41	33	0	6	0	1	0	1	0	0	0
.....TATGCTACGGCGGATAGGAGCCC.....	23	2	1	34.00	34	27	0	4	1	0	2	0	0	0	0
.....TATGCTACGGCGGATAGGAGCCT.....	23	2	1	26.00	26	22	0	1	0	0	2	1	0	0	0
.....ATCCTATCTGCTGTGGTTT.....	19	0	3	19.67	59	11	42	6	0	0	0	0	0	0	0
.....TATGCTACGGCGGATAGGAGCT.....	22	1	1	19.00	19	9	1	6	0	0	3	0	0	0	0
.....ATCCTATCTGCTGTGGTTTATC.....	22	1	3	17.33	52	8	41	3	0	0	0	0	0	0	0
.....TATGCTACGGCGGATAGGA.....	19	0	1	17.00	17	9	1	3	1	0	0	3	0	0	0
.....TATGCTACGGCGGATAGGAGA.....	21	1	1	11.00	11	5	1	2	1	1	1	0	0	0	0
.....TATGCTACGGCGGATAGGAGCAA.....	23	0	1	10.00	10	7	0	2	0	1	0	0	0	0	0
.....ATCCTATCTGCTGTGGTTTATT.....	22	1	3	9.00	27	3	23	1	0	0	0	0	0	0	0
.....TATGCTACGGCGGATAGGAGCAT.....	23	1	1	8.00	8	6	0	2	0	0	0	0	0	0	0
.....ATCCTATCTGCTGTGGTTTATGA.....	23	1	3	7.67	23	0	21	0	0	0	2	0	0	0	0
.....ATCCTATCTGCTGTGGTTTATGTAG.....	25	0	1	6.00	6	0	6	0	0	0	0	0	0	0	0
.....ATCCTATCTGCTGTGGTTTAA.....	21	1	3	5.67	17	0	17	0	0	0	0	0	0	0	0
.....TATGCTACGGCGGATAGGAA.....	20	1	1	4.00	4	3	0	1	0	0	0	0	0	0	0
.....ATGCTACGGCGGATAGGAGCA.....	21	0	1	4.00	4	0	0	4	0	0	0	0	0	0	0
.....ATCCTATCTGCTGTGGTTTATGTG.....	24	1	3	3.67	11	1	10	0	0	0	0	0	0	0	0
.....ATCCTATCTGCTGTGGTTTATGT.....	23	0	3	3.67	11	1	9	1	0	0	0	0	0	0	0
.....ATCCTATCTGCTGTGGTTTC.....	20	1	3	3.33	10	0	10	0	0	0	0	0	0	0	0
.....TATGCTACGGCGGATAGGAGCCCC.....	24	3	1	3.00	3	3	0	0	0	0	0	0	0	0	0
.....ATGCTACGGCGGATAGGAGC.....	20	0	1	3.00	3	0	0	3	0	0	0	0	0	0	0
.....TATCCTATCTGCTGTGGTTTATG.....	23	0	3	3.00	9	1	6	2	0	0	0	0	0	0	0
.....ATCCTATCTGCTGTGGTTTCC.....	21	2	3	2.33	7	1	6	0	0	0	0	0	0	0	0
.....TATGCTACGGCGGATAGGAGCTT.....	23	2	1	2.00	2	0	0	1	0	0	1	0	0	0	0
.....TATGCTACGGCGGATAGGAA.....	21	2	1	2.00	2	1	1	0	0	0	0	0	0	0	0
.....ATGCTACGGCGGATAGGAGCAA.....	22	0	1	2.00	2	0	1	1	0	0	0	0	0	0	0
.....TATGCTACGGCGGATAGGAGTCC.....	23	3	1	2.00	2	2	0	0	0	0	0	0	0	0	0
.....TATGCTACGGCGGATAGGAGTT.....	22	2	1	2.00	2	0	0	0	1	0	0	1	0	0	0
.....TATGCTACGGCGGATAGGT.....	19	1	1	2.00	2	2	0	0	0	0	0	0	0	0	0
.....ATGCTACGGCGGATAGGAG.....	19	0	1	2.00	2	0	0	2	0	0	0	0	0	0	0
.....TATGCTACGGCGGATAGGAGTTT.....	23	3	1	2.00	2	1	0	1	0	0	0	0	0	0	0
.....TATGCTACGGCGGATAGG.....	18	0	1	2.00	2	0	0	1	1	0	0	0	0	0	0
.....ATCCTATCTGCTGTGGTTTAAA.....	22	2	3	2.00	6	0	6	0	0	0	0	0	0	0	0
.....ATCCTATCTGCTGTGGTTTATGTA.....	24	0	3	1.67	5	0	5	0	0	0	0	0	0	0	0
.....TATCCTATCTGCTGTGGTTTATAA.....	24	2	3	1.33	4	0	4	0	0	0	0	0	0	0	0
.....ATCCTATCTGCTGTGGTTTATTAT.....	24	3	3	1.33	4	0	4	0	0	0	0	0	0	0	0
.....TCCTATCTGCTGTGGTTTATG.....	21	0	3	1.33	4	0	2	2	0	0	0	0	0	0	0
.....ATCCTATCTGCTGTGGTT.....	18	0	3	1.33	4	0	4	0	0	0	0	0	0	0	0
.....ATGCTACGGCGGATAGGAA.....	19	1	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....TATGCTACGGCGGATAGGAGAC.....	22	2	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....ATCCTATCTGCTGTGGTTTATGTAGAATA.....	29	1	1	1.00	1	0	1	0	0	0	0	0	0	0	0
.....ATCCTATCTGCTGTGGTTTATGTAGA.....	26	0	1	1.00	1	0	1	0	0	0	0	0	0	0	0
.....TATGCTACGGCGGATAGGAGCATA.....	24	2	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....TATGCTACGGCGGATAGGG.....	19	1	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....TATGCTACGGCGGATAGGAGTCT.....	23	3	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....TGTAGAATTCGAAAGTCATATGCTAC.....	26	0	1	1.00	1	0	1	0	0	0	0	0	0	0	0
.....TCCTATCTGCTGTGGTTTATGTAGAAT.....	27	0	1	1.00	1	0	1	0	0	0	0	0	0	0	0
.....TATGCTACGGCGGATAGGAGCG.....	22	1	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....TATGCTACGGCGGATAGGAGCAC.....	23	1	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....TATCCTATCTGCTGTGGTTTATGTAG.....	26	0	1	1.00	1	0	1	0	0	0	0	0	0	0	0
.....TCCTATCTGCTGTGGTTTATGTAGAA.....	26	0	1	1.00	1	0	0	1	0	0	0	0	0	0	0
.....TATGCTACGGCGGATAGGTT.....	20	2	1	1.00	1	0	0	1	0	0	0	0	0	0	0
.....TATGCTACGGCGGATAGGAGCAAA.....	24	1	1	1.00	1	0	0	1	0	0	0	0	0	0	0
.....TATGCTACGGCGGATAGGAT.....	20	1	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....ATGCTACGGCGGATAGGA.....	18	0	1	1.00	1	0	0	1	0	0	0	0	0	0	0
.....TATGCTACGGCGGATAGGAGCAAG.....	24	1	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....ATGCTACGGCGGATAGGAGCAAA.....	23	1	1	1.00	1	0	0	1	0	0	0	0	0	0	0
.....TATGCTACGGCGGATAGGAGTC.....	22	2	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....TATCCTATCTGCTGTGGTTTA.....	21	0	3	1.00	3	0	3	0	0	0	0	0	0	0	0
.....ATCCTATCTGCTGTGGTTTT.....	20	1	3	1.00	3	1	2	0	0	0	0	0	0	0	0
.....ATCCTATCTGCTGTGGTTTAAAA.....	23	3	3	1.00	3	0	3	0	0	0	0	0	0	0	0
.....ATCCTATCTGCTGTGGTTTATA.....	22	1	3	1.00	3	0	3	0	0	0	0	0	0	0	0
.....CCAGAGAGGGCTTTTGGTTT.....	20	0	5	0.80	4	0	4	0	0	0	0	0	0	0	0
.....TATCCTATCTGCTGTGGTTT.....	20	0	3	0.67	2	1	1	0	0	0	0	0	0	0	0
.....ATCCTATCTGCTGTGGTTCC.....	20	2	3	0.67	2	0	2	0	0	0	0	0	0	0	0
.....TATGCTACGGCGGATAGGAGTTC.....	23	3	2	0.50	1	1	0	0	0	0	0	0	0	0	0
.....ATCCTATCTGCTGTGGTTTATCCT.....	24	3	3	0.33	1	0	0	0	0	0	1	0	0	0	0
.....TATCCTATCTGCTGTGGTTTATT.....	23	1	3	0.33	1	0	1	0	0	0	0	0	0	0	0
.....CTATCTGCTGTGGTTTATG.....	19	0	3	0.33	1	0	1	0	0	0	0	0	0	0	0
.....ATCCTATCTGCTGTGGTTA.....	19	1	3	0.33	1	0	1	0	0	0	0	0	0	0	0
.....ATCCTATCTGCTGTG.....	15	0	3	0.33	1	0	1	0	0	0	0	0	0	0	0
.....TATCCTATCTGCTGTGGTTTATC.....	23	1	3	0.33	1	0	0	0	0	0	0	1	0	0	0
.....TATCCTATCTGCTGTGGTTTAT.....	22	0	3	0.33	1	1	0	0	0	0	0	0	0	0	0
.....ATCCTATCTGCTGTGGTTTATTC.....	23	2	3	0.33	1	0	1	0	0	0	0	0	0	0	0
.....TCCTATCTGCTGTGGTTTA.....	19	0	3	0.33	1	0	0	1	0	0	0	0	0	0	0
.....ATCCTATCTGCTGTGGTTTATGGC.....	24	2	3	0.33	1	0	1	0	0	0	0	0	0	0	0
.....ATCCTATCTGCTGTGGTTTATAA.....	23	2	3	0.33	1	0	1	0	0	0	0	0	0	0	0
.....ATCCTATCTGCTGTGGT.....	17	0	3	0.33	1	0	1	0	0	0	0	0	0	0	0
.....TCCTATCTGCTGTGGTTT.....	18	0	3	0.33	1	0	0	1	0	0	0	0	0	0	0
.....TCCTATCTGCTGTGGTTTAT.....	20	0	3	0.33	1	0	0	1	0	0	0	0	0	0	0
.....ATCCTATCTGCTGTGGTTTATCC.....	23	2	3	0.33	1	0	1	0	0	0	0	0	0	0	0
.....ATCCTATCTGCTGTGGTTTATGTA.....	25	1	3	0.33	1	0	1	0	0	0	0	0	0	0	0
.....ATCCTATCTGCTGTGG.....	16	0	3	0.33	1	0	1	0	0	0	0	0	0	0	0
.....ATCCTATCTGCTGTGGTTTATCG.....	23	2	3	0.33	1	1	0	0	0	0	0	0	0	0	0
.....ATCCTATCTGCTGTGGTTTATGC.....	23	1	3	0.33	1	0	1	0	0	0	0	0	0	0	0
.....ATCCTATCTGCTGTGGTTTTCT.....	22	3	4	0.25	1	0	1	0	0	0	0	0	0	0	0
.....TCTGCAAACCTGCCAGAGAGGGC.....	23	0	5	0.20	1	0	1	0	0	0	0	0	0	0	0
.....ATCCTATCTGCTGTGGTTTCAA.....	22	3	5	0.20	1	0	1	0	0	0	0	0	0	0	0
.....ATCCTATCTGCTGTGGTTATC.....	21	3	6	0.17	1	0	1	0	0	0	0	0	0	0	0

Anti-sense strand reads

TTGGAAATAGAGTTTTAAAGACGTTTGGACGGTCTCTCCCGAAAACCAAATAGGATAGACGACACCAAATACATCTTAAGCTTTCAGTATACGATGCCGCCTATCCTCGTTAGTAATCGGTGTTTCGGTTGATAGGCACCTATAGATCAAGCAACCCGC **********...((((..(((((..((((((((((((((((.((((.....))))).))))))))))))))..)))))..))))...**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M040 female body	GSM444067 head	M059 embryo
.....ATAGGATAGACGACACCAAAT.....	21	0	3	0.33	1	0	1	0
.....TAGGATAGACGACACCAAAT.....	20	0	3	0.33	1	1	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
dp5	XL_group1e:8374709-8374867 -	dps_131	AACCTT---TATCTCAAAATTTCTGCAAACCTGCCAG----------AGAGGGC----TTTTGGTTTATCCTATCTGCTGTGGTTTATGTAGAATTCGAAAGTCATATGCTACGGCGGATAGGAGCAATCATTAGCCACAAAGCCAACTATCCGTG-GATATCTAGTTCGTTGGGCG
droPer2	scaffold_13:187400-187541 +	dpe_295	TCT---------GCAAACCTGCCAG----------AGAGGGC----TTTTGGTTTATCCTATGCGCTGTGGTTTATGTACAATTCGCAAGTCATATGCAACGGCGGATAGGAGCAATCATTAGCCACAAAGCCAACTATCCGTGGATATCTAGTTCGTTGGGCG
droWil2	scf2_1100000004540:2074013-2074077 +		AAGTAT---CAAA-----TTTGATCCAAATGCGACAAAAAAT----------AAT----------GCCG-GAGTTGGC----CGTTG---------TCTGCTGGG----------GT
droVir3	scaffold_12963:13009175-13009216 +		TATCAT-------------AATCCGCTGGGAGTTATGTCGTTTTGAACGTCAT----------AT
droMoj3	scaffold_6500:30311469-30311597 +		TTTCGGTT-TATGTAAAA--ATTTAGCCTCCACCCCT----------AATTTACCCCCTCACTCTCATTTG-TAAAAGG----CGTATT----------TCAAATAGTAGAGACTGTGCTTTGGCAAATATATGCAT-----ATCCATGTATCCAAGTT------TC
droAna3	scaffold_13248:3645039-3645059 +		AATGTT---TATCTTAATTTTT----------AT
droBip1	scf7180000396589:813486-813537 -		ATTTTA---CAATTCAAAATTTCTTCTAGCCTCCTCG----------AGGGTAT----TGTTGTCTT----------AT
droEle1	scf7180000488688:12809-12862 -		TTCAGT---A----------TAGCTGCTGA----------AGATAGC----TTTTGGGTTGCTGCAGCTGCTATGCTCT----------AT
droRho1	scf7180000766583:28058-28077 +		AAATTT---TATCTTAAAATT----------TC
droBia1	scf7180000301480:16654-16710 -		CAAAGT---T----------TTTACAAACTTATTCG----------CGAGGGT----TTTGTTTTGTTGTTAGCTGCTGTTG----------TT
droTak1	scf7180000415367:223606-223646 +		TTTCTT---TAG----------AATTCGAAATTTATATGCTAATTCAGGTAGA----------A
droEug1	scf7180000408984:232937-232971 +		CACATT---TTTCTCAATA--TCTATCGATTTACCAA----------AGA-----------
dm3	chrX:559401-559458 -		AACGGA---TATCTAA----------TAGCCCG----------AGAACGC----GATTGTAGCATTCTCTCTTCTTTTTTTA----------TG
droSec2	scaffold_8:1009858-1009924 +		ATGTAACATTGGCACAAA----------AACCAGAAGCTAAGGCAAAAAGGAGCAAAAGGCAGCCAGAGAGTCA----------AC
droYak3	v2_chrUn_5178:8735-8826 +		ATTTGC---CAAAAACT--TTT-------TGCCAAAAACTTTTTGTTCCTAAT----------GTCTGGTGATGGTGTGCGGTTGATG---------TAATGTATTTTATGT----------TCATATA----------TT
droEre2	scaffold_4843:66651-66706 -		ATTTGT---CTTGTAAAT--TTCTAGTGATTTCCCAC----------ATAATCC----TTTTGGCCCACTATA----------TC

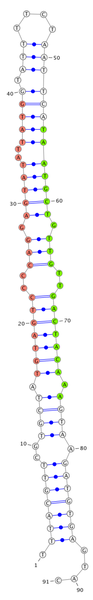
Generated: 09/08/2015 at 08:39 PM

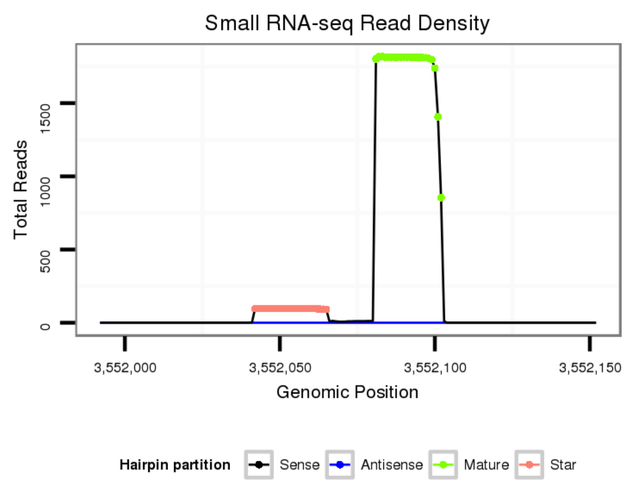
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	4
rescue.confident	2
rescue.candidate	0

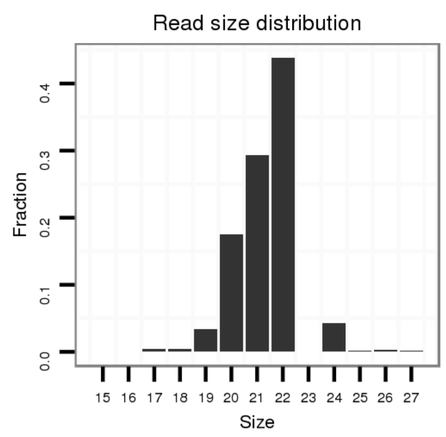
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dps_18	**4_group4:3552042-3552102 +**	**confident**	**Testes-restricted**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

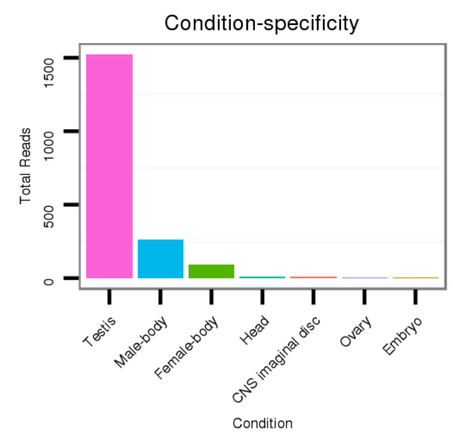
Legend: mature star mismatch in alignment mismatch in read

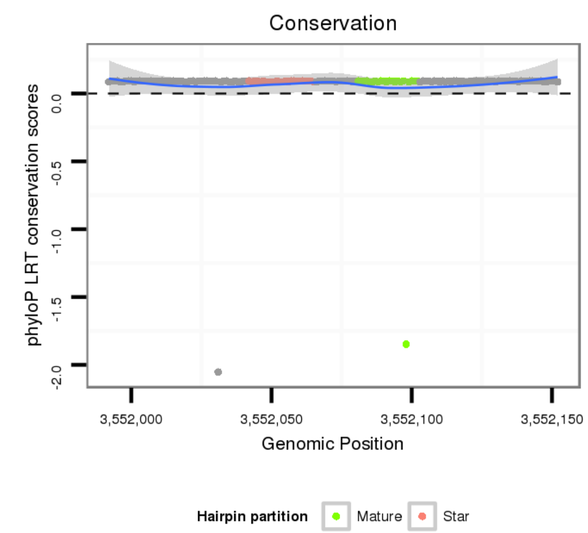
Predicted structure











Show Alternate Folds

Flybase annotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

CAATCCAATCAATAATAAAAAGTTTTTGCATCTAATTTACGTTCGTGCTATGTAGTCCCCAGGAGTATATTATGGTATTTTCTAATTCATAATGCTGTTGTTGACTACAAAGTAAGATGTGAGTACTCCACAAAGAATGATTAAATGAAAATTAAGCAAAC ********** .(((((((..((((.(((((((..(((.(((((..(((((.(((....)))))))))))))).))).)))))))).)))).)))))))....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	SRR902011 testis	M022 male body	V112 male body	M040 female body	GSM444067 head	SRR902012 CNS imaginal disc	GSM343916 embryo	M062 head	SRR902010 ovaries
.....TAATGCTGTTGTTGACTACAAA.....	22	0	1	836.00	836	757	14	42	15	2	3	0	0	3
.....TAATGCTGTTGTTGACTACAA.....	21	0	1	549.00	549	448	54	14	26	0	4	1	0	2
.....TAATGCTGTTGTTGACTACA.....	20	0	1	329.00	329	213	49	30	32	0	2	2	1	0
.....TAATGCTGTTGTTGACTACAAAA.....	23	1	1	243.00	243	225	5	9	4	0	0	0	0	0
.....TAATGCTGTTGTTGACTACAAAAA.....	24	2	1	92.00	92	83	0	7	1	0	0	0	1	0
.....TGTAGTCCCCAGGAGTATATTATG.....	24	0	1	81.00	81	32	0	42	3	4	0	0	0	0
.....TAATGCTGTTGTTGACTAC.....	19	0	1	58.00	58	47	3	1	5	0	0	0	2	0
.....TAATGCTGTTGTTGACTACCCC.....	22	3	1	38.00	38	33	0	2	2	1	0	0	0	0
.....TAATGCTGTTGTTGACTAA.....	19	1	1	37.00	37	23	4	6	1	3	0	0	0	0
.....TAATGCTGTTGTTGACTACC.....	20	1	1	25.00	25	20	3	1	1	0	0	0	0	0
.....TAATGCTGTTGTTGACTACC.....	21	2	1	25.00	25	25	0	0	0	0	0	0	0	0
.....TAATGCTGTTGTTGACTACG.....	20	1	1	19.00	19	17	1	1	0	0	0	0	0	0
.....TAATGCTGTTGTTGACTAT.....	19	1	1	15.00	15	14	0	0	1	0	0	0	0	0
.....TAATGCTGTTGTTGACTACAAAT.....	23	1	1	9.00	9	8	1	0	0	0	0	0	0	0
.....TAATGCTGTTGTTGACTA.....	18	0	1	8.00	8	5	2	0	0	1	0	0	0	0
.....TAATGCTGTTGTTGACTACTC.....	21	2	1	8.00	8	8	0	0	0	0	0	0	0	0
.....AATGCTGTTGTTGACTACAAA.....	21	0	1	8.00	8	4	0	0	4	0	0	0	0	0
.....TAATGCTGTTGTTGACTACAAAG.....	23	0	1	8.00	8	6	1	1	0	0	0	0	0	0
.....TAATGCTGTTGTTGACTACCT.....	21	2	1	7.00	7	6	1	0	0	0	0	0	0	0
.....TATTTTCTAATTCATAA.....	17	0	2	5.50	11	11	0	0	0	0	0	0	0	0
.....TAATGCTGTTGTTGACTACAAC.....	22	1	1	5.00	5	5	0	0	0	0	0	0	0	0
.....AATGCTGTTGTTGACTACAAAA.....	22	1	1	5.00	5	5	0	0	0	0	0	0	0	0
.....TAATGCTGTTGTTGACTATT.....	20	2	2	5.00	10	10	0	0	0	0	0	0	0	0
.....TAATGCTGTTGTTGACTG.....	18	1	2	4.50	9	0	3	1	0	5	0	0	0	0
.....TAATGCTGTTGTTGACTACAAATCT.....	25	3	1	4.00	4	4	0	0	0	0	0	0	0	0
.....TAATGCTGTTGTTGACTACTCC.....	22	3	1	4.00	4	4	0	0	0	0	0	0	0	0
.....AATGCTGTTGTTGACTACAA.....	20	0	1	3.00	3	0	1	0	2	0	0	0	0	0
.....TGTAGTCCCCAGGAGTATATTATGGTA.....	27	0	1	3.00	3	1	0	1	0	1	0	0	0	0
.....AATGCTGTTGTTGACTACA.....	19	0	1	3.00	3	0	0	0	3	0	0	0	0	0
.....TGTAGTCCCCAGGAGTATATTATGGT.....	26	0	1	3.00	3	0	0	3	0	0	0	0	0	0
.....TAATGCTGTTGTTGACTACCCT.....	22	3	2	2.50	5	5	0	0	0	0	0	0	0	0
.....TGTAGTCCCCAGGAGTATATTAT.....	23	0	1	2.00	2	1	0	1	0	0	0	0	0	0
.....TAATGCTGTTGTTGACTACTT.....	21	2	1	2.00	2	2	0	0	0	0	0	0	0	0
.....TAATGCTGTTGTTGACTACAATT.....	23	2	1	2.00	2	2	0	0	0	0	0	0	0	0
.....TAATGCTGTTGTTGACTACAAAC.....	23	1	1	2.00	2	2	0	0	0	0	0	0	0	0
.....TAATGCTGTTGTTGACT.....	17	0	1	2.00	2	2	0	0	0	0	0	0	0	0
.....TGTAGTCCCCAGGAGTATATTATGG.....	25	0	1	2.00	2	0	0	2	0	0	0	0	0	0
.....TAATGCTGTTGTTGACTACT.....	20	1	1	2.00	2	2	0	0	0	0	0	0	0	0
.....TGTAGTCCCCAGGAGTATATTAA.....	23	1	1	2.00	2	2	0	0	0	0	0	0	0	0
.....TGTAGTCCCCAGGAGTATATT.....	21	0	1	2.00	2	2	0	0	0	0	0	0	0	0
.....TAATGCTGTTGTTGACTACAAAAC.....	24	2	1	2.00	2	2	0	0	0	0	0	0	0	0
.....TGTAGTCCCCAGGAGTATATTATGA.....	25	1	1	2.00	2	2	0	0	0	0	0	0	0	0
.....TAATGCTGTTGTTGACTACCTC.....	22	3	2	2.00	4	3	0	1	0	0	0	0	0	0
.....TAATGCTGTTGTTGACTACCTT.....	22	3	2	1.50	3	2	0	0	1	0	0	0	0	0
.....TTTTCTAATTCATAA.....	15	0	3	1.33	4	4	0	0	0	0	0	0	0	0
.....TAATGCTGTTGTTGACTACAACC.....	23	2	1	1.00	1	1	0	0	0	0	0	0	0	0
.....TAATGCTGTTGTTGACTACAAATA.....	24	2	1	1.00	1	1	0	0	0	0	0	0	0	0
.....GTAGTCCCCAGGAGTATATTATGGTAT.....	27	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....TCTAATTCATAATGCTGTTGTTGAC.....	25	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....TAATGCTGTTGTTGACTACAACCC.....	24	3	1	1.00	1	0	0	0	0	0	0	0	1	0
.....TGTAGTCCCCAGGAGTATATTATA.....	24	1	1	1.00	1	1	0	0	0	0	0	0	0	0
.....TAATGCTGTTGTTGACTATG.....	20	2	1	1.00	1	1	0	0	0	0	0	0	0	0
.....TGCTGTTGTTGACTACAAA.....	19	0	1	1.00	1	0	0	0	1	0	0	0	0	0
.....TAATGCTGTTGTTGACTACCG.....	21	2	1	1.00	1	1	0	0	0	0	0	0	0	0
.....TAATGCTGTTGTTGACTACATT.....	22	2	1	1.00	1	1	0	0	0	0	0	0	0	0
.....TAATGCTGTTGTTGACTACAAAAAT.....	25	3	1	1.00	1	1	0	0	0	0	0	0	0	0
.....TAATTCATAATGCTGTTGTTGACT.....	24	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....TAATGCTGTTGTTGACTACAAG.....	22	1	1	1.00	1	0	1	0	0	0	0	0	0	0
.....TGTAGTCCCCAGGAGTATAT.....	20	0	1	1.00	1	0	0	1	0	0	0	0	0	0
.....TAATGCTGTTGTTGACTACAATC.....	23	2	1	1.00	1	1	0	0	0	0	0	0	0	0
.....TCTAATTCATAATGCTGTTGTTGACT.....	26	0	1	1.00	1	0	1	0	0	0	0	0	0	0
.....AATGCTGTTGTTGACTACAAAT.....	22	1	1	1.00	1	1	0	0	0	0	0	0	0	0
.....TAATGCTGTTGTTGACTACAAGA.....	23	2	1	1.00	1	1	0	0	0	0	0	0	0	0
.....TAATGCTGTTGTTGACTACAAT.....	22	1	1	1.00	1	1	0	0	0	0	0	0	0	0
.....AATGCTGTTGTTGACTACAAAAA.....	23	2	1	1.00	1	1	0	0	0	0	0	0	0	0
.....TAATGCTGTTGTTGACTAG.....	19	1	1	1.00	1	1	0	0	0	0	0	0	0	0
.....ATGTAGTCCCCAGGAGTATATTATG.....	25	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....TAATGCTGTTGTTGACTACAAAAAG.....	25	3	1	1.00	1	1	0	0	0	0	0	0	0	0
.....TATGTAGTCCCCAGGAGTATATT.....	23	0	1	1.00	1	0	0	0	0	0	0	1	0	0
.....ATGCTGTTGTTGACTACAAAG.....	21	0	1	1.00	1	0	1	0	0	0	0	0	0	0
.....AATGCTGTTGTTGACTACAAAG.....	22	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....TAATGCTGTTGTTGACTACAAATG.....	24	2	1	1.00	1	1	0	0	0	0	0	0	0	0
.....ATGCTGTTGTTGACTACAA.....	19	0	1	1.00	1	0	0	0	1	0	0	0	0	0
.....TCATAATGCTGTTGTTGACT.....	20	0	1	1.00	1	0	1	0	0	0	0	0	0	0
.....TGTAGTCCCCAGGAGTATA.....	19	0	1	1.00	1	0	0	0	0	1	0	0	0	0
.....TAATGCTGTTGTTGACTACCTG.....	22	3	1	1.00	1	1	0	0	0	0	0	0	0	0
.....TAATGCTGTTGTTGACTC.....	18	1	1	1.00	1	1	0	0	0	0	0	0	0	0
.....TAATGCTGTTGTTGACTACAG.....	21	1	1	1.00	1	0	1	0	0	0	0	0	0	0
.....TTCTAATTCATAATGCTGTTGTTGA.....	25	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....TGTAGTCCCCAGGAGTATATTATGT.....	25	1	1	1.00	1	0	0	1	0	0	0	0	0	0
.....TATTTTCTAATTCATAATGCTGTTGT.....	26	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....TAATGCTGTTGTTGACTACATTT.....	23	3	2	1.00	2	2	0	0	0	0	0	0	0	0
.....TAATGCTGTTGTTGACTATC.....	20	2	2	1.00	2	2	0	0	0	0	0	0	0	0
.....TAATGCTGTTGTTGACTACTCT.....	22	3	3	1.00	3	3	0	0	0	0	0	0	0	0
.....TAATGCTGTTGTTGACTACAACAA.....	24	3	2	0.50	1	1	0	0	0	0	0	0	0	0
.....TAATGCTGTTGTTGACTAAG.....	20	2	2	0.50	1	1	0	0	0	0	0	0	0	0
.....TAATGCTGTTGTTGACTATCC.....	21	3	3	0.33	1	1	0	0	0	0	0	0	0	0
.....TAATGCTGTTGTTGACTTT.....	19	2	7	0.29	2	2	0	0	0	0	0	0	0	0
.....TAATGCTGTTGTTGACTATCG.....	21	3	4	0.25	1	1	0	0	0	0	0	0	0	0
.....TAATGCTGTTGTTGACTGA.....	19	2	5	0.20	1	0	1	0	0	0	0	0	0	0

Anti-sense strand reads

GTTAGGTTAGTTATTATTTTTCAAAAACGTAGATTAAATGCAAGCACGATACATCAGGGGTCCTCATATAATACCATAAAAGATTAAGTATTACGACAACAACTGATGTTTCATTCTACACTCATGAGGTGTTTCTTACTAATTTACTTTTAATTCGTTTG ********** .(((((((..((((.(((((((..(((.(((((..(((((.(((....)))))))))))))).))).)))))))).)))).)))))))....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M040 female body	SRR902011 testis
.....AAAATGCAAGCACGATACATCAGGGG.....	26	1	1	1.00	1	0	1

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
dp5	4_group4:3551992-3552152 +	dps_18	CAATCCAAT-CAATAATAAAAAGTTTTTGCATCTAATTTACGTTCGTGCTATGTAGTCCCCAGGAGTATATTATGGTATTTTCTAATTCATAATGCTGTTGTTGACTACAAAGTAAGATGTGAGTACTCCACAAAGAATGATTAAATGAAAATTAAGCAAAC
droPer2	scaffold_10:2579840-2580001 +	dpe_273	CAATCCAATCCAATAATAAAAAGTTTTTGCATCTAATTTAAGTTCGTGCTATGTAGTCCCCAGGAGTATATTATGGTATTTTCTAATTCATAATGCTGTTGTTGACTGCAAAGTAAGATGTGAGTACTCCACAAAGAATGATTAAATGAAAATTAAGCAAAC

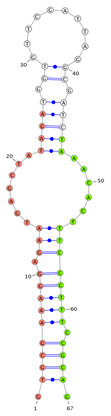
Generated: 09/08/2015 at 08:36 PM

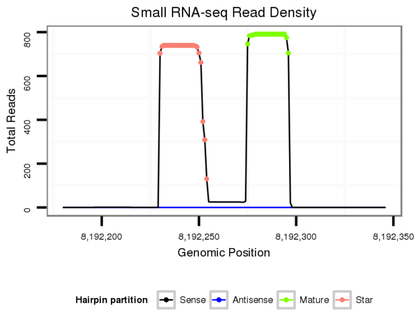
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	2
rescue.candidate	0

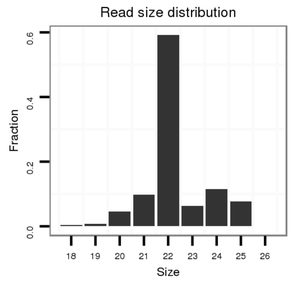
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dps_2749	**XL_group1e:8192230-8192296 +**	**confident**	**Mirtron**	**intron**	[View on UCSC Genome Browser [Cornell Mirror]]

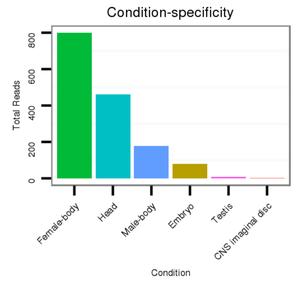
Legend: mature star mismatch in alignment mismatch in read

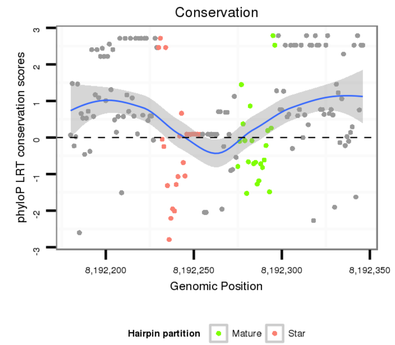
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dpse\GA23034-in]; CDS [Dpse\GA23034-cds]; CDS [Dpse\GA23034-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

AAGCTGCGGGACGCCGGCTGCCATGCCGTCCTCTTCCTGAACATACCCAGGTGCGAAAGGGAGAATGAGCTATAGATGGTGTTCGATTAGGCGATCTAAACACTTTCCCTTTCCGCAGCTATGGCGGCGGCACCCACCCGTGGAACGACTCGTTCGGGGCGACGAAGC	Read size	# Mismatch	Hit Count	Total Norm	Total	M040 female body	GSM444067 head	M062 head	V112 male body	M059 embryo	GSM343916 embryo	SRR902011 testis	SRR902012 CNS imaginal disc
.....TAAACACTTTCCCTTTCCGCAG.....	22	0	1	640.00	640	504	10	74	1	36	11	4	0
.....GTGCGAAAGGAGAATGAGCTAT.....	22	0	1	262.00	262	54	113	13	78	0	3	0	1
.....TAAACACTTTCCCTTTCCGCAGT.....	23	1	1	166.00	166	66	26	35	20	15	4	0	0
.....GTGCGAAAGGAGAATGAGCTATAG.....	24	0	1	165.00	165	40	94	9	20	0	1	1	0
.....GTGCGAAAGGAGAATGAGCTATAGA.....	25	0	1	117.00	117	29	27	16	33	4	5	1	2
.....GTGCGAAAGGAGAATGAGCTATA.....	23	0	1	82.00	82	16	34	10	18	0	2	2	0
.....TAAACACTTTCCCTTTCCGCA.....	21	0	1	67.00	67	47	2	11	0	6	1	0	0
.....GTGCGAAAGGAGAATGAGCTA.....	21	0	1	42.00	42	15	16	1	10	0	0	0	0
.....AAACACTTTCCCTTTCCGCAG.....	21	0	1	33.00	33	29	1	3	0	0	0	0	0
.....GTGCGAAAGGAGAATGAGCT.....TGGTGTTCGATTAGGCGATC.....	20	0	1	26.00	26	6	4	2	14	0	0	0	0
.....TGGTGTTCGATTAGGCGATC.....	20	0	1	24.00	24	3	8	1	1	2	9	0	0
.....TAAACACTTTCCCTTTCCGCAGC.....	23	0	1	20.00	20	1	0	12	0	7	0	0	0
.....TAAACACTTTCCCTTTCCGC.....	20	0	1	14.00	14	14	0	0	0	0	0	0	0
.....TGCGAAAGGAGAATGAGCTATAGA.....	24	0	1	11.00	11	8	1	1	1	0	0	0	0
.....TAAACACTTTCCCTTTCCGCAGA.....	23	1	1	11.00	11	8	0	2	1	0	0	0	0
.....TGCGAAAGGAGAATGAGCTATAG.....	23	0	1	9.00	9	7	0	0	1	0	0	0	1
.....GTGCGAAAGGAGAATGAGCTATAA.....	24	1	1	8.00	8	3	4	1	0	0	0	0	0
.....TGCGAAAGGAGAATGAGCTAT.....	21	0	1	7.00	7	6	1	0	0	0	0	0	0
.....GTGCGAAAGGAGAATGAGC.....	19	0	1	6.00	6	2	2	1	1	0	0	0	0
.....TAAACACTTTCCCTTTCCGCAC.....	22	1	1	5.00	5	0	0	3	0	2	0	0	0
.....AAACACTTTCCCTTTCCGCAGT.....	22	1	1	5.00	5	5	0	0	0	0	0	0	0
.....CACTTTCCCTTTCCGCAG.....	18	0	1	4.00	4	4	0	0	0	0	0	0	0
.....CTAAACACTTTCCCTTTCCGCAG.....	23	0	1	4.00	4	2	0	2	0	0	0	0	0
.....TAAACACTTTCCCTTTCCGCAGTA.....	24	2	1	3.00	3	3	0	0	0	0	0	0	0
.....GCGAAAGGAGAATGAGCTATAG.....	22	0	1	3.00	3	3	0	0	0	0	0	0	0
.....GTGCGAAAGGAGAATGAG.....	18	0	1	2.00	2	0	2	0	0	0	0	0	0
.....GTGCGAAAGGAGAATGAGCTATAGAN.....	26	1	1	2.00	2	1	1	0	0	0	0	0	0
.....TGCGAAAGGAGAATGAGCTATA.....	22	0	1	2.00	2	1	1	0	0	0	0	0	0
.....AACACTTTCCCTTTCCGCAGT.....	21	1	1	2.00	2	1	0	0	0	0	1	0	0
.....AACACTTTCCCTTTCCGCAG.....	20	0	1	2.00	2	2	0	0	0	0	0	0	0
.....AAACACTTTCCCTTTCCGC.....	19	0	1	2.00	2	2	0	0	0	0	0	0	0
.....CTAAACACTTTCCCTTTCCGCAGT.....	24	1	1	2.00	2	0	0	1	0	1	0	0	0
.....AAACACTTTCCCTTTCCGCA.....	20	0	1	2.00	2	2	0	0	0	0	0	0	0
.....TGCGAAAGGAGAATGAGCTATT.....	22	1	1	1.00	1	1	0	0	0	0	0	0	0
.....GTGCGAAAGGAGAATGAGCTTT.....	21	1	1	1.00	1	0	0	0	1	0	0	0	0
.....TAAACACTTTCCCTTTCCGCC.....	21	1	1	1.00	1	1	0	0	0	0	0	0	0
.....GATGGTGTTCGATTAGGCG.....	19	0	1	1.00	1	0	1	0	0	0	0	0	0
.....ACACTTTCCCTTTCCGCAG.....	19	0	1	1.00	1	1	0	0	0	0	0	0	0
.....AAACACTTTCCCTTTCCGCAGA.....	22	1	1	1.00	1	1	0	0	0	0	0	0	0
.....AAACACTTTCCCTTTCCGCAGC.....	22	0	1	1.00	1	0	0	1	0	0	0	0	0
.....GCTGCCATGCCGTCCTCTTC.....	20	0	1	1.00	1	1	0	0	0	0	0	0	0
.....GTGCGAAAGGAGAATGAGCTATT.....	23	1	1	1.00	1	0	0	1	0	0	0	0	0
.....TGCGAAAGGAGAATGAGCTA.....	20	0	1	1.00	1	1	0	0	0	0	0	0	0
.....GTGCGAAAGGAGAATGAGCTATAGAT.....	26	0	1	1.00	1	0	0	0	1	0	0	0	0
.....GCGAAAGGAGAATGAGCTATAGA.....	23	0	1	1.00	1	1	0	0	0	0	0	0	0
.....TGCGAAAGGAGAATGAGCTATAGANA.....	26	2	1	1.00	1	1	0	0	0	0	0	0	0
.....CACTTTCCCTTTCCGCAGT.....	19	1	1	1.00	1	1	0	0	0	0	0	0	0
.....TAAACACTTTCCCTTTCCGCAGTC.....	24	2	1	1.00	1	0	0	1	0	0	0	0	0
.....GCGAAAGGAGAATGAGCTAT.....	20	0	1	1.00	1	1	0	0	0	0	0	0	0
.....TGGTGTTCGATTAGGCGATT.....	20	1	1	1.00	1	1	0	0	0	0	0	0	0
.....GTGCGAAAGGAGAATGAGCTATG.....	23	1	1	1.00	1	0	0	1	0	0	0	0	0
.....TAAACACTTTCCCTTTCCGCC.....	21	1	1	1.00	1	0	0	1	0	0	0	0	0
.....TGCGAAAGGAGAATGAGCT.....	19	0	1	1.00	1	0	0	0	0	0	1	0	0
.....TGCGAAAGGAGAATGAGCTATAA.....	23	1	1	1.00	1	1	0	0	0	0	0	0	0
.....CTAAACACTTTCCCTTTCCGCA.....	22	0	1	1.00	1	0	0	1	0	0	0	0	0
.....GTGCGAAAGGAGAATGAGCG.....	20	1	1	1.00	1	0	1	0	0	0	0	0	0
.....GGTGCGAAAGGAGAATGAGCTATAG.....	25	0	1	1.00	1	0	1	0	0	0	0	0	0
.....TGCGAAAGGAGAATGAGCTATAGAN.....	25	1	1	1.00	1	0	0	0	1	0	0	0	0

Anti-sense strand reads

TTCGACGCCCTGCGGCCGACGGTACGGCAGGAGAAGGACTTGTATGGGTCCACGCTTTCCTCTTACTCGATATCTACCACAAGCTAATCCGCTAGATTTGTGAAAGGGAAAGGCGTCGATACCGCCGCCGTGGGTGGGCACCTTGCTGAGCAAGCCCCGCTGCTTCG	Read size	# Mismatch	Hit Count	Total Norm	Total	GSM343916 embryo	GSM444067 head

Show Alignment With Reads

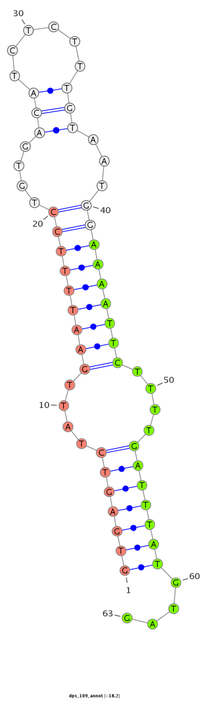
Re-alignment of all predicted orthologs

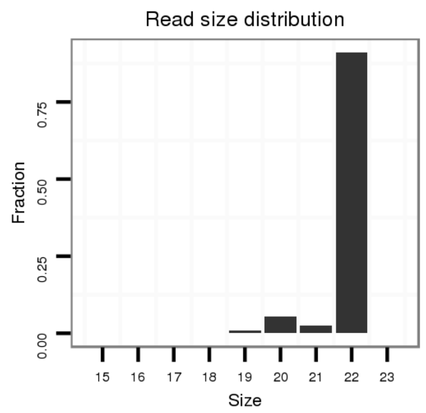
Species	Coordinate	ID	Alignment
dp5	XL_group1e:8192180-8192346 +	dps_2749	AAGCTGCGGGACGCCGGCTGCCATGCCGTCCTCTTCCTGAACATACCCAGGTGCGAAAGG----------AG-AATGAGCTATAGATGGTGTTCGATTAGGCGAT----------CTAA--AC---ACTTT----------CCC-TTTCCGCAGCTATGGCGGCGGCACCCACCCGTGGAAC----------GACTCGTTCGGGGCGACGAAGC
droPer2	scaffold_13:375028-375194 -	dps_736	AAGCTGCGGGACGCCGGCTGCCATGCCGTCCTCTTCCTGAACATACCCAGGTGCGAAAGG----------AG-AATGAGCTATAGATTTGTTCGATTAGGCGAT----------CTAA--AC---ACTTT----------CCC-TTTCCGCAGCTATGGCGGCGGCACCCACCCGTGGAAC----------GACTCGTTCGGGGCGACGAAGC
droWil2	scf2_1100000004963:750366-750553 -		AAACTGCGGAAGCCGGCTGCATGCCGTCTCTTCTGAACATACCCAGGTGAGAGAA----------T-----------ATCGATTAAATTGAAATGAAGATTAAGTGGTAGTAGGAAGTAATT----------GCATCGACTAA-ATCAAC----TAT----------C-TAA-A-CGCACAGCTATGCGGCGGCACCCACCCGTGGAAC----------GACTCGTTCGAGCCAATCAAAGC
droVir3	scaffold_12726:2811755-2811910 +		AAGCTACGCGAAGCCGGCTGCCATGCCGTCTCTTCTGAACATACCAGGTGACTTTTC----------T-----------T-----------T----T--T-----CCTCTCGCTCTTAC-----AATAGATTGCTA----ACAT----------T-TGT-GATGCACAGCTATGGCGGCGGCACCACTCGTGGAAC----------GACTCGTTCGGCCACGACGAAGC
droMoj3	scaffold_6473:5674512-5674669 -		AAGCTCCGCGAAGCCGGCTGCCATGCCGTCCTCTTCTGAACATACCCAGGTAGCGCGAG----------CC-----------A--CT----------GT----------G----------T----T--T-----TGTCTAGCTCCATC-----ATTTGCTT----GACT----------GA----------T-TGC-GATGCACAGCTATGGCGGCGGCACCACTCGTGGAAC----------GACTCGTTCGGCCACGACGAAGC
droGri2	scaffold_15203:6409733-6409893 +		AAGCTGCGGAGCCGGCTGCCATGCCGTCCTCTTCTGAACATACCCAGGTGACCAAC----------AC-----------TGTAACC----------T----T--AGC--CGCT----------CA--TATTTATTAGTTC----------T---GACCA----------A-ATAC-ACTTTGAGCTATGGCGGCGGCACCACTCCGTGGAAC----------GACTCGTCGGGCCGACGAAGC
droAna3	scaffold_13047:734629-734782 +		AAGCTCCGCGAGCCGGCTGCCATGCCGTCCTCTTCCTGAACATCCCAGGTAGGGTT----------T-----------PC----------T----------T----------TCTCCAC----------T----T--T-----TACC-----AAGAGA-GGTACTA----------ACCA----------T-TTC-CCCCACAGCTATGGCGGCGGCACCCATCCGTGGAAC----------GACTCCTTCGGCTTCACGAAGC
droBip1	scf7180000039643 1:522461-522614 +		AAGCTGCGGCGACGCCGGCTGCCACGCCGTCCTGTTCCTGAACATACCCAGGTAAGGGTT----------T-----------PC----------T----------T----------CCTCTTT----------T----T--T-----TCTCA----------CAGGGGCAGTAA----------CCAT----------C-TTC-CCCCTCAGCTATGGCGGCGGCACCCATCCGTGGAAC----------GACTCATTCGCTTCACGAAGC
droKik1	scf7180000302698:162585-162802 -		AAGCTACGGGAAGCGGCTGCCATGCCGTCTCTTCCTGAACATCCCAGGTGCGTGAT----------GCGC-CT----------TTCC--T----------TT----------G----------T----T--T-----AATCTAGCTTTTAA-----ATTAGTTG----AATTATTAGCTAAAATTTAGCTAAAATTATTAGTAAAAATATATAATAATTCATAAATAACCCTATTCTTTAGCTATGGCGGCGGCACCACTCGTGGAAC----------GACTCCTTTGCTTCGCAAGC
droFic1	scf7180000453800:1984898-1985077 +		GAGTGCCACCCGCGC-----ATCCAATCATCCTGAAGATTTGAGTAAACTGGAACATAAAG------T-----------AT--GCA----------ATTATATAGGTTT-AAT----------AATTCGT----TATCCAAATTAAA--ATCCGGTH----------T----------TA----------A-T-AT-TTTTCAGCTGGCGAAGTGGCACCATCCCTGGGGTCCGGACAAGGAGGAGCAGT-----TCT-CAGC
droEle1	scf7180000491008:102791-102978 +		GAATGCCACCCGCA-----TGTATCATCATCCTGAAGATTTGAGTAACCTGCC----------AG-AAAA----------TCCTA--CTGCTTGA----------TTGTTTTTATATTGTTG----------T----T--T-----TGAATA----------TTTTGTTTGGATCATTAA----AACCT----------ATAA--ACTTTCAGCTGGCGGCACGCGTGCCATCCCTGGGGTCCCGACAAGGAGGAGCAGT-----TCT-CAGC
droRho1	scf7180000779169:97157-97345 -		CGTGATGGGA----------TTATCATCCTGAACATTTAAGTAACCTAG----------AAGA-AA----------TTGA--TTGCTATT----------TTGTTTGTTATATTATTTTGTATTACTTTATGATTATGAATAA-ACATTAAAAC---AT----------TAT----------T-ACC-CTTTCCAGCTGGCGGCACGCGTGCCATCCCTGGGGTCCCGACAAGGAGGAGCAGT-----TCT-CAGC
droBia1	scf7180000301760:2644076-2644253 +		AAGCTCCGCGACGCCGGCTGCCATGCCGTCCTCTTCCTGAACATCCCAGGTGCATTCCG----------GAGA-CC----------T--GTGGGGATATACCACCGATCATAC----------CA----ATAGCATATCCCA--ATCC--TTTH----------CCC----------C-TTAT-CCCCCCAGCTATGGCGGCGGCACCCATCCGTGGAAC----------GACTCCTTCGGCGCCTCAAGC
droTak1	scf7180000415169:1005755-1005827 -		CACTTT----------T----------T----------T

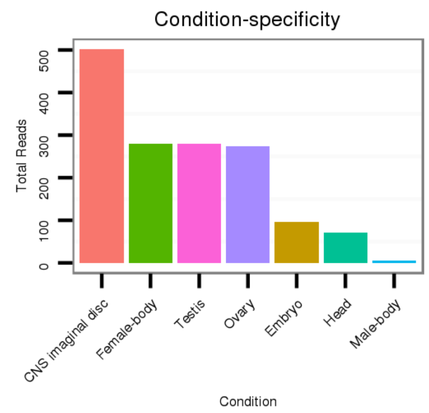
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dps_109	**4_group5:488334-488396 -**	**confident**	**Mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

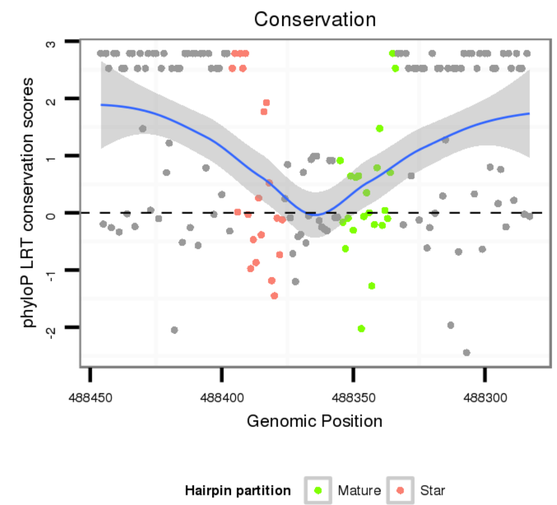
Legend: mature star mismatch in alignment mismatch in read

Predicted structure









Show Alternate Folds

Flybase annnotation

intron [Dpse\GA10922-in]; CDS [Dpse\GA10922-cds]; CDS [Dpse\GA10922-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TCACGTTCCCCAAACATCACTTTGATGCTGGTTTCATCATTACCGCTTTCGTGAGTCTATTGAATTTTCCTGTGACATCTCTTTGTAATGGAAAATTCTTTTGATTTATGTAGATCTGCGCGGCCTTGGGACGGGCCGTGAATGTATATCCCTTGTCCTGGTT ********** (((((((....(((((((((....(((.....)))...)))))))))....)))))))....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	SRR902012 CNS imaginal disc	M040 female body	SRR902011 testis	SRR902010 ovaries	M059 embryo	M062 head	GSM444067 head	GSM343916 embryo	V112 male body	M022 male body
..AAAATTCTTTTGATTTATGTAG..	22	0	1	1372.00	1372	498	217	273	272	55	40	9	6	2	0
..GTGAGTCTATTGAATTTTCC..	20	0	1	58.00	58	2	17	0	0	21	5	5	5	3	0
..AAAATTCTTTTGATTTATGTAGA..	23	0	1	21.00	21	4	5	6	4	1	0	0	1	0	0
..AAATTCTTTTGATTTATGTAG..	21	0	1	20.00	20	0	14	3	1	1	1	0	0	0	0
..AAAATTCTTTTGATTTATGT..	20	0	1	20.00	20	0	7	0	0	1	4	7	1	0	0
..AAAATTCTTTTGATTTATGTA..	21	0	1	13.00	13	1	9	0	1	2	0	0	0	0	0
..AAATTCTTTTGATTTATGTAGA..	22	0	1	8.00	8	4	2	0	2	0	0	0	0	0	0
..AAAATTCTTTTGATTTATG..	19	0	1	7.00	7	0	4	2	0	1	0	0	0	0	0
..AATTCTTTTGATTTATGTAG..	20	0	1	5.00	5	0	5	0	0	0	0	0	0	0	0
..AAATTCTTTTGATTTATGTAGT..	22	1	1	5.00	5	0	4	0	0	0	0	0	0	1	0
..AAAATTCTTTTGATTTATGTAGT..	23	1	1	4.00	4	1	0	3	0	0	0	0	0	0	0
..GTGAGTCTATTGAATTTTC..	19	0	1	3.00	3	0	1	0	0	1	0	0	0	0	1
..TTCTTTTGATTTATGTAG..	18	0	1	2.00	2	0	0	1	0	0	0	0	1	0	0
..TGAGTCTATTGAATTTTCC..	19	0	1	2.00	2	0	2	0	0	0	0	0	0	0	0
..AAAATTCTTTTGATTTATGTAC..	22	1	1	2.00	2	0	0	0	0	2	0	0	0	0	0
..GTGAGTCTATTGAATTTTCCTG..	22	0	1	2.00	2	0	1	0	0	1	0	0	0	0	0
..GTGAGTCTATTGAATTTTCA..	20	1	1	2.00	2	0	1	0	0	0	0	0	0	1	0
..GTGAGTCTATTGAATTTTCCA..	21	1	1	2.00	2	0	1	0	0	0	0	0	1	0	0
..TGTGACATCTCTTTGTAATGG..	21	0	1	2.00	2	0	2	0	0	0	0	0	0	0	0
..AAAATTCTTTTGATTTATGTAA..	22	1	1	2.00	2	0	2	0	0	0	0	0	0	0	0
..AAAATTCTTTTGATTTATGTAGAA..	24	1	1	1.00	1	1	0	0	0	0	0	0	0	0	0
..GAAAATTCTTTTGATTTATGTAG..	23	0	1	1.00	1	0	0	1	0	0	0	0	0	0	0
..AAAATTCTTTTGATTTATGC..	20	1	1	1.00	1	0	0	0	0	1	0	0	0	0	0
..TTTTGATTTATGTAGA..	16	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0
..GAAAATTCTTTTGATTTATGT..	21	0	1	1.00	1	0	1	0	0	0	0	0	0	0	0
..AAATTCTTTTGATTTATGTAGC..	22	1	1	1.00	1	0	1	0	0	0	0	0	0	0	0
..TCTTTTGATTTATGTAGA..	18	0	1	1.00	1	0	1	0	0	0	0	0	0	0	0
..TTTTGATTTATGTAG..	15	0	2	0.50	1	1	0	0	0	0	0	0	0	0	0
..CTTTTGATTTATGTAG..	16	0	2	0.50	1	1	0	0	0	0	0	0	0	0	0

Anti-sense strand reads

AGTGCAAGGGGTTTGTAGTGAAACTACGACCAAAGTAGTAATGGCGAAAGCACTCAGATAACTTAAAAGGACACTGTAGAGAAACATTACCTTTTAAGAAAACTAAATACATCTAGACGCGCCGGAACCCTGCCCGGCACTTACATATAGGGAACAGGACCAA ********** (((((((....(((((((((....(((.....)))...)))))))))....)))))))....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M040 female body

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
dp5	4_group5:488283-488446 -	dps_109	TCACGTTCCCCAAACATCACTTTGATGCTGGTTTCATCATTACCGCTTTCGTGAGTCTAT----------TGA------ATT-T-----TCCTGTGACATCTCTTTGTAATGGAAA----------A--TTCT----T----T-TGATTTATGTAGATCTGCGCGGCCTTGGGACGGGCCGTGAATGTATATCCCTTGTCCTGGTTG
droPer2	scaffold_5:4988554-4988717 -	dpe_112	TCACGTTCCCCAAACATCACTTTGATGCTGGTTTCATCATTACCGCTTTCGTGAGTCTAT----------TGA------ATT-T-----TCCTGTGACATCTCTTTGTAATGGAAA----------A--TTCT----T----T-TGATTTATGTAGATCTGCGCGGCCTTGGGACGGGCCGTGAATGTGTATCCCTTGTCCTGGTTG
droWil2	scf2_1100000004577:2571118-2571281 -		TTACGTTCCCTAAACATCATTTTGATGCGGGTTCATTATTAACAGCTTTGTAAGTTATA------A------TTA------ATCAA-T---CGAAAAAT---A----------CTTCTAAATGG----------TTAATT----TGTTA----T-TGTTTTTTTAGATCTGCGCGGATTTGGGCCGAGGTGTCAATGTTTATCGTTTGTCTTGGCTC
droVir3	scaffold_12963:14698072-14698235 -		TTACATTCCCCAAACATCATTTCGATGCTGGCTTCATAATAACCGCTTTTGTAAGTTCGT----------A--TTCA---AA-A-----TTATATAA----------T-TTG-----TCAAC--TAACAGAT----TAC--ATTT-TTTTTTATAGATTTGCGCGGATTGGGACGTGGTGTTAATGTGTATCGTTTGTCCTGGCTG
droMoj3	scaffold_6500:17627220-17627380 -		TCACCTTTCCTAAGCATCATTTCGATGCAGGCTTCATAATAAGAGCTTTCGTGAGTGATA----------TAA------ATA-G----GTGTAAATA----------ATA--TTTTC-A---T--AAATAACT----TGT------A-TTTCTTGTATAGATCTGCGCTGCTCTAGGACGTGCTGTCAATGTCTATCGTTTATCCTGGCTA
droGri2	scaffold_15126:1868129-1868302 +		TCAGATTTCCCAAGCATCATTTCGATGCTGGCTTTATTATTAACCGCGTTTGTAAGTCTAATGAAATATATAATATA--TATATATATA-C-----TTATATTA----------AT--TT-T---T--GTATTATT----AA---------TTTATTTAATAGATTTGTGCTGCTCTGGGACGTGCCGTTAATGTGTATCCTTTGTCCTGGCTG
droAna3	scaffold_12916:8572267-8572425 -		TTACCTTCCCGAAGCATCATTTTGATGCCGGATTTATTATTAACAGCTTTTGTGAGTTCTT----------A---AA---TA-A-----TTTATTT---GTCTTAAACATAAAAT----------AACGA----C-TTGAATTTGTAGATCTGCGCCGCGCTGGGACGTGCCGTCAACGTGTATCCCTTATCCTGGTTG
droBip1	scf7180000396535:1089823-1089981 -		TTACCTTTCCAAAACATCATTTTGATGCAGGATTCATTATTAACAGCTTTTGTGAGTTCTC----------T---AA---TC-T-----TGATATTT---A----------CTTTAAAAA----------TTAATT----AAAGA----C-TTTAATTTGTAGATCTGCGCCGCGATAGGTGCGCGTGTCAACGTTTATCCCTTATCCTGGCTG
droKik1	scf7180000302473:486006-486160 -		TTACCTTCCCCAAGCACACTTTGATGCTGGTTTCATCATAACCGCTTTCGTAAGTCTTA----------TAA------AT--------AATAGACA-------ATA--TGATT-A---T--GAA---T-TACT----A----C-TGTTTTGCTTAGATCTGTGCCGCTTTGGGACGTGCCGTGAACGTGTATCCCTTATCCTGGCTG
droFic1	scf7180000453815:362258-362419 -		TTACCTTCCCCAAGCATCACTTCGACGCAGGATTCATTATTAACAGCTTTTGTAAGTTTAC----------TTA------AAA-T-----TTAAAATC---G----------CTTC---------T--GC-C---C--ATCTAATA----ATTTA----T-TTGTTTATTCAGATTTGCGCCGCTAATAGGACGCGCCGTAAATGTTTACGCATTGTCCTGGCTT
droEle1	scf7180000490970:242358-242522 -		TTACCTTTCCCAAGCATCATTTCGACGCAGGATTTATCATTAACAGCATTCGTGAGTTTAT----------T--AAAATAT---T-AGT-A-------A---A----------CACTAGGAG-TTTT--TC-G---C--TCATAG-----ATAC----T-GTTTTCTTTCAGATTTGCGCCGCGTAATAGGACGCGCTGTAAATGTGTACCCCTGTCGTGGTTTA
droRho1	scf7180000780014:189898-190060 -		TTACCTTTCCCAAGCATCATTTTGACGCAGGATTTATCATTAACAGCTTTCGTAAGTTT--------------TTAATAT---T-AGATA-------A---A----------CATCGAAAGTG-TT--TCGC---T--CAATA-----ATAC----T-TAACATTTCAGATCTGCGCCGCTAATAGGACGTGCGGTAAACGTGTATCCCTTGTCCTGGTTG
droBia1	scf7180000302422:2777640-2777807 -		TTACCTTCCCCAAACATCATTTCGACGCCGGATTCATCATTAACAGCTTTCGTAAGTTTAA----------TTA------ATG-GACATC-------A---A----------ATTCAAAAG-GTTTT--CC-C---TTTAAACAAGG----AATA-----T-CTTTTTTACAGATCTGCGCCGCCATAGGTCGTGCCGTGAATGTGTATCCCTTATCCTGGCTG
droTak1	scf7180000415104:132998-133157 -		TCACCTTTCCCAAGCATCATTTCGACGCCGGATTTATCATTAACAGCTTTCGTAAGTTTAT----------T--TCTATAT---T-TAATT-------A---A----------AATCCCAAG-G--------C---T--AAACA-----ATAT----T-TTACTTTCATAGATCTGCGCCGCGTAATAGGACGTGCCGTGAATGTGTATCCTTTATCCTGGCTG
droEug1	scf7180000409463:2115716-2115878 +		TTACGTTTCCCAAGCATCACTTCGATGCTGGATTCATTATTACAGCTTTCGTAAGTTCAT----------T--TAAA---TA-T-----GCATATGTGCTCCCTTT----------C--AAGCCATT----AACAC----T-TTATTTTTACAGATCTGCGCTGCAATAGGACGGGCCGTAAATGTGTATCCCTTATCCTGGTTG
dm3	chr2L:6681340-6681513 -		TCACCTTTCCCAAGCATCATTTTGACGCCGGTTTCATTATAACAGCTTTTGTAAGTTATT----------T--TCAGCAT---T-AGAAA-------T---A----------CTTAAAAAG-GCGT--TC-C---C--AAACAGAA----AGTTATTTTCTTTTTTCACAGATTTGCGCTGCCATTGGAAGGGCCGTGAATGTGTATCCCTTGTCCTGGCTG
droSim2	2L:6455057-6455229 -		TCACCTTTCCCAAGCATCATTTTGACGCCGGTTTCATTATAACAGCTTTTGTAAGTTATT----------T--TCAGCAT---T-AGAAA-------C---A----------CTTCAAAAG-GTTT--TC-C---C--AAACAGCA----AGTTATTTTTCTTTTTTCACAGATTTGCGCTGCCATTGGAAGGGCCGTAAATGTGTATCCCTTGTCCTGGCTG
droSec2	scaffold_3:2220372-2220535 -		TCACCTTTCCCAAGCATCATTTTGACGCCGGTTTCATTATAACAGCTTTTGTAAGTTATT----------T--TCAGCAT---T-AGAAA-------C---A----------CTTCAAAAG-GAGT--G----------TTATTT----ATTTC----T-CTTTTTCACAGATTTGCGCTGCCATTGGAAGAGCCGTCAATGTGTATCCCTTGTCCTGGCTG
droYak3	2L:6231850-6232018 +		TCACCTTTCCCAAGCATCATTTTGACGCTGGCTTTATTATTAACAGCTTTTGTAAGTTCAT----------T--TCCATAT---T-GGAAA-------C---A----------CGTTAAAAG-GCGT--GC-C---C--GAACAACT----AGACT----A-TTTTTCCACAGATTTGCGCTGCCATAGGAAGGGCCGTGAATGTGTATCCCTTGTCGTGGCTG
droEre2	scaffold_4929:15591481-15591645 -		TCACCTTTCCCAAGCATCATTTTGACGCTGGCTTCATTATTAACAGCTTTTGTAAGTTTAT----------TTA------ATT-TCGAAA-------C---A----------CTTTAAAAG-GCAT--TC-C---T--GAACAACT----AG---T----T-TCTTTCACAGATTTGCGCTGCCATAGGAAGGGCCGTGAATGTGTATCCCTTGTCGTGGCTG

Generated: 09/08/2015 at 07:00 PM

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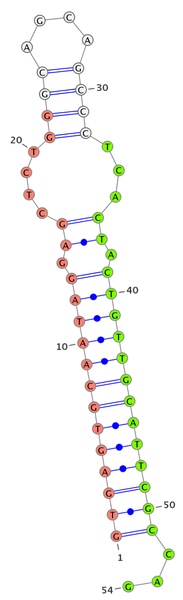
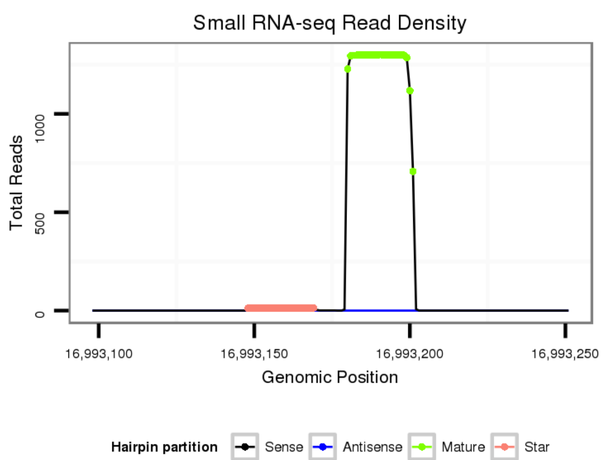
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	2
rescue.candidate	0

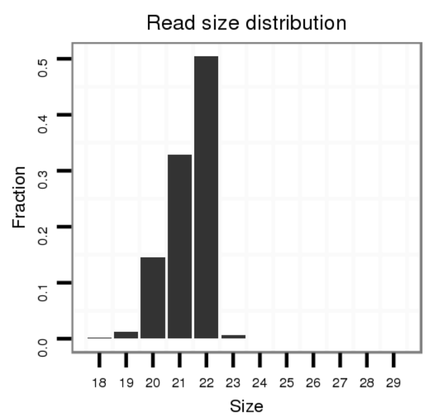
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dps_53	**3:16993148-16993201 +**	**confident**	**Mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

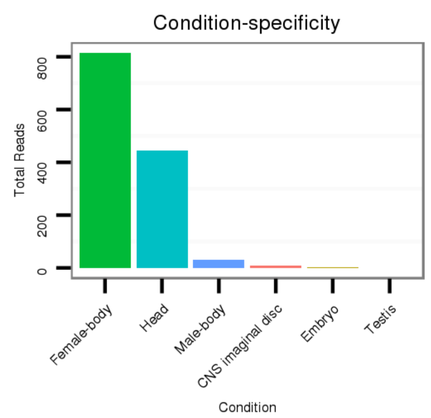
Legend: mature star mismatch in alignment mismatch in read

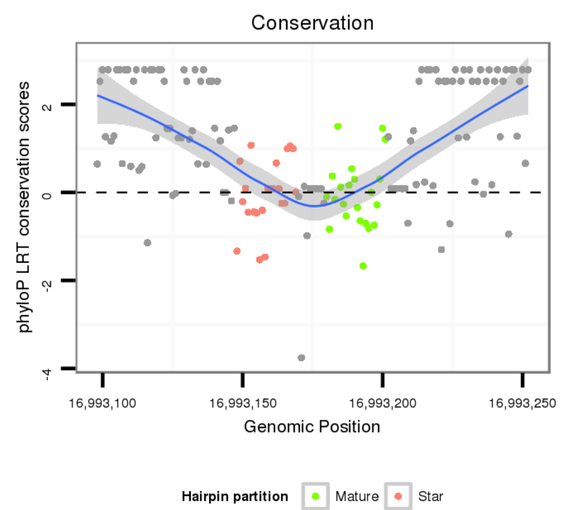
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dpse\GA20945-in]; CDS [Dpse\GA20945-cds]; CDS [Dpse\GA20945-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

AGAGTCCAAGAACCATCTGAACTACTACACCAGCAAGCAGCCAGCAGCAGGTGAGTGCAATAGGAGCTCTGGGCAGCAGCCCTCACTACTGTTGCATTCGCCAGCACGACAAGACGACAAGTCGGCGCAGGAGAGCGACGACGAGGTGAAGGAC **********((((((((((((.((....((((....))))...)).)))))))))))...**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M040 female body	M062 head	GSM444067 head	M022 male body	V112 male body	SRR902012 CNS imaginal disc	M059 embryo	SRR902011 testis
.....TCACTACTGTTGCATTCGCCAG.....	22	0	1	651.00	651	418	201	10	14	1	4	2	1
.....TCACTACTGTTGCATTCGCCA.....	21	0	1	387.00	387	255	117	5	6	0	3	1	0
.....TCACTACTGTTGCATTCGCC.....	20	0	1	164.00	164	66	80	8	10	0	0	0	0
.....CACTACTGTTGCATTCGCCAG.....	21	0	1	40.00	40	38	2	0	0	0	0	0	0
.....CACTACTGTTGCATTCGCCA.....	20	0	1	23.00	23	23	0	0	0	0	0	0	0
.....TCACTACTGTTGCATTCGCCAGT.....	23	1	1	17.00	17	3	14	0	0	0	0	0	0
.....TCACTACTGTTGCATTCGC.....	19	0	1	12.00	12	3	6	1	0	0	2	0	0
.....TCACTACTGTTGCATTCGCCAC.....	22	1	1	9.00	9	0	8	0	1	0	0	0	0
.....GTGAGTGCAATAGGAGCTCTGG.....	22	0	1	8.00	8	1	0	6	0	0	0	1	0
.....TCACTACTGTTGCATTCGCCAGC.....	23	0	1	7.00	7	1	6	0	0	0	0	0	0
.....CTCACTACTGTTGCATTCGCCAG.....	23	0	1	5.00	5	3	2	0	0	0	0	0	0
.....CACTACTGTTGCATTCGCC.....	19	0	1	4.00	4	4	0	0	0	0	0	0	0
.....TCACTACTGTTGCATTCGCCT.....	21	1	1	4.00	4	0	4	0	0	0	0	0	0
.....ACTACTGTTGCATTCGCCAG.....	20	0	1	3.00	3	2	1	0	0	0	0	0	0
.....GTGAGTGCAATAGGAGCTCTGGG.....	23	0	1	3.00	3	0	0	2	0	1	0	0	0
.....TCACTACTGTTGCATTCGCCAGA.....	23	1	1	2.00	2	2	0	0	0	0	0	0	0
.....CTCACTACTGTTGCATTCGCC.....	21	0	1	1.00	1	1	0	0	0	0	0	0	0
.....CTACTGTTGCATTCGCCAG.....	19	0	1	1.00	1	0	1	0	0	0	0	0	0
.....TCACTACTGTTGCATTCGCCG.....	21	1	1	1.00	1	0	1	0	0	0	0	0	0
.....TGAGTGCAATAGGAGCTCTGG.....	21	0	1	1.00	1	1	0	0	0	0	0	0	0
.....CACTACTGTTGCATTCGCCAGT.....	22	1	1	1.00	1	1	0	0	0	0	0	0	0
.....GTGAGTGCAATAGGAGCTCTGGGCAGCAG.....	29	0	1	1.00	1	0	0	0	0	0	1	0	0
.....TCACTACTGTTGCATTCGCCAT.....	22	1	1	1.00	1	1	0	0	0	0	0	0	0
.....TCACTACTGTTGCATTCG.....	18	0	1	1.00	1	0	1	0	0	0	0	0	0
.....TCACTACTGTTGCATTCGCCAGG.....	23	1	1	1.00	1	1	0	0	0	0	0	0	0
.....TACTGTTGCATTCGCCAG.....	18	0	1	1.00	1	0	1	0	0	0	0	0	0
.....ACTACTGTTGCATTCGCCAGT.....	21	1	1	1.00	1	1	0	0	0	0	0	0	0
.....TCACTACTGTTGCATTCGCCAA.....	22	1	1	1.00	1	1	0	0	0	0	0	0	0

Anti-sense strand reads

TCTCAGGTTCTTGGTAGACTTGATGATGTGGTCGTTCGTCGGTCGTCGTCCACTCACGTTATCCTCGAGACCCGTCGTCGGGAGTGATGACAACGTAAGCGGTCGTGCTGTTCTGCTGTTCAGCCGCGTCCTCTCGCTGCTGCTCCACTTCCTG **********((((((((((((.((....((((....))))...)).)))))))))))...**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M040 female body	V112 male body	M022 male body	SRR902010 ovaries

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
dp5	3:16993098-16993252 +	dps_53	AGAGTCCAAGAACCATCTGAACTACTACACCAGCAAGCAGCCAGCAGC-----AGGTGAG-------TG--CAATAGGAGCTCTGGGC-AGCAGCC----------CTCA-----CTACT----------GTTGCATTCGCCAGCACGACAAGACGACAAGTCGGCGCAGGAGAGCGACGACGAGGTGAAGGACA
droPer2	scaffold_31:765303-765457 -	dpe_103	AGAGTCCAAGAACCATCTGAACTACTACACCAGCAAGCAGCCAGC--TGC---AGGTGAG-------TG--CAATAGGAGCTCTGGGC-AGCAGCC----------CTCA-----CTACT----------GTTGCATTCGCCAGCACGACAAGACGACAAGTCGGCGCAGGAGAGCGACGACGAGGTGAAGGACA
droWil2	scf2_1100000004822:208360-208503 -		AGAATCCAAGAATCATATAAACTACATGGCCAGCCAACAACAGCAG--TGAATTT-T----CAACTTATCTA----------------CCTAATTAGAA-----TTGAA---GTTATTC----------AACTA--ACATGTT------TCCAGACAAATCAGCTCAGGAGAGCGATGATGAAGTCAAGGATA
droVir3	scaffold_12875:5390240-5390386 +		GGAGTGCAAGAATCATCTAAACTACTAGGCCAGCAAGCAGCCAGG--TGAGTCT------TTTGGTCCAATGAT----------G-CA-----ATAATCA-------------AAAGCCCAAA-------TCGATTGCAT-TACCAGC------GCAAGACAAGTCGGCGCAGGAAAGTGATGATGAGGTGAAGGACA
droMoj3	scaffold_6496:24700984-24701130 -		GGAGTGCAAGAATCATCTGAACTACTAGGCCAGCAAGCAGCCAGG--TGAGTTA------------------------CTGGGC-AT-----AGGCCAAAGCAATTCATG-----CTGCA----GTTGTTC----------AT--TGCTCGCCAGC------TCAAGACAAGTCGGCGCAGGAGAGCGATGATGAGGTGAAGGACA
droGri2	scaffold_15112:385491-385636 +		GGAGTGCAAAAATCACTTGAACTACTAGTCCAGCAAGCAACCTGG--TGAGTTCGA---TT-AT-------CGAT----------T-CG-----ATTTATG-------------CATATTTAATATATACTT----GGCTTTTGCAGC------GCAAGATAAATGTGCGCAGGAGAGCGATGATGAGGTCAAGGACA
droAna3	scaffold_13266:13167633-13167779 -		GGAGTCCAAGAATCATCTCAACTACTATGCCAGCAAGCAGCCAGG--TAGGAG--A-----CGCTTCATTAGA---A-TCCTGATT-AG-----------A-------------AACCATA-AT-------AACATTATACATTGTAGC------CCAGGATAAATCAGCTCAAGAGAGCGACGACGAGGTCAAGGACA
droBip1	scf7180000396730:761523-761664 +		GGAGTCCAAGAATCATCTCAATTACTATGCCAGCAAGCAGCCAGG--TAGGAG--A---T--------TC-TTCATT----------G-AG-----AATTCTG-------------AATAGAAACT-------AACATCATCCATTATAGC------TCAGGACAAATCAGCCCAGGAGAGTGACGACGAGGTCAAGGACA
droKik1	scf7180000302386:304722-304870 +		GGAGTCCAAGAATCACCTTAACTACTATAACAGCAAGCAGCCAGG--TGAGTCA-A-----G-------------------C-AC-----AAGGAAAAATGTTTCTTAGGAAACTAAA----CTAGATTA----------TTCCCCTTTAGC------CCAGGACAAATCGGCTCAGGAGAGCGATGACGAGGTTAAGGACA
droFic1	scf7180000453948:865308-865457 +		GGAGTCCAAGAACCACCTTAACTACTAGGCCAGCAAGCAGCCAGG--TACTGAA-T----CAACTGATTCAACTTG----------T-G------AATCTTC-------------AATATTAATC-------TTAATTTTGTACCTAGC------CCAGGACAAATCGGCTCAGGAGAGCGATGATGAGGTGAAAGACA
droEle1	scf7180000491214:3230912-3231058 +		GGAGTCCAAGAACCACCTTAACTACTATTCCAGCAAGCAGCCAGG--TGGTGTAGC----------CAGATCTTTTG----------T-AC-----ATTTATA-------------AATGTTAAAT-------CTCATTCTATAGATTAGC------CCATGATAAATGTGCCCAGGAGAGCGATGACGAGGTGAAGGACA
droRho1	scf7180000779932:135852-135997 +		GGAGTCCAAGAACCACCTTAACTACTATGCCAGCAAACAGCCAGG--TGGGGTAGT----------TGAATCCTTAA----------C-AG-----AATTCTG-------------AGTATTAAGG-------CA-GATATATTCCTTAGC------ACATGACAAATCGGCTCAGGAGAGCGACGACGAGGTGAAGGACA
droBia1	scf7180000302292:525697-525843 +		GGAGTCCAAGAACCACCTCAACTACTATGCCAGCAAGCAGCCAGG--TGGGCCAGA----------TATATTTATTT----------C-AG-----ATTTTTT-------------AATATTAAAT-------CCCATTTTATACCTTAGC------CCAGGACAAATCGGCCCAGGAGAGCGACGACGAGGTAAGGACA
droTak1	scf7180000415820:90788-90936 +		GGAGTCCAAGAACCACCTTAACTACTATGCCAGCAAGCAGCCAGG--TGGGTA-GC----------GA-ATTATATA----------------TAATATCTATAATATGTATACTCCAAGT--C----------TAAACCCTTAGC------CCAGGACAAATCGCGTCAGGAGAGCGACGACGAGGTGAAGGACA
droEug1	scf7180000409462:746744-746887 -		GGAGTCCAAGAACCACCTTAACTACTACGCCAGCAAGCAGCCAGG--TGAGGCAGATA---AG----TG--TTC----------C-AA-----TGTCCTC-------------ATTACTTAAT-------CGAAT-TTTTACCTCAGC------CCAGGACAAATCAGCTCAGGAGAGCGACGACGAGGTGAAGGACA
dm3	chr2R:7737879-7738026 +		GGAGTCCAAGAACCACCTGAACTACTATGCCAGCAAGCAGCCAGG--TGGGAGT------ATTATTTCATCGAG----------G-AA-----AACTCCA-------------AATAATAAAT-------CCCATTTGGTTACTTAGC------CCAGGACAAGTGAGCGCAGGAGAGTGACGACGAGGTAAAGGATA
droSim2	2r:8443207-8443354 +	dsi_19333	GGAGTCCAAGAACCACCTGAACTACTATGCCAGCAAGCAGCCAGG--TGGGAGT------ATTATTTCATCGAG----------G-AA-----AATTTCA-------------AATAATAAGG-------CCCATTTGGTTACTTAGC------CCAGGACAAGTGAGCGCAGGAGAGCGACGATGAGGTAAAGGATA
droSec2	scaffold_1:5289610-5289758 +		GGAGTCAAAGAACCACCTGAACTACTATGCCAGCAAGCAGCCAGG--TGGGAGT------ATTATTTCATCGAG----------A-AA-----AGCTCCA-------------AATAATAAGTC------CCCATTTGGTTACTTAGC------CCAGGACAAGTCAGCGCAGGAGAGCGACGATGAGGTAAAGGATA
droYak3	2R:9213320-9213467 -		GGAGTCCAAAAACCACCTGAACTACTATGCCAGTAAGCAGCCAGG--TGGGAAT------A-TATTTCGTTAAA----------AAAA-----AATTACA-------------AATAATAAAT-------GCCTTTTGGCTCCTTAGC------CCAGGACAAGTCGGCGCAGGAGAGCGACGACGAGGTGAAGGATA
droEre2	scaffold_4845:18056520-18056666 -		GGAGTCCAAGAACCACCTAAACTACTATGCCAGTAAGCAGCCAGG--TGGGTA-GA----TATTTCTTTAAT----------G-AA-----AATTACA-------------AATAATAAAT-------ACCATTTGGGTCCTTAGC------CCAGGACAAGTCAGCGCAGGAGAGCGACGACGAGGTGAAGGATA

Generated: 09/08/2015 at 07:00 PM

	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
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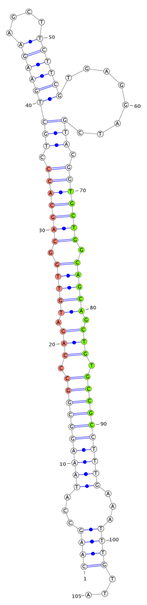
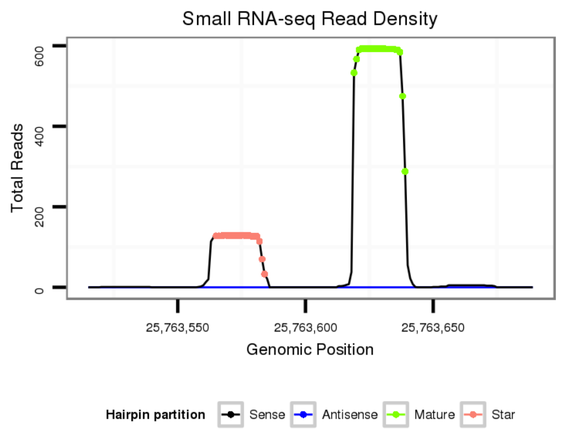
rescue.known	0
rescue.confident	2
rescue.candidate	0

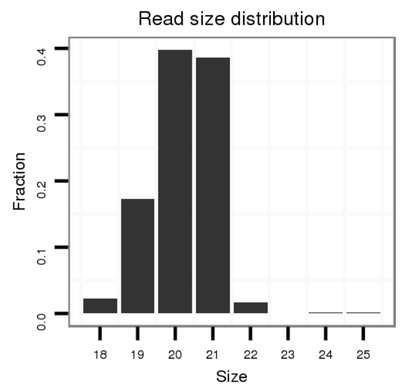
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dps_123	**2:25763565-25763639 +**	**confident**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

