

Supplemental Table 1 All candidate piRNAs from *P. olivaceus* gonads

Sequence	ID	Reads number (ovary)	Reads number (testis)
CTCGCCTTAGGACACCTGCGTTACC	25_138820_4	0	4
ACATGAGAGGTGTAGAATAAGTGGGAGGCCG	31_14304_3	3	0
CATGAGAGGTGTAGAATAAGTGGGAGGCCG	30_28247_3	3	0
ACATGAGAGGTGTAGAATAAGTGGGAGGCCA	31_7735_5	4	1
TGAGAGGTGTAGAATAAGTGGGAGGCC	28_113342_4	4	0
ATGAGAGGTGTAGAATAAGTGGGAGGCCTCG	31_5035_8	7	1
CATGAGAGGTGTAGAATAAGTGGGAGGCCA	30_11346_7	7	0
ATGAGAGGTGTAGAATAAGTGGGAGGCCA	29_22065_9	8	1
ATGAGAGGTGTAGAATAAGTGGGAGGCCG	29_24740_8	8	0
TGAGAGGTGTAGAATAAGTGGGAGGCCA	28_52102_9	8	1
TGAGAGGTGTAGAATAAGTGGGAGGCCTCG	30_6769_12	8	4
CATGAGAGGTGTAGAATAAGTGGGAGGCCTC	31_2671_16	15	1
TGAGAGGTGTAGAATAAGTGGGAGGCCTC	29_6481_33	31	2
TGAGAGGTGTAGAATAAGTGGGAGGCCTCGG	31_1351_33	31	2
GACATGAGAGGTGTAGAATAAGTGGGAGGC	30_1983_42	37	5
CATGAGAGGTGTAGAATAAGTGGGAGGC	28_11222_47	45	2
ATGAGAGGTGTAGAATAAGTGGGAGGCCTC	30_1713_49	48	1
CATGAGAGGTGTAGAATAAGTGGGAGG	27_16978_55	49	6
TGAGAGGTGTAGAATAAGTGGGAGGC	26_14285_74	58	16
ACATGAGAGGTGTAGAATAAGTGGGAGGC	29_3287_65	59	6
GACATGAGAGGTGTAGAATAAGTGGGAGG	29_3120_68	62	6
ATGAGAGGTGTAGAATAAGTGGGAGGC	27_11876_79	71	8
TGAGAGGTGTAGAATAAGTGGGAGG	25_9954_78	73	5
GACATGAGAGGTGTAGAATAAGTGGGAGGCC	31_586_78	74	4
ACATGAGAGGTGTAGAATAAGTGGGAGG	28_5769_91	81	10
ATGAGAGGTGTAGAATAAGTGGGAGG	26_11706_91	82	9
CATGAGAGGTGTAGAATAAGTGGGAGGCC	29_2001_105	99	6
ACATGAGAGGTGTAGAATAAGTGGGAGGCC	30_737_109	100	9
TGAGAGGTGTAGAATAAGTGGGAGGCC	27_9006_105	103	2
ATGAGAGGTGTAGAATAAGTGGGAGGCC	28_3748_142	132	10
ACATGAGAGGTGTAGAATAAGTGGGAGGCCT	31_221_186	174	12
CATGAGAGGTGTAGAATAAGTGGGAGGCCT	30_372_197	183	14
TGAGAGGTGTAGAATAAGTGGGAGGCCT	28_2269_226	207	19
ATGAGAGGTGTAGAATAAGTGGGAGGCCT	29_755_260	243	17
GTATTGACTACAGAGGTCTCAACGATG	27_237437_3	3	0
CTATTGAAAGTCAGCCCTCGATCCAAG	27_312411_2	0	2
GAAAGTCAGCCCTCGATCCAA	21_29046_2	1	1
GAAAGTCAGCCCTCGATCCAAGCTTTGT	28_215235_2	1	1
TTGAAAGTCAGCCCTCGATCCAAG	24_125849_2	1	1
GAAAGTCAGCCCTCGATCCAAG	22_52007_2	2	0

TGAAAGTCAGCCCTCGATCCAA	22_50852_2	2	0
TGAAAGTCAGCCCTCGATCCAAGC	24_26782_11	2	9
TTGAAAGTCAGCCCTCGATCCAAGCTTT	28_128270_3	2	1
GAAAGTCAGCCCTCGATCCAAGCTTT	26_125751_6	3	3
TGAAAGTCAGCCCTCGATCCAAGCT	25_188449_3	3	0
TGAAAGTCAGCCCTCGATCCAAGCTT	26_256753_3	3	0
TTGAAAGTCAGCCCTCGATCCAAGCTT	27_247368_3	3	0
ATTGAAAGTCAGCCCTCGATCCAAGCTT	28_89219_5	4	1
TTGAAAGTCAGCCCTCGATCCAAGCT	26_158330_5	4	1
GAAAGTCAGCCCTCGATCCAAGCTT	25_71386_9	8	1
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TTGAAAGTCAGCCCTCGATCCAAGC	25_30781_23	9	14
ATTGAAAGTCAGCCCTCGATCCAAG	25_65781_10	10	0
ATTGAAAGTCAGCCCTCGATCCAAGCT	27_58685_14	10	4
GAAAGTCAGCCCTCGATCCAAGCT	24_15956_20	14	6
ATTGAAAGTCAGCCCTCGATCCAAGC	26_35749_27	18	9
TATTGAAAGTCAGCCCTCGATCCAAG	26_36985_26	19	7
GAAAGTCAGCCCTCGATCCAAGC	23_2049_74	21	53
TATTGAAAGTCAGCCCTCGATCCAAGC	27_20488_45	25	20
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TTTGATCCTTCGATGTCGGCTCTTCCTATCAT	32_6789_4	2	2
TTTTGATCCTTCGATGTCGGCTCTTCCTATCA	32_17297_2	2	0
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TCCTTCGATGTCGGCTCTTCCTATCAT	27_137921_5	3	2
TCGATGTCGGCTCTTCCTATCATGT	26_187269_4	3	1
TGATCCTTCGATGTCGGCTCTTCCTATCA	29_68351_3	3	0
TTGATCCTTCGATGTCGGCTCTTCCTATCA	30_26469_3	3	0
TTTGATCCTTCGATGTCGGCTCTTCCTATCA	31_9085_4	3	1
TTGATCCTTCGATGTCGGCTCTTCCTATCAT	31_7307_5	4	1
TTGATCCTTCGATGTCGGCTCTTCCTATCATT	32_4848_6	4	2
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TCCTTCGATGTCGGCTCTTCCTATCATT	28_42636_11	7	4
TCGATGTCGGCTCTTCCTATCAT	23_12676_11	7	4
TGATCCTTCGATGTCGGCTCTTCCTATC	28_57806_8	7	1
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TCCTTCGATGTCGGCTCTTCCTATCA	26_73439_12	9	3

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ATCCTTCGATGTCGGCTCTTCCTATCA	27_52338_16	13	3
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CTTCGATGTCGGCTCTTCCTATCAT	25_36423_19	15	4
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CTTCGATGTCGGCTCTTCCTATCATTG	27_40897_21	18	3
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CCTTCGATGTCGGCTCTTCCT	21_1183_55	44	11
ATCCTTCGATGTCGGCTCTTCCT	23_2292_68	60	8
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GATCCTTCGATGTCGGCTCTTCCT	24_3043_108	63	45
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TTTTGATCCTTCGATGTCGGCTCTTCCT	28_3462_153	125	28

