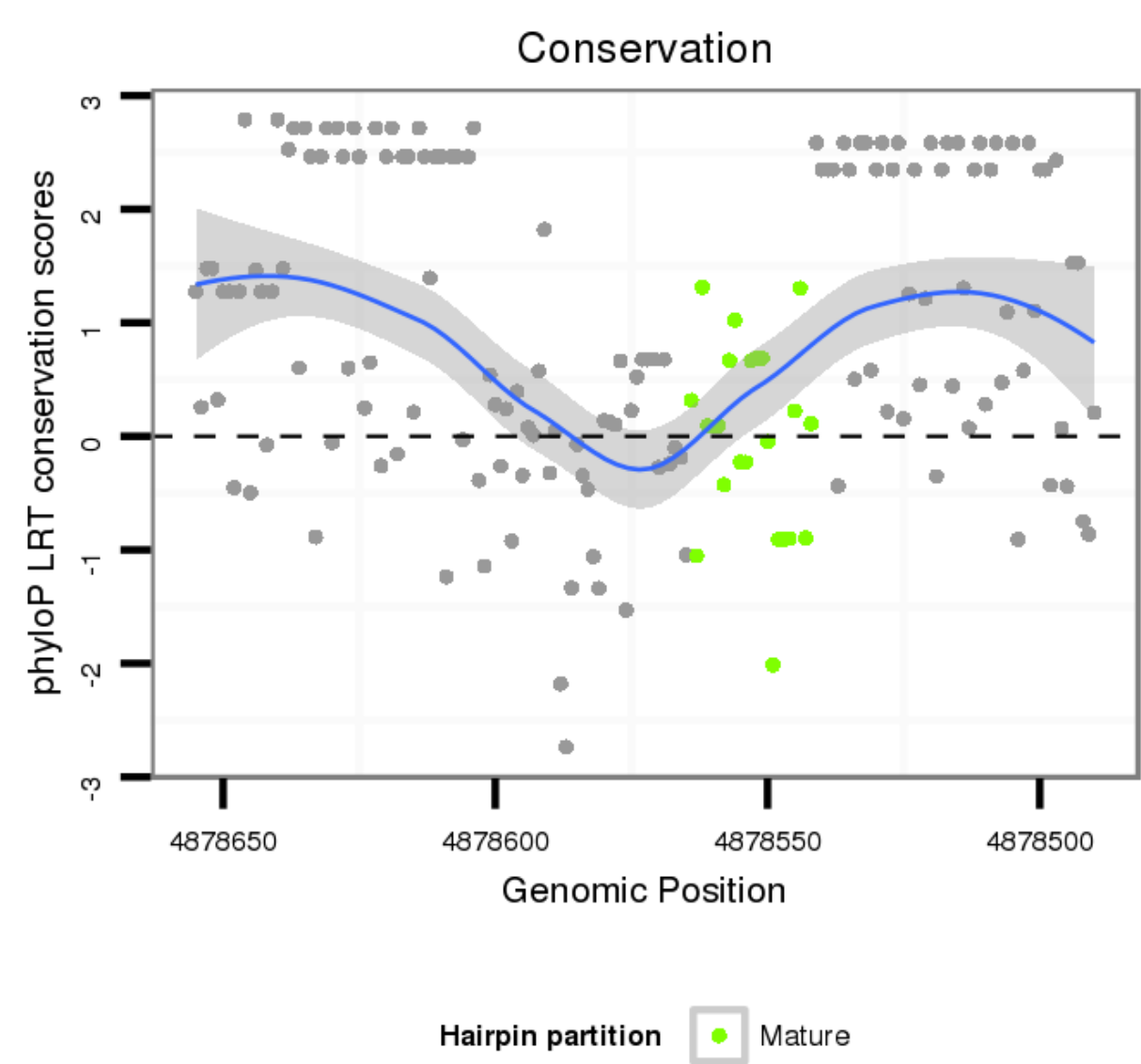
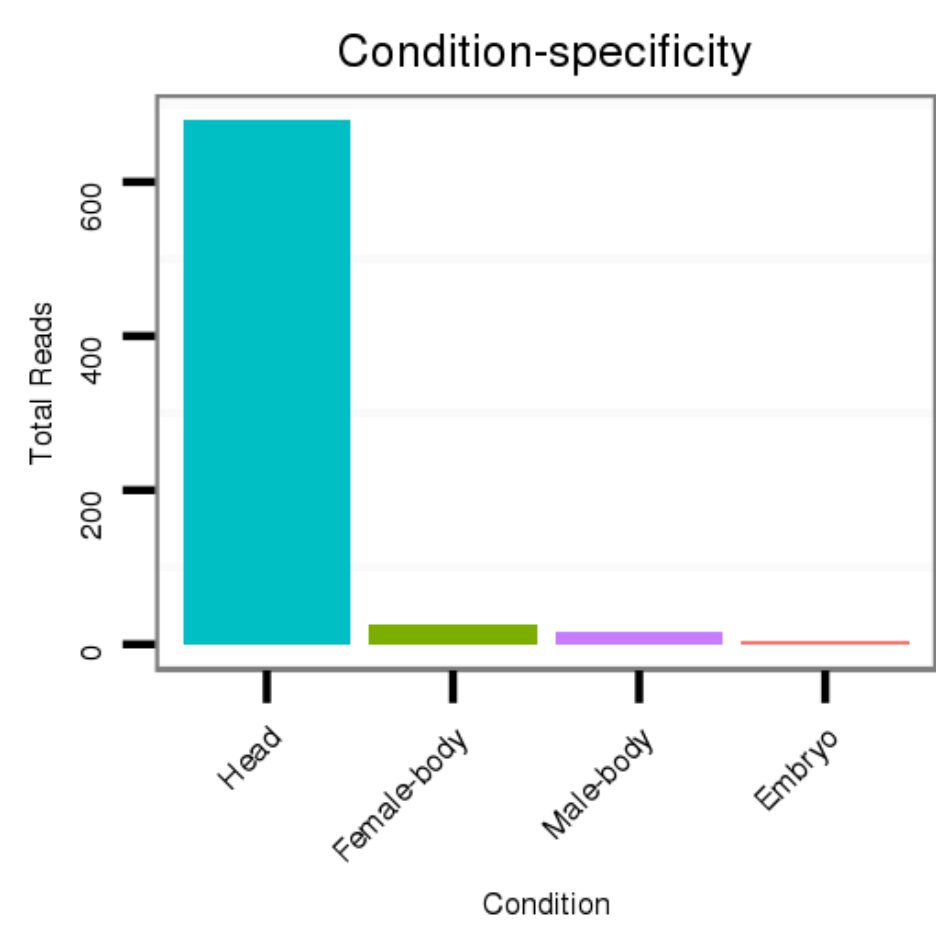
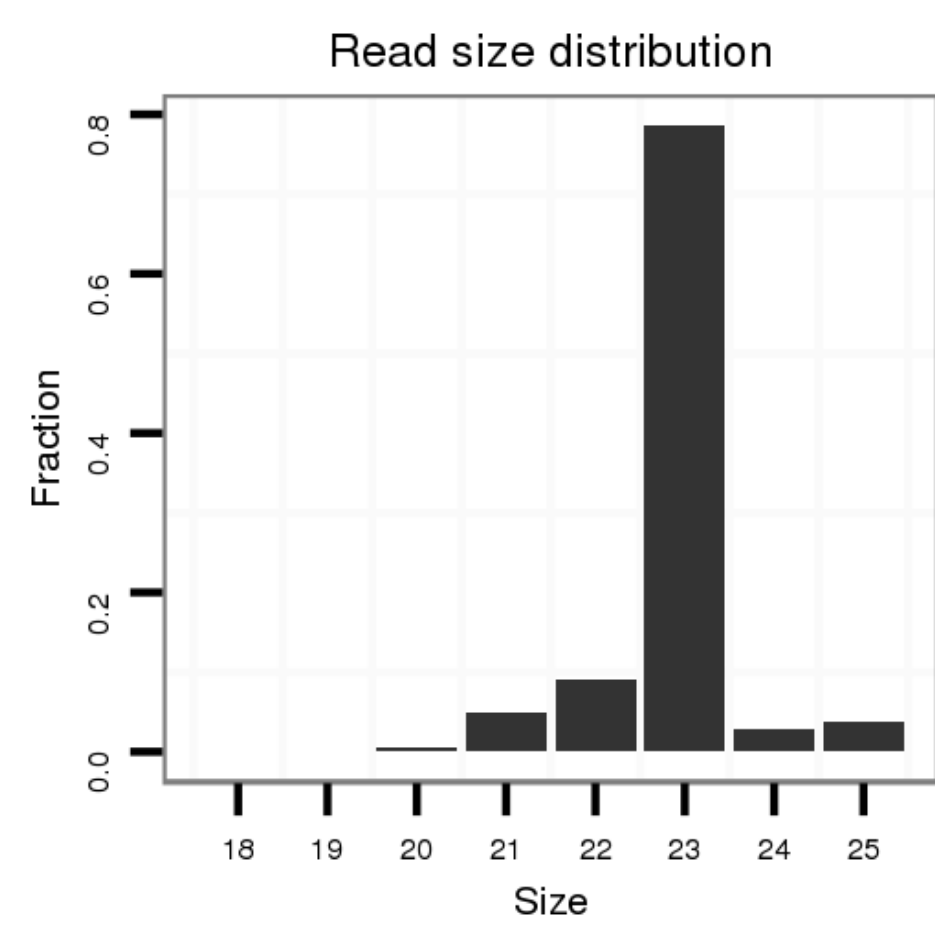
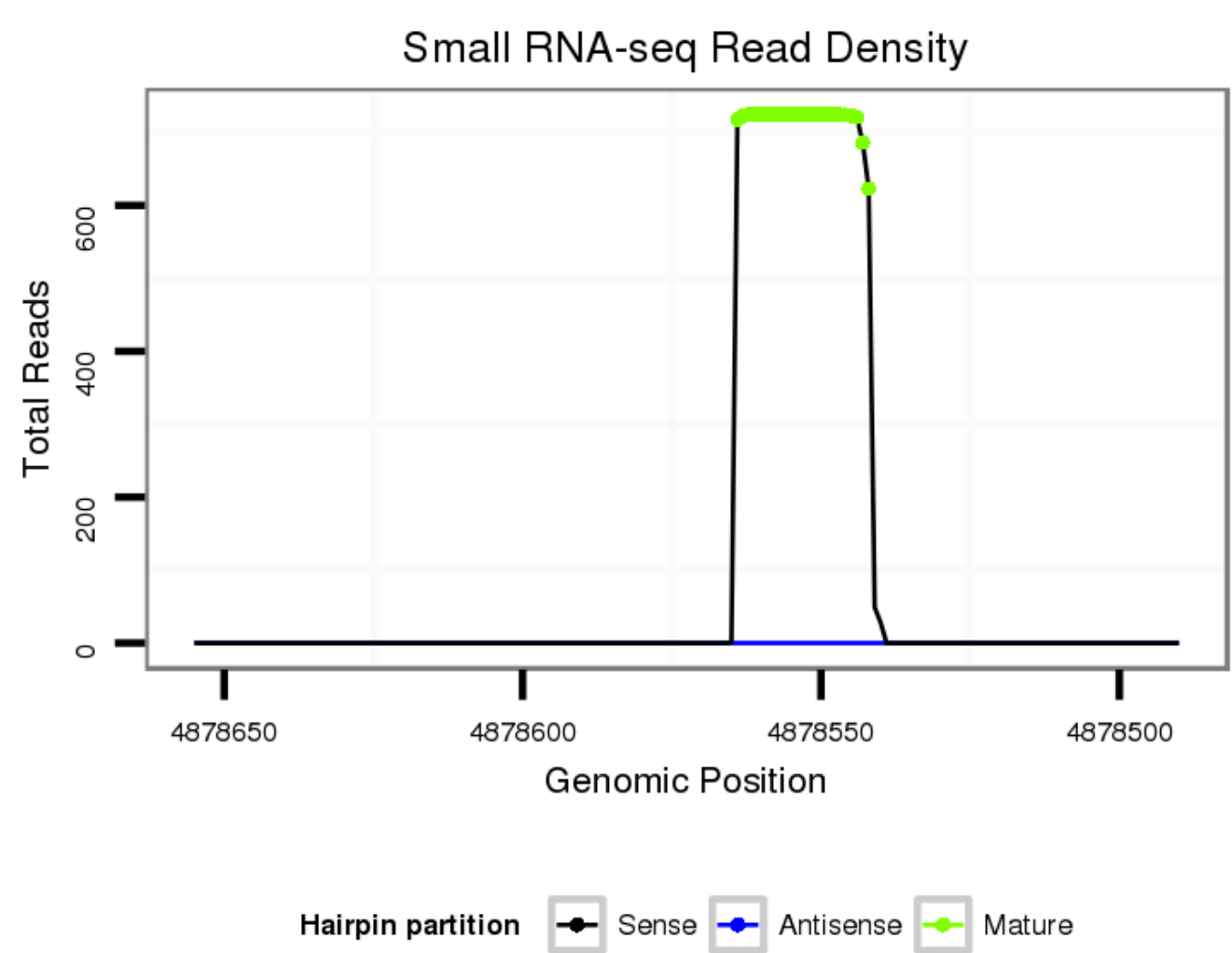
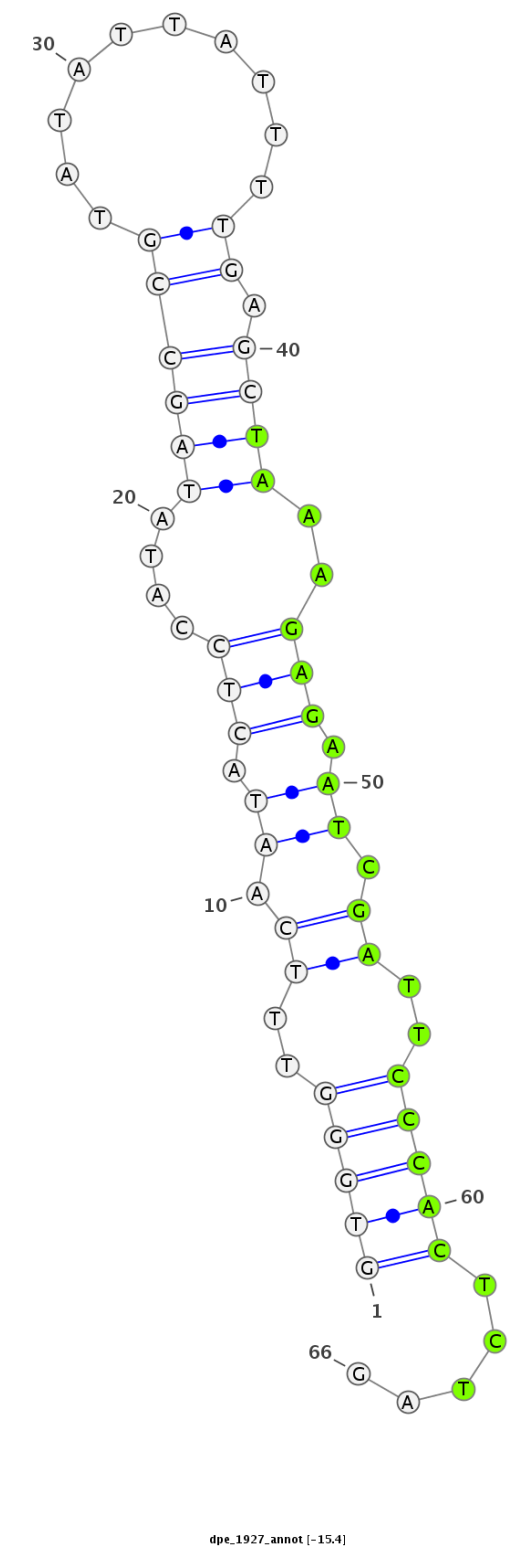


ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dpe_1927	scaffold_6:4878540-4878605 -	candidate-rescued	Mirtron	intron	[View on UCSC Genome Browser (Cornell Mirror)]

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Show Alternate Folds

Flybase annotation

intron [Dper^ΔGL11973-in]; CDS [Dper^ΔGL11973-cds]; CDS [Dper^ΔGL11973-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads

show mid mismatch reads

[illegible]

Anti-sense strand reads

[illegible]

