

<u>RNAi ID</u>	<u>Gene Symbol</u>	<u>Accession number</u>	<u>GI number</u>	<u>21mer NA(n19)</u>	<u>CDS start</u>	<u>CDS end</u>	<u>RNAi start</u>	<u>RNAi end</u>
5031804_1	IRS1	NM_005544	5031804	CACAAACGCTTCTTCGTA	1021	4749	1096	1116
5031804_10	IRS1	NM_005544	5031804	GATAATCGGTTCCGAAAGAGA	1021	4749	2572	2592
5031804_14	IRS1	NM_005544	5031804	CAGATCATCAATCCCATCAGA	1021	4749	2953	2973
5031804_16	IRS1	NM_005544	5031804	TACTCATTGCCAAGATCCTTT	1021	4749	3313	3333
5031804_32	IRS1	NM_005544	5031804	CAGAATGAAGACCTAAATGAC	1021	4749	4768	4788
11068002_1	IGF1R	NM_000875	11068002	CATCTTCGAGATGACCAATCT	46	4149	399	419
11068002_12	IGF1R	NM_000875	11068002	CATGTA	46	4149	999	1019
11068002_38	IGF1R	NM_000875	11068002	CATCTTACTACATGGGCTGAA	46	4149	1740	1760
11068002_63	IGF1R	NM_000875	11068002	GAGAATCCCAATGGATTGATT	46	4149	2611	2631
11068002_111	IGF1R	NM_000875	11068002	AAACACATTTGGGATGTTCTT	46	4149	4308	4328
19923111_1	IGF1	NM_000618	19923111	GATTTCTTGAAGGTGAAGATG	167	628	218	238
19923111_4	IGF1	NM_000618	19923111	GAAGGAAGTACATTTGAAGAA	167	628	565	585
19923111_7	IGF1	NM_000618	19923111	CAAGTAGAGGGAGTGCAGGAA	167	628	588	608
19923111_12	IGF1	NM_000618	19923111	CAAGAACTACAGGATGTAGGA	167	628	610	630
19923111_36	IGF1	NM_000618	19923111	CACAAATGCATGGGTGTTGTA	167	628	930	950
4885060_5	AKT1	NM_005163	4885060	CATGAACGAGTTTGAGTACCT	199	1641	636	656
4885060_10	AKT1	NM_005163	4885060	CACATTAAGATCACAGACTTC	199	1641	1057	1077
4885060_12	AKT1	NM_005163	4885060	GATCATGCAGCATCGCTTCTT	199	1641	1401	1421
4885060_14	AKT1	NM_005163	4885060	CAAGATGACAGCATGGAGTGT	199	1641	1558	1578
4885060_16	AKT1	NM_005163	4885060	TATTTTCATCCAGTTTGTCTC	199	1641	1852	1872
6715585_17	AKT2	NM_001626	6715585	GACAAAGATGGCCACATCAAG	204	1649	1053	1073
6715585_22	AKT2	NM_001626	6715585	GACTTTGGCCTCTGCAAAGAG	204	1649	1080	1100
6715585_23	AKT2	NM_001626	6715585	GACACAAGGTACTTCGATGAT	204	1649	1506	1526
6715585_24	AKT2	NM_001626	6715585	CAAGTACTTCGATGATGAAT	204	1649	1510	1530
19923313_1	AKT3	NM_005465	19923313	AAAAACTGGAGGCCAAGATAC	1	1440	58	78
19923313_30	AKT3	NM_005465	19923313	GAATGAATTGTAGTCCA	1	1440	347	367
19923313_65	AKT3	NM_005465	19923313	CACGTTTCTATGGTGCAGAAA	1	1440	743	763
19923313_84	AKT3	NM_005465	19923313	GAAATGATGTGTGGGAGGTTA	1	1440	1012	1032
19923313_12	AKT3	NM_005465	19923313	CATTCTGCTACTTCACTGTCA	1	1440	1449	1469
4505694_7	PDPK1	NM_002613	4505694	CAAAATCGGTTTCAATCGATGA	81	1751	596	616
4505694_12	PDPK1	NM_002613	4505694	AAATGAAGATATGCACATCCA	81	1751	719	739
4505694_17	PDPK1	NM_002613	4505694	CAGAAGATCATTAAAGTTGGAA	81	1751	954	974
4505694_28	PDPK1	NM_002613	4505694	CAACATAGAGCAGTACATTCA	81	1751	1310	1330
4505694_34	PDPK1	NM_002613	4505694	GATAAGCGGAAGGGTTATTT	81	1751	1470	1490
5453891_1	PIK3CA	NM_006218	5453891	GAATGTTTACTACCAAATGGA	13	3219	79	99

5453891_54	PIK3CA	NM_006218	5453891	AAACTAGAAAGTATGTTGCTA	13	3219	694	714
5453891_104	PIK3CA	NM_006218	5453891	AAAATGGCTTTGAATCTTTGG	13	3219	1330	1350