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CCCGTGGACGGTGTGAGGCCGGTA	24_63434_4	2	2
CTCAGCCCGTGGACGGTGTGAGGCCGGTA	29_106217_2	2	0
GCCCGTGGACGGTGTGAGGCCGGTAAC	27_115678_6	2	4
TCAGCCCGTGGACGGTGTGAGGCCGGT	27_230459_3	2	1
AGCCCGTGGACGGTGTGAGGCCGGTAAC	28_108141_4	3	1
CAGCCCGTGGACGGTGTGAGGCCGG	25_132634_4	3	1
CCCGTGGACGGTGTGAGGCCGG	22_29447_3	3	0
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GCCCGTGGACGGTGTGAGGCCGG	23_46432_3	3	0
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CCCGTGGACGGTGTGAGGCCG	21_2317_28	24	4
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TTGGATTGTTCACCCCTAATGGGG	25_231872_2	0	2
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AAGCGTTGGATTGTTCACCCCTAATT	27_172763_4	1	3
CACGAAGCGTTGGATTGTTCACCCCTAATAGG	33_11810_2	1	1
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AAGCGTTGGATTGTTCACCCCTAAG	26_248078_3	2	1
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ACCAAGCGTTGGATTGTTACCCCA	24_14964_21	18	3
CCAAGCGTTGGATTGTTACCCACTAA	27_35826_24	18	6
TTGGATTGTTACCCACTAATAGGGAACG	29_11607_18	18	0
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CCAAGCGTTGGATTGTTACCCACTA	26_39608_24	20	4
ACCAAGCGTTGGATTGTTACCCACTAA	28_15661_33	21	12
CGTTGGATTGTTACCCACTAATAGG	26_40581_24	21	3
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CGTTGGATTGTTACCCACTAATAGGG	27_27905_32	29	3
ACCAAGCGTTGGATTGTTACCCACTA	27_27848_32	30	2
CAAGCGTTGGATTGTTACCCACTA	25_18637_40	30	10
TTGGATTGTTACCCACTAAT	21_1967_33	32	1
AGCGTTGGATTGTTACCCACTAATAGG	28_11698_45	35	10

CACCAAGCGTTGGATTGTTCACCCCTAATAG	32_721_50	36	14
AAGCGTTGGATTGTTCACCCCTAAT	26_21083_49	38	11
ACCAAGCGTTGGATTGTTCACCCCTAATAGGGA	34_731_39	38	1
CAAGCGTTGGATTGTTCACCCAC	23_2926_52	41	11
ACCAAGCGTTGGATTGTTCACCCAC	25_13274_57	42	15
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CCAAGCGTTGGATTGTTCACCCCTAATAG	30_1539_54	47	7
AAGCGTTGGATTGTTCACCCCTAA	25_6800_114	50	64
CAAGCGTTGGATTGTTCACCCCTAATAGGGA	32_659_55	52	3
ACCAAGCGTTGGATTGTTCACCCCTAATAG	31_729_64	53	11
AGCGTTGGATTGTTCACCCCTAATAGGG	29_3906_55	54	1
CAAGCGTTGGATTGTTCACCCCTAAT	27_14554_64	54	10
CAAGCGTTGGATTGTTCACCCCTAA	26_17439_60	55	5
CACCAAGCGTTGGATTGTTCACCCAC	26_14129_75	59	16
AAGCGTTGGATTGTTCACCCCTAATA	27_9732_97	64	33
CAAGCGTTGGATTGTTCACCCCTAATA	28_7489_71	64	7
AAGCGTTGGATTGTTCACCCAC	22_1194_82	65	17
CCAAGCGTTGGATTGTTCACCCA	23_1702_88	65	23
CCAAGCGTTGGATTGTTCACCCCTAATA	29_2433_88	73	15
ACCAAGCGTTGGATTGTTCACCCCTAAT	29_2288_93	76	17
CAAGCGTTGGATTGTTCACCCCTAATAG	29_2377_90	79	11
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CGTGCAAATCGGTCTCCGACC	22_492_200	155	45
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TTGCATCGGAAAGACGGTTTCTCTTTGG	28_212460_2	0	2
TTGCATCGGAAAGACGGTTTCTCTTTGGT	29_87969_2	0	2
GCATCGGAAAGACGGTTTCTCTTTGGTC	28_131098_3	2	1
TGCATCGGAAAGACGGTTTCTCTTTGGT	28_73441_6	5	1
TGCATCGGAAAGACGGTTTCTCTTTGG	27_77197_10	6	4
TGCATCGGAAAGACGGTTTCTCTTTGGTC	29_8200_26	20	6
TATCTAGCGAAACCACAGCCAAGGG	25_170300_3	1	2
AGCGAAACCACAGCCAAGGGA	21_14464_4	2	2
ATCTAGCGAAACCACAGCCAAG	22_25139_3	2	1
CTATCTAGCGAAACCACAGCCAAGGGA	27_367360_2	2	0
TACTATCTAGCGAAACCACAGCCAA	25_172930_3	2	1
TAGCGAAACCACAGCCAAGGGA	22_28179_3	2	1
TCTAGCGAAACCACAGCCAAGG	22_26646_3	2	1
ACTATCTAGCGAAACCACAGCCA	23_24289_5	3	2
ATCTAGCGAAACCACAGCCAAGG	23_25057_5	3	2
ATCTAGCGAAACCACAGCCAAGGGA	25_105863_5	3	2
CTATCTAGCGAAACCACAGCCAAG	24_101807_3	3	0
TATCTAGCGAAACCACAGCCAAG	23_45654_3	3	0
TCTAGCGAAACCACAGCCAAGGG	23_47091_3	3	0

ACTATCTAGCGAAACCACAGCCAAGGGA	28_113782_4	4	0
ATCTAGCGAAACCACAGCCAAGGG	24_48559_6	4	2
CTACTATCTAGCGAAACCACAGCCAAG	27_177760_4	4	0
CTACTATCTAGCGAAACCACAGCCAAGGG	29_48359_4	4	0
CTATCTAGCGAAACCACAGCCA	22_17302_5	4	1
CTATCTAGCGAAACCACAGCCAAGGG	26_126199_6	4	2
TACTATCTAGCGAAACCACAGCCAAGGGA	29_38730_5	4	1
TATCTAGCGAAACCACAGCCA	21_12339_5	4	1
TATCTAGCGAAACCACAGCCAAGGGA	26_197761_4	4	0
TCTAGCGAAACCACAGCCAAGGGA	24_56786_5	4	1
ACTATCTAGCGAAACCACAGCCAAG	25_97119_6	5	1
ACTATCTAGCGAAACCACAGCCAAGGG	27_146824_5	5	0
CTAGCGAAACCACAGCCAAGGGA	23_22971_6	5	1
TACTATCTAGCGAAACCACAGCCA	24_48630_6	5	1
TACTATCTAGCGAAACCACAGCCAAG	26_160267_5	5	0
CTACTATCTAGCGAAACCACAGCCA	25_103597_6	6	0
CTACTATCTAGCGAAACCACAGCCAAGG	28_65867_7	6	1
CTACTATCTAGCGAAACCACAGCCAAGGGA	30_13437_6	6	0
TACTATCTAGCGAAACCACAGCCAAGGG	28_76821_6	6	0
TAGCGAAACCACAGCCAAGGG	21_8133_7	6	1
TCTAGCGAAACCACAGCCAAG	21_7715_8	7	1
CTAGCGAAACCACAGCCAAGGG	22_7025_13	10	3
CTATCTAGCGAAACCACAGCCAAGG	25_56135_12	12	0
ACTATCTAGCGAAACCACAGCCAAGG	26_59159_15	14	1
TACTATCTAGCGAAACCACAGCCAAGG	27_51925_16	15	1
CTAGCGAAACCACAGCCAAGG	21_3562_18	17	1
AAAGAAACTAACCAGGATTCCTCAG	25_230108_2	0	2
AAAAGAAACTAACCAGGATTCCTCAGTAGC	31_7609_5	1	4
AAGAAACTAACCAGGATTCCTCAGT	26_361237_2	1	1
AAGAAACTAACCAGGATTCCTCAGTAGC	29_9809_21	1	20
AGAAACTAACCAGGATTCCTCAG	24_135300_2	1	1
AGAAACTAACCAGGATTCCTCAGTAGC	28_123605_3	1	2
AGAAACTAACCAGGATTCCTCAGTAGCG	29_29718_6	1	5
AGGGAAAGAAACTAACCAGGATTCCT	27_309395_2	1	1
AAACTAACCAGGATTCCTCA	21_34759_2	2	0
AAACTAACCAGGATTCCTCAGTAG	25_135025_4	2	2
AAACTAACCAGGATTCCTCAGTAGC	26_56477_16	2	14
AAAGAAACTAACCAGGATTCCT	23_72080_2	2	0
AAAGAAACTAACCAGGATTCCTCAG	26_156601_5	2	3
AAAGAAACTAACCAGGATTCCTCAGTAGCG	31_6090_6	2	4
AACTAACCAGGATTCCTCAGTAG	24_145231_2	2	0
AAGAAACTAACCAGGATTCCT	22_26205_3	2	1
AAGAAACTAACCAGGATTCCTCAG	25_142117_4	2	2