Show Alignment With Reads

Re-alignment of all predicted orthologs

Accession	Coordinate	ID	Alignment
droPer2	scaffold_6:4878490-4878655	dps_1927	CCATACCAGAGAGCATCTCTCGGACAGCACCCTGCATGGC---AGTGCACCGGTGGGTTTCA---ATA-CTCC-----ATAT--A-----G-----CGGTATATTATTTTG---AGC A -----A-----AGAGAAATCGATCCCACT A AGGGTCCTTTGATGACACCATACACTTTGAGGATGTGATGCC---C-----ACCCGCAA
dps5	2:29507873-29508038 -	dps_872	CCATACCAGAGAGCATCTCTCGGACAGCACCCTGCATGGC---AGTGCACCGGTGGGTTTCA---ATA-CTCC-----ATAT--A-----G-----CGGTATATTATTTTG---AGC A -----A-----AGAGAAATCGATCCCACT A AGGGTCCTTTGATGACACCATACACTTTGAGGATGTGATGCC---C-----ACCCGCAA
droW112	scaf2_1100000004343:3802459-3802628 -		CCATACCAGAGAGCATCTCTCGGAGAGCACTCTCATGGCAGCAGTGCACCTGCTGCT CT ---A---AAGAGAG---A---G---CGGTATATTATTTTG---AGC A -----A-----AATTCCATAGATAGTATTGGCACT TTA GTCTCCCTAACTCTC C -----TA CTG AGGGTCCTTTGATGACACCATACACTTTGATGTGTCGCC C -----A-----ACCCGCAA
droVir3	scaffold_13047:16588070-16588248 +		CCATACCAGAGAGCATCTCTCGAGAGCACTCTCATGGCAGCAGTGCACCTGCTGCT CT ---A---AAGAGAG---A---G---CGGTATATTATTTTG---AGC A -----A-----AATTCCATAGATAGTATTGGCACT TTA GTCTCCCTAACTCTC C -----TA CTG AGGGTCCTTTGATGACACCATACACTTTGATGTGTCGCC C -----A-----ACCCGCAA
droMo3	scaffold_6540:12906002-12906175 +		CCATACCAGAGAGCATCTCTCGGACAGCACTCTCATGGCAGCAGTGCACCTGCTGCT CT ---A---AAGAGAG---A---G---CGGTATATTATTTTG---AGC A -----A-----AATTCCATAGATAGTATTGGCACT TTA GTCTCCCTAACTCTC C -----TA CTG AGGGTCCTTTGATGACACCATACACTTTGATGTGTCGCC C -----A-----ACCCGCAA
droGr12	scaffold_15116:1545367-1545427 +		CCATACCAGAGAGCATCTCTCGGACAGCACTCTCATGGCAGCAGTGCACCTGCTGCT CT ---A---AAGAGAG---A---G---CGGTATATTATTTTG---AGC A -----A-----AATTCCATAGATAGTATTGGCACT TTA GTCTCCCTAACTCTC C -----TA CTG AGGGTCCTTTGATGACACCATACACTTTGATGTGTCGCC C -----A-----ACCCGCAA
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droFiCl	scaf7180000454126:37557-37802 -		CCATACCAGAGAGCATCTCTCGGACAGCACTCTCATGGCAGCAGTGCACCTGCTGCT CT ---A---AAGAGAG---A---G---CGGTATATTATTTTG---AGC A -----A-----AATTCCATAGATAGTATTGGCACT TTA GTCTCCCTAACTCTC C -----TA CTG AGGGTCCTTTGATGACACCATACACTTTGATGTGTCGCC C -----A-----ACCCGCAA
droE1e1	scaf7180000490934:829608-829667 -		CCATACCAGAGAGCATCTCTCGGACAGCACTCTCATGGCAGCAGTGCACCTGCTGCT CT ---A---AAGAGAG---A---G---CGGTATATTATTTTG---AGC A -----A-----AATTCCATAGATAGTATTGGCACT TTA GTCTCCCTAACTCTC C -----TA CTG AGGGTCCTTTGATGACACCATACACTTTGATGTGTCGCC C -----A-----ACCCGCAA
droRho1	scaf7180000777405:10900-11066 +		CCATACCAGAGAGCATCTCTCGGACAGCACTCTCATGGCAGCAGTGCACCTGCTGCT CT ---A---AAGAGAG---A---G---CGGTATATTATTTTG---AGC A -----A-----AATTCCATAGATAGTATTGGCACT TTA GTCTCCCTAACTCTC C -----TA CTG AGGGTCCTTTGATGACACCATACACTTTGATGTGTCGCC C -----A-----ACCCGCAA
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droBui1	scaf7180000409804:1323414-1323472 -		CCATACCAGAGAGCATCTCTCGGACAGCACTCTCATGGCAGCAGTGCACCTGCTGCT CT ---A---AAGAGAG---A---G---CGGTATATTATTTTG---AGC A -----A-----AATTCCATAGATAGTATTGGCACT TTA GTCTCCCTAACTCTC C -----TA CTG AGGGTCCTTTGATGACACCATACACTTTGATGTGTCGCC C -----A-----ACCCGCAA
dm3	Chr3R:15060226-15060389 -		CCATACCAGAGAGCATCTCTCGGACAGCACTCTCATGGCAGCAGTGCACCTGCTGCT CT ---A---AAGAGAG---A---G---CGGTATATTATTTTG---AGC A -----A-----AATTCCATAGATAGTATTGGCACT TTA GTCTCCCTAACTCTC C -----TA CTG AGGGTCCTTTGATGACACCATACACTTTGATGTGTCGCC C -----A-----ACCCGCAA
droSiM2	3:6202105-6202269 +	ds1_22114	CCATACCAGAGAGCATCTCTCGGACAGCACTCTCATGGCAGCAGTGCACCTGCTGCT CT ---A---AAGAGAG---A---G---CGGTATATTATTTTG---AGC A -----A-----AATTCCATAGATAGTATTGGCACT TTA GTCTCCCTAACTCTC C -----TA CTG AGGGTCCTTTGATGACACCATACACTTTGATGTGTCGCC C -----A-----ACCCGCAA
droSeC2	scaffold_25:7055570-7055642 -		CCATACCAGAGAGCATCTCTCGGACAGCACTCTCATGGCAGCAGTGCACCTGCTGCT CT ---A---AAGAGAG---A---G---CGGTATATTATTTTG---AGC A -----A-----AATTCCATAGATAGTATTGGCACT TTA GTCTCCCTAACTCTC C -----TA CTG AGGGTCCTTTGATGACACCATACACTTTGATGTGTCGCC C -----A-----ACCCGCAA
droYaK3	3R:3762747-3762910 -		CCATACCAGAGAGCATCTCTCGGACAGCACTCTCATGGCAGCAGTGCACCTGCTGCT CT ---A---AAGAGAG---A---G---CGGTATATTATTTTG---AGC A -----A-----AATTCCATAGATAGTATTGGCACT TTA GTCTCCCTAACTCTC C -----TA CTG AGGGTCCTTTGATGACACCATACACTTTGATGTGTCGCC C -----A-----ACCCGCAA
droEre2	scaffold_4770:6571506-6571669 +		CCATACCAGAGAGCATCTCTCGGACAGCACTCTCATGGCAGCAGTGCACCTGCTGCT CT ---A---AAGAGAG---A---G---CGGTATATTATTTTG---AGC A -----A-----AATTCCATAGATAGTATTGGCACT TTA GTCTCCCTAACTCTC C -----TA CTG AGGGTCCTTTGATGACACCATACACTTTGATGTGTCGCC C -----A-----ACCCGCAA

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Predicted structure

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

Anti-sense strand reads

Show Alignment With Reads

Re-alignment of all predicted orthologs

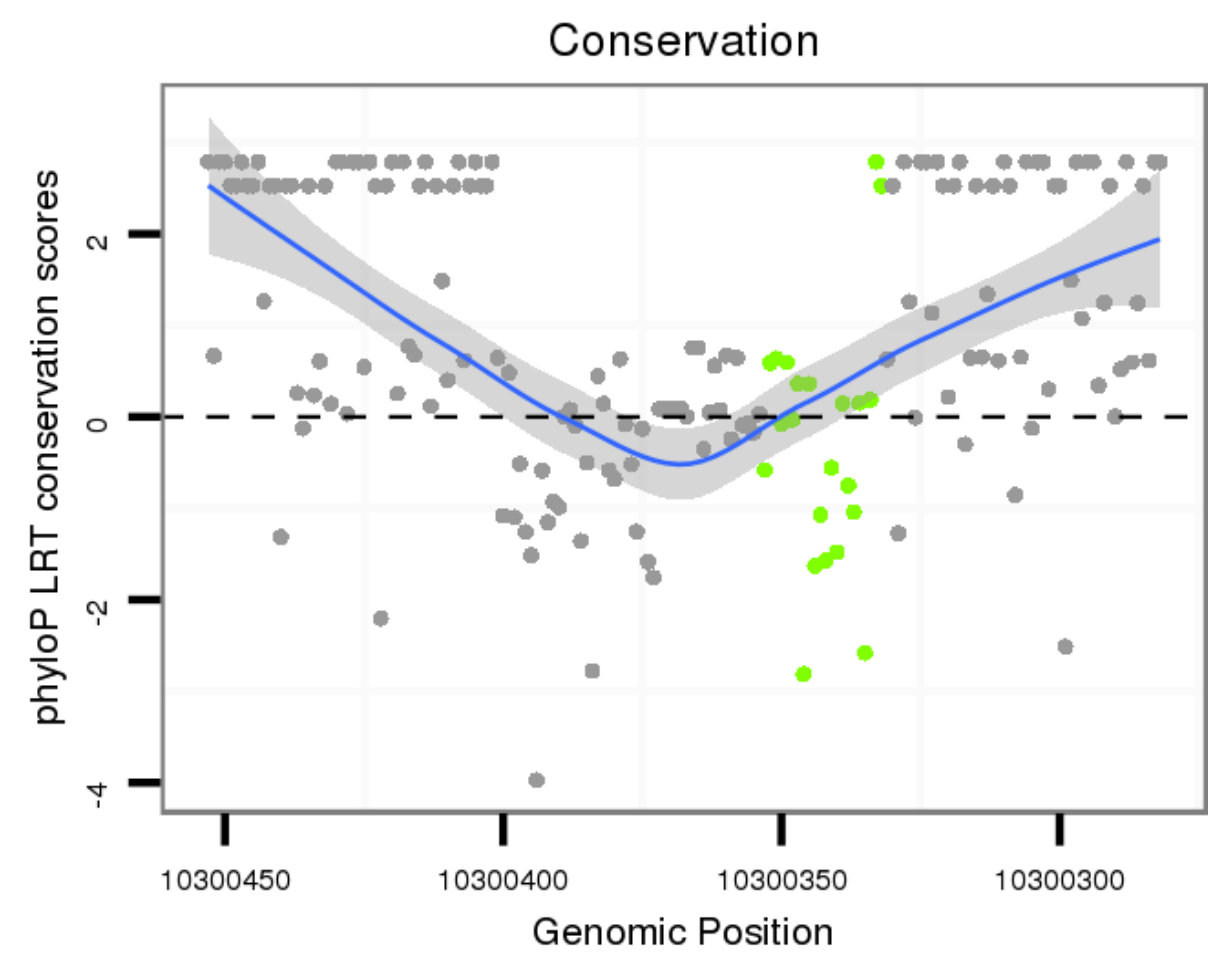
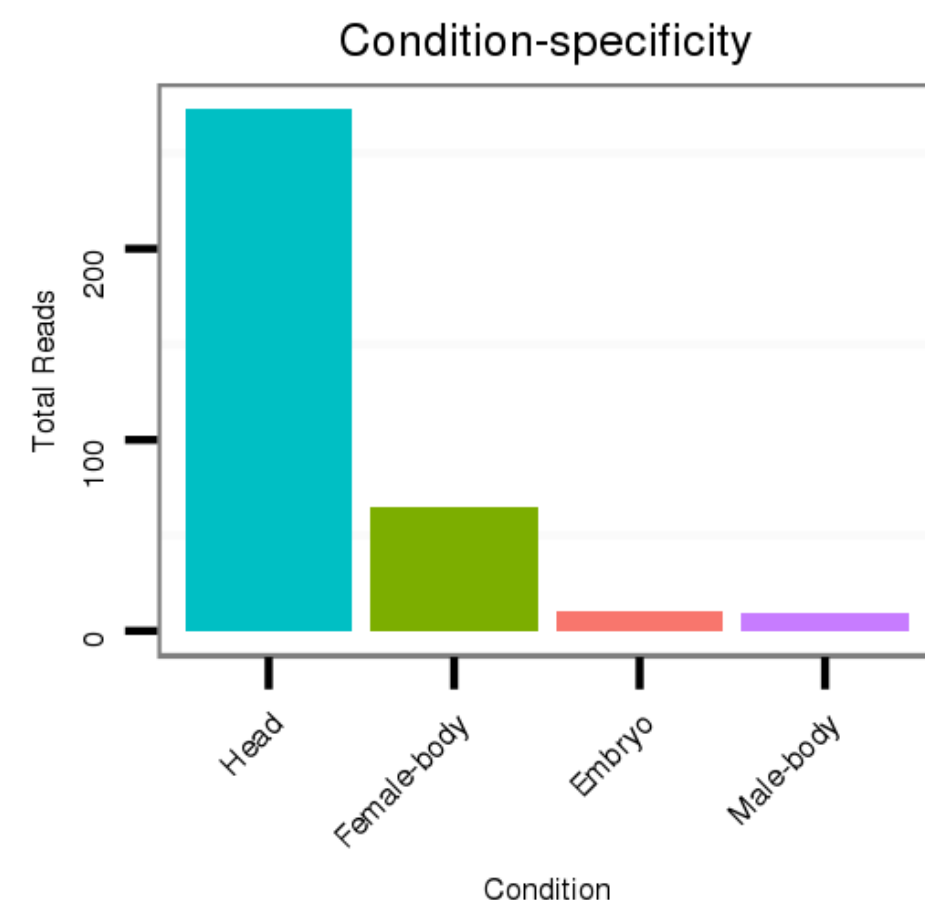
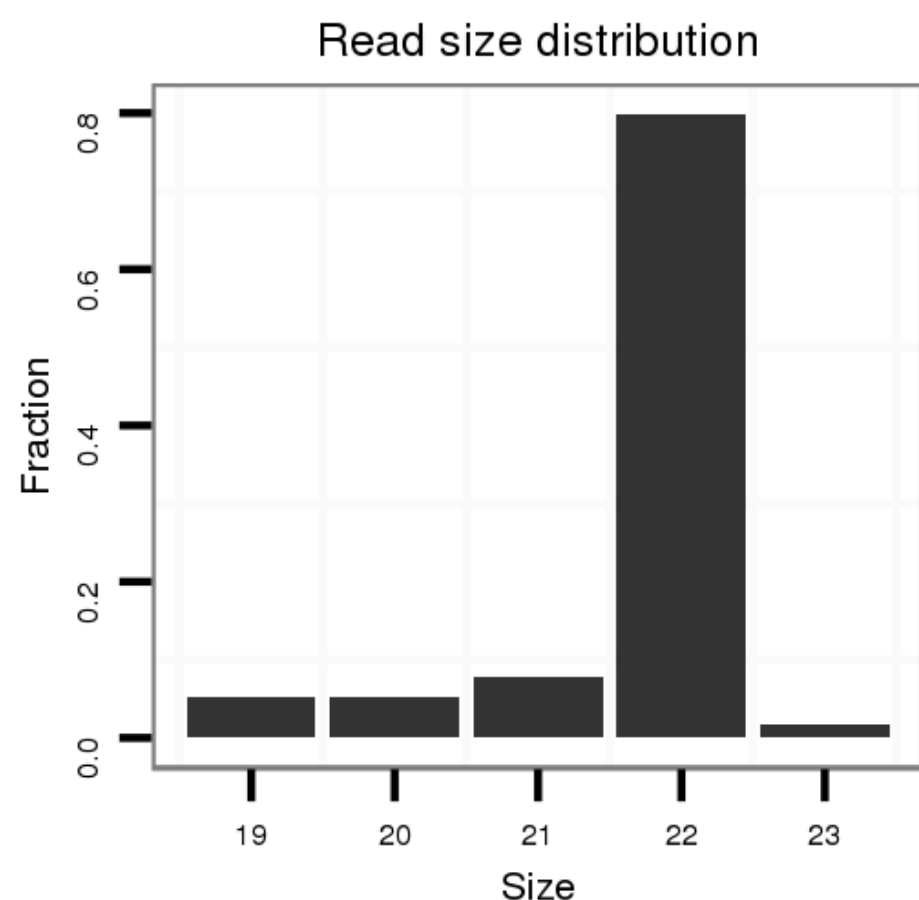
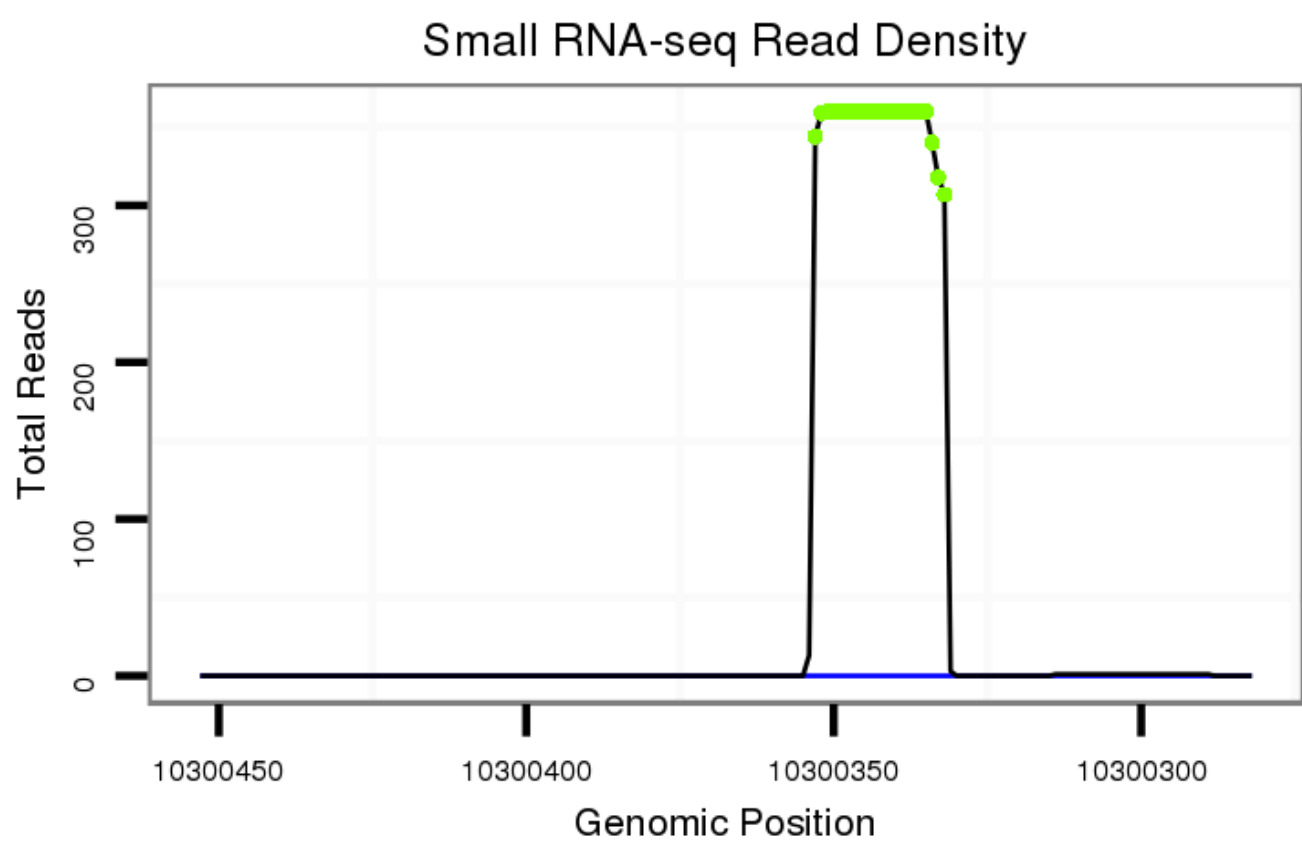
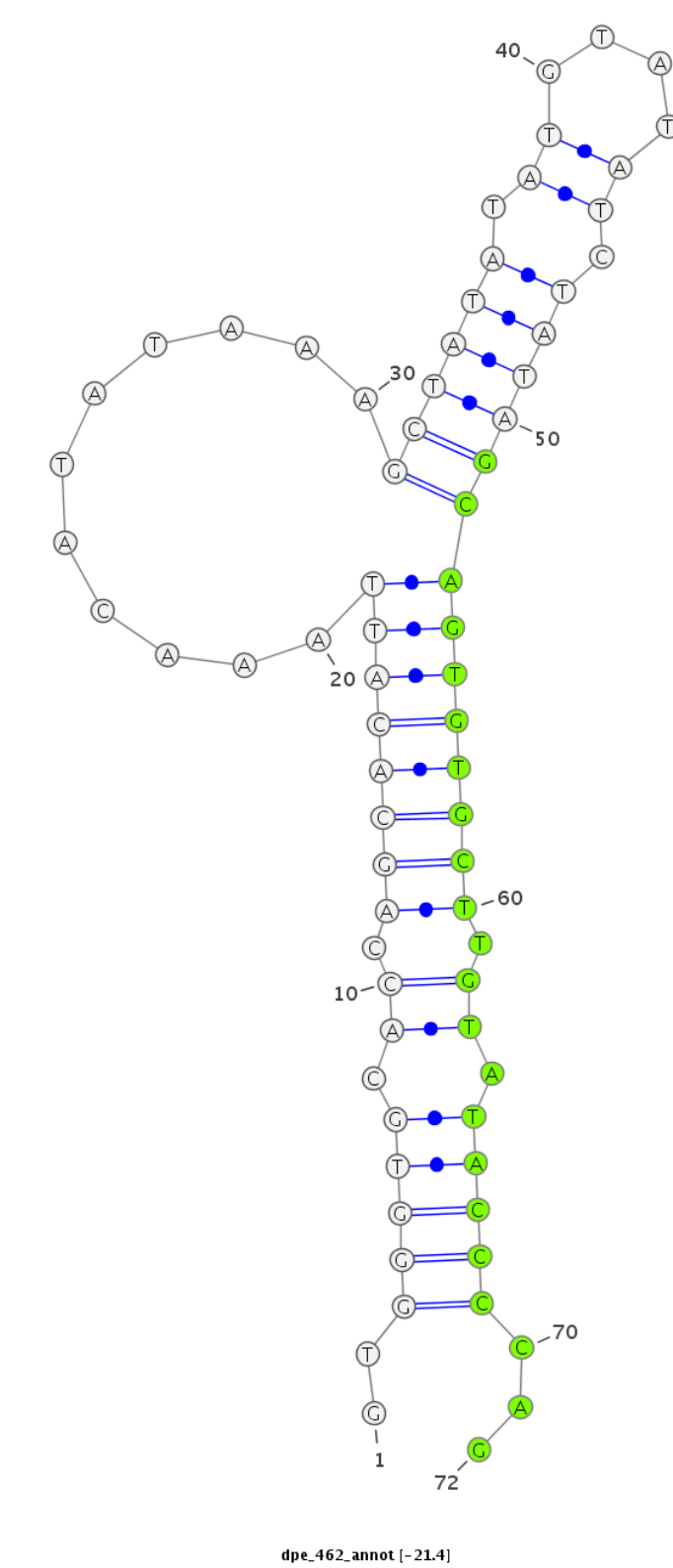
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rescue.confident	1
rescue.candidate	1

