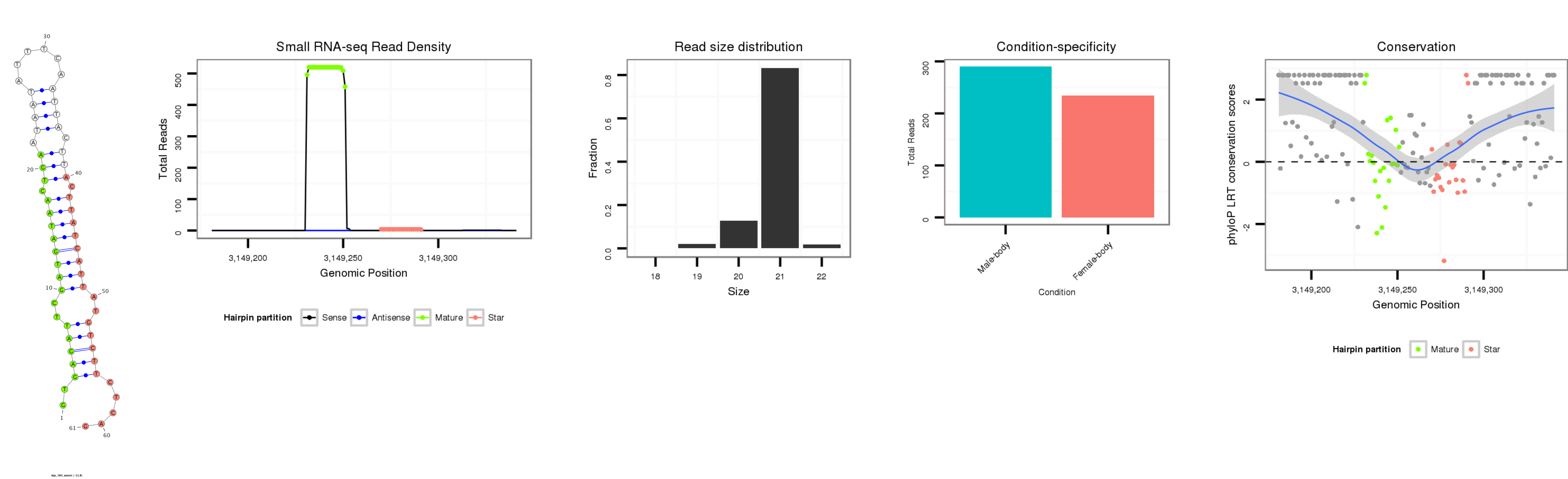


ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dgr_284	scaffold_15110:3149231-3149291 +	confident	Mirtron	intron	[View on UCSC Genome Browser (Concell Mirrot)]

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

Predicted structure



Show Alternate Folds

Flybase annotation

intron [Dgri/GH15934-inj]; CDS [Dgri/GH15934-cds]; CDS [Dgri/GH15934-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

	Read #	Hit	Total	V109	M041
	size	Mismatch	Count	male	female
AGATCTTTCTGATAGATCAGACCAGTTACTTTCTCAACTTTACGACAAGGTGAGATTGCGATGATAACTGAGATAAATAATTTACTTACTTACTATCATTAATGCTTCTCTCAGACGCGCAACAAGGTATTACCACAAAATCGTCGGTCTTCCCTTACCAAAATAT	21	0	1	435.00	435
GTGAGATTTCGATGATAACTG	20	0	1	50.00	50
GTGAGATTTCGATGATAACTG	20	0	1	17.00	17
GTGAGATTTCGATGATAACTG	19	0	1	10.00	10
GTGAGATTTCGATGATAACTG	22	0	1	6.00	6
GTGAGATTTCGATGATAACTG	22	0	1	3.00	3
GTGAGATTTCGATGATAACTG	21	1	1	2.00	2
GTGAGATTTCGATGATAACTG	22	1	1	2.00	2
GTGAGATTTCGATGATAACTG	23	1	1	2.00	2
GTGAGATTTCGATGATAACTG	21	0	1	1.00	1
GTGAGATTTCGATGATAACTG	19	0	1	1.00	1
GTGAGATTTCGATGATAACTG	21	0	1	1.00	1
GTGAGATTTCGATGATAACTG	24	2	1	1.00	1
GTGAGATTTCGATGATAACTG	18	0	1	1.00	1

Anti-sense strand reads

	Read #	Hit	Total	V109	M041
	size	Mismatch	Count	male	female
TCTAGAAAGCATCTAGTCTGTCATGAAGAGGTTGAAATGCTGGTCTCCACTCTAAGCTACTATTGACTTATTATAAAGTTAATGAATGAATAGTAATACAGAAGAGTTCGCGGTTGTTCCTAAGTGGTTTTAGACGCCAGAGGGAATGGTTTATA	24	0	1	1.00	1
TCTAGAAAGCATCTAGTCTGTCATGAAGAGGTTGAAATGCTGGTCTCCACTCTAAGCTACTATTGACTTATTATAAAGTTAATGAATGAATAGTAATACAGAAGAGTTCGCGGTTGTTCCTAAGTGGTTTTAGACGCCAGAGGGAATGGTTTATA	18	0	1	1.00	1