AGAAACTAACCAGGATTCCCTC	22_27913_3	2	1
AGAAACTAACCAGGATTCCCTCA	23_81167_2	2	0
AGGGAAAGAACTAACCAGGATTCCCTC	28_239125_2	2	0
GAAAAGAACTAACCAGGATTCCCTCA	27_349448_2	2	0
GAAAAGAACTAACCAGGATTCCCTCAG	28_223595_2	2	0
GAAACTAACCAGGATTCCCTCA	22_48251_2	2	0
AAAAGAACTAACCAGGATTCCCTCA	26_184371_4	3	1
AAAAGAACTAACCAGGATTCCCTCAGTAG	30_26667_3	3	0
AAAGAACTAACCAGGATTCCCTCA	25_144882_4	3	1
AAAGAACTAACCAGGATTCCCTCAGT	27_101524_7	3	4
AACTAACCAGGATTCCCTCAGT	22_29935_3	3	0
AAGAACTAACCAGGATTCCCTCA	24_45115_6	3	3
AAGAACTAACCAGGATTCCCTCAGTA	27_233707_3	3	0
GAAAAGAACTAACCAGGATTCCCTCAGT	29_44524_4	3	1
GAAAAGAACTAACCAGGATTCCCTCAGTA	30_28208_3	3	0
GAAAAGAACTAACCAGGATTCCCTCAGTAG	31_9013_4	3	1
GAAACTAACCAGGATTCCCTCAGTAGC	27_99921_7	3	4
AAAAGAACTAACCAGGATTCCCTCAGTA	29_49930_4	4	0
AAAGAACTAACCAGGATTCCCTC	24_55584_5	4	1
AAAGAACTAACCAGGATTCCCTCAGTAGC	30_6203_13	4	9
AAGAACTAACCAGGATTCCCTCAGTAG	28_60747_7	4	3
AAGAACTAACCAGGATTCCCTCAGTAGCG	30_10684_7	4	3
AAAAGAACTAACCAGGATTCCCTC	25_95899_6	5	1
AAAAGAACTAACCAGGATTCCCTCAGT	28_90304_5	5	0
AAACTAACCAGGATTCCCTCAGTAGCG	27_105479_7	5	2
AAAGAACTAACCAGGATTCCCTCAGTA	28_93194_5	5	0
AACTAACCAGGATTCCCTCAGTAGC	25_87611_7	5	2
AAAGAACTAACCAGGATTCCC	22_7399_12	6	6
AAGAACTAACCAGGATTCCCTC	23_19584_7	6	1
AACTAACCAGGATTCCCTCAGTAGCG	26_105638_8	7	1
CACCAGCCTGTCTTCTCTCTGAGTT	27_303727_2	0	2
CTGAGGAGCCAATGGTGCGAAGCTAC	26_380460_2	2	0
GAGGAGCCAATGGTGCGAAGCTACC	25_296382_2	2	0
CTGAGGAGCCAATGGTGCGAAGCTACC	27_177521_4	3	1
CTGAGGAGCCAATGGTGCGAAGCTACCA	28_75832_6	5	1
TGAGGAGCCAATGGTGCGAAGCTACC	26_165906_5	5	0
CCCTAGAGATGGTTGTGCATGAAAATC	27_166372_4	0	4
TAGAGATGGTTGTGCGTGAAAATCCCA	27_328880_2	0	2
TAGTTAATGATGTGCTCCGTGACA	24_63213_4	0	4
TAGTTAATGATGTGCTCCGTGACATGCT	28_53426_8	0	8
TAGTTAATGATGTGCTCCGTGACATG	26_90284_9	3	6
TGACAGTGAAATGGGTGTAACCTAGC	26_100355_8	3	5
TAACTCTGAGATGGTCAACCAGTAACG	27_325847_2	0	2

ATAACTCTGAGATGGTCAACCAGTAAC	27_354141_2	2	0
TAACTCTGAGATGGTCAACCAGTAA	25_18060_41	9	32
TAACTCTGAGATGGTCAACCAGTAAC	26_4952_217	64	153
CTGGTGTCTCTGGCAAATGTCAT	24_105453_2	0	2
TTCTGGTGTCTCTGGCAAATGTC	24_43543_6	1	5
TTCTGGTGTCTCTGGCAAATGTCAA	26_227493_3	1	2
TTCTGGTGTCTCTGGCAAATGTCA	25_110097_5	2	3
TGACATGATAGCATCACGCAGTTGCA	26_340347_2	1	1
TGACATGATAGCATCACGCAGTTGCTG	27_104832_7	6	1
TGACATGATAGCATCACGCAGTTGCT	26_81525_11	11	0
TGGAATACCAGGTGCTGTATGCTT	25_82652_7	0	7
TTGGAATACCAGGTGCTGTATGCTT	26_173605_4	0	4
TAGATGCCTAAATGCATTGAGTTGCT	26_294460_2	0	2
TAGATGCCTAAATGCATTGAGTTGCTGC	28_105994_4	0	4
TAGATGCCTAAATGCATTGAGTTGCTG	27_50600_16	5	11
CACAGTCATAGGGACGATGAGG	22_33766_2	0	2
CACAGTCATAGGGACGATGAGGGGG	25_254967_2	0	2
CACAGTCATAGGGACGATGAGGGG	24_120575_2	1	1
CACAGTCATAGGGACGATGAGGGGGC	26_308468_2	1	1
TAGTCTATTCGAGAGGCTCTGGTGCC	26_219449_3	0	3

ID abbreviation stands for the sequencing identity of piRNA.