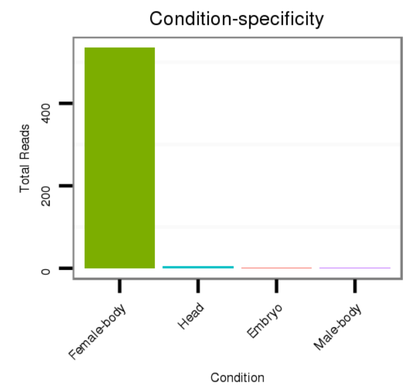
Legend: mature star mismatch in alignment mismatch in read

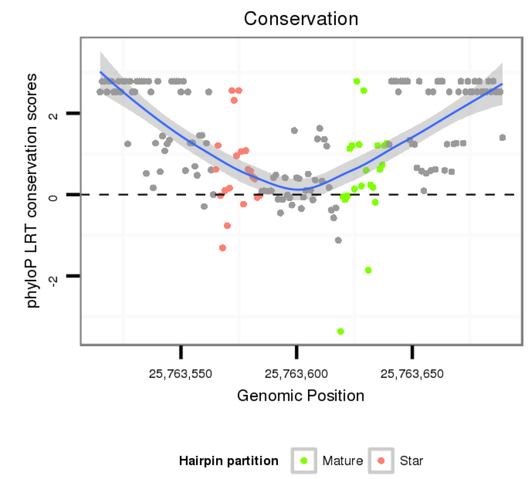
Predicted structure











Show Alternate Folds

Flybase annotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

GTACAAGGACTTTTGGTAAATTCTCAAACAAATTTCAAGCCATAAAGGCGGCCCAGATGTTGGCAGCACCCTGCTGAAGAAGCTTCTTCGTGAGGATCGTACGGTGCTGGCAGCAGCTGTGCCGCCTTTGAAATTTGTTAAAGAGTTTATCGAAGGTCCTGCTGAGCGTCACCCA **********(((((...(((((((((((.(((.(((((.(((((((.(((((((((....)))))).....))).))))))).)))))).))).))))))))))...)))))...**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M040 female body	M059 embryo	GSM444067 head	M062 head	GSM343916 embryo	V112 male body
.....TGCTGGCAGCAGCTGTGCCGC.....	21	0	1	206.00	206	206	0	0	0	0	0
.....TGCTGGCAGCAGCTGTGCCG.....	20	0	1	178.00	178	173	0	4	0	0	1
.....TGCTGGCAGCAGCTGTGCC.....	19	0	1	83.00	83	83	0	0	0	0	0
.....TGCTGGCAGCAGCTGTGCCGT.....	21	1	1	46.00	46	42	0	3	0	0	1
.....CGGCCCAGATGTTGGCAGCA.....	20	0	1	41.00	41	41	0	0	0	0	0
.....CGGCCCAGATGTTGGCAGCAC.....	21	0	1	33.00	33	33	0	0	0	0	0
.....TGCTGGCAGCAGCTGTGCCGCC.....	22	0	1	18.00	18	17	1	0	0	0	0
.....GCTGGCAGCAGCTGTGCCGC.....	20	0	1	17.00	17	17	0	0	0	0	0
.....GTGCTGGCAGCAGCTGTGCC.....	20	0	1	16.00	16	16	0	0	0	0	0
.....CTGGCAGCAGCTGTGCCGCC.....	20	0	1	14.00	14	14	0	0	0	0	0
.....CGGCCCAGATGTTGGCAGC.....	19	0	1	12.00	12	11	0	0	1	0	0
.....GTGCTGGCAGCAGCTGTGCCGC.....	22	0	1	9.00	9	9	0	0	0	0	0
.....GCTGGCAGCAGCTGTGCC.....	18	0	1	9.00	9	9	0	0	0	0	0
.....GCTGGCAGCAGCTGTGCCGT.....	20	1	1	7.00	7	7	0	0	0	0	0
.....CGGCCCAGATGTTGGCAGCACC.....	22	0	1	7.00	7	7	0	0	0	0	0
.....TGCTGGCAGCAGCTGTGCCGCCT.....	23	0	1	6.00	6	6	0	0	0	0	0
.....GCGGCCCAGATGTTGGCAGCACCC.....	24	0	1	6.00	6	1	4	0	1	0	0
.....GCTGGCAGCAGCTGTGCCG.....	19	0	1	6.00	6	6	0	0	0	0	0
.....TGCTGGCAGCAGCTGTGCCGTT.....	22	2	2	6.00	12	12	0	0	0	0	0
.....CTGGCAGCAGCTGTGCCGCCT.....	21	0	1	5.00	5	5	0	0	0	0	0
.....GGCCCAGATGTTGGCAGCACCC.....	22	0	1	4.00	4	3	0	0	1	0	0
.....GGCCCAGATGTTGGCAGCAC.....	20	0	1	3.00	3	3	0	0	0	0	0
.....AGAGTTTATCGAAGGTCCT.....	19	0	1	3.00	3	0	0	0	0	3	0
.....GTGCTGGCAGCAGCTGTGCCG.....	21	0	1	3.00	3	3	0	0	0	0	0
.....TGGCAGCAGCTGTGCCGCCTT.....	21	0	1	3.00	3	3	0	0	0	0	0
.....TGCTGGCAGCAGCTGTGCCT.....	20	1	1	3.00	3	3	0	0	0	0	0
.....GGCGGCCCAGATGTTGGCAGCACCC.....	25	0	1	3.00	3	0	3	0	0	0	0
.....AGGCGGCCCAGATGTTGGCAGCACCC.....	26	0	1	3.00	3	2	0	0	1	0	0
.....TGCTGGCAGCAGCTGTGCCGCCA.....	23	1	1	3.00	3	3	0	0	0	0	0
.....CTGGCAGCAGCTGTGCCGCCTT.....	22	0	1	3.00	3	3	0	0	0	0	0
.....GTGCTGGCAGCAGCTGTGCCGT.....	22	1	1	2.00	2	1	0	1	0	0	0
.....TGCTGGCAGCAGCTGTGC.....	18	0	1	2.00	2	2	0	0	0	0	0
.....GCCCAGATGTTGGCAGCACC.....	20	0	1	2.00	2	2	0	0	0	0	0
.....GGCCCAGATGTTGGCAGCA.....	19	0	1	2.00	2	2	0	0	0	0	0
.....GTGCTGGCAGCAGCTGTGC.....	19	0	1	2.00	2	2	0	0	0	0	0
.....GGCGGCCCAGATGTTGGC.....	18	0	1	2.00	2	1	1	0	0	0	0
.....TGCTGGCAGCAGCTGTGCCGA.....	21	1	1	2.00	2	2	0	0	0	0	0
.....TGCTGGCAGCAGCTGTGCCTT.....	21	2	2	1.50	3	3	0	0	0	0	0
.....CGGCCCAGATGTTGGCAGCT.....	20	1	1	1.00	1	1	0	0	0	0	0
.....CTGCTGGCAGCAGCTGTGCCGCT.....	20	1	1	1.00	1	1	0	0	0	0	0
.....CAGATGTTGGCAGCACCC.....	18	0	1	1.00	1	0	1	0	0	0	0
.....GGCGGCCCAGATGTTGGCAGCACC.....	24	0	1	1.00	1	0	1	0	0	0	0
.....CTGGCAGCAGCTGTGCCGC.....	19	0	1	1.00	1	1	0	0	0	0	0
.....CGGCCCAGATGTTGGCAGT.....	19	1	1	1.00	1	1	0	0	0	0	0
.....GTACGGTGCTGGCAGCAGC.....	19	0	1	1.00	1	1	0	0	0	0	0
.....GGCGGCCCAGATGTTGGCAGCA.....	22	0	1	1.00	1	1	0	0	0	0	0
.....GGTGCTGGCAGCAGCTGTGCCGCCT.....	25	0	1	1.00	1	0	1	0	0	0	0
.....GGCCCAGATGTTGGCAGCACC.....	21	0	1	1.00	1	1	0	0	0	0	0
.....GGTGCTGGCAGCAGCTGTGC.....	20	0	1	1.00	1	1	0	0	0	0	0
.....AAAGGCGGCCCAGATGTTGGCAGCACCC.....	28	0	1	1.00	1	0	1	0	0	0	0
.....GGCGGCCCAGATGTTGGCAGC.....	21	0	1	1.00	1	1	0	0	0	0	0
.....GCCCAGATGTTGGCAGCAC.....	19	0	1	1.00	1	1	0	0	0	0	0
.....TGCTGGCAGCAGCTGTGCCGCT.....	22	1	1	1.00	1	1	0	0	0	0	0
.....TGTTAAAGAGTTTATCGAAGG.....	21	0	1	1.00	1	1	0	0	0	0	0
.....GTACGGTGCTGGCAGCAGCTGTGCC.....	25	0	1	1.00	1	0	0	0	1	0	0
.....TGCTGGCAGCAGCTGTGCCGCCTTT.....	25	0	1	1.00	1	1	0	0	0	0	0
.....AGGACTTTTGGTAAATTCTC.....	20	0	1	1.00	1	1	0	0	0	0	0
.....CGGTGCTGGCAGCAGCTGTGCCGCCT.....	26	0	1	1.00	1	1	0	0	0	0	0
.....AAGGCGGCCCAGATGTTGGCAGCACCC.....	27	0	1	1.00	1	0	1	0	0	0	0
.....GCTGGCAGCAGCTGTGCCGCCT.....	22	0	1	1.00	1	1	0	0	0	0	0
.....AGAGTTTATCGAAGGTCCC.....	19	1	1	1.00	1	0	1	0	0	0	0
.....TGCTGGCAGCAGCTGTGCCGCCTT.....	24	0	1	1.00	1	1	0	0	0	0	0
.....CGGTGCTGGCAGCAGCTGTG.....	20	0	1	1.00	1	1	0	0	0	0	0
.....TGCTGGCAGCAGCTGTGCCGCCC.....	23	1	1	1.00	1	1	0	0	0	0	0
.....GCTGGCAGCAGCTGTGCCGCC.....	21	0	1	1.00	1	1	0	0	0	0	0
.....TAAAGAGTTTATCGAAGGTCC.....	21	0	1	1.00	1	0	0	0	0	0	1
.....GTACGGTGCTGGCAGCAGCTGTGC.....	24	0	1	1.00	1	0	1	0	0	0	0
.....CGGCCCAGATGTTGGCAGCACCC.....	23	0	1	1.00	1	0	1	0	0	0	0
.....GGTGCTGGCAGCAGCTGTGCCGCCC.....	25	1	1	1.00	1	0	1	0	0	0	0
.....ACGGTGCTGGCAGCAGCTGT.....	20	0	1	1.00	1	1	0	0	0	0	0
.....GCGGCCCAGATGTTGGCAGCACC.....	23	0	1	1.00	1	1	0	0	0	0	0
.....GCCCAGATGTTGGCAGCACCC.....	21	0	1	1.00	1	1	0	0	0	0	0
.....CGGCCCAGATGTTGGCAGCACCA.....	23	1	1	1.00	1	1	0	0	0	0	0
.....GCTGGCAGCAGCTGTGCCGTT.....	21	2	2	0.50	1	1	0	0	0	0	0
.....TGCTGGCAGCAGCTGTGCT.....	19	1	2	0.50	1	1	0	0	0	0	0
.....CTGGCAGCAGCTGTGCCGTT.....	20	2	3	0.33	1	1	0	0	0	0	0
.....GCTGGCAGCAGCTGTGTT.....	18	2	19	0.05	1	1	0	0	0	0	0

Anti-sense strand reads

CATGTTCCTGAAAACCATTTAAGAGTTTGTTTAAAGTTCGGTATTTCCGCCGGGTCTACAACCGTCGTGGGACGACTTCTTCGAAGAAGCACTCCTAGCATGCCACGACCGTCGTCGACACGGCGGAAACTTTAAACAATTTCTCAAATAGCTTCCAGGACGACTCGCAGTGGGT **********(((((...(((((((((((.(((.(((((.(((((((.(((((((((....)))))).....))).))))))).)))))).))).))))))))))...)))))...**********	Read size	# Mismatch	Hit Count	Total Norm	Total	GSM343916 embryo	M040 female body
.....AGAGTTTATCGAAGGTCCT.....	19	0	1	3.00	3	0	0
.....GCTGGCAGCAGCTGTGCCG.....	21	0	1	3.00	3	3	0
.....TGGCAGCAGCTGTGCCGCCTT.....	21	0	1	3.00	3	3	0
.....TGCTGGCAGCAGCTGTGCCT.....	20	1	1	3.00	3	3	0
.....GGCGGCCCAGATGTTGGCAGCACCC.....	25	0	1	3.00	3	0	3
.....AGGCGGCCCAGATGTTGGCAGCACCC.....	26	0	1	3.00	3	2	0
.....TGCTGGCAGCAGCTGTGCCGCCA.....	23	1	1	3.00	3	3	0
.....CTGGCAGCAGCTGTGCCGCCTT.....	22	0	1	3.00	3	3	0
.....GTGCTGGCAGCAGCTGTGCCGT.....	22	1	1	2.00	2	1	0
.....TGCTGGCAGCAGCTGTGC.....	18	0	1	2.00	2	2	0
.....GCCCAGATGTTGGCAGCACC.....	20	0	1	2.00	2	2	0
.....GGCCCAGATGTTGGCAGCA.....	19	0	1	2.00	2	2	0
.....GTGCTGGCAGCAGCTGTGC.....	19	0	1	2.00	2	2	0
.....GGCGGCCCAGATGTTGGC.....	18	0	1	2.00	2	1	1
.....TGCTGGCAGCAGCTGTGCCGA.....	21	1	1	2.00	2	2	0
.....TGCTGGCAGCAGCTGTGCCTT.....	21	2	2	1.50	3	3	0
.....CGGCCCAGATGTTGGCAGCT.....	20	1	1	1.00	1	1	0
.....CTGCTGGCAGCAGCTGTGCCGCT.....	20	1	1	1.00	1	1	0
.....CAGATGTTGGCAGCACCC.....	18	0	1	1.00	1	0	1
.....GGCGGCCCAGATGTTGGCAGCACC.....	24	0	1	1.00	1	0	1
.....CTGGCAGCAGCTGTGCCGC.....	19	0	1	1.00	1	1	0
.....CGGCCCAGATGTTGGCAGT.....	19	1	1	1.00	1	1	0
.....GTACGGTGCTGGCAGCAGC.....	19	0	1	1.00	1	1	0
.....GGCGGCCCAGATGTTGGCAGCA.....	22	0	1	1.00	1	1	0
.....GGTGCTGGCAGCAGCTGTGCCGCCT.....	25	0	1	1.00	1	0	1
.....GGCCCAGATGTTGGCAGCACC.....	21	0	1	1.00	1	1	0
.....GGTGCTGGCAGCAGCTGTGC.....	20	0	1	1.00	1	1	0
.....AAAGGCGGCCCAGATGTTGGCAGCACCC.....	28	0	1	1.00	1	0	1
.....GGCGGCCCAGATGTTGGCAGC.....	21	0	1	1.00	1	1	0
.....GCCCAGATGTTGGCAGCAC.....	19	0	1	1.00	1	1	0
.....TGCTGGCAGCAGCTGTGCCGCT.....	22	1	1	1.00	1	1	0
.....TGTTAAAGAGTTTATCGAAGG.....	21	0	1	1.00	1	1	0
.....GTACGGTGCTGGCAGCAGCTGTGCC.....	25	0	1	1.00	1	0	0
.....TGCTGGCAGCAGCTGTGCCGCCTTT.....	25	0	1	1.00	1	1	0
.....AGGACTTTTGGTAAATTCTC.....	20	0	1	1.00	1	1	0
.....CGGTGCTGGCAGCAGCTGTGCCGCCT.....	26	0	1	1.00	1	1	0
.....AAGGCGGCCCAGATGTTGGCAGCACCC.....	27	0	1	1.00	1	0	1
.....GCTGGCAGCAGCTGTGCCGCCT.....	22	0	1	1.00	1	1	0
.....AGAGTTTATCGAAGGTCCC.....	19	1	1	1.00	1	0	1
.....TGCTGGCAGCAGCTGTGCCGCCTT.....	24	0	1	1.00	1	1	0
.....CGGTGCTGGCAGCAGCTGTG.....	20	0	1	1.00	1	1	0
.....TGCTGGCAGCAGCTGTGCCGCCC.....	23	1	1	1.00	1	1	0
.....GCTGGCAGCAGCTGTGCCGCC.....	21	0	1	1.00	1	1	0
.....TAAAGAGTTTATCGAAGGTCC.....	21	0	1	1.00	1	0	0
.....GTACGGTGCTGGCAGCAGCTGTGC.....	24	0	1	1.00	1	0	1
.....CGGCCCAGATGTTGGCAGCACCC.....	23	0	1	1.00	1	0	1
.....GGTGCTGGCAGCAGCTGTGCCGCCC.....	25	1	1	1.00	1	0	1
.....ACGGTGCTGGCAGCAGCTGT.....	20	0	1	1.00	1	1	0
.....GCGGCCCAGATGTTGGCAGCACC.....	23	0	1	1.00	1	1	0
.....GCCCAGATGTTGGCAGCACCC.....	21	0	1	1.00	1	1	0
.....CGGCCCAGATGTTGGCAGCACCA.....	23	1	1	1.00	1	1	0
.....GCTGGCAGCAGCTGTGCCGTT.....	21	2	2	0.50	1	1	0
.....TGCTGGCAGCAGCTGTGCT.....	19	1	2	0.50	1	1	0
.....CTGGCAGCAGCTGTGCCGTT.....	20	2	3	0.33	1	1	0
.....GCTGGCAGCAGCTGTGTT.....	18	2	19	0.05	1	1	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
dp5	2:25763515-25763689 +	dps_123	GTACAAGGACTTTTGGTAAATTCTCAA-ACAAATTTCAAGCCA-TAA-AGGCGGCCC---AGATGTTGGCAGCACCCTGCTGAAG------AA-------GCTTCTTC----------GTGAGGA----------TCGTACGGTGCTGGC-AGCAGCTG-----TGCCGCCTTT---GAAATTTGTTAAAGAGTTTATCGAAGGTCCTGCTGAGCGTCAC---CCA
droPer2	scaffold_6:1162988-1163162 -	dpe_2243	GTACAAGGACTTTTGGTAAATTCTCAA-ACAAATTTCAAGCCA-TAA-AGGCGGCCC---AGATGTTGGCAGCACCCTGCTGAAG------AA-------GCTTCTTC----------GTGAGGA----------TCGTACGGTGCTGGC-AGCAGCTG-----TGCCGCCTTT---GAAATTTGTTAAAGAGTTTATCGAAGGTCCTGCTGAGCGTCAC---CCA
droWil2	scf2_1100000004902:6588055-6588266 +		GTACAAGGACTTTTGGTAAATTCTCAT-ACAAATTTCAAGCCA-TTAGAAGAAAAAGAAA---------AGAAAG-----AGA------**--**-------**-------**-------AAAGGAATTCATCCAAACTATTTGCCAGTAATTGGAATTCAAATTAAATTGCTGCCAA----AAAGCTTTGA-TGTTTCCTTCTCTAGT-TTCT-----GTTTTTCTTT---GAAATTTGTTA-AGAGTTTACCGAAGGTCCTGCTGAGCGTCAC---CCC
droVir3	scaffold_12855:7690636-7690802 -		GTACAAGGACTTTTGGTAAATTCACAA-ATACATTTCAGGCCC-CAAAAGGCGGCTA---AGTTGTTGCTAA--A-----AAAT------TG------**-------**----------AAGCCGC----AAATTGTGCA---TTTTTGTTTGGC-TAAAGCTG-----AGCTGGTTTT---GAAATGTGTTT-GGAGTTTACCGAAGGTCCTGCTGAGCGTCAC---CCA
droMoj3	scaffold_6540:24975419-24975568 +	dmo_2782	GTACAAGGACTTTTGGTAAATTCTTAA-ATACATTTCATGTCA-CAAAGGGCGGCTA---AATTGTTGCCAACAG-------AC------A-------**-------**----------**------**----------**-T**GTAAGCTGTTGGC-AACAATTT-----AGCTGCTTTT---GAAATGTTTTA-AGAGTTTACCGGAAGTCCTGCTGAGCGTCAC---CCA
droGri2	scaffold_15074:5197884-5198052 +		GTACAAGGACTTTTGGTAAACTCTCAACACACATTTCATGCCCGGAAAAGGCGGCTT---AGTTGTTGCCAA--G-----AAAT------CG------**-------**----------**CTGCCAT---**--AAA------TTGCGAATTGTTGGT-AAAAGCTG-----AGCTGCTTTTTGGAAATGTGTTA-AGAGTTTACCGAAGGTTGTGCTGAGCGTCACC--CCA
droAna3	scaffold_13340:14074537-14074695 -		GTACAAGGACTTCTGGTAAACTCCCAG-ACCAATTTCAAGCCA-**-**ATAAGGCATCCGG---GACTGTTGACGGCAGG-----GGGC------AG----T--**-------**----------**-------**TAGA------TTGCCCGCCATCGGG-AGCAGACT-----GCAGGCCTTT---GAAATTCGCTG-GGGCCTTACCGGGGGTCCTGCTGAGCGTCAC---CCA
droBip1	scf7180000395971:1084818-1084976 +		GTACAAGGACTTCTGGTAAACTCCCAG-ACCAATTTCAAGCCA-**-**ATGAGGCCTCCG---GCCTGTTGACGGGG-----GGGC------AG----T--**-------**----------**-------**TAGA------TTGCTCGCCGTTGGT-AGCAGACT-----GCAGGCCTTT---GAAATTCGCTG-GGGCCTTACCGGGGGTCCTGCTGAGCGTCAC---CCA
droKik1	scf7180000302706:1794332-1794520 +		GTACAAGGACTTCTGGTAAACTCCCAG-ACCAATTTCAAGCCA-TAAGGGGCGGCCA---GGCTGCTGGCCGGGGG-----GGGCAT---AG----A-TAGATCCACATCCGA-AT----------**-CGGAT**----------**---**CGGATCGCA------TTGCCTGTGGCCGGG-AGCAGCCG-----AGCTGCCTTT---GAAATTCGTTG-GGGCCTTACCGGGGGTCCTGCTGAGCGTCAC---CCA
droFic1	scf7180000453488:226151-226337 +		GTACAAGGACTTCTGGTAAACTCCCAG-ACCAATTTCAAGCCA-TAAGAGGCAGCCGACGAACTGCTGGCCGGCGG-----GGGC------GG----G-GGATCCGGG----------**-------**----------**GATACGGATC-----TCGGACTGCCGGCCGCGGG-AGCAGCG-----GGCTGCCTTT---GAAATTCGCTG-GGGTTTAGCGGGGGTCCTGCTGAGCGTCACCACCA
droEle1	scf7180000491080:2089094-2089268 +		GTACAAGGACTTCTGGTAAACTCCCAG-ACCAATTTCAAGCCA-TAAGAGGCGGCTG---GGCTGCTGGCCGTGTG-----GGAT------AG------GGATCCGT----------**-------**----------**ATACGGATCGGC------CTACCTGGTGCCGGG-AGCAGACG-----AGCTGCCTTT---GAAATTCGCTG-GGAGCTTACTGGGGGTCCTGCTGAGCGTCAC---CCA
droRho1	scf7180000779338:48680-48854 +		GTACAAGGACTTCTGGTAAACTCCCAG-ACCAATTTCAAGCCA-TAAGGGGCGGCTG---GACTGCTGGCCGGGGT-----GGGC------GG------GGATCCGT----------**-------**----------**ATACGGATCGGA------CTGCCTGTGGCCGGG-AGCAGTCG-----AGCTGCCTTT---GAAATTCGCTG-GGAGCTTACTGGGGGTCCTGCTGAGCGTCAC---CCA
droBia1	scf7180000302113:3465611-3465799 -		GTACAAGGACTTCTGGTAAACTCCCAG-ACCAATTTCAAGCCA-TAAGGGGCGGCCG---GGCTGCTCCCACCGGGA-----GGCT------AG----G-GGGATCCGTGTATCACAGGG----------**-------**----------**----AGATCTCAA------CTGACCACCATTGGG-AGCAGTCTCTGCGGCTGCCTTT---GAAATTCGCTG-GGGCCTTACCGGGGGTCCTGCTGAGCGTCAC---CCA
droTak1	scf7180000410579:64955-65153 +		GTACAAGGACTTCTGGTAAACTCCCAG-ACCAATTTCAAGCCA-TAAGGGGCGGCCT---GGCTGCTGGCCGGGGT-----T---TAGACAGTTGAT-GAGATCCATATACCATATAAGGATCTAATCCAA----------**-------**----------**-------**ACAA------TTGACTGCCGTCGGG-AGCAGCCG-----AGCTGCCTTT---GAAATTCGCTG-GGGCCTTACCGGGGGTCCTGCTGAGCGTCAC---CCA
droEug1	scf7180000409797:1238135-1238297 -		GTACAAGGACTTCTGGTAAACTCCCAG-ACCAATTTCAAGCCA-TAAATGGTAGCCC---AATTGCTGCCCGGGGG-----GGAC------AG----TT--**-------**----------**------**----------**------**ATAGAA------CTGACTACCGGCCGGG-AGCAGTAG-----AGCTGCCTTT---GAAATTCGCTG-GGGCCTTACCGGGGGTCCTGCTGAGCGTCAC---CCA
dm3	chr3R:7594379-7594556 -		GTACAAGGACTTCTGGTAAACTCCCAG-ACCAATTTCAAGCCA-TAAGGGGCGGCCA---GGCTGCTGGCCGGGGT-----GGAC------AG----GTGGTGTTCGT----------**-------**----------**ATACGGATACGA------CTGACTGCCGCCGGG-AGCAGCGG-----AGCTGCCTTT---GAAATTCGCTG-GGGCCTTACCGGGGGTCCTGCTGAGCGTCAC---CCA
droSim2	3r:13505772-13505949 +		GTACAAGGACTTCTGGTAAACTCCCAG-ACCAATTTCAAGCCA-TAAGGGGCGGCTA---GGCTGCTGGCCGGGGT-----GGAC------AT----GTGGTTTCCGT----------**-------**----------**ATACGGATACGA------CTGACTGCTGCTGGG-AGCAGGCG-----AGCTGCCTTT---GAAATTCGCTG-GGGCCTTACCGGGGGTCCTGCTGAGCGTCAC---CCA
droSec2	scaffold_0:14371279-14371456 +		GTACAAGGACTTCTGGTAAACTCCCAG-ACCAATTTCAAGCCA-TAAGGGGCGGCTA---GGCTGCTGGCCGGGGT-----GGAC------AT----GTGGTTTCCGT----------**-------**----------**ATACGGATACGA------CTGACTGCTGCTGGG-AGCAGGCG-----AGCTGCCTTT---GAAATTCGCTG-GGGCCTTACCGGGGGTCCTGCTGAGCGTCAC---CCA
droYak3	3R:16823670-16823847 +		GTACAAGGACTTCTGGTAAACTCCCAG-ACCAATTTCAAGCCA-TAAGAGGCGGCCA---GGCTGCTGGCCGGGGT-----GGAC------AG----TAGTATCCGT----------**-------**----------**ATACGGATTCGA------CTGACTGAGGCCGGG-AGCAGGCG-----AGCTGCCTTT---GAAATTCGCTG-GGGCCTTACCGGGGGTCCTGCTGAGCGTCAC---CCA
droEre2	scaffold_4770:14021958-14022135 +		GTACAAGGACTTCTGGTAAACTCCCAG-ACCAATTTCAAGCA-TAAGGGGCGGCCA---GGCTGCTGGCCGGGGT-----GGAC------AG----TAAGTATCCGT----------**-------**----------**ATACGGATTCGA------CTGACTGCGGCCGGG-AGCAGGCG-----AGCTGCCTTT---GAAATTCGCTG-GGGCCTTACCGGGGGTCCTGCTGAGCGTCAC---CCA

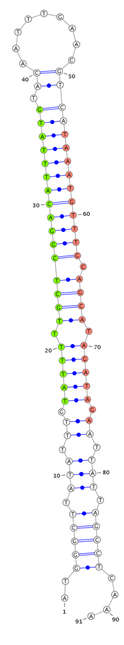
Generated: 09/08/2015 at 08:13 PM

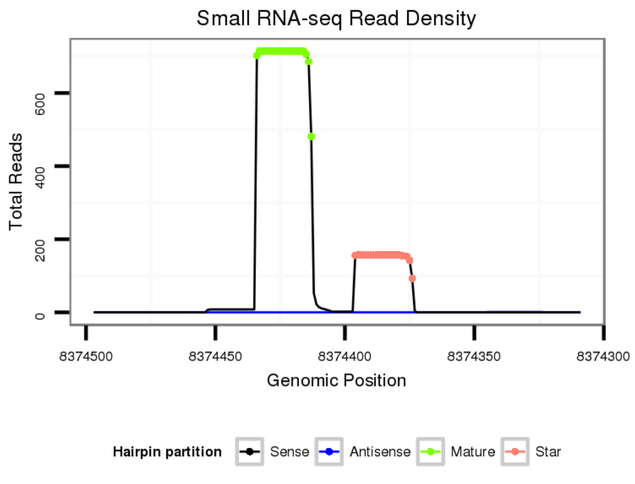
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	1

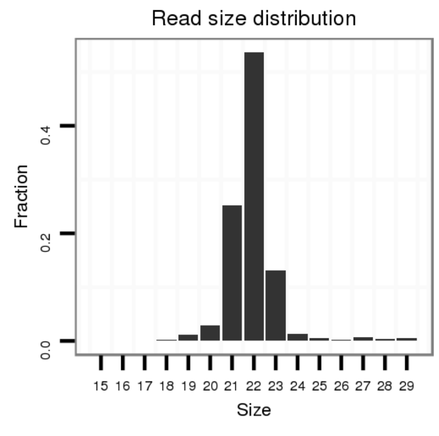
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dps_3415	**XL_group1e:8374359-8374447 -**	**confident**	**Testes-restricted**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

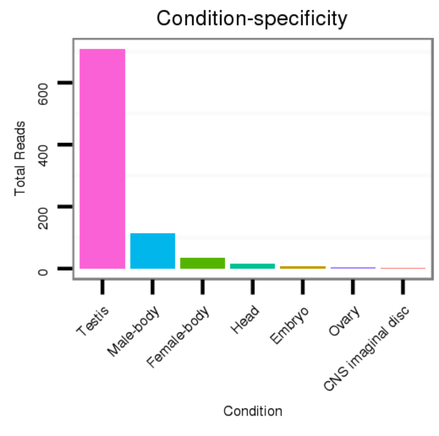
Legend: mature star mismatch in alignment mismatch in read

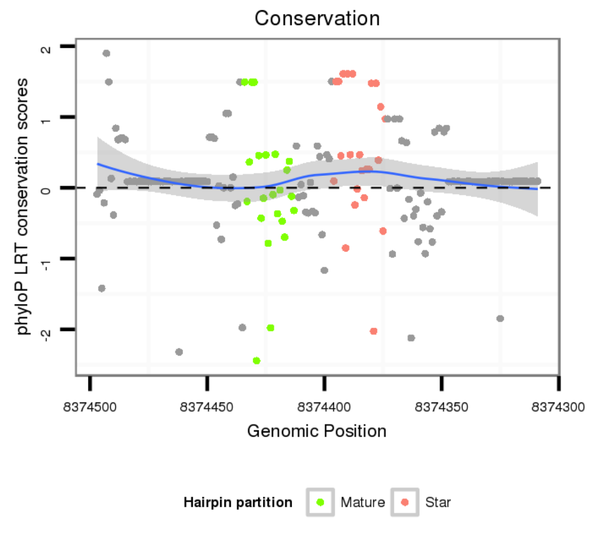
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

mature	star
1. dps-mir-2542-1 XL_group1e:8373664-8373685 - 2. dps_3415 XL_group1e:8374413-8374434 - 3. dps-mir-2542-2 XL_group1e:8377011-8377032 - 4. dps_3417 XL_group1e:8377859-8377880 - 5. dps-mir-2542-3 XL_group1e:8378629-8378650 - 6. Unknown_singleton_1920:1845-1866 +	1. dps_3415 XL_group1e:8374374-8374396 - 2. XL_group1e:8381735-8381757 -

Sense Strand Reads

hide 3p reads show mid mismatch reads

AAATTTTAGGATCGAGTGATTCCGATTCGTTAGGGCAGAATATATTTCATGGGCTTATATTTGTATTTTTGCTCGGACATTTATGTACAATTTGAACGTCATAAATGTTTGCAGCATAGATAGAATTATTAGCCTCAAAACCAACCATGAGCTCTCCGTTCCGCGGGTGAAAATGCGCTAAAATGATCT **********..(((((.(((.((.(((((.((((((((((((((((.((.....)))))))))))))).))))).)))))..)).))).))))).....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	SRR902011 testis	V112 male body	M040 female body	GSM444067 head	M022 male body	GSM343916 embryo	SRR902010 ovaries	M062 head	SRR902012 CNS imaginal disc	M059 embryo
.....TATTTTTGCTCGGACATTTATG.....	22	0	6	422.67	2536	2223	219	35	18	8	6	20	1	4	2
.....TATTTTTGCTCGGACATTTAT.....	21	0	6	204.83	1229	950	228	10	18	8	3	9	1	2	0
.....TAAATGTTTGCAGCATAGATAGA.....	23	0	2	89.50	179	111	25	26	4	0	5	0	1	4	3
.....TAAATGTTTGCAGCATAGATAG.....	22	0	2	49.50	99	60	12	17	8	0	1	0	1	0	0
.....TATTTTTGCTCGGACATTTATC.....	22	1	6	36.17	217	161	44	1	2	9	0	0	0	0	0
.....TATTTTTGCTCGGACATTTATGT.....	23	0	6	27.00	162	83	63	2	2	1	9	1	0	1	0
.....TATTTTTGCTCGGACATTTATGA.....	23	1	6	21.67	130	88	32	1	1	6	0	2	0	0	0
.....TATTTTTGCTCGGACATTTA.....	20	0	6	20.67	124	115	8	1	0	0	0	0	0	0	0
.....TATTTTTGCTCGGACATTTATT.....	22	1	6	18.33	110	97	10	0	1	2	0	0	0	0	0
.....TATTTTTGCTCGGACATTTAA.....	21	1	6	13.50	81	75	4	0	1	1	0	0	0	0	0
.....TAAATGTTTGCAGCATAGATA.....	21	0	2	11.00	22	18	3	0	1	0	0	0	0	0	0
.....TATTTTTGCTCGGACATTTATCC.....	23	2	6	10.33	62	52	7	0	0	3	0	0	0	0	0
.....TATTTTTGCTCGGACATTT.....	19	0	6	9.17	55	49	0	2	2	1	0	0	1	0	0
.....TATTTTTGCTCGGACATTTATGTA.....	24	0	6	8.17	49	45	4	0	0	0	0	0	0	0	0
.....TTTCATGGGCTTATATTTG.....	19	0	6	7.67	46	44	0	1	1	0	0	0	0	0	0
.....ATTTTTGCTCGGACATTTATG.....	21	0	6	7.17	43	36	2	5	0	0	0	0	0	0	0
.....TATTTTTGCTCGGACATTTATGTACAATT.....	29	0	6	4.83	29	20	9	0	0	0	0	0	0	0	0
.....TATTTTTGCTCGGACATTTATGTC.....	24	1	6	4.50	27	18	6	0	0	3	0	0	0	0	0
.....TATTTTTGCTCGGACATTTATA.....	22	1	6	4.17	25	23	2	0	0	0	0	0	0	0	0
.....TATTTTTGCTCGGACATTTATCCC.....	24	3	6	4.00	24	19	1	0	0	4	0	0	0	0	0
.....TATTTTTGCTCGGACATTTATGTAC.....	25	0	6	3.83	23	23	0	0	0	0	0	0	0	0	0
.....ATTTTTGCTCGGACATTTATGT.....	22	0	6	3.67	22	4	9	5	0	0	4	0	0	0	0
.....TATTTTTGCTCGGACATTTATCA.....	23	2	6	3.50	21	19	2	0	0	0	0	0	0	0	0
.....TATTTTTGCTCGGACATTTT.....	20	1	6	3.50	21	20	1	0	0	0	0	0	0	0	0
.....TATTTTTGCTCGGACATTTAAA.....	22	2	6	3.33	20	19	1	0	0	0	0	0	0	0	0
.....TAAATGTTTGCAGCATAGATAGAA.....	24	0	2	3.00	6	6	0	0	0	0	0	0	0	0	0
.....TATTTTTGCTCGGACATTTATGTACAA.....	27	0	6	2.67	16	15	1	0	0	0	0	0	0	0	0
.....TGAACGTCATAAATGTTTGCAGCATAG.....	27	0	2	2.50	5	5	0	0	0	0	0	0	0	0	0
.....TAAATGTTTGCAGCATAGATAA.....	22	1	2	2.50	5	4	1	0	0	0	0	0	0	0	0
.....TATTTTTGCTCGGACATTTATGTACAAT.....	28	0	6	2.50	15	15	0	0	0	0	0	0	0	0	0
.....TATTTTTGCTCGGACATTTATGTACA.....	26	0	6	2.17	13	13	0	0	0	0	0	0	0	0	0
.....TATTTTTGCTCGGACATTTATA.....	23	2	6	1.67	10	10	0	0	0	0	0	0	0	0	0
.....ATTTTTGCTCGGACATTTAT.....	20	0	6	1.67	10	7	2	1	0	0	0	0	0	0	0
.....TATTTTTGCTCGGACATTTATAA.....	23	2	6	1.67	10	10	0	0	0	0	0	0	0	0	0
.....TAAATGTTTGCAGCATAGATC.....	21	1	2	1.50	3	2	1	0	0	0	0	0	0	0	0
.....TAAATGTTTGCAGCATAGAT.....	20	0	2	1.50	3	2	0	1	0	0	0	0	0	0	0
.....TATTTTTGCTCGGACATTTATGTT.....	24	1	6	1.50	9	0	4	0	0	1	0	4	0	0	0
.....TTCATGGGCTTATATTTG.....	18	0	6	1.33	8	7	0	0	0	0	0	1	0	0	0
.....ATTTTTGCTCGGACATTTATGTACAATT.....	28	0	6	1.17	7	6	1	0	0	0	0	0	0	0	0
.....TATTTTTGCTCGGACATTTATGTTT.....	25	2	6	1.17	7	6	0	0	0	1	0	0	0	0	0
.....TATTTTTGCTCGGACATTTG.....	20	1	6	1.17	7	5	2	0	0	0	0	0	0	0	0
.....AAATGTTTGCAGCATAGATAGA.....	22	0	2	1.00	2	0	0	2	0	0	0	0	0	0	0
.....TAAATGTTTGCAGCATAGA.....	19	0	2	1.00	2	2	0	0	0	0	0	0	0	0	0
.....TAAATGTTTGCAGCATAGATAGAG.....	24	1	2	1.00	2	1	1	0	0	0	0	0	0	0	0
.....TAAATGTTTGCAGCATAGATAGT.....	23	1	2	1.00	2	0	0	1	0	0	0	0	1	0	0
.....TAAATGTTTGCAGCATAGATCT.....	22	2	2	1.00	2	2	0	0	0	0	0	0	0	0	0
.....TATTTTTGCTCGGACATTTAAAA.....	23	3	6	0.83	5	5	0	0	0	0	0	0	0	0	0
.....TATTTTTGCTCGGACATTTTC.....	21	2	6	0.83	5	5	0	0	0	0	0	0	0	0	0
.....TATTTTTGCTCGGACATTTATTC.....	23	2	6	0.83	5	5	0	0	0	0	0	0	0	0	0
.....TATTTTTGCTCGGACATT.....	18	0	6	0.83	5	3	1	0	0	1	0	0	0	0	0
.....TATTTTTGCTCGGACATTA.....	19	1	6	0.83	5	5	0	0	0	0	0	0	0	0	0
.....TATTTTTGCTCGGACATTTCCC.....	22	3	8	0.75	6	6	0	0	0	0	0	0	0	0	0
.....TATTTTTGCTCGGACATTTCC.....	21	2	6	0.67	4	3	0	0	0	1	0	0	0	0	0
.....TATTTTTGCTCGGACATTTATCG.....	23	2	6	0.67	4	4	0	0	0	0	0	0	0	0	0
.....GTATTTTTGCTCGGACATTT.....	20	0	6	0.67	4	4	0	0	0	0	0	0	0	0	0
.....ATTTTTGCTCGGACATTTATGTC.....	23	1	6	0.67	4	1	3	0	0	0	0	0	0	0	0
.....TGAACGTCATAAATGTTTGCAGCAT.....	25	0	2	0.50	1	1	0	0	0	0	0	0	0	0	0
.....AACGTCATAAATGTTTGCAGC.....	21	0	2	0.50	1	0	0	1	0	0	0	0	0	0	0
.....TAAATGTTTGCAGCATAGAA.....	20	1	2	0.50	1	1	0	0	0	0	0	0	0	0	0
.....ATAAATGTTTGCAGCATAGATAGA.....	24	0	2	0.50	1	1	0	0	0	0	0	0	0	0	0
.....AATGTTTGCAGCATAGATAG.....	20	0	2	0.50	1	1	0	0	0	0	0	0	0	0	0
.....ATAAATGTTTGCAGCATAGATAG.....	23	0	2	0.50	1	1	0	0	0	0	0	0	0	0	0
.....TAAATGTTTGCAGCATAGATAGAT.....	24	1	2	0.50	1	0	1	0	0	0	0	0	0	0	0
.....TATTTTTGCTCGGACAT.....	17	0	6	0.50	3	3	0	0	0	0	0	0	0	0	0
.....ATTTTTGCTCGGACATTTG.....	19	1	6	0.50	3	2	0	0	0	1	0	0	0	0	0
.....TATTTTTGCTCGGACATTTATTCC.....	24	3	6	0.50	3	0	0	0	0	0	0	3	0	0	0
.....TATTTTTGCTCGGACA.....	16	0	6	0.50	3	3	0	0	0	0	0	0	0	0	0
.....TTTGCTCGGACATTTATG.....	18	0	6	0.50	3	3	0	0	0	0	0	0	0	0	0
.....TATTTTTGCTCGGACATTTATGTGAG.....	26	3	6	0.50	3	3	0	0	0	0	0	0	0	0	0
.....TATTTTTGCTCGGACATTTATGC.....	23	1	6	0.50	3	0	1	0	0	0	0	0	0	0	2
.....TATTTTTGCTCGGACATTTTG.....	21	2	6	0.50	3	3	0	0	0	0	0	0	0	0	0
.....TATTTTTGCTCGGACATTTATCCT.....	24	3	6	0.33	2	2	0	0	0	0	0	0	0	0	0
.....TATTTTTGCTCGGACATTTATTG.....	23	2	6	0.33	2	2	0	0	0	0	0	0	0	0	0
.....TATTTTTGCTCGGACATTTATGTACC.....	26	1	6	0.33	2	2	0	0	0	0	0	0	0	0	0
.....TATTTTTGCTCGGACATTTC.....	19	1	6	0.33	2	1	0	0	1	0	0	0	0	0	0
.....GTATTTTTGCTCGGACATTTATT.....	23	1	6	0.33	2	2	0	0	0	0	0	0	0	0	0
.....TATTTTTGCTCGGACATTTATTCT.....	24	3	6	0.33	2	2	0	0	0	0	0	0	0	0	0
.....TATTTTTGCTCGGACATTTCT.....	20	2	6	0.33	2	2	0	0	0	0	0	0	0	0	0
.....TTTTGCTCGGACATTTAT.....	18	0	6	0.33	2	2	0	0	0	0	0	0	0	0	0
.....TATTTTTGCTCGGACATTTATGAC.....	24	2	6	0.33	2	2	0	0	0	0	0	0	0	0	0
.....TTTTTGCTCGGACATTTATGTACAATT.....	27	0	6	0.33	2	2	0	0	0	0	0	0	0	0	0
.....TATTTTTGCTCGGACATTTAC.....	21	1	6	0.33	2	2	0	0	0	0	0	0	0	0	0
.....ATTTTTGCTCGGACATTTATGC.....	22	1	6	0.33	2	2	0	0	0	0	0	0	0	0	0
.....TATTTTTGCTCGGACATTTATGTCT.....	25	2	6	0.17	1	0	1	0	0	0	0	0	0	0	0
.....TTTTGCTCGGACATTTATG.....	19	0	6	0.17	1	1	0	0	0	0	0	0	0	0	0
.....TATTTTTGCTCGGACATTTATGTAT.....	25	1	6	0.17	1	1	0	0	0	0	0	0	0	0	0
.....TTTGCTCGGACATTTATGT.....	19	0	6	0.17	1	1	0	0	0	0	0	0	0	0	0
.....TTTTTGCTCGGACATTTAT.....	19	0	6	0.17	1	0	1	0	0	0	0	0	0	0	0
.....TATTTTTGCTCGGACATTTCG.....	21	2	6	0.17	1	1	0	0	0	0	0	0	0	0	0
.....TATTTCATGGGCTTATATTTG.....	21	0	6	0.17	1	1	0	0	0	0	0	0	0	0	0
.....TATTTTTGCTCGGAC.....	15	0	6	0.17	1	1	0	0	0	0	0	0	0	0	0
.....TATTTTTGCTCGGACATTTATGTAG.....	25	1	6	0.17	1	1	0	0	0	0	0	0	0	0	0
.....TATTTTTGCTCGGACATTTATGAG.....	24	2	6	0.17	1	1	0	0	0	0	0	0	0	0	0
.....TATTTTTGCTCGGACATTTATGTCTT.....	26	3	6	0.17	1	1	0	0	0	0	0	0	0	0	0
.....TTTGCTCGGACATTTAT.....	17	0	6	0.17	1	1	0	0	0	0	0	0	0	0	0
.....TATTTTTGCTCGGACATTTAATC.....	23	3	6	0.17	1	1	0	0	0	0	0	0	0	0	0
.....GTATTTTTGCTCGGACATTTATGTA.....	25	0	6	0.17	1	1	0	0	0	0	0	0	0	0	0
.....ATTTTTGCTCGGACATTTATGAT.....	23	2	6	0.17	1	1	0	0	0	0	0	0	0	0	0
.....ATTTTTGCTCGGACATTTATGTACAAT.....	27	0	6	0.17	1	1	0	0	0	0	0	0	0	0	0
.....ATTTTTGCTCGGACATTTATT.....	21	1	6	0.17	1	0	1	0	0	0	0	0	0	0	0
.....TATTTTTGCTCGGACATTG.....	19	1	6	0.17	1	1	0	0	0	0	0	0	0	0	0
.....TTTTTGCTCGGACATTTATG.....	20	0	6	0.17	1	1	0	0	0	0	0	0	0	0	0
.....ATTTCATGGGCTTATATTTG.....	20	0	6	0.17	1	1	0	0	0	0	0	0	0	0	0
.....ATTTTTGCTCGGACATTTATGTAA.....	24	1	6	0.17	1	0	0	0	0	0	0	0	1	0	0
.....TATTTTTGCTCGGACATTTATGTAA.....	25	1	6	0.17	1	1	0	0	0	0	0	0	0	0	0
.....ATTTTTGCTCGGACATTTATGA.....	22	1	6	0.17	1	1	0	0	0	0	0	0	0	0	0
.....TATTTTTGCTCGGACATTCG.....	20	2	6	0.17	1	1	0	0	0	0	0	0	0	0	0
.....TATTTTTGCTCGGACATTTATGTCA.....	25	2	6	0.17	1	1	0	0	0	0	0	0	0	0	0
.....ATTTTTGCTCGGACATTTAA.....	20	1	6	0.17	1	1	0	0	0	0	0	0	0	0	0
.....TATTTTTGCTCGGACATTTG.....	20	1	6	0.17	1	1	0	0	0	0	0	0	0	0	0
.....TTTTGCTCGGACATTTAA.....	18	1	7	0.14	1	0	0	1	0	0	0	0	0	0	0
.....TATTTTTGCTCGGACATTTATCCG.....	24	3	7	0.14	1	0	1	0	0	0	0	0	0	0	0
.....TATTTTTGCTCGGACATTTCA.....	21	2	7	0.14	1	1	0	0	0	0	0	0	0	0	0
.....TATTTTTGCTCGGACATTCCC.....	21	3	8	0.13	1	1	0	0	0	0	0	0	0	0	0
.....TATTTTTGCTCGGACATTTTCC.....	22	3	8	0.13	1	1	0	0	0	0	0	0	0	0	0
.....TATTTTTGCTCGGACATTTTAA.....	22	3	9	0.11	1	1	0	0	0	0	0	0	0	0	0

Anti-sense strand reads

TTTAAAATCCTAGCTCACTAAGGCTAAGCAATCCCGTCTTATATAAAGTACCCGAAATATAAACATAAAAACGAGCCTGTAAATACATGTTAAACTTGCAGTATTTACAAACGTCGTATCTATCTTAATAATCGGAGTTTTGGTTGGTACTCGAGAGGCAAGGCGCCCACTTTTACGCGATTTTACTAGA **********..(((((.(((.((.(((((.((((((((((((((((.((.....)))))))))))))).))))).)))))..)).))).))))).....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M040 female body	V112 male body	SRR902012 CNS imaginal disc
.....AGAGGCAAGGCGCCCACTTTTA.....	22	0	1	1.00	1	1	0	0
.....TGGTTGGTACTCGAGAGGCAA.....	21	0	5	0.20	1	0	0	1
.....TAAGGCTAAGCAATCCCGTCTTATA.....	25	0	6	0.17	1	1	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
dp5	XL_group1e:8374309-8374497 -	dps_3415	AAATTTTAGGATCGAGTGATTCCGATTCGTTAGGGCAGAATATATTTCATGGGCTTATATTTGTATTTTTGCTCGGACATTTATGTACAATTTGAA---------CGTCATAAATGTTTGCAGCATAGATAGAATTATTAGCCTCAAAACCAACCATGAGCTCTCCGTTCCGCGGGTGAAAATGCGCTAAAATGATCT
droPer2	scaffold_13:190619-190807 +	dpe_101	AAATTTTAGGATCGAGTGATTCCGATTCGTTAGGGGAGAATATATTTCATGGGCTTATATTTTTATTTGTACTCAGACATTTATGTACAATTTGAA---------CGTCATAAATGTTTGCAGCATAAATAGAATTATTAGCCACAAAACCAACCATGAGCTCTCCGTTCCGCGGGTGAAAGTGCGCTAAAATGATCT
droWil2	scf2_1100000004956:478712-478771 -		CTTAT----------ATATATTTTTCCAGTAGTACGCTTAGATTGTATTCAAA---------CCTCAAAGATTTTTAGA----------
droMoj3	scaffold_6654:191719-191803 +		TACTTTT----------ATGTATATAACATTGTAATTTTTGAGATCA----GTTTTA-AATAAAAATTTGAATGTTAAAAATGTTTACAAAATAAAT----------
droKik1	scf7180000302476:2941025-2941091 +		TATAT----------ATATATTTGTGTTAATGTATATATATATACGTGTAC---------AGACATAAATATATGTAGTATATATA----------
droFic1	scf7180000453253:12898-12980 +		TGTTTTTAG----------AGGTTATAATTGTGTTTTTGGTACGATACATATGTACAAGATGG---------AAACAAAATCATT---ACAGCTCGTATCAAAGA----------
droEle1	scf7180000486869:1577-1625 +		TAA----------ATGTTTATAGTATAATATAACTAATATCATCATTAACCCCATGA----------
droRho1	scf7180000779410:414089-414125 -		TATTTT----------TGTTCAGACATCCTTGTCCATTTTGAA---------CCTC----------
droTak1	scf7180000415867:270369-270418 +		TT----------ACAAACTTTTTGAA---------ATTCATAAATTTTTGCGTGCAGATAAAATAATT----------
droEug1	scf7180000409110:1386289-1386294 -		AAGTTT----------AA----------
droYak3	3L:17003534-17003546 -		TAAATTCTGGATC----------TAA----------

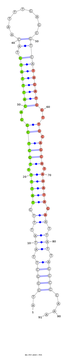
Generated: 09/08/2015 at 08:41 PM

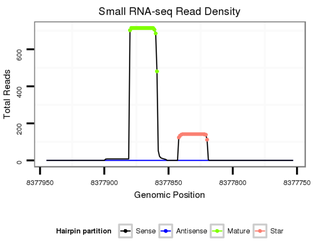
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	3
rescue.confident	3
rescue.candidate	0

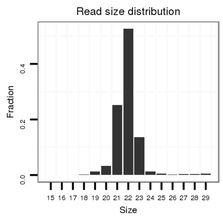
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dps_3417	**XL_group1e:8377803-8377895 -**	**confident**	**Testes-restricted**	**intergenic**	[View on UCSC Genome Browser (Cornell Mirror)]

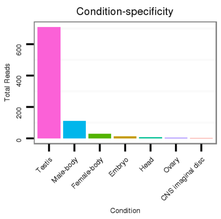
Legend: mature star mismatch in alignment mismatch in read

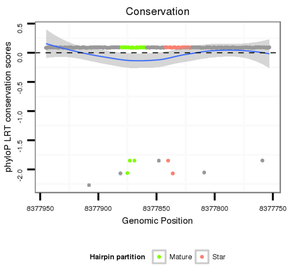
Predicted structure











Show Alternate Folds

Flybase annotation

intergenic

No Repeatable elements found

mature	star
1. dps-mir-2542-1 XL_group1e:8373664-8373685 - 2. dps_3415 XL_group1e:8374413-8374434 + 3. dps-mir-2542-2 XL_group1e:8377011-8377032 - 4. dps_3417 XL_group1e:8377859-8377880 - 5. dps-mir-2542-3 XL_group1e:8378629-8378650 - 6. Unknown_singleton_1920:1845-1866 +	1. dps-mir-2542-1 XL_group1e:8373625-8373647 - 2. dps-mir-2542-2 XL_group1e:8376972-8376994 - 3. dps_3417 XL_group1e:8377820-8377842 - 4. dps-mir-2542-3 XL_group1e:8378590-8378612 -

Sense Strand Reads

hide 3p reads show mid mismatch reads

CGAAATTTTAGGATCGAGTGATTCCGATTCGTTAGGGCAGAATATATTTCATGGGCTTATATTTGTATTTTGCTCGGACATTTATGTACAATTTGAGCGTCAFAGATGGTTGCAGCATAAATAGAATTATTAGCCCCAAAACCAACCATGAGCTCTCCGTTCCGCGGGTGAAAGTGCGCTAAAATAATCTGT	Read size	# Mismatch	Hit Count	Total Norm	Total	SRR902011 testis	V112 male body	M040 female body	GSM343916 embryo	GSM444067 head	M022 male body	SRR902010 ovaries	M059 embryo	M062 head	SRR902012 CNS imaginal disc
..(.(((.(.(.(.((((.((((((.(.(((((((.((.....))))))))))..)).))))).))))).)).)))).)))))....															
.....TATTTTGCTCGGACATTTATG.....	22	0	6	422.67	2536	2223	219	35	6	18	8	20	2	1	4
.....TATTTTGCTCGGACATTTAT.....	21	0	6	204.83	1229	950	228	10	3	18	8	9	0	1	2
.....TATTTTGCTCGGACATTTATGTAGATGGTTGCAGCATAAATAGA.....	23	1	4	92.25	369	266	24	38	33	1	0	2	4	1	0
.....TATTTTGCTCGGACATTTATG.....	22	1	6	36.17	217	161	44	1	0	2	9	0	0	0	0
.....TATTTTGCTCGGACATTTATGT.....	23	0	6	27.00	162	83	63	2	9	2	1	1	0	0	1
.....TATTTTGCTCGGACATTTATGTAGATGGTTGCAGCATAAATAG.....	22	0	4	26.25	105	84	5	14	2	0	0	0	0	0	0
.....TATTTTGCTCGGACATTTATGTAG.....	23	1	6	21.67	130	88	32	1	0	1	6	2	0	0	0
.....TATTTTGCTCGGACATTTATA.....	20	0	6	20.67	124	115	8	1	0	0	0	0	0	0	0
.....TATTTTGCTCGGACATTTATG.....	22	1	6	18.33	110	97	10	0	0	1	2	0	0	0	0
.....TATTTTGCTCGGACATTTATA.....	21	1	6	13.50	81	75	4	0	0	1	1	0	0	0	0
.....TATTTTGCTCGGACATTTATGC.....	23	2	6	10.33	62	52	7	0	0	0	3	0	0	0	0
.....AGATGGTTGCAGCATAAATAGA.....	22	0	4	9.75	39	27	4	6	0	1	0	0	0	1	0
.....TATTTTGCTCGGACATTT.....	19	0	6	9.17	55	49	0	2	0	2	1	0	0	1	0
.....TATTTTGCTCGGACATTTATGTA.....	24	0	6	8.17	49	45	4	0	0	0	0	0	0	0	0
.....TTTCATGGGCTTATATTTG.....	19	0	6	7.67	46	44	0	1	0	1	0	0	0	0	0
.....ATTTTGCTCGGACATTTATG.....	21	0	6	7.17	43	36	2	5	0	0	0	0	0	0	0
.....GATGGTTGCAGCATAAATAGA.....	21	0	4	6.25	25	18	3	4	0	0	0	0	0	0	0
.....TATTTTGCTCGGACATTTATGTAGAATT.....	29	0	6	4.83	29	20	9	0	0	0	0	0	0	0	0
.....TATTTTGCTCGGACATTTATGTT.....	24	1	6	4.50	27	18	6	0	0	0	3	0	0	0	0
.....TATTTTGCTCGGACATTTATG.....	22	1	6	4.17	25	23	2	0	0	0	0	0	0	0	0
.....TATTTTGCTCGGACATTTATGCC.....	24	3	6	4.00	24	19	1	0	0	0	4	0	0	0	0
.....TATTTTGCTCGGACATTTATGTAC.....	25	0	6	3.83	23	23	0	0	0	0	0	0	0	0	0
.....TATTTTGCTCGGACATTTATGT.....	22	0	6	3.67	22	4	9	5	4	0	0	0	0	0	0
.....TATTTTGCTCGGACATTTT.....	20	1	6	3.50	21	20	1	0	0	0	0	0	0	0	0
.....TATTTTGCTCGGACATTTATGA.....	23	2	6	3.50	21	19	2	0	0	0	0	0	0	0	0
.....TATTTTGCTCGGACATTTAG.....	22	2	6	3.33	20	19	1	0	0	0	0	0	0	0	0
.....TAGATGGTTGCAGCATAAATAGAA.....	24	0	4	3.00	12	8	3	0	1	0	0	0	0	0	0
.....ATGGTTGCAGCATAAATAGA.....	20	0	4	2.75	11	0	10	1	0	0	0	0	0	0	0
.....TATTTTGCTCGGACATTTATGTACAA.....	27	0	6	2.67	16	15	1	0	0	0	0	0	0	0	0
.....TAGATGGTTGCAGCATAAATA.....	21	0	4	2.50	10	3	3	1	2	1	0	0	0	0	0
.....TATTTTGCTCGGACATTTATGTACAAT.....	28	0	6	2.50	15	15	0	0	0	0	0	0	0	0	0
.....TATTTTGCTCGGACATTTATGTACA.....	26	0	6	2.17	13	13	0	0	0	0	0	0	0	0	0
.....TAGATGGTTGCAGCATAAATAT.....	22	1	4	1.75	7	2	5	0	0	0	0	0	0	0	0
.....ATTTTGCTCGGACATTTAT.....	20	0	6	1.67	10	7	2	1	0	0	0	0	0	0	0
.....TATTTTGCTCGGACATTTATGA.....	23	2	6	1.67	10	10	0	0	0	0	0	0	0	0	0
.....TATTTTGCTCGGACATTTATGA.....	23	2	6	1.67	10	10	0	0	0	0	0	0	0	0	0
.....TAGATGGTTGCAGCATAAAT.....	20	0	4	1.50	6	0	3	3	0	0	0	0	0	0	0
.....TATTTTGCTCGGACATTTATGT.....	24	1	6	1.50	9	0	4	0	0	0	1	4	0	0	0
.....TTTCATGGGCTTATATTTG.....	18	0	6	1.33	8	7	0	0	0	0	1	0	0	0	0
.....ATTTTTGCTCGGACATTTATGTACAATT.....	21	0	4	1.25	5	2	0	3	0	0	0	0	0	0	0
.....AGATGGTTGCAGCATAAATAG.....	22	1	4	1.25	5	2	2	1	0	0	0	0	0	0	0
.....TAGATGGTTGCAGCATAAATAGA.....	23	1	4	1.25	5	1	2	2	0	0	0	0	0	0	0
.....TATTTTGCTCGGACATTTATGTAGAATT.....	28	0	6	1.17	7	6	1	0	0	0	0	0	0	0	0
.....TATTTTGCTCGGACATTTATGTTT.....	25	2	6	1.17	7	6	0	0	0	0	1	0	0	0	0
.....TATTTTGCTCGGACATTTT.....	20	1	6	1.17	7	5	2	0	0	0	0	0	0	0	0
.....TATTTTGCTCGGACATTTA.....	19	1	6	0.83	5	5	0	0	0	0	0	0	0	0	0
.....TAGATGGTTGCAGCATAAAG.....	18	0	6	0.83	5	3	1	0	0	0	1	0	0	0	0
.....TATTTTGCTCGGACATTTAAAA.....	23	3	6	0.83	5	5	0	0	0	0	0	0	0	0	0
.....TATTTTGCTCGGACATTTATGC.....	23	2	6	0.83	5	5	0	0	0	0	0	0	0	0	0
.....TATTTTGCTCGGACATTTG.....	21	2	6	0.83	5	5	0	0	0	0	0	0	0	0	0
.....TGGTTGCAGCATAAATAGA.....	19	0	4	0.75	3	0	3	0	0	0	0	0	0	0	0
.....GATGGTTGCAGCATAAATAG.....	20	0	4	0.75	3	1	0	2	0	0	0	0	0	0	0
.....TATTTTGCTCGGACATTTCCC.....	22	3	6	0.75	6	6	0	0	0	0	0	0	0	0	0
.....TGAGCGTCATAGATGGTTGCAG.....	22	0	3	0.67	2	1	1	0	0	0	0	0	0	0	0
.....TGAGCGTCATAGATGGTTGCAGCA.....	24	0	3	0.67	2	1	1	0	0	0	0	0	0	0	0
.....ATTTTTGCTCGGACATTTATGTT.....	23	1	6	0.67	4	1	3	0	0	0	0	0	0	0	0
.....GTATTTTTGCTCGGACATTTATGTA.....	25	0	6	0.67	4	4	0	0	0	0	0	0	0	0	0
.....TATTTTGCTCGGACATTTCC.....	21	2	6	0.67	4	3	0	0	0	0	1	0	0	0	0
.....TATTTTGCTCGGACATTTATGC.....	23	2	6	0.67	4	4	0	0	0	0	0	0	0	0	0
.....TACAATTTGAGCGTCATAGATGGTT.....	22	2	4	0.50	2	0	2	0	0	0	0	0	0	0	0
.....TAGATGGTTGCAGCATAAAT.....	19	0	4	0.50	2	2	0	0	0	0	0	0	0	0	0
.....TAGATGGTTGCAGCATAAATAGAA.....	25	1	4	0.50	2	2	0	0	0	0	0	0	0	0	0
.....TAGATGGTTGCAGCATAAATAGAT.....	24	1	4	0.50	2	2	0	0	0	0	0	0	0	0	0
.....TAGATGGTTGCAGCATAAAG.....	20	1	4	0.50	2	0	2	0	0	0	0	0	0	0	0
.....TAGATGGTTGCAGCATAAAT.....	21	1	4	0.50	2	0	2	0	0	0	0	0	0	0	0
.....ATAGATGGTTGCAGCATAA.....	19	0	4	0.50	2	0	2	0	0	0	0	0	0	0	0
.....ATTTTTGCTCGGACATTTG.....	19	1	6	0.50	3	2	0	0	0	0	1	0	0	0	0
.....TATTTTGCTCGGACATTTTG.....	21	2	6	0.50	3	3	0	0	0	0	0	0	0	0	0
.....TTTGCTCGGACATTTATG.....	18	0	6	0.50	3	3	0	0	0	0	0	0	0	0	0
.....TATTTTGCTCGGACATTTATGTG.....	23	1	6	0.50	3	0	1	0	0	0	0	2	0	0	0
.....TATTTTGCTCGGACA.....	16	0	6	0.50	3	0	0	0	0	0	0	0	0	0	0
.....TATTTTGCTCGGACATTTATGCC.....	24	3	6	0.50	3	0	0	0	0	0	0	3	0	0	0
.....TATTTTGCTCGGACATTTATGTGAG.....	26	3	6	0.50	3	3	0	0	0	0	0	0	0	0	0
.....TATTTTGCTCGGACAT.....	17	0	6	0.50	3	3	0	0	0	0	0	0	0	0	0
.....TGAGCGTCATAGATGGTTGCAGCATAAA.....	29	1	3	0.33	1	0	1	0	0	0	0	0	0	0	0
.....TGAGCGTCATAGATGGTTGCAGCAT.....	25	0	3	0.33	1	0	1	0	0	0	0	0	0	0	0
.....TACAATTTGAGCGTCATAGATGGTT.....	25	0	3	0.33	1	1	0	0	0	0	0	0	0	0	0
.....ATTTTTGCTCGGACATTTATG.....	22	1	6	0.33	2	2	0	0	0	0	0	0	0	0	0
.....TATTTTGCTCGGACATTTATG.....	21	1	6	0.33	2	2	0	0	0	0	0	0	0	0	0
.....TATTTTGCTCGGACATATGTTAT.....	26	1	6	0.33	2	2	0	0	0	0	0	0	0	0	0
.....TATTTTGCTCGGACATTTG.....	19	1	6	0.33	2	1	0	0	0	1	0	0	0	0	0
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.....GTATTTTTGCTCGGACATTTATG.....	23	1	6	0.33	2	2	0	0	0	0	0	0	0	0	0
.....TTTTGCTCGGACATTTT.....	18	0	6	0.33	2	2	0	0	0	0	0	0	0	0	0
.....TATTTTGCTCGGACATTTCC.....	20	2	6	0.33	2	2	0	0	0	0	0	0	0	0	0
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.....TTTTTGCTCGGACATTTATGTACAATT.....	27	0	6	0.33	2	2	0	0	0	0	0	0	0	0	0
.....AGATGGTTGCAGCATAAATA.....	20	0	4	0.25	1	0	1	0	0	0	0	0	0	0	0
.....TAGATGGTTGCAGCATAAATAG.....	23	1	4	0.25	1	0	0	0	0	0	0	0	1	0	0
.....TAGATGGTTGCAGCATAAATAGAAT.....	25	0	4	0.25	1	1	0	0	0	0	0	0	0	0	0
.....TAGATGGTTGCAGCATAAA.....	19	0	4	0.25	1	0	1	0	0	0	0	0	0	0	0
.....ATAGATGGTTGCAGCATAAAT.....	23	0	4	0.25	1	1	0	0	0	0	0	0	0	0	0
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.....GATGGTTGCAGCATAAAG.....	18	1	4	0.25	1	1	0	0	0	0	0	0	0	0	0
.....ATGGTTGCAGCATAAATAGAA.....	21	0	4	0.25	1	0	1	0	0	0	0	0	0	0	0
.....TGGTTGCAGCATAAATAG.....	18	0	4	0.25	1	0	0	1	0	0	0	0	0	0	0
.....GATGGTTGCAGCATAAATAGAA.....	22	0	4	0.25	1	0	0	1	0	0	0	0	0	0	0
.....ATGGTTGCAGCATAAATAGAA.....	22	1	4	0.25	1	0	1	0	0	0	0	0	0	0	0
.....TAGATGGTTGCAGCATAAATGCC.....	23	3	4	0.25	1	1	0	0	0	0	0	0	0	0	0
.....TAGATGGTTGCAGCATAAATAGAAAA.....	26	3	4	0.25	1	1	0	0	0	0	0	0	0	0	0
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.....ATAGATGGTTGCAGCATAAATAGA.....	24	0	4	0.25	1	0	1	0	0	0	0	0	0	0	0
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.....AGATGGTTGCAGCATAAATAGAA.....	23	0	4	0.25	1	0	1	0	0	0	0	0	0	0	0
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.....TATTTTGCTCGGACATTTCC.....	21	2	6	0.17	1	1	0	0	0	0	0	0	0	0	0
.....GTATTTTTGCTCGGACATTTATGTA.....	25	0	6	0.17	1	1	0	0	0	0	0	0	0	0	0
.....ATTTTTGCTCGGACATTTAG.....	22	1	6	0.17	1	1	0	0	0	0	0	0	0	0	0
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.....TTTTTGCTCGGACATTTAT.....	21	1	6	0.17	1	1	0	0	0	0	0	0	0	0	0
.....ATTTCATGGGCTTATATTTG.....	20	0	6	0.17	1	1	0	0	0	0	0	0	0	0	0
.....ATTTTTGCTCGGACATTTATGTACAAT.....	27	0	6	0.17	1	1	0	0	0	0	0	0	0	0	0
.....TTTTGCTCGGACATTTATGT.....	19	0	6	0.17	1	1	0	0	0	0	0	0	0	0	0
.....TATTTTGCTCGGACATTTATGTAG.....	25	1	6	0.17	1	1	0	0	0	0	0	0	0	0	0
.....TATTTTGCTCGGACATTTATGC.....	25	2	6	0.17	1	1	0	0	0	0	0	0	0	0	0
.....ATTTTTGCTCGGACATTTAG.....	20	1	6	0.17	1	1	0	0	0	0	0	0	0	0	0
.....TATTTTGCTCGGACATATGT.....	19	0	6	0.17	1	1	0	0	0	0	0	0	0	0	0
.....TATTTTGCTCGGACATTTAGTCC.....	26	3	6	0.17	1	1	0	0	0	0	0	0	0	0	0
.....TTTTGCTCGGACATTTAT.....	17	0	6	0.17	1	1	0	0	0	0	0	0	0	0	0
.....TATTTTGCTCGGACATTTATGAG.....	24	2	6	0.17	1	1	0	0	0	0	0	0	0	0	0
.....TATTTTGCTCGGACATTTATGTAG.....	25	1	6	0.17	1	1	0	0	0	0	0	0	0	0	0
.....TATTTCATGGGCTTATATTTG.....	21	0	6	0.17	1	1	0	0	0	0	0	0	0	0	0
.....TATTTTGCTCGGACATTTAAAA.....	23	3	6	0.17	1	1	0	0	0	0	0	0	0	0	0
.....TATTTTGCTCGGACATTTAG.....	20	1	6	0.17	1	1	0	0	0	0	0	0	0	0	0
.....TATTTTGCTCGGACATTTATGTAG.....	25	1	6	0.17	1	1	0	0	0	0	0	0	0	0	0
.....ATTTTTGCTCGGACATTTATGTAG.....	24	1	6	0.17	1	1	0	0	0	0	0	0	1	0	0
.....TATTTTGCTCGGACATTTATGTGA.....	25	2	6	0.17	1	1	0	0	0	0	0	0	0	0	0
.....TTTTTGCTCGGACATTTAT.....	19	0	6	0.17	1	1	0	1	0	0	0	0	0	0	0
.....ATTTTTGCTCGGACATTTATGCAT.....	23	2	6	0.17	1	1	0	0	0	0	0	0	0	0	0
.....TATTTTGCTCGGACATTTG.....	19	1	6	0.17	1	1	0	0	0	0	0	0	0	0	0
.....TATTTTTGCTCGGACATTTATGCC.....	24	3	7	0.14	1	0	1	0	0	0	0	0	0	0	0
.....TATTTTGCTCGGACATTTCA.....	21	2	7	0.14	1	1	0	0	0	0	0	0	0	0	0
.....TTTTGCTCGGACATTTAG.....	18	1	7	0.14	1	0	0	1	0	0	0	0	0	0	0
.....TATTTTTGCTCGGACATTTCC.....	22	3	8	0.13	1	1	0	0	0	0	0	0	0	0	0
.....TATTTTTGCTCGGACATTTCCC.....	21	3	8	0.13	1	1	0	0	0	0	0	0	0	0	0
.....TATTTTTGCTCGGACATTTAAA.....	22	3	9	0.11	1	1	0	0	0	0	0	0	0	0	0

Anti-sense strand reads

GCTTTAAAATCCTAGCTCACTAAGGCTAAGCAATCCCGTCTTATATAAAGTACCCGAATATAAACATAAAAACGAGCCTGTAAATACATGTTAAACTCGCAGTATCTACCAACGTCGTATTTATCTTAATAATCGGGGTTTTGGTTGGTACTCGAGAGGCAAGGCGCCCACTTTCACGCGATTTTATTAGACA	Read size	# Mismatch	Hit Count	Total Norm	Total	M040 female body	SRR902012 CNS imaginal disc	V112 male body
..(.(((.(.(.(.((((.((((((.(.(((((((.((.....))))))))))..)).))))).))))).)).)))).)))))....								
.....TATCTACCAACGTCGTATTTA.....	21	0	4	0.25	1	1	0	0
.....TGGTTGGTACTCGAGAGGCAA.....	21	0	5	0.20	1	0	1	0
.....TAAGGCTAAGCAATCCCGTCTTATA.....	25	0	6	0.17	1	1	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
dp5	XL_group1e:8377753-8377945 -	dps_3417	CGAAATTTTAGGATCGAGTGATTCCGATTCGTTAGGGCAGAATATATTTCATGGGCTTATATTTGTATTTTGCTCGGACATTTATGTACAATTTGAGCGTCAAAGATGGTTGCAGCATAAATAGAATTATTAGCCCAAAACCAACCATGAGCTCTCCGTTCCGCGGGTGAAAGTGCGCTAAAATAATCTGT
droPer2	scaffold_13:190617-190809 +	dps_101	CGAAATTTTAGGATCGAGTGATTCCGATTCGTTAGGGCAGAATATATTTCATGGGCTTATATTTGTATTTGCTCGGACATTTATGTACAATTTGAGCGTCAAAGATGGTGCAGCATAAATAGAATTATTAGCCCAAAACCAACCATGAGCTCTCCGTTCCGCGGGTGAAAGTGCGCTAAAATAGTCCTGT

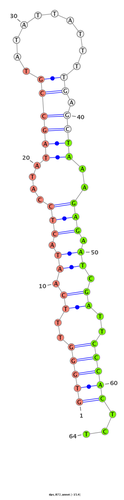
Generated: 09/08/2015 at 08:42 PM

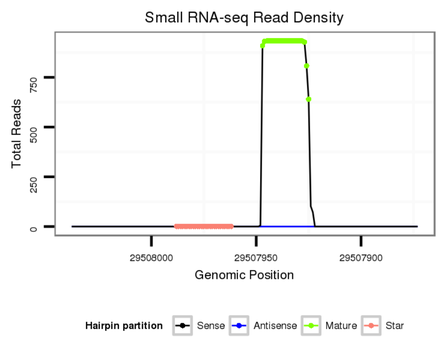
	PASS/FAIL
crit.star	3
crit.loop	3
crit.mor	0
crit.half	0
crit.total	1
crit.mismatch	1
crit.top3	3
crit.tptop3	3
crit.uri	0
crit.back	0
rescue.genome	0
rescue.dominant	0
rescue.known	3
rescue.confident	3
rescue.candidate	0

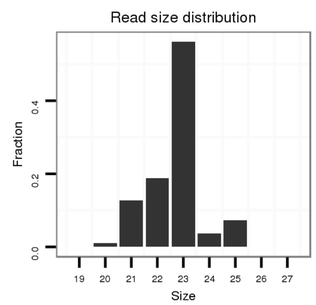
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dps_872	**2:29507923-29507988 -**	**candidate-rescued**	**3p_tailed_mirtron**	**intron**	[View on UCSC Genome Browser [Cornell Mirror]]

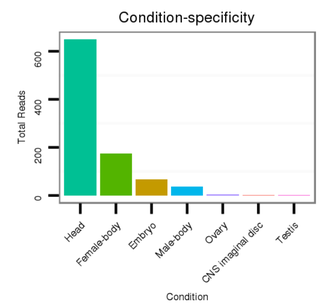
Legend: mature star **mismatch in alignment** mismatch in read

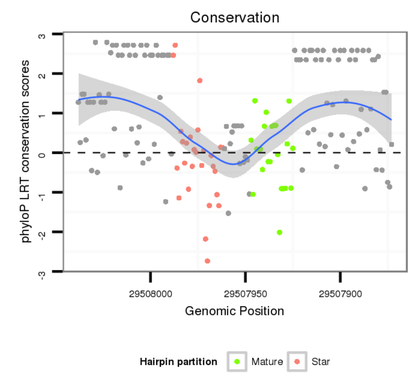
Predicted structure











Show Alternate Folds

Flybase annotation

intron [Dpse\GA18756-in]; CDS [Dpse\GA18756-cds]; CDS [Dpse\GA18756-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

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CCATACCAGAGAGCGATCTCTCGGACAGCACCCTGCATGGCAGTGCACCGGTGGGTTTCAATACTCCATATAGCCGTATATTATTTTGAGCTAAAGAGAATCGATTCCCACTCTAGGGCTCCTTTGATGACACCATACACTTTGAGGATGTGATGCCCACCCGCAA
**********************************************(((((..((.((.(((.....(((((((.........)).)))).)))..)))).)).))..)))))...**********************************************
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Read size	# Mismatch	Hit Count	Total Norm	Total	M062 head	GSM444067 head	M040 female body	M059 embryo	V112 male body	GSM343916 embryo	SRR902010 ovaries	SRR902011 testis	SRR902012 CNS imaginal disc
23	0	1	522.00	522	214	181	77	35	11	4	0	0	0
22	0	1	162.00	162	104	20	18	10	8	1	0	1	0
21	0	1	115.00	115	33	42	26	1	13	0	0	0	0
23	1	1	74.00	74	60	3	1	10	0	0	0	0	0
25	0	1	68.00	68	17	11	23	10	2	0	4	0	1
24	0	1	29.00	29	3	11	8	4	2	1	0	0	0
21	1	1	13.00	13	12	1	0	0	0	0	0	0	0
22	0	1	12.00	12	1	0	10	1	0	0	0	0	0
20	0	1	6.00	6	5	0	1	0	0	0	0	0	0
24	0	1	4.00	4	0	0	4	0	0	0	0	0	0
21	0	1	3.00	3	0	0	3	0	0	0	0	0	0
24	1	1	3.00	3	0	1	0	0	0	0	0	2	0
24	0	1	2.00	2	1	1	0	0	0	0	0	0	0
20	0	1	2.00	2	0	0	2	0	0	0	0	0	0
23	0	1	2.00	2	1	0	0	0	1	0	0	0	0
24	1	1	2.00	2	1	0	1	0	0	0	0	0	0
22	0	1	2.00	2	1	0	1	0	0	0	0	0	0
23	0	1	1.00	1	0	0	1	0	0	0	0	0	0
25	1	1	1.00	1	1	0	0	0	0	0	0	0	0
24	1	1	1.00	1	0	0	1	0	0	0	0	0	0
19	0	1	1.00	1	0	0	0	0	1	0	0	0	0
20	0	1	1.00	1	0	1	0	0	0	0	0	0	0
21	0	1	1.00	1	1	0	0	0	0	0	0	0	0
23	2	1	1.00	1	1	0	0	0	0	0	0	0	0
26	1	1	1.00	1	0	1	0	0	0	0	0	0	0
20	0	1	1.00	1	1	0	0	0	0	0	0	0	0
22	1	1	1.00	1	1	0	0	0	0	0	0	0	0
27	0	1	1.00	1	1	0	0	0	0	0	0	0	0

Anti-sense strand reads

```
GGTATGGTCTCTCGCTAGAGAGCCTGTCGTGGGACGTACCGTCACGTGGCCACCCAAAGTTATGAGGTATATCGGCATATAATAAAACTCGATTTCTCTTAGCTAAGGGTGAGATCCCGAGGAAACTACTGTGGTATGTGAAACTCCTACACTACGGGTGGGCGTT
**************************************************(((((..((.((.(((.....(((((((.........)).)))).)))..)))).)).))..)))))...**************************************************
```

Read size	# Mismatch	Hit Count	Total Norm	Total	M040 female body

Show Alignment With Reads

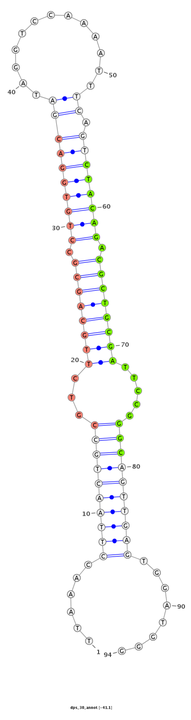
Re-alignment of all predicted orthologs

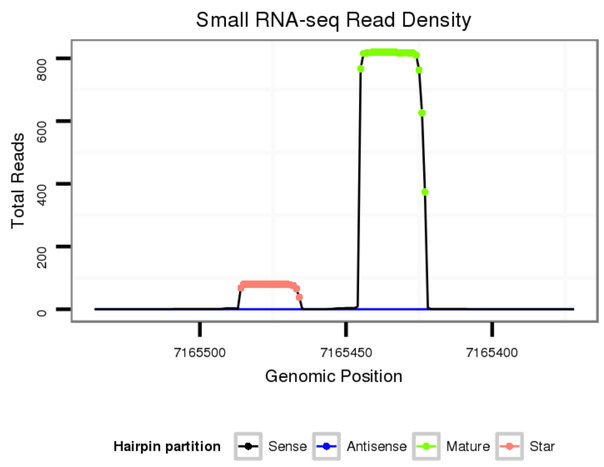
Species	Coordinate	ID	Alignment
dp5	2:29507873-29508038 -	dps_872	CCATACCAGAGAGCGATCTCTCGGACAGCACCCTGCATGGC---AGTGCACCGGTGGGTTTCA----ATA-CTCC-------ATAT---A----------G----------CCGTATATTATTTTG-------AGCTA----------A----------AGAGAATCGATTCCCACTCTAGGGCTCCTTTGATGACACCATACACTTTGAGGATGTGATGCC---C----------ACCCGCAA-
droPer2	scaffold_6:4878490-4878655 -	dpe_1927	CCATACCAGAGAGCGATCTCTCGGACAGCACCCTGCATGGC---AGTGCACCGGTGGGTTTCA----ATA-CTCC-------ATAT---A----------G----------CCGTATATTATTTTG-------AGCTA----------A----------AGAGAATCGATTCCCACTCTAGGGCTCCTTTGATGACACCATACACTTTGAGGATGTGATGCC---C----------ACCCGCAA-
droWil2	scf2_1100000004943:3802459-3802628 -		CCATACCAGAGAGTGATCTCTCGGATAGCACCTTCATGGCAGGCAGTGCACCATGAGTCGT-----------AAGAAC----------A----------G----------GTCCTCCCTAACTCTC-----A----------TAACTCTAGGGCTCCTTCGATGATACCATACACTTTGAGATGTTTGCCGCGC----------A------
droVir3	scaffold_13047:16588070-16588248 +		CCATACCCGAGAGTGATCTCTCGATAGCACCTTCATGGCAGGCAGTGCGCCGTAGGTTTCT-----GTG-CGTGT-------CCAACTCT----------GG-------GCTATATAACA----------GCTGATTGATTTCTCAGGGCTCCTTCGATGACACAGTTCACTTTGAGATGTCCTGCCTCGAAAACAGAATCGCTGCGGTATCTC-
droMoj3	scaffold_6540:12906002-12906175 +		CCATACCCGAGAGTGATCTCTCGGACAGCACCTTCATGGCAGGCAGTGCGCCGTAGATCCAATTACTTAGAGTGTCA-----GGCACCAGACTAATTG----------GTTTCTCAGGGCTCCTTTGATGATGCCATTCACTTTGAGGATGCGTGCCACAAAAATAGAGTCACTGAG-----GAA-
droGri2	scaffold_15116:1545367-1545427 +		CCATACCCGAGAAGTGATCTCTCGACAGCACCTTCACGGCAGCAGCGCACCGGTAAGATT----------A----------G----------
droAna3	scaffold_13340:15326419-15326593 +		CCATTCCAGAAAGTGATCTTCTCGACAGTACTTTGCAGGCAGTAGTGCACCGGTAAGTGAT----------A----------G---GGCAGTTAATGAATTATCTATCT-------AGAAATAT-------TTGATATTT-----TTT--CT----------AA-----AATCATTCAGGGCTCCTTTGATGACACCATTCACTTCGAGGATGTCATGCCGCGT----------ACTCGCAG-
droBip1	scf7180000396708:4707902-4708087 -		CCATTCCAGAAAGCGATCTTCTCGACAGTACTTTGCATGGCAGTAGTGCTCCGTAACGA--------AAA-CTTT-------A----------T----------TTATCTATTTTAAGATTAAATTTAATTTAA----------TTTAATTCTA----------TAATAA-CAATAATAAT----------AATTTTCAGGGCATCCTTTGATGACACCATTCACTTCGAGGATGTCATGCCACGC----------ACTCGCAC-
droKik1	scf7180000302707:278796-278965 -		CCATACCGGAGAGCGATCTCTCGACAGCACCTTCATGGCAGGAGTGCCCGTAGCTGTC-----GTT-----GAGTCTCATA----------A----------ACT-------AAAAATTTTAAAATTTTA----------TCATCATTTCC----------TA-TTTCAGGGCATCCTTTGATGACACCATTCATTCGAGGATGTCATGCCGCGC----------AATCGCGC-
droFic1	scf7180000454126:37557-37802 -		CCATTCCGGAAAGCGATCTCTCGGACAGCACTTTCATGGCAGGCAGTGCACCATAAGTTTGA----TAT-TTT----------A----------G----------TTTTAATTTTAATACATAAATGTAATTTTTAATACAAAGCGCTTTTAGAATATCGAAATTATTTGGTTTATGGTTTACTCTTTTATTTCCTCAAAAACCCAATATTT-------CATTATACAT----------ATTTTCAGGGCATCATTGATGACACCATTCATTCGAGGATGTCATGCCGCGC----------AA------
droEle1	scf7180000490994:829608-829667 -		CCATTCCGGAGAGCGATCTCTCGGACAGCACTTTCATGGCAGGCAGTGCTCCGTATGTT----------A----------G----------A----------CCATTCCCAGAA