Show Alignment With Reads

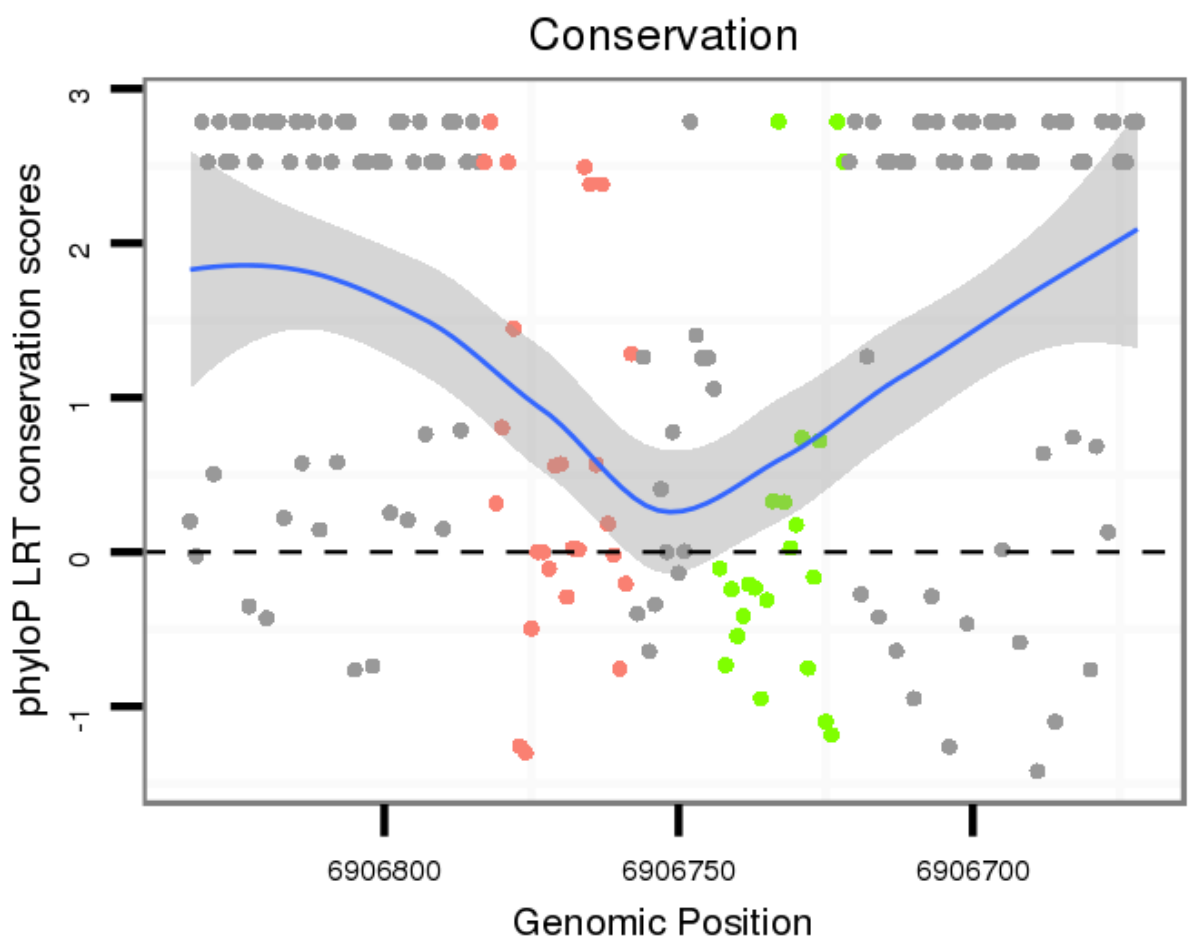
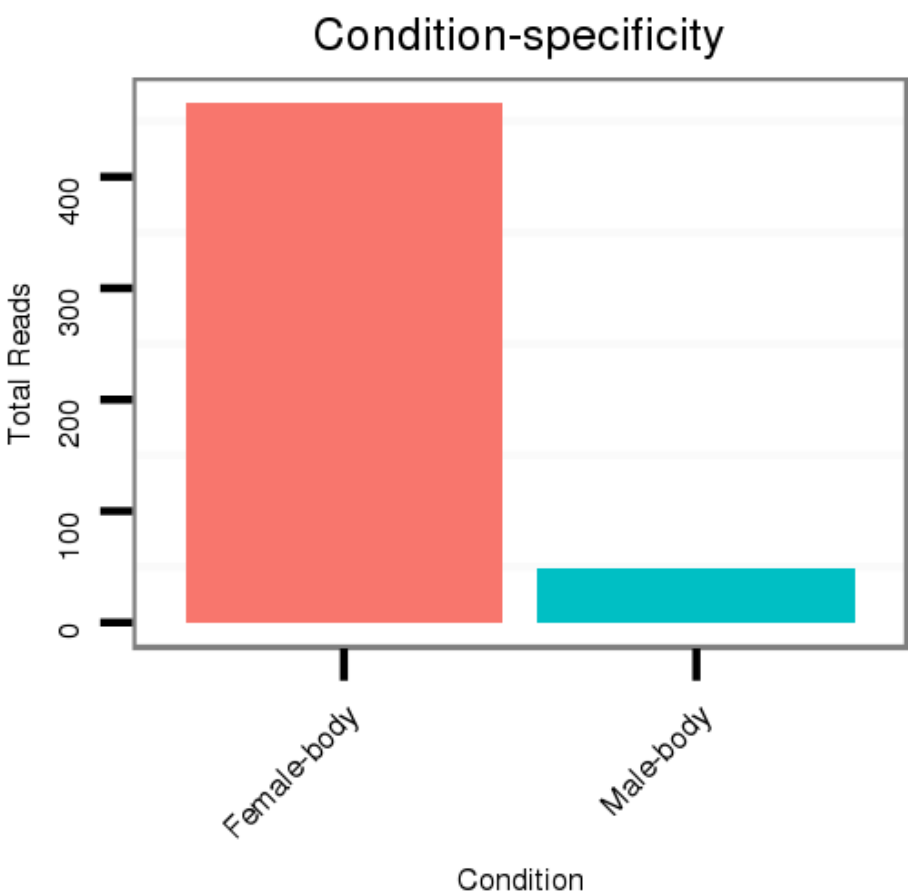
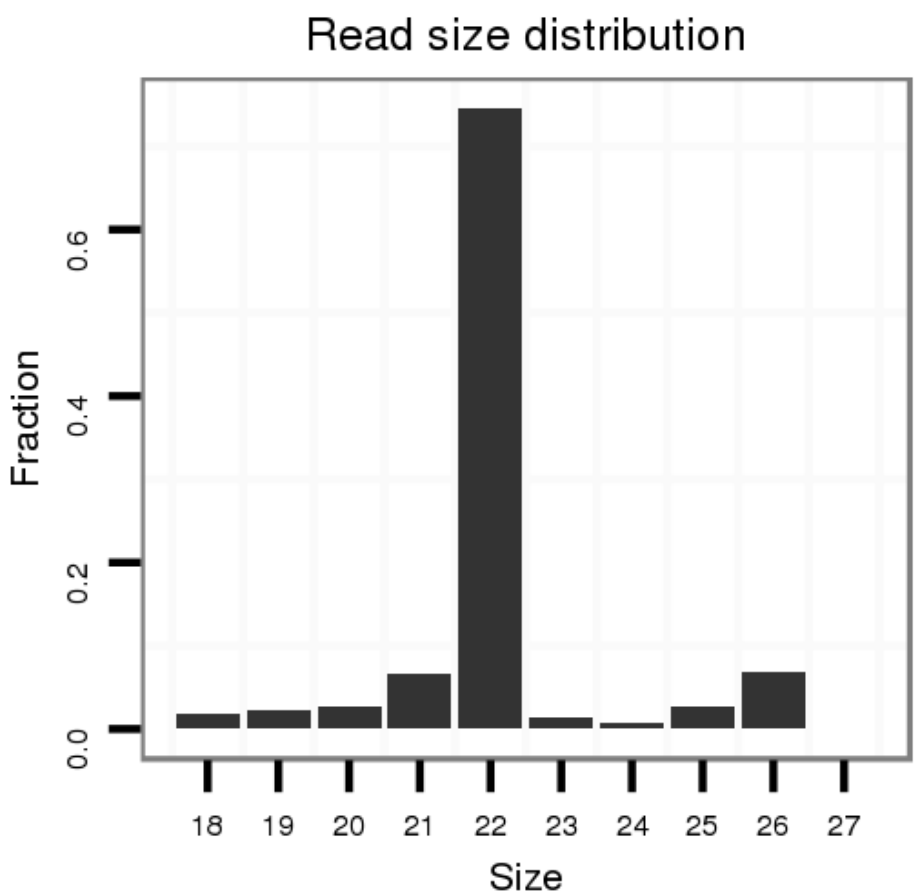
Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droGri12	scaffold_15110:3149181-3149341 +	dgr_284	AGATCTTTCTGATAGATCAGACCAGTTACTTTCTCAACTTTACGACCAAGGTGAGATTGCGATGATAACTGAGATAAATAATTTACTTACTTACTATCATTAATGCTTCTCTCAGACGCGCAACAAGGTATTACCACAAAATCGTCGGTCTTCCCTTACCAAAATAT
droBir3	scaffold_13049:2100079-2100296 +	dvi_17966	AGATCTTTCTGATAGATCAGACCAGTTACTTTCTCAACTTTACGACCAAGGTGAGATTGCGATGATAACTGAGATAAATAATTTACTTACTTACTATCATTAATGCTTCTCTCAGACGCGCAACAAGGTATTACCACAAAATCGTCGGTCTTCCCTTACCAAAATAT
droMoJ3	scaffold_5978:589-763 -		AGATCTTTCTGATAGATCAGACCAGTTACTTTCTCAACTTTACGACCAAGGTGAGATTGCGATGATAACTGAGATAAATAATTTACTTACTTACTATCATTAATGCTTCTCTCAGACGCGCAACAAGGTATTACCACAAAATCGTCGGTCTTCCCTTACCAAAATAT
droW12	scf2_1100000004762:3971807-3971977 +		AGATCTTTCTGATAGATCAGACCAGTTACTTTCTCAACTTTACGACCAAGGTGAGATTGCGATGATAACTGAGATAAATAATTTACTTACTTACTTACTATCATTAATGCTTCTCTCAGACGCGCAACAAGGTATTACCACAAAATCGTCGGTCTTCCCTTACCAAAATAT
dp5	XR_group8:8384530-8384690 +		AGATCTTTCTGATAGATCAGACCAGTTACTTTCTCAACTTTACGACCAAGGTGAGATTGCGATGATAACTGAGATAAATAATTTACTTACTTACTTACTATCATTAATGCTTCTCTCAGACGCGCAACAAGGTATTACCACAAAATCGTCGGTCTTCCCTTACCAAAATAT
droPer2	scaffold_40:576585-576745 +		AGATCTTTCTGATAGATCAGACCAGTTACTTTCTCAACTTTACGACCAAGGTGAGATTGCGATGATAACTGAGATAAATAATTTACTTACTTACTTACTATCATTAATGCTTCTCTCAGACGCGCAACAAGGTATTACCACAAAATCGTCGGTCTTCCCTTACCAAAATAT
droAna3	scaffold_13337:14640730-14640888 +		AGATCTTTCTGATAGATCAGACCAGTTACTTTCTCAACTTTACGACCAAGGTGAGATTGCGATGATAACTGAGATAAATAATTTACTTACTTACTTACTATCATTAATGCTTCTCTCAGACGCGCAACAAGGTATTACCACAAAATCGTCGGTCTTCCCTTACCAAAATAT
droBip1	scf718000039641:669731-669895 -		AGATCTTTCTGATAGATCAGACCAGTTACTTTCTCAACTTTACGACCAAGGTGAGATTGCGATGATAACTGAGATAAATAATTTACTTACTTACTTACTATCATTAATGCTTCTCTCAGACGCGCAACAAGGTATTACCACAAAATCGTCGGTCTTCCCTTACCAAAATAT
droRik1	scf7180000302383:608119-606271 +		AGATCTTTCTGATAGATCAGACCAGTTACTTTCTCAACTTTACGACCAAGGTGAGATTGCGATGATAACTGAGATAAATAATTTACTTACTTACTTACTATCATTAATGCTTCTCTCAGACGCGCAACAAGGTATTACCACAAAATCGTCGGTCTTCCCTTACCAAAATAT
droRiC1	scf718000045413:1451310-1451478 +		AGATCTTTCTGATAGATCAGACCAGTTACTTTCTCAACTTTACGACCAAGGTGAGATTGCGATGATAACTGAGATAAATAATTTACTTACTTACTTACTATCATTAATGCTTCTCTCAGACGCGCAACAAGGTATTACCACAAAATCGTCGGTCTTCCCTTACCAAAATAT
droRiE1	scf7180000491249:5086826-5086982 +		AGATCTTTCTGATAGATCAGACCAGTTACTTTCTCAACTTTACGACCAAGGTGAGATTGCGATGATAACTGAGATAAATAATTTACTTACTTACTTACTATCATTAATGCTTCTCTCAGACGCGCAACAAGGTATTACCACAAAATCGTCGGTCTTCCCTTACCAAAATAT
droRho1	scf7180000779786:8982-9147 +		AGATCTTTCTGATAGATCAGACCAGTTACTTTCTCAACTTTACGACCAAGGTGAGATTGCGATGATAACTGAGATAAATAATTTACTTACTTACTTACTATCATTAATGCTTCTCTCAGACGCGCAACAAGGTATTACCACAAAATCGTCGGTCTTCCCTTACCAAAATAT
droBial1	scf7180000302428:927147-927319 -		AGATCTTTCTGATAGATCAGACCAGTTACTTTCTCAACTTTACGACCAAGGTGAGATTGCGATGATAACTGAGATAAATAATTTACTTACTTACTTACTATCATTAATGCTTCTCTCAGACGCGCAACAAGGTATTACCACAAAATCGTCGGTCTTCCCTTACCAAAATAT
droTak1	scf7180000415707:3729-3963		AGATCTTTCTGATAGATCAGACCAGTTACTTTCTCAACTTTACGACCAAGGTGAGATTGCGATGATAACTGAGATAAATAATTTACTTACTTACTTACTATCATTAATGCTTCTCTCAGACGCGCAACAAGGTATTACCACAAAATCGTCGGTCTTCCCTTACCAAAATAT
droEug1	scf7180000409466:1982819-1982984 +		AGATCTTTCTGATAGATCAGACCAGTTACTTTCTCAACTTTACGACCAAGGTGAGATTGCGATGATAACTGAGATAAATAATTTACTTACTTACTTACTATCATTAATGCTTCTCTCAGACGCGCAACAAGGTATTACCACAAAATCGTCGGTCTTCCCTTACCAAAATAT
dm3	chr3L:4217129-4217286 +		AGATCTTTCTGATAGATCAGACCAGTTACTTTCTCAACTTTACGACCAAGGTGAGATTGCGATGATAACTGAGATAAATAATTTACTTACTTACTTACTATCATTAATGCTTCTCTCAGACGCGCAACAAGGTATTACCACAAAATCGTCGGTCTTCCCTTACCAAAATAT
droSim2	31:4137180-4137334 +	dsi_591	AGATCTTTCTGATAGATCAGACCAGTTACTTTCTCAACTTTACGACCAAGGTGAGATTGCGATGATAACTGAGATAAATAATTTACTTACTTACTTACTATCATTAATGCTTCTCTCAGACGCGCAACAAGGTATTACCACAAAATCGTCGGTCTTCCCTTACCAAAATAT
droSec2	scaffold_2:4213939-4214093		AGATCTTTCTGATAGATCAGACCAGTTACTTTCTCAACTTTACGACCAAGGTGAGATTGCGATGATAACTGAGATAAATAATTTACTTACTTACTTACTATCATTAATGCTTCTCTCAGACGCGCAACAAGGTATTACCACAAAATCGTCGGTCTTCCCTTACCAAAATAT
droYak3	31:4791508-4791663 +		AGATCTTTCTGATAGATCAGACCAGTTACTTTCTCAACTTTACGACCAAGGTGAGATTGCGATGATAACTGAGATAAATAATTTACTTACTTACTTACTATCATTAATGCTTCTCTCAGACGCGCAACAAGGTATTACCACAAAATCGTCGGTCTTCCCTTACCAAAATAT
droFre2	scaffold_4784:6929488-6929646 +		AGATCTTTCTGATAGATCAGACCAGTTACTTTCTCAACTTTACGACCAAGGTGAGATTGCGATGATAACTGAGATAAATAATTTACTTACTTACTTACTATCATTAATGCTTCTCTCAGACGCGCAACAAGGTATTACCACAAAATCGTCGGTCTTCCCTTACCAAAATAT

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

Predicted structure



Flybase annotation

intron [Dgr\GH15276-in]; CDS [Dgr\GH15276-cds]; CDS [Dgr\GH15276-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

Anti-sense strand reads									
CGAGTGCCTAACCAACAAGAGCAGTCTTAACGCCCGATGCTACGTAAGCTC CATTACCCATTAACTCAAAGTCA ATTTCGAACATAAAAT GGTAGATGAATAGATGAATTC GATGAGCCGCGGATGAGACACTCGTTCTGCCGTGACTAGCCACAGCTGTT									
*****.(((((((((((.(((((((...(((((((...)))))).)))))).)))))).)))))).*****									
Read #	Hit	Total	size	Mismatch	Count	Norm	Total		

Anti-sense strand reads

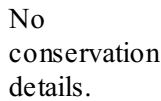
[illegible]

Re-alignment of all predicted orthologs

Generated: 09/08/2015 at 06:57 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

Legend: mature star mismatch in alignment mismatch in read



No Repeatable elements found

hide 3p reads | show mid mismatch reads

Read #	size	Mismatch	Hit Count	Total Norm	Total	male body
21	0		1	62.00	62	62
22	0		1	24.00	24	24
20	0		1	13.00	13	13
22	1		1	8.00	8	8
22	0		1	7.00	7	7
21	0		1	5.00	5	5
23	1		1	2.00	2	2
20	0		1	2.00	2	2
23	2		1	1.00	1	1
23	2		1	1.00	1	1
25	3		1	1.00	1	1

No data available in table

Show Alignment With Reads

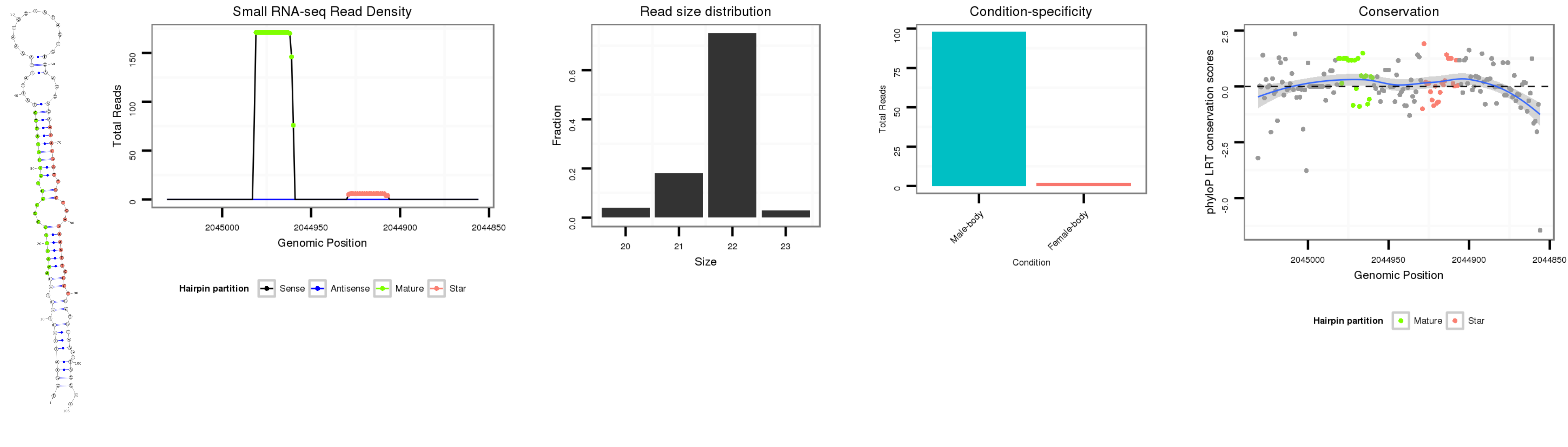
Re-alignment of all predicted orthologs

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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

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

[illegible]

Anti-sense strand reads

[illegible]

Show Alignment With Reads

[illegible]