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dpe_462	scaffold_0:10300332-10300403 -	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 [Dper^hGL23095-in]; CDS [Dper^hGL23095-cds]; CDS [Dper^hGL23095-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TGAAGGTCGAGCGTCCAGGCGCAATTACACGAGTCCAGGAAGACGAGTGGGTGCACACGACATTAAACATATAAAGCTATATATGTATATCTATAAGCAGTGCTTGTATACCCCGACACACCAAGACAGCTGCTCACCCTGTATCCCGATCAATCGATTGCCCAT	Read #	size mismatch	Hit Count	Total Count	Total	V057	V050	M042	V042	V111	M021
						head	head	female body	embryo	male body	embryo
.....(((((((.....(((((((.....)))))))))))))))).....*****.....	22	0	1	284.00	284	139	81	48	9	7	0
.....GCGAGTGTGCTTGTATACCCGAG.....	22	1	1	37.00	37	22	9	2	1	3	0
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.....GCGAGTGTGCTTGTATACCCGAG.....	23	1	1	19.00	19	14	3	2	0	0	0
.....GCGAGTGTGCTTGTATACCC.....	19	0	1	17.00	17	8	3	4	1	1	0
.....GCGAGTGTGCTTGTATACCC.....	20	0	1	13.00	13	4	6	2	0	1	0
.....GCGAGTGTGCTTGTATACCCGAG.....	21	0	1	10.00	10	2	1	7	0	0	0
.....GCGAGTGTGCTTGTATACCCGAG.....	21	0	1	6.00	6	3	2	1	0	0	0
.....GCGAGTGTGCTTGTATACCCGAG.....	21	0	1	5.00	5	2	3	0	0	0	0
.....GCGAGTGTGCTTGTATACCC.....	21	0	1	3.00	3	2	1	0	0	0	0
.....GCGAGTGTGCTTGTATACCCGAG.....	22	1	1	2.00	2	1	1	0	0	0	0
.....GCGAGTGTGCTTGTATACCCGAG.....	22	1	1	2.00	2	2	0	0	0	0	0
.....GCGAGTGTGCTTGTATACCCGAG.....	22	2	1	1.00	1	0	1	0	0	0	0
.....GCGAGTGTGCTTGTATACCC.....	22	2	1	1.00	1	1	0	0	0	0	0
.....GCGAGTGTGCTTGTATACCC.....	20	0	1	1.00	1	0	0	0	0	0	1
.....GCGAGTGTGCTTGTATACCCGAG.....	23	0	1	1.00	1	1	0	0	0	0	0
.....GCGAGTGTGCTTGTATACCC.....	20	1	1	1.00	1	1	0	0	0	0	0
.....GCGAGTGTGCTTGTATACCCGAG.....	22	0	1	1.00	1	0	0	1	0	0	0
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.....GCGAGTGTGCTTGTATACCCGAG.....	23	2	1	1.00	1	1	0	0	0	0	0
.....GCGAGTGTGCTTGTATACCCGAG.....	22	1	1	1.00	1	0	1	0	0	0	0
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.....GCGAGTGTGCTTGTATACCCGAG.....	24	2	1	1.00	1	0	0	0	0	1	0
.....GCGAGTGTGCTTGTATACCCGAG.....	20	1	1	1.00	1	0	0	1	0	0	0
.....GCGAGTGTGCTTGTATACCCGAG.....	20	1	1	1.00	1	1	0	0	0	0	0
.....GCGAGTGTGCTTGTATACCC.....	19	1	1	1.00	1	1	0	0	0	0	0
.....GCGAGTGTGCTTGTATACCC.....	20	2	2	0.50	1	0	1	0	0	0	0

Anti-sense strand reads

Show Alignment With Reads

Re-alignment of all predicted orthologs

Accession	Coordinate	ID	Alignment
droPer2	scaf102_010300282-10300453	dpe_462	TGAAGTCTGAGCGTCCAGCGCAATTACACGAGTTCAG-GAAGACGAGTGGGTGCACC--A-GCA-----CA--TTAAACATA---TAAAGCTATATAT-GTATATC-----T-----ATAACG-AAG-G-----TGT-GCTTTGA-TAC---CCGACACCAACAGACAGCTGCTCCAT-CTGATCCCGATCAATGATGCCCAT
dp5	210181330-10181497	dpe_455	TGAAGTCTGAGCGTCCAGCGCAATTACACGAGTTCAG-GAAGACGAGTGGGTGCACC--A-GCA-----CA--TTAAACATA---TAAAGCTATATAT-GTATATC-----T-----ATAACG-AAG-G-----TGT-GCTTTGA-TAC---CCGACACCAACAGACAGCTGCTCCAT-CTGATCCCGATCAATGATGCCCAT
droW112	scaf2_11000000490219022539-9022701		TGAAGTCTGAGCGTCCAGCGCAATTACACGAGTTCAG-GAAGACGAGTGGGTGCACC--A-GCA-----CA--TTAAACATA---TAAAGCTATATAT-GTATATC-----T-----ATAACG-AAG-G-----TGT-GCTTTGA-TAC---CCGACACCAACAGACAGCTGCTCCAT-CTGATCCCGATCAATGATGCCCAT
droV13	scaf102_128223790401-3790564		TGAAGTCTGAGCGTCCAGCGCAATTACACGAGTTCAG-GAAGACGAGTGGGTGCACC--A-GCA-----CA--TTAAACATA---TAAAGCTATATAT-GTATATC-----T-----ATAACG-AAG-G-----TGT-GCTTTGA-TAC---CCGACACCAACAGACAGCTGCTCCAT-CTGATCCCGATCAATGATGCCCAT
droMo3	scaf102_654017099575-17099735		TGAAGTCTGAGCGTCCAGCGCAATTACACGAGTTCAG-GAAGACGAGTGGGTGCACC--A-GCA-----CA--TTAAACATA---TAAAGCTATATAT-GTATATC-----T-----ATAACG-AAG-G-----TGT-GCTTTGA-TAC---CCGACACCAACAGACAGCTGCTCCAT-CTGATCCCGATCAATGATGCCCAT
droGr12	scaf102_149061382895-1383059		TGAAGTCTGAGCGTCCAGCGCAATTACACGAGTTCAG-GAAGACGAGTGGGTGCACC--A-GCA-----CA--TTAAACATA---TAAAGCTATATAT-GTATATC-----T-----ATAACG-AAG-G-----TGT-GCTTTGA-TAC---CCGACACCAACAGACAGCTGCTCCAT-CTGATCCCGATCAATGATGCCCAT
droAna3	scaf102_1334017149374-7149395		TGAAGTCTGAGCGTCCAGCGCAATTACACGAGTTCAG-GAAGACGAGTGGGTGCACC--A-GCA-----CA--TTAAACATA---TAAAGCTATATAT-GTATATC-----T-----ATAACG-AAG-G-----TGT-GCTTTGA-TAC---CCGACACCAACAGACAGCTGCTCCAT-CTGATCCCGATCAATGATGCCCAT
droB1p1	scaf11800000296424652032-652199		TGAAGTCTGAGCGTCCAGCGCAATTACACGAGTTCAG-GAAGACGAGTGGGTGCACC--A-GCA-----CA--TTAAACATA---TAAAGCTATATAT-GTATATC-----T-----ATAACG-AAG-G-----TGT-GCTTTGA-TAC---CCGACACCAACAGACAGCTGCTCCAT-CTGATCCCGATCAATGATGCCCAT
droK1k1	scaf11800000202256110322-110486		TGAAGTCTGAGCGTCCAGCGCAATTACACGAGTTCAG-GAAGACGAGTGGGTGCACC--A-GCA-----CA--TTAAACATA---TAAAGCTATATAT-GTATATC-----T-----ATAACG-AAG-G-----TGT-GCTTTGA-TAC---CCGACACCAACAGACAGCTGCTCCAT-CTGATCCCGATCAATGATGCCCAT
droF1c1	scaf11800000453581272813-272965		TGAAGTCTGAGCGTCCAGCGCAATTACACGAGTTCAG-GAAGACGAGTGGGTGCACC--A-GCA-----CA--TTAAACATA---TAAAGCTATATAT-GTATATC-----T-----ATAACG-AAG-G-----TGT-GCTTTGA-TAC---CCGACACCAACAGACAGCTGCTCCAT-CTGATCCCGATCAATGATGCCCAT
droE1e1	scaf118000004912803591270-3591445		TGAAGTCTGAGCGTCCAGCGCAATTACACGAGTTCAG-GAAGACGAGTGGGTGCACC--A-GCA-----CA--TTAAACATA---TAAAGCTATATAT-GTATATC-----T-----ATAACG-AAG-G-----TGT-GCTTTGA-TAC---CCGACACCAACAGACAGCTGCTCCAT-CTGATCCCGATCAATGATGCCCAT
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droTak1	scaf11800000415383115705-115865		TGAAGTCTGAGCGTCCAGCGCAATTACACGAGTTCAG-GAAGACGAGTGGGTGCACC--A-GCA-----CA--TTAAACATA---TAAAGCTATATAT-GTATATC-----T-----ATAACG-AAG-G-----TGT-GCTTTGA-TAC---CCGACACCAACAGACAGCTGCTCCAT-CTGATCCCGATCAATGATGCCCAT
droEug1	scaf118000004097871235183-1235345		TGAAGTCTGAGCGTCCAGCGCAATTACACGAGTTCAG-GAAGACGAGTGGGTGCACC--A-GCA-----CA--TTAAACATA---TAAAGCTATATAT-GTATATC-----T-----ATAACG-AAG-G-----TGT-GCTTTGA-TAC---CCGACACCAACAGACAGCTGCTCCAT-CTGATCCCGATCAATGATGCCCAT
droM12	chr3R:24345661-24345822		TGAAGTCTGAGCGTCCAGCGCAATTACACGAGTTCAG-GAAGACGAGTGGGTGCACC--A-GCA-----CA--TTAAACATA---TAAAGCTATATAT-GTATATC-----T-----ATAACG-AAG-G-----TGT-GCTTTGA-TAC---CCGACACCAACAGACAGCTGCTCCAT-CTGATCCCGATCAATGATGCCCAT
droS2c2	scaf102_22948938-949100		TGAAGTCTGAGCGTCCAGCGCAATTACACGAGTTCAG-GAAGACGAGTGGGTGCACC--A-GCA-----CA--TTAAACATA---TAAAGCTATATAT-GTATATC-----T-----ATAACG-AAG-G-----TGT-GCTTTGA-TAC---CCGACACCAACAGACAGCTGCTCCAT-CTGATCCCGATCAATGATGCCCAT
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droEre2	scaf102_482013689926-3690090		TGAAGTCTGAGCGTCCAGCGCAATTACACGAGTTCAG-GAAGACGAGTGGGTGCACC--A-GCA-----CA--TTAAACATA---TAAAGCTATATAT-GTATATC-----T-----ATAACG-AAG-G-----TGT-GCTTTGA-TAC---CCGACACCAACAGACAGCTGCTCCAT-CTGATCCCGATCAATGATGCCCAT

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Show Alignment With Reads

Re-alignment of all predicted orthologs

Genomic Coordinates	ID	Alignment
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chr10p22.3:6540-17099574-17099735		TGAAGCTGAGCGTGCAGGCGCAATTACACAGCTTCACG-GAAGCAGCGTGGTGCCACC-A-BCA-----CA-TTAAACATA-----TAAAGCTATATAT-ATATATC-----T-----ATATAGC-A-A-G-----TGT-GCTTTGTA-TAG-----CGCAGACACACAGACAGAGCTGCTCACT-CTGATCCCGATCAATCATGTCGCAT
chr10p22.3:14906-1382895-1383059		TGAAGCTGAGCGTGCAGGCGCAATTACACAGCTTCACG-GAAGCAGCGTGGTGCCACC-A-BCA-----CA-TTAAACATA-----TAAAGCTATATAT-ATATATC-----T-----ATATAGC-A-A-G-----TGT-GCTTTGTA-TAG-----CGCAGACACACAGACAGAGCTGCTCACT-CTGATCCCGATCAATCATGTCGCAT
chr10p22.3:13340-7149374-7149541		TGAAGCTGAGCGTGCAGGCGCAATTACACAGCTTCACG-GAAGCAGCGTGGTGCCACC-A-BCA-----CA-TTAAACATA-----TAAAGCTATATAT-ATATATC-----T-----ATATAGC-A-A-G-----TGT-GCTTTGTA-TAG-----CGCAGACACACAGACAGAGCTGCTCACT-CTGATCCCGATCAATCATGTCGCAT
chr10p22.3:18000039624-652032-652199		TGAAGCTGAGCGTGCAGGCGCAATTACACAGCTTCACG-GAAGCAGCGTGGTGCCACC-A-BCA-----CA-TTAAACATA-----TAAAGCTATATAT-ATATATC-----T-----ATATAGC-A-A-G-----TGT-GCTTTGTA-TAG-----CGCAGACACACAGACAGAGCTGCTCACT-CTGATCCCGATCAATCATGTCGCAT
chr10p22.3:18000030256-110322-110486		TGAAGCTGAGCGTGCAGGCGCAATTACACAGCTTCACG-GAAGCAGCGTGGTGCCACC-A-BCA-----CA-TTAAACATA-----TAAAGCTATATAT-ATATATC-----T-----ATATAGC-A-A-G-----TGT-GCTTTGTA-TAG-----CGCAGACACACAGACAGAGCTGCTCACT-CTGATCCCGATCAATCATGTCGCAT
chr10p22.3:180000453581-272813-272965		TGAAGCTGAGCGTGCAGGCGCAATTACACAGCTTCACG-GAAGCAGCGTGGTGCCACC-A-BCA-----CA-TTAAACATA-----TAAAGCTATATAT-ATATATC-----T-----ATATAGC-A-A-G-----TGT-GCTTTGTA-TAG-----CGCAGACACACAGACAGAGCTGCTCACT-CTGATCCCGATCAATCATGTCGCAT
chr10p22.3:180000491280-3591270-3591445		TGAAGCTGAGCGTGCAGGCGCAATTACACAGCTTCACG-GAAGCAGCGTGGTGCCACC-A-BCA-----CA-TTAAACATA-----TAAAGCTATATAT-ATATATC-----T-----ATATAGC-A-A-G-----TGT-GCTTTGTA-TAG-----CGCAGACACACAGACAGAGCTGCTCACT-CTGATCCCGATCAATCATGTCGCAT
chr10p22.3:180000779501-61345-61505		TGAAGCTGAGCGTGCAGGCGCAATTACACAGCTTCACG-GAAGCAGCGTGGTGCCACC-A-BCA-----CA-TTAAACATA-----TAAAGCTATATAT-ATATATC-----T-----ATATAGC-A-A-G-----TGT-GCTTTGTA-TAG-----CGCAGACACACAGACAGAGCTGCTCACT-CTGATCCCGATCAATCATGTCGCAT
chr10p22.3:180000302075-144004-1440269		TGAAGCTGAGCGTGCAGGCGCAATTACACAGCTTCACG-GAAGCAGCGTGGTGCCACC-A-BCA-----CA-TTAAACATA-----TAAAGCTATATAT-ATATATC-----T-----ATATAGC-A-A-G-----TGT-GCTTTGTA-TAG-----CGCAGACACACAGACAGAGCTGCTCACT-CTGATCCCGATCAATCATGTCGCAT
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chr10p22.3:2435661-24345822		TGAAGCTGAGCGTGCAGGCGCAATTACACAGCTTCACG-GAAGCAGCGTGGTGCCACC-A-BCA-----CA-TTAAACATA-----TAAAGCTATATAT-ATATATC-----T-----ATATAGC-A-A-G-----TGT-GCTTTGTA-TAG-----CGCAGACACACAGACAGAGCTGCTCACT-CTGATCCCGATCAATCATGTCGCAT
chr10p22.3:2372760-23723921		TGAAGCTGAGCGTGCAGGCGCAATTACACAGCTTCACG-GAAGCAGCGTGGTGCCACC-A-BCA-----CA-TTAAACATA-----TAAAGCTATATAT-ATATATC-----T-----ATATAGC-A-A-G-----TGT-GCTTTGTA-TAG-----CGCAGACACACAGACAGAGCTGCTCACT-CTGATCCCGATCAATCATGTCGCAT
chr10p22.3:225948938-349100		TGAAGCTGAGCGTGCAGGCGCAATTACACAGCTTCACG-GAAGCAGCGTGGTGCCACC-A-BCA-----CA-TTAAACATA-----TAAAGCTATATAT-ATATATC-----T-----ATATAGC-A-A-G-----TGT-GCTTTGTA-TAG-----CGCAGACACACAGACAGAGCTGCTCACT-CTGATCCCGATCAATCATGTCGCAT
chr10p22.3:2251563-22515827		TGAAGCTGAGCGTGCAGGCGCAATTACACAGCTTCACG-GAAGCAGCGTGGTGCCACC-A-BCA-----CA-TTAAACATA-----TAAAGCTATATAT-ATATATC-----T-----ATATAGC-A-A-G-----TGT-GCTTTGTA-TAG-----CGCAGACACACAGACAGAGCTGCTCACT-CTGATCCCGATCAATCATGTCGCAT
chr10p22.3:4820-3688926-3690090		TGAAGCTGAGCGTGCAGGCGCAATTACACAGCTTCACG-GAAGCAGCGTGGTGCCACC-A-BCA-----CA-TTAAACATA-----TAAAGCTATATAT-ATATATC-----T-----ATATAGC-A-A-G-----TGT-GCTTTGTA-TAG-----CGCAGACACACAGACAGAGCTGCTCACT-CTGATCCCGATCAATCATGTCGCAT