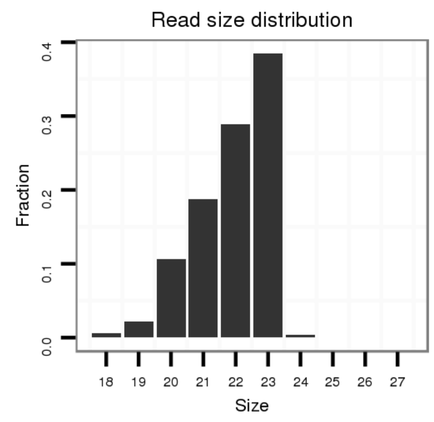
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dps_30	**4_group3:7165422-7165486 -**	**confident**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

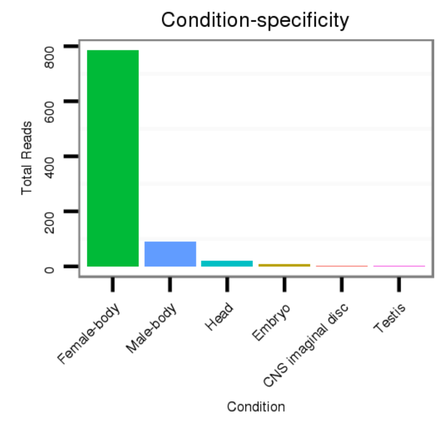
Legend: mature star **mismatch in alignment** mismatch in read

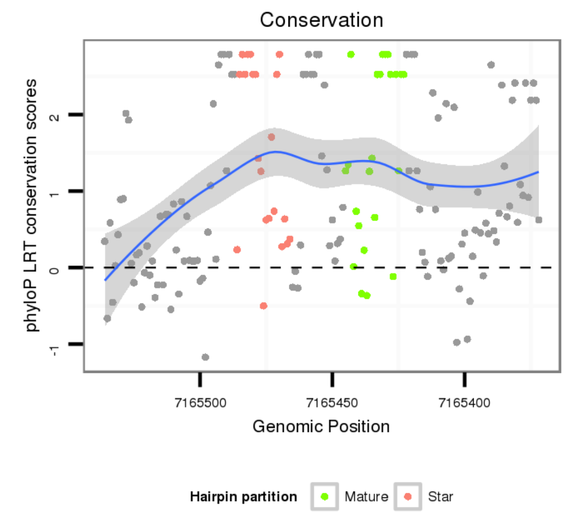
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

mature	star
1. dps_30 4_group3:7165423-7165445 - 2. dps_31 Unknown_singleton_3046:125-147 +	1. dps_30 4_group3:7165466-7165486 - 2. dps_31 Unknown_singleton_3046:84-104 +

Sense Strand Reads

hide 3p reads show mid mismatch reads

ACAAAAGATAAAACTAATCTCGGATCGGATGTTCCTTAAACCTTAACTGCCGTCTTGCAGCGCCTGTGGACGATAGGTCCAAAATTTCAGTCTACAGACGCTGCGATTCCGGGCAGTTGAGTGGATGGGATCCACCTTTAAATCACACTTAAAGCTATGTGCACA **********.....((((((((((...((((((((.((((((((((.....)).)))))))).)))))))).....)))))))))).....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M040 female body	V112 male body	M062 head	M059 embryo	GSM444067 head	GSM343916 embryo	M022 male body	SRR902011 testis	SRR902012 CNS imaginal disc	SRR902010 ovaries
.....CTACAGACGCTGCGATTCCGGGC.....	23	0	2	347.00	694	592	63	16	1	4	1	11	3	3	0
.....CTACAGACGCTGCGATTCCGGG.....	22	0	2	235.50	471	446	22	1	0	2	0	0	0	0	0
.....CTACAGACGCTGCGATTCCGG.....	21	0	2	122.00	244	227	14	1	1	0	1	0	0	0	0
.....CTACAGACGCTGCGATTCCG.....	20	0	2	45.00	90	35	49	0	0	6	0	0	0	0	0
.....CGTCTTGCAGCGCCTGTGGAC.....	21	0	2	28.50	57	47	4	2	1	2	0	1	0	0	0
.....CGTCTTGCAGCGCCTGTGGA.....	20	0	2	26.00	52	39	8	0	0	5	0	0	0	0	0
.....TACAGACGCTGCGATTCCGGGC.....	22	0	2	21.50	43	43	0	0	0	0	0	0	0	0	0
.....TACAGACGCTGCGATTCCGGG.....	21	0	2	14.00	28	28	0	0	0	0	0	0	0	0	0
.....TACAGACGCTGCGATTCCGG.....	20	0	2	13.00	26	24	2	0	0	0	0	0	0	0	0
.....CGTCTTGCAGCGCCTGTGG.....	19	0	2	9.00	18	18	0	0	0	0	0	0	0	0	0
.....GTCTTGCAGCGCCTGTGGAC.....	20	0	2	8.50	17	14	0	3	0	0	0	0	0	0	0
.....CTACAGACGCTGCGATTCC.....	19	0	2	7.00	14	12	0	1	0	1	0	0	0	0	0
.....CTACAGACGCTGCGATTCCGGGCT.....	24	1	2	4.00	8	6	0	0	0	0	1	1	0	0	0
.....CTACAGACGCTGCGATTCCGGGT.....	23	1	2	3.50	7	7	0	0	0	0	0	0	0	0	0
.....TCTACAGACGCTGCGATTCCGGG.....	23	0	2	2.00	4	4	0	0	0	0	0	0	0	0	0
.....TCTACAGACGCTGCGATTCCGG.....	22	0	2	2.00	4	4	0	0	0	0	0	0	0	0	0
.....GTCTTGCAGCGCCTGTGGA.....	19	0	2	2.00	4	4	0	0	0	0	0	0	0	0	0
.....CTACAGACGCTGCGATTCCGGGCA.....	24	0	2	2.00	4	1	0	0	2	0	1	0	0	0	0
.....CGTCTTGCAGCGCCTGTG.....	18	0	2	2.00	4	4	0	0	0	0	0	0	0	0	0
.....ACTGCCGTCTTGCAGCGCCTGT.....	22	0	2	1.50	3	0	0	0	0	0	3	0	0	0	0
.....AATTTCAGTCTACAGACGCTGC.....	22	0	2	1.50	3	0	0	0	0	0	3	0	0	0	0
.....CTACAGACGCTGCGATTCCGGGCTTT.....	25	2	2	1.50	3	3	0	0	0	0	0	0	0	0	0
.....CGTCTTGCAGCGCCTGTGGT.....	20	1	2	1.50	3	3	0	0	0	0	0	0	0	0	0
.....CTACAGACGCTGCGATTCCGGT.....	22	1	2	1.50	3	3	0	0	0	0	0	0	0	0	0
.....AGACGCTGCGATTCCGGGCA.....	20	0	2	1.50	3	3	0	0	0	0	0	0	0	0	0
.....TTCCGGGCAGTTGAGTGGATGG.....	22	0	2	1.00	2	0	0	0	0	0	0	0	2	0	0
.....AAAATTTCAGTCTACAGACGCTGC.....	24	0	2	1.00	2	0	0	0	2	0	0	0	0	0	0
.....AACTGCCGTCTTGCAGCGCCTGT.....	23	0	2	1.00	2	0	0	0	1	0	1	0	0	0	0
.....CAGACGCTGCGATTCCGGGCA.....	21	0	2	1.00	2	0	0	0	1	0	1	0	0	0	0
.....GATGTTCCTTAAACCTTAACTG.....	22	0	2	1.00	2	1	0	0	1	0	0	0	0	0	0
.....ATTTCAGTCTACAGACGCTGC.....	21	0	2	1.00	2	1	0	0	0	0	1	0	0	0	0
.....CGTCTTGCAGCGCCTGTGGTT.....	21	2	2	1.00	2	1	1	0	0	0	0	0	0	0	0
.....GTCTTGCAGCGCCTGTGGACG.....	21	0	2	1.00	2	2	0	0	0	0	0	0	0	0	0
.....TACAGACGCTGCGATTCCGGGCT.....	23	1	2	1.00	2	2	0	0	0	0	0	0	0	0	0
.....ACAGACGCTGCGATTCCGGGC.....	21	0	2	1.00	2	2	0	0	0	0	0	0	0	0	0
.....AGACGCTGCGATTCCGGG.....	18	0	2	1.00	2	1	1	0	0	0	0	0	0	0	0
.....TCAGTCTACAGACGCTGCGATT.....	22	0	2	1.00	2	2	0	0	0	0	0	0	0	0	0
.....GTCTTGCAGCGCCTGTGG.....	18	0	2	1.00	2	2	0	0	0	0	0	0	0	0	0
.....CTACAGACGCTGCGATTCT.....	19	1	2	1.00	2	2	0	0	0	0	0	0	0	0	0
.....CGTCTTGCAGCGCCTGTGGAT.....	21	1	2	1.00	2	2	0	0	0	0	0	0	0	0	0
.....CTACAGACGCTGCGATTCCGGA.....	22	1	2	1.00	2	2	0	0	0	0	0	0	0	0	0
.....CGTCTTGCAGCGCCTGTGGACG.....	22	0	2	1.00	2	2	0	0	0	0	0	0	0	0	0
.....CTACAGACGCTGCGATTCCGGGCC.....	24	1	2	1.00	2	2	0	0	0	0	0	0	0	0	0
.....TACAGACGCTGCGATTCCG.....	19	0	2	1.00	2	2	0	0	0	0	0	0	0	0	0
.....TCTACAGACGCTGCGATTCCG.....	21	0	2	1.00	2	0	0	0	0	0	0	0	0	2	0
.....CTTAACTGCCGTCTTGCAGCGCCTGC.....	26	1	2	1.00	2	0	0	0	2	0	0	0	0	0	0
.....CGTCTTGCAGCGCCTGTGGACT.....	22	1	2	1.00	2	2	0	0	0	0	0	0	0	0	0
.....TCTACAGACGCTGCGATTCCGGGA.....	24	1	2	0.50	1	1	0	0	0	0	0	0	0	0	0
.....CCTTAAACCTTAACTGCCGTC.....	21	0	2	0.50	1	0	0	1	0	0	0	0	0	0	0
.....CTACAGACGCTGCGATTC.....	18	0	2	0.50	1	0	0	0	0	0	0	1	0	0	0
.....GACGCTGCGATTCCGGGCA.....	19	0	2	0.50	1	0	0	0	0	0	1	0	0	0	0
.....CAGACGCTGCGATTCCGGGC.....	20	0	2	0.50	1	1	0	0	0	0	0	0	0	0	0
.....ATAGGTCCAAAATTTCAGTCTAC.....	23	0	2	0.50	1	0	0	0	0	0	1	0	0	0	0
.....AAAACTAATCTCGGATCGGATG.....	22	0	2	0.50	1	1	0	0	0	0	0	0	0	0	0
.....CAGCGCCTGTGGACGATAGGT.....	21	0	2	0.50	1	0	0	0	0	0	1	0	0	0	0
.....TACAGACGCTGCGATTCCGGGT.....	22	1	2	0.50	1	1	0	0	0	0	0	0	0	0	0
.....CTACAGACGCTGCGATTCCGGGA.....	23	1	2	0.50	1	1	0	0	0	0	0	0	0	0	0
.....AAAACTAATCTCGGATCGGATGTC.....	24	1	2	0.50	1	0	0	0	1	0	0	0	0	0	0
.....GTTGAGTGGATGGGATCCACCTT.....	23	0	2	0.50	1	0	0	0	0	0	1	0	0	0	0
.....TTGCAGCGCCTGTGGACGATA.....	21	0	2	0.50	1	1	0	0	0	0	0	0	0	0	0
.....CCGTCTTGCAGCGCCTGTGGAC.....	22	0	2	0.50	1	1	0	0	0	0	0	0	0	0	0
.....CTACAGACGCTGCGATTCCGGC.....	22	1	2	0.50	1	1	0	0	0	0	0	0	0	0	0
.....AATCTCGGATCGGATGTTCCTTAAACCTT.....	29	0	2	0.50	1	0	0	0	1	0	0	0	0	0	0
.....TACAGACGCTGCGATTCCGGGCA.....	23	0	2	0.50	1	1	0	0	0	0	0	0	0	0	0
.....CTTAAACCTTAACTGCCGTCTTGCAGC.....	27	0	2	0.50	1	0	0	0	1	0	0	0	0	0	0
.....TACAGACGCTGCGATTCCGGGCTTT.....	24	2	2	0.50	1	1	0	0	0	0	0	0	0	0	0
.....CTACAGACGCTGCGATTCCGGGTT.....	24	2	2	0.50	1	1	0	0	0	0	0	0	0	0	0
.....TTCAGTCTACAGACGCTGCG.....	20	0	2	0.50	1	1	0	0	0	0	0	0	0	0	0
.....TTAAACCTTAACTGCCGTCTTGCAGCGCC.....	29	0	2	0.50	1	0	0	0	1	0	0	0	0	0	0
.....GATTCCGGGCAGTTGAGTGGATGGG.....	25	0	2	0.50	1	0	0	0	0	0	1	0	0	0	0
.....AAACCTTAACTGCCGTCTTGCAGC.....	24	0	2	0.50	1	0	0	0	1	0	0	0	0	0	0
.....GTCTTGCAGCGCCTGTGGTT.....	20	2	2	0.50	1	0	1	0	0	0	0	0	0	0	0
.....ATAAAACTAATCTCGGATCGGAC.....	23	1	2	0.50	1	0	0	0	1	0	0	0	0	0	0
.....ATCGGATGTTCCTTAAACCTTAACTGC.....	27	0	2	0.50	1	0	0	0	1	0	0	0	0	0	0
.....CCGGGCAGTTGAGTGGATG.....	19	0	2	0.50	1	0	0	0	0	1	0	0	0	0	0
.....TCTTGCAGCGCCTGTGGAC.....	19	0	2	0.50	1	1	0	0	0	0	0	0	0	0	0
.....GCAGCGCCTGTGGACGATAG.....	20	0	2	0.50	1	0	1	0	0	0	0	0	0	0	0
.....GTTGAGTGGATGGGATCCACCT.....	22	0	2	0.50	1	0	0	0	0	0	1	0	0	0	0
.....TAAACCTTAACTGCCGTCTTGCAG.....	24	0	2	0.50	1	0	0	0	0	0	1	0	0	0	0
.....GATAAAACTAATCTCGGATC.....	20	0	2	0.50	1	0	0	0	1	0	0	0	0	0	0
.....AGTTGAGTGGATGGGATCCACCTT.....	24	0	2	0.50	1	0	0	0	0	0	1	0	0	0	0
.....TTGCAGCGCCTGTGGACGATAG.....	22	0	2	0.50	1	1	0	0	0	0	0	0	0	0	0
.....ATCTCGGATCGGATGTTCCTTAAACC.....	26	0	2	0.50	1	0	0	0	1	0	0	0	0	0	0
.....ATTTCAGTCTACAGACGCTGCGATTCC.....	27	0	2	0.50	1	1	0	0	0	0	0	0	0	0	0
.....TTAAACCTTAACTGCCGTCTTGCAGCGC.....	28	0	2	0.50	1	0	0	0	1	0	0	0	0	0	0
.....CGTCTTGCAGCGCCTGTGT.....	19	1	2	0.50	1	1	0	0	0	0	0	0	0	0	0
.....CTACAGACGCTGCGATTCCGGTTT.....	24	3	2	0.50	1	1	0	0	0	0	0	0	0	0	0
.....CTGCCGTCTTGCAGCGCCTGT.....	21	0	2	0.50	1	1	0	0	0	0	0	0	0	0	0
.....TACAGACGCTGCGATTCCGGGTC.....	23	2	2	0.50	1	1	0	0	0	0	0	0	0	0	0
.....AAAATTTCAGTCTACAGACGCTGCGA.....	26	0	2	0.50	1	0	0	0	1	0	0	0	0	0	0
.....CCGGGCAGTTGAGTGGATGGG.....	21	0	2	0.50	1	1	0	0	0	0	0	0	0	0	0
.....GATTCCGGGCAGTTGAGTGGATGG.....	24	0	2	0.50	1	1	0	0	0	0	0	0	0	0	0
.....TCTTGCAGCGCCTGTGGACGATAGG.....	25	0	2	0.50	1	1	0	0	0	0	0	0	0	0	0
.....CTGCCGTCTTGCAGCGCCTGTG.....	22	0	2	0.50	1	1	0	0	0	0	0	0	0	0	0
.....TCTTGCAGCGCCTGTGGA.....	18	0	2	0.50	1	1	0	0	0	0	0	0	0	0	0
.....TCTTGCAGCGCCTGTGGACG.....	20	0	2	0.50	1	1	0	0	0	0	0	0	0	0	0
.....TTCCGGGCAGTTGAGTGGATGGA.....	23	1	2	0.50	1	1	0	0	0	0	0	0	0	0	0
.....ACAGACGCTGCGATTCCGGG.....	20	0	2	0.50	1	1	0	0	0	0	0	0	0	0	0
.....TACAGACGCTGCGATTCC.....	18	0	2	0.50	1	1	0	0	0	0	0	0	0	0	0
.....TCTACAGACGCTGCGATTCC.....	20	0	2	0.50	1	1	0	0	0	0	0	0	0	0	0
.....GATTCCGGGCAGTTGAGTGGAT.....	22	0	2	0.50	1	0	0	0	0	0	1	0	0	0	0
.....GTCTTGCAGCGCCTGTGGACC.....	21	1	2	0.50	1	1	0	0	0	0	0	0	0	0	0
.....AGACGCTGCGATTCCGGGCAGT.....	22	0	2	0.50	1	0	0	0	1	0	0	0	0	0	0
.....TTGCAGCGCCTGTGGACGATAGG.....	23	0	2	0.50	1	0	1	0	0	0	0	0	0	0	0

Anti-sense strand reads

TGTTTTCTATTTTGATTAGAGCCTAGCCTACAAGGAATTTGGAATTGACGGCAGAACGTCGCGGACACCTGCTATCCAGGTTTTAAAGTCAGATGTCTGCGACGCTAAGGCCCGTCAACTCACCTACCCTAGGTGGAAATTTAGTGTGAATTTCGATACACGTGT **********.....((((((((((...((((((((.((((((((((.....)).)))))))).)))))))).....)))))))))).....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M040 female body	V112 male body	GSM444067 head
.....GATGTCTGCGACGCTAAGGC.....	20	0	2	0.50	1	1	0	0
.....CTACCCTAGGTGGAAATTTAG.....	21	0	2	0.50	1	1	0	0
.....TCGCGGACACCTGCTATCCA.....	20	0	2	0.50	1	0	1	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
dp5	4_group3:7165372-7165536 -	dps_30	ACA-AAAGATAAAAC---TAAT-C-TCGGATCGG----------ATGTTCCTTAAACC---------T--TAACTGCCGTCTTGCAGCGCCT--GTGGAGG--ATAGGTCCAAA---ATTTCAGTCTACAGACGCTGCGATTCCG-GGCAGTTGAGT-GG---AT--------GGGAT---CCA--CCTTTAAATCACACTTAAAGCTA--TGTGCACA----------
droPer2	scaffold_1:8612784-8612948 -	dpe_229	ACA-AAAGATAAAAC---TAAT-C-TCGGATCGG----------ATGTTCCTTAAACC---------T--TAACTGCCGTCTTGCAGCGCCT--GTGGAGG--ATAGGTCCAAA---ATTTCAGTCTACAGACGCTGCGATTCCG-GGCAGTTGAGT-GG---AT--------GGGAT---CCA--CCTTTAAATCACACTTAAAGCTA--TGTGCACA----------
droWil2	scf2_1100000004945:407286-407437 +	dwi_5419	AAA-CAAGATAAATCTCCAAA--TGTGAATTAGATAT----AAGTTATATCCA-------GTGATC------GATT--TAATTGCCGTCTTGCAGGGTGTTTGTAAAGAATCCAGGTCCAAATT-AAAA-TCTTTATAGATCCTGCGATTCTG-GGCAATTGAAT-GA---------------------CACACTGAA------------------------------
droVir3	scaffold_12963:14467473-14467585 -	dvi_24646	AGT-CTATGTA--ATG--TAACTGCCGTCTTGCAAGGCCT--GTGGATA-CAAAGGTCCAAA---AATT-AATCCACACGAGTTGCGATTCTG-GGCAGTTGA---------------------TTTTACTAAAATCTT--TATGCACA----------
droMoj3	scaffold_6500:15423853-15423994 -	dmo_3155	GACAACAG----CACAGCAGC--C------GGCACTC----------G-----------TCTT--TAACTGCCGTCTTGCAGCTCCT--GTGGATG-CCCAGGTCCAAT---AAGT-AATGCACACGTGCTGCGATTCCG-GGCAGTTGAGG-GG---A-GCAA-CAGG--AT--TCCT--TTAA-GAACTACAGCT------A---------
droGri2	scaffold_15252:2029231-2029386 +	dgr_469	AAA-GAGGA---ATCATCATAAT-T------TGTAT---------ATCAATCTA-T-----ATAATGTTACAATGAT--TAACTGCCGTCTTGCCGGGCCT--GTGGGCA-CCCAGGTCCAAACAAAAGT-TGCCCACATGCTGGCGATTCTG-AGCAGTTAAA-------------------TTAA--CTT--CATTCACAACT-------
droAna3	scaffold_12916:9588080-9588226 -	dan_4042	TTA-AG---------------------GAACCGTA-----T--ATC-----TCCCATTAACTGCTGTCTTGCAGAGTCT--GTGGAGC--G-TGGTCCAAA---TTT--TGTCTACAGCCACTGCGATTCCG-GGCAGTTGAAAGTG---AT--AA-TACGG-AC--TCCCCAAAAACACATCACATCT-GCGCTT--TGTGCAC----------
droBip1	scf7180000396580:1442858-1443004 +		TTA-AG---------------------GATCAGCA-T----T---TC-----TCCCATTAACTGCCGTCTTGCAGCGTCT--GTGGAGC--G-TGGTCCAAA---TTT--TGTCTACAGCCGCTGCGATTCCG-GGCAGTTGCAAGTG---AAACCA-TACGG-AT--TCCT--CAAATACATCACATCT-GCGCTT--TGTGCAC----------
droKik1	scf7180000302246:274527-274648 +		A--TTA-AGTCTACAGACGCTGCGATTCCG-GGCAGTTGAGT-GGCCCATGCTG-G--------------ATGCCACTTAACGCTTCCTGTGCAGC--GCAGAGAA
droFic1	scf7180000453924:1051732-1051906 +		ACA-AGAGATAGG--ATCGGA--T------TGGAGTG-----G-ATCGATCGCCT-----GGGATC-----TGCC--TAACTGCCGTCTTGCAGCGC-C--GTAGAG---TTTGGTCCAAA---ATTT-AGCCTACGCCCGCTACGATTCCG-GGCAGTTGAAA-GG---ATCCAG-GATCCGAGT-CGC--CCAACCCTTCACACTTAACGCTT--TGTGCAC----------
droEle1	scf7180000491046:1758551-1758727 +		ACA-AGAGATAAGTCAACGGA--T------CGGATTG-----GAGTGGATCGGAT------TGCGTC------TGCC--TAACTGCCGTCTTGCAGCAC-T--GTAGTG---TTTGGTCCAAA---ATTT-AGTCTACAGCCGCTGCGATTCTG-GGCAGTTGAAA-GG---ATGCAATGATGACAG---GC--CCAGACCATCACACTTAACGCTT--TGTGCAC----------
droRho1	scf7180000780028:158230-158404 +		ACA-GGAGATAAGTCAACGGA--T------CGGATTG-----GAATGGATTGGAT------TGGATC------TGCC--TAACTGCCGTCTTGCAGCGC-T--GTATTG---TTTGGTCCAAA---ATTT-AGTCTATAGTCGCTACGATTCTG-GGCAGTTGAAA-TG---ATCCAA-GACGAGAG---GC--CCAATCCATCACACTTAACGCTT--TGTGCAC----------
droBia1	scf7180000302188:2122009-2122188 +		ACA-GGAGATAAGTAAACAGA--T------CGGATTGGACTGGAGTGGATCGGAT------TGCATC------GGCC--TAACTGCTGTCTTGCAGCGC-C--GTAGAG---TTTGGTCCAAA---ATTT-AGTCTACGCTCGCTGCGATTCCG-GGCAGTTGAAA-GG---ATGCAA-GACGAGAG---AC--TCAGTCCACTAGACTTAACGCTT--TGTGCAC----------
droTak1	scf7180000415438:753082-753217 -		G--TGGATCGGAT------GGCATC------TGCC--TAACTGCTGTCTTGCAGCGC-C--GTGGAGC--TTTGGTCCAAA---ATTT-AGTCTATGCTCGCTGCGATTCCG-GGCAGTTGAAA-GG---ATGCCA-AATGAGAG---AC--CCA---------ACCTAACGCTT--TGTGCAC----------
droEug1	scf7180000409554:3024279-3024455 -		AAA-AGAGATAACTCAACAGG--T------CGGATTG-----GAGCGGATCGGAT------TGAATC------TGAT--TAACTGCTGTCTTGCAGCGC-T--GTAGAG---TGTGGTCCAAA---ATTT-AGTCTATAGTCGCTGCGATTCTG-GGCAGTTGTAA-GG---ATAAAAAGATGAGAG---GC--CCAAACCATCACACTTAACGCTT--TGTGCAC----------
dm3	chr2L:3067716-3067891 +	dme_436	ACA-AGAGATAAGTTAACAGA--T------TGGATTT-----GCGTCGATCGGAT------TGAATC------TGCC--TAACTGCTGTCTTGCAGCGC-T--GTAGCG---TTCGGTCCAAA---ATTA-AGTCTACAGTCTCTGCGATTCCG-GGCAGTTGAAA-TG---ATGCAA-GATGAGAG---GC--TCAGTCCATAACACTTAACGCTT--TGTGCAC----------
droSim2	2L:2946901-2947076 +	dsi_32463	ACA-AGAGATAAGTCAACAGA--T------TGGATTT-----GCGCCGATCGGCT------TGAATC------TGCC--TAACTGCTGTCTTGCAGCGC-T--GTAGCG---TTCGGTCCAAA---ATTT-AGTCTACAGTCGCTGCGATTCCG-GGCAGTTGAAA-TG---ATGCAA-GATGAGAG---GC--CCAGTCCATAACACTTAACGCTT--TGTGCAC----------
droSec2	scaffold_5:1224959-1225134 +	dse_1854	ACA-AGAGATAAGTCAACAGA--T------TGGATTT-----GCGTCGATCGGCT------TGAATC------TGCC--TAACTGCTGTCTTGCAGCGC-T--GTAGCG---TTCGGTCCAAA---ATTT-AGTCTACAGTCATCGCGATTCCG-GGCAGTTGAAA-TG---ATGCAA-GATGAGAG---GC--CCAGTCCATAACACTTAACGCTT--TGTGCAC----------
droYak3	2L:3063715-3063881 +	dya_1801	ACA-AGAGAT-----------------------TGGATCG-----GCGTCGATCGGAT------TAAGTC------TGCC--TAACTGCTGTCTTGCAGCGC-T--GTAGCG---TTTGGTCCAAA---ATTT-AGTCTACAGTCGCTGCGATTCCG-GGCAGTTGAAA-TG---ATGCAA-GATGAAAGAGAGC--CCGGTCCATAACACTTAACGCTT--TGTGCAC----------
droEre2	scaffold_4929:3115459-3115621 +	der_1527	ACA-AGAGAT-----------------------TGGATTG-----GCGTCAATCGGAT------TGAATC------TGCC--TAACTGCTGTCTTGCAGCGC-T--GTAGCG---TTCGGTCCAAA---ATTT-AGTCTACAGTCGCTGCGATTCCG-GGCAGTTGAAA-GG---ATGCAA-GATGAGAG---GC--CCAGTCCATCACACTTAACGCTT--TGTGCAC----------

Generated: 09/08/2015 at 08:19 PM

	PASS/FAIL
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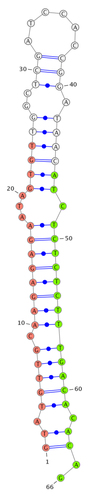
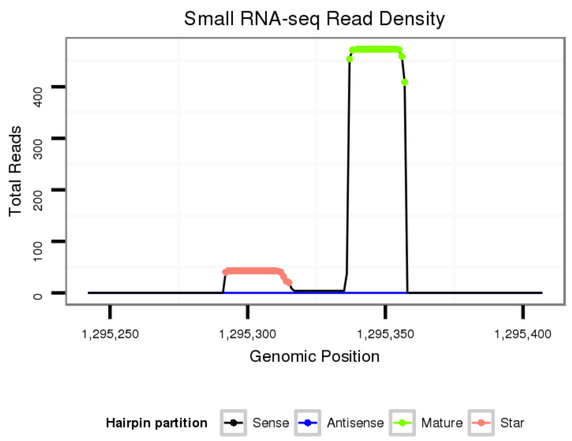
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	2
rescue.candidate	10

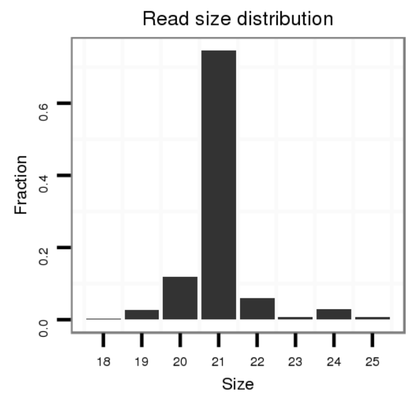
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dps_22	**XR_group6:1295292-1295357 +**	**confident**	**Mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

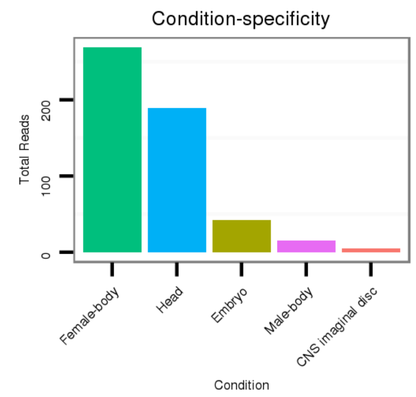
Legend: mature star mismatch in alignment mismatch in read

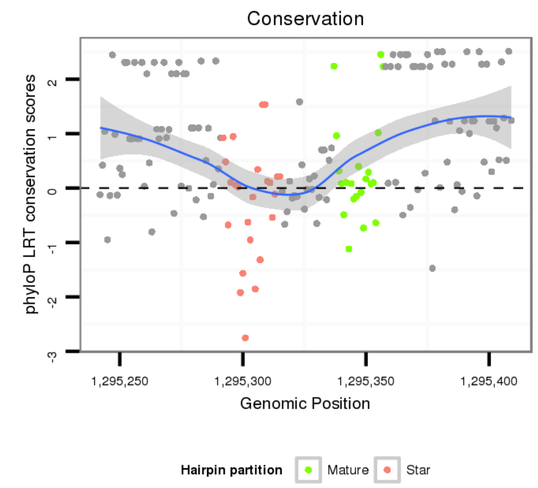
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dpse\GA23669-in]; CDS [Dpse\GA23669-cds]; CDS [Dpse\GA23669-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

GTCGCTGGCCAAGGACGAGCAGAACTACACCGAGCCCAAGTACTATCTGGGTATGTTGCAAGAGAGAATAGTGTTGGCTCGATCCACCGGATAACATCTCTCTCTTTGACACACAGGGGATCTCATTCCGGGCACTTACTGCTCGAGGATCTTTAGTGACTGCGAC **********((.(((((.(((((((((...(((((((..(((.....))).)))))).)))))))))))))).))..	Read size	# Mismatch	Hit Count	Total Norm	Total	M040 female body	GSM444067 head	M062 head	M059 embryo	GSM343916 embryo	V112 male body	SRR902012 CNS imaginal disc
ATCTCTCTCTTTGACACACAG	21	0	1	369.00	369	211	70	58	12	8	6	4
ATCTCTCTCTTTGACACACAGT	22	1	1	196.00	196	19	123	33	8	9	3	1
ATCTCTCTCTTTGACACACA	20	0	1	41.00	41	30	6	4	1	0	0	0
CATCTCTCTCTTTGACACACAG	22	0	1	23.00	23	4	6	7	2	4	0	0
TCTCTCTCTTTGACACACAG	20	0	1	15.00	15	15	0	0	0	0	0	0
GTATGTTGCAAGAGAGAATAGTGT	24	0	1	15.00	15	1	2	0	2	4	5	1
ATCTCTCTCTTTGACACAC	19	0	1	10.00	10	0	0	10	0	0	0	0
TCTCTCTCTTTGACACACAGT	21	1	1	10.00	10	2	6	2	0	0	0	0
ATCTCTCTCTTTGACACACAGC	22	1	1	8.00	8	0	0	6	2	0	0	0
GTATGTTGCAAGAGAGAATAGT	22	0	1	8.00	8	1	5	0	1	0	1	0
ATCTCTCTCTTTGACACACAGTT	23	2	1	7.00	7	3	2	2	0	0	0	0
CATCTCTCTCTTTGACACACA	21	0	1	7.00	7	0	3	1	3	0	0	0
GTATGTTGCAAGAGAGAATAG	21	0	1	7.00	7	0	5	0	0	0	2	0
GTATGTTGCAAGAGAGAATAGTGTT	25	0	1	4.00	4	1	0	0	0	2	1	0
TGGCTCGATCCACCGGATAAC	21	0	1	4.00	4	0	0	2	1	1	0	0
CATCTCTCTCTTTGACACAC	20	0	1	3.00	3	1	1	0	1	0	0	0
GTATGTTGCAAGAGAGAATAGTG	23	0	1	3.00	3	1	2	0	0	0	0	0
ATCTCTCTCTTTGACACACAGA	22	1	1	3.00	3	2	0	1	0	0	0	0
GTATGTTGCAAGAGAGAATA	20	0	1	2.00	2	0	2	0	0	0	0	0
TCTCTCTTTGACACACAGT	19	1	1	2.00	2	0	2	0	0	0	0	0
TCTCTCTCTTTGACACACA	19	0	1	2.00	2	2	0	0	0	0	0	0
ATCTCTCTCTTTGACACACAA	21	1	1	1.00	1	0	1	0	0	0	0	0
GTATGTTGCAAGAGAGAATAGTT	23	1	1	1.00	1	0	0	0	0	0	1	0
TATGTTGCAAGAGAGAATAGTGT	23	0	1	1.00	1	0	1	0	0	0	0	0
TATGTTGCAAGAGAGAATAGT	21	0	1	1.00	1	0	1	0	0	0	0	0
ATCTCTCTCTTTGACACACT	20	1	1	1.00	1	0	1	0	0	0	0	0
ATCTCTCTCTTTGACACA	18	0	1	1.00	1	0	0	1	0	0	0	0
TCTCTCTTTGACACACAG	18	0	1	1.00	1	1	0	0	0	0	0	0
CTCTCTCTTTGACACACAG	19	0	1	1.00	1	1	0	0	0	0	0	0
CTCTCTCTTTGACACACAGT	20	1	1	1.00	1	1	0	0	0	0	0	0
GTATGTTGCAAGAGAGAAT	19	0	1	1.00	1	0	1	0	0	0	0	0
TATGTTGCAAGAGAGAATAG	20	0	1	1.00	1	0	1	0	0	0	0	0
CATCTCTCTCTTTGACACACAC	22	1	1	1.00	1	0	0	0	1	0	0	0
ATCTCTCTCTTTGACACACAC	21	1	1	1.00	1	0	0	1	0	0	0	0
TCTCTCTCTTTGACACACAGA	21	1	1	1.00	1	0	1	0	0	0	0	0
ATCTCTCTCTTTGACACACAGTTT	24	3	2	0.50	1	0	0	0	1	0	0	0
ATCTCTCTCTTTGACACACAAT	22	2	2	0.50	1	0	1	0	0	0	0	0

Anti-sense strand reads

CAGCGACCGGTTCCTGCTCGTCTTGATGTGGCTCGGGTTCATGATAGACCCATACAACGTTCTCTCTTATCACAACCGAGCTAGGTGGCCTATTGTAGAGAGAGAAACTGTGTGTCCCCTAGAGTAAGGCCCGTGAATGACGAGCTCCTAGAAATCACTGACGCTG **********((.(((((.(((((((((...(((((((..(((.....))).)))))).)))))))))))))).))..	Read size	# Mismatch	Hit Count	Total Norm	Total
No data available in table					

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
dp5	XR_group6:1295242-1295409 +	dps_22	GTCGCTGG---CCAAGGACGAGCAGAACTACACCGAGCCCAAGTACTATCTGGGTATG----------TTG-CAAGA-G----------AGAA----------TA-------GT--GTTGGCTCGATCCACCGGATAACATCTCTC----------TCTTTGACACACAGGGGATCTCATTCCGGGCACTTACTGCTCGAGGATCTTTAGTGACTGCGACAA
droPer2	scaffold_12:1984752-1984919 +	dpe_77	GTCGCTGG---CCAAGGACGAGCAGAACTACACCGAGCCCAAGTACTATCTGGGTATG----------TTG-CAAGA-G----------AGAA----------TA-------GT--GTTGGCTCGATCCACCGGATAACATCTCTC----------TCTTTGACACACAGGGGATCTCATTCCGGGCACTTACTGCTCGAGGATCTTCAGTGACTGCGACAA
droWil2	scf2_1100000004762:5597924-5598087 +		ACCATTGA---TCAAGGATGAGTTAATTACACCGAACCGAAATATTATTGGGTAG----------CTCGATTT-A----------GAA--------------AC-------TC--GTAAATTTTATGTATTCT---ATATTCCTA----------TTCCTTGGTTTAGGTGATCTCATTCCTGGCACTATATGCTCACGCATATTCAGTGATTGCGACAA
droVir3	scaffold_13049:1777254-1777410 -	dvi_17904	GCCGCTGC---CAAGGACGAGCACAACTACACCGAGCCCAAATACTATCTGGGTAG----------TGGG-CCCCAA-------GTTGAA--------------ACCCAGACTT--TT----------ATACTTGAA----------CCCCAC-TTCACAGGCGACCTAATACCGGGCACCTATTGCTCCGCGCATCTTCAGCGATTGCGACAA
droMoj3	scaffold_6654:2055092-2055254 +		GCCGCTGC---CCAAGGACGAGCACAACTACACAGAACCCAAATATATCTGGGTAG----------CGCA-TTT-T----------GAA--TCACATCTCTCAAGTCTCCT---C----GTTATATCGAAATCTTG------TTTCAGGTGATCTTATACCAGGCACCTACTGCTCGCGCATCTTTAGCGACTGCGACAA
droGri2	scaffold_15110:2847521-2847608 -		ACCAATTTA----------
droAna3	scaffold_13337:8836599-8836777 +		GTCGCTGG---CGAAGGACGAGCAAAACTACACTGAGCCCAAATACTATCTAGGTGAG----------TCTCATACA-------GCT-CTCAACAACTCATTAAGTACAATT--TGCAAGT---GTTTTGTCTGAT----------TCTG----------ACTCTGATTCGCAGGTGACCTTATTCCGGGCACCTACTGCTCCAGGATCTTCAGCGACTGCGACAA
droBip1	scf7180000396541:978415-978594 +		GTCGCTGG---CGAAGGACGAACAGAACTACACTGAGCCCAAATACTACCTGGGTGAGTGTTG----------CTT-CCAGA-----A---CT-CTTAACAACTCATTAAGTACCATT--TGCGAGTG--TC----------ACATCTGTT----------TGTCTGATTCGCAGGTGACCTTATTCCGGGCACCTACTGCTCCAGGATCTTCAGCGACTGCGACAA
droKik1	scf7180000302697:523799-524022 -		GTCGCTGG---CCAAGGACGAGCAGAACTACACGGAGCCCAAATACTATCTAGGTGGGATATACATTTACACACAATATTTCTAAATGAAATTTTCTAATTAAATTT-TCAGA-----ACACTT-TTTAAGGACTCATTAAATATAATT--CTTGGCTG--TG----------ACATCTGTT----------TCCCGCATTCACAGGTGACCTCATACCCGGCACCTACTGCTCGAGGATCTTTAGCGACTGCGACAA
droFic1	scf7180000453819:101262-101338 -		--------
droEle1	scf7180000491193:2530222-2530298 +		--------
droRho1	scf7180000779741:122561-122633 -		GTCTCTGG---CCAAGGACGAGCAAAACTACACGGAGCCCAAATACTATTTGGGTAG----------TTTAGAAAA-T----------AAAA----------TA-------AT--
droBia1	scf7180000302193:5200991-5201062 +		GTCACTGG---CCAAGGACGAGCAGAACTACACGGAGCCCAAATACTACCTGGGTGAG----------TTG-TGGT-G----------TAAA----------TA-------AT--
droTak1	scf7180000415664:65956-66027 +		GTCACTGG---CCAAGGACGAGCAAAACTACACGGAGCCCAAGTATTATCTGGGTGAG----------TTGC-TGGA-A----------TAAA----------TA-------AT--
droEug1	scf7180000409711:5150944-5151020 +		--------
dm3	chr3L:20847236-20847383 -		GCA-----TGAGTATGCACTGGGCATG----------TCC-CCACA-GTAGAAT-GTC-CTTAATGGTTAATTGAATATTATT--TCTGACTG--TG----------ACATCTGCC----------TTCCGCT-TTCCAGGTGACCTCATACCCGGAACGTACTGCTCCAGGATCTTCAGCGACTGCGACAA
droSim2	3L:20405333-20405408 -		--------
droSec2	scaffold_11:743433-743497 -		ATCCTTGG---CCAAGGACGAGCAGAACTACACGGAGCCCAAGTACTATCTGGGTGAG----------TTA-----------------------------TA-------AT--
droYak3	3R:25536509-25536635 -		GTCGCTGCAGCACAACCCACCAACTGAGCCACCCCGAACCAATCCATCAGTTGCCCCAA----------TTAC-AGCG-T------CCG-GTG----------GC--------CGATCCACCAGATGCC----------TTCGA----------CAACTGTCCGATCTTCCCGAGCCCGGCCGCG--
droEre2	scaffold_4784:20534547-20534613 -		ATCCTTGG---CCAAGGACGAGCAGAACTATACGGAGCCCAAGTACTATCTGGGTAG----------TTGCC-----------------------------TA-------AT--

Generated: 09/08/2015 at 10:31 PM

	PASS/FAIL
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crit.mor	0
crit.half	0
crit.total	1
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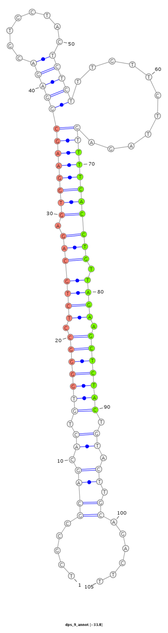
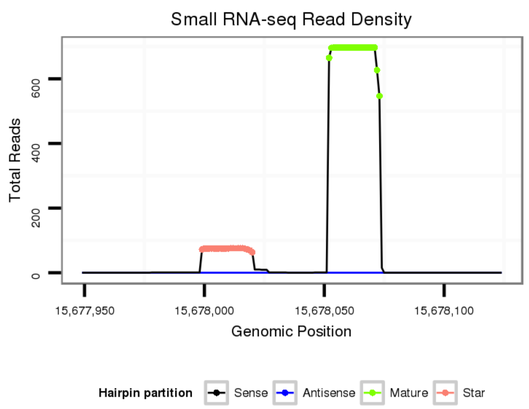
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	3
rescue.candidate	0

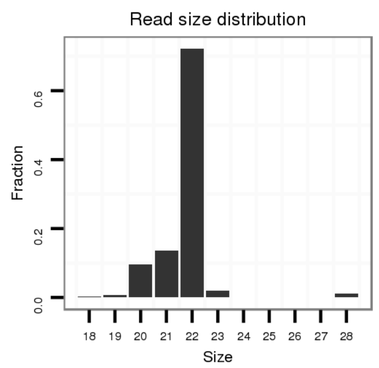
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dps_9	**3:15677999-15678074 +**	**confident**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser [Cornell Mirror]]

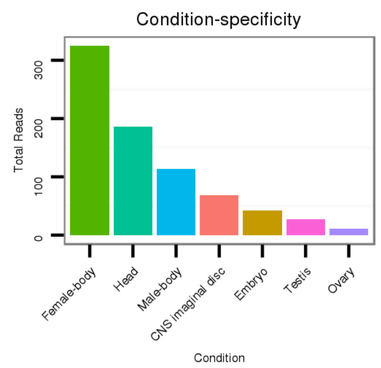
Legend: mature star mismatch in alignment mismatch in read

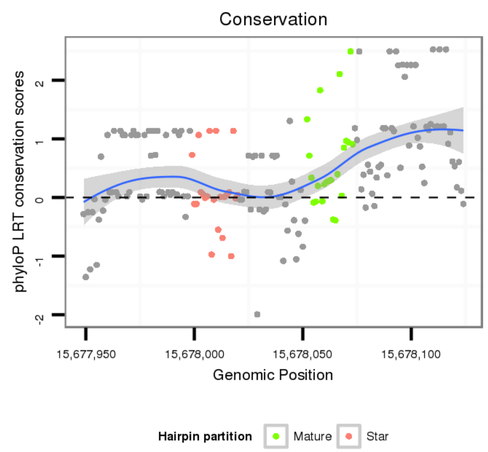
Predicted structure











Show Alternate Folds

Flybase annotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

CGTTTTCCCAGCTCTAAACGACCTCCAGCAAAACTTCGCCGCAGCACTGTGGGGCCTCTGCAGAGTGGAAGCGGAGACGTGCTACTCTCTTTGTTCTTAGAGTTTTCACCTGTTAGAAGCTCTACTGTACTTGCAGACTTGTTATTTGCTGTTTTGTGAAATTTTATTGCTCTCTA **********.....((((.((.(((((((.(((((((.(((((((((((((.....)))))).....)))))))))))).))))).)))))))..)).)).)).....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M040 female body	M062 head	GSM444067 head	V112 male body	M022 male body	SRR902012 CNS imaginal disc	M059 embryo	SRR902011 testis	GSM343916 embryo	SRR902010 ovaries
.....TTTCACCTGTTAGAAGCTCTAC.....	22	0	1	507.00	507	185	69	39	34	45	67	28	25	4	11
.....TTTCACCTGTTAGAAGCTCTA.....	21	0	1	76.00	76	47	4	14	6	2	0	3	0	0	0
.....TTTCACCTGTTAGAAGCTCT.....	20	0	1	66.00	66	18	12	15	13	6	0	0	2	0	0
.....GGGGCCTCTGCAGAGTGGAAGC.....	22	0	1	51.00	51	20	9	9	6	0	2	2	0	3	0
.....TTTCACCTGTTAGAAGCTCTACG.....	23	1	1	48.00	48	15	11	4	4	3	3	4	0	2	2
.....TTCACCTGTTAGAAGCTCTAC.....	21	0	1	23.00	23	23	0	0	0	0	0	0	0	0	0
.....TTTCACCTGTTAGAAGCTCTACT.....	23	0	1	15.00	15	8	4	1	0	0	0	2	0	0	0
.....TTTCACCTGTTAGAAGCTCTAA.....	22	1	1	15.00	15	6	1	1	2	2	0	0	0	3	0
.....TTTCACCTGTTAGAAGCTCTACA.....	23	1	1	11.00	11	6	1	1	0	2	1	0	0	0	0
.....TTTCACCTGTTAGAAGCTCTACCA.....	24	2	1	8.00	8	8	0	0	0	0	0	0	0	0	0
.....GGGGCCTCTGCAGAGTGGAAGCGGAGAC.....	28	0	1	8.00	8	0	8	0	0	0	0	0	0	0	0
.....GGGGCCTCTGCAGAGTGGAAG.....	21	0	1	5.00	5	5	0	0	0	0	0	0	0	0	0
.....TTTCACCTGTTAGAAGCTCTTT.....	22	2	1	4.00	4	2	1	1	0	0	0	0	0	0	0
.....TTCACCTGTTAGAAGCTCT.....	19	0	1	4.00	4	4	0	0	0	0	0	0	0	0	0
.....TTCACCTGTTAGAAGCTCTA.....	20	0	1	4.00	4	4	0	0	0	0	0	0	0	0	0
.....GGGGCCTCTGCAGAGTGGAA.....	20	0	1	3.00	3	1	0	1	1	0	0	0	0	0	0
.....GGGCCTCTGCAGAGTGGAAGC.....	21	0	1	2.00	2	2	0	0	0	0	0	0	0	0	0
.....GGGGCCTCTGCAGAGTGGA.....	19	0	1	2.00	2	2	0	0	0	0	0	0	0	0	0
.....TTTCACCTGTTAGAAGCTCC.....	20	1	1	2.00	2	0	2	0	0	0	0	0	0	0	0
.....GGGGCCTCTGCAGAGTGG.....	18	0	1	2.00	2	2	0	0	0	0	0	0	0	0	0
.....TTCACCTGTTAGAAGCTCTACG.....	22	1	1	2.00	2	2	0	0	0	0	0	0	0	0	0
.....TTTCACCTGTTAGAAGCTCTAT.....	22	1	1	2.00	2	0	0	0	1	0	0	0	0	1	0
.....TTTCACCTGTTAGAAGCTCTT.....	21	1	1	2.00	2	1	0	0	1	0	0	0	0	0	0
.....TTCACCTGTTAGAAGCTCTAA.....	21	1	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....GGGGCCTCTGCAGAGTGGAAA.....	21	1	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....GGGCCTCTGCAGAGTGGAAG.....	20	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....TCACCTGTTAGAAGCTCC.....	18	1	1	1.00	1	0	1	0	0	0	0	0	0	0	0
.....TCACCTGTTAGAAGCTCTAC.....	20	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....AAAACTTCGCCGCAGCACTGT.....	21	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....TTCACCTGTTAGAAGCTCTACCA.....	23	2	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....GAGTGGAAGCGGAGACGTGCTACT.....	24	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....TTCACCTGTTAGAAGCTCTACA.....	22	1	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....TTTCACCTGTTAGAAGCTCTACCAA.....	25	3	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....TTTCACCTGTTAGAAGCTCTACG.....	23	1	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....TAGAGTTTTCACCTGTTAGAAGCTCTAC.....	28	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....GGGGCCTCTGCAGAGTGGAAGCGGA.....	25	0	1	1.00	1	0	1	0	0	0	0	0	0	0	0
.....GGGGCCTCTGCAGAGTGGT.....	19	1	1	1.00	1	0	0	1	0	0	0	0	0	0	0
.....TTCACCTGTTAGAAGCTCTTT.....	21	2	1	1.00	1	0	0	0	1	0	0	0	0	0	0
.....GAGTTTTCACCTGTTAGAAGCTCTACCA.....	28	2	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....GGGGCCTCTGCAGAGTGGTTT.....	21	3	3	0.33	1	1	0	0	0	0	0	0	0	0	0

Anti-sense strand reads

GCAAAAGGGTCGAGATTTGCTGGAGGTCGTTTTGAAGCGGCGTCGTGACACCCCGGAGACGTCTCACCTTCGCCTCTGCACGATGAGAGAAACAAGAATCTCAAAAGTGGACAATCTTCGAGATGACATGAACGTCTGAACAATAAACGACAAAACACTTTAAAATAACGAGAGAT **********.....((((.((.(((((((.(((((((.(((((((((((((.....)))))).....)))))))))))).))))).)))))))..)).)).)).....**********	Read size	# Mismatch	Hit Count	Total Norm	Total
No data available in table					

Show Alignment With Reads

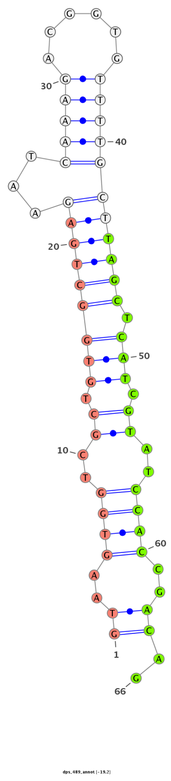
Re-alignment of all predicted orthologs

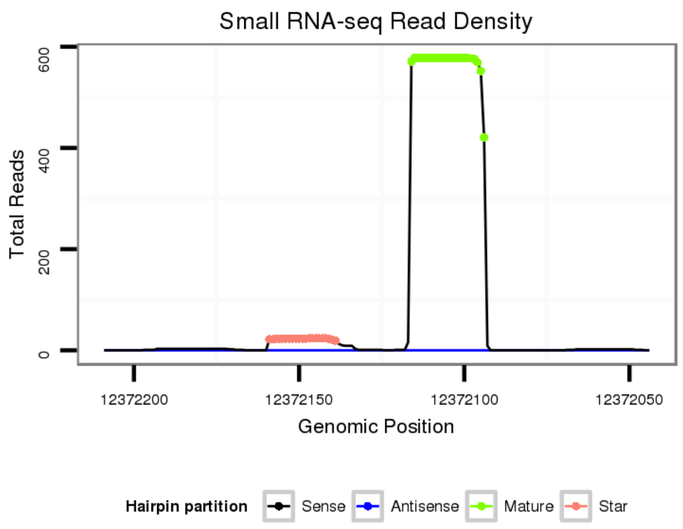
Species	Coordinate	ID	Alignment
dp5	3:15677949-15678124 +	dps_9	CGTTTTCCCAGCTCTAAACGACCTCCAGCAAAACTTCGCCGCAG----------CACTGTGGGGCCTCT---GCAGAGTGG-----AAGC--GGAGACGTGCTACTCTCTTTGTTCTTAGAGTT--------T----------T-CACCTGTTAGAAGC-TCTACTGT------AC-TT-G--CAGA--CTTGTTATTTGCTGTTTTGTGAAATTTTATTGCTCTCTA---
droPer2	scaffold_4:3375401-3375576 -	dpe_28	CGTTTTCCCAGCTCTAAACGACCTCCAGCAAAACTTCGCCGCAG----------CACTGTGGGGCCTCT---GCAGAGTGG-----AAGC--GGAGACGTACTACTCTCTTTGTTCTTAGAGTT--------T----------T-CACCTGTTAGAAGC-TCTACTGT------AC-TT-G--CAGA--CTTGTTATTTGCTGTTTTGTGAAATTTTATTGCTCTCTA---
droWil2	scf2_1100000004510:1723387-1723483 +		CTCTCTGT----------***

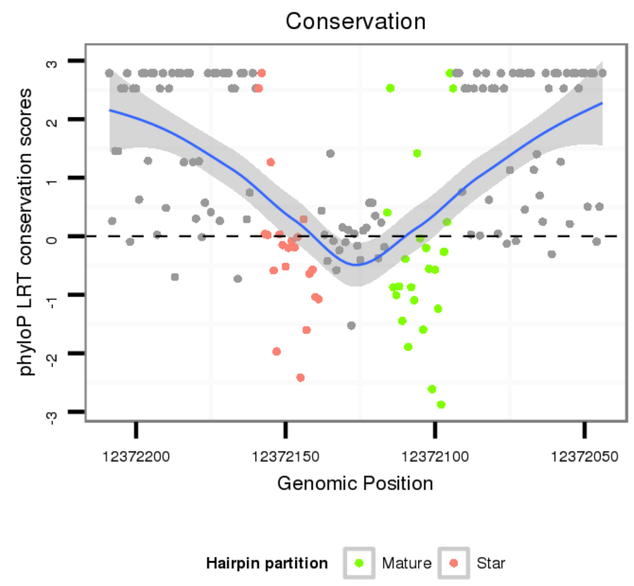
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dps_489	**2:12372094-12372159 -**	**confident**	**Mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

Legend: mature star **mismatch in alignment** mismatch in read

Predicted structure







Show Alternate Folds

Flybase annnotation

intron [Dpse\GA19705-in]; CDS [Dpse\GA19705-cds]; CDS [Dpse\GA19705-cds]; utr3 [utr3_plus_6113]; utr3 [utr3_plus_6114]; utr5 [utr5_plus_10978]; utr5 [utr5_plus_10979]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

TTAGGGACCGCTTGAATGTGGATAAGATCAGGCAGAAGAATGCCAATATGGTAAGTGGTCGCTGTGGCTGAGAATCAAAGACGGTGTTTTGCTTAGCTCATCGTATCCACCGACAGATTGCTCAAGTGCCGACCGTCAACAACAACACGTTCCTGTACTTCAACGT **********((..((((..((.(((((((((...(((((.....)))))))))).))).))..)))).))..))..	Read size	# Mismatch	Hit Count	Total Norm	Total	GSM343916 embryo	M059 embryo	M040 female body	GSM444067 head	M062 head	V112 male body	SRR902012 CNS imaginal disc	SRR902011 testis	M022 male body
.....TAGCTCATCGTATCCACCGACAG.....	23	0	1	399.00	399	194	91	56	19	25	6	5	2	1
.....TAGCTCATCGTATCCACCGACA.....	22	0	1	121.00	121	16	8	30	52	11	4	0	0	0
.....TAGCTCATCGTATCCACCGACAGT.....	24	1	1	118.00	118	26	50	11	19	8	4	0	0	0
.....TAGCTCATCGTATCCACCGACAGC.....	24	1	1	19.00	19	0	14	0	0	5	0	0	0	0
.....TAGCTCATCGTATCCACCGAC.....	21	0	1	17.00	17	0	0	7	4	5	1	0	0	0
.....TAGCTCATCGTATCCACCGACAGA.....	24	0	1	9.00	9	2	5	1	0	1	0	0	0	0
.....AGCTCATCGTATCCACCGACAGT.....	23	1	1	8.00	8	2	1	1	3	1	0	0	0	0
.....TTAGCTCATCGTATCCACCGACA.....	23	0	1	8.00	8	2	1	2	2	1	0	0	0	0
.....TAGCTCATCGTATCCACCGA.....	20	0	1	7.00	7	0	0	1	4	1	1	0	0	0
.....TTAGCTCATCGTATCCACCGACAG.....	24	0	1	7.00	7	6	0	1	0	0	0	0	0	0
.....GTAAGTGGTCGCTGTGGCTGA.....	21	0	1	6.00	6	2	1	2	1	0	0	0	0	0
.....AGCTCATCGTATCCACCGACAG.....	22	0	1	6.00	6	0	1	4	0	1	0	0	0	0
.....GTAAGTGGTCGCTGTGGCTGAGAATC.....	26	0	1	5.00	5	0	2	0	0	2	1	0	0	0
.....TAGCTCATCGTATCCACCGACAC.....	23	1	1	5.00	5	1	4	0	0	0	0	0	0	0
.....GTAAGTGGTCGCTGTGGCTGAG.....	22	0	1	3.00	3	1	1	0	0	0	1	0	0	0
.....GTAAGTGGTCGCTGTGGCT.....	19	0	1	2.00	2	0	0	2	0	0	0	0	0	0
.....GTAAGTGGTCGCTGTGGCTGAGAATCA.....	27	0	1	2.00	2	1	0	1	0	0	0	0	0	0
.....GTAAGTGGTCGCTGTGGCTG.....	20	0	1	2.00	2	0	0	0	1	0	1	0	0	0
.....TAGCTCATCGTATCCACCGACAT.....	23	1	1	1.00	1	1	0	0	0	0	0	0	0	0
.....GTAAGTGGTCGCTGTGGC.....	18	0	1	1.00	1	0	1	0	0	0	0	0	0	0
.....TAGCTCATCGTATCCACCG.....	19	0	1	1.00	1	0	0	0	1	0	0	0	0	0
.....GTAAGTGGTCGCTGTGGT.....	18	1	1	1.00	1	0	0	1	0	0	0	0	0	0
.....TAGCTCATCGTATCCACC.....	18	0	1	1.00	1	0	1	0	0	0	0	0	0	0
.....TGTGGATAAGATCAGGCAGAAGAA.....	24	0	1	1.00	1	0	0	0	0	0	0	0	1	0
.....TGTGGATAAGATCAGGCAGAAGAATGC.....	27	0	1	1.00	1	0	0	0	0	0	0	1	0	0
.....AGCTCATCGTATCCACCGACAGC.....	23	1	1	1.00	1	0	1	0	0	0	0	0	0	0
.....AGCTCATCGTATCCACCGACA.....	21	0	1	1.00	1	0	0	1	0	0	0	0	0	0
.....TTGCTTAGCTCATCGTATCCACCGACA.....	27	0	1	1.00	1	0	0	0	0	0	1	0	0	0
.....TAGCTCATCGTATCCACCGACAA.....	23	1	1	1.00	1	0	1	0	0	0	0	0	0	0
.....TGTGGCTGAGAATCAAAGACGGT.....	23	0	1	1.00	1	0	1	0	0	0	0	0	0	0
.....AAGTGGTCGCTGTGGCTGAGAATC.....	24	0	1	1.00	1	0	0	1	0	0	0	0	0	0
.....AACACGTTCCTGTACTTCAAC..	21	0	1	1.00	1	0	0	0	0	1	0	0	0	0
.....GTAAGTGGTCGCTGTGGCTGAGA.....	23	0	1	1.00	1	0	0	0	0	0	1	0	0	0
.....TAGCTCATCGTATCCACCGACG.....	22	1	1	1.00	1	0	0	0	1	0	0	0	0	0
.....AACAACACGTTCCTGTACTTC.....	21	0	1	1.00	1	0	1	0	0	0	0	0	0	0
.....TAGCTCATCGTATCCACCGACCT.....	23	2	1	1.00	1	0	0	0	1	0	0	0	0	0
.....TGAATGTGGATAAGATCAGGCAGAAG.....	26	0	1	1.00	1	0	0	0	0	0	0	1	0	0

Anti-sense strand reads

AATCCCTGGCGAACTTACACCTATTCTAGTCCGTCTTCTTACGGTTATACCATTCACCAGCGACACCGACTCTTAGTTTCTGCCACAAAACGAATCGAGTAGCATAGGTGGCTGTCTAACGAGTTCACGGCTGGCAGTTGTTGTTGTGCAAGGACATGAAGTTGCA **********((..((((..((.(((((((((...(((((.....)))))))))).))).))..)))).))..))..	Read size	# Mismatch	Hit Count	Total Norm	Total	GSM343916 embryo	M040 female body	GSM444067 head	SRR902011 testis	V112 male body

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
dp5	2:12372044-12372209 -	dps_489	TTAGGGACCGCTTGAATGTGGATAAGATCAGGCAGAAGAATGCCAATATGGTAAGT--GGTCGCTGT----------G-GCTGA-GAATC-AAAGACGGTGTT-TTGCTTAGCTCA--TCGTATCCACCGACAGATTGCTCAAGTGCCGACCGTCAACAACAACACGTTCCTGTACTTCAACGT
droPer2	scaffold_0:8096624-8096789 +	dpe_65	TTCGGGACCGCTTGAATGTGGATAAGATCAGGCAGAAGAATGCCAATATGGTAAGT--GGTCGCTGT----------G-GCTGA-GAATC-AAAGACGGTGTT-TTGCTTAGCTCA--TCGTATCCACCGACAGATTGCTCAAGTGCCGACCGTCAACAACAACACGTTCCTGTACTTCAACGT
droWil2	scf2_1100000004921:855072-855239 -		TTAAGGATCGTTTGAATGTCGAAAAATTAGGCAAAGAATGCCAATTTGGTAAGATCTT-TGAATG----------T-TTTTT-GCTTT-TAGT-TAACGTTTTTAA-ACATGGGATTCTTCTTTTCGACAGATTGCTCAAGTGCCCACTCTCAATAATCATACGTTCCTATACTTCAATGT
droVir3	scaffold_13047:13870896-13871055 +		TCAAGGATCGCTTGAATGTCGAGAAGATCAGACAGAAAAATGCTAATATGGTATGA--TCTGATTTA----------A-AAATA-T-TTT-AAAATCA-CATT--T-C-AAGTTA--CTTTATTCACTTCTAGATTGCTCAGGTGCCAACGGTGAATAATAGAACGTTCCTTTACTTTAATAT
droMoj3	scaffold_6540:26217900-26218060 -		TCAAGGAGCGCTTGAACGTCGAGAAGATCAGGCAAAAGAATGCAAATATGGTAAGA--ATTTGCTCG----------A-AATCA-TATTT-AAACTCA-CACAT----T-AAGCTC--ATATTCTTGCTTCCAGATCGCTCAGGTTCCCACCGTCAACAATAGAACGTTCCTGTACTTTAACAT
droGri2	scaffold_14830:6086385-6086546 -		TCAAGGATCGCTTGAACGTCGAGAAGATCAGAGAAAAGAATGCAAACATGGTAAAA--CTTCACCAT----------A-AGA-- --ATC-ACATCAATCATT-GCCCTAAATTTC--TGTTCTTCGCGCTCAGATCGCTCAGGTGCCGAGCGTAAATAATAGAACATTCCTGTACTTCAATGT
droAna3	scaffold_13340:7418990-7419144 -		TCAAGGACCGCTTGAACGTGGAAAAGATCCGGCAGAAGAATGCCAACTTGGTAGGT--AT--AAATTGGGTCATAGATTTCTTAAATTATACTT---------- ------ ------ ---------- ---------- --ACTTTTGCCGACAGATTGCCCAGGTACCCACAGTCAACAACAACACTTCCTGTACTTCAACGT
droBip1	scf7180000396708:1434346-1434513 +		TCAAGGACCGCTTGAACGTGGAGAAGATCCGGCAGAAGAATGCCAATTTGGTAAGTTCAT--AAATCAAGTCATAGCTTTCTAGAAGGATACTTACCA-GCCTC-TTTTC-GGAT-------- ---------- --------GGGGACAGATTGCCCAGGTACCCACAGTCAACAACAACACATTCCTGTACTTCAACGT
droKik1	scf7180000302475:80107-80270 -		TCAAGGACCGCTTGAATGTTGAGAAGATCCGACAGAAGAATGCCAATTTGGTAGGT--ATCTCCTAG----------A-ACTAA---CCAAAGATTAAGAGT-CGCTAATTGAA-GACCTTCATGCTTGCAGATTGCCCAAGTGCCCAGTGTCAACAACAACACCTTCCTGTACTTCAATGT
droFic1	scf7180000453796:120985-121149 -		TTAAGGACCGCTTGAATGTGGATAAGATCAGGCAGAAGAATGCTAATTTGGTGTGT--TT-CTCTTT----------A-ACAATTTATTT-AAATTCAATATT-TTCTAATTAAA--GCATTGTTACCAACAGATTGCTCAGGTGCCCAGTGTCAACAACAGCACCTTCCTGTACTTCAATAT
droEle1	scf7180000486474:1479887-1480050 +		TCAAGGACCGCTTGAACGTGGATAAGATCAGACAGAAAAATGCCAACTTGGTAAGG--ATCTACTTC----------A-GCTAT-TTTTT-CAGTTCGT-CCTTTTTGC-AAACAA--TACTTTTTCACACAGATTGCTCAAGTGCCCAGTGTCAACAACAACACCTTCCTGTACTTCAATGT
droRho1	scf7180000778413:22560-22724 -		TCAAGGACCGCTTGAATGTGGATAAGATCAGACAGAAGAATGCCAACTTGGTGAGG--ATCTACATA----------A-GTATT-TAATT-AGGTTTGATATT-TTCTAACTGAA--CCATCTGTATCAACAGATTGCCAGGTGCCCAGTGTCAACAACAATACCTTTCTCTACTTCAATGT
droBia1	scf7180000299102:394622-394781 +		TCAAGGACCGCTTGAATGTGGATAAGATCAGGCAGAAGAATGCCAATTTGGTGAGC--GTCCACTTA----------A-ACCACTTATTT-AA-T-TA-TATT-T--T-AATTTA--ATCTTTCTGACCCCAGATTGCTCAGGTGCCCAGTGTCAACAACAACACCTTCCTGTACTTCAACGT
droTak1	scf7180000415580:214042-214202 -		TCAAGGACCGCTTGAATGTGGATAAGATCAGGCAGAAGAATGCCAATTTGGTAAGG--ATTTAGTTA----------T-TTTTA-TATTT-TCATTT------ATTTCTAATTTGT--TTGTTTTATCCCCCAGATTGCTCAGGTGCCCAGTGTCAACAACAACACCTTCCTGTACTTCAACGT
droEug1	scf7180000409557:68501-68658 -		TCAAGGATCGATTGAATGTGGATAAGATCAGGCAGAAGAATGCCAATTTGGTAAGA--CATTACTTA----------A-GCTTT-TATTT-GG--------TT-TTGGCAAATTAA--CCATTATGGCCCACAGATTGCTCAGGTGCCCAGTGTCAACAACAACACCTTCCTGTACTTTAACGT
dm3	chr3R:12461530-12461693 +		TCAAGGACCGCTTAAATGTGGACAAGATCAGGCAGAAAAATGCAAATTTGGTGAGC--TT-TACATG----------A-GCTTA-TAATC-AAAT-GGAAATTTTTTAC-AAATCA--CCATTCTTTTCAAAAGATTGCCCAGGTGCCCAGTGTCAACAACAACACTTTCCTGTACTTCAACGT
droSim2	3r:8788525-8788688 -		TCAAGGACCGCTTAAATGTGGACAAGATCAGGCAGAAAAATGCTAATTTGGTGAGC--TT-TACATG----------A-GCTTA-TATTC-AAAT-GGAAATTTTTTAC-AATTAA--CCATTTATTTGAAAAGATTGCCCAGGTGCCCAGTGTTAACAACAACACTTTCCTGTACTTCAACGT
droSec2	scaffold_12:1685871-1686034 -		TCAAGGACCGCTTAAATGTGGACAAGATCAGGCAGAAAAATGCTAATTTGGTGAGC--TT-TACATG----------A-GCTTA-TATTC-AAAT-GGAAATTTTTTAC-AAATAA--CCATTCTTTTTGAAAAGATTGCCCAGGTGCCCAGTGTCAACAACAACACTTTCCTGTACTTCAACGT
droYak3	3R:11929890-11930052 -		TCAAGGATCGCTTAAATGTGGATAAGATCAAGCAGAAAAATGCCAATTTGGTGAGG--CT-TA-ATG----------ACTCTTT-TACTT-CAAT-GAACATATTTTAC-AATTTA--GATTTTACATTTTAGATTGCCCAGGTGCCCAGTGTCAACAACAACACCTTCCTGTACTTCAACGT
droEre2	scaffold_4770:9173011-9173174 -		TCAAGGACCGCTTAAATGTGGACAAGATCCGGCAGAAAAATGCAAATTTGGTGAGG--CG-TACATG----------A-CGTTT-TACTT-CAAT-AAACATTTTTTAC-AATCTG--CCATTCTTGTCAAAAGATTGCCCAGGTGCCCAGTGTCAACAACAACACCTTCCTGTACTTCAACGT

Generated: 09/08/2015 at 06:08 PM

	PASS/FAIL
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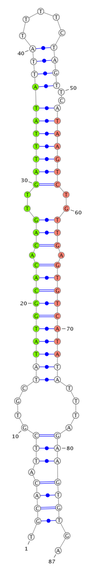
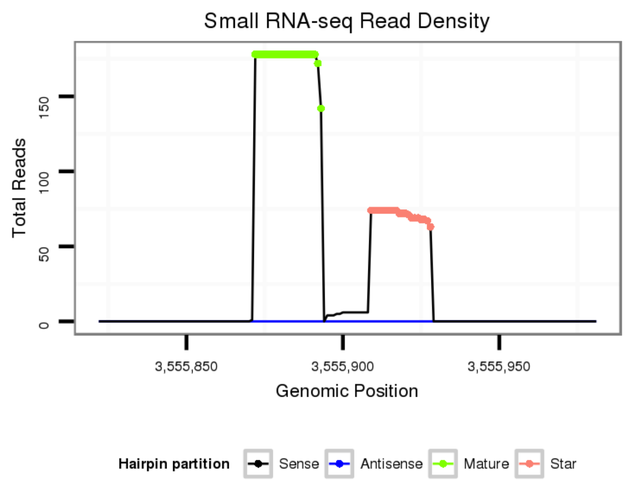
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	2
rescue.candidate	0

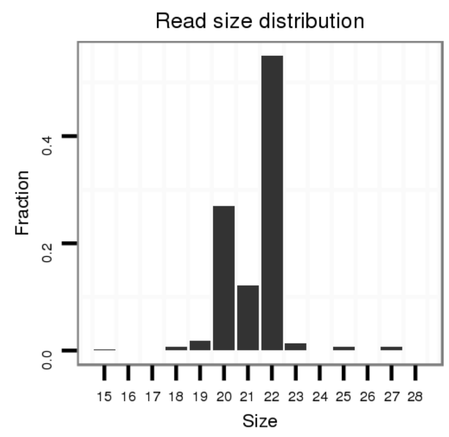
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dps_23	**4_group4:3555872-3555931 +**	**confident**	**Testes-restricted**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

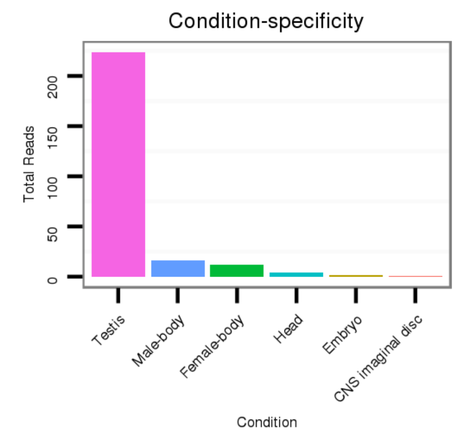
Legend: mature star mismatch in alignment mismatch in read

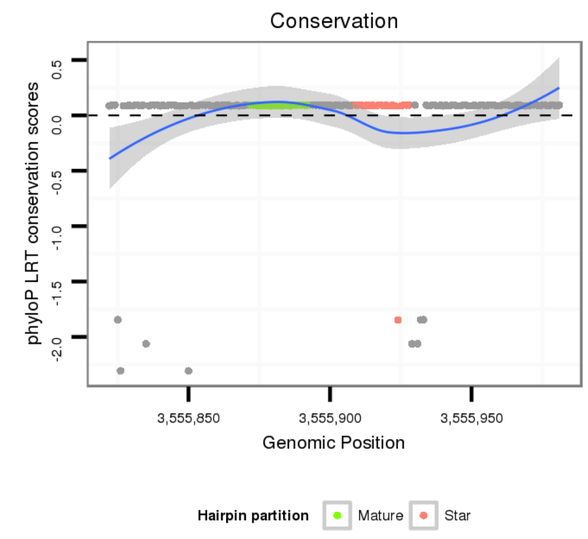
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

mature	star
1. dps-mir-2511-1 4_group4:3552572-3552593 + 2. dps-mir-2511-2 4_group4:3554152-3554173 + 3. dps_23 4_group4:3555872-3555893 +	

Sense Strand Reads

hide 3p reads show mid mismatch reads

GTATGCGTGTTGATGAAAGTGTTTCCCCGACCAAATGCACATTCGTGCTATATGGCACACAGTTGATTTATATTATTTTCTAGTTCATAAGTCTGTTGAGTGTCATATATTTAGAAGTGTGATGCATCCTCATGTATCCTTAGCATGGCTTAGATCAAGA **********.((((.(((....((((((((((.(((..(((((((((((.....))))..)))))))..))))..))))))))))....)))))))..**********	Read size	# Mismatch	Hit Count	Total Norm	Total	SRR902011 testis	V112 male body	M040 female body	SRR902010 ovaries	M062 head	SRR902012 CNS imaginal disc	M022 male body	M059 embryo	GSM444067 head	GSM343916 embryo
.....TAAGTCTGTTGAGTGTCATAG.....	21	1	3	322.67	968	901	44	10	3	1	6	0	0	3	0
.....TATGGCACACAGTTGATTTATA.....	22	0	3	141.00	423	391	2	15	0	10	1	0	4	0	0
.....TAAGTCTGTTGAGTGTCATA.....	20	0	1	63.00	63	52	10	1	0	0	0	0	0	0	0
.....TATGGCACACAGTTGATTTAT.....	21	0	3	30.67	92	63	13	13	0	2	0	1	0	0	0
.....TAAGTCTGTTGAGTGTCATAA.....	21	1	1	19.00	19	18	1	0	0	0	0	0	0	0	0
.....TATGGCACACAGTTGATTTATAA.....	23	1	3	16.67	50	48	0	2	0	0	0	0	0	0	0
.....TAAGTCTGTTGAGTGTCATT.....	20	1	1	7.00	7	3	4	0	0	0	0	0	0	0	0
.....TAAGTCTGTTGAGTGTCATC.....	20	1	1	6.00	6	6	0	0	0	0	0	0	0	0	0
.....TATGGCACACAGTTGATTTA.....	20	0	3	6.00	18	17	0	1	0	0	0	0	0	0	0
.....TAAGTCTGTTGAGTGTCAT.....	19	0	1	4.00	4	4	0	0	0	0	0	0	0	0	0
.....TAAGTCTGTTGAGTGTCATAGT.....	22	2	3	4.00	12	9	3	0	0	0	0	0	0	0	0
.....TAAGTCTGTTGAGTGTCATAGG.....	22	2	3	3.33	10	10	0	0	0	0	0	0	0	0	0
.....TAAGTCTGTTGAGTGTCATATAA.....	23	1	1	3.00	3	3	0	0	0	0	0	0	0	0	0
.....TATGGCACACAGTTGATTTATAAA.....	24	2	3	3.00	9	8	0	1	0	0	0	0	0	0	0
.....TATGGCACACAGTTGATTTATC.....	22	1	3	2.33	7	6	1	0	0	0	0	0	0	0	0
.....TATTTTCTAGTTCATAAGTCTGT.....	23	0	3	2.33	7	7	0	0	0	0	0	0	0	0	0
.....TAAGTCTGTTGAGTGTCATG.....	20	1	1	2.00	2	1	1	0	0	0	0	0	0	0	0
.....TATTTTCTAGTTCATAAGTCTGTTGAG.....	27	0	3	2.00	6	6	0	0	0	0	0	0	0	0	0
.....TAAGTCTGTTGAGTGTCATAGCC.....	23	3	3	1.67	5	5	0	0	0	0	0	0	0	0	0
.....AAGTCTGTTGAGTGTCATAG.....	20	1	3	1.67	5	5	0	0	0	0	0	0	0	0	0
.....TAAGTCTGTTGAGTGTCATATT.....	22	1	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....TAAGTCTGTTGAGTGTCATCCG.....	22	3	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....TAAGTCTGTTGAGTGTCATCC.....	21	2	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....TCTAGTTCATAAGTCTGTTGAGTGT.....	25	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....TAAGTCTGTTGAGTGTCA.....	18	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....ATATGGCACACAGTTGATTTATA.....	23	0	3	1.00	3	3	0	0	0	0	0	0	0	0	0
.....TTTCTAGTTCATAAGTCTGTTGA.....	23	0	3	1.00	3	3	0	0	0	0	0	0	0	0	0
.....ATGGCACACAGTTGATTTATAAAT.....	24	3	3	1.00	3	3	0	0	0	0	0	0	0	0	0
.....TAAGTCTGTTGAGTGTCATAGG.....	22	2	3	0.67	2	2	0	0	0	0	0	0	0	0	0
.....TCATAAGTCTGTTGAGTGTCATAGT.....	25	2	3	0.67	2	2	0	0	0	0	0	0	0	0	0
.....TATGGCACACAGTTGATTTATCA.....	23	2	3	0.67	2	2	0	0	0	0	0	0	0	0	0
.....TATGGCACACAGTTGATT.....	18	0	3	0.67	2	1	0	0	0	0	0	1	0	0	0
.....TATTTTCTAGTTCATAAGTCTGTA.....	24	1	3	0.67	2	2	0	0	0	0	0	0	0	0	0
.....TAAGTCTGTTGAGTG.....	15	0	3	0.67	2	2	0	0	0	0	0	0	0	0	0
.....TATGGCACACAGTTGATTTATATTATC.....	27	1	3	0.67	2	2	0	0	0	0	0	0	0	0	0
.....TATGGCACACAGTTGATTTATATTA.....	25	0	3	0.67	2	2	0	0	0	0	0	0	0	0	0
.....ATATGGCACACAGTTGATTTAT.....	22	0	3	0.67	2	0	1	1	0	0	0	0	0	0	0
.....TATGGCACACAGTTGATTTAA.....	21	1	3	0.67	2	2	0	0	0	0	0	0	0	0	0
.....TATGGCACACAGTTGATTT.....	19	0	3	0.67	2	0	1	1	0	0	0	0	0	0	0
.....TAAGTCTGTTGAGTGTCATCG.....	21	2	3	0.67	2	2	0	0	0	0	0	0	0	0	0
.....TATGGCACACAGTTGA.....	16	0	3	0.33	1	1	0	0	0	0	0	0	0	0	0
.....ATGGCACACAGTTGATTTAT.....	20	0	3	0.33	1	0	0	1	0	0	0	0	0	0	0
.....TGGCACACAGTTGATTTATAA.....	21	1	3	0.33	1	1	0	0	0	0	0	0	0	0	0
.....TTCTAGTTCATAAGTCTGTTG.....	21	0	3	0.33	1	1	0	0	0	0	0	0	0	0	0
.....TATGGCACACAGTTGATTTATATTATTT.....	28	0	3	0.33	1	1	0	0	0	0	0	0	0	0	0
.....ATGGCACACAGTTGATTTATAT.....	22	0	3	0.33	1	1	0	0	0	0	0	0	0	0	0
.....TTTTCTAGTTCATAAGTCTGTTGAG.....	25	0	3	0.33	1	1	0	0	0	0	0	0	0	0	0
.....AAGTCTGTTGAGTGTCATAGT.....	21	2	3	0.33	1	0	1	0	0	0	0	0	0	0	0
.....ATGGCACACAGTTGATTTATA.....	21	0	3	0.33	1	0	0	1	0	0	0	0	0	0	0
.....ATATGGCACACAGTTGATTTATATTAT.....	27	0	3	0.33	1	1	0	0	0	0	0	0	0	0	0
.....TATGGCACACAGTTGATTTATT.....	22	1	3	0.33	1	0	0	1	0	0	0	0	0	0	0
.....TATGGCACACAGTTGATTTATAAAT.....	25	3	3	0.33	1	1	0	0	0	0	0	0	0	0	0
.....ATGGCACACAGTTGATTTATC.....	21	1	3	0.33	1	0	0	1	0	0	0	0	0	0	0
.....TAAGTCTGTTGAGTGTCATAGTC.....	23	3	3	0.33	1	0	1	0	0	0	0	0	0	0	0

Anti-sense strand reads

CATACGCACAACTACTTTCACAAAGGGGCTGGTTTACGTGTAAGCACGATATACCGTGTGTCAACTAAATATAATAAAAGATCAAGTATTCAGACAACTCACAGTATATAAATCTTCACACTACGTAGGAGTACATAGGAATCGTACCGAATCTAGTTCT **********.((((.(((....((((((((((.(((..(((((((((((.....))))..)))))))..))))..))))))))))....)))))))..**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M040 female body