Supplemental Table 2 All piRNA clusters from *P. olivaceus* gonads

ID	piRNA cluster sequence	Reads number (testis)	Reads number (ovary)	Fold change (testis)	Fold change (ovary)	Log(fold change) (testis/ovary) ²
26_19472_53	TGAACCAGGTGAAGCCCTCCTCTCTG	0	191	0	81.01723372	NA
28_7074_75	CAAGATGATGATGATGATGATGCTGACC	0	98	0	41.56905186	NA
21_2169_30	CTGGGAATACCAGGTGCTGTA	0	34	0	14.42191595	NA
26_74432_12	TAGTCTATGCGAGAGGCTCTGGTACC	0	23	0	9.756001967	NA
26_53651_17	TACCACACAGTGATGCAGCTGGACAG	0	23	0	9.756001967	NA
26_101150_8	TCGCTTACGGCCATACCACCCTTGAA	0	17	0	7.210957975	NA
22_6619_13	CCTGGGAATACCAGGTGCTGTA	0	15	0	6.362609978	NA
24_39862_7	TCATACAGTAACTGTGTCCACAGC	0	11	0	4.665913984	NA
25_82652_7	TGGGAATACCAGGTGCTGTATGCTT	0	11	0	4.665913984	NA
26_242069_3	TATCTCTTGATGACCTCCTCAGGATG	0	8	0	3.393391988	NA
26_216419_3	AACTGACGGGACAAGGCATCTGGTTT	0	7	0	2.96921799	NA
27_191425_3	TGTGATGGTGCTGGATGTGTTGCTGCC	0	7	0	2.96921799	NA
27_166372_4	CCCTAGAGATGGTTGTGCATGAAAATC	0	6	0	2.545043991	NA
25_168120_3	TCCCTGTGGGAACCTTTCTGACACC	0	5	0	2.120869993	NA
25_138820_4	CTCGCCTTAGGACACCTGCGTTACC	0	4	0	1.696695994	NA
27_217272_3	GATACGTCTGTACCGCTGCCGGACAGG	0	3	0	1.272521996	NA
26_214922_3	TGCGAGATTGAGGAGGATATATGCCT	0	3	0	1.272521996	NA
25_173498_3	TGGAGACAAGGGGATCTGCCAGTAG	0	3	0	1.272521996	NA
26_219727_3	TGGGAATACCAGGTGCTGTATGCTTT	0	3	0	1.272521996	NA
26_219449_3	TAGTCTATTCGAGAGGCTCTGGTGCC	0	3	0	1.272521996	NA
26_273717_2	CAACCAGTGTCTCCATTCCTCTAGTG	0	2	0	0.848347997	NA
34_8703_2	GCCTGGCTAGCTCAGTCGGTAGAGCATGAC ACTC	0	2	0	0.848347997	NA

26_342986_2	TGTGTGACCAAGGACGATGAGGAACT	0	2	0	0.848347997	NA
25_243044_2	TGAATACTTATGACCATGTGATATT	0	2	0	0.848347997	NA
27_288865_2	TAGGACGGTGAAATGTGGATGTTGCTG	0	2	0	0.848347997	NA
24_105874_2	CCACACAGTGATGCAGCTGGTCAG	0	2	0	0.848347997	NA
28_184633_2	TATCATGGAGGGCAGATGTTTCAGGCCT	0	2	0	0.848347997	NA
26_281452_2	CCTTGTTACAGGTGTGCCCCGTGGCTC	0	2	0	0.848347997	NA
27_313465_2	CGGACCATTCTCTGTAAACCTTAGAGA	0	2	0	0.848347997	NA
26_343310_2	TAGGCGGGATTCTGACTTAGAGGCGT	0	2	0	0.848347997	NA
29_96787_2	TGGGTGAAGATGGGGGCCAGCTGGTCAGC	0	2	0	0.848347997	NA
25_211581_2	CAAGATGATGATGATGATGCTGACC	0	2	0	0.848347997	NA
25_211237_2	CCTGAGCCTCCCCCTTACCTGCCC	0	2	0	0.848347997	NA
26_308394_2	GTGTGTGTGTGTGTGTGTGTGTGTGC	0	2	0	0.848347997	NA
27_270096_2	AAAAAGCCAGAAGGATCGTGAGGCCCC	0	2	0	0.848347997	NA
25_242223_2	TGCAGTCGTTGCTGTGGTGTATGAG	0	2	0	0.848347997	NA
26_342107_2	TTTAACTGGCATTGTGTGGATGTAAC	0	2	0	0.848347997	NA
27_303727_2	CACCAGCCTGTCTTCCTCCTCTGAGTT	0	2	0	0.848347997	NA
26_5210_206	TTCACAGTGCCAGACTAGAGTCAAGC	2	434	0.9139478	184.0915154	-7.654095728
28_5968_88	CACCACTGAACCAGGTGAAGCCCTCCTC	1	214	0.4569739	90.77323569	-7.634011482
23_606_221	TCCATTTTCAGGGCTAGTTGATT	5	529	2.2848694	224.3880452	-6.617740312
27_1505_587	TATCATCCAGGTACACAAAGACAAACT	9	658	4.1127649	279.106491	-6.084563267
21_278_209	CAAATCCCGGACGAGCCCCCA	13	638	5.9406604	270.6230111	-5.509517391
24_943_317	TACCGTTTGACAGGTGTACCGCCC	28	998	12.795269	423.3256506	-5.048085578
27_10710_88	TATCCCTGTGGTAACTTTTCTGACACC	5	170	2.2848694	72.10957975	-4.980007336
21_2093_31	TAAGAGTAGTGGTATTTCACC	2	64	0.9139478	27.14713591	-4.892544495
32_3666_8	ACGCGGAAGACCGGGGTTCAATCCCCGAC GA	1	30	0.4569739	12.72521996	-4.799435091
25_32891_21	GACTGCCTGGGAATACCAGGTGCTG	3	87	1.3709216	36.90313787	-4.75052549