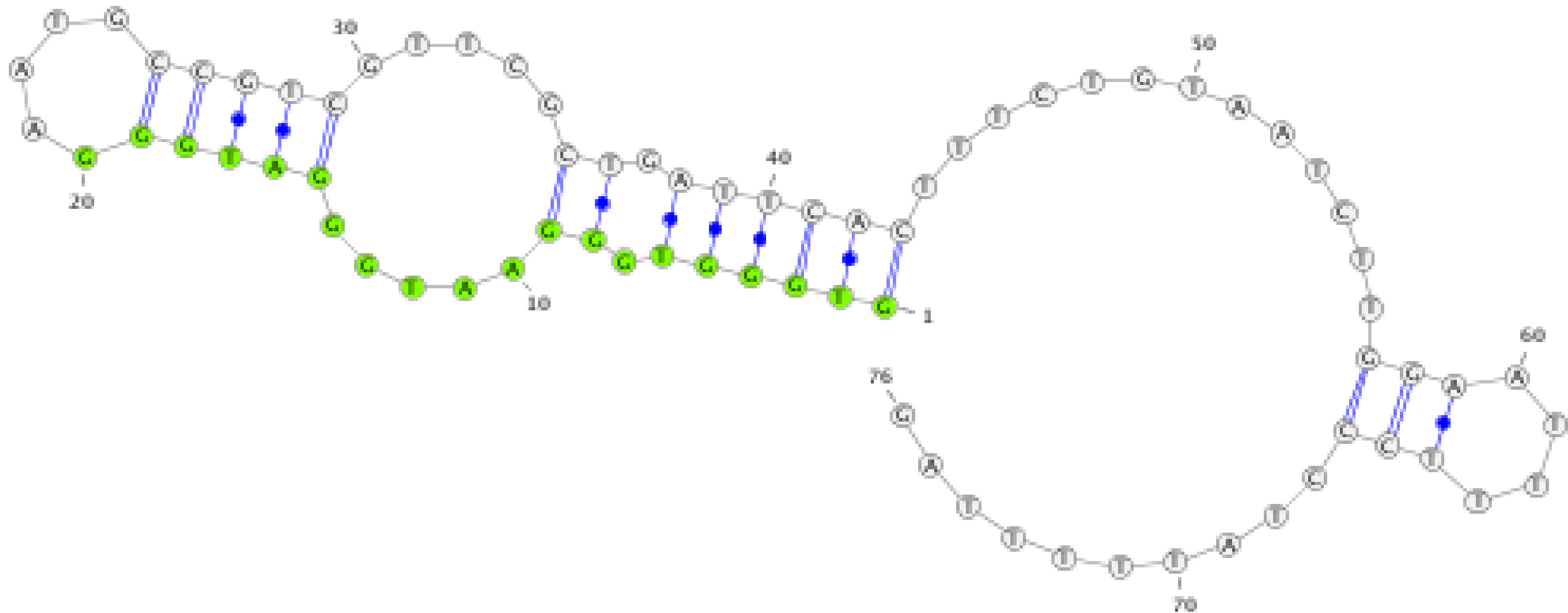
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	PASS/FAIL
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crit_mor	0
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crit_total	1
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crit_top3	1
crit_top3	1
crit_uri	0
crit_back	1
rescue_total	1
rescue_dominant	1
rescue_known	0
rescue_confident	1
rescue_candidate	2

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dpe_1364	scaffold_3:1906654-1906729 -	candidate-rescued	Mitron	intron	[View on UCSC Genome Browser (Cornell Minot)]

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



dpe_1364_annot [-17.0]

Show Alternate Folds

Flybase annotation

intron [Dper¹GL21825-in]; CDS [Dper¹GL21825-cds]; CDS [Dper¹GL21825-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

[illegible]

Anti-sense strand reads

										V111	M021	M042	V057					
										female	male	embryo	body	female	body	head		
										Read #	Hit	Total	Count	Norm	Total	Count	Norm	
GTTTAAAGCTCGCAGGATTACGGGCTGTGTGTACCGGGTCGGTAACTTGCACCCACGCTTACCGTACGCTCTGTGTACTTGGCGTGCACTTAGAGGGGTGTT										21	0	1	1.00	1	0	1	0	0
#####(((((((.....(((((((.....)))))).....))))))#####										19	0	1	2.00	2	0	0	0	0
.....GCTCGAGGTTACGGGCTCTG.....										20	0	1	2.00	2	0	0	0	0
.....CGAGATTACGGGCTGTGTG.....										20	0	1	2.00	2	0	2	0	0
.....CGGGTCGGTAACTTTCAGCC.....										20	0	1	2.00	2	0	0	0	0
.....CTCGAGGTTACGGGCTCTG.....										21	0	1	1.00	1	1	0	0	0
.....GTCGAGGTTACAGGGCTCTGTG.....										21	0	1	1.00	1	1	0	0	0
.....GTCGAGGTTACAGGGCTCTGCTGA.....										21	0	1	1.00	1	0	1	0	0
.....CGAGATTACGGGCTCTGTGTT.....										21	0	1	1.00	1	1	0	0	0
.....CAGGGCTCTGTGTTACCGGGT.....										21	0	1	1.00	1	1	0	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

[illegible]

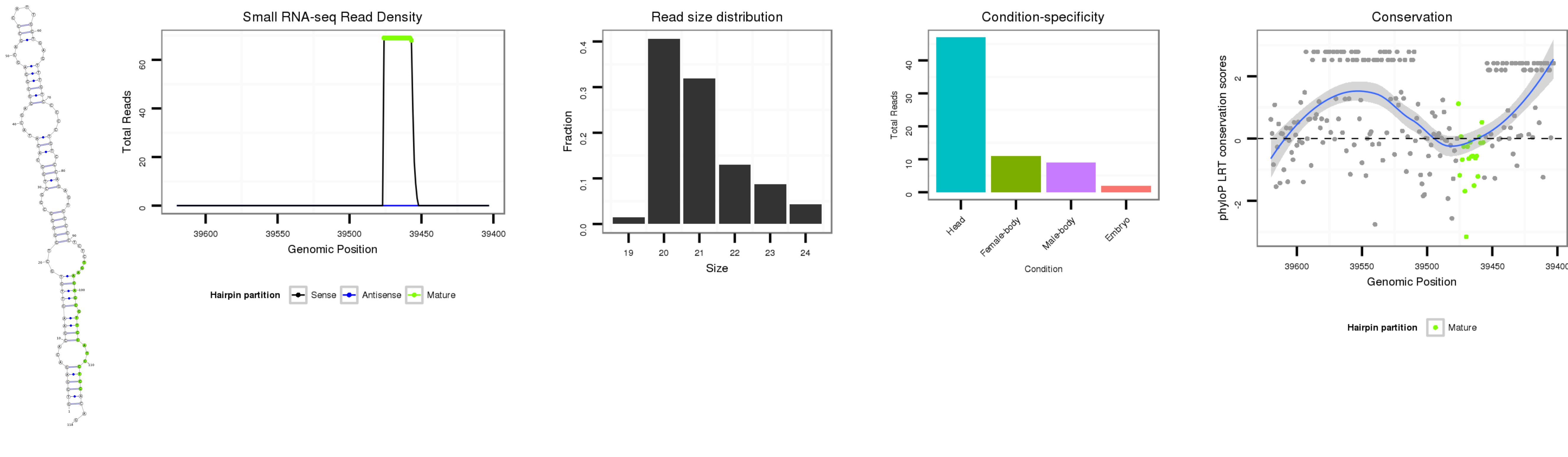
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crit.mor	0
crit.half	0
crit.total	1
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crit.top3	1
crit.tptop3	0
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	2

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

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Show Alternate Folds

Flybase annotation

intron [Dper¹GL16639-in]; CDS [Dper¹GL16639-cds]; CDS [Dper¹GL16639-cds]

No Repeatable elements found

Sense Strand Reads

[illegible]

Anti-sense strand reads

[illegible]

Re-alignment of all predicted orthologs

[illegible]

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

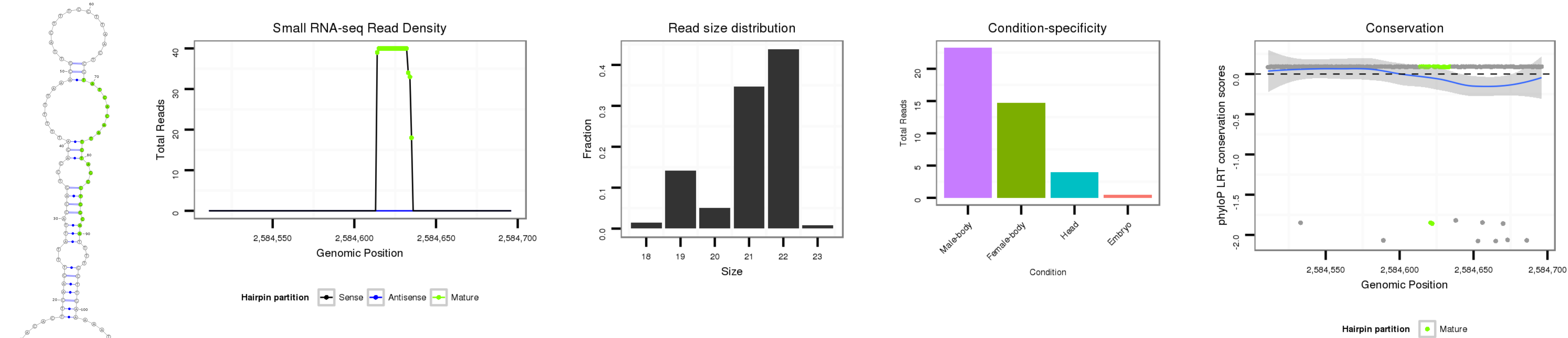
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crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	1
rescue.candidate	1

	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	0
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	2

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dpe_330	scaffold_10:2584561-2584646 +	candidate-rescued	Testes-restricted	intergenic	[View on UCSC Genome Browser (Cornell Mirror)]

Legend: ■ mature ■ star ■ mismatch ■ h in alignment ■ mismatch in read

Predicted structure



Show Alternate Folds

Flybase annotation

intergenic

No Repeatable elements found

mature	star
1. dpe_324 scaffold_10:2581754-2581775 + 2. dpe_331 scaffold_10:2583602-2583623 + 3. dpe_330 scaffold_10:2584614-2584635 + 4. dpe_2513 scaffold_8:5851007-1028 + 5. dpe_327 scaffold_7:193795-816 + 6. dpe_2512 scaffold_9:415170-191 + 7. dpe_2511 scaffold_9:415890-911 + 8. dpe_332 scaffold_7:821713-734 +	

Sense Strand Reads

hide 3p reads

show mid mismatch reads

GCAAGATATGAGTACTCCACAAATAATGATTAAATGAAAATTAAGCAAAACACTTCAAGTTTATTACCAGTCCAGATTTTTTAAACGTTACTTTCCTTAACTCGTATCACAATTCTAGCCTGGCAATTTTGCTTGAAAAATACCTCCTTTTAGAACATTTTGAGATAAGCGCACAAATTTTCAAGTGA	Read #																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																
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Anti-sense strand reads

CGTTCATATCATGAGGTGTTTATTACTAATTACTTTTAATTCGTTTGTGAAGTTCAAATAATGGTCAGGTCATAAAAAATTGCAATTGAAAGGAATTGAGCATAGTGTTTAAGATCGGACCGTTAAACGAACCTTTTATGGAGGAAAACTCTTGTAACACTCTATTCGCGTGTAAAAAGTTCACAT	Read #	Hit	Total		V057	M042
*****	size	Mismatch	Count	Norm	head	female
.....	22	2	10	0.10	1	0
.....	22	2	10	0.10	1	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droPer2	scaffold_10:2584511-2584696 +	dpe_330	GCAAGATATGAGTACTCCACAAATAATGATTAAATGAAAATTAAGCAAAACACTTCAAGTTTATTACCAGTCCAGATTTTTTAAACGTTACTTTCCTTAACTCGTATCACAATTCTAGCCTGGCAATTTTGCTTGAAAAATACCTCCTTTTAGAACATTTTGAGATAAGCGCACAAATTTTCAAGTGA
dp5	4_group4:3553695-3553880 +	dps_83	GCAAGATATGAGTACTCCACAAATGAATGATTAAATGAAAATTAAGCAAAACACTTCAAGTTTATTACCAGTCCAGATTTCTAAACGTTACTTTCCTTAACTCGTATCACAAGCTTAGCCTGGCAATTTAGCTTGAAAAATACCTCTTTTAGAAATTTCGATAAGCGCACAACTTCAAGTGA

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

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

Show Alternate Folds

No Repeatable elements :

Sense Strand Reads

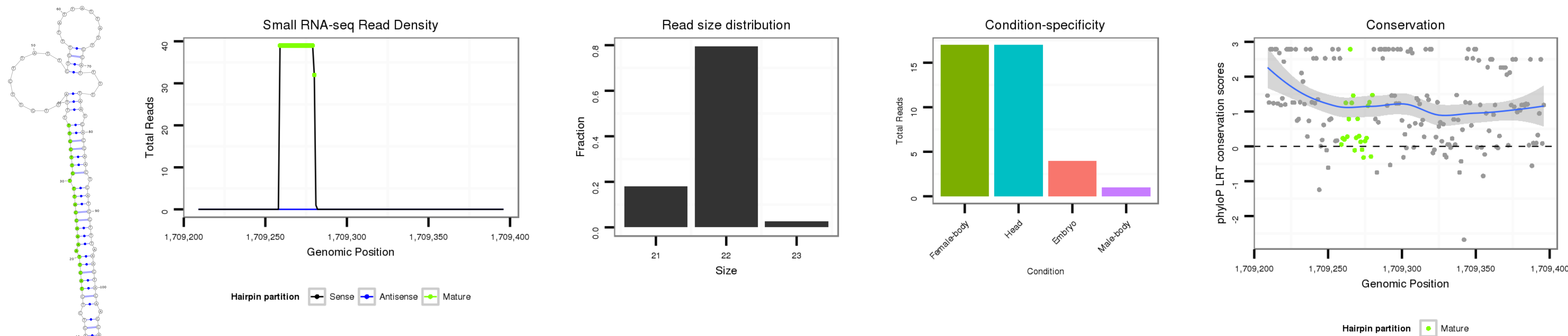
Re-alignment of all predicted orthologs

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crit.uri	1
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	1
rescue.candidate	1

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Show Alternate Folds

Flybase annotation

intergenic

No Repeatable elements found

Sense Strand Reads

[illegible]

Anti-sense strand reads

Show Alignment With Reads

Re-alignment of all predicted orthologs

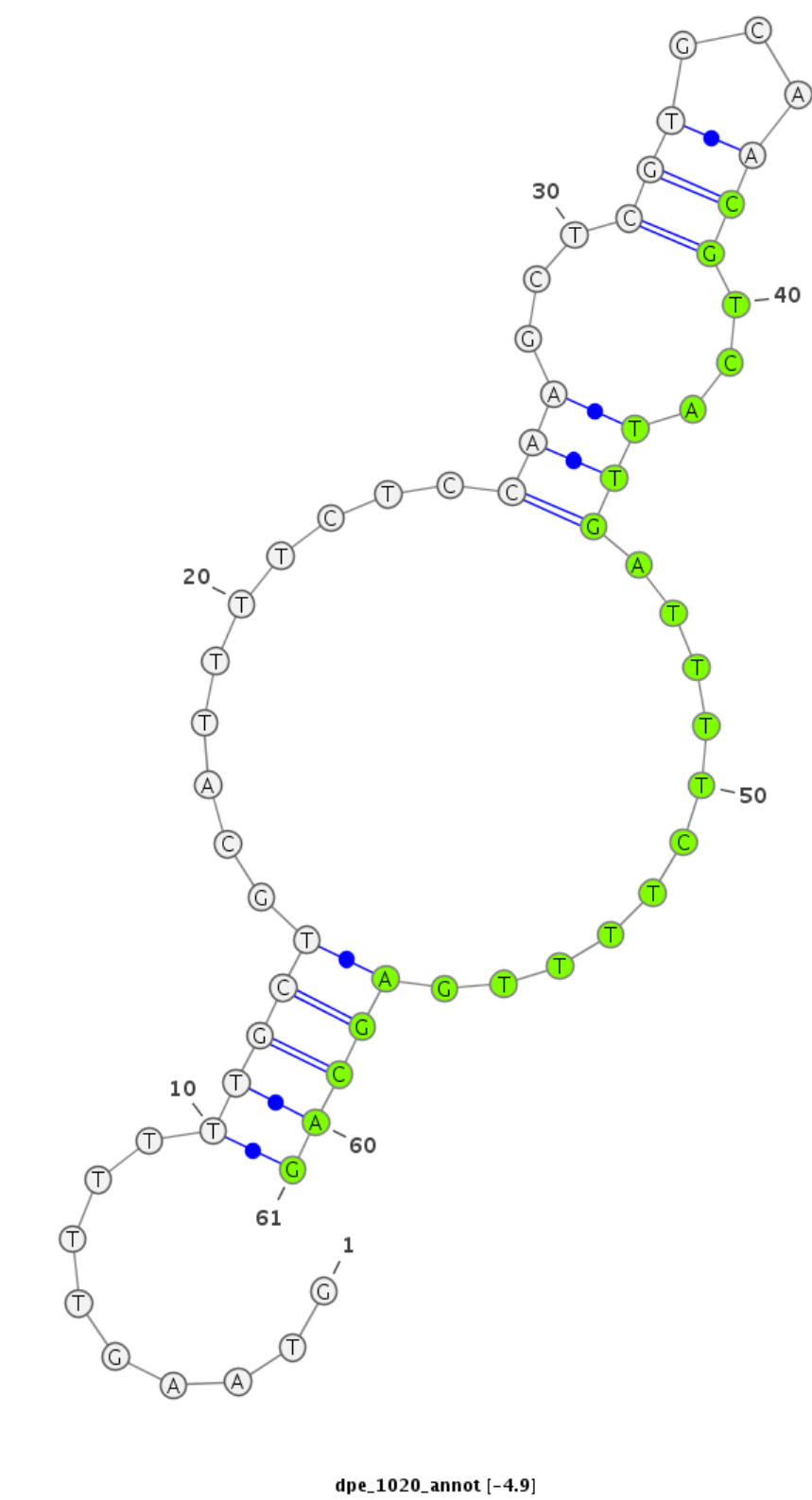
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crit.mor	0
crit.half	0
crit.total	1
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crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	2
rescue.candidate	1

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Show Alternate Folds

Flybase annotation

intron [Dper\GL11168-in]; CDS [Dper\GL11168-cds]; CDS [Dper\GL11168-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

[illegible]

Anti-sense strand reads

[illegible]