5453891_170	PIK3CA	NM_006218	5453891	TACTGAAGAAAGCATTGACTA	13	3219	1970	1990
5453891_293	PIK3CA	NM_006218	5453891	AATGAAAGCTCACTCTGGATT	13	3219	3234	3254
18560516_1	PIK3R1	XM_043865	18560516	AAGAGAAGAAGATATTGACTT	43	2217	93	113
18560516_24	PIK3R1	XM_043865	18560516	CAGAATTACGACAGCTTCTTG	43	2217	518	538
18560516_56	PIK3R1	XM_043865	18560516	TACTGTAGCCAACAACGGTAT	43	2217	987	1007
18560516_92	PIK3R1	XM_043865	18560516	TACATGAATATAACACTCAGT	43	2217	1388	1408
18560516_16	PIK3R1	XM_043865	18560516	GATCCTTCTCCTGAAGTTCAG	43	2217	2232	2252
4826907_2	PIK3R2	NM_005027	4826907	CATTCAAGGGGAGGAGTGAA	242	2428	1243	1263
4826907_4	PIK3R2	NM_005027	4826907	CAATAAGCTGATCAAGTCTT	242	2428	1363	1383
4826907_7	PIK3R2	NM_005027	4826907	CAAATACCAGCAGGACCAGAT	242	2428	1519	1539
4826907_12	PIK3R2	NM_005027	4826907	CAGATGAAGCGTACTGCAATT	242	2428	1664	1684
4826907_24	PIK3R2	NM_005027	4826907	GAAAGAGATGCAAAGGATCCT	242	2428	1786	1806
5453893_1	PIK3CB	NM_006219	5453893	GATTCACAGATAGCATCTGAT	1	3213	61	81
5453893_52	PIK3CB	NM_006219	5453893	AAAAACGTTTGACTATTTCATG	1	3213	686	706
5453893_99	PIK3CB	NM_006219	5453893	GAC TTAAAGGACAATTGAGA	1	3213	1339	1359
5453893_146	PIK3CB	NM_006219	5453893	GATTGTGCCCTCTCTAGATTC	1	3213	1957	1977
5453893_189	PIK3CB	NM_006219	5453893	CATTCAGCTGAACAGTAGCAA	1	3213	2586	2606
4506248_1	PTEN	NM_000314	4506248	GATGGATTCGACTTAGACTTG	1035	2246	1089	1109
4506248_27	PTEN	NM_000314	4506248	AAGATCTTGACCAATGGCTAA	1035	2246	1351	1371
4506248_41	PTEN	NM_000314	4506248	TATTATAGCTACCTGTTAAAG	1035	2246	1563	1583
4506248_61	PTEN	NM_000314	4506248	GATATCAAAGTAGAGTTCTTC	1035	2246	1788	1808
4506248_118	PTEN	NM_000314	4506248	CAATAGGACATTGTGTCAGAT	1035	2246	2327	2347
9257221_1	FOXO1A	NM_002015	9257221	GATCTACGAGTGGATGGTCAA	386	2353	940	960
9257221_13	FOXO1A	NM_002015	9257221	AACAACAGTAAATTTGCTAAG	386	2353	1160	1180
9257221_23	FOXO1A	NM_002015	9257221	CAAAGATGGCCTCTACTTTAC	386	2353	1443	1463
9257221_40	FOXO1A	NM_002015	9257221	TATACAAACACTTCAGGACAA	386	2353	1699	1719
9257221_63	FOXO1A	NM_002015	9257221	TAAAAGTACTTCAGATTGTCT	386	2353	2376	2396
4503738_2	FOXO3A	NM_001455	4503738	GACAATAGCAACAAGTATACC	925	2946	1687	1707
4503738_6	FOXO3A	NM_001455	4503738	GATGAAGTCCAGGACGATGAT	925	2946	1924	1944
4503738_13	FOXO3A	NM_001455	4503738	CATGTCACACTATGGTAACCA	925	2946	2307	2327
4503738_17	FOXO3A	NM_001455	4503738	CATGTTCAATGGGAGCTTGGA	925	2946	2766	2786
4503738_28	FOXO3A	NM_001455	4503738	CAAAGTACACAAGACCTACA	925	2946	2986	3006
5174578_1	MLLT7	NM_005938	5174578	GAAATCAGTCATATGCAGAAT	183	1688	475	495
5174578_13	MLLT7	NM_005938	5174578	CAGTTCAAATGCCAGCAGTGT	183	1688	950	970

5174578_20	MLLT7	NM_005938	5174578	CAAGACAGAATGCCTCAGGAT	183	1688	1557	1577
5174578_29	MLLT7	NM_005938	5174578	CATCAGTGACCTCATGGATGA	183	1688	1628	1648
5174578_36	MLLT7	NM_005938	5174578	CACTTAGGCTTTGTAGCAAGA	183	1688	1975	1995
11995473_1	GSK3A	NM_019884	11995473	GACATCAAAGTGATTGGCAAT	115	1566	475	495
