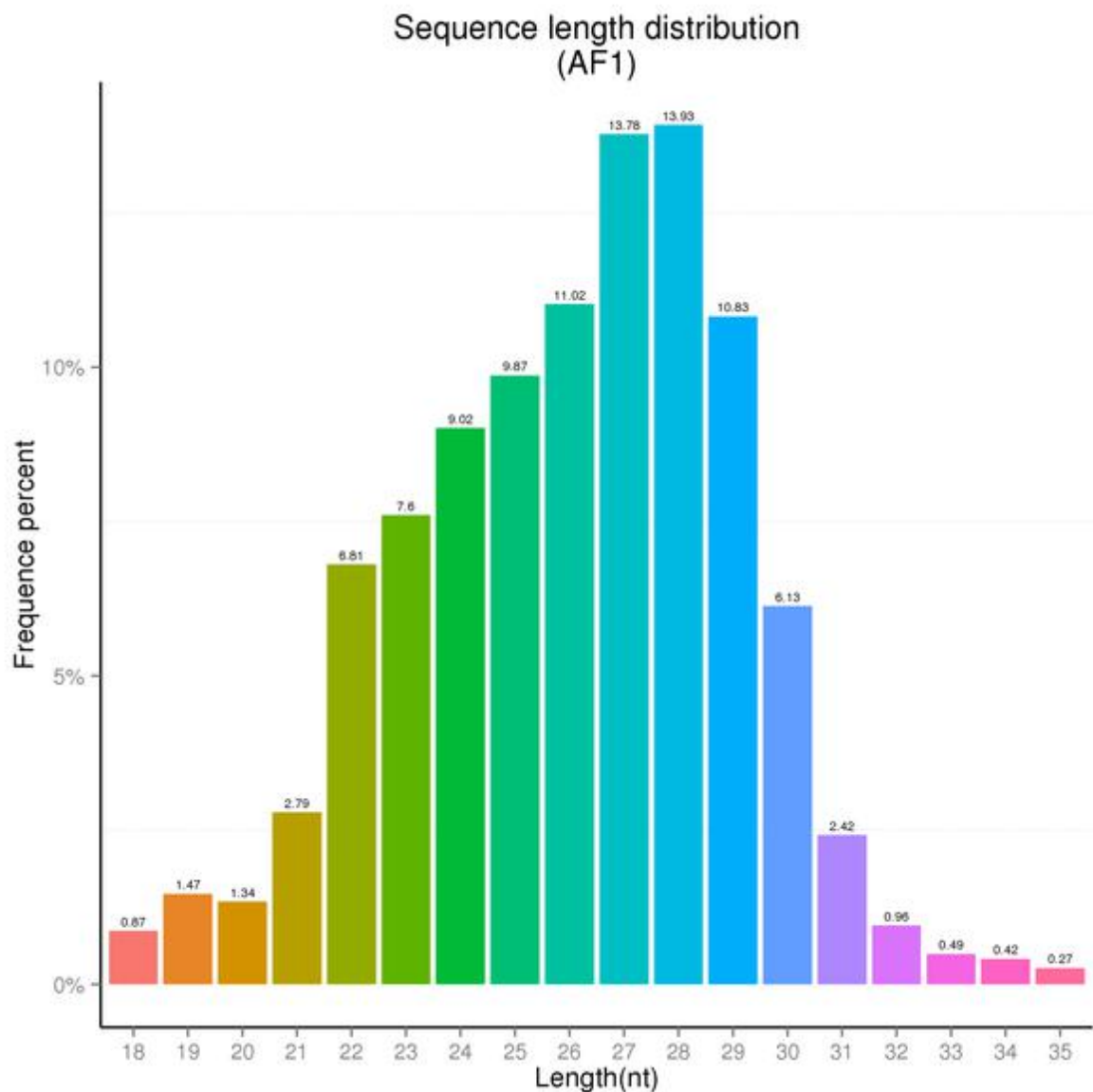


# Discovery and Characterization of piRNAs in male and female gonads of Amur sturgeon (*Acipenser schrenckii*)

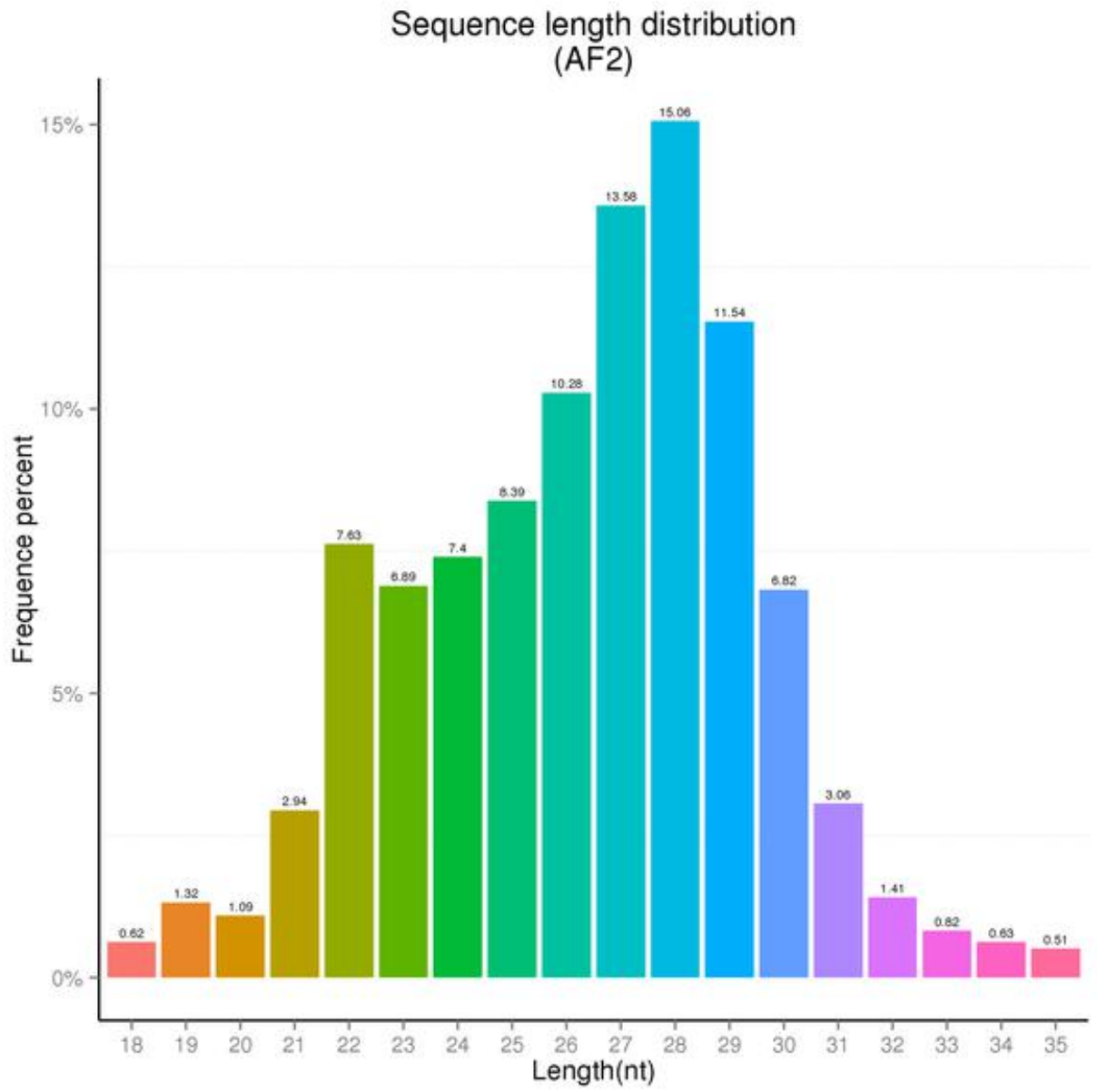
Lihong Yuan, Linmiao Li, Xiujuan Zhang, Jinping Chen\*

**Figure S1** - The sequence length distribution and frequency percentage of small RNA reads of *Acipenser schrenckii*. The x-axis indicates the length of small RNA reads. The y-axis indicates the percentage of small RNA reads with specific length. Different color suggests different type of small RNAs. A) and B), Ovary 1 and 2; C) and D), Testis 1 and 2.

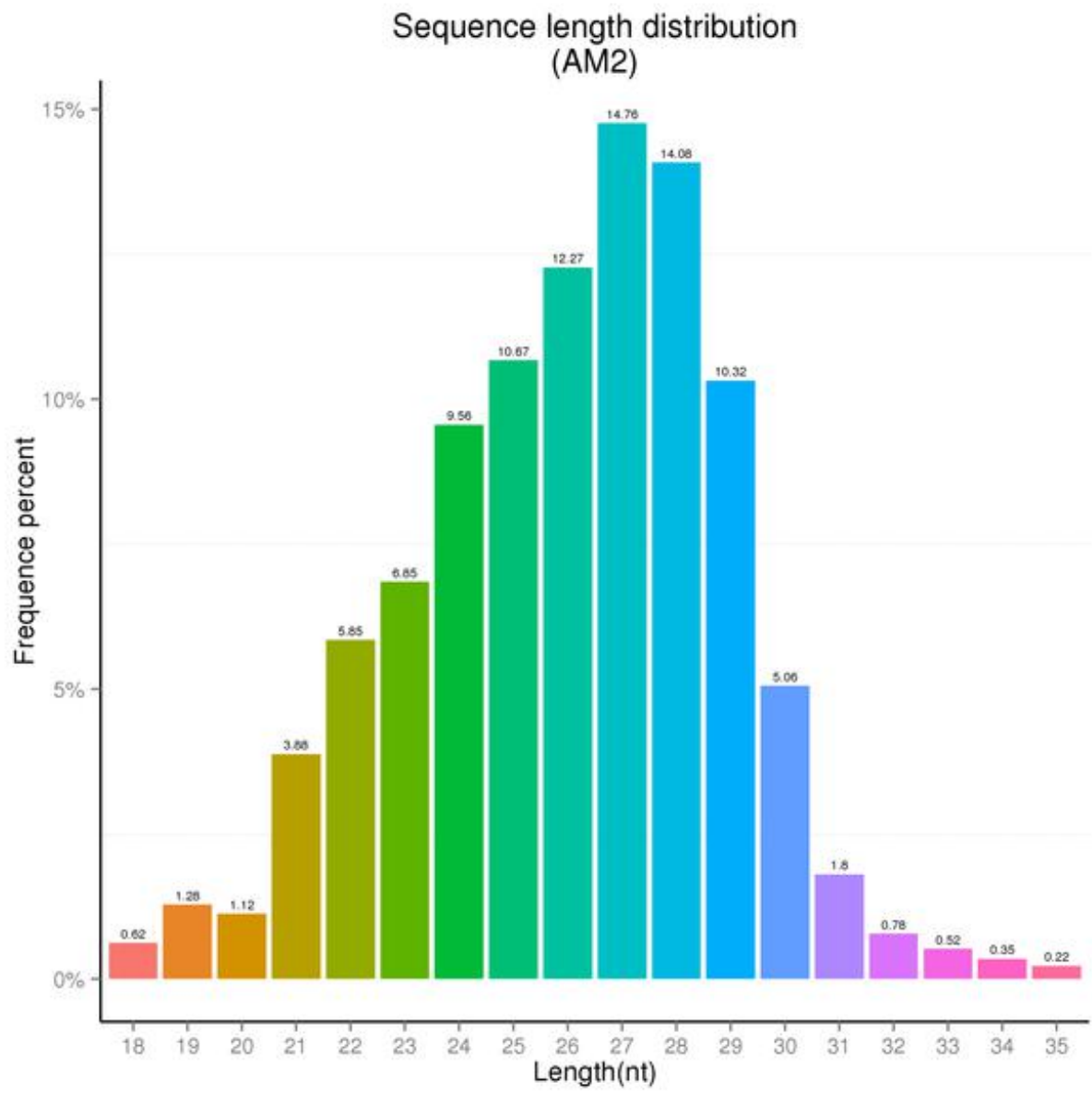
A



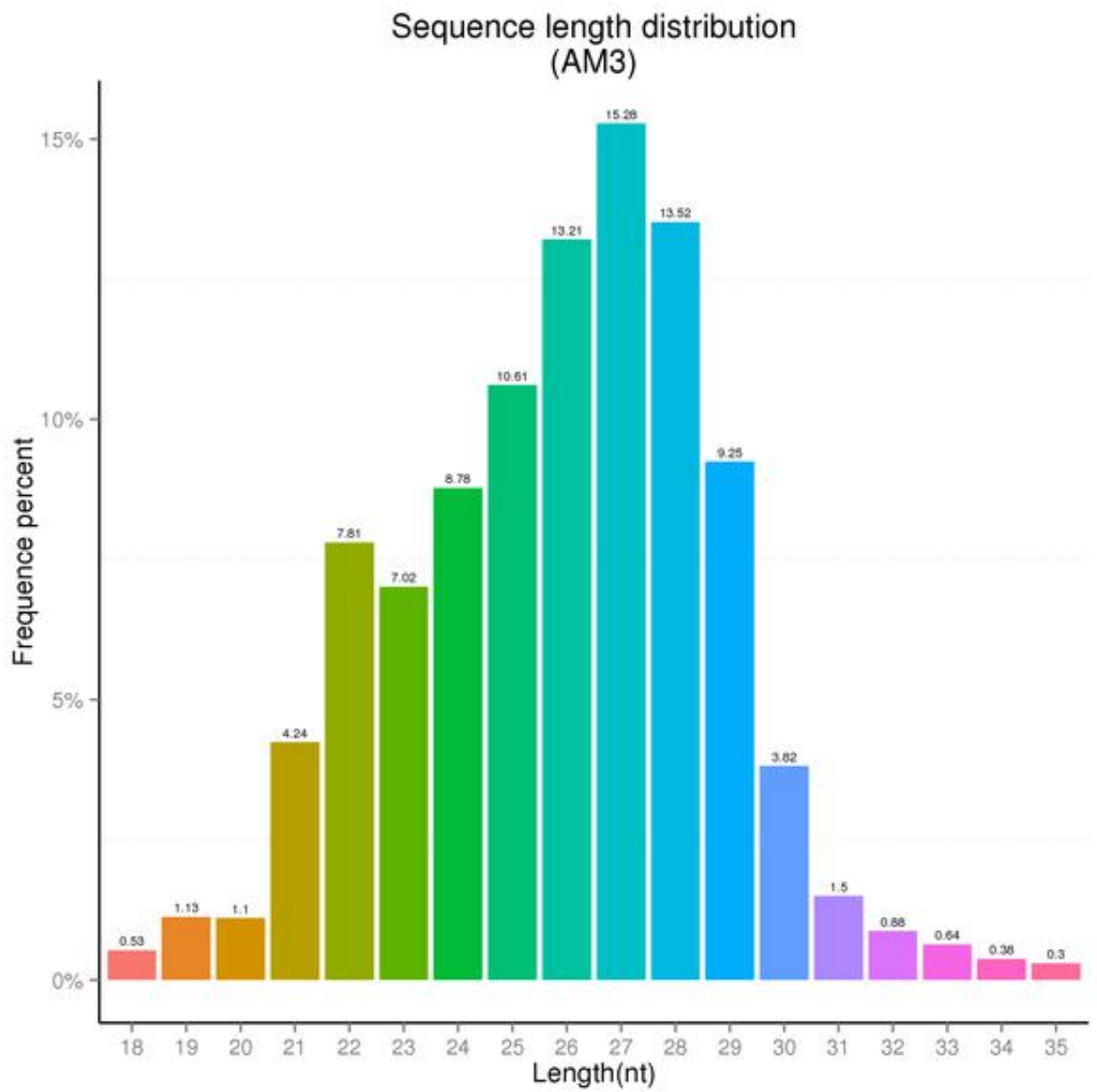
**B**



C



D



**Figure S2. Expression pattern of sex-biased putative piRNAs validated by microarray.** The expression of 311 sex-biased putative piRNAs is reflected as Log2FC. The heat map showed the putative piRNAs clustered into ten clades based on sexes, including five clades up-regulated in ovaries and five up-regulated in testes. For detailed information see Table S5.