Show Alignment With Reads

Re-alignment of all predicted orthologs

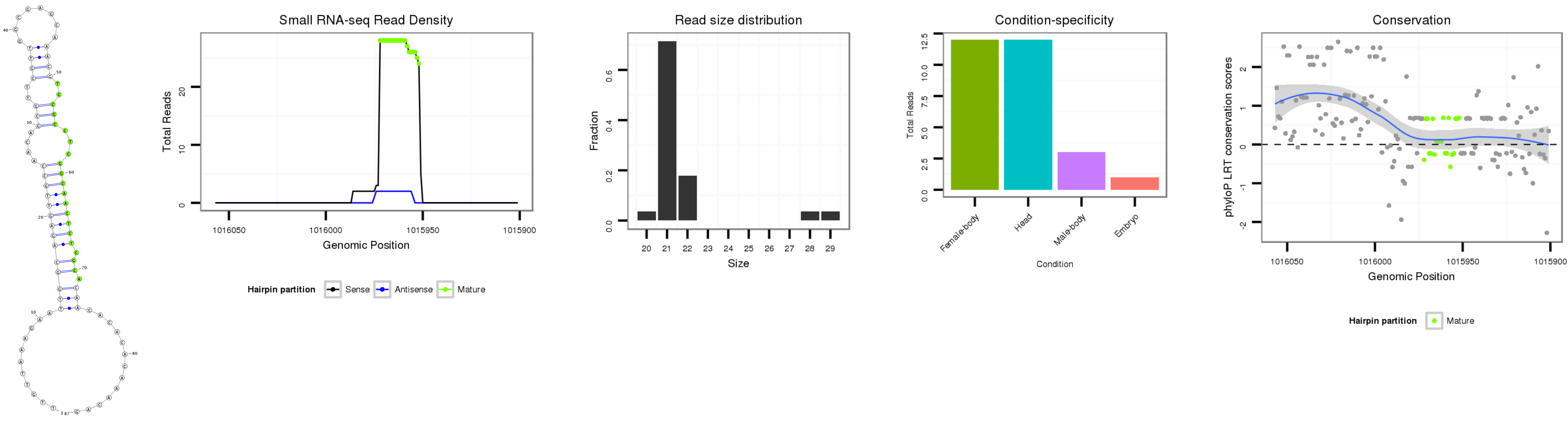
Species	Coordinate	ID	Alignment
droPer2	scaffold_2:1816101-1816261 +	dpe_1020	AGCCAGCGTC-----AACCAAGC---CATCATGCGACGCCGCCACCAGCAATGAGCGTAAGTTT---TTG-CT-GCATT---TCTCC-----AA-----GCTC-G---TG---CAA--CGTCAT-T---GAT-----T---TTCT--TTTG-----AGCAGCTGTGCTCGGAGGACTACGTTCTTCATGTGCATATGCCGAACAAAAGTTTC
dp5	3:1639101-1639261 +	dps_945	AGCCAGCGTC-----AACCAAGC---CATCATGCGACGCCGCCACCAGCAATGAGCGTAAGTTT---TTG-CT-GCATT---TCTCC-----AA-----GCTC-G---TG---CAA--CGTCAT-T---GAT-----T---TTCT--TTTG-----AGCAGCTGTGCTCGGAGGACTACGTTCTTCATGTGCATATGCCGAACAAAAGTTTC
droW112	scf2_11000000004514:1283679-1283849 -		GCCGAGGCTGCCGCCAACCAAGCCCAAGTAATGAGTTT-----GACGCTTCCCAATGAAATGAGAGATT---CATAT-GCATT---TTAT-------TTATTATTAT---CAA--TTGAT-T---AC-----TTT-C-TA--TGAT---TTCA--TCAAACTCGAGGACTATGTAATCATGATCATATGCCAACAAGATTTC
droVir3	scaffold_12875:11833059-11833208 +		AGCCAAAG---CAA---AGCGATCA-----GCCGATAGGAACAATGATGTAAGTACA---TATAT-GCAGCGC---AAAAG---CAAATN-G---GA---TAA--TAA--C---CCT---TTTGT--ATT---TTAGCCCAATTAAGATACGTTCTTCATGTACATGCCAACAAAGATTTC
droMo3	scaffold_6496:15028016-15028174 -		GCCGAGGCTGCCGCCAACCAAGCCCAAGTAATGAGTTT-----GACGCTTCCCAATGAAATGAGAGATT---CATATGCAAT---AATGAATGT---AACATATN-A---TA---TAA--CAAT-A--TAT---TTATT-TGTT---TTAGCCCACTTAAGATTAATGTTCTTCAATGATCATATGCCAACAAGATTTC
droGr12	scaffold_15245:11681558-11681718 +		AGCCAAAG---CAA---AGCAATCA-----GCCGATAGCAATGAGTGAAGTAA---TTT---GC---AT--CAATTT---GG---AACATTTTTTA--AT---TGT--TAA--T-A--ATTGAC---TAAATTTGAAAATCTTACCATCGAAGATTAATGTTCTCATGTGCATATGCCAACAAGATTTC
droAna3	scaffold_13266:1940695-1940860 +		A---AGC---AGTAAAC-----GCCGCCACCAGCATGACTGTAAGTAGGAGTTCTGGT-TT-G---CCTCTCAATTTTCAGATTTTCCCC-AA---A-A---AA---ACA--CCAC--GATT-CA-----TGATCT--CTTC---TCAGCGCTCTCGACGACGACGTCACTCATGTGCAATGCCAACAAAGCTTC
droBip1	scf7180000396730:2926943-2927108 +		A---AGC---AGTAAAC-----GCCGCCACCAGCATGACTGTAAGTAGGAGTTCTGGT-TT-GA---GCTGTCAATTTTCAGATTTTCCCC-GA---A-A---AA---AAA--CCCTTGATT-A---TGATCT--CTTC---TCAGCGCTCTCGACGACGACGTCACTCATGTGCAATGCCAACAAAGCTTC
droKik1	scf7180000302471:1581974-1582135 -		AGCCAGCGCT-----AGCCAAAGAGTGTAC-----GCCGCCACCCAAAATGAGCTGTAAGTACAGATGAGGAC-----TTTG-----GCTC-G---TCGATATCTCAAG---G---CTGCTT--CTTC---CCCATGTCTCGAGGACTATGTAATCACTGCTATATATGCCGAACAAAGCTTC
droFic1	scf7180000454039:613684-613831 -		AGCCAGCGCT-----AGTAAAC-----GCCGCCACTAAATGAGCTGTAAGTTT---GGG-TTCTT---CCAA--T---ATT---CTAGCTC-A---GA---AAA--CTAAT-A--AA---TGTCTT--CTTT---TTCACTATTCCCGAGGATACCTCATGCAATGTGCATATGCCGAACAAAGCTTC
droEle1	scf7180000491201:1770649-1770804 -		AGCCAGCGCT-----AGTAAAC-----GCCGCCACTAAATGAGCTGTAAGTTT---GGG-TTCTT---CCCGAT---GG---GCCATCCCTC-A---TA---AAA--CTGCAAG---TC---GTTT-TT---TTTC---TACCTACTCCCGAGGAGTACTCATGCAATGTGCATATGCCGAACAAAGCTTC
droRho1	scf7180000780066:321261-321413 -		AGCCAGCGCT-----AGTAAAC-----GCCGCCACTAAATGAGCTGTAAGTTT---GGG-TTCTT---CTTCGCTC---GG---ATCATCTTAC-A---CA---AATATACAA-A--AC---A--CT--CTTT---TTCACTACTCCCGAGGAGTACTCATGCAATGTGCATATGCCGAACAAAGCTTC
droBia1	scf7180000302143:2798240-2798388 -		AGCCAGCGCT-----AGTAAAC-----GCCGCCACTAAATGAGCTGTAAGTTT---CAG-TGTC---CTCC-----GATTGTTTC-G---TG---TAA--TGA--TC--AATGACAC---TTC-TATC---CTTACTATCTCCCGAGGAGTACTCATGCAATGTGCATATGCCGAACAAAGCTTC
droTak1	scf7180000415379:181556-181704 -		AGCCAGCGCT-----AGTAAAC-----GCCGCCACTAAATGAGCTGTAAGTTT---GAG-ATGSG---CCCTCTCC-----GATTGTTTC-A---CA---AAG--ATAA--T---CTCGA--T---TTC--TTTC---TCATATCTCCCGAGGAGTACTCATGCAATGTGCATATGCCGAACAAAGCTTC
droEug1	scf7180000409474:2632373-2632522 +		AGCCAGCGCT-----AGTAAAC-----GCCGCCACTAAATGAGCTGTAAGTTT---GGTCTTCT---ACTTC-----GATT---TCGSAC-A---CA---AAA--TAAAT-G--AA---TATATGT--CTTC---ACATATCTCTCGAGGAGTACTCATGCAATGTGCATATGCCGAACAAAGCTTC
dm3	chr2R:15323935-15324087 -		AGCCAGCGCT-----AGTAAAC-----GCCGCCACTAAATGAGCTGTAAGTTT---GCCATCTG---CCCGCATC-----CACCACATC-A---TA---AAA--TAAAT-G--AA---TCTATTT---CCCC---GCCATTAATCTCGAGGAGTACTCATGCAATGTGCATATGCCGAACAAAGCTTC
droSim2	2r:15975683-15975833 -		AGCCAGCGCT-----AGTAAAC-----GCCGCCACTAAATGAGCTGTAAGTTT---GCCATCTG---CCCGCATC-----CACCACATC-A---TA---AAA--TAAAT-G--AA---TCTATTT---CCCC---GCCATTAATCTCGAGGAGTACTCATGCAATGTGCATATGCCGAACAAAGCTTC
droSec2	scaffold_1:12839940-12840091 -		AGCCAGCGCT-----AGTAAAC-----GCCGCCACTAAATGAGCTGTAAGTTT---GGTCTTCT---CCCGCATC-----CACCACATC-A---TA---AAA--TAAAT-G--AA---TCTATTT---CCCC---GCCATTAATCTCGAGGAGTACTCATGCAATGTGCATATGCCGAACAAAGCTTC
droYak3	2R:13852461-13852609 +		AGCCAGCGCT-----AGTAAAC-----GCCGCCACTAAATGAGCTGTAAGTTT---ACA-CTTGC---CCAA--T---AG--CCCC---TC-A---TA---ACA--TAAATG--AATGCG--TAATTT---TCTC---GCCAGCACAATCTCGAGGAGTACTCATGCAATGTGCATATGCCGAACAAAGCTTC
droEre2	scaffold_4845:9522588-9522735 -		AGCCAGCGCT-----AGTAAAC-----GCCGCCACTAAATGAGCTGTAAGTTT---GCA-CTTGC---CCAA--T---AG--CCCC---TGCACCAATC---TA---AAA--TAAAT-A--TATCG--TAATTT---GCTC---GCCAGCACAATCTCGAGGAGTACTCATGCAATGTGCATATGCCGAACAAAGCTTC

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

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

	M042	V057	V050	M021	V111	V042
	female body	head	head	embryo	male body	embryo
GAAACTGGCCCAAGAATTTTCACCAAATGGAAGATTGTAAAGAATTGGCAGAGTGCACAACGCGTCTGTGGCGAGCAAACTCGGCCCTCGGCAACTCTCGCAACAACACACAACAAGAGCCACACTACTCGCTCGTTCGCTCACTCACTC	Read #					
***** ((((((((((.....((..(((.....))))))....)))))))).)..... *****	Mismatch	Hit Count	Total Norm	Total		
.....TCGCGCTCGGCAACTCTCGCA.....	21	0	19.00	19	10	4
.....TCGCGCTCGGCAACTCTCGCAC.....	22	0	5.00	5	1	0
.....TCGCGCTCGGCAACTCTCGCAC.....	23	1	3.00	3	0	1
.....TCGCGCTCGGCAACTCTCGCAC.....	22	1	1.00	1	0	1
.....CGTTCGCGCTCGGCAACTCTCG.....	21	0	1.00	1	0	1
.....TTGGCGAGCAAACTCGCGCTCGGCAACT.....	29	0	1.00	1	0	1
.....TTGGCGAGCAAACTCGCGCTCGGCAAC.....	28	0	1.00	1	0	1
.....TCGCGCTCGGCAACTCTCGC.....	20	0	1.00	1	1	0
.....TCGCGCTCGGCAACTCTCGTT.....	21	2	1.00	1	1	0

Anti-sense strand reads

[illegible]

Show Alignment With Reads

Re-alignment of all predicted orthologs

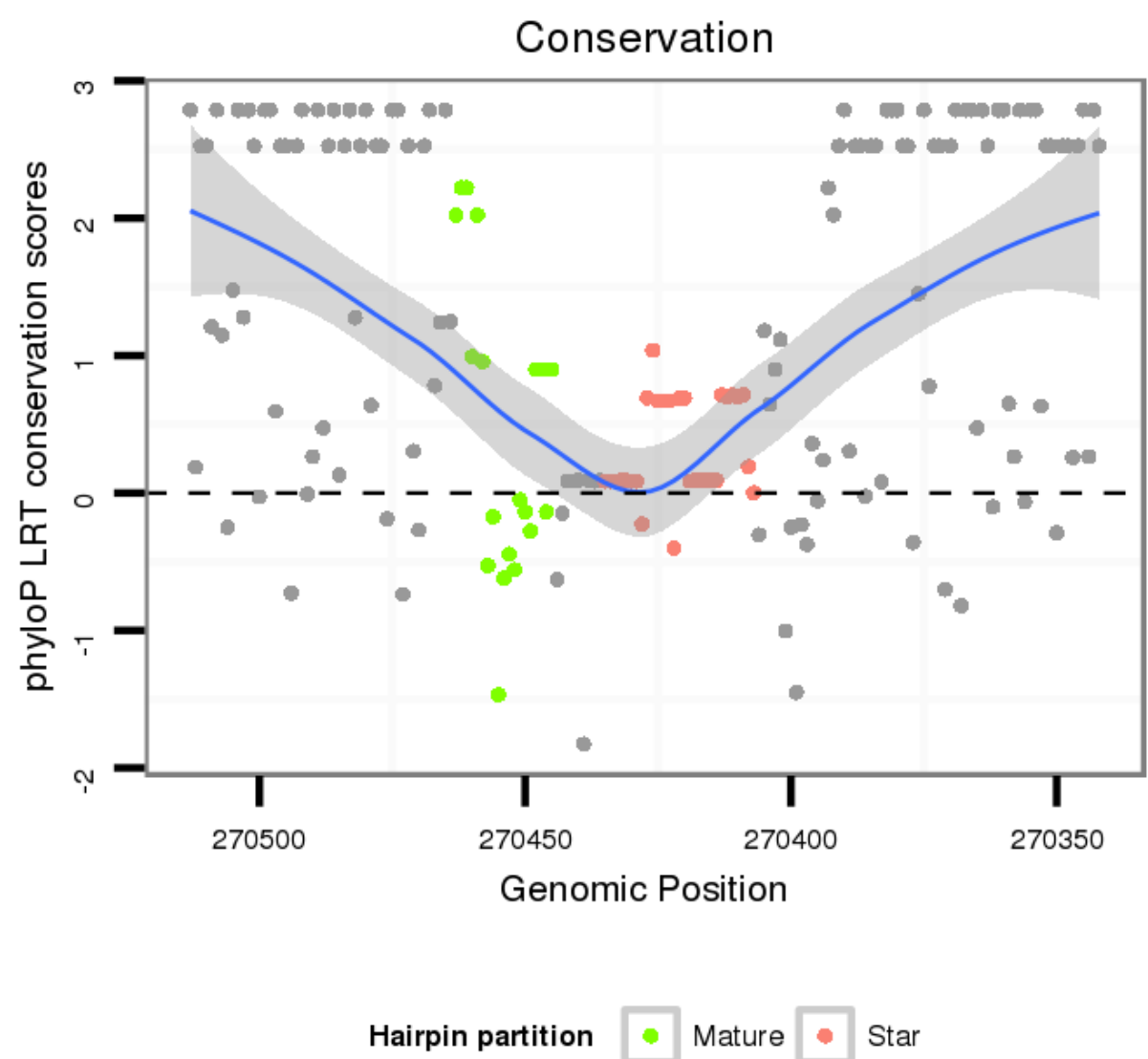
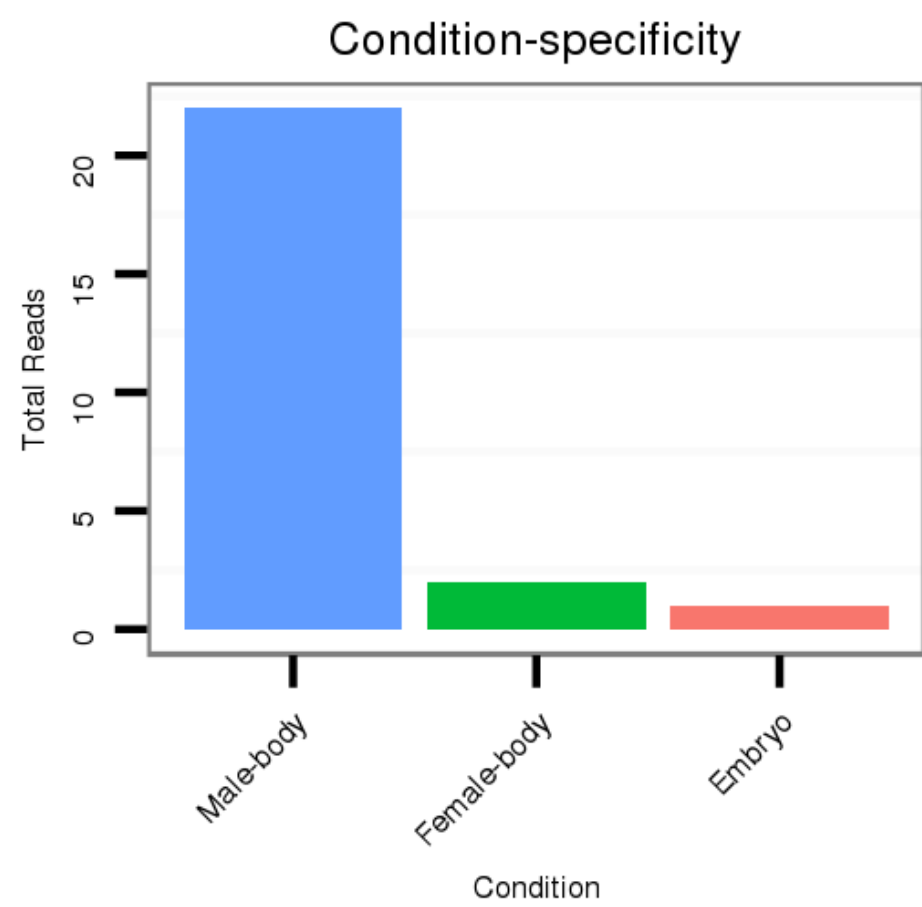
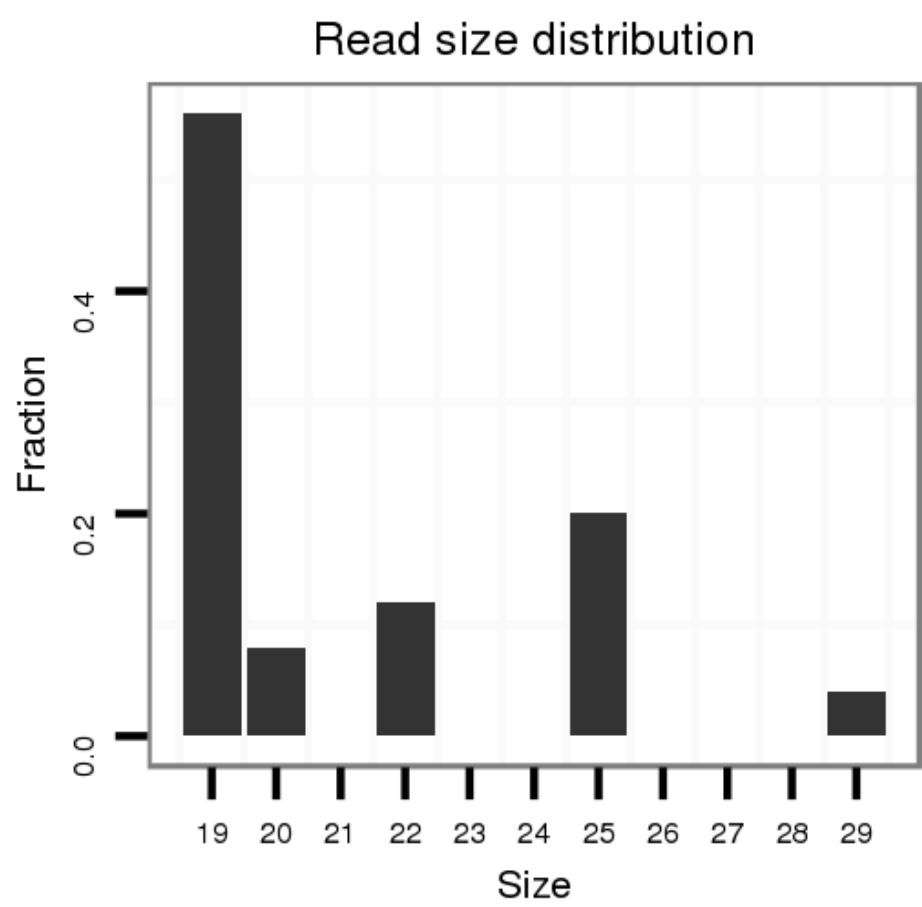
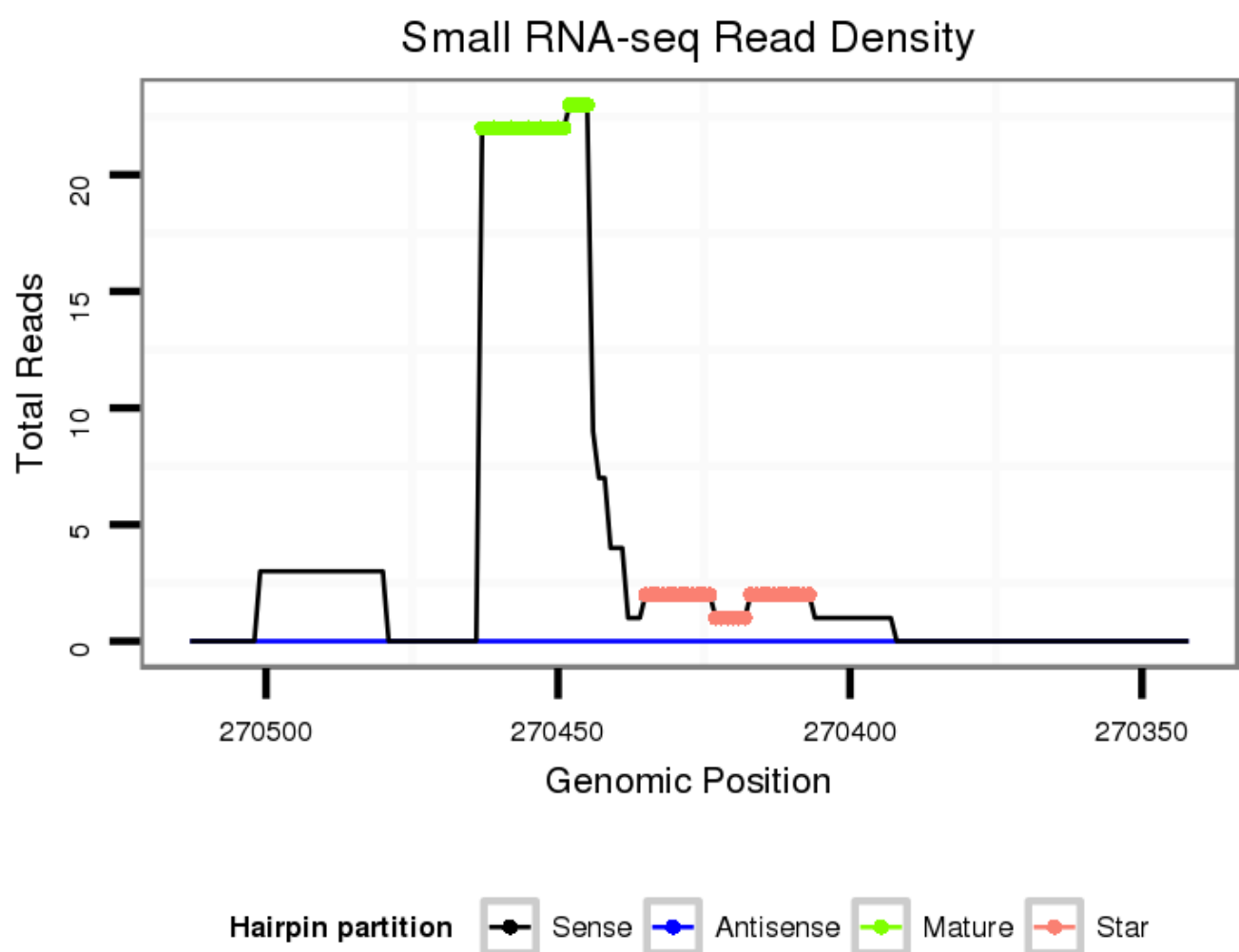
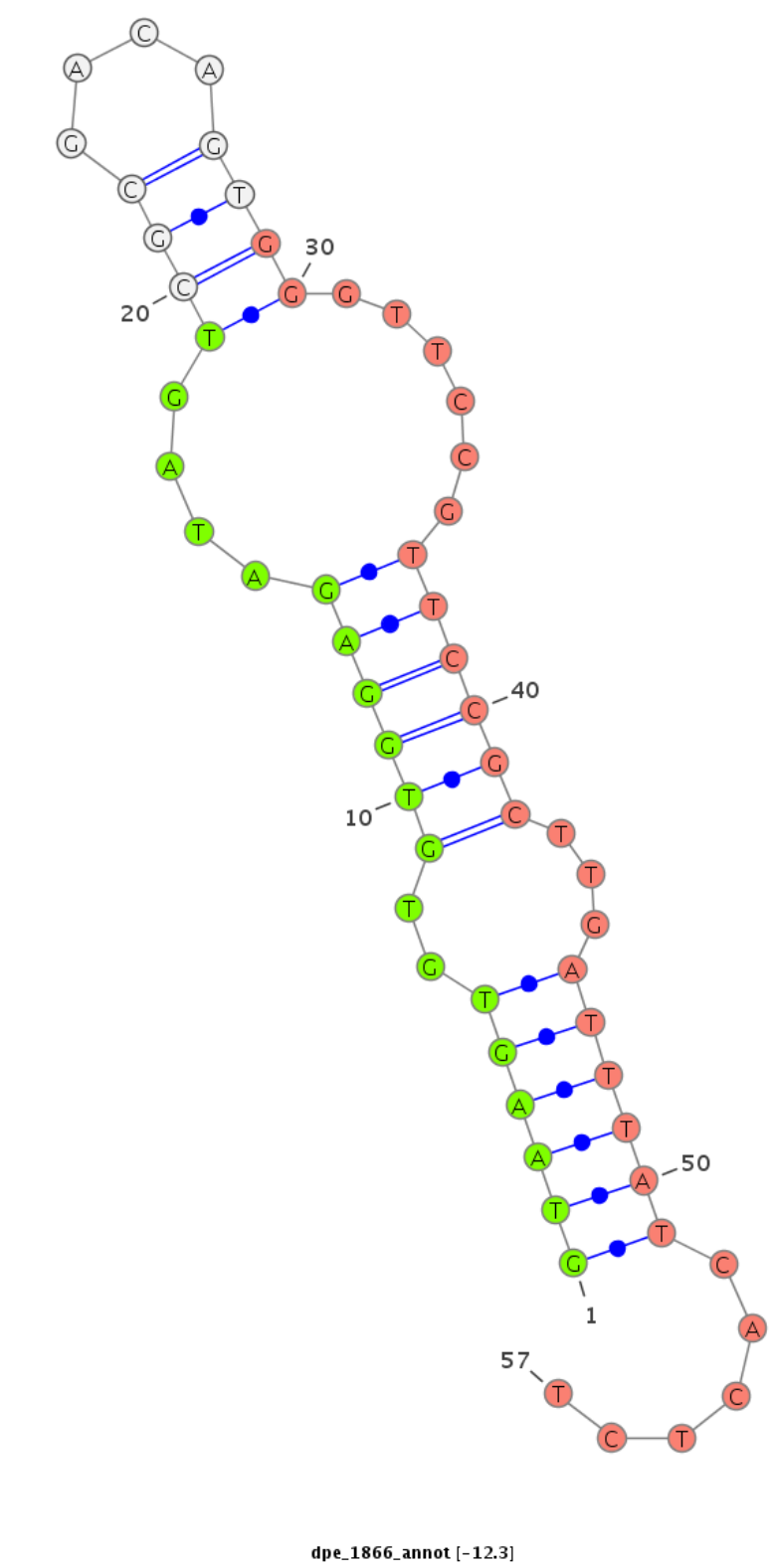
[illegible]