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
dp5	4_group4:3555822-3555981 +	dps_23	GTATGCGTGTTGATGAAAGTGTTTCCCCGACCAAATGCACATTCGTGCTATATGGCACACAGTTGATTTATATTATTTTCTAGTTCATAAGTCTGTTGAGTGTCATATATTTAGAAGTGTGATGCATCCTCATGTATCCTTAGCATGGCTTAGATCAAGA
droPer2	scaffold_9415:491-650 +	dpe_39	GTAACCGTGTTGACGAAAGTGTTTCCCCCACCAAATGCACATTCGTGCTATATGGCACACAGTTGATTTATATTATTTTCTAGTTCATAAGTCTGTTGAGTGCCATACAGCAAGAAGTGTGATGCATCCTCATGTATCCTTAGCATGGCTTAGATCAAGA

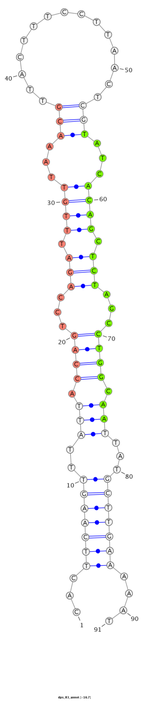
Generated: 09/08/2015 at 08:39 PM

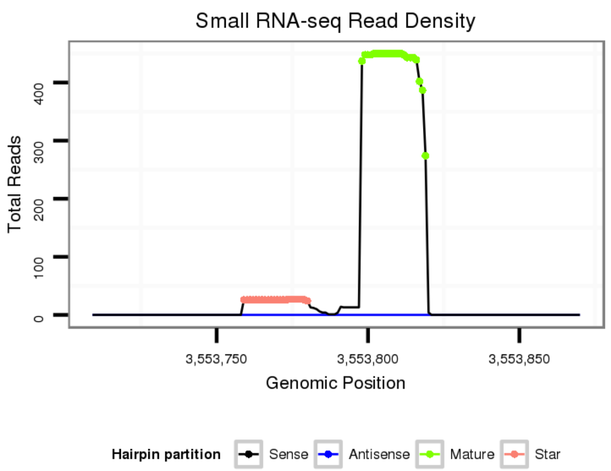
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	4
rescue.candidate	0

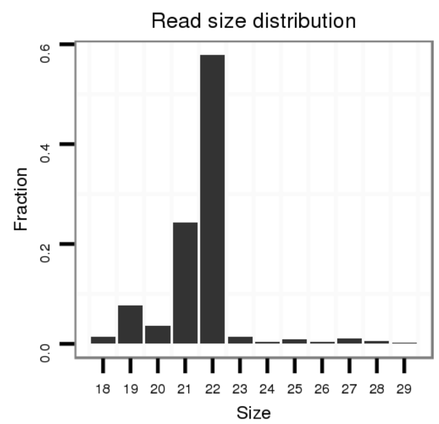
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dps_83	**4_group4:3553759-3553820 +**	**confident**	**Testes-restricted**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

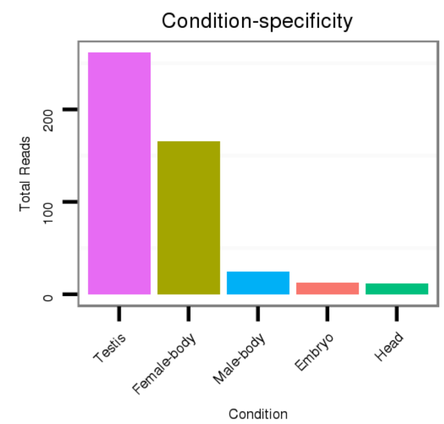
Legend: mature star mismatch in alignment mismatch in read

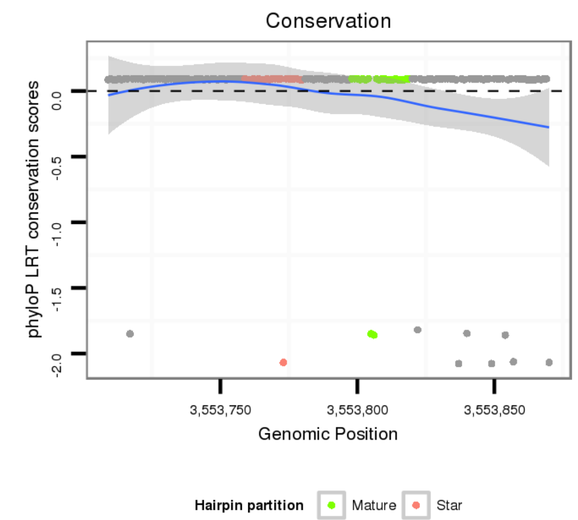
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

CTCCACAAGTAATGATTAAATGAAAATTAAGCAAACACTTCAAGTTTATTACCAGTCCAGATTTGTTAAACGTTACTTTCCTTAACTCGTATCACAGCTCTAGCCTGGCAATTATGCTTGAAAAATACATCTTTTTAGAAAATTTCGATATAAGCGCACAAG **********...(((((((..(((.((((...(((.((((...(((.....)))...)))).)))...)))).)))...)))))))....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	SRR902011 testis	M040 female body	M022 male body	M062 head	M059 embryo	V112 male body	GSM343916 embryo	GSM444067 head	SRR902010 ovaries
.....TATCACAGCTCTAGCCTGGCAA.....	22	0	1	262.00	262	149	91	2	4	9	6	1	0	0
.....TATCACAGCTCTAGCCTGGCA.....	21	0	1	107.00	107	61	38	2	4	1	1	0	0	0
.....TATCACAGCTCTAGCCTGG.....	19	0	1	37.00	37	10	22	4	1	0	0	0	0	0
.....TATCACAGCTCTAGCCTGGCAT.....	22	1	1	12.00	12	10	2	0	0	0	0	0	0	0
.....ACCAGTCCAGATTTGTTAAACG.....	22	0	1	11.00	11	10	0	0	0	0	1	0	0	0
.....TATCACAGCTCTAGCCTGGC.....	20	0	1	10.00	10	3	4	2	1	0	0	0	0	0
.....TATCACAGCTCTAGCCTGGCAAA.....	23	1	1	9.00	9	7	0	0	1	0	0	0	1	0
.....TATCACAGCTCTAGCCTGGCAAAA.....	24	2	1	7.00	7	7	0	0	0	0	0	0	0	0
.....ATCACAGCTCTAGCCTGGCA.....	20	0	1	6.00	6	1	5	0	0	0	0	0	0	0
.....ATCACAGCTCTAGCCTGGCAA.....	21	0	1	5.00	5	0	5	0	0	0	0	0	0	0
.....TAACTCGTATCACAGCTCTAGCCTGGC.....	27	0	1	5.00	5	5	0	0	0	0	0	0	0	0
.....TATCACAGCTCTAGCCTGGCAAT.....	23	0	1	4.00	4	3	0	0	0	0	0	0	1	0
.....ACCAGTCCAGATTTGTTAAACGTTA.....	25	0	1	4.00	4	4	0	0	0	0	0	0	0	0
.....TATCACAGCTCTAGCCTG.....	18	0	1	4.00	4	0	0	4	0	0	0	0	0	0
.....ACCAGTCCAGATTTGTTAAACGTTACTT.....	28	0	1	3.00	3	2	0	0	0	0	1	0	0	0
.....ACCAGTCCAGATTTGTTAAACGTT.....	24	0	1	2.00	2	0	0	0	0	0	2	0	0	0
.....TAACTCGTATCACAGCTCTAG.....	21	0	1	2.00	2	2	0	0	0	0	0	0	0	0
.....TAACTCGTATCACAGCTCTAGC.....	22	0	1	2.00	2	2	0	0	0	0	0	0	0	0
.....TATCACAGCTCTAGCCTGGCATA.....	23	2	1	2.00	2	1	0	1	0	0	0	0	0	0
.....ACCAGTCCAGATTTGTTAAACGTTAC.....	26	0	1	2.00	2	2	0	0	0	0	0	0	0	0
.....TTAACTCGTATCACAGCTCTAGC.....	23	0	1	2.00	2	2	0	0	0	0	0	0	0	0
.....TATCACAGCTCTAGCCTGGCAAG.....	23	1	1	2.00	2	2	0	0	0	0	0	0	0	0
.....TATCACAGCTCTAGCCTGGT.....	20	1	1	2.00	2	1	1	0	0	0	0	0	0	0
.....TTAACTCGTATCACAGCTCTC.....	21	1	1	2.00	2	2	0	0	0	0	0	0	0	0
.....ACCAGTCCAGATTTGTTAAAC.....	21	0	1	2.00	2	0	0	0	0	2	0	0	0	0
.....ACAGCTCTAGCCTGGCAA.....	18	0	2	2.00	4	1	1	0	2	0	0	0	0	0
.....ACCAGTCCAGATTTGTTAAACGT.....	23	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....ATCACAGCTCTAGCCTGGCAAAA.....	23	2	1	1.00	1	0	1	0	0	0	0	0	0	0
.....TATCACAGCTCTAGCCTGGCC.....	21	1	1	1.00	1	0	0	1	0	0	0	0	0	0
.....ACCAGTCCAGATTTGTTAG.....	19	1	1	1.00	1	1	0	0	0	0	0	0	0	0
.....TATCACAGCTCTAGCCTGGA.....	20	1	1	1.00	1	0	0	0	0	0	1	0	0	0
.....TATCACAGCTCTAGCCTGGCAG.....	22	1	1	1.00	1	0	0	0	1	0	0	0	0	0
.....TTAACTCGTATCACAGCTCTAG.....	22	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....TATCACAGCTCTAGCCTGGCAACA.....	24	2	1	1.00	1	1	0	0	0	0	0	0	0	0
.....TATCACAGCTCTAGCCTGGCAATCC.....	25	2	1	1.00	1	1	0	0	0	0	0	0	0	0
.....ACCAGTCCAGATTTGTTAAA.....	20	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....TTAAACGTTACTTTCCTT.....	18	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....TATCACAGCTCTAGCCTGGCCG.....	22	2	1	1.00	1	1	0	0	0	0	0	0	0	0
.....TAACTCGTATCACAGCTCTAGCCTGGCAA.....	29	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....TATCACAGCTCTAGCCTGGCT.....	21	1	1	1.00	1	1	0	0	0	0	0	0	0	0
.....CAGCTCTAGCCTGGCAAC.....	18	1	3	0.33	1	0	0	0	1	0	0	0	0	0

Anti-sense strand reads

GAGGTGTTCATTACTAATTTACTTTTAATTCGTTTGTGAAGTTCAAATAATGGTCAGGTCTAAACAATTTGCAATGAAAGGAATTGAGCATAGTGTCGAGATCGGACCGTTAATACGAACTTTTTATGTAGAAAAATCTTTTAAAGCTATATTCGCGTGTTC **********...(((((((..(((.((((...(((.((((...(((.....)))...)))).)))...)))).)))...)))))))....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M040 female body	GSM343916 embryo

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
dp5	4_group4:3553709-3553870 +	dps_83	CTCCACAAGTAATGATTAAATGAAAATTAAGCAAACACTTCAAGTTTATTACCAGTCCAGATTTGTTAAACGTTACTTTCCTTAACTCGTATCACAGCTCTAGCCTGGCAATTATGCTTGAAAAATACATCTTTTTAGAAAATTTCGATATAAGCGCACAAG
droPer2	scaffold_10:2584525-2584686 +	dpe_330	CTCCACAAATAATGATTAAATGAAAATTAAGCAAACACTTCAAGTTTATTACCAGTCCAGATTTTTTTAAACGTTACTTTCCTTAACTCGTATCACAATTCTAGCCTGGCAATTTTGCTTGAAAAATAGCTCCTTTTAGAACATTTTGAGATAAGCGCACAAT

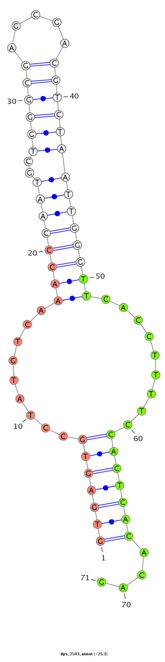
Generated: 09/08/2015 at 08:37 PM

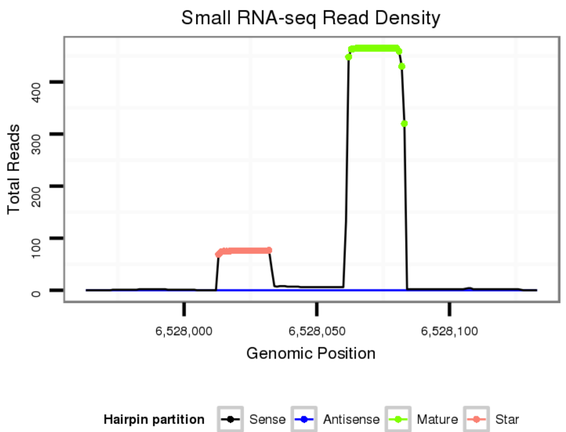
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	1

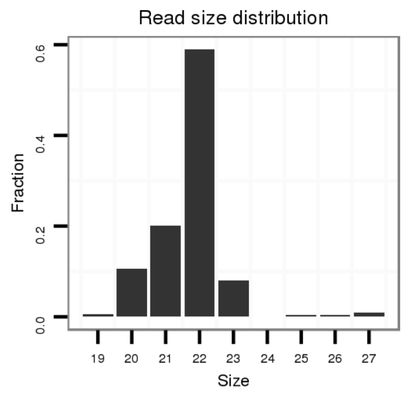
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dps_2543	**XL_group1a:6528013-6528083 +**	**confident**	**Mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

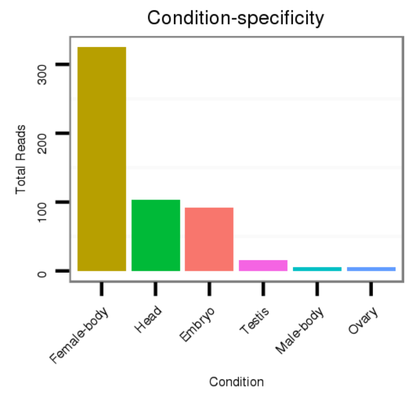
Legend: mature star mismatch in alignment mismatch in read

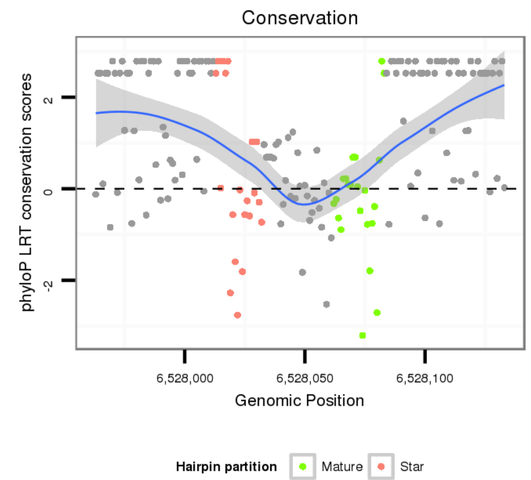
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dpse\GA18237-in]; CDS [Dpse\GA18237-cds]; CDS [Dpse\GA18237-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

GGCCGGTTGCGTGGCCTTGTTCGATCTGAGGAGCCAAAAGGAGATCTTCTGTGAGTGCCTATGTCAAACCCAATGCTGGGCGAGCGACGTCTAATTGGGTTCACCTTTTCCACTCACACAGCCAACAATGAGCATCCCGAGGTGATACAGTCGGCCAGTTGGCGCGAGGAT **********(((((((.....(((((((..((((((.....)))))))))))))).....)))))))....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M040 female body	M062 head	M059 embryo	GSM343916 embryo	SRR902011 testis	GSM444067 head	V112 male body	SRR902010 ovaries
.....TTCACCTTTTCCACTCACACAG.....	22	0	1	260.00	260	148	47	19	25	12	5	1	3
.....GTTCACCTTTTCCACTCACACA.....	22	0	1	61.00	61	43	8	6	2	0	2	0	0
.....TTCACCTTTTCCACTCACACA.....	21	0	1	45.00	45	28	9	2	0	3	2	1	0
.....GTTCACCTTTTCCACTCACACAG.....	23	0	1	44.00	44	25	9	6	1	1	2	0	0
.....GTGAGTGCCTATGTCAAACC.....	20	0	1	36.00	36	16	5	13	2	0	0	0	0
.....GTGAGTGCCTATGTCAAACCC.....	21	0	1	32.00	32	20	4	8	0	0	0	0	0
.....GTTCACCTTTTCCACTCACAC.....	21	0	1	20.00	20	10	5	2	0	0	0	1	2
.....TCACCTTTTCCACTCACACAG.....	21	0	1	13.00	13	13	0	0	0	0	0	0	0
.....TTCACCTTTTCCACTCACAC.....	20	0	1	9.00	9	5	3	1	0	0	0	0	0
.....TTCACCTTTTCCACTCACACCA.....	22	2	1	7.00	7	6	0	1	0	0	0	0	0
.....GTTCACCTTTTCCACTCACA.....	20	0	1	5.00	5	5	0	0	0	0	0	0	0
.....TTCACCTTTTCCACTCACACAGT.....	23	1	1	5.00	5	2	1	0	0	0	2	0	0
.....TGAGTGCCTATGTCAAACCC.....	20	0	1	4.00	4	3	0	1	0	0	0	0	0
.....AATGCTGGGCGAGCGACGTCTAATTGG.....	27	0	1	4.00	4	2	0	1	0	0	0	1	0
.....TCACCTTTTCCACTCACACA.....	20	0	1	3.00	3	3	0	0	0	0	0	0	0
.....GTTCACCTTTTCCACTCACACC.....	22	1	1	3.00	3	1	0	2	0	0	0	0	0
.....GTTCACCTTTTCCACTCACACT.....	22	1	1	2.00	2	0	0	0	0	2	0	0	0
.....TTCACCTTTTCCACTCACACT.....	21	1	1	2.00	2	2	0	0	0	0	0	0	0
.....TTCACCTTTTCCACTCACACAA.....	22	1	1	2.00	2	1	0	1	0	0	0	0	0
.....TTCACCTTTTCCACTCACACAGA.....	23	1	1	2.00	2	1	0	0	0	1	0	0	0
.....GTTCACCTTTTCCACTCACACAGT.....	24	1	1	1.00	1	0	1	0	0	0	0	0	0
.....GTGGCCTTGTTCGATCTGAGG.....	21	0	1	1.00	1	1	0	0	0	0	0	0	0
.....GTGAGTGCCTATGTCAAACCCA.....	22	0	1	1.00	1	1	0	0	0	0	0	0	0
.....CAACAATGAGCATCCCGAGGTGAT.....	24	0	1	1.00	1	1	0	0	0	0	0	0	0
.....TTCACCTTTTCCACTCACA.....	19	0	1	1.00	1	0	1	0	0	0	0	0	0
.....TTCACCTTTTCCACTCACACAC.....	22	1	1	1.00	1	0	1	0	0	0	0	0	0
.....TGCCTATGTCAAACCCAATGCTGGGC.....	26	0	1	1.00	1	0	0	1	0	0	0	0	0
.....TTCACCTTTTCCACTCACACCT.....	22	2	1	1.00	1	0	0	1	0	0	0	0	0
.....TGCTGGGCGAGCGACGTCTAATTGGGT.....	27	0	1	1.00	1	0	0	0	0	0	0	1	0
.....GTTCACCTTTTCCACTCACACAC.....	23	1	1	1.00	1	0	1	0	0	0	0	0	0
.....TCGATCTGAGGAGCCAAAAGGA.....	22	0	1	1.00	1	1	0	0	0	0	0	0	0
.....ATACAGTCGGCCAGTTGGCGC.....	21	0	1	1.00	1	1	0	0	0	0	0	0	0
.....ACCTTTTCCACTCACACAG.....	19	0	1	1.00	1	0	0	1	0	0	0	0	0
.....CACCTTTTCCACTCACACAG.....	20	0	1	1.00	1	1	0	0	0	0	0	0	0
.....TGAGTGCCTATGTCAAACCCAATGC.....	25	0	1	1.00	1	1	0	0	0	0	0	0	0
.....GTTCACCTTTTCCACTCACACAA.....	23	1	1	1.00	1	1	0	0	0	0	0	0	0
.....GATACAGTCGGCCAGTTGGCG.....	21	0	1	1.00	1	0	0	0	0	0	0	1	0
.....TTCACCTTTTCCACTCACACCAA.....	23	3	1	1.00	1	0	0	1	0	0	0	0	0
.....GAGTGCCTATGTCAAACCC.....	19	0	1	1.00	1	0	1	0	0	0	0	0	0
.....TTCACCTTTTCCACTCACACAGC.....	23	0	1	1.00	1	0	1	0	0	0	0	0	0
.....CCAATGCTGGGCGAGCGACGTCTAAT.....	26	0	1	1.00	1	0	0	1	0	0	0	0	0
.....CCAACAATGAGCATCCCGAGGTGAT.....	25	0	1	1.00	1	0	0	0	0	0	0	1	0
.....TGGGTTCACCTTTTCCACTCACACA.....	25	0	1	1.00	1	1	0	0	0	0	0	0	0
.....TTCACCTTTTCCACTCACACAAAA.....	24	3	2	0.50	1	0	0	1	0	0	0	0	0

Anti-sense strand reads

CCGGCCAACGCACCGGAACAAGCTAGACTCCTCGGTTTTCCTCTAGAAGACACTCACGGATACAGTTTGGGTTACGACCCGCTCGCTGCAGATTAACCCAAGTGGAAAAGGTGAGTGTGTCGGTTGTTACTCGTAGGGCTCCACTATGTCAGCCGGTCAACCGCGCTCCTA **********(((((((.....(((((((..((((((.....)))))))))))))).....)))))))....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M040 female body

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
dp5	XL_group1a:6527963-6528133 +	dps_2543	GGCCGGTTGCGTGGCCTTGTTCGATCTGAGGAGCCAAAAGGAGATCTTCTGTGAGTGCC-TATG----------TCAAACCCAATGCTG----------GGC--------G----AGC------GACGTCTAATTGGGTTCA-CCTTTT----------CC-A-CTCA----CA---CAGCCAACAATGAGCATCCCGAGGTGATACAGTCGGCCAGTTGGCGCGAGGAT
droPer2	scaffold_25:785638-785808 -	dpe_1260	GGCCGGTTGCGTGGCCTTGTTCGATCTGAGGAGCCAAAAGGAGATCTTCTGTGAGTGCC-TATG----------TCAAACCCAATGCTG----------GGC--------G----AGC------GCCGTCTAATTGGGTTCA-CCTTTT----------CC-A-CTCA----CA---CAGCCAACAATGAGCATCCCGAGGTGATACAGTCGGCCAGTTGGCGCGAGGAT
droWil2	scf2_1100000004401:904031-904195 -		TGCAGGATGTGTGGCACTCTTTGATCTGAGCGTGCAGAAGGAGATATTCTGTAAGTTTT-AAACATTTT----------ATTCTC---T----------GCAT--------GGT-TCCCTGTTGTA--ATCCATTTGA-TT----------T-T-TTTT----TC---CAGCGAACAATGAGCATCCGGAGGTCATACAATCGGCCAGTTGGCGGGAGGAC
droVir3	scaffold_12928:4070365-4070529 +		GGCTGGCTGTGTGGCGCTCTTCGATGTTGCTGCCCAAAAGGAGATCTTCTGTGAGTAAT-G----------CGAGACGCAATGCTT----------AG-------T----TT------T----TTCGACTTACATTAATCTGCCATTCATAT-AATC----TG---CAGCAAACAATGAGCATCCGAGGTGATACAATCGGCCAGTTGGCGCGAAGAT
droMoj3	scaffold_6359:662123-662289 +		GGCTGGCTGTGTGGCGCTCTTCGATATTGCGGCCCAAAAGGAATCTTCTGTGAGTAGCACAAAAC----------TT----------G----------GGGATTCGAAT-TGTA---ACTGTAGCTAATT-GA-CACGTG-CTT----T-T-CTCT----C---CAGCTAACAATGAACATCCCGAGGTAATTCAATCCGCCAGCTGGCGAGAGGAT
droGri2	scaffold_14853:596522-596685 -		AGCCGGTTGTGTGGCACTTTTGATATTGCCGCCCAGAAGGAAATATTCTGTGAGTAAA-ATCAAT----------TTCTAATTTTAT-GTCTATA-TA----------AAAA--------AAA-TTTC--------T-A-----TTT----T-T-CCTG----TG---CAGCAAACAATGAGCACCGGAAGTATACAATCGGTCAGCTGGCGCGAGGAT
droAna3	scaffold_13335:2206581-2206743 -		AGCCGGTTGTGTGGCTCTCTTCGATCTAAGCGCCCAAAAGGAGATATTCTGTAAGTGCCTTG----------CCAGAGTC----CTT--CGA--------GAA-A--AT-AATATTAAAG-AG-T-----CTC----T-T-G--CCA---TCCTTTAGCTAACAATGAACATCCGAGGTCATACAGTCGGCCAGTTGGCGCGAAGAT
droBip1	scf7180000393717:38592-38753 -		AGCCGGTTGTGTGGCTCTCTTCGATCTCAGTGCCCAAAAGGAGATATTCTGTAAGTCCA-AGGACG----------AGTCCT---T----------T----------TGAAGG--------GAT-TTC-ACTCCTATAATGC-AG-A-----AT----CC-T-TCCC----TC---CAGCTAACAATGAACATCCGAGGTCATACAGTCGGCCAGTTGGCGCGAGGAT
droKik1	scf7180000302610:412331-412496 +		CGCCGGCTGTGTGGCCCTCTTCGATCTCAGCACCCAAAAGGAGATCTTCTGTGAGTTGT-ATACTC---TCCGAGTCACCCCCCCACT---CG----------TAA--GTCTAA----CAC-AA-A-----TCT----T-T-TCTC----TC---CAGCAAACAATGAACATCCCGAGGTGATTCAATCCGCCAGCTGGCGCGAAGAT
droFic1	scf7180000454072:707233-707396 -		CGCTGGTTGTGTGGTCTCTTCGATCTTAGCACTCAAAAGGAGATCTTCTGTAAGTAAA-AAGCAA----------TT----------ACATATGTGCAC--------T----AGC------GATCTTTAACT--TCGGGTTT----T-C-A-TTGC----G---CAGCGAACAATGAACATCCTGAGGTGATACAATCGGCCAGTTGGCGTGAGGAT
droEle1	scf7180000491006:1296775-1296956 -		CGCCGGCTGCGTGGCACTCTTGATCTCAGCACCCAGAAGGAGATCTTCTGTGAGTCAA-CAGCTC----------CTGCTC---T----TCAT-T----------T-AAAACAAACTCAAAC--------T----AAC------ACCAACTAACT--CCAACTTC----TT-T-TCCCCGCGAA---TAGCGAACAATGAGCATCCCGAGGTGATACAGTCGGCTAGTTGGCGCGAGGAC
droRho1	scf7180000763611:421203-421362 +		CGCCGGTTGCGTGGCTCTCTTGATCTCAGCACCCAGAAGGAGATCTTCTGTGAGTCAC-AAGCTC----------CTCTCT---T----------AAAA--------TAA-TTTCAATCTGAAT-GT-T-----TTT----TT-T-GCCC----G---CAGCGAACAATGAGCATCCCGAGGTGATACAGTCGGCCAGTTGGCGCGAGGAC
droBia1	scf7180000301760:1902349-1902510 -		CGCCGGCTGCGTGGCTCTCTTCGATCTCAGCACCCAAAAGGAGATCTTCTGTGAGTCAA-CAGCTC----------CCCTTT---TG----------C-AAAT--------GA-TTTCACTTAGTAAAT-GC-C-----CT----TT-GTTTTC----G---CAGCGAACAATGAGCATCCCGAGGTGATACAGTCGGCCAGTTGGCGCGAGGAC
droTak1	scf7180000415873:314726-314888 +		CGCCGGCTGTGTGGCCCTCTTCGATCTCAGCACCCAAAAGGAGATCTTCTGTGAGTCAC-TACCTTT----------CACTTT---TG----------CAAG--------AGA-TTTCTGTAATAAAT-AT-C-----CT----TT-CTTCTC----T---CAGCGAACAACGAGCACCGGAGGTGATACAGTCGGCCAGTTGGCGCGAGGAT
droEug1	scf7180000409095:29002-29162 +		CGCCGGTTGCGTAGCTCTTTTGATCTCAGCACCCAAAAGGAGATCTTCTGTAAGTTAA-CACCTC----------CTCTTT---T----------GCTA--------TGA-TTTACATAAAATATAG-GT-A-----ATT----TG-GTTTTC----G---CAGCTAACAATGAGCATCCCGAGGTTATACAGTCGGCCAGTTGGCGCGAGGAT
dm3	chrX:6700788-6700963 +		CGCCGGCTGCGTGGCTCTCTTCGATCTCAGCACTCAAAAGGAGATATTCTGTGAGTAAA-CACATT----------CTTTTTTTTTTTTTTTTTTT-T----------T-AAAT--------AAA-TTTACCCTAACTAAAT-AT-G-----TTT----T----------TT-C-TCTC----TA---CAGCGAACAATGAGCACCCGAGGTGATACAGTCGGCCAGTTGGCGCGAGGAC
droSim2	x:6303630-6303792 +		CGCCGGCTGTGTGGCTCTCTTTGATCTCAGCACTCAAAAGGAGATATTCTGTGAGTAAA-CACATC----------TTTCCT---T----------A----------TAAAAT--------AAT-TTTACCCTAACTAAAT-AT-G-----TTT----TT-G-TCCT----TT---CAGCGAACAATGAGCACCCGAGGTGATACAGTCGGCCAGTTGGCGCGAGGAC
droSec2	scaffold_4:95128-95290 -		CGCCGGCTGTGTGGCTCTCTTTGATCTCAGCACTCAAAAGGAGATATTCTGTGAGTAAA-CACATC----------TTTCCT---T----------T----------TAAAAT--------AAT-TTTACCCTAACTAAAT-AT-G-----TTT----TT-G-TCCT----TT---CAGCGAACAATGAGCACCCGAGGTGATACAGTCGGCCAGTTGGCGCGAGGAC
droYak3	X:2668188-2668347 +		CGCCGGCTGCGTGGCTCTCTTCGATCTCAGCACCCAAAAGGAGATATTCTGTGAGTAAA-ACACATC----------CTTTTT---C----------AAAT--------GGA-TTTACCCTTACTAAAT-GT-A-----TTT----TT-G-TCAC----TA---CAGCGAACAATGAGCATCCCGAGGTGATACAGTCGGCCAGTTGGCGCGAGGAT
droEre2	scaffold_4690:15628870-15629029 +		CGCCGGCTGCGTGGCTCTCTTTGATCTCAGCACCCAAAAGGAGATATTCTGTGAGTGAA-CACATC----------CTTTTT---T----------AAAT--------GGT-TTTACCCAAACTAAAT-GT-A-----TTT----TT-G-TCCC----TA---CAGCGAACAATGAGCATCCCGAGGTGATACAGTCAGCCAGTTGGCGGGAGGAT

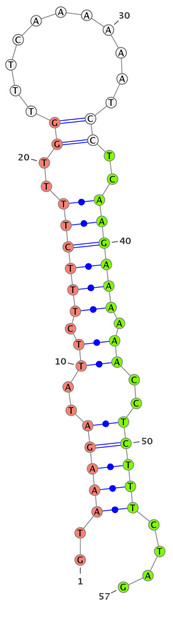
Generated: 09/08/2015 at 07:01 PM

	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	0
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	2
rescue.candidate	0

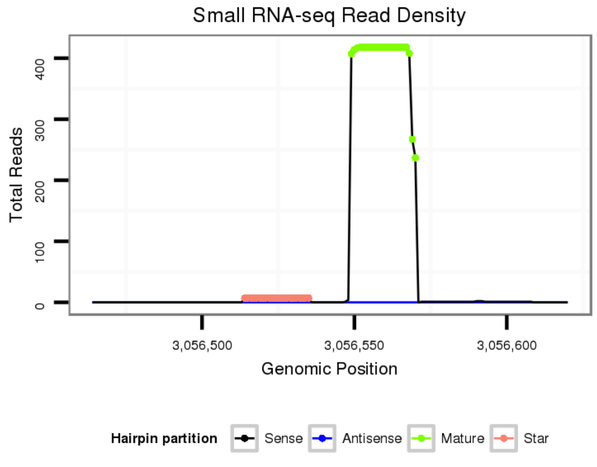
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dps_1668	**4_group4:3056514-3056570 +**	**confident**	**Mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

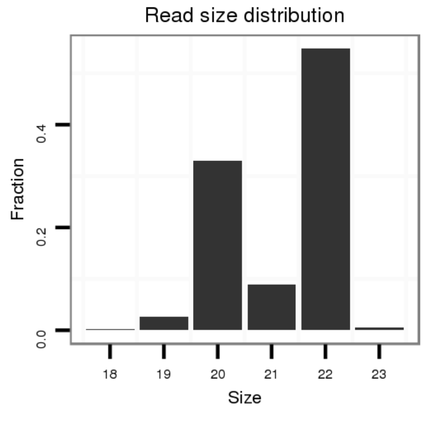
Legend: mature star mismatch in alignment mismatch in read

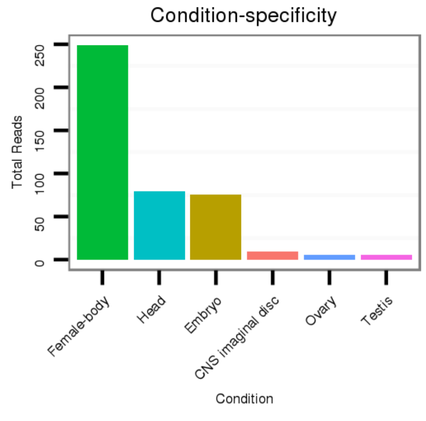
Predicted structure

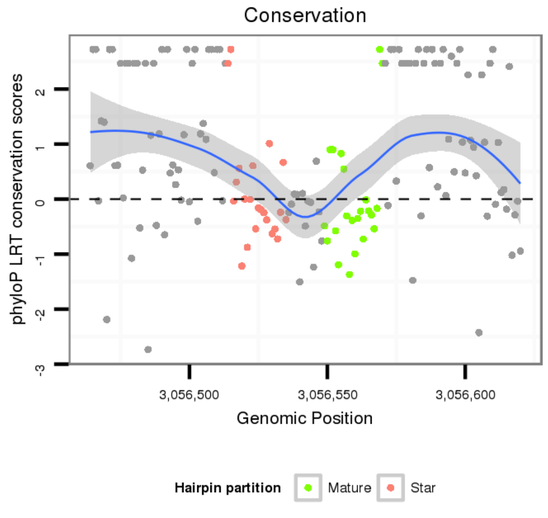


dps_1668_amot [-2.8]









Show Alternate Folds

Flybase annotation

intron [Dpse\STIP-in]; CDS [Dpse\STIP-cds]; CDS [Dpse\STIP-cds]; utr5 [utr5_plus_824]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

CAACACAAACAGACCACGGGGGCGCCACAGCAAACATCAACAGATTTATGGTAAAGATATTCTTTCTTTTGGTTTCAAAAAATCCTCAAGAAAAAACCTCTTTCTAGGCATTTGGGCGGACGACAGTGACGAGGAGGGCCCCGGTGATGGTGGCGGC **********..(((((..((.((((((..((.....))..)))))).))..)))))....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M040 female body	M062 head	M059 embryo	SRR902012 CNS imaginal disc	SRR902010 ovaries	SRR902011 testis	GSM444067 head	GSM343916 embryo	V112 male body
.....TCAAGAAAAAACCTCTTTCTAG.....	22	0	1	225.00	225	168	5	35	5	6	4	1	1	0
.....TCAAGAAAAAACCTCTTTCT.....	20	0	1	138.00	138	52	59	25	1	0	1	0	0	0
.....TCAAGAAAAAACCTCTTTCC.....	20	1	1	31.00	31	0	22	9	0	0	0	0	0	0
.....TCAAGAAAAAACCTCTTTCTA.....	21	0	1	30.00	30	16	5	8	1	0	0	0	0	0
.....TCAAGAAAAAACCTCTTTCTAGA.....	23	1	1	15.00	15	14	0	1	0	0	0	0	0	0
.....TCAAGAAAAAACCTCTTTC.....	19	0	1	10.00	10	0	6	3	1	0	0	0	0	0
.....CAAGAAAAAACCTCTTTCTAG.....	21	0	1	7.00	7	7	0	0	0	0	0	0	0	0
.....GTAAAGATATTCTTTCTTTTGG.....	22	0	1	7.00	7	5	1	1	0	0	0	0	0	0
.....TCAAGAAAAAACCTCTTTCTAGAA.....	24	2	1	2.00	2	1	0	0	0	1	0	0	0	0
.....AAGAAAAAACCTCTTTCTAG.....	20	0	1	2.00	2	0	0	0	1	0	1	0	0	0
.....CTCAAGAAAAAACCTCTTTCTAG.....	23	0	1	2.00	2	0	0	2	0	0	0	0	0	0
.....AGAAAAAACCTCTTTCTAG.....	19	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....CCTCAAGAAAAAACCTCTTTCT.....	22	0	1	1.00	1	0	0	1	0	0	0	0	0	0
.....TCAAGAAAAAACCTCTTTCTAGT.....	23	1	1	1.00	1	0	0	1	0	0	0	0	0	0
.....CTCAAGAAAAAACCTCTTTCT.....	21	0	1	1.00	1	0	1	0	0	0	0	0	0	0
.....AAGAAAAAACCTCTTTCT.....	18	0	1	1.00	1	0	1	0	0	0	0	0	0	0
.....TGACGAGGAGGGCCCCGGT.....	19	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....CATTTGGGCGGACGACAGTGA.....	21	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....TCAAGAAAAAACCTCTTTCTAGC.....	23	1	1	1.00	1	0	0	1	0	0	0	0	0	0
.....CAAGAAAAAACCTCTTTCTAGA.....	22	1	1	1.00	1	1	0	0	0	0	0	0	0	0
.....CAAGAAAAAACCTCTTTCTAGAA.....	23	2	1	1.00	1	1	0	0	0	0	0	0	0	0
.....TCAAGAAAAAACCTCTTTCTAAAA.....	24	3	3	0.33	1	1	0	0	0	0	0	0	0	0

Anti-sense strand reads

GTTGTGTTTGTCTGGTGCCCCCGCGGTGTCGTTTGTAGTTGTCTAAATACCATTTCTATAAGAAAGAAAACCAAAGTTTTTTAGGAGTTCTTTTTTGGAGAAAGATCCGTAAACCCGCCTGCTGTCACTGCTCCTCCCGGGGCCACTACCACCGCCG **********..(((((..((.((((((..((.....))..)))))).))..)))))....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M040 female body

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
dp5	4_group4:3056464-3056620 +	dps_1668	CAACACAAACAGACCACGGGGGCGCCACAGCAAACATCAACAGATTTATGGTAAAGAT---------A---TTC---TTTCTT-TTGGT--TTCAAA----AAATCCTCAA----------GAAA----------AA---A---CCTC-TTTCTAGGCATTTGGGCGG------ACGACAGTGACGAGGAGGGCCCCGGTGATGGTGGCGGC--------
droPer2	scaffold_10:2074166-2074322 +	dpe_621	CAACACAAACAGACCACGGGGGCGCCACAGCAAACATCAACAGATTTATGGTAAAGAT---------A---TTC---TTTCTT-TTGGT--TTCAAA----AAATCCTCAA----------GAAA----------AA---A---CCTC-TTTCTAGGCATTTGGGCGG------ACGACAGTGACGAGGAGGGCCCCGGTGATGGTGGCGGC--------
droWil2	scf2_1100000004521:8469408-8469555 +		CAATAATAAACAGACCGCGGGCAGGCAGCAGCAAGCACGCAAATTTATGGTAAGGCGAA----------AA--AT---------C------ ----------TGTCT---------CTGTTCATTAAA----------TTTA-TTGTGTTT-GTTTTAGGTATTTGGGCCATGGGGATGACAGTGAGGAGA---------TGAAGGAAGCGGC--------
droVir3	scaffold_12963:3760424-3760580 -		CAACATTAACAGGCCACGCAGACGCCACACAAGCACCAACAAATTTACGGTAAGCAA----------AAG-TTA---CAA-ATGTT--A--T--ACAAAAATTGTGAA----------ATAT----------TT---A---TGTTTCTGTCAGGCATTTGGGCGG------ACGACAGCGAGAATGAGGGCGAGGACGAAAGCGGCGGT--------
droMoj3	scaffold_6500:14214183-14214338 -		TAACATAAACAGGCCACGCAGACGCCAACCAAGCATCAACAATTTATGGTATGAATG----------AA----TA---------------------CGCAAAACAAAATTGTAGAAT------TTAATTAA----------TCT--------A-TT-TGTTTAGGCATTTGGGCTG------ATGACAGTGACAATGAGGGCGAAGGCGAGACGCGGT--------
droGri2	scaffold_15252:3266367-3266527 -		CAATAATAAATCGACCACGCCGTCGTCAAACCAAACATCACAATCTACGGTAAGCAA----------AAGCAAA---C---A-CAA-AATTT--GTT----TGT------ ----------TTTCAATT---------T-GTT---------TTC---TTTTTTCC-TTTCCAGGCATTTGGGCCG------ATGACAGCGACAATGAAAGCGAGGAGAAGCCAGCGGT--------
droAna3	scaffold_12916:11166866-11167022 -		TAACATGAACAGGCCCCGCGGGCGTCACAGCAAGCACCAGCAGATCTATGGTGATGTGC----------GTCCTCC---C---T-CCT-ATTTT--ATT----AGT------ ----------T------TTTCATGATTT----------TT---A---TCCG-ATTCTAGGCATTTGGGCTG------ATGACAGCGAGGAGGAGAGCGGCGGAGAGGCAGACAG--------
droBip1	scf7180000396572:824624-824778 -		TAATAATAAACAGGCCGCGTGGTCGCAACACCAAGGAGAGATGATCTACGGTAACTGC----------AGCCT-CTTAC---TCCTT-AGT-T-----------C------ ----------CTTGAAT---------TTACATTTTTTTT-T---A---TCGG-ATTCTAGGTATTTGGGCAG------ATGAGAGCGATGAGGAGAGCGGTGGAGAGGGC------ --------
droKik1	scf7180000302389:332507-332671 +		CAACATCAACAGGCCCGCGGACGCCAGAGTCGGCACCAGCAGATCTACGGTGAGCAGTG----------G-CTTAGC---ACCCT-ATT-T--CTT----AAT------ ----------AT---------TGATAATATAAAT-TA---ATGCATTT-TTTGCAGGCATTTGGGCGG------ATGACAGCGAGGAGGAGAGCGCGGCGAGGGTGGCAAA--------
droFic1	scf7180000454023:19549-19705 +		CAATGTGAACCGGCCGCGGGACGCGACAGCAGCACACCAGCAGATCTACGGTAAGTGA----------GAGGTTC---C---G-GCG-TTATT-----------GCCAGAT------TTGATTAGCCA----------GT---T---TCTA-TCCGCAGGCATCTGGGCGG------ATGACAGCGAGGAAGAGAGCGGTGGCGAGGGCGGTGGC--------
droEle1	scf7180000491024:422827-422999 -		CAACATGAACCGGCCTCGTGGACGCCACAGCAGACACCAACAGATCTACGGTGAGTAGCGCAGTGGAAAGTAA--GTTG---------T------ ----------GGCCAGAT------TTGGTTAGTAAA----------CAGACC---ACTA-TTCGCAGGCATTTGGGCCG------ACGACAGCGAGGAGGAGAGCGCGGCGAGGCCGCGGGCGGGGGCGG
droBia1	scf7180000302422:3926452-3926608 +		CAACATCAACCGGCCCGTGGACGCCAGAGCAGGCACCAACAGATCTACGGTGAGCAG----------GAGGTCC---C---T-TAA-TTCTA--A-G----CAA------ ----------CTCCAATA---------A-GCC---------CTC---C---CCAC-TTTGCAGGCATCTGGGCGG------ATGACAGCGAGGAGGAGAGCGGTGGTGAGGGCGGTGGA--------
droTak1	scf7180000415871:500698-500855 +		CAACATGAACCGGCCCGCGGGCGCGACAGCAGGCACCAGCAGATCTACGGTGAGCGG----------GGAGTCC---T---C-TAA-TCCTG--G--CCAGC---------- ----------AA------TTAAAT-----G-GAA---------ATC---C---CTTT-TCCGCAGGCATTTGGGCGG------ACGACAGCGAGGAGGAGAGCGCGGCGAGGGCGGCGGGGC--------
droEug1	scf7180000409004:276099-276252 -		CAACATTAACCGGCCCGTGGGCGCCAGAGCCGGCACCAGCAGATCTACGGTGAGCAGTG----------AA--GTCC---TAGCTT-C----TTT-----------GTCCGAG------CTTCTTAATTAA----------TTA--------A-CT-ACTGCAGGTATATGGGCGG------ACGACAGCGAG---GAGAGCGGTGGCGAGGGCGGCAGC--------
dm3	chr2L:5721195-5721345 +		CAACATCAATCGGCCCGAGGCGCCAGAGCAGGCACCAACAGATCTACGGTATGTATTG----------AA--ATAC---------A------ ----------TGCCGGAA------TTTGTTTGTAAA----------CGA--------ACTT-TCTGTAGGTATTTGGGCGG------ATGACAGCGAGGAGAGAGTGGTGGCGAGGGCGGAACT--------
droSim2	2L:5526108-5526257 +		CAACATCAATCGACCCCGTGGCCGCCAGAGCAGCAAGCACCAACAGATCTACGGTATGTATTA----------AA--ATAT---------C------ ----------TGCCGAAA------TTAGTTTTTGAA----------CGA--------A-TT-TTTACAGGTATTTGGGCGG------ATGACAGCGAGGAGAGAGTGGCGGCGAGGGCGGAAGT--------
droSec2	scaffold_5:3800248-3800398 +		CAACATCAATCGACCCCGTGGCCGCCAGAGCAGCACCAACAGATCTACGGTATGTATTG----------AA--ATAC---------C------ ----------TGCCGGAA------TTATTTTTTAAA----------CGA--------ACTT-TTTGCAGGTATTTGGGCTG------ATGACAGCGAGGAGAGAGTGGTGGCGAGGGCGGAAAC--------
droYak3	2L:13470288-13470437 -		CAACATCAACCGGCCTCGTGGGCGCCAGAGCCGGCACCAACAGATCTACGGTAGCGTATTG----------AA--GTTC---------C------ ----------GGCCAGAA------TTAGTTAGTAAA----------CTA--------ACTT-TTCACAGGCATTTGGGCGG------ATGATAGCGAGGAGGAGAGTGGCGGCGAGGCCGCGG-AGC--------
droEre2	scaffold_4929:5811578-5811727 +		CAACATCAACCGGCCTCGTGGCCGCCAGAGTCGGCACCAACAGATCTACGGTACGTAGAG----------AA--GTTC---------C------ ----------GCCGAGAT------TTAGTTAGAAAA----------GTA--------ACTT-TTCGCAGGTATTTGGGCGG------ATGACAGCGAGGAGGAGAGTGGTGGCGAGG-CCGCGAGC--------

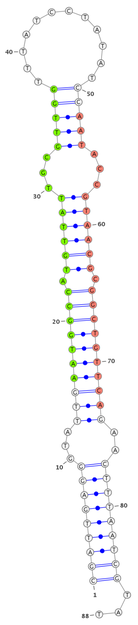
Generated: 09/08/2015 at 07:01 PM

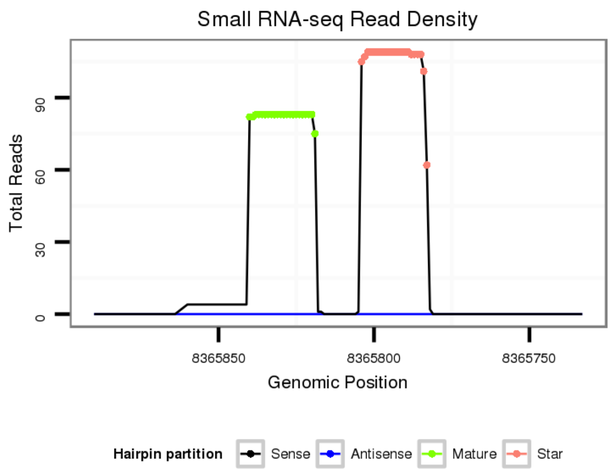
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	2
rescue.candidate	0

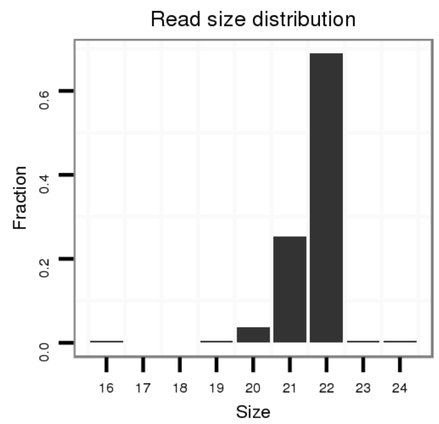
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dps_55	**XL_group1e:8365783-8365840 -**	**confident**	**Testes-restricted**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

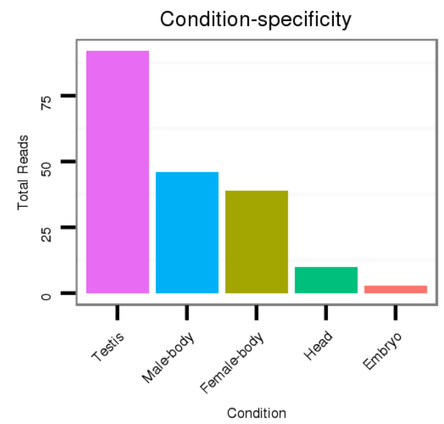
Legend: mature star **mismatch in alignment** mismatch in read

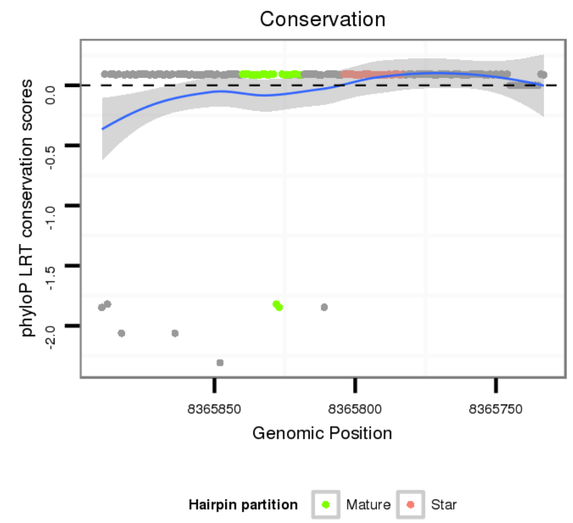
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

ATATTCTTCAGTGAAATGTGTACTCTTTTTTGAGCCGATTGAGGGTATTGAATGGCCATGTTATTGCGTTGGTTTATCCTATATCCAATACCGTAACGCGGCTGTTCAGAACTTTAATCGTATTCTATCCCAATATCCTGTGAGTGTCCAAAAAAATG	Read size	# Mismatch	Hit Count	Total Norm	Total	M040 female body	SRR902011 testis	V112 male	GSM444067 head	M022 male	M062 head body	M059 embryo	GSM343916 embryo
********************************(((((((((...(((((((((.((((((...(((((.....)))))...)))))).))))))))))..)))))))))...********************************													
.....AATGGCCATGTTATTGCGTTGG.....	22	0	1	73.00	73	5	28	35	3	0	0	1	1
.....AATACCGTAACGCGGCTGTTCA.....	22	0	1	58.00	58	21	35	0	0	2	0	0	0
.....AATACCGTAACGCGGCTGTTC.....	21	0	1	39.00	39	9	23	1	0	2	3	1	0
.....AATACCGTAACGCGGCTGTTT.....	21	1	1	13.00	13	1	9	1	0	1	1	0	0
.....AATACCGTAACGCGGCTGTTCG.....	22	1	1	9.00	9	1	5	0	0	1	2	0	0
.....AATGGCCATGTTATTGCGTTG.....	21	0	1	8.00	8	2	0	3	3	0	0	0	0
.....AATACCGTAACGCGGCTGTT.....	20	0	1	6.00	6	0	4	1	1	0	0	0	0
.....AATACCGTAACGCGGCTGTTCCC.....	23	2	1	6.00	6	0	5	0	0	1	0	0	0
.....AATACCGTAACGCGGCTGTTA.....	21	1	1	5.00	5	0	3	0	0	2	0	0	0
.....AATACCGTAACGCGGCTGTTCAA.....	23	1	1	4.00	4	1	3	0	0	0	0	0	0
.....AATACCGTAACGCGGCTGTTTTT.....	23	3	1	4.00	4	0	4	0	0	0	0	0	0
.....AATACCGTAACGCGGCTGTTCT.....	22	1	1	3.00	3	0	2	0	0	1	0	0	0
.....AATACCGTAACGCGGCTGTG.....	20	1	1	3.00	3	0	3	0	0	0	0	0	0
.....TACCGTAACGCGGCTGTTCAG.....	21	0	1	2.00	2	1	1	0	0	0	0	0	0
.....ATACCGTAACGCGGCTGTTCCC.....	22	2	1	2.00	2	0	2	0	0	0	0	0	0
.....TTTTGAGCCGATTGAGGGTATTG.....	23	0	1	1.00	1	0	0	1	0	0	0	0	0
.....AATACCGTAACGCGGCTGTTTTA.....	23	3	1	1.00	1	0	1	0	0	0	0	0	0
.....AATACCGTAACGCGGCTGTTAG.....	22	2	1	1.00	1	0	1	0	0	0	0	0	0
.....TTTGAGCCGATTGAGGGTATTG.....	22	0	1	1.00	1	0	0	0	1	0	0	0	0
.....AATACCGTAACGCGGCTGTTCATC.....	24	2	1	1.00	1	0	1	0	0	0	0	0	0
.....TTGAGCCGATTGAGGGTATTG.....	21	0	1	1.00	1	0	0	1	0	0	0	0	0
.....TGAGCCGATTGAGGGTATTG.....	20	0	1	1.00	1	0	0	1	0	0	0	0	0
.....AATACCGTAACGCGGCTGTTCATCT.....	25	3	1	1.00	1	0	1	0	0	0	0	0	0
.....AATACCGTAACGCGGCTGTTAT.....	22	2	1	1.00	1	0	1	0	0	0	0	0	0
.....AATACCGTAACGCGGCTGTTCTC.....	23	2	1	1.00	1	0	1	0	0	0	0	0	0
.....ATACCGTAACGCGGCTGTTTTT.....	22	3	1	1.00	1	0	1	0	0	0	0	0	0
.....CAATACCGTAACGCGGCTGTTCA.....	23	0	1	1.00	1	1	0	0	0	0	0	0	0
.....AATACCGTAACGCGGC.....	16	0	1	1.00	1	0	1	0	0	0	0	0	0
.....AATGGCCATGTTATTGCGTTGGTT.....	24	0	1	1.00	1	0	0	1	0	0	0	0	0
.....AATGGCCATGTTATTGCGTTGGA.....	23	1	1	1.00	1	0	0	1	0	0	0	0	0
.....TGGCCATGTTATTGCGTTGG.....	20	0	1	1.00	1	0	0	1	0	0	0	0	0
.....ATACCGTAACGCGGCTGTTCA.....	21	0	1	1.00	1	0	1	0	0	0	0	0	0
.....ATACCGTAACGCGGCTGTT.....	19	0	1	1.00	1	1	0	0	0	0	0	0	0
.....AATACCGTAACGCGGCTGTTCTTT.....	24	3	1	1.00	1	0	1	0	0	0	0	0	0
.....AATACCGTAACGCGGCTGTTCAAC.....	24	2	1	1.00	1	0	1	0	0	0	0	0	0

Anti-sense strand reads

TATAAGAAGTCACTTTACACATGAGAAAAAACTCGGCTAACTCCCATAACTTACCGGTACAATAACGCAACCAAATAGGATATAGGTTATGGCATTGCGCCGACAAGTCTTGAAATTAGCATAAGATAGGGTTATAGGACACTCACAGGTTTTTTTAC	Read size	# Mismatch	Hit Count	Total Norm	Total	M040 female body	GSM444067 head
********************************(((((((((...(((((((((.((((((...(((((.....)))))...)))))).))))))))))..)))))))))...********************************							

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
dp5	XL_grouple:8365733-8365890 -	dps_55	ATATTCTTCAGTGAAATGTGTACTCTTTTTTGAGCCGATTGAGGGTATTGAATGGCCATGTTATTGCGTTGGTTTATCCTATATCCAATACCGTAACGCGGCTGTTCAGAACTTTAATCGTATTCTATCCCAATATCCTGTGAGTGTCCAAAAAAATG-------
droPer2	scaffold_13:198509-198662 +	dpe_122	GTTTTTCTCCAGTGAAATGTGTACTCTGTTTTGAGCCGATTGACGGTATTGAATGGCCATGTTTCTGCGTTGGTTTATCCCATATCCAATACCGTAACGCGGCTGTTCAGAACTTTAATCGTATTCTATCCCAATATCCTGTGAGT----------TGATGATAC

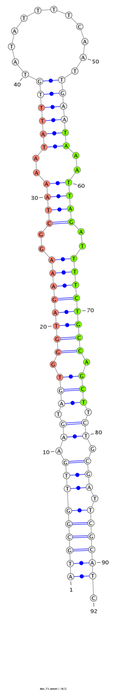
Generated: 09/08/2015 at 08:37 PM

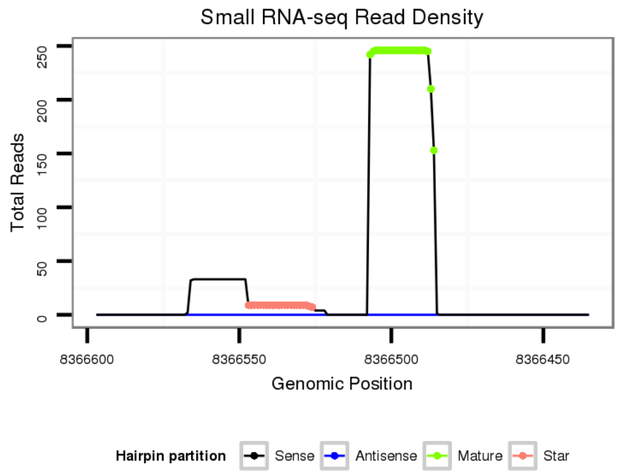
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	2
rescue.candidate	0

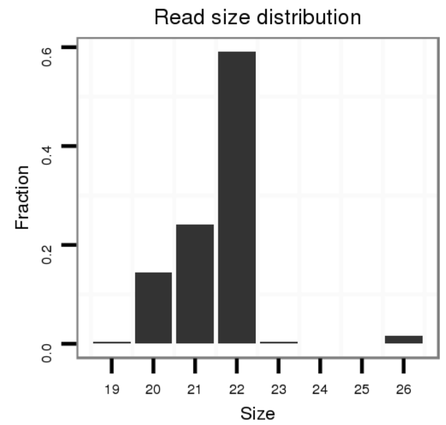
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dps_73	**XL_group1e:8366485-8366547 -**	**confident**	**Testes-restricted**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

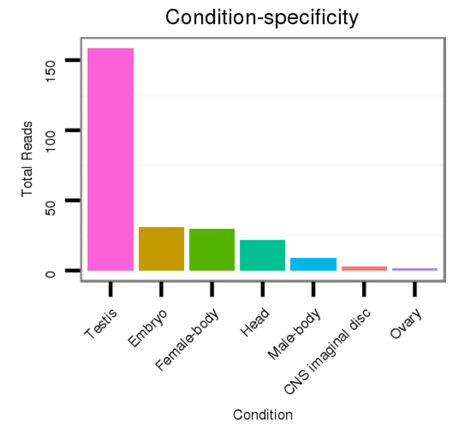
Legend: mature star mismatch in alignment mismatch in read

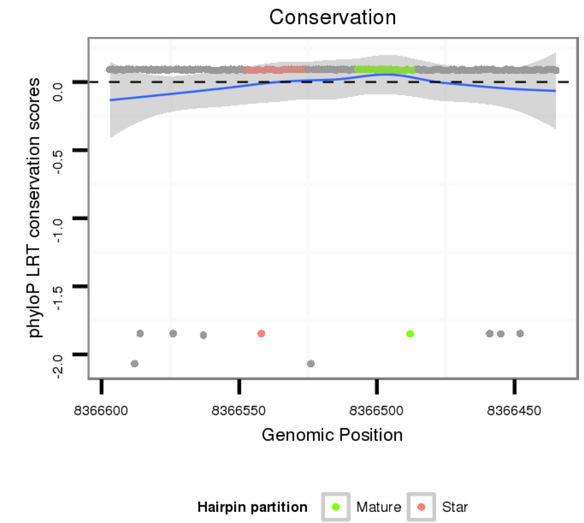
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

ATCATCATAGTATACTGTGAAGAAAACACTGTTTCATGCGGTTGAAGTAGTGGGTAGAAAGGCTAAAATATTTGTATATTTTCAATTGAATAAATTAGATTTTCTGCCAGCTTCTGCGATTCGCATCGACCCCTGTTTATGCGCTCTCGAGAGCGATCGTTTC **********(((((((((.((.(((.(((((((((..((((..((((((.....))))))..))))..)))))))).))).)).))).)))))).**********	Read size	# Mismatch	Hit Count	Total Norm	Total	SRR902011 testis	M059 embryo	M040 female body	M062 head	V112 male body	GSM444067 head	GSM343916 embryo	SRR902012 CNS imaginal disc	M022 male body	SRR902010 ovaries
.....TAAATTAGATTTTCTGCCAGCT.....	22	0	1	148.00	148	74	18	19	11	5	8	9	2	2	0
.....TAAATTAGATTTTCTGCCAGC.....	21	0	1	57.00	57	41	3	6	2	1	1	0	1	0	2
.....TAAATTAGATTTTCTGCCAG.....	20	0	1	35.00	35	33	0	2	0	0	0	0	0	0	0
.....TTTCATGCGGTTGAAGTAG.....	19	0	1	30.00	30	28	0	0	0	2	0	0	0	0	0
.....TAAATTAGATTTTCTGCCAGCC.....	22	1	1	16.00	16	3	12	0	1	0	0	0	0	0	0
.....TAAATTAGATTTTCTGCCAGT.....	21	1	1	5.00	5	5	0	0	0	0	0	0	0	0	0
.....TGGGTAGAAAGGCTAAAATATTTGTA.....	26	0	1	4.00	4	4	0	0	0	0	0	0	0	0	0
.....AAATTAGATTTTCTGCCAGCT.....	21	0	1	3.00	3	0	0	3	0	0	0	0	0	0	0
.....TGGGTAGAAAGGCTAAAATATT.....	22	0	1	3.00	3	3	0	0	0	0	0	0	0	0	0
.....TGGGTAGAAAGGCTAAAATATC.....	22	1	1	2.00	2	2	0	0	0	0	0	0	0	0	0
.....TAAATTAGATTTTCTGCCAGCTTCC.....	25	1	1	2.00	2	2	0	0	0	0	0	0	0	0	0
.....TAAATTAGATTTTCTGCCAGCTCT.....	24	2	1	2.00	2	2	0	0	0	0	0	0	0	0	0
.....GTTTCATGCGGTTGAAGTAG.....	20	0	1	2.00	2	2	0	0	0	0	0	0	0	0	0
.....TAAATTAGATTTTCTGCCAGCA.....	22	1	2	2.00	4	3	0	0	0	0	1	0	0	0	0
.....AATTAGATTTTCTGCCAGCT.....	20	0	1	1.00	1	0	1	0	0	0	0	0	0	0	0
.....TAAATTAGATTTTCTGCCAGCCG.....	23	2	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....TGGGTAGAAAGGCTAAAATAT.....	21	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....TAAATTAGATTTTCTGCCAGCTG.....	23	1	1	1.00	1	0	0	1	0	0	0	0	0	0	0
.....TAGATTTTCTGCCAGCTA.....	18	1	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....TAAATTAGATTTTCTGCCAGCTT.....	23	0	1	1.00	1	0	0	0	0	1	0	0	0	0	0
.....TAAATTAGATTTTCTGCCAGCG.....	22	1	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....TAAATTAGATTTTCTGCCAGA.....	21	1	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....TTCATGCGGTTGAAGTAG.....	18	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....TAAATTAGATTTTCTGCCA.....	19	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....TGGGTAGAAAGGCTAAAATA.....	20	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....TAAATTAGATTTTCTGCCAGCTG.....	23	1	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....GAATAAATTAGATTTTCTGCC.....	21	0	2	0.50	1	1	0	0	0	0	0	0	0	0	0
.....TAAATTAGATTTTCTGA.....	17	1	4	0.25	1	1	0	0	0	0	0	0	0	0	0

Anti-sense strand reads

TAGTAGTATCATATGACACTTCTTTTGTGACAAAGTACGCCAACTTCATCACCCATCTTTCCGATTTTATAAACATATAAAAGTTAACTTATTTAATCTAAAAGACGGTCGAAGACGCTAAGCGTAGCTGGGGACAAATACGCGAGAGCTCTCGCTAGCAAAG **********(((((((((.((.(((.(((((((((..((((..((((((.....))))))..))))..)))))))).))).)).))).)))))).**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M040 female body

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
dp5	XL_group1e:8366435-8366597 -	dps_73	ATCATCATAGTATACTGTGAAGAAAACACTGTTTCATGCGGTTGAAGTAGTGGGTAGAAAGGCTAAAATATTTGTATATTTTCAATTGAATAAATTAGATTTTCTGCCAGCTTCTGCGATTCGCATCGACCCCTGTTTATGCGCTCTCGAGAGCGATCGTTTC
droPer2	scaffold_13:197817-197979 +	dpe_144	ATCATCATATTTGTACTGTGAAGAGAACACTGTTTTATGCGGTTGAAGTAGTGGGTGGAAAGGCTAAAATATTTTTATATTTTCAATTGAATAAATTAGATTTTCTGCCAACTTCTGCGATTCGCATCGACCCCTGTTTGTGCACTCTCGGGAGCGATCGTTTC

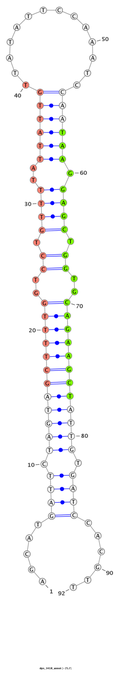
Generated: 09/08/2015 at 08:41 PM

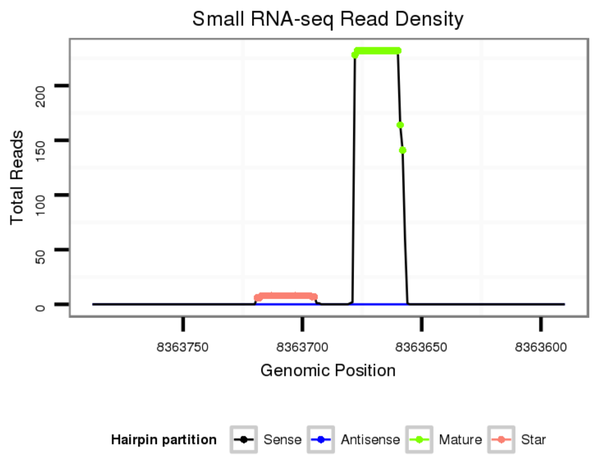
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	2
rescue.candidate	0

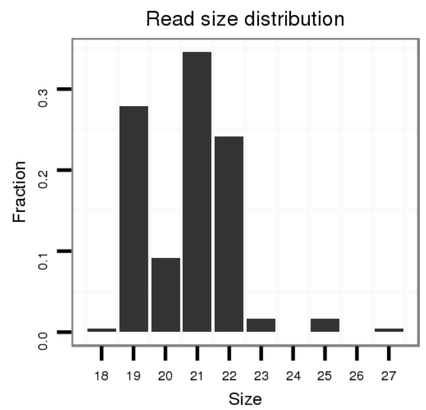
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dps_3418	**XL_group1e:8363640-8363738 -**	**confident**	**Testes-restricted**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

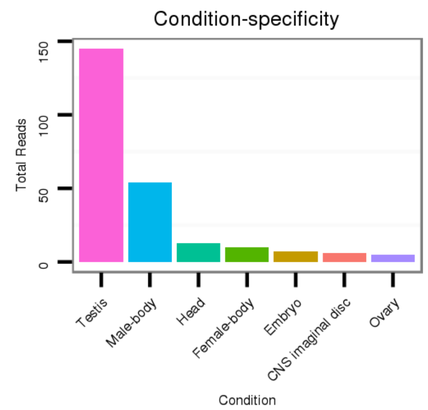
Legend: mature star mismatch in alignment mismatch in read

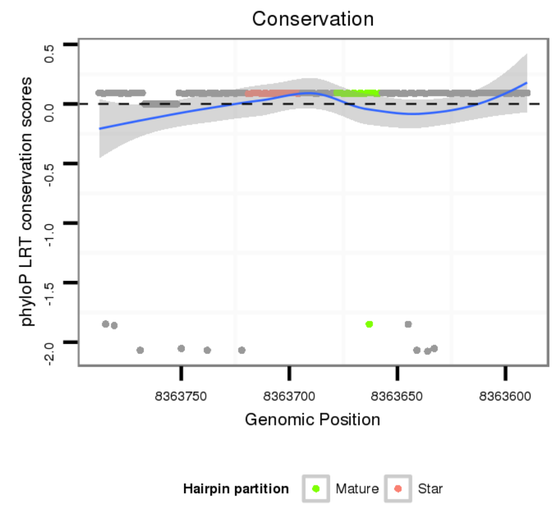
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

ATCATAACAAGAACCAATTGTGTCAAGTTGTGACTCCACGGAAGTTTCTGGTTGAGCATGATTCTAGTAGCTTTTGGTCCTGTTTTATTATTGTTATATTCCAAATCCAATAAGGAGCTGGTGCAGAAGCTATTGTGATCCACGTTGGATTCAAACATTTATCGAAAAGTATCCGAAAAATATTATAAGTGATGTTCAT **********.....((((.(((((((((((..((.((((..((((((.....))))))..))))..))..))))))))))).))))......**********	Read size	# Mismatch	Hit Count	Total Norm	Total	SRR902011 testis	V112 male body	M040 female body	GSM444067 head	SRR902012 CNS imaginal disc	M059 embryo	SRR902010 ovaries	GSM343916 embryo	M062 head	M022 male body
.....TAAGGAGCTGGTGCAGAAGCT.....	21	0	1	80.00	80	41	18	7	6	2	3	0	1	2	0
.....TAAGGAGCTGGTGCAGAAG.....	19	0	1	67.00	67	59	6	0	0	0	0	2	0	0	0
.....TAAGGAGCTGGTGCAGAAGCTA.....	22	0	1	56.00	56	17	29	3	3	1	1	0	2	0	0
.....TAAGGAGCTGGTGCAGAAGC.....	20	0	1	22.00	22	17	0	0	1	3	0	1	0	0	0
.....TAAGGAGCTGGTGCAGAAGCG.....	21	1	1	10.00	10	9	0	0	0	0	1	0	0	0	0
.....TAAGGAGCTGGTGCAGAAGCT.....	22	1	1	8.00	8	0	6	1	0	0	0	0	1	0	0
.....TAAGGAGCTGGTGCAGAAGCTAA.....	23	1	1	5.00	5	3	1	0	1	0	0	0	0	0	0
.....GCTTTTGGTCCTGTTTTATTATTGT.....	25	0	1	4.00	4	4	0	0	0	0	0	0	0	0	0
.....TAAGGAGCTGGTGCAGAAGCTC.....	22	1	1	4.00	4	4	0	0	0	0	0	0	0	0	0
.....AAGGAGCTGGTGCAGAAGCTA.....	21	0	1	3.00	3	1	1	0	1	0	0	0	0	0	0
.....TTTTGGTCCTGTTTTATTATTGT.....	23	0	1	2.00	2	0	0	0	0	0	0	2	0	0	0
.....TAAGGAGCTGGTGCAGAAGCTAAA.....	24	2	1	2.00	2	1	1	0	0	0	0	0	0	0	0
.....TAAGGAGCTGGTGCAGAAGA.....	20	1	1	2.00	2	2	0	0	0	0	0	0	0	0	0
.....TAAGGAGCTGGTGCAGAAGCA.....	21	1	1	2.00	2	2	0	0	0	0	0	0	0	0	0
.....TAAGGAGCTGGTGCAGAAGCCG.....	22	2	4	2.00	8	8	0	0	0	0	0	0	0	0	0
.....TAAGGAGCTGGTGCAGAAGTC.....	21	2	4	1.50	6	6	0	0	0	0	0	0	0	0	0
.....TAAGGAGCTGGTGCAGAAA.....	19	1	1	1.00	1	0	1	0	0	0	0	0	0	0	0
.....AAGGAGCTGGTGCAGAAG.....	18	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....TTTTGGTCCTGTTTTATTATTGTG.....	24	1	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....TAAGGAGCTGGTGCAGAAGT.....	20	1	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....ATAAGGAGCTGGTGCAGAAGCT.....	22	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....AATAAGGAGCTGGTGCAGAAGC.....	22	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....TAAGGAGCTGGTGCAGAAGCG.....	21	1	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....AAGGAGCTGGTGCAGAAGCTC.....	21	1	1	1.00	1	0	0	0	0	0	0	0	0	0	1
.....GCTTTTGGTCCTGTTTTATTATTGTTA.....	27	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....TAAGGAGCTGGTGCAGAAGCTAT.....	23	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....GCTTTTGGTCCTGTTTTATTATT.....	23	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....TAAGGAGCTGGTGCAGAAGAA.....	21	2	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....TAAGGAGCTGGTGCAGAAAA.....	20	2	2	0.50	1	0	1	0	0	0	0	0	0	0	0

Anti-sense strand reads

TAGTATTGTTCTTGGTTAACACAGTTCAACACTGAGGTGCCTTCAAAGACCAACTCGTACTAAGATCATCGAAAACCAGGACAAAATAATAACAATATAAGGTTTAGGTTATTCCTCGACCACGTCTTCGATAACACTAGGTGCAACCTAAGTTTGTAAATAGCTTTTCATAGGCTTTTTATAATATTCACTACAAGTA **********.....((((.(((((((((((..((.((((..((((((.....))))))..))))..))..))))))))))).))))......**********	Read size	# Mismatch	Hit Count	Total Norm	Total	GSM343916 embryo	M040 female body

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
dp5	XL_grouple:8363590-8363788 -	dps_3418	ATCATAACAAGAACCA----------ATTGTGTCAAGTTGTGACTCCACGGAAGTTTCTGGTTGAGCATGATTCTAGTAGCTTTTGGTCCTGTTTTATTATTGTTATATTCCAAATCCAATAAGGAGCTGGTGCAGAAGCTATTGTGATCCACGTTGGATTCAAACATTTATCGAAAAGTATCCGAAAAATATTATAAGTGATGTTCAT
droPer2	scaffold_13:200666-200860 +	dpe_335	ATCGTAATAAGAACCATTAATAAGATCCATTTT----------AAGGAAGTTTCTGTTTGAGCATGATTCTAATAGCTTTTGGTCCTGTTTTATTATTGTTATATTCCAAATCCAATAAGGAGCTGGTGCAAAAGCTATTGTGATCCACATTGTATTCCAAAATTTATCGAAAAGTATCCGAAAAATATTATAAGTGATGTTCAT

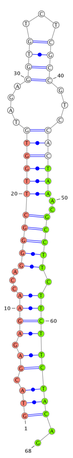
Generated: 09/08/2015 at 08:37 PM

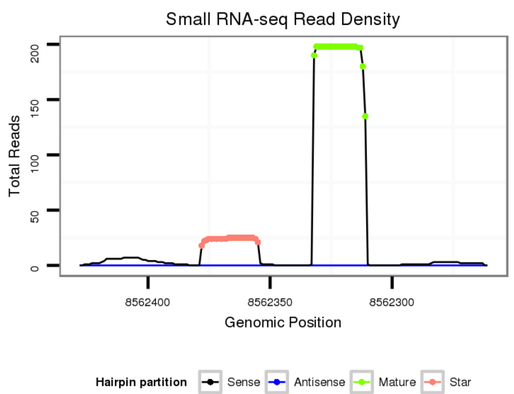
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	1

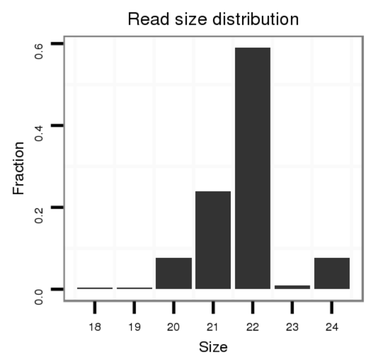
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dps_87	**2:8562311-8562378 -**	**confident**	**Mirtron**	**intron**	[View on UCSC Genome Browser (Cornell Mirror)]

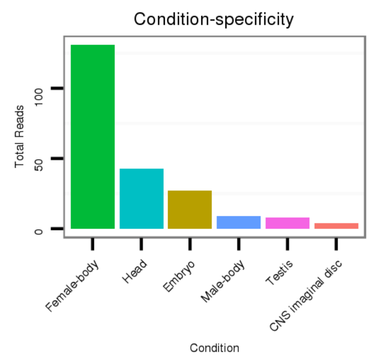
Legend: mature star mismatch in alignment mismatch in read

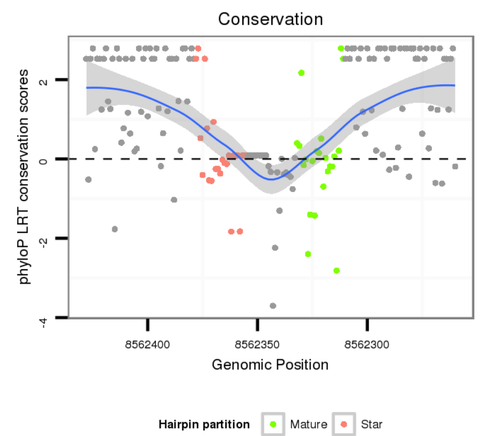
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dpse\GA19323-in]; CDS [Dpse\GA19323-cds]; CDS [Dpse\GA19323-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

CAGAGCCGGATCGATGCTCCCGATTGGTCAGCAGACTGCGACAGAATCAGGTACGAGAGAACCAGGGGCTTGGTGTAGAGGTGTCTCGCCGTCCACTAAACGCCTTCTTCTTCTACAGGACAAGGTGCTGTCGATCACGAATCTGATTATGGAGGAGCTGCTCGGCGA **********(((.(((.((((...((((((((((....((((...))))...))))))..)))))).)))))))))..**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M040 female body	M062 head	M059 embryo	SRR902011 testis	V112 male body	GSM444067 head	SRR902012 CNS imaginal disc	M022 male body	GSM343916 embryo
.....TAAACGCCTTCTTCTTCTACAG.....	22	0	1	127.00	127	76	15	20	8	0	5	2	0	1
.....TAAACGCCTTCTTCTTCTACA.....	21	0	1	44.00	44	28	13	3	0	0	0	0	0	0
.....GTACGAGAGAACCAGGGGCTTGGT.....	24	0	1	17.00	17	4	1	1	0	7	0	2	2	0
.....TAAACGCCTTCTTCTTCTAC.....	20	0	1	16.00	16	9	6	1	0	0	0	0	0	0
.....AAACGCCTTCTTCTTCTACAG.....	21	0	1	7.00	7	6	1	0	0	0	0	0	0	0
.....TAAACGCCTTCTTCTTCTACAGT.....	23	1	1	6.00	6	4	0	2	0	0	0	0	0	0
.....TACGAGAGAACCAGGGGCTTGG.....	22	0	1	2.00	2	2	0	0	0	0	0	0	0	0
.....AAACGCCTTCTTCTTCTACA.....	20	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....GTACGAGAGAACCAGGGGCTTGG.....	23	0	1	1.00	1	0	0	1	0	0	0	0	0	0
.....TAAACGCCTTCTTCTTCTACAGCC.....	24	2	1	1.00	1	0	0	1	0	0	0	0	0	0
.....CGAGAGAACCAGGGGCTTGGTG.....	22	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....CGATGCTCCCGATTGGTCAGCAGACTGC.....	28	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....TAAACGCCTTCTTCTTCTACAGG.....	23	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....TAAACGCCTTCTTCTTCTACAGG.....	23	1	1	1.00	1	0	0	1	0	0	0	0	0	0
.....GTACGAGAGAACCAGGGGCTTGAG.....	24	2	1	1.00	1	0	0	1	0	0	0	0	0	0
.....ACGAGAGAACCAGGGGCTTGGT.....	22	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....TACGAGAGAACCAGGGGCTTGGT.....	23	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....TCGATGCTCCCGATTGGTCAGC.....	22	0	1	1.00	1	0	0	1	0	0	0	0	0	0
.....CCGGATCGATGCTCCCGATTG.....	21	0	1	1.00	1	0	0	0	0	0	0	0	0	1
.....TAAACGCCTTCTTCTTCTACG.....	21	1	1	1.00	1	0	0	1	0	0	0	0	0	0
.....ATTATGGAGGAGCTGCTCGGC..	21	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....CCAGGGGCTTGGTGTAGAG.....	19	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....ATCGATGCTCCCGATTGGT.....	19	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....TAAACGCCTTCTTCTTCTACAGTTT.....	25	3	1	1.00	1	1	0	0	0	0	0	0	0	0
.....TACGAGAGAACCAGGGGCTTGAC.....	23	2	1	1.00	1	0	0	1	0	0	0	0	0	0
.....CCCGATTGGTCAGCAGACTGCGACAGA.....	27	0	1	1.00	1	1	0	0	0	0	0	0	0	0
..GAGCCGGATCGATGCTCCCGATT.....	23	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....CTAAACGCCTTCTTCTTCTAC.....	21	0	1	1.00	1	0	1	0	0	0	0	0	0	0
.....GTACGAGAGAACCAGGGGCTTGGG.....	24	1	1	1.00	1	0	1	0	0	0	0	0	0	0
.....TAAACGCCTTCTTCTTCTACAC.....	22	1	1	1.00	1	0	1	0	0	0	0	0	0	0
.....GATTATGGAGGAGCTGCTCGGC..	22	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....TAAACGCCTTCTTCTTCT.....	18	0	1	1.00	1	0	1	0	0	0	0	0	0	0
.....TACGAGAGAACCAGGGGCTTG.....	21	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....GTACGAGAGAACCAGGGGCTTGGA.....	24	1	1	1.00	1	1	0	0	0	0	0	0	0	0
.....CGATGCTCCCGATTGGTCAGCAGA.....	24	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....GATCACGAATCTGATTATGGAGGA.....	24	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....TAAACGCCTTCTTCTTCTACAGA.....	23	1	1	1.00	1	1	0	0	0	0	0	0	0	0

Anti-sense strand reads

GTCTCGGCCTAGCTACGAGGGCTAACCAGTCGTCTGACGCTGTCTTAGTCCATGCTCTCTTGGTCCCCGAACCACATCTCCACAGAGCGGCAGGTGATTTGCGGAAGAAGAAGATGTCCTGTTCCACGACAGCTAGTGCTTAGACTAATACCTCCTCGACGAGCCGCT **********(((.(((.((((...((((((((((....((((...))))...))))))..)))))).)))))))))..**********	Read size	# Mismatch	Hit Count	Total Norm	Total
No data available in table					