11995473_19	GSK3A	NM_019884	11995473	CAAGTTGACCATCCCTATCCT	115	1566	750	770
11995473_25	GSK3A	NM_019884	11995473	CACTGATTACACCTCATCCAT	115	1566	996	1016
11995473_35	GSK3A	NM_019884	11995473	CATTCTCATCCCTCCTCACTT	115	1566	1428	1448
11995473_37	GSK3A	NM_019884	11995473	GACTAGAGGGCAGAGGTAAT	115	1566	1667	1687
21361339_1	GSK3B	NM_002093	21361339	CATGAAAGTTAGCAGAGACAA	233	1534	307	327
21361339_33	GSK3B	NM_002093	21361339	GAGAAAGCTAGATCACTGTAA	233	1534	535	555
21361339_63	GSK3B	NM_002093	21361339	CAATGTTTCGTATATCTGTTC	233	1534	868	888
21361339_74	GSK3B	NM_002093	21361339	GAGCAAATCAGAGAAATGAAC	233	1534	1067	1087
21361339_97	GSK3B	NM_002093	21361339	AAAAACCACCAGTTACTTGAG	233	1534	1562	1582
4507692_2	TSC1	NM_000368	4507692	TATGCTTGAAACACCTTGGT	1	3495	117	137
4507692_27	TSC1	NM_000368	4507692	TAGAAACTCATGATGTTGTGA	1	3495	749	769
4507692_62	TSC1	NM_000368	4507692	AAAGAAGAAGCTGCAATATCT	1	3495	1429	1449
4507692_80	TSC1	NM_000368	4507692	CATAATGCTGCCATGAAAGAT	1	3495	2194	2214
4507692_128	TSC1	NM_000368	4507692	AAAAGGATAACCCAGGTGTTT	1	3495	2854	2874
10938006_1	TSC2	NM_000548	10938006	TAAACAGACGGAGTTTATCAT	19	5442	117	137
10938006_32	TSC2	NM_000548	10938006	CATCAACAGGCAGTTCTATGA	19	5442	1440	1460
10938006_42	TSC2	NM_000548	10938006	CAGCATTAAATCTCTTACCATA	19	5442	2330	2350
10938006_62	TSC2	NM_000548	10938006	CAATGAGTCACAGTCCTTTGA	19	5442	4581	4601
10938006_75	TSC2	NM_000548	10938006	CAGACATAGAGGCACAGATTG	19	5442	5522	5542
19924298_2	FRAP1	NM_004958	19924298	CACTATGTCACCATGGAACTC	80	7729	215	235
19924298_38	FRAP1	NM_004958	19924298	CAGATTCCACAGCTAAAGAAG	80	7729	1658	1678
19924298_92	FRAP1	NM_004958	19924298	GATGAAATAGTCACCCTCATG	80	7729	3173	3193
19924298_15	FRAP1	NM_004958	19924298	GAGGTTATCCAGTACAAACTT	80	7729	4880	4900
19924298_26	FRAP1	NM_004958	19924298	TAGTAAATGCTTCCACTAAAC	80	7729	7779	7799
20149546_1	RPS6KA1	NM_002953	20149546	CATTTGAGCTCCTCAAGGTT	157	2364	337	357
20149546_9	RPS6KA1	NM_002953	20149546	TATCATTTACAGAGACCTCAA	157	2364	702	722
20149546_17	RPS6KA1	NM_002953	20149546	CATGTCTTCTACTCCACCATT	157	2364	1108	1128
20149546_30	RPS6KA1	NM_002953	20149546	GAAGAGATTGAGATTCTTCTG	157	2364	1528	1548
20149546_44	RPS6KA1	NM_002953	20149546	AAAAATGGCATCAACCACCAT	157	2364	2608	2628
4759049_1	RPS6KA3	NM_004586	4759049	GAGAATGGACAGCAAATTATG	1	2223	67	87
4759049_41	RPS6KA3	NM_004586	4759049	CAGAAGAAGATGTCAAATTCT	1	2223	497	517
4759049_69	RPS6KA3	NM_004586	4759049	CAACGATAGACTGGAATAAAC	1	2223	983	1003

4759049_98	RPS6KA3	NM_004586	4759049	AAAAGCAAGAGAGACCCAACA	1	2223	1363	1383
4759049_153	RPS6KA3	NM_004586	4759049	GATATTTGGATCCATGGTGTA	1	2223	2238	2258
17158043_1	RPS6	NM_001010	17158043	GATGAACGCAAACCTTCGTA	43	792	100	120
17158043_3	RPS6	NM_001010	17158043	AACTTCGTA	43	792	109	129
17158043_4	RPS6	NM_001010	17158043	TACTTTCTATGAGAAGCGTAT	43	792	117	137
17158043_9	RPS6	NM_001010	17158043	GAAAATCAGTTCGTGGTTGCA	43	792	323	343