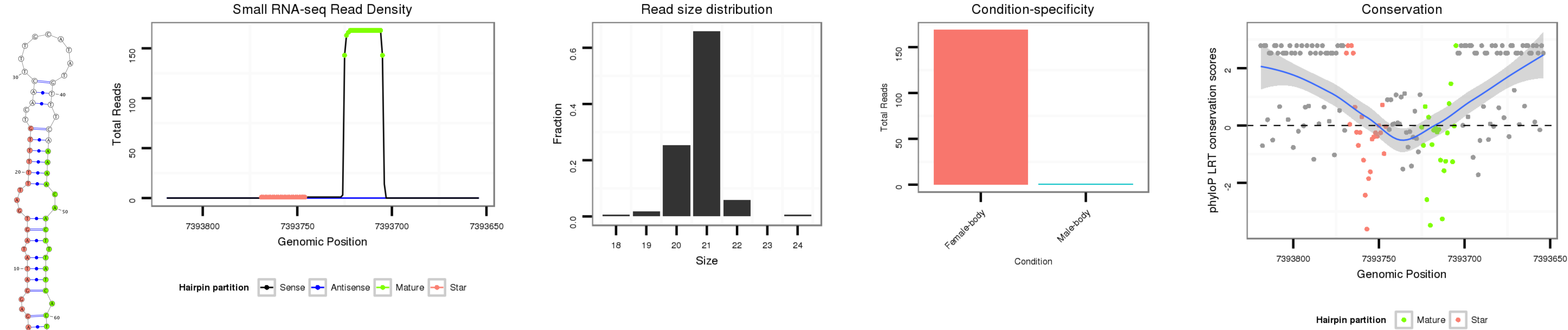
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	PASS/FALL
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crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	1
rescue.confident	5
rescue.candidate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

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:
dgr_51	scaffold_15245:7393704-7393769 -	confident-exception	Mirtron	intron

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Show Alternate Folds

Flybase annnotation

intron [Dgri|GH20497-in]; CDS [Dgri|GH20497-cds]; CDS [Dgri|GH20497-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

						M041	V109
TGAAGCCGATGCTGGCGACACAGCAGCTGCTGCAACAGGGCGCCGATATCGTAAAGAGGATATAGTGATTTTTTGTCAACTTTGCATATGTTTCAAAAACAACTTTATCACTTACAGGAGAAGATACGACTGGCGCTCAGCGAGGCGAATGCCACATGGAAACGTC	Read #					female	
*****(((((((.....(((((((.....(((((((.....)))))))))).....)))))).....))))*****	size	Mismatch	Hit	Total	Total	body	male
.....AAAACAACCTTTATCACTTACAG.....	21	0	1	110.00	110	110	0
.....AAAACAACCTTTATCACTTAC.....	20	0	1	23.00	23	23	0
.....AAACAACCTTTATCACTTACAG.....	20	0	1	16.00	16	16	0
.....AAAACAACCTTTATCACTTACAG.....	22	0	1	8.00	8	8	0
.....AAACAACCTTTATCACTTACAG.....	21	1	1	6.00	6	6	0
.....AAACAACCTTTATCACTTACAG.....	20	0	1	3.00	3	3	0
.....AAAACAACCTTTATCACTTACAG.....	23	1	1	3.00	3	3	0
.....ACAACCTTTATCACTTACAG.....	20	1	1	2.00	2	2	0
.....AAAACAACCTTTATCACTTACAG.....	22	0	1	2.00	2	2	0
.....AAACAACCTTTATCACTTACAG.....	21	0	1	2.00	2	2	0
.....AAACAACCTTTATCACTTAC.....	19	0	1	2.00	2	2	0
.....GTAAGAGGATATAGTGATTTTTTGT.....	24	0	1	1.00	1	0	1
.....AAAACAACCTTTATCACTTACAG.....	23	1	1	1.00	1	1	0
.....ACAACCTTTATCACTTACAG.....	19	0	1	1.00	1	1	0
.....ACAACCTTTATCACTTACAG.....	18	0	1	1.00	1	1	0
.....AAACAACCTTTATCACTTACAG.....	21	1	1	1.00	1	1	0
.....TCAACTTTGCATATGTTTCA.....	20	0	1	1.00	1	1	0
.....AAAACAACCTTTATCACTTACAG.....	23	1	1	1.00	1	1	0

Anti-sense strand reads

ACTTCGGCTACGACCGCTGTGCTGCTGACGAGCTTGTCCCGCGGCTATAG CATTCTCCTATATCACTAAAAAC AGTTGAACGTATACAAAGT TTTGTGAAATAGTGAATGT CCTCTTCTATGCTGACCGGAGTGCCTCCGCTTACGGGTGTACCTTTGCGAG	Read #	Hit	Total	
*****(((((((.....(((((((.....(((((((.....)))))))))).....)))))).....))))*****	size Mismatch	Count	Norm	Total
No data available in table				

No data available in table

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droGr12	scaffold_15245:7393654-7393819 -	dgr_51	TGAAGCCGATGCTGGCGACACAGCAGCTGCTGCAACAGGGCGCCGATATC GTAAGAGG --ATATAGTATGTTTTT-----GTCAACTTTGCAT--ATGT--TTCA AAA -----A--CA-----ACTTTAT-CA-CTTAC AG GGAGAAGATACGACTGGCGCTCAGCGAGGCGAATGCCACATGGAAACGTC
droV1r3	scaffold_12875:12972527-12972682 +		TGAAGCCATGCTGGCGAC CC CAGCAGT CG CTCAACAGGGCG CG AGCAT GT TAAG GCT --ATA CG CT CG C CTG -----GT AC CTT GC ---G---GCTAAT TGC ---G-----TT TA TTT G GA GGAAAGATAC CG TGGCGCT AG CGAGGCG TAA GG ACACATGGAAACGTC
droMoJ3	scaffold_6496:20237788-20237942 +		TGAAGCCATGCTGGCGACACAGCAGCTGCTGCAACAGGGCGCCGATAT GTAAAGATA -- CTG -- CCG -- CT ACT TAAAGT -----GTT CTC -- C ATT G AGGAGAAGAT CG CTGGCGCT AG CGAGGCG AA GG ACACATGGAAACGTC
droW112	scf2_1100000004558:1887030-1887185 +		TA AA CC ATGCTGGCGAC CC CAGCAGT CG CTCAACAGGG CG CGATAT GTAAAGTAA TTT--TAC-----CTAGG-----T AT --CCTAT CG T AA CTAAT CTCT --T-----CT CG CT TT T CTT AGGAGAAGAT CG CTGGCGCT AG CGAGGCG AA GG ACACATGGAAAC CTC
dp5	3:4663596-4663771 -		TA AA CC CGATGCTGGCGAC CC CAGCAGT CG CTCAACAGGG CG CGATAT GTAAAGTAA TTT CTCTAC CCCCAA-----GGATC--CCCAGG GA TC CTG AT--A--G-----T--TTGCTGAAC TTTCTC TTT CT -CA TTT CG AGGAGAAGAT CG CTGGCG CT AGCGAGGCG AA TG CG ACATGGAAAC ATC
droPer2	scaffold_2:4851954-4852122 -		TA AA CC CGATGCTGGCGAC CC CAGCAGT CG CTCAACAGGG CG CGATAT GTAAAGTAA TTT CTCTAC CCCCAA-----GGATC--CCCAGG GA TC CTG AT--A--G-----T--TTGCTGAAC TTTCTC TTT CT -CA TTT CG AGGAGAAGAT CG CTGGCG CT AGCGAGGCG AA TG CG ACATGGAAAC ATC
droAna3	scaffold_13266:1190459-1190620 -		TGAAGCCATGCTGGCGAC CC CAGCAGT CG CTCAACAGGG CG CGATAT GTAAAGTAA TTT CTCTAC CCCCAA-----GGATC--CCCAGG GA TC CTG AT--A--G-----T--TTGCTGAAC TTTCTC TTT CT -CA TTT CG AGGAGAAGAT CG CTGGCG CT AGCGAGGCG AA TG CG ACATGGAAAC ATC
droB1p1	scf7180000396730:2184666-2184825 -		TGAAGCCATGCTGGCGAC CC CAGCAGT CG CTCAACAGGG CG CGATAT GTAAAGTAA TTT CTCTAC CCCCAA-----GGATC--CCCAGG GA TC CTG AT--A--G-----T--TTGCTGAAC TTTCTC TTT CT -CA TTT CG AGGAGAAGAT CG CTGGCG CT AGCGAGGCG AA TG CG ACATGGAAAC ATC
droK1k1	scf7180000402386:411574-411733 +		TGAAGCCATGCTGGCGAC CC CAGCAGT CG CTCAACAGGG CG CGATAT GTAAAGTAA TTT CTCTAC CCCCAA-----GGATC--CCCAGG GA TC CTG AT--A--G-----T--TTGCTGAAC TTTCTC TTT CT -CA TTT CG AGGAGAAGAT CG CTGGCG CT AGCGAGGCG AA TG CG ACATGGAAAC ATC
droF1c1	scf7180000453773:406646-406804 -		TGAAGCCATGCTGGCGAC CC CAGCAGT CG CTCAACAGGG CG CGATAT GTAAAGTAA TTT CTCTAC CCCCAA-----GGATC--CCCAGG GA TC CTG AT--A--G-----T--TTGCTGAAC TTTCTC TTT CT -CA TTT CG AGGAGAAGAT CG CTGGCG CT AGCGAGGCG AA TG CG ACATGGAAAC ATC
droE1e1	scf7180000491214:2937961-2938120 -		TGAAGCCATGCTGGCGAC CC CAGCAGT CG CTCAACAGGG CG CGATAT GTAAAGTAA TTT CTCTAC CCCCAA-----GGATC--CCCAGG GA TC CTG AT--A--G-----T--TTGCTGAAC TTTCTC TTT CT -CA TTT CG AGGAGAAGAT CG CTGGCG CT AGCGAGGCG AA TG CG ACATGGAAAC ATC
droRho1	scf7180000779263:68798-68956 +		TGAAGCCATGCTGGCGAC CC CAGCAGT CG CTCAACAGGG CG CGATAT GTAAAGTAA TTT CTCTAC CCCCAA-----GGATC--CCCAGG GA TC CTG AT--A--G-----T--TTGCTGAAC TTTCTC TTT CT -CA TTT CG AGGAGAAGAT CG CTGGCG CT AGCGAGGCG AA TG CG ACATGGAAAC ATC
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droTak1	scf7180000415991:772642-772796 -		TGAAGCCATGCTGGCGAC CC CAGCAGT CG CTCAACAGGG CG CGATAT GTAAAGTAA TTT CTCTAC CCCCAA-----GGATC--CCCAGG GA TC CTG AT--A--G-----T--TTGCTGAAC TTTCTC TTT CT -CA TTT CG AGGAGAAGAT CG CTGGCG CT AGCGAGGCG AA TG CG ACATGGAAAC ATC
droEug1	scf7180000409462:1022378-1022537 +		TGAAGCCATGCTGGCGAC CC CAGCAGT CG CTCAACAGGG CG CGATAT GTAAAGTAA TTT CTCTAC CCCCAA-----GGATC--CCCAGG GA TC CTG AT--A--G-----T--TTGCTGAAC TTTCTC TTT CT -CA TTT CG AGGAGAAGAT CG CTGGCG CT AGCGAGGCG AA TG CG ACATGGAAAC ATC
dm3	chr2R:7476091-7476252 -		TA AA CC ATGCTGGCGAC CC CAGCAGT CG CTCAACAGGG CG CGATAT GTAAAGTAA TTT CTCTAC CCCCAA-----GGATC--CCCAGG GA TC CTG AT--A--G-----T--TTGCTGAAC TTTCTC TTT CT -CA TTT CG AGGAGAAGAT CG CTGGCG CT AGCGAGGCG AA TG CG ACATGGAAAC ATC
droSim2	2r:8180634-8180794 -		TA AA CC ATGCTGGCGAC CC CAGCAGT CG CTCAACAGGG CG CGATAT GTAAAGTAA TTT CTCTAC CCCCAA-----GGATC--CCCAGG GA TC CTG AT--A--G-----T--TTGCTGAAC TTTCTC TTT CT -CA TTT CG AGGAGAAGAT CG CTGGCG CT AGCGAGGCG AA TG CG ACATGGAAAC ATC
droSec2	scaffold_1:5026910-5027070 -		TA AA CC ATGCTGGCGAC CC CAGCAGT CG CTCAACAGGG CG CGATAT GTAAAGTAA TTT CTCTAC CCCCAA-----GGATC--CCCAGG GA TC CTG AT--A--G-----T--TTGCTGAAC TTTCTC TTT CT -CA TTT CG AGGAGAAGAT CG CTGGCG CT AGCGAGGCG AA TG CG ACATGGAAAC ATC
droYak3	2R:9479078-9479237 +		TA AA CC ATGCTGGCGAC CC CAGCAGT CG CTCAACAGGG CG CGATAT GTAAAGTAA TTT CTCTAC CCCCAA-----GGATC--CCCAGG GA TC CTG AT--A--G-----T--TTGCTGAAC TTTCTC TTT CT -CA TTT CG AGGAGAAGAT CG CTGGCG CT AGCGAGGCG AA TG CG ACATGGAAAC ATC
droEre2	scaffold_4845:18319983-18320139 +		TA AA CC ATGCTGGCGAC CC CAGCAGT CG CTCAACAGGG CG CGATAT GTAAAGTAA TTT CTCTAC CCCCAA-----GGATC--CCCAGG GA TC CTG AT--A--G-----T--TTGCTGAAC TTTCTC TTT CT -CA TTT CG AGGAGAAGAT CG CTGGCG CT AGCGAGGCG AA TG CG ACATGGAAAC ATC