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	PASS/FAIL
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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	1
rescue.dominant	0
rescue.known	1
rescue.confident	1
rescue.candidate	1

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Show Alternate Folds

Flybase annotation

intron [Dper\GL12297-in]; CDS [Dper\GL12297-cds]; CDS [Dper\GL12297-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

[illegible]

Anti-sense strand reads

TAGGGTGGATGAGCAAGGCTCTTGACCAGCTCGTCCGATAAGACGTTACAC CATTACACACCTCTATCA GCCTGTGCA CCCAAGGCAAGCGCACTAAATAGTGAGA AATAGTGAGAAATGTCCTCCACGAAACGGTAAACGGCACTTCAGGTTTGTAAGGGSCCTCTCAC										Read #	Hit	Total		M042	
*****((((((.....(((.....)))).....)))).....*****										size	Mismatch	Count	Norm	Total	female body

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
dpePer2	scaffold_6:270342-270513 -	dpe_1866	ATCCCACTACTCGTTCCGAGAAGCTGGTCGAGCAGGCTATTCTGCAAGTG STAAGTGTGTGGA -----GATAGTGGCGACAGT SGGTTCGGTTCGCGTTGATTATCACTCT TTA-----TCACTCTTACAGGAAGTGCCTTTGCCATTGCCGTGAAGTCCAAACACTTCCCCGGAGAGTG
dp5	2:242971653-24971824 -	dps_776	ATCCCACTACTCGTTCCCG GA CTGGTCGAGCAGGCTATTCTGCAAGTG STAAGTGTGTGGA -----GATAGTGGCGAG AGTGGTTCGGTTCGCGTTGATTATCACTCT TTA-----TCACTCTTACAGGAAGTGCCTTTGCCATTGCCGTGAAGTCCAAACACTTCCCCGGAGAGTG
drow112	scf2_1100000004943:13604433-13604603 +		ATCC CA ATACTACTCGTTCCCG GA ACT CT GTGAGCAGGC CA ATTCTCAAGTG STAAGTGCAT TT -----ACTG CA -----TAGGCGGTATCAGGCTACTA AGCACTTA -----ATTCCG ATT -----GCTG AT -----TATTACAGGAAGG SC ATTTGCCATTGCCGTAAAGTCCAA CTA ATTCCCCGG AGATG
drowir3	scaffold_13047:13614705-13614885 +	dvi_16838	ATCCCA CA TA CT ACTCGTTCCCG GA CTGGT CT GAGCAGGC CA ATTCTCAAGTG STAAGAACCC TTGAT GTG AAAACCAAGGT CT CATTAT G -----AGCA CTTGATTATGT GGCTATTATCG -----TG T -----T CTCGT TTAAAGGA G GGT G ATTGG CA ATTGG CT AAAT CT CAAC CA ATTCC AG CG S AGTG
drowoj3	scaffold_6540:10860849-10861032 +		ATCCCA CA TA CT ACTCGTTCCCG GA CT CT GT CT GAGCAGGC CA ATTCTCAAGTG STAAGTCA CCCTCAG GTG AAAACCGAAT CT CATTAT G -----GTTATAGA ACTCTCATGATGTGT ----- T -----TCAC TG T -----T CTGTCT ACAGGAAGG SC ATTTGCCATTGG CA ATT CT AAAT CT CAAC CA ATTCC AG CG S AGTG
drowri2	scaffold_15074:401940-402113 -		ATCCCA CA TA CT ACTCGTTCCCG GA ACTGGT CT GAGCAGGC CA ATTCTCAAGTG STAAGTAA TC -----AAACCTAA ACTTATTAA GGACA AACT -----CTTATGATG CTATGAC TTT T GA -----T-----G TTTG AGGA G GG SC ATTTGCCATTGG CT AAAGT CT CAAC CA ATTCCCCGG CG SAGTG
drowana3	scaffold_12911:1983818-1983981 +		A CTCCACTACTCGTT CCG GA CT GGT CT GAGCA CA CTAT CA CA CT GT GA TAAGTTGCCGA T GCT AGAATTAA AG TC A -----CCACATTACACATAT TC AAAA AT ----- CA T TC AGGAAGGT G CTTT GG AG CT AAAT CT CAAC CA ATT CT CG CG SAGTG
drowip1	scf7180000396714:1067973-1068136 -		A CTCCACTACT CT CTT CCG GA CT GGT CT GAGCAGGCTAT CA CA CT GT GA TAAGTTCACCTA CT T GAG AGCA TTGAAGT TA A -----ACACAT GA ACTTAT TC CA AAAC ----- GT AC CG AGGAAGG SC ATT TTG CA CT CT AAAT CT CAAC CA ATT CT CG CG SAGAGTG
drowik1	scf7180000302297:46177-46331 -		A CTCCCA CA TA CT ACTCGTTCCCG GA CTGGT CT GAGCAGGCTATTCTGCAAGTG STAAGTCTGCC ATGGA CTG T -----G ATA CA ACTTAA AT TC -----GGCC TT -----T CT CTACAGGAAGG SC ATT TTG CCATTGCCGTGAAGT CT AA G CA CTT CCCCGGAGAGTG
drowic1	scf7180000454068:15701-15862 -		A CTCCCA CA TA CT ACTCGTTCCCG GA CTGGT CT GAGCAGGCTAT CA CT CT CAAGTG STATGT TGTCCA C GGTATCAGCC CT CGAC CA A -----CCAACTAA ATT TG CA AA CC CT ----- CT GT CT AGGAAGG SC ATT TTG CA CT CT AAAT CT CAAC CA S CA CT TT CCCGGAG ATG
drowel1	scf7180000491278:33183-33345 +		A CTCCCA CA TA CT ACT CA TTCCCG GA CTGGT CT GAGCAGGCTAT CA CT CT CAAGTG STAAGTGT TT T TGCTCTAG CTAA -----GGAGCA ACTCT CAG TC AGTG A -----CCAC CT GA AA -----T CT AGGAAGG SC CTTTG CA ATTGG CT GAAGTCC AA S CA CT TT CCCGGAG ATG
drowho1	scf7180000775729:3799-3959 +		A CTCCCA CA TA CT ACTCGTTCCCG GA CTGGT CT GAGCAGGCTAT CA CT CT CAAGTG STAAGTGT CTCT -----GGGCGAG CTAT ATAG TC A -----CCAC CT AA AT AT GA -----ATA AT CT GT CT AGGAAGG SC CTTTGCCATT TC GTGAAGTCC AA S CA CT TT CCCGGAG ATG
drowia1	scf7180000301256:49076-49175 +		ATCCCA CA TA CT ACTCGTT CCG GA ACTGGT CT GAGCAGGCTATTCTCAAGTG----- CA AGG SC CTTTGCCATTGCCGTGAAGTCC AA S CA TT CT CCCGGAG ATG
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drowug1	scf7180000409540:3761-3860 +		A CTCCCA CA TA CT ACT CT CCCG GA CT GGT CT GAGCAGGCTAT CT CA CT CA CT CT ----- CA AGG SC CTTTGCCATTGG CT GAAGTCC AA S CA TT CT CCCGGAG ATG
dm3	chr38Het:2477494-2477593 +		A CTCCCACTACT CT CTCCCG GA CTGGT CT GAGCAG CA CTAT CT CAAGTG----- CA AGG SC CTTTGCCATTGCCGTGAAGTCC AA ACT TT CCCGGAG ATG
drowim2	21:22493057-22493156 -		A CTCCCACTACTCGTTCCCG GA CTGGT CT GAGCAG CA CTAT CT CAAGTG----- CA AGG SC CTTTGCCATTGCCGTGAAGTCC AA ACT TT CCCGGAG ATG
drowec2	scaffold_6:105530-105629 +		A CTCCCACTACTCGTTCCCG GA CTGGT CT GAGCAG CA CTAT CT CAAGTG----- CA AGG SC CTTTGCCATTGCCGTGAAGTCC AA ACT TT CCCGGAG ATG
drowak3	3R:327480-327579 +		ATCCCACTACTCGTTCCCG GA CTGGT CT GAGCAG CA CTAT CT CAAGTG----- CA AGG SC CTTTGCCATTGCCGTGAAGTCC AA S CA CT TT CCCGGAG ATG
drower2	scaffold_4770:334345-334444 +		A CTCCCACTACTCGTTCCCG GA CTGGT CT GAGCAG CA CTAT CT CAAGTG----- CA AGG SC CTTTGCCATTGCCGTGAAGTCC AA S CA CT TT CCCGGAG ATG

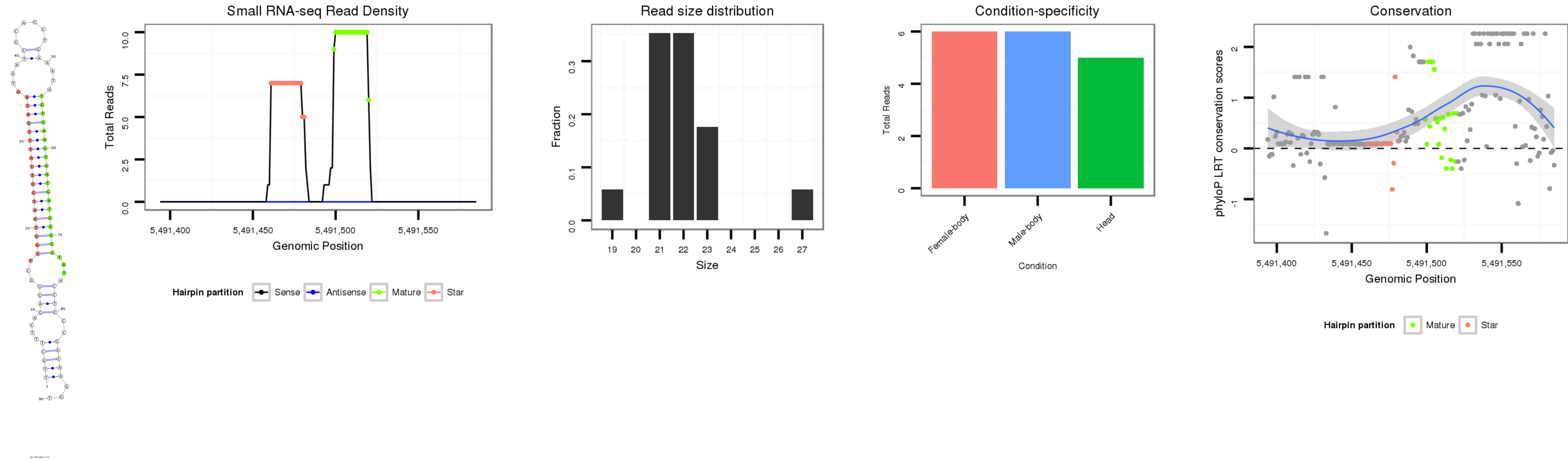
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	PASS/FAIL
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crit.mor	0
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crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident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

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dpe_2495	scaffold_1:5491444-5491535 +	Known Ortholog	Canonical miRNA	intergenic	[View on UCSC Genome Browser {Cornell Mirror}]

Legend: ■ **nature** ■ **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

Read #	size	Mismatch	Hit	Total	Count	Norm	Total	V111	male	M042	female	V057	V050
22	0	1	4.00	4	3	1	0	0	0	0	0	0	0
21	0	1	3.00	3	1	0	1	1	1	1	1	1	1
25	1	1	2.00	2	2	0	0	0	0	0	0	0	0
21	0	1	2.00	2	0	1	1	0	0	0	0	0	0
23	0	1	1.00	1	0	1	0	0	0	0	0	0	0
23	0	1	1.00	1	0	1	0	0	0	0	0	0	0
23	0	1	1.00	1	0	0	1	0	0	0	0	0	0
27	0	1	1.00	1	1	0	0	0	0	0	0	0	0
19	0	1	1.00	1	0	1	0	0	0	0	0	0	0
22	0	1	1.00	1	0	0	1	0	0	0	0	0	0
21	0	1	1.00	1	0	1	0	0	0	0	0	0	0
22	0	1	1.00	1	1	0	0	0	0	0	0	0	0