17158043_16	RPS6	NM_001010	17158043	AATCTGAGCGTTCCTCAACTTG	43	792	355	375
20070179_1	EIF4EBP1	NM_004095	20070179	GATCATCTATGACCGGAAATT	65	421	217	237
20070179_2	EIF4EBP1	NM_004095	20070179	CATCTATGACCGGAAATTCCT	65	421	220	240
20070179_3	EIF4EBP1	NM_004095	20070179	GAAGAGTCACAGTTTGAGATG	65	421	392	412
20070179_6	EIF4EBP1	NM_004095	20070179	GACAAGAACGAACCCCTCCTT	65	421	694	714
4885116_1	CBL	NM_005188	4885116	GACAAGAAGATGGTGGAGAAG	149	2869	302	322
4885116_30	CBL	NM_005188	4885116	AAAAGACAATAGTCCCTTGA	149	2869	735	755
4885116_62	CBL	NM_005188	4885116	GATAAGGATGTAAAGATTGAG	149	2869	1310	1330
4885116_79	CBL	NM_005188	4885116	TATTCTGTTGGAGCAGAATCC	149	2869	1802	1822
4885116_113	CBL	NM_005188	4885116	GATATCACATCAGTGGTCCA	149	2869	2991	3011
4757919_1	CBLB	NM_004351	4757919	GATGCTATTCAGGATGCAGTT	323	2635	401	421
4757919_41	CBLB	NM_004351	4757919	CAAACTATCGTACCATGGAA	323	2635	886	906
4757919_63	CBLB	NM_004351	4757919	TAATCCTGATTTAACTGGATT	323	2635	1333	1353
4757919_86	CBLB	NM_004351	4757919	CAGAACTACCCAGTCACATCA	323	2635	1742	1762
4757919_137	CBLB	NM_004351	4757919	TACATCTTAATGGTCAGAATT	323	2635	2650	2670
5032090_1	SGK	NM_005627	5032090	CAATTCTCATCGCTTTCATGA	43	1338	107	127
5032090_18	SGK	NM_005627	5032090	GAAAGGTTCTTCTAGCAAGAC	43	1338	371	391
5032090_47	SGK	NM_005627	5032090	CACTGAACATCGTTTATAGAG	43	1338	686	706
5032090_54	SGK	NM_005627	5032090	GAAATGTACGACAACATTCTG	43	1338	952	972
5032090_71	SGK	NM_005627	5032090	TATGTGTGTTCCGAATGTTT	43	1338	1369	1389
4557883_1	INSR	NM_000208	4557883	CATGGATATCCGGAACAACCT	107	4255	217	237
4557883_30	INSR	NM_000208	4557883	CACCAATACGTCATTACAAC	107	4255	1010	1030
4557883_60	INSR	NM_000208	4557883	CAGTATGCCATCTTTGTGAAG	107	4255	1868	1888
4557883_80	INSR	NM_000208	4557883	CACCTATTTCTACGTGACAGA	107	4255	2923	2943
4557883_111	INSR	NM_000208	4557883	GAGTTCAGAGATCGTTCCTAT	107	4255	4362	4382
8051634_1	XPO1	NM_003400	8051634	TAGATAATGTGGTGAATTGCT	39	3254	121	141
8051634_61	XPO1	NM_003400	8051634	GACCAAATTAATCAGCACATT	39	3254	767	787
8051634_132	XPO1	NM_003400	8051634	GAGAGAATTCATGAAGGATAC	39	3254	1361	1381
8051634_196	XPO1	NM_003400	8051634	AAAGTACATGTTACTCCCTAA	39	3254	2003	2023
8051634_322	XPO1	NM_003400	8051634	AAATCAAATTCATGCTGTTT	39	3254	3254	3274

4758953_1	PPP2R2B	NM_004576	4758953 GACATTATCTCTACGGTAGAA	526	1857	598	618
4758953_13	PPP2R2B	NM_004576	4758953 CAGCTTACTTTCTTCTGTCTA	526	1857	833	853
4758953_28	PPP2R2B	NM_004576	4758953 GAGGATTAACCTATGGA ACTT	526	1857	1107	1127
4758953_39	PPP2R2B	NM_004576	4758953 GAAATTATCTCTTCGATTTTCG	526	1857	1360	1380
4758953_70	PPP2R2B	NM_004576	4758953 TAATCTCACATACTGAATACT	526	1857	1878	1898
5031798_1	INPP5D	NM_005541	5031798 GAATTGCGTTTACACTTACAG	141	3707	281	301
5031798_12	INPP5D	NM_005541	5031798 CATCAACATGGTGTCCAAGCT	141	3707	911	931
5031798_38	INPP5D	NM_005541	5031798 CATCTGTACTGACAACGTGAA	141	3707	1649	1669
5031798_58	INPP5D	NM_005541	5031798 GATTGAGTTTCTCAGGTGCTA	141	3707	2327	2347
5031798_69	INPP5D	NM_005541	5031798 GATTTGAGGGTGGAGATATAG	141	3707	4021	4041

<u>CDS length-50</u>	<u>Relative RNAi</u>	<u>% of CDS</u>	<u>GC content</u>	<u>rule</u>	<u>sense 19 mer</u>	<u>antisense 19 mer</u>	
3678	25	0.67971724	0.47368422	2	CAAACGCTTCTTCGTA	CAGTACGAAGAAGCGTTG	0
3678	1501	40.8102229	0.42105263	2	TAATCGGTTCCGAAAGAGA	TCTCTTTCGGAACCGATTA	0
3678	1882	51.1691136	0.42105263	2	GATCATCAATCCCATCAGA	TCTGATGGGATTGATGATC	0
3678	2242	60.9570419	0.42105263	2	CTCATTGCCAAGATCCTTT	AAAGGATCTTGGCAATGAG	2
3678	3697	100.516585	0.36842105	2	GAATGAAGACCTAAATGAC	GTCATTTAGGTCTTCATTC	0
4053	303	7.47594375	0.42105263	2	TCTTCGAGATGACCAATCT	AGATTGGTCATCTCGAAGA	0
4053	903	22.2797927	0.47368422	2	TGTA	TCACAAGGGATGCAGTACA	1
4053	1644	40.5625463	0.42105263	2	TCTTACTACATGGGCTGAA	TTCAGCCCATGTAGTAAGA	0
4053	2515	62.0528004	0.36842105	2	GAATCCCAATGGATTGATT	AATCAATCCATTGGGATTC	1
4053	4212	103.92302	0.42105263	1	ACACATTTGGGATGTTCTT	AGGAACATCCCAAATGTGT	0
411	1	0.243309	0.36842105	2	TTTCTTGAAGGTGAAGATG	CATCTTCACCTTCAAGAAA	1
411	348	84.6715328	0.31578946	2	AGGAAGTACATTTGAAGAA	TTCTTCAAATGTA	0
411	371	90.2676399	0.5263158	2	AGTAGAGGGAGTGCAGGAA	TTCCTGCACTCCCTCTACT	0 manually
411	393	95.620438	0.42105263	2	AGAACTACAGGATGTAGGA	TCCTACATCCTGTAGTTCT	1
411	713	173.479319	0.42105263	2	CAAATGCATGGGTGTTGTA	TACAACACCCATGCATTTG	0
1392	387	27.8017241	0.42105263	2	TGAACGAGTTTGAGTACCT	AGGTA	0
1392	808	58.045977	0.36842105	2	CATTAAGATCACAGACTTC	GAAGTCTGTGATCTTAATG	0
1392	1152	82.7586207	0.47368422	2	TCATGCAGCATCGCTTCTT	AAGAAGCGATGCTGCATGA	0
1392	1309	94.0373563	0.47368422	2	AGATGACAGCATGGAGTGT	ACACTCCATGCTGTCATCT	2
1392	1603	115.158046	0.36842105	2	TTTCATCCAGTTTGT	GAGAACAACTGGATGAAA	1
1395	799	57.2759857	0.47368422	2	CAAAGATGGCCACATCAAG	CTTGATGTGGCCATCTTTG	1
1395	826	59.2114695	0.5263158	2	CTTTGGCCTCTGCAAAGAG	CTCTTTGCAGAGGCCAAAG	1
1395	1252	89.7491039	0.42105263	2	CACAAGGTACTTCGATGAT	ATCATCGAAGTACCTTG	0
1395	1256	90.0358423	0.36842105	2	AGGTACTTCGATGATGAAT	ATTCATCATCGAAGTACCT	0
1389	7	0.50395968	0.47368422	1	AAACTGGAGGCCAAGATAC	GTATCTTGGCCTCCAGTTT	1
1389	296	21.3102952	0.31578946	2	ATGAATTGTAGTCCA	AAGTTGACTACAATTCAT	0
1389	692	49.8200144	0.42105263	2	CGTTTCTATGGTGCAGAAA	TTTCTGCACCATAGAAACG	0
1389	961	69.1864651	0.42105263	2	AATGATGTGTGGGAGGTTA	TAACCTCCCACACATCATT	0
1389	1398	100.647948	0.42105263	2	TTCTGCTACTTCACTGTCA	TGACAGTGAAGTAGCAGAA	0
1620	465	28.7037037	0.36842105	2	AAATCGGTTTCATTCGATGA	TCATCGAATGAACCGATTT	0
1620	588	36.2962963	0.36842105	1	ATGAAGATATGCACATCCA	TGGATGTGCATATCTTCAT	2
1620	823	50.8024691	0.31578946	2	GAAGATCATTAAGTTGGAA	TTCCA	0
1620	1179	72.7777778	0.36842105	2	ACATAGAGCAGTACATTCA	TGAATGTA	0
1620	1339	82.654321	0.36842105	2	TAAGCGGAAGGGTTTATTT	AAATAAACCTTCCGCTTA	0
3156	16	0.50697085	0.31578946	2	ATGTTTACTACCAAATGGA	TCCATTTGGTAGTAAACAT	0

3156	631	19.9936629	0.31578946	1	AACTAGAAGTATGTTGCTA	TAGCAACATACTTCTAGTT	0
3156	1267	40.1457541	0.36842105	1	AATGGCTTTGAATCTTTGG	CCAAAGATTCAAAGCCATT	0
3156	1907	60.4245881	0.36842105	2	CTGAAGAAAGCATTGACTA	TAGTCAATGCTTCTTTCAG	1
3156	3171	100.475285	0.42105263	1	TGAAAGCTCACTCTGGATT	AATCCAGAGTGAGCTTTCA	1
2124	0	0	0.31578946	1	GAGAAGAAGATATTGACTT	AAGTCAATATCTTCTTCTC	1
2124	425	20.0094162	0.42105263	2	GAATTACGACAGCTTCTTG	CAAGAAGCTGTCGTAATTC	0
2124	894	42.0903955	0.47368422	2	CTGTAGCCAACAACGGTAT	ATACCGTTGTTGGCTACAG	0
2124	1295	60.9698682	0.31578946	2	CATGAATATAACACTCAGT	ACTGAGTGTTATATTCATG	1
2124	2139	100.706215	0.47368422	2	TCCTTCTCCTGAAGTTCAG	CTGAACTTCAGGAGAAGGA	2
2136	951	44.5224719	0.47368422	2	TTTCAAGGGAGGAGGTGAA	TTCACCTCCTCCCTTGAAA	2
2136	1071	50.1404494	0.36842105	2	ATAAGCTGATCAAGGTCTT	AAGACCTTGATCAGCTTAT	1
2136	1227	57.4438202	0.47368422	2	AATACCAGCAGGACCAGAT	ATCTGGTCTGCTGGTATT	0
2136	1372	64.2322097	0.42105263	2	GATGAAGCGTACTGCAATT	AATTGCAGTACGCTTCATC	0
2136	1494	69.9438202	0.42105263	2	AAGAGATGCAAAGGATCCT	AGGATCCTTTGCATCTCTT	1
3162	10	0.31625553	0.36842105	2	TTCACAGATAGCATCTGAT	ATCAGATGCTATCTGTGAA	0
3162	635	20.0822264	0.31578946	1	AAACGTTTGACTATTCATG	CATGAATAGTCAAACGTTT	0
3162	1288	40.7337128	0.31578946	2	CTTTAAAGGACAATTGAGA	TCTCAATTGTCTTTAAAG	0
3162	1906	60.2783049	0.47368422	2	TTGTGCCCTCTCTAGATTC	GAATCTAGAGAGGGCACAA	0
3162	2535	80.170778	0.42105263	2	TTCAGCTGAACAGTAGCAA	TTGCTACTGTTGAGCTGAA	1
1161	4	0.34453058	0.42105263	2	TGGATTGCACTTAGACTTG	CAAGTCTAAGTCGAATCCA	0
1161	266	22.9112834	0.42105263	1	GATCTTGACCAATGGCTAA	TTAGCCATTGGTCAAGATC	0
1161	478	41.171404	0.31578946	2	TTATAGCTACCTGTTAAAG	CTTTAACAGGTAGCTATAA	0
1161	703	60.5512489	0.31578946	2	TATCAAAGTAGAGTTCTTC	GAAGAACTCTACTTTGATA	1
1161	1242	106.976744	0.36842105	2	ATAGGACATTGTGTCAGAT	ATCTGACACAATGCCTAT	0
1917	504	26.2910798	0.47368422	2	TCTACGAGTGGATGGTCAA	TTGACCATCCACTCGTAGA	1
1917	724	37.7673448	0.31578946	1	CAACAGTAAATTTGCTAAG	CTTAGCAAATTTACTGTTG	0
1917	1007	52.5299948	0.42105263	2	AAGATGGCCTCTACTTTAC	GTAAGTAGAGGCCATCTT	0
1917	1263	65.8841941	0.36842105	2	TACAAACACTTCAGGACAA	TTGTCCTGAAGTGTTTGTA	1
1917	1940	101.199791	0.31578946	2	AAAGTACTTCAGATTGTCT	AGACAATCTGAAGTACTTT	0
1971	712	36.123795	0.36842105	2	CAATAGCAACAAGTATAACC	GGTATACTTGTGCTATTG	0
1971	949	48.1481481	0.47368422	2	TGAAGTCCAGGACGATGAT	ATCATCGTCTGGACTTCA	2
1971	1332	67.5799087	0.42105263	2	TGTCACACTATGGTAACCA	TGGTTACCATAGTGTGACA	0
1971	1791	90.8675799	0.47368422	2	TGTTCAATGGGAGCTTGGA	TCCAAGCTCCCATTGAACA	0
1971	2011	102.029427	0.42105263	2	AACTGACACAAGACCTACA	TGTAGGTCTTGTGTCAGTT	0
1455	242	16.6323024	0.31578946	2	AATCAGTCATATGCAGAAT	ATTCTGCATATGACTGATT	1
1455	717	49.2783505	0.47368422	2	GTTCAAATGCCAGCAGTGT	ACACTGCTGGCATTGAAAC	0

1455	1324	90.9965636	0.47368422	2	AGACAGAATGCCTCAGGAT	ATCCTGAGGCATTCTGTCT	0
1455	1395	95.8762887	0.47368422	2	TCAGTGACCTCATGGATGA	TCATCCATGAGGTCACTGA	0
1455	1742	119.725086	0.42105263	2	CTTAGGCTTTGTAGCAAGA	TCTTGCTACAAAGCCTAAG	0
1401	310	22.1270521	0.36842105	2	CATCAAAGTGATTGGCAAT	ATTGCCAATCACTTTGATG	1
1401	585	41.7558887	0.47368422	2	AGTTGACCATCCCTATCCT	AGGATAGGGATGGTCAACT	0
1401	831	59.3147752	0.42105263	2	CTGATTACACCTCATCCAT	ATGGATGAGGTGTAATCAG	0
1401	1263	90.1498929	0.47368422	2	TTCTCATCCCTCCTCACTT	AAGTGAGGAGGGATGAGAA	4
1401	1502	107.209136	0.47368422	2	CTAGAGGGCAGAGGTAAT	ATTTACCTCTGCCCTCTAG	1
1251	24	1.91846523	0.36842105	2	TGAAAGTTAGCAGAGACAA	TTGTCTCTGCTAACTTTCA	0
1251	252	20.1438849	0.36842105	2	GAAAGCTAGATCACTGTAA	TTACAGTGATCTAGCTTTC	0
1251	585	46.7625899	0.31578946	2	ATGTTTCGTATATCTGTTC	GAACAGATATACGAAACAT	0
1251	784	62.6698641	0.36842105	2	GCAAATCAGAGAAATGAAC	GTTCAATTTCTCTGATTTGC	0
1251	1279	102.238209	0.42105263	1	AAACCACCAGTTACTTGAG	CTCAAGTAACTGGTGGTTT	0
3444	66	1.91637631	0.42105263	2	TGCTTGTAACACCTTGGT	ACCAAGGTGTTTACAAGCA	0
3444	698	20.2671312	0.36842105	2	GAAACTCATGATGTTGTGA	TCACAACATCATGAGTTTC	1
3444	1378	40.0116144	0.36842105	1	AGAAGAAGCTGCAATATCT	AGATATTGCAGCTTCTTCT	1
3444	2143	62.224158	0.36842105	2	TAATGCTGCCATGAAAGAT	ATCTTTCATGGCAGCATT	0
3444	2803	81.387921	0.42105263	1	AAGGATAACCCAGGTGTTT	AAACACCTGGGTATCCTT	1
5373	48	0.89335567	0.36842105	2	AACAGACGGAGTTTATCAT	ATGATAAACTCCGTCTGTT	0
5373	1371	25.5164712	0.42105263	2	TCAACAGGCAGTTCTATGA	TCATAGAACTGCCTGTTGA	0
5373	2261	42.0807742	0.31578946	2	GCATTAATCTCTTACCATA	TATGGTAAGAGATTAATGC	0
5373	4512	83.9754327	0.42105263	2	ATGAGTCACAGTCCTTTGA	TCAAAGGACTGTGACTCAT	0
5373	5453	101.488926	0.47368422	2	GACATAGAGGCACAGATTG	CAATCTGTGCCTCTATGTC	2
7599	85	1.11856823	0.47368422	2	CTATGTCACCATGGAACTC	GAGTTCATGGTGACATAG	0
7599	1528	20.1079089	0.42105263	2	GATTCCACAGCTAAAGAAG	CTTCTTTAGCTGTGGAATC	2
7599	3043	40.0447427	0.42105263	2	TGAAATAGTCACCCCTCATG	CATGAGGGTGACTATTTCA	0
7599	4750	62.5082248	0.36842105	2	GGTTATCCAGTACAAACTT	AAGTTTGTACTGGATAACC	0
7599	7649	100.657981	0.36842105	2	GTAATGCTTCCACTAAAC	GTTTAGTGAAGCATTTAC	0
2157	130	6.0268892	0.47368422	2	TTTCGAGCTCCTCAAGGTT	AACCTTGAGGAGCTCGAAA	1
2157	495	22.9485396	0.36842105	2	TCATTTACAGAGACCTCAA	TTGAGGTCTCTGTAAATGA	1
2157	901	41.7709782	0.42105263	2	TGTCTTCTACTCCACCATT	AATGGTGGAGTAGAAGACA	1
2157	1321	61.2424664	0.36842105	2	AGAGATTGAGATTCTTCTG	CAGAAGAATCTCAATCTCT	2
2157	2401	111.312007	0.42105263	1	AAATGGCATCAACCACCAT	ATGGTGGTTGATGCCATTT	0
2172	16	0.73664825	0.36842105	2	GAATGGACAGCAAATTATG	CATAATTTGCTGTCCATTC	0
2172	446	20.53407	0.31578946	2	GAAGAAGATGTCAAATTCT	AGAATTTGACATCTTCTTC	1
2172	932	42.9097606	0.36842105	2	ACGATAGACTGGAATAAAC	GTTTATTCCAGTCTATCGT	0



2172	1312	60.4051565	0.47368422	1	AAGCAAGAGAGACCCAACA	TGTTGGGTCTCTTTGCTT	1
2172	2187	100.690608	0.36842105	2	TATTTGGATCCATGGTGTA	TACACCATGGATCCAAATA	0
699	7	1.00143062	0.42105263	2	TGAACGCAAACCTTCGTA	AGTACGAAGTTTGCCTTCA	0
699	16	2.28898426	0.36842105	1	ACTTCGTA	CTCATAGAAAGTACGAAGT	0 manually
699	24	3.43347639	0.36842105	2	CTTTCTATGAGAAGCGTAT	ATACGCTTCTCATAGAAAG	0 manually
699	230	32.9041488	0.42105263	2	AAATCAGTTCGTGGTTGCA	TGCAACCACGAACTGATTT	0
699	262	37.4821173	0.47368422	1	TCTGAGCGTTCTCAACTTG	CAAGTTGAGAACGCTCAGA	1 manually
306	102	33.3333333	0.36842105	2	TCATCTATGACCGGAAATT	AATTTCCGGTCATAGATGA	0
306	105	34.3137255	0.42105263	2	TCTATGACCGGAAATTCCT	AGGAATTTCCGGTCATAGA	0
306	277	90.5228758	0.42105263	2	AGAGTCACAGTTTGAGATG	CATCTCAA	1
306	579	189.215686	0.47368422	2	CAAGAACGAACCTTCCTT	AAGGAAGGGTTCGTTCTTG	0
2670	103	3.8576779	0.47368422	2	CAAGAAGATGGTGGAGAAG	CTTCTCCACCATCTTCTTG	7
2670	536	20.0749064	0.42105263	1	AAGACAATAGTCCCTTGA	TCCAAGGGACTATTGTCTT	0
2670	1111	41.6104869	0.31578946	2	TAAGGATGTAAAGATTGAG	CTCAATCTTTACATCCTTA	3
2670	1603	60.0374532	0.47368422	2	TTCTGTTGGAGCAGAATCC	GGATTCTGCTCCAACAGAA	1
2670	2792	104.569288	0.42105263	2	TATCACATCAGTGGTTCCA	TGGAACCACTGATGTGATA	0
2262	28	1.23784262	0.42105263	2	TGCTATTCAGGATGCAGTT	AACTGCATCCTGAATAGCA	1
2262	513	22.6790451	0.36842105	2	AACTATCGTACCATGGAA	TTCCATGGTACGATAGTTT	0
2262	960	42.4403183	0.31578946	2	ATCCTGATTTAACTGGATT	AATCCAGTTAAATCAGGAT	1
2262	1369	60.5216622	0.47368422	2	GA	TGATGTGACTGGT	1
2262	2277	100.66313	0.31578946	2	CATCTTAATGGTCAGAATT	AATTCTGACCATTAAGATG	3
1245	14	1.12449799	0.36842105	2	ATTCTCATCGCTTTTATGA	TCATGAAAGCGATGAGAAT	0
1245	278	22.3293173	0.42105263	2	AAGGTTCTTCTAGCAAGAC	GTCTTGCTAGAAGAACCTT	0
1245	593	47.6305221	0.36842105	2	CTGAACATCGTTTATAGAG	CTCTATAAACGATGTTTACAG	0
1245	859	68.9959839	0.36842105	2	AATGTACGACAACATTCTG	CAGAATGTTGTCGTACATT	0
1245	1276	102.48996	0.36842105	2	TGTGTGTTTCCGAATGTTT	AAACATTCGAAACACACA	0
4098	60	1.46412884	0.47368422	2	TGGATATCCGGAACAACCT	AGGTTGTTCCGGATATCCA	0
4098	853	20.8150317	0.42105263	2	CCAATACGTCATTCACAAC	GTTGTGAATGACGTATTGG	0
4098	1711	41.7520742	0.42105263	2	GTATGCCATCTTTGTGAAG	CTTCACAAAGATGGCATA	1
4098	2766	67.4963397	0.42105263	2	CCTATTTCTACGTGACAGA	TCTGTACGTAGAAATAGG	0
4098	4205	102.61103	0.42105263	2	GTTCAGAGATCGTTCCTAT	ATAGGAACGATCTCTGAAC	0
3165	32	1.01105845	0.36842105	2	GATAATGTGGTGAATTGCT	AGCAATTCACCACATTATC	0
3165	678	21.4218009	0.31578946	2	CCAAATTAATCAGCACATT	AATGTGCTGATTAATTTGG	0
3165	1272	40.1895735	0.36842105	2	GAGAATTCATGAAGGATAC	GTATCCTTCATGAATTCTC	0
3165	1914	60.4739336	0.36842105	1	AGTACATGTTACTCCCTAA	TTAGGGAGTAACATGTA	0
3165	3165	100	0.31578946	1	ATCCAATTCATGCTGTTT	AAACAGCATGAATTTGGAT	0

1281	22	1.71740827	0.36842105	2	CATTATCTCTACGGTAGAA	TTCTACCGTAGAGATAATG	0
1281	257	20.0624512	0.36842105	2	GCTTACTTTCTTCTGTCTA	TAGACAGAAGAAAGTAAGC	2
1281	531	41.4519906	0.36842105	2	GGATTAACCTATGGAACCTT	AAGTTCCATAGGTTAATCC	0
1281	784	61.2021858	0.31578946	2	AATTATCTCTTCGATTTTCG	CGAAATCGAAGAGATAATT	0
1281	1302	101.639344	0.31578946	2	ATCTCACATACTGAATACT	AGTATTCAGTATGTGAGAT	0
3516	90	2.55972696	0.36842105	2	ATTGCGTTTACACTTACAG	CTGTAAGTGAAACGCAAT	0
3516	720	20.4778157	0.47368422	2	TCAACATGGTGTCCAAGCT	AGCTTGGACACCATGTTGA	1
3516	1458	41.4675768	0.42105263	2	TCTGTAAGTGTCCAAGCT	TTCACGTTGTCAGTACAGA	0
3516	2136	60.7508532	0.42105263	2	TTGAGTTTCTCAGGTGCTA	TAGCACCTGAGAACTCAA	0
3516	3830	108.930603	0.42105263	2	TTTGAGGGTGGAGATATAG	CTATATCTCCACCCTCAA	0