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
dp5	2:8562260-8562428 -	dps_87	CAGAGCCGGATCGATGCTCCCGATTGGTCAGCAGACTGCGACAGAATCAGGTACGAGA-----GAACCAGGGGCTTGGTGTAGAGGTGTCTCGCCGT----------CC----------AC----------TAAAC----------GC-------CTTCTTC-TT----------CTACAGGACAAGGTGCTGTCGATCACGAATCTGATTATGGAGGAGCTGCTCGGCGAG
droPer2	scaffold_0:2391156-2391325 -	dpe_132	CAGAGCCGGATCGATGCTCCCGATTGGTCAGCAGACTGCGACAGAATCAGGTACGAGAGG---AACAAGGAGCTCGGTGTAGAGGTGTCTCGCCGT----------CC----------AC----------TAAAC----------CC-------CTTCTTC-TT----------CTACAGGACAAGGTGCTGTCGATCACGAATCTGATTATGGAGGAGCTGCTCGGCGAG
droWil2	scaffold_1100000004921:1460518-1460682 -		CGGAGCCGGATCGATGTTCCCGTTTGGTCAGCAGATTGCGACAAAATCAGGTAAGAGGAGAATGCCGCTT----------TTGAG----------GTGAAA----AGC----GC----------**----------**-----**----------CAGAACTAAGACT----TG--T----CA---TT-TG----------TTTTAGGACAAGTGCTGGCGATAACAAATTTAATAATGGAAGAACTACTCGGCGAA
droVir3	scaffold_13047:9834112-9834269 -		CGGAGCCGGATCGTGCAGCGCCTGGTTAGCAGACTGCGCAGAATCAGGTGAGTG-----**----------CGAGGCTA----------GTAG----------**----------TAAAC----------G-ATTCATAATTAATATG-------TTTAATC-TG----------TTGCAGGACAAAGTGTTGCGCATAACGAACTTGATTATGGAGGAGCTGCTGGCGAA
droMoj3	scaffold_6540:9545044-9545210 +		CGGAGCCGGATCGTTGTAGCGCTCTGGTTAGCAGCTGCGACAGAATCAGGTAAGTG-----**----------TGC------**----------T-G----------**----------TT----------TGATTCCCTATTTTCCCTAGCTTATCC-----ATAACTAAC----GG------TATTGCATA-TA----------TTGCAGGACAAAGTGCTGGCGATAACAAATTTGATTATGGAAGAGCTGCTGGCGAC
droGri2	scaffold_14906:2694910-2695089 -		CGGAGCCGGATCGTTGTAGCGCTCTCGTCAGCAGACTGCGTCAAAATCAGGTAAGTTT----GAAGCTG----------GGAA----------GTGAAA----AGC----------**----------**----------TGTC----------AACG--GAACTGATT----TTG------TTTTTTTTTTGGGGGGGGGGTGTGCAGGACAAAGTGCTGGCGATTACGAACATGATAATGGAGGAGCTGCTGGCGAA
droAna3	scaffold_12911:3879294-3879452 -		CAGAGCCGGACCGTGCACCCGACTGGTCAGCAAGCTGCGGTCAACCAGGTGGGTG-----**----------TTTCAATTG----------C---TTCAAAACAAGTT----------**----TA-----A--TGCTAATC----------CC-------CCCTTTT-CT----------TTCAAGGACAAAGTGCTGGCGATCACAAACCTGATCATGGAGGAGCTGTTGGCGAG
droBip1	scf7180000396640:727828-727993 -		CGGAACCGGACCGTGCACCAGACTGGTCAGCAAGCTGCGGTGAACCAGGTGAGTC-----**----------CGCAACGAA----------CCAC-TCTGGCGGGAGTT----------**----TG-----C--CGCTAATC----------CTTC--G----------A-------CCCTTTT-TT----------TTGCAGGACAAAGTGCTGGCGATCACAAACCTGATCATGGAGGAGCTACTGGCGAG
droKik1	scf7180000302810:448982-449144 +		CAGAGCCGGATCGTGCACCAGACTGGTCAGCAGCTGCGACAGAATCAGGTGAGTC-----**----------TCGGGAAA----------**----------GTC----------**----TG-----ATACACCAATC----------AGTG--GATCATAAT----TTC------GATTTCT-C----------TTAAAGGACAAAGTGCTGGCGATCACGAACTTGATCATGGAGGAGCTGCTAGGCGAT
droFic1	scf7180000453776:134382-134569 -		CGGAACCGGATCGATGCACCAGACTGGTCAGCAGACTGCGACAGAATCAGGTGGGTC-----**----------TCAGGAAAAGTATATTTAAAACGGGTTCTTTAAATGT----------TCGAATTTAAATAAGGTTATC----------TAATC----------AA------CTTTTTT-GT----------GGACAGGACAAAGTGCTGGCGATCACAAATTTGATCATGGAGGAGCTGCTCGGCGAG
droEle1	scf7180000491280:1006383-1006539 -		CGGAGCCGGATCGATGCACCAGACTGGTCAGCAGCCTGCGTCAGAATCAGGTGGGTT-----**----------ACCAAAAG----------GCG---CTTATTTGAACAT----------**----------**-----**----------AAGTAAAAC-----AG------TA---TT-AT----------CTACAGGACAAAGTGCTGGCGATCACGAATTGATAATGGAGGAACTGCTGGCGAA
droRho1	scf7180000780109:19788-19997 +		CGGAGCCGGATCGTGCACCAGACTGGTCAGCAGACTGCGGCAGAATCAGGTGGGTC-----**----------TCAGGAAATATATTTTA-ATGGATTATTCAAGAGTGTT---TCTACTTGAATATAAATAAAATGAC-AATTTGAATGCTA--TGCTAATT----------**----------CC-------TTAATCT-TT----------CTCCAGGACAAAGTGCTGGCGATCACGAATTGATTATGGAGGAGCTGCTCGGCGAA
droBia1	scf7180000302113:3232441-3232602 -		CGGAGCCGGATCGTGCACCAGACTGGTCAGCAGACTGCGACAGAATCAGGTGGGTT-----**----------CTTAG--GA----------TC-ACATTATAATA----------**----------**-----**----------CAGCATT-ATACTTATGCAAGGCTTCT-TT----------CCCAGGACAAAGTGCTGGCGATCACGAACTTGATAATGGAGGAGCTCCTGGCGAA
droTak1	scf7180000410579:311740-311897 +		CGGAACCGGATAGATGCACCAGACTGGTCAGCAGATTGCGACAGAATCAGGTGGGTT-----**----------TTCCGAGAA----------CCA----------**----------**--AAT----------AATG--AAATATTATTCATATT------TATTTAT-TT----------CTTCAGGACAAAGTGCTGGCGATCACGAACTTGATAATGGAGGAGCTGCTCGGCGAA
droEug1	scf7180000409770:424944-425101 -		CAGAGCCTGATCGTGCACCAGCTGGTCAGCAGACTGCGGCAGAATCAGGTGAGTT-----**----------TCTAA--AA----------TTGATAT----------**----------TAAAC----------CATA--TATCTTAAT----ACG------CTTTTCT-TT----------TTTCAGGACAAAGTGCTGGCTATCACGAACTTGATAATGGAGGAGTTACTCGGAGAA
dm3	chr3R:22954249-22954410 -		CGGAGCCGGATCGATGCACCAGACTGGTCAGCAGACTGCGGCAGAATCAGGTGAGTT-----**----------TCTGGAAGA----------GTGGAATAGTAACTGGAG----------**----------**-----**----------C-----AAAAATAAT----TG------CATTCGT-GT----------TCCCAGGACAAAGTGCTGGCGATCACGAACTTGATAATGGAGGAACTACTCGGCGAA
droSim2	3r:22403879-22404040 -		CGGAGCCGGATCGATGCACCAGACTGGTCAGCAGACTGCGGCAGAATCAGGTGGGTT-----**----------TCTGGAAGA----------GTGGCATCATAACTGGAG----------**----------**-----**----------A-----AAATATAAT----TG------CATCGCT-GT----------TCCCAGGACAAAGTGCTGGCGATCACGAACTTGATAATGGAGGAACTGCTCGGCGAA
droSec2	scaffold_13:1717232-1717393 -		CGGAGCCGGATCGATGCACCAGACTGGTCAGCAGCTGCGGCAGAATCAGGTGGGTT-----**----------TCTGGAAGA----------GTGGCATCATATCTGGAG----------**----------**-----**----------A-----AAATATAAT----TG------CATCGCT-GT----------TCCCAGGACAAAGTGCTGGCGATCACGAACTTGATAATGGAGGAACTGCTCGGCGAA
droYak3	3R:23533190-23533355 +		CAGAGCCGGATCGATGCACCAGACTGGTCAGCAGACTGCGGCAGAATCAGGTGGGTT-----**----------TCGGCAAGA----------GTGGAATCTTAAGTGAACAT----------**----------**-CA---**----------A---AAACATAAT----TG------CATTCGT-GT----------TTACAGGACAAAGTGCTGGCGATCACGAACTTGATAATGGAGGAACTACTCGGCGAA
droEre2	scaffold_4820:5075759-5075923 +		CGGAGCCGGATCGTGCACCAGACTGGTCAGCAGACTGCGGCAGAATCAGGTGGGTT-----**----------TGGGGCAGA----------GTGGAATCCTGAGTGAACA----------**----------**-CA---**----------A---ACCAACAAT----TG------CATTTC-AA----------TCCCAGGACAAGGTGCTGGCGATATTACGAACTTGATAATGGAGGAACTGCTCGGCGAA

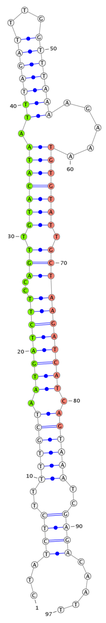
Generated: 09/08/2015 at 07:01 PM

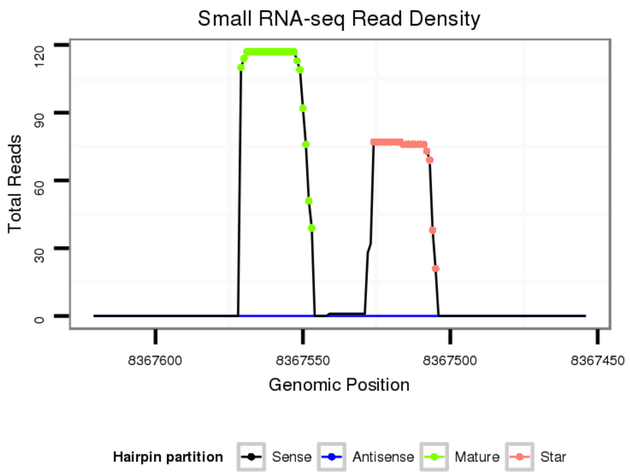
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	2
rescue.candidate	0

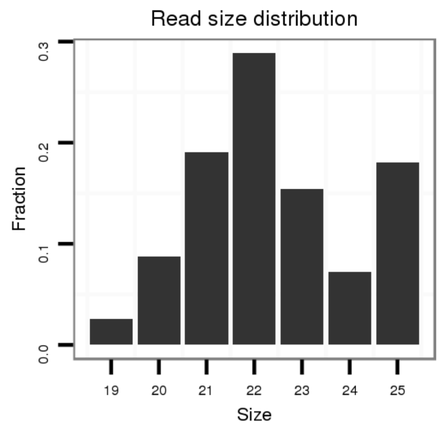
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dps_61	**XL_group1e:8367504-8367571 -**	**confident**	**Testes-restricted**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

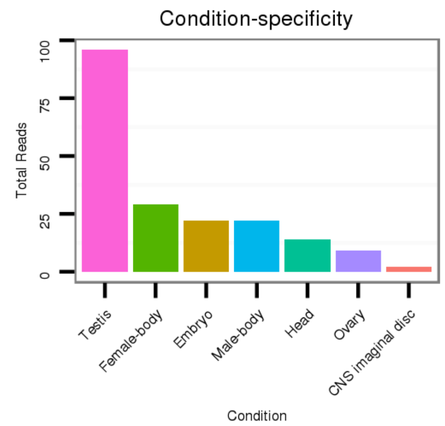
Legend: mature star mismatch in alignment mismatch in read

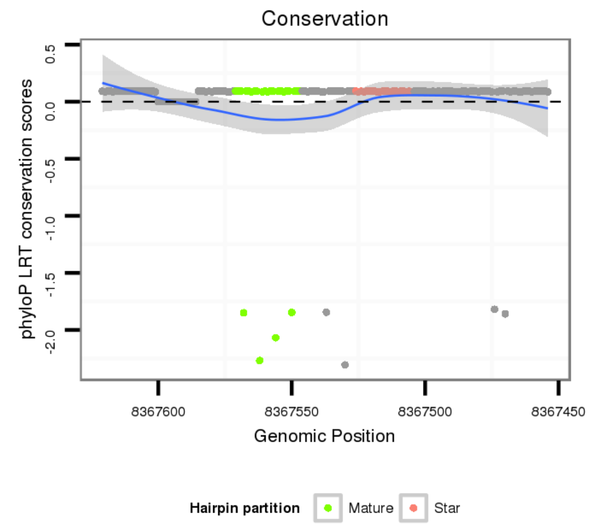
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

AGAACATTTTTTTTTAAATACTGTTTCGATTCAATCTATCTCTTTTTGCTAATGATCTTCCAGTTGTACATAATTTAGATTTGGTTTAAAAGAAATGTGTATTGCTAAGATCATCAGTAAATCGAGACAATTCGCTACAAAGATATGACAACTCAACCAATCAATTAG						SRR902011	M040 female	V112	GSM444067	M059	SRR902010	GSM343916	M062	SRR902012 CNS imaginal	M022
********...((((..((((((.(((((((..(((.(((((((.(((((((...)))))))).....)))))))).)))))))))))).))))))..)))).....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	testis	body	male body	head	embryo	ovaries	embryo	head	disc	male body
.....AATGATCTTCCAGTTGTACATAATT.....	25	0	1	34.00	34	18	3	0	1	5	2	3	0	2	0
.....AATGATCTTCCAGTTGTACATAA.....	23	0	1	25.00	25	17	1	0	0	0	7	0	0	0	0
.....TGTGTATTGCTAAGATCATCAG.....	22	0	1	21.00	21	12	2	6	1	0	0	0	0	0	0
.....AATGTGTATTGCTAAGATCATC.....	22	0	1	19.00	19	2	3	0	3	7	0	2	2	0	0
.....AATGATCTTCCAGTTGTACATA.....	22	0	1	16.00	16	13	1	2	0	0	0	0	0	0	0
.....AATGATCTTCCAGTTGTACAT.....	21	0	1	15.00	15	13	1	0	1	0	0	0	0	0	0
.....TGTGTATTGCTAAGATCATCA.....	21	0	1	15.00	15	2	5	5	1	0	0	2	0	0	0
.....AATGATCTTCCAGTTGTACATAAT.....	24	0	1	12.00	12	6	4	0	0	1	0	0	0	0	1
.....TGTGTATTGCTAAGATCATC.....	20	0	1	8.00	8	0	2	3	2	0	0	1	0	0	0
.....AATGATCTTCCAGTTGTACATAATTCG.....	27	2	1	7.00	7	7	0	0	0	0	0	0	0	0	0
.....AATGATCTTCCAGTTGTACATAAA.....	24	1	1	6.00	6	6	0	0	0	0	0	0	0	0	0
.....AATGATCTTCCAGTTGTACATAATTC.....	26	1	1	6.00	6	6	0	0	0	0	0	0	0	0	0
.....AATGATCTTCCAGTTGTACATAATTCCC.....	28	3	1	4.00	4	4	0	0	0	0	0	0	0	0	0
.....ATGTGTATTGCTAAGATCATC.....	21	0	1	4.00	4	0	3	1	0	0	0	0	0	0	0
.....AATGATCTTCCAGTTGTACA.....	20	0	1	4.00	4	4	0	0	0	0	0	0	0	0	0
.....AATGATCTTCCAGTTGTAC.....	19	0	1	4.00	4	3	0	1	0	0	0	0	0	0	0
.....AATGTGTATTGCTAAGATCAT.....	21	0	1	3.00	3	0	1	1	1	0	0	0	0	0	0
.....AATGATCTTCCAGTTGTACATAATCCC.....	27	3	1	3.00	3	3	0	0	0	0	0	0	0	0	0
.....AATGATCTTCCAGTTGTACATAAAA.....	25	2	1	3.00	3	3	0	0	0	0	0	0	0	0	0
.....AATGATCTTCCAGTTGTAA.....	19	1	1	3.00	3	2	1	0	0	0	0	0	0	0	0
.....AATGTGTATTGCTAAGATCA.....	20	0	1	3.00	3	0	0	2	1	0	0	0	0	0	0
.....TGATCTTCCAGTTGTACATAATT.....	23	0	1	3.00	3	3	0	0	0	0	0	0	0	0	0
.....AATGATCTTCCAGTTGTACATAATTCTC.....	28	3	1	3.00	3	3	0	0	0	0	0	0	0	0	0
.....ATGATCTTCCAGTTGTACAT.....	20	0	1	2.00	2	1	1	0	0	0	0	0	0	0	0
.....ATGATCTTCCAGTTGTACATAATT.....	24	0	1	2.00	2	0	1	0	0	0	0	0	1	0	0
.....AATGTGTATTGCTAAGATCATCA.....	23	0	1	2.00	2	0	1	0	0	0	0	1	0	0	0
.....AATGATCTTCCAGTTGTACATAATTA.....	26	1	1	2.00	2	2	0	0	0	0	0	0	0	0	0
.....AATGATCTTCCAGTTGTACATAATA.....	25	1	1	2.00	2	2	0	0	0	0	0	0	0	0	0
.....AATGTGTATTGCTAAGATT.....	19	1	1	1.00	1	0	0	0	1	0	0	0	0	0	0
.....AATGATCTTCCAGTTGTACATC.....	22	1	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....TTGGTTTAAAAGAAATGTGTATTGC.....	25	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....AATGTGTATTGCTAAGATCATCT.....	23	1	1	1.00	1	0	0	0	1	0	0	0	0	0	0
.....AATGATCTTCCAGTTGTACATAATTTTC.....	28	2	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....AATGATCTTCCAGTTGTACT.....	20	1	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....TGTGTATTGCTAAGATCAT.....	19	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0

Anti-sense strand reads

TCTTGTAAAAAAAAATTTATGACAAAGCTAAGTTAGATAGAGAAAAACGATTACTAGAAGGTCAACATGTATTAAATCTAAACCAAATTTTCTTTACACATAACGATTCTAGTAGTCATTTAGCTCTGTTAAGCGATGTTTCTATACTGTTGAGTTGGTTAGTTAATC					M040 female body
********...((((..((((((.(((((((..(((.(((((((.(((((((...)))))))).....)))))))).)))))))))))).))))))..)))).....**********	Read size	# Mismatch	Hit Count	Total Norm	Total

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
dp5	XL_group1e:8367454-8367621 -	dps_61	AGAACATTTTT-----TTTTAAATACTGTTTCGATTCAATCTATCTCTTTTTGCTAATGATCTTCCAGTTGTACATAATTTAGATTTGGTTTAAAAGAAATGTGTATTGCTAAGATCATCAGTAAATCGAGACAATTCGCTACAA-AGATATGACAACTCAACCAATCAATTAG
droPer2	scaffold_13:196869-197027 +		AGAACATTTTTTTTTTTTTAAATAC----------TATCTCTTTTTGCTAATAATCTTGCAGTTATACATGATTTAGATTTGGATTAAAACAAATGTGTATTGCTAAGATCATCAGTAAATCGAGACAATTCGCTACAAAAGATATGTCAATTCAACCAATCAATTAG

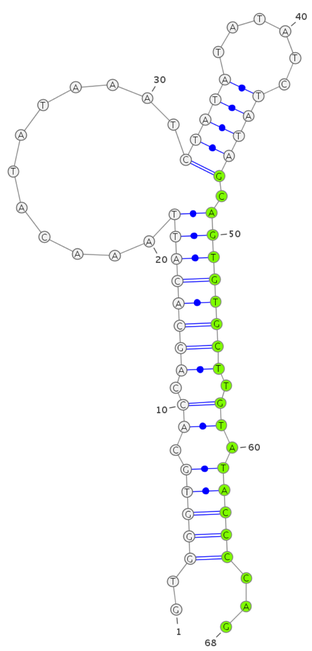
Generated: 09/08/2015 at 08:37 PM

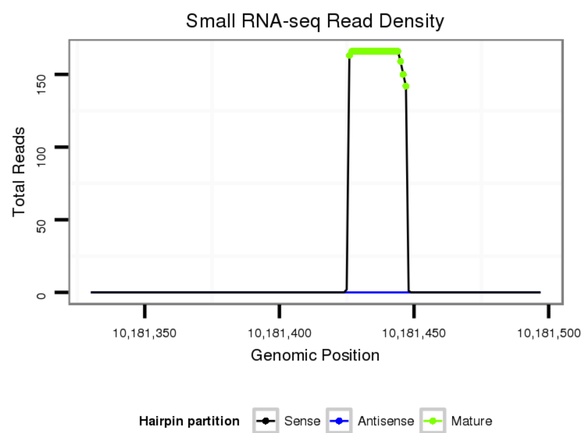
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

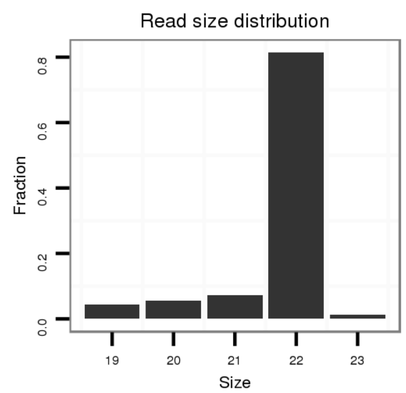
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dps_455	**2:10181380-10181447 +**	**candidate-rescued**	**Mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

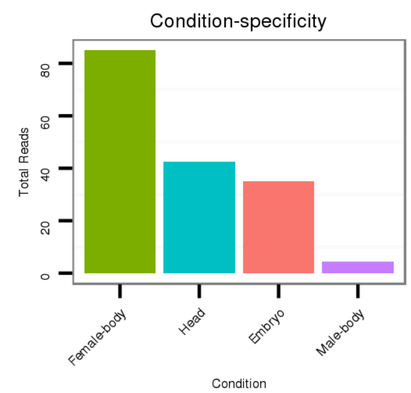
Legend: mature star mismatch in alignment mismatch in read

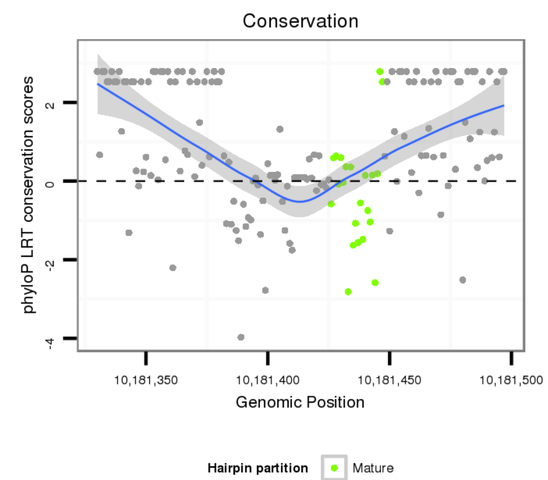
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dpse\GA27138-in]; CDS [Dpse\GA27138-cds]; CDS [Dpse\GA27138-cds]

No Repeatable elements found

mature	star
1. dps_455 2:10181426-10181447 + 2. dps_2346 Unknown_singleton_294:18519-18540 -	

Sense Strand Reads

hide 3p reads show mid mismatch reads

TGAAGGTCGAGCGTGCCAGGCGCAATTACACTCAGTTCCAGGAAGAGCAGGTGGGTGCACCAGCACATTAAACATATAAATCTATATATATCTATAGCAGTGTGCTTGTATACCCCAGACAACCAAGACACAGTCGTCCACTCTGATCCCCATCAATCGATTGACCAT **********..(((((.((.((((((((.....(((((.....)))))*)))))))*)).)).)))))...**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M040 female body	GSM444067 head	M059 embryo	GSM343916 embryo	M062 head	V112 male body
.....GCAGTGTGCTTGTATACCCCAG.....	22	0	2	136.00	272	131	45	33	33	22	8
.....GCAGTGTGCTTGTATACCCC.....	20	0	2	9.00	18	12	2	1	0	2	1
.....GCAGTGTGCTTGTATACCCCA.....	21	0	2	8.50	17	12	1	3	0	1	0
.....GCAGTGTGCTTGTATACCC.....	19	0	2	7.00	14	4	4	0	0	6	0
.....GCAGTGTGCTTGTATACCCCAGT.....	23	1	2	5.00	10	5	1	2	1	1	0
.....CAGTGTGCTTGTATACCCCAG.....	21	0	2	3.50	7	7	0	0	0	0	0
.....AGCAGTGTGCTTGTATACCCCAG.....	23	0	2	2.00	4	2	2	0	0	0	0
.....CAGTGTGCTTGTATACCCCAGT.....	22	1	2	1.50	3	1	0	1	0	1	0
.....GCAGTGTGCTTGTATACCCCAC.....	22	1	2	1.50	3	0	0	3	0	0	0
.....GCAGTGTGCTTGTATACCCCAGA.....	23	0	2	1.00	2	2	0	0	0	0	0
.....GCAGTGTGCTTGTATACCCCAGC.....	23	1	2	1.00	2	1	0	0	1	0	0
.....GCAGTGTGCTTGTATACCCCAT.....	22	1	2	0.50	1	0	1	0	0	0	0
.....CAGTGTGCTTGTATACCCCAGC.....	22	1	2	0.50	1	0	0	0	0	1	0
.....CAATTACACTCAGTTCCAGGAAGAGCAG.....	28	0	2	0.50	1	1	0	0	0	0	0
.....AGTGTGCTTGTATACCCCAG.....	20	0	2	0.50	1	1	0	0	0	0	0
.....CAGTGTGCTTGTATACCCC.....	19	0	2	0.50	1	1	0	0	0	0	0
.....GCAGTGTGCTTGTATACCCCAGTA.....	24	2	2	0.50	1	1	0	0	0	0	0

Anti-sense strand reads

ACTTCCAGCTCGCACGGTCCGCGTTAATGTGAGTCAAGGTCCTTCTCGTCCACCCACGTGGTCGTGTAATTTGTATATTTAGATATATATAGATATCGTCACACGAACATATGGGGTCTGTTGGTTCTGTGTCAGCAGGTGAGACTAGGGGTAGTTAGCTAACTGGTA **********..(((((.((.((((((((.....(((((.....)))))*)))))))*)).)).)))))...**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M040 female body

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
dp5	2:10181330-10181497 +	dps_455	TGAAGGTCGAGCGTGCCAGGCGCAATTACACTCAGTTCCAG-GAAGAGCAGGTGGGTGCACC--A-GCA-----CA--TTAAA----CATATAAATCTATA-----TATATC----------T------ATAGC--A----G----------TGT-GCTTGTA--TAC----CCCAGACAACCAAGACACAGTCGTCCACT-CTGATCCCCATCAATCGATTGACCAT
droPer2	scaffold_0:10300282-10300453 -	dpe_462	TGAAGGTCGAGCGTGCCAGGCGCAATTACACGCAGTTCCAG-GAAGAGCAGGTGGGTGCACC--A-GCA-----CA--TTAAACATA----TAAAGCTATATAT-GTATATC----------T------ATAGC--A----G----------TGT-GCTTGTA--TAC----CCCAGACAACCAAGACACAGTCGTCCACT-CTGATCCCGATCAATCGATTGCCCAT
droWil2	scf2_1100000004902:9022539-9022701 -		TGAAGGTCGAACGAGCTAGACGTAATTATACAAATTCCAA-GAGGAACAGGTACCA-----**-**---------CACACATATCAAG-----AATT----------GTTTTGTACTCAA---------TGTAA----CAC--A----AAT---------**---**ACTTTTC--TTT----TGTAGCGCACCAAAACTCAGTCGTCCAGA-CTTATTCCAATCAATCGTTTGCCCAT
droVir3	scaffold_12822:3790401-3790564 -		TGAAGGTCGAGCGTGCCAGGCGCAATTATACCCAGTTTCAG-GAGGAGCAGGTGGGTGCAGT--**-**---------A----AATCA----A---------AATTG--AAA--GTCTCTG----AG---------CTAA----**-----**--TGATATAT-----AGT--TC-ATCTA-TTG----TCTAGCCAATTAAAACACAGCGGCAAGA-CTAATACCTATTAATCGTTTGCCCAT
droMoj3	scaffold_6540:17099574-17099735 -		TGAAGGTCGAGCGTGCCAGGCGCAATTATACGCAATACCAA-GAGGAGCAGGTGGGTGCACT--TAGCA-----AA--TGAAA----**----------**-----**------**AGTGTGCTGG----AG---------CTAA----**--**TGCCGA----GAT---------**---**CCGGTCC--AT----TTTAGCGCACCAAAACACAGACGCCAGC-CTCATACCCATTAATCGTTGCCCAT
droGri2	scaffold_14906:1382895-1383059 -		TGAAGGTCGAGCGGCCCGGCGCAACTATACACAGTACCAA-GAGGAGCAGGTGTGTACACT--C-GGC-----TATA----AATCA----A---------GTTG----ATGTCCTTG----AA---------CTAA----**--**TAC--A----ATT---------**---**G-CGGTC--AAT----TTCAGCCAAGTAAAACACAGCAGCCAGA-CTCATACCTATCAATCGGCTGCCCAT
droAna3	scaffold_13340:17149374-17149541 -		TGAAGGTCGAGCGCGCTCGAAGGAACTACACGCAGTTCCAA-GAAGAACAGGTACGAGTCGC-TA-GCC-----CA--AGAGG----TTCACAAAC-----AT-ACTT----------GG---------TG----AAGAGT--A----ATG---------**---**A-CGTTTATTTT----CACAGCTACAAAGACACAGTCGTCCACT-TTGATACCCATCAATCGACTGCCCAT
droBip1	scf7180000396424:652032-652199 -		TGAAGGTCGAGCGCGCTCGAAGGAACTACACCAGTTCCAA-GAAGAGCAGGTAGGAGTCAC-TG-GCC-----CA--CCCAG----TTCACAATC-----AT-GGTTACC----------T-----AAGAGT--A----ATG---------**---**A-CGTTTATTTT----GCAGGCCACAAAGACACAGTCGTCCAGC-TTGATACCCATCAATCGACTGCGTAT
droKik1	scf7180000302256:110322-110486 -		TGAAGGTCGAGCGGCTCGGCGGAATTACACCAGTTCCAG-GAAGAGCAGGTGACTTAACC--**-**---------ACA----GTCCT----C-TT-------AGTT----------GGTCCGTTCAAAT---------CGCA----**---**AT--A----AAC---------**---**CCTTCTC-ATTT----TACAGCCACCAAGACACAGTCGTCCAGC-CTGATACCGATCAACCGACTTCCCAT
droFic1	scf7180000453581:272813-272965 +		TGAAGGTCGAGCGTGCCAGGAGGAATTACACCAGTTTCAG-GAGGAGCAGGTGGGCTTAGC--T-**---**------GCA----ATA--**----------**-----**------**----------GG---------TGTATCTGACTATT--A----**-**----------**---**---ATCTATTTTTGTAGACAGTCGACCAAGACACAATCGTCCACT-TTGATACCGATCAACCGACTTCCCAT
droEle1	scf7180000491280:3591270-3591445 +		TGAAGGTCGAGCGAGCCCGCCGGAATTACACTCAGTTTCAG-GAGGAGCAGGTGGGGTTCTACTT-TGCTACTAGT--ACTAC----TTTAC--C------**------**----------AA---------TAAAT----**-----**CAGTGGTATATAACAGCGTT-CCT--TA--ATG----CACAGCCACCAAGAGCCAATCGTCAACG-CTGATTCCAATCAATCGACTTCCCAT
droRho1	scf7180000779501:61345-61505 -		TGAAGGTCGAGCGAGCCCGGCGCAATTACACTCAGTTTCAG-GAGGAGCAGGTGGGCATGGG--T-**---**------GTA----CAC-C----C-TG------**------**----------GG---------CCAGT----**-----**CACTTATA----ACAGAATAC-CTCTCCC--AAC----GCCAGCCCACCAAGAGCCAGTCGTCCACT-CTGATACCCATCAATCGACTTCCCAT
droBia1	scf7180000302075:2440004-2440169 +		TGAAGGTCGAGCGTGCCCGGCGCAACTACACTCAGTTTCAG-GAGGAGCAGGTGGGCCACCT--T-**---**------**---**--G--**----**----------**------**----------GGTCTACTCAATTCAAT----**-----**TGATTATCTATGACAGACTAT-ACCTCTC--ATC----GCCAGCCCACCAAGAGCCAATCGTCCACT-CTGATACCGATCAATCGACTTCGAAT
droTak1	scf7180000415383:115705-115865 +		TGAAGGTCGAGCGTGCCAGGCGCAATTACACTCAGTTTCAG-GAGGAGCAGGTGGGTTCTTC--T-CTC-----CA--CTTAA----T----------**------**----------ACAAC----**-----**AAGATATCTAT-----AATATATAACCTA-TTA----CATAGCCACCAAGAGCCAATCGTCCACT-CTGATACCGATCAATCGACTTCCCAT
droEug1	scf7180000409787:1235183-1235345 +		TGAAGGTCGAGCGTGCCCGGCGCAATTATACTCAATTTCAG-GAGGAGCAGGTGGGTTTTTG--G-T-----**-TT-**----ACTCA----ATAC------**------**----------CG---------CCGA----**-----**--TTATTTATAACATCCCAT-CCTTTGT--ACC----AACAGCCACCAAGAGCCAATCGTCCACT-CTTATACCAATCAATAGACTTCCCAT
dm3	chr3R:24345661-24345822 -		TGAAGGTCGAGCGGCCCGGCGCAACTACACTCAGTTTCAG-GCGGAGCAGGTGGGTTAAGG--T-**---**------ACA----ACCCA----CAAC------**------**----------GG---------TCAAT----**-----**ATGTTATATAT-----AGTAT-GCAACCT--ACT----GCAGGCCACCAAGAGCCAGTCGTCCACT-CTGATACCAATCAACCGCTCTACCCAT
droSim2	3r:23723760-23723921 -		TGAAGGTCGAGCGGCCCGGCGCAACTACACTCAGTTTCAG-GAGGAGCAGGTGAGTAGAGG--T-**---**------ACA----ACCCA----CAAC------**------**----------GG---------TCAAT----**-----**ATGTTATATAT-----AGTAT-CCAACCT--ACT----GCAGGCCACCAAGAGCCAGTCGTCCACT-CTGATACCAATCAACCGCTCTACCCAT
droSec2	scaffold_22:948938-949100 -		TAAAGGTCGAGCGCCCCGGCGCAACTACACTCAGTTTCAGCGAGGAGCAGGTGAGTACAGG--T-**---**------ACA----ACCCA----C-AC------**------**----------GG---------TCAAT----**-----**ATGTTATATAT-----AGTAT-CCAACCT--ACT----GCAGGCTACTAAGAGCCAGTCGTCCACTCCTGATACCATTCAACCGCTCTACCCAT
droYak3	3R:22151663-22151827 +		TGAAGGTCGAGCGCCCCGGCGCAACTACACTCAGTTTCAG-GAGGAGCAGGTGCGCTAACC--C-**---**------ACATCC-ACCCA----CTAC------**------**----------GG---------TCAAT----**-----**ATGTTATATAG-----AGTAT-CTATCC--AAT----GCCAGCCCACCAAGAGCCAGTCATCCAGC-CTGATACCGATCAACCGACTTCCCAT
droEre2	scaffold_4820:3689926-3690090 +		TAAAGGTCGAGCGCCCCGGCGCAACTACACCAGTTTCAG-GAGGAGCAGGTGGCTAG--**-**--C-----CACTT-AAACCCT----CCTT------**------**----------GG---------TCAAT----**-----**ATGCTATATAT-----AGTAT-CCTAACT--AAT----GCCAGCCCACCAAGACACAGTCGTCCACT-CTGATACCGATCAACCGACTTCCCAT

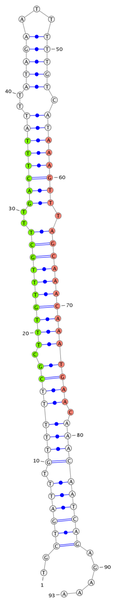
Generated: 09/08/2015 at 07:08 PM

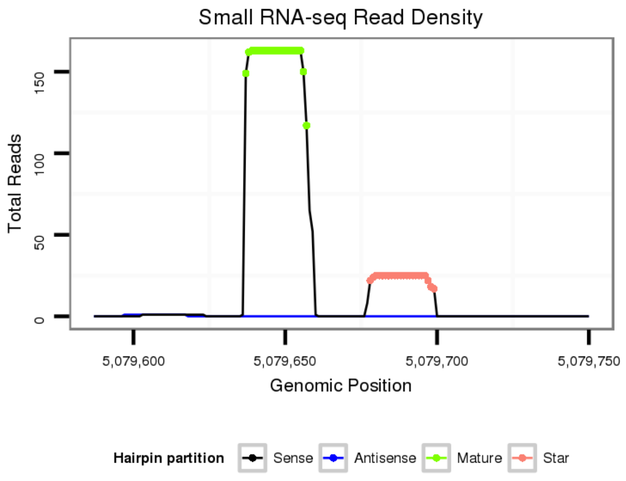
	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	2

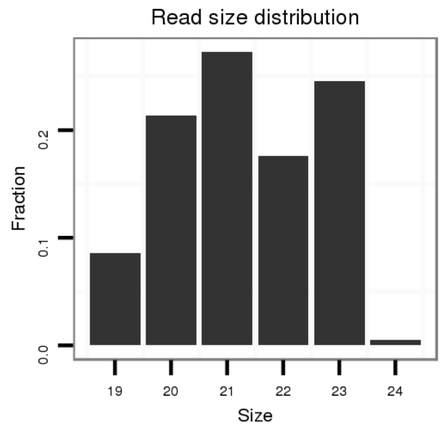
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dps_187	**4_group3:5079637-5079700 +**	**confident**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

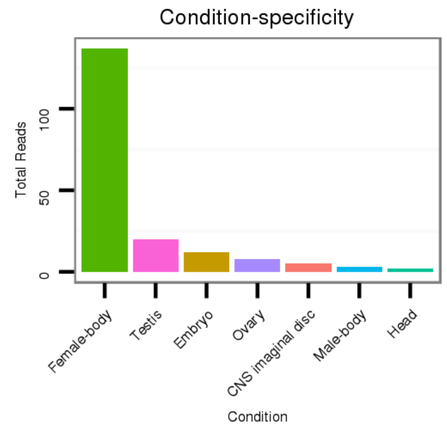
Legend: mature star mismatch in alignment mismatch in read

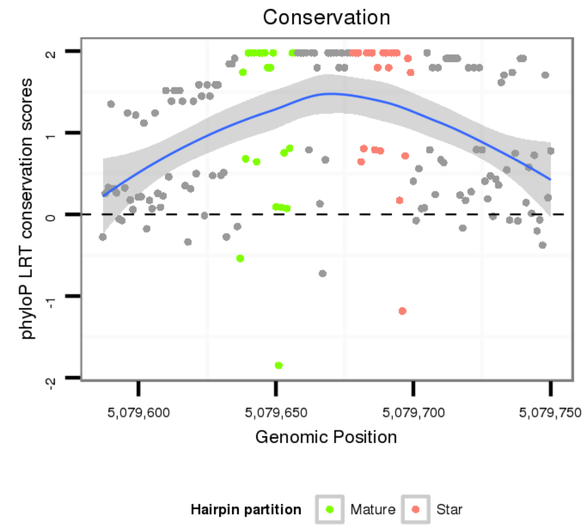
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

ATATTCGAAGCGATCCGTAGACGAACAAAGCACGTTGCTGATTTGTTTTTCGCTTTGTTTGCTTTGACTTTATTTATAGAATTTTTGTCATAAAGTTTAGCAAACAAATGAACAAACAATCAGAGAAAAATCGCTGACTATTTCAATTTGTTTTCGTTGAATTT **********..(((((((.(((((((((.((((((((((..((((((((..(((((...))))).)))))))).)))))))))))))).))))))))))).....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M040 female body	SRR902011 testis	M059 embryo	SRR902010 ovaries	SRR902012 CNS imaginal disc	GSM343916 embryo	V112 male body	M022 male body	M062 head	GSM444067 head
.....CGCTTTGTTTGCTTTGACTTT.....	21	0	1	46.00	46	44	1	0	0	0	0	1	0	0	0
.....CGCTTTGTTTGCTTTGACTTTAT.....	23	0	1	44.00	44	24	10	1	3	5	0	0	0	0	1
.....CGCTTTGTTTGCTTTGACTT.....	20	0	1	31.00	31	27	3	0	0	0	0	0	1	0	0
.....AAAGTTTAGCAAACAAATGAAC.....	22	0	1	13.00	13	5	0	8	0	0	0	0	0	0	0
.....CGCTTTGTTTGCTTTGACT.....	19	0	1	13.00	13	11	0	0	0	0	1	0	0	1	0
.....CGCTTTGTTTGCTTTGACTTTA.....	22	0	1	13.00	13	8	5	0	0	0	0	0	0	0	0
.....GCTTTGTTTGCTTTGACTTTAT.....	22	0	1	6.00	6	1	0	0	5	0	0	0	0	0	0
.....GCTTTGTTTGCTTTGACTTT.....	20	0	1	6.00	6	6	0	0	0	0	0	0	0	0	0
.....TAAAGTTTAGCAAACAAATGA.....	21	0	1	3.00	3	1	0	1	0	0	0	1	0	0	0
.....TAAAGTTTAGCAAACAAATG.....	20	0	1	2.00	2	2	0	0	0	0	0	0	0	0	0
.....TAAAGTTTAGCAAACAAATGAAC.....	23	0	1	2.00	2	2	0	0	0	0	0	0	0	0	0
.....CGCTTTGTTTGCTTTGACA.....	19	1	2	1.50	3	2	0	0	1	0	0	0	0	0	0
.....AGTTTAGCAAACAAATGAAC.....	20	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....TCGCTTTGTTTGCTTTGACTT.....	21	0	1	1.00	1	0	1	0	0	0	0	0	0	0	0
.....CGCTTTGTTTGCTTTGACTTTT.....	22	1	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....GTAGACGAACAAAGCACGTTG.....	21	0	1	1.00	1	0	1	0	0	0	0	0	0	0	0
.....CGCTTTGTTTGCTTTGACTTTATA.....	24	1	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....TAAAGTTTAGCAAACAAATGAA.....	22	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....AAAGTTTAGCAAACAAATG.....	19	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....CTTTGTTTGCTTTGACTTTAT.....	21	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....AAGTTTAGCAAACAAATGAAC.....	21	0	1	1.00	1	0	0	1	0	0	0	0	0	0	0
.....GCTTTGTTTGCTTTGACTT.....	19	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....AAGTTTAGCAAACAAATGA.....	19	0	1	1.00	1	0	1	0	0	0	0	0	0	0	0
.....CGCTTTGTTTGCTTTGACTTTATT.....	24	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0

Anti-sense strand reads

TATAAGCTTCGCTAGGCATCTGCTTGTTTCGTGCAACGACTAAACAAAAAGCGAAACAAACGAAACTGAAATAAATATCTTAAAAACAGTATTTTCAAATCGTTTGTTTACTTGTTTGTTAGTCTCTTTTTAGCGACTGATAAAGTTAAACAAAAGCAACTTAAA **********..(((((((.(((((((((.((((((((((..((((((((..(((((...))))).)))))))).)))))))))))))).))))))))))).....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M040 female body
.....GCTAGGCATCTGCTTGTTTCG.....	21	0	1	1.00	1	1

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
dp5	4_group3:5079587-5079750 +	dps_187	ATATTCGAAGCGATCCGTAGACGAACAAAGCAC-GTTGCTGATTT----------GT---------TTT-TCGCTTTGTTTGCTTTGACTTTATTTATAGAAT--TTTTGTCAT-AAAGTTTAGCAAACAAATGAAC--------A----AACAATCAGA-GAAAAA---TCGCTG----ACTAT----------TTCAATTTGTTTTCGTTGA-ATTT
droPer2	scaffold_1:6570970-6571133 +		ATATTCGAAGCGATCCGTAGACGAACAAAGCAC-GTTGTTGATTTG----------T---------TTT-TCGCTTTGTTTGCTTCGACTTTATTTATAGAAT--TTTTGTCAT-AAAGTTTAGCAAACAAATGAAC--------A----AACAATCAGT-GAAAAA---TCGCTG----ACTAT----------TTCGATTTGTTTTCGTTGA-ATTT
droAna3	scaffold_12916:5704769-5704878 -		----------\----------\----------\--\---------\--\--\--\--\--CTTTATTTGCT---GTTTTATTTTTAGAATTTTTTTGTCAT-AAAATTTAACAAACAAATATAC--------C----TGGGAACTG-\------\--CTGCTG----AGAATCTGTGCCATTAAAT----------\-------TGTATTTTTCCA-A-CT
droBip1	scf7180000396568:1135145-1135246 +		T----------\----------\----------\--\---------TTT-TTGCTTTGTTTGCT---AGTTTATTTTTAGCG--TTTTGTCAT-AAAGTTTAACAAACAAACATAC--------CTGTTGGGGAACTGTTGAAAAATTTCGCTG----AGAAT----------\----------\--CT
droKik1	scf7180000302270:961344-961521 +		C----------GAACAAAGGTCAGTTGTTGTTTTAGTTATGGCTGTTCATAAGCATTTTTTT-CTGCTTTGTTTGCT---AGTTTATTTTTAGCT--TTTTGTCATTAAAGTTTAACAAACAAACAAACAAAGCAACG----GGGGAACAGT-GAAAAA---TCGCTG----AGACG----------TTGTC------TTGGGATATGTTTTCGATCG-GTTT
droFic1	scf7180000453924:1637394-1637550 -		\----------\----------\-----TTGCTGTTCAG------TTTTTT-TCGCTTTGTTTGCT---AGCTTATTTTTAGCA--TTTTGTCAT-AAAGTTTAACAAACAAACAAACCA------\-ACCAGGCAACAGT-GAAAAA---TCGCTG----AGACTT--TGCCATTAAAA---TGTGTTGTTGTT------TTGTGATTTGTTTTCGATTG-GTTT
droEle1	scf7180000490728:367238-367423 -		ACATTCATAGCGAATGACAGG-GAACAAAGGTGAGTTGTTGTTTTAGTTATTGCTGATCAT-------TTTTT-TCGTTTTGTTTGCT---AGTTTATTTTTAGCT--TTTTGTCAT-AAAGCTTAACAAACAAACAAACAAACAAACC----A-TCAACAGT-AAAAAA---TAGCTG----AGACTAAGC----------GGGATTGTTTTCGATCG-GTCT
droRho1	scf7180000779523:357408-357553 -		\----------\-TTGCTGTTTTATTTA--------\--\---------\--T-TTGCTTTGTTTGCT---AGTTTATTTTTAGCT--TTTTGTCAT-AAAGTTTAACAAACAAACC---\--------\-----\----AACAGT-GAAAAA---TAGCAG----CGACTTTGTGCCATTAAAA---TGTCTGGTTGTT------TCGGGATTTGCTTTCGATCG-GTCT
droBia1	scf7180000302408:1950159-1950358 -		ACATCCAAAGCAAATGCCTGG-GAACAAAGACCGCTGTTGTTTTAGTTATTGCTGCTCAT---------TTTTCTGCTTTGTTTGCT---AGTTTATTTTTAGCT--TTTTGTCAT-AAAGTTTAACAAACAAACCAAC--------C----AGGCAACAGT-GAAAAA---TAGCTG----ACACTGTGCGCCATTAAA----TGTGTGGTTGTT------TTGGGATTGTTTTCGATCG-\TTT
droTak1	scf7180000415399:638509-638711 -		ACATTCATAGCAAATGACTGG-GAACAAAGGTCAGTTGTTGTTTTAGTTATTGGTGCTCAT-------TTTTT-CTGCTTTGTTTGCT---AGTTTATTTTTAGC--TTTTGTCAT-AAAGTTTAACAAACAAACCAAC--------C----AGGCAACAGT-GAAAAA---TAGCTG----ACACTTTGTGTTATTAAAA---TGTGTAGTTGTT------TTTCGATTTGTTTTCGCTTGTATTT
droEug1	scf7180000409554:2433155-2433338 +		ACATTCATAG---------GG-AAACAAAGGTCGTTGTTGTTTTGGTTATTGCTGTTCAT---------TTT-CCGCTTTGTTTGCT---AGTTTATTTTTAGCT--TTTTGTCAT-AAAGTTTAACCAACAAACAAACCA------\-ACCAGGCAACAGT-GAAAAA---CATCCAG----ACACTTGGTGCCATTAAAAA----------TGGGATTTGTGTTCGATCC-GTTG
dm3	chr2L:3649385-3649564 -		ACATTCTTAGCGAATGACAGG-AAACAAAGGTCAGTTGTTGTTTTCAGTTACTGCTGCTCAC---------TTT-TCGCTTTGTTTGCT---AGTTTATTTTTAGCA--TTTTGTCAT-AAAGTTTAACAAACAAACCAAC--------C----AGGCAACAGT-GAAAAA---TTGCTG----ACACT--GTGCCATTAAA----------\-----TTTGTATTCGATCG-ATTT
droSim2	2L:3507764-3507943 -		ACATTCATAGCGAATGACAGG-AATCAAAGGTCAGTTGTTGTTTCAGTTACCGCTGCTCAC---------TTT-TCGCTTTGTTTGCT---AGTTTATTTTTAGCA--TTTTGTCAT-AAAGTTTAACAAACAAACCAAC--------C----AGGCAACGGT-GAAAAA---TTGCTG----ACACT--GTGCCATTAAA----------\-----TTTGTATTCGATCG-ATTT
droSec2	scaffold_5:1750263-1750442 -		ACGTTCATAGCGAATGACAGG-AAACAAAGGTCAGTTGTTGTTTCAGTTACTGCTGCTCAC---------TTT-TCGCTTTGTTTGCT---AGTTTATTTTTAGCA--TTTTGTCAT-AAAGTTTAACAAACAAACCAAC--------C----AGGCAACGGT-GAAAAA---TTGCTG----ACACT--GTGCCATTAAA----------\-----TTGTATTCGATCG-ATTT
droYak3	2L:3643502-3643709 -		GCATTTATTGCGAATGACAGG-AAACAAAGGCCAGTTGTTGTTTCAGTTACTGCCGCTCAA---------TTT-TCGCTTTGTTTGCT---AGTTTATTTTTAGCA--TTTTGTCAT-AAAGTTTAACAAACAAACCAAC--------C----AGGCAACAGT-GAAAAA---TTGCTG----ACACG--GTGCCATTAAAAAACTGTGGTGTTGTTTGTATTTTGGGATTTGTATTGGATCG-ATTT
droEre2	scaffold_4929:3688596-3688801 -		ACATTCATAGTGAATGACAGG-AAACAAAGGTCAGTTGTTGTTTCGGTTACTGCTGCTCAA---------TTT-TCGCTTTGTTTGCT---AGTTTATTTTTAGCA--TTTTGTCAT-AAAGTTTAACAAACAAACGAAC--------C----AGGCAACAGT-GAAAAA---TTCCTGACTGAGACCC-CGTGCCATTAAAAA-CTGTGGTGTTGTT------TTGGGATTTGTATTCGATCG-ATTT

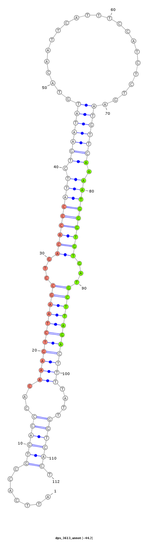
Generated: 09/08/2015 at 08:13 PM

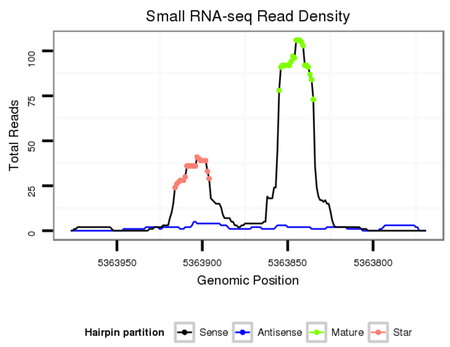
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

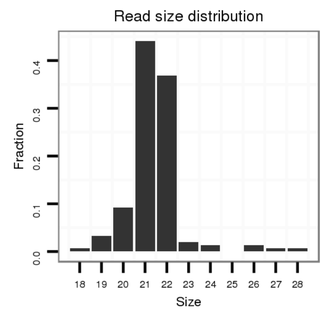
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dps_3613	**3:5363819-5363927 -**	**confident**	**Canonical miRNA**	**CDS**	[View on UCSC Genome Browser [Cornell Mirror]]

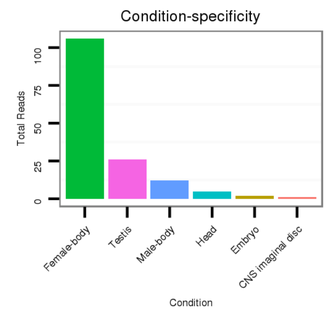
Legend: mature star mismatch in alignment mismatch in read

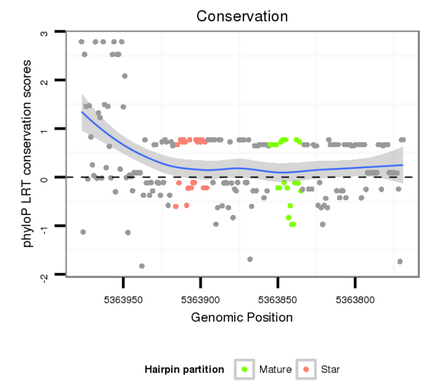
Predicted structure











Show Alternate Folds

Flybase annnotation

CDS [Dpse\GA19635-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

TTCAGAAATTGGCTAAATGTGATGCATAATCCATAGAATGCATACCATTCACCGTGACCCACAAAGTCTAAGCCTGACACCCATTCTCGAATGTTCAAAATGGGTGTGATGCTTAGACTTTTATTGGTCACTGTATTATTTGTAAGTAAGCTTTTCATGAACAAAAAAGCAATTTTACCAATT **********.....((((((...((((((((((...(((((((((.(((((((.....)))))))).))))))))))...)))))))))))....)))))))..**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M040 female body	SRR902011 testis	V112 male body	GSM444067 head	M059 embryo	M062 head	M022 male body	SRR902010 ovaries	SRR902012 CNS imaginal disc
.....AAAATGGGTGTGATGCTTAGA.....	21	0	1	22.00	22	13	6	3	0	0	0	0	0	0
.....CAAAATGGGTGTGATGCTTAGA.....	22	0	1	15.00	15	13	0	1	0	0	0	0	0	1
.....AATGTTCAAAATGGGTGTGATG.....	22	0	1	11.00	11	8	0	3	0	0	0	0	0	0
.....CAAAGTCTAAGCCTGACACCC.....	21	0	1	9.00	9	9	0	0	0	0	0	0	0	0
.....AAAATGGGTGTGATGCTTAGAC.....	22	0	1	7.00	7	7	0	0	0	0	0	0	0	0
.....TGATGCTTAGACTTTTATTGG.....	21	0	1	6.00	6	2	4	0	0	0	0	0	0	0
.....AAATGGGTGTGATGCTTAGACT.....	22	0	1	5.00	5	4	0	1	0	0	0	0	0	0
.....AAAATGGGTGTGATGCTTAG.....	20	0	1	4.00	4	2	1	0	1	0	0	0	0	0
.....AAATGGGTGTGATGCTTAGAC.....	21	0	1	4.00	4	3	1	0	0	0	0	0	0	0
.....CAAAATGGGTGTGATGCTTAG.....	21	0	1	4.00	4	3	1	0	0	0	0	0	0	0
.....TGATGCTTAGACTTTTATTGGT.....	22	0	1	3.00	3	2	1	0	0	0	0	0	0	0
.....ACAAAGTCTAAGCCTGACACC.....	21	0	1	3.00	3	3	0	0	0	0	0	0	0	0
.....TGTGATGCTTAGACTTTTATTG.....	22	0	1	3.00	3	2	0	1	0	0	0	0	0	0
.....AAATGGGTGTGATGCTTAG.....	19	0	1	3.00	3	2	1	0	0	0	0	0	0	0
.....TTCAAAATGGGTGTGATGCTT.....	21	0	1	3.00	3	2	0	0	1	0	0	0	0	0
.....TGACACCCATTCTGAATATGTA.....	22	0	1	3.00	3	0	2	0	0	1	0	0	0	0
.....TAAGCCTGACACCCATTCTGA.....	21	0	1	3.00	3	1	2	0	0	0	0	0	0	0
.....CCACAAAGTCTAAGCCTGACAC.....	22	0	1	3.00	3	0	3	0	0	0	0	0	0	0
.....CTAAGCCTGACACCCATTCTG.....	21	0	1	2.00	2	1	1	0	0	0	0	0	0	0
.....GTGTGATGCTTAGACTTTTAT.....	21	0	1	2.00	2	2	0	0	0	0	0	0	0	0
.....AATGTTCAAAATGGGTGTGAT.....	21	0	1	2.00	2	2	0	0	0	0	0	0	0	0
.....ACAAAGTCTAAGCCTGACAC.....	20	0	1	2.00	2	0	1	0	0	0	1	0	0	0
.....TAAGCCTGACACCCATTCTGAA.....	22	0	1	2.00	2	2	0	0	0	0	0	0	0	0
.....TTCAAAATGGGTGTGATGCTTA.....	22	0	1	2.00	2	1	0	0	0	0	1	0	0	0
.....AAATGGGTGTGATGCTTAGACTT.....	23	0	1	2.00	2	2	0	0	0	0	0	0	0	0
.....ACACCCATTCTGAATATGTACAATTCA.....	27	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....AATGGGTGTGATGCTTAGAC.....	20	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....CAAAATGGGTGTGATGCTTA.....	20	0	1	1.00	1	0	0	1	0	0	0	0	0	0
.....TGAATGTTCAAAATGGGTGTG.....	21	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....TGGGTGTGATGCTTAGACTTTT.....	22	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....TTGGTCACTGTATTATTTGTA.....	21	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....CACAAAGTCTAAGCCTGACAC.....	21	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....AATGTTCAAAATGGGTGTGATGA.....	23	1	1	1.00	1	0	0	0	0	0	0	1	0	0
....GAAATTGGCTAAATGTGATGC.....	21	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....TTCAAAATGGGTGTGATGCT.....	20	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....TGTGATGCTTAGACTTTTATTGGTT.....	25	1	1	1.00	1	1	0	0	0	0	0	0	0	0
.....ATTTCCATCTCTGAATGTTCA.....	21	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....AAAATGGGTGTGATGCTTAGAA.....	22	1	1	1.00	1	0	0	1	0	0	0	0	0	0
.....CTAAGCCTGACACCCATTCTGA.....	22	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....AGTCTAAGCCTGACACCCATT.....	21	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....AATGTTCAAAATGGGTGTGA.....	20	0	1	1.00	1	0	0	1	0	0	0	0	0	0
.....CACCGTGACCCACAAAGTCTAAGCCTG.....	27	0	1	1.00	1	0	0	0	0	1	0	0	0	0
.....TGATGCTTAGACTTTTATTG.....	20	0	1	1.00	1	0	1	0	0	0	0	0	0	0
.....AAGTCTAAGCCTGACACCCAT.....	21	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....AAAGTCTAAGCCTGACACC.....	19	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....TCATTTCCATCTCTGAATGTTCAAAA.....	26	0	1	1.00	1	0	1	0	0	0	0	0	0	0
.....TGACACCCATTCTGAATATG.....	20	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....CAATTCATTTCCATCTCTGA.....	20	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....CCACAAAGTCTAAGCCTG.....	18	0	1	1.00	1	0	0	0	0	0	0	1	0	0
.....TGACCCACAAAGTCTAAGCCT.....	21	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....TTTCCATCTCTGAATGTTCAAAATGGGT.....	28	0	1	1.00	1	0	0	0	0	1	0	0	0	0
..CAGAAATTGGCTAAATGTGATG.....	22	0	1	1.00	1	0	0	0	1	0	0	0	0	0
.....ATTCACCGTGACCCACAAAGT.....	21	0	1	1.00	1	0	0	1	0	0	0	0	0	0
.....ATGCTTAGACTTTTATTGGTC.....	21	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....CAAAATGGGTGTGATGCTTCT.....	21	2	1	1.00	1	0	0	1	0	0	0	0	0	0
.....TGACACCCATTCTGAATATGTACA.....	24	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....TCACTGTATTATTTGTAAGTA.....	21	0	1	1.00	1	0	1	0	0	0	0	0	0	0
.....AAAATGGGTGTGATGCTTAGACA.....	23	1	1	1.00	1	1	0	0	0	0	0	0	0	0
.....TTCAAAATGGGTGTGATGCTTT.....	22	1	1	1.00	1	1	0	0	0	0	0	0	0	0
.....CACAAAGTCTAAGCCTGACACCCA.....	24	0	1	1.00	1	0	0	0	0	0	1	0	0	0
.....TAAGCCTGACACCCATTCTGAATATG.....	26	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....CAAAATGGGTGTGATGCTT.....	19	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....AAAGTCTAAGCCTGACACCC.....	20	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....CACAAAGTCTAAGCCTGACACCC.....	23	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....CACAAAGTCTAAGCCTGTTT.....	19	2	4	0.25	1	1	0	0	0	0	0	0	0	0

Anti-sense strand reads

AAGTCTTTAACCGATTTACACTACGTATTAGGTATCTTACGTATGGTAAGTGGCACTGGGTGTTTCAGATTCGGACTGTGGGTAAGACTTATACATGTTAAGTAAAGGTAGAGACTTACAAGTTTTACCCACACTACGAATCTGAAAATAACCAGTGACATAATAAACATTCATTCGAAAAGTACTTGTTTTTTCGTTAAAATGGTTAA **********.....((((((...((((((((((...(((((((((.(((((((.....)))))))).))))))))))...)))))))))))....)))))))..**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M040 female body	SRR902011 testis	V112 male body	GSM343916 embryo
.....CGGACTGTGGGTAAGACTTAT.....	21	0	1	1.00	1	1	0	0	0
.....GGACTGTGGGTAAGACTTAT.....	20	0	1	1.00	1	1	0	0	0
.....ACCAGTGACATAATAAACATT.....	21	0	1	1.00	1	1	0	0	0
.....GATTCGGACTGTGGGTAAGAC.....	21	0	1	1.00	1	1	0	0	0
.....GGTAAGTGGCACTGGGTGTT.....	20	0	1	1.00	1	0	1	0	0
.....ACTTGTTTTTTCGTTAAAATG.....	21	0	1	1.00	1	1	0	0	0
.....AGTTTTACCCACACTACGAAT.....	21	0	1	1.00	1	1	0	0	0
.....GTACTTGTTTTTTCGTTAAAA.....	21	0	1	1.00	1	1	0	0	0
.....TTGGGTGTTTCAGATTCGGAC.....	21	1	1	1.00	1	1	0	0	0
.....CTTGTTTTTTCGTTAAAATG.....	20	0	1	1.00	1	1	0	0	0
.....GTATCTTACGTATGGTAAGTG.....	21	0	1	1.00	1	1	0	0	0
.....GGACTGTGGGTAAGACTTATA.....	21	0	1	1.00	1	1	0	0	0
.....CTGAAAATAACCAGTGACATA.....	21	0	1	1.00	1	1	0	0	0
.....GTTTTACCCACACTACGAAT.....	20	0	1	1.00	1	1	0	0	0
.....GGTAGAGACTTACAAGTTTTA.....	21	0	1	1.00	1	0	1	0	0
.....ACATGTTAAGTAAAGGTAGA.....	20	0	1	1.00	1	1	0	0	0
.....ACTGGGTGTTTCAGATTCGG.....	20	0	1	1.00	1	1	0	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
dp5	3:5363769-5363977 -	dps_3613	TTCAGAAATTGGCTAAATGTGATGCATAATCCATAGAA-TGCAT--ACCATT----------CACCGTGACCCACAAAGTCTAAGC----------CTGACAC--CC----------ATTCTGAATATGTACAATTCATTTCCATCTCTGAATGTTCAAAATGGGTGTGATGCTTAGACTTTTATTGGTCACTGTATTATTTGTA--AGT----------AAGCTTTTCATGAACAAAAAAGCAATTTTACCAA--------TT
droPer2	scaffold_2:5568985-5569201 -	dps_2446	TTCAGAAATTGGCTAAATGTGATGCATAATCCATAGAACTACAT--ACCATT----------CACCGTGACCCACAAAGTCTAAGC----------CTGACAC--CC----------ATTCTGAATATGTACAATTCATTCCACCTCTGAATGTTCAAAATGGGTGTGATGCTTAGACTTTTATTGGTCACTGTATTATTTGTA--AGT----------AAGCTTTTCATGAACAAAAAAGCAATTTTACCATTTTTCATTT
droWil2	scf2_1100000004382:418516-418543 -		TAACGCAAAGTTGGCAAGTACGAGAGCTTA---------.....----------.....----------.....--**--**----------.....--**--**----------.....--
droVir3	scaffold_12875:4556931-4556959 -		TGCAAAAGTTGGCAAATGCGAGGCATGA---------.....----------.....----------.....--**--**----------.....--**--**----------.....--
droMoj3	scaffold_6496:25512899-25512926 +		TGCAAAAGTGGCAAGTGCGAGGCATA---------.....----------.....----------.....--**--**----------.....--**--**----------.....--
droGri2	scaffold_15245:394780-394812 +		TACAAAAGTTGGCAAGTGCGAGGCATAACTCA-----.....----------.....----------.....--**--**----------.....--**--**----------.....--
droAna3	scaffold_13266:10784919-10785192 +		TGCAGAAGTTGGCAAATGTGATGCATAAACTG-----GAC--GGTTTTCAATGTCAATTGCCCTTGGCACGGATTTATTCCAAGTTGCATGACCCAGAGTGTCCATTCAATTTTGAAAAAATCCGTTAAAGCGCCTTTTGACAAATCAATTATAAATTTTTTTATATATGTAATATTTTATATGAAATCTC--TATTTTTA--------TACAAAATTTGTATTCCTTCTTTTTTCGCTGGTTTATGCAA-------.....--**--**----------ATACTCTCTTATTCACGAAGCTTTTAATA------AAACAAT----------.....TT
droBip1	scf7180000396428:1212079-1212349 +		TGCAGAAGTTGGCAAATGTGATGCATAAAGTGA----GACTTGGT---GGATGTCAACAGCCCTTGCCACGGATTTATTCCAAATTGCATGGG----GAGTGCCCATTCAATTTCGAAAAAATCCGTAAAAGAGGTATATGACAA--CAATT----------CGCAATATTTTTAATAAAAGTACATATTTTTATGACAGAATT--------TTGTATTATAACTC----------CTATCATTATTATTATATTATGCTATTATATTTATAACTTGCTGTTATATGAAATACTC-CGTATTAAC----------.....GA-------TT
droKik1	scf7180000302476:3285425-3285452 -		TGCAAAAGTTGGCAAATGCGATGCCTA---------.....----------.....----------.....--**--**----------.....--**--**----------.....--
droFic1	scf7180000453948:1991273-1991300 +		TTCAGAAGTTAAGTAAATGCGATGCCTA---------.....----------.....----------.....--**--**----------.....--**--**----------.....--
droEle1	scf7180000491214:817734-817762 +		TGCAGAAGTTGAGCAAATGTGATGCCTAA---------.....----------.....----------.....--**--**----------.....--**--**----------.....--
droRho1	scf7180000778035:79547-79575 +		TACAGAAGTTGAGCAAGCCTGAGGCCTAA---------.....----------.....----------.....--**--**----------.....--**--**----------.....--
droBia1	scf7180000301754:5713570-5713599 -		TGCAGAAGTTGAGTAAATGTGAGGCCTAAT---------.....----------.....----------.....--**--**----------.....--**--**----------.....--
droTak1	scf7180000415138:275323-275350 +		TGCAGAAGTTGAGTAAATGTGATGCCTA---------.....----------.....----------.....--**--**----------.....--**--**----------.....--
droEug1	scf7180000409672:1647492-1647520 +		TGCAGAAGTTGAGCAAATGTGAGGCCTAA---------.....----------.....----------.....--**--**----------.....--**--**----------.....--
dm3	chr2R:13462899-13462928 -		TTCAGCAGCTAAGCAAATGCGAGGCCTAAT---------.....----------.....----------.....--**--**----------.....--**--**----------.....--
droSim2	scf1111157713119578 -		
droSec2	scf1111157713119578 - 10962423 +		TTCAGCGGCTAAGCAATACGAGGCCTAAT---------.....----------.....----------.....--**--**----------.....--**--**----------.....--
droYak3	2R:15723089-15723118 +		TTCAAAAGTTAAGTAAATGTGAGGCCTAAT---------.....----------.....----------.....--**--**----------.....--**--**----------.....--
droEre2	scaffold_4845:7691017-7691046 -		TTCAGAAGTTAAGCAAATGTGAGGCCTAAT---------.....----------.....----------.....--**--**----------.....--**--**----------.....--

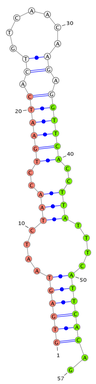
Generated: 09/08/2015 at 08:15 PM

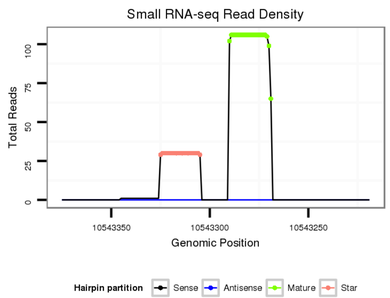
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

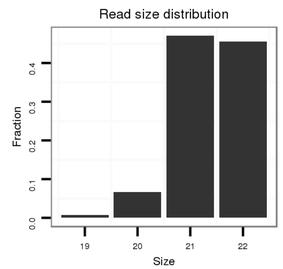
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dps_463	**2:10543269-10543325 -**	**confident**	**Mirtron**	**intron**	[View on UCSC Genome Browser [Cornell Mirror]]

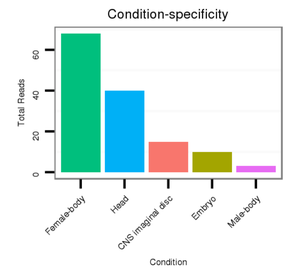
Legend: mature star mismatch in alignment mismatch in read

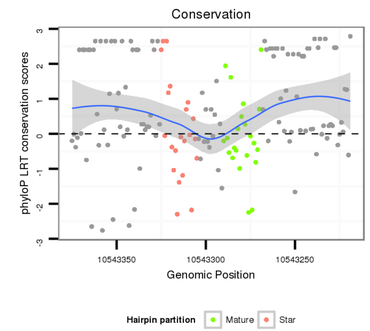
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dpse\GA26611-in]; CDS [Dpse\GA26611-cds]; CDS [Dpse\GA26611-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

```
ACGCGACGCGGCGACCTGGAACTCTTCCTTACATCCCCCATGGGCACCAAGTGAGTAATCTAACCTGAATCACTGTCAACAAGAGGTTCACCTTATTTCATTCACAGATCAATGATCCTGTCGCGTCGCGCCAATGATGATGACCATCGCGATGGCT Read size | # Mismatch | Hit Count | Total Norm | Total | M040 female body | M062 head | GSM444067 head | SRR902012 CNS imaginal disc | M059 embryo | GSM343916 embryo | V112 male body
**********************************************((((((.....(((..(((((((.((.......)).)))))).))))....))))))..********************************************
.....................................................................GTTCACCTTATTTCATTCACAG..... 22  0  1  62.00 62  40  9  1  5  3  2  2
.....................................................................GTTCACCTTATTTCATTCACA...... 21  0  1  33.00 33  18  8  5  0  1  0  1
.....................................GTGAGTAATCTAACCTGAATC.......................................... 21  0  1  28.00 28  3  9  2  10  3  1  0
.....................................................................TTCACCTTATTTCATTCACAG..... 22  1  1  15.00 15  3  3  7  0  1  1  0
.....................................................................GTTCACCTTATTTCATTCAC....... 20  0  1  6.00 6  2  4  0  0  0  0  0
.....................................................................TTCACCTTATTTCATTCACAG..... 21  0  1  3.00 3  2  0  1  0  0  0  0
.....................................................................TTCACCTTATTTCATTCACAG..... 22  1  1  2.00 2  0  2  0  0  0  0  0
.....................................................................GTTCACCTTATTTCATTCACAG..... 23  1  1  2.00 2  0  2  0  0  0  0  0
.....................................TGAGTAATCTAACCTGAATC.......................................... 20  0  1  1.00 1  1  0  0  0  0  0  0
.....................ACATCCCCCATGGGCACCAA.......................................................... 20  0  1  1.00 1  1  0  0  0  0  0  0
.....................................................................TTCACCTTATTTCATTCACA...... 20  0  1  1.00 1  1  0  0  0  0  0  0
.....................GTGAGTAATCTAACCTGAAT.......................................................... 20  0  1  1.00 1  1  0  0  0  0  0  0
.....................................................................GTTCACCTTATTTCATTCACAG..... 22  1  1  1.00 1  0  1  0  0  0  0  0
.....................................................................GTTCACCTTATTTCATTCA........ 19  0  1  1.00 1  0  0  1  0  0  0  0
```

Anti-sense strand reads

```
TGCGCTGCGCCGCTGGACCTTGAGAAGGAATGTAGGGGGTACCCGTGGTTCACTCATTAGATTGGACTTAGTGACAGTTGTTCTCCAAGTGGAATAAAGTAAGTGTCTAGTTACTAGGACAGCGCAGCGCGGTTACTACTCTGGTAGCGCTACCGA Read size | # Mismatch | Hit Count | Total Norm | Total | M040 female body | M059 embryo | GSM343916 embryo
**********************************************((((((.....(((..(((((((.((.......)).)))))).))))....))))))..********************************************
```

Show Alignment With Reads

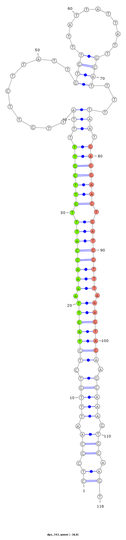
Re-alignment of all predicted orthologs

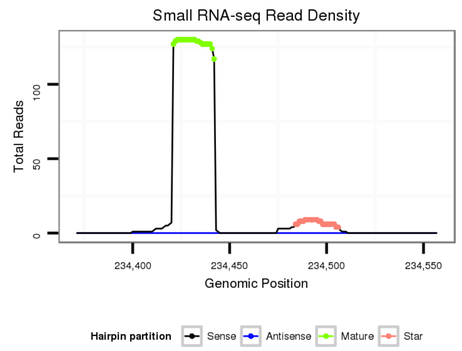
Species	Coordinate	ID	Alignment
dp5	2:10543219-10543375 -	dps_463	ACGCGACGCGGCGACCTGGAACTCTTCCTTACATCCCCCATGGGCACCAA----------GTGAGTAATCTAA----------CCTGAATCACTG----------TCAA----------CAAGAG----------G-TTCACC----------TTA---------T---TTCA--TT-CACAGATCAATGATCCTGTCGCGTCGCGCCAATGATGATGACCATCGCGATGGCT
droPer2	scaffold_0:9937683-9937839 +	dps_456	TCGCGACGCGGCGACCTGGAACTCTTCCTTACATCCCCCATGGGCACCAA----------GTGAGTAATCTAA----------CCTGAATCACTG----------TCAA----------CAAGAG----------G-TTCACC----------TTA---------T---TTCA--TT-CACAGATCAATGATCCTGTCGCGTCGCGCCAATGATGATGACCATCGCGATGGCT
droWil2	scf2_1100000004943:6660556-6660718 +		T-CAGACGAGGTGACCTGAGTCTTTCCTTACTCACCATGGGCACAA----------GAAGTGGTTCCTTCTGA----------TT-TG----------G-AAGTCT----------|----------|----------|-----|----------|-|-----|----------CTTAA--ATA---ATGTGTAATTTTA---------|---|-TG--TT-TTCAGCTCTATGATTCTGTCCGACGCGCCAATGATGATGACATCGCGATGGCT
droVir3	scaffold_12822:3383957-3384115 +	dvi_2702	TCGCGACGCGGCGACCTGAACTCTTCCTGACTCCACATGGGCACCAA----------GTGAGTGTGTCTC----------TATAATAT---|----------|----------ATTA-|-----|----------AA-TCAA-CCAACCCTGATA----------ATT---|---|----------|---CTCG--TT-GTTAGATCGATGATCTGTCCGACGCGCCAATGATGATGACCATCGCGATGGCT
droMoj3	scaffold_6540:16703828-16703984 +		TCGCGACGCGGCGACCTGGACTCTTCCTGACTCCCCCATGGGCACCAA----------GTAGTGTTA--G----------TCTAGATCT--|----------AA----------|----------|---GTCGAA----------CA---|----------|-G-T-|-----|-----TTATACT----------|----------CA----------T---|-CTG--CATGCTAGATCGATGATCTGTCGCGACGCGCTAA-GAGATGAGCATCGCGATGGCT
droGri2	scaffold_14906:1022590-1022751 +		TCGCGACGCGGCGACCTGGACTCTTCTGACTCCCCATGGGCACCAA----------GTGAGTGGAGAGT--AT----------A-|-----CG--|----------|----------TA----------|----------|---CTTGAACT-|-----AAGCAA--T----------|----------AT-TTCA-ATTATAC----------|----------CC----------|---TTCG--CA-TCCAGATCGATGATTGTCGCGTCGCGCCAATGATGATGACATCGCGATGGCT
droAna3	scaffold_13340:16810058-16810212 +		TCGCGCGCGGCGACTTGGAACTCTTCCTTACTCACATGGGCAACAA----------GTAGTGTCAAAAAAAAG----------|----------TT----------|----------|---TTTTAAT-|-----TTTATAT--A----------|----------AT-T-T--|----------|----------T----------|----------|---AT-GTC--G-TCCAGATCGATGATCCTGTCGCGCGCGCAATGATGATGACATCGCGATGGCT
droBip1	scf7180000396424:325475-325641 +		TCGCGCGCGGCGACTTGGAACTCTTCCTTACTCACCCATGGGCAACAA----------GTAGTGTCAAAA---AG----------A----------|----------GC-GT----------|----------|---TTTGAAT-|-----TTTGGGAT--A----------|----------AT-T-T--TTATAT----------|----------CTTT----------|----------TA----------|----TAT--G-ACAGATCGATGATCCTGTCGCGCGCAATGATGATGACATCGCGATGGCT
droKik1	scf7180000302253:169054-169116 +		AT----------|----------|----------|

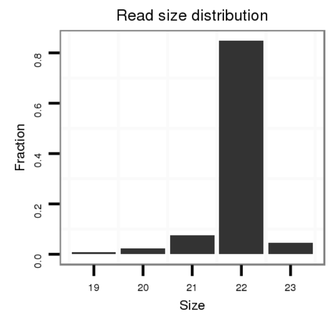
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dps_243	**4_group3:234421-234507 +**	**confident**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

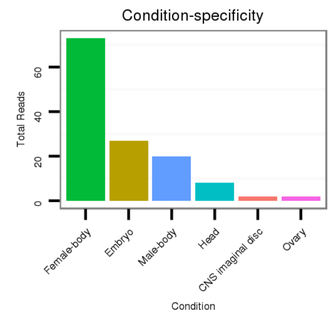
Legend: mature star mismatch in alignment mismatch in read

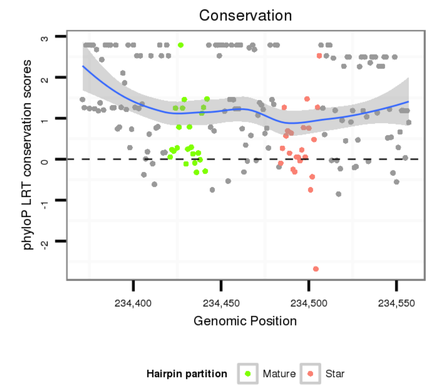
Predicted structure











Show Alternate Folds

Flybase annotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

TCTTGTTAACAGCTTTTGCTTTTTTGTTTACCTCACTCGCAATTTGTCTGTACTTAAAACCATTTGTTCGTTTTTATTGTTCTTATTGTGTTTATTATTATTGCATTTTTAATGACGAACTGATGGTTTAAAGTACAAGCAAAGTGCAAGTTTCACCTTTTTCGAAATTGCCAATTATTATGAAAAT **********((.(((.((((((.(((((((.(((((((.(((((((.(((.....(((((.....)))))...))).)))))))).)))))))).)))))))).))))).))).**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M040 female body	V112 male body	M059 embryo	GSM343916 embryo	GSM444067 head	M062 head	SRR902010 ovaries	SRR902012 CNS imaginal disc
....TACTTAAAACCATTTGTTCGTT....	22	0	1	111.00	111	59	18	12	12	4	2	2	2
....TACTTAAAACCATTTGTTCGT....	21	0	1	7.00	7	4	0	1	1	0	1	0	0
....TACTTAAAACCATTTGTTCGTTA....	23	1	1	3.00	3	3	0	0	0	0	0	0	0
....TACTTAAAACCATTTGTTCG....	20	0	1	2.00	2	2	0	0	0	0	0	0	0
....TACTTAAAACCATTTGTTCGTTAAA....	25	3	1	2.00	2	2	0	0	0	0	0	0	0
....GACGAACTGATGGTTTAAAGTAC....	23	0	1	2.00	2	0	0	1	0	0	1	0	0
....TACTTAAAACCATTTGTTCGG....	21	1	1	2.00	2	0	0	0	0	0	2	0	0
....ACTTAAAACCATTTGTTCGTT....	21	0	1	2.00	2	2	0	0	0	0	0	0	0
....ATTTTTAATGACGAACTGATG....	23	0	1	2.00	2	2	0	0	0	0	0	0	0
....ACTGATGGTTTAAAGTACAAGC....	22	0	1	1.00	1	0	0	1	0	0	0	0	0
....CGAACTGATGGTTTAAAGTACA....	22	0	1	1.00	1	1	0	0	0	0	0	0	0
....GTCTGTACTTAAAACCATTT....	20	0	1	1.00	1	1	0	0	0	0	0	0	0
....ATTTGTCTGTACTTAAAACCATT....	23	0	1	1.00	1	1	0	0	0	0	0	0	0
....CGAACTGATGGTTTAAAGT....	19	0	1	1.00	1	1	0	0	0	0	0	0	0
....ATGACGAACTGATGGTTTAAAGT....	23	0	1	1.00	1	1	0	0	0	0	0	0	0
....TGTACTTAAAACCATTTGTTCG....	22	0	1	1.00	1	1	0	0	0	0	0	0	0
....ACCTCACTCGCAATTTGTCTG....	21	0	1	1.00	1	0	0	1	0	0	0	0	0
....TCTGTACTTAAAACCATTTGTTCGTTTT....	28	0	1	1.00	1	0	0	1	0	0	0	0	0
....AATTTGTCTGTACTTAAAACCA....	22	0	1	1.00	1	1	0	0	0	0	0	0	0
....GTACTTAAAACCATTTGTTCGTT....	23	0	1	1.00	1	1	0	0	0	0	0	0	0
....TACTTAAAACCATTTGTTCGTTT....	23	0	1	1.00	1	1	0	0	0	0	0	0	0
....CTTAAAACCATTTGTTCGTT....	20	0	1	1.00	1	0	1	0	0	0	0	0	0
....TACTTAAAACCATTTGTTCGTG....	22	1	1	1.00	1	0	0	1	0	0	0	0	0

Anti-sense strand reads

AGAACAATTGTCGAAAACGAAAAAACAAATGGAGTGAGCGTTAAACAGACATGAATTTTGGTAAACAAGCAAAAATAACAAGAATAACACAAATAATAATAACGTAAAAATTACTGCTTGACTACCAAATTTCATGTTCGTTTCACGTTCAAAGTGGAAAAAGCTTTAACGGTTAATAATACTTTTA **********((.(((.(((((.(((((((.(((((((.(((((((.(((.....(((((.....)))))...))).)))))))).)))))))).)))))))).))))).))).**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M040 female body