26_4587_233	TGATGATAGGTGTGAGTGCTACAGGG	10	287	4.5697388	121.7379376	-4.735523327
22_1845_53	TGAGCTCGCCTTAGGACACCTG	3	84	1.3709216	35.63061588	-4.699899417
28_21331_23	TATCGTTACGTCTAGGCGGGATTCTGAC	2	43	0.9139478	18.23948194	-4.31880925
26_31972_31	TGAGAATAGGTTGAGATCGTTTCGGC	4	63	1.8278955	26.72296191	-3.869824419
26_100439_8	TGTTGTAAATGTCCTGAAGGGAGGGG	1	14	0.4569739	5.93843598	-3.699899417
25_4460_173	ATACCACCCTGAACACGCCCAGTCT	53	705	24.219615	299.042669	-3.626103488
25_74670_8	GAATCCAGTTTGTTCCTCTGAAACA	2	22	0.9139478	9.331827968	-3.351976114
29_6372_33	TACTTAGTAAACCAGACCCGAGCTACAAC	3	30	1.3709216	12.72521996	-3.21447259
27_74475_10	TGAAGAGAAAGAAGATGCACCAGGAAA	3	25	1.3709216	10.60434996	-2.951438184
25_5909_131	TTGGTGTAAAGGGAGAAGAGCAGTG	36	290	16.45106	123.0104596	-2.902528584
26_90284_9	TAGTTAATGATGTGCTCCGTGACATG	3	18	1.3709216	7.635131974	-2.477506996
24_571_519	TACCTCGTTGGCTGCATGCTATGA	109	643	49.810152	272.7438811	-2.453035098
28_22475_22	CACACTTCTTCGGGTTGGCCGTGAGCCC	8	45	3.655791	19.08782993	-2.384397591
26_91429_9	CAGTCGTTGCTGTGGTGTATGAGCAA	5	27	2.2848694	11.45269796	-2.325503902
25_96275_6	TAACAGATGGTGTCTCGGATCAGCA	1	5	0.4569739	2.120869993	-2.21447259
30_1316_62	TTCATGATGATAGGTGTGAGTGCTACAGGG	24	111	10.967373	47.08331384	-2.101997861
26_143639_5	TACAGGACTATGCTGAGTATGTGACT	1	4	0.4569739	1.696695994	-1.892544495
28_109_3076	TAACTCTGAGATGGTCAACCAGTAACTC	670	2644	306.1725	1121.516052	-1.873033671
26_92335_9	TTCTTGACCAGGCTGGAGGTGTTGGT	3	11	1.3709216	4.665913984	-1.767013613
29_12530_16	TCATACAGCACAGGAAGTGTGATGTCCTC	4	14	1.8278955	5.93843598	-1.699899417
26_5425_199	TGCTTTGTTTCATCTGAGCGTTCAGGA	85	289	38.842779	122.5862856	-1.658079241
27_50600_16	TAGATGCCTAAATGCATTGAGTTGCTG	5	17	2.2848694	7.210957975	-1.658079241
27_3384_282	TAACTCTGAGATGGTCAACCAGTAACT	69	218	31.531197	92.46993168	-1.552204363
24_43543_6	TTCTGGTGTTCCTCTGGCAAATGTC	4	12	1.8278955	5.090087983	-1.477506996
26_308468_2	CACAGTCATAGGGACGATGAGGGGGC	2	6	0.9139478	2.545043991	-1.477506996
26_352311_2	TGTGCTTTTGATGTGGAGATGGAAGC	1	3	0.4569739	1.272521996	-1.477506996
29_1578_131	GCATTGACTACCGAGGACTTAATGATATC	65	191	29.703302	81.01723372	-1.44760551

27_40807_21	AATCGATAGAATAATCCGCCACCGTGC	12	33	5.4836865	13.99774195	-1.351976114
26_43517_22	TCTTCTGCTGCTGTAGCCCATCTGCT	15	41	6.8546081	17.39113394	-1.343205904
25_66399_9	TTATAGTTGTGCAAATATGGGCTGA	11	30	5.0267126	12.72521996	-1.340003472
25_2329_310	TGTGCTGTAGGCCTGTGCATCCCCCT	224	598	102.36215	253.6560511	-1.309191247
26_112456_7	TTGTAGCAGTGCTTGGCCTTCTTGAT	3	8	1.3709216	3.393391988	-1.307581994
25_125268_4	TGTGATTGACAGTGAAATGGGTGTA	2	5	0.9139478	2.120869993	-1.21447259
26_4952_217	TAACTCTGAGATGGTCAACCAGTAAC	75	187	34.273041	79.32053773	-1.210620265
26_153941_5	TGGATGATTGTGTGGATCGTGTAGGG	6	13	2.7418433	5.514261981	-1.008021713
31_913_50	TTGTAGCAGTGCTTGGCCTTCTTGATGCCCC	43	90	19.649877	38.17565987	-0.958132837
26_1554_628	TGAAGTCCACAATGAGCTCCTTGGTC	422	858	192.84298	363.9412908	-0.916279144
26_219032_3	TGACATGATAGCATCATGCAGTCGCT	1	2	0.4569739	0.848347997	-0.892544495
28_6116_86	TTCAGGATTATGGAGGCCACTGTGCTCT	90	178	41.127649	75.50297174	-0.87642483
25_28176_25	TGGTCAAGAAAGCTCACCAGCGCCT	13	22	5.9406604	9.331827968	-0.651536396
26_140427_5	TCTGTACGATTCCCCCTGAGTCTCCA	3	5	1.3709216	2.120869993	-0.629510089
26_100355_8	TGACAGTGAAATGGGTGTAACCTAGC	3	5	1.3709216	2.120869993	-0.629510089
26_34840_28	TCAAACGGTAACGCAGGTGTCCTAAG	21	33	9.5964514	13.99774195	-0.544621192
27_215451_3	TGAGCTGTAAGGTCTTATATAGACAGG	2	3	0.9139478	1.272521996	-0.477506996
25_28498_25	TCGCAGCTTTTGAGCCATCTTGGAC	19	27	8.6825036	11.45269796	-0.399504484
27_17378_53	TTCATGATGATAGGTGTGAGTGCTACA	22	31	10.053425	13.14939396	-0.387309187
26_6826_159	TGTGTTGAAACCTGTCCTGGAGTACA	155	208	70.830951	88.2281917	-0.316859808
27_116961_6	TGGGACATTGACTATAGCCCTGTGGCC	7	9	3.1988171	3.817565987	-0.255114575
27_86617_9	TTGGTCTTGCTGGTGTTAAGGAGCAGG	7	9	3.1988171	3.817565987	-0.255114575
27_1371_639	TGACTGTGTTGAACCAATTGGTTGGCC	694	875	317.13987	371.1522487	-0.226891849
22_7243_12	ATGCAGCCCAAAGCGGGTGGTA	16	20	7.311582	8.483479971	-0.21447259
25_139699_4	TGGATTGAGAGCTGGTGACTGTGGA	4	5	1.8278955	2.120869993	-0.21447259
25_41991_16	TGGTGTTGAATGCTGAACTGAAGTC	23	28	10.510399	11.87687196	-0.176337461
25_9407_82	CCATCATGAAGTGCTTCGAGCGGCT	177	190	80.884376	80.59305972	0.005205447

25_1548_461	TAATTTGACAGTCAGTGCTTTGGTA	317	324	144.86072	137.4323755	0.075944532
25_94091_6	TACTTGCCAAACTGAAGCTTGCAGT	4	4	1.8278955	1.696695994	0.107455505
26_166198_4	TATAGGACGGTGAAATGTGGATGTTG	4	4	1.8278955	1.696695994	0.107455505
26_172543_4	CAGGAAGTGTGATGTCCTCCATGGCC	2	2	0.9139478	0.848347997	0.107455505
27_340570_2	CACTCGTCGTGTGACCACAAAGGGCCC	2	2	0.9139478	0.848347997	0.107455505
27_325073_2	AGCAAAGTGTGATGTGGATCCAGTGTGGG	1	1	0.4569739	0.424173999	0.107455505
33_10408_2	TCCTCTTTAGTATAGTGGTCAGTATCCCCGC CT	1	1	0.4569739	0.424173999	0.107455505
27_294436_2	TGAGTGTGACAGTGGTGGAGCAGATGT	1	1	0.4569739	0.424173999	0.107455505
28_179708_2	TGGACATGGTCAGCAACAATACTCAGGT	1	1	0.4569739	0.424173999	0.107455505
30_31512_2	TGACAGAAGATGGTCGTTTCAGGCTAGTTCC	1	1	0.4569739	0.424173999	0.107455505
26_364537_2	TATGTTGTGCAATTGGTCCAAGAATG	1	1	0.4569739	0.424173999	0.107455505
27_65850_12	TGCTGAAACCAGTTCTGAACCAGAGCA	14	13	6.3976343	5.514261981	0.214370709
29_42364_4	ATGGCCCCCTGCGCAAGGATGACACGCAAA	17	15	7.7685559	6.362609978	0.288027751
23_11865_12	TCAAACGGTAACGCAGGTGTCCT	31	27	14.16619	11.45269796	0.306764313
27_64043_12	TGAAGTCCACAATGAGCTCCTTGGTCT	14	12	6.3976343	5.090087983	0.329847926
22_5461_17	TACGACCTCAGCTCAGACGAGA	20	17	9.1394775	7.210957975	0.341920759
27_46431_18	TGACTGTGTTGAACCAATTGGTTGGAC	13	11	5.9406604	4.665913984	0.348463604
25_94627_6	TGAGTGTGACAGTGGTGGAGCAGAT	5	4	2.2848694	1.696695994	0.4293836
23_5486_27	GGGTTAAGGCGCCCGATGCCGAC	117	93	53.465943	39.44818187	0.438661413
22_8139_11	AAAGTCAGCCCTCGATCCAAGC	9	7	4.1127649	2.96921799	0.470025584
23_2049_74	GAAAGTCAGCCCTCGATCCAAGC	182	139	83.169245	58.9601858	0.496309072
25_110947_5	TGCAGAAGTTCACTCTGGACTGGGC	4	3	1.8278955	1.272521996	0.522493004
26_220266_3	TGTGACACAGTTTGTTAGGATGCTCT	4	3	1.8278955	1.272521996	0.522493004
26_25226_40	TTCATGATGATAGGTGTGAGTGCTAC	27	20	12.338295	8.483479971	0.540414912
24_79691_3	TATCCGGTAAAGCGAATGACTAGA	3	2	1.3709216	0.848347997	0.692418006
22_17477_5	GAAGAGCCCAGCGCCGAATCCC	15	10	6.8546081	4.241739985	0.692418006