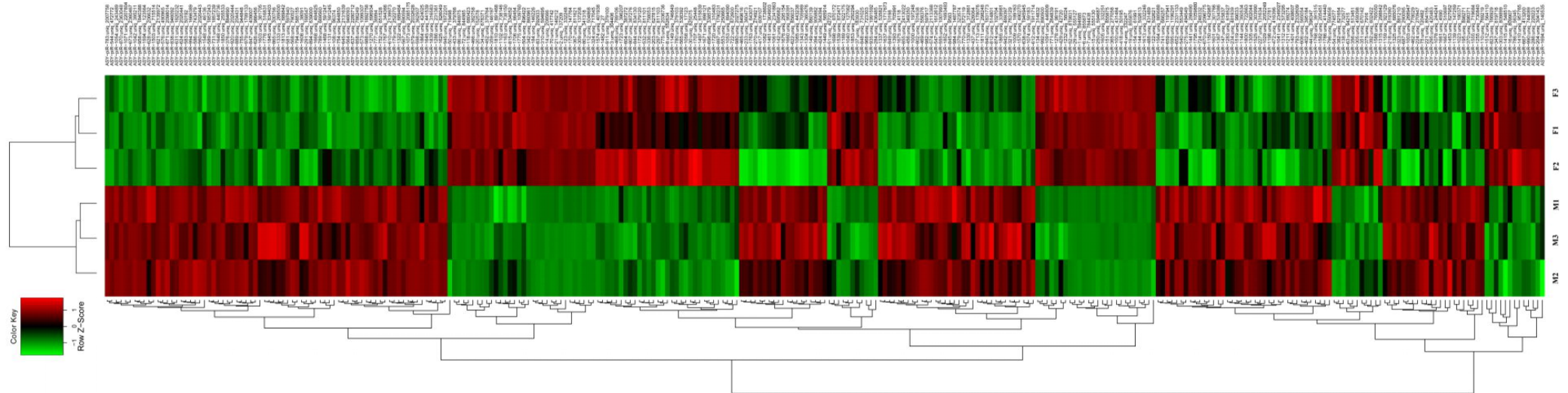


Table S1 - Summary of library quality control and the ambiguous reads filter.

Sample ID	Sample description	Reads	Bases	Error rate	Q20	Q30	GC content	N% > 10%	low quality	5 adapter contamination	3 adapter null or insert null	with ployA/T/G/C	clean reads	Total sRNA	Mapped sRNA	"+" Mapped sRNA	"-" Mapped sRNA
AF1	Ovary 1	8374222 (100.00%)	0.419G	0.01%	98.61%	97.28%	47.74%	20 (0.00%)	775 (0.01%)	1251 (0.01%)	347039 (4.14%)	47700 (0.57%)	7977437 (95.26%)	7719149 (92.18%)	3367185 (40.21%)	1663800 (19.87%)	1703385 (20.34%)
AF2	Ovary 2	7762049 (100.00%)	0.388G	0.01%	98.63%	97.29%	48.10%	26 (0.00%)	703 (0.01%)	1224 (0.02%)	388225 (5.00%)	40969 (0.53%)	7330902 (94.45%)	7012600 (90.34%)	3303306 (42.56%)	1661237 (21.40%)	1642069 (21.16%)
AM2	Testis 1	7717550 (100.00%)	0.386G	0.01%	98.71%	97.44%	48.13%	23 (0.00%)	657 (0.01%)	1005 (0.01%)	317293 (4.11%)	42664 (0.55%)	7355908 (95.31%)	7129325 (92.39%)	3164300 (41.00%)	1583153 (20.51%)	1581147 (20.49%)
AM3	Testis 2	8557963 (100.00%)	0.428G	0.01%	98.65%	97.32%	48.03%	25 (0.00%)	723 (0.01%)	1245 (0.01%)	451253 (5.27%)	48639 (0.57%)	8056078 (94.14%)	7803509 (91.18%)	3126400 (36.53%)	1550844 (18.12%)	1575556 (18.41%)

**Table S2 - List of orthologs to known piRNAs**

piRNA	piRNA sequence	known piRNA	known piRNA sequence	known piRNA description
uniq_231483	TCTGCCAGTGCTCTGAATGTCAAAGT	dme_piR_009519	TCTGCCAGTGCTCTGAATGTCAAAGT	Drosophila_melanogaster:U:825171:825198:Plus
uniq_1332959	TCTGCCAGTGCTCTGAATGTCAAAA	dme_piR_009519	TCTGCCAGTGCTCTGAATGTCAAAGT	Drosophila_melanogaster:U:825171:825198:Plus
uniq_1596260	CTGCCAGTGCTCTGAATGTCAAAGT	dme_piR_009519	TCTGCCAGTGCTCTGAATGTCAAAGT	Drosophila_melanogaster:U:825171:825198:Plus
uniq_2785878	GCATCGGTGGTTCAGTGGTAGAATGC	dme_piR_010919	GCATCGGTGGTTCAGTGGTAGAATGCTC	Drosophila_melanogaster:2L:2031692:2031719:Plus
uniq_519316	TGGAATACCAGGTGCTGTAAGCTA	dre_piR_0001123	TGGAATACCAGGTGCTGTAAGCTA	Danio_rerio:4:38948896:38948920:Minus
uniq_783379	TAGACAGCAGGACGGTGGCCATGGA	dre_piR_0002388	TAGACAGCAGGACGGTGGCCATGGAAGTC	Danio_rerio:14:34501105:34501129:Minus
uniq_1641194	AGACAGCAGGACGGTGGCCATGGAAGT	dre_piR_0002388	TAGACAGCAGGACGGTGGCCATGGAAGTC	Danio_rerio:14:34501105:34501129:Minus
uniq_2370819	AGACAGCAGGACGGTGGCCATGGAAGTC	dre_piR_0002388	TAGACAGCAGGACGGTGGCCATGGAAGTC	Danio_rerio:14:34501105:34501129:Minus
uniq_521643	GCATTGGTGGTTCAGTGGTAGAATTCTCGC	dre_piR_0002593	GCATTGGTGGTTCAGTGGTAGAATTCTCGC	Danio_rerio:6:47439166:47439190:Minus
uniq_738146	GCATTGGTGGTTCAGTGGTAGAATTCTC	dre_piR_0002594	GCATTGGTGGTTCAGTGGTAGAATTCTCG	Danio_rerio:24:891219:891243:Plus
uniq_296661	GCATTGGTGGTTCAGTGGTAGAATTCT	dre_piR_0002595	GCATTGGTGGTTCAGTGGTAGAATTCTC	Danio_rerio:8:39868444:39868472:Plus
uniq_82822	TGGAATACCAGGTGCTGTGAGCTT	dre_piR_0004353	TGGAATACCAGGTGCTGTGAGCTT	Danio_rerio:4:37882405:37882429:Minus
uniq_2400385	ACCCGAAAGATGGTGAAGTATGCCTGGGC	dre_piR_0006070	ACCCGAAAGATGGTGAAGTATGCCTGGGC	Danio_rerio:6:31619152:31619176:Plus
uniq_3024074	CCGAAAGATGGTGAAGTATGCCTGGGC	dre_piR_0006070	ACCCGAAAGATGGTGAAGTATGCCTGGGC	Danio_rerio:6:31619152:31619176:Plus
uniq_2097900	GAAAGATGGTGAAGTATGCCTGGGC	dre_piR_0006070	ACCCGAAAGATGGTGAAGTATGCCTGGGC	Danio_rerio:6:31619152:31619176:Plus
uniq_295323	CCGAAAGATGGTGAAGTATGCCTGGG	dre_piR_0012448	ACCCGAAAGATGGTGAAGTATGCCTGGG	Danio_rerio:12:12717727:12717750:Plus
uniq_941207	TTGGTGAATTCTGCTTACAATGACA	dre_piR_0013017	TTGGTGAATTCTGCTTACAATGACAGG	Danio_rerio:21:16628981:16629004:Minus
uniq_606128	TTGGTGAATTCTGCTTACAATGAC	dre_piR_0013019	TTGGTGAATTCTGCTTACAATGACAG	Danio_rerio:10:8985377:8985400:Minus
uniq_1114509	CTACCATCTGTGGATTATGACTGAACGC	dre_piR_0016672	CTACCATCTGTGGATTATGACTGAACGC	Danio_rerio:5:64168419:64168447:Plus
uniq_442139	TACCATCTGTGGATTATGACTGAACGC	dre_piR_0016672	CTACCATCTGTGGATTATGACTGAACGC	Danio_rerio:5:64168419:64168447:Plus
uniq_295268	TGGTGAAGTATGCCTGGGCAGGGCGAA	dre_piR_0019149	TGGTGAAGTATGCCTGGGCAGGGCGAAG	Danio_rerio:5:64165746:64165773:Plus
uniq_457625	GCATTGGTGGTTCAGTGGTAGAATTCTCGCC	dre_piR_0029993	GCATTGGTGGTTCAGTGGTAGAATTCTCGCCT	Danio_rerio:21:34775365:34775396:Minus
uniq_1968022	TGGTGGTTCAGTGGTAGAATTCTCGCCT	dre_piR_0029993	GCATTGGTGGTTCAGTGGTAGAATTCTCGCCT	Danio_rerio:21:34775365:34775396:Minus
uniq_962627	TTGGTGGTTCAGTGGTAGAATTCTCGCCT	dre_piR_0029993	GCATTGGTGGTTCAGTGGTAGAATTCTCGCCT	Danio_rerio:21:34775365:34775396:Minus
uniq_800856	TGGTGGTTCAGTGGTAGAATTCTCGCC	dre_piR_0029993	GCATTGGTGGTTCAGTGGTAGAATTCTCGCCT	Danio_rerio:21:34775365:34775396:Minus
uniq_258265	TTGGTGGTTCAGTGGTAGAATTCTCGCC	dre_piR_0029993	GCATTGGTGGTTCAGTGGTAGAATTCTCGCCT	Danio_rerio:21:34775365:34775396:Minus
uniq_2611026	TCCGAAGTTCCCTCAGGATAGCTGG	dre_piR_0031044	TCCGAAGTTCCCTCAGGATAGCTGGCG	Danio_rerio:5:64165882:64165909:Plus
uniq_77832	CCCGAAAGATGGTGAAGTATGCCTGG	dre_piR_0032495	ACCCGAAAGATGGTGAAGTATGCCTGG	Danio_rerio:5:64165736:64165762:Plus
uniq_142422	AGCAGGACGGTGGCCATGGAAGTCGGC	dre_piR_0035551	AGCAGGACGGTGGCCATGGAAGTCGGC	Danio_rerio:4:39613435:39613461:Minus
uniq_707926	TTGGTGGTTCAGTGGTAGAATTCTC	dre_piR_0037750	GCATTGGTGGTTCAGTGGTAGAATTCTCGCC	Danio_rerio:21:34775366:34775396:Minus
uniq_334052	GCATTGGTGGTTCAGTGGTAGAATTCTCGC	dre_piR_0037750	GCATTGGTGGTTCAGTGGTAGAATTCTCGCC	Danio_rerio:21:34775366:34775396:Minus
uniq_524388	GCATTGGTGGTTCAGTGGTAGAATTCTC	dre_piR_0037750	GCATTGGTGGTTCAGTGGTAGAATTCTCGCC	Danio_rerio:21:34775366:34775396:Minus
uniq_845610	TTGGTGGTTCAGTGGTAGAATTCTCG	dre_piR_0037750	GCATTGGTGGTTCAGTGGTAGAATTCTCGCC	Danio_rerio:21:34775366:34775396:Minus
uniq_2505226	GCATTGGTGGTTCAGGGTAGAATTCT	dre_piR_0043343	GCATTGGTGGTTCAGGGTAGAATTCTCGC	Danio_rerio:14:34777330:34777359:Minus
uniq_2073500	CCCTGTTGAGCTTGACTCTAGTCTGGC	dre_piR_0045878	ACCCTGTTGAGCTTGACTCTAGTCTGGCCC	Danio_rerio:4:34937644:34937673:Minus
uniq_2208829	CCTGTTGAGCTTGACTCTAGTCTGGC	dre_piR_0045878	ACCCTGTTGAGCTTGACTCTAGTCTGGCCC	Danio_rerio:4:34937644:34937673:Minus
uniq_2423014	GCATTGGTGGTTCAGTGGTAGAATGC	dre_piR_0047433	AGCATTGGTGGTTCAGTGGTAGAATGC	Danio_rerio:5:42102943:42102969:Plus

uniq_12	TGATGATGATGATGATGCTGATG	dre_piR_0053487	TGATGATGATGATGATGCTGATG	Danio_rerio:18:3129142:3129167:Plus
uniq_2325806	TTATGACTGAACGCCTCTAAGTCAGAA	dre_piR_0055038	GATTATGACTGAACGCCTCTAAGTCAGAAT	Danio_rerio:5:64168432:64168461:Plus
uniq_689009	TTATGACTGAACGCCTCTAAGTCAGA	dre_piR_0055038	GATTATGACTGAACGCCTCTAAGTCAGAAT	Danio_rerio:5:64168432:64168461:Plus
uniq_1887516	ATGACTGAACGCCTCTAAGTCAGAAT	dre_piR_0055038	GATTATGACTGAACGCCTCTAAGTCAGAAT	Danio_rerio:5:64168432:64168461:Plus
uniq_2412492	TATGACTGAACGCCTCTAAGTCAGAAT	dre_piR_0055038	GATTATGACTGAACGCCTCTAAGTCAGAAT	Danio_rerio:5:64168432:64168461:Plus
uniq_2576353	TGTCAAACGGTAACGCAGGTGTCCTAAGGGC	dre_piR_0058848	TGTCAAACGGTAACGCAGGTGTCCTAAGGGC	Danio_rerio:5:64167959:64167989:Plus
uniq_1515257	TGGGAATACCAGGTGCTGTAAGCTTA	dre_piR_0059985	CCGCCTGGGAATACCAGGTGCTGTAAGCTTA	Danio_rerio:7:1187692:1187722:Minus
uniq_2355707	CCTGGGAATACCAGGTGCTGTAAGCTTA	dre_piR_0059987	CCTGGGAATACCAGGTGCTGTAAGCTTA	Danio_rerio:7:1187692:1187719:Minus
uniq_66021	CAGAAGGGCAAAAGCTCGCTTGATCT	dre_piR_0061523	CAGAAGGGCAAAAGCTCGCTTGATCT	Danio_rerio:5:64168021:64168046:Plus
uniq_231639	TTGGTGAATTCTGCTTCAACAATGATA	dre_piR_0064967	TTGGTGAATTCTGCTTCAACAATGATA	Danio_rerio:5:64168214:64168239:Minus
uniq_1979803	AAGGGAACGGGCTTGGCAGAATCAGC	dre_piR_0065052	AAGGGAACGGGCTTGGCAGAATCAGC	Danio_rerio:5:64167652:64167677:Plus
uniq_1947476	GCATTGGTGGTTCAGTGGTAGAGTTC	dre_piR_0065738	GCATTGGTGGTTCAGTGGTAGAGTTC	Danio_rerio:14:29865313:29865338:Minus
uniq_58521	AGCAGTTGAACATGGGTCAGTCGGTC	hsa_piR_000753	AGCAGTTGAACATGGGTCAGTCGGTCCTG	gb DQ570940 Homo
uniq_707672	AGCAGTTGAACATGGGTCAGTCGGT	hsa_piR_000753	AGCAGTTGAACATGGGTCAGTCGGTCCTG	gb DQ570940 Homo
uniq_785489	AGCAGTTGAACATGGGTCAGTCGGTCC	hsa_piR_000753	AGCAGTTGAACATGGGTCAGTCGGTCCTG	gb DQ570940 Homo
uniq_805840	GCAGTTGAACATGGGTCAGTCGGTC	hsa_piR_000753	AGCAGTTGAACATGGGTCAGTCGGTCCTG	gb DQ570940 Homo
uniq_832647	AGCAGTTGAACATGGGTCAGTCGGTCCT	hsa_piR_000753	AGCAGTTGAACATGGGTCAGTCGGTCCTG	gb DQ570940 Homo
uniq_1321030	GCAGTTGAACATGGGTCAGTCGGTCCT	hsa_piR_000753	AGCAGTTGAACATGGGTCAGTCGGTCCTG	gb DQ570940 Homo
uniq_2069273	CAGTTGAACATGGGTCAGTCGGTCC	hsa_piR_000753	AGCAGTTGAACATGGGTCAGTCGGTCCTG	gb DQ570940 Homo
uniq_2606757	GCAGTTGAACATGGGTCAGTCGGTCC	hsa_piR_000753	AGCAGTTGAACATGGGTCAGTCGGTCCTG	gb DQ570940 Homo
uniq_2868282	AGCATTGGTGGTTCAGTGGTAGAATTCT	hsa_piR_000765	AGCATTGGTGGTTCAGTGGTAGAATTCTCGC	gb DQ570956 Homo
uniq_921388	TTGGTGGTTCAGTGGTAGAATTCTCGC	hsa_piR_001311	ATTGGTGGTTCAGTGGTAGAATTCTCGCC	gb DQ571812 Homo
uniq_460176	TTGGTGGTTCAGTGGTAGAATTCTCGCCTG	hsa_piR_001312	ATTGGTGGTTCAGTGGTAGAATTCTCGCCTG	gb DQ571813 Homo
uniq_4440	ATTTGGTGTATGTGCTTGGCTGAGGAG	hsa_piR_001318	ATTTGGTGTATGTGCTTGGCTGAGGAGCCAA	gb DQ571823 Homo
uniq_712635	ATTTGGTGTATGTGCTTGGCTGAGGA	hsa_piR_001318	ATTTGGTGTATGTGCTTGGCTGAGGAGCCAA	gb DQ571823 Homo
uniq_855423	TTGGTGTATGTGCTTGGCTGAGGAGC	hsa_piR_001318	ATTTGGTGTATGTGCTTGGCTGAGGAGCCAA	gb DQ571823 Homo
uniq_873648	ATTTGGTGTATGTGCTTGGCTGAGG	hsa_piR_001318	ATTTGGTGTATGTGCTTGGCTGAGGAGCCAA	gb DQ571823 Homo
uniq_1028233	ATTTGGTGTATGTGCTTGGCTGAGGAGC	hsa_piR_001318	ATTTGGTGTATGTGCTTGGCTGAGGAGCCAA	gb DQ571823 Homo
uniq_1319892	TTTGGTGTATGTGCTTGGCTGAGGAGC	hsa_piR_001318	ATTTGGTGTATGTGCTTGGCTGAGGAGCCAA	gb DQ571823 Homo
uniq_2165327	ATTTGGTGTATGTGCTTGGCTGAGGAGCCA	hsa_piR_001318	ATTTGGTGTATGTGCTTGGCTGAGGAGCCAA	gb DQ571823 Homo
uniq_2230646	ATTTGGTGTATGTGCTTGGCTGAGGAGCCAA	hsa_piR_001318	ATTTGGTGTATGTGCTTGGCTGAGGAGCCAA	gb DQ571823 Homo
uniq_1911329	TGAAGGTGTTCTGGAGAACGTGATT	hsa_piR_006658	TGAAGGTGTTCTGGAGAACGTGATTC	gb DQ579110 Homo
uniq_777048	CAGTTGAACATGGGTCAGTCGGTCTCT	hsa_piR_009228	CAGTTGAACATGGGTCAGTCGGTCTCT	gb DQ582496 Homo
uniq_683343	TGTATGTGCTTGGCTGAGGAGCCAAT	hsa_piR_014923	TGGTGTATGTGCTTGGCTGAGGAGCCAATGG	gb DQ590404 Homo
uniq_450946	TGGTTCAGTGGTAGAATTCTCGCCTGC	hsa_piR_018570	TTGGTGGTTCAGTGGTAGAATTCTCGCCTGCC	gb DQ595536 Homo
uniq_562695	TTGGTGGTTCAGTGGTAGAATTCTCGCCTGC	hsa_piR_018570	TTGGTGGTTCAGTGGTAGAATTCTCGCCTGCC	gb DQ595536 Homo
uniq_1134381	GTGGTTCAGTGGTAGAATTCTCGCCTGCC	hsa_piR_018570	TTGGTGGTTCAGTGGTAGAATTCTCGCCTGCC	gb DQ595536 Homo
uniq_1865339	GGTTCAGTGGTAGAATTCTCGCCTGC	hsa_piR_018570	TTGGTGGTTCAGTGGTAGAATTCTCGCCTGCC	gb DQ595536 Homo
uniq_531703	TTGGTGGTTCAGTGGTAGAATTCTCGCCTGCC	hsa_piR_018570	TTGGTGGTTCAGTGGTAGAATTCTCGCCTGCC	gb DQ595536 Homo