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
dp5	4_group3:234371-234557 +	dps_243	T----CTTGTTAACAGCTTT-TGCT----------TTTTTG----TTTACCTCA--CTCGC-----AATTTGTCTGTACTTAAAACCATTTG-TTC-GTTT-----TTATTGTTCTT-ATTGTGTTTATT--AT--TA---TTG--CAT----------T--TTTAATGACGAACTGATGGTT--TAAAGTACAAGCAAAGTGCA------AGTTTCA----------CCT--TTTTCG---------AAATTGCCAATTATTATGAAAAT
droPer2	scaffold_1:1709209-1709395 +	dpe_322	T----CTTGTTAACAGCTTT-TGCT----------TTTTTG----TTTACCTCA--CTCGC-----AATTTGTCTGTACTTAAAACCATTTG-TTC-GTTT-----TTATTGTTCTT-ATTGTGTTTATT--AT--TA---TTG--CAT----------T--TTTAATGACGAACTGATGGTT--TAAAGTACAAGCAAAGTGCA------AGTTTCA----------CCT--TTTTCG---------AAATTGCCAATTATTATGAAAAT
droWil2	scf2_1100000004521:12231584-12231847 -		C----CTTGTTAAAAGCTTTTGCT----------TT----T----TTTACCTCA--TCAAG-----ACTTTGATTGTAAATTGAAAGTGTTTAAAG-ATTT-----CCCTTGTTGTCAATATGTGTTCAATTT-TT--TCTTTTTT--TATTAATTTAATTTAATTATTTTTGCA--TATAACCCTTAAC-TGCTCG---TCAAAAGCAATCAAAGTGTTTTTGC---CCTTGT---ACGTTTTCATTGTATACATATATATTTATAC----------TATTATAAAATAGTTTAAATTTTTTCA---------AAATTGCCAATTATTCG-GAGA-
droVir3	scaffold_12723:4015059-4015323 +	dvi_23304	T----TTTTTTG----GTTT-TATT----------TTTTTTCT---TAAACGAGTTTTGTG-----GCCTTGCTTGCGATTAAAAGCAGTCCAACG-GTT-----TCATTGTTGTATATTATTTTATT--TT--T----------G-T----------T--TTGAAAAGCGTTT-GATTGTT--TTGAATGCAAGCAAGGTGTTATTA---CCTTTGATCCCATGTTTTTAACATACTACATACACATGCAGACATCCAGACAGGCAAACATAAATTTATAAACTAGTTTTGTT--TTATTGAATGAAAAACAAATGCCAACTTCTTCGATTT-
droMoj3	scaffold_6500:14710021-14710198 -		TTCTGCCTTGTTGACAGCTTTGTGCTTTCATTTTCTTACATTTGT---TTCATTAGAATTGGC-----GCCTTGCTTGCGCTTAAAACTTATTGAACG-GTT-----TCATTGTTGTATATTATTTTATT--AT--TGTT-TTAATTTTA----------TTTTTGAAATGCGTTC-AATTAGAGGTTTGCCAGCAAGCAAGGTGC-------\-------\----------\----\-----\--------\----------\
droGri2	scaffold_15252:3644378-3644525 -		T----CTTGTTAACAGCTTT-TGCT----------CTTTTT----TTTACCTCGATTCAGC-----GCCTTGCTTGCGCTTAAAGCCATTTA-AAAGTGTT-----TCATTGTTGTATATTATTATAT--TT--TA---TTT--GTT----------T--TTGAATGCGCTTT-AATAGTT--TTGGATGCAAGCAAGGTGC--------\-------\----------\----\-----\--------\----------\
droAna3	scaffold_12916:13774631-13774831 -	dan_4040	T----CTTGTTAACAGCTTT-TGCT----------TTTTTTTTTATGTACCTCA--GAGGCGC----TTTTTTGTGTGCTAAGACTTCCCGCCCCGTT-----TGCTTGTTGTATTGTGTGTTTGTAT--TATT-TTT--TATTA----------TTTTTAAGAGTGGC-CGAAGTT--TTAGCGGGAGACAAAGCTATGCCATACAGATTCA----------ACT--TTTTCA---------AAATTGCCAATTTTGT-G-AAGA-
droBipl	scf7180000396535:738654-738840 -		T----CTTGTTAACAGCTTT-TGCT----------TTTTTT----TGTACCTCA--TAGGC-----CCCTTGTTGCGCCAAGACTTCCCGCCCCGATT-----TGCTTGTTGTCCATTGTGTTCTTTTAT--TA---TTT--TATTTTTTTT----------C--TTTAAGTACGGGC-CGCATTT--TTAGCGGAGACAAA-----------GATTCA----------AGT--TTTTCA---------AAATTGCCAATTTTAT-G-AAGA-
droKikl	scf7180000302677:189885-190084 +		T----CTTGTTAACAGCTTT-TGCT----------TATTTT----TATACCTCA--CTGGCCCC---TAGTTGTCTGCGCTAAGATTCATCGCCTCCGCCTGATTATCATTGTTGTCCATTGTGTTGTGT--AT--TA---TTT--TATTT----------T--TTTAAGACGAACCGATAAGTG--TTAGCGGAGCAAGCAAGCAAAGCCAAATAGATTCA----------CCG--TTTTCG---------AAATTGCCAATTATT-G-AAGAT
droFic1	scf7180000454144:360272-360465 -		T----CTTGTTAACAGCTTT-TGCT----------TTTTTT----TTTACCTCA--CTGGC-----TTTTTGCTTGCGCCAAGATTCGCCAGCTCCGTTT-----TCATTGTTGTCCATTGTGTTCTATATAT--TA---TTT--TATTA----------T--TTTAAGACGAGCCATATGGTG--TTCGCGGGAGCAAAGCCAGGCCATAGATTCA----------CCG--TTTTCA---------AAATTGCCAATTATT-G-AAGA-
droEle1	scf7180000491186:2985986-2986176 -		T----CTTGTTAACAGCTTT-TGCT----------TTTTTT----TTTACCTCA--CTGGCGC----GCTGTGCTTGCGCCAAGACCATCCAGCTCCGTTT-----TCATTGTTGTACATTGTGTTCTAT--AT--TG---TTT--TATTA----------T--TTTAAGACGAGCAATGGTG--TTTGGCGGGAGCAAAGCCAGGCCATAGATTCA----------CCG--TTTTCA---------AAATTGCCAATTAGT-G-AAGA-
droRho1	scf7180000779234:260078-260265 +		T----CTTGTTAACAGCTTT-TGCT----------TTT----T----TTTACCTCA--CTGGC-----TTTTTGCTTGCGCCAAGATTCATTCAGCTCCGTTT-----TCATTGTTGTACATTGTGTTCTAT--AT--TA---TTT--TATTA----------T--TTTAAGACGAGCAATGGTG--TTAGCGGGAGCAAAGCCGAGCCATAGATTCA----------CCG--TTTTCA---------AAATTGCCAATTAGT-G-AAGA-
droBia1	scf7180000301468:35130-35323 -		T----CTTGTTAACAGCTTT-TGCT----------TTT----T----TTTACCTCA--GCGGCTTGCATTTGCTGCTCGCGCCAAGATTCATCCAGCTCCGTTT-----TCATTGTTGTCCATTGTGTTCTATATAT--TA---TTT--TATTA----------G--TTTAAGACGAGCGCGAGGTG--TTAGCGGGAGCAAGCGCAAGCCTATAGATTCA----------AAGTTTTTCA---------AAATTGCCAATTAGT-G-AAGAT
droTak1	scf7180000415667:579347-579537 +		T----CTTGTTAACAGCTTT-TGCT----------TTT----T----TTTACCTCA--GCGGC-----TTTTTGCTTGCGCCAAGATTCATCCAGCTCCGTTT-----TCATTGTTGTACATTGTGTTCTAT--ATTATA---TTT--TATTA----------T--TTTAAGACGAGCGCGATGATG--TTCGCAGCAGCAAGCGCAAGGCCTATAGATTCA----------AGG--TTTTCA---------AAATTGCCAATTAGT-G-AAGA-
droEug1	scf7180000409554:4977650-4977841 +		T----CTTGTTAACAGCTTT-TGCT----------TTT----T----TTTACCTCA--GCGGC-----TTTTTGCTTGCGCCAAGATTCATGCAGCTCCGATT-----TCATTGTTGTACATTGTGTTCCAT--ATTTTT---TATT-TATTA----------T--TTTAAGACGAGCGCAATGGTG--TTAGCAGCAGCAAAGCGAAGCCAAATAGATTCA----------AGG--TTTTCA---------AAATTGCCAATTAGT-G-AAGA-
dm3	chr2L:9935027-9935218 -		T----CTTGTTAACAGCTTT-TGCT----------TTTTTG----TTTACCTCA--GCGGC-----TATTTGCTTGCGACACAGACCATGCAGCTCCGTTT-----TCATTGTTGTACATTGTGTTCTAT--AT--TATT-TTT--TATTA----------T--TTTAAGACGAGC-TCTGGTG--CTCAGAGCAGCAAAGCACAGCCATAGATTCA----------AGG--TTTTCA---------AAATTGCCAATTAGT-G-AAGA-
droSim2	2L:9633178-9633370 -		T----CTTGTTAACAGCTTT-TGCT----------TTTTTTT---TTTACCTCA--GCGGC-----TATTTGCTTGCGCACAGACCATGCAGCTCCGTTT-----TATTGTTGTACATTGTGTTCTAT--AT--TATT-TTT--TATTA----------T--TTTAAGACGAGC-TCTGGTG--CTGGCAGCAGCAAAGCGCAGCCATAGATTCA----------AGG--TTTTCA---------AAATTGCCAATTAGT-G-AAGA-
droSec2	scaffold_3:5381854-5382047 -		T----CTTGTTAACAGCTTT-TGCT----------TTTTTTTT---TTTACCTCA--GCGGC-----TATTTGCTTGCGCAACGACCATGCAGCTCCGTTT-----TATTGTTGTACATTGTGTTCTAT--AT--TATT-TTT--TATTA----------T--TTTAAGACGAGC-TCTGGTG--CTGGCAGCAGCAAAGCGCAGCCATAGATTCA----------AGG--TTTTCA---------AAATTGCCAATTAGT-G-AAGA-
droYak3	2L:12625727-12625915 -		T----CTTGTTAACAGCTTT-TGCT----------TTT----T----TTTACCTCA--GCGGC-----TATTTGCTTGCGCCAAGACCATGCAGCTCCGTTT-----TCATTGTTGTACATTGTGTTCTAT--AT--TA---TTT--TATTA----------T--TTTAAGACGAGC-AATGGTG--TTGGCGGCAGCAAAGCGCAGCCATAGATTCA----------AGG--TTTTCA---------AAATTGCCAATTAGT-G-AAGA-
droEre2	scaffold_4929:10555277-10555465 -		T----CTTGTTAACAGCTTT-TGCT----------TTT----T----TTTACCTCA--GCGGC-----TATTTGCTTGCGCCAAGACCATGCAGCTCCGTTT-----TCATTGTTGTACATTGTGTTCTAT--AT--TA---GTT--TATTA----------T--TTTAAGACGAGC-AATGGTG--TTGGCGGCAGCAAAGCGCAGCCATAGATTCA----------AGG--TTTTCG---------AAATTGCCAATTAGT-G-AAGA-

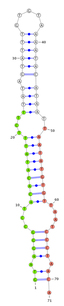
Generated: 09/08/2015 at 08:14 PM

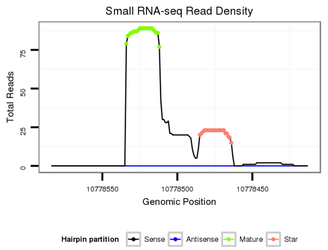
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	0
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	2
rescue.candidate	1

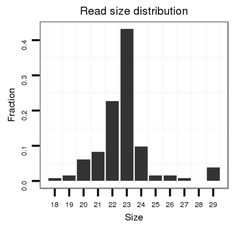
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dps_2791	**XL_group1e:10778463-10778534 -**	**confident**	**Mirtron**	**intron**	[View on UCSC Genome Browser [Cornell Mirror]]

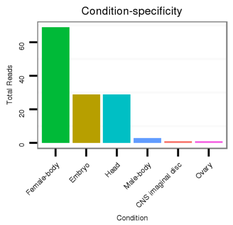
Legend: mature star mismatch in alignment mismatch in read

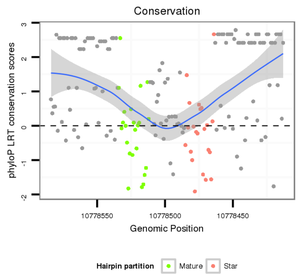
Predicted structure











Show Alternate Folds

Flybase annotation

intron [Dpse\GAI1485-in]; CDS [Dpse\GAI1485-cds]; CDS [Dpse\GAI1485-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

ATGCAGATATTTTCAAAATGTGGCCATTTTATGCGCAAAATTGCCATTAGGTAAGGGCCTACACATATTTCTTTATAGTATTTGTGTAAAATACATAATTAATATGTGTTAATCCCTAACAGATATATTGATATTGTTGCCGGACTGGCCGTCACCGCAAAGGGTCACATTG	Read # size	Mismatch	Hit Count	Total Norm	Total	M040 female body	M062 head	M059 embryo	GSM444067 head	GSM343916 embryo	V112 male body	SRR902010 ovaries	SRR902012 CNS imaginal disc	SRR902011 testis	M022 male body
**********															
....GTAAGGGCCTACACATATTTCTT	23	0	1	43.00	43	12	12	18	0	1	0	0	0	0	0
....GTAAGGGCCTACACATATTTCT	22	0	1	15.00	15	7	4	3	0	0	1	0	0	0	0
....GTAAGGGCCTACACATATTTCTTT	24	0	1	11.00	11	8	1	1	0	0	0	1	0	0	0
....GTAAGGGCCTACACATATTTCTTTATAGT	29	0	1	5.00	5	4	0	1	0	0	0	0	0	0	0
....TTATAGTATTTGTGTAAAATAC	22	0	1	4.00	4	2	2	0	0	0	0	0	0	0	0
....TAATATGTGTTAATCCCTAACA	22	0	1	4.00	4	1	1	0	0	1	1	0	0	0	0
....TAATATGTGTTAATCCCTAACAG	23	0	1	4.00	4	3	1	0	0	0	0	0	0	0	0
....TATAGTATTTGTGTAAAATA	20	0	1	3.00	3	3	0	0	0	0	0	0	0	0	0
....TATAGTATTTGTGTAAAATAC	21	0	1	3.00	3	0	3	0	0	0	0	0	0	0	0
....TAATATGTGTTAATCCCTAACAG	23	0	1	3.00	3	3	0	0	0	0	0	0	0	0	0
....GTAAGGGCCTACACATATTTCTTT	22	1	1	3.00	3	0	0	3	0	0	0	0	0	0	0
....GTAAGGGCCTACACATATTTCTTT	23	1	1	3.00	3	0	1	2	0	0	0	0	0	0	0
....TATAGTATTTGTGTAAAATACA	22	0	1	2.00	2	0	1	0	1	0	0	0	0	0	0
....TAATATGTGTTAATCCCTAAC	21	0	1	2.00	2	2	0	0	0	0	0	0	0	0	0
....TAAGGGCCTACACATATTTCTT	22	0	1	2.00	2	1	0	0	0	0	0	0	1	0	0
....TAAGGGCCTACACATATTTCT	21	0	1	2.00	2	2	0	0	0	0	0	0	0	0	0
....TATAGTATTTGTGTAAAATACAT	23	0	1	2.00	2	2	0	0	0	0	0	0	0	0	0
....CATAATTAATATGTGTTAATCCC	23	0	1	2.00	2	0	0	2	0	0	0	0	0	0	0
....GTAAGGGCCTACACATATTTCTTTAT	26	0	1	2.00	2	2	0	0	0	0	0	0	0	0	0
....TATATGTATTTGTGTAAAATACA	23	0	1	2.00	2	2	0	0	0	0	0	0	0	0	0
....TGCCGGACTGGCCGTCACCGCAAAG	25	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0
....CTACACATATTTCTTTATAGT	21	0	1	1.00	1	1	0	0	0	0	1	0	0	0	0
....TTAATATGTGTTAATCCCTA	20	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0
....TAAGGGCCTACACATATTTCTT	23	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0
....AATATGTGTTAATCCCTAACA	21	0	1	1.00	1	0	0	1	0	0	0	0	0	0	0
....TACACATATTTCTTTATAGTAT	22	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0
....TATTTGTGCCGGACTGGCCGTCA	24	1	1	1.00	1	1	0	0	0	0	0	0	0	0	0
....TTAATATGTGTTAATCCCTAAC	22	0	1	1.00	1	0	0	1	0	0	0	0	0	0	0
....GTAAGGGCCTACACATATT	19	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0
....TATTTGTGTAAAATACATAATT	22	0	1	1.00	1	0	1	0	0	0	0	0	0	0	0
....TTAATATGTGTTAATCCCTAACAG	24	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0
....ATATGTGTTAATCCCTAACAG	21	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0
....AAGGGCCTACACATATTTCTTTATAGT	27	0	1	1.00	1	0	0	1	0	0	0	0	0	0	0
....AATATGTGTTAATCCTAA	19	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0
....GGCCTACACATATTTCTTTATAGT	24	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0
....TGATATTGTTGCCGGACTGGCCGTCA	26	0	1	1.00	1	0	0	1	0	0	0	0	0	0	0
....TTATAGTATTTGTGTAAAAT	20	0	1	1.00	1	0	0	1	0	0	0	0	0	0	0
....GTAAGGGCCTACACATATTTCTTTA	24	1	1	1.00	1	0	0	1	0	0	0	0	0	0	0
....TATGTGTTAATCCCTAACAG	20	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0
....GTAAGGGCCTACACATAT	18	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0
....TTAATATGTGTTAATCCCTAACAG	25	1	1	1.00	1	0	0	1	0	0	0	0	0	0	0
....TTATAGTATTTGTGTAAAATA	21	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0
....GTAAGGGCCTACACATATTT	20	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0
....ATTAATATGTGTTAATCCCTAACAG	26	1	1	1.00	1	0	1	0	0	0	0	0	0	0	0
....CATAATTAATATGTGTTAATCCCTA	25	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0
....TATAGTATTTGTGTAAAATACATAA	25	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0
....TGTGGCCATTTTATGCGCA	19	0	2	0.50	1	0	0	0	1	0	0	0	0	0	0

Anti-sense strand reads

TACGTCTATAAAAGTTTTACACCGGTAAAATACGCGTTTTAACGGTAATCCATTCCCGGATGTGTATAAAGAAATATCATAAACACATTTTATGTATTAATTTATACACAATTAGGGATTGCTCTATATAACTATAACAACGGCCTGACCGGCAGTGGCGTTTCCCAGTGTAAC	Read # size	Mismatch	Hit Count	Total Norm	Total	M040 female body	SRR902010 ovaries
**********							
....TTATAGTATTTGTGTAAAATACATAATTAATATGTGTTAATCCCTAACAGATATATTGATATTGTTGCCGGACTGGCCGTCACCGCAAAGGGTCACATTG	25	0	1	1.00	1	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
dp5	XL_group1e:10778413-10778584 +	dps_2791	ATGCAGATATTTTCAAAATGTGGCCATTTTATGCGCAAAATTGCCATTAGGTAAGGGCC----------TACACATATTTC----------T----------TATAGTATTTGTGTAAAATACATAATTAATATGTGTTAA---------TC----------CCTAACAGATATATTGATATTGTTGCCGGACTGGCCGTCACCGCAAAGGGTCACATTG
droPer2	scaffold_14:222397-222568 -	dpe_759	ATGCAATATTTTCAAAATGTGGCATTTTATGCGCAAAATTGCGATTAGGTAAGGGCC----------TACACATATTTC----------T----------TATAGTATTTGTGTAAAATACATAATTAATATGTGTTAA---------TC----------CCTAACAGATATATTGATATTGTTGCCGGACTGGCCGTCACCGCAAAGGGTCACATTG
droW112	scf2_1100000004909:18283636-18283795 -		ATGCAGATTTTTCAAATGTGGCATTTTATGCGCAAAATTGCCATTAGGTAAGGGCC----------CAGA----------GAAAAAAAGGATATCCT------CATGAT----------CAACACCAA----------T----------TTT----------C----------AT----------TCCTTTGATATATTGATATTGTTGCCGGACTGGCCGTCACCGCAAAGGGTCACATTG
droVir3	scaffold_12726:1033945-1034134 +	dvi_1861	ATGCAATTTTTCAAATGTGGCATTTTATGCGCAAAATTGCATTAGGTAGTGTGTGTGTGTGTGCGTGTGTGTATTGAATTTTGAATTTCTTATTGCAATAAA----------ATTTGCC----------T----------TATGTATGATATTGATATTTGTTGCCGGACTGGCCGTCACCGCAAGGGTCACATTG
droMoj3	scaffold_6473:9128895-9129080 +		ATGCAATTTTTCAAATGTGGCCATTTTATGCGCAAAATTGCATTAGGTGCTGTGCGAATGATTGTGAATGTGCC----------CTCTTATCC----------T----------TATATTGATATTGATATTGTTGCCGGACTGGCCGTCACCGCAAGGGTCACATTG
droGri2	scaffold_14853:5466268-5466436 -		ATGCAGATTTTTCAAATGTGGCATTTTATGCGCAAAATTGCATTAGGTGCCACC----------CAAC----------TAACAGCAGCATTCATTTCAATTCAATTGCTTA--------ACATA----------T----------TTT----------C----------TTTTGTGATATATTGATATTGTTGCCGGACTGGCCGTCACCGCAAGGGTCACATTG
droAna3	scaffold_13248:3479812-3479982 -		ATGCAGATTTTTCAAATGTGGCATTTTATGCGCAAATATGCCATTAGGTGCTAAGC----------A--------TTAGTAAGGT----------GTATTAGTT----------T----------TTT----------C----------TATCCTTCTATATGTTTGTGTCTTCATCTTTGTATATATTGATATTGTTGCCGGACTGGCCGTCACCGCAAGGGTCACATTG
droRip1	scf7180000396431:788686-788850 +		ATGCAGATTTTTCAAATGTGGCATTTTATGCGCAAATATTGCCATTAGGTAAGCAGC----------T----------TTT----------C----------GCCAAATAATTGTCCATCTCCCAACCTTCTATATTCTTGTCTTGTGTATCTTTGATATTGATATTGTTGCCGGACTGGCCGTCACCGCAAGGGTCACATTG
droKik1	scf7180000302344:1432665-1432863 +		ATGCAGATATTTTCAAATGTGGCATTTTATGCGCAATATTGCCATTAGGTGTGGCTA----------TAATAACTATAATTATTACATTAATTTATTATATAAA----A----------T----------TAGT----AAACACGAATTTAATTAATTTC----------TA----------ATGTTGTT----TA----------TC----------ATCAATTGATATATTATTGTTGCCGGACTGGCCGTCACCGCAAGGGTCACATTG
droPic1	scf7180000453829:1036147-1036336 +		ATGCAGATTTTTCAAATGTGGCATTTTATGCGCAAATATGCCATTAGGTGCTATC----------ATATTAAAAT----------GCTTGTCATTTGTGGCAATTAGCATACTGCT----------T----------GA----TGTGCTTTATTTATATGTTT----TA----------T----------GTTTTTATATTGATATTGTTGCCGGACTGGCCGTCACCGCAAAGGGTCACATTG
droEle1	scf7180000491006:2592959-2593057 +		TG----------GATTATAAATATAA----------AAGT----------GATT----------T----------TTCGGTGATATTGATATTGTTGCCGGACTGGCCGTCACCGCAAGGGTCACATTG
droRho1	scf7180000076361:11556-11666 -		TTATAGATTTTTAAAATA----------T----------TAAATTTAAA----------T----------TTCGGTGATATTGATATTGTTGCCGGACTGGCCGTCACCGCAAGGGTCACATTG
droRia1	scf7180000301760:5024855-5024943 +		TAAAA----------T----------AAG----------T----------TAATTTAAA----------T----------TTCGGTGATATTGATATTGTTGCCGGACTGGCCGTCACCGCAAGGGTCACATTG
droTak1	scf7180000415211:143319-143447 +		AGA----------TTTATTT----------T----------T----------T----------TATTCTTTCTTATAATGTGATTAATTTC----------T----------TTCGTGATATTGATATTGTTGCCGGACTGGCCGTCACCGCAAGGGTCACATTG
droEug1	scf7180000409032:907681-907763 +		ATGCAGATTTTTCAAATGTGGCATTTTATGCGCAATTGCCATTAGGTAATATA----------GTTGC----ATTC----------T----------NTGTTGTATAATATA----------T----------TTT----------C----------ATCCAGTGATATTGATATTGTTGCCGGACTGGCCGTCACCGCAAGGGTCACATTG
dm3	chrX:9063969-9064141 +		ATGCAATTTTTCAAATGTGGCATTTTATGCGCAAATATGCGATTAGGTAAGTTA----------AATA----------TATTAAAAACTAAACAATTGGGGAAATAAGTTAATAACACAAA----------T----------TTT----------CA----TGT----TC----------ATCCAGTGATATTGATATTGTTGCCGGACTGGCCGTCACCGCAAGGGTCACATTG
droSim1	scaffold_14514:1-423594 +		ATGCAATTTTTCAAATGTGGCATTTTATGCGCAAATATGCCATTAGGTAATATA----------AATA----------ACTAAACAATTAGGAAACTAAGTTAATAACACAAA----------T----------TTT----------CA----TGT----TC----------ATCCAGTGATATTGATATTGTTGCCGGACTGGCCGTCACCGCAAGGGTCACATTG
droYak3	Ki:12252637-12252920 -		ATGCAATTTTTCAAATGTGGCATTTTATGCGCAAATATGCCATTAGGTAATATAATTTTCATGACATGTACATCTAAAAACTAAATGAAGTTGTTAACCTTTTAAAATCTGAGGGAAGTTTATTAATGAGATGAATTTTAAATTGTTGTTGAAAGGCATGTCTAAGAATAGGCA----------CG-AATATC-T----------TAGTAATTAATACAAA----------T-AATTAATAAACA----------TTT----------CA----TGT----TC----------ATCCAGTGATATTGATATTGTTGCCGGACTGGCCGTCACCGCAAGGGTCACATTG
droKre2	scaffold_4690:6053676-6053901 -		ATGCAATTTTTCAAATGTGGCATTTTATGCGCAAATATGCCATTAGGTAATATA----------TATAAATATATA----------GTAATTAGA----TTAGCAAGGCGGTATTTAATGATATATGTACATTCAAGAAAAAA----------T-GTAATCACCATTTGCGAAATATATTT----------TTA----TGT----TC----------ATCCAGTGATATTGATATTGTTGCCGGACTGGCCGTCACCGCAAGGGTCACATTG

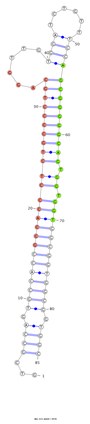
Generated: 09/08/2015 at 10:31 PM

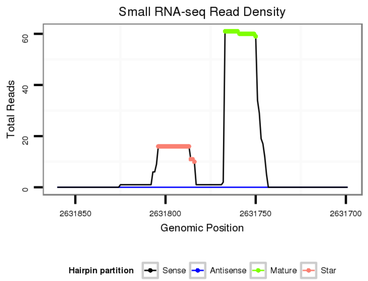
	PASS/FAIL
crit.star	1
crit.mat	1
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.loop1	1
crit.loop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.pairing	0
rescue.known	0
rescue.confident	1
rescue.candidate	1

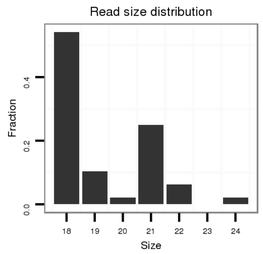
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dps_113	**XL_group1a:2631749-2631810 -**	**confident**	**Canonical miRNA**	**intron**	[View on UCSC Genome Browser [Cornell Mirror]]

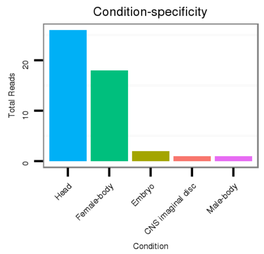
Legend: mature star mismatch in alignment mismatch in read

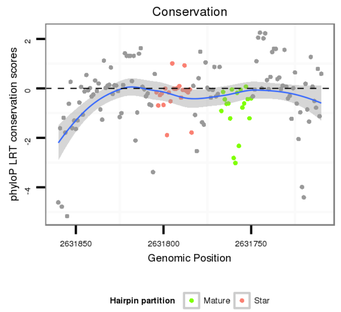
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dpse\GA18086-in]; CDS [Dpse\GA18086-cds]; CDS [Dpse\GA18086-cds]

Repeatable elements

Name	Class	Family	Strand
(CTG)n	Simple_repeat	Simple_repeat	+

Sense Strand Reads

hide 3p reads show mid mismatch reads

```
GTCAGTCACAAAAAGGAGCAGGCCCGACCCACCGAGGGGTCGTCGCCAGTGCCACCGCCACCCTCTGCCCCTGCAGGTTGTGGATCTGTTTCCAGCGGGGGCAGTGGTGGTGGCGGTGGCGGTGGCAGCAGCAGCAGCTCCAGCCGCTTGCTCTACAAGAGC
**********************************************...((((.((((((((((((((((((((((((((.......((((.....))))))))))))))).)).))))))))))))).))))**********************************
```

Read size	# Mismatch	Hit Count	Total Norm	Total	GSM444067 head	M040 female body	M062 head	V112 male body	M059 embryo	SRR902012 CNS imaginal disc	GSM343916 embryo
18	0	1	25.00	25	19	5	0	1	0	0	0
20	1	1	21.00	21	19	1	1	0	0	0	0
20	0	1	10.00	10	1	4	3	1	0	0	1
21	0	1	7.00	7	1	3	3	0	0	0	0
23	0	1	7.00	7	3	2	1	0	1	0	0
19	1	1	6.00	6	4	1	1	0	0	0	0
21	0	1	5.00	5	0	3	1	0	1	0	0
24	0	1	5.00	5	0	2	2	1	0	0	0
19	0	1	5.00	5	0	5	0	0	0	0	0
22	0	1	5.00	5	1	3	0	1	0	0	0
20	2	1	1.00	1	0	1	0	0	0	0	0
22	0	1	3.00	3	1	1	0	0	1	0	0
21	1	1	3.00	3	0	0	3	0	0	0	0
21	0	1	2.00	2	0	1	0	0	1	0	0
23	1	1	1.00	1	0	1	0	0	0	0	0
20	0	1	1.00	1	0	0	1	0	0	0	0
21	0	1	1.00	1	0	0	0	0	1	0	0
24	0	1	1.00	1	0	0	0	0	0	1	0
19	1	1	1.00	1	0	0	1	0	0	0	0
22	1	1	1.00	1	1	0	0	0	0	0	0
21	1	1	1.00	1	0	0	1	0	0	0	0
23	1	1	1.00	1	0	0	0	1	0	0	0
20	2	1	1.00	1	0	1	0	0	0	0	0
21	1	1	1.00	1	0	0	0	0	0	0	0
18	0	1	1.00	1	0	1	0	0	0	0	0
20	1	2	1.00	2	1	0	1	0	0	0	0
18	1	2	1.00	2	2	0	0	0	0	0	0
19	2	7	0.86	6	6	0	0	0	0	0	0
23	2	2	0.50	1	1	0	0	0	0	0	0
20	2	2	0.50	1	1	0	0	0	0	0	0
22	0	8	0.13	1	0	1	0	0	0	0	0
20	3	20	0.05	1	1	0	0	0	0	0	0

Anti-sense strand reads

```
CAGTCAGTGTTTTTCCTCGTCCGGGCTGGGTGGCTCCCCAGCAGCGGTCACGGTGGCGGTGGGAGACGGGGACGTCCAACACCTAGACAAAGGTCGCCCCCGTCACCACCACCGCCACCGCCACCGTCGTCGTCGAGGTCGGCGAACGAGATGTTCTCG
************************************...((((.((((((((((((((((((((((((((.......((((.......))))))))))))))).)).))))))))))))).))))************************************
```

Read size	# Mismatch	Hit Count	Total Norm	Total	GSM343916 embryo	M059 embryo	M040 female body	V112 male body

Show Alignment With Reads

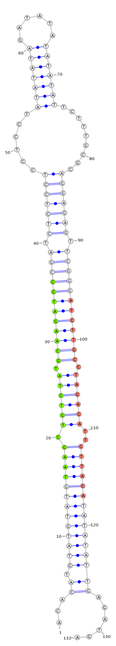
Re-alignment of all predicted orthologs

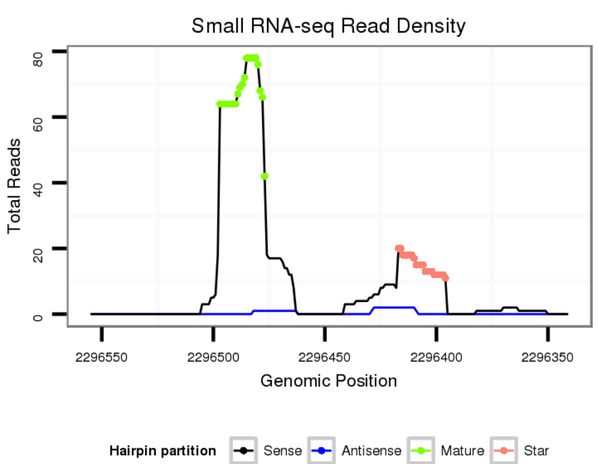
Species	Coordinate	ID	Alignment
dp5	XL_group1a:2631699-2631849 -	dps_113	AAAGGAGCA------GGC-CCGAC-----CCACCGAGGGTCGTCGCCAGTGCCA-----C----------CGC-CACCCTCTGC----CCCT----------GCAGGTTGTGGATCT---GTTTCCAGCGGGGGCAGTGGTGGT----------GGCGGTGG----------CGGTGG-----GGGTGTTGGTGGCAGCAGC----------AGCAG--------CTC-----CAGCCGCTTG--------C----------TCTACAAGAGC
droPer2	scaffold_28:1069088-1069250 +		AAAGGAGCA------GGC-CCGAC-----CCACCGAGGGTCGTCGCCAGTGCCA-----C----------CGC-CACCCTCTGC----CCCT----------GCAGGTTGTGGATCT---GTTTCCAGCGGGGGCAGTGGTGGT----------GGCGGTGG----------CGGTGG-----GGGTGTTGGTGGCAGCAGC----------AGCAG--------CTC-----CAGCCGCTTG--------C----------TCTACAAGAGC
droWil2	scf2_1100000004909:11934516-11934641 +		GG-TCAGCA------C--A-----------------------------------A--------CAGCAACAC----------GG----A----------CA-TGATGC----TCC----------GCCACAAG-----G----------A-----AGCCA----------ATTATTATA----------AGTA----------GTAGTAGTAGTAGTAA-A-------------AGCAGCAGCAG---CTGCAAT---TCTG-GAAC--------A----------CAT-CAA-GG
droVir3	scaffold_12932:1375034-1375207 -		ACCA-CC-A------C--TA-GAC-----CA-A-AAGGGTCGGGA-------------A----------GCGGCCGCGGCCGTTACGCAGCAA----------------------------------GCAC-----------GCAC-----CAGCAGCAGCA----GGCCGTTGTCCAGCAGGCCGTCGTGCAA-A-CA-G----------AGCAA----CAGCAACAACAGCA----------GCAG----------CA---CAGC----------AGCAG---TTCGTG-A-----CAGCAGCAA--------T----------GCAGCAAGTAC
droMoj3	scaffold_6473:2960137-2960282 -		AGGAGA-AGCCCTCAAGGAAGGACGGGCGG----------GCG-AAGAGTGCCA-----C----------GGC-CAC-AA-G-TGC--TGT----------G----------GCC--GACCAGCAG----------CAGCAG-----TGGAG----------GCGCGTTGG-G----------AGCAA----------CAGCA----------ACAACA----------ACAACA---G-A----------CAGCAGCAGC----------A----------CAGCAAGAG
droGri2	scaffold_14398:28187-28325 +		GCCTCGG-C------C-----------------------TCCACCA-C----------A----------CAG----------CGCCGCCGCCA--GCCTCC--CCATCAG----------CC---C----------A----------A----------AGCAG-CACCA----------CAACAGCACCA----------GTT-CA-CA-C----------AGCAATCGCGTTGGGC--CAGCA--GCA----------ATGGT----------TGCCA---G----------CAGCAGCAGC----------A----------CGCAGCAAG
droAna3	scaffold_12929:1950952-1951096 -		GAAGGAGCA------AAG-AATG----------A----------G----------ATC----------TGGATCTGGTTCTGGATCT--GC----------AGCTACCTG---A----------A----------A----------

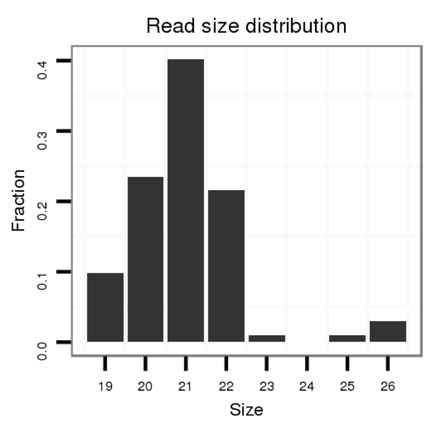
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dps_3750	**XL_group1a:2296391-2296505 -**	**confident**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

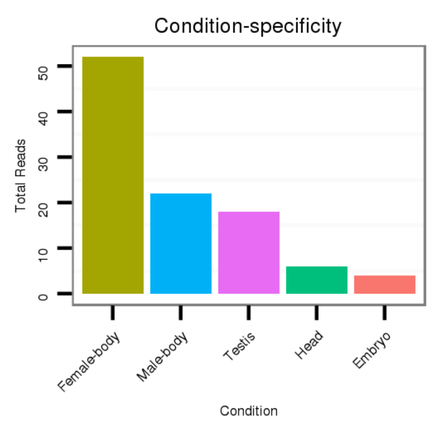
Legend: mature star **mismatch in alignment** mismatch in read

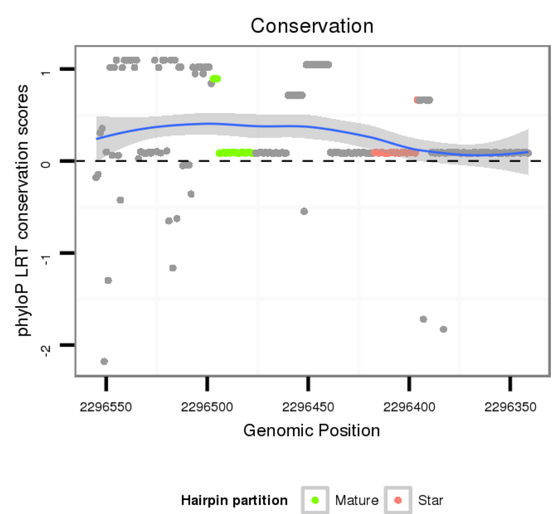
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

ACCTGTGGCCACGGTATTTCACTTGCACTTTCCATTTACATTTACACATGTATGTATGTAAGCTGTCTATGCAAGATCCCGATCTCTCCTCCTCCTATATATAGATATATATATATTCTTTGCGCAGGAGAGTTCGGGATCTTGCCTAGACATTCTTACATATATATTGAGATGAAAATAGCTGGCGATCATTATCCTTCCCTCCTCCAAGAAAG	Read size	# Mismatch	Hit Count	Total Norm	Total	M040 female body	V112 male body	SRR902011 testis	M062 head	M059 embryo	GSM444067 head	M022 male body	GSM343916 embryo
...((.(((((((((((((.((((((.(((((((((((((.(((((((.....(((((((.....)))))))).....)))))))).))))))))))))).)))))).).))))))))))))))))).....													
.....TAAGCTGTCTATGCAAGATCC.....	21	0	1	24.00	24	22	0	1	1	0	0	0	0
.....TAAGCTGTCTATGCAAGATC.....	20	0	1	20.00	20	3	10	4	1	0	0	2	0
.....ATCTTGCCTAGACATTCTTACA.....	22	0	1	11.00	11	2	0	9	0	0	0	0	0
.....GTAAGCTGTCTATGCAAGA.....	19	0	1	7.00	7	2	3	2	0	0	0	0	0
.....GTAAGCTGTCTATGCAAGATC.....	21	0	1	4.00	4	1	2	0	0	0	1	0	0
.....GCAAGATCCCGATCTCTCCTCC.....	22	0	1	4.00	4	2	0	0	0	2	0	0	0
.....CAAGATCCCGATCTCTCCTCC.....	21	0	1	3.00	3	3	0	0	0	0	0	0	0
.....TATGTATGTAAGCTGTCTATG.....	21	0	1	3.00	3	1	2	0	0	0	0	0	0
.....TATGCAAGATCCCGATCTCTCC.....	22	0	1	2.00	2	2	0	0	0	0	0	0	0
.....TTGCCTAGACATTCTTACATAC.....	22	1	1	2.00	2	2	0	0	0	0	0	0	0
.....TGCAAGATCCCGATCTCTCCTC.....	22	0	1	2.00	2	2	0	0	0	0	0	0	0
.....GCAAGATCCCGATCTCTCCTC.....	21	0	1	2.00	2	1	1	0	0	0	0	0	0
.....CTATGCAAGATCCCGATCTCT.....	21	0	1	2.00	2	2	0	0	0	0	0	0	0
.....ATTCTTTGCGCAGGAGAGTTCGGGAT.....	26	0	1	2.00	2	2	0	0	0	0	0	0	0
.....AGTTCGGGATCTTGCCTAGA.....	20	0	1	2.00	2	1	0	1	0	0	0	0	0
.....TTCGGGATCTTGCCTAGACATT.....	22	0	1	1.00	1	1	0	0	0	0	0	0	0
.....TATGTAAGCTGTCTATGCAAG.....	21	0	1	1.00	1	0	1	0	0	0	0	0	0
.....GAAAATAGCTGGCGATCAT.....	19	0	1	1.00	1	1	0	0	0	0	0	0	0
.....GAGAGTTCGGGATCTTGCC.....	19	0	1	1.00	1	1	0	0	0	0	0	0	0
.....TAAGCTGTCTATGCAAGAT.....	19	0	1	1.00	1	0	0	1	0	0	0	0	0
.....ATTCTTTGCGCAGGAGAGTTCGG.....	23	0	1	1.00	1	1	0	0	0	0	0	0	0
.....TATGTAAGCTGTCTATGCAAGA.....	22	0	1	1.00	1	1	0	0	0	0	0	0	0
.....CGATCATTATCCTTCCCTCC.....	20	0	1	1.00	1	1	0	0	0	0	0	0	0
.....CTATGCAAGATCCCGATCTC.....	20	0	1	1.00	1	0	0	0	1	0	0	0	0
.....GTAAGCTGTCTATGCAAGAT.....	20	0	1	1.00	1	0	0	0	0	0	1	0	0
.....CTATGCAAGATCCCGATCTCC.....	21	1	1	1.00	1	0	1	0	0	0	0	0	0
.....ATCTTGCCTAGACATTCTTAC.....	21	0	1	1.00	1	0	0	0	1	0	0	0	0
.....AGTTCGGGATCTTGCCTAGAA.....	21	1	1	1.00	1	0	0	1	0	0	0	0	0
.....AGGAGAGTTCGGGATCTTGCC.....	21	0	1	1.00	1	0	0	0	0	1	0	0	0
.....TAAGCTGTCTATGCAAGATT.....	20	1	1	1.00	1	0	0	0	0	0	1	0	0
.....ATGCAAGATCCCGATCTCTCCTCCT.....	25	0	1	1.00	1	0	0	0	0	1	0	0	0
.....ATGCAAGATCCCGATCTCTCCTT.....	23	1	1	1.00	1	1	0	0	0	0	0	0	0
.....GTAAGCTGTCTATGCAAGAC.....	20	1	1	1.00	1	1	0	0	0	0	0	0	0
.....TAAGCTGTCTATGCAAGATCCC.....	22	0	1	1.00	1	1	0	0	0	0	0	0	0
.....TTGCGCAGGAGAGTTCGGGATCTTGC.....	26	0	1	1.00	1	1	0	0	0	0	0	0	0
.....TGTAAGCTGTCTATGCAAG.....	19	0	1	1.00	1	0	1	0	0	0	0	0	0

Anti-sense strand reads

TGGACACCGGTGCCATAAAGTGAACGTGAAAGGTAAATGTAAATGTGTACATACATACATTCGACAGATACGTTCTAGGGCTAGAGAGGAGGAGGATATATATCTATATATATATAAGAAACGCGTCCTCTCAAGCCCTAGAACGGATCTGTAAGAATGTATATATAACTCTACTTTTATCGACCGCTAGTAATAGGAAGGGAGGAGGTTCTTTC	Read size	# Mismatch	Hit Count	Total Norm	Total	M040 female body	SRR902011 testis	GSM444067 head	V112 male body	M022 male body
...((.(((((((((((((.((((((.(((((((((((((.(((((((.....(((((((.....)))))))).....)))))))).))))))))))))).)))))).).))))))))))))))))).....										
.....CCTCTCAAGCCCTAGAACGG.....	20	0	1	1.00	1	1	0	0	0	0
.....CTCTCAAGCCCTAGAACGGA.....	20	0	1	1.00	1	0	1	0	0	0
.....TCTAGGGCTAGAGAGGAGGA.....	20	0	1	1.00	1	1	0	0	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
dp5	XL_group1a:2296341-2296555 -	dps_3750	ACCTGTG----------GC---C----------ACGGTA-TTTCACTTGCACTTTCCATTTACATTTACACATGTATGTATGTAAGCTGTCTATGCAAGATCCCGATCTCTCCTCCTCCTATATATAGATATATATATATTCTTTGCGCAGGAGAGTTCGGGATCTTGCCTAGACATTCTTACATATATATTGAGATGAAAATAGCTGGCGATCATTATCCTTCCCTCCTCCAAGAAAG
droPer2	scaffold_28:732673-732887 -	dpe_2298	ACCTGTG----------GC---C----------ACGGTA-TTTCACTTGCACTTTCCATTTACATTTACACATGTATGTATGTAAGCTGTCTATGCAAGATCCCGATCTCTCCTCCTCCTATATATAGATATATATATATTCTTTGCGCAGGAGAGTTCGGGATCTTGCCTAGACATTCTTACATACATATTGAGACGAAAATAGCTGGCGATCATTATCCTTCCCTCCTCCAAGAAAG
droMoj3	scaffold_6473:872940-872965 +		CCCTC--**----------**--**---**----------**------**----------TATATATAAATATATATATAT----------
droEle1	scf7180000491023:551327-551386 -		GCCTCCG**----------CAGCCAC**----------ACTGTA-TTTCACT**-----CTTGTATATATA----------TATATATATATAT----------ATATATA----------
droRho1	scf7180000777256:41825-41879 -		AACCGCA**----------GCCAC**----------ACTGTA-TTTCACT**-----CTTCCATTCAAACTTTTGTG**TGTATGTAT----------
droEug1	scf7180000409528:26826-26912 -		AGTTTCCGGCGCATCCGCAGACATGTCATGCAACCAACCAAACGTATTTTCACT**-----CTTCCATTCATAATTTTGT**ATGTATGTATGTAA----------
droEre2	scaffold_4690:3569997-3570050 -		ATCTACA**----------GCCAC**----------ACTGTA-TTTCAGC**-----CTACCATTTACAATT-----**TGTATGTATGTAA----------

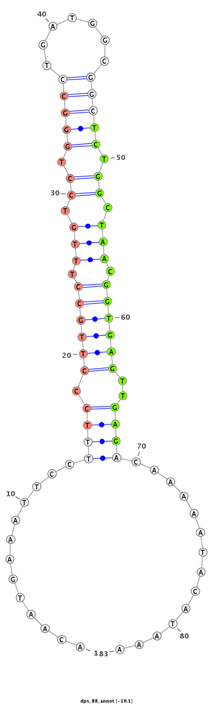
Generated: 09/08/2015 at 08:14 PM

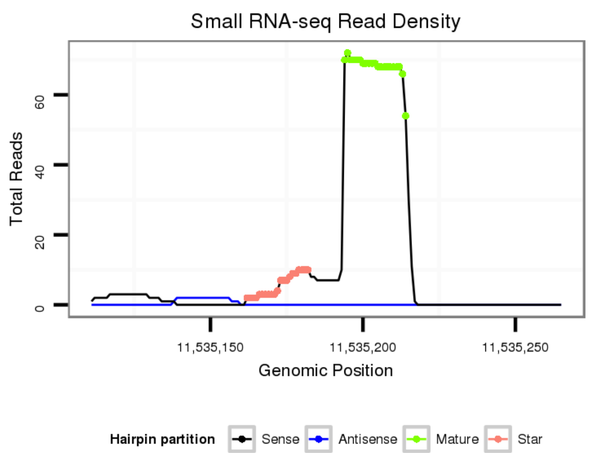
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

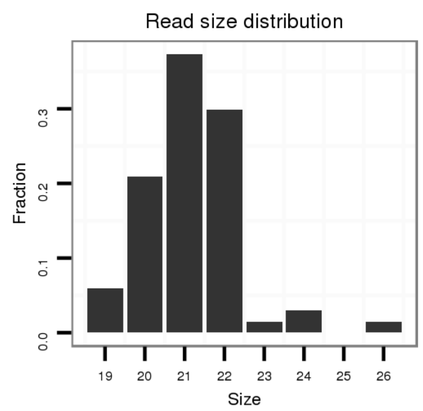
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dps_88	**3:11535161-11535215 +**	**confident**	**Canonical miRNA**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

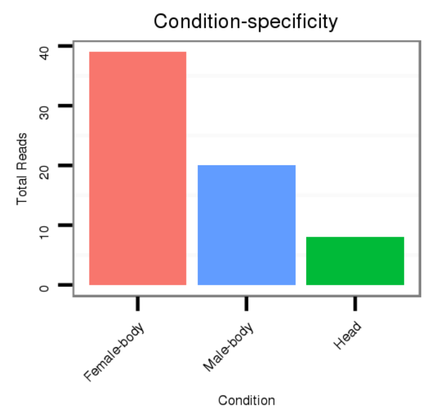
Legend: mature star mismatch in alignment mismatch in read

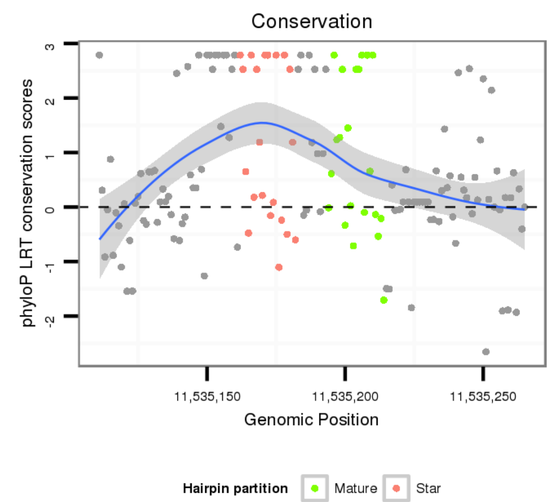
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dpse\GA24904-in]; CDS [Dpse\GA24904-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

TTGTCTGCCTGCCGTGCACCAAATCTTCACTAATCCACAATGAAATTCCTTTCCCTTGCCTTTGTCCTGGGCCTGATGGCGGCTCTGGCTAACGGTGAGTTGAGACAAAAATACATAAAAGTGTATTTAAATTTAATTATGATATTTATTTGTGT **********.....((((.(((((((.(((.((.(((((.....)))))).)).))).)))))))..))))).....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M040 female body	V112 male body	GSM444067 head	M062 head	M022 male body
.....TCTGGCTAACGGTGAGTTGAG.....	21	0	1	20.00	20	10	8	1	0	1
.....TCTGGCTAACGGTGAGTTGAGA.....	22	0	1	19.00	19	12	4	3	0	0
.....TCTGGCTAACGGTGAGTTGAGAC.....	23	0	1	10.00	10	7	1	1	0	1
.....TCTGGCTAACGGTGAGTTGA.....	20	0	1	10.00	10	5	4	1	0	0
.....TCCCTTGCCTTTGTCCTGGGC.....	21	0	1	2.00	2	1	0	1	0	0
.....CTCTGGCTAACGGTGAGTTGA.....	21	0	1	2.00	2	1	1	0	0	0
.....CTGGCTAACGGTGAGTTGAG.....	20	0	1	2.00	2	1	1	0	0	0
TTGTCTGCCTGCCGTGCAC.....	19	0	1	1.00	1	0	0	0	1	0
.....TCTGGCTAACGGTGAGTTG.....	19	0	1	1.00	1	1	0	0	0	0
.....TGTCCTGGGCCTGATGGCGGC.....	21	0	1	1.00	1	1	0	0	0	0
.....GGGCCTGATGGCGGCTCTGGCTAACG.....	26	0	1	1.00	1	1	0	0	0	0
.....GCCTGCCGTGCACCAAATCTTC.....	22	0	1	1.00	1	1	0	0	0	0
.....CTCTGGCTAACGGTGAGTTG.....	20	0	1	1.00	1	0	1	0	0	0
.....TGTCCTGGGCCTGATGGCG.....	19	0	1	1.00	1	1	0	0	0	0
.....TTGCCTTTGTCCTGGGCCT.....	19	0	1	1.00	1	1	0	0	0	0
.....CTGGGCCTGATGGCGGCTC.....	19	0	1	1.00	1	1	0	0	0	0
.....TCTGGCTAACGGTGAGTTGAGACA.....	24	0	1	1.00	1	1	0	0	0	0
.TGTCTGCCTGCCGTGCACCAAA.....	22	0	1	1.00	1	1	0	0	0	0
.....GCTCTGGCTAACGGTGAGTTGAG.....	23	0	1	1.00	1	1	0	0	0	0
.....TCTGGCTAACGGTGAGTTGAGAA.....	23	1	1	1.00	1	1	0	0	0	0
.....TGTCCTGGGCCTGATGGCGG.....	20	0	1	1.00	1	1	0	0	0	0
.....TTGTCCTGGGCCTGATGGCGGCTC.....	24	0	1	1.00	1	0	0	0	1	0
.....CTCTGGCTAACGGTGAGTTGAG.....	22	0	1	1.00	1	1	0	0	0	0
.....CCTGGGCCTGATGGCGGCTCTGGC.....	24	0	1	1.00	1	0	0	0	1	0
.....TCTGGCTAACGGTGAGTTGAGT.....	22	1	1	1.00	1	1	0	0	0	0

Anti-sense strand reads

AACAGACGGACGGCACGTGGTTTAGAAGTGATTAGGTGTTACTTTAAGGAAAGGGAACGGAAACAGGACCCGGACTACCGCCGAGACCGATTGCCACTCAACTCTGTTTTTATGTATTTTCACATAAATTTAAATTAATACTATAAATAAACACA **********.....((((.(((((((.(((.((.(((((.....)))))).)).))).)))))))..))))).....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M040 female body	V112 male body
.....GTGATTAGGTGTTACTTTA.....	19	0	1	1.00	1	1	0
.....TGATTAGGTGTTACTTTAAGG.....	21	0	1	1.00	1	1	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
dp5	3:11535111-11535265 +	dps_88	TTGTCTGCC---------TGCCGTGCACCAAA----------TCTT---CACTAATCC----------ACAATGAAATTCCTTTCCCTTGCCTTTGTCCTGGGCCTGATGGCGGCTCTGGCTAACGGTGAGTTGAGACAAA---------AATACATAAAAGTGTATT----------TA---AATTTAATTATGATA----------TTTAT---TTGT---GT
droPer2	scaffold_4:6935835-6935989 +	dpe_123	TTGGCTGCC---------TGCCGTGCACCAAA----------TCTT---CACTAATCC----------ACAATGAAATTCCTTTCCCTTGCCTTTGTCCTGGGCCTGATGGCGGCTCTGGCTAACGGTGAGTTGAGACAAA---------AATATATAAAAGTGTATT----------TA---AATTTAATTATTATA----------TTTAT---TTGT---GT
droWil2	scf2_1100000004954:3517015-3517154 -		TTTTCCGCA-ACAAC---------GAC-----A----------ACTA---CAACAAACCAC---------AAAAACATGAAATTCCTTTCGGTTGCTTCGTTCTGGGTCTGCTGGCGGCTTTGGCCAATGGTGAGTTCTCC--ACT-------A----------ATTTA------TA----TATACTGTATATACTTATGA--------------------------------CT
droVir3	scaffold_12875:19998284-19998442 -		TCTTC----------TTCAGTC-----TTTCAAGCAATCAAACAAAACAA-CAAAACCAAAATC--AATCAACATGAAATTCCTGTCGCTCGCATTTCTGCTCGGTCTCCTGG---CGCTGGCTACGGGTAAGTCTGCGCTTC---------T----------CAA---GAGCA---------CCAACT----------GCAGGCTAA-------TT-GA---TTCTTTTGC
droMoj3	TGC--AATC-GCAAGTGCTCGAGTC-----TTCACAGCAGTCGTGC--AAACCCAAAAACAAA-GCCAAGTCAATATGAAATTCCTGTCGCTCGCTTTCTGCTCGGGCTGCTGG---CTCTGGCCAGTGGTAAGTCGA----ACTATTCAAGAG----------ATTTCGCAATTG-----AG---CATTCAACTA-AAT-----------TTTAA---TCCT---C
droGri2	scaffold_15252:7673893-7674051 -		TTCA--GCT-TT--ATTCGCAGAGCA-----A----------TACT---AATTAACCA-----C--TAAGAAAATGAAATTCCTATCGATTGGATTTGTCTCCCACTTCTGG---CATTTGCAAGTGGTAAGTTTTCTAAAC--------A-T--------ACGAATTC---AAATTA----ATTGGCT---GTACTAATCG--------------TCTACTATTTGT---GG
droAna3	scaffold_13266:4265763-4265946 -		TTGTCGGCA-ACAAAACCTAGAGAGTT-----CACTCCGCGAGT-ACCTCAGAAAACAAAAACCAAAAA--ACTCACAATGAAATTCCTGTCGCTTGCCTTTGTCTCGGTCTGTTGG---CCCTGGCTGGTGGTAAGTAAACTAAACT-------T----------AATTACCTTCTT----AAGACATAAGTAAA-TATTCT-------------TCACC---TTGTTTAGT
droBip1	scf7180000395751:79802-79972 -		TTGTCAGAG-CTAACTCC--CCGAGTACCAT----------AGCTCGAAAAACAAAACCAAA-AC--T--CACAATGAAATTCCTGTGCCTCGCCTTTGTCTAGGTCTGCTGG---CCCTGGCTGGTGGTAAGTAAACGAAGCT-------T----------GTTTTC-TTATTT----AACACATAACTTAAT-ATTAT-------------TTACT---TTGCTTAGT
droKik1	scf7180000302412:730049-730199 -		TTCA--GTT-CTCGCTTCTGTTCAGCT-----A----------A---------------------TACAAAGATGAAATTCCTCTCGGTTGCCTTCCTGCTCGGCCTCCTGG---CTCTGGCTACGGGTAATATAAA----------T----------ATTTAT-AATCAATATAATATACAGTGATT----------GCAAGTTAACAATCAATTTAA---TCT---AT
droFic1	scf7180000453851:9436-9604 -		TTGTCTTCT-GAAAATCCTCTTCCTTC-----A----------ACCGGCAACAACAAACCACAAA-AC--CAACAACATGAAATTCCTGTCCTTGCCTTTGTTTGGGTCTGCTGG---CTCTGGCCAACGGTAAGTAAATTAAATAA----AACT----------ATTTGA-GAACTG----TAT---TTTATTTATATTG----------TCAAT---GTTT---GC
droEle1	scf7180000489694:114612-114786 +		TTGTCACCT-GCA-ATCCTCTCCAGTC-----A----------ACCGGCAAAAACAAACCACAAA-AT--CAACAACATGAAATTCCTGTCGCTTGCCTTTGTTTGGGATCTGCTGG---CTCTGGCCAATGGTGAGTGAACTCAACTAAA----T----------ATTTGC-AAACAA----CGTAAGTCATTTAACTCTGAT----------TTCCA---TTCTACAGT
droRho1	scf7180000777700:1193-1369 -		TTCTCACTG-GCAAATCCTCTCCAGTC-----A----------ACCGGCAAAAACAAACCACAAA-AT--CAACAACATGAAGTTCCTGTCCTTGCCTTTGTTTGGGTCTGCTGG---CTCTGGCCAATGGTGAGTAAACTAAACTATA----T----------ATTTACTAAACAA----TAACTGTCATTTAATTCTTAT----------TTCAA---TCCTTTAGT
droBia1	scf7180000302292:2305402-2305580 +		TTGTCGGCT-GCAAATCCCCTCCAGTC-----A----------ACCTCAAAAACCAACCACAAA-AC--CAAGAAAATGAAATTCCTGTCGCTTGCCTTTGTCTGGGTCTGCTGGCTGCTGGCCAATGGTGAGTAAATTGAACGAAC----T----------GACTGC-GAACTG----CATAAGTTATTTAATTATTAT----------CACAA---CTATTTTCC
droTak1	scf7180000413920:71637-71780 +		TTCA--GTTTGCAC-TTCTGTTCTAGC-----T----------ACTTC--------------------AAAGATGAAATTCTTTCGGTTGCCTCCTGCTCGGCCTTTGG---CTCTCACCAGCGGTAAATATGAGTTT--------A----------ATAAAT-TAATTA----TACCAGT---CTAGTAATAATA----------ATAAT---ATTC---CT
droEug1	scf7180000409672:3286466-3286632 +		TTGTCAGCT-GCAAATCCTACCCAGTC-----A----------ACCTCA-----AACCACAAAAACATCAACAACATGAAATTCCTGTCGCTTGCCTTTGTCTGGGTCTGCTGG---CTCTGGCTAATGGTGAGTTAACTAAAG--------T----------ATTTAC-GAACTT----TATAAGTTATTAAATGATTATA----------TTAAT---TTCC---TT
dm3	chr2R:14275632-14275801 +		TTGTCAACG-GCTAATACGCGGGAGTC-----A----------AGCTCAGATTCAACCACAAAAAC--CAACAACATGAAATTCCTATCACTCGCCTTCGTTTTGGGTCTGCTGG---CTCTGGCCAACGGTGAGTAATGCCAAC--------T----------ATTTAC-AAACTA----AATAAGTTATTTAATTATGAT----------TTTAA---TTAT---AT
droSim2	2r:14943076-14943245 +		TTGTCAACT-GCAAATTCTTTGCAGTC-----A----------AGCTCAGCATTCAACCACAAAAAC--CAACAACATGAAATTCCTATCACTCGCCTTCGTTCTGGGTCTGCTGG---CTCTGGCCAACGGTGAGTAATGCCAAC--------T----------ATTCAC-CAACTA----AATAAGTTATTTAATTATGAT----------TTTAA---TTAT---AT
droSec2	scaffold_1:11750840-11751009 +		TTGTCAACT-GCAAATTCTCTGCAGTC-----A----------AGCTCAGCATTCAACCACAAAAAC--CAACAACATGAAATTCCTATCACTCGCCTTCGTTCTGGGTCTGCTGG---CTCTGGCCAACGGTGAGTAATGCCAAC--------T----------ATTCAC-CAACTA----CATAAGTTATTTAATTATGAT----------TTAAA---TTAT---AT
droYak3	2R:14912646-14912814 -		TTGTTAGCT-GCATATCCTCTGCAGTC-----A----------AGCTCAGAAACCAACCACAAA-AC--CAAAAACATGAAATTCCTATCAGTTGCCTTTGTTCTGGGTCTGCTGG---CCCTGGCCAACGGTGAGTAATCCCAGA--------T----------ATTCGC-AAGCTA----AATATGTTATTTAATTATGAT----------TTCAA---TTAT---AT
droEre2	scaffold_4845:8481609-8481755 +		TC-------------------------A----------AGCTCAGAATCCAACCACAAA-AC--CAACAACATGAAATTCCTATCAGTTGCCTTCGTTCTGGGTCTGCTGG---CTCTGGCCAACGGTGAGTAATCCCAGC--------T----------ATTCCC-AAACTAT---ATATATGTTATTTAATTATGAT----------TTCAT---TTAT---AT

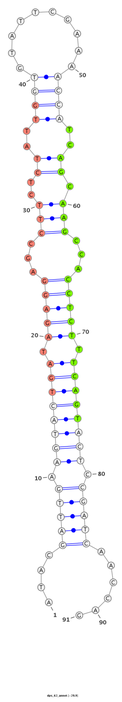
Generated: 09/08/2015 at 08:14 PM

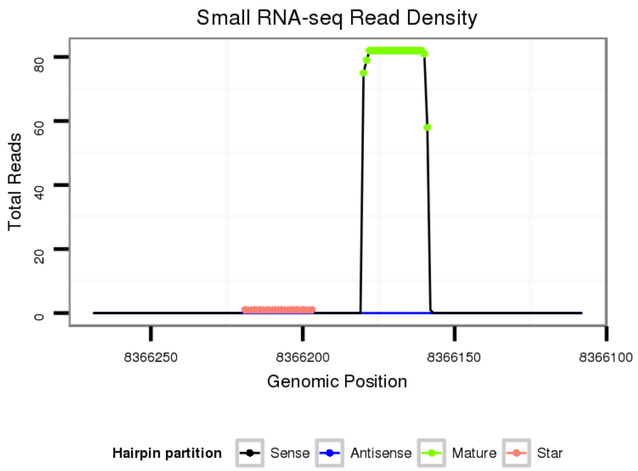
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	2
rescue.candidate	0

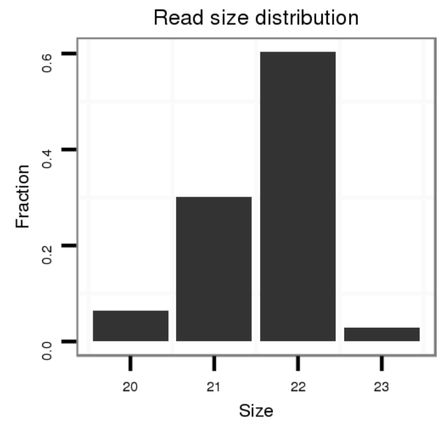
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dps_62	**XL_group1e:8366158-8366219 -**	**confident**	**Testes-restricted**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

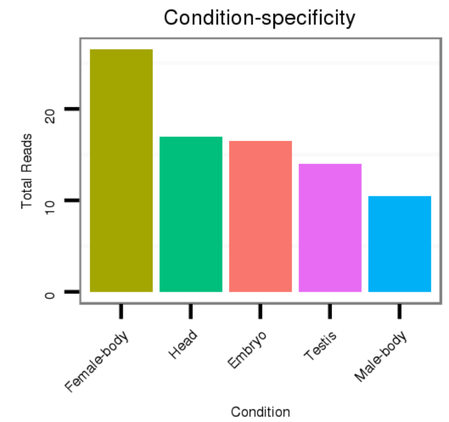
Legend: mature star mismatch in alignment mismatch in read

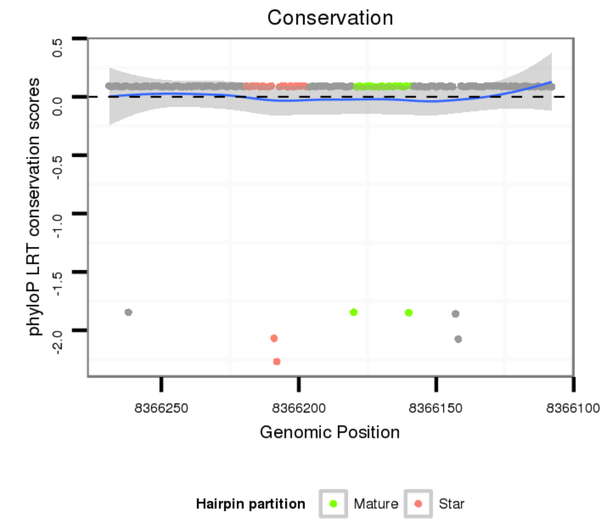
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

mature	star
	1. dps_3831 XL_group1e:8363078-8363100 - 2. dps_62 XL_group1e:8366197-8366219 -

Sense Strand Reads

hide 3p reads show mid mismatch reads

AGATCGATCGACGATCTATGGAGGATCCCTGTTTCATACGATTGAAGTACTGATAGAGGAGCCTTCTCTATTGGTGTATTCGAAAACCATCAGCAAGCCACCTCTTTCAGTACTCCGATCAACCAGCATGGTATCCCAATATTCTGTGACGAACGCTGGAGG **********....(((((.(((((((((.(((((...(((..((..((((.....))))..)).)))...)))))).)))))))).)))))......**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M040 female body	SRR902011 testis	GSM444067 head	M059 embryo	V112 male body	GSM343916 embryo	M062 head
.....TCAGCAAGCCACCTCTTTCAGT.....	22	0	1	51.00	51	10	5	11	7	8	8	2
.....TCAGCAAGCCACCTCTTTCAG.....	21	0	1	22.00	22	12	6	2	1	1	0	0
.....TCAGCAAGCCACCTCTTTCAGC.....	22	1	1	5.00	5	0	0	0	1	0	1	3
.....TCAGCAAGCCACCTCTTTCAGTT.....	23	1	1	4.00	4	1	2	0	0	1	0	0
.....CAGCAAGCCACCTCTTTCAGT.....	21	0	1	3.00	3	1	1	1	0	0	0	0
.....AGCAAGCCACCTCTTTCAGT.....	20	0	1	3.00	3	1	2	0	0	0	0	0
.....TGATAGAGGAGCCTTCTCTATTG.....	23	0	2	1.50	3	1	0	0	1	1	0	0
.....TCAGCAAGCCACCTCTTTCA.....	20	0	1	1.00	1	0	0	0	0	0	0	1
.....CAGCAAGCCACCTCTTTCAG.....	20	0	1	1.00	1	1	0	0	0	0	0	0
.....TCAGCAAGCCACCTCTTTCAGTA.....	23	0	1	1.00	1	1	0	0	0	0	0	0
.....TCAGCAAGCCACCTCTTTCAGA.....	22	1	1	1.00	1	0	0	0	0	0	0	1
.....TCAGCAAGCCACCTCTTTCAGTAA.....	24	1	1	1.00	1	0	1	0	0	0	0	0
.....TGATAGAGGAGCCTTCTCTT.....	20	1	2	0.50	1	0	0	1	0	0	0	0
.....TGATAGAGGAGCCTTCTCTAT.....	21	0	2	0.50	1	0	0	0	0	1	0	0
.....TGATAGAGGAGCCTTCTCTA.....	20	0	2	0.50	1	0	0	0	0	1	0	0

Anti-sense strand reads

TCTAGCTAGCTGCTAGATACCTCCTAGGGACAAAGTATGCTAACTTCATGACTATCTCCTCGGAAGAGATAACCACATAAGCTTTTGGTAGTCGTTCGGTGGAGAAAGTCATGAGGCTAGTTGGTCGTACCATAGGGTTATAAGACACTGCTTGCGACCTCC **********....(((((.(((((((((.(((((...(((..((..((((.....))))..)).)))...)))))).)))))))).)))))......**********	Read size	# Mismatch	Hit Count	Total Norm	Total	GSM444067 head	GSM343916 embryo	V112 male body	M040 female body
.....GGAAGAGATAACCACATAAGC.....	21	0	2	0.50	1	0	0	1	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
dp5	XL_group1e:8366108-8366269 -	dps_62	AGATCGATCGACGATCTATGGAGGATCCCTGTTTCATACGATTGAAGTACTGATAGAGGAGCCTTCTCTATTGGTGTATTCGAAAACCATCAGCAAGCCACCTCTTTCAGTACTCCGATCAACCAGCATGGTATCCCAATATTCTGTGACGAACGCTGGAGG
droPer2	scaffold_13:198129-198290 +	dpe_138	AGATCGACCGACGATCTATGGAGGATCCCTGTTTCATACGATTGAAGTACTGATAGAGGATGCTTCTCTATTGGTGTATTCGAAAACCAACAGCAAGCCACCTCTTTCAATACTCCGATCAACCAGTCTGGTATCCCAATATTCTGTGACGAACGCTGGAGG

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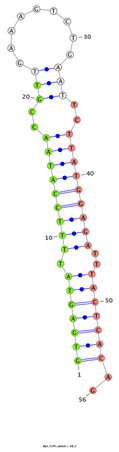
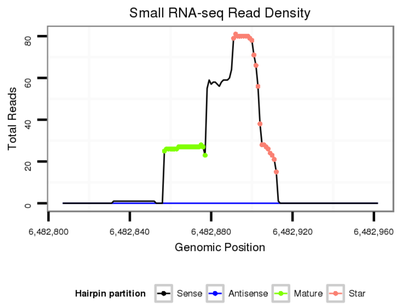
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	2
rescue.candidate	0

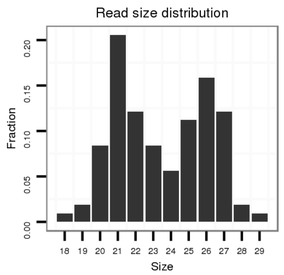
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dps_1595	**4_group3:6482857-6482912 +**	**confident**	**Mirtron**	**intron**	[View on UCSC Genome Browser [Cornell Mirror]]

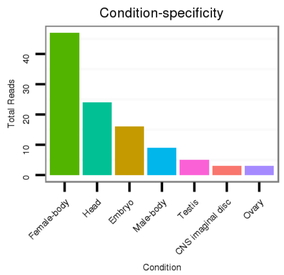
Legend: mature star mismatch in alignment mismatch in read

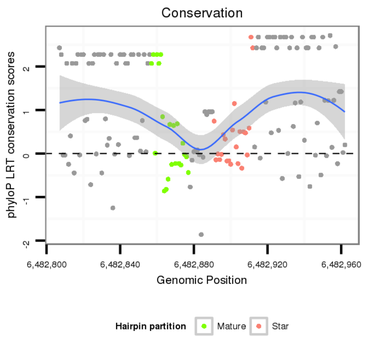
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dpse\GA18404-in]; CDS [Dpse\GA18404-cds]; CDS [Dpse\GA18404-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

AAGAGGACTGTTTTCGCACACAACAGCATATCGAATCGGAATATTGTTCAGTGAGTATTTTCCATAACCGTTGAAAGTCTGAATTCTTATGGAGATTTACTCACAGCGATGCCAACATGCTCATTGAGTCCGTGCCGTTCACGTCTGTGGGTAAAC	Read size	# Mismatch	Hit Count	Total Norm	Total	M040 female body	M062 head	M059 embryo	GSM444067 head	GSM343916 embryo	V112 male body	SRR902011 testis	SRR902012 CNS imaginal disc	SRR902010 ovaries
....GTGAGTATTTTCCATAACCGT....	21	0	1	16.00	16	8	1	3	0	3	1	0	0	0
....TGAAAGTCTGAATTCTTATGGAGATT....	26	0	1	16.00	16	6	4	0	2	0	3	0	1	0
....TCTTATGGAGATTTACTCACAG....	22	0	1	10.00	10	6	0	0	1	3	0	0	0	0
....TGAAAGTCTGAATTCTTATGGAGATTT....	27	0	1	10.00	10	4	4	1	1	0	0	0	0	0
....TGAAAGTCTGAATTCTTATGGAGAT....	25	0	1	9.00	9	2	0	0	2	0	2	2	1	0
....TCTTATGGAGATTTACTCACAGG....	23	1	1	6.00	6	1	0	0	1	2	0	0	2	0
....TGAAAGTCTGAATTCTTATGGAG....	23	0	1	6.00	6	2	1	0	1	0	1	1	0	0
....TGAAAGTCTGAATTCTTATGGAGA....	24	0	1	5.00	5	1	0	0	0	0	0	2	0	2
....GTGAGTATTTTCCATAACCGG....	21	1	1	5.00	5	0	2	3	0	0	0	0	0	0
....TCTTATGGAGATTTACTCACA....	21	0	1	4.00	4	2	0	0	1	0	0	0	0	1
....GTGAGTATTTTCCATAACCG....	20	0	1	4.00	4	0	0	2	1	1	0	0	0	0
....TCTTATGGAGATTTACTCACAGG....	23	1	1	2.00	2	1	0	0	0	1	0	0	0	0
....CTGAATTCTTATGGAGATTTACTCACAG....	28	0	1	2.00	2	2	0	0	0	0	0	0	0	0
....GTGAGTATTTTCCATAACCGTTG....	23	0	1	2.00	2	2	0	0	0	0	0	0	0	0
....GAAAGTCTGAATTCTTATGGAGATT....	25	0	1	2.00	2	2	0	0	0	0	0	0	0	0
....AAGTCTGAATTCTTATGGAGATTTACT....	27	0	1	1.00	1	0	0	1	0	0	0	0	0	0
....GTGAGTATTTTCCATAACC....	19	0	1	1.00	1	0	0	0	1	0	0	0	0	0
....GTGAGTATTTTCCATAACCGTTGAAAG....	27	0	1	1.00	1	0	0	0	0	0	1	0	0	0
....TGAATTCTTATGGAGATTTACTCAC....	25	0	1	1.00	1	0	1	0	0	0	0	0	0	0
....TTTTCCATAACCGTTGAAAGTCTGAAT....	27	0	1	1.00	1	1	0	0	0	0	0	0	0	0
....TTCTTATGGAGATTTACTCACAG....	23	0	1	1.00	1	1	0	0	0	0	0	0	0	0
....TTCTTATGGAGATTTACTCA....	20	0	1	1.00	1	0	0	0	0	0	1	0	0	0
....TCTTATGGAGATTTACTCAC....	20	0	1	1.00	1	1	0	0	0	0	0	0	0	0
....GTGAGTATTTTCCATAACCGTTGAAA....	26	0	1	1.00	1	1	0	0	0	0	0	0	0	0
....TGAGTATTTTCCATAACCGT....	20	0	1	1.00	1	1	0	0	0	0	0	0	0	0
....GAAAGTCTGAATTCTTATGGAG....	23	1	1	1.00	1	1	0	0	0	0	0	0	0	0
....CGTTGAAAGTCTGAATTC....	18	0	1	1.00	1	0	0	0	0	0	0	0	1	0
....TTCTTATGGAGATTTACTCACA....	22	0	1	1.00	1	0	0	0	0	1	0	0	0	0
....GAAAGTCTGAATTCTTATGGAG....	22	0	1	1.00	1	0	0	0	0	0	0	0	0	0
....TGAAAGTCTGAATTCTTATGGA....	22	0	1	1.00	1	0	0	0	0	1	0	0	0	0
....CTTATGGAGATTTACTCACAG....	21	0	1	1.00	1	0	0	0	1	0	0	0	0	0
....ATTCTTATGGAGATTTACTCACAGG....	25	1	1	1.00	1	0	0	0	1	0	0	0	0	0
....TGAAAGTCTGAATTCTTATGG....	21	0	1	1.00	1	1	0	0	0	0	0	0	0	0
....TGAAAGTCTGAATTCTTATGGAGATTTAC....	29	0	1	1.00	1	0	1	0	0	0	0	0	0	0
....TCTTATGGAGATTTACTCACAGC....	23	0	1	1.00	1	0	1	0	0	0	0	0	0	0
....ATTCTTATGGAGATTTACTC....	20	0	1	1.00	1	0	0	0	1	0	0	0	0	0
....GCATATCGAATCGGAATATTG....	21	0	1	1.00	1	0	0	0	0	0	0	1	0	0
....TTCTTATGGAGATTTACTC....	19	0	1	1.00	1	1	0	0	0	0	0	0	0	0
....CTTATGGAGATTTACTCACA....	20	0	1	1.00	1	1	0	0	0	0	0	0	0	0
....GAAAGTCTGAATTCTTATGGAGAT....	24	0	1	1.00	1	1	0	0	0	0	0	0	0	0

Anti-sense strand reads

TTCTCCTGACAAAAGCGTGTGTTGTCGTATAGCTTAGCCTTATAACAAGTCACTCATAAAAGGTATTGGCAACTTTCAGACTTAAGAATACCTCTAAATGAGTGTGGCTACGGTTGTACGAGTAACTCAGGCACGGCAAGTGCAGACACCCATTTG	Read size	# Mismatch	Hit Count	Total Norm	Total	M059 embryo	GSM343916 embryo	M062 head

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
dp5	4_group3:6482807-6482962 +	dps_1595	AAGAGGACTGTTTTCGCACACAACAGCATATCGAATCGGAATATTGTTCAGTGAGTAT----------TTTCCATAACCGTTGAAAG----------TCTGAATTC----------TTATGGAG----------ATTTACTCACAGCGATGCCAACATGCTCATTGAGTCCGTGCCGTTCACGTCTGTGGGTAAAC
droPer2	scaffold_1:7974292-7974447 +	dpe_589	AAGAGGACTGTTTTCGCACACAACAGCATATCGAATCGGAATATTGTTCAGTGAGTAT----------TTTCCATAACCGTTGAAAG----------TCTGAATTC----------TTATGGAG----------ATTTACTCACAGCGATGCCAACATGCTCATTGAGTCCGTGCCGTTCACGTCTGTGGGTAAAC
droWil2	scf2_1100000004521:4668422-4668579 -		AAAAGTTT-GGTTTTGC-CATAAAGCTATA-GAATCGGAATGTTATTCATGAAGTAA----------TGTGCC---CA----------TCT-------AAAAGGAGTCTTAATTACTTATCGAAGCGATGCCAATATGCTATTGAGCCATGCCGTTCACGTCTGTGGTAAAC
droVir3	scaffold_12963:2360541-2360695 -	dvi_10140	AAAGGGCGATTTTCGCACAAACTTGTAGCGAATCGGAATATAATTCATGAAGTTTCAAATA---GTTTTTAGT----------AAA-----ATATGATCGATTAATG----------TGTAATACAAGTGATGCCAATATGCTATTGAGCCCGTTGCCATTCACTCGTTGGCAAAC
droMoj3	scaffold_6500:27609007-27609165 -		AAAGGAACGTTTTCGCACACAACACGGTTGCGAATCGGAATATAATTCATGAAGTTGCAATAAAGAGGATTTCCTCAACGCATGATT----------TAATG----------TGATTTTGCAGTGATGCCAATATGCTATTGAGCCGTTGCCATTCACTCGTTGGCAAAC
droGri2	scaffold_15252:2049290-2049454 -		AAGGGAACGTTTTCGCACAAACTTGTGCGAATCGGAATATAATTCATGAAGTTTAATTGG----------G-GTTTGTTGAGTCACTGGAGA----------ATCTGATT--TAATG----------GTCTTTTTTGCAGTGATGCCAATATGCTATTGAGCCGTGCCGTTCACTCGTTGGTAAAC
droAna3	scaffold_12916:4317236-4317404 -		AAGAGAACGTTTTCGCACAACAGGTTCGCGAATCGGAATGTTCATGAAGTAGA-----AAGGATTAAAGCAAAGGATCCTAGCAGGCAAATAACTGTTTTT-CTT----------AATAATCTCTAGCGATGCCAACATGCTCATGGATCCGTGCCGTTCACTCGTTGGCAAGC
droBip1	scf1800000396737:463692-463854 +		AAGGGAACTGTTTCGCCATAACAGGTATCGAATCGGAATATGTTCATGAAGTAGA-----AAGGATTAAATTAAAGAGTTATAGCAGGGAAGTAATT-----G----------TCTATAATCTCTAGCGATGCCAACATGCTCATGGATCCGTGCCGTTCACTCGTTGGCAAAC
droKik1	scf1800000302677:369726-369933 +		AAAAGAACGTTTTCGCACACAATAGGTGGCGAATCGGAATATGTTCATGTGAGTAA----------CCAGGGAAAA------ATATATATTTGTGGTTTTTGGGAAGATATT----------CCTCCTTTAGCTCTTTTTGACTTTGTAATTAACAAATTCATTTGTTT------TGATCTTTAGCGAGCCAACATGCTCATTGAGTCCGTGCCGTTCACTCGTTGGCAAAC
droFic1	scf1800000454111:621009-621066 +		A----------CGACAGCGAGCCAACATGCTCATTGAGTCCGTGCCGTTCACTCGTTGGCAAGC
droEle1	scf1800000490644:378755-378815 -		----------TTCACCACAGTGATGCCAACATGCTATTGAATCCGTGCCATTTACTCGTTGGCAAAC
droRho1	scf1800000779170:60678-60738 +		----------TTTACCACAGTGAGCCAACATGCTATTGAATCCGTGCCGTTTACTCGTTGGCAAGC
droBia1	scf1800000302422:1964195-1964270 -		AAGGGAACGTTTTCGCACATAAATAGGTATCGAATCGAAATGTTCATGTAAGTAA----------CCAATTG---CA----------ACCTGAATT----------TTCACCACAGTGAGCCAACATGCTAATGAATCCGTGCCGTTCACTCGTTGGCAAAC
droTak1	scf1800000415871:65518-65578 -		----------TTCACCACAGTGAGCCAACATGCTAATGAATCCGTGCCGTTCACTCGTTGGCAAAC
droEug1	scf1800000407253:566302-566362 +		----------TTCACTCACAGCGATGCCAACATGCTATTGAATCCATGCCGTTCACTCGTTGCCAAAC
dm3	chr2L:11131713-11131936 +		AAGGGAACGTTTTCGCACATAAATAGGTATCGAATCGGAATGGTATCATGTGAGTAGA----------CCAAATG---CG----------TATCTGAATTTGGGGGTGGTTGGTTCTTTAAAAGAATAGTCTGGCTTGCTTTTAGTTTAAATCTATATGCTGGATC----------GTATTTTAATCCAATTCTATTTATCCACAGCGAGCCAACATGCTATTGAATCCGTGCCGTTTACTCGTTGGCAAAC
droSim2	21:10789926-10790144 +	dsi_19703	AAGGGAACGTTTTCGCACATAAATAGGTATCGAATCGGAATGGTATCATGTGAGTAGA----------CCAAATG---CA----------TCCTGAATTTTGAAAGGGAGTTTAGT----------TTAGTTTAAATCTAAATACTGGATGGTGAATATATACTAAGATTGGTATTTTAATCCAATTCTATTTACCACAGCGAGCCAACATGCTATTGAATCCGTGCCGTTTACTCGTTGGCAAAC
droSec2	scaffold_3:6533093-6533306 +		AAGGGAACGTTTTCGCACATAAATAGGTATCGAATCGGAATGGTATCATGTGAGTAGA----------CCAAATG---TT----------GT-------TTTTTTAAGTATAGTC----------TTTTAGTTTAAATCTAAATGCTGGATGGTGAATATATACTAAGATTGGTATTTTAATCCAATTCTATTTACCACAGCGAGCCAACATGCTATTGAATCCGTGCCGTTTACTCGTTGGCAAAC
droYak3	2L:7528167-7528228 +		A----------TTTACCTACAGCGATGCCAACATGCTATTGAATCCATGCCGTTCACTCGTTGGCAAAG
droEre2	scaffold_4929:14311774-14311861 -		AAGGGAACGTTTTCGCACATAACAGGTATCGAATCGGAATGTTCATGTGAGTAGA----------CCAAGTG---CA----------TCCTGAATT----------TGTAAGGGGGT