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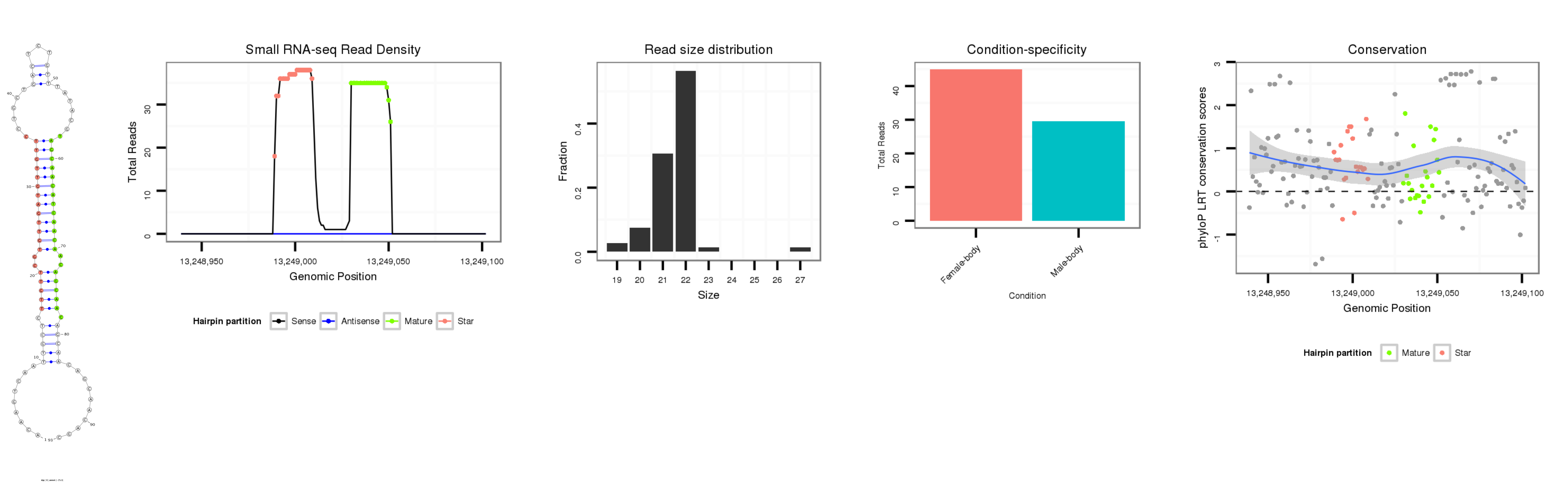
PASS/Fail	
crit.star	0
crit.loop	1
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.ptop3	1
crit.uri	1
crit.back	0
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

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	3
rescue.candidate	0

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dgr_52	scaffold_15252:13248989-13249052 +	confident	Canonical miRNA	5pUTR	[View on UCSC Genome Browser (Cornell Mirror)]

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Show Alternate Folds

Flybase annotation

utr5 [utr5_plus_2224]

Repeatable elements

Name	Class	Family	Strand
(CAA)n	Simple_repeat	Simple_repeat	+

mature	star
1. scaffold_15203:3827780-3827801- 2. dgr_52_scaffold_15252:13249030-13249051+	

Sense Strand Reads

hide 3p reads show mid mismatch reads

[illegible]

Anti-sense strand reads

TATACCGTGACTAGATAATAAATCCGCTGTTGGGTGTGTCAGTTAAACAGACAACAGACAGACAGACATGAGACAAATATGATCGTTGTAGTTGTTGCGTTGTGTTGTGCTGTGCTGTTGTTGTGTTCCGAGTTAAATAATGACTTGGCC					Read #	Hit	Total
*****.((							

Re-alignment of all predicted orthologs

[illegible]

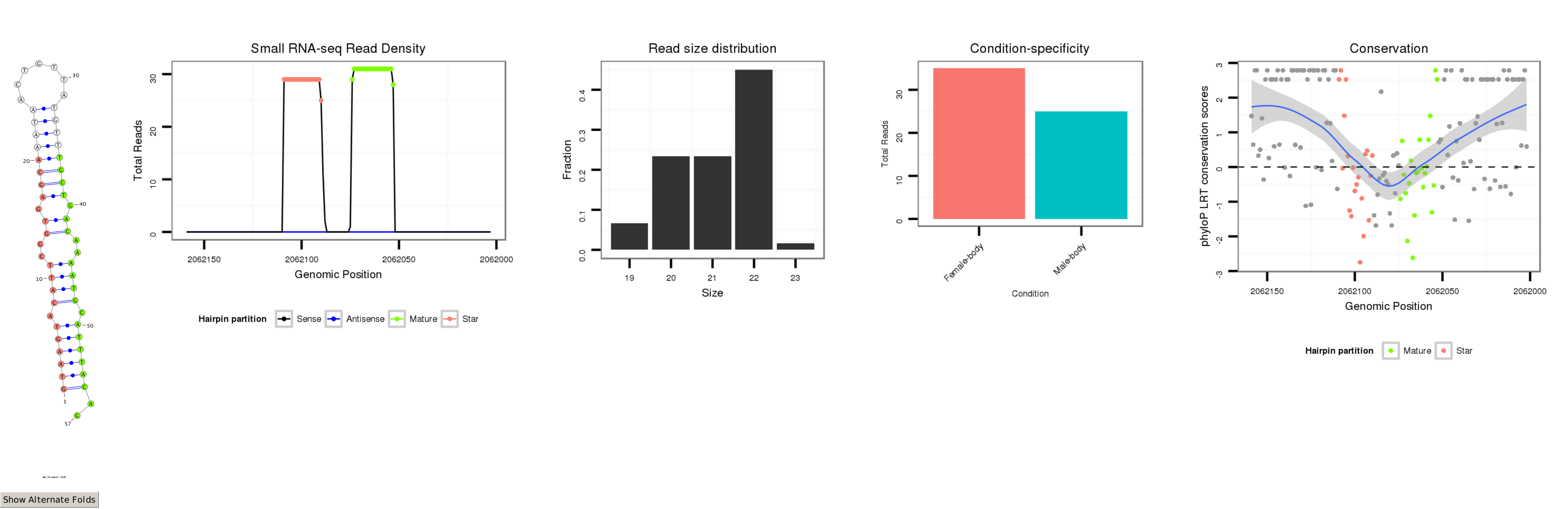
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	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dgr_56	scaffold_14906:2062053-2062109 -	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 [DgriGH18673-in]; CDS [DgriGH18673-cds]; CDS [DgriGH18673-cds]

No Repeatable elements found

Sense Strand Reads

	Read size	# Mismatch	Hit Count	Total Norm	Total	M041 female body	V109 male body
AATTCCATCACGGCGAGGAGCGCAAAATCATAGTATTCCACAAAGGGCAACGTAAGTACATTCGGTGAGCAAAATAACTGTTATGTTTGCTGACAAAATGCATTTTACAGGAAGAGATTGCAGAAGCACGAGGAGCAGGCGCCTCCCTTGTGGGTGGCGT	22	0	1	25.00	25	24	1
*****(((((((.(((.(((.(((((((.....)))))))).)).)).)).)).).*****	20	0	1	14.00	14	2	12
.....GTAAGTACATTCGGTGAGCA.....	21	0	1	9.00	9	2	7
.....GTAAGTACATTCGGTGAGCAA.....	19	0	1	4.00	4	0	4
.....GTAAGTACATTCGGTGAGC.....	21	0	1	3.00	3	3	0
.....GTAAGTACATTCGGTGAGCAA.....	22	0	1	2.00	2	1	1
.....TGCTGACAAAATGCATTTTACAG.....	22	1	1	2.00	2	2	0
.....GCTGACAAAATGCATTTTACAG.....	22	1	1	2.00	2	2	0
.....GCTGACAAAATGCATTTTACAG.....	21	0	1	2.00	2	2	0
.....GTAAGTACATTCGGTGAGCAA.....	23	1	1	1.00	1	0	1
.....TTGCTGACAAAATGCATTTTACAG.....	23	0	1	1.00	1	1	0
.....TGCTGACAAAATGCATTTTACAG.....	23	1	1	1.00	1	0	1
.....GCTGACAAAATGCATTTTACAG.....	24	3	1	1.00	1	1	0
.....GTAAGTACATTCGGTGAGCAA.....	22	1	1	1.00	1	0	1

Anti-sense strand reads

	Read #	# Mismatch	Hit Count	Total Norm	Total	M041 female body
TTAAGGTAGTCCGCTCCTCGCGTTTTAGTATCATAAAGTGTTCGCCGTTCATTTCATGAAGCCAATCGTTATTAGACAATACAAAGCACTGTTTTACGTAAGTGTCTTCTCTAACGCTCTTCGTGCTCCTCGTCCGCGGAGGGAACACCCACCGCA						
*****(((((((.(((.(((.(((.(((((((.....)))))))).)).)).)).)).).*****						