uniq_556109	TGGTTCAGTGGTAGAATTCTCGCCTGCC	hsa_piR_018570	TTGGTGGTTCAGTGGTAGAATTCTCGCCTGCC	gb DQ595536 Homo
uniq_7740	TTGGTGTATGTGCTTGGCTGAGGAGCC	hsa_piR_018573	TTGGTGTATGTGCTTGGCTGAGGAGCC	gb DQ595539 Homo
uniq_2761330	TGGTGTATGTGCTTGGCTGAGGAGC	hsa_piR_018573	TTGGTGTATGTGCTTGGCTGAGGAGCC	gb DQ595539 Homo
uniq_66454	GCATTGGTGGTTCAGTGGTAGAATTCTCA	hsa_piR_019825	GCATTGGTGGTTCAGTGGTAGAATTCTCAC	gb DQ597218 Homo
uniq_183491	GCATTGGTGGTTCAGTGGTAGAATTCTCAC	hsa_piR_019825	GCATTGGTGGTTCAGTGGTAGAATTCTCAC	gb DQ597218 Homo
uniq_860961	GGGGATGTAGCTCAGTGGTAGAGCGCA	hsa_piR_020485	GGGGATGTAGCTCAGTGGTAGAGCGCATGCT	gb DQ598159 Homo
uniq_446107	GGGGATGTAGCTCAGTGGTAGAGCGC	hsa_piR_020485	GGGGATGTAGCTCAGTGGTAGAGCGCATGCT	gb DQ598159 Homo
uniq_642070	GGTGTGACGCGATGTGATTCTGCC	mmu_piR_000622	CGGGTGTGACGCGATGTGATTCTGCC	gb DQ540988 Mus_musculus:3:5843428:5843455:Plus
uniq_201553	GGGTGTGACGCGATGTGATTCTGCC	mmu_piR_000622	CGGGTGTGACGCGATGTGATTCTGCC	gb DQ540988 Mus_musculus:3:5843428:5843455:Plus
uniq_952674	CGAAAGATGGTGAAGTATGCCTGGGC	mmu_piR_018323	CGAAAGATGGTGAAGTATGCCTGGGC	gb DQ698371 Mus_musculus:15:86022679:86022704:Plus
uniq_2246269	TCAGACCCAGAAAAGGTGTTGGTTGAT	mmu_piR_038323	ATCAGACCCAGAAAAGGTGTTGGTTGATAT	gb piRNA-T34 Mus_musculus:13:44880547:44880577:Minus
uniq_965909	GCATGGGTGGTTCAGTGGTAGAATTCTCGCC	rno_piR_005567	GCATGGGTGGTTCAGTGGTAGAATTCTCGCC	gb DQ614031 Rattus
uniq_73519	GCATGGGTGGTTCAGTGGTAGAATTCTC	rno_piR_005567	GCATGGGTGGTTCAGTGGTAGAATTCTCGCC	gb DQ614031 Rattus
uniq_1569095	GCATGGGTGGTTCAGTGGTAGAATTCT	rno_piR_005567	GCATGGGTGGTTCAGTGGTAGAATTCTCGCC	gb DQ614031 Rattus
uniq_2757252	GCATGGGTGGTTCAGTGGTAGAATTCTCG	rno_piR_005567	GCATGGGTGGTTCAGTGGTAGAATTCTCGCC	gb DQ614031 Rattus
uniq_1603788	TTGACGCGATGTGATTCTGCCCAGT	rno_piR_005787	GGGTGTGACGCGATGTGATTCTGCCCAGT	gb DQ614419 Rattus
uniq_2330815	TGACGCGATGTGATTCTGCCCAGT	rno_piR_005787	GGGTGTGACGCGATGTGATTCTGCCCAGT	gb DQ614419 Rattus

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Table S3 - Summary of 265 enriched GO annotations and 29 enriched KEGG pathways that may associate with sturgeon putative piRNA.

Enriched GO accession	Description	Term type	Over-represented pValue	Corrected pValue
GO:0015074	DNA integration	biological_process	3.01E-171	2.00E-167
GO:0006313	transposition, DNA-mediated	biological_process	3.67E-50	8.10E-47
GO:0032196	transposition	biological_process	3.67E-50	8.10E-47
GO:0006310	DNA recombination	biological_process	1.77E-32	2.93E-29
GO:0006259	DNA metabolic process	biological_process	2.63E-29	3.48E-26
GO:0034641	cellular nitrogen compound metabolic process	biological_process	1.58E-28	1.75E-25
GO:0071704	organic substance metabolic process	biological_process	1.53E-23	1.26E-20
GO:0044238	primary metabolic process	biological_process	8.25E-23	6.08E-20
GO:0006807	nitrogen compound metabolic process	biological_process	1.22E-22	8.09E-20
GO:0046483	heterocycle metabolic process	biological_process	4.42E-20	2.66E-17
GO:0022613	ribonucleoprotein complex biogenesis	biological_process	4.93E-20	2.72E-17
GO:0042254	ribosome biogenesis	biological_process	4.53E-19	2.31E-16
GO:0006139	nucleobase-containing compound metabolic process	biological_process	1.21E-18	5.73E-16
GO:0044237	cellular metabolic process	biological_process	1.35E-18	5.95E-16
GO:0008152	metabolic process	biological_process	1.44E-18	5.97E-16
GO:1901135	carbohydrate derivative metabolic process	biological_process	1.77E-18	6.89E-16
GO:0006725	cellular aromatic compound metabolic process	biological_process	2.29E-18	8.43E-16
GO:1901360	organic cyclic compound metabolic process	biological_process	1.20E-17	4.18E-15
GO:0044710	single-organism metabolic process	biological_process	1.61E-17	5.32E-15
GO:1901564	organonitrogen compound metabolic process	biological_process	9.98E-17	3.15E-14
GO:0055086	nucleobase-containing small molecule metabolic process	biological_process	6.28E-16	1.89E-13
GO:0009116	nucleoside metabolic process	biological_process	1.64E-15	4.73E-13
GO:1901657	glycosyl compound metabolic process	biological_process	2.15E-15	5.93E-13
GO:1901566	organonitrogen compound biosynthetic process	biological_process	3.49E-15	9.25E-13
GO:0072527	pyrimidine-containing compound metabolic process	biological_process	5.29E-15	1.30E-12
GO:0042278	purine nucleoside metabolic process	biological_process	7.36E-15	1.63E-12
GO:0046128	purine ribonucleoside metabolic process	biological_process	7.36E-15	1.63E-12
GO:0009141	nucleoside triphosphate metabolic process	biological_process	3.27E-14	6.98E-12
GO:0043170	macromolecule metabolic process	biological_process	4.98E-14	1.03E-11

GO:0009123	nucleoside monophosphate metabolic process	biological_process	7.48E-14	1.50E-11
GO:0009119	ribonucleoside metabolic process	biological_process	7.71E-14	1.50E-11
GO:0009199	ribonucleoside triphosphate metabolic process	biological_process	1.39E-13	2.56E-11
GO:0009205	purine ribonucleoside triphosphate metabolic process	biological_process	1.39E-13	2.56E-11
GO:0072521	purine-containing compound metabolic process	biological_process	1.61E-13	2.87E-11
GO:0009144	purine nucleoside triphosphate metabolic process	biological_process	1.70E-13	2.97E-11
GO:0006753	nucleoside phosphate metabolic process	biological_process	3.31E-13	5.62E-11
GO:0046034	ATP metabolic process	biological_process	5.35E-13	8.86E-11
GO:0009161	ribonucleoside monophosphate metabolic process	biological_process	5.78E-13	9.33E-11
GO:0009117	nucleotide metabolic process	biological_process	7.96E-13	1.23E-10
GO:0009126	purine nucleoside monophosphate metabolic process	biological_process	9.14E-13	1.35E-10
GO:0009167	purine ribonucleoside monophosphate metabolic process	biological_process	9.14E-13	1.35E-10
GO:0006518	peptide metabolic process	biological_process	2.15E-12	3.10E-10
GO:0043603	cellular amide metabolic process	biological_process	3.85E-12	5.42E-10
GO:0006412	translation	biological_process	3.94E-12	5.42E-10
GO:0090304	nucleic acid metabolic process	biological_process	4.72E-12	6.25E-10
GO:0009259	ribonucleotide metabolic process	biological_process	5.83E-12	7.57E-10
GO:0006206	pyrimidine nucleobase metabolic process	biological_process	6.78E-12	8.64E-10
GO:0044711	single-organism biosynthetic process	biological_process	7.40E-12	9.25E-10
GO:0009150	purine ribonucleotide metabolic process	biological_process	8.10E-12	9.94E-10
GO:0044260	cellular macromolecule metabolic process	biological_process	1.22E-11	1.47E-09
GO:0043043	peptide biosynthetic process	biological_process	1.60E-11	1.89E-09
GO:0006163	purine nucleotide metabolic process	biological_process	1.84E-11	2.14E-09
GO:0019637	organophosphate metabolic process	biological_process	1.87E-11	2.14E-09
GO:0019693	ribose phosphate metabolic process	biological_process	2.01E-11	2.26E-09
GO:0009058	biosynthetic process	biological_process	2.06E-11	2.28E-09
GO:1901576	organic substance biosynthetic process	biological_process	2.79E-11	3.03E-09
GO:0043604	amide biosynthetic process	biological_process	2.47E-10	2.48E-08
GO:0044249	cellular biosynthetic process	biological_process	5.24E-10	5.04E-08
GO:0006118	obsolete electron transport	biological_process	4.58E-09	4.27E-07
GO:0055114	oxidation-reduction process	biological_process	6.84E-09	6.12E-07
GO:0044281	small molecule metabolic process	biological_process	1.54E-08	1.34E-06
GO:0006352	DNA-templated transcription, initiation	biological_process	2.50E-08	2.15E-06
GO:0072528	pyrimidine-containing compound biosynthetic process	biological_process	2.92E-08	2.48E-06
GO:0042775	mitochondrial ATP synthesis coupled electron transport	biological_process	4.57E-08	3.83E-06

GO:0006091	generation of precursor metabolites and energy	biological_process	5.05E-08	4.19E-06
GO:0006119	oxidative phosphorylation	biological_process	5.72E-08	4.68E-06
GO:0045333	cellular respiration	biological_process	7.14E-08	5.77E-06
GO:0006733	oxidoreduction coenzyme metabolic process	biological_process	9.60E-08	7.67E-06
GO:0006732	coenzyme metabolic process	biological_process	1.37E-07	1.07E-05
GO:0044283	small molecule biosynthetic process	biological_process	1.56E-07	1.16E-05
GO:0015980	energy derivation by oxidation of organic compounds	biological_process	1.73E-07	1.28E-05
GO:0042773	ATP synthesis coupled electron transport	biological_process	2.86E-07	2.08E-05
GO:0070647	protein modification by small protein conjugation or removal	biological_process	8.94E-07	6.17E-05
GO:0010467	gene expression	biological_process	1.13E-06	7.66E-05
GO:0044271	cellular nitrogen compound biosynthetic process	biological_process	1.29E-06	8.54E-05
GO:0016567	protein ubiquitination	biological_process	1.78E-06	0.00011541
GO:0006220	pyrimidine nucleotide metabolic process	biological_process	1.92E-06	0.00012335
GO:0022904	respiratory electron transport chain	biological_process	2.14E-06	0.00013362
GO:0032446	protein modification by small protein conjugation	biological_process	2.70E-06	0.00016654
GO:0006120	mitochondrial electron transport, NADH to ubiquinone	biological_process	2.71E-06	0.00016654
GO:0006743	ubiquinone metabolic process	biological_process	5.58E-06	0.00032981
GO:0006744	ubiquinone biosynthetic process	biological_process	5.58E-06	0.00032981
GO:0009064	glutamine family amino acid metabolic process	biological_process	8.58E-06	0.00048603
GO:0019915	lipid storage	biological_process	9.86E-06	0.0005536
GO:0033057*	multicellular organismal reproductive behavior	biological_process	1.14E-05	0.00061935
GO:0045924*	regulation of female receptivity	biological_process	1.14E-05	0.00061935
GO:0046008*	regulation of female receptivity, post-mating	biological_process	1.14E-05	0.00061935
GO:0060180*	female mating behavior	biological_process	1.14E-05	0.00061935
GO:0006818	hydrogen transport	biological_process	1.26E-05	0.00067398
GO:0015992	proton transport	biological_process	1.26E-05	0.00067398
GO:0022900	electron transport chain	biological_process	1.30E-05	0.00068736
GO:0009112	nucleobase metabolic process	biological_process	1.62E-05	0.00084947
GO:0006165	nucleoside diphosphate phosphorylation	biological_process	1.68E-05	0.00086969
GO:0046939	nucleotide phosphorylation	biological_process	1.68E-05	0.00086969
GO:0006814	sodium ion transport	biological_process	1.91E-05	0.00098201
GO:0006221	pyrimidine nucleotide biosynthetic process	biological_process	1.97E-05	0.0010037
GO:0009132	nucleoside diphosphate metabolic process	biological_process	2.79E-05	0.0013906
GO:0042181	ketone biosynthetic process	biological_process	3.34E-05	0.0016288
GO:1901661	quinone metabolic process	biological_process	3.34E-05	0.0016288