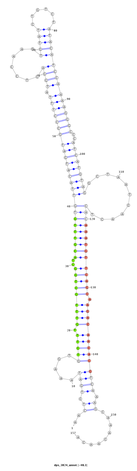
Generated: 08/18/2015 at 04:03 PM

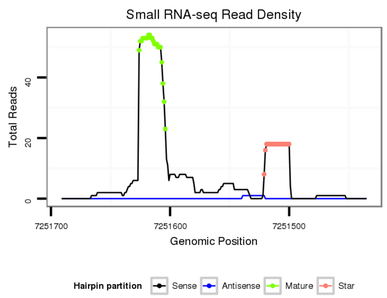
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	1

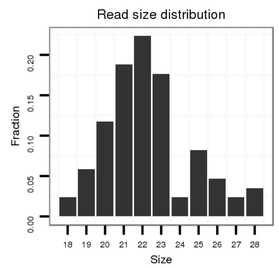
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dps_3824	**2:7251485-7251641 -**	**confident**	**Canonical miRNA**	**intron**	[View on UCSC Genome Browser [Cornell Mirror]]

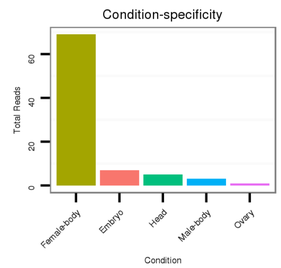
Legend: mature star mismatch in alignment mismatch in read

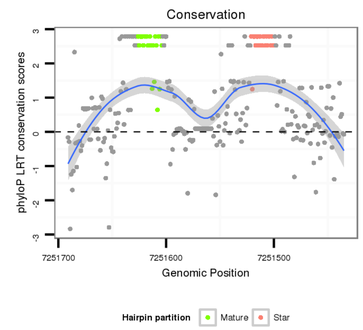
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dpse\GA14324-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

```
TCCCCCAGTGACCAAGTGATAAGTGTGCGTGTGCGTGTGTCTTACCAAAGAACTCTGATAAAGTGTGTTTGTTTGCTGGCTACGTTTGTGTTACATGATGCCCTTTATGGACTCCAAGTGTATCTGTCTATACATCCAAAAGGGCCCATCATGTAGGCTAATCAACTCACAAATGTTCAGCAAGACAACACGTCAAAGCAAACAACAAGTAAATGTATCTAATAAACTGCCAGTATGATATATCTTTCTCCAAATAA
**********..((.((((.....(((((.(((((((((..(((((((((((((((((((((((((((.(((.......((((.....)))))))))))))))))..))))))))).....))))))))))))).))))))))))..)).........**********
```

Read size	# Mismatch	Hit Count	Total Norm	Total	M040 female body	GSM343916 embryo	M059 embryo	V112 male body	GSM444067 head	M062 head	SRR902010 ovaries
23	0	1	10.00	10	9	0	0	1	0	0	0
22	0	1	8.00	8	8	0	0	0	0	0	0
21	0	1	7.00	7	7	0	0	0	0	0	0
22	0	1	6.00	6	4	0	0	0	2	0	0
25	0	1	6.00	6	4	1	1	0	0	0	0
20	0	1	6.00	6	5	0	0	0	0	1	0
21	0	1	5.00	5	5	0	0	0	0	0	0
19	0	1	4.00	4	4	0	0	0	0	0	0
26	0	1	3.00	3	3	0	0	0	0	0	0
22	0	1	3.00	3	1	0	0	1	1	0	0
20	0	1	2.00	2	2	0	0	0	0	0	0
24	0	1	2.00	2	1	0	0	1	0	0	0
27	0	1	1.00	1	1	0	0	0	0	0	0
20	0	1	1.00	1	0	0	1	0	0	0	0
21	0	1	1.00	1	0	0	0	0	0	1	0
23	0	1	1.00	1	0	0	0	0	0	0	1
18	0	1	1.00	1	1	0	0	0	0	0	0
21	0	1	1.00	1	1	0	0	0	0	0	0
21	0	1	1.00	1	1	0	0	0	0	0	0
22	0	1	1.00	1	1	0	0	0	0	0	0
23	0	1	1.00	1	1	0	0	0	0	0	0
23	0	1	1.00	1	1	0	0	0	0	0	0
22	1	1	1.00	1	1	0	0	0	0	0	0
28	0	1	1.00	1	1	0	0	0	0	0	0
22	0	1	1.00	1	1	0	0	0	0	0	0
20	0	1	1.00	1	1	0	0	0	0	0	0
28	0	1	1.00	1	0	0	1	0	0	0	0
21	0	1	1.00	1	0	1	0	0	0	0	0
28	0	1	1.00	1	1	0	0	0	0	0	0
23	0	1	1.00	1	0	1	0	0	0	0	0
19	0	1	1.00	1	1	0	0	0	0	0	0
26	0	1	1.00	1	1	0	0	0	0	0	0
18	0	1	1.00	1	1	0	0	0	0	0	0
25	0	1	1.00	1	1	0	0	0	0	0	0
22	0	1	1.00	1	1	0	0	0	0	0	0
25	0	1	1.00	1	0	0	1	0	0	0	0
21	0	1	1.00	1	1	0	0	0	0	0	0
28	0	1	1.00	1	1	0	0	0	0	0	0
27	0	1	1.00	1	0	0	1	0	0	0	0
18	0	2	0.50	1	0	1	0	0	0	0	0
18	0	12	0.08	1	1	0	0	0	0	0	0

Anti-sense strand reads

```
AGGGGGTCACTGGTTCACTATTCACACGCACACGCACACAGAATGGTTTCTTGAGACTATTTCACACAAACAAACGACCGATGCAAACACAATGTACTACGGGAAATACCTGAGGTTCACATAGACAGATATGTAGGTTTCCCCGGGTAGTACATCCGATTAGTTGAGTGTTTACAAGTCGTTCTGTTGTGCAGTTTCGTTTGTTGTTCATTTACATAGATTATTTGACGGTCATACTATATAGAAAGAGGTTTATT
**********..((.((((.....(((((.(((((((((((((((((((((((((((.(((.......((((.....)))))))))))))))))..))))))))).....))))))))))))).))))))))))..)).........**********
```

Read size	# Mismatch	Hit Count	Total Norm	Total	M040 female body
19	0	1	1.00	1	1

Show Alignment With Reads

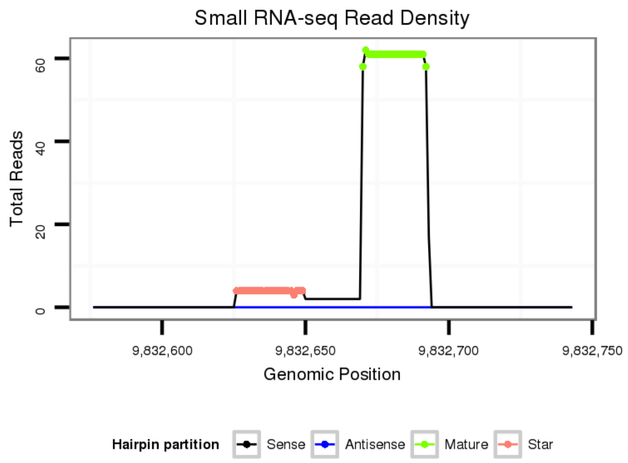
Re-alignment of all predicted orthologs

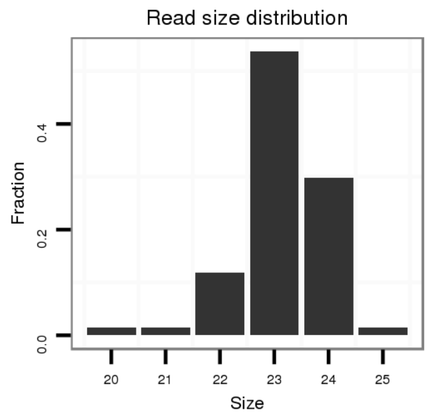
Species	Coordinate	ID	Alignment
dp5	2:7251435-7251691 -	dps_3824	TCCC------CC-AGTGACCAAGTGATAA----------GTGTGCGTG----------TGCGTGTG----------TCC--T---TACCAAAGAACTCTGAT-AAAGTGTGTTTGTTTGCTGG-CTACGTTTGTGTTACATGA----------TGCCCTTTATGGACTCCA----------AGTGTATCTGTCTATACATCCAAAAGGGCCCATCATGTAGGCTA-ATCAACTCACAAATGTTCAGCAAGACAACACGTCAAAGCAAACAACAAGTAA----------ATGTA--TCTA----------ATAAACTGCCAGTATGA----------TATAT-CT-TTCTC---CAAATAA----------
droPer2	scaffold_0:1112031-1112293 -	dpe_2478	TCCC------CC-AGTGACCAAGTGATAA----------GTGTGCGTGGCGTG----------TGCGTGTG----------TCC--T---TACCAAAGAACTCTGAT-AAAGTGTGTTTGTTTGCTGG-CTACGTTTGTGTTACATGA----------TGCCCTTTATGGACTCCA----------AGTGTATCTGTCTATACATCCAAAAGGGCCCATCATGTAGGCTA-ATCAACTCACAAATGTTCAGCAAGACAACACGTCAAAGCAAACAACAAGTAA----------ATGTA--TCTA----------ATAAACTGCCAGTATGA----------TATAT-CT-TTCTC---CAAATAA----------
droWil2	scf2_1100000004902:91361-91556 -	dwi_5413	C-GA-----TT-A----------TTAAAGTGTG-----|--------|----------TGCAATGT-----------|---GAAG-CTA-GAGAACTCTAG-AAAGTGTGTTTGTTTGCTGG-CTACGTTTGTGTTACATGATTCA-------AT-GTTT----------|----------T-TATTGG-CATC-TGTAGGCTTAATGAATCAGAAATGTTCAGCAAGACAACACGTCAGAGAAACAACAAGATA--CAAA-----|-----|-----|----------AA-GAA----------A----------GATAT-CT-GTCTC---T-----|----------
droVir3	scaffold_13047:936572-936831 -	dvi_24633	TCCG------C-AA----------TTGTGATATGTAATAATGT-------|----------GCCTCTTCGATAATAC-------|----------C---G---TG-GAGAAGTCTGAG-AAAGTGTGTTTGTCTGA-CTACGTTTGTGTTACATGCGAAGTCTCGAT-------CGGCT-------|----------|----------G-TGG-G-AT-TCTCATGTAGATA-AG-TAC-G-GAAATGTTCAGCAAGACAACACGTCGAAGCAAGCGCGAATATGTCGCGTTA--TTA----------|----------ATAGAC-A-TTCAGTGA----------TGTAT-G-TTA-GCTTATATGAATAATAGCAATGTTT----------
droMoj3	scaffold_6540:4939432-4939649 -	dmo_3125	TTG-G-----TG-AA----------TTATGATTTGTGATTT-G-TG-AA-CTGCATTTCAGTGGCTATCGATGAGAG-------|----------A---CTGCAACGAGAGAAATCTAG-AAAGTGTGTTTGTTTGCTGG-CCACGTTTGTGTTACATGTGAAATCCTGT-------CGCTGTGTCA----------A----------|----------TTTGTCTCATGTAGATA-AGCAACCACAAATGTTCAGCAAGACAACACGTCAAAGCTGTGCGCAAATAATCGAAT-----|-----|-----|----------|----------|----------|-----|-----|-----|-----TGA----------
droGri2	scaffold_14906:5355619-5355890 +	dgr_460	TCGG------CC-ATGACCGAGTGATAATGTGATATGTGATTG-|-------|----------|-------TG-------|-CTCGCGACGAGCAGAATCTCTGAG-AAAGTGTGTTTGTTTGCTGG-CTACGTTTGTGTTACATTTCGAACTAACGG-|------CGCAGTTGTGTGCTGCTCCTGCTGCGG-|----------|----------TG-|-----TTTGTCTCATGTAGGTTA-AGCAACCACAAATGTTCAGCAAGACAACACGTCAAAGCAAGCGCGAATAGGTCGGGTTTATAATATGTG--TTA----------ATACATAAAAAATAT----------|----------ATTTATGT-GTTTA-TCT-----GTTT----------
droAna3	scaffold_13340:938945-939173 +	dan_4036	TCTG-----|--|----------|----------|-------|----------|-----CATC-TGAAGTGAA-------|-TCTGGAGCAGATGAGAACTCTGAG-AAAGTGTGTTTGTTTGCTGG-CTACGTTGTGTTACATG-|----------AGTTCC----------|----------|----------T-TTCGGGG-TTC-TGTAGGCTTAGAATCAGAAATGTTCAGCAAGACAACACGTCAAAGCAAACACAGCAGCACTACTACATCAATGTGAGTCGATTCAAACAAATGGAC----------AAATAA----------|----------ACTTTCAT--TTATA-GCT-----|-AATAT----------
droBip1	scf7180000394085:58581-58786 -		GA-|-----|--|----------|----------|-------|----------|----------|-------|----------|-CTGGATCTGATGAGAACTCTGAG-AAAGTGTGTTTGTTTGCTGG-CTACGTTGTGTTACAGTG-|----------AGTTCC----------|----------|----------TCC-AAAGGGCCCTCTGTAGGCTTA-CCAACTCACAGATGTTCAGCAAGACAACACGTCAAAGCAAACACAGAGGCTACTCCCCCAATGTGACTGCCCATCCAAGCAGTGGATACTCCACTCCAAAAATAT----------|----------|----------|-----|-----|-----AA----------
droKik1	scf7180000302475:1404899-1405140 +		TATTTACGGTGGA-AATATT-|-------|----------|-------|----------|-CAATGGAAA-|----CTCAAAATGATCAACAGTGCACCGGCCTGAGAACTCTGAG-AAAGTGTGTTTGTTTGCTGG-CTACGTCGTGTTACAGTG-|----------A----------|----------TCCAAAATGGATTTCTGTGGGCTTA-CCAACTCACAGATGTTCAGCAAGACAACACGTCTAAAAATCAACAACAGCTTTGCAA-----|----|-----|----------A-TTAAGCAAGAAAGCTCAGTGGAAATTCGCTAATCC-CCT-TTTC---CA---AA----------
droFic1	scf7180000453800:2293575-2293756 +		TATTTACAGCTTTA-CAGTT-|-------|----------|-------|----------|-CAAAAAAACTGCAATGGAAA-|----ACTTTA-|-CTGGAGCAGATGAGACTCTGAG-AAAGTGTGTTTGTTTGCTGG-CTACGTCGTGTTACAGTG-|----------A----------|----------TCCAAATGGATTTCTGTGGGCTTA-CCAACTCACAGATGTTCAGCAAGACAACACGTCAAAAATACAACACAGTG-|----------|----------|-----|-----|----------|----------|-----|-----|-----|----------|----------|----------|-----|-----|-----|----------|----------|----------|-----|-----|-----|----------

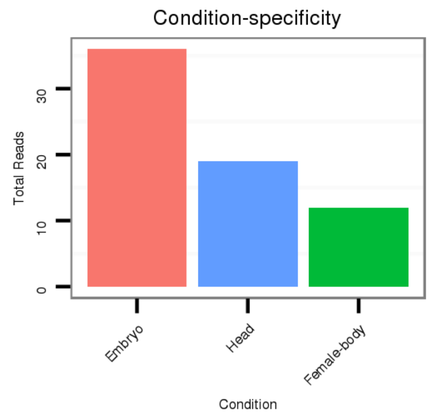
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dps_86	**XL_group1e:9832626-9832693 +**	**confident**	**Mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

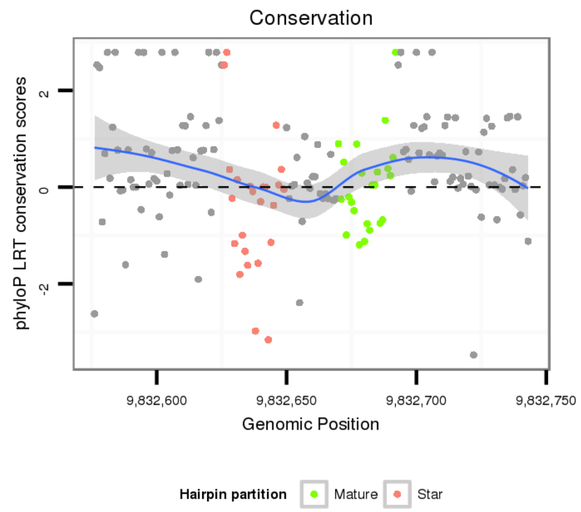
Legend: mature star **mismatch in alignment** mismatch in read

Predicted structure









Show Alternate Folds

Flybase annotation

intron [Dpse\GA17005-in]; CDS [Dpse\GA17005-cds]; CDS [Dpse\GA17005-cds]; utr3 [utr3_plus_8424]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

```
CCCGCTAGAAGTGTGCCTTAAATGGTTACGAAACGAACTACACGAAATTGGTAAGAGGTGAATACATACTTATTTGGATCCCGTTAAGGGCTAATAATGTGTGTTAAATTTCTTACAGACTGTCTTAAAATCGAGGACGTTGCACTCCCAGCGAAGACATTTCTGCTG
***************************************************(((((((((....((((((....((((..(((.....)))))))....))))))...)))))))))).**************************************************
.......................................................................................TAATGTGTGTTAAATTTCTTACA.......................................................
.......................................................................................AATGTGTGTTAAATTTCTTACA........................................................
.......................................................................................TAATGTGTGTTAAATTTCTTAC........................................................
.....................................................GTAAGAGGTGAATACATACTTATT.........................................................................
.......................................................................................TAATGTGTGTTAAATTTCTTACAGT.....................................................
.............................................................................ATTTGGATCCCGTTAAGGGCTAATA.........................................................
.....................................................GTAAGAGGTGAATACATACTTATG.........................................................................
.....................................................GTAAGAGGTGAATACATACT.............................................................................
.............................................................................TGGATCCCGTTAAGGGCTAAT.........................................................
```

Read size	# Mismatch	Hit Count	Total Norm	Total	M059 embryo	GSM343916 embryo	M040 female body	M062 head	GSM444067 head	V112 male body	M022 male body
23	0	1	17.00	17	3	1	6	1	6	0	0
22	0	1	5.00	5	0	0	3	2	0	0	0
22	0	1	3.00	3	1	2	0	0	0	0	0
24	0	1	3.00	3	1	1	0	0	1	0	0
25	1	1	1.00	1	1	0	0	0	0	0	0
25	0	1	1.00	1	0	0	1	0	0	0	0
24	1	1	1.00	1	0	0	0	1	0	0	0
20	0	1	1.00	1	0	0	0	1	0	0	0
21	0	1	1.00	1	0	0	1	0	0	0	0

Anti-sense strand reads

```
GGGCGATCTTCACACGGAATTTACCAATGCTTTGCTTGATGTGCTTTAACCATTCTCCACTTATGTATGAATAAACCTAGGGCAATTCCCGATTATTACACACAATTTAAAGAATGTCTGACAGAATTTTAGCTCCTGCAACGTGAGGGTCGCTTCTGTAAAGACGAC
***************************************************(((((((((....((((((....((((..(((.....)))))))....))))))...)))))))))).**************************************************
```

Read size	# Mismatch	Hit Count	Total Norm	Total	GSM444067 head	GSM343916 embryo

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
dp5	XL_grouple:9832576-9832743 +	dps_86	CCCGCTAGAAGTGTGCCTTAAATGGTTACGAAACGAACTACACGAAATTGGTAAGAGGTGA----------ATAC---ATA----C-TTATT----------TGGATCCCGT----------TAAG----GGCTAATAA-TGTGTGTTAAATTTCTTACAGACTGTCTTAAAATCGAGGACGTTGCACTCCCAGCGAAGACATTTC-TGCTG
droPer2	scaffold_22:369107-369274 -	dpe_114	CCCGCTAGAAGTGTGCCTTAAATGGCTACGAAACGAACTACACGAAATTGGTAAGAGGTGA----------ACAC---ATA----C-TTATT----------TGGATCCCGT----------TAAG----GGCTAATAA-TGTGTGTTAAATTTCTTACAGACTGTCTTAAAATCGAGGACGTTGCACTCCCAGCGAAGACATTTC-TGCTG
droWil2	scf2_1100000004909:9139795-9139964 -		TCCAATTGAAACTCGCATTAAATGGATTACAAAGGCATTTTATGAAATTGGTAATAAATATT--------TA-----AACC-----------------------CACAGACT-TATGTATG----------CAT-ATACATATA----------TTTATGTCTTTATTTTCTTACAGATAGCCTTAGTCTGCAAGATGTGTCAACGCAAAGCAACCATTTT-ATACA
droVir3	scaffold_12970:7630167-7630329 -		TCCAATAGAAATGTTTCTTAAATACATTAAAAGGCATTCTATGAAATTGGTAAGCGAAACTATTATTTAAAGTA---TAC----------A--------------------CCTATTA----------CTTA----------ACGCGTTTTCTTTTAAATATAGATTGCCTAAGAGTGCTGGACATCCACTTCAAAACCATTATTTT-TATT
droMoj3	scaffold_6482:2058412-2058615 +		GCCGATCGAAGTTTCCTTAAGTATATAAAAGAGCATTTTATGATATTGGTAAGCTAATATT--------T-AAACATAGTATCA-CTGACCAACAGCAGTTTGGTCA--GTT-----ATAGTATT----------TATCTA----TAT-ATTCATTTTTTT-----------TTTATATTTATATATATATAGATTGCCTAAGAGTGCTGGACATCCACTTCAAAACAATTATTTT-TTACT
droGri2	scaffold_15203:6986556-6986713 +		TCCCATCGACATTTTCTTAAATACTTTAGAAAAGCGCTTTAATGAAATTGGTAAGCAGTCA----------AACT---ATTCAATTC-----------------------AAATTATTT--------AAATTTA----------TAT-----------------------F-------CTGTTTCGATTTAGATTCCCTAAGAGTGCTGGACATCCCACTCCAAAAACAATTAGTTT-TTACA
droAna3	scaffold_13137:1019359-1019514 -		CC-AATTAAAAGTATCATAATATTTTTATCAAAGCATCTTGTAAAATAGGTATTCAAATA----------AGCG---TT----C-TTAAA----------TATTTTCCAT----------TA-----------ACAGT--TTTTTTTCCTTTCAGACTGCCTTAAAATCAAGAGGATCTTTCCTGTGCATAAAGAGTTTTTTGTTG
droBip1	scf7180000395390:1446-1599 +		CCCA-TTGAAAGTATCATGATATGGTTTGTCAAAGCATTTTGTAAATTAGGTATTCAGTTA----------ACCC---TTAAAAAT-----------------------ATTTG----------CAATAA----------AATATCCATTCTTCTTTTCAGATTGCCTTAAAATCAAGAGCAATTTTCGCGTAGATAAAGAATTTT-TTATT
droKik1	scf7180000302698:50023-50194 -		GCCCATTGAAGAATGCATCAAGTGGTTGATAAAGCATGCAACGAAATAGGTTTGTGAATATT--------CT-----AATG-----------------------CTAAAATTA--------AACTTTA---TATAATTCATTTA----------TTA-AAGTGCCATTTTATTTTTAGATAGTCTTCAAATGATGGATGTTGTCTTGGAAGAAAAGCCTTTTC-TAATG
droFic1	scf7180000453495:521053-521226 +		ACCGATTGAGGGGTGGATAAACGGTTAACGAAAGGGTGTTATGAAATAGGTAAATACGTG----------CTTA---ATTGTGACA-----------------------AA----------ATTTTATAAGATA-ATACATTTTTTGAAA----------ATCAT---TTATTTATTTTTCAGATTGTCTTCAAATCAAGGATGTTTTACCGCATGAAAAGATTTTTC-TAATA
droEle1	scf7180000491182:2012-2173 -		TCCGCTTGAAGGATGCATAAAATGGTTTATAAAAAGATGTGTTGATATAGGTGCGTGAATTG---------GAAA---ATGCGGACC-----------------------CAAAAAAG--------TTAAAAA----------TTTT----------AAAA----TTTCCCTTTTTCAGATTGCCTTCAAATCAAGGATGTTTCACCACACGAAAAGCCTTGTG-TAATA
droRho1	scf7180000779395:18559-18723 +		TCCGATTGAAGGATGTATCAAATGGTTTATAAAAGCATGTGTTGAAATAGGTACATACATATA--------A-TAAAAATGGGGACC-ATAAA----------TGGTTGA---------AGTTT----------TATA----------AT------TATCTATTTTTCAGATTGCCTTCAAATCAAGGATGTTTCACCTAATGACAAGCCTTTTT-TAAAA
droBia1	scf7180000302126:754344-754506 -		ACCGATTGAAGGGTGTATGAGACCGTTCTTAAAAGCATGCCATGATATAGGTGCCTCTCAA----------AATA---AGTTCTTTA---AA----------TTATAACGAGTTTGTAATAATGTTCTATT---TTCTCAGATTGCCTGCAAATCAAGGATGTCTCACCCCAAGAAAGCGCGTTTC-TGATA
droTak1	scf7180000413933:24392-24544 -		TCCGATTGAAGGGTGTGTCAAACGGCTTTTAAAAGCATGTAATGACATAGGTAATTTTATA----------AGTA---AGC----------A--AAA----------TAGTAGG---------CGATTT----------TTA----------ATGA-------TTTTTTTTTCAGATTGTCTTCAAATCAAGGATGTTTTACCTGACGAAACGGATTTCC-TAATG
droEug1	scf7180000409008:1363113-1363264 -		TCCGATTGAAAGTTGTTTAAAGCGGTTATTAAAAGCATGTCATGACATAGGTAGCTATTCA----------GATA---ATT----------GAA----------TGTTTTACAA----------TAAT----GA-------------CGATAATGTTTCAGATTGTCTTCAAATTAAGGATTTTTCATCACACGAAAAGCTTTTC-TGATA
dm3	chrX:16255030-16255196 +		CCCGATTGAAGTCTGTATAAAACGGTTATTAAGAGCATGTCATGAAATAGGTAATTGTGTA----------AAGA---ATGTGGATG-----------------------CACAAAATG---------ATATTTA----------TATA----------ATGATTTTCTATTGACTCGCAGATTGTATTCAAATCAAGATGTTCACATCACGAAAGCGCTTCC-TGATG
droSim2	x:15365160-15365332 +	dsi_12559	GCCGATTGAAGTCTGTATAAAGCGGTTATTAAGAGGGTGTCATGAAATAGGTAATTGTAA----------AAA---TAAA--TAA-----------------------AAA----------TAATAAAA-TATAAAATAATATTTA----------AATA----------ATGATTTTCTATTGACTTGCAGATTGTATTCAAATCAAGATGTTCACATCACGAAAGCGCTTCC-TGATG
droSec2	scaffold_12:72547-72719 +		ACCGATTGAAGTCTGTATAAAGCGGTTATTAAGAGGGTGTCATGAAATAGGTAATTGTAA----------AAA---TAAA--TAA-----------------------AAA----------TAATAAAA-TATAAAATAATATTTA----------AATA----------ATGATTTTCTATTGACTTGCAGATTGTATTCAAATCAAGATGTTCACATCACGAAAGCGCTTCC-TGATG
droYak3	X:10376325-10376495 +		CCCGATTGAAGTCTATATAAACGGCTTTTAAAGAGGGTGTAATGATTTAGGTAATTGTAAG----------AGA---ATGTGGATG-----------------------GATG----CATAAATAG---------ATATTTA----------TATC----------ATGATTTCTCCATTGACTTTCAGATTCTATTCAAATCAAGATGTTCACACACGAAAACGCTTTTC-TGTTG
droEre2	scaffold_4690:10842419-10842585 -		CCCAATTGAAGTCTATATAAACGGATATTAAGAGGGTGTAATGATTAGGTAATTGTATG----------AGGA---ATGTGGATG-----------------------CATAAAAGG---------ATATTTA----------TATT----------ATGACTTTCCATTTACTTTCAGATTGTATTCAAATCAAGATGTTCACATTATGAAAAGCCTTCC-TGCTG

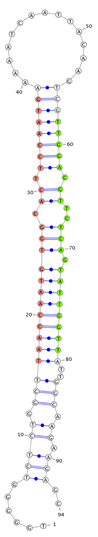
Generated: 09/08/2015 at 10:31 PM

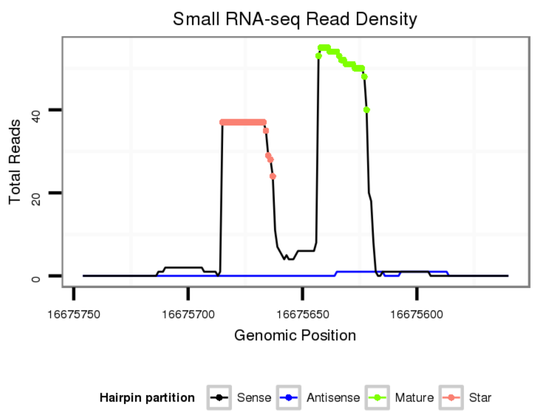
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	2
rescue.candidate	0

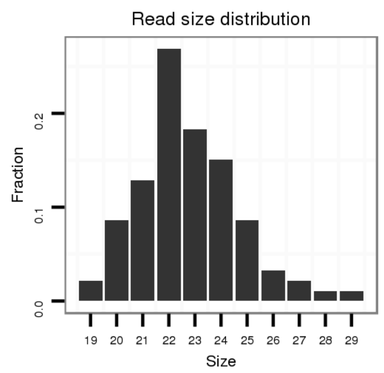
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dps_3828	**2:16675610-16675696 -**	**confident**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser [Cornell Mirror]]

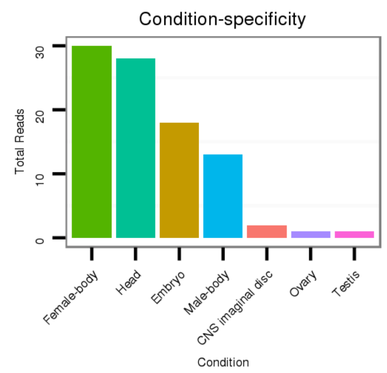
Legend: mature star **mismatch in alignment** mismatch in read

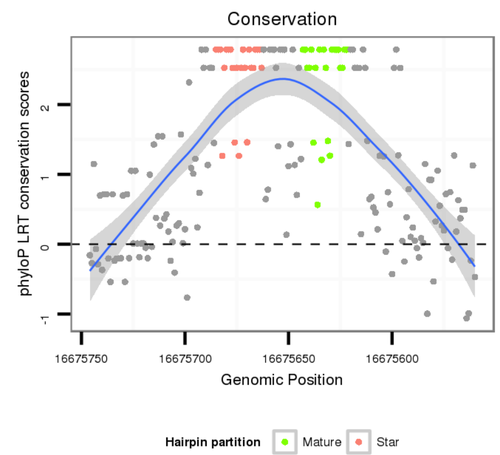
Predicted structure











Show Alternate Folds

Flybase annotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

CGGTTCTTTCCATGCTCCAATAAAGAAACGTGAAAAGTGTACAAGTTGGGGGTCTCTGGCTTAACCAATGTGGCACTTCCAATGAAAAATCAATTACAAGTCGTTGGACGTTCTCAGTATTGGTTATTGGCAAGAAGAGCCCACAGGCAGCTATAAGAGTTACAATTGTAAAGATAGATTAGCGCTT ********** .....(((((.(((((((((((((((.((.(((((((.....)))))))).))..))).).))))))))).))..))).))))..**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M040 female body	GSM444067 head	V112 male body	M059 embryo	GSM343916 embryo	M062 head	SRR902012 CNS imaginal disc	SRR902010 ovaries	SRR902011 testis
.....TTGGACGTTCTCAGTATTGGTT.....	22	0	1	20.00	20	5	7	6	0	0	1	1	0	0
.....TAACCAATGTGGCACTTCCAATG.....	23	0	1	13.00	13	5	0	1	1	4	2	0	0	0
.....TTGGACGTTCTCAGTATTGGTTAT.....	24	0	1	8.00	8	1	3	2	0	2	0	0	0	0
.....TTGGACGTTCTCAGTATTGGT.....	21	0	1	7.00	7	2	4	1	0	0	0	0	0	0
.....TTGGACGTTCTCAGTATTGGTTATT.....	25	0	1	6.00	6	0	3	1	0	0	2	0	0	0
.....TAACCAATGTGGCACTTCCA.....	20	0	1	5.00	5	2	0	0	1	0	2	0	0	0
.....TAACCAATGTGGCACTTCCAATGA.....	24	0	1	4.00	4	1	0	0	2	0	0	1	0	0
.....TAACCAATGTGGCACTTCCAAT.....	22	0	1	4.00	4	0	0	1	1	1	1	0	0	0
.....TTGGACGTTCTCAGTATTGG.....	20	0	1	2.00	2	1	1	0	0	0	0	0	0	0
.....TAACCAATGTGGCACTTCCAATGAAA.....	26	0	1	2.00	2	0	0	0	2	0	0	0	0	0
.....TAACCAATGTGGCACTTCC.....	19	0	1	2.00	2	1	0	0	1	0	0	0	0	0
.....TAACCAATGTGGCACTTCCAA.....	21	0	1	2.00	2	1	0	0	0	1	0	0	0	0
.....TTGGACGTTCTCAGTATTGGTTT.....	23	1	1	2.00	2	1	1	0	0	0	0	0	0	0
.....TTGGACGTTCTCAGTATTGGTTA.....	23	0	1	2.00	2	1	0	1	0	0	0	0	0	0
.....TGGACGTTCTCAGTATTGGTTAT.....	23	0	1	1.00	1	0	1	0	0	0	0	0	0	0
.....TAACCAATGTGGCACTTCCAATGAA.....	25	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....TTGGACGTTCTCAGTATTGGTTAA.....	24	1	1	1.00	1	0	0	1	0	0	0	0	0	0
.....GTTGGACGTTCTCAGTATTGGT.....	22	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....AAAGTGTACAAGTTGGGGGT.....	20	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....TTACAAGTCGTTGGACGTTCTCAGTA.....	26	0	1	1.00	1	0	0	0	0	0	0	0	1	0
.....TCAATTACAAGTCGTTGGACGTTC.....	24	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....TTGGACGTTCTCAGTATTGGTTATC.....	25	1	1	1.00	1	0	0	0	1	0	0	0	0	0
.....TAACCAATGTGGCACTTCCAATGAAAA.....	27	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....TAACCAATGTGGCACTTCCAATGAAAAA.....	28	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....GTGTACAAGTTGGGGGTCTCTGG.....	23	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....AATCAATTACAAGTCGTTGGA.....	21	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....AAGAAGAGCCCACAGGCAGCT.....	21	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....TGGACGTTCTCAGTATTGGTTATT.....	24	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....TCAATTACAAGTCGTTGGACGTT.....	23	0	1	1.00	1	0	0	0	0	0	0	0	0	1
.....TGAAAAATCAATTACAAGTCGTTGGAC.....	27	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....TAACCAATGTGGCACTTCCAAC.....	22	1	1	1.00	1	0	0	0	1	0	0	0	0	0
.....GTTGGACGTTCTCAGTATTGGTTAT.....	25	0	1	1.00	1	0	0	0	0	1	0	0	0	0
.....GTTCTCAGTATTGGTTATTG.....	20	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....TAACCAATGTGGCACTTCCAATGAAAAAT.....	29	0	1	1.00	1	0	0	0	0	0	1	0	0	0
.....TACAAGTCGTTGGACGTTCTC.....	21	0	1	1.00	1	0	0	0	1	0	0	0	0	0
.....TTAACCAATGTGGCACTTCCA.....	21	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....TAACCAATGTGGCACTTCCAATGAAAAAA.....	29	1	1	1.00	1	0	0	0	1	0	0	0	0	0

Anti-sense strand reads

GCCAAGAAAGGTACGAGGTTATTTCTTTGCACTTTTCACATGTTCAACCCCCAGAGACCGAATTGGTTACACCGTGAAGGTTACTTTTTAGTTAATGTTCAGCAACCTGCAAGAGTCATAACCAATAACCGTTCTTCTCGGGTGTCCGTCGATATTCTCAATGTTAACATTTCTATCTAATCGCGAA ********** .....(((((.(((((((((((((((.((.(((((((.....)))))))).))..))).).))))))))).))..))).))))..**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M040 female body	GSM444067 head	GSM343916 embryo	M059 embryo
.....GGGTGTCCGTCGATATTCTCA.....	21	0	1	1.00	1	1	0	0	0
.....AGAGTCATAACCAATAACCGT.....	21	0	1	1.00	1	1	0	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
dp5	2:16675560-16675746 -	dps_3828	CGGTTCTTTCCATGCTCCAA-TAAAGAAACGT----------GA----------AAAGTGTACAAGTTGGGGGTCTCTGGCTTAACCAATGTGGCACTTCCAATGAAAAATCAATTACAAGTCGTTGGACGTTCTCAGTATTGGTTATTGGCAAGAAGAGCCCACAGGCAGCTATAAG--A-----GTT----------ACAATTGTAAAGATAGATTAGCG----------CTT---
droPer2	scaffold_0:3721604-3721790 +	dpe_2482	CGGTTCTTTCCATGCTCCAA-TAAAGAAACGT----------GA----------AAAGTGTACAAGTTGGGGGTCTCTGGCTTAACCAATGTGGCACTTCCAATGAAAAATCAATTACAAGTCGTTGGACGTTCTCAGTATTGGTTATTGGCAAGAAGAGCCCACAGGCAGCTATAAG--A-----GTT----------ACAATTGTAAAGATAGATTAGCG----------CTT---
droWil2	scf2_1100000004902:9400240-9400380 +	dwi_5416	----------GCTTCTAGCTTAATGAATGCGACACTTCCAATGAGGAATCCATTCGAAATCGTTGGATGATATCAGTATTGGTTATTGGCGAGAAGCATCTAAAGCAGCTTTAAG--T-----TAA----------CAAACAAT-TAGATTGTTAAGC----------A------TTATA-AGTT---
droVir3	scaffold_13047:9559433-9559595 -	dvi_24635	----------GGGTTTTCTTAGCTTAACCAATGTGGCACTTCCAATGAAAAATCAATTCGAAATCGTTGGATGTTCTCAGTATTGGTTATTGGCGAGAAGAACCCAAACACAGCTATAAG--A-----AAC----------CAAA-AAT--AAAATAA----------ACAACAAAAGACACCTAACAAAATAGCATAA-----G-TTTT---
droMoj3	scaffold_6540:7667621-7667843 -	dmo_270	AAGTGCGTTTGAATCGGAGCTGAGAGGAGT----------GAACCCTCGACGACAAAGCGA--ACGATTGAGTTTCTTAGCTTAACCAATGTGGCACCTCCAATGAAAAATCAATTCGAAATCGTTGGATGTTCTCATATTGGTTATTGGCGAGAAGAGCTCAAACACAGCTATAAG--A-----AAC----------CAAA-GAACCATCAAATATATG----------ATATAAACTCTGAAATTAAATAGCATAG-----A-TTTT---
droGri2	scaffold_14906:2448908-2449070 -	dgr_463	A----------GATTGGGTTTCTTAGCTTAACCAATGTGGCACTTCCAATGAAAAATCAATTTGCAATCGTTGGATGTTCTCAGTATTGGTTATTGGCGAGATGAATCCAAACACAGCAATAAT--T-----AAAAC------CAAATACA----------ACAACAAAAAACT-GTAA-AATATAGTATAA-----GTTTTT---
droAna3	scaffold_12911:3664247-3664417 -	dan_200	----------GA----------AAAGTT-ATACGCGCGGGCGATCTCTGGCCTAACCAATGTGGCACTTCCAATGAGAAATCAATTGCAAGTCGTTGGATGCTCTCAGTATTGGTTATTGGCGAGATTGGCGCGGAGACACTGTTGTCCA-----CCC----------ACTC-----TAGTCCGTTCTAGTTTGACTCTCGCC----------CC-----G-CTTTGAA
droBip1	scf7180000396640:523304-523461 -		----------GA----------AAAGTT-ATACGCGCGGGCGACTCTGGCCTAACCAATGTGGCACTTCCAATGAGAAATCAATTGCAAGTCCTTGGATGCTCTCAGTATTGGTTTTTGGCGAGATTGGCCCGGCGGCAACTGTGTCTA-----CCC----------AGTC-----TAGTCCATTCTAGGTT----------GC-----G-CCTT---
droKik1	scf7180000302810:681870-682038 +		CGGCG----------C-----GGGGCTTCTGGCTTAACCAATGTGGCACTTCCAATGAGGAATCAATTGCAAGTCGTTGGATGCTCTCAGTATTGGTTATTGGCGAGATTGGCCCGCAGGCAGCTATAGT--T-----GT-----TGTTCCGCTTAGTCCGAG----------TAATTTTCCCCCAATTTAGTTGTCGCACCACT-----G-C---
droFic1	scf7180000454114:125769-125955 +		CAG----------TAAAAAATCGCGAAAGTGCAGTCGA----------AGAGTT-TACCGG-CGGGGCTTCTGGCTTAACCAATGTGGCACTTCCAATGAGAAATCAATTGCAAGCGCTTGGATGCTCTCAGTATTGGTTATTGGCGAGATTGGCCCGGAGGCAGGGGTATT--G-----GGCACTAG------ACCGTATAGTTCCGATCAGTCCGAA----------TTT---
droEle1	scf7180000491194:1479876-1480031 +		----------GGGGGCTTCTGGCTTAACCAATGTGGCACTTCCAATGAGAAATCAATTGCAAGACGTTGGATGCTCTCAGTATTGGTTATTGGCAAGATTGGCCCGGAGACAGCAGTATTCTA-----GGCACTTGGATACCAATCCAATAGTTCCGATCAGTCCGAG----------TTT---
droRho1	scf7180000779322:264802-264948 -		----------GGGGGCTTCTGGCTTAACCAATGTGGCACTTCCAATGAGAAATCAATTGCAAGCGCTTGGATGCTCTCAGTATTGGTTATTGGCGAGATAGGCCCGTAGGCAGGAATAATT--A-----GGCACTGG------TACGCATAGTTCCGATCAGTCCGAA----------TT-----A--
droBia1	scf7180000302035:101939-102078 +		----------GGGGGCTTCTGGCTTAACCAATGTGGCACTTCCAATGAGAAATCAATTGCAAGCGCTTGGATGCTCTGTGATTGGTTATTGGCGAGATTGGCCCGGAGGCAGGGTCACT--AGGTCTAGGC----------AGTTCCGATCAGTCCGAG----------TT-----A--
droTak1	scf7180000415712:510701-510827 +		----------GGGGGCTTCTGGCTTAACCAATGTGGCACTTCCAATGAGAAATCAATTGCAAGCGCTTGGATGCTCTCAGTATTGGTTATTGGCGAGTTTGGCCCGGAGGCAGGATAACT--ATATCTAG------------AATCCGG----------TTC---
droEug1	scf7180000409488:463410-463580 -		A----------AAGT-----GC----------AGAATT-TTCCGGCCGGGGCTTCTGGCTTAACCAATGTGGCACTTCCAATGAGAAATCAATTGCAAGCGCTTGGATGCTCTCAGTATTGGTTATTGGCGAGATTGGCCCGGAGACAGCAATTCTT--A-----AGC----------AGTTTCGTCAGTCCGAG-----TTAAAACTCCCC----------TC-----G-ATTT---
dm3	chr3R:27444091-27444224 +		----------GGGGGCTTCTGGCTTAACCAATGTGGCACTTCCAATGAGAAATCAATTGCAAGCGCTTGGATGCTCTCAGTATTGGTTATTGGCGAGATTGGCCCGGGACAGCAATTACT--A-----GAC----------AGTTCCGATCAGTCCGCA----------CT-----A--
droSim2	3r:26724064-26724197 +		----------GGGGGCTTCTGGCTTAACCAATGTGGCACTTCCAATGAGAAATCAATTGCAAGCGCTTGGATGCTCTCAGTATTGGTTATTGGCGAGATTGGCCCGGGACAGCAATTACT--A-----GAC----------AGTTCCGATCAGTCCGCA----------CT-----A--
droSec2	scaffold_2807:1133-1266 +		----------GGGGGCTTCTGGCTTAACCAATGTGGCACTTCCAATGAGAAATCAATTGCAAGCGCTTGGATGCTCTCAGTATTGGTTATTGGCGAGATTGGCCCGGGACAGCAATTACT--A-----GAC----------AGTTCCGATCAGTCCGCA----------CT-----A--
droYak3	3R:28380205-28380344 +		----------GGGGGCTTCTGGCTTAACCAATGTGGCACTTCCAATGAGAAATCAATTGCAAGCGCTTGGATGCTCTCAGTATTGGTTATTGGCGAGATTGGCCCGGGACAGCAATTACC--A-----GAC----------CGTTCCGATTAGTCCGAA----------TTAAA-G-CC---
droEre2	scaffold_4820:530483-530616 -		----------GGGGGCTTCTGGCTTAACCAATGTGGCACTTCCAATGAGAAATCAATTGCAAGCGCTTGGATGCTCTCAGTATTGGTTATTGGCGAGATTGGCCCGGGGCAGCAATACT--A-----GAC----------AGTTCCGATCAGTCCGCA----------CT-----A--

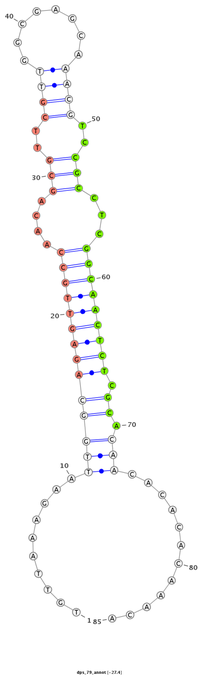
Generated: 09/08/2015 at 08:15 PM

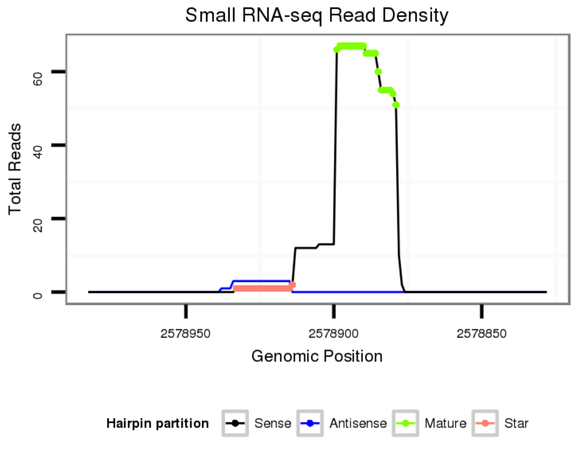
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	7
rescue.candidate	5

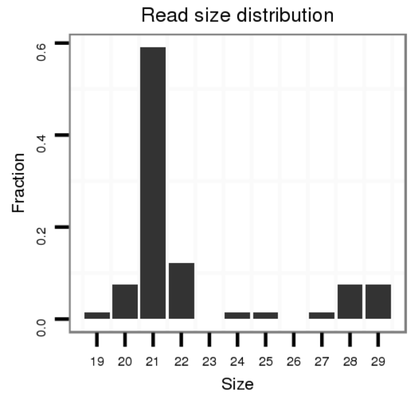
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dps_79	**XL_group1a:2578878-2578933 -**	**candidate**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

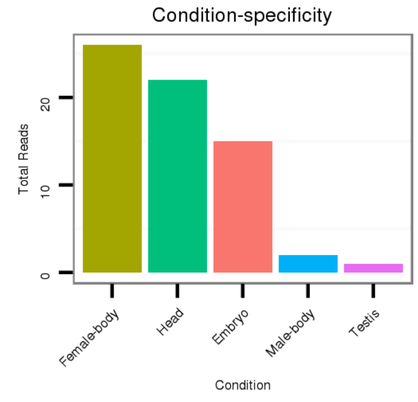
Legend: mature star mismatch in alignment mismatch in read

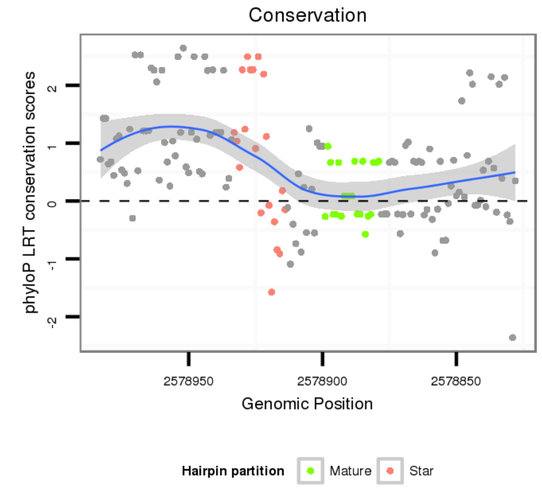
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

AAACTGGCCCAAGAATTTTCACCAAATGGAAAAGTTGTTAAAGAATTGGCAGAGTTGCCAACAGCGTTCGTTGGCGAGCAAACGTCCGCCTCGGCAACTCTCGCACAACACACACAAACAGAGAGCCACACTACTCGCTCGTTCGCTCACTCACTC **********.....(((((((((((((....(((..((((.....))))..)))...)))))))))).))..))).....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M040 female body	M062 head	M059 embryo	GSM343916 embryo	GSM444067 head	V112 male body	SRR902010 ovaries	SRR902011 testis
.....TCCGCCTCGGCAACTCTCGCA.....	21	0	1	39.00	39	15	2	4	6	9	2	0	1
.....TCCGCCTCGGCAACTCTCGCAC.....	22	0	1	8.00	8	1	4	2	1	0	0	0	0
.....TTGGCGAGCAAACGTCCGCCTCGGCAACT.....	29	0	1	5.00	5	2	2	1	0	0	0	0	0
.....TTGGCGAGCAAACGTCCGCCTCGGCAAC.....	28	0	1	5.00	5	0	5	0	0	0	0	0	0
.....TCCGCCTCGGCAACTCTCGCT.....	21	1	1	4.00	4	1	0	0	0	2	1	0	0
.....TCCGCCTCGGCAACTCTCGC.....	20	0	1	3.00	3	3	0	0	0	0	0	0	0
.....TCCGCCTCGGCAACTCTCGCC.....	21	1	1	2.00	2	0	0	2	0	0	0	0	0
.....TCCGCCTCGGCAACTCTCGCACA.....	23	0	1	2.00	2	0	0	2	0	0	0	0	0
.....CAAACGTCCGCCTCGGCAACTCTCGCA.....	27	0	1	1.00	1	1	0	0	0	0	0	0	0
.....GTTGGCGAGCAAACGTCCGCCTCGG.....	25	0	1	1.00	1	1	0	0	0	0	0	0	0
.....AGAGTTGCCAACAGCGTTCG.....	20	0	1	1.00	1	0	0	0	1	0	0	0	0
.....TTGGCGAGCAAACGTCCGCCTCGG.....	24	0	1	1.00	1	1	0	0	0	0	0	0	0
.....TCCGCCTCGGCAACTCTCGTT.....	21	2	1	1.00	1	0	0	0	0	1	0	0	0
.....CCGCCTCGGCAACTCTCGCA.....	20	0	1	1.00	1	1	0	0	0	0	0	0	0
.....TCCGCCTCGGCAACTCTCG.....	19	0	1	1.00	1	1	0	0	0	0	0	0	0

Anti-sense strand reads

TTTGACCGGGTTCTTAAAAGTGGTTTACCTTTTCAACAATTTCTTAACCGTCTCAACGGTTGTCGCAAGCAACCGCTCGTTTGCAGGCGGAGCCGTTGAGAGCGTGTTGTGTGTGTTTGTCTCTCGGTGTGATGAGCGAGCAAGCGAGTGAGTGAG **********.....(((((((((((((....(((..((((.....))))..)))...)))))))))).))..))).....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	SRR902011 testis	M040 female body	V112 male body	M022 male body
.....GTCTCAACGGTTGTCGCAAG.....	20	0	1	2.00	2	2	0	0	0
.....AACCGTCTCAACGGTTGTCGCAAG.....	24	0	1	1.00	1	0	1	0	0

Show Alignment With Reads

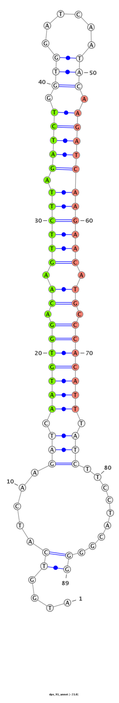
Re-alignment of all predicted orthologs

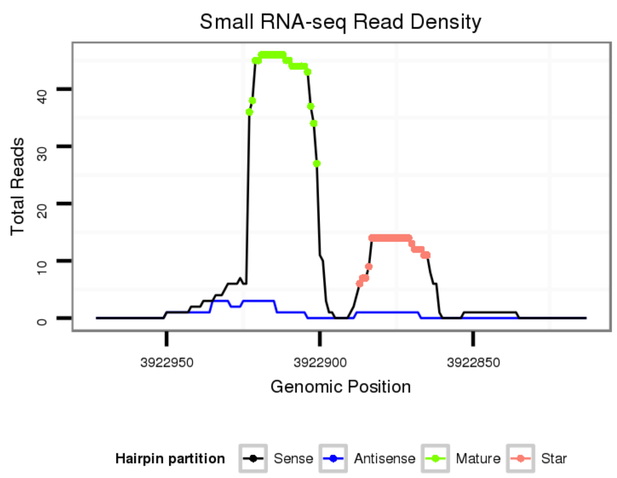
Species	Coordinate	ID	Alignment
dp5	XL_groupla:2578828-2578983 _	dps_79	AAACTGGCCC------AAGAATTTTCACCA-AA------TGGAAAAGTTGTTA-AAGAATTG------GCAGAGTTGCCAACAGCGTTCGTTGGCG-AGCAAACGTCCGCCTCGGCAACTCTCGCACAACACACACAAACAGAG----------AGCCACACTACTCGCTCGTTCGCTCACTC----------ACTC
droPer2	scaffold_28:1015901-1016056 _	dpe_321	AAACTGGCCC------AAGAATTTTCACCA-AA------TGGAAAAGTTGTTA-AAGAATTG------GCAGAGTTGCCAACAGCGTTCGTTGGCG-AGCAAACGTCCGCCTCGGCAACTCTCGCACAACACACACAAACAGAG----------AGCCACACTACTCGCTCGTTCGCTCACTC----------ACTC
droWil2	scf2_1100000004909:6990733-6990921 +		AAACTAGCAAAAGTAAAAGAATTTTCAGAA-AACAACGGGCAAAATGTTGTTA-AGAATTATTAGCAGCAGAGTTGCCACCAATACCAATGTTTGTAGGTTACGTC----------TCTCGCTCGCT--CTGGCTGTCCCATACACACACACACGCACACACACAAACGCACCAACA-----ACAGAGGCCCATTCACTCACACAGCA
droVir3	scaffold_13042:4560291-4560437 +		AAAT------------------------AAACACGCTGCCA-ACGGTC-ATA---ACGAAGTTGCCAACAGAG-------GC-ACCACACGGCCATCA----AGTTGATGCATGGCACGGGCAGACAGAGCTTGTCACTCAGTCAGTCATTCATTCATTT-ACTCATTCATTCATTCATTCACTC----------ACTC
droMoj3	scaffold_6500:10189327-10189371 _		CACCCAACCCA-----TACACTCACC----------------------------CAACACACACACAC

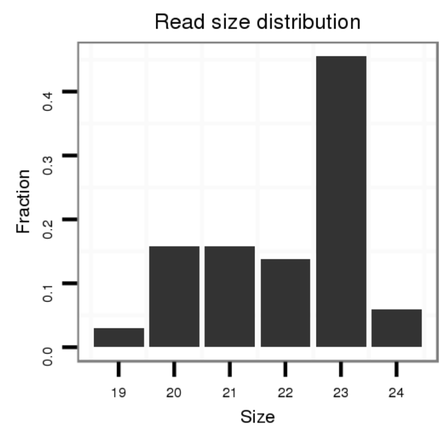
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dps_91	**XL_group1a:3922863-3922923 -**	**confident**	**Canonical miRNA**	**CDS**	[View on UCSC Genome Browser {Cornell Mirror}]

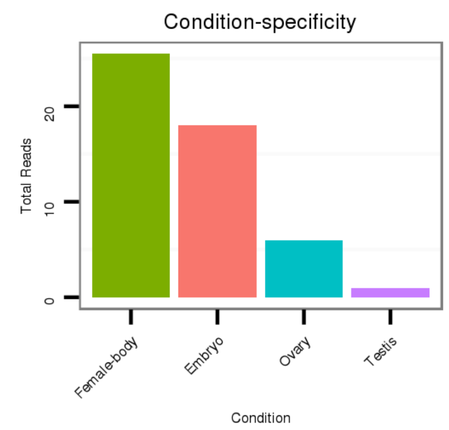
Legend: mature star mismatch in alignment mismatch in read

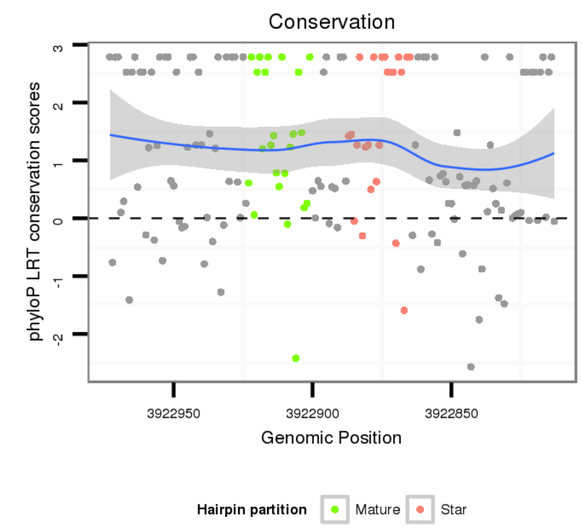
Predicted structure











Show Alternate Folds

Flybase annnotation

CDS [Dpse\dhd-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

TCAAGTCCCTGGCCCGCAAGTACTCCACAAAGGCGATGGTCATCAAGATCAATGTGGACAAGTTCTTAGATCTGGTGGATCAATACAAGATCAAGAACATGCCCACATTTATCTTCCTACGGGGCACGACGCGCCTTGCCCGCTTCAGCGGCGCCGATGAG **********....((.....(((.(((((((.((.((((((.(((((.(((.....))).))))))))))).)).)).))))))).))).....))**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M040 female body	M059 embryo	GSM343916 embryo	SRR902010 ovaries	SRR902011 testis
.....AATGTGGACAAGTTCTTAGATCT.....	23	0	1	16.00	16	8	4	4	0	0
.....AATGTGGACAAGTTCTTAGATC.....	22	0	1	6.00	6	2	2	1	1	0
.....TGTGGACAAGTTCTTAGATCTGG.....	23	0	1	5.00	5	4	0	0	1	0
.....TCAAGAACATGCCCACATTTAT.....	22	0	1	5.00	5	3	2	0	0	0
.....AATGTGGACAAGTTCTTAGA.....	20	0	1	5.00	5	1	0	1	3	0
.....AATGTGGACAAGTTCTTAGAT.....	21	0	1	3.00	3	2	0	0	1	0
.....AAGATCAAGAACATGCCCACATT.....	23	0	1	2.00	2	2	0	0	0	0
.....ATCAAGAACATGCCCACATTT.....	21	0	1	2.00	2	1	0	1	0	0
.....ATCAAGAACATGCCCACATTTAAA.....	24	2	1	2.00	2	2	0	0	0	0
.....ATCAAGAACATGCCCACATTTAA.....	23	1	1	2.00	2	2	0	0	0	0
.....AGATCAAGAACATGCCCACA.....	20	0	1	1.00	1	1	0	0	0	0
.....GGCGATGGTCATCAAGATCAATGTGG.....	26	0	1	1.00	1	1	0	0	0	0
.....ATGTGGACAAGTTCTTAGATCTGG.....	24	0	1	1.00	1	0	0	1	0	0
.....TCAATGTGGACAAGTTCTTAGT.....	22	1	1	1.00	1	0	1	0	0	0
.....ACAAGTTCTTAGATCTGGT.....	19	0	1	1.00	1	1	0	0	0	0
.....AATGTGGACAAGTTCTTAGATAA.....	23	2	1	1.00	1	1	0	0	0	0
.....AATGTGGACAAGTTCTTAGATC.....	23	1	1	1.00	1	0	1	0	0	0
.....TCAAGATCAATGTGGACAAGTTCTTAGA.....	28	0	1	1.00	1	1	0	0	0	0
.....ATGTGGACAAGTTCTTAGATC.....	21	0	1	1.00	1	0	1	0	0	0
.....ACAAGTTCTTAGATCTGGTGG.....	21	0	1	1.00	1	0	0	1	0	0
.....ACAAGATCAAGAACATGCCC.....	20	0	1	1.00	1	0	0	0	0	1
.....ATCAATGTGGACAAGTTCTTAG.....	22	0	1	1.00	1	1	0	0	0	0
.....CAATGTGGACAAGTTCTTAGATAA.....	24	2	1	1.00	1	1	0	0	0	0
.....TGTGGACAAGTTCTTAGATCTGGT.....	24	0	1	1.00	1	1	0	0	0	0
.....TCCACAAAGGCGATGGTCATCAAGA.....	25	0	1	1.00	1	1	0	0	0	0
.....TGTGGACAAGTTCTTAGATCTG.....	22	0	1	1.00	1	0	0	1	0	0
.....TACAAGATCAAGAACATGCC.....	20	0	1	1.00	1	0	1	0	0	0
.....CAAGATCAAGAACATGCCCACATT.....	24	0	1	1.00	1	1	0	0	0	0
.....CAATGTGGACAAGTTCTTAGATA.....	23	1	1	1.00	1	1	0	0	0	0
.....TGGACAAGTTCTTAGATCTGG.....	21	0	1	1.00	1	1	0	0	0	0
.....TCATCAAGATCAATGTGGACAAGTT.....	25	0	1	1.00	1	1	0	0	0	0
.....CAAGATCAAGAACATGCCCACATTTATC.....	28	0	1	1.00	1	0	1	0	0	0
.....AATGTGGACAAGTTCTTAGATCTA.....	24	1	1	1.00	1	0	0	0	1	0
.....CAAGATCAATGTGGACAAG.....	19	0	1	1.00	1	1	0	0	0	0
.....GGGGCACGACGCGCCTTG.....	18	0	1	1.00	1	1	0	0	0	0
.....ATGGTCATCAAGATCAATGTGG.....	22	0	1	1.00	1	1	0	0	0	0
.....GATCTGGTGGATCAATACA.....	19	0	2	0.50	1	1	0	0	0	0

Anti-sense strand reads

AGTTCAGGGACCGGGCGTTCATGAGGTGTTTCCGCTACCAGTAGTTCTAGTTACACCTGTTCAAGAATCTAGACCACCTAGTTATGTTCTAGTTCTTGTACGGGTGTAAATAGAAGGATGCCCCGTGCTGCGCGGAACGGGCGAAGTCGCCGCGGCTACTC **********....((.....(((.(((((((.((.((((((.(((((.(((.....))).))))))))))).)).)).))))))).))).....))**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M040 female body	M059 embryo	V112 male body	GSM343916 embryo
.....CAGTAGTTCTAGTTACACCTG.....	21	0	1	2.00	2	2	0	0	0
.....AGTTACACCTGTTCAAGAATC.....	21	0	1	1.00	1	1	0	0	0
.....AGGTGTTTCCGCTACCAGTAG.....	21	0	1	1.00	1	1	0	0	0
.....GTTCTAGTTCTTGTACGGGTG.....	21	0	1	1.00	1	1	0	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
dp5	XL_group1a:3922813-3922973 -	dps_91	TCAAGTCCCTGGCCCGCAAGTACTCCACAAAGGCGATGGTCATCAAGATCAATGTGGACAAGTTCTTAGATCTGGTGGATCAATACAAGATCAAGAACATGCCCACATTTATCTTCCTACGGGGCACGACGCGCCTTGCCCGCTTCAGCGGCGCCGATGAG
droPer2	scaffold_11:485777-485937 -	dpe_147	TCAAGTCCCTGGCCCGCAAGTACTCCACAAAGGCGATGGTCATCAAGATCAATGTGGACAAGTTCTTAGATCTGGTGGATCAATACAAGATCAAGAACATGCCCACATTTATCTTCCTACGGGGCACGACGCGCCTTGCCCGCTTCAGCGGCGCCGATGAG
droWil2	scf2_1100000004909:8002048-8002208 +		TTAAATCTCTGGCCCGTCAATATGCCGGCAAGGCGTGTTCATTAAAATCAATGTGGATAATTTGAAGAGCTCACGGAGAATATAATGTCCGCAGCATGCCCACTTTGTATTTCTCAAGGGTATGAGACGTGTCAGCATTTCTCCGGAGCCGATGAT
droVir3	scaffold_12928:3292529-3292689 +		TCAAATCCCTGGCACGCCAATACGCCAGCAAGGCGATCGTTATCAAAGTCAACGTCGACAAATTTGACGAGCTGGTGGAAAAGTACAAGGTGCGCAGCATGCGAACGTTTGTCTTCCTCAAGGGCAATCGCAGCTTGGGCAAAATCATTGGCGCCGACGAG
droMoj3	scaffold_6482:2461584-2461744 +		TGAAAGCATCGGCGCGCCAGTACGCCAACAAGGTGGACGTAATTAAGATTAATGTGGACCGATTCGATGATTTGGTGGAAACCTACAAGGTGCGCAGCATGCCTACATTTGTGTTCATCAAGAACAATCGAAAAATTGCCCGAGTCATTGGAGCAGATGAG
droGri2	scaffold_14853:2402374-2402534 +		TCAAATCGTAGCTCGTCAATACCCAGCAAAGCCATCGTACTCAAGATTAATGTGGACAATATGACGAGCTCGTCGAAAGTACAAGGTGCGCAATATGCCAACATTTGTGTTCCTCAAGGGCAACCGCAGCATGCGCAAAGTCATCGGCGCCGATGAT
droAna3	scaffold_13117:3988392-3988552 +		TCAAGTCCCTGGCACGCAAATACTCCACCAAGGCGGTGGTCATCAAGATCAATGTGGACAAGTTCGATGATCTGACGGAGAAGTATCGTGTCCGGAGCATGCCCACCTTTGTCTTCTTGAAGAACAATCGCAAAGTGGGCCGATTGTCCGGCGCCGATGAG
droBip1	scf7180000396383:390102-390262 -		TCAAGTCGCTGGCGCGAAGTACTCCACCAAGGCGGTGGTCGTCAAGGTCAATGTGGACAAGTTCGAGGAGCTGTCGGAGAAGTATCGCGTCCGGAGCATGCCCACGTTCGTCTTCCTCAAGAACAATCGCAAGGTGGGCCGCGCTTGTCCGGCGCCGACGAG
droKik1	scf7180000302610:67155-67315 +		TCAAGCCGCTGGCCAGCAAGTATCCTCCAAGGCCGTGGTCCTCAAGGTCGATGTGGACAAGTATGACGAGTTGACGGAGCGCTACAAGGTGCGCAGCATGCCGACCTTTGTCTTCCTGAAGAACAACCGCGCAGTGCGATCCTTCAGCGGCGCCGATGAA
droFic1	scf7180000454045:321894-322054 +		TCAAGTCACTGGCCAGCAAGTACTCGTCCAAGGCTGTCGTAATCAAGGTCAACGTGGACAAGTTCGAAGGCTGTCGGAACGCTACAATGTCCGCAGCATGCCCACGTTCGTCTTCCTTAAGAGCACCACCGCGTGGCGCTCGTTTCCGGTGCCGATGAG
droEle1	scf7180000491272:227422-227582 -		TGAAATCGCTGGCCAGCAAGTACTCGACCAAGGCCGTGGTCCTCAAGATCGATGTGGACAAGTTTGAGGAGTTGACGGAGCGCTACAAGGTGCGCAGCATGCCCACCTTCGTTTTCATCAAGAACAATCGCCGTTGGCATCTTTTTCTGGCGCCGATGAC
droRho1	scf7180000779588:245009-245169 +		TGAAATCGCTGGCCAGCAAGTACTCCTCCAAGGCCGTGGTCTCTCAAGATCGATGTGGACAGGTTCGACGAGCTGACGGAGCGCTACAAGGTGCGCAGCATGCCCACCTTCGTCTTCATCAAGAACAATCGTCGTGTGGCTGCTTTTTCTGGAGCGGATGAG
droBia1	scf7180000301345:302254-302414 -		TGAAGTCGCTGGCCAGCAAGTACTCCACCAAGGCGGTGGTCCTCAAGATCGACGTGGACAAGTTCGAGGAGCTGACCGAGCGCTACAAGGTGCGCAGCATGCCCACCTTCGTCTTCCTCAAGAACAACCGCCGCGTGGCCGCCTTGTCCGGCGCCGACGAG
droTak1	scf7180000415769:421271-421431 +		TGAAATCGCTGGCCAGCAAGTACTCATCCAAGGCCGTCGTCCTCAAGATCGATGTGGACAAGTTCGAGGAGCTGACGGAGCGCTACAAGGTGCGCAGCATGCCGACCTTCGTCTTCCTCAAGAACAATCGTCGCGTGGCCGCATTTTCCGGCGCGGATGAG
droEug1	scf7180000409182:131962-132122 +		TAAAAGCACTGGCCAGCAAATACTCAACCAAGGCCGTAGTTCTCAAGATTGATGTGGACAAGTTCGACGAGCTGACGGAGCGCTACAAGGTGCGCAGCATGCCCACTTTGTGTTCCTCAAAAAGGATCGTCGTGTGGCCGCATTCTCCGGCGCTGATGAG
dm3	chrX:5206614-5206774 +		TCAAATCGCTGGCCAGAAATACTCCAGCAAGGCGGTGGTGCTCAAGATCGATGTGGACAAATTCGAGGAGCTGACGGAGCGCTACAAGGTGCGCAGCATGCCAACGTTTGTCTTTTGCGCCAAAATCGACGCTTGGCCTCCTTGCCGGCGCCGACGAG
droSim2	x:4855173-4855333 +		TCAAATCGCTGGCCAGAAAGTACTCCAGCAAGGCGGTGGTGCTCAAGATCGACGTGGACAAGTTCGAGGAGCTGACGGAGCGCTACAAGGTGCGCAGCATGCCCACCTTCGTCTTTCTGCGCCCAGAATCGCCGCCTGGCGCTCCTTGGCCGGCGCCGACGAG
droSec2	scaffold_4:1545844-1546004 -		TCAAATCGCTGGCCAGAAAGTACTCCAGCAAGGCGGTGGTGCTCAAGATCGACGTGGACAAGTTCGAGGAGCTGACGGAGCGCTACAAGGTGCGCAGCATGCCCACCTTCGTCTTTCTGCGCCCAGAATCGCCGCCTGGCGCTCCTTGGCCGGCGCCGACGAG
droYak3	X:3259288-3259448 -		TCAAATCGCTGGCCAGAAATACTCCAGCAAGGCCGTGGTGCTCAAGATCGATGTGGACAAGTTCGAGGAGCTGACGGAACGCTACAAGGTGCGCAGCATGCCCACCTTTGTCTTTCTGCGCAACAATCGCCGCCTGGCGCGCCTTGTCCGGCGCCGACGAG
droEre2	scaffold_4690:2561716-2561876 +		TGAAATCGCTGGCCAGAAAGTACTCCAGCAAGGCGATCGTCCTCAAGATCGATGTGGACAAGTTCGAGGAGCTGACGGAACGCTACAAGGTCCGCAGCATGCCCACCTTCGTCTTTTGCGCAACAATCGCCGCCTGGCGCGCCTTGTCCGGCGCCGACGAG

Generated: 09/08/2015 at 08:16 PM

	PASS/FAIL
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crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
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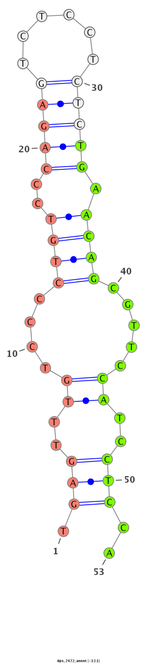
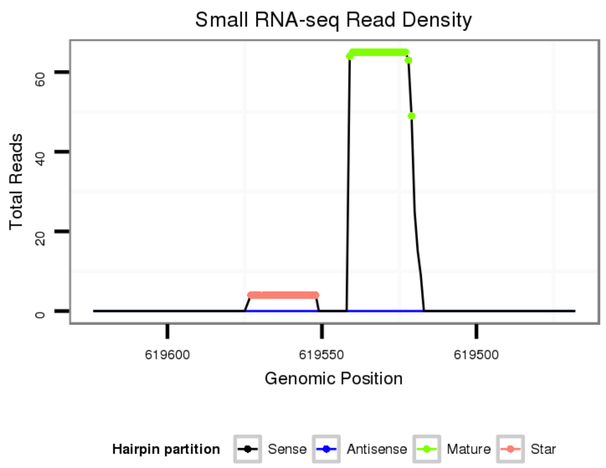
crit.tptop3	0
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	1

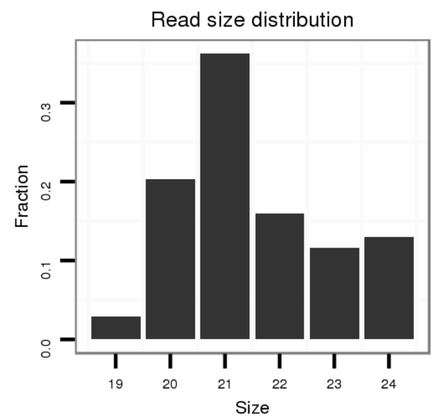
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dps_2422	**XL_group1a:619518-619574 -**	**confident**	**Mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

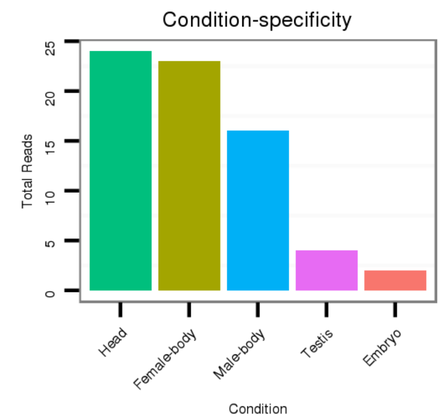
Legend: mature star mismatch in alignment mismatch in read

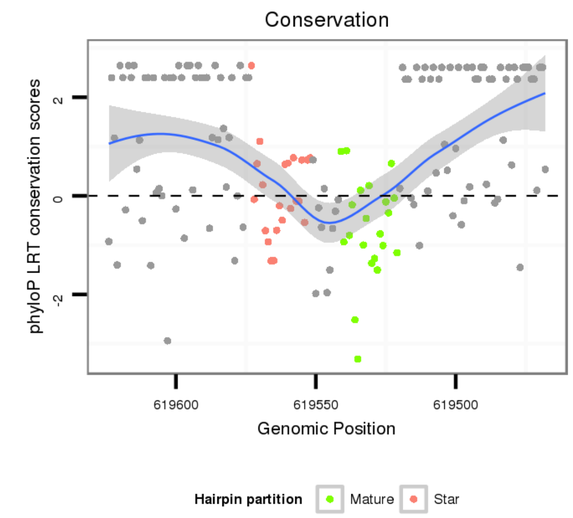
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dpse\GA22838-in]; CDS [Dpse\GA22838-cds]; CDS [Dpse\GA22838-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

```
AGGAAGTTGTGCTGGGGCGGCTGGCACATACGAGGCGGAGCAGCCCATTGGTGAGTTTGTCCCCTGTCCCAGAGTCTCCTCTCTGAACAGCGTTCCATCCTCCACAGCTTTCCACCAGCAGGTCCTTCTATGCTTTGCACTACAGACAAATGCCAAA
**************************************************.(((..((....((((..(((((.....)))))).))))).....)).))).**************************************************
```

Read size	# Mismatch	Hit Count	Total Norm	Total	M040 female body	GSM444067 head	V112 male body	M062 head	SRR902011 testis	M059 embryo	M022 male body	GSM343916 embryo
21	0	1	24.00	24	8	3	10	1	0	0	1	1
20	0	1	14.00	14	9	3	2	0	0	0	0	0
24	0	1	9.00	9	0	4	1	1	2	1	0	0
22	0	1	9.00	9	1	5	0	3	0	0	0	0
23	0	1	6.00	6	2	2	2	0	0	0	0	0
22	0	1	2.00	2	1	1	0	0	0	0	0	0
23	0	1	2.00	2	0	0	0	0	2	0	0	0
20	1	1	2.00	2	2	0	0	0	0	0	0	0
19	0	1	2.00	2	1	1	0	0	0	0	0	0
21	0	1	1.00	1	1	0	0	0	0	0	0	0
22	1	1	1.00	1	1	0	0	0	0	0	0	0
23	1	1	1.00	1	0	0	1	0	0	0	0	0

Anti-sense strand reads

```
TCCTTCAACACGACCCCGCCGACCGTGTATGCTCCGCCTCGTCGGGTAACCACTCAAACAGGGGACAGGGTCTCAGAGGAGAGACTTGTCGCAAGGTAGGAGGTGTCGAAAGGTGGTCGTCCAGGAAGATACGAAACGTGATGTCTGTTTACGGTTT
**************************************************.(((..((....((((..(((((.....)))))).))))).....)).))).**************************************************
```

Read size	# Mismatch	Hit Count	Total Norm	Total	M040 female body	V112 male body	GSM343916 embryo

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
dp5	XL_group1a:619468-619624 -	dps_2422	AGGAAGTTGTGCTGGG-GCGGCTGGCACATACGAGGCGGAGCAGCCCATTGGTGAGTTTGTCC----------CCTG----------TCCCAGAGT----------CTCC-------TCTCTGAACAGC-GTT---CCATCCTCCACAGCTTTCCAC-CAGCAG-GTCCTTCTATGCTTTGCACTACAGACAAATGCCAAA
droPer2	scaffold_157:39402-39562 -		AGGAAGTTGTGCTGGGCGCGGCTGGCACATACGAGGCGGAGCAGCCCATTGGTGAGTTTGTC--CCC----------CTG----------TCCCAGAG----------TCCCCC--TCTCTGAACAGC-GTT---CCATCCTCCACAGCTTTCCACCAGCAGGGTCCTTCTATGCTTTGCC-TACAGACAAATGCCAAA
droWil2	scf2_1100000004909:10021302-10021478 +		GGGTAGTTGTACGGC-GTGGCCGGACATATGAGGCTGAGCAACCTGTGGGTAAGTCCAA--ATCCATATT------------A----------TATGTCATTTTCC----------ATGTCATTTTG-AGTGA----------TCTGTGATCTCC-TGT---TTTCAGATCAAGCTCTTCAT-CAGCAG-CTTTGCTGTGCTTTGCATTGCAGACCAATGCAAAG
droVir3	scaffold_12932:1231700-1231755 -		GGGCAGCTGTGCGGGC-GTACCGGGCACCTACGAGGCCGAACAGCCCATAGGTAGGT--TCTCTGAACAGC-GTT---CCATCCTCCACAGCTTTCCAC-CAGCAG-GTCCTTCTATGCTTTGCACTACAGACAAATGCCAAA
droMoj3	scaffold_6473:15048959-15049029 -		C--TCTC--ATTCT-----------AC-----CCCCTTCTTACAGCAGTGCAT-CAGCAG-CTGTTGTTGTGCTTTGCACTGCAAACCAATGCCAAG
droGri2	scaffold_14853:4516626-4516794 +		GGGCAGCTGTAGGGGT-GTGCAGGCACCTACGAGGCCGAGCAGCCAATAGGTGATACACA--------T------TGA----------GAATCCAGTCA----------AAAA----------TGTTAGTTACGAAAATATATATTGTCA---AACTTTGTTGCAGCTTTGCAT-CAGCAG-CTGTTGCTGTGCTTTGCCTGCAAACAAATGCCAAG
droAna3	scaffold_12929:1760283-1760438 +		TGGCAGCTGTGCCGGA-GCGGCAGGGCACCTACGAGGCAGAGCAGCCCATTGGTAAGAGTCCTG-AGAGGT--------------------------CCTTGG----------AGCTT---AAATACTAAAACT---------T---AATCCTTTTTCAGCTCTCCAT-CAGCAG-ATACTCTTGTGCTTTGCCTGCAAACCAATGCCAAG
droBip1	scf7180000396543:223675-223831 +		TGGCAGCTGTGCCGGT-GCGGCCGGCACCTACGAGGCAGAGCAGCCCATTGGTGAGAGTCCTT-AGAGGT--------------------------CCTTGG----------AGTTC---AAATCTTATAGTT--------TT-----TTCCATTTTTTAGCTCTTCAT-CAGCAG-ATCCTCCTGTGCTTTGCCTTGCAAACAAATGCCAAG
droKik1	scf7180000302610:279024-279197 -		GGGCAGTTGTGCTGGG-GTGAGGGGAACCTATGAGGCAGAGCAGCCAATTGGTGGTGGTGATT-ACCATGAC------------TAA----------CCTCACTTCTC----------CTTGA----------TCTCG-------TCTTGAAACCC-TTT---TTTATTGTACTAGCTCTGCAT-CACACA-ATACTTTTGTGCTTTGCCTTGCAAACCAATGCAAAG
droFic1	scf7180000453927:488192-488394 -		GGGCAGCTGTGCCGGA-GGCACCGGAACCTATGAGGCTGAGCAGCCCATCGGTGAGTGATGGTT--CCAGACT------------TGATACCCTATTA--------AGAAGT------TCTTGCTTTAGCA----------AGTGATGTG-TTTATCACTCAACCTCCTCCTTACAAACT---------GGATATTTTCCAGCCCTGCAC-CACACA-ATACTCTTGTGCTTCGCCTTGCAAACCAATGCCAAG
droEle1	scf7180000491011:1038796-1038952 -		TGGAAGCTGTGCCGGA-GGCACCGGAACTTATGAGGCAGAGCAACCTGTTGGTAAGTTAGG----------------------------TTTCAGAGTTTACCACAT----------GCTAAGAAGT-GATTAAGCCCCTTTTCAGCTTTGCAC-CACACA-ATACTGTTGTGCTTTGCCTTGCAAACCAATGCCAAG
droRho1	scf7180000779506:830439-830636 -		TGGCAGCTGTGCTGGA-GGCACTGGAACTTATGAGGCGGAGCAACCCATCGGTGAGTCCTTA--AGTGATTGTAAGCTTACTA----------TTTCGGAG----------ATATAACGTAT-AGTAG----ATTACGATTCATCCTGCTCCTTACACACTTAA---TCGTCTTTTCCAGCCTTTCAC-CACACA-ATTCTGTTGTGCTTTGCCTTGCAAACCAATGCCAAA
droBia1	scf7180000301760:1008563-1008714 -		CGGCAGCTGTGCCGGA-GGCACGGGCACCTACGAGGCAGAGCAGCCCATAGGTGAGTGCAGTTC----------------------A----------CAGCCCATTTG------C----------A------TCTCTAACCAGC-----CCATCTCCTCCAGCCCTGCAC-CAGCAA-ATACTCCTGTGCTTCGCCTGCAAACCAATGCCAAG
droTak1	scf7180000415151:99031-99086+		GGGAAGCTGTGCCGGC-GGCACTGGAACCTATGAGGCAGAGCAGCCTATTGGTGAGT--TCTCTAACCAGC-CCTTCCTCCTCCAGCCCTGCAC-CAACAA-ATACTCTTATGCTTTGCCTTGCAAACCAATGCAAAG
droEug1	scf7180000409277:377003-377157 -		TGGAAGTTGTGCCGGG-GGCACCGGAACGTATGAGGCAGAGCAGCCGCATTGGTGAGTGTTC--AATTT--TCCCAGTCATCCTGCAGCTTCCCTACT---TTTACTTTTCCAGCTTTGCAC-CAACAA-ATACTCTTATGCTTTGCCTTGCAAACCAATGCAAAG
dm3	chrX:41717-41892 -		TGGCAGTTGTGCTGGA-GGCACTGGAACTTATGAGGCGAAGCAATCTGTTGGTGAGCATCA--AGCCATACC------------A----------TGGTTCATTTA----------CCTAA----------TACCAGTCGGCCTGTCCCTAATCGACT---TTACCCTTCGCAGCTTTGCAC-CAACAA-ATACTATTGTGCTTCGCATTGCAAACCAATGCCAAG
droSim2	x:31615-31792 -		TGGCAGTTGTGCTGGA-GGCACTGGAACTTATGAGGCGAAGCAATCTGTTGGTGAGCATTA--AACCATACC------------TGA----------GCATTCATTTA----------CCTAA----------TACCAGTCACTCTGTCCCTAATCGCCT---TTACCCTTCGCAGCTTTCCAT-CAACAA-ATACTATTGTGCTTCGCATTGCAACAAATGCCAAG
droSec2	scaffold_108:31565-31742 -		TGGCAGTTGTGCTGGA-GGCACTGGAACTTATGAGGCGAAGCAATCTGTTGGTGAGCATTA--AACCATACC------------TGA----------GCATTCATTTA----------CCTAA----------TACCAGTCACTCTGTCCCTAATCGCCT-----TTACCCTTCGCAGCTTTCCAT-CAACAA-ATACTATTGTGCTTCGCATTGCAACAAATGCCAAG
droYak3	X:31599-31774 -		TGGCAGCTGTGCTGGA-GGCACTGGAACTTATGAGGCGAAGCAATCTGTCCGGTGAGCATTA--AACCATAAG------------A----------TTGTTCATATA----------TTTAA----------TACTATTCACCCTCCTCCTAATCCTCT---TCACCCTTCGCAGCTTTGCAC-CAACAA-ATACTATTATGCTTCGCCTTGCAAACCAATGCCAAG
droEre2	scaffold_4644:26051-26226 -		TGAGAGCTGTGCTGGA-GGAGCTGGAACATATGAGGCGAAGCGATGTCTTGGTGAGCATTA--AACCATATC------------A----------TGCCCATGTA----------CCTAA----------TGGCATTCATCCTACTCCTAATCCTCA---TCACTCTTGCAGCTTTGCAC-CAACAA-ATACTATTGTGCTTCGCCTTGCAAACCAATGCCAAG