Show Alignment With Reads

Re-alignment of all predicted orthologs

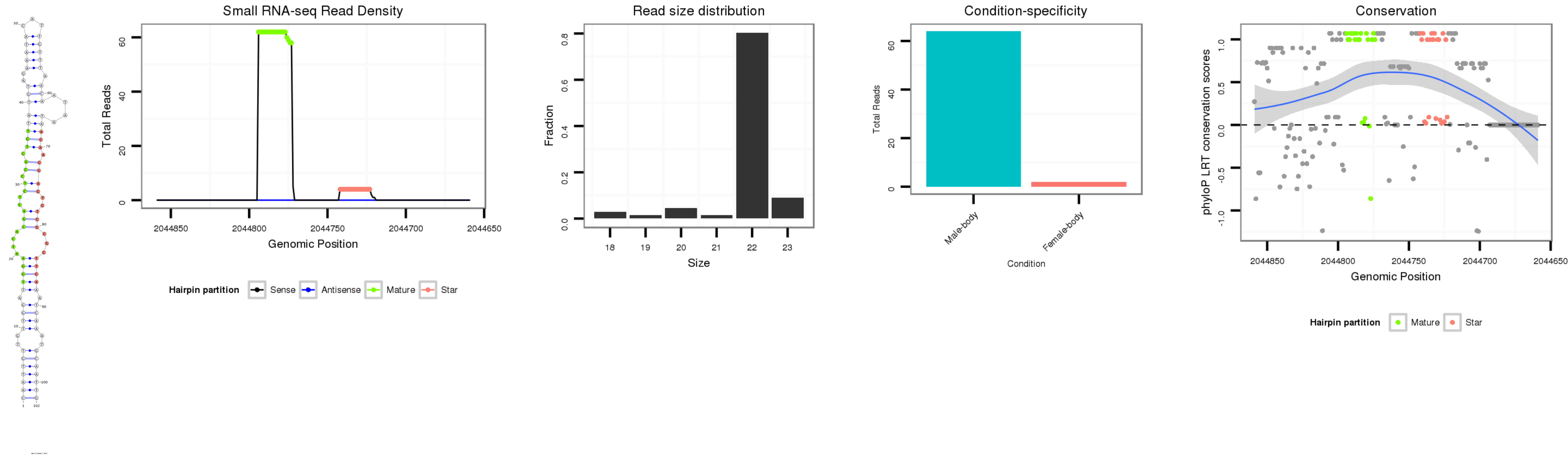
Species	Coordinate	ID	Alignment
droGri2	scaffold_14906:2062002-2062159 -	dgr_56	AATTCCATCACGGCGAGGAGCGCAAAATCATAGTATTCCACAAAGGGCAACGTAAGTAC-----ATTCGGTGAGCAA-ATAACTGTTATGTTTGCTGACAAAATGCATTTTACAGGAAGAGATTGCAGAAGCACGAGGAGCAGGCGCCTCCCTTGTGGGTGGCGTG
droV1r3	scaffold_12855:971762-971918 -		AGTTTCATCACGGCGGAGGACGCAAAATCATAGTATTTCACCAAGGCAAAAGTAAAGTATTTTAAAGAACAAAACAAATGTTA-----TGCTCGCT-----TACCCATGCAATTCAGAGCAATTACAGCGCCCGCAAGCGCGCCCTTGTGGGCAGCGTG
droMej3	scaffold_6540:7562333-7562494 +		AATTTCATCACGGCGAGGAGCGCAATCATAGTATTCCACAAAGGGCAAGTAAAGTCTGACAAATGACAAATATATATTAG-----T-----GCATCTAT-----ACACAAATATTTAGGATTCGAAATTCGAAAGCCCGCAAGCAGCGCGCTTGTGGGTGGCGTG
droW112	scf2_1100000004902:2799355-2799512 -		AGTTTCGCCAAGGCGAGGAGCGCAATCATAGTTCACCAAGGCAAAAGTAAAGTAT-----CTTACCTTTTATGTAAGTTCGAATACCAAAACCCCTTGAATGTAAAGCAATTATTGAAGCCCGCAAGCAGCGCGCTTGTGGGTGGCGTG
dp5	2:14649380-14649531 +		AGTTTCGCCAAGGCGAGGAGCGCAATCATAGTTCACCAAGGCAAAAGTAAAGTAT-----CATATCTTAACCTTG-----GATTACTTAT-----TGAATAATCGTTTTCAGAGCAATCTTAGAGCCAGAGAGAGCGCGCTTGTGGGTGGCGTG
droPer2	scaffold_0:5768207-5768362 -		AGTTTCGCCAAGGCGAGGAGCGCAATCATAGTTCACCAAGGCAAAAGTAAAGTAT-----TATATTTTAACCTTGATTGATTACTTAT-----TGAATAATCGTTTTCAGAGCAATCTTAGAGCCAGAGAGAGCGCGCTTGTGGGTGGCGTG
droAna3	scaffold_13340:13225427-13225584 +		AGTTTCGCCAAGGCGAGGAGCGCAATCATAGTTCACCAAGGCAAAAGTAAAGTAT-----CTCCTATATATCTTATATACATTTACCTTTATATCTATCTACAAATGAAATTCGGAAGCCAGAGAGCGCGCTTGTGGGTGGCGTG
droBip1	scf718000039691:2097859-2098015 +		AGTTTCGCCAAGGCGAGGAGCGCAATCATAGTTCACCAAGGCAAAAGTAAAGTAT-----CTCCTATATATCTTATATACATTTACCTTTATATCTATCTACAAATGAAATTCGGAAGCCAGAGAGCGCGCTTGTGGGTGGCGTG
droK1k1	scf7180000302810:178176-178330 -		GGTTTCGCCAAGGCGAGGAGCGCAATCATAGTTCACCAAGGCAAAAGTAAAGTAT-----CTCCTATATATCTTATATACATTTACCTTTATATCTATCTACAAATGAAATTCGGAAGCCAGAGAGCGCGCTTGTGGGTGGCGTG
droF1c1	scf7180000454073:3320294-3320452 -		AGTTTCGCCAAGGCGAGGAGCGCAATCATAGTTCACCAAGGCAAAAGTAAAGTAT-----AGTTTGTGTATTTATGATCCCTATACCTCCCTTTCTATCTTTACAGATCAGATTCTCAGCTAGCGCAAGCGCGCTTGTGGGTGGCGTG
droE1e1	scf7180000491212:1701107-1701265 -		AGTTTCGCCAAGGCGAGGAGCGCAATCATAGTTCACCAAGGCAAAAGTAAAGTAT-----ATCTAATAGATCTTGAACCCCAATAACTCTCTGTCTCTCTCACAGAGAGCTTCGAGCGCAAGCGCGCTTGTGGGTGGCGTG
droRho1	scf7180000779955:90519-90577 +		AGTTTCATCACGGCGAGGAGCGCAATCATAGTTCACCAAGGCAAAAGTAAAGTAT-----ATCTCCATATTTCCAGAAATCCCGCAATTACTCAATTCTCTCTCACAGAGAGCTTCGAGCGCAAGCGCGCTTGTGGGTGGCGTG
droB1a1	scf7180000302402:6816972-6817130 +		AGTTTCGCCAAGGCGAGGAGCGCAATCATAGTTCACCAAGGCAAAAGTAAAGTAT-----AGATTCTCTATTTTGTGATTTCTCAATACACTTTTGAATCTCTCTCACAGAGAGCTTCGAGCGCAAGCGCGCTTGTGGGTGGCGTG
droTak1	scf7180000415750:38162-38320 +		AGTTTCGCCAAGGCGAGGAGCGCAATCATAGTTCACCAAGGCAAAAGTAAAGTAT-----TAGTCCATCTTTGTGATTCCTTTCAACCACTTCTCTCTCTCTCACAGAGAGCTTCGAGCGCAAGCGCGCTTGTGGGTGGCGTG
droEug1	scf7180000409490:593660-593818 -		AGTTTCGCCAAGGCGAGGAGCGCAATCATAGTTCACCAAGGCAAAAGTAAAGTAT-----AACTACCTATTTCTCAATCCCAATTAATCTTTAAATCTCTCTCTCTCACAGAGAGCTTCGAGCGCAAGCGCGCTTGTGGGTGGCGTG
dm3	chr3R:4127739-4127896 +		AGTTTCGCCAAGGCGAGGAGCGCAATCATAGTTCACCAAGGCAAAAGTAAAGTAT-----AGTTCTTATGATC-AAAATCATAAAAAACAACCTTGAAATTTTTCAGAAATGAGCTTCGAGCGCAAGCGCGCTTGTGGGTGGCGTG
droSim2	3r:16839013-16839170 -		AGTTTCGCCAAGGCGAGGAGCGCAATCATAGTTCACCAAGGCAAAAGTAAAGTAT-----AGTCCCTTATGATC-AAAAGCTTAATAAACAACCTTTAAATCTATTTCAGAAATGAGCTTCGAGCGCAAGCGCGCTTGTGGGTGGCGTG
droSec2	scaffold_0:17701297-17701454		AGTTTCGCCAAGGCGAGGAGCGCAATCATAGTTCACCAAGGCAAAAGTAAAGTAT-----AGTCCCTTATGATC-AAAAGCTTAATAAACAACCTTTAAATCTATTTCAGAAATGAGCTTCGAGCGCAAGCGCGCTTGTGGGTGGCGTG
droYak3	3R:8202977-8203135 +		AGTTTCGCCAAGGCGAGGAGCGCAATCATAGTTCACCAAGGCAAAAGTAAAGTAT-----AGTCCCTTATGATGATCATCAACAAACAACCTTGAAATTTTTCAGAAATGAGCTTCGAGCGCAAGCGCGCTTGTGGGTGGCGTG
droEre2	scaffold_4770:17445722-17445880 -		AGTTTCGCCAAGGCGAGGAGCGCAATCATAGTTCACCAAGGCAAAAGTAAAGTAT-----AGTCCCTTATGATGATCATCAAAAAACAATTTAAATCTATTTCAGAAATGAGCTTCGAGCGCAAGCGCGCTTGTGGGTGGCGTG

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

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

[illegible]

Anti-sense strand reads

[illegible]

No data available in table

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droGr12	scaffold_15081:2044659-2044859_-	dgr_45	TATCCCGACTCTATCGATAGACAA--CGATTGTCAGTTAGG-----CTATTCCG---GCTAACAAATTGTTGTGGAT TGGAATCACGACTCTCCGCTGT TATGTAGAAATACATTGTTTAAC-----AATAATA ACAACGAGTCTCGCGCTTCA AAATCAAATGCAATTGGTTCCTCAGCAATGCAAAGTGTAACAATATGATTTTGGATTATGTTACC
droVir3	scaffold_13042:907078-907225=	dvi_343	GC----- CTATCGATA AACTAT CGA TAAGCA T--- ----- AGCGCC CCAA TCG ATTAG CT ACAATTCT CGTTG ATTGGAATCACGACACTCACTGT TATGTAGAA ----- -----AA CGATAACA GTGAGTCTCGCGTTC CAACTCAAA CGCAAT-AA TTCT CGAGCAA-----
droMoJ3	scaffold_6328:2901283-2901391_-	dmo_204	TC-----C----- ----- ----- ----- ----- ----- CTT ACAATT CTGT GT ATTGGAATCACGAACTCATCTGT TATGTAG CG----- -----AA CGATAACA GTGAGTCTCGCAT CCAACTCAAA CGCAAT-AA TT CA GTAGCA ACG-----
droW112	scf2_11000000004909:7956558-7956706_+		TG----- ATC A TATACAT TGTGTG -TGT GAGTGT TTTTGTGTGGGATCCG CATATT--- ----- GT TTGT AGATG TG TGGAATCACGACATCACTGT TATGT TT ACATA --- FGT CTAACATTCTGTTATA GTATAACAGTCTCTCTTCCGCTTCTCT C CA
droEle1	scf7180000490751:1118639-1118647_+		TTTCC GAGT ----- ----- ----- ----- ----- ----- -----

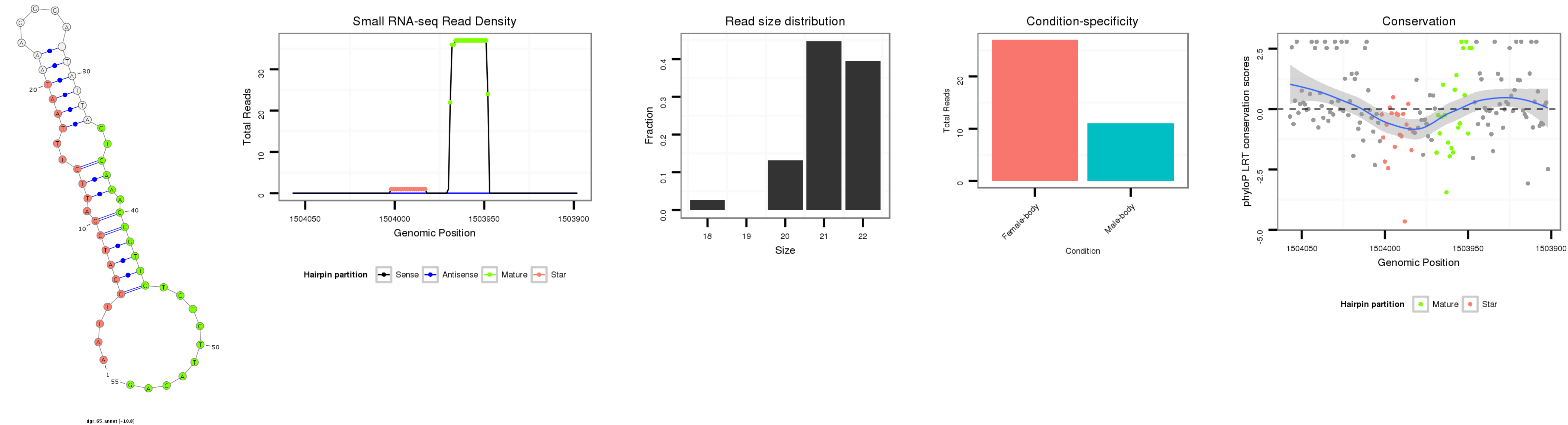
Generated: 09/08/2015 at 06:12 PM **PASS/FAIL**

crit.star	2
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	4
rescue.candidate	0

	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	0

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Show Alternate Folds

Flybase annnotation

intron [Dgri\GH15675-in]; CDS [Dgri\GH15675-cds]; CDS [Dgri\GH15675-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

										Read #		Hit	Total			M041	V109
										size	Mismatch	Count	Norm	Total	female body	male body	
GAACGGAAATTGAGTTCCTCATGATTTGCAAGTGCTACAACATTTGATGACGTAAGAAATTGGATGGATCTTTAATAAAGGGATTATTACTGAACCGTCTCTCTTACAGCTACCGGATACCAGCTACTATCTGAAGGCCATGGACATATCATTTACGAA																	
***** (((((((((((((((((((.....))))))))) *****																	
.....TGAAACCGTTCCTCTTTACAGT										22	1	1	15.00	15	12	3	
.....CTGAACCGGTTCTCTCTTACAG.....										22	0	1	14.00	14	6	8	
.....TGAAACCGTTCCTCTTTACAG.....										21	0	1	10.00	10	10	0	
.....CTGAACCGTTCCTCTCTTACA.....										21	0	1	7.00	7	6	1	
.....TGAAACCGTTCCTCTTACA.....										20	0	1	4.00	4	4	0	
.....AAACCGTTCCTCTTACA.....										18	0	1	1.00	1	1	0	
.....ACTGAACCGGTTCTCTTACA.....										22	0	1	1.00	1	0	1	
.....AATTGGATGGATCTTTAAT.....										20	0	1	1.00	1	0	1	
.....CTGAACCGGTTCTCTTACAG.....										22	1	1	1.00	1	1	0	
.....CTGAACCGTTCCTCTTACAGT										23	1	1	1.00	1	1	0	
.....CTGAACCGTTCCTCTTACAGG										23	2	1	1.00	1	1	0	
.....CTGAACCGGTTCTCTTACAGA.....										23	1	1	1.00	1	1	0	

Anti-sense strand reads

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

Re-alignment of all predicted orthologs

[illegible]

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

Predicted structure

Show Alternate Folds

Flybase annotation

intron [Dgn⁺GH24062-in]; CDS [Dgn⁺GH24062-cds]; CDS [Dgn⁺GH24062-cds]