GO:1901663	quinone biosynthetic process	biological_process	3.34E-05	0.0016288
GO:0007618*	mating	biological_process	3.58E-05	0.0017297
GO:0090407	organophosphate biosynthetic process	biological_process	5.01E-05	0.002371
GO:0045454	cell redox homeostasis	biological_process	5.53E-05	0.0025961
GO:0007617*	mating behavior	biological_process	5.93E-05	0.0026927
GO:0019098*	reproductive behavior	biological_process	5.93E-05	0.0026927
GO:0044705*	multi-organism reproductive behavior	biological_process	5.93E-05	0.0026927
GO:1901137	carbohydrate derivative biosynthetic process	biological_process	8.77E-05	0.0039267
GO:0051186	cofactor metabolic process	biological_process	9.65E-05	0.0042893
GO:0009108	coenzyme biosynthetic process	biological_process	9.81E-05	0.004333
GO:0042180	cellular ketone metabolic process	biological_process	0.00012845	0.0054551
GO:0010883	regulation of lipid storage	biological_process	0.00013348	0.005597
GO:0010884	positive regulation of lipid storage	biological_process	0.00013348	0.005597
GO:0009059	macromolecule biosynthetic process	biological_process	0.00015638	0.00645
GO:0006006	glucose metabolic process	biological_process	0.00016012	0.0064681
GO:0044706	multi-multicellular organism process	biological_process	0.00018404	0.0073893
GO:0006144	purine nucleobase metabolic process	biological_process	0.00019364	0.0076362
GO:0048609*	multicellular organismal reproductive process	biological_process	0.00020382	0.007943
GO:0002200	somatic diversification of immune receptors	biological_process	0.0002182	0.0083052
GO:0002562	somatic diversification of immune receptors via germline recombination within a single locus	biological_process	0.0002182	0.0083052
GO:0016444	somatic cell DNA recombination	biological_process	0.0002182	0.0083052
GO:0033151	V(D)J recombination	biological_process	0.0002182	0.0083052
GO:0034645	cellular macromolecule biosynthetic process	biological_process	0.00027445	0.010236
GO:0015947	methane metabolic process	biological_process	0.00027656	0.010236
GO:0043446	cellular alkane metabolic process	biological_process	0.00027656	0.010236
GO:0009229	thiamine diphosphate biosynthetic process	biological_process	0.00031778	0.011632
GO:0042357	thiamine diphosphate metabolic process	biological_process	0.00031778	0.011632
GO:0006096	glycolytic process	biological_process	0.0003288	0.011839
GO:0006757	ATP generation from ADP	biological_process	0.0003288	0.011839
GO:0046031	ADP metabolic process	biological_process	0.0003288	0.011839
GO:0006974	cellular response to DNA damage stimulus	biological_process	0.00035712	0.012789
GO:0042435	indole-containing compound biosynthetic process	biological_process	0.00036713	0.013014
GO:0034470	ncRNA processing	biological_process	0.00036929	0.013014
GO:0006094	gluconeogenesis	biological_process	0.0004126	0.014237

GO:0019319	hexose biosynthetic process	biological_process	0.0004126	0.014237
GO:0046364	monosaccharide biosynthetic process	biological_process	0.0004126	0.014237
GO:0006541	glutamine metabolic process	biological_process	0.00045278	0.015452
GO:0009135	purine nucleoside diphosphate metabolic process	biological_process	0.00047319	0.015833
GO:0009179	purine ribonucleoside diphosphate metabolic process	biological_process	0.00047319	0.015833
GO:0044724	single-organism carbohydrate catabolic process	biological_process	0.00052945	0.017451
GO:0009185	ribonucleoside diphosphate metabolic process	biological_process	0.00060607	0.019682
GO:0042430	indole-containing compound metabolic process	biological_process	0.00062269	0.019929
GO:0009147	pyrimidine nucleoside triphosphate metabolic process	biological_process	0.00062951	0.020006
GO:0042451	purine nucleoside biosynthetic process	biological_process	0.0007396	0.023004
GO:0046129	purine ribonucleoside biosynthetic process	biological_process	0.0007396	0.023004
GO:0006629	lipid metabolic process	biological_process	0.00075402	0.023272
GO:1901607	alpha-amino acid biosynthetic process	biological_process	0.00075523	0.023272
GO:0000380	alternative mRNA splicing, via spliceosome	biological_process	0.00075981	0.023304
GO:0022414*	reproductive process	biological_process	0.00077751	0.023628
GO:0008610	lipid biosynthetic process	biological_process	0.00078755	0.023824
GO:0001819	positive regulation of cytokine production	biological_process	0.00079315	0.023885
GO:0009142	nucleoside triphosphate biosynthetic process	biological_process	0.0008372	0.024542
GO:0009145	purine nucleoside triphosphate biosynthetic process	biological_process	0.0008372	0.024542
GO:0009201	ribonucleoside triphosphate biosynthetic process	biological_process	0.0008372	0.024542
GO:0009206	purine ribonucleoside triphosphate biosynthetic process	biological_process	0.0008372	0.024542
GO:0051705	multi-organism behavior	biological_process	0.0010251	0.029786
GO:0008652	cellular amino acid biosynthetic process	biological_process	0.0010565	0.030409
GO:0046500	S-adenosylmethionine metabolic process	biological_process	0.0010854	0.030995
GO:0006825	copper ion transport	biological_process	0.0011031	0.031365
GO:0019953*	sexual reproduction	biological_process	0.001153	0.032644
GO:0044272	sulfur compound biosynthetic process	biological_process	0.0013301	0.037182
GO:0007610	behavior	biological_process	0.0014508	0.039882
GO:0019538	protein metabolic process	biological_process	0.0014662	0.04014
GO:0034660	ncRNA metabolic process	biological_process	0.0014957	0.040778
GO:0033554*	cellular response to stress	biological_process	0.0015323	0.041604
GO:0006487	protein N-linked glycosylation	biological_process	0.0015724	0.04252
GO:0019362	pyridine nucleotide metabolic process	biological_process	0.0016549	0.044317
GO:0009309	amine biosynthetic process	biological_process	0.001659	0.044317
GO:0042401	cellular biogenic amine biosynthetic process	biological_process	0.001659	0.044317

GO:0044703*	multi-organism reproductive process	biological_process	0.0017665	0.046625
GO:0006525	arginine metabolic process	biological_process	0.0018271	0.047572
GO:0001816	cytokine production	biological_process	0.0018383	0.047572
GO:0001817	regulation of cytokine production	biological_process	0.0018383	0.047572
GO:0006123	mitochondrial electron transport, cytochrome c to oxygen	biological_process	0.0019811	0.049862
GO:0072524	pyridine-containing compound metabolic process	biological_process	0.001987	0.049862
GO:0000150	recombinase activity	molecular_function	6.33E-24	5.99E-21
GO:0003735	structural constituent of ribosome	molecular_function	4.21E-15	1.07E-12
GO:0003676	nucleic acid binding	molecular_function	5.86E-15	1.39E-12
GO:0004842	ubiquitin-protein transferase activity	molecular_function	5.04E-11	5.30E-09
GO:0019787	ubiquitin-like protein transferase activity	molecular_function	5.04E-11	5.30E-09
GO:0016491	oxidoreductase activity	molecular_function	1.22E-10	1.26E-08
GO:0004803	transposase activity	molecular_function	2.61E-10	2.58E-08
GO:0046914	transition metal ion binding	molecular_function	3.43E-10	3.35E-08
GO:0008270	zinc ion binding	molecular_function	5.19E-09	4.78E-07
GO:0034062	RNA polymerase activity	molecular_function	5.89E-09	5.34E-07
GO:0003899	DNA-directed RNA polymerase activity	molecular_function	1.44E-08	1.27E-06
GO:0000990	transcription factor activity, core RNA polymerase binding	molecular_function	1.42E-07	1.07E-05
GO:0000996	core DNA-dependent RNA polymerase binding promoter specificity activity	molecular_function	1.42E-07	1.07E-05
GO:0016987	sigma factor activity	molecular_function	1.42E-07	1.07E-05
GO:0016651	oxidoreductase activity, acting on NAD(P)H	molecular_function	4.72E-07	3.33E-05
GO:0003954	NADH dehydrogenase activity	molecular_function	1.06E-06	7.27E-05
GO:0016655	oxidoreductase activity, acting on NAD(P)H, quinone or similar compound as acceptor	molecular_function	1.37E-06	8.96E-05
GO:0008137	NADH dehydrogenase (ubiquinone) activity	molecular_function	1.99E-06	0.00012586
GO:0050136	NADH dehydrogenase (quinone) activity	molecular_function	1.99E-06	0.00012586
GO:0016860	intramolecular oxidoreductase activity	molecular_function	7.23E-06	0.00042391
GO:0004523	RNA-DNA hybrid ribonuclease activity	molecular_function	7.48E-06	0.00043459
GO:0009055	electron carrier activity	molecular_function	4.03E-05	0.0019333
GO:0003824	catalytic activity	molecular_function	4.43E-05	0.0021105
GO:0016779	nucleotidyltransferase activity	molecular_function	5.75E-05	0.002682
GO:0000988	transcription factor activity, protein binding	molecular_function	0.00010908	0.0047543
GO:0030975	thiamine binding	molecular_function	0.00015119	0.0062996
GO:0008234	cysteine-type peptidase activity	molecular_function	0.00015675	0.00645
GO:0004298	threonine-type endopeptidase activity	molecular_function	0.00015941	0.0064681

GO:0070003	threonine-type peptidase activity	molecular_function	0.00015941	0.0064681
GO:0004576	oligosaccharyl transferase activity	molecular_function	0.00018869	0.0075304
GO:0015078	hydrogen ion transmembrane transporter activity	molecular_function	0.00020245	0.0079364
GO:0016776	phosphotransferase activity, phosphate group as acceptor	molecular_function	0.00023975	0.0090247
GO:0030058	amine dehydrogenase activity	molecular_function	0.00036807	0.013014
GO:0042302	structural constituent of cuticle	molecular_function	0.00045496	0.015452
GO:0016151	nickel cation binding	molecular_function	0.00054346	0.017824
GO:0043169	cation binding	molecular_function	0.00059876	0.019541
GO:0017176	phosphatidylinositol N-acetylglucosaminyltransferase activity	molecular_function	0.00061852	0.019929
GO:0005173	stem cell factor receptor binding	molecular_function	0.00076568	0.023376
GO:0097159	organic cyclic compound binding	molecular_function	0.00081101	0.024202
GO:1901363	heterocyclic compound binding	molecular_function	0.00081101	0.024202
GO:0046872	metal ion binding	molecular_function	0.0008857	0.025849
GO:0061630	ubiquitin protein ligase activity	molecular_function	0.0010603	0.030409
GO:0061659	ubiquitin-like protein ligase activity	molecular_function	0.0010603	0.030409
GO:0005198	structural molecule activity	molecular_function	0.0013187	0.03702
GO:0051536	iron-sulfur cluster binding	molecular_function	0.0014352	0.039617
GO:0051540	metal cluster binding	molecular_function	0.0014352	0.039617
GO:0016530	metallochaperone activity	molecular_function	0.0017478	0.046316
GO:0016531	copper chaperone activity	molecular_function	0.0017478	0.046316
GO:0015002	heme-copper terminal oxidase activity	molecular_function	0.001829	0.047572
GO:0003723	RNA binding	molecular_function	0.0018342	0.047572
GO:0016863	intramolecular oxidoreductase activity, transposing C=C bonds	molecular_function	0.0018504	0.0477
GO:0016894	endonuclease activity, active with either ribo- or deoxyribonucleic acids and producing 3'-phosphomonoesters	molecular_function	0.0018655	0.047902
GO:0004129	cytochrome-c oxidase activity	molecular_function	0.0019811	0.049862
GO:0016675	oxidoreductase activity, acting on a heme group of donors	molecular_function	0.0019811	0.049862
GO:0016676	oxidoreductase activity, acting on a heme group of donors, oxygen as acceptor	molecular_function	0.0019811	0.049862
GO:0005840	ribosome	cellular_component	6.35E-13	1.00E-10
GO:0030529	ribonucleoprotein complex	cellular_component	4.01E-12	5.42E-10
GO:0005730	nucleolus	cellular_component	2.20E-10	2.24E-08
GO:0044444	cytoplasmic part	cellular_component	1.25E-09	1.18E-07
GO:0044432	endoplasmic reticulum part	cellular_component	1.23E-07	9.71E-06
GO:0005789	endoplasmic reticulum membrane	cellular_component	4.50E-07	3.24E-05



GO:0031974	membrane-enclosed lumen	cellular_component	4.68E-07	3.33E-05
GO:0042175	nuclear outer membrane-endoplasmic reticulum membrane network	cellular_component	8.50E-07	5.92E-05
GO:0005737	cytoplasm	cellular_component	1.27E-06	8.48E-05
GO:0031981	nuclear lumen	cellular_component	4.11E-06	0.00024995
GO:0044428	nuclear part	cellular_component	4.69E-06	0.00028271
GO:0043233	organelle lumen	cellular_component	8.36E-06	0.00047724
GO:0070013	intracellular organelle lumen	cellular_component	8.36E-06	0.00047724
GO:0005839	proteasome core complex	cellular_component	2.26E-05	0.0011413
GO:0008250	oligosaccharyltransferase complex	cellular_component	2.34E-05	0.0011742
GO:1990234	transferase complex	cellular_component	5.93E-05	0.0026927
GO:0071013	catalytic step 2 spliceosome	cellular_component	6.30E-05	0.0028397
GO:0031090	organelle membrane	cellular_component	0.00010086	0.004425
GO:0043189	H4/H2A histone acetyltransferase complex	cellular_component	0.00011551	0.0049692
GO:1902562	H4 histone acetyltransferase complex	cellular_component	0.00011551	0.0049692
GO:0000502	proteasome complex	cellular_component	0.00012509	0.0053464
GO:0070069	cytochrome complex	cellular_component	0.00019103	0.0075782
GO:0005783	endoplasmic reticulum	cellular_component	0.00021938	0.0083052
GO:0045261	proton-transporting ATP synthase complex, catalytic core F(1)	cellular_component	0.00040839	0.014237
GO:0005758	mitochondrial intermembrane space	cellular_component	0.00045714	0.015452
GO:0031970	organelle envelope lumen	cellular_component	0.00045714	0.015452
GO:0031300	intrinsic component of organelle membrane	cellular_component	0.00049743	0.016477
GO:0031301	integral component of organelle membrane	cellular_component	0.00049743	0.016477
GO:0042765	GPI-anchor transamidase complex	cellular_component	0.00062153	0.019929
GO:0098803	respiratory chain complex	cellular_component	0.00063113	0.020006
GO:0030176	integral component of endoplasmic reticulum membrane	cellular_component	0.00073851	0.023004
GO:0031227	intrinsic component of endoplasmic reticulum membrane	cellular_component	0.00073851	0.023004
GO:0098588	bounding membrane of organelle	cellular_component	0.001313	0.037014
GO:0031967	organelle envelope	cellular_component	0.0014042	0.039089
GO:0045277	respiratory chain complex IV	cellular_component	0.0019811	0.049862

Enriched KEGG pathway	Description		P-Value	Corrected P-Value
ko03010	Ribosome		4.35E-16	1.30E-13
ko00190	Oxidative phosphorylation		3.74E-09	5.59E-07
ko05012*	Parkinson's disease		6.34E-09	6.32E-07

ko05322	Systemic lupus erythematosus	1.27E-07	9.53E-06
ko04141	Protein processing in endoplasmic reticulum	1.16E-05	0.000692643
ko05010	Alzheimer's disease	2.05E-05	0.001013298
ko03050	Proteasome	2.38E-05	0.001013298
ko03008	Ribosome biogenesis in eukaryotes	2.71E-05	0.001013298
ko00020	Citrate cycle (TCA cycle)	4.08E-05	0.001356803
ko03013	RNA transport	5.73E-05	0.001714131
ko00510	N-Glycan biosynthesis	0.000132394	0.003598708
ko03040	Spliceosome	0.00022511	0.005608982
ko04612*	Antigen processing and presentation	0.000317536	0.007303327
ko03060	Protein export	0.000573958	0.011707161
ko04392	Hippo signaling pathway - multiple species	0.000587316	0.011707161
ko04932*	Non-alcoholic fatty liver disease (NAFLD)	0.000729371	0.013071093
ko04145	Phagosome	0.000743173	0.013071093
ko04142	Lysosome	0.001216221	0.019600913
ko00240	Pyrimidine metabolism	0.001245543	0.019600913
ko05130*	Pathogenic Escherichia coli infection	0.001534493	0.022940664
ko00563	Glycosylphosphatidylinositol (GPI)-anchor biosynthesis	0.00172479	0.023823211
ko05310	Asthma	0.001752878	0.023823211
ko04120	Ubiquitin mediated proteolysis	0.003450748	0.044649459
ko03018	RNA degradation	0.003649776	0.044649459
ko05416*	Viral myocarditis	0.003733232	0.044649459
ko00983	Drug metabolism - other enzymes	0.003990382	0.045582732
ko05169*	Epstein-Barr virus infection	0.004282308	0.045582732
ko05330	Allograft rejection	0.004307584	0.045582732
ko00010	Glycolysis / Gluconeogenesis	0.004421068	0.045582732

\*: Enriched GO/KEGG terms may involve in reproduction and aquaculture.