26_100513_8	TGGGTTTCAAGCAGGAGGTGTCAGAA	19	12	8.6825036	5.090087983	0.770420518
26_79850_11	AAGGGAACGGGCTTGCGGAATCAGC	27	17	12.338295	7.210957975	0.774880166
28_21168_24	CCATCATGAAGTGCTTCGAGCGGCTGGT	15	9	6.8546081	3.817565987	0.844421099
27_349150_2	TTGGTGAGCCTGTGTGAATTGTAGCCT	5	3	2.2848694	1.272521996	0.844421099
25_12446_61	ACGCGCGCGGAGTCAGAGGGCTCG	425	239	194.2139	101.3775857	0.937907728
22_7203_12	GTAACGCAGGTGTCCTAAGGCG	34	19	15.537112	8.059305972	0.946990833
25_6510_119	TGGATTGAGATCTGGTGACTGTGGA	463	240	211.5789	101.8017597	1.055433293
27_865_941	TAAGGATTATGGAGGCCACTGTGCTCT	1070	537	488.96205	227.7814372	1.102072308
26_190482_4	TCATCATGAAGTGCTTCGAACGGCTA	4	2	1.8278955	0.848347997	1.107455505
26_134016_6	CACACAGTGATGCAGTTGGTCAGGAC	4	2	1.8278955	0.848347997	1.107455505
26_227068_3	GAAGATATAGGACGGTGAAATGTGGA	2	1	0.9139478	0.424173999	1.107455505
29_8200_26	TGCATCGGAAAGACGTTTCTCTTTGGTC	33	16	15.080138	6.786783977	1.151849624
25_25828_28	TTCATGATGATAGGTGTGAGTGCTA	19	9	8.6825036	3.817565987	1.185458017
21_1793_36	CCATCTAGTAGCTGGTTCCCT	249	117	113.7865	49.62835783	1.197092717
26_351_2165	TAAGGATTATGGAGGCCACTGTGCTC	3241	1513	1481.0523	641.7752598	1.206482538
27_7088_134	ACTACTCTTATCGTTTCCTCACTTACC	822	382	375.63253	162.0344674	1.213021261
24_28255_11	AATGAAGCGCGGGTAAACGGCGGG	77	35	35.186988	14.84608995	1.244959029
24_7528_44	CTTATCGTTTCCTCACTTACCCGG	276	118	126.12479	50.05253183	1.333336912
21_5357_11	GATAACTGGCTTGTGGCGGCC	35	14	15.994086	5.93843598	1.4293836
25_38566_18	TCTTGGACAGGGTTGCTGAGCTTCC	15	6	6.8546081	2.545043991	1.4293836
26_146893_5	GAAATGTGGATGTTGCTGAAACCAGT	10	4	4.5697388	1.696695994	1.4293836
23_4870_31	CGAAGAGGGAAGAGCCCAGCGCC	115	45	52.551996	19.08782993	1.461092459
24_10992_30	TGGGAATGCAGCCCAAAGCGGGTG	41	16	18.735929	6.786783977	1.465007509
23_11118_13	CACCTGTCAAACGGTAACGCAGG	27	10	12.338295	4.241739985	1.540414912
23_21434_6	AGGGATAACTGGCTTGTGGCGGC	11	4	5.0267126	1.696695994	1.566887124
21_3393_19	GTAACGCAGGTGTCCTAAGGC	55	19	25.133563	8.059305972	1.640887705
27_79289_10	TTGTAGCCTCAGTTTCCTGTTCTTAGC	12	4	5.4836865	1.696695994	1.692418006

27_176405_4	CTTGCCAAACTGAAGCTTGCAGTGAGC	3	1	1.3709216	0.424173999	1.692418006
32_14226_2	GCATTTGTGATTTCAGTGGTAGAATTCTCGCC T	3	1	1.3709216	0.424173999	1.692418006
27_152435_4	TGTACCTGATGAGGGCCTGGGCCTCCT	3	1	1.3709216	0.424173999	1.692418006
26_279798_2	TCTTGAAGAAACATGTCCAGTTGTCT	3	1	1.3709216	0.424173999	1.692418006
25_10796_71	CTCACCTGCCGAATCAACTAGCCCT	748	244	341.81646	103.4984556	1.723612627
22_2472_39	TATTGAAAGTCAGCCCTCGATC	172	55	78.599507	23.32956992	1.752360546
28_47502_10	TACCATGACAGACCCTGACTTTTGGACT	19	6	8.6825036	2.545043991	1.770420518
22_693_143	GAAATACCACTACTCTTATCGT	561	176	256.36234	74.65462374	1.779880847
25_47967_14	CTGGGTCAGGGTTTCGTGCGTAGCA	76	23	34.730015	9.756001967	1.831821062
29_1560_133	AGGGTGTAATCTCGCGCCAGGCCGTACC	411	124	187.81626	52.59757582	1.836253778
23_332_377	ACGTGCAAATCGGTCGTCCGACC	1538	446	702.82582	189.1816034	1.893395393
24_1500_212	CCGAAGTTTCCCTCAGGATAGCTG	1557	442	711.50832	187.4849074	1.924106175
28_46333_10	ATCTAGCGAAACCACAGCCAAGGGAACG	150	41	68.546081	17.39113394	1.978722191
25_296_1891	GCAAATCGGTCGTCCGACCTGGGTA	4355	1171	1990.1212	496.7077523	2.002387148
32_1064_34	TTCTGATCGAGGCTCAGCCCGTGGACGGTG TG	98	26	44.78344	11.02852396	2.021725631
24_2814_117	GCCAAGCGTTCATAGCGACGTCGC	175	46	79.970428	19.51200393	2.035104661
25_420_1434	TTGGATTGTTCACCCACTAATAGGG	9775	2512	4466.9196	1065.525084	2.067715743
27_228900_3	TAAAGTCCACCGCTATATGCGACCAGG	4	1	1.8278955	0.424173999	2.107455505
23_3457_44	CTCACGATCCTTCTGGCTTTTTG	433	108	197.86969	45.81079184	2.110791217
21_99_599	CTGCGGGATGAACCGAACGCC	2127	527	971.98343	223.5396972	2.120400671
29_13616_15	CTAAGTCAGAATCCCGCCTAGACGTAACG	73	18	33.359093	7.635131974	2.127355062
26_9915_108	GAAGATTGGAAAACTTTGCCTGGTC	351	86	160.39783	36.47896388	2.13651797
26_26203_39	GGGAGTTTGACTGGGGCGGTACACCT	409	99	186.90232	41.99322586	2.154055918
23_7365_20	CTGCTCAGTACGAGAGGAACCGC	34	8	15.537112	3.393391988	2.194918346
21_197_303	CGGGATGAACCGAACGCCGGG	1924	448	879.21774	190.0299514	2.209993667