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

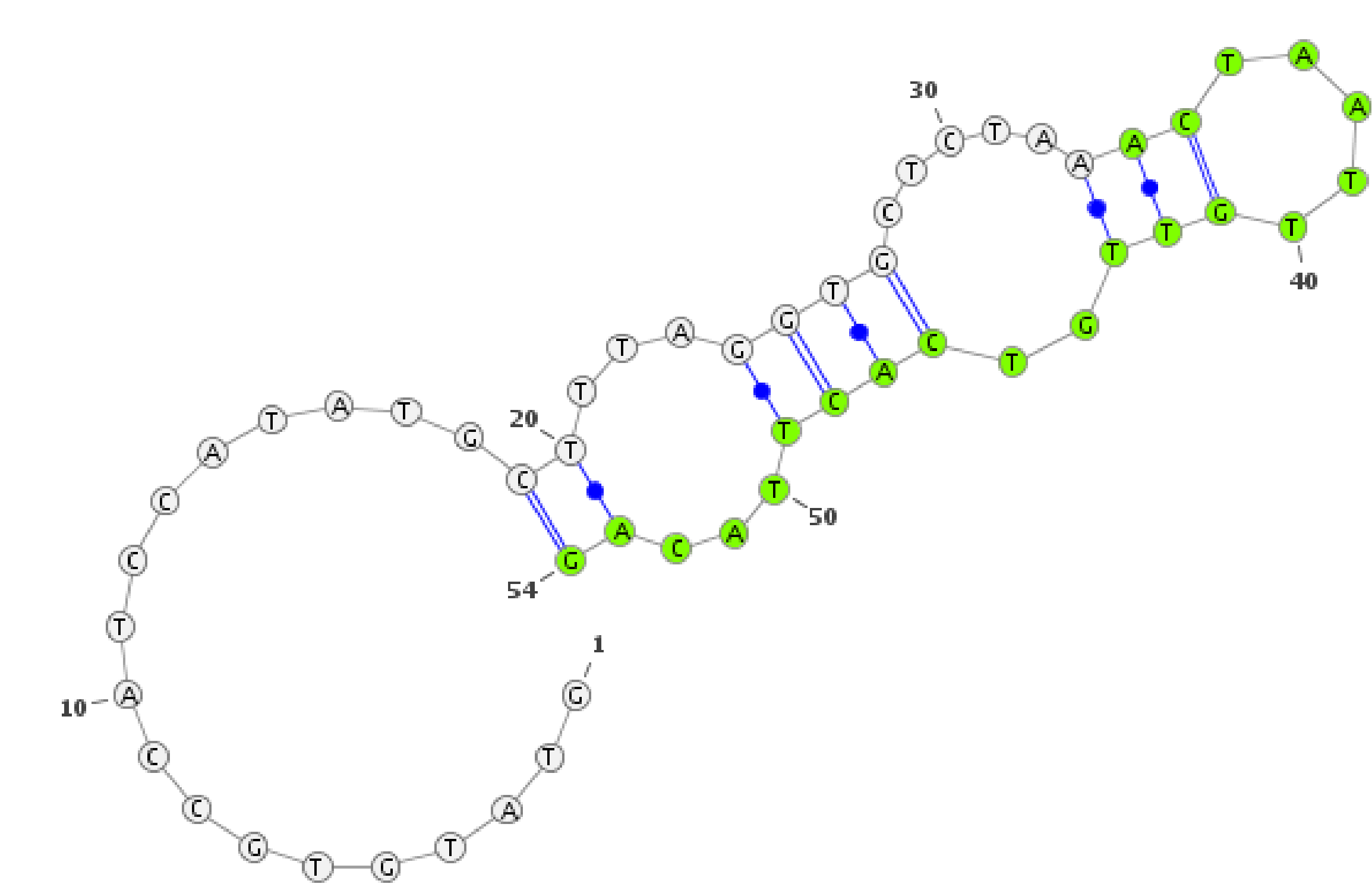
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	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	2
rescue.candidate	0

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dgf_258	scaffold_15081:119802-119855 +	confident-exception	Mirtron	intron	[View on UCSC Genome Browser (Cornell Mirror)]

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

Predicted structure



dgf_258_annot [-1.0]

Show Alternate Folds

Flybase annotation

intron [Dgri/GH17761-in]; CDS [Dgri/GH17761-cds]; CDS [Dgri/GH17761-cds]

No Repeatable elements found

Sense Strand Reads

	Read #		Hit	Total		M041	V109
	size	Mismatch	Count	Norm	Total	female body	male body
CGAGGTGGACTCCAATCCAATCAGACGAGGAGTCTTCGATTGTCTGGGTATGTGCCATCCATGCTTTAGGTGCTCTAAACTPAATTTGTGCTACCTACAGACACAAATGAGACGAACTCGCTGGCCAAATGGAGTTCGCTGGAGCTGTTC	21	0	1	15.00	15	13	2
*****(((((.....(((.....)))))).....))*****	20	0	1	12.00	12	11	1
.....ACTAATTGTTGTCACTTACAG.....	22	1	1	9.00	9	8	1
.....ACTAATTGTTGTCACTTACAG.....	20	0	1	3.00	3	3	0
.....CTAATTGTTGTCACTTACAG.....	18	0	1	1.00	1	1	0
.....TAATTGTTGTCACTTACAG.....	20	0	1	1.00	1	1	0
.....AATGAGACGAACTCGCTGGC.....	23	2	1	1.00	1	1	0
.....ACTAATTGTTGTCACTTACAGTT.....	20	0	1	1.00	1	0	1
.....CGAGGAGTCTTCGATTGTC.....	21	0	1	1.00	1	1	0
.....GACGAACTCGCTGGCCAAATG.....	19	1	2	0.50	1	1	0
.....TAATTGTTGTCACTTACAG.....							

Anti-sense strand reads

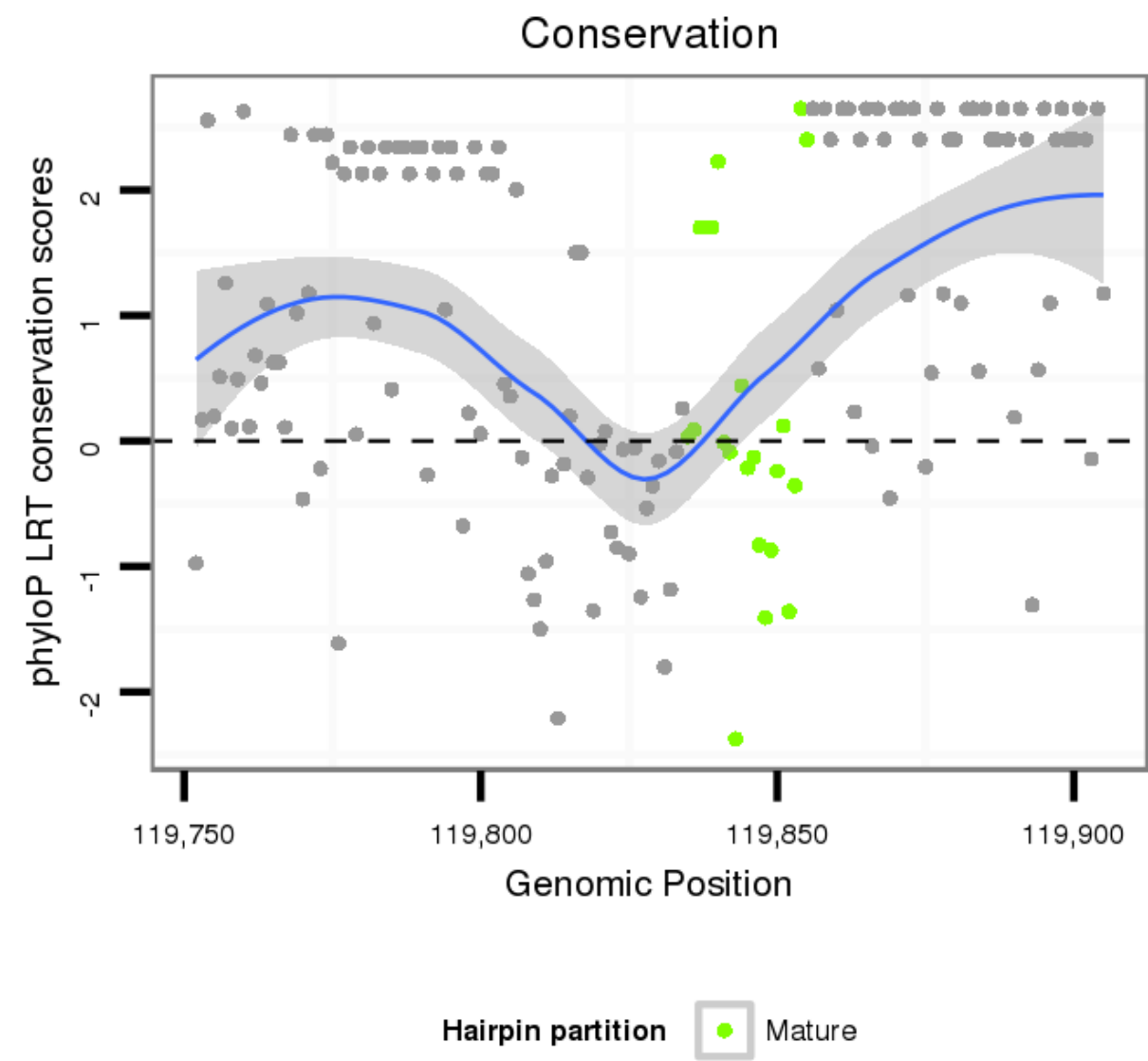
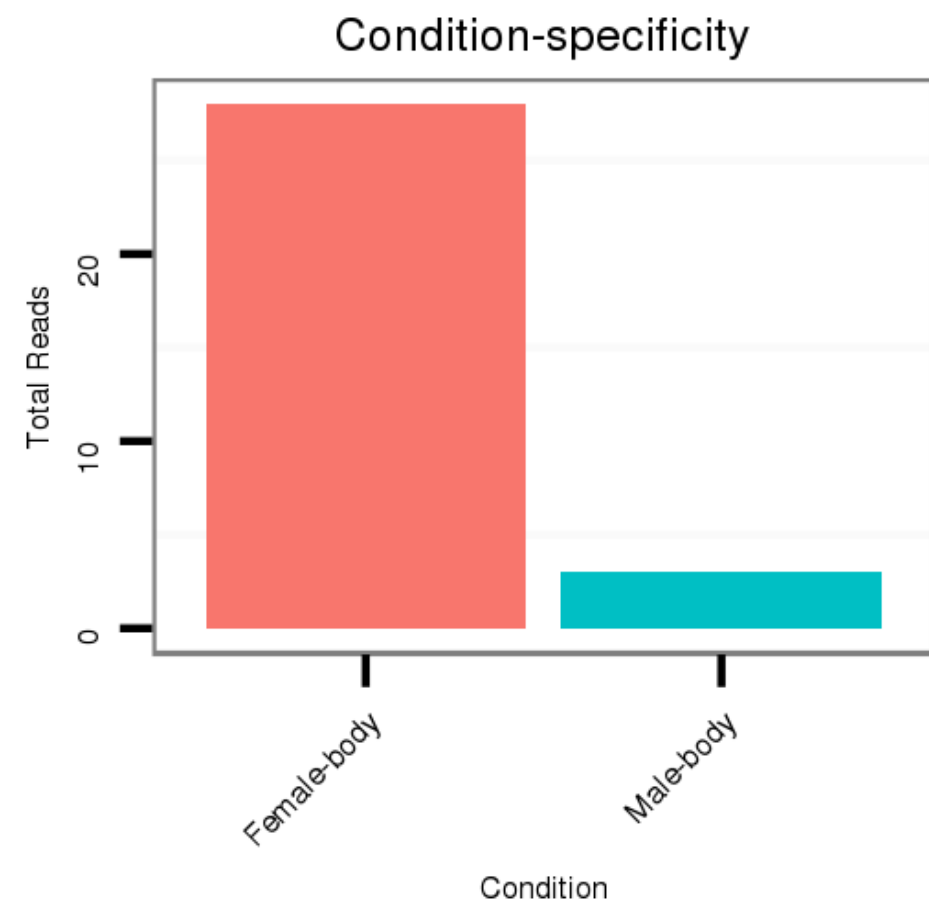
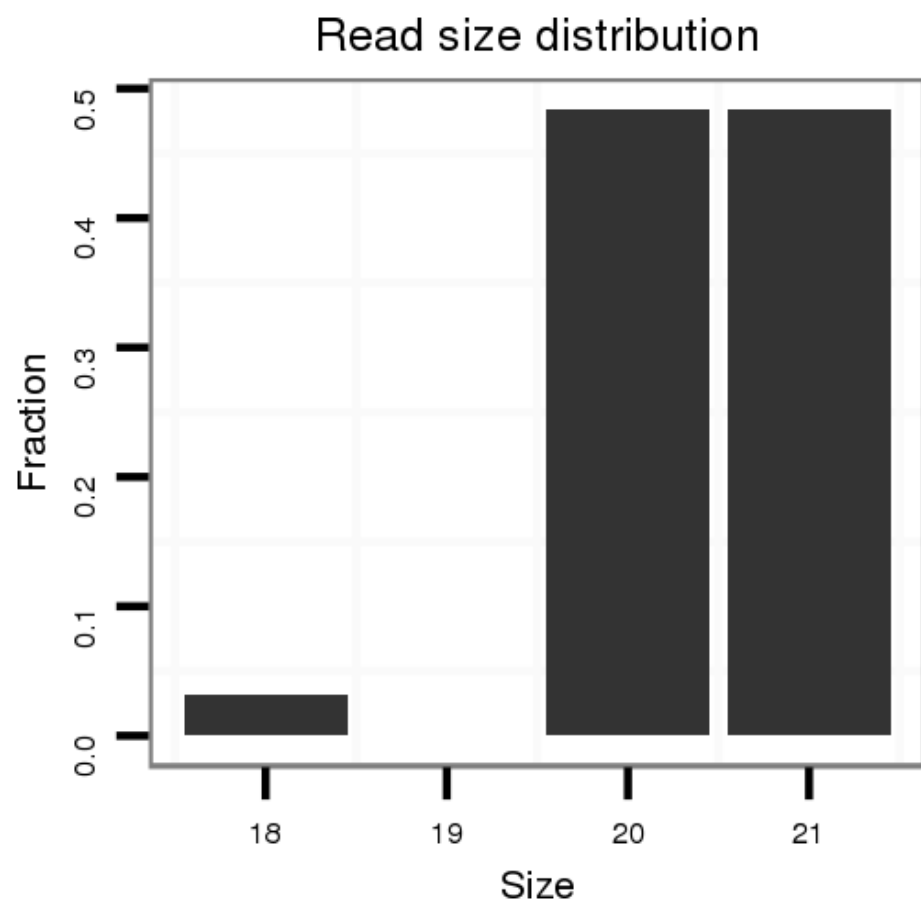
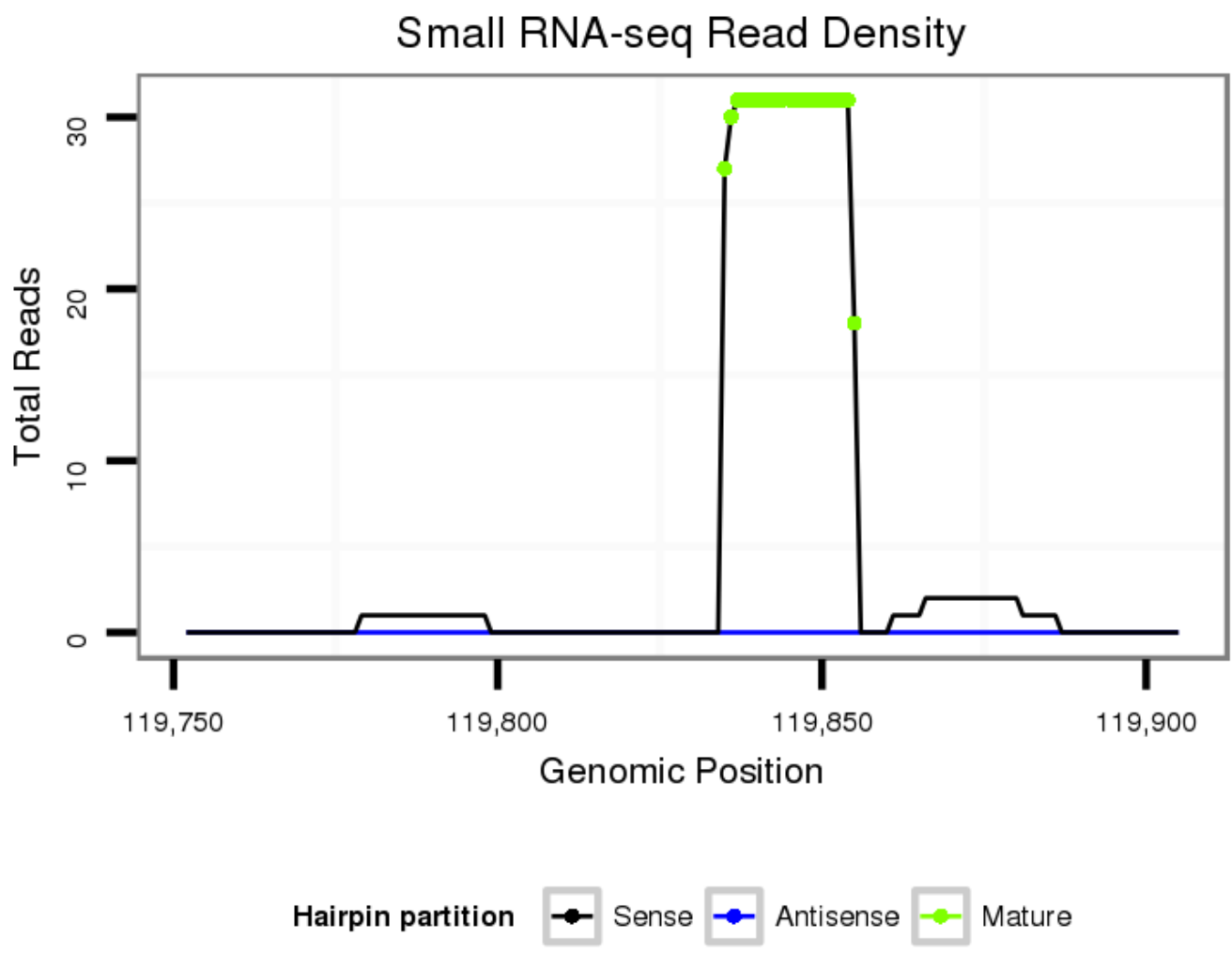
GCTCCACCTGAGGTTTAGGTTGAGTCTGCTCTCCAGAACTAACAGACCCATACACGGTAGGTATACGAAATCCACGAGATTGGATTAAACACAGCTGAATGCTGTGTTTACTCTGCTTGAGCGACCGGTTTACCTCAAGCGACCTCGACAAC					Read #	Hit	Total	
*****(((((.....(((.....)))))).....))*****					size Mismatch	Count	Norm	Total
No data available in table								
Show Alignment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