Table S4 – Summary of 130 enriched GO annotations and 2 enriched KEGG pathways that may associate with sex-specific putative piRNA.

Enriched GO accession	Description	Term type	Over-represented pValue	Corrected pValue
GO:0015074	DNA integration	biological_process	5.9564E-90	3.9461E-86
GO:0006259	DNA metabolic process	biological_process	2.3659E-37	7.8371E-34
GO:0006313	transposition, DNA-mediated	biological_process	4.1082E-33	6.8041E-30
GO:0032196	transposition	biological_process	4.1082E-33	6.8041E-30
GO:0090304	nucleic acid metabolic process	biological_process	9.9349E-29	1.3164E-25
GO:0006310	DNA recombination	biological_process	1.1764E-23	9.742E-21
GO:0006139	nucleobase-containing compound metabolic process	biological_process	3.3515E-23	2.4671E-20
GO:0006725	cellular aromatic compound metabolic process	biological_process	5.665E-21	3.753E-18
GO:0046483	heterocycle metabolic process	biological_process	2.0314E-20	1.2234E-17
GO:1901360	organic cyclic compound metabolic process	biological_process	3.1654E-19	1.6132E-16
GO:0034641	cellular nitrogen compound metabolic process	biological_process	1.6349E-17	7.7364E-15
GO:0044260	cellular macromolecule metabolic process	biological_process	1.0795E-16	3.764E-14
GO:0043170	macromolecule metabolic process	biological_process	5.9295E-15	1.7079E-12
GO:0019219	regulation of nucleobase-containing compound metabolic process	biological_process	9.8293E-15	2.7133E-12
GO:0006355	regulation of transcription, DNA-templated	biological_process	1.1774E-14	3.0001E-12
GO:1903506	regulation of nucleic acid-templated transcription	biological_process	1.1774E-14	3.0001E-12
GO:2001141	regulation of RNA biosynthetic process	biological_process	1.2706E-14	3.1178E-12
GO:0051252	regulation of RNA metabolic process	biological_process	1.4687E-14	3.475E-12
GO:2000112	regulation of cellular macromolecule biosynthetic process	biological_process	6.9074E-14	1.578E-11
GO:0010556	regulation of macromolecule biosynthetic process	biological_process	7.4778E-14	1.6237E-11
GO:0031326	regulation of cellular biosynthetic process	biological_process	7.5975E-14	1.6237E-11
GO:0009889	regulation of biosynthetic process	biological_process	8.2933E-14	1.717E-11
GO:0051171	regulation of nitrogen compound metabolic process	biological_process	9.0128E-14	1.8094E-11
GO:0006807	nitrogen compound metabolic process	biological_process	1.1637E-13	2.2675E-11
GO:0006351	transcription, DNA-templated	biological_process	2.4768E-13	4.4348E-11
GO:0097659	nucleic acid-templated transcription	biological_process	2.4768E-13	4.4348E-11
GO:0010468	regulation of gene expression	biological_process	2.6742E-13	4.6622E-11
GO:0080090	regulation of primary metabolic process	biological_process	3.2747E-13	5.5629E-11

GO:0032774	RNA biosynthetic process	biological_process	3.4505E-13	5.715E-11
GO:0060255	regulation of macromolecule metabolic process	biological_process	4.8941E-13	7.9082E-11
GO:0006352	DNA-templated transcription, initiation	biological_process	2.2197E-12	3.5013E-10
GO:0031323	regulation of cellular metabolic process	biological_process	4.4759E-12	6.8959E-10
GO:0016070	RNA metabolic process	biological_process	1.0846E-11	1.633E-09
GO:0044238	primary metabolic process	biological_process	1.9094E-11	2.8111E-09
GO:0034654	nucleobase-containing compound biosynthetic process	biological_process	3.1926E-11	4.5981E-09
GO:0008284	positive regulation of cell proliferation	biological_process	5.1106E-11	7.2038E-09
GO:0010883	regulation of lipid storage	biological_process	8.0205E-11	1.0844E-08
GO:0010884	positive regulation of lipid storage	biological_process	8.0205E-11	1.0844E-08
GO:0042127	regulation of cell proliferation	biological_process	9.9786E-11	1.3222E-08
GO:0019222	regulation of metabolic process	biological_process	5.0553E-10	6.567E-08
GO:0019438	aromatic compound biosynthetic process	biological_process	6.2309E-10	7.9384E-08
GO:0071704	organic substance metabolic process	biological_process	8.1527E-10	1.0191E-07
GO:0046660*	female sex differentiation	biological_process	1.0912E-09	1.3292E-07
GO:0010467	gene expression	biological_process	1.1058E-09	1.3292E-07
GO:0001819	positive regulation of cytokine production	biological_process	1.1235E-09	1.3292E-07
GO:0044237	cellular metabolic process	biological_process	1.3125E-09	1.5255E-07
GO:0018130	heterocycle biosynthetic process	biological_process	1.5314E-09	1.737E-07
GO:0019915	lipid storage	biological_process	1.5469E-09	1.737E-07
GO:0001816	cytokine production	biological_process	1.6869E-09	1.8321E-07
GO:0001817	regulation of cytokine production	biological_process	1.6869E-09	1.8321E-07
GO:0034645	cellular macromolecule biosynthetic process	biological_process	1.9225E-09	2.0543E-07
GO:0009059	macromolecule biosynthetic process	biological_process	2.8751E-09	3.0234E-07
GO:1901362	organic cyclic compound biosynthetic process	biological_process	3.4087E-09	3.5285E-07
GO:0007548*	sex differentiation	biological_process	9.4071E-09	9.588E-07
GO:0022414*	reproductive process	biological_process	1.0036E-08	1.0074E-06
GO:0044271	cellular nitrogen compound biosynthetic process	biological_process	2.6321E-07	0.000025643
GO:0003006*	developmental process involved in reproduction	biological_process	2.8044E-07	0.000026926
GO:0051240	positive regulation of multicellular organismal process	biological_process	3.0061E-07	0.000028399
GO:0044249	cellular biosynthetic process	biological_process	3.0435E-07	0.000028399
GO:1901576	organic substance biosynthetic process	biological_process	5.2502E-07	0.000048309
GO:0009058	biosynthetic process	biological_process	2.9591E-06	0.00026138
GO:0051235	maintenance of location	biological_process	3.1333E-06	0.00027313
GO:0008152	metabolic process	biological_process	4.8208E-06	0.00041478

GO:0048609*	multicellular organismal reproductive process	biological_process	0.000026904	0.0022005
GO:0008283	cell proliferation	biological_process	0.000029569	0.002389
GO:0019953*	sexual reproduction	biological_process	0.000065602	0.0050537
GO:0033057*	multicellular organismal reproductive behavior	biological_process	0.000076352	0.0056204
GO:0045924*	regulation of female receptivity	biological_process	0.000076352	0.0056204
GO:0046008*	regulation of female receptivity, post-mating	biological_process	0.000076352	0.0056204
GO:0060180*	female mating behavior	biological_process	0.000076352	0.0056204
GO:0010876	lipid localization	biological_process	0.000083716	0.0059131
GO:0044703*	multi-organism reproductive process	biological_process	0.000084389	0.0059131
GO:0007339*	binding of sperm to zona pellucida	biological_process	0.000085313	0.0059131
GO:0009988	cell-cell recognition	biological_process	0.000085313	0.0059131
GO:0035036*	sperm-egg recognition	biological_process	0.000085313	0.0059131
GO:0032879	regulation of localization	biological_process	0.0001056	0.0071387
GO:0032504*	multicellular organism reproduction	biological_process	0.00010949	0.0073269
GO:0009253	peptidoglycan catabolic process	biological_process	0.00014936	0.0097971
GO:0008037	cell recognition	biological_process	0.00017013	0.010943
GO:0032501	multicellular organismal process	biological_process	0.000192	0.012231
GO:0007610	behavior	biological_process	0.00020986	0.013241
GO:0044706	multi-multicellular organism process	biological_process	0.00028622	0.017889
GO:0007617*	mating behavior	biological_process	0.0002961	0.017997
GO:0019098*	reproductive behavior	biological_process	0.0002961	0.017997
GO:0044705*	multi-organism reproductive behavior	biological_process	0.0002961	0.017997
GO:0048522	positive regulation of cellular process	biological_process	0.00030863	0.018588
GO:0051239	regulation of multicellular organismal process	biological_process	0.00044101	0.025629
GO:0048518	positive regulation of biological process	biological_process	0.00049265	0.028136
GO:0007618*	mating	biological_process	0.00050449	0.028566
GO:0034755	iron ion transmembrane transport	biological_process	0.00061795	0.033284
GO:0000003*	reproduction	biological_process	0.00067096	0.035848
GO:0051705	multi-organism behavior	biological_process	0.00069986	0.037092
GO:0006397	mRNA processing	biological_process	0.00074343	0.039089
GO:0005667	transcription factor complex	cellular_component	1.7834E-19	9.8456E-17
GO:0043234	protein complex	cellular_component	7.6312E-06	0.00064816
GO:0016592	mediator complex	cellular_component	0.000046159	0.0035976
GO:0032991	macromolecular complex	cellular_component	0.00048251	0.027797
GO:0032865	ERMES complex	cellular_component	0.0005445	0.030061

GO:0044232	organelle membrane contact site	cellular_component	0.0005445	0.030061
GO:0044233	ER-mitochondrion membrane contact site	cellular_component	0.0005445	0.030061
GO:0030904	retromer complex	cellular_component	0.00092602	0.047426
GO:0001071	nucleic acid binding transcription factor activity	molecular_function	1.6629E-24	1.5739E-21
GO:0003700	transcription factor activity, sequence-specific DNA binding	molecular_function	1.6629E-24	1.5739E-21
GO:0003676	nucleic acid binding	molecular_function	2.2209E-17	9.809E-15
GO:0000990	transcription factor activity, core RNA polymerase binding	molecular_function	4.0429E-17	1.488E-14
GO:0000996	core DNA-dependent RNA polymerase binding promoter specificity activity	molecular_function	4.0429E-17	1.488E-14
GO:0016987	sigma factor activity	molecular_function	4.0429E-17	1.488E-14
GO:0000988	transcription factor activity, protein binding	molecular_function	5.9104E-16	1.9578E-13
GO:0008270	zinc ion binding	molecular_function	1.4319E-15	4.5172E-13
GO:0000150	recombinase activity	molecular_function	2.0914E-15	6.2979E-13
GO:0046914	transition metal ion binding	molecular_function	1.3735E-13	2.5999E-11
GO:0003677	DNA binding	molecular_function	5.3374E-08	5.2777E-06
GO:0046872	metal ion binding	molecular_function	0.000001781	0.00016163
GO:0043169	cation binding	molecular_function	2.1589E-06	0.00019328
GO:0097159	organic cyclic compound binding	molecular_function	0.000014807	0.0012262
GO:1901363	heterocyclic compound binding	molecular_function	0.000014807	0.0012262
GO:0001076	transcription factor activity, RNA polymerase II transcription factor binding	molecular_function	0.000034209	0.002698
GO:0001104	RNA polymerase II transcription cofactor activity	molecular_function	0.000034209	0.002698
GO:0003712	transcription cofactor activity	molecular_function	0.000085684	0.0059131
GO:0000989	transcription factor activity, transcription factor binding	molecular_function	0.000090022	0.0061484
GO:0003796	lysozyme activity	molecular_function	0.00014828	0.0097971
GO:0004523	RNA-DNA hybrid ribonuclease activity	molecular_function	0.00016809	0.010918
GO:0003995	acyl-CoA dehydrogenase activity	molecular_function	0.00042335	0.02494
GO:0061630	ubiquitin protein ligase activity	molecular_function	0.00042539	0.02494
GO:0061659	ubiquitin-like protein ligase activity	molecular_function	0.00042539	0.02494
GO:0004842	ubiquitin-protein transferase activity	molecular_function	0.00055631	0.030209
GO:0019787	ubiquitin-like protein transferase activity	molecular_function	0.00055631	0.030209
GO:0016783	sulfurtransferase activity	molecular_function	0.00077379	0.040365
GO:0004803	transposase activity	molecular_function	0.00081919	0.0424
GO:0005173	stem cell factor receptor binding	molecular_function	0.00093061	0.047426

Enriched KEGG pathway	Description	P-Value	Corrected P-Value
ko00534	Glycosaminoglycan biosynthesis - HS/Hep	1.06E-08	3.82E-07
ko00532	Glycosaminoglycan biosynthesis - CS/DS	2.07E-07	3.72E-06

\*: Enriched GO/KEGG terms may involve in reproduction and aquaculture.

Table S5 - Validation of the expression of 311 sex-biased putative piRNAs by microarray.

Up-regulated piRNAs in testes	piRNA ID	After normalization		Statistical analysis (F vs. M)		Length of piRNA	piRNA seq
		Median_Male	Median_Female	log2Ratio	P-value		
ASY-piR-1029	uniq_2052249	7.046214555	6.483815777	-1.001820436	0.044194439	26	UAUCAAACUGGUAGGCCCUUGGUCAGU
ASY-piR-741	uniq_666257	6.79224803	5.8475794	-1.002171099	0.037021376	29	UAUGUCCUCUUUAGAGCCUGCAGGUGGU
ASY-piR-1312	uniq_573295	7.410097966	6.22881869	-1.008545109	0.025129032	29	UUGGUCUUUGGAUGCAUCUGGUGGGCACA
ASY-piR-218	uniq_819390	5.574908836	4.564784619	-1.010124217	0.004859692	29	UCCUGAUGUAUGAACUGAUUAAAGCUUC
ASY-piR-849	uniq_10198	9.448632568	8.435323	-1.013309568	0.028664238	28	UAAUGUCAGAACAGUGCAUGCUGGUGCU
ASY-piR-1786	uniq_414440	6.087462841	5.073248982	-1.014213859	0.042775187	26	UGUACUGCUGUAGCCGAUCUGACCAU
ASY-piR-1648	uniq_440736	12.25949809	11.22370008	-1.019870634	4.11E-05	29	UACAGGAAUCUCUGCAGGGUCUGGAGGCG
ASY-piR-1503	uniq_715514	12.71999481	11.57230548	-1.021435773	0.005270714	26	UUCUUAGAGGGACUGGUGGCUCUCAG
ASY-piR-147	uniq_615837	6.942514505	5.920849053	-1.021665452	0.03724273	26	UCUGCGUACAGGAAUCUCUGCAGGGA
ASY-piR-394	uniq_905882	7.903379777	6.759333407	-1.024210554	0.036299574	29	UCUGCGUACAGGAAUCUCUGCAGGGUCUG
ASY-piR-628	uniq_206632	13.15963486	11.83499768	-1.025248705	0.015767096	26	UCUUAGAGGGACUGGUGGCUCUCAGC
ASY-piR-1645	uniq_441539	14.59828517	13.57070563	-1.027579544	0.002493845	27	UGGUUCGAUCAGCAGGACCGGAGAGC
ASY-piR-942	uniq_469397	10.43549664	9.279223644	-1.029291636	0.001698626	27	UUAGAACUUCUUAAACAGGGUGUGUG
ASY-piR-227	uniq_131634	7.342815461	6.336878436	-1.029932506	0.016602762	27	UGAGUACGUUAAAAUGUUGAGACUGC
ASY-piR-1713	uniq_178076	10.06933787	9.038461789	-1.030876085	3.42E-05	27	UACAGGUAUCUCUGCAGGGUCUGGAGU
ASY-piR-1570	uniq_490270	10.55722435	9.434628228	-1.036708286	0.040059604	28	UCACUGUGACUGGAUCUGUGUUGUAUGC
ASY-piR-1449	uniq_565914	7.749310785	6.502500341	-1.037357078	0.040756391	29	UCUGCGUACAGGUAUCUCUGCAGGGUCUA
ASY-piR-812	uniq_514801	10.08192721	9.033423002	-1.038335304	0.047673195	27	UGAUUGCAUUGCUGUAGAACUGUGUGU
ASY-piR-1000	uniq_197248	9.926790153	8.82336724	-1.038882661	0.018409005	27	UCCUGAUCUGUUGGACUGUUCGGGAGU
ASY-piR-1603	uniq_381705	12.17923526	11.12142559	-1.040216917	0.047685	28	UGCGCUGUGCUGUGUUGUGCUCUGUGGU
ASY-piR-1343	uniq_705989	8.41080465	7.120669887	-1.042560462	0.024541161	30	UCUGCGUACAGGUAUCUCUGCAGGGUCUGU
ASY-piR-567	uniq_690594	14.11695308	12.95222556	-1.052575187	0.014609949	29	UUCUUCCAUGAACGAGGAAUCCAGU
ASY-piR-802	uniq_101638	9.7474937	8.693486957	-1.054006743	0.002729213	27	UAAAGCAUCUCUGGUCUGUCAGAGAGU
ASY-piR-544	uniq_472772	13.23159621	12.28115729	-1.060732258	0.000903716	29	UUUCAGGAUGGACCAGAACGUGGAGGUGU
ASY-piR-1009	uniq_189163	10.45780836	9.406205005	-1.061025212	0.009321026	27	UAGCUGUAUGAGAGGCUGUGGUCUAUU
ASY-piR-1337	uniq_535821	9.599912842	8.537218401	-1.062694442	0.044479264	26	UUUGCAGGAUUUGAAGAUUUGUGUGC
ASY-piR-540	uniq_553449	6.805206455	5.741466986	-1.063739469	0.019718027	27	UCCUGAUGUAUGAACUGAUUAAAGCAU
ASY-piR-1800	uniq_722663	7.204571144	6.241585987	-1.064475703	0.005157236	26	UGGAAACUGGAGACAUCUUGAGACG
ASY-piR-564	uniq_946093	13.55322929	12.48863517	-1.064594117	0.009050068	26	ACCGAUUGGAUGGUUAGUGAGGUCU
ASY-piR-379	uniq_323574	9.341148141	8.276512174	-1.064635967	0.036353451	30	UAUUGUUGAACUUCUGCCAUGAGGGUGGA
ASY-piR-1519	uniq_99033	6.932706887	6.06608919	-1.064910299	0.001810808	30	UCUCGGCCAAGGUGACCAGAGUCUGGGAUC
ASY-piR-547	uniq_1612612	9.117210185	8.17450962	-1.066001244	0.001035413	30	UACUGUUGGACCAUCCCGGCUGUGGAGGU
ASY-piR-645	uniq_2131639	13.42307213	12.35590164	-1.067170489	0.00018769	31	UUUCAGGAUGGACCAGAACGUGGAGGUGACU