28_1037_461	TGTTTGGGAATGCAGCCCAAAGCGGGTG	617	143	281.95288	60.65688179	2.216710847
25_4141_186	GATATAGACAGCAGGACGGTGGCCA	256	59	116.98531	25.02626591	2.224812456
27_691_1165	ACCCTGTTGAGCTTGA CTCTAGTCTGG	6863	1563	3136.2117	662.9839597	2.241977081
22_1037_94	AGCCCGTGGACGGTGTGAGGCC	350	79	159.94086	33.50974589	2.254885869
27_1107_775	GGGATTATGACTGAACGCCTCTAAGTC	3646	821	1666.1268	348.2468528	2.258315939
25_33786_21	TCTGAGATGTGGGTCCCCAGGAACT	40	9	18.278955	3.817565987	2.259458598
24_9294_36	ACAGTGGCAGGTGGGGAGTTTGAC	175	39	79.970428	16.54278594	2.273264398
23_740_189	CGTCGCTTTTTGATCCTTCGATG	1908	425	871.90616	180.2739494	2.27398193
30_6636_12	CTGGGCAGGGCGAAGCCAGAGGAACTCTG	41	9	18.735929	3.817565987	2.295082508
28_6803_78	AAGGCGAGCTCAGGGAGGACAGAAACCT	256	56	116.98531	23.75374392	2.300100583
28_1558_320	TTGGTAAGCAGAACTGGCGCTGCGGGAT	442	95	201.98245	40.29652986	2.325502456
23_3786_40	CTCAGATCAGACGAGACAACCCG	554	118	253.16353	50.05253183	2.338554622
24_251_1071	CTGTGGGATTATGACTGAACGCCT	8898	1868	4066.1535	792.3570293	2.359442148
28_687_664	TAGTCTGGCACTGTGAAGAGACATGAGA	2645	549	1208.6959	232.8715252	2.375845173
25_3095_241	ACTGGCGCTGCGGGATGAACCGAAC	1679	347	767.25914	147.1883775	2.382050167
23_14164_10	CACTTACCCGGTGAGGCGGGGAG	98	20	44.78344	8.483479971	2.400237254
30_2530_32	TGAGCGCGTGCGATAGGACCCGAAAGATGG	90	18	41.127649	7.635131974	2.4293836
32_3958_8	AGGGAAGAGCCCAGCGCCGAATCCCCGTCC GA	50	10	22.848694	4.241739985	2.4293836
26_269215_3	TGTGTGTCTCTGAAGAGTGACCGGTC	5	1	2.2848694	0.424173999	2.4293836
32_17788_2	GTCGGGCTGGGGTGCGAAGCGGGGCTGGGC AC	5	1	2.2848694	0.424173999	2.4293836
32_7016_4	GCATTTGTGGTTCAGGGGTAGAATTCTCGCC T	5	1	2.2848694	0.424173999	2.4293836
23_529_255	AGATGGTGA ACTATGCCTGGGCA	315	61	143.94677	25.87461391	2.475926186
27_56314_14	CGGGGGAGAGGGTGTAATCTCGCGCC	78	15	35.643962	6.362609978	2.485967128
25_14705_51	CGAGCTCAGGGAGGACAGAAACCTC	163	31	74.486742	13.14939396	2.501987349

23_3872_39	TTACCACAGGGATAACTGGCTTG	197	37	90.023854	15.69443795	2.520053959
31_9308_4	TAGTACCCGAAAGATGGTGAACATATGCCTG G	16	3	7.311582	1.272521996	2.522493004
25_1283_550	GCTGTGTGTCTCTGAAGAGTGACCA	630	118	287.89354	50.05253183	2.524020474
23_1529_98	GCGGCCAAGCGTTCATAGCGACG	379	70	173.1931	29.6921799	2.544226526
28_752_611	GATGAACCGAACGCCGGTTAAGGCGCC	5943	1054	2715.7957	447.0793945	2.602772019
24_11397_29	TTTGA CTGGGGCGGTACACCTGTC	206	36	94.136618	15.27026395	2.624031031
21_3562_18	CTAGCGAAACCACAGCCAAGG	201	34	91.851749	14.42191595	2.671044355
23_5232_28	ACGTGAGCTGGGTTTAGACCGTC	150	25	68.546081	10.60434996	2.692418006
24_1119_273	CGTGGACGGTGTGAGGCCGGTAAC	1763	284	805.64494	120.4654156	2.741525145
25_5157_151	CCGGCGGCGTCCGGTGAGCTCTCGC	887	142	405.33583	60.23270779	2.75049868
28_4233_125	ATCGGTCGTCCGACCTGGGTATAGGGGC	591	91	270.07156	38.59983387	2.806675185
22_634_154	CGAAGCTACCATCTGTGGGATT	541	83	247.22287	35.20644188	2.811900857
34_46_501	AAGCTACCATCTGTGGGATTATGACTGAAC GCCT	6646	1014	3037.0484	430.1124345	2.819884146
26_2929_356	TGACGTGCAAATCGGTCTCCGACCT	617	92	281.95288	39.02400787	2.853020228
21_1031_63	CTCCATCTAAGGCTAAATACC	1107	165	505.87008	69.98870976	2.853572797
26_57964_16	CTAAGTCAGAATCCCGCCTAGACGTA	27	4	12.338295	1.696695994	2.862343007
27_63055_13	TGTGCTTGGCTGAGGAGCCAATGGTGC	61	9	27.875406	3.817565987	2.868267841
26_9405_114	CTTGAGCCGGGCGTGGAATGCGAGC	1508	219	689.11661	92.89410568	2.891089159
28_22978_22	TCTGGTGGAGGCCCGCAGCGGTCCTGAC	124	18	56.664761	7.635131974	2.891726814
26_24798_41	CAGACGACCTGATTCTGGGTCAGGGT	166	24	75.857663	10.18017597	2.897532435
21_792_80	CCGAAAGATGGTGAACATATGC	154	22	70.373977	9.331827968	2.914810427
28_47321_10	CAATAGTAATCCTGCTCAGTACGAGAGG	21	3	9.5964514	1.272521996	2.914810427
25_81117_7	TTGTAGCTCAGATCCAGTTCTCTCA	14	2	6.3976343	0.848347997	2.914810427
27_182117_4	TATCTAGCGAAACCACAGCCAAGGGAA	14	2	6.3976343	0.848347997	2.914810427
26_185522_4	TTTCAGTAGATCCAGACAGATCGAAC	7	1	3.1988171	0.424173999	2.914810427