Generated: 09/08/2015 at 10:31 PM

	PASS/FAIL
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crit.mor	0
crit.half	0
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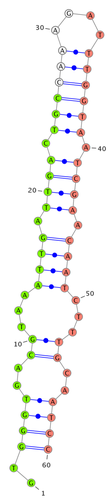
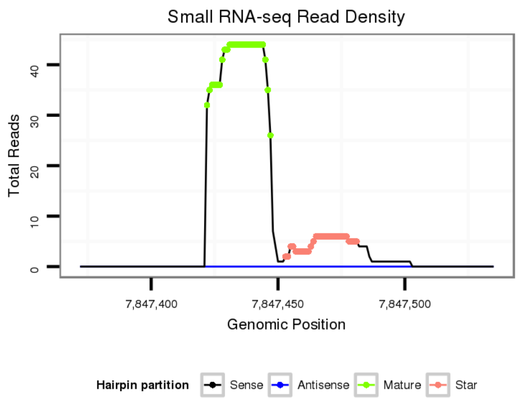
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	1

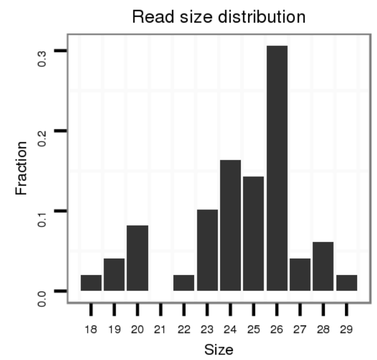
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dps_2568	**XL_group1a:7847422-7847485 +**	**confident**	**Mirtron**	**intron**	[View on UCSC Genome Browser [Cornell Mirror]]

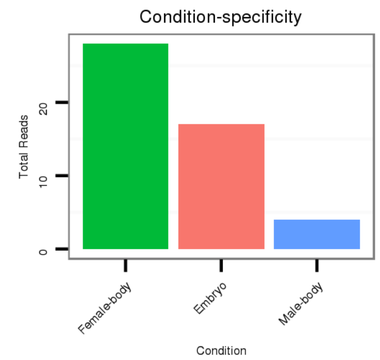
Legend: mature star mismatch in alignment mismatch in read

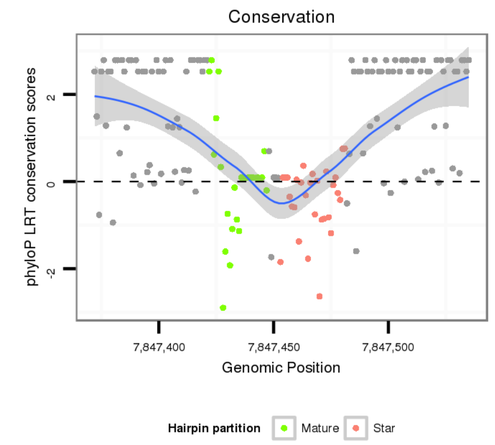
Predicted structure











Show Alternate Folds

Flybase annotation

intron [Dpse\GA14513-in]; CDS [Dpse\GA14513-cds]; CDS [Dpse\GA14513-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

```
GACCAGGCGTACTGCATATGTCGCACTTCCGACTGTTCTAGGTTTATGATGTGGGTGACGTAAATTGATTGACTGCCAAAGATTTGGTAATCGAACAATCTTTGCAATCCACAGAGGCTGCGATGGATGTGAGGAATGGTACCATGGCGATTGCATTGGCATCA
************************************************..((((..((...((((.((((.((((((....)))))).)))))..)))))...))..))))**************************************************
```

Read size	# Mismatch	Hit Count	Total Norm	Total	M040 female body	GSM343916 embryo	M059 embryo	V112 male body	M062 head
26	0	1	13.00	13	4	7	1	1	0
25	0	1	6.00	6	5	1	0	0	0
24	0	1	5.00	5	5	0	0	0	0
20	0	1	4.00	4	0	3	1	0	0
28	0	1	3.00	3	1	0	0	2	0
24	0	1	3.00	3	3	0	0	0	0
23	0	1	3.00	3	2	0	0	1	0
19	0	1	2.00	2	2	0	0	0	0
27	0	1	2.00	2	1	0	1	0	0
26	0	1	1.00	1	1	0	0	0	0
22	0	1	1.00	1	1	0	0	0	0
20	0	1	1.00	1	1	0	0	0	0
29	0	1	1.00	1	0	0	1	0	0
24	1	1	1.00	1	0	0	1	0	0
27	1	1	1.00	1	1	0	0	0	0
22	0	1	1.00	1	0	0	1	0	0
23	0	1	1.00	1	1	0	0	0	0
23	0	1	1.00	1	1	0	0	0	0
25	0	1	1.00	1	0	0	1	0	0
26	0	1	1.00	1	1	0	0	0	0
22	0	1	1.00	1	1	0	0	0	0
18	0	1	1.00	1	0	1	0	0	0
24	2	1	1.00	1	0	0	1	0	0

Anti-sense strand reads

```
CTGGTCCGCATGACGTATACAGCGTGAAGGCTGACAAGATCCAAATACTACACCCACTGCATTTAACTAACTGACGGTTTCTAAACCATTAGCTTGTTAGAAACGTTAGGTGTCTCCGACGCTACCTACACTCCTTACCATGGTACCGCTAACGTAACCGTAGT
****************************************************..((((..((...((((.((((.((((((....)))))).)))))..)))))...))..))))**************************************************
```

Read size	# Mismatch	Hit Count	Total Norm	Total	GSM444067 head	SRR902010 ovaries

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
dp5	XL_group1a:7847372-7847535 +	dps_2568	GACCAGGCGTACTGCATATGTCGCACTTCCGACTGTTCTAGGTTTATGATGTGGGTGACGT--------------AAATTGATTGACT----------GCCAAAGATTT---GG--TAATCGAAC---AA------TC-TTTGC-AA----------TCCACAGAGGCTGCGATGGATGTGAGGAATGGTACCATGGCGATTGCATTGGCATCA
droPer2	scaffold_15:201323-201486 +		GACCAGGCGTACTGCATATGTCGCACTTCCGACTGCTCTAGGTTTATGATGTGGGTGACGT--------------AAATTGATTGACT----------GCCGAAGGTTT---GGTAAT-----CCAACCA------TC-TTTGC-AA----------TCCACAGCGGCTGCGATGGCTGTGAGGAATGGTACCATGGCGATTGCATTGGAATCA
droWil2	scf2_1100000004909:2923645-2923821 +		GATCAGGCTTATTGCATATGCCGCACATCCGACTGTTCCAGGTTTATGATGTGAGTATAAACT----------GGTTTAG----------ATCAATTTAA----------CCATAAAGGCATAACCATA----------ACATT--------GAC---TGTTTGTTATT-G--TTTTAGCGGTTGCGATGGCTGTGAGGAGTGGTATCATGGCGATTGCATTGGCATCA
droVir3	scaffold_12970:6437641-6437807 +		GATCAGGCCTACTGCATATGTCGCACATCCGACTGCTCCAGATTCATGATGTAAGTTGTA-A----------TA----------TAGCTACTTG-ACAATTGTT------G----TCA-----ATCAATTGCGACT----------AATT---GA-AC---TTTTTGCAGTGGCTGCGAGGAATGGTATCATGGCGACTGCATTGGCATCA
droMoj3	scaffold_6473:1170523-1170681 +		GACCAGGCCTACTGCATATGTCGCACATCGATTGCCTCTAGGTTCATGATGTAAGTAACTAA----------TAA----TTCCT------G----TCA-----AACAATTTCGACT----------GTCA------TTTTAATTT---CA-ATCTG--TTTGTAGTGGCTGCGATGGCTGCGAGGAATGGTATCACGGCGACTGCATTGGAATCA
droGri2	scaffold_15203:9300678-9300882 -		GATCAGGCCTACTGCATATGCCGCACATCCGACTGCTCCCGATTCATGATGTAAGTGTGTGATGGA---------TTG----------A-----TGGA----------TTCA----------TTCAACCAATT----------GCATTGAGATTCCGTTT---TTTTTCT-TTTTGTTTTGTTTTGTTTTATTTTTTATATTTTTGCAGCGGCTGCGATGGCTGCGAGGAATGGTATCATGGCAATTGCATTGGCATCA
droAna3	scaffold_13047:1227922-1228091 +		GACCAGGCCTACTGCATCTGCCGCACCTCTGACTGCTCCAGGTTCATGATGTCACCACC--------CCT---A----------GACGA----------CTCCC------G----TCACCCTTGG----------CACTCTGTA---AACAATA----------AC----------AACG-TCCAT--TTTTCAGAGGCTGCGATGGCTGTGAGGAATGGTACCACGGAGATTGCATTGGCATCA
droBip1	scf7180000396575:169642-169833 -		GACCAGGCCTACTGTATCTGCCGAACATCTGACTGCTCCCGGTTTATGATGTCATCCTCC----------GCCCC----------CCGCCGCCCG-CTCCCTGCCGA----GTCCAAACACCTGTGG----------CCATCTGTA---AACAATA----------AC----------AATTCATTCCTTT-CTTCC--ATTTCAGAGGCTGCGATGGCTGTGAAGATGGTATCACGGCGATTGCATTGGCATCA
droKik1	scf7180000302696:2005885-2006044 -		GACCAGGCCTACTGCATCTGCCGCACCTCAGACTGTTCCCGGTTTATGATGTCATCATG------------GCCCG----------GAGGCACCCC-ATCTCCCTC------G----T----------TACTCACT-----TT----CTTGTGCGCTTCCAGAGGCTGTGATGGCTGCGAGGATGTGGTATCATGGCGACTGCATTGGCATCA
droFic1	scf7180000454073:2076804-2076971 -		GATCAGGCGTACTGCATATGCCGCACCTCCGACTGCTCTAGATTTATGATGTGAGTCCTCCGG----------GCCCG----AAA----------GTCC----------TTCAGC------TGGAA----------TGCAGATGC--CCTAACC--CGTTCCCTTCAC--TTTTCAGCGGCTGCGATGGCTGTGAGGAATGGTATCACGGCGACTGCATCGGGCATCA
droEle1	scf7180000491018:100996-101154 +		GATCAGGCCTACTGCATCTGCCGCACCTCCGACTCCGACAGGTTTATGATGTCAGTTCCACA-G----------GCCCG----ACA----------GTCAGTACA----------AATATGATCCTCAACT---A------ACATT-GATT------CGGCCAGCGGTTGCGATGGCTGTGAGGAATGGTACCACGGCGACTGCATCGGGCATCA
droRho1	scf7180000780067:53511-53676 -		GACCAGGCGTACTGCATCTGCCGCACTTCCGACTCCGACGAGGTTCATGATGTCAGTCCTTAATG----------GAGTCCCATT-AGA----------ACT----------CC-CACTG-ACTAACCCCTTT---AT-TTATC--TTCCTGCCAGCGGCTGCGATGGCTGTGAGGATGGTACCACGGCGACTGCATCGGGCATCA
droBia1	scf7180000301760:5136255-5136414 -		GATCAGGCCTACTGCATCTGCCGCACCTCCGACTGCTCCAGGTTCATGATGTCAGTT----CGCCGCTGCCCAT----------CAAGGG---G----------TCCTCGCTAACCAGC-----CT----TGTCATTCTTTCCAGTGGCTGCGATGGCTGTGAGGATGGTACCACGGCGACTGCATCGGGCATCA
droTak1	scf7180000415696:124009-124161 -		GATCAGGCGTACTGCATCTGCCGCACCTCCGACTGCTCCAGGTTCATGATGTCAGTTGTGT-------AT---CGCCTC----------AGAGATAT----------TCCCTCCTAACCCCTAATC---T----C--CTTCCAGCGGCTGCGATGGCTGCGAGGATGGTACCACGGCGACTGCATCGGGCATCA
droEug1	scf7180000409032:794529-794689 +		GATCAGGCATATTGCATATGTCGCACCTCCGACTGCTCCAGGTTCATGATGTCACCC----------CAAT---GATTCT----------CGAGACCAAG----------ACCA----------TGT----------TGTTCATTTGATTCC-GATGC--TTTCCAGAGGCTGCGATGGTTGTGAGGATGGTACCACGGCGATTGCATTGGTGATCA
dm3	chrX:9166587-9166748 -		GACCAGCGCTACTGCATATGCCGCTCCGACTGCTCCAGGTTCATGATGTCAGTT----------GAAT---GGCCTT----------AAAGGGCTAG----------ATCCCGGCTAACTACTTGTACCC-TTCGC--TTTCCAGAGGCTGCGATGGTTGCGAGGATGGTACCACGGCGACTGTATAGGGCATCA
droSim2	x:8714011-8714172 -		GACCAGGCGTACTGCATATGCCGCTCCGACTGCTCCAGGTTCATGATGTCAGTT----------TATT---AGCCCT----------TAAGATCTAG----------ATCCCGCCTAACCGCTTGTCCGC-ATCGC--TTTCCAGAGGCTGCGATGGTTGCGAGGATGGTACCACGGTGACTGTATAGGGCATCA
droSec2	scaffold_2196:1492-1653 -		GGCCAGGCGTACTGCATATGCCGCTCCCGACTGCTCCAGGTTCATGATGTCAGTT----------GAAT---AGCCCT----------TAAGATCTAG----------ATCCCGCCTAACCGCTTGTCAGC-ATCGC--TTTCCAGAGGCTGCGATGGTTGCGAGGATGGTACCACGCAGACTGTTATAGGGCATCA
droYak3	X:17758838-17759013 -		GATCAGGCGTACTGCATATGTCGCACCTCCGACTGCTCCAGGTTCATGATGTCAGTT----------CCCT---GGCCCT----------CAAGTGGGA----------GTCCT----------TGGCG----------TGGAGATTCCGCCTAAACACTTCTACCC-TTCGC--ATTCCAGAGGCTGCGATGGCTGTGAGGATGGTACCACGGCGACTGCATAGGGCATCA
droEre2	scaffold_4690:5952661-5952837 +		GATCAGGCGTACTGCATATGCCGCTCCGACTGCTCCAGGTTCATGATGTAAGTT----------GTCTT---GGCCCT----------CCAGAGTGA----------GTCTT----------TCGCA----------TGGAGATCCGCCCCAACCACTTGTCCACTTCGC--TTTCCAGAGGCTGCGATGGCTGCGAGGATGGTACCACGGCGACTGCATAGGGCATCA

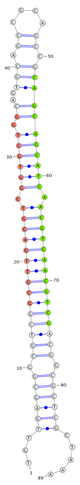
Generated: 09/08/2015 at 07:03 PM

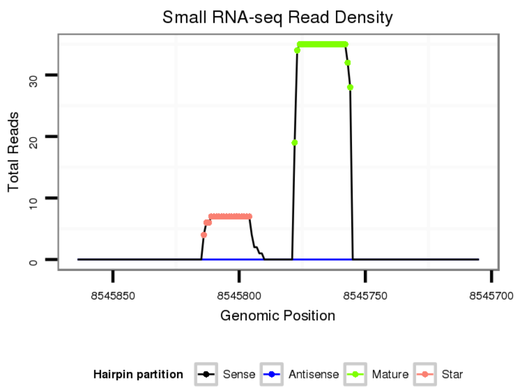
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

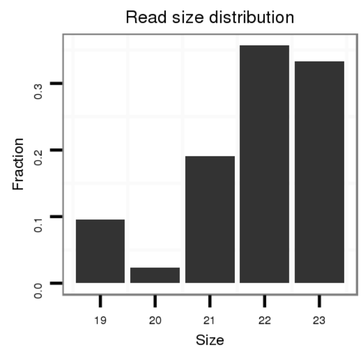
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dps_72	**XL_group1a:8545755-8545814 -**	**confident**	**Canonical miRNA**	**intron**	[View on UCSC Genome Browser [Cornell Mirror]]

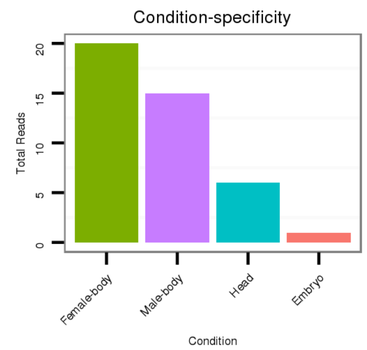
Legend: mature star mismatch in alignment mismatch in read

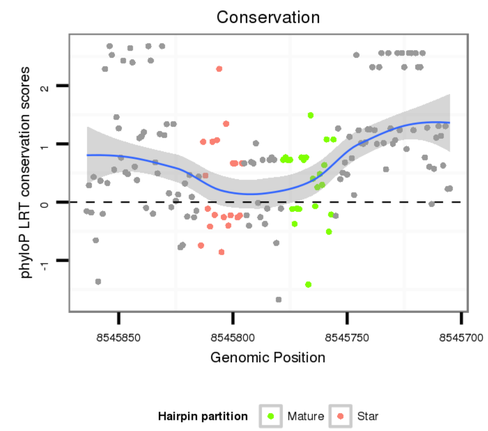
Predicted structure











Show Alternate Folds

Flybase annotation

intron [Dpse\sog-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

```
ATATATACTGTGTTGTGTGTGTCATGCTGCTGCTATGTTGAGCGGCGTCGGCGTTGACGTCGGTGCTGGCAGTGCAGCCGCAGCCGCAGCAGCATCAACGTCAACGTCGACGGCGCTCGCTAAAACTACATAAATCAAAGGAAAAGCAATTTTCTGTTTT
**********************************...((((((.(((((((((((((((.(((((((.((..(((.((....)).)))))))))))).)))))))))))))))).)))))).....**********************************
```

Read size	# Mismatch	Hit Count	Total Norm	Total	M040 female body	V112 male body	GSM444067 head	GSM343916 embryo	M059 embryo
23	0	1	14.00	14	6	5	3	0	0
22	0	1	13.00	13	5	7	1	0	0
19	0	1	3.00	3	2	0	1	0	0
21	0	1	3.00	3	2	1	0	0	0
22	0	1	2.00	2	1	1	0	0	0
21	0	1	2.00	2	1	1	0	0	0
21	0	1	1.00	1	0	0	0	1	0
23	1	1	1.00	1	1	0	0	0	0
23	1	1	1.00	1	0	1	0	0	0
19	0	1	1.00	1	1	0	0	0	0
20	0	1	1.00	1	0	0	1	0	0
21	0	1	1.00	1	1	0	0	0	0
21	0	1	1.00	1	1	0	0	0	0
21	1	3	0.33	1	0	0	0	0	1

Anti-sense strand reads

```
TATATATGACACAACACACACAGTACGACGACGATACAACTCGCCGCAGCCGCAACTGCAGCCACGACCGTCACGTCGGCGTCGGCGTCGTCGTAGTTGCAGTTGCAGCTGCCGCGAGCGATTTTGATGTATTTAGTTTCCTTTTCGTTAAAAGACAAAA
**********************************...((((((.(((((((((((((((.((((((.((..(((.((....)).)))))))))))).)))))))))))))))).)))))).....**********************************
```

Read size	# Mismatch	Hit Count	Total Norm	Total	M040 female body
22	1	1	1.00	1	1

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
dp5	XL_group1a:8545705-8545864 -	dps_72	ATATA---------TAC----------TGTGTTGTGTGTGTCATGCTGCTGCTATGTTGA-GC----------GGC----GTC----------GG----------CGTTGACGTCGGTGCTGGCAGTGCAG----------CCGCAGC----------C---GCAGCAGCATCAACGTCAACGTCGACGGCGCTCGCTAAAACTACATAAATCAAAGGAAAAGCA-ATTTTCTGTTTT
droPer2	scaffold_15:941173-941344 -		ATATA---------TAC----------TATGTTGTGTGTGTCATGCTGCTGCTATGTTGG-AC----------GGC----GTC----------GG----------CGTTGACGTCGGTGCTGGCAGTGCAG----------CCGCAGC-----CGCAGCCGCAGCTGCAGCAGCATCACGTCAACGTCGACGGCACTCGCTAAAACTACATAAATCAAAGGAAAAGCA-ATTCTCTGTTTT
droWil2	scf2_1100000004515:859272-859356 -		GTGT---TGTTGAGCGTGCT--GCTGCTGCTGTGTGTG-TT----------GCT-GCTGCT----------GA----------TGTTGTTG---------- ------- ---- ----------TTGCTGTTGCTGCTGCT-GG----------TGGTGCTGTGC
droVir3	scaffold_12970:6843997-6844135 -		ATGCT---------GG---C----GCTGTGGCTGG----------GCTTTAACTTTGACTGGC---ACA----------GC----------CGCTGTCGCATCGCAAGCGTTGCGCCAACAGCA---------- ------- ---- ----------GGAGCAGCAGCAGCAGCAGGCAGCGGGGGCAACAACAACAGCAAAAGCATTTGCAAAAACAA
droMoj3	scaffold_6473:2417720-2417833 -		TGTCA---------TG---CAAATGCTGCAAAGGG----AGGTGGCGTGCATAAATAA----------C----GAC--------AACAGCAG----------GATCA---------- ------- ---- ----------AGAGCAATAAGAACAGGAGATGAAGCAACTGCAATAGCCAAGCAAGAGCA-A----------
droGri2	scaffold_14853:6483291-6483419 -		TGT-TC---TG-TGTGTGTGTTGCTGCTCCTGTGATTGCCA----------C-TGCGGCTGTGGCAGCGAAGTCAG----------CGTCGACG---------- ------- ---- ----------TTAACGTTGACGTCGCTCGCTAAAACTACATAAATCAAAGGAAAAGCA-TTTTTCTGTTGT
droAna3	scaffold_12929:2766688-2766885 +		ATATA---------TATTTT----------ACAA----------TCTATGTATATGAACATAAATATGCTGTGTGTGTCATGTTGCTGCTATGCTAGCA----------GA----GTT----------GA----------CGCTGACGTCG----------ACAGAGACCAGCGACAGGACTGAGAACAGCGA--ACAGCGCTCTCAACGTCAACGTCGACGGCGCTCGCTAAAACTACATAAATCAAAGGAAAAGCA-TTTTTCTGTTTT
droBip1	scf7180000395909:17683-17888 +		ATACATATGCACCATAGTATGTAGTGTGTATATATTGTAGAA----------TC---TATATGAACATAAATATGCTGTGTGTGTCATGTTGCTGCTATGCTACCGA----------C----GTT----------GA----------CGTTGACGCGG----------ACAGAGACTAGCGACAGC----------GA--ACAGCGCTCTCAACGTCAACGTCGACGGCGCTCGCTAAAACTACATAAATCAAAGGAAAAGCA-TTTTTCTGTTTT
droKik1	scf7180000302517:886975-887085 -		ATATG---------GA---CATAAATATGCTGTGTGTGTCATGTTGCTGCTATGTTGGCGA----------C----GTT----------GA----------CG----------CG---------- ------- ---- ----------TCGCACGCTCGCAGCGCTCGCTAAAACTACATAAATCAAAGGAAAAGCA-TTTTTCTGTTTT
droFic1	scf7180000454038:779949-780071 -		ATATG---------GA---CATAAATATGCTGTGTGTGTCATGTTGCTGCTATGTTGGCGA----------C----GTT----------GA----------CGTCGACG---------- ------- ---- ----------TCGCACGCTCGCAGCGCTCGCTAAAACTACATAAATCAAAGGAAAAGCA-TTTTTCTGTTTT
droEle1	scf7180000491006:1190452-1190574 +		ATATA---------TA---CATAGATATGCTGTGTGTGTCATGTTGCTGCTATGTTGGCGA----------C----TTT----------GA----------CTTCGACG---------- ------- ---- ----------TCGCACGTCGGCAGCGCTCGCTAAAACTACATAAATCAAAGGAAAAGCA-TTTCTCTGTTTT
droRho1	scf7180000779985:1656776-1656890 +		AT---AAATATGCTGTGTGTGTCATGATGGTACTATGTTGGCAG----------C----GTC----------GA----------CGTTGACG---------- ------- ---- ----------TCGCACGTCGGCAGCGCTCGCTAAAACTACATAAATCAAAGGAAAAGCA-TTTTTCTGTTTT
droBia1	scf7180000302421:2323096-2323258 -		GACTA---------CAGTATGCTGTGTGGATATTATGCTGAGCGGATATCTGGATATCTGGA---------TAGGTGGACACACATGCTGT--GTGTCATGTTGCTGCTATGTTGGCGA----------C----GTT----------GA----------CG----------CG---------- ------- ---- ----------G-GCACGCGGGCAGCGCTCGCTAAAACTACATAAATCAAAGGAAAAGCA-TTTCTCTGTTTT
droTak1	scf7180000415909:170245-170355 +		ATATG---------GA---CATAAATATGCTGTGTGTGTCATGTTGCTGCTATGTTGGCGA----------C----GTT----------GA----------CG----------CG---------- ------- ---- ----------TCGCACGCGGGCAGCGCTCGCTAAAACTACATAAATCAAAGGAAAAGCA-TTTTTCTGTTTT
droEug1	scf7180000409533:687860-688028 -		GTGTA---------TAT----------ATATATATATATATGGA---------TATATGGACATAAATATGCTGTGTGTGTCATGTTGCTGCTATATTGGCGA----------TGT----TTT----------GACGTTGGCGTCGACGTTGACGTTG----------CAG---------- ------- ---- ----------CGGGCCTCGCAGCGCTCGCTAAAACTACATAAATCAAAGGAAAAGCA-TTTTTCTGTTTT
dm3	chrX:15523360-15523482 -		ATA--TAGATATGCTGTGTGTGTCATGTTGCTGCTATGCTGGCGA----------C----GCT----------GG----------CGCTGACGCTG---------- ------- ---- ----------GCGTGCACGTCGGCAGCGCTAGCTAAAACTACATAAATCAAAGGAAAAGCA-TTTTTCTGTTTT
droSim2	x:14688915-14689037 -		ATA--TAGCATATGCTGTGTGTGTCATGTTGCTGCTATGCTGGCGA----------C----GTT----------GA----------CGCCGACGCTG---------- ------- ---- ----------CGCGTGCACGTCGGCAGCGCTAGCTAAAACTACATAAATCAAAGGAAAAGCA-TTTTTCTGTTTT
droSec2	scaffold_37:101222-101338		ATA--TAGATATGCTGTGTGTGTCATTTTGCTGCTATGCTGGCGA----------C----GCT----------GA----------CGCTGCG---------- ------- ---- ----------TCGCACGTCGGCAGCGCTAGCTAAAACTACATAAATCAAAGGAAAAGCA-TTTTTCTGTTTT
droYak3	X:9713019-9713146 -		ATA--CATAGATATGCTGTGTGTGTCATGATGCTGCTATGCTGGCGA----------C----G--------------------ACTGCGACGTCGACGTTGACG---------- ------- ---- ----------CTGCACGTCGACAGCGCTAGCTAAAACTACATAAATCAAAGGAAAAGCA-TTTTTCTGTTTG
droEre2	scaffold_4690:11517411-11517588 +		ATATA---------TGTATATGG----------CTGCATGGACATATGTACATACAGGTATGTACATGTGTATGTACATAGATATGCTGT--GTGTCATGATGCTGCTATGCTGGCGA----------C----GCT----------GG----------CGCTGCGTCG---------- ------- ---- ----------ACGCGGACGTCGACAGCGCTAGCTAAAACTACATAAATCAAAGGAAAAGCA-TTTTTCTGTTTT

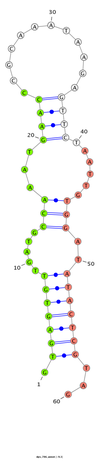
Generated: 09/08/2015 at 08:16 PM

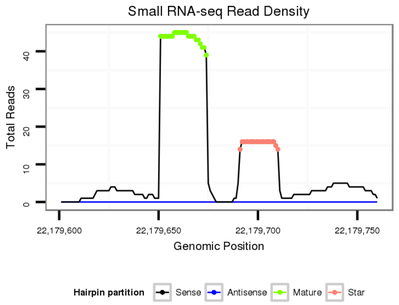
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

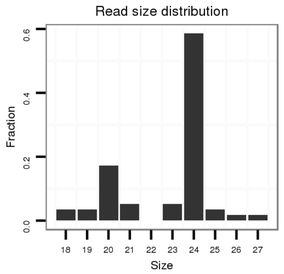
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dps_706	**2:22179651-22179710 +**	**confident**	**Mirtron**	**intron**	[View on UCSC Genome Browser (Cornell Mirror)]

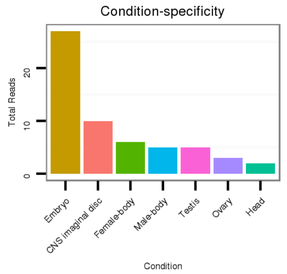
Legend: mature star mismatch in alignment mismatch in read

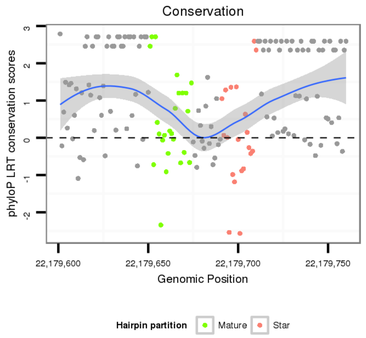
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dpse\GA30193-in]; CDS [Dpse\GA30193-cds]; CDS [Dpse\GA30193-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

AATATCTCCTGTCCGATCCCAACCTGGATGCCATGGAGAAGACAGAGAAGGTGAGTGTTGATGCCAAATGAACCCGCAA (((((((.....(((...((((.....))))).....))))..)))))))	Read size	# Mismatch	Hit Count	Total Norm	Total	M059 embryo	M040 female body	GSM343916 embryo	SRR902012 CNS imaginal disc	V112 male body	SRR902011 testis	SRR902010 ovaries	GSM444067 head
.....GTGAGTGTTGATGCCAAATGAACC.....	24	0	1	34.00	34	9	1	11	9	2	2	0	0
.....AATTGTGGATATACTCGTAG.....	20	0	1	8.00	8	1	1	0	0	1	3	2	0
.....GTGAGTGTTGATGCCAAATGAACCC.....	25	0	1	2.00	2	1	0	0	0	1	0	0	0
.....ATTGTGGATATACTCGTAG.....	19	0	1	2.00	2	0	1	1	0	0	0	0	0
.....GTGAGTGTTGATGCCAAATGAAC.....	23	0	1	2.00	2	1	0	0	0	1	0	0	0
.....TAATTGTGGATATACTCGTAGA.....	22	0	1	2.00	2	0	0	0	1	0	0	1	0
.....GAGAAGGTGAGTGTTGATGC.....	20	0	1	1.00	1	0	0	1	0	0	0	0	0
.....TCGACGGCTGTCCCATAGC.....	19	0	1	1.00	1	0	1	0	0	0	0	0	0
.....CCAACCTGGATGCCATGGAGAAGA.....	24	0	1	1.00	1	1	0	0	0	0	0	0	0
.....GTGAGTGTTGATGCCAAATGAACCCGC.....	27	0	1	1.00	1	1	0	0	0	0	0	0	0
.....GTGAGTGTTGATGCCAAATGA.....	21	0	1	1.00	1	0	0	1	0	0	0	0	0
.....ATTGAGCAACTGGATCTCGACGGCT.....	25	0	1	1.00	1	0	0	0	1	0	0	0	0
.....CCCAACCTGGATGCCATGGA.....	20	0	1	1.00	1	0	0	0	0	0	0	0	0
.....GTCCCATAGCCGATTTGGGGCTGGA	25	0	1	1.00	1	0	1	0	0	0	0	0	0
.....TGTCCCATAGCCGATTTGG.....	19	0	1	1.00	1	0	0	0	0	0	0	0	0
.....GTGAGTGTTGATGCCAAATG.....	20	0	1	1.00	1	0	0	0	0	0	0	0	1
.....TAATTGTGGATATACTCGTA.....	20	0	1	1.00	1	0	0	1	0	0	0	0	0
.....GGATGCCATGGAGAAGACAGAG.....	22	0	1	1.00	1	0	1	0	0	0	0	0	0
.....GTCCGATCCCAACCTGGA.....	18	0	1	1.00	1	0	1	0	0	0	0	0	0
.....CCCATAGCCGATTTGGGGCTGG.	22	0	1	1.00	1	0	1	0	0	0	0	0	0
.....AACTGGATCTCGACGGCTGTCCCATAGCCGATTTGGGGCT...	40	0	1	1.00	1	0	0	0	1	0	0	0	0
.....TCTAATTGTGGATATACTCGTAG.....	23	0	1	1.00	1	0	0	0	0	0	0	0	0
.....AATTGTGGATATACTCGT.....	18	0	1	1.00	1	0	0	0	0	0	0	1	0
.....GTGAGTGTTGATGCCAAA.....	18	0	1	1.00	1	0	0	0	0	0	0	0	1
.....TAATTGTGGATATACTCGTAGA.....	22	1	1	1.00	1	0	0	0	1	0	0	0	0
.....TTGATGCCAAATGAACCCGCA.....	21	0	1	1.00	1	0	1	0	0	0	0	0	0
.....GTGAGTGTTGATGCCAAATGAACCCG.....	26	0	1	1.00	1	0	1	0	0	0	0	0	0
.....TAATTGTGGATATACTCGTAG.....	21	0	1	1.00	1	0	0	0	1	0	0	0	0

Anti-sense strand reads

TTATAGAGGACAGGCTAGGGTTGGACCTACGGTACCTCTTCTGTCTCTTCCACTCACAACTACGGTTTACTTGGGCGTTTATTCTCAAGATTAACACCTATATGAGCATCTAACTCGTTGACCTAGAGCTGCCGACAGGGTATCGGCTAAACCCCGACCT (((((((.....(((...((((.....))))).....))))..)))))))	Read size	# Mismatch	Hit Count	Total Norm	Total
No data available in table					

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
dp5	2:22179601-22179760 +	dps_706	AATATCTCCTGTCCGATCCCAACCTGGATGCCATGGAGAAGACAGAGAAGGTGAGTG---TTGATGCCAAATGAACCCGCAA
droPer2	scaffold_3:4960716-4960875 +	dps_2493	AATATCTCCTGTCCGATCCCAACCTGGATGCCATGGAGAAGACAGAGAAGGTGAGTG---TTGATGCCAAATGAACCCGCAA
droWil2	scf2_1100000004943:15077084-15077253 +		AATATATTTCCTGATCCAAATATGATGCCATGGAGAAGACGAAAAGGTAAGAACG--------A------T----T
droVir3	scaffold_12855:8364538-8364707 -		AGCATATCCAAACGATCCAATCTGGATGCCATGGAGAAAAATGAAAAGGTAAACA---TCC
droMoj3	scaffold_6540:23582424-23582584 -		AGCATATCCAAATGGATCCCAATCTGATGCATGGAGAAGAAGAGAAGGTAACT---TTAATGTATCTCAATTAAATT
droGri2	scaffold_15074:4959332-4959493 -		AGCATATAAAGTGATCCCAATGAGGATGCCATGGAGAAGAAGAAAGGTCAGTCAA-------------AAGCAAAG
droAna3	scaffold_13340:22833576-22833737 -		AGTATATCCTGCTGATCCAAACATGATGCCATGGAGAAGACGAAAAGGTAACAC---TT-----A-----T---T
droBip1	scf7180000396424:1108431-1108594 -		AGTATATCCTGCTGATCCAAACATGAGCCATGGAGAAGACGAAAAGGTAGATAA-------------CCT----
droKik1	scf7180000302634:306069-306230 -		AGTATATATTTCCGATCCCAACATGATGCCATGGAAAGACGAAAAGGTGAGTG---CCA----------
droFic1	scf7180000453903:220266-220432 -		AATATATTTCTGTCCGATCCAAACATGAGCCATGGAGAAAACAGAGAAAGGTAGTAA-------------TAA---
droEle1	scf7180000491104:2385502-2385557 -		AGTATATTTCTGTCCGATCCAAACATGATGCATGGAGAAGACGAGAAGGTGAGTT----------
droRho1	scf7180000777661:30991-31045 -		AATATATTCTGTCTGATCCAAACATGATGCATGGAGAAGACAGAGAAGGTAAG----------
droBia1	scf7180000302411:344662-344740 -		ATTATAGT-----------
droTak1	scf7180000415261:515776-516001 +		AGTATATTCTGACCGATCCAAACATGATGCCATGGAAAGACAGAAAAGGTGAGTAAG-------------TATAACAG
droEug1	scf7180000409759:548067-548325 -		AGTATATTTGTCCGATCCAAACATGATGCCATGGAGAAGACAGAAAAGGTGAGTAATGCAT----------
dm3	chr3R:614248-614452 -		AGTATATTCTATCCGATCCAAACATGATGCCATGGAAAGACGAAAAGGTAGTTACGCTTTACCAACGTAA
droSim2	3r:548757-548961 -	dsi_17146	AGTATATTCTATCCGATCCAAACATGATGCCATGGAAAGACGAAAAGGTAGTTGGGCTTTACCAAAATA
droSec2	scaffold_6:714161-714365 -		AGTATATTCTATCCGATCCAAACATGATGCCATGGAAAGACGAAAAGGTAGTTGGGCTTTACCAAAATA
droYak3	3R:933342-933537 -		AGTCATTCTATCCGATCCAAACATGATGCCATGGAAAGACGAAAAGGTAGTTACGTGCACAAATA
droEre2	scaffold_4770:922206-922261 -		AGTATATTCTAGCCGATCCAAACATGATGCATGGAAAGACGAAAAGGTAGTT----------

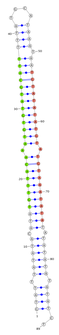
Generated: 09/08/2015 at 10:31 PM

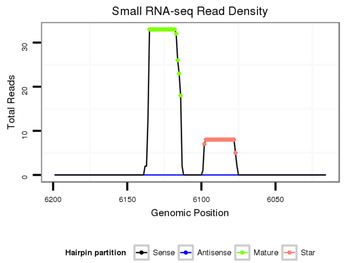
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.ptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	1

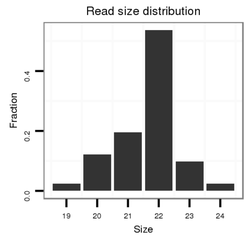
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dps_3529	**Unknown_singleton_1502:6066-6149 -**	**confident**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser [Comell Mirror]]

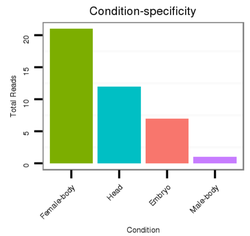
Legend: mature star mismatch in alignment mismatch in read

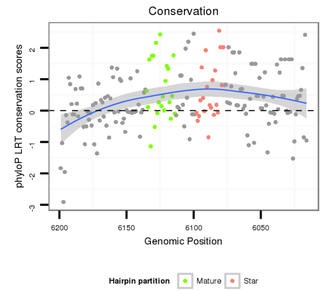
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

Repeatable elements

Name	Class	Family	Strand
Gypsy7-I_Dya-int	LTR	Gypsy	+

Sense Strand Reads

hide 3p reads show mid mismatch reads

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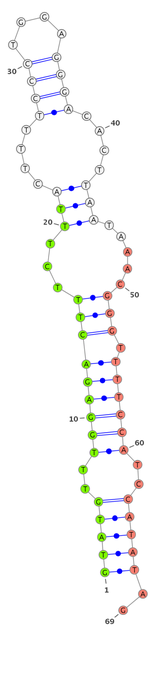
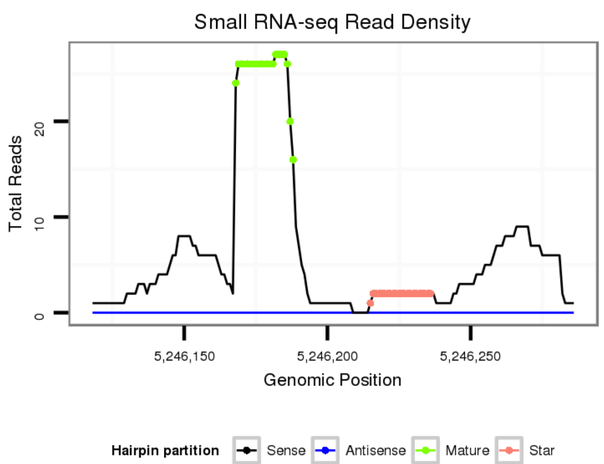
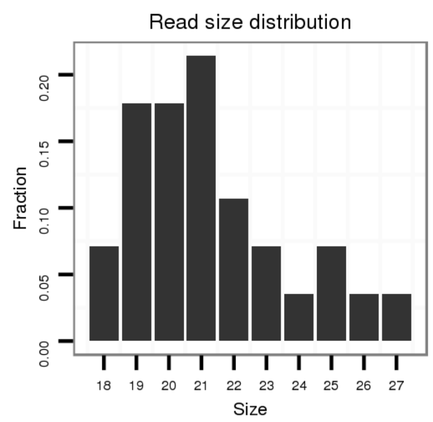
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dps_1563	**4_group3:5246168-5246236 +**	**confident**	**Mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

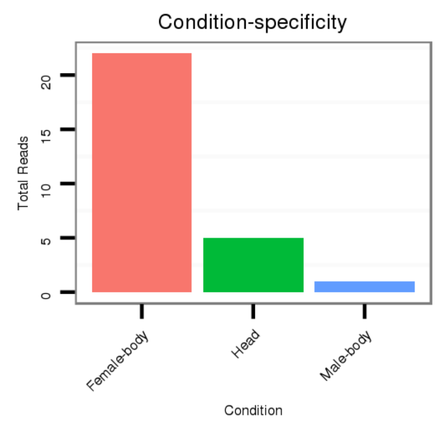
Legend: mature star mismatch in alignment mismatch in read

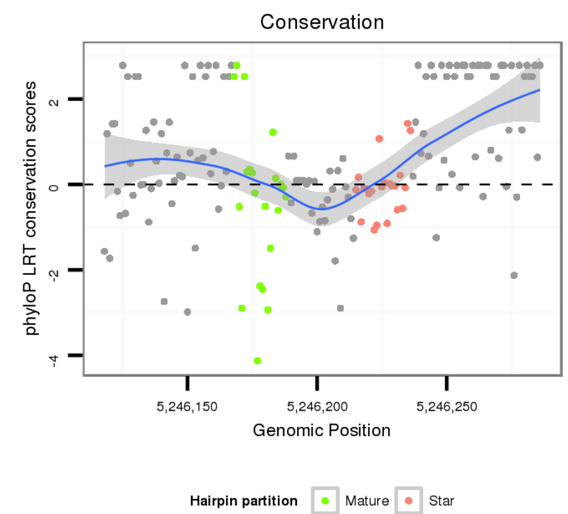
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dpse\GA16835-in]; CDS [Dpse\GA16835-cds]; CDS [Dpse\GA16835-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

CCACAGCTGGATGGCAAAAAGACCGAAAATCTAACACAGCACGTTGCACAGTATGTTTGGAGACTTTCTTTACTTTTCCCTGGAGGGACACTTAATAAACGGGTTTTCCATCCATATAGATTCGCCACTTTGGAGGTAATGCATTACTATGGCATCCTACTGGAGGACT **********(((((..(((((((((...(((....((((....))))....)))).....))).)))))))..)))))..	Read size	# Mismatch	Hit Count	Total Norm	Total	M040 female body	M062 head	V112 male body	GSM444067 head	M022 male body	GSM343916 embryo
.....GTATGTTTGGAGACTTTCTTT.....	21	0	1	6.00	6	4	2	0	0	0	0
.....GTATGTTTGGAGACTTTCT.....	19	0	1	5.00	5	4	0	0	1	0	0
.....GTATGTTTGGAGACTTTCTT.....	20	0	1	4.00	4	3	0	0	0	1	0
.....AACGGGTTTTCCATCCATATAGT.....	23	1	1	3.00	3	1	2	0	0	0	0
.....GTATGTTTGGAGACTTTCTTTA.....	22	0	1	2.00	2	2	0	0	0	0	0
.....ACGGGTTTTCCATCCATATAGT.....	22	1	1	2.00	2	1	0	1	0	0	0
.....GTATGTTTGGAGACTTTCTTTAC.....	23	0	1	2.00	2	2	0	0	0	0	0
.....GTATGTTTGGAGACTTTCTTTACTT.....	25	0	1	2.00	2	1	0	0	1	0	0
.....TATGTTTGGAGACTTTCTTT.....	20	0	1	1.00	1	1	0	0	0	0	0
.....ATTACTATGGCATCCTACTGGA.....	22	0	1	1.00	1	1	0	0	0	0	0
.....CATTACTATGGCATCCTACTGGA.....	23	0	1	1.00	1	1	0	0	0	0	0
.....CTAACACAGCACGTTGCACA.....	20	0	1	1.00	1	1	0	0	0	0	0
.....GACCGAAAATCTAACACAGCACGT.....	24	0	1	1.00	1	1	0	0	0	0	0
.....CTAACACAGCACGTTGCAC.....	19	0	1	1.00	1	1	0	0	0	0	0
.....TTTGGAGGTAATGCATTACTATGGCATCC.....	29	0	1	1.00	1	0	1	0	0	0	0
.....GTATGTTTGGAGACTTTCTTTT.....	22	1	1	1.00	1	1	0	0	0	0	0
.....TATGTTTGGAGACTTTCT.....	18	0	1	1.00	1	1	0	0	0	0	0
.....AATGCATTACTATGGCATCCTACTGGAG.....	28	0	1	1.00	1	1	0	0	0	0	0
.....CGAAAATCTAACACAGCACGTT.....	22	0	1	1.00	1	1	0	0	0	0	0
.....GTATGTTTGGAGACTTTCTTTACTTT.....	26	0	1	1.00	1	1	0	0	0	0	0
.....AATCTAACACAGCACGTTGC.....	20	0	1	1.00	1	1	0	0	0	0	0
.....ATTCGCCACTTTGGAGGTAATGC.....	23	0	1	1.00	1	1	0	0	0	0	0
.....TACTATGGCATCCTACTGGA.....	20	0	1	1.00	1	1	0	0	0	0	0
.....TTTCTTTACTTTTCCCTGGAGGGACAC.....	27	0	1	1.00	1	1	0	0	0	0	0
.....GTATGTTTGGAGACTTTC.....	18	0	1	1.00	1	1	0	0	0	0	0
.....AAAAGACCGAAAATCTAAC.....	19	0	1	1.00	1	0	1	0	0	0	0
.....ACGGGTTTTCCATCCATATAGA.....	22	0	1	1.00	1	0	1	0	0	0	0
.....AACGGGTTTTCCATCCATATAG.....	22	0	1	1.00	1	0	1	0	0	0	0
.....GGCAAAAAGACCGAAAATCTAACAC.....	25	0	1	1.00	1	1	0	0	0	0	0
.....ATGGCATCCTACTGGAGGACT	21	0	1	1.00	1	1	0	0	0	0	0
.....GCATTACTATGGCATCCTACTGGA.....	24	0	1	1.00	1	0	1	0	0	0	0
.....GTATGTTTGGAGACTTTCTTTACT.....	24	0	1	1.00	1	1	0	0	0	0	0
.....ATCTAACACAGCACGTTGCACA.....	22	0	1	1.00	1	0	0	1	0	0	0
CCACAGCTGGATGGCAAAA.....	19	0	1	1.00	1	1	0	0	0	0	0
.....GGTAATGCATTACTATGGC.....	19	0	1	1.00	1	1	0	0	0	0	0
.....ACTTTGGAGGTAATGCATTACTATGGC.....	27	0	1	1.00	1	1	0	0	0	0	0

Anti-sense strand reads

GGTGTCGACCTACCGTTTTTCTGGCTTTTAGATTGTGTCGTGCAACGTGTCATACAAACCTCTGAAAGAAATGAAAAGGGACCTCCCTGTGAATTATTTGCCCAAAAGGTAGGTATATCTAAGCGGTGAAACCTCCATTACGTAATGATACCGTAGGATGACCTCCTGA **********(((((..(((((((((...(((....((((....))))....)))).....))).)))))))..)))))..	Read size	# Mismatch	Hit Count	Total Norm	Total
No data available in table					

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
dp5	4_group3:5246118-5246286 +	dps_1563	CCA-CAGCTGGATGGCAAAAAGACCGAAAATCTAACACAGCACGTTGCACAGTATGTTTGGAGAC----------TTTCTTTACTTTTCCCTGGAGG----------GACACTTA--ATAA---ACGGGTTTTCC--ATCCATATAGATTCGCCACTTTGGAGGTAATGCATTACTATGGCATCCTACTGGAGGACT
droPer2	scaffold_1:6737974-6738141 +		CCA-CAGCTGGATGGCAAAAAGACCGAAAATCTAACACAGCACGTTGCACAGTATGTTTAGAGAC----------TTTCTTTACTTTTC-CTGGAGG----------GACACTTA--ATAA---ACGGGTGTTCC--ATCTATATAGATTCGCCACTTTGGAGGTAATGCATTACTATGGCATCCTACTGGAGGACT
droWil2	scf2_1100000004521:8975675-8975830 -		GCT-AAATTGGAGGGTGGCGAGGCTATAAAACTCTCCGAGCATGTGTGCGATAAGTTTTCTTGCA-AAATATAAGAATTG----------GTTTTCTTTG----------ACT-T-ACCCTT---CC---CC---TT-TTGTTAACCCTAACAGATTTGCCACCTTGGAGGTGATGCATTACTATGGCATCCTCTTGGAGGACT
droVir3	scaffold_12963:15280852-15281015 +		CC--AAATTGGAAGGCGGCCAGACCATTGGACTCTCGGAGCACATCTCACAGTAGGTTACCCAATGA-ATATCTAAT-----------GTTTTCTTTG----------G-AAGCCCTT--AAAC---TT-GTGGTACTCCCACTAGATTTGCCACTCTGGAGGTAATGCATCTACTATGGCATCCTCTGGAGGACT
droMoj3	scaffold_6500:18257675-18257834 +		CC--AAGCTGGAAGGCGGCCAGACCATCGGATTGTCCGAGCATATTGCACAGTGAGTCAAAGCATGA-ATGCCCAATTGAAT----------GTTTTCTTTG----------G-AAGCCCTT--AAAC---TT-GTGGTACTCCCACTAGATTTGCCACTCTGGAGGTAATGCATCTACTATGGCATCCTCTGGAGGACT
droGri2	scaffold_8317:2086-2257 -		TGGCAAATTGGAAGGCGGTCATAGTATTGGAATAGGGATCACATCTCACAGTGAGTTATCAAAAA--GAAACGAAATATATTT----------GGCT--------TT----------TAAATGTT--TATT-TTGTTTTT-TTGC--TTGCTTATCAGATTCCCACTTTGGAGGTGATGCATCTACTATGGCATCTTCCTGGAGGATT
droAna3	scaffold_12916:5548424-5548577 -		GCC-AGGATTGATGGAGGACAGAGAGTACGACTATCCGAGCACATATCACAGTGGGTTCTAGTAC--------ATATTATTTCTT----------AAGTTTTA--CTAA-AAATATGTTA---------TTTTTAGGTTCGCCACCTTAGAGGTAATGCATCTATTATGGTATCCTCCTGGAGGACT
droBip1	scf7180000396568:1289822-1289979 +		CC--AAGATCGATGGAGGGCAGAGTGTCAGAATTTCAGAGCAGATATCACAGTGGGTTTTCAAAA---AACAAAATCATTTTA----------AAGTTGTA--TTGA-AAATATACCA---------TCTATAGGTTTGCCACCTTGGAAGTCATGCACTATTATGGTATCCTTCTGGAGGACT
droKik1	scf7180000302270:1139884-1140046 +		GCC-AAGTTGGGAGGAGGTCAAAGCATACCTCTATCGGAGCATATATCACAGTGGGTTTTTTTGGA----------TTTAAATAAATAATTTATATATTTTA--TAAA-TATATATTTT---------TCCGCAGATTTGCCACTTTGGAGGTAATGCATCTATTATGGAATCTTCCTGGAGGACT
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droEle1	scf7180000490728:175150-175309 -		GCG-AAACTAGCTGGAAGTCAATCTATACGCCTTTCAGAGCACATAACACAGTATGTTTTTAACTTA-ATAGCAAATCATTA----------A-AAAATATT--ATCA-AAATATTTAT---------TATAAAGGTTTGCCACCCTGGAGGTAATGCATCTACTATGGCATCCTTTTGGAGGACT
droRho1	scf7180000779523:182467-182621 -		CC--AAACTTGCTGGAGGTCAATCGATTCGCCTTCTCAGAGCACATAACACAGTAAGTTTTGACT----------TTTAATAAAT------TAAAGT----------AAAATATA--ACGT---ATCTGTAA---------TCCAAAGGTTTGCCACCCTGGAAGTAATGCATCTATTATGGCATCCTGTTGGAGGACT
droBia1	scf7180000302261:1051661-1051817 -		CC--AAATTTGAAGGAGGCACATCGATTCGCCTATCAGAGCACATTACACAGTGAGATTTTAATC--ATTATTAATATTTT----------AAAATCTA--ACCA-AAATATTTTC---------TTTGAAGGTTTGCCACTTTGGAGGTAATGCATCTATTATGGCATCCTGTTAGAGGACT
droTak1	scf7180000415438:402727-402884 +		CC--AAAGTTGAAGGAGGTCAATCAATTCGCCTTTCAGAACACATTACACAGTGAGATTTAACATTA-ACAAATAATTTTTA----------AAAATGTA--ATCA-CATATTTAA---------TTTAAAGGTTTGCCACTTTGGAGGTAATGCATCTATTACGGCATTCTCTTGGAGGACT
droEug1	scf7180000409554:2587126-2587284 +		GCT-AAGCTTGCTGGAGGTCAAGCGATTCGCCTGTCGGAGCACATTACACAGTGAGAATTAACTTG--GTAATAATTAATCT----------A-TAAATATA--ATAA-CTATATTTTA---------TTTGAAGGTTTGCCACCCTCGAGGTAATGCATCTATTATGGCATCCTGCTGGAGGACT
dm3	chr2L:3501512-3501666 -		CC--AAACTTGCTGGATGTCAAACCATTCGCCTGTCGGAGCACATAACACAGTAGCGTTATATGGTA-TTATATTATATTAT----------A-GA-TTAT--TAA-TGCATTAAT---------ATTACAGGTTTGCCACGCTGGAGGTGATGCATCTACTATGGCATCCTCTGTGGAGGACT
droSim2	2L:3361133-3361289 -	dsi_12601	CC--AAACTGGCTGGATGTCAAACCATTCGCCTGTCGGAGCACATTACACAGTACGATTATACCTT--ACAGCGAATTCTTTTC----------GA-CT-TTAT--TAA-TGGAATAAT---------ATTACAGGTTTGCCACGCTGGAGGTGATGCATCTACTATGGCATCCTCTTGGAGGACT
droSec2	scaffold_5:1603857-1604013 -		CC--AAACTTGCTGGATGTCAAAGTATTCGCCTGTCGGAGCACATTAACACAGTATCATTAAACCAT--ACAGCGAATCCTTTTC----------GA-CT-TTAT--TAA-TGAACTAAT---------ATTACAGGTTTGCCACGCTGGAGGTGATGCATCTACTATGGCATCCTCTTGGAGGACT
droYak3	2L:3489961-3490118 -		CC--AAACTTGCTGGCGGTCAATCCATTCGCCTGTCGGAGCACATTACCCAGTACGATATATCTTT--ATAACTTATTCTTTTC----------GAAATG-TAT--TAA-TGCATTCAT---------GTTACAGGTTTGCCACGCTGGAGGTGATGCATCTACTATGGCATCCTGTTGGAGGACT
droEre2	scaffold_4929:3536549-3536711 -		TCC--AAACTCGCTGGGGGTCAATCCATTCGCCTGTCGGAGCACATTGCCCAGTAAGATTTTACCCC--ACAACTAATCATTTCC----------AATGAATT----------CA-G---TGC--TAA-TGATTGAT---------ATTACAGGTTTGCTACGCTGGAGGTGATGCATCTACTATGGCATCCTCCTGGAGGACT

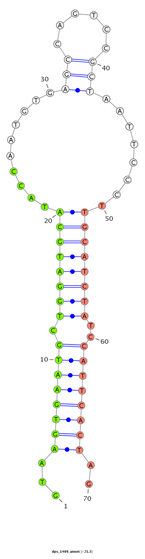
Generated: 09/08/2015 at 10:31 PM

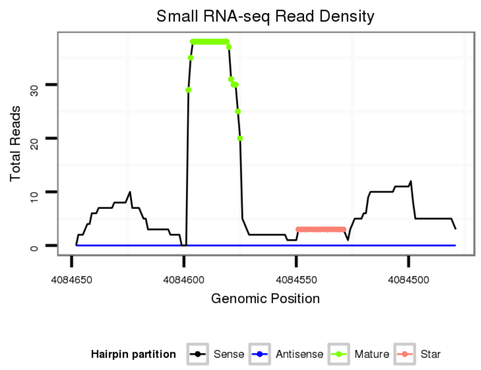
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

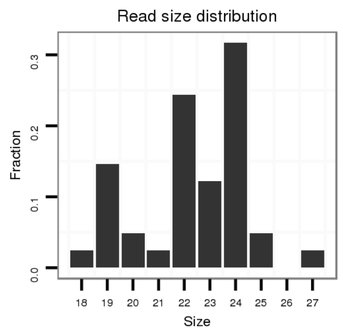
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dps_1409	**4_group1:4084529-4084598 -**	**confident**	**Mirtron**	**intron**	[View on UCSC Genome Browser [Cornell Mirror]]

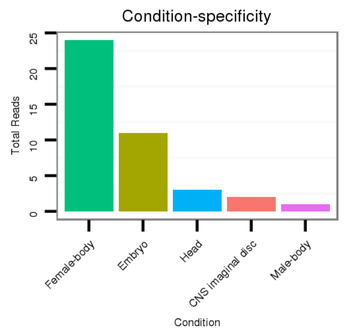
Legend: mature star **mismatch in alignment** mismatch in read

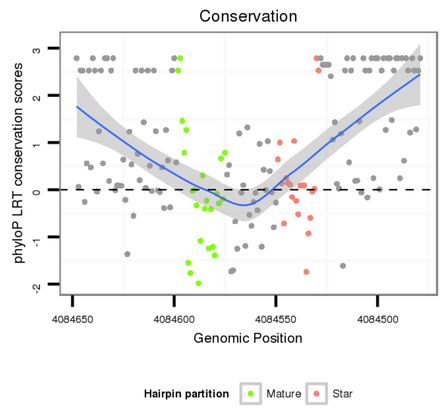
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dpse\GA25200-in]; CDS [Dpse\GA25200-cds]; CDS [Dpse\GA25200-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

ATGCGGCCACGCCCAAGGAGTCGGCTGGTGAGGAAGGAGCGGCCGGCGAGGTAAGTGAATGCTGGATGCATACCAATGTGAGCCAGTCCGCTAATTCCCTTGCATCTATCCATTCACTAGAAAAAGGAGTCTGAGGAGCACTCGGAGAACGATAAAGATCTGACCACCGA **********...(((((((((.(((((((((.....(((.....)))).....)))))))).)))))))))..**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M040 female body	M059 embryo	M062 head	GSM343916 embryo	V112 male body	SRR902012 CNS imaginal disc	GSM444067 head
.....GTAAGTGAATGCTGGATGCATACC.....	24	0	1	12.00	12	6	4	1	1	0	0	0
.....GTAAGTGAATGCTGGATGC.....	19	0	1	6.00	6	5	0	0	1	0	0	0
.....GTAAGTGAATGCTGGATGCATA.....	22	0	1	5.00	5	5	0	0	0	0	0	0
.....TTGCATCTATCCATTCACTAGT.....	22	1	1	5.00	5	1	0	0	3	1	0	0
.....TAAGTGAATGCTGGATGCATACC.....	23	0	1	3.00	3	2	1	0	0	0	0	0
.....TAAGTGAATGCTGGATGCATAC.....	22	0	1	3.00	3	1	0	0	0	0	2	0
.....CTGAGGAGCACTCGGAGAACG.....	21	0	1	3.00	3	3	0	0	0	0	0	0
.....AAAGGAGTCTGAGGAGCACTCGGAGAAC.....	28	0	1	2.00	2	0	1	1	0	0	0	0
.....GATAAAGATCTGACCACCGA	20	0	1	2.00	2	2	0	0	0	0	0	0
.....TTGCATCTATCCATTCACTAGC.....	22	1	1	2.00	2	0	0	2	0	0	0	0
.....AAGTGAATGCTGGATGCATACC.....	22	0	1	2.00	2	1	1	0	0	0	0	0
.TGCGGCCACGCCCAAGGAGTCGGC.....	24	0	1	2.00	2	2	0	0	0	0	0	0
.....GTAAGTGAATGCTGGATGCATAC.....	23	0	1	2.00	2	0	1	1	0	0	0	0
.....TTGCATCTATCCATTCACTAGA.....	22	0	1	2.00	2	0	1	0	0	0	1	0
.....CTGGTGAGGAAGGAGCGGCCGGC.....	23	0	1	1.00	1	0	0	0	0	0	1	0
.....TGAGGAGCACTCGGAGAAC.....	19	0	1	1.00	1	1	0	0	0	0	0	0
.....GAACGATAAAGATCTGACCACCGA	24	0	1	1.00	1	1	0	0	0	0	0	0
.....AAAAGGAGTCTGAGGAGCACTCGGA.....	25	0	1	1.00	1	1	0	0	0	0	0	0
.....GTAAGTGAATGCTGGATGCATACCAAT.....	27	0	1	1.00	1	1	0	0	0	0	0	0
.....GTCTGAGGAGCACTCGGAGAAC.....	22	0	1	1.00	1	1	0	0	0	0	0	0
.....AAGTGAATGCTGGATGCATACCAA.....	24	0	1	1.00	1	1	0	0	0	0	0	0
.....GTAAGTGAATGCTGGATGCATACCA.....	25	0	1	1.00	1	1	0	0	0	0	0	0
.....CACGCCCAAGGAGTCGGCTGGTGAG.....	25	0	1	1.00	1	1	0	0	0	0	0	0
.....GTAAGTGAATGCTGGATGCA.....	20	0	1	1.00	1	1	0	0	0	0	0	0
.....AATGTGAGCCAGTCCGCTAATTCCC.....	25	0	1	1.00	1	0	0	1	0	0	0	0
.....CTTGCATCTATCCATTCACTAGT.....	23	1	1	1.00	1	0	1	0	0	0	0	0
.....AGGAGTCTGAGGAGCACTCGGAGAAC.....	26	0	1	1.00	1	0	0	0	0	1	0	0
.....GCCACGCCCAAGGAGTCGGC.....	20	0	1	1.00	1	1	0	0	0	0	0	0
.....GCCCAAGGAGTCGGCTGGTG.....	20	0	1	1.00	1	1	0	0	0	0	0	0
....GGCCACGCCCAAGGAGTCGGCTGGTGAG.....	28	0	1	1.00	1	1	0	0	0	0	0	0
.....GTAAGTGAATGCTGGATG.....	18	0	1	1.00	1	0	0	0	1	0	0	0
.....AAGGAGTCTGAGGAGCACTCGGAGAAC.....	27	0	1	1.00	1	0	0	0	0	1	0	0
.....GAGTCGGCTGGTGAGGAAGGAGCGG.....	25	0	1	1.00	1	1	0	0	0	0	0	0
.....CGGAGAACGATAAAGATCTGACCACCG.	27	0	1	1.00	1	1	0	0	0	0	0	0
.....GCTGGTGAGGAAGGAGCGGCCGGC.....	24	0	1	1.00	1	1	0	0	0	0	0	0
.....CGATAAAGATCTGACCACC..	19	0	1	1.00	1	1	0	0	0	0	0	0
.....AATGTGAGCCAGTCCGCTAA.....	20	0	1	1.00	1	0	0	0	0	1	0	0
.....TTGCATCTATCCATTCACTAG.....	21	0	1	1.00	1	0	0	0	1	0	0	0
.....CACGCCCAAGGAGTCGGCTGGT.....	22	0	1	1.00	1	1	0	0	0	0	0	0
.....GCATCTATCCATTCACTAGC.....	20	1	1	1.00	1	0	0	1	0	0	0	0

Anti-sense strand reads

TACGCCGGTGCGGGTTCCTCAGCCGACCACTCCTTCCTCGCCGGCCGCTCCATTCACTTACGACCTACGTATGGTTACACTCGGTCAGGCGATTAAGGGAACGTAGATAGGTAAGTGATCTTTTTCCTCAGACTCCTCGTGAGCCTCTTGCTATTTCTAGACTGGTGGCT **********...(((((((((.(((((((((.....(((.....)))).....)))))))).)))))))))..**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M040 female body

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
dp5	4_group1:4084479-4084648 -	dps_1409	ATGCGGCCACGCCCAAGGAGTCGGCT----------GGTGAG---GAAGGAGCG----------GCCGGCGAGGTAAGTGAA----------TG---C----TGGATG----------CATACCAATGTGAG-------C-----CAGTCC--G----------CTAATT----------CC----------CTTGCATCTAT----------CCATTCACTAGAAAAAGGAGTCTGAGGAGCACTCGGAGAACGATAAAGATCTGACCACCGA
droPer2	scaffold_5:1180140-1180309 +	dpe_1746	ATGCGGCCACGCCCAAGGAGTCGGCT----------GGTGAG---GAAGGAGCG----------GCCGGCGAGGTAAGTGAA----------TG---C----TGGATG----------CATACCAATGTGAG-------C-----CAGTCC--G----------CTAATT----------CC----------CTTGCATCTAT----------CCATTCACTAGAAAAAGGAGTCTGAGAGCACTCGGAGAACGATAAAGATCTGACCACCGA
droWil2	scf2_1100000004945:317420-317584 +		ATGCAGCCACTCCCAAAGAG---GT----------GGTGA---GAAGCAGCA----------AGTAATGAGGTAGCATAAATCCCACA---AA----------AAA---------TTATTCC------ -----------AA--TTTGTGTAA----------CTTTAAAT----------TC------ ----------TAATTT-----GA---AATGTAGAAAAAGGACACGAGACCATCGGAAATGACAAAGATTGTGACACCGA
droVir3	scaffold_12723:3023769-3023945 +		ATGCGGGAACGAAAAGGA---AAGAGTCCCGGCGGCACGAG---GAAGCAGCG---------G---GGCCGGAGAGGTAAGTCCC------AACCAGCAAGCA----------GGG---------TAGTCGC------ -----------T----- GTTTA----------AACTCA-TT----------T------ --GAATGA-----TG------CA---ATTGCAGAAAAAGGAGACGAGAGAACTCTGAAAACGACAAAGATTTAACCACCGA
droMoj3	scaffold_6500:6844475-6844649 -		ATGCGGGCACGCCAAAGGAA---GCA----------AACGAGGATCGCGCTGCA----------GCGGGCGAGTCAGAAACC----------TC---G----AACGGG----------AA----CATAAT--TACGAAAC-------GAGTTT-AAA---A-------GATT-------C----------TCCC-SATT----------TC------ ----------TAATTG------TA---ATTGCAGAAAAAGCCGACGAGAGAACTCTGAGAACGACAAAGATCTAACCACCGA
droGri2	scaffold_15126:459183-459350 -		ATGCATGCACGCCAAAGGAA---AAG----------ACGGAG---GATGCAGCGTCAGCAGCTGCTGCTGCGGGCGAGGTAATTGCC------AACA---------------------------------AAGCGGAG-------T------AAA---- -----TCAATGTGA----------CATGA-ATT----------TA------ ---TGTT-----TTT-----GCT---TTGCAGA------AGGGCGAGAGAACTCGGAGAATGACAAAGATCTAACCACCGA
droAna3	scaffold_12916:10082180-10082333 +		ATGCAGCCACTCCCAAGGAG---GGC----------GGAGATG---GAAGCAGCA----------GCTGGAGAGGTAAGATAC----------TG---A----AATCT----------TT----TATAGA--AGATTCTC-------------- -----TA----------AATT-GGAG----------TT------ ----------ATAT-------------TTCGCAGAAAAAGGATACAGAGGAGAGTTCGGAGAACGACAAAGATCTGACCACCGA
droBip1	scf7180000396580:953518-953674 -		ATGCAGCCACTCCGAAGGAG---GGC----------GGCGATG---GAAGCTGCG----------GCTGGCGAGGTAAGACTT----------G---G----AACA----------C--TTC--- -----C--TTC--T----------TTATTTTGAAAAACTTCCTC------ ----------TCAATGGGAATGTT---CTTACAGAAAAAGGAACCGAGGAGAGCTCTGAGAACGACAAAGATCTGACCACCGA
droKik1	scf7180000302412:560591-560769 +		ATGCGCCCACACCCAAGAG---GCT----------GGTGCA---GATGGAGAAGTAGCAGCGGGAACACCCGGAGAGGTATTGCCAA----------CTACTA----------AAATGA-------T---GGC--TTC--T----------GAATT----------TT-AATG----------TAATAT--TTTGTA------TAT----GTG---CACACAGAAAAAGGAACCGAGGAGACTCTGAGAATGACAAAGATCTGACCACCGA
droFic1	scf7180000454117:77580-77738 +		AGGCTGCCACGCCCAAGAA---GT----------GGCGATG---GAAGCGGCG----------TGAGAGACGTAAGAAA----------AG---A----AATTTA----------GG----TATTGT--TAAGATTT-------------- -----GA----------AAAT-AACC----------TT------ ----------TTGTTT----TCG---CCACAGAAAAAGGAATCGAGGAGCACTCTGAGAACGACAAAGATTTGACCACCGA
droEle1	scf7180000491186:1216468-1216686 +		ATGCTGCCACGCCCAAGAA---GGA----------GGCGATG---GAAGCAGCG---------C---GGA-GGGAGAGGTAAGCAAA----------AG---G----AAT-AAATAATTTAAGGGGCTCTTAAAAA-AACCAAATGGA-------C-----TAGGATAAACATAAATATTCT-TA--TTACG----TACCATTCTAAACACA----------TT---------- ----------TTATTT----CGC---CTCCACAGAAAAAGGAATCGAGGAACATCTGAGAACGACAAAGATCTGACCACCGA
droRho1	scf7180000771933:93771-93961 +		AGGCTGCCACGCCCAAGAG---GA----------GGCGATG---GAAGCGGCG----------AGGGAGAGGTAAGCAAA----------AT---G----AATTTG----------AT----AAGATT--TGAAAAAC-------CAGACC--AAC-TAAATAAGTCG-AT--GTATT----TACCATTCTAATTATG----------TT---------- ----------TAATAT-----CG---CCATAGAAAAAGGAATCGAGGAGCATCTGAGAACGACAAAGATCTAACCACCGA
droBia1	scf7180000301500:215619-215776 -		ATGCTGCCACGCCCAAGGAA---GGC----------GGAGATG---GAGCCGGCG----------AGGGAGAGGTAAGTAA----------AT---AGTGAATTTA----------TGACCTG--------- -----C-------- -----AT----------GACTTA-CT----------T------ ---A-AACTACCCATAT-----TA---CTCAGAGAAAAAGGAAACGAGGAGCATCGGAGAACGACAAAGATCTGACCACCGA
droTak1	scf7180000415629:144566-144723 +		ATGCAGCCACGCCCAAGAG---GA----------GGCGATG---GAAGCGGCG----------AGGGCTGAGGTAAGAGAA----------AT---C----ATTTTA----------GA----AATATA--GAAGAAAT-------C-----TAAT-SACT----------TC------ ----------CTATTT----CCG---CCACAGAAAAAGGAAACTGAGGAGCATCTGAGAACGACAAGGATCTGACCACCGA
droEug1	scf7180000409461:452762-452917 +		AGGCTGCCACACCCAAGAG---GT----------GGCGATG---GAAGCGGCG----------GCGGGAGATGTAAGCAAA----------AA---C----AATATA----------AA----AATGTA--AAAACA-------C-----AA----------GACT-GATT----------TC------ ----------TCATTT-----TG---GTAGAGAAAAAGGAAACGAGGAGCATCTGAGAACGACAAAGATCTGACCACCGA
dm3	chr2L:8427047-8427207 +		AGGCTGCCACGCCCAAGAG---GT----------GGTGAT---GAAGCGGCG----------GCGGTAGAGGTAAGCAAA----------TC---A----TATCCT----------CA----AATGTC--TACGTCTC-------C-----AT----------GACT-GATG----------TG---TT----------TAATTT----ACG---CCATATAGAAAAAGGAAACTGAGGAGCATCTGAGAACGACAAAGATCTGACCACCGA
droSim2	2L:8153996-8154154 +	dsi_13205	AGGCTGCCACGCCCAAGAG---GT----------GGTGAT---GAAGCGGCG----------GCGGTAGAGGTAAGCAAA----------TC---A----TATCCT----------CA----AATGTC--TGCGGCTC-------C-----AT----------GATT-GATG----------TA------ ----------TAACTT----TCG---TCATATAGAAAAAGGAAACTGAGGAGCATCTGAGAACGACAAAGATCTGACCACCGA
droSec2	scaffold_3:3923337-3923495 +		AGGCTGCCACGCCCAAGAG---GT----------GGTGAT---GAAGCGGCG----------GCGGTAGAGGTAAGCAAC----------TC---A----TATCCT----------CA----AATGTC--TTTGGCTC-------C-----AT----------GATT-GATG----------TA------ ----------TAATTT----TCG---TCATATAGAAAAAGGAAACTGAGGAGCATCTGAGAACGACAAAGATCTGACCACCGA
droYak3	2L:11064995-11065153 +		ATGCTGCCACGCCCAAGAG---GT----------GGTGAT---GAAGCGGCG----------GCGGTAGAGGTAAGAAAA----------TC---A----TATTTA----------CA----ATATGTC--TACGGCCC-------C-----AT----------GACT-GATG----------TC------ ----------TCATTC----CAG---ACATATAGAAAAAGGAAACAGAGGAGCATCTGAGAACGACAAAGATCTGACCACCGA
droEre2	scaffold_4929:17335770-17335928 +		ATGCTGCCACGCCCAAGAG---GGC----------GGTGAT---GAAGCGGCG----------GCGGTAGAGGTAAGCAAA----------TC---A----TATTTA----------CA----AATGTC--TACGGGTC-------C-----AT----------GACT-GATG----------TA------ ----------TCATTT----GCG---TTGATAGAAAAAGGAAACTGAGGAGCATCTGAGAAATGACAAAGATCTGACCACCGA

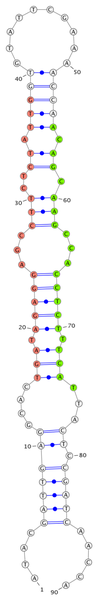
Generated: 09/08/2015 at 10:31 PM

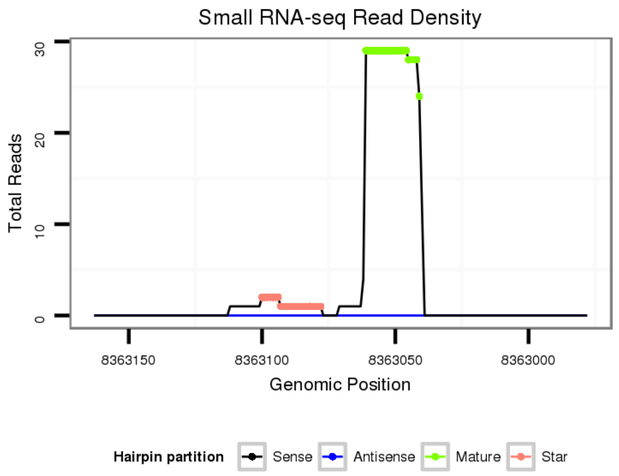
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	1

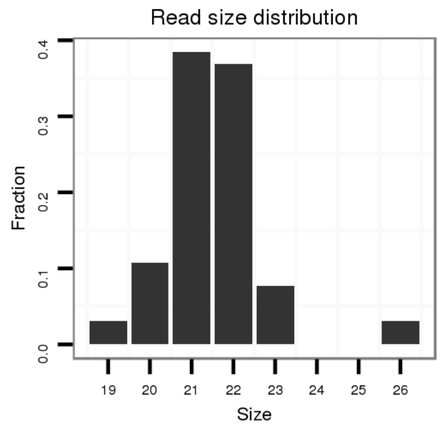
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dps_3831	**XL_group1e:8363028-8363113 -**	**confident**	**Testes-restricted**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

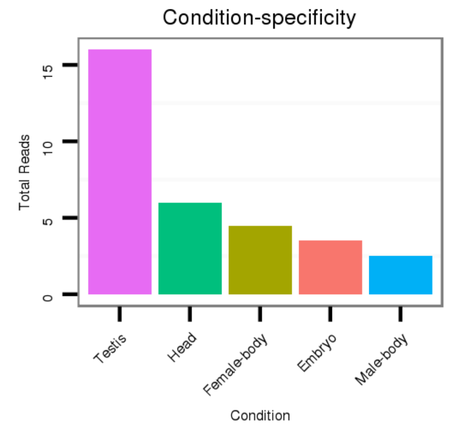
Legend: mature star mismatch in alignment mismatch in read

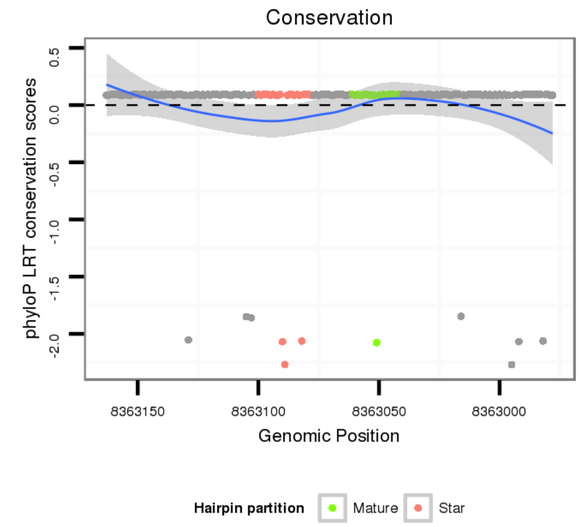
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

mature	star
	1. dps_3831 XL_group1e:8363078-8363100 - 2. dps_62 XL_group1e:8366197-8366219 -

Sense Strand Reads

hide 3p reads show mid mismatch reads

CCATATCGACCTATGTTCTGTGCACTATCTATCGCGGATCACTGTTTCATACGATTGAGGCACTGATAGAGGAGCCTTCTCTATTGGTGTATTCGAAAACCAACAGCAAGCCACCTCTTTCATTACTCCGATCAACCAGTATGGTATTGCAATATTCTGTGAGTGAGGCCTGGTAAAATAATATCG **********....(((((((....(((.(((((...(((..((.(((((.....)))))).)).)))...)))))).)))...)).)))))).....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	SRR902011 testis	M062 head	M040 female body	M059 embryo	V112 male body	GSM343916 embryo	GSM444067 head
.....ACAGCAAGCCACCTCTTTCAT.....	21	0	1	11.00	11	6	3	1	0	0	1	0
.....ACAGCAAGCCACCTCTTTCATT.....	22	0	1	11.00	11	5	2	2	2	0	0	0
.....ACAGCAAGCCACCTCTTTCA.....	20	0	1	3.00	3	3	0	0	0	0	0	0
.....ACAGCAAGCCACCTCTTTCATTCA.....	24	2	1	3.00	3	3	0	0	0	0	0	0
.....ACAGCAAGCCACCTCTTTCATTAA.....	24	1	1	3.00	3	3	0	0	0	0	0	0
.....ACAGCAAGCCACCTCTTTCATTT.....	23	1	1	2.00	2	2	0	0	0	0	0	0
.....TGATAGAGGAGCCTTCTCTATTG.....	23	0	2	1.50	3	0	0	1	1	1	0	0
.....CGATTGAGGCACTGATAGA.....	19	0	1	1.00	1	0	0	0	0	0	0	1
.....AACAGCAAGCCACCTCTTTCAT.....	22	0	1	1.00	1	0	0	0	0	1	0	0
.....AACAGCAAGCCACCTCTTTCATT.....	23	0	1	1.00	1	0	0	1	0	0	0	0
.....AACAGCAAGCCACCTCTTTCA.....	21	0	1	1.00	1	1	0	0	0	0	0	0
.....TCGAAAACCAACAGCAAGCCACCTCT.....	26	0	1	1.00	1	1	0	0	0	0	0	0
.....TGATAGAGGAGCCTTCTCTA.....	20	0	2	0.50	1	0	0	0	0	1	0	0
.....TGATAGAGGAGCCTTCTCTT.....	20	1	2	0.50	1	0	0	0	0	0	0	1
.....TGATAGAGGAGCCTTCTCTAT.....	21	0	2	0.50	1	0	0	0	0	1	0	0

Anti-sense strand reads

GGTATAGCTGGATACAAGACACGTGATAGATAGCGCCTAGTGACAAAGTATGCTAACTCCGTGACTATCTCCTCGGAAGAGATAACCACATAAGCTTTTGGTTGTCGTTCGGTGGAGAAAGTAATGAGGCTAGTTGGTCATACCATAACGTTATAAGACACTCACTCCGGACCATTTTATTATAGC **********....(((((((....(((.(((((...(((..((.(((((.....)))))).)).)))...)))))).)))...)).)))))).....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M040 female body	V112 male body	GSM343916 embryo
.....GGAAGAGATAACCACATAAGC.....	21	0	2	0.50	1	0	1	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
dp5	XL_group1e:8362978-8363163 -	dps_3831	CCATATCGACCTATGTTCTGTGCACTATCTATCGCGGATCACTGTTTCATACGATTGAGGCACTGATAGAGGAGCCTTCTCTATTGGTGTATTCGAAAACCAACAGCAAGCCACCTCTTTCATTACTCCGATCAACCAGTATGGTATTGCAATATTCTGTGAGTGAGGCCTGGTAAAATAATATCG
droPer2	scaffold_13:201282-201467 +	dpe_107	CCATATCGACCTATGTTCTGTGCACTATCTATCGAGGATCACTGTTTCATACGATTGAAGTACTGATAGAGGATGCTTCTCGATTGGTGTATTCGAAAACCAACAGCAAGCGCCCTCTTTCATTACTCCGATCAACCAGTATGGTATCGCAATATTCTGTGAGTGAGGGCTTGTAAAATAAGATCG

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PARSEFAIL	
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	2
rescue.candidate	0