ASY-piR-234	uniq_481939	7.108524457	6.033423002	-1.071612469	0.031609833	26	UCUCCUUGGUCCUGUAGAGCUUGGA
ASY-piR-142	uniq_695682	8.830779268	7.552028611	-1.076113108	0.038533686	31	UCUGCGUACAGGAAUCUCUGCAGGGUCUGGA
ASY-piR-979	uniq_1789133	12.46147945	11.3777528	-1.083726652	0.01154684	26	UUUCAGGAUGGACCAGAACGUGGAGA
ASY-piR-783	uniq_2007758	13.34810569	12.25949809	-1.088607605	0.000267572	31	UUUCAGGAUGGACCCGAACAUGGAGGUGACC
ASY-piR-233	uniq_360473	8.764318728	7.687667284	-1.090129896	0.019918671	30	UCUGCGUACAGGAAUCUCUGCAGGGUCUGG
ASY-piR-1330	uniq_312861	9.119157288	7.919359948	-1.09046867	0.048832653	27	UUUGCAGGAUUUGAAGAUUUGUGUGCA
ASY-piR-1813	uniq_689842	11.12142559	10.01657618	-1.092598628	0.004067055	29	UGCUC AUGUGUCAGGGCUUGGUAGGCUGC
ASY-piR-1637	uniq_1717673	9.609178738	8.526825235	-1.094843978	0.004276381	29	UAAUUGACGGUGCAGUGAGAGUUUCCUUU
ASY-piR-1304	uniq_360476	8.182394353	7.084808388	-1.097585966	0.031870061	30	UCUGCGUACAGGAAUCUCUGCAGGGUCUGU
ASY-piR-984	uniq_1487787	9.113308077	8.01355531	-1.099752767	0.04359303	27	ACUACUCCAAAGUCCGAGAGCUGGUGU
ASY-piR-1144	uniq_350534	7.016808288	6.037089319	-1.109267212	0.001067661	27	UGGUCUUGUAGAUGGCGAGUCUAGCAA
ASY-piR-1811	uniq_298248	10.09583653	8.984418459	-1.111418075	0.01324668	30	UACAGGUAUCUCUGCAGGGUCUGUAGGCGU
ASY-piR-1286	uniq_231361	14.8623387	13.74917109	-1.113167612	0.008897623	26	UGUUGGUUGAUUAUAGACAGCAGGACA
ASY-piR-865	uniq_300756	11.37368083	10.19926336	-1.114186581	0.016011893	28	UUAGAACUUCUUUAAACAGGGUGUGUGC
ASY-piR-1564	uniq_885688	6.828665428	5.886712714	-1.114419911	0.026188651	29	UACGAGUGUACUGUCUGACUUUGAUAGUC
ASY-piR-1074	uniq_59183	10.73541499	9.647758207	-1.117641449	0.000193587	28	UACAGGUAUCUCUGCAGGGUCUGGAGGU
ASY-piR-1865	uniq_338981	10.24317398	9.18404882	-1.120872849	0.00095528	27	UCUGUAAUCCAGGGAUUGUGGUGAGU
ASY-piR-1305	uniq_902044	7.330916878	6.209453366	-1.121463512	0.003291343	26	UCCGACUGGUGACAAUGGUAGUCCGC
ASY-piR-456	uniq_349350	9.652546247	8.526825235	-1.125721012	0.0066261	27	UCUACUCCCCUCUCACUGUGGUGCUGU
ASY-piR-1625	uniq_826049	14.70643306	13.36365568	-1.131891388	0.000348873	29	UAGGAGUUGUAAGAUAAAGGCGAGACGGC
ASY-piR-606	uniq_565054	6.46760555	5.348728154	-1.132398536	0.002797567	26	UCCUGAUGAACAGUGCCCUGGUGAUC
ASY-piR-1211	uniq_69274	6.199672345	5.523561956	-1.137028249	0.025386495	26	UUCUACCAAUCUAGUUCGGACAGGU
ASY-piR-291	uniq_168547	11.57230548	10.31891935	-1.137850994	0.022984394	30	UGAGACUGAUUACUGCUGUCUGAGUGUGUU
ASY-piR-1159	uniq_923129	5.705056346	4.564784619	-1.140271727	0.048906595	25	UCCGUCUGCAGGGUGAACCCUCUUGC
ASY-piR-1852	uniq_1693483	9.265810362	8.121533517	-1.144276844	0.022278136	26	AAAGCAUCUCUGGUCUGUCUGAGAGU
ASY-piR-889	uniq_204431	12.62411004	11.60933267	-1.154298659	0.001323123	27	UUUGAAAUGUUACCGCGGGAGGCUGGC
ASY-piR-659	uniq_1197941	6.785724906	5.684164178	-1.156368286	0.00095596	25	UGGGCAAGUUGCAGUUCUGAGACAA
ASY-piR-295	uniq_420483	5.115477217	3.857980995	-1.156969346	0.01503692	29	UCCGGAUCGUGCUGACCCUGUCGACAGCU
ASY-piR-1461	uniq_904903	8.763489037	7.614709844	-1.158154537	0.014728483	25	UCUGUGAACAUAGAGCUGAUGUGAC
ASY-piR-1763	uniq_643071	9.094737505	7.977756926	-1.167178878	0.03115636	28	UGAGCGUGGUUCCUGGUGACGUAGAACG
ASY-piR-855	uniq_2413022	9.671835885	8.59058705	-1.167875926	0.041863979	27	UGGGUGUAAAUUGCUGCACAGGUGUGU
ASY-piR-1768	uniq_391515	6.044394119	5.080373416	-1.169925001	0.017412766	26	UGUUGAAAAGUCAUAACUGUGAAUG
ASY-piR-945	uniq_1872201	14.6783067	13.39063921	-1.170330438	0.000267945	32	UCUAAGUACACACGGGCUGUACAGUGAAACUG
ASY-piR-179	uniq_252270	14.1582415	12.98355776	-1.17468374	0.000249431	30	UCUGAUGUCAGGAGUUGCGGAGGAACGAGU
ASY-piR-1082	uniq_1738602	8.688250309	7.511752654	-1.176497655	0.03721423	27	UAAGGUUCUGGCUUGUGUAGCGAAUGU
ASY-piR-1041	uniq_2349027	7.637832402	6.286942737	-1.183875914	0.015064519	28	UACUGUUGGACCAUUCCCGCUGUGGAU
ASY-piR-402	uniq_395184	6.309855263	4.754887502	-1.187458631	0.004844041	28	UCCAUGAUGUUCGAUAGGAUUCAGAUC
ASY-piR-1839	uniq_316583	14.48413058	13.54004729	-1.188152437	0.01311882	26	UGGUGAACUAUGCCUGGGCAGGGCGU
ASY-piR-754	uniq_944850	13.53237622	12.38082178	-1.189883846	0.005252411	26	UUGUAAAAGUGCCAGUAGGCGGAGGC

ASY-piR-465	uniq_849616	8.79658045	7.606096714	-1.191294619	0.031658378	29	UACAAACACAGACGGUUGUUGUGAUGAGU
ASY-piR-1582	uniq_205451	5.910892526	4.709658248	-1.192074279	0.021527753	26	GAGAAUCGUGUGCAAUAGUCUCCACU
ASY-piR-1845	uniq_834403	11.34272288	9.949826711	-1.194353528	0.007952377	28	UUAGAACUUCUUUAACAGGGUGUGUGU
ASY-piR-1065	uniq_443238	8.233619677	7.14635653	-1.196320736	0.037706265	27	UGUCAGGACGGUGCAUGCUGGUACUCC
ASY-piR-1061	uniq_2341863	8.657616189	7.479780264	-1.196819028	0.010756538	27	UAUUUCCCAGGAUCAAGGGCUGGUUU
ASY-piR-555	uniq_1007993	9.026984441	7.919359948	-1.198310986	0.000490431	26	UAUUUCCCAGGAUCAAGGGCUGGUU
ASY-piR-1864	uniq_424025	13.83323601	12.87504536	-1.199529338	0.037642417	29	UGGGAUUAUGACUGAACGCCUCUAAGUCA
ASY-piR-652	uniq_2331133	7.018663844	5.828665428	-1.200161535	0.009531207	27	UGUCAAGAUUGUCCAUCUGGAGGCUG
ASY-piR-1676	uniq_295154	8.879072651	7.675369018	-1.203703634	0.026601648	27	UCGGUCUGGAGAUGUCACUUGGACAGU
ASY-piR-1401	uniq_408607	6.513069582	5.303780748	-1.209288834	0.009982771	25	UCCGACUGGUGACAAUGGUAGUCCG
ASY-piR-874	uniq_102704	10.48683502	9.235216462	-1.21547931	0.000433135	26	UUACAUACUCAGGGCUGGGUAGCUGU
ASY-piR-670	uniq_2096775	6.963859408	5.790076931	-1.216482915	0.031112632	27	UAAUGAAAAUGUACAACUGAGAUGUGU
ASY-piR-1283	uniq_618527	7.286942737	6.186526969	-1.217195217	0.041095747	27	UUGUUUAGGUCUUGCUUCAGUAGAGUC
ASY-piR-595	uniq_1196291	6.8475794	5.62935662	-1.21822278	0.004366266	29	UGAUGUUGGGCUGCACGAUGCCCUGGGCU
ASY-piR-221	uniq_854155	4.709658248	3.95419631	-1.219445137	0.02590274	29	UCCGAGCUUGCCGUUUCUGAACUUUGGCA
ASY-piR-1198	uniq_72781	7.770388596	6.573647187	-1.226068079	0.020117607	28	UCUGCGUACAGGUAUCUCUGCAGGGUCU
ASY-piR-149	uniq_660139	8.002815016	6.894817763	-1.235734091	0.034172985	29	UGACCUUGUUGCCUUGCUGAAUGAAAGU
ASY-piR-1333	uniq_269500	11.35342254	9.980615636	-1.238603313	0.009917237	26	UGCGUGCGCUGUGCUGUGAAGUGCUG
ASY-piR-321	uniq_763129	10.67581005	9.601151739	-1.240560544	0.019345498	30	UGAGACUGAUUACAGCUGUCUGAGUGUGUC
ASY-piR-1393	uniq_705991	9.491185027	8.347990391	-1.24197279	0.005577858	30	UCUGCGUACAGGUAUCUCUGCAGGGUCUGG
ASY-piR-1322	uniq_689464	14.32708477	13.14749645	-1.245916358	0.004603608	26	UCAGCUAGGAAUAAUGGAAUAGGACU
ASY-piR-847	uniq_409007	12.56188457	11.44553222	-1.25715299	0.010077583	26	UAGAGGUGAAAUUCUUGGACCGGUGU
ASY-piR-598	uniq_362507	14.08558311	12.82641608	-1.259167033	0.000518773	27	UUUCAGGAUGGACCCGAACGUGGAGGU
ASY-piR-1668	uniq_484825	11.50490173	10.19690944	-1.261727744	0.003608853	27	UCUGAUGAAGGUCGGCGUCGGAUGUGU
ASY-piR-568	uniq_790527	11.09759324	9.968666793	-1.26215425	0.006160916	30	UACUGUUGGACCAUUCCCGCUGUGGAGGC
ASY-piR-1767	uniq_344366	13.48158923	12.43371583	-1.265205832	0.005463106	29	UCCGGUUCUGUUUGUGGGUUUCCCGAAC
ASY-piR-1525	uniq_303990	7.581200582	6.309855263	-1.271345319	0.001158914	27	UGAGUACGUUGAAAUGUUGAGACGGU
ASY-piR-472	uniq_416396	7.65224746	6.276124405	-1.272055306	0.016729925	28	UUGAACUUUUGGCUCUGAAAUGGUCAGU
ASY-piR-1850	uniq_255533	12.02571634	10.72827485	-1.27654525	0.007721739	30	UCUUAGAGGGACUGGUGGCUCUCAGCCACA
ASY-piR-840	uniq_1831773	10.32239765	8.945687679	-1.280686649	0.002243177	27	UGACAUAGGACUCUGUGAGUUGGCGGU
ASY-piR-1608	uniq_38091	11.74209887	10.42504102	-1.281813636	0.0206631	30	UGAGACUGAUUACUGCUGUCUGAGUGUGUC
ASY-piR-755	uniq_944848	12.55310927	11.36431708	-1.287893029	0.000117638	26	UUGUAAAAGUGCCAGUAGGCGGAGGU
ASY-piR-982	uniq_597917	9.858240077	8.669475648	-1.288080324	0.000692916	27	UCCUUUGGUCGGUUUCCAGAUGGCGGU
ASY-piR-622	uniq_856037	8.117210185	6.865217746	-1.288544756	0.018728526	29	UACUGUUGGACCAUUCCCGCUGUGGAGU
ASY-piR-870	uniq_2363048	13.07795617	11.78252051	-1.29543566	0.001234833	26	UAGAGGUGAAAUUCUUGGACCGGUGG
ASY-piR-1054	uniq_243489	13.14749645	11.77848786	-1.301483774	0.000487013	27	UUGUAAAAGUGCCAGUAGGCGGAGGUG
ASY-piR-417	uniq_609107	8.872418378	7.461479447	-1.302839281	0.04917403	28	UUGGAAAGUGUGAGCUCUGGUUCAAGUG
ASY-piR-610	uniq_2139973	14.25898308	12.9659045	-1.312399748	0.002123888	31	UUUCAGGAUGGACCCGAUGUGGAGGUGACC
ASY-piR-1675	uniq_4118	9.580572641	8.380821784	-1.316435411	0.026763019	25	UGAGCGUGGUUCCUGGUGACGUAGA