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droGr12	scaffold_15081:119752-119905 +	dgf_258	CGAGGTGGACTCCAATCCAATCAGACGAGGAGTCTTCGATTGTCTGGGTATGTGC-----CATC-C-----ATA-----TGCTTTAG-----GTGC--T-----CT---AACTAATTGC--TT-----GTCACTT-ACAGACACAAATGAGACGAACTCGCTGGCCAAATGGAGTTCGCTGGAGCTGTTC
droVir2	scaffold_12970:5224751-5224909 -	dvi_13172	GAGGTGGACTCCAATCCAATCAGACGAGGAGTCTTCGATTGTCTGGGTATGTGC-----SCPG-#-----TGGCAT-#-GTTCAATATGGATGTC-#-CGACTAATTATGTC-#-TTCTTT-#-GAGACACAAAGSAACGAAGTCTGTCGCAATGGAGCTCCTCAGCTC#PG
droMoJ3	scaffold_6473:4793264-4793434 -		GAGGTGGACTCCAATCCAATCAGACGAGGAGTCTTCGATTGTCTGGGTATGTGC-----SCPG-#-----TGGCAT-#-GTTCAATATGGATGTC-#-CGACTAATTATGTC-#-TTCTTT-#-GAGACACAAATGAGACGAACTCGCTGGCCAAATGGAGTTCGCTGGAGCTGTTC
droW112	scf7_1100000004590:1162638-1162806 -		GAGGTGGACTCCAATCCAATCAGACGAGGAGTCTTCGATTGTCTGGGTATGTGC-----SCPG-#-----TGGCAT-#-GTTCAATATGGATGTC-#-CGACTAATTATGTC-#-TTCTTT-#-GAGACACAAATGAGACGAACTCGCTGGCCAAATGGAGTTCGCTGGAGCTGTTC
dp5	Al_group1e:1311887-1312041 +		GAGGTGGACTCCAATCCAATCAGACGAGGAGTCTTCGATTGTCTGGGTATGTGC-----SCPG-#-----TGGCAT-#-GTTCAATATGGATGTC-#-CGACTAATTATGTC-#-TTCTTT-#-GAGACACAAATGAGACGAACTCGCTGGCCAAATGGAGTTCGCTGGAGCTGTTC
droPer2	scaffold_18:157908-158062 +		GAGGTGGACTCCAATCCAATCAGACGAGGAGTCTTCGATTGTCTGGGTATGTGC-----SCPG-#-----TGGCAT-#-GTTCAATATGGATGTC-#-CGACTAATTATGTC-#-TTCTTT-#-GAGACACAAATGAGACGAACTCGCTGGCCAAATGGAGTTCGCTGGAGCTGTTC
droAna3	scaffold_13248:2890139-2890298 +		GAGGTGGACTCCAATCCAATCAGACGAGGAGTCTTCGATTGTCTGGGTATGTGC-----SCPG-#-----TGGCAT-#-GTTCAATATGGATGTC-#-CGACTAATTATGTC-#-TTCTTT-#-GAGACACAAATGAGACGAACTCGCTGGCCAAATGGAGTTCGCTGGAGCTGTTC
droBip1	scf7180000396429:123062-123219 -		GAGGTGGACTCCAATCCAATCAGACGAGGAGTCTTCGATTGTCTGGGTATGTGC-----SCPG-#-----TGGCAT-#-GTTCAATATGGATGTC-#-CGACTAATTATGTC-#-TTCTTT-#-GAGACACAAATGAGACGAACTCGCTGGCCAAATGGAGTTCGCTGGAGCTGTTC
droRik1	scf7180000302344:225820-225872 +		GAGGTGGACTCCAATCCAATCAGACGAGGAGTCTTCGATTGTCTGGGTATGTGC-----SCPG-#-----TGGCAT-#-GTTCAATATGGATGTC-#-CGACTAATTATGTC-#-TTCTTT-#-GAGACACAAATGAGACGAACTCGCTGGCCAAATGGAGTTCGCTGGAGCTGTTC
droPic1	scf7180000454073:1303342-1303423 -		GAGGTGGACTCCAATCCAATCAGACGAGGAGTCTTCGATTGTCTGGGTATGTGC-----SCPG-#-----TGGCAT-#-GTTCAATATGGATGTC-#-CGACTAATTATGTC-#-TTCTTT-#-GAGACACAAATGAGACGAACTCGCTGGCCAAATGGAGTTCGCTGGAGCTGTTC
droHel1	scf7180000491044:45899-45952 -		GAGGTGGACTCCAATCCAATCAGACGAGGAGTCTTCGATTGTCTGGGTATGTGC-----SCPG-#-----TGGCAT-#-GTTCAATATGGATGTC-#-CGACTAATTATGTC-#-TTCTTT-#-GAGACACAAATGAGACGAACTCGCTGGCCAAATGGAGTTCGCTGGAGCTGTTC
droRho1	scf718000077352:24135-24198 -		GAGGTGGACTCCAATCCAATCAGACGAGGAGTCTTCGATTGTCTGGGTATGTGC-----SCPG-#-----TGGCAT-#-GTTCAATATGGATGTC-#-CGACTAATTATGTC-#-TTCTTT-#-GAGACACAAATGAGACGAACTCGCTGGCCAAATGGAGTTCGCTGGAGCTGTTC
droBia1	scf7180000302041:694568-694653 +		GAGGTGGACTCCAATCCAATCAGACGAGGAGTCTTCGATTGTCTGGGTATGTGC-----SCPG-#-----TGGCAT-#-GTTCAATATGGATGTC-#-CGACTAATTATGTC-#-TTCTTT-#-GAGACACAAATGAGACGAACTCGCTGGCCAAATGGAGTTCGCTGGAGCTGTTC
droTak1	scf7180000414562:491234-491320 -		GAGGTGGACTCCAATCCAATCAGACGAGGAGTCTTCGATTGTCTGGGTATGTGC-----SCPG-#-----TGGCAT-#-GTTCAATATGGATGTC-#-CGACTAATTATGTC-#-TTCTTT-#-GAGACACAAATGAGACGAACTCGCTGGCCAAATGGAGTTCGCTGGAGCTGTTC
droBug1	scf7180000409008:87079-87241 +		GAGGTGGACTCCAATCCAATCAGACGAGGAGTCTTCGATTGTCTGGGTATGTGC-----SCPG-#-----TGGCAT-#-GTTCAATATGGATGTC-#-CGACTAATTATGTC-#-TTCTTT-#-GAGACACAAATGAGACGAACTCGCTGGCCAAATGGAGTTCGCTGGAGCTGTTC
dm3	chrX:13665187-13665359 +		GAGGTGGACTCCAATCCAATCAGACGAGGAGTCTTCGATTGTCTGGGTATGTGC-----SCPG-#-----TGGCAT-#-GTTCAATATGGATGTC-#-CGACTAATTATGTC-#-TTCTTT-#-GAGACACAAATGAGACGAACTCGCTGGCCAAATGGAGTTCGCTGGAGCTGTTC
droSim2	node_24415:70784-70972 -		GAGGTGGACTCCAATCCAATCAGACGAGGAGTCTTCGATTGTCTGGGTATGTGC-----SCPG-#-----TGGCAT-#-GTTCAATATGGATGTC-#-CGACTAATTATGTC-#-TTCTTT-#-GAGACACAAATGAGACGAACTCGCTGGCCAAATGGAGTTCGCTGGAGCTGTTC
droBeet2	scaffold_20:303894-304094 +		GAGGTGGACTCCAATCCAATCAGACGAGGAGTCTTCGATTGTCTGGGTATGTGC-----SCPG-#-----TGGCAT-#-GTTCAATATGGATGTC-#-CGACTAATTATGTC-#-TTCTTT-#-GAGACACAAATGAGACGAACTCGCTGGCCAAATGGAGTTCGCTGGAGCTGTTC
droTak3	X7:957837-958034 +		GAGGTGGACTCCAATCCAATCAGACGAGGAGTCTTCGATTGTCTGGGTATGTGC-----SCPG-#-----TGGCAT-#-GTTCAATATGGATGTC-#-CGACTAATTATGTC-#-TTCTTT-#-GAGACACAAATGAGACGAACTCGCTGGCCAAATGGAGTTCGCTGGAGCTGTTC
droPer2	scaffold_4690:13219266-13219495 -		GAGGTGGACTCCAATCCAATCAGACGAGGAGTCTTCGATTGTCTGGGTATGTGC-----SCPG-#-----TGGCAT-#-GTTCAATATGGATGTC-#-CGACTAATTATGTC-#-TTCTTT-#-GAGACACAAATGAGACGAACTCGCTGGCCAAATGGAGTTCGCTGGAGCTGTTC