Anti-sense strand reads

Read #	size	Mismatch	Hit	Total	Count	Norm	Total	M042	female	V057
22	0	1	1.00	1	1	0	0	0	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droPer2	scaffold_1:5491394-5491585 +	dpe_2495	AA-AAGTTTCAGTTGTCCAATAAAAAACAATCTTTGGATGAACCAGCAATACATTGCTTTCAGAGGGCTCGCTCATCGTTATTGATAGTAATCGCACCTGAAATATGTCGAAGTAATGATGGGCGTATACC--TCCCGGCAAGGTCAAACCTCAATAACATTGTGAAATAAACCGATTTCCTTCTGTAAATTAAGA
dp5	4_group3:4018551-4018742 +	dps-mir-2560	AA-AAGTTTCAGTTGTCCAATAAAAAACAATCTTTGGATGAACCAGCAATACATTGCTTTCAGAGGGCTCGCTCATCGTTATTGATAGTAATCGCACCTGAAATATGTCGAAGTAATGATGGGCGTATACC--TCCCGGCAAGGTCAAACCTCAATAACATTGTGAAATAAACCGATTTCCTTCTGTAAATTAAGA
droWil2	scf71800004521:2360386-2360506 -		ATTTCA---TAA-TAATCAATGCAAA-TCATATTT---TTTTCGGATTAAC-----ATGGTTTTCATTTTTCCTTAAGGTCAAACCTCAATAACATTGTGAAATATTAACAATT---AATTTCGCGCGATTGGCT
droAna3	scaffold_12916:6082150-6082205 +		ATTCAGTAATGATGGGCGTATACC--TCCCGGCAAGGTCAAACCTCAATAACATTGTGAAATAAACCGATTTCCTTCTGTAAATTAAGA
droBipl	scf7180000396568:758124-758187 -		ATTCAGTAATGATGGGCGTATACC--TCCCGGCAAGGTCAAACCTCAATAACATTGTGAAATAAACCGATTTCCTTCTGTAAATTAAGA
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droPic1	scf7180000453924:287081-287166 -		ATTCAGTAATGATGGGCGTATACC--TCCCGGCAAGGTCAAACCTCAATAACATTGTGAAATAAACCGATTTCCTTCTGTAAATTAAGA
droEie1	scf7180000491273:865547-865632 +		ATTCAGTAATGATGGGCGTATACC--TCCCGGCAAGGTCAAACCTCAATAACATTGTGAAATAAACCGATTTCCTTCTGTAAATTAAGA
droRho1	scf7180000779970:32987-33118 -		ATTCAGTAATGATGGGCGTATACC--TCCCGGCAAGGTCAAACCTCAATAACATTGTGAAATAAACCGATTTCCTTCTGTAAATTAAGA
droBial	scf7180000302261:149631-149716 -		ATTCAGTAATGATGGGCGTATACC--TCCCGGCAAGGTCAAACCTCAATAACATTGTGAAATAAACCGATTTCCTTCTGTAAATTAAGA
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droBak3	21:2264903-2264988 -		ATTCAGTAATGATGGGCGTATACC--TCCCGGCAAGGTCAAACCTCAATAACATTGTGAAATAAACCGATTTCCTTCTGTAAATTAAGA
droBak3	21:2264903-2264988 -		ATTCAGTAATGATGGGCGTATACC--TCCCGGCAAGGTCAAACCTCAATAACATTGTGAAATAAACCGATTTCCTTCTGTAAATTAAGA
droBre2	scaffold_4929:2413348-2413478 -		ATTCAGTAATGATGGGCGTATACC--TCCCGGCAAGGTCAAACCTCAATAACATTGTGAAATAAACCGATTTCCTTCTGTAAATTAAGA

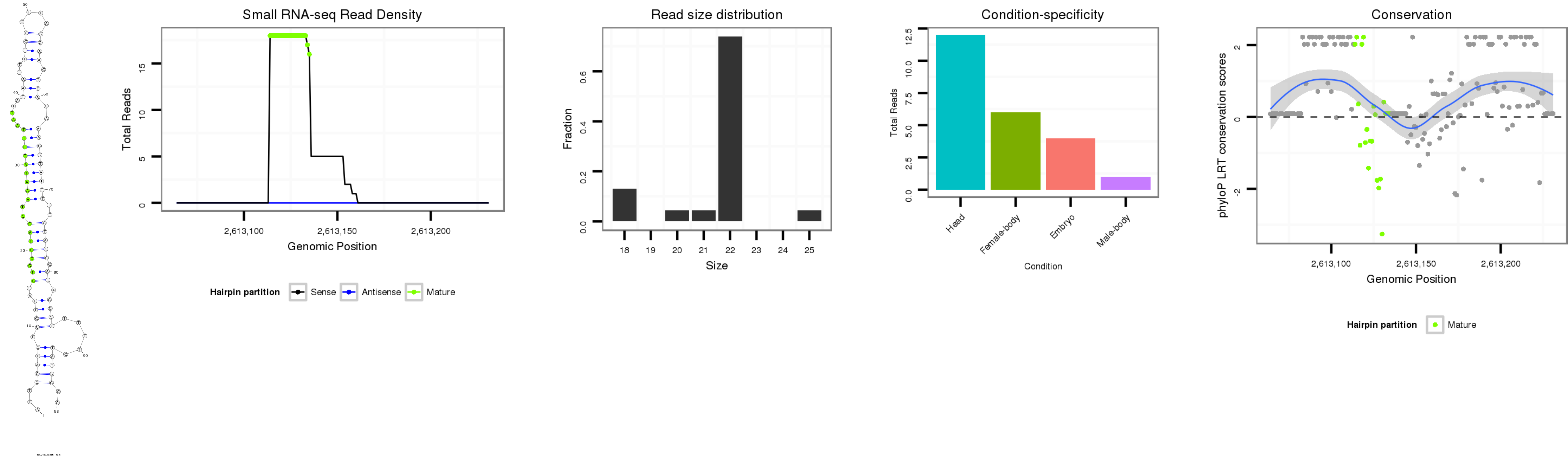
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PASS/FAIL	
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crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.ltop3	1
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	1
rescue.confident	0
rescue.candidate	1

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dpe_2487	scaffold_5:2613114-2613181 +	confident-exception	Mirtron	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

	Read #		Hit	Total		V057	M042	V050	M021	V042	V111
	size	Mismatch	Count	Norm	Total	head	female body	head	embryo	embryo	male body
CTTTTGTAGATTTTTCATATGTGAAAGTCAACGCAATTCCATGTGGTTAGGTGGGTACCTAAATATCTTAATTATAATTTTCCGTTAGGAACCTACAAAGGTATTTTGTACCGACAGGCCTTTTCTATGGCGCTAAAAGCATAATCTGGTGTTGGCATACATCTA	22	0	1	16.00	16	6	5	3	0	1	1
*****(((.(((.(.(((.(.((((((.....((.(.(((.....)))..))..))))))..))))..))))..))))..*****	18	0	1	3.00	3	0	0	0	3	0	0
.....GTGGGTACCTAAATATCTTAAT.....	21	0	1	1.00	1	0	0	1	0	0	0
.....TATAATTTTCCGTTAGGAACCTT.....	22	0	1	1.00	1	1	0	0	0	0	0
.....GTGGGTACCTAAATATCTTA.....	20	0	1	1.00	1	0	1	0	0	0	0
.....TATAATTTTCCGTTAGGAACCTTACA.....	25	0	1	1.00	1	0	0	1	0	0	0

Anti-sense strand reads

GAAAACATCTAAAAAGTATACACTTTCAGTTGCGTTAAGGTACACCAATCCACCCATGGATTATAGAATTATATATAAAGGCAATCCTTGAATGTTCCATAAAAACATGGCTGTCCGGAAAAGATACCGCGATTTTCGTATTAAAGACCACAAACCGTATGTAGAT	Read #		Hit	Total	
*****(((.(((.(.(((.(.((((((.....((.(.(((.....)))..))..))))))..))))..))))..))))..*****	size	Mismatch	Count	Norm	Total
No data available in table					
Show Alignment With Reads					

Re-alignment of all predicted orthologs

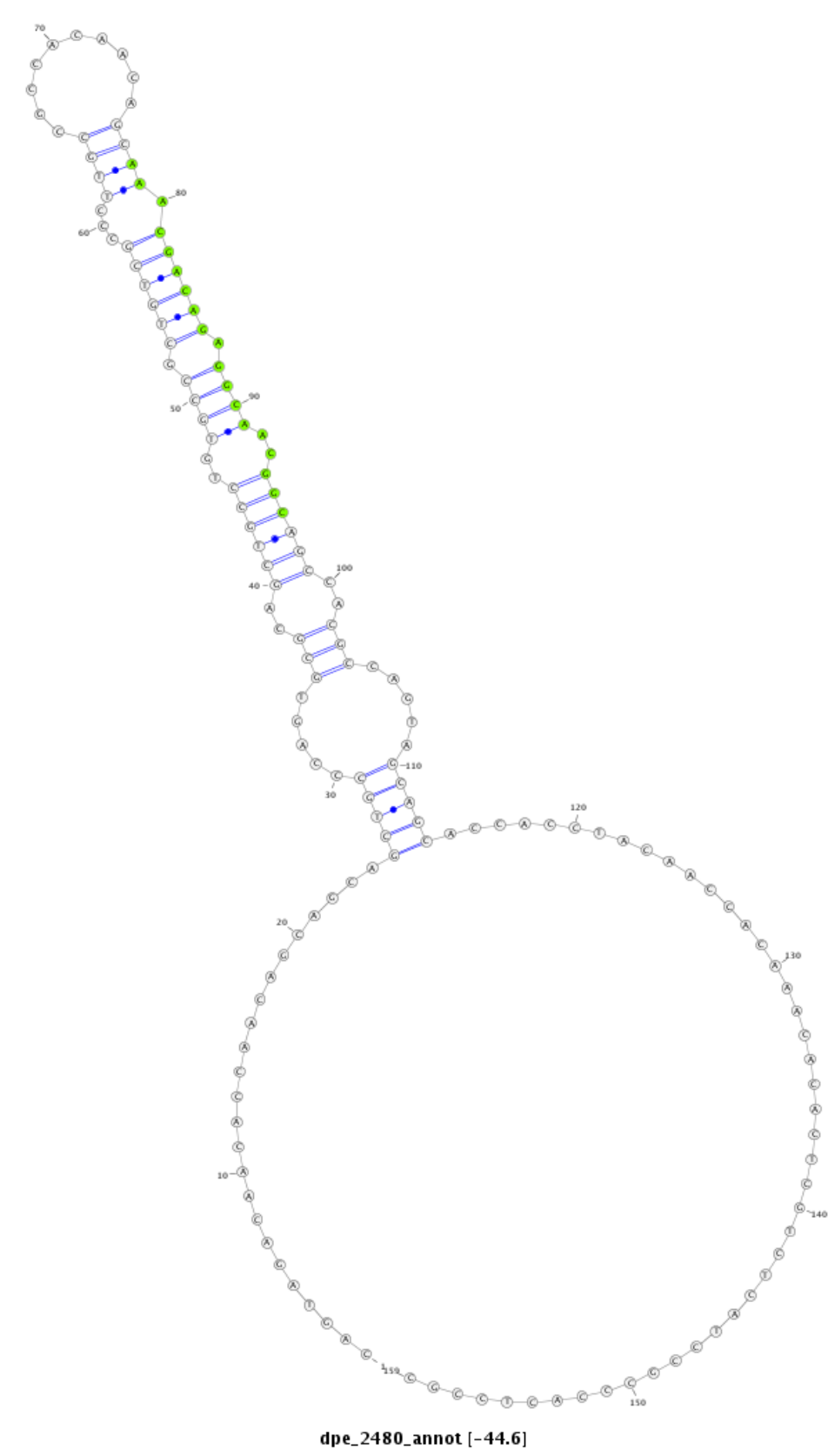
Species	Coordinate	ID	Alignment
droPer2	scaffold_5:2613064-2613231 +	dpe_2487	CTTTTGTAGATTTTTCATATGTGAAAGTCAACGCAATTCCATGTGGTTAGGTGGGTACCTAAATATCTTAATTATAATTTTCCG---TTAGGAAC-----TAC-----AAAGG---T-----ATTTTG-----TACCGACAGGCCTTTTCTATGGCGCTAAAAGCATAATCTGGTGTTGGCATACATCTA
dp5	4_group1:2592719-2592886 -	dps_239	CTTTTGTAGATTTTTCATATGTGAAAGTCAACGCATTCCATGTGGTTAGGTGGGTACCTAAATATCTTAATTATAATTTTCCG---TTAGGAAC-----TAC-----AAAGG---T-----ATTTTG-----TACCGACAGGCCTTTTCTATGGCGCTAAAAGCATAATCTGGTGTTGGCTACATCTA
droVir3	scaffold_12963:4588919-4589061 -		-----TGCGAAAGTCAACGCAATTCCATGTGGTTAGGTATGTGCCAGCA-----ACA---TTTATATC---TTTGTATATAC---ATT---GATTAT-----T---TTTTATTTTT---TGA---TTTTCGAGGACTTGCTATGGCGTTAAAGGCTCTATCTTATTCCGG-----
droMoJ3	scaffold_6500:8495816-8495947 -		-----TGCGAAAGTCAACGCAATTCTATGTGGTTAGGTAAATGTCGAATATCT-----ATT---CAAAATT---CG-TTTTAATTAATCG-----TCCACT-----T-----ACCTTTTCAGGACTTGCTATGGCGTTAAAGGCTCTATATGGTAATTGG-----
droBiP1	scf7180000396554:1423059-1423191 +		-----TGTGAAAGTCAACGCAATCCATGTGGTTGSGTGGGTACCTCAACATA-----TCN---TAGTTAGT-CCTTTGAC---TAAATAG-----TAAATC-----TGTGTTTCAGGCTTGCTACGGCTTCAAAGGCTTAATCTGGTAATTGGC-----
droKiK1	scf7180000302235:132564-132702 -		-----TGTGAAAGTCAACGCAATCATGTGGTTGSGTACGTACCTATTCAAT-----TSTTATTAGAAAT-----TCCTTTATATAAAGT-----ATC---TGGACTTTTTTTCAGGCTTGCTATATGGCTTCAAGGCTCATCTGGTGTTTGG-----
droPiC1	scf7180000453316:79293-79433 +		-----TGTGAAAGTCAACGCAATCCATGTGGTTGSGTATGTTTTAATCTGT-----TCN---TTAGGAAT---TTA---TG-TTACTATTAATTA-----T---ATGAA---TT-----ATCCCTTCAGGCTTGCTATGGCTTCAAGGCTCAATCTGGTGTTTGGTCA-----
droE1e1	scf7180000491046:1482269-1482404 +		-----TGTGAAAGTCAACGCAATCCATGTGGTTGSGTATGTACCAAAAGCGCT-----CCN---TTTCGAAC---AA---AA---CTCTACTAT-----TAAATTCAGGCTTGCTATGGCTTCAAGGCTCAATCTGGTGTTTGGC-----
droB1a1	scf7180000302261:1570770-1570902 -		-----TGTGAAAGTCAACGCAATCCATGTGGTTGSGTAAAGCTTACATATAA-----TCN---TTAGGAGC---CG---AACTAATAG-----TAAATATTAC-----TTG---TSTTTTCAGGCTCGCTACGGCTTCAAGGCTCATCTGGTGTTGGC-----
droTak1	scf7180000412373:124394-124532 +		-----TGTGAAAGTCAACGCAATCCATGTGGTTGSGTATGCATATAACATA-----ACN---GTACCAAT-TTTTGTAT-TA---ATATTAT-----T---AATTTAATATT-----TAATTACAGGCTCGTTATGGCTTCAAGGCTCAATCTGGTGTTTGGC-----
droEug1	scf7180000409452:1590826-1590965 +		-----TGTGAAAGTCAACGCAATCATGTGGTTAGGTATGCTAAAACTAAT-----TCN---TAAATATC-TTTCGGAA-CTC---TTATAAT-----T---ACTTAAATTTA-----TCATCAATAGGCTTGCTATGGCTTCAAGGCTCAATCTGGTGTTTGGC-----
droSim2	21:14581968-14582099 +		-----TGTGAAAGTCAACGCAATCCATGTGGTTGSGTATGTGTGATTCGAAT-----ACA---TTAGGATC---ATTTAAT---AA---TA---ATATTATATAT-----A---STTTTCAGGCTTGCTACGGCTTCAAGGCTCAATCTGGTGTTTGGC-----
droSec2	scaffold_3:1292333-1292464 +		-----TGTGAAAGTCAACGCAATCCATGTGGTTGSGTATGTGTGATTCGGT-----ACA---TTAGGAACA-----TAC-----ATATAAT---ATATTAAATAT-----TACTTTCAGGCTTGCTATGGCTTCAAGGCTCAATCTGGTGTTTGGC-----
droYak3	21:15139031-15139157 +		-----TGTGAAAGTCAACGCAATCCATGTGGTTGSGTATGTGAATAATGC-----ACA---TTATCAC-----T---ATATAAT---ATTTATATAT-----T---ATTTTTTCAGGCTTGCTATATGGCTTCAAGGCTCAATCTGGTGTTTGG-----

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	PASS/FAIL
crit.star	0
crit.loop	1
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.ptop3	0
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	0
rescue.known	0
rescue.confident	0
rescue.candidate	2

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Show Alternate Folds

Flybase annotation

CDS [Dper\GL16840-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

[illegible]

Anti-sense strand reads

[illegible]

Show Alignment With Reads

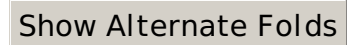
Re-alignment of all predicted orthologs

[illegible]

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

Predicted structure



Flybase annnotation

intron [Dper\GL22604-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

[illegible]

Anti-sense strand reads

[illegible]