ASY-piR-1073	uniq_2085175	14.21963492	12.90250074	-1.317134185	0.001386888	29	UUUCAGGAUGGACCAGAACGUGGAGGUGG
ASY-piR-894	uniq_639000	11.73287404	10.43749201	-1.317673763	0.000377437	28	UAGCAGUGAUGGCUGGGCGGUCUGACGU
ASY-piR-958	uniq_1840388	12.86024638	11.53219356	-1.328052822	2.70E-06	27	UUGUAAAAGUGCCAGUAGGUGGAGGCA
ASY-piR-1601	uniq_301766	6.996238081	5.62935662	-1.340269731	0.040338389	26	UACUCUGGGUUGACGGUCUGAAUAUC
ASY-piR-275	uniq_494549	6.864186145	5.523561956	-1.340624189	0.029515785	28	UGAGUGCAGCAUACUCUAGGUUGACGGU
ASY-piR-1776	uniq_516831	11.35342254	9.986079047	-1.357419908	0.007289783	29	UUAGAACUUCUUAAACAGGGUGUGUGCU
ASY-piR-589	uniq_1857243	12.31830743	10.95079888	-1.367508548	0.000573828	29	UUUCAGGAUGGACCCGAACAUGGAGGUGU
ASY-piR-270	uniq_274921	8.774237984	7.409390936	-1.377423207	0.006321019	27	UGAAUCAUCGGGUGCUGAAGCGUCAGA
ASY-piR-44	uniq_396347	6.499845887	5.464886049	-1.380555825	0.020033537	27	UAAUCCGAGCUUGCCGUUUCUGAGCA
ASY-piR-752	uniq_651528	13.8255551	12.44143126	-1.384123841	0.001021593	27	UCUAUUCUGUGGGUGGUGGUGCAUGGC
ASY-piR-1042	uniq_395211	12.99641464	11.60563384	-1.390780799	6.56E-05	29	UGAUGUUGAGACGGCGGAGAAUGGCCAGU
ASY-piR-731	uniq_1857239	12.35590164	10.96229355	-1.393608086	0.000626825	29	UUUCAGGAUGGACCCGAACAUGGAGGUGA
ASY-piR-424	uniq_364394	8.110265791	6.701595261	-1.40867053	0.015164495	28	UUUUAGUGCAAACGGCUGGAUAUGAUGC
ASY-piR-560	uniq_2020443	13.00501043	11.5075469	-1.442124174	0.008706172	26	UGAUUGUGGAUCAUCCGGGGCUGGGG
ASY-piR-75	uniq_120482	5	3.700439718	-1.442518236	0.019887784	26	UCCGAUUCGGUCUGAAAUAACAACC
ASY-piR-1468	uniq_591247	11.56811447	10.36322219	-1.446681937	0.014494838	29	UCCUUUGAUCGCUCCAAAGUUACUUGGAC
ASY-piR-1660	uniq_958391	8.258566034	6.743712427	-1.453359578	0.005560937	27	AUAUCUGGAAAAUUACUGAUGAUGUG
ASY-piR-574	uniq_2113368	9.943979914	8.459431619	-1.484548296	0.009106156	29	UACACUCACAGCAGCCAUCGGGGUCUGGG
ASY-piR-671	uniq_2098014	13.26079705	11.61371274	-1.48738751	0.001266962	29	UUUCAGGAUGGACCCGAAUGUGGAGGUGA
ASY-piR-1071	uniq_2207804	13.51422091	12.02571634	-1.488504569	3.03E-05	26	UUUCAGGAUGGACCCGAAUGUGGAGG
ASY-piR-469	uniq_558376	10.13699111	8.65731845	-1.493486597	0.004460522	28	UCCGAAAUGAUGGUGAUUGUAGAAGGU
ASY-piR-1325	uniq_685076	5.741466986	4.247927513	-1.493539473	0.006826677	25	UCCGUCUGCAGGGUGAACCUUUAC
ASY-piR-1270	uniq_696934	13.95625514	12.43371583	-1.51717129	0.005042723	26	UGAUUCAACUCGAACAGCUGGAGGGC
ASY-piR-920	uniq_2020444	12.268542	10.74216906	-1.526372938	0.002539457	26	UGAUUGUGGAUCAUCCGGGGCUGGGA
ASY-piR-988	uniq_1892758	14.0331792	12.49901537	-1.534163837	0.001373807	29	AUUUUCAGGAUGGACCCGAAUGUGGAGGU
ASY-piR-637	uniq_2280712	13.74023753	12.16715676	-1.535672056	0.001265726	27	UGAUUGUGGAUCAUCCGGGGCUGGGGU
ASY-piR-1441	uniq_298490	7.358284895	6.173260714	-1.568207965	0.020712889	28	UAAUGAUCUGCAUGUUUUGUUGAAUAGU
ASY-piR-994	uniq_1666389	12.83335133	11.38563775	-1.581178704	0.000978403	26	UAAUUGUGGAUCAGCCGGGGCUGGGG
ASY-piR-687	uniq_290095	5.303780748	3.700439718	-1.584962501	0.027074218	29	UGCAUUUGGUGAAAUCUGUUUAUGACUG
ASY-piR-579	uniq_2032628	14.32708477	12.74185317	-1.585231598	3.80E-06	28	UUUCAGGAUGGACCCGAAUGUGGAGGUG
ASY-piR-1150	uniq_142987	7.16155182	5.303780748	-1.586642984	0.022053631	27	UGUGCUGAAUAAAUGCUGUAUAGGUU
ASY-piR-770	uniq_572119	9.244958393	7.914883386	-1.625742906	0.004126481	26	UUAGAACUUCUUAAACAGGGUGUGU
ASY-piR-724	uniq_248332	7.28077077	5.741466986	-1.625989769	0.00585617	26	UUUGUAAUUUUCAGUUUCUGUGAGG
ASY-piR-673	uniq_2360467	13.37223025	11.76563143	-1.628307493	0.000746197	29	UAAUUGUGGAUCAGCCGGGGCUGGGGAGU
ASY-piR-1594	uniq_123564	12.98841842	11.35342254	-1.634995873	0.002666139	29	UAGGAGUUGUAAGUAAGGCUGAGACGGU
ASY-piR-1453	uniq_627952	5.609794354	3.874469118	-1.638600464	0.035939113	25	UCCUGAUGUAUGAACUGAUUAAAGU
ASY-piR-583	uniq_50192	12.88734756	11.24396733	-1.643380236	0.000542303	27	UGAUUGUGGAUCAUCCGGGGCUGGGGA
ASY-piR-858	uniq_786249	13.603182	11.95679963	-1.646382368	0.002129472	26	UCUAUUCUGUGGGUGGUGGUGCAUGU
ASY-piR-573	uniq_1099307	13.67748108	12.02928723	-1.648193854	0.000953648	27	UUUCAGGAUGGACCCGAAUGUGGAGGU

ASY-piR-581	uniq_597840	11.42870911	9.672425342	-1.652276081	0.000270704	27	UUCUCUGGAUUGUAGUAGGUGUGAGGU
ASY-piR-845	uniq_9583	9.627533884	8.080817528	-1.654174282	0.00250344	26	UACAGAAAUGUAGGCUGGGCAUUAGU
ASY-piR-612	uniq_1911714	10.74216906	9.236811481	-1.669295768	0.017391062	31	UACACUCUCAGCAGCCAUCGGGGUCUGGGCA
ASY-piR-794	uniq_585155	11.22068062	9.666815756	-1.673305615	0.014617535	27	UCCUUUGAUCGCUCCAAAGUUACUUGG
ASY-piR-789	uniq_669560	11.90350531	10.46947224	-1.680911634	0.01282572	27	UUCAACUCGAACAGCUGGAGGGUGGUC
ASY-piR-626	uniq_986456	12.68642757	11.00093895	-1.685488625	0.000308881	27	UAAUUGUGGAUCAGCCGGGGCUGGGGA
ASY-piR-624	uniq_2020441	13.08425476	11.39178061	-1.692474155	0.000354716	26	UGAUUGUGGAUCAUCCGGGGCUGGGU
ASY-piR-793	uniq_2332609	6.912889336	5.235216462	-1.733113269	0.007172954	26	UGACAAUGUUUCGGACAGUUGAAAUU
ASY-piR-638	uniq_1945945	11.13249973	9.375039431	-1.757460298	0.000707698	30	UACACUCUCAGCAGCCAUCGGGGUCUGGGC
ASY-piR-1003	uniq_268947	5.297680549	3.700439718	-1.7589919	0.016863069	27	UACAGUUGUUUAAACUGUGAGACUUU
ASY-piR-376	uniq_884690	12.49901537	10.70108982	-1.760219389	0.001398891	27	UUGGAAUACAGCCGUAGACAUGGGGC
ASY-piR-777	uniq_36994	14.19323016	12.24931101	-1.774670925	0.002692004	27	UCUAUUCUGUGGGUGGUGUGCAUGGU
ASY-piR-576	uniq_490965	13.15429071	11.66073875	-1.804825172	0.000927818	29	UUUCAGGAUGGACCCGAAUGUGGAGGUGU
ASY-piR-1131	uniq_591245	11.92140707	10.16406888	-1.819817335	0.0327572	29	UCCUUUGAUCGCUCCAAAGUUACUUGGAU
ASY-piR-1661	uniq_4590	5.68182404	3.857980995	-1.823843045	0.032892944	25	CUGUAUAAACUGUUCUUAUGGUGACU
ASY-piR-586	uniq_743479	12.95222556	11.10841555	-1.843810007	0.008836778	29	UGCUGUUGAACUAGCCUUGGAGAGGGCGU
ASY-piR-631	uniq_1820232	13.11582939	11.2177558	-1.8980736	0.000163483	25	UGCAGAUGGGAACAUGGCUGGCAGU
ASY-piR-621	uniq_2139972	13.15429071	11.54673372	-1.902118087	0.002141446	31	UUUCAGGAUGGACCCGAAUGUGGAGGUGACU
ASY-piR-1795	uniq_1059880	7.410097966	5.431845787	-1.978252179	0.01441268	26	UACUGUUGUUGAUUCAUGACGAUGU
ASY-piR-838	uniq_946092	13.20480037	11.39803107	-1.987449397	0.000365814	26	ACCGAUUGGAUGGUUUAGUGAGGUCA
ASY-piR-1023	uniq_180371	3.700439718	1.659079432	-2.041360286	0.007717421	26	UAGCUUCAGAUUUAGGAUUAUCAACU
ASY-piR-1078	uniq_244241	5.247927513	3.273018494	-2.078002512	0.006725692	28	UGAGAUUGUCAUAGGAGUCCUUCAGAU
ASY-piR-796	uniq_550658	6.981091537	5.014950341	-2.084282596	0.035526633	27	UUUCCUGAUUAGCAGACUCUUGACGGG
ASY-piR-1667	uniq_510697	6.257387843	4.169925001	-2.087462841	0.033048722	27	UGUUUGUCGGGUCUCUUCAGAGACGGU
ASY-piR-1548	uniq_46136	13.74023753	10.57947309	-2.106788157	0.011360204	27	UUGGUGUUUUUCUCUGUAUUUGCAGGA
ASY-piR-1367	uniq_534386	7.614709844	5.667702932	-2.125629423	0.015170855	25	UCAGCUCUGAAUGUGGAAAUACAGG
ASY-piR-323	uniq_881210	6.132713922	3.938599455	-2.194114467	0.002889558	29	UGAAGUUUGACUAUGCAGUAAAUCUGUGU
ASY-piR-462	uniq_778029	5.080373416	3.415037499	-2.239071162	0.040175029	27	AACUGGUAGAGGUCCUUGAUUGAAACA
ASY-piR-224	uniq_270947	5.62935662	3.36923381	-2.26012281	0.042606517	28	UGAGCUUGUAAAGGUCCUGAAACAGUGU
ASY-piR-1555	uniq_719684	3.700439718	1.315295612	-2.385144106	0.005075997	25	UCUAGACUGAUGAGCAUCAUAACA
ASY-piR-1139	uniq_147259	3.772589504	1.315044421	-2.457545083	0.034484453	26	UCUGAUCAUUCUGUAAAUAUGAAGC
ASY-piR-370	uniq_898371	4.044394119	0.720129867	-2.728738414	0.047212337	30	UAACAUAUUUACUGCCAUCUAUUUUGAACU
ASY-piR-108	uniq_96374	12.570923	10.04621455	-2.759193455	0.011158346	28	UAAUGUACAGAUACUAAGGCGGGUAGU
ASY-piR-195	uniq_898271	4.448460501	1.580237514	-2.868222987	0.01920801	28	UGAAGUUUGACUAUGCAGUAAAUCUGUG
ASY-piR-437	uniq_526064	10.78108645	8.088346575	-2.877206382	0.01771982	25	UAAUGUACAGAUACUAAGGCGGGU
ASY-piR-110	uniq_769219	5.222392421	2.543918318	-3.906736716	0.044421583	27	UAAAGACUUAUCUCUGCAAGGUGUUA
ASY-piR-1255	uniq_730840	4.044394119	0.719794633	-4.140112546	0.000477559	27	UCUGAUCAUUCUGUAAAUAUGAAGCU

Up-regulated piRNAs in ovaries	piRNA ID	After normalization		Statistical analysis (F vs. M)		Length of piRNA	piRNA seq
		Median_Male	Median_Female	log2Ratio	P-value		
ASY-piR-122	uniq_502621	4.906890596	13.32685077	8.465339655	0.001871969	26	UGGGAUAUCAAGUGCUGCAGGCACU
ASY-piR-303	uniq_809899	-0.083249726	8.026523443	8.102841167	0.001898777	31	UGAAAGGACAGAUUUACUCCACUGCAGUGC
ASY-piR-19	uniq_855876	5.357552005	13.35567227	7.998120267	9.84E-05	27	CCUGGGAAUAUCAAGUGCUGCAGGCAC
ASY-piR-4	uniq_332247	5.790076931	13.24019505	7.772753923	0.000399719	25	UGGGAUAUCAAGUGCUGCAGGCAA
ASY-piR-144	uniq_502613	5.339850003	13.09206888	7.623015886	1.07E-07	26	UGGGAUAUCAAGUGCUGCAGGCACC
ASY-piR-151	uniq_855875	6.360481336	13.95625514	7.595773805	8.22E-06	27	CCUGGGAAUAUCAAGUGCUGCAGGCAA
ASY-piR-100	uniq_431484	6.321928095	13.79818488	7.552140717	0.000340795	26	UGGGAUAUCAAGUGCUGCAGGCAUU
ASY-piR-365	uniq_277058	6.675957033	14.56096965	7.550894144	5.38E-06	26	UUGAAUAAGCCUGAUCUCGUCUGAUU
ASY-piR-488	uniq_431489	5.247927513	12.73089465	7.482967133	2.62E-05	26	UGGGAUAUCAAGUGCUGCAGGCAUA
ASY-piR-1613	uniq_332246	5.136136688	12.95222556	7.465725698	1.01E-05	25	UGGGAUAUCAAGUGCUGCAGGCAC
ASY-piR-1605	uniq_332251	6.420662048	13.74917109	7.222997921	2.38E-05	25	UGGGAUAUCAAGUGCUGCAGGCAU
ASY-piR-16	uniq_809907	0.18355396	7.424866117	7.104927652	0.020238546	31	UGAAAGGACAGAUUUACUCCACUGCAGUGU
ASY-piR-29	uniq_555127	7.046214555	14.12199211	7.075777556	2.13E-05	29	CACCUGGGAAUAUCAAGUGCUGCAGGCAC
ASY-piR-990	uniq_744089	3	9.45532722	7.039156751	0.000168531	27	UCCUUCAGGUAGGACCACUUCGAUGC
ASY-piR-418	uniq_50195	6.011227255	13.02161621	6.959120288	4.70E-05	29	ACCUGGGAAUAUCAAGUGCUGCAGGCACC
ASY-piR-6	uniq_855873	6.732450113	13.67748108	6.945030968	0.000127695	27	CCUGGGAAUAUCAAGUGCUGCAGGCAU
ASY-piR-15	uniq_555130	7.283860054	14.25898308	6.906667251	8.51E-06	29	CACCUGGGAAUAUCAAGUGCUGCAGGCAU
ASY-piR-7	uniq_784438	7.327178356	14.21963492	6.866051803	1.81E-05	26	CCUGGGAAUAUCAAGUGCUGCAGGCA
ASY-piR-21	uniq_146212	7.668884984	14.31834274	6.649457751	6.49E-06	26	ACCUGGGAAUAUCAAGUGCUGCAGGC
ASY-piR-1	uniq_594685	6.87036472	13.54848078	6.607922469	0.000184234	27	ACCUGGGAAUAUCAAGUGCUGCAGGCA
ASY-piR-70	uniq_417742	7.86727874	14.30452958	6.353244865	6.93E-06	25	CCUGGGAAUAUCAAGUGCUGCAGGC
ASY-piR-184	uniq_146226	7.868308133	14.11695308	6.351326787	7.55E-06	26	ACCUGGGAAUAUCAAGUGCUGCAGGU
ASY-piR-154	uniq_61991	6.241585987	12.69439416	6.340830454	0.00022779	27	ACCUGGGAAUAUCAAGUGCUGCAGACA
ASY-piR-310	uniq_594695	7.647458426	13.94295734	6.295498911	1.32E-05	27	ACCUGGGAAUAUCAAGUGCUGCAGGCU
ASY-piR-52	uniq_819831	7.548179712	13.82009584	6.271916128	0.000101385	28	CACCUGGGAAUAUCAAGUGCUGCAGGCA
ASY-piR-83	uniq_292933	7.880603904	14.00266854	6.122064632	7.11E-06	27	ACCUGGGAAUAUCAAGUGCUGCAGGUA
ASY-piR-667	uniq_413200	3.95419631	10.02040126	6.066204953	0.000248017	26	UCCUUCAGGUAGGACCACUUCGAUGC
ASY-piR-250	uniq_594687	7.35974956	13.54848078	6.004451504	0.000108907	27	ACCUGGGAAUAUCAAGUGCUGCAGGCG
ASY-piR-112	uniq_504868	9.360481336	14.99628958	5.885588784	4.00E-05	29	ACCACCUGGGAAUAUCAAGUGCUGCAGGC
ASY-piR-2	uniq_137209	8.318919345	14.09345883	5.774539486	2.44E-06	29	CCACCUGGGAAUAUCAAGUGCUGCAGGCA
ASY-piR-309	uniq_137208	8.91064273	14.3934128	5.724231786	7.95E-05	29	CCACCUGGGAAUAUCAAGUGCUGCAGGCG
ASY-piR-170	uniq_147764	8.933198855	14.59828517	5.665086319	2.23E-05	27	CACCUGGGAAUAUCAAGUGCUGCAGGC
ASY-piR-14	uniq_208566	7.692324899	13.53237622	5.535343789	3.02E-05	31	ACCACCUGGGAAUAUCAAGUGCUGCAGGCAC
ASY-piR-367	uniq_811621	8.642352599	14.37558251	5.516565471	2.24E-06	29	CCACCUGGGAAUAUCAAGUGCUGCAGGCU