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PASS/FAIL	
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.pairing	0
crit.top3	1
crit.prop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	1
rescue.confident	0
rescue.candidate	0



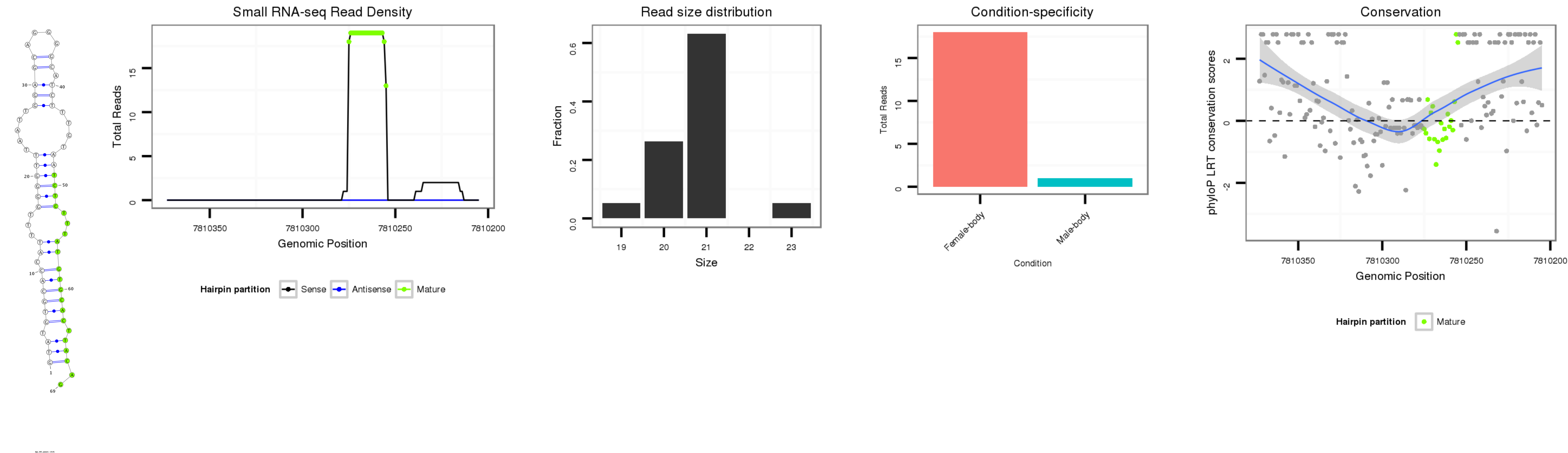
Hairpin partition ☐ Sense ☐ Antisense ☒ Mature

Hairpin partition ☒ Mature

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dgr_305	scaffold_15110:7810255-7810323 -	confident-exception	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 [Dgrñ\GH15201-in]; CDS [Dgrñ\GH15201-cds]; CDS [Dgrñ\GH15201-cds]; utr3 [utr3_minus_4500]; utr3 [utr3_minus_4499]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

CATTCCATTGTGCGTCACATTTTACCGGATGGCGCCGCCCTCTTCGATGGTATGTGCACCATTTTGGGGTTAATTGGAGCAGGGGCATCTTTGTAA	TCTCTTTATGTGCACTTTACGAGTTCCCGAGAATAGCCGTTCCGATCGCATGCTCTTCTCGAGGAGACC	Read #	Mismatch	Hit	Total	female body	V109
size	Count	Norm	Total		male body		
.....TCTCTTTATGTGCACTTACAGT.....	22	1	1	36.00	36	36	0
.....TCTCTTTATGTGCACTTACAG.....	21	0	1	12.00	12	11	1
.....TCTCTTTATGTGCACTTACAG.....	20	0	1	4.00	4	4	0
.....TCTCTTTATGTGCACTTACAG.....	21	1	1	4.00	4	4	0
.....TCTCTTTATGTGCACTTACAGTT.....	23	2	1	2.00	2	2	0
.....TCTCTTTATGTGCACTTACAG.....	20	0	1	1.00	1	1	0
.....GCCGTTCCGATCGCATGCTCTTCC.....	24	0	1	1.00	1	0	1
.....TCTCTTTATGTGCACTTACAG.....	21	1	1	1.00	1	1	0
.....TTCCGATCGCATGCTCTTCTCG.....	22	0	1	1.00	1	1	0
.....TAATCTCTTTATGTGCACTTAC.....	23	0	1	1.00	1	1	0
.....TCTCTTTATGTGCACTTAC.....	19	0	1	1.00	1	1	0

Anti-sense strand reads

[illegible]

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droGr12	scaffold_15110:7810205-7810373 -	dgr_305	CATTCCATTGTGCGTCACATTTTACCGGATGGCGCCGCCCTCTTCGATGGTATGTGCACCAT-----T-----TTGGGGT-T-----TAAT-TG--GAGCAGGGGCATCT-----TTGTA-ACTCT-----TTATGT--GCAC-TTACAGAGTCCCCGAGAATAGCCGTTCGCATCGCATGCTCTTCTGCAGGAGACC
droVit3	scaffold_13049:3662227-3662383 -		CATTCCA T GTGCGTCAC C TTTT G CC A AAATGGCGCC A ST T CTCTT G ACGGT T GT T ACAG C CC-----G-CTCTGATC T TT-CT T CTGCT T -----G-CTTA-CT-GT T T-TTCA-TT C AGAA T TTCCCGAG C AGCCGCT C AGATCGCATGCTCTTCTGCAGGAG G CT
droMoJ3	scaffold_6654:387608-387771 +		CATTCC C TTATGCGTCAC A CTTTTT G CC A AGAGGG A AG G CCCTCTTTGATGGTAC S CTGTAT T GTCTCAA A C-----TCTT---G-TCAT-TG S T-----AA-CTATATAG--CC-------A-AT-----AAT C C-AAT-T T CAGAA T TTCTT S AGG C AGCCGCC C CTGATCGCATGCTCTTCTGCAGGAG G CT
droW112	scf2_1100000004511:2414102-2414256 +		CATTCCATTGTGCT T ST A C C TTTT G CC A SATGG T SG T GT T TTT T GATGGTAA S CTATAATG-----T-----AT--ATTAACCAT-----A-----TG--CG-----ATTTA-AG-GCAATATAT T TT T GTTAGAA T TTCTT S AGC A ATCCGATCTGATCGTATGTTT T TTT T CAAGAA T CC
dpB5	XR_group3a:1100924-1101084 -		CATTCCA C CT C CT T STACATT C CT G CC C CAACGGA S CGGCT T TTTCGATGGTATG C AGGAGGA-----TAT--AGAT---G-TCAT-TG--AAATCAT S ATATG-----TCAG-AAA G -----TTTT-CCG C AGAA T TTCCCGAG C AAAGCA T ATCCGATCGCATGCT T CTCTT T CAAGAG C CC
droPer2	scaffold_23:1128473-1128633 -		CATTCCA C CT C CT T STACATT C CT G CC C CAACGGA S CGGCT T TTTCGATGGTATG C AGGAGGA-----TAG--AGAT---G-TCAT-TG--AAATCAT S AGATC-----TCAG-AAA G -----TTTT-CCG C AGAA T TTCCCGAG C AAAGCA T ATCCGATCGCATGCT T CTCTT T CAAGAG C CC
droAna3	scaffold_13337:1932168-1932329 +		CATTCCA C TT T GC A CTACATT C CT G CC C SATGGA S CTATCT T TTT T GAGGTAT T TTAGAT-----C--ATTTTA-SA--AC-TTT-----AAGATATTAACTT-----T-A--C-----TGCT-T-TGTT-GTTAGAA T TCCCT S AGC A ATCCTTCATCGCATGCT T CTCTC T AGGAG C CC
droBip1	scf7180000396569:1976618-1976728 +		CATTCCA C TT T GC A CTACATT C CT G CC C SATGGA S CT T GCACT A TTT T GAGGTAT C TTASATC-----GAT-----TTT T GGAAAT-C---G-----AACAG-ATATTTAA-----G---AC-T T CAC A ATTGTT C T C AGAA T TCCCT S AGC A ATCCTTCATCGCATGCT T CTCTT T CAAGAG C CC
droKi1k	scf7180000302510:987788-987948 +		CAT T CC C CTGTGC A CTAC T TT T CT G CC C CAATGGA S CGGCC T TTT T GAA S GTAT T TC C AAATA-----T-----CTGTTT-GT--AT-AT-TTT-----TA-GCTTCTCG-----G---A-TGTT-C--T T GGT--ATT T T C AGAGTTTCCCGAG C AAAGCCG C AGC S ATCGATGCT T CTCTGCAGGAG G CC
droFio1	scf7180000454113:561561-561724 +		TATTCCT T CTGTCTAC A CTATT C CT G CC C CAATG C AS T CT S GA S CTTTTCGATGGTAT T TCAGATA-----T-----TTTTTG-TT--AA-A--561561-----G-AG---TCG---CTGGTTTATTTAA-CT T T T GT T C--TTT C C C AGAGTTTCCCGAG C AAAGCCG C ATCGATCGCATGCT T CTCTGCAGGAG A CT
droEle1	scf7180000491249:4075068-4075228 +		CATTCC G CTGTGC A CTACATT C CT G CC C CAATGGA S CTGCT T TTTCGAGGTAT T AA T TTA-----A-----ATATTT-TG--AA-A-------G-TG---T-G---CCT-ATTTA-TTAA--TT T T T TAACA--A G T T CAGAGTTCCCCGAG C AAAGCA T ATCGATCGATGCT T CTCTT T GCAGGAG G CC
droRho1	scf7180000776850:437727-437885 +		CATTCC G CTGTGC A CTACATT C CT C CAATGGA S GA S CT T TTT T GATGGTAT T TTA T TAAT-----A-T-----TTTT---G-TCAT-TTAA-----AA-GCATCTAG-----G---TTA-TTGA-C-----TATAA T T T ACAGAGTCCCC T SAG C AAAGCA T ATCCGA S CGTATGCT T CTCTT T GCAGGAG G CC
droBia1	scf7180000300910:1631407-1631567 -		CATTCC G CTGTGC A CTACATT C CT G CC C CAACGGA S CCGCT T TTTCGAAGGTAT T CGAAGGA-----CTAACCATAATA T AA--TT T CATATC-----G---A-TTTA-CT-TGTATC--ATT T T G CAGAGTTCCCCGAG C AGCA T ATCGATCGCATGCT T CTCTT T GCAGGAG G CC
droTak1	scf7180000415095:292111-292277 +		CATTCC G CTGTGC A CCACATT C CT G CC C CAATGGA S CGGCT T TTTGAAGGTACT T TA C CTTA-----A-----TTATTT-TA--AC-A-------G-TT---TA T ---CATCTTTTA-TTAATTAATATTGTAT--TATT-T T CAGAGTTCCCCGAG C ATAGCA T ATCGATCGCATGCT T CTCTT T GCAGGAG G CC
droEug1	scf7180000409007:336418-336573 -		CATTCC G CTGTGC A CCACATT C CT G CC C CAATGCT T TTCTCT T TTT T GATGGTAT T TC T CTTA A -----G-CTACTT-TACATTAT T C---G------ACC-----G---A-TTAA-CC-TGTAT--ATT T C C AG A TTTCCCGAG C AAAGCA T ATCCGATCGATGCT T CTCTT T GCAGGAG G CC
dm3	chr31:1524090-1524244 -		CATTCC G CTGTGC A CTACATT C CT G CC C CAATGGCG C GCCCTCTTCGATGGTAT T TA T ASATA-----T-----TTGTAT-TT--A---G-----AAC-----AG---G-----TTTAA-AC-T G ACT--ATGA-T T CAGAGTTTCCCGAG C AGCA T ATCGATGCT T CTCTT T GCAGGAG C CC
droSim2	31:1434300-1434454 -	dsi_20520	CATTCC G CTGTGC A CTACATT C CT G CC C CAATGGCG C GCCCTCTTCGATGGTACT T TA T ASATA-----T-----TTGTCT-TT--A---G-----AAC-----AG---G-----TTTAA-AC-T

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