Show Alignment With Reads

Re-alignment of all predicted orthologs

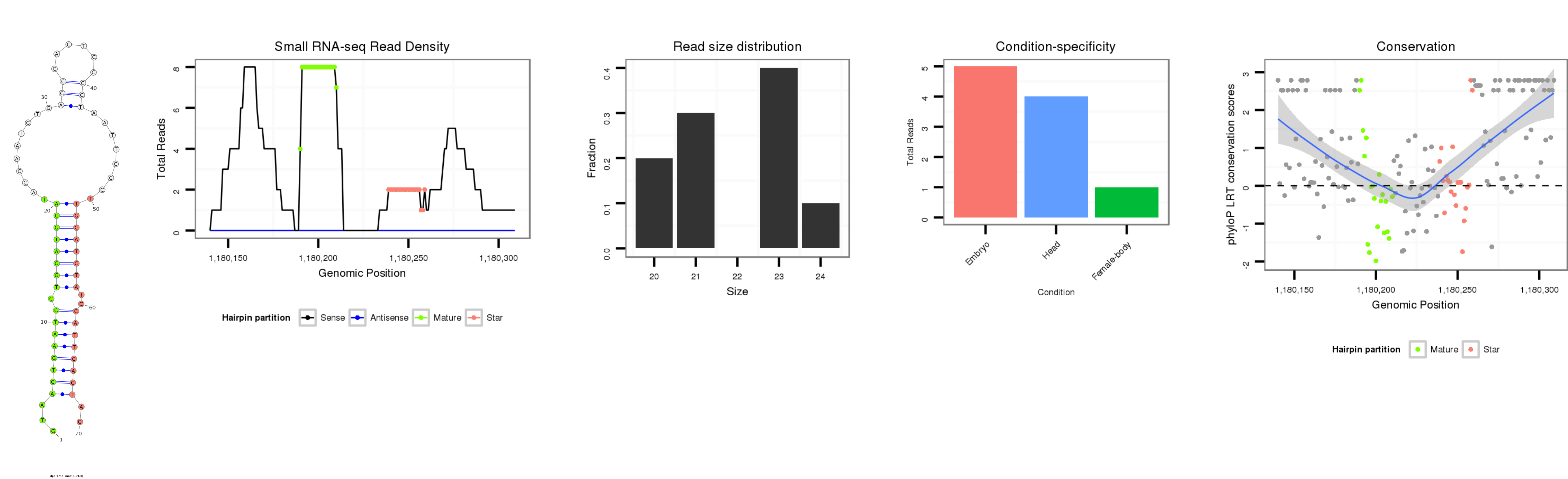
Species	Coordinate	ID	Alignment
droPer2	scaffold_56:124044-124205 +	dpe_157	GACA---AAAGCGTGGTACTTGT-TGAAAGAACAT-----AT-C-GAA--G-GTTGGTAGT SATGGGACTCGTCTAGAACGAGCGGAATTC--AAACATTGC TGC-ACCTTCAGAGCCTCAACAT TACGCC-TAGAGAAC-GCAAGC-AGCTTTCGACCAT-GCATAC-CACCAGCGAAGC
dp5	Xl_group3b:100238-100400 +	dps_110	GACA---AAAGCGTGGTACTTGT-TGAAAGAACAT-----AT-C-GAA--G-GTTGGTAGT SATGGGACTCGTCTAGAACGAGCGGAATTC--AAACATTGC TGC-ACCTTCAGAGCCTCAACAT TACGCC-TAGAGAAC-GCAAGC-AGCTTTCGACCAT-GCATAC-CACCAGCGAAGC
droW12	scf2_1100000004515:1719065-1719070 -		GACA---AAAGCGTGGTACTTGT-TGAAAGAACAT-----AT-C-GAA--G-GTTGGTAGT SATGGGACTCGTCTAGAACGAGCGGAATTC--AAACATTGC TGC-ACCTTCAGAGCCTCAACAT TACGCC-TAGAGAAC-GCAAGC-AGCTTTCGACCAT-GCATAC-CACCAGCGAAGC
droVi3	scaffold_12970:5369119-5369199 -	dvi_24642	-----GGTAGT SATGGGACTCACTAGAACGAGTGGAAATTTC--AAACATTGC TGC-ACCTTCAGAGCCTCAACAT TACGCC-TAGAGAAC-GCAAGC-AGCTTTCGACCAT-GCATAC-CACCAGCGAAGC
droMo3	scaffold_6473:4951753-4951833 -	dmo_3154	-----GGTAGT SATGGGACTCACTAGAACGAGTGGAAATTTC--AAACATTGC TGC-ACCTTCAGAGCCTCAACAT TACGCC-TAGAGAAC-GCAAGC-AGCTTTCGACCAT-GCATAC-CACCAGCGAAGC
droGr12	scaffold_15203:9467769-9467849 +		-----GGTAGT SATGGGACTCACTAGAACGAGTGGAAATTTC--AAACATTGC TGC-ACCTTCAGAGCCTCAACAT TACGCC-TAGAGAAC-GCAAGC-AGCTTTCGACCAT-GCATAC-CACCAGCGAAGC
droAna3	scaffold_13334:472139-472306 +	dan_4039	TATC---GAAGC---GGGACTTGTTCGAAAGAGT CAAA--ACAAT-TTAA--G-AGCTGGTAGT SATGGGACTCGTCTAGAACGAGCGGAATTC--AAACATTGC TGC-ACCTTCAGAGCCTCAACAT TACGCC-TAGAGAAC-GCAAGC-AGCTTTCGACCAT-GCATAC-CACCAGCGAAGC
droBip1	scf7180000396433:1081260-1081392 -		-----GC---GGGACTTGTTCGAAAGAGT CAAA--ACAAT-TTAA--G-AGCTGGTAGT SATGGGACTCGTCTAGAACGAGCGGAATTC--AAACATTGC TGC-ACCTTCAGAGCCTCAACAT TACGCC-TAGAGAAC-GCAAGC-AGCTTTCGACCAT-GCATAC-CACCAGCGAAGC
droKik1	scf7180000302698:307832-307977 -		ACA---TAAGC---GGGACTTGTTCGAAAGAGT CAAA--ACAAT-TTAA--G-AGCTGGTAGT SATGGGACTCGTCTAGAACGAGCGGAATTC--AAACATTGC TGC-ACCTTCAGAGCCTCAACAT TACGCC-TAGAGAAC-GCAAGC-AGCTTTCGACCAT-GCATAC-CACCAGCGAAGC
droFic1	scf7180000454073:1443011-1443147 +		-----GC---GGGACTTGTTCGAAAGAGT CAAA--ACAAT-TTAA--G-AGCTGGTAGT SATGGGACTCGTCTAGAACGAGCGGAATTC--AAACATTGC TGC-ACCTTCAGAGCCTCAACAT TACGCC-TAGAGAAC-GCAAGC-AGCTTTCGACCAT-GCATAC-CACCAGCGAAGC
droEle1	scf7180000491044:215078-215220 +		AAAT---TAAGC---GGGACTTGTTCGAAAGAGT CAAA--ACAAT-TTAA--G-AGCTGGTAGT SATGGGACTCGTCTAGAACGAGCGGAATTC--AAACATTGC TGC-ACCTTCAGAGCCTCAACAT TACGCC-TAGAGAAC-GCAAGC-AGCTTTCGACCAT-GCATAC-CACCAGCGAAGC
droRho1	scf7180000779510:38401-38550 +		ACTC---TAAGC---GGGACTTGTTCGAAAGAGT CAAA--ACAAT-TTAA--G-AGCTGGTAGT SATGGGACTCGTCTAGAACGAGCGGAATTC--AAACATTGC TGC-ACCTTCAGAGCCTCAACAT TACGCC-TAGAGAAC-GCAAGC-AGCTTTCGACCAT-GCATAC-CACCAGCGAAGC
droBia1	scf7180000302041:563683-563823 +		ACTC---TAAGC---GGGACTTGTTCGAAAGAGT CAAA--ACAAT-TTAA--G-AGCTGGTAGT SATGGGACTCGTCTAGAACGAGCGGAATTC--AAACATTGC TGC-ACCTTCAGAGCCTCAACAT TACGCC-TAGAGAAC-GCAAGC-AGCTTTCGACCAT-GCATAC-CACCAGCGAAGC
droTak1	scf7180000414393:30846-30988 -		-----GC---GGGACTTGTTCGAAAGAGT CAAA--ACAAT-TTAA--G-AGCTGGTAGT SATGGGACTCGTCTAGAACGAGCGGAATTC--AAACATTGC TGC-ACCTTCAGAGCCTCAACAT TACGCC-TAGAGAAC-GCAAGC-AGCTTTCGACCAT-GCATAC-CACCAGCGAAGC
droEug1	scf7180000408958:35963-36101 -		-----GC---GGGACTTGTTCGAAAGAGT CAAA--ACAAT-TTAA--G-AGCTGGTAGT SATGGGACTCGTCTAGAACGAGCGGAATTC--AAACATTGC TGC-ACCTTCAGAGCCTCAACAT TACGCC-TAGAGAAC-GCAAGC-AGCTTTCGACCAT-GCATAC-CACCAGCGAAGC
dm3	ChrX:13553568-13553711 +	dme_424	ACCA---TAAGC---GGGACTTGTTCGAAAGAGT CAAA--ACAAT-TTAA--G-AGCTGGTAGT SATGGGACTCGTCTAGAACGAGCGGAATTC--AAACATTGC TGC-ACCTTCAGAGCCTCAACAT TACGCC-TAGAGAAC-GCAAGC-AGCTTTCGACCAT-GCATAC-CACCAGCGAAGC
droSim2	x:12890287-12890429 +	dsi_32459	ACCA---TAAGC---GGGACTTGTTCGAAAGAGT CAAA--ACAAT-TTAA--G-AGCTGGTAGT SATGGGACTCGTCTAGAACGAGCGGAATTC--AAACATTGC TGC-ACCTTCAGAGCCTCAACAT TACGCC-TAGAGAAC-GCAAGC-AGCTTTCGACCAT-GCATAC-CACCAGCGAAGC
droYak3	X:12890287-12890429 +	dys_1935	ACCA---TAAGC---GGGACTTGTTCGAAAGAGT CAAA--ACAAT-TTAA--G-AGCTGGTAGT SATGGGACTCGTCTAGAACGAGCGGAATTC--AAACATTGC TGC-ACCTTCAGAGCCTCAACAT TACGCC-TAGAGAAC-GCAAGC-AGCTTTCGACCAT-GCATAC-CACCAGCGAAGC
droEre2	scaffold_4690:13329686-13329820 -	der_1524	-----GC---GGGACTTGTTCGAAAGAGT CAAA--ACAAT-TTAA--G-AGCTGGTAGT SATGGGACTCGTCTAGAACGAGCGGAATTC--AAACATTGC TGC-ACCTTCAGAGCCTCAACAT TACGCC-TAGAGAAC-GCAAGC-AGCTTTCGACCAT-GCATAC-CACCAGCGAAGC

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	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	2
rescue.candidate	9

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Show Alternate Folds

Flybase annotation

intron [Dper^ΔGL25947-in]; CDS [Dper^ΔGL25947-cds]; CDS [Dper^ΔGL25947-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads

show mid mismatch reads

[illegible]

Anti-sense strand reads

[illegible]

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droPer2	scaffold_51180140~1180309	dpe_1746	ATGCGGCCACGCCCAAGGATCGGCT-----GGTGAG--GAAGSAGCG-----GCCGGCGAGTAAGTGAA-----TG--C--TGGAATG-----CATACCAATGTGAG--C-----CAGTCC--G-----CTAATT-----CC-----CTGCATCTAT-----CCATTCAGTAAGAAAGGATGCTGAAGAGCACTCGGAGACGATAAAGATCTGACCACCGA
dp5	4_group14084479~4084648	dpe_1409	ATGCGGCCACGCCCAAGGATCGGCT-----GGTGAG--GAAGSAGCG-----GCCGGCGAGTAAGTGAA-----TG--C--TGGAATG-----CATACCAATGTGAG--C-----CAGTCC--G-----CTAATT-----CC-----CTGCATCTAT-----CCATTCAGTAAGAAAGGATGCTGAAGAGCACTCGGAGACGATAAAGATCTGACCACCGA
droW112	scf7_1100000004945~317420~317584		ATGCGGCCACGCCCAAGGATCGGCT-----GGTGAG--GAAGSAGCG-----GCCGGCGAGTAAGTGAA-----TG--C--TGGAATG-----CATACCAATGTGAG--C-----CAGTCC--G-----CTAATT-----CC-----CTGCATCTAT-----CCATTCAGTAAGAAAGGATGCTGAAGAGCACTCGGAGACGATAAAGATCTGACCACCGA
droV1r3	scaffold_12723~3023769~3023945		ATGCGGCCACGCCCAAGGATCGGCT-----GGTGAG--GAAGSAGCG-----GCCGGCGAGTAAGTGAA-----TG--C--TGGAATG-----CATACCAATGTGAG--C-----CAGTCC--G-----CTAATT-----CC-----CTGCATCTAT-----CCATTCAGTAAGAAAGGATGCTGAAGAGCACTCGGAGACGATAAAGATCTGACCACCGA
droMo3	scaffold_6500~6844475~6844649		ATGCGGCCACGCCCAAGGATCGGCT-----GGTGAG--GAAGSAGCG-----GCCGGCGAGTAAGTGAA-----TG--C--TGGAATG-----CATACCAATGTGAG--C-----CAGTCC--G-----CTAATT-----CC-----CTGCATCTAT-----CCATTCAGTAAGAAAGGATGCTGAAGAGCACTCGGAGACGATAAAGATCTGACCACCGA
droGr12	scaffold_15126~459183~459350		ATGCGGCCACGCCCAAGGATCGGCT-----GGTGAG--GAAGSAGCG-----GCCGGCGAGTAAGTGAA-----TG--C--TGGAATG-----CATACCAATGTGAG--C-----CAGTCC--G-----CTAATT-----CC-----CTGCATCTAT-----CCATTCAGTAAGAAAGGATGCTGAAGAGCACTCGGAGACGATAAAGATCTGACCACCGA
droAna3	scaffold_12916~10082180~10082333		ATGCGGCCACGCCCAAGGATCGGCT-----GGTGAG--GAAGSAGCG-----GCCGGCGAGTAAGTGAA-----TG--C--TGGAATG-----CATACCAATGTGAG--C-----CAGTCC--G-----CTAATT-----CC-----CTGCATCTAT-----CCATTCAGTAAGAAAGGATGCTGAAGAGCACTCGGAGACGATAAAGATCTGACCACCGA
droBip1	scf7180000396580~953518~953674		ATGCGGCCACGCCCAAGGATCGGCT-----GGTGAG--GAAGSAGCG-----GCCGGCGAGTAAGTGAA-----TG--C--TGGAATG-----CATACCAATGTGAG--C-----CAGTCC--G-----CTAATT-----CC-----CTGCATCTAT-----CCATTCAGTAAGAAAGGATGCTGAAGAGCACTCGGAGACGATAAAGATCTGACCACCGA
droK1k1	scf7180000302412~560591~560763		ATGCGGCCACGCCCAAGGATCGGCT-----GGTGAG--GAAGSAGCG-----GCCGGCGAGTAAGTGAA-----TG--C--TGGAATG-----CATACCAATGTGAG--C-----CAGTCC--G-----CTAATT-----CC-----CTGCATCTAT-----CCATTCAGTAAGAAAGGATGCTGAAGAGCACTCGGAGACGATAAAGATCTGACCACCGA
droF1c1	scf7180000454117~17580~17729		ATGCGGCCACGCCCAAGGATCGGCT-----GGTGAG--GAAGSAGCG-----GCCGGCGAGTAAGTGAA-----TG--C--TGGAATG-----CATACCAATGTGAG--C-----CAGTCC--G-----CTAATT-----CC-----CTGCATCTAT-----CCATTCAGTAAGAAAGGATGCTGAAGAGCACTCGGAGACGATAAAGATCTGACCACCGA
droEle1	scf7180000491186~1216468~121666		ATGCGGCCACGCCCAAGGATCGGCT-----GGTGAG--GAAGSAGCG-----GCCGGCGAGTAAGTGAA-----TG--C--TGGAATG-----CATACCAATGTGAG--C-----CAGTCC--G-----CTAATT-----CC-----CTGCATCTAT-----CCATTCAGTAAGAAAGGATGCTGAAGAGCACTCGGAGACGATAAAGATCTGACCACCGA
droRho1	scf718000071933~93771~93961		ATGCGGCCACGCCCAAGGATCGGCT-----GGTGAG--GAAGSAGCG-----GCCGGCGAGTAAGTGAA-----TG--C--TGGAATG-----CATACCAATGTGAG--C-----CAGTCC--G-----CTAATT-----CC-----CTGCATCTAT-----CCATTCAGTAAGAAAGGATGCTGAAGAGCACTCGGAGACGATAAAGATCTGACCACCGA
droBia1	scf7180000301500~215619~215776		ATGCGGCCACGCCCAAGGATCGGCT-----GGTGAG--GAAGSAGCG-----GCCGGCGAGTAAGTGAA-----TG--C--TGGAATG-----CATACCAATGTGAG--C-----CAGTCC--G-----CTAATT-----CC-----CTGCATCTAT-----CCATTCAGTAAGAAAGGATGCTGAAGAGCACTCGGAGACGATAAAGATCTGACCACCGA
droTak1	scf7180000415629~144566~144723		ATGCGGCCACGCCCAAGGATCGGCT-----GGTGAG--GAAGSAGCG-----GCCGGCGAGTAAGTGAA-----TG--C--TGGAATG-----CATACCAATGTGAG--C-----CAGTCC--G-----CTAATT-----CC-----CTGCATCTAT-----CCATTCAGTAAGAAAGGATGCTGAAGAGCACTCGGAGACGATAAAGATCTGACCACCGA
droEug1	scf7180000409461~452762~452917		ATGCGGCCACGCCCAAGGATCGGCT-----GGTGAG--GAAGSAGCG-----GCCGGCGAGTAAGTGAA-----TG--C--TGGAATG-----CATACCAATGTGAG--C-----CAGTCC--G-----CTAATT-----CC-----CTGCATCTAT-----CCATTCAGTAAGAAAGGATGCTGAAGAGCACTCGGAGACGATAAAGATCTGACCACCGA
dm3	chr21:8427047~8427207		ATGCGGCCACGCCCAAGGATCGGCT-----GGTGAG--GAAGSAGCG-----GCCGGCGAGTAAGTGAA-----TG--C--TGGAATG-----CATACCAATGTGAG--C-----CAGTCC--G-----CTAATT-----CC-----CTGCATCTAT-----CCATTCAGTAAGAAAGGATGCTGAAGAGCACTCGGAGACGATAAAGATCTGACCACCGA
droS1m2	21:8153996~8154154	Hs1_13205	ATGCGGCCACGCCCAAGGATCGGCT-----GGTGAG--GAAGSAGCG-----GCCGGCGAGTAAGTGAA-----TG--C--TGGAATG-----CATACCAATGTGAG--C-----CAGTCC--G-----CTAATT-----CC-----CTGCATCTAT-----CCATTCAGTAAGAAAGGATGCTGAAGAGCACTCGGAGACGATAAAGATCTGACCACCGA
droSec2	scaffold_313923337~3923495		ATGCGGCCACGCCCAAGGATCGGCT-----GGTGAG--GAAGSAGCG-----GCCGGCGAGTAAGTGAA-----TG--C--TGGAATG-----CATACCAATGTGAG--C-----CAGTCC--G-----CTAATT-----CC-----CTGCATCTAT-----CCATTCAGTAAGAAAGGATGCTGAAGAGCACTCGGAGACGATAAAGATCTGACCACCGA
droYak3	21:11064995~11065153		ATGCGGCCACGCCCAAGGATCGGCT-----GGTGAG--GAAGSAGCG-----GCCGGCGAGTAAGTGAA-----TG--C--TGGAATG-----CATACCAATGTGAG--C-----CAGTCC--G-----CTAATT-----CC-----CTGCATCTAT-----CCATTCAGTAAGAAAGGATGCTGAAGAGCACTCGGAGACGATAAAGATCTGACCACCGA
droEre2	scaffold_4929~17335770~17335928		ATGCGGCCACGCCCAAGGATCGGCT-----GGTGAG--GAAGSAGCG-----GCCGGCGAGTAAGTGAA-----TG--C--TGGAATG-----CATACCAATGTGAG--C-----CAGTCC--G-----CTAATT-----CC-----CTGCATCTAT-----CCATTCAGTAAGAAAGGATGCTGAAGAGCACTCGGAGACGATAAAGATCTGACCACCGA

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	PASS/FAIL
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crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
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crit.top3	1
crit.ttop3	1
crit.uri	0
crit.back	0
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	1
rescue.candidate	1