23_2902_53	AAGGGCAAAAGCTCGCTTGATCT	823	117	376.0895	49.62835783	2.921839406
24_185_1392	GATGAACCGAACGCCGGGTAAAGG	4698	663	2146.8633	281.227361	2.932421443
27_33035_27	TGTCCCTACCTACTATCTAGCGAAACC	202	28	92.308723	11.87687196	2.958312066
27_11421_82	GTTTGGGAATGCAGCCCAAAGCGGGTG	161	22	73.572794	9.331827968	2.978940764
28_4899_108	ACAGAAACCTCCCGTGGAGCAGAAGGGC	467	61	213.4068	25.87461391	3.043996907
27_27195_33	TGTGCTTATAGTTGTGCAAATATGGGC	46	6	21.020798	2.545043991	3.04605496
25_55618_12	CAGGAGGTGTCAGAAAAGTTACCAC	39	5	17.821981	2.120869993	3.070929629
28_22958_22	AAAGCGGGGCCTCACGATCCTTCTGGCT	125	16	57.121735	6.786783977	3.07323979
30_3447_24	AAAGCATCGCGAAGGCCACGGTGGGTGTT	63	8	28.789354	3.393391988	3.084735428
24_458_638	AAGATGGTGAACCTATGCCTGGGCA	6136	758	2803.9917	321.5238909	3.124484234
23_5362_28	AGCCCAAAGCGGGTGGTAAACTC	312	38	142.57585	16.11861194	3.14493021
28_75832_6	CTGAGGAGCCAATGGTGCGAAGCTACCA	17	2	7.7685559	0.848347997	3.194918346
21_574_113	GTGGCCATGGAAGTCGGAATC	319	37	145.77467	15.69443795	3.215414753
29_3762_57	TCAGGGTTTCGTGCGTAGCAGAGCAGCTC	193	22	88.195958	9.331827968	3.240480924
26_81525_11	TGACATGATAGCATCACGCAGTTGCT	18	2	8.2255298	0.848347997	3.277380506
23_6907_21	CAAGCGTTCATAGCGACGTCGCT	93	10	42.49857	4.241739985	3.324686221
23_877_165	ATGGTGAACCTATGCCTGGGCAGG	1229	132	561.62089	55.99096781	3.326330586
26_3364_316	AGAGGTGTAGAATAAGTGGGAGGCCT	2567	270	1173.0519	114.5269796	3.356507488
27_21403_43	TCTTGGGGCCGAAACGATCTCAACCTA	300	31	137.09216	13.14939396	3.382077885
28_154023_3	ACATCAGGACGGTGGCCATGGAAGTCGG	10	1	4.5697388	0.424173999	3.4293836
28_35180_14	CAGAAATCCCGCCTAGACGTAACGATACC	103	10	47.068309	4.241739985	3.472027937
28_1469_338	TTTGTAAGCAGAACTGGCGCTGCGGGA	1496	143	683.63292	60.65688179	3.494478628
26_44053_22	TTGGATTGAGATCTGGTGA CTGCGGC	75	7	34.273041	2.96921799	3.528919273
26_107827_8	TTCCAGAGCTCCGCCGTCATGGCGCT	22	2	10.053425	0.848347997	3.566887124
31_92_388	CGGAGGAAAAGAACTAACCAGGATTCCCT C	3121	283	1426.2155	120.0412416	3.570589904
27_13721_68	CGACCTGATTCTGGGTCAGGGTTTCGT	354	31	161.76875	13.14939396	3.620864745

29_755_260	ATGAGAGGTGTAGAATAAGTGGGAGGCCT	2117	180	967.4137	76.35131974	3.663407963
32_3561_9	GCCCACGGTGGGTGTTGACGCGATGTGATT TC	27	2	12.338295	0.848347997	3.862343007
26_33045_30	CCGAAAGATGGTGAACCTATGCCTGGG	56	4	25.590537	1.696695994	3.914810427
26_165158_5	TGTGCTTGGCTGAGGAGCCAATGGTG	14	1	6.3976343	0.424173999	3.914810427
29_12169_17	CCAATGGTGCGAAGCTACCATCTGTGGGA	35	2	15.994086	0.848347997	4.236738522
32_1776_20	CATCGCGAAGGCCACGGTGGGTGTTGACG CG	19	1	8.6825036	0.424173999	4.355383018
21_6889_9	GTGCGAAGCTACCATCTGTGG	20	1	9.1394775	0.424173999	4.4293836
27_3559_268	CGGTCGGGCTGGGGTGCGAAGCGGGGC	944	43	431.38334	18.23948194	4.5638338
25_2864_259	TTACCTGGTCGGCCTGTTTCGAGGAC	740	30	338.16067	12.72521996	4.73194637
25_2129_338	TAAATCCGGGATCTGCAGAGATGCT	551	20	251.79261	8.483479971	4.891435919
26_396429_2	AAGTAGATGCAGCAGGATGAAGATCT	2	0	0.9139478	0	NA
25_284412_2	TGATGATTATGATGATGATGACAAA	2	0	0.9139478	0	NA
27_359123_2	TGACATGATGGCATCACACAGTTGCTG	2	0	0.9139478	0	NA
27_371183_2	TCTGGGTGAACTATCCCTTTAAGGAGC	2	0	0.9139478	0	NA
24_153401_2	GGGTGTAGAATAAGTGGGAGGCCT	2	0	0.9139478	0	NA
29_109705_2	TTGCTGGTGTTAAGGAGCAGGTTATTGTC	2	0	0.9139478	0	NA
26_400260_2	GCATGACGGTGGCCATGGAAGTCGGA	2	0	0.9139478	0	NA
25_316351_2	GCATGTTTGTGGGGAACCTGGTGCT	2	0	0.9139478	0	NA
24_164831_2	CATGAAAGCATGGATCCATCCTGC	2	0	0.9139478	0	NA
28_250842_2	TACCTAATAAAGTGGCTGGTGACTGTAT	2	0	0.9139478	0	NA
29_113141_2	TGCAATTGGTCCAAGAATGTAAGTATGAG	2	0	0.9139478	0	NA
22_49747_2	ACGGTGGCCATGGAAGTCGGCT	2	0	0.9139478	0	NA
24_165923_2	TACTCAGGTAGGCTGTGGCGTTTA	2	0	0.9139478	0	NA
26_400620_2	CCAGGAAGTGGATGTACATCTCCGTC	2	0	0.9139478	0	NA
27_237437_3	GTATTGACTACAGAGGTCTCAACGATG	3	0	1.3709216	0	NA

27_352996_2	CAGGTTCTATTGGCCAAGGATGGCATT	4	0	1.8278955	0	NA
25_292832_2	TCTGGTGACTGTGGAGGCCATTGGA	4	0	1.8278955	0	NA
30_44312_2	GAAGGCCCCACGGTGGGTGTTGACGCGATGT	4	0	1.8278955	0	NA
28_149725_3	CATGGACGGTGTGAGGCCGGTGGCGGCC	5	0	2.2848694	0	NA
29_69003_3	GCATGTGGTTCCGTGGTAGAATTCTCGCC	5	0	2.2848694	0	NA
25_188773_3	TGGATTGAGGTCTGGTGACTGTGGA	8	0	3.655791	0	NA
27_73228_11	TCGCTGAACATGCATGGAGAGTTGCCT	11	0	5.0267126	0	NA
27_146858_5	CACAGTTGCTGCAGATTTGTCTGGCTGC	14	0	6.3976343	0	NA
26_88224_10	TTACTCAGGTCCAGCTCTCTCAGCCT	19	0	8.6825036	0	NA

ID abbreviation stands for the identity of piRNA cluster.