ASY-piR-324	uniq_717045	9.384244122	14.3719581	5.257092667	2.17E-05	27	CCACCUGGAAUAUCAAGUGCUGCAGG
ASY-piR-284	uniq_436485	5.969626351	11.08214904	5.11252269	4.57E-05	25	UGGGAUAUCAAGUGCUGUAGGCAC
ASY-piR-80	uniq_341318	9.084586963	13.79818488	4.914529117	3.35E-05	29	CCACCUGGAAUAUCAAGUGCUGCAGGUA
ASY-piR-204	uniq_304143	3.922832139	8.20701432	4.902686156	0.000873607	31	UGAAAGGACAGAUUUACUCCACUGCCGUGU
ASY-piR-286	uniq_228223	3.544320516	8.452584453	4.828544544	0.00209855	29	UGAAAGGACAGAUUUACUCCACUGCAGU
ASY-piR-786	uniq_56345	-0.111457181	4.624490865	4.735948046	0.014889764	26	UGGAUUGUGGACACAGUCUCGACUGU
ASY-piR-20	uniq_152578	10.31628153	14.92802481	4.611743277	0.000124614	31	AGACCACCUGGAAUAUCAAGUGCUGCAGGC
ASY-piR-123	uniq_332248	8.083922484	12.90704713	4.538453509	0.000172711	25	UGGGAUAUCAAGUGCUGCAGGCAG
ASY-piR-466	uniq_382758	10.78299821	15.30128183	4.518283624	2.33E-05	31	AGACCACCUGGAAUAUCAAGUGCUGCAGAC
ASY-piR-72	uniq_844985	10.94275884	15.36512061	4.422361763	9.65E-05	32	GAGACCACCUGGAAUAUCAAGUGCUGCAGGC
ASY-piR-86	uniq_846975	11.38685046	15.54531142	4.2931388	1.06E-06	31	UGC GCCACACCACCUUGAAUAAGCCUGAUC
ASY-piR-1410	uniq_957765	-0.13245417	3.95419631	4.176848289	0.002644438	27	UCCAAUGAUUGAAACUCUGGCCAGUUC
ASY-piR-34	uniq_678371	10.19023623	14.1030692	4.142825875	0.000495955	30	GACCACCUGGAAUAUCAAGUGCUGCAGGU
ASY-piR-1694	uniq_140535	5.431845787	9.422765614	4.055519949	0.035397598	29	UGUCAAUAAAAACUGGGAAGUGAUCCACU
ASY-piR-118	uniq_680423	10.98892133	14.96402493	3.975103598	7.68E-05	31	GACCACCUGGAAUAUCAAGUGCUGCAGGUA
ASY-piR-433	uniq_379766	11.45284181	15.37814807	3.764435328	1.53E-05	31	GACCACCUGGAAUAUCAAGUGCUGCAGGAC
ASY-piR-359	uniq_146197	10.68284832	13.99034037	3.739449839	0.001502969	26	ACCUGGAAUAUCAAGUGCUGCAGGA
ASY-piR-823	uniq_166929	3.285402219	6.886712714	3.601310495	0.001464917	27	UCCACGUAUUGACCAGCCAGUCUGGCU
ASY-piR-1512	uniq_564110	3.142957954	6.743712427	3.600754473	0.046530871	25	UGACUCAGUAGCUACCAUUAUUUUGU
ASY-piR-968	uniq_723303	7.675957033	11.09912861	3.50891831	0.000509023	27	UUUUGAACUGUGACAAUAGGAAGAUC
ASY-piR-1415	uniq_548510	3.142957954	6.894817763	3.505699222	0.031177821	29	UUCGAUCUGUGACUUAAGGUAAGCUACC
ASY-piR-452	uniq_379764	10.78299821	13.99246633	3.209468118	0.000163421	31	GACCACCUGGAAUAUCAAGUGCUGCAGGAA
ASY-piR-935	uniq_1991592	7.272240971	10.40921412	3.136973154	0.000213761	31	UCCAGCUGAUUCAGCACGUGACCCGACCAGC
ASY-piR-897	uniq_1790231	6.723376529	9.724798044	3.001421515	0.003461984	28	UGGACUUGUUUGCAGAUUCGAGGAUGC
ASY-piR-1671	uniq_898121	6.273018494	9.198240389	2.941887262	0.002472557	28	UCCAGCUGAUUCAGUACGUGACCCGACC
ASY-piR-696	uniq_338579	6.360481336	8.625708843	2.907085673	0.00216095	31	UCCAGCUGAUUCAGCACGUGACCCGACCAGU
ASY-piR-553	uniq_250665	6.115477217	8.779992878	2.869100352	0.00426826	28	UCCAGCUGAUUCAGCACGUGACCCGACC
ASY-piR-722	uniq_872600	5.888743249	8.669475648	2.818615883	0.001238356	29	UCCAGCUGAUUCAGCACGUGACCCGACCA
ASY-piR-347	uniq_619718	1.99770178	5.348728154	2.804834846	0.027935801	25	UUUGUCUUAUCUUCUGUCCAAUGAUA
ASY-piR-1053	uniq_894090	5.878561873	8.660590206	2.784106503	0.021705902	26	CGGAUUGUGGAGCCUCCAGUGACGC
ASY-piR-1720	uniq_310483	6.456696651	8.251876859	2.761527573	0.007274778	26	UCAUCAUGUGACUCUUCAGAGUGAGC
ASY-piR-980	uniq_2027275	6.502500341	8.703903573	2.432722958	0.025478396	29	UGAUGUUGGGCUGCACGAUCCUGAGCA
ASY-piR-771	uniq_264839	8.471336514	10.7968508	2.383531869	2.32E-05	26	UGGACGUGCUGGUACCUGGGACACC
ASY-piR-3	uniq_304406	6.206200388	8.549463819	2.343263432	0.00407124	27	UCUGCGUACAGGAAUCUCUGCAGGCAC
ASY-piR-468	uniq_789106	6.648657176	8.835524112	2.333023772	0.002487475	29	UUCAUUCACUAGACCUGCUCUGAACCAAGC
ASY-piR-1574	uniq_401938	6.386581053	8.627837834	2.224115648	0.003820257	29	UGAACGCGGUAGGGAACCGGACCCUCC
ASY-piR-342	uniq_860961	10.69537331	12.85610126	2.183603586	0.000162304	27	GGGGAUGUAGCUCAGUGGUAGAGCGCA
ASY-piR-1482	uniq_27	6.539158811	8.54303182	2.178768169	0.015324725	27	UUCAUCGUGUGACUCUUCAGAGUGAGC
ASY-piR-356	uniq_513451	4.763765654	6.759333407	2.086908065	0.001217699	25	UAUUUGCAACUGUUGUCACAGGAAC

ASY-piR-8	uniq_552634	6.115477217	7.892289823	2.005624549	0.018833179	27	UCUGCGUACAGGUAUCUCUGCAGGCAC
ASY-piR-1091	uniq_446809	9.101756865	10.9944713	1.892714434	0.004365335	27	UCCGACUGUAAGGCAACAUCAUCCACC
ASY-piR-992	uniq_890500	8.9522559	10.54101593	1.888845335	0.001281159	26	UUACAUGAACUAGGACAGAACCCUUC
ASY-piR-911	uniq_379100	6.372139541	8.054378208	1.851057731	0.000594409	28	UGACGUCUCUGCACCAGCCAGAUGGCCA
ASY-piR-1723	uniq_396207	6.549463819	8.423466121	1.831208462	0.03003906	26	UGAUGACGAAGAGACUACUCGAAGCU
ASY-piR-1497	uniq_615839	6.996238081	8.820178962	1.823940881	0.038682257	26	UCUGCGUACAGGAAUCUCUGCAGGGC
ASY-piR-1775	uniq_109760	11.22811721	13.04732276	1.819205548	0.010993917	31	GCAUUUGUGGUUCAGUGGUAGAAUUCUCGCC
ASY-piR-780	uniq_379103	6.924812504	8.688250309	1.802716027	0.004287667	28	UGACGUCUCUGCACCAGCCAGAUGGCC
ASY-piR-382	uniq_821654	5.398031074	7.183221824	1.78519075	0.000367175	27	UCCGGCUGGCAGAUUCUAAUCCACC
ASY-piR-1040	uniq_127062	7.577428828	9.32305476	1.762085115	0.014064128	26	UGUGGAUUUCCUUCCAGUAGACACC
ASY-piR-63	uniq_94215	5.273018494	6.981091537	1.708073043	0.000294217	28	UGACCAGAGCUUAGCCAGAACUUAGCCU
ASY-piR-775	uniq_2036736	6.241585987	7.892289823	1.650703837	0.0033281	29	UGACGUCUCUGCACCAGCCAGAUGGACUG
ASY-piR-1189	uniq_622175	7.557144557	9.151862198	1.64232331	0.000210385	27	UGGACGUGCUGGUACCUGGGACACCA
ASY-piR-297	uniq_811103	6.342815461	7.968666793	1.625851332	0.001828678	29	CGAUGAUGAUGAAGGUAACCUUACUGACG
ASY-piR-1315	uniq_298842	4.574908836	5.942514505	1.62058641	0.029278261	26	AGACUGUAGCUGGAUCCAUCUCCAC
ASY-piR-565	uniq_538392	7.151439431	8.203348003	1.593786351	0.034513331	28	UGAUGUUGGGCUGCACGAUGCCUGAGC
ASY-piR-1278	uniq_98191	8.786814144	10.49868303	1.551365106	0.005071774	25	UCUGUGGUGAUGGGAGAACAUAUA
ASY-piR-848	uniq_731025	8.249508549	9.783271111	1.544771923	0.000425297	26	UGAAUCCACUUCUGACACCACGUGU
ASY-piR-305	uniq_459398	4.837102265	6.156504486	1.532013621	0.018484887	28	UACCUAUGGAGACCAUCUGCAUCUGAGC
ASY-piR-134	uniq_314832	9.13442632	10.64835758	1.513931262	0.005543388	29	UCCGAUUCGGUCUGAAAUAACAAACCAGC
ASY-piR-1163	uniq_738150	11.73978061	13.10110025	1.509266272	0.000179455	28	GCAUUGGUGGUUCAGUGGUAGAAUUCU
ASY-piR-1853	uniq_250294	7.460797161	8.587465008	1.498721861	0.002930814	26	UGACGUCUCUGCACCAGCCAGAUGGU
ASY-piR-604	uniq_387272	6.772589504	8.223197272	1.490747159	0.003993106	27	UGACGUCUCUGCACCAGCCAGAUGGCC
ASY-piR-138	uniq_732577	5.639039173	6.949340382	1.488100961	0.016415502	27	UGACCAGAGCUUAGCCAGAACUUAGCC
ASY-piR-375	uniq_7916	4.321928095	5.781359714	1.459431619	0.006560045	30	UCUUCGUACUGCACUGUGCCUACUAAAGGU
ASY-piR-807	uniq_387276	6.822305264	7.892289823	1.424684273	0.019407452	27	UGACGUCUCUGCACCAGCCAGAUGGCA
ASY-piR-1698	uniq_870172	7.941536738	9.098690097	1.399406848	0.043927263	29	UCCUGAUGCACACCAACCCUUGUCCUCC
ASY-piR-1102	uniq_738146	11.84601267	12.76500977	1.390007262	0.022788885	28	GCAUUGGUGGUUCAGUGGUAGAAUUCUC
ASY-piR-1588	uniq_765050	5.014950341	6.26366044	1.389191322	0.03219886	26	UCUGGUAGAUCUUCUACUCUCUGCA
ASY-piR-351	uniq_670142	4.044394119	5.431845787	1.387451668	0.046363884	29	UACAGAAUUCUCCAGACAGCCUUGUGUC
ASY-piR-1706	uniq_66454	11.46258748	13.14749645	1.373463371	0.035277018	29	GCAUUGGUGGUUCAGUGGUAGAAUUCUCA
ASY-piR-30	uniq_825575	7.283860054	8.633600735	1.349740681	0.008754835	31	AGGCGAUGAUGAUGAAGGUAACCUUACUGAC
ASY-piR-54	uniq_774577	5.781359714	7.122396631	1.341036918	0.000523558	28	GAUGAUGAUGAAGGUAACCUUACUGACG
ASY-piR-429	uniq_42720	9.810571635	11.11829223	1.331960934	0.023683193	27	UGACUAUGUGAAGACCCUCUGCACAAC
ASY-piR-50	uniq_719498	13.25064385	14.57474134	1.324097487	0.015856868	29	UCUCGUCUGAUCUCAGAAGCUAAGCAACA
ASY-piR-1149	uniq_746849	7.228016971	8.525520809	1.297503839	0.010707308	27	UGAAACACGGUCUCUCUCUGAGCACAG
ASY-piR-1058	uniq_17123	7.181566408	8.279997414	1.290901199	0.024985751	28	UGGACGUGCUGGUACCUGGGACACCAU
ASY-piR-336	uniq_758053	6.50779464	7.770388596	1.280809108	0.010775512	25	UCAGACAGCCUCUGUAGCAGACGGU
ASY-piR-51	uniq_42723	7.892795766	9.100224296	1.270644262	0.018748922	27	UGACUAUGUGAAGACCCUCUGCACAUA

ASY-piR-815	uniq_334052	11.43484538	12.87897689	1.26849882	0.011131668	29	GCAUUGGUGGUUCAGUGGUAGAAUUCUCG
ASY-piR-504	uniq_496422	11.18249781	12.78115477	1.19783424	0.031180419	29	UCCCAUAUGGUCUAGUGGUUAGGAUCCU
ASY-piR-532	uniq_811101	6.227214805	7.407975835	1.180761031	0.010969513	29	CGAUGAUGAUGAAGGUAACCUUACUGACU
ASY-piR-1539	uniq_872471	7.848101264	8.960967268	1.166849077	0.022816103	29	UCAAUACUGUGGAGAGCCUGAUCUUUCUC
ASY-piR-1232	uniq_56024	9.8008999	10.95419631	1.15329641	0.003192227	28	UAGGAAUGGAAACAGACCAAGGACUUCU
ASY-piR-1810	uniq_891468	12.0832577	13.15429071	1.071033014	0.026132319	31	GCAUUGGUGGUUCAGUGGUAGAAUUCUCGUC
ASY-piR-203	uniq_627815	6.569855608	7.614709844	1.044854236	0.037967235	28	CGAUGAUGAUGAAGGUAACCUUACUGAC
ASY-piR-37	uniq_183930	8.533978572	9.752101838	1.031758216	0.023308314	30	UCCGAUUCGGUCUGAAAUAACAACCAGCA
ASY-piR-1707	uniq_25448	7.189000868	8.223197272	1.029261297	0.02619858	26	UACUGUAGUCAUGAACCAGCUGACAC
ASY-piR-844	uniq_834130	7.112005026	8.122396631	1.010391606	0.002109874	29	UGACGUCUCUGCACCAGCCAGAUGGCCCG
ASY-piR-392	uniq_602422	4.709658248	5.714245518	1.004587269	0.041358187	26	UUCUUACCUGUUACUGCUGACCAGGA
ASY-piR-172	uniq_379120	6.440177062	7.64385619	1.004347653	0.01446724	29	CGAUGAUGAUGAAGGUAACCUUACUGGCA

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