sgRNA	Gene	CP	CL
CTACAAAGACCACGTCACTG	ABTB1	742	763
GGGCTCGGAAGTAGTCACTG	ABTB1	591	618
TGTAATCGCGTAGAGCCCGG	ABTB1	865	917
TGTTGAAGCCGTCAGGACAA	ABTB1	947	958
AGACTCATCTTGTTGCATCA	AHR	873	807
ATCGCAAACAAAGCCAACTG	AHR	661	744
CTTACTTCGGATATGGGACT	AHR	1033	1089
TTATAACAGACTACTGTCTG	AHR	681	656
AGTTCGAAGACTCCGGCAGT	AIRE	577	658
CCACCTGAAACTTGTCCTCG	AIRE	729	883
CCCCGCTCACCGTTCCCGAG	AIRE	1125	1201
GTGGCGGTACCAAAGCCTTG	AIRE	1512	1667
CCATAATATCTATATTACGG	AMBRA1	458	548
GCTGCTCTGGACTGTACTGA	AMBRA1	1423	1656
GGAGCTGGGGACCTGCCAAG	AMBRA1	497	603
GGATGATCCAGTATCTCTCA	AMBRA1	981	986
ACAGGGACAGGACTCGACCG	AMFR	452	481
CCTCAACCACGAAGGGACGT	AMFR	1288	1060
GCACAAGAACTATCTACGTG	AMFR	1090	1151
TGCCGACAATAATCGTGTCA	AMFR	2116	1977
AGGAATAGTGATCCTAACCA	ANAPC1	601	527
GTCCCAGCTCCAGTTACGGT	ANAPC1	1787	2012
GTTGTCTGGATGACTAATGT	ANAPC1	1194	1230
TCTGGAAAGGTGAAGTCACA	ANAPC1	1282	1233
AGCAAGATCTCAGTCAGAGT	ANAPC10	521	520
GATGTTCACTAAATGAGGCT	ANAPC10	1193	1212
GGAACATGAATCCAGCCACT	ANAPC10	1463	1627
TGGTGCTGACCCCAAGCAGT	ANAPC10	697	720
ACCAGCGGGCAGTCGTCGCC	ANAPC11	739	810
GAGCACTGGCCCCACACCAG	ANAPC11	950	1135
GATTAAGTGCTGGAACGGCG	ANAPC11	904	985
GTGGCCAACGATGAGAACTG	ANAPC11	1383	1195
CCTGAACCTGAACAAGACAA	ANAPC13	1037	915
GATGTCGCAATACCACTGGT	ANAPC13	540	526
GGTATTGCGACATCCTCATA	ANAPC13	970	1038
GTGAGGTTCAGAGAGATGGA	ANAPC13	739	773
AGCCTATCCGCCGCTACCTG	ANAPC2	1039	1156
CTGACAGTGGATCGAGCGGG	ANAPC2	802	922
GAAGTCCACACTATGTTGCG	ANAPC2	1020	998
GGAGCCGGTAGTACCGGCGA	ANAPC2	363	509
ACATACTACCTTATTCAGCT	ANAPC4	1394	1253
CCTGCAGCATCTAGTCCAAG	ANAPC4	1148	1202
GTCACAGAAGTCTCTACCAA	ANAPC4	410	536
GTGTCACCCCCTAACACAGA	ANAPC4	843	1006
AAAAGCTCTCTGTTGAACAA	ANAPC5	561	728
AAACTTACTAGTGACCGAAG	ANAPC5	649	667
CCACCTCGCAGAGCTACACG	ANAPC5	702	661
GCTGAAAGAAAGCTTACTGT	ANAPC5	693	741
GCTGGCAAACCTGTACAAGA	ANAPC7	157	226
TACTTAAGGGAGCAGCACTT	ANAPC7	1173	1123
TCATACCCAGAAACCACCCA	ANAPC7	836	891
TGAATGTGATAGACCACGTG	ANAPC7	1488	1292
GGGAGTTAGTGAAGCCTACG	ANKIB1	692	747
GTCCACAGGGCATATCCACA	ANKIB1	1392	1512
TGAAGTCATTCAACACGTGG	ANKIB1	923	968
TGCTGCATTAGACAAACGAG	ANKIB1	1089	1100
ACTATTTATGACTACGTGCG	AREL1	1215	1210
CATGCCTTGTTGGAATCGGT	AREL1	1095	1114
GGATTATCATACTCATCTCG	AREL1	536	524
TGATGGCATTCAACCTCCTG	AREL1	801	835
AAGATATCACAACCATGAGC	ARIH1	1458	1714
GGAGGAGGATTACCGCTACG	ARIH1	550	663
TCACTTAACAGCTTTAACTG	ARIH1	1087	1174
TTCAAGTAGCAGATCTGACA	ARIH1	2138	2055
AAGTTTCAGAGATATTGGAC	ARIH2	478	514
CCTGTACCCGAATAACCATG	ARIH2	616	666
GGACATAGAGGACTATTACG	ARIH2	568	616
GTTCTCGTCAAGGACGGCGT	ARIH2	1270	1274
AGATGTCTAACGATAAGGAG	ARNT	1022	1020
CAAGCTAACCATCTTACGCA	ARNT	1083	1059
TGGATTGTGTTGGAGAGTGT	ARNT	2233	2159
TGGGGAACCTCACTTCGTGG	ARNT	1236	1411
AGACAGACTTCTCGTTGATG	ASB1	1506	1466
AGGCTGCGCTGATGTACAAG	ASB1	860	845
CCATGATGCAGCTTACGTCG	ASB1	937	907
GCGAGAGGCGTGGTAGACAG	ASB1	1289	1328
CACCAGCAGCACATGAACAC	ASB10	1713	1630
CTGGTCTCTGACATACGAAG	ASB10	1122	1164
GAGAGTGGATGGTCGGTCCG	ASB10	1046	1195
GGCCAGTACTGGAGTCCGCG	ASB10	570	617
ACACCCGGTTAATTGTCACA	ASB11	958	1177
ATAGCAGAAGAGATCTATGG	ASB11	829	845
CTGCAGCAAGCATTGAAGAG	ASB11	634	697
TCTTCACACAGTCTACCCTC	ASB11	1154	1133
AGACTGCGGCCAAATAGAGG	ASB12	870	1050
CAAAAGCTGGTCCAAAGTAT	ASB12	1020	1182
TGGTAGTTTAGCTTTGACGT	ASB12	1339	1493
TTGTTGTAGATGCTACCACC	ASB12	798	807

AAGCTTTGCCGCATTCACGT	ASB13	1672	1631
CTGCAACAGCTGATCGAGAG	ASB13	1097	1323
GAGGCTTCTTATTGACGTCG	ASB13	407	489
GTGGATGCTCGCAACATCGA	ASB13	1625	1722
AACATGCACCTAAGGATGAG	ASB14	1364	1258
AATACAAAGCTGACTTCCTG	ASB14	850	917
ATCTGCGTTGTGCCAACGAG	ASB14	2025	1906
ATGGAAATGTTACTGCGGAA	ASB14	1122	1158
CCCAGAGCTATGACGATGAG	ASB15	1020	1112
CTGCAACAAGTAGACAGTTG	ASB15	1186	1045
GTGCTGTTTGAGGCAGCAGG	ASB15	910	920
TACACCGAGCTGCCTATGAG	ASB15	979	1046
AGAGGCCGCCAACATGATTG	ASB16	321	397
CAAGGCTAATGTGCTGACTG	ASB16	756	733
GCTCGACACCTGATCCGGCA	ASB16	637	666
GGGGACTTGACGGGCACCTG	ASB16	678	909
ATTGTTAAGACAATGTTGAT	ASB17	1238	1187
CACATATTTCAGTGAAGTCG	ASB17	868	936
TCAAGACAGAAGTTGTAACC	ASB17	616	684
TGACCCAAAAACTGTAGGGA	ASB17	486	635
CCGAGGTCCTTACCCGAGCG	ASB18	537	649
CTGCACTGAAATCACGCCTG	ASB18	433	406
GGTACCTGATAGTCCAAACG	ASB18	612	671
GGTGTCGCACGCAGGCGGTG	ASB18	1227	1149
AGGTGCTGACATCAACACGC	ASB2	1716	1483
CGACGCCAACAAGACCAACA	ASB2	1260	1290
GAATCTCGCAGAGCCCAACA	ASB2	1120	1368
GTGGAATCCAAGAACGCCTA	ASB2	726	889
CAAGGGTGTAGCTTTGTCCA	ASB3	955	942
TATCAGCAACATCGACACTT	ASB3	1849	1788
TGTGTGCATGGCTTTCCAAA	ASB3	1146	1224
TTAAGGCTGTTGCTTCAACA	ASB3	1423	1427
GATCTTAACACAATCCACAT	ASB4	614	555
GCGCTAAAGTCCAATGACTT	ASB4	346	464
TACAGTTGATTGTAGCATTG	ASB4	1262	1258
TTGGCACAGAGAATGGAACT	ASB4	2028	2128
TAGTGGTGATCGATCTGCCC	ASB5	318	281
TCACTATGTAGAAATGACTG	ASB5	1042	977
TCTTCCATCCCCAACGCATG	ASB5	2402	2231
TGGGAGCATGCGTTGAATAA	ASB5	1374	1432
ATGCCGCTGACAAGCATGGT	ASB6	1637	1511
CCCATGCCGCAAGAGAACGT	ASB6	1162	1103
CCGGTCCCTCCGATTAACGT	ASB6	1238	1352
GCCCAGTTATGTCGCCAGCG	ASB6	641	684
AGAGGGGCAGACACAAACTT	ASB7	1163	1259
AGCTCGCCATTATCCGAGAG	ASB7	559	618
ATTCGCATCTCGGCCATTCG	ASB7	786	701
CTAACATCAAGCGTGCAATG	ASB7	1233	1047
AATTGTTCGGATTAAGCGCT	ASB8	1014	1113
CAATGATACACCGCTCAGCT	ASB8	949	1018
CCTTCTGGATTATGGCGCAG	ASB8	730	865
TGTTCGGTTATACCCATCCA	ASB8	453	426
AATAGAGTGGAGTGCCCAGG	ASB9	601	696
ATGCATGAAGCTGCAATCCA	ASB9	1079	980
CTGACACAAGCATTAAACAG	ASB9	564	602
GAGAGTTGACACACTCCACG	ASB9	704	716
CATCTAGGAGCATCTACCCA	ATG10	622	637
CTTGCCCTAAAGTAAAGTAC	ATG10	674	693
GAAACACAGGACTGTTCTGA	ATG10	543	640
TGAATTCTGCACAATAACGT	ATG10	1157	1082
CATACTTACGAAGACACACA	ATG16L1	821	784
CTTCCCAAAGCTTAACCCTG	ATG16L1	730	812
GAATAACCAAATGCAGCGGA	ATG16L1	696	722
TGCAAGCCGAATCTGGACTG	ATG16L1	739	777
AAAGCCAAAACTGATGCTGG	ATG3	563	573
GTAGATACATATCACAACAC	ATG3	927	802
TAGTCCACCACTGTCCAACA	ATG3	1262	1353
TGTTTGCACCGCTTATAGCA	ATG3	990	1053
AGGAATGTTAGACGAAGATG	ATXN3	491	441
CTGTCATCCATATTTCCAGA	ATXN3	974	1042
TCAACAGTCCAGAGTATCAG	ATXN3	740	782
TGCCTGAATAACTTATTGCA	ATXN3	800	872
AATCCTGAATATCAGAAGCT	ATXN3L	449	496
ATCGAGCCAAGAAATTTGCA	ATXN3L	989	1115
TGGAACATCAGACCAAGATG	ATXN3L	1371	1326
TGTCTGAACAATCTATTGCA	ATXN3L	1398	1439
CTTCGAATGACAGTAAGACA	AURKA	319	357
TGAACCTGAAAACTCACCGA	AURKA	610	654
TGAGTCACGAGAACACGTTT	AURKA	2065	1798
TGCTTGCAAAGGAATGCGCT	AURKA	1460	1398
AACTGACAGAGTCCGTACTG	BACH1	823	915
CCTGGCCTACGATTCTTGAG	BACH1	837	874
CTAATCCTGATACCTAACCA	BACH1	1273	1290
GAAATCCGACTTGGGCACCA	BACH1	755	911
CCCAGAATAAGAATGCACCG	BACH2	908	1052
CTCTTCCTATTCCTACGCGG	BACH2	473	537
GAATTATGGACAGCCCCACG	BACH2	428	487
GTTCAGCATAACGAAAAGTG	BACH2	650	642
AAGGTCTACCCCATTGACCA	BAP1	1184	1147
CACGGACGTATCATCCACCA	BAP1	1484	1438

CTGTCCATCAAGACTAGCAG	BAP1	956	980
GAACCGTCAGACAGTACTAG	BAP1	1325	1418
ACTTTACGTTTGCATGAAGG	BARD1	1100	1081
ATGTCCAGTGTGTTACACCC	BARD1	1140	1061
GACTGGAAAGTCTATTGTGA	BARD1	813	907
GCTGTGAAAAGAAATCATAG	BARD1	307	368
CACTGCACCAGCAGTCCTAG	BCL6B	665	660
CCCACATTTGAACTGCACAG	BCL6B	1044	1190
CCCGGGGGTCCCGAAGCGAG	BCL6B	314	401
CCTCTGGATCACCCTCTGAA	BCL6B	543	655
AAGATGCCCACCATAAAGCA	BFAR	494	609
ATTCCTTTAGCTCCTAACAC	BFAR	1514	1450
GGCTGTGGCCAAATGGACGG	BFAR	934	1004
TGACACGTTCTAGCTCCATG	BFAR	1502	1274
ATATTCAACTTTCCCCGCCG	BIRC2	767	937
ATGCTATGTCAGAACACCGG	BIRC2	996	1120
CAAGCTACTATGTTCCAAGG	BIRC2	1026	1158
TTCTGAATAAAGCTACAGCT	BIRC2	601	694
ACCCGGAAGTAATGAGTGTG	BIRC3	1303	1271
AGGATTAACTAGAACACTAG	BIRC3	1227	1236
CATGGGTTCAACATGCCAAG	BIRC3	556	570
TTTCGTTATTCATTGCACAG	BIRC3	979	840
AACAGAGAGTATCCAACACA	BIRC6	585	563
GAGGCCAAGTCTCCACAAGT	BIRC6	924	996
GCCCACCTATAGCCTACATG	BIRC6	741	885
TTGCACTCAAGGATTCAACA	BIRC6	1235	1135
AGCCGGTGATGGTCCCACGC	BIRC7	1653	1534
CCAGGATCTGCCCATCCACG	BIRC7	529	520
CCTGGACGGAGCATGCCAAG	BIRC7	1696	1580
GGTGGCACCTCAGCAGTCAG	BIRC7	674	551
CATTTAACCCGTTCACTTGA	BIRC8	1118	1153
GAGCAACTATAAAACGCTTG	BIRC8	869	1091
GGACGTTAAGAAAATAATGG	BIRC8	625	753
TCTAGCAGATATTTGCAACC	BIRC8	698	878
AATGGCTCTAATGAAGATAG	BMI1	710	762
CTAGATTGATGTCATGTATG	BMI1	1084	1109
GTGGTCTGGTCTTGTGAACT	BMI1	692	741
TTGTATACAAATTAGTTCCA	BMI1	434	507
GCGGCCACATAGGATGTGGA	BRAP	739	996
TCACATCTGTCATTTCTCGA	BRAP	1047	1145
TGTGGTTACATAACGTTGTG	BRAP	1526	1296
TTGGTGTACATAGGCTGATG	BRAP	1767	1722
AGAAACCTACAACTCATGGA	BRCA1	691	787
AGGAAACATGTAATGATAGG	BRCA1	601	630
GCAGCATTTGAAAACCCCAA	BRCA1	541	716
GGCTCAGGGTTACCGAAGAG	BRCA1	307	383
ACCTTGACAGACACACAGGT	BRCC3	1618	1644
GAGCGTGGTTGAGACAAACG	BRCC3	1002	1157
GCTCTGGAGAAATTTCTACT	BRCC3	397	521
TCTAGTTGAACGATGATACA	BRCC3	1657	1489
ACAAACCTAAATATGCCTAG	BRWD1	1011	923
AGATATTATAGATACCCCAA	BRWD1	435	523
GGTATGTACACAAATCAACA	BRWD1	737	775
TTCCTAGTGGAGATACATCG	BRWD1	1234	1301
CAGCTCGATCTCGGCCGACG	BTBD1	1323	1362
CGGTCAATGTATTCAACTCG	BTBD1	680	711
GTTCCCACTGATGACAATTG	BTBD1	942	1040
TGGATGCAATAAGTGCAGAA	BTBD1	828	922
ACGAGTTTATGTGCCCATGT	BTRC	1349	1188
AGTGCAGAACTGCTTCACAA	BTRC	1329	1476
TAAAATTATACAAGACATTG	BTRC	754	774
TGCGATGCCTGTATAACCCA	BTRC	1701	1561
AAAACATAGAAAAACGTGTG	CADPS2	691	667
ACAAGCAGCCCAGATCAGAA	CADPS2	643	753
AGCTCTACGTCTTCGTCGTG	CADPS2	1425	1363
GGTGAATGACAGTACCACGT	CADPS2	1865	1698
CCTGTCGAAAGCTCTTCCAA	CBL	565	647
CTATCTTGTCAAGATATGAG	CBL	614	728
GGTGGAAGATCTCGAAGTGT	CBL	1042	1057
GTAGATCCGTTTGATCCTAG	CBL	903	1005
CTTCATCTCTTGGATCAAAG	CBLB	1066	1188
TGAATTAGATCCAGGCGAGG	CBLB	757	831
TGTGGGATGTCGACTCCTAG	CBLB	1547	1528
TTCCGCAAAATAGAGCCCCA	CBLB	1109	1250
GAAGACGTCGAACTCGAAGA	CBLC	600	602
GAGAGGTGGCCCATTCTCGG	CBLC	472	648
GGCCCAGCTGTACTCGCCTG	CBLC	1538	1702
GTCCACAGTACTTTCCCCCG	CBLC	866	959
CGAATTGAGCAGTGTACACG	CBLL1	949	877
GGCTGATTATAGTGCTCATG	CBLL1	723	792
GTGGCATTATAAAACGCTCA	CBLL1	649	803
GTTTCCTGACTGACCGATCG	CBLL1	368	377
CCTTGCAAGATATAACACGT	CBX4	1464	1323
CGGTCAGGACATTGGAACGA	CBX4	445	357
GGGCTGCGGATCGCTAACCC	CBX4	727	770
TAAAAGTCCTGTCGGCAGGA	CBX4	529	638
AGGCGGCCAAAGATAACAGG	CCIN	377	444
AGTCGTTACAGTGAACTCGA	CCIN	1030	1081
CAATTGGGTGTACTTCCGGA	CCIN	361	422
GTGTGGAAGACAAGCCCGAT	CCIN	711	769

ACTGCGACCAGAGATCGTGT	CCNB1IP1	1489	1387
ATTGACCTCTATGAAAGGGG	CCNB1IP1	813	903
CAAACTCTCTGGCTATGCAT	CCNB1IP1	1314	1287
TCAAGAATACAATTTCAGCA	CCNB1IP1	805	929
AGGGACTCAATGACACAATG	CCNF	1212	1293
CTTCATAGGAGAATCCGGTG	CCNF	746	864
GCAGGGACTTACAGCTCGGA	CCNF	851	971
GGACAACACTTACAAGTACG	CCNF	1371	1230
AAATACTTGAAGGACGAAAG	CDC16	471	540
ACGACATGCTTCATACAACT	CDC16	747	642
TCATTACACAGCTTGCTAAG	CDC16	1533	1420
TGCTCTAGATAACCGAACCC	CDC16	754	775
CAGTCTGTTCTGATAACCTG	CDC20	1640	1744
GGCCAAATGTCGTCCATCTG	CDC20	1080	1048
TCCCAGAACTCCAATCCACA	CDC20	963	1019
TGGGGAATATATATCCTCTG	CDC20	605	629
ACTAATGGGACATGAGTACA	CDC23	1182	1213
GATATTTATCAATCTCACAG	CDC23	734	916
GGCGCTTAGAGAATTGAGAG	CDC23	294	364
GTTGCCTATCACAATATCAG	CDC23	497	577
GAACATTCGAAAGGACCTGG	CDC26	890	947
TCAGACCCGTAAGAAACAGA	CDC26	472	467
TGTCATCAAGCTTTAGCTCT	CDC26	1525	1674
TTAGCAGTGATCCCAAGAGC	CDC26	609	671
ATGATTCAAAGGGAGACCAG	CDC27	787	867
CTGTTATTACCGCTCAGGAA	CDC27	808	959
GATGGCACATCAATTACAGG	CDC27	1068	1170
TGAATCAATATAAGACACTG	CDC27	850	940
CATCTTGGTCAGGAACCGAA	CDC34	839	909
CCCAACACCTACTACGAGGG	CDC34	1006	1015
CGAGGGCGATCTATACAACT	CDC34	1017	976
TCAGGAGGGAGATCACACTC	CDC34	1164	1060
ACACCTATGAAGACCAGCAG	CDCA3	922	998
ACAGATAACTGGGTACCCAG	CDCA3	532	730
ATACCAAGAGTAGGAGAGCG	CDCA3	639	752
TGCCAGCACTAGGTGAACGG	CDCA3	1269	1209
AACAGTGATTAACAAGCTGA	CHFR	683	641
ACGGTTTGGGCATTTCTACG	CHFR	1223	1367
AGCGGGAGTGGACCATCGGG	CHFR	781	861
GGATGAGGTATGCTTCCACG	CHFR	771	747
ACAGTGTGTAACCACTCTCG	CIAO1	1261	1207
AGGGCCATGAATCCACTGTG	CIAO1	1581	1639
GACCGGAGAATCCGCATCTG	CIAO1	1132	1420
GGCCAGGTAATTACCGCAGG	CIAO1	384	514
AAGGCTGACCACATCCGGAA	CISH	707	879
ACAAGCAGTTGGAGTCCAGA	CISH	1121	1358
CTCACCAGATTCCCGAAGGT	CISH	690	862
CTGTCAGTGAAAACCACTCG	CISH	904	985
ATAAACCTACAACAAAGACG	CNOT4	1022	1099
CATGTATCTTCATGAATTGG	CNOT4	1376	1404
GTTATATACCTGATGTGAAG	CNOT4	735	724
GTTCATCCAATCACAGTGCA	CNOT4	620	535
CCAACAAGAACAATATCCGC	COPS5	797	854
CCTCCTCACTCCTTAGTCCA	COPS5	1506	1631
GCCTTGAAAATGCAATCGGG	COPS5	466	576
GTGATGCATGCCAGATCGGG	COPS5	575	633
AGCCACATCACCAACCTCAA	CORO7	1725	1654
AGGACGCCAGGATCCGACTG	CORO7	973	1141
GCAGCTGTACTGTTACGAGG	CORO7	858	889
TGTGTCTACTGGATTCAACC	CORO7	951	1006
ACCAATGTTCATATAAATGG	CRBN	708	823
CTGACTGTGTTCTTAGCTCA	CRBN	1923	1914
TGAAGAGGTAATGTCTGTCC	CRBN	1593	1514
TTACATACTGTATGTGATGT	CRBN	2054	1815
ATTGCCCCCCTCCAAACACG	CREBBP	1373	1322
CTTAGCCCACTGATGAACGA	CREBBP	935	928
TAATTAATCAGGCTTCACAA	CREBBP	936	959
TGGCAACTGGACGTTCCCCA	CREBBP	1446	1347
GGAAGAAACCTATATCCCAA	CSH1	375	423
GGATAAGGGAACGGTTTGGA	CSH1	1028	1248
TCCGACACCCTCCAACATGG	CSH1	1561	1522
TGTTGGCGAACATACTCCTG	CSH1	1108	1024
CACCAGTCAAACCAAGCACG	CUL1	852	928
CTTTATACACTGTTAACGTA	CUL1	1307	1403
GTTCGCCGTGAATGTGACGA	CUL1	1435	1269
TCGCTTCATAAACAACAACG	CUL1	574	752
ACTGACTCCACAAATAGTGT	CUL2	1076	942
AGATATCTATGCTTTATGTG	CUL2	1002	1001
CACCACCATAGCCATACTGA	CUL2	408	385
GCTGGTAAACTCATAACCAC	CUL2	659	736
ATAACTTGTACATGCAACCA	CUL3	1519	1505
ATCCAGCGTAAGAATAACAG	CUL3	572	617
GAGCATCTCAAACACAACGA	CUL3	1521	1644
TATCATCAATAAATAATGAG	CUL3	457	427
AGTTCTGCAGCACATAGGTG	CUL4A	858	785
GAAACCACTGATTGCTTGTG	CUL4A	2105	2169
GCTGCCCGACAACTACACGC	CUL4A	1293	1189
TATGCTCACAGCAAAGCATG	CUL4A	1357	1191
AGCATGTGGTACTTACTGGG	CUL4B	1271	1413
CTCTTCAGTAGAGTTCGAGG	CUL4B	698	782

GCTGTTAGCAAAGCTAGAGA	CUL4B	430	511
GCTTCTTCTGTATCGGTACG	CUL4B	892	1181
AGCTTGTTTACATAATCCGC	CUL5	924	930
ATTGGAGTAAGAGAATCCTA	CUL5	828	955
CCATGTATCAAGCATAAGCT	CUL5	1264	1303
GAGGAACATATCATTAGTGC	CUL5	1310	1291
CACTTGCGAACTCAGAACGA	CUL7	1485	1466
CTGAATGAGGGACTTCACGT	CUL7	1122	1070
GAATGCCCTCGAAAGACATG	CUL7	1343	1299
GCATTGATACGCGCATTCGG	CUL7	877	776
AGCATAGTCCTTATGCATCG	CUL9	727	713
CTCGGCCAGTAACAAAAGTG	CUL9	867	881
GAGAGTGGGATATCTGACCC	CUL9	1022	1171
TCATAGAGTTTACAGTAACG	CUL9	720	816
GACTCGGCAACAGAATCTGA	CYLC2	842	1037
TCCACCTCGACAGTACGAGT	CYLC2	1636	1468
TCGGAATCAGAATTAAAACA	CYLC2	571	698
TTCTCAAATACGGGACAACA	CYLC2	1295	1240
AAAGGCCTCCAAATAGACGT	CYLD	966	1074
GGATAACCCTATTGGCAACT	CYLD	440	520
TCACTGACGGGGTGTACCAA	CYLD	988	976
TGAGACTGAATGGTAAAGAG	CYLD	719	741
ATGACCTGACCTGGTGAATG	DAZ2	904	845
GTGACCTGAAATGCTGAATC	DAZ2	1412	1490
TCAGCATTTCAGGTCACCAC	DAZ2	1366	1196
TCTGCTTATCCACATTCACC	DAZ2	1052	1001
AATGCCATTAGCGATACGAG	DCAF1	1012	937
AATGTGGTTCAGTCCAACAA	DCAF1	696	752
ATTGGAAGACCTATTATGCA	DCAF1	1133	1188
TAATTGGTGCCAATCACCCA	DCAF1	1204	1287
ACCATGTAAAGTGCATACTT	DCAF10	1583	1565
ACCCGAACAGCCTAGCGCCA	DCAF10	419	391
GAGGTTGAAGACGGCGCCGT	DCAF10	521	601
GTGTGAAAGAATTTCTTATG	DCAF10	362	475
AGACGCTCCAGCCTACGTCG	DCAF11	107	110
AGAGGGTAAGTTACCTGCGG	DCAF11	764	956
CGCCTAGATTGAGTCCCATG	DCAF11	796	865
TGTGGGATCGACGCACCATG	DCAF11	2186	1966
AGCTACTCTCGAGTGTTGCA	DCAF12	1133	1207
ATGCGAGACACAATGTGTCA	DCAF12	1419	1215
CATCTATCGACTACCTACGC	DCAF12	1222	1150
GTGTGGCACAAAATGCAACA	DCAF12	1517	1664
ACCAAGTTGGACTTACAGAG	DCAF13	559	577
ATATAGTACTGTACGATATG	DCAF13	1894	1719
ATTACATACAATATTAGGAA	DCAF13	523	633
GGTGACCATCCAGCGAAGCA	DCAF13	683	752
CGCAGGGCCTACCTGCCGAG	DCAF15	722	743
TGCTGACGTAGATGTCACGG	DCAF15	818	688
TGTACCTGACCGTATGCGAG	DCAF15	1547	1532
TTGAGGGACACGCACACCCG	DCAF15	859	845
CAGTTTAGCATGATACAACC	DCAF16	1212	1220
CTTGTCAGAATCAGAAAGTG	DCAF16	367	371
TGCCAGGCAAGACTCTCAAG	DCAF16	626	633
TGGCATGATCTCTAGAGAGC	DCAF16	1355	1471
AATCAGTATTCCATGAGACA	DCAF17	1245	1360
ATGCAACAGAAACTTGACTT	DCAF17	1049	1129
GGTGTGACGATGTAGTGCCA	DCAF17	1314	1095
TCACCTATAGCCTATGAGAG	DCAF17	790	989
AAATCGGTCGCTTGCCAAGG	DCAF4	626	749
ACGGAGACTCGTCATCACCG	DCAF4	405	377
GAGTCTCTGCGAGTCCCATG	DCAF4	691	942
TGCATGAACACCTTGAGCGT	DCAF4	1894	1717
GGAGGATAGTACTCTCACTG	DCAF5	931	971
GTACTGGAGACCTCGACGGT	DCAF5	710	841
TCCACCAACACCCACGTGTG	DCAF5	902	851
TGTGCCATAGCAGAACCCGG	DCAF5	564	755
ATGTCACTTGACGAGCAACA	DCAF6	1591	1554
GGGAGCCATTGCAAATCTGA	DCAF6	1000	1140
TCAGGACTTGATGGGACCGT	DCAF6	1055	1070
TGGGCAAATAGCAACAGACG	DCAF6	752	814
CTATGATATTGCATTTAGCC	DCAF7	2027	2167
GCATGTCGTATCAATGCTTG	DCAF7	2153	2010
GCGGTGACTATCTCCGTGTG	DCAF7	1640	1671
TTCATCGCGTAGACTGTCCA	DCAF7	1939	1743
AGGACTCATCAGATGATGAG	DCAF8	1115	1113
CGCACCAGCACAGAAAGTCG	DCAF8	1072	1031
GCTACACTTACGACGCTGGG	DCAF8	1174	1196
TGGTGTGGGATTGGGTACGG	DCAF8	1007	1019
AAAGGCCCAGATACCCAAGA	DCUN1D1	583	798
ACAGTGCGAGTTCTCCAAAC	DCUN1D1	401	429
GTGTAAAAGGATCATTGGAC	DCUN1D1	1077	1110
TTAGTGTGTTGATTATTGCG	DCUN1D1	1245	1280
GAATGAGTGGAGACTAGACG	DCUN1D2	640	739
GAGTGCACGCCATAAACTGG	DCUN1D2	800	881
TCACCTTCGCTAAGAACCCA	DCUN1D2	542	582
TCAGTGTATTGGTCATAGCG	DCUN1D2	685	838
GCAGCACTCGAAATTCTGTG	DCUN1D3	577	593
GCATTGACGGAATCTGTGCA	DCUN1D3	1566	1527
TCAGGCGCTACAAGGATGAG	DCUN1D3	768	820
TTGACGAGGATATCTCCACC	DCUN1D3	856	754

CATTAGGGTCCACTCGATTG	DDB1	1032	1120
CATTGTCGATATGTGCGTGG	DDB1	1947	1606
GCGGCACGTAAAAACCTATG	DDB1	281	319
GGATAGCCATCTGAATTGAG	DDB1	887	838
ACTGCTCACCCCTTTGATGA	DDB2	1339	1456
ATGTAGCCCTCCTGTCAAAG	DDB2	1054	1149
CAAAAAGAAAGTGACGCATG	DDB2	1048	1146
TGGTCACAGGAGACAACGTG	DDB2	1435	1372
ACAGCTGTATTCTGTACGGG	DTL	629	810
AGGTGATAAACTTTCCACGG	DTL	419	522
GAGAATACCTTAGTCTCAGC	DTL	889	974
TGAAGCTGCCTACATATGGA	DTL	905	980
ACGTCGCTCTTGCTCACGGG	DTX1	665	746
GGTTCGAAGATACATGCAGA	DTX1	538	524
GTGCTGAAGGAGGACGCTCG	DTX1	764	829
GTGTGGGAGTGGGAGAACGA	DTX1	616	704
CAGAAGCGGTCCTGTGTGGG	DTX2	812	992
CTCCAGATAGTCACAGACGC	DTX2	1430	1498
CTGAACACCACCAACGCCTG	DTX2	1044	1171
GGGGAGGTCAATAATGTAAG	DTX2	848	966
CAGAAGTCTCGCCATCTATG	DTX3	865	920
GACTGTGTCCAAGCCCGTGT	DTX3	1038	892
GTGCCGGCATTCATTCTGCG	DTX3	639	754
TAGGTAGAGCCCATTTGGAG	DTX3	802	1027
AGAAAAATGGAAGGTCACGA	DTX3L	818	1050
CAGGTCACCTGATCGACTTG	DTX3L	936	914
GGTGATATGCATCAACATGA	DTX3L	1281	1264
TTCTCTCATCAACTGACATG	DTX3L	1116	1060
CGATGATGTAGGGCGCGAGA	DTX4	909	877
GACCCATTTAGGTTCTTCAC	DTX4	1023	1049
TGAAATAAAATCCATCCCAG	DTX4	402	443
TGGAAGTGAGGTCGATCCAG	DTX4	1422	1379
ACTAGGTTAAGAGTAAACAA	DZIP3	515	541
ATGCCTTTCAGATATAATGG	DZIP3	534	561
CACAGCTAGAAGCAGCACTT	DZIP3	942	932
TGCGGTAACTCCTTGTTAGG	DZIP3	1012	1104
AGGTGGTGGGCACATCAAAG	E4F1	1532	1706
CTGAACAAAATCCTCCAAGG	E4F1	369	509
GGCACAGCGCACACACATAG	E4F1	855	752
GGGAAGGTCTCACTGCACTG	E4F1	843	748
AAGAGAATGATCCATACCAC	EED	1033	970
ACGATTATGGAATATCCAGA	EED	970	1246
ATGGCTCGTATTGCTATCAT	EED	1733	1816
TTGTGAATGACATTCATACA	EED	2030	1947
AGCGGCCTCCTGACGAGCAG	ELOB	504	524
CGAACTGAAGCGCATCGTCG	ELOB	1271	1419
CTTGGCGTCCGTGAAGATGG	ELOB	1404	1293
GCTTCACCAGTCAAACAGCA	ELOB	601	590
ACTTTCGATAGCACATGTGA	ELOC	1247	1138
AGGTCCTTCACAGCCACCAT	ELOC	1226	1204
TGGGAATTCAGGAATCTCGG	ELOC	827	924
TTACTTTACTTTAGATGGAG	ELOC	1257	1352
GCTGGAGTTTCAAGACATCC	ENC1	693	838
GGAAGGTCCTATTTCCGGCA	ENC1	566	721
TGAAAGTCTGTCCTCCCAGA	ENC1	900	1061
TGCAAAGTGTACATTACTGG	ENC1	691	750
ATGGTGAACCATAAGGATTG	EP300	2165	2125
CCTGACCCAAGTATGATCCG	EP300	880	807
CTGTAATAAGTGGCATCACG	EP300	1117	1051
GGTACGACTAGGTACAGGCG	EP300	988	955
ACCTGCTACCAAACAGTGCT	ERCC8	1130	1123
GATGTTGAAAGAATCCACGG	ERCC8	522	637
GCCAAGATATAGTCATAACG	ERCC8	786	829
TGTGTAATAAGATTGTCTGC	ERCC8	1449	1476
AAGTCGATATCCCTCAGTAC	F9	922	875
AGGAAAAACAGTCTCAGCAC	F9	1002	1044
CCAAACCAGGTCAATTCCCT	F9	1147	1144
TTTAAATGGCGGCAGTTGCA	F9	802	838
ATAAGGCTTGAGTAGAACTG	FANCL	1093	1130
ATTTACAACTGAAGAATGCA	FANCL	726	757
ATTTACCTGAGGTGTCCAGG	FANCL	815	805
CGAGATGAATCCCTCATACA	FANCL	840	992
AGATGCGACCTAAAGTCATG	FBXL12	591	527
CAGCACGATGCATTCAAGCA	FBXL12	732	679
CCTACCGTGTGACCGAGACA	FBXL12	1343	1175
GGATCCGGTCCCGTACCGGG	FBXL12	618	873
CCGCCTACCACAAGTCGGTG	FBXL14	793	839
CGATGCCCACATCCGAAAGG	FBXL14	1531	1456
CTCTAAAGCACATCTCCCGA	FBXL14	1327	1354
TGCAGCAACATCACCAACAC	FBXL14	1643	1379
CCGCAGCAGCCGGGCCAATG	FBXL15	642	834
CCTCTGCGCCAGGTACACGA	FBXL15	588	595
GGACCCGGTTCAGGACGTGT	FBXL15	1009	1026
TCACGAATGGCTGTCAGACG	FBXL15	1130	1066
AGAAGCTAGAGCGTTTCAAG	FBXL19	711	853
CGCCGTTGTCGGCCCTACGG	FBXL19	678	814
TCACCCTGGTAGGTGAAAGG	FBXL19	784	805
TGCAACGAGATCGTCCACCC	FBXL19	1371	1105
CCTTCATCCGTGATACGCTG	FBXL2	1845	1708
GTTTGTAATAGACACACAGG	FBXL2	763	817

TTCTTGATTAAAGGGTCGAG	FBXL2	688	776
TTGGTGTGATCAGATCACGA	FBXL2	1314	1241
AAGCTTTATGGATTTACCAA	FBXL3	959	1169
GACACTGATCAGCCACACAA	FBXL3	1020	995
GATGTAGTCAGTGAGAATCC	FBXL3	1302	1301
TCCATCTCTCAAAGTACTAG	FBXL3	691	687
AAGTCTGTGCTAATCTACAC	FBXL4	1470	1413
AGTTGTGCTACATGGTGTGA	FBXL4	1816	1659
TGTTTCGAACTTATGGGACA	FBXL4	887	919
TTGGTCAGAGAGACCTACGA	FBXL4	1095	1145
GAACGTTATGAATTAAGCCA	FBXL5	1010	1019
GAAGTGTCAGAACACTCCAC	FBXL5	1013	1007
GTGCAAACAGGCATACTGCT	FBXL5	1834	1703
TACCTCTGGCCCAATGAACA	FBXL5	909	920
AATGCTATTACGGTTGATGC	FBXL6	1560	1420
ATTGGGCATAAGCCACTCCA	FBXL6	1076	1137
GAGCGTCAGCAGTCACACCG	FBXL6	810	896
TGGGACCGGCTGGCGCCGAG	FBXL6	341	428
CAAGGGTGACAGTTTAATGG	FBXL7	1066	1239
CCAGCATGAGACACACGTTG	FBXL7	1598	1370
CTGTTACAATATCTCCAACG	FBXL7	559	597
TGCGTCCGCCTGACCGACGA	FBXL7	1269	1377
GGCTGGAATTTGAGCCATCG	FBXL8	683	755
TCTGGACAACAGTACCCTAG	FBXL8	691	664
TGGCGTGCGACAAACTGGCT	FBXL8	1011	964
TGTGCACGCTGTATGCGGGG	FBXL8	953	950
ATACCCACCTTATACATGAT	FBXO10	1704	1444
GCAGCACACACCTCACAACG	FBXO10	712	825
GCGGTGTATACATAATAGCA	FBXO10	419	517
GGGCCTACAAGTATCTACTA	FBXO10	780	920
AACCACTGTAGGGTTAGCAT	FBXO11	1033	1025
AGAGCCTTCCATAAAAACGA	FBXO11	917	1066
AGTATGAACATCCAAATCCC	FBXO11	1070	1106
ATATATAACAGATCATGCAC	FBXO11	825	681
AAGATGAGATTGCGGCCGAA	FBXO17	783	918
CCTGGCGCGACATAGTGGAC	FBXO17	917	878
GGGCCGCGCACTCTACGCAG	FBXO17	962	1089
TTGGGCCACTCACTCGAAAG	FBXO17	876	946
AAGCAGAGGACAGTACGTCT	FBXO18	1334	1324
CACTGGGAAGACCTCAACGC	FBXO18	1048	983
CCGTGCTTCTCTACGCCATG	FBXO18	1960	1954
GACGGCATCCTGTCTAACTG	FBXO18	1132	1181
ACCCCCTTCTCCTTACTCAA	FBXO2	1085	1220
CCTTCTGCGTAACCCGTGTG	FBXO2	1623	1584
GCACTTGAGCAGCCACAGCG	FBXO2	595	742
GGAAGTAGAACTGCTGCCAG	FBXO2	407	447
AAAAAGCTGGGTTAGAAGCG	FBXO21	463	654
GTGTGTATCCTAAATATGGA	FBXO21	1473	1533
TGAACTTCAGTTGGTCGTAA	FBXO21	1423	1428
TGGGGTGGTCAATGTCAAGA	FBXO21	715	724
AGCAATTATAACCAAAGACA	FBXO22	566	628
CGATTGCTACCTGATCCCAT	FBXO22	1549	1571
CGCCAGGTTACTCAACACGA	FBXO22	459	540
GCAGAGTATTGCGGACCCAT	FBXO22	721	767
CTTGGGTCCGAGGCAAACTG	FBXO24	1464	1400
GAGATCGCGATACACCCCTG	FBXO24	1142	1182
GGAAGGTGTACAGTTCAGAA	FBXO24	758	855
TCTTCATTCTTGACTACGTG	FBXO24	831	839
AGAAGATCTTTGATTAAGCG	FBXO25	666	816
GATTAGAAACTATTCTCGCC	FBXO25	616	685
GTTAACTTCATTGAGTGGCG	FBXO25	1265	1348
TGTCCATAAAGAAAGCACAA	FBXO25	1006	1057
AAAACAGGACAACCGTGCCT	FBXO27	1591	1516
AAGTGGATGGTGCAACACGG	FBXO27	1033	943
CGAATAAGGTTGCGTCCGAT	FBXO27	1412	1434
GCAGGTCTTGGACCTAGAGG	FBXO27	919	1041
TATCAAGTCATGATCCGCTG	FBXO3	947	997
TGTTCATACCGAATTCACAA	FBXO3	1174	1134
TTCAGAGATAAAACCATCCG	FBXO3	333	430
TTTGAGTCAGTACATAGCAG	FBXO3	905	913
CCAAAGTCACTATTTAAGCA	FBXO30	759	773
GACACTAAACCATTAGCATG	FBXO30	652	621
GGGTATATCTGATAGCCGCA	FBXO30	382	429
TTCATGTTGGTCTAAACCAA	FBXO30	1289	1344
AGACAGTGGAGATCGACCTG	FBXO31	996	900
ATCAGGTGGATCCTGAACAG	FBXO31	753	873
ATGGTGTTTGCGAAAACTTG	FBXO31	880	970
CCAGATATCGGGCCATACGG	FBXO31	1045	1144
AAATGGATCTATGTTCACAA	FBXO32	1242	1256
GAACAACATTCAGATCACCA	FBXO32	1320	1272
TATTCATAGTTACTGCAACA	FBXO32	467	460
TTCCAGAAGATTTAACTACG	FBXO32	682	763
AAATACATACCTCAGCAAGG	FBXO33	1018	1042
AGAAGAGACAGTCGTTGCAA	FBXO33	906	1063
CAGTAAACTGAGGTGCTCCA	FBXO33	850	923
GCCGCTCAGATAGTTCTCGG	FBXO33	706	965
AAAGGAAAGAGATAGAGCAA	FBXO4	497	523
CTTAAAAAAGCCTATATCTG	FBXO4	423	594
GGCGCGTACGACCTCACGGG	FBXO4	801	940
GGTCCAAACATAGCAAATCG	FBXO4	440	517

AGATTTGGGGATCACTGTGG	FBXO40	836	854
CCATATTCGGAGTTGAGGCA	FBXO40	1048	1237
GATATCGGTTTGGTACCACA	FBXO40	1446	1511
TGTATCTAGTGCACAATGGG	FBXO40	1506	1444
ACTGCATTGTGACAACCCAT	FBXO42	1725	1736
ATGGGCGAGAGTTCAAACTG	FBXO42	772	741
CAACTATCTTAATCCTCGGA	FBXO42	474	574
TGTTTAGGTCAAGTCTCCAG	FBXO42	545	553
AGAGGGTCACGAGGTCGATG	FBXO44	1335	1171
AGGAGCTGATGGATACCACA	FBXO44	690	773
AGGATCTCTCTCGAGACCAG	FBXO44	752	919
TGGAGCCTGGATGTGAATGG	FBXO44	1082	1060
ACCACACTTCCCATGCATGG	FBXO45	1214	1142
CATCAGTGCTCTGAGCAATG	FBXO45	1243	1233
CCAGCAATGCCACATAACCT	FBXO45	2143	2189
GTACCAGTGCTTGCACACCA	FBXO45	711	823
CAACACGAAGTAGTCAGCCG	FBXO6	1150	1194
CACATTCCGGCCGGACATCG	FBXO6	1204	1314
GCAAATTGATTTCAATGGTG	FBXO6	727	813
GGTTCCTATGCAGGCTCCGT	FBXO6	446	611
CCCAGCGTACCTGTACCCCC	FBXO7	1106	1124
TACATGCATCCTCTCTGCGA	FBXO7	1550	1502
TCTGTAGTGAATCGGTGGAA	FBXO7	746	845
TTGGAATGACGACAGTATGG	FBXO7	1114	1022
AAGGTCAGTTGCATTCAGGT	FBXO8	1740	1616
AGGTTGTGCAAATCCACTTG	FBXO8	1734	1553
CATCGTAAACAAGTCCAAGG	FBXO8	1054	1185
TATCCTGGATGATTCGCCAA	FBXO8	774	794
AAAACATCGGCAGATACCAA	FBXO9	512	612
ACTTATACCCGGTCTCCAGA	FBXO9	739	990
AGTCACTAGACACCACCCAT	FBXO9	663	669
TTACCATCAAACCGAACACG	FBXO9	892	894
AAACAGGACTCTGATCACAT	FBXW10	968	995
AGAAAATGAACACTTGCTTG	FBXW10	1046	1032
GAAGTGGAAGCTGAGAACGA	FBXW10	770	808
GGCCATCAGTACTTCCTGAG	FBXW10	1095	1218
AAAGTGTTAACAGGACACAC	FBXW11	757	745
AGACTATAGAATCTAACTGG	FBXW11	650	766
AGTGCAATACAGCCTCATTG	FBXW11	1031	991
GACACGGCGTAAAGTGATGT	FBXW11	1446	1430
ACTGTGTCCAATTAATGACG	FBXW2	1062	1114
AGACTTCACTGTGAAAGTAT	FBXW2	1298	1260
CAGCATGTGAGTAAAGTCTG	FBXW2	854	893
TCACCTGATTAGTCTGAGTG	FBXW2	1000	1015
ATAGGGCTTGTTCCGCACGC	FBXW5	1453	1306
CAGGAACTCGTCCCGCGACA	FBXW5	1164	1228
GGAGTCAGAGAACGTCAACG	FBXW5	974	1103
TGACCTGGGCAGCGACAACG	FBXW5	1385	1303
AAGAGCGGACCTCAGAACCA	FBXW7	601	689
ACAGAATTGATACTAACTGG	FBXW7	709	811
ACATTAGTGGGACATACAGG	FBXW7	1284	1378
GTTGGAGTAGAACCTAGACC	FBXW7	666	826
AGAAACCAGAAGGTACCCTG	FBXW8	759	1007
AGTGTGGGACACCCGCACCT	FBXW8	880	873
CATGTTACGAACCAACTGGA	FBXW8	1340	1320
GGGCCAGAGGAGAACGTGAG	FBXW8	850	873
AGGTAACAGGAACACCCACA	FEM1B	1026	1041
ATATAAGGGACACACTGATG	FEM1B	1245	1257
CTATAGTAGTGAATGGCCAT	FEM1B	1722	1609
GATGTACCTACCCGTCGAAG	FEM1B	1166	1235
ACTTGGTGCCAAACTCTGAA	FOXD4L4	793	928
ATTGTCGAACATGTCCTGGG	FOXD4L4	1627	1606
GCCCTGCACAACCCCCACCC	FOXD4L4	884	941
TGCGGCGGTAGTATGGGAAG	FOXD4L4	954	1012
AACACCACCGTACCTTCCCG	FUS	1657	1652
CAAAGCTATAATCCCCCTCA	FUS	670	841
CCAGTCGAGCCATATCCCTG	FUS	1594	1511
GCCACCACCACTACTCATGG	FUS	990	993
CCGCTCAGACCAGCCCACGG	FZR1	362	459
CCTCACCGACGCGTGCCGTG	FZR1	1467	1304
GGCACTCCACAGGTACACGC	FZR1	1127	1173
TGTCTCCCGTCAGCAACAAG	FZR1	2103	1906
AAATTACCCAGACAGTCACC	G2E3	886	972
AACCAAGCGTTCTTACAACA	G2E3	922	1052
GCCATTTCTTTAGTTCACGG	G2E3	561	726
TGATAACTTCGTTTACATCG	G2E3	1616	1605
AGCATGCCGAGAATTAACCA	GAN	744	748
AGGATGTTATGTCAGCTCTG	GAN	768	847
CTGGCCAACTTCAAACCCCG	GAN	682	793
TTTCAGGCAAGACATAACTT	GAN	1073	1018
AGGCGCCTGACACAAACGTG	GNB2	1061	1185
GCAACACGACAGGTACCCTG	GNB2	1289	1296
GTAGGCACAGGTCATTACCC	GNB2	1135	1263
TCTACCTCCAGATCACAGCT	GNB2	1861	1805
AACATTCCGGACATTCATCG	GPR50	1337	1422
GGTGCGAGGATCGTACTCGA	GPR50	722	733
TGAAGATCCGTTCGTACTGG	GPR50	821	810
TGATATTCGTGAGATGCAGG	GPR50	1705	1623
CTCTGGACACCTACGGACGG	GRWD1	838	951
GGACCATACTTACCCGAACT	GRWD1	823	807

GTGGTCACCGACTGAGAACA	GRWD1	1444	1610
TCCGGCGACACAAGTTCCGA	GRWD1	823	933
ATTGTGCAAAGCTAAAGCAA	HACE1	867	897
CATATCAATTCCATTACTGG	HACE1	692	826
GGCTTCACAGATACATTGGC	HACE1	986	1275
TATTAATTCAATATCACCCG	HACE1	1002	1180
ACTTACCCGTACCAGTAGCG	HDAC4	1110	1136
GCATCAGCGTGTCATACACG	HDAC4	661	636
GGAGCCCATTGAGAGCGATG	HDAC4	542	588
GGGGCTGACTTACCGCAGAG	HDAC4	574	610
ACTACCACTTGAATACATGG	HECTD1	1083	1101
AGTGTTACCACTACTCCACG	HECTD1	1083	1109
GCTGACCGATTTACCCGTCG	HECTD1	462	566
TGGGTTCGACCAAAACGGAA	HECTD1	359	402
AATACTTACAGTATTAAGTA	HECTD2	1063	1213
ATTTAATCAGCAAAGTCTGG	HECTD2	666	746
CAGTATAAGGAATAAGGGGA	HECTD2	925	949
GTAGATGTGTTATTAAACTG	HECTD2	871	898
AGCTTGTAGAGCACCTCTCG	HECTD3	830	958
CGGCGGTTGATGTATAGGCG	HECTD3	657	704
GGCCCATGCGCTATGACCAG	HECTD3	1242	1265
TTAGCTATGTACCCCCGACA	HECTD3	1115	1139
ACACTCCTGATAAAGCCATG	HECTD4	956	924
AGCACACAGAGACACAACAG	HECTD4	627	602
GATGGATCGAGACATGACCA	HECTD4	629	539
GTATGCACATCGCACCAACG	HECTD4	1577	1332
CAAAATTGCGAGCATCCCGT	HECW1	1011	1121
CCACATAAAAGACCCGCCCG	HECW1	195	256
CTTCTCCTCGCAAGACGACG	HECW1	968	1017
GCACATTCTACTCACCAATG	HECW1	616	588
ACGTAAACAGAACCACGACG	HECW2	537	532
AGGCCTGATCATGTTTAGCA	HECW2	1213	1226
GGTAAGGGCTGATTACCCGA	HECW2	550	659
TATGCTGGTAGCGTTCAAAG	HECW2	1282	1319
CAATACGTTTAGCAGACCAG	HERC1	759	670
GCAGTTCTTGATGCGACACA	HERC1	892	959
GGAAGTGGACCATCAGCTAG	HERC1	788	744
GTTCTATAGTAGCAATCCAG	HERC1	505	486
AAAAGATAATTCGAGAACGA	HERC2	559	621
AAGCTCGTTGTCTTGTGGAA	HERC2	1083	1185
AGCAGCTACGATAAGAACCA	HERC2	767	926
GATGTGGTCAAAGTCCGCTG	HERC2	1019	1081
GAAGTAACTCAAATTGCTTG	HERC3	1247	1287
GATTGACCTGAACTCAACTA	HERC3	990	904
GGTTGTTCCTGCGAACGTGA	HERC3	1477	1480
TGTGGTTCTTGCATCAAGCA	HERC3	1520	1461
ACTATCTTGAGGAATAGTGG	HERC4	834	766
CAGACCTGCTGAGATATCTG	HERC4	772	809
GATATGTACAGATTGTAACA	HERC4	1196	1265
GATTCACAGATTCAATCACT	HERC4	753	784
CTGATGTGGAGACTAAACGG	HERC5	1050	1069
GATGCATATTTCCAACAACT	HERC5	863	938
GTACTTGTGGAAAATGACTG	HERC5	1235	1365
TTACTGGGATGAAAGTGCTG	HERC5	978	1018
AAGCCGAATTAGCCAGTCCA	HERC6	1052	1270
AGTGGTGTGCACATATGCCA	HERC6	182	143
ATTGTTGATCTCGTGAGCTG	HERC6	1418	1398
TGGGACATTACGCCCACTGA	HERC6	1769	1690
AAGGCAGATGGACTAAGCAA	HLTF	1466	1419
ATAGTCCATTACATAGCATA	HLTF	1460	1367
CATTTATTGATAGAGAATGG	HLTF	352	376
GTTGGACTACGCTATTACAC	HLTF	1214	1125
AAACCCCAATTACGCCGGCG	HOXB4	536	678
CCCCAAGTTCCCTCCATGCG	HOXB4	741	848
GACGACGGGCTCTTTGCACG	HOXB4	647	848
TCGCCCGGGTACTACGCCGG	HOXB4	305	401
AATCTTAACAACTTACCAAG	HUWE1	NA	NA
CACCCTCCTCCAATCATGGG	HUWE1	NA	NA
GCTGAACTTCACCTGAATCG	HUWE1	NA	NA
TCTGCATGGCGCACCATCAG	HUWE1	NA	NA
AGGAGGGCCTTGATACTCCT	IFNA10	738	720
ATCACAGCCTAGAGAACAGA	IFNA10	1132	1190
CTTCAATCTCTTCAGCACAG	IFNA10	571	561
TGATTTCCGAATCCCCCAGG	IFNA10	685	892
AGACATCTAAGGTTCGACCT	IPP	489	472
ATGATCCAGTTACTAAACAG	IPP	896	850
GAATTCCAAGAGATCATGGC	IPP	880	915
TCACTTCATCAGGCTCGAAG	IPP	1337	1252
ATTTATCCCACAGAAAGACC	IRAK1	1285	1344
CCCCGGGAAATCTCACAGAG	IRAK1	269	334
GATCAACCGCAACGCCCGTG	IRAK1	595	693
TGGGGCTGGACCCGGCAAAG	IRAK1	664	823
CATCTCATGTGCCAAGAAAG	IRAK4	1240	1352
CTACGTAAATAACACAACTG	IRAK4	1348	1457
GGCACCACAAATTGCACAGT	IRAK4	847	950
TGTAAACATATACTAAGCAG	IRAK4	609	752
AGCTCGAACTCGTATCCTGG	IRF2BP1	1371	1500
AGTACCTCGAATATGAACGC	IRF2BP1	943	898
ATGATGTGGCCCTGTCATAG	IRF2BP1	920	1017
CTGTCTGGCAGAACTGAACG	IRF2BP1	486	536

CGACGTGGCCGATACACCCG	IRF2BPL	712	677
CGGCGTCGAAGGCGAAAACG	IRF2BPL	1011	984
GCTTGCTGGAACCATCAACG	IRF2BPL	415	497
GGGCCGTTAAGCAGCGTCTG	IRF2BPL	620	774
AATACAAACCTGGTCTACGT	ITCH	1266	1255
ACAACACACGAATTACACAA	ITCH	1325	1355
GAACGGCGGGTTGACAACAT	ITCH	989	1101
TCCCGAACATAGGCTATCTG	ITCH	703	731
CCTCACAAGAAGAGCATGCT	JOSD1	1461	1404
GAAGCCCATGACGTTAGTGA	JOSD1	1189	1235
GGACAGCAATGCCTTCACCC	JOSD1	1840	1828
TTTCTCATGGTAGATTTGTG	JOSD1	1200	1135
AGGATCAGCCCCAGTACCTG	JOSD2	867	918
CCTCCTGTCCCACCACACGG	JOSD2	1071	1146
CTGCCGATGAGATCTGCAAG	JOSD2	1122	1175
CTGCCGTTCGTGGTACACGG	JOSD2	1200	1157
ACCTCGGTACGAAACCACAC	KAT2B	1792	1619
GCGAGCGCGTACCTTGCAGG	KAT2B	1110	1119
GGAATATCCCCCATAACTCG	KAT2B	297	393
TGCCAAAAGAATACATCACA	KAT2B	886	802
GATGTGGTCCTCGTCAACTG	KATNB1	1722	1732
GCTGAACCGGAGACACCGCA	KATNB1	501	548
GGACGAGCGCGAGTCCCGCG	KATNB1	823	1044
TCACACGGGGCCTGTCAACG	KATNB1	825	1008
AACTACCTCTTCGTGGCGGG	KBTBD11	713	713
AGGTCCTGAGCGCGGCCAAG	KBTBD11	791	1005
GGCCGTCTACTGCTTCCACG	KBTBD11	1372	1456
GGGTCCTCAAGCCAAACGCG	KBTBD11	392	396
AATGACCTTTATGTTATAGG	KBTBD12	955	1039
ATCAAGACATAGGAGCTATG	KBTBD12	478	386
CATCACAGCAGAAAGTGTGT	KBTBD12	1801	1690
TTTATATCAGCACTTTGCCG	KBTBD12	1258	1367
CAGGTAACACAGCGTGCGCG	KBTBD13	576	614
CGTGCCACGTGCCGCCGTCG	KBTBD13	1089	1075
GTAAAGCTTGTTGCCCAGCG	KBTBD13	775	920
TCTGGAGCACAACCTCACGT	KBTBD13	1016	936
ATAATAACTTATGCATACAC	KBTBD2	1220	1167
TAATGATATCTACATAGCAG	KBTBD2	1206	1288
TACTGAGAATATCTATCAGT	KBTBD2	1346	1434
TAGGTGGAGAACTTAATCGG	KBTBD2	721	827
CTAACACACAACGATGACAC	KBTBD3	973	824
GAGATTACATCAGTTATCTG	KBTBD3	957	1083
GTAGCACCAGGTTTGATCAG	KBTBD3	847	933
TTGTGGATGGTCGAGCATCA	KBTBD3	1979	1901
CCTCCCGAATTGAACCCATG	KBTBD6	1004	1071
CTGCTGTGATCCATACTCGG	KBTBD6	1116	1228
GTCTCTCAGTGAGGCCAACG	KBTBD6	392	471
TCAAGTCCTTCTACGATGCG	KBTBD6	2352	2198
CGCGTACAGGCGCTGCACAT	KBTBD7	1376	1458
GACTCTAGCAGATCTAACCC	KBTBD7	703	793
TCAAGTCCTTCTACGACGCG	KBTBD7	2349	2217
TCTGCTATGACCCTTACTCG	KBTBD7	1204	1153
ACAGTTGACAGACATTGTAG	KBTBD8	844	910
ATGACATTTACATTGCAGGA	KBTBD8	907	1071
CCTGTGACTATATCTAGACA	KBTBD8	1217	1234
TGATCATATACTTAGCACAT	KBTBD8	960	982
AATGCAGTGCATATTAACAA	KCMF1	675	674
AGGCGATCCTAATCATGTCA	KCMF1	1246	1238
GTACGTAGAATGTTTCACCC	KCMF1	1165	1276
GTTGTAACTGAGAAGCGGAA	KCMF1	655	723
ACAACAAATACTCATATACC	KCTD10	916	913
GCTTCCCACAGCGGTCAATG	KCTD10	569	626
TCTGCATGGTGGTATAGTAG	KCTD10	1361	1256
TGTCTCTGCGCTTTAACGGA	KCTD10	824	872
AGCACCTAGACACTCAGAGT	KCTD11	1156	1266
CCCAACCTCAATTCCCAAGG	KCTD11	1045	1235
GCTGTCTCTCCGTACCCACG	KCTD11	1105	1145
GTGCACTTCTCTGCTCGCCG	KCTD11	1171	1310
CAGCGGCTTGAGACCGTAGG	KCTD13	634	730
CATGGTGTCCTGTCCCGTGA	KCTD13	1065	1010
GGAGAGTACGAGAGAACTGG	KCTD13	980	1110
TGGGTGCTGATTGACCGGAG	KCTD13	749	825
AGTGGACCGTCTGCACACGC	KCTD21	1446	1322
GCTATATCCTCAACTTCCTG	KCTD21	569	580
GGTAGAAGTCGGCCTCCCTG	KCTD21	437	632
TGGCGCCTAGCATGGAGTCA	KCTD21	897	887
AAGTGGGTCCGACTCAACGT	KCTD5	1477	1462
ACGAGACAGCAAAACATCGC	KCTD5	1104	1036
CTGGCATAAGCGGTACAGGA	KCTD5	732	802
TCCCGACCTGGACTCAGACA	KCTD5	1593	1447
ATCCGGGTAACGCGTCAATG	KCTD6	856	928
GCAACTAACCATCACCACTA	KCTD6	603	640
TCAATAAAGTAATTGCCTTG	KCTD6	573	574
TTCTAAGTACTCCAACCCAG	KCTD6	820	925
CTTGGTCAAGCGTCCGACTG	KDM2B	992	999
GCTGCGGATCTACGAGATCG	KDM2B	1139	1144
GGGGGACGTTTGAAGCGATG	KDM2B	901	958
TGTCCGAAGTGTAACCACGC	KDM2B	1075	953
ACAACCCCATGACCAATCAG	KEAP1	1182	1213
AGTACGACTGCGAACAGCGA	KEAP1	1264	1379

GAGGCTTACAACCCCAGTGA	KEAP1	462	536
TGACAGCACCGTTCATGACG	KEAP1	1546	1339
ACCGAAAGATACCTGCACAT	KLHL1	736	814
GCGTCACACATCATTACCTG	KLHL1	960	1012
GGAGGAATGGATAACAACAA	KLHL1	476	507
GGTGGCCCACAGCTACACAA	KLHL1	748	892
AGGATGGCATAGGGCAAGCG	KLHL10	726	674
ATGGGTGAATGTTACTTGTG	KLHL10	1576	1571
GCAACGTCTGGAGTGCATCG	KLHL10	1289	1375
TCATTGAGTATGCATACACC	KLHL10	1105	960
AGAAACAGTACATGTGACAG	KLHL12	1174	1149
CCACTGAACTAAGGCGGGAA	KLHL12	636	720
CCCTGCATTGTAAACTACAG	KLHL12	822	901
CTCTCAATGTCACATCACAG	KLHL12	1602	1609
ACTCACTTGGTTACACTAGG	KLHL13	713	698
CATTAATTACGTGCAAACGG	KLHL13	921	874
CCATCATGACTCTATGCACA	KLHL13	1701	1632
TAAAGTGTTTCTCATATCTG	KLHL13	586	658
AATACTGAACCAAATTGCTG	KLHL14	939	1101
CCAGCAGTTCCATTGCCACA	KLHL14	715	735
GCACCGAGATCTGGTCGTTG	KLHL14	920	1033
TGAATCCAGCTATTAAATCG	KLHL14	822	983
CAAAATTATTGACGATAGCA	KLHL15	457	509
CCCAGAGATAGAGCTGTACG	KLHL15	842	883
GATTTCGGCGTAAACATCGA	KLHL15	796	864
TCTGAAGTAATCACTCTGGG	KLHL15	719	769
ACGACCCCGTGACTAACACG	KLHL17	557	568
CACCACAATCTCAGCCGTGT	KLHL17	1204	1131
GAGCTGGGTGAAACACGACG	KLHL17	857	1056
GGAGATCCGTGCGCACAAAG	KLHL17	908	968
GCTGCACATTCCTTCGAGAA	KLHL18	806	896
GGCTGCTAAGACAATCCGGT	KLHL18	328	327
TAATGCAAGGAATGGACCCA	KLHL18	1408	1267
TCACCACAGCCACGCCAACG	KLHL18	528	552
AAACAGATCCTACTTTGGGA	KLHL2	1018	1204
AGCATGGGTGAACCATGACA	KLHL2	845	931
GGTACTTCATTGCTTCAATG	KLHL2	780	928
TGGTCCACTGGTCCTTCACA	KLHL2	505	503
AAGACGTCCTCAATTACCCC	KLHL20	1006	1136
ACGGAAACCTATCCGATGTG	KLHL20	835	858
GGCTGACAAAATGACTCGAT	KLHL20	1374	1471
TGATCCGAGACATTGACGAG	KLHL20	1598	1560
ACAACCCGCAGACGGGTCAG	KLHL21	659	713
ACAACTCAAGCGTGAATGAG	KLHL21	1661	1649
GACGGGCGAGGACGCATTCG	KLHL21	475	431
GGTGGGCAGCGCGCCACCAG	KLHL21	582	590
CAATGTACAAGAGACACTGG	KLHL22	993	1064
CTTCGTATACTTGATTGGAG	KLHL22	484	434
GCGAGACCGAGGTATATGAG	KLHL22	1043	1054
GTACCTGCCTACAACACACA	KLHL22	678	684
AGAAATACCAGATTATACCA	KLHL23	843	954
CAGTAAAGAAGGCTTGTGAG	KLHL23	610	661
GACTGCACAGTGGTAATACC	KLHL23	1071	979
TGCATAAAGAGATTTCCCAG	KLHL23	480	542
ACGATAGACCCAACGCATGA	KLHL24	1444	1542
AGAACTTGGCACATGCATCA	KLHL24	1276	1190
AGTTATAAATCCAGACATCA	KLHL24	507	606
TATCACCTCAGAATAGCCAG	KLHL24	703	669
AGTGCTTGCGAAGCGTGTTG	KLHL25	1600	1516
CTCACGCATCGCCATCAACG	KLHL25	1302	1180
GGCCTCAAAATAGCGGCTAG	KLHL25	312	328
GGTGTACGACACCGTACATG	KLHL25	1007	1040
CAGCACGGCCGACAAGAACG	KLHL26	1228	1168
GTGCCGAGAAGGTGCACTTG	KLHL26	1851	1706
TAATAGTCAGCACAACATCG	KLHL26	804	808
TGTGCTGACTATTAACAGAG	KLHL26	851	985
AGTACTTTGGGAGCACAGCG	KLHL28	1051	1076
CATATTCCAAATTCATAGCG	KLHL28	682	840
TGTATAGGCATACTCCACAA	KLHL28	1132	1057
TGTGACATCATTCTTCGAGT	KLHL28	1535	1457
AGTATGAGTTCACCGACCCG	KLHL29	845	983
CATGTGGCCGTTGCCCACAG	KLHL29	908	897
GGGGGTCACCCCAATGACCG	KLHL29	374	436
TATCAATCAGTCCACACCCT	KLHL29	1680	1548
CATCTATACTGCTGAAATCG	KLHL3	1202	1263
CGAGATAGAAGCCCACCGTG	KLHL3	483	573
GACTATTGATTAAGAACCCA	KLHL3	1280	1437
GGAGTGCTATGATTTCGAGG	KLHL3	953	1008
AACCCCACTTGTGATAGTCG	KLHL30	1374	1389
ATGGCGCACCCAGCGCATCA	KLHL30	1007	922
GCCCACCAGCAGTGTGACGT	KLHL30	1295	1163
GGCCGGCTGACCATCACGCA	KLHL30	980	984
AGGCGAACAAGAATCCGAGG	KLHL31	604	654
CTTCAACACCTGGATACACC	KLHL31	1084	1130
GATCCACCCTCTGAATTGAC	KLHL31	1725	1653
TACCAATGACTAAGTCACAT	KLHL31	561	500
AGAGTGTCTGACTGGAATCG	KLHL32	1481	1504
CCACATCCATTAGGCCAAAG	KLHL32	861	831
CCCCCATGACTGCCACACAA	KLHL32	1175	1152
TCTGCCCAGGAATTACTGCG	KLHL32	1105	1099

CGGGTCGTAACGGTGCACTT	KLHL34	578	634
GCGGTGATTGTACACATCGA	KLHL34	832	927
GCTCAACCCTACATCGCTGA	KLHL34	1763	1732
GTACACGCGCCGCAGTACGT	KLHL34	1048	1002
ATGACCCCCGCTGTAAACAG	KLHL36	1175	1401
GGACGCCAAGAGCGAGCAGT	KLHL36	648	673
TGAAGGCATCAAGCCGCTTG	KLHL36	791	795
TTCAACTCCATGTTCACCAT	KLHL36	2970	2535
CCCTGAAACTCAATCAGTGG	KLHL38	704	724
CTACTGTACAGCAAACAGAC	KLHL38	949	1065
GGCACTGACGTCCTTCCCAG	KLHL38	1361	1363
TGCCTCCCCCGTATACACGT	KLHL38	1271	1237
AAAGCCTAGAAAATCAACTG	KLHL4	497	623
CTTCAACCTGCCCTGAACCG	KLHL4	782	834
TGTGTAAGCATACTGCACCA	KLHL4	1585	1479
TTGGCACCATGAATGGCCGT	KLHL4	1146	971
CAAAAATGCCGCGAAGACTG	KLHL41	834	991
GAAATGGGTGCGAACAGACA	KLHL41	592	591
GGAGGTAGTGCTAGACAATG	KLHL41	1359	1475
TGTGGTAGGAGGACTATATG	KLHL41	1369	1280
ACAACCCCAGCACCAACGAG	KLHL42	1099	1158
ACGAGGAGATGACTGAGCGT	KLHL42	665	645
CATGGTCGTCCACTTCCACG	KLHL42	1610	1754
TGAGTGTTACAACCCCGAGC	KLHL42	756	953
AAGATTGTGGCGGTGCACAT	KLHL5	1136	1127
ATGATCTCCGTACAAATATG	KLHL5	1754	1740
GACAGACTGGAGCAAACGGT	KLHL5	912	908
GTGTAGAACCAAATTCGTTG	KLHL5	728	834
GAGGAAACCTGACTTTAGCA	KLHL7	664	746
TGGGCGTCATGAATAACATG	KLHL7	1376	1376
TTAAAATATCTACAAGACTG	KLHL7	856	1006
TTTAGGTATAAGTGTGCTAG	KLHL7	1157	1205
AATAGTCGAAGGCGACATGT	KLHL8	1648	1642
ACTCCATTCGGACTACCCCA	KLHL8	947	1053
GATGAAACACTTGCACAGGT	KLHL8	1094	1226
TGGAGGACAAAAGCTTATGG	KLHL8	806	973
ATTGCTTTGTGATGTGACCC	KLHL9	1449	1473
GCAATACCATGCTGGTAACG	KLHL9	1507	1448
GTGAGTGGAGTCAGATCGAA	KLHL9	315	409
TTGCAGCATAATCCATCCGA	KLHL9	1102	1184
AAGGACAACACATTTGGATA	LITAF	1093	1176
GGCTGGGTATAATACGAAGG	LITAF	485	487
TCCATCCTATGAAGAGACAG	LITAF	1311	1217
TTCATCAGTTACCGTGCAGA	LITAF	810	889
AATAAAACTGGTGCGCAAGG	LNX1	758	809
GAACCTGGCGGGACACGACG	LNX1	815	894
GTCCACACGGAGTGTCCAGG	LNX1	1008	1062
TGGTTTGAAAGTGATGCTCG	LNX1	1308	1395
ACAGAACGAATGTCCGCAAG	LONRF1	1501	1517
AGAAATAAGCTGAAAAAACA	LONRF1	371	392
TACAGAGCGGAATCATATGC	LONRF1	1413	1327
TAGACTGTGCTGACTGAGCA	LONRF1	819	844
AAAGCATACGCATATCAACT	LRR1	1069	958
AGGCTCCTTTAACCGAACAG	LRR1	383	515
GACAGAGGCTCAACACGGCT	LRR1	1076	1257
TAAGTTCTTGAAGGTGTATG	LRR1	870	812
AATGGTCCCACGTAGAACAT	LRRC41	801	801
AGCGTTTCAAGCGAGCTGCA	LRRC41	639	743
GCTCCGGCGTGTTACCCGAG	LRRC41	362	484
TGGAACTGTGAATAGCTCCA	LRRC41	1135	1176
AGATGGCCTACGAATCTCAG	LRSAM1	1277	1253
GCCCACGGACAGATTCTCAA	LRSAM1	800	879
GGGAAGTGAGGTGATTCGTG	LRSAM1	1507	1459
TCAGGTTCCCAATGGAACGT	LRSAM1	1192	1243
AAGACCCAGGATTGCAACAT	LTN1	850	821
ACGTGTACTTGGTAATACGT	LTN1	1636	1514
AGAGACACAGAAACTGTGAA	LTN1	491	554
CTATCAACTGTGATTCGTGA	LTN1	1341	1335
AGGTGGCAAAGATGTACACG	MAGEA6	1148	1049
CTCTAGTTGAAGTCACCCTG	MAGEA6	899	842
GGAACTCAGACTCCAGGTCA	MAGEA6	524	613
TCATAGGATTGGCTCCAGAG	MAGEA6	472	563
AAGAAGATCACACTCAGTAG	MAGEB4	961	926
AGGCGACGAGAGCCAAGATG	MAGEB4	784	771
AGTATCCCTCAAAACAGATG	MAGEB4	1270	1218
CAGGAAAGTCTCTCAGCGCA	MAGEB4	1037	1235
AATTCGTACACATCCACCAA	MALT1	1436	1344
ATATCCAAACACAATATTGG	MALT1	681	702
ATGGATTTGGAGCATCAACG	MALT1	1168	1321
TGAGACCAAAAAGCTATACA	MALT1	721	866
CAAGATGGATGATCGTCCAG	MAP3K1	1133	1050
CCTGAGGCCCAATAAACACC	MAP3K1	699	664
CTTTCCGCTAAACTGTGGCA	MAP3K1	1729	1772
TTTCACTGTGCGACCTGATG	MAP3K1	2624	2282
AGATGACCACAAGTGAAAGG	MARCHF1	743	776
CAGAATCTGTCACTGCGAAG	MARCHF1	933	1154
CGTAATCGCGATCACCTGTG	MARCHF1	1609	1528
GCGAACACCCGAGATCTCAG	MARCHF1	453	550
AAGTATTGAGTGAGTTCTCG	MARCHF10	899	909
ATTCTCAATGAGCCATGACT	MARCHF10	1066	1071

CAAATCCGAGCCCAGACAAG	MARCHF10	619	657
CACCTGGAGAGGGTTCGCTG	MARCHF10	1695	1828
AGGTCCGAGGCGCCTCCCGG	MARCHF11	439	636
TCGTCCGCTCCCCTGCACCG	MARCHF11	1349	1504
TCTATAACAGCAAAGTTCAC	MARCHF11	990	1056
TGAACCCCTGCCGATGTGAT	MARCHF11	1644	1620
CTCCAGACAGCTCTTATGCA	MARCHF2	798	874
GCGGACACTGTGCTGCGACA	MARCHF2	1225	1223
GCTGCCGGAGCAGTCACACA	MARCHF2	693	690
TCCGTGCCTTGGACACACCG	MARCHF2	1424	1240
AAGGTCCCTGTACATTCACA	MARCHF3	1267	1401
CAAACCCAGGCCGTTAGTGG	MARCHF3	678	797
GAAACTTGCATGACATACTG	MARCHF3	946	966
TCGTGGCAGATCCTGCACAT	MARCHF3	1066	886
ACTTGACCGAGCCATCACAG	MARCHF4	1425	1354
CTGGTGGCGCAACATCTGGG	MARCHF4	1194	1282
CTTCTGTAAGGAGAAGACCG	MARCHF4	1020	1124
TTGTTGGCCGCCAAACCGGG	MARCHF4	755	1014
AGGACTATGTGCTTAGACTG	MARCHF5	1188	1064
AGGTATTCAGCATTGCACTG	MARCHF5	1362	1319
ATCAGCATGACAGGAATAGT	MARCHF5	1222	1227
CCAGGCCTGTCTACAACGCT	MARCHF5	1107	1136
CCCCACCGTTCAATGCTGCG	MARCHF6	889	827
TCGAGAACTGAGCTTTCAGT	MARCHF6	1142	1164
TGTCCCTGTTCGAGTAATGC	MARCHF6	1069	1052
TTGGTTTCATTATACACTTG	MARCHF6	1109	1198
AGATCTAGATGATGTATCAG	MARCHF7	946	950
ATGAAGGTAGGCGGACAACG	MARCHF7	697	651
ATGGATTATAGTCACCGAAG	MARCHF7	535	564
GATGTTCAGAAGGCAATTGG	MARCHF7	777	749
CTGCAAGTATGAGTTCATCA	MARCHF8	1281	1369
GCTCATTGACCGTACTGCTG	MARCHF8	2075	1981
GGCAGGCCTGGTGCACGAAG	MARCHF8	861	755
TTCTATCACGCCATCCAGCC	MARCHF8	923	927
ATCCGCTGGATCAGCGAGAG	MARCHF9	299	335
CGAGGAGGAGTACTACGGGT	MARCHF9	341	419
TGGAAGCAGATCCGGCACTG	MARCHF9	827	912
TTCAGCCAAGTGGCAACGAC	MARCHF9	1772	1630
AGGAGAACTTTCAAGCACTT	MBD3L1	568	691
CTTGTCCCTAGTTACACAGG	MBD3L1	1753	1762
GGTCAGATACCATCAATGGG	MBD3L1	883	1105
TGTCCAGTTACACATTCAAG	MBD3L1	1017	1003
AGACACTTATACTATGAAAG	MDM2	438	553
GAGAACATTACCGGATTCGA	MDM2	432	497
TACCATGATCTACAGGAACT	MDM2	1243	1282
TGTTGCAATGTGATGGAAGG	MDM2	875	896
ATGTATGCATTTATGCTCTG	MDM4	1195	1147
CAGCATATGGTATATTGTGG	MDM4	1278	1246
CTCAGAGGTAACCTCTACAT	MDM4	910	983
TCCAAGTCAAGACCAACTGA	MDM4	1665	1659
ACAGCGGCAGACTGAAGGAC	MED8	650	686
ACAGCTGAACACTCTGAACA	MED8	665	712
AGTTGGAGAACGAGTATGGC	MED8	940	1007
CGGTCTGGAGACAACACCAG	MED8	1243	1389
AGTCAGGGTCCCTTATCGTG	MEX3C	843	1028
GCCACCTTCAAAGCTTACAT	MEX3C	1078	1184
TATATCAAGACTCCTGTTCG	MEX3C	1789	1800
TCCCACGCCTACGGCCCCGG	MEX3C	959	1059
AAGTTACCTCACCAGCCGCA	MGRN1	1493	1502
CAAAGAGGTAACCTTCAGGG	MGRN1	402	534
GAGACCGTCCACTACAAGAG	MGRN1	944	994
TCGCTGTTCTCGTCGTCCGA	MGRN1	1943	1858
ATTGTAGTACAGTATCCAAG	MIB1	1173	1211
GTTATAGAAGTACTACATCG	MIB1	976	1057
TAGCGCAGCATATGTCCTCT	MIB1	984	986
TATCTAAATTACCAAGACCA	MIB1	807	814
CAGGTGGACACCAAGAACCA	MIB2	770	774
GCATCGTATCACGGACCGCG	MIB2	770	776
GCGAGTGAGCGGTCTCGTAG	MIB2	418	501
TACCACCAATGTGTACCGTG	MIB2	1194	1094
CCTTGTGTAAACTGGTTGGG	MID1	879	951
GAATTGGCTCAATCAGACGA	MID1	923	996
GAGATACTCACTAACGACGT	MID1	481	458
GTGTGATACTAGGATGCGGT	MID1	1371	1235
AGCAGAGGCTGTGAGCACAA	MID2	826	851
CTGTGAGCAGGACCCGCCAA	MID2	622	688
GTTATCTCGCTGAACCACCG	MID2	796	877
TGATCGATTTGAGAAACTCA	MID2	1357	1431
AGTGGGAGAGTGCCGATACG	MKRN1	1033	973
CCTTCTCTAGTCGTGCATTG	MKRN1	1958	1926
TAAACAGGTCACCTGCAGGT	MKRN1	412	500
TCCCGAAGCGGCGCTCACTG	MKRN1	804	1011
AAAACTAACTCACATGAACC	MKRN2	826	819
AGGAATGCGGCTTCATCTCG	MKRN2	882	980
GTTGACGTTCGAACACGAGA	MKRN2	1096	1123
TGTTTAGATATGACCACACG	MKRN2	1033	973
ATTCGCACGACCTTTCTGGT	MKRN3	1227	1306
GAGAGAGACAATGCAGACCG	MKRN3	782	828
GGAGACATATGCGACATGTG	MKRN3	771	809
TGTGCAGCGTGGTATGGACA	MKRN3	2244	1955

GAGCCAAAAGCAGAGCAACA	MNAT1	1010	1134
TCATTGTATTCTCTTAGACT	MNAT1	648	747
TGAGTGGAGTACCACACTCA	MNAT1	1583	1504
TTTCAACTTGACCAACAATG	MNAT1	1350	1188
ACAAGAGTCGGAGACCACTG	MPND	948	1070
AGCCAGACGGAAGGATCATG	MPND	1055	1008
AGTCTGACCTGGCCAAGTCG	MPND	1437	1314
CTGACACGGAGTGAGGTCGT	MPND	1785	1686
ACTGCCAATAGCAATGCTGA	MSL2	945	942
CCAATTTCTACCATTATCCG	MSL2	872	999
GCTACTGTGTCACAAACGGG	MSL2	939	1051
GTATATAACACAGACTACAC	MSL2	413	353
ACATCCACGCCATCCTCGTG	MUL1	692	651
ACTGCAAGGGGGTAATTCAG	MUL1	720	840
CGGTGAAGGACTGAATCGAG	MUL1	682	710
GGAGAAGTGATACATACCAA	MUL1	721	742
AGAGTGCATCGACCCCTCGG	MYC	970	998
CTATGACCTCGACTACGACT	MYC	1557	1434
CTGCGGGGAGGACTCCGTCG	MYC	552	581
CTTCGGGGAGACAACGACGG	MYC	1055	1253
GATATGCCATTCTTGCGAGG	MYCBP2	1144	1054
GCTTCAGCCAGATTCATATG	MYCBP2	544	585
GGTTGACTGAGATATCCTTG	MYCBP2	1557	1562
GTGGAGAACTAGCACCCGAT	MYCBP2	942	979
ATTCTGTGCGGGATAGCGAA	MYLIP	1061	1116
CTGCAGTTTACGGGTAGCAA	MYLIP	1162	1296
GGAGGCGAAAGCCAACGGCG	MYLIP	758	941
TCTTAGGATAGCTTATCCTG	MYLIP	1301	1352
AAAATGCATGAAACCAATCA	MYSM1	1020	1022
CGTAGGGTCCGAGACCCATG	MYSM1	747	903
GAGATGTTAATTGTATTGGA	MYSM1	1447	1674
TGGCGCCCCTCAAAAAACTC	MYSM1	802	1018
CAGAGCCCGGGTCATCTTCT	NA	394	534
GTGGTGACCTGAAATGCTGA	NA	1	1028
AGCCCGATGTCTGCGCCACG	NACC1	985	1126
CGAGTCCCGAAATCGCATCC	NACC1	1067	714
GGCCGGCTGAGCATGAACGT	NACC1	795	1304
GTACTGTGACGTGTCAGTGG	NACC1	1623	1053
ATGGACTAGTTGGTTATATG	NAE1	1170	1301
CACAGCACTAAATACAACTC	NAE1	1317	903
TAGCTAAATATTTAGCACAG	NAE1	781	1105
TCAAAGAAGCAGTATCGGCA	NAE1	1059	396
AAGATGAACAGGAAAACAAA	NANOGNB	433	467
AAGCAGAAATGGAGAGAAGA	NANOGNB	347	2023
AGAAACAATCAGCTATGCCT	NANOGNB	1883	750
TTGCCCAGAGAGTATGCATG	NANOGNB	814	1491
ACATCCAAGTTACTTGACGG	NEDD4	1334	303
ATTACAGGATACCTGTACAG	NEDD4	295	1077
ATTGCTACATTCTCCAACCG	NEDD4	978	1524
GTGGAACATCCACTTGACCT	NEDD4	1500	687
AGAACAGGGCCATCTACCAC	NEDD4L	711	1125
ATAACACAAAGACTACAACC	NEDD4L	996	1043
GATGTTATTGTCCGACTCCG	NEDD4L	964	1960
TTGGACTCGACCTATCATGC	NEDD4L	2289	1403
CATCCTCGACGAGCAGACGG	NEURL1	1602	1643
CTTCCACCGCATCAACGACT	NEURL1	1767	1636
GGCATCGGTGAGAAGTGACG	NEURL1	1627	1527
TGGTGCTCCCGGACTGTCTG	NEURL1	1447	1706
ATGGCGTCACGTTCACGCAG	NEURL1B	1885	839
CATGAGCGACGGATCGTGCG	NEURL1B	794	776
CCTGTCGGCCGACCGCAAAG	NEURL1B	656	792
GTGTTCTACAGCGTGAACGA	NEURL1B	808	851
CTGCCCGATCTGGTCAACCT	NEURL2	832	1132
GGTCTTCCTGGTCGAGATCG	NEURL2	1012	772
TGCACCCGATGGAAGCGGGT	NEURL2	725	721
TGCGCAGATATGGTTCCACG	NEURL2	724	1644
AGGCGCACCACGTTCCACGA	NEURL3	1739	1424
CTCTTCGCCAAGGTCAACGC	NEURL3	1581	1347
GGACGTGTATGGGACCACTA	NEURL3	1321	725
TGGAAGCGAAGTGCCTCTCG	NEURL3	777	686
AAGAGAAATGCACTGTACGG	NFX1	538	1448
CTACATTTATGTGTGACAAG	NFX1	1423	1499
CTTACCACAGAAACAAGTGT	NFX1	1419	1259
TCCACATAACACATCTCGGG	NFX1	1091	1117
CATCACCAACGACTGCCATG	NHLRC1	1226	671
CCTGCAGAATGGGCACTCGA	NHLRC1	692	1420
TGGCGCTTTGTCCCAAGACG	NHLRC1	1121	1343
TGGTAACTGATGCGGAGGCA	NHLRC1	1388	512
CGGACTCTGAAGATAGCCTG	NLE1	472	831
GAGGTCTTGGGGATTAACTG	NLE1	683	1008
GTCCACGGGCACGTCGAACG	NLE1	1024	1000
TTTCTTAGGACACAGACACT	NLE1	975	1292
CCACAGATGATGTCCAACCT	NOSIP	1379	504
CTCACGTGACAACAGGATCG	NOSIP	450	1118
GCCCCGCACATGGTCCTGCG	NOSIP	1100	1770
GTCAGGTCCGACATGCGCAG	NOSIP	1803	783
AGAAGTTTGTTCAAAACAAG	NSMCE1	641	1088
GATGACCCATGGCGTGCTAG	NSMCE1	1201	310
GTCCTCCAACTTATCTACGG	NSMCE1	247	1045
TGGGAGACCCATTTATGCGT	NSMCE1	952	1325

AGCAGACTCTACACCACTGA	NSMCE2	1277	1246
AGTGAGTAGTGAATATAGTA	NSMCE2	1074	1065
GCAACTAAACCATTATGTAA	NSMCE2	917	1380
GTCCATACCAGAGTTGATAC	NSMCE2	1377	1459
ACTACAGCTCACTACCACAC	NUP43	1552	1019
GTAAATCCATTACATCACCA	NUP43	1076	545
TCCGGGAAGTTTACAGACCG	NUP43	492	1077
TGGGATGTCTATCAACACAG	NUP43	959	220
ACAACATCAGCCGAGCCGCG	OSTM1	216	546
ACAGCAGCGCAGAGCTGACA	OSTM1	614	1308
AGGTCGTGGAAGACCCTGTG	OSTM1	1369	677
GTTATGTTCAAAGCAGGTCA	OSTM1	659	836
AGGCCAGACAGTTAACACCT	OTUB1	837	1226
CATCTATCAACAGAAGATCA	OTUB1	1138	1253
GAGCACCTCCGACTACCTTG	OTUB1	1194	623
GCAGGACCGAATTCAGCAAG	OTUB1	540	1159
AGTGCCGGAAGAAGTCTGCT	OTUB2	1050	855
CGCCATCCGCAAGACCAAAG	OTUB2	768	425
GATTTACCGGAGGAAAATCG	OTUB2	391	1329
GTTCAACGACCAGAGTGCCT	OTUB2	1277	594
CTCCGCCGCACTACTCGGGG	OTUD1	617	915
GCCAAGTGCTCTTCGCCCCA	OTUD1	834	1250
GCGGTGGACGTGTAGTGCGG	OTUD1	1182	1217
GCTCAGTCGGAAGTTCCGAT	OTUD1	1045	853
AAGACCCGAACCAAGCACAT	OTUD4	825	1580
ACAACAGATGTGGATTACAG	OTUD4	1536	1863
AGAGGTACATCTAACTCCTG	OTUD4	1966	868
AGGGATTATGAGGATAAACA	OTUD4	770	723
CCATGGGATACATCAAAACG	OTUD5	681	896
CCTGCCATCATTCAAACCAG	OTUD5	877	1024
CGGCGCAGGCTACAACAGTG	OTUD5	1070	828
GGTTGTGCGAAAGCATTGCA	OTUD5	780	1524
ATTCAATGCTACTGTCGTCT	OTUD6A	1434	1073
CCAAGACGTGGCCCGCATGG	OTUD6A	1180	973
GGCCGGCTTCAAGCGCGAGG	OTUD6A	801	1767
TGCGCCGCCACCAACGCGAG	OTUD6A	1760	1455
AAAGGATTGTGCTCTGACTG	OTUD6B	1587	823
GAAGCAACTCACCGAAGATG	OTUD6B	830	333
GCGCTAGAAGAAACCTGCAC	OTUD6B	307	664
TGCTTGAGAATCAGCCACCT	OTUD6B	702	649
AAGCTGAAGAAAAACATGGG	OTUD7A	574	1035
AATTGCTGCACACCGAATCG	OTUD7A	964	635
TATGGGCTAGGACAAAAACG	OTUD7A	745	1408
TGTGCTCAGAATCCGTCAGG	OTUD7A	1233	1094
AAGCGTTGAAAAGGCGCTGG	OTUD7B	906	935
CTCCCCTCACTAAAGGATGG	OTUD7B	917	757
TAGGAGGCCCATAGTCGTCG	OTUD7B	591	880
TAGTGTAATTCTGTCCCTAG	OTUD7B	804	907
AAGAGTCCCTTACTCTGCTG	OTULIN	735	1033
ATTGCTTATACATGAAAGAG	OTULIN	1007	588
GTGATAATTACTGTGCACTG	OTULIN	541	850
TGAACTATTCACAAATGAGG	OTULIN	819	1039
ACACAGAGAATGGGTACGTA	PAFAH1B1	979	798
GAATGCATCAGAACCATGCA	PAFAH1B1	824	1012
GACATTTCATTCGACCACAG	PAFAH1B1	924	1130
TGTATGGGTCGTAGCAACAA	PAFAH1B1	1154	852
AGCTTCAAAACAAACCCTTG	PARP11	731	970
GACACGTCAGATACCCAGTG	PARP11	1019	1272
GCTAACTGAACACTGACTGT	PARP11	1184	496
GTATTCACATTCTCCCAGTG	PARP11	415	1332
CCAGTCCCGAGGTTTGGACC	PCGF1	1253	1080
CCTTGCACCTCGTTCCGTAG	PCGF1	1088	1365
GCTCATCATAGCGATAGTAG	PCGF1	1293	1258
TGGATCTTAATGTTGCACAT	PCGF1	1230	892
AACGGCTCCAATGAGGACCG	PCGF2	758	1219
CATCGACGCCACCACTATCG	PCGF2	1152	607
CTCTCCATCGAATTCTACGA	PCGF2	559	1387
TGGACCTGCACGTCACACAT	PCGF2	1535	1199
AGAAATTGATTGGACACACC	PDE4D	1210	1678
ATGGATGGTTGGTTGCACAT	PDE4D	1857	669
CAAACAGCGGCGTTTCACGG	PDE4D	552	750
GCTGTCGGATCGATACAGGA	PDE4D	655	803
CCGGCCTGGAGACATAATCG	PDLIM2	829	901
CTGCCGTCTACCCGACTCTG	PDLIM2	746	533
CTGGGGCTTCCGTATCACAG	PDLIM2	425	1000
TCCGAGGGCAAAGTACCCTG	PDLIM2	884	387
CAGAAGAAGCACGACGAAGA	PDZRN3	336	637
CATTGGGATTTATATCAGTG	PDZRN3	589	1199
CTTCACTGGATGATCCATCG	PDZRN3	1125	1036
TACGGCCTGTACTACCCTAG	PDZRN3	1082	1040
AACTTCGTCGGCGACCTCGG	PDZRN4	880	957
CAATGTATTCACCAGATACG	PDZRN4	849	1913
CAGTGCGACTACCGCGCCCG	PDZRN4	1830	900
TAGTAGACCAGCCTATGGGA	PDZRN4	783	758
GGCTCGTTAATTGACCTCTG	PELI1	617	517
TAAAAGACCTAAGGCAAATG	PELI1	545	1497
TAGCCTACGTGAAACCAGAT	PELI1	1443	1105
TCTTCTGTGAACCCATTGCG	PELI1	989	697
GTAGATTTGCCCTCTACAAG	PELI2	477	555
TGTACACCTTGCGAGAAACC	PELI2	535	492

TTTGGAAGAGTCAAATCCGG	PELI2	454	1150
TTTGTCAAGGAATCAGACTG	PELI2	1293	786
CAATGGTTGTCTGGCAAGTG	PELI3	681	1261
CACCAGGCACTGAGTAACCG	PELI3	1064	978
GAAGTCAATCATGTTCTCTG	PELI3	953	573
TAGATGCGGGCAGTATAGGG	PELI3	410	958
AGGCAACATGTAGCCGCTGG	PEX10	761	1218
CAGAAGGACGAGTACTACCG	PEX10	1147	777
GGAGCTTCTACCTGCAAGTG	PEX10	641	1016
TCATCCAGGTGGACCCATCG	PEX10	967	979
CAACAACTTCGATACATCCT	PEX12	1154	743
CTTAAAGAGAATTGTAATGG	PEX12	602	1541
GAGACCCGCTCTTCAGCATG	PEX12	1265	1077
TCTGTAAAATCGTTTCCAGC	PEX12	987	684
AAAATACAGAATGAATACCT	PEX2	674	641
CTACTCCAAAAATGCCACAG	PEX2	542	595
GCTTTCATGGATTTAAACCT	PEX2	476	981
TGGCTGATATCTCAGGTTAG	PEX2	913	1033
GTTCATTCACCACCAAACGT	PHIP	997	1897
TAGGCTGCAAGCATGTTGTG	PHIP	2017	622
TCAACATCAACCAAAAAAGG	PHIP	525	1257
TGATGGAAACGTGATAGTGT	PHIP	1562	1040
GAACATGTAAGGGCCCGACA	PIAS1	893	880
TAGGACTTGAATGTACGTTG	PIAS1	923	718
TGATGAAATACAATTTAAGG	PIAS1	566	499
TGTGGACAGTCGGACAAGTG	PIAS1	584	1730
ATACAGTCCAAGTTCAGTTG	PIAS2	1752	1099
CAAACACTTACCTAAACTCG	PIAS2	1018	651
CTAAAGATGTAATATTCAAG	PIAS2	574	787
GATGTGTACAAGTCACTGCA	PIAS2	733	888
ACCACAAAGAGCCATACCAA	PIAS3	754	1498
AGTGGCTGAGAGTCGAGCCA	PIAS3	1463	494
TCTTCCGGGGAAAGCGTCGT	PIAS3	491	1026
TGACACCCGGAGACTTGTAG	PIAS3	826	1528
GAAGCACGAGCTCGTCACCA	PIAS4	1437	1883
GACCACTCACCTAATTCGGT	PIAS4	1662	426
GATGAGGGACACCCGCACAC	PIAS4	424	956
GCACGGGGTAGTCAATATTG	PIAS4	857	742
GAGTAGTGGAAAATGGCGAT	PJA1	734	1029
GCTCCTGTGAGTATTTGTGG	PJA1	701	548
GTGCGTCCAGAAGTCAGGGT	PJA1	472	1315
TTCTTGCCAGGCCATCCGAG	PJA1	1402	815
ACTGATAAGTTCAAGCCAGG	PJA2	806	1222
CAGTTAAATGAGGGAACTGG	PJA2	1132	1216
GTAATAACTCTTGAGTATGG	PJA2	1184	1778
TTCAATGCTGAACCACAAGT	PJA2	1791	675
AGTGCTTCGAGGCACACCAG	PML	826	1539
GCAGGATAGTGCCTTTGGCG	PML	1326	663
GCGGTACCAGCGCGACTACG	PML	658	1007
TTGATGGAGAAGGCGTACAC	PML	1116	875
AGATGAGCCTTCCTTCTAAG	POC1B	845	2080
CTTGTATCGACATACACACT	POC1B	2396	1094
TATCTGTAAGCTCTAGCATG	POC1B	1117	1284
TTCTACAAATCAGTTCACAG	POC1B	1135	948
CACCAACAACACCCACATCG	PPIL2	972	1520
GGCAGGCCCACTATTCCACA	PPIL2	1428	1380
TGAACTTGTCCAAATTGGTG	PPIL2	1292	1267
TGAAGAAGAAGGGCTACGTG	PPIL2	1458	711
CTGAAGAAAAGCCCTCGCCG	PPM1D	489	905
GCCAGTGTGGTCATCATTCG	PPM1D	934	983
GGTCCATTGTGAGTGAGTCG	PPM1D	878	1517
TTGAGGGTATGACTACACCT	PPM1D	1625	914
AAAAGATTTGCGCACCCAAG	PRC1	858	838
AATCGATTTACAAACCGAGG	PRC1	754	1221
ACCGCACAATCTCAGCATCG	PRC1	1285	993
GCGGTTACAAAGAACTGAGG	PRC1	815	1243
AGGTGGTTGCTAAGCGACAG	PRKN	1165	1127
AGTCTAAGCAAATCACGTGG	PRKN	1156	1324
ATGCTAGACTTACCCACACA	PRKN	1465	1715
TACTTACTGCACTAGTCCCA	PRKN	1838	1114
AAATCCTGATAGTGGCATCG	PRPF19	1097	1017
CAAAGCCACTGTGCTAACCA	PRPF19	1031	437
CTAATCATGTTTATGAGCGG	PRPF19	373	1438
GCTCCTCCGATGATCAGGTG	PRPF19	1166	1043
AAACACATCAATCACTCTGA	PSMD14	1141	779
AAAGCCAACAACCAAAGCCA	PSMD14	741	603
AGACAAACAACTTCGAATCT	PSMD14	489	757
ATCAAACCCATAACTTCCAT	PSMD14	784	1120
CCTCGCTGTACACACAGACA	PWP1	997	866
CGACTTAGATAAATATGATG	PWP1	793	783
GTATCTTTCAGAGTAACGTA	PWP1	715	1877
GTCCCACACTTCAATAACAG	PWP1	1678	918
CCATACCCTCGAAAGACCAG	RAB40A	921	1081
CCTCAAAGAAGGTCACACCC	RAB40A	1159	1437
TCCCCGTACAGCCATCTCGG	RAB40A	1370	641
TGAAGCTCTGGGATACGTCG	RAB40A	561	483
ACCCGCCGGGTGGCCGTACG	RAB40B	451	655
ATGGATTAAGGAGATCGATG	RAB40B	716	1027
CAACATCACAGAGTCGTTCA	RAB40B	885	1486
CATAGACCAGGATCACACCC	RAB40B	1509	1165

ACCGTTACTGTAGGCGTACG	RAB40C	1234	1186
GATGCGGGATAGCTCCGTGA	RAB40C	1074	416
GCCGTCAAAGGACCAGCGGT	RAB40C	355	313
GGTTTCCAACCAAGATCCGG	RAB40C	230	1067
AGGAAGTCATCCGCTGACGC	RABGEF1	937	803
AGTGTCTGATATGGTGGTGA	RABGEF1	786	561
CAGGCAGAAGCAGATTCAGG	RABGEF1	483	592
TCAGGATTTCTACCACAATG	RABGEF1	591	711
ACCTTAGTCCGTACCTCGAG	RACK1	661	1264
AGTGTATTTGCACACACCCA	RACK1	1323	959
CCACACAGGCTATCTGAACA	RACK1	867	488
CTTGCGTTGTGAGATCCCAG	RACK1	512	1547
AGGATGCAAAGCATCGCATT	RAD18	1612	2001
AGTGGATTGTCCTGTTTGCG	RAD18	1900	1131
CAAATTCAGCCCTCAAAAAG	RAD18	955	1074
TCCAGACAGTCTTTAAAGCA	RAD18	916	599
AGATGCGGCAGAGATGTCGA	RAG1	593	708
CAGTGGACACCATTGCAAAG	RAG1	633	1595
CATGTGAGGTTTACTTCCCG	RAG1	1533	1018
GGACTGTGAAAGCCATCACA	RAG1	914	1023
ACGGGAATTCTATCGCCCAG	RANBP2	896	192
CGAAACGAAACAATTTCGCG	RANBP2	166	915
TGGTACTTCAGAGACAAGCA	RANBP2	918	909
TGTGAACATCCGGCTAGTGG	RANBP2	824	1331
CAAAAACTCATACCGCATGG	RASD2	1299	1058
CCAGTACACACCCACCATCG	RASD2	1018	1112
TAACCGGGAGTCCTTCGATG	RASD2	939	713
TGTGGCAACAAGAACGACCA	RASD2	704	1882
ATTGCCGTTACAGACCAGAA	RBBP4	1898	734
CACTACGACAGTGAGAAAGG	RBBP4	755	747
CAGTGTGAGCATCAACTGAG	RBBP4	746	614
TCTTGGAACCCAAATCTCAG	RBBP4	526	1506
AAGATTCTCCATGGGACGAG	RBBP5	1486	961
CCAGATAGATACCACTCCAC	RBBP5	1013	799
GGCAGCAATAGGGTCCACGC	RBBP5	743	838
TGGGGATGGGGAATACATCG	RBBP5	917	871
AAGTCGAACTGAACCAGCGA	RBBP6	790	1148
GATATCATCGATCTAGGTCA	RBBP6	1130	916
TGAGACACAACAATTCATCT	RBBP6	928	1151
TTAATTGGAGGTTCAGATCG	RBBP6	1039	1434
CATGGTCATCAGATGCACTT	RBBP7	1490	1341
GAATGAGAGGCAGTTGACTT	RBBP7	1369	751
GGCCCAGTCTTACCGTTCAG	RBBP7	701	769
TCTGCGGCATGTAACGAGCA	RBBP7	764	1027
AGTGCGCCCTGATATGACAG	RBCK1	1120	966
CCAGCACCGAGTAGCACACG	RBCK1	1007	1016
CGCCTCATACCAGCCCGACG	RBCK1	939	1578
GGAGACCCTGCACTCCCATG	RBCK1	1491	1160
AGTACACTCTTCTGAAGTAG	RBX1	1138	845
ATGGATGTGGATACCCCGAG	RBX1	733	795
CAGAAGAGTGTACTGTCGCA	RBX1	725	1079
GTTATCAACCACAATATCCC	RBX1	1078	922
ACGGAGCAGGGTACACTCGA	RC3H1	1006	743
GGATATAACTGAGAACCTCG	RC3H1	650	1168
TAACACAGCTTATTCCGCGA	RC3H1	1183	925
TTAGAGGCTTGAGGAAACCG	RC3H1	750	214
AGAATTCATTCGATCTCGAG	RC3H2	251	487
CAAATCACCATACAAAAGAG	RC3H2	406	1207
GGTTGCAAAGAAATGCGTTG	RC3H2	1194	817
TCATTTGAAGACCAGTTGCG	RC3H2	713	915
ATTTACTTGCAGATTGTCTG	RCBTB1	912	1204
CTGAACTATAGTAACTGTCT	RCBTB1	1004	798
GGGAATGGGACGACCAACCA	RCBTB1	811	1592
GTGGTCCACTCCCGTAACTG	RCBTB1	1479	1080
ACATATTGGACAATTCTGTC	RCHY1	1088	1190
ATCCAGCTGTCTCCAATACC	RCHY1	1128	1025
GTTGCTCATGTCTTGCCATG	RCHY1	943	1376
TTCTGATATTCTGATGGCAT	RCHY1	1328	1316
ACCAAGCTGCAAGTCCTGTG	RFFL	1324	793
AGGCTGTAGCTCGAAACCGT	RFFL	702	1195
CAGCTTTGTCCCAGGCCGAA	RFFL	1082	1195
TTTCGGTAGAGATGTCATGG	RFFL	1200	737
AGGAATCTGTGAACCGACAG	RFPL4A	670	1781
AGTGGATATGACGTTCGATG	RFPL4A	2013	574
CCTGAGGAGTTTCCGAAGTG	RFPL4A	478	938
GAAGCCGTGCAACTGAAATG	RFPL4A	835	606
ATCACTAGCATATGACAATG	RFWD2	656	709
GATTCTTATGGAATTCCTCA	RFWD2	581	936
GCTAACGTGCTATTATACCA	RFWD2	917	678
TACCAATCTAGACAACTCAG	RFWD2	682	644
ACAAGTACGAAAATGTCCCC	RFWD3	732	1577
ACTTCAGAACAACATAGGCA	RFWD3	1484	1245
GAAGTTACATGTATCGATGG	RFWD3	1357	1074
GAGGGTATCTGCTTCACGGA	RFWD3	892	842
CAAGGATAACGGGTGTTCGA	RHOBTB1	836	973
CGCCCACACTGTTGGCACGT	RHOBTB1	1189	1322
GGATTCCTCAGGCCGACCAG	RHOBTB1	1293	566
TCCTCAAATCGAACATCTCG	RHOBTB1	595	1380
AGCACCTCCTACCTAGCCAA	RHOBTB2	1258	1191
CCAATATCGTGTGTGCCAGG	RHOBTB2	1321	796

CGTCGCTGGTGGAAGCACGG	RHOBTB2	771	1620
TCCACCATGTCAAGACCATG	RHOBTB2	1701	336
ACTTCTCGAAATCTAATTGG	RHOBTB3	272	835
GCACCTGGTTGTTCAAGTTG	RHOBTB3	688	1197
GCCTGATACTCGGTGAACAC	RHOBTB3	1342	904
TTAACAATGACTCGTAATGG	RHOBTB3	907	1062
AAAGTAGTGTTGACTAAGGG	RICTOR	952	674
GGCATAGTCGCAAACATCTG	RICTOR	635	607
GTGCCAAATAATTATCCATG	RICTOR	534	1167
TGTCTTCACATGCTTCATCG	RICTOR	1231	809
ACTGCATTGTCACAGCCCTA	RING1	925	1101
GACCACAACGATGAGTGGGG	RING1	1238	671
GGGGGAGCAGTGTAGGGACA	RING1	687	594
TAAGATCTATCCTAGCCGGG	RING1	619	469
CCCGGCACCATGTGACATTG	RLIM	451	587
GTCACCTATGAAAGTGAACG	RLIM	473	1253
TGATCCTGTAGATTCACCAC	RLIM	1431	1258
TTCAACTGAAGCGTTAACAG	RLIM	1179	1263
GAAGTGCCGAGCATAGCTGA	RMND5B	1196	960
GCCCTGCACGAACAAGACCT	RMND5B	1002	645
GTGGAACACCTGTATCAGCA	RMND5B	556	1072
TCACAGCAGTGTATCCCGAG	RMND5B	1110	970
CAGATGACAATCTTAAAGAG	RNF10	817	1351
CGAGGCAGCGCACATTCACA	RNF10	1360	841
TGCATAAGAAGGATCTCAAG	RNF10	897	753
TGGGGAAAGAGGAACAAGTG	RNF10	872	380
AGCTGTAAAAAGCCCAACAC	RNF103	394	1003
CAATTAGTAAACCATGACCA	RNF103	929	1604
CACCGGATCCACCAGCTGGG	RNF103	1433	1164
TTTGCGCTCATTACAACCCG	RNF103	1111	1040
ACCCAACACCTAGCCAGACT	RNF11	1002	708
ATGGATCAGAAAAAAAGATC	RNF11	696	1349
CCCTCCCCTACCTGATATGG	RNF11	1384	924
TCACGAGTCTCAGTCCGACC	RNF11	869	1462
GAGGATGTCCTAATGCATGG	RNF111	1544	951
TAACAGTAGAAATCCTACTG	RNF111	824	1019
TCTTCATTGGCAGTAACCTG	RNF111	1101	1529
TGATGATAAAGGTTGACTTG	RNF111	1579	1414
ATACAGAAGACCCGTGACAG	RNF113A	1044	781
GAGGATGACAAGATCTATCG	RNF113A	803	776
TGAGCCCGAGAGTCTCGGCG	RNF113A	712	1762
TGTAATCTGAACGGTCATGG	RNF113A	1789	446
AGGGCCCCATACGTGCGCCA	RNF113B	324	807
GAGCACGACCACATCTACCG	RNF113B	868	556
TGGACCTGTACACCACGTCG	RNF113B	663	1322
TGGCTGCACTTGAGGATGGT	RNF113B	1321	999
ATACATTCTTACGGCAGCCA	RNF114	1083	1279
GCCGCTTACACGTGTCCGCA	RNF114	1205	808
GGACACGTGAAGCGTCCTAG	RNF114	688	1237
GTCCAAGATCCGGTCCCACG	RNF114	1080	1241
CTCTGCAAAATGTGTTGTTG	RNF115	1196	691
GCTCTATTATCTTGGTCCAG	RNF115	550	811
GGTCGGAGATACAGATCTCG	RNF115	729	1581
TTAGGACAACTGGAAAACAC	RNF115	1732	988
ACCACTTATAAACCAACCTG	RNF121	879	1111
CGCATGCATGCCAAGCACCG	RNF121	1177	1442
GACTACATGGCATCTACCAT	RNF121	1383	1075
GGCTTACATTGTAGGAGCGT	RNF121	1126	508
ATGACCATATAGATGTTGAG	RNF122	473	781
CAAGAAGTTACAATTATATG	RNF122	687	1208
TGAGCGATACGGATATAAGG	RNF122	1133	962
TGTTGGTGCTAACCAGTCCC	RNF122	1058	1112
CCAGTGATACACCGTTCCTG	RNF123	951	1072
GCAGCGCAAGGTGTATCTGG	RNF123	1045	1113
TTCATCCCAATAGTAGCGCA	RNF123	1094	945
TTGAGCACGGTGATCGCACA	RNF123	1194	1170
GTGGACCTGTCCTTATTGCC	RNF125	1233	1047
GTGTAACACCTCAAGGCACA	RNF125	1096	1934
TATGTGCCCTCATTTCACTG	RNF125	2099	1125
TGGACCACTACAAGAACTTG	RNF125	1185	229
CCTGGATGCCATCATCACAC	RNF126	267	1302
GGGAGAGAGACCATCCGTCC	RNF126	1142	613
GGGCGACTCACCTCCAACGG	RNF126	562	1266
TGCGCCCCAGGAGGGAACGT	RNF126	1420	1296
ATTCTGCAATCTATTCAAAG	RNF128	1055	912
GCACACGGGAGTGAACCGTA	RNF128	814	887
GCACCGTGAAATTCGTGTGC	RNF128	896	937
TGGTTGGCCCTCATCCAACG	RNF128	997	854
GGAATTAGGTAGTATTCCAA	RNF13	804	504
TATAACCAAATCTTGCAGGG	RNF13	467	1066
TCTGATGACCTCATTAGCAT	RNF13	1315	915
TGGAGGCACTATGGGTTCAC	RNF13	1020	846
CCACCGAAGAACTTCAGCCG	RNF130	679	1115
CTCACGTTTCGCATCGACCG	RNF130	1235	1267
GTCATGATAACAGAATTGAG	RNF130	1155	1684
TGACTACAGCAACTGCATTG	RNF130	1611	746
AACTTCGAGTAGTAAAAGAG	RNF133	621	976
CTTGCACTTATTGAACGGGG	RNF133	911	686
CTTTCTCCCCACCTCAACCA	RNF133	633	812
TCCTGCCACTCTCTTCAAAG	RNF133	759	795

AATTACAAGAAAGCGTCACC	RNF135	733	709
GCCCGCCTGTATCTCGCGTG	RNF135	804	382
TCAGAAGCCTGCAGAATCAG	RNF135	366	1029
TCTTCAAGTTAAAGGTTGGA	RNF135	942	1313
CAAAACGCCCGTGCGGACCA	RNF138	1073	674
CACAGGGGACACTTAAAAGT	RNF138	604	1303
CAGATCTCTCAAGATTCAGT	RNF138	1136	1577
GTCACATTTCCACGACATAG	RNF138	1534	235
ACCCGGATTCCAGCCAAAGC	RNF139	187	744
CACTGAGAGACATTAATACA	RNF139	684	631
CCCCAAATAATGGGCTACTG	RNF139	560	558
GTTAATGTACATCTTAAGGA	RNF139	559	599
AATTTCAAGATATTTGTGAG	RNF14	545	736
GGAAGAACACCGTGGCAGCG	RNF14	677	838
TCAGGTCCAAGGAGGACTGG	RNF14	847	1403
TGGATCTGATGTAGACCAAG	RNF14	1470	860
AAAGCAGAGGAATCAGACCC	RNF141	752	1032
AGTAGCAAAACATGTTACGT	RNF141	1062	1103
GCTGAGCTTAATGATGTGTA	RNF141	1097	745
TGTACGGGTGGTCTGTACCA	RNF141	674	727
CAGAGCTTGCAAGACACCAG	RNF144A	627	977
CCAGAGTACAGAAGATGCAT	RNF144A	962	455
GCAGTGCAAAGCCTGCCGTA	RNF144A	416	517
GCCGGGCACCAAGTCCGACA	RNF144A	410	891
AACACGAGCAGAATTTCAGG	RNF144B	739	1211
ATCTGGACCCCTACCGAACA	RNF144B	993	955
ATGCAGCTGGCAATCCGAGA	RNF144B	817	1203
CTGGTCCACAGGTACCAAAC	RNF144B	1109	1260
ACTGGAGGCAGTGTTAAATG	RNF145	1335	1316
ATCAGCCTGCATCACGTGAG	RNF145	1467	1113
ATTCCACAGGGACATTCCCA	RNF145	1154	694
TAAGAAGCCAAAAATCCATG	RNF145	559	806
CATTCAGGGACGGTTAAAGA	RNF146	664	578
GAAATGAACATGGACGTCGC	RNF146	572	1093
TGACCATCTACTGATGTTAG	RNF146	1230	783
TTGTCGACAAGAAATTCCCG	RNF146	721	1460
ACCTTGCCCATGTCTCACGC	RNF149	1704	1419
CGTGGTAAACATCGAGTACG	RNF149	1570	838
GGCTAACGAGATAATCATCA	RNF149	776	835
TCCAGTAACGATGACCATAG	RNF149	974	1562
AGACAAACACAACCGAAGTG	RNF150	1522	1117
CAAGGGCAACTGCACGTACA	RNF150	1247	834
GCTCTGCCTGGACTTTACCG	RNF150	768	1361
GTTTCGATATGCAAATGCCA	RNF150	1239	659
CACACGAAGTTGCTGTCAGG	RNF151	603	606
GCAAAAAGTGCATCCTCCGG	RNF151	423	1084
TCTGCCATGGGGTTCTCAAG	RNF151	904	1278
TTGTCCACATGAATAAACTC	RNF151	1241	452
CCAGCAGAAGTCCGTCACCG	RNF152	387	507
GGGAAGTTTGATGAAGACCG	RNF152	434	640
GTTTCAATTACTACAGCCCC	RNF152	535	894
TTGGTGACACCGCGGCACCA	RNF152	935	1523
AAAGTGGTGCATTCGAGGAG	RNF165	1477	1148
AGGAGGGACCTGTGACGTCC	RNF165	1045	741
AGTTGGCCGAAGTCGAAGCT	RNF165	733	1320
TTTGGCTCTGTGCGAAACAG	RNF165	1405	1276
ACCTTCGCCTGCCCGTACTG	RNF166	1320	691
CCACATCACAGCCTATCCCC	RNF166	664	1110
TCCTACAAAGCGCCCTGTCG	RNF166	1046	1465
TCTGCCTGGAGGTCTATCAC	RNF166	1511	467
AAAGACTGACCCATTGACCG	RNF167	397	1295
CCTACACATGACTATCAGAA	RNF167	1274	526
GATCCCGTCTGTATTTATTG	RNF167	471	1168
TGGATACAACGAGCTATCTG	RNF167	1153	831
AAGAAATTCTCTCGTCAACG	RNF168	721	982
CAGCGTGTGGTTACACGGGA	RNF168	918	440
GCACCACAGGCACATAACCA	RNF168	401	1000
TCGTCTGCTCAGTAAACCTG	RNF168	933	1252
AATCCACAAGCTGTTACCAG	RNF169	1182	673
GATGACACAGACACATCGCT	RNF169	688	710
TCAAAACAACCGCTGCGTCT	RNF169	563	1271
TGCGGCCACTCGCTTTGCCG	RNF169	1126	863
AAACATTCACCCAGAAAACC	RNF170	810	1057
ATTATAACCGGAGATTCTCA	RNF170	896	965
GCGATATGGTTCATGGCTTG	RNF170	1013	1078
TTCCCGGTGGAGACCAACTG	RNF170	1112	1491
AGCTTTCTGCAGAAGACACA	RNF175	1348	1896
GACAACCCACATCTGCAACA	RNF175	1896	806
TCCCCATTACTCCATAGTAG	RNF175	794	895
TTTCCACGTGCATGGAATCG	RNF175	874	1465
ACTGAATTGTCCTTTCTGTG	RNF180	1421	664
CAAGCTGGGGAACAAAAAGC	RNF180	588	964
CATTGGGCAGCATTAATCAG	RNF180	930	1127
GACTGATTATCAGCCAACAC	RNF180	1203	1472
CAAATTCCAAAAGACACACG	RNF181	1284	767
GTGATGGCAAGGCATCTCAA	RNF181	926	893
TCCTATTGAAAAGTGACCTG	RNF181	880	1463
TGAACACGACTGCGAGCCGT	RNF181	1352	1277
ACAGACAATGACACCTTGTG	RNF182	1398	770
ATAAAATTCTACCACAGGAG	RNF182	623	1314

ATCCTTGTAAACTTGACTTG	RNF182	1225	676
CCTGGTCATAACCATCATGG	RNF182	652	1173
CATCTTACCTGATGTAAACA	RNF185	1264	1347
CTGAGAACTCCAGTGCAGGG	RNF185	1928	1149
GGAGACCAGACCTAACAGAC	RNF185	1006	271
GGTCATCCCCCTCTATGGAA	RNF185	237	1266
CTGCAGCCTGCGCGACCATG	RNF186	1383	1071
GCGGTGACCTTGCGGCACAG	RNF186	995	473
GCTGGCCCAGCCATGCACAG	RNF186	484	919
TGAAGTAAGTGCAAACCACG	RNF186	1002	875
AGCAGTCGTCGGCGCACTCG	RNF187	828	1322
CAGCGCGGTTCCCACTCGGG	RNF187	978	1146
CGCACGCCCGACAGAAGCGG	RNF187	886	928
GAAAGGACTTGAATGACGCC	RNF187	870	406
ACACAACCCAAGCATAGGGG	RNF19A	365	1519
ATTATATAAGCAGCACATCG	RNF19A	1535	650
GGTGCCAAATCTGTTTACAG	RNF19A	548	1003
TGTCTTTAGAATGCCGCAAA	RNF19A	962	1578
ATAATGTATGCACTGCATCG	RNF19B	1733	789
CTTGTGCATAAGCGGCGGGT	RNF19B	769	717
GCCCGAAGCTAACTTGTGAG	RNF19B	716	578
GGAAAACCTCCAAACACAAG	RNF19B	525	536
ACAAAGAATGTCCTACCTGT	RNF2	465	982
CCCTTGACTAGACTGCAGCG	RNF2	916	981
GCTTCATACTCATCACGACT	RNF2	909	1205
TGCTTCCTGATTGCTATGTG	RNF2	1363	741
GCACAATCACTATCAATGCT	RNF20	792	1060
GCATCGCACCATGTCTCAGG	RNF20	1022	1201
GGAGGGCACTACCACTACGC	RNF20	1188	865
TGGCAGAAATGTTGGATCAG	RNF20	868	1174
AATCAGTACGTGATTCGGCC	RNF208	1279	1370
ACTCCTACAATGTCACCCAG	RNF208	1259	977
CTGCCACGGCGGCCCCGTAA	RNF208	738	630
TCCATCTTGAGGATGACATG	RNF208	818	2339
AACCAGTACTACGTCCACCT	RNF213	2630	1325
ACTTAAGATCATGTGCACCG	RNF213	1226	531
GCAACATCTGAAAAAACACG	RNF213	498	292
GGTGGAAATCCAATTCCCCG	RNF213	203	1614
AGCAGCGACACTCAATCAGC	RNF216	1566	1135
GAAGCAGCGCTGGTCAAGAG	RNF216	1090	371
GCCCCGTGAAATAACAAACC	RNF216	353	702
TCTGAATTCACTAAGCCAAG	RNF216	671	1115
CCCGGCACATCAGCACCATG	RNF217	1052	747
GAATTCAAAACACTCTGTGA	RNF217	650	243
GATTCCCTCTCCCCCGACGG	RNF217	180	822
GTTGTAAAGTGCTTGCACTG	RNF217	733	740
CATCAACCTTTAGTGAACCG	RNF220	715	1285
GCTGAATCATAGTGGTGTGG	RNF220	1267	374
GGCAAAGGTATAGGAACCGT	RNF220	313	872
GTTGGCTCGTACTCGCAGAA	RNF220	762	795
AAAAGAATTGAATTTACATG	RNF24	730	786
ACCACAATATATATGTTGAG	RNF24	702	435
AGCAACAGAAGAGTAAACTA	RNF24	406	1291
TCAAGCCTCGAGATGAGTTG	RNF24	1333	1052
AACGCAAGCGGCTCTACCAG	RNF25	777	1032
ACAGATAACAACATCCCTCA	RNF25	1044	872
CCCCCACTAGTATCCCCATG	RNF25	827	903
GAGGCAAGATCATACACGAG	RNF25	965	771
AGACTAGTCAGTACCGTGTG	RNF26	868	826
AGCAGGGAGATACTGCACCG	RNF26	758	1346
CCCACATGTGAACCGGACCA	RNF26	1222	907
GTCTTCGAGAGGATGTCATG	RNF26	936	1542
CTAGAACCTGATCTTGCACG	RNF31	1569	985
GAGCAATCTCTCTCAATAGG	RNF31	870	1051
GGATCATGCTCACTAGCTGG	RNF31	1107	960
TTGACACCACGCCAGTACCG	RNF31	1017	668
ACGAAGACATAGTAGCAGAG	RNF34	706	1360
CCATCATGGACTAGGCTCTG	RNF34	1311	1501
CCTTCAGTCGCATTAACTGA	RNF34	1387	747
TGTAAATCTGAATGGACCGG	RNF34	613	768
ACACAGCAATCACGATCGGT	RNF38	751	97
AGACGGGGAGATACATTCGG	RNF38	91	1337
AGCCTCCGAGGCATAAATGG	RNF38	1167	1142
TAACAACAGTGGCACCACAT	RNF38	1259	703
CCATACTCCCAGAAACGCCA	RNF4	575	1627
GACTCACAATGACTCTGTTG	RNF4	1684	1504
TGCTTCCAAGGAGATCTCGG	RNF4	1441	692
TGTGGTGAGCAGTGACGATG	RNF4	858	549
CAGTACCCCCGACAACAGAA	RNF40	449	894
GCAGAAGAAGCTACGCACAG	RNF40	792	1060
GCTCCAGGATAAAGTGACAT	RNF40	896	1005
GGGACGCCCAGCGATACAAG	RNF40	942	833
ACTGTGAGCACAACCCGAAG	RNF41	759	916
CATTAAGCACCTGCGCTCAG	RNF41	856	613
GGGCGACCGTCACAACACTA	RNF41	594	1383
TCCTGAGTGACACTCACTCT	RNF41	1526	901
GCACGGACATCAGCCTACAG	RNF43	864	937
GCCCAGCACCCCTATGCACA	RNF43	876	491
GGTTCTTGGTAAGATCGAGA	RNF43	368	594
TTACCCCAGATCAACACCAC	RNF43	674	529

ACCTCCACACCTCCCCGTAG	RNF44	530	596
AGAGACACAAACTGCCCCAG	RNF44	490	1924
GACAACGACGTGGACCTGCG	RNF44	2063	784
GTCACCACAGTGACGACCCA	RNF44	798	1031
ACCAAATGGCTGGAATCCCT	RNF5	902	817
AGTGTCCAGTATGTAAAGCT	RNF5	765	814
GCTCGCGATTTGGCCCTTCG	RNF5	734	845
GTACGCACCTGATGAAGACA	RNF5	850	1194
ACAAAGGTCAACTAGTCCTG	RNF6	1160	1185
ACAGCGGTTAGATGGCGTCA	RNF6	1215	769
CTAGAAGTAATGTTACAGTG	RNF6	810	730
GTGCGTGAAGCGTTAGCTCG	RNF6	660	1338
AACAAACAAGAGGACTGTGT	RNF7	1385	972
AGCTCAGGCTCCAAGTCGGG	RNF7	745	1046
CCTCAAGAAGTGGAACGCGG	RNF7	962	1124
TTCAGCTTGACATCTAAGAC	RNF7	1261	454
CAGGGAGACTACATCCAACT	RNF8	430	1001
GTGGTTTCGAGAAATCATCA	RNF8	923	905
TGAGCCAAGTAAGACCACAG	RNF8	898	1197
TTCAGTTTGGATGAATTAGC	RNF8	1234	1054
AAGCTCAAATGGTCCAAAGT	RNFT1	1071	1335
AATCTTGTGTGGACACACTG	RNFT1	1562	1150
AATTCCGCTATCTCTTCAAG	RNFT1	971	1100
TGTGTACACAGTCGCTTACG	RNFT1	1155	752
ATCTCTTCTGCAGATTGAGG	RPL12	766	765
GACCCCAACGAGATCAAAGT	RPL12	701	561
GGATAACGTACCAGACCCAG	RPL12	504	1052
TCTTCTGCAGTTAAACACAG	RPL12	998	1224
AGAAGTATGTCCGACAAGCC	RPL14	1183	1267
ATGAGGTCCAAAGGAGACAT	RPL14	1219	1691
GTGTTCTAGGCTTTGGTCGA	RPL14	1649	1367
GTTACCTGTGCGGAAACTTG	RPL14	1269	1309
ACAACCTCTTCAACACAACC	RPL18	1237	603
AGCCACTCACCATCCGGGAA	RPL18	480	1304
CCGCCATAACAAGGACCGAA	RPL18	1265	650
GGACCATAACTGATGATGTG	RPL18	655	1291
AATGGACCGTCACAGGCTTG	RPL19	1346	1352
GAATGCCAGAGAAGGTCACA	RPL19	1223	680
GCTTCCGGATCTGCTGACCT	RPL19	543	1791
TGTACCCTTCCGCTTACCTG	RPL19	1836	1295
AGGCGCTACGCCAGGACCGA	RPL24	1322	1069
AGTCGGCTTTCCTTTCCAAG	RPL24	848	974
GAAGCACAAAAAGGGACAGT	RPL24	999	868
GCCGAGCAGTCAAATTCCAG	RPL24	780	2085
ACGCAAAGCTGTCATCGTGA	RPL27	2184	685
GGGATATCCACAGAGTACCT	RPL27	661	710
GTTCATGAAACCTGGGAAGG	RPL27	555	1012
TGGCAGCTGTCACTTTGCGG	RPL27	809	1266
CCACCGAGGCCTGCGCAAGG	RPL3	1044	1387
CCGTGTCATTGCCCACACCC	RPL3	1411	1172
GGCTACGTGGAAACCCCTCG	RPL3	1004	1160
TGAGATGATCGACGTCATCG	RPL3	1255	1261
ACGAAGGGAACGTCATCGTT	RPL37	1333	823
AGGCCTTAGAGCCACAGCGG	RPL37	749	817
CCTCATTCGACCAGTTCCGG	RPL37	742	724
TTTAGATAACTGGAGTGCCA	RPL37	644	1421
CAGACTAGTGCTGAGTCTTG	RPL4	1356	740
GAAAAATAGATGTGTCGTGG	RPL4	657	1458
TCCTCATTATAGATGATGCA	RPL4	1483	1191
TTTGTTAGGTCATCGTATTG	RPL4	1218	728
AGTGAGCCCAAAGGTTCGAA	RPL7	650	715
CGTTTGTCATCAGAATCAGA	RPL7	629	1125
TATCAATGGAGTGAGCCCAA	RPL7	1121	2084
TTCAGCTTCGAAAGGCAAGG	RPL7	2110	672
AAATGGAACACCAATTCCAG	RWDD3	717	1048
AGAACCAGCTCATGAACCAT	RWDD3	1191	506
CGCGCGGGTAGTCACCTGAG	RWDD3	410	865
TCAGAGTTAATCGAGATACC	RWDD3	726	1342
CTCAGGCGTGAGGTATTCGG	SART1	1358	713
GAAGATAAAGACCCTAGGAG	SART1	562	875
GAAGCGCGATGACGGCTACG	SART1	794	1002
GCCGTCGGACGACACCCGAG	SART1	942	818
ACAGCTGGCCAGACAAGTCG	SH3RF1	781	282
CGGGGTCACAATTAACCCGG	SH3RF1	199	980
TCTGACTGTGATCCGAAGAG	SH3RF1	801	1587
TGCAACAAGACCTTAGCCTG	SH3RF1	1555	1241
ACACAGGCGTCCTGCATTCG	SH3RF2	1168	1177
CTCTACAACTTCGACCTACG	SH3RF2	1192	902
GCAACACGTCTACCCTCCGT	SH3RF2	956	1072
GGAGGTGGATAACGTCCATG	SH3RF2	1078	1063
CCTCCGACTACATTATTCCG	SH3RF3	963	513
CGTGGGGGTAGATCCCGCCG	SH3RF3	490	1038
GCACAAGGGAGAGATGTACC	SH3RF3	997	1698
TCTGTGCGTCACACTGAGCG	SH3RF3	2007	833
ACACTCAAAGCGGTAATCAG	SHPRH	744	743
AGAAACGCAGTCCATCCAAG	SHPRH	713	818
ATTAATCGATGGTGTATCAG	SHPRH	843	1081
TTTCTATCACCGTCAGCATG	SHPRH	1175	917
AACTGCATCCAACAATGACT	SIAH1	1001	751
AAGTTGCGAATGGATCCCAA	SIAH1	710	1253

CAGAAGACGCATATTTACAG	SIAH1	1159	730
TAAGTCCATTACAACCCTAC	SIAH1	715	721
AAGAGCATTACCACCCTTCA	SIAH2	746	929
GACCGGACACTCGAAGAGCG	SIAH2	752	455
GGTCAGGGAACAGCCCGTGG	SIAH2	355	1530
TGCAGGAAGCACCAGGACAT	SIAH2	1576	1565
AAGACTTTGTGATTGTCCGC	SKP2	1459	1053
AGGTCTCTGGTGTTTGTAAG	SKP2	867	1077
CTGAGACAGTATGCCGTGGA	SKP2	986	789
GTTGGTCCATAAATGATCGT	SKP2	901	1185
CCACTCTTACCTGTTCATAG	SMU1	1059	882
CTTGCCTCGAAACAAATCTA	SMU1	901	825
GTTTGGTCAGAAATCACATG	SMU1	699	1630
TACCACAGTCATACCTCACG	SMU1	1789	771
ATTCGATAACCATTAGCGTG	SMURF1	795	1523
CACAGACTGGAGTTAGCACG	SMURF1	1468	314
CGAGACAGAATAGGAACCGG	SMURF1	260	1074
GAAGAAGGTTTGGATTACGG	SMURF1	803	682
AGAATACGCTTGATCCAAAG	SMURF2	702	765
CTTCCCTGGAAACCTCAATG	SMURF2	742	1152
GAACAGAGGACAACGCAACA	SMURF2	1102	1324
GTATTACGGATCTCCCATCC	SMURF2	1249	1137
AAGCTAACCTACACCATGAG	SNRNP40	1015	939
AGCATCCACAGATAAAACCG	SNRNP40	827	850
ATTTGACCGACTGATATGTG	SNRNP40	852	1096
GACATTTCAGAACACGTACC	SNRNP40	1115	2097
AAGTGCACGCGGATGCTCGT	SOCS1	2385	1053
ACGCCTGCGGATTCTACTGG	SOCS1	742	794
CGAAAAAGCAGTTCCGCTGG	SOCS1	593	877
CGGCGTGCGAACGGAATGTG	SOCS1	935	618
AAAACCCCAGGATGGTACTG	SOCS2	545	449
AAATTAAAAGAGGCACCAGA	SOCS2	395	956
CTTCGAATCGAATACCAAGA	SOCS2	835	1061
GGAAGGGACGCGGAGCCAGT	SOCS2	1156	788
ACCTACTGAACCCTCCTCCG	SOCS3	631	1123
TACTGGAGCGCAGTGACCGG	SOCS3	1091	578
TCAGCGTCAAGACCCAGTCT	SOCS3	646	1205
TTGAGCACGCAGTCGAAGCG	SOCS3	1248	1054
ACAGAAAAGACGGTTATGTG	SOCS4	993	2058
ACTTGTCTCAGACTGAATTG	SOCS4	2106	874
GCCTAAAAATCGATGCCCAC	SOCS4	786	2213
TTGTCGGTGGTTATGACACA	SOCS4	2175	624
AACAATTTGAGGGATTTCTG	SOCS5	538	1125
AAGTTTGGTAGAACTCGAAG	SOCS5	975	671
GAAGTCGCTCTCTAAGACAG	SOCS5	648	1076
TCCACAAGCTAATTGTGACT	SOCS5	1104	1226
ATCACTACAGTCCCGCGCCG	SOCS6	1050	514
GCGCATACTTTCAGCCACGT	SOCS6	432	1051
TGATGGGTACGCTAAAAAGG	SOCS6	1000	718
TGGCTTGTTGATTGGCACCA	SOCS6	724	843
GATGTGGACATTTCTCAGCG	SOCS7	756	1050
GCGCGTCGCTCGTTTCCGTG	SOCS7	1036	937
GCTCGGATGGGAGCAATCCG	SOCS7	923	857
TGCAGCTCTTGGTGCGAAAG	SOCS7	911	717
ACAAGGCTATCTTAGCAGGT	SPOP	648	822
AGAGGGTAAGCTTGTCATCA	SPOP	857	1292
AGATGAGTTAGGAGGACTGT	SPOP	1342	648
TGTTTGCGAGTAAACCCCAA	SPOP	637	1249
CAGAGCACGGACGCTATCAG	SPSB1	1325	966
GCACGTGTGGCAGATCACGT	SPSB1	1030	1052
GCTGGACATCATAGGACACA	SPSB1	1110	1486
TCGGGTACACAACCCTCGTG	SPSB1	1453	721
AGTCTTTGGGGTTCCAACCG	SPSB2	604	945
AGTTCCCGCTGGATACTGGG	SPSB2	796	699
GCAGAGGGGCACGCATGCCG	SPSB2	608	1316
GCTGCAGACTGACCACTACG	SPSB2	1354	1460
ACAGTCACAGAAGGACTCGC	SPSB3	1496	1309
CTAGCAGGCTCCACTAACTG	SPSB3	1187	978
GCCGAAGCAACTTACCATGT	SPSB3	938	1463
TTCCACATGGAGTACAGCTG	SPSB3	1563	1417
CAGCACCACGAGCAGCGAGT	SPSB4	1420	1021
GCGGCACGCGTGGAACCCCG	SPSB4	813	422
GGCAGTGACGCCGAGTCGTG	SPSB4	362	993
TGGCCACACCAACTACAGCG	SPSB4	975	1858
AATCGATGGATTGCGCCATG	STAMBP	1992	1176
ATACTTGTTATAGAGGATGA	STAMBP	1085	369
CCAGAGCGGAAGTACCGACG	STAMBP	346	749
GAGTTTGGGAAGGTAGACCC	STAMBP	709	964
AAGAAGCAAGAGTTAGCCCG	STAMBPL1	890	1804
ATCTGCAAATACATTCAGCA	STAMBPL1	1879	676
CCAGACCTAAAGTAACGTCG	STAMBPL1	572	665
GGAGCATCAGAGATTGATAG	STAMBPL1	612	1387
ATGTGTGCAGCATCGCCAAG	STC1	1366	451
CTCAACAGTGCTCTACAGGT	STC1	354	804
GAGCCCCAGGAAATCCCGAG	STC1	573	846
TGGAGCACCTCCGAATGGCG	STC1	842	1462
GAAGCGCTGGAACAGCATTG	STUB1	1321	367
GGAGATGGAGAGCTATGATG	STUB1	342	1226
GGCCGTGTATTACACCAACC	STUB1	1059	1978
GTCCCACCTCTCACGCTCCG	STUB1	1854	960

AGGACATCCATACGGCAGGT	SYVN1	1025	551
CCTCCAGAGTGAGAACCCCT	SYVN1	451	1021
CTTGACTCACAAAGTCCACA	SYVN1	995	574
TCAGGATGCTGTGATAGGCG	SYVN1	485	1052
ATATAGCAAGCTGTTGCAAG	TAF1D	1077	1294
CCAGCCAACAGGAAGACCAC	TAF1D	1451	807
CTGTGGAACTTGCAAATCGA	TAF1D	732	1218
TCATTGAAGCAAATGAATGT	TAF1D	1342	826
ATAATTTGGGATGCCCACAC	TBL1X	786	1114
GGCCGAGATCAGTATCAACG	TBL1X	1057	920
GTTCTCTTCCCCATTCACCG	TBL1X	655	943
TGAGGCACTGTATACGAGAG	TBL1X	887	1050
AGGGCCTTTATGCTGCCCTA	TBL1XR1	857	816
ATGCTAGGAGATCACTAACA	TBL1XR1	870	348
TAGAAATCAATGCAGCGGGT	TBL1XR1	315	725
TATTGGTCGACCATCAAACA	TBL1XR1	794	780
CATGTTGTGTAAACTGGCGT	TLE1	903	787
GAGCACTAGACAGCGCAAGA	TLE1	746	1055
GTACCCGCTTGGTTAACGAG	TLE1	1053	1422
TCTGACCGTCTGCAGTAACG	TLE1	1397	935
CAAGAGTGATTACAATCTGG	TLE2	869	438
CGCCTACCAGTGCATCCGAG	TLE2	430	869
GAGATTGTGAAGCGTCTGAG	TLE2	712	1485
TAGAGAGACTCACCCCGATG	TLE2	1302	1332
AGACCCCACATACATGACCA	TLE3	1346	804
CCCACGAGGCACGTCTACAC	TLE3	964	693
CGGGCCAGTGAGAAGCACCG	TLE3	599	843
GGGAGCCGTTCATCTCATGG	TLE3	770	1117
AACATTAGTTATACCCACTG	TMF1	1075	548
GAGGATGGGATACTTCAACC	TMF1	541	634
GATGAAAAGGTACTAACAGG	TMF1	624	1576
TTACATGAATCCTTGCACAT	TMF1	1573	1733
AAGTATGTCCAGCTCAACGT	TNFAIP1	1982	1464
ACAACAAGTATTCCTACACC	TNFAIP1	1345	1393
CTGTGTCGCACAGGACAAGA	TNFAIP1	1422	1265
TGGATCCTCATAGACCGTTG	TNFAIP1	1227	960
AGTTGTACTGAAGTCCACTT	TNFAIP3	1063	724
CCACTTGTTAACAGAGACCG	TNFAIP3	626	653
CTTGTGGCGCTGAAAACGAA	TNFAIP3	551	1035
TGAGAGACTCCAGTTGCCAG	TNFAIP3	887	1312
CAGCTGAAATATCCCTGTAG	TOPORS	1053	956
CCATGGTGCCTGACTAACAG	TOPORS	942	1043
GGACAGTTCAACAAGTTCTG	TOPORS	972	1069
GTAGCGAAATCGTCGATCAG	TOPORS	1024	1729
ACTTGCCACAAGTCTTGACG	TRAF2	1992	643
GGGGACCCTGAAAGAATACG	TRAF2	502	955
TGGGAGACCAGAGCCACGCG	TRAF2	874	1582
TGTGCTGCCTGTGTTCACGA	TRAF2	1721	881
CAACTCGCTCGAAAAGAAGG	TRAF3	866	568
CAGCCAAGCAGAGAAACTGA	TRAF3	557	711
GCCCGAAGCAGACCGAGTGT	TRAF3	782	1894
TGTGCAGAGCAGTTAATGCT	TRAF3	1835	562
AGCTTGAGAAAAGTCTCCGG	TRAF3IP2	413	923
CCTGCGCACTCAAGTTCTGG	TRAF3IP2	896	408
GATAGTTCCATGGAGCATGT	TRAF3IP2	454	533
GGATCTGCCAACCATAGACA	TRAF3IP2	466	1199
AGTGTGCAGGTAGATCACGG	TRAF4	1189	849
CTCTGCCCATTCAAAGACTC	TRAF4	877	1101
GTCTACTGTGAGAATAAGTG	TRAF4	1025	952
GTTGCCTGCCCCAACCAATG	TRAF4	913	1127
AGAGGTCATCAAATCTCAGG	TRAF5	966	1073
GAGTAATACCAACCTGGTAC	TRAF5	977	546
GGGGGTTGTGAAGCACCGAG	TRAF5	505	635
TCATATTGAAGGATAAACGG	TRAF5	665	978
ACAAAAGATGATAGTGTGGG	TRAF6	873	1198
ATGGTGAAATGTCCAAATGA	TRAF6	1037	1067
CAACATTCTCATGTGTGACT	TRAF6	1125	1575
GAAGCAGTGCAAACGCCATG	TRAF6	1435	1000
AGCTGTCCCACATCAACGCG	TRAF7	1002	926
CAACGTCAAACTGACCGTGG	TRAF7	895	841
CCCTGGCACAGGGACCACGA	TRAF7	841	1530
CCGCTTCCACGAGATGCACG	TRAF7	1556	1099
AGGTCATCATCGACACTCTG	TRAIP	1247	802
ATGATCCGAGACATGGGTGT	TRAIP	746	1151
CTGAGGACCTACTTTCAGTG	TRAIP	1058	563
GGTTTGAGACAGCACCAAGT	TRAIP	547	1061
CACTGCGGAGGTTTCGAGGT	TRIM11	927	818
CGGCCATCTTAGCAAGCGGG	TRIM11	696	900
GATCCGGTGATGACCGACTG	TRIM11	934	1080
TCCATAGGCACAACTTCTGG	TRIM11	1099	1629
CAAGTGTCCTACATGCCGTA	TRIM13	1729	1674
CAGTATGCAAAGGACACTTG	TRIM13	1761	658
TGGGAGCAAGGCAAAACCCG	TRIM13	695	1229
TGGGATCTGTGCTACTCGTG	TRIM13	1202	838
AATCACGGATCTTCTTGACA	TRIM15	836	935
AGCTACACTTCTTACCCGGT	TRIM15	880	1030
GATGCGGTGACCATTCCCTG	TRIM15	1017	432
GCTGGGAGAAACTTACTGCG	TRIM15	326	891
CGTGAGTGTGCAGTGCCCAG	TRIM17	928	835
GGCCACAGGTGGTCATCACA	TRIM17	777	774

GGGAGCAGATCACCAGGACA	TRIM17	743	727
TCTGGCGGCTCTCATACAGG	TRIM17	574	935
AGAGGCGCGTTAAGTCCCCG	TRIM2	838	1407
AGCCACTTACATTCCCATCG	TRIM2	1475	484
CCGAACTGAGCACCCCCGAC	TRIM2	383	830
TGGTGGTTAAGATCGTCCCG	TRIM2	866	970
ATCCAGACACAGCCAATCCG	TRIM21	895	1101
GAAACACCGTGACCACGCCA	TRIM21	1121	1194
GAGCCTGTGAGCATCGAGTG	TRIM21	1202	1128
TCATCTCAGAGCTAGATCGA	TRIM21	1056	974
AGAAATAGCAACATTCGAAG	TRIM22	887	985
CCAAACATTCCGCATAAACG	TRIM22	864	918
GAACCTCTGAGCCTAGATTG	TRIM22	808	577
TCCGAGTACCAGATCTGAGT	TRIM22	568	642
ACACACAGTGCAATATACAG	TRIM23	607	1522
GATCGACAAGTAACAGACCT	TRIM23	1545	1262
TGAAGGAGGAGAACAAATCG	TRIM23	1282	1047
TGGCCACAAAGCAAAAGACG	TRIM23	1050	1360
ATGCATCACACCTTGCACGA	TRIM24	1507	1037
CTGCTGCACTAGTAATCGTG	TRIM24	1150	830
GCACTAGGTGAACGTATTGG	TRIM24	737	937
GGCAACGAATGACTCCAACT	TRIM24	906	676
CAGAAAGCATCAAAACTGCG	TRIM25	573	1019
CATGTACAGTCAGATCAACG	TRIM25	1037	1321
CCTCAGAGACCACCTCGACA	TRIM25	1108	1137
TGTTCCGGGGCTCCAAACGT	TRIM25	995	825
GAGCGGCTGAAGGTGGACAA	TRIM26	719	943
GGACCAGAGGCAGTACATTG	TRIM26	967	970
TGAACCACCTGAGTACCCTA	TRIM26	958	917
TGGACCCACAGTCGGCCAGT	TRIM26	855	1044
CCAAGTCTAGCTCCTCAAGG	TRIM27	896	964
CCTTCCCGCAGAGGCACATG	TRIM27	1101	948
CTTGCCGCAGATTATCAGAG	TRIM27	792	1376
GAGCCCATGATGCTCGACTG	TRIM27	1477	1091
AGTTCTTAGAGGATGCAGTG	TRIM28	1149	675
CCAGCGGGTGAAGTACACCA	TRIM28	600	461
CTTCCCAGGCAGTACCACTG	TRIM28	472	1838
TGAAACTTCATCTCGCCATG	TRIM28	1909	410
ACGAAAGGACAACCCAATTG	TRIM3	399	816
ACGGCGCTTCACATCGTCCG	TRIM3	698	1361
CGCCACTGCACACGAAACGG	TRIM3	1454	600
GCAGCAATTGCCTTAGTCGG	TRIM3	497	666
AGAAGATGACCCGGGCTCTG	TRIM31	466	846
CTTACCTGCAGAAGATGACC	TRIM31	895	799
GAGCCCGGGTCATCTTCTGC	TRIM31	543	1339
TGAACAAAACCTCAGAGCCC	TRIM31	1000	1049
CAGCTCCGGCAGAATTGCCG	TRIM32	849	513
GAAGCCCCGGACAGTTAACG	TRIM32	364	1130
GAAGTACTAGTCGCTGACCG	TRIM32	1104	1262
GGCAGATGTAGCACTACTGG	TRIM32	1349	657
CGGGGGCGCAGTATCGACGC	TRIM33	639	1276
CTCAGCGTGCCCATCCCGGG	TRIM33	1190	1043
GTGTTGTGTACCGATACTAC	TRIM33	1098	1226
GTTTGCACACTGATCAATCG	TRIM33	1198	820
GAACCCTTGAGTCTAGACTG	TRIM34	625	899
GAGTAACTGATACCACACAC	TRIM34	911	533
GTCAAGTTGAGCCCAGACAA	TRIM34	537	1141
TCATCTCAGATGTGGAGTGT	TRIM34	1180	887
GCAGACATCGATAAGCATGC	TRIM35	1093	391
GCTGGTGAGGTCGTCAGACA	TRIM35	387	582
GCTTCGCGAGTTCTTGAGAG	TRIM35	519	1221
TGCTGGCACATGAGATCGAG	TRIM35	1201	843
AAGGTCACACATAATGGCTG	TRIM36	873	1071
ATTGACCGAATTAACAGACC	TRIM36	933	638
GCCTACAAAACCTTAAAGGT	TRIM36	474	1401
TGGAATGAGATAGAAGTGTG	TRIM36	1494	681
CATTTGCGAGTAAGTCCAAA	TRIM37	702	477
CTCTAATTTAAATAGCATGG	TRIM37	341	936
GGAAACACTTACCGGCAATG	TRIM37	741	1050
TACTGGAACCCACATAACCA	TRIM37	968	659
AAAATGTTAAGGAGTCATCA	TRIM38	652	1164
ACAGACTCTGAGTAGACTGA	TRIM38	1080	1054
AGAAGTCTGTTATACACAAG	TRIM38	915	983
GGATCAAGAAATGTCATGTG	TRIM38	910	815
AATATTCCTAGAAAGTTCGG	TRIM39	721	1008
ACATCAAGGTGAAACCCAAG	TRIM39	849	1397
AGGAGAGCCTTATGATCCCG	TRIM39	1084	1406
TTTCACCTTGATGTGCAAAG	TRIM39	1639	996
CCGATGGGTGCCGACATTCG	TRIM4	905	534
GAAGAAGCTCATCTTAGAGG	TRIM4	431	947
GGAGCACCAGACTCACGCCA	TRIM4	861	1966
TAAGTCTCAGCGTAATCTCG	TRIM4	1984	861
AGTGTGCCTGACACAGCATG	TRIM40	1078	1082
ATGATGAGACATGTGTTCAG	TRIM40	1145	1315
GAGGCCGTGAGCACCAACTG	TRIM40	1245	1095
TTTAGGAACGACTCAATCGC	TRIM40	1130	1417
AGATGCCCTGATCGGTCACG	TRIM41	1500	1665
AGGGGCACGTGGAACCACTG	TRIM41	1714	1076
GGACAACATGGACTATGTGT	TRIM41	1143	1068
GTAGTCTTCATCCCGCATGG	TRIM41	1007	785

AGAGGCAGCTGAGGAAGACC	TRIM43B	724	1022
CATATCCCTACAGGGCGATG	TRIM43B	1046	542
GGAAATGTGTCATAAACCAG	TRIM43B	460	1308
TCCCACGAAAGGCAGAGACA	TRIM43B	1213	1850
AACGACTTACCACACCATGG	TRIM45	1816	927
GATGCTGGAGAGCCTACGTG	TRIM45	774	676
GATGTCCGGACATTCTCGGA	TRIM45	569	617
TCAGTAGTGGACATCCGAGG	TRIM45	571	1156
ACGGGAACATGATCACTTGG	TRIM46	1256	1448
CGCCATTGCCAGCTCGACGT	TRIM46	1542	1127
TACCGCCAGAGTGTGAGTGT	TRIM46	1136	879
TCTGGGCACATAAGGCCCTA	TRIM46	939	312
CTGCTCCCACTGGTTGACGC	TRIM47	375	845
GAGGACCGCATGGACGAGCT	TRIM47	751	1205
GCGCGGCAGTAGCGCTCGAG	TRIM47	1148	910
TGGCCGCATCGTGGCGCGAG	TRIM47	976	960
AAGAAGTCCATGCTAGACAA	TRIM5	901	1184
AGGTCAAGTTGAGCCCAGAG	TRIM5	1065	719
CCACACGTTCCTCACAGAGG	TRIM5	776	813
TTTCGAGCTCCTGATCTGAA	TRIM5	654	2787
CACCGTCTACAGCCGCATGA	TRIM50	2655	704
CTGACATCAAGCTGACCGTG	TRIM50	790	1991
GGCAACACGGTGGTGCAGTG	TRIM50	2215	706
TGTGGCCACTCTTACTGCAA	TRIM50	700	1045
AAATCTCAGAAATCTGAACA	TRIM51	825	2189
ACTCACCTCTGAATCCACTG	TRIM51	2035	691
CTGAATGCAAGAAGACAACG	TRIM51	660	940
TCACTTGGAAAGGCTGCGAA	TRIM51	765	1517
ACAACCTCATGCCTGCACGA	TRIM54	1735	732
AGAAGCAGTTGTTAAACCAG	TRIM54	633	256
GGAGATGTTCTCCAAACCAG	TRIM54	240	986
GTGTGATCACTGCTTGCACG	TRIM54	916	606
CACCAGGTTATTGTCCACAC	TRIM56	542	788
CAGGGCCCAGACACCCCACG	TRIM56	716	954
GCAGCTACGAGCCCACGTGG	TRIM56	934	901
TGGAAGGGGCGATCGCACAG	TRIM56	801	1288
CAGCATGCTGCATCCCTGGG	TRIM58	1223	385
CGGTTGGGGCGAAAGCCCGA	TRIM58	314	1445
CTTGACTCAGGAGGCCAACG	TRIM58	1512	1201
TTGGAGTTTGAGAAGCATCG	TRIM58	1037	405
CAACATCACAGAGAGCCGTT	TRIM59	368	517
GAAAATGATCCAAGGCGATA	TRIM59	445	597
TGAGAGCATGGCAGTACACG	TRIM59	660	1125
TGTGGTCATTGCCTTACCAT	TRIM59	1304	865
AGCTAATTTAAATCTTGTCC	TRIM6	775	800
GAACCCCTGAGCATAGACTG	TRIM6	714	842
GCGAAATATCCTAGACAGAG	TRIM6	698	1467
TGGTCACCACACGTTCCTCG	TRIM6	1809	1019
AGAAGAAGCAGAGAAGCGCG	TRIM62	946	1076
AGTGCTCCGTGATGCAGCGG	TRIM62	1121	1501
GCGTTGAGGATGGCGTCCAG	TRIM62	1383	1431
GCTGCTCAAGCGACAACTGG	TRIM62	1189	1630
CATCTACTGTCTCACGTGTG	TRIM63	1750	1071
CTGGAAGACACTCTGCAATG	TRIM63	989	955
GAGGTGATCATGGATCGTCA	TRIM63	1034	841
GGAGATGTTTACCAAGCCAG	TRIM63	710	1024
TACAGCACACGACAGCACTG	TRIM65	1247	633
TGCACACGCTGCACACACAG	TRIM65	825	803
TGGGATGAAGACCAACAGCT	TRIM65	832	564
TGGGGTCAGTCTTACCCACG	TRIM65	559	930
ACTCTGCAATCATCCTCCAC	TRIM68	1003	1116
CCTCCATTGGCACAACACTG	TRIM68	1293	711
GCTGGACAGGAGCTCGACAG	TRIM68	666	1130
TGACCTGTGTGAGCGCCATG	TRIM68	1085	699
AAGAAGTTACCCTTACTCAA	TRIM69	656	1172
CAAAGGTCCTATCCAGTACA	TRIM69	1187	538
CGGAACCAATCATTGCACAG	TRIM69	536	1075
GGAGCAATGTCTCTTAGCCA	TRIM69	964	784
AAGGACCACTACATCGAGCG	TRIM71	731	778
AGGTCAAAGCCGTGACGGCG	TRIM71	659	396
CCAGAAAGTAGTGCTAGCCG	TRIM71	303	730
GTCATTGGTTATGACCACGA	TRIM71	648	703
CAGCTGGATGTCCAGACGGG	TRIM72	584	922
GCGCCCGTGACAGCCGAGTG	TRIM72	641	653
GCTCCGAGCACTCCACGCGG	TRIM72	485	1436
TGCTCGCAGTAGATGCTCAG	TRIM72	1515	1472
CCACCACCTGCCAGCACATG	TRIM73	1661	1481
CCTCACTCCCCACCTTCATG	TRIM73	1564	1673
GAGTCCCTAATGCTACAGTG	TRIM73	1510	650
GGCAGATGGGACACTGAAGC	TRIM73	623	1209
GGCTTCGATCACCCAGGCCA	TRIM74	963	1015
GTCCTACCACCTGGACACCA	TRIM74	1002	1733
TCTGCAGCCGCATGAAGGTG	TRIM74	1624	876
TGCGGCCACTCCTACTGCAA	TRIM74	798	1092
CAGGTGGCCGATCTTAGTGG	TRIM8	954	998
GACAGTGGAGGTCCTAGACA	TRIM8	883	765
GGGACACTCGGTGTGCGACG	TRIM8	746	1051
TGCACGTGGGACTGGCAGCA	TRIM8	1214	994
AAGAAGAGTGCACCTGACTG	TRIM9	965	1219
CAGGTGATACAGGAGTTGCG	TRIM9	1124	789

GCTGAACGGACTGTCAGACA	TRIM9	733	741
GGCGCTGGCGAACCCCCCGT	TRIM9	575	842
GCAACTCCAGCTACTAGAAC	TRIML1	715	1177
GCGGCACAGACTCAGCTCTG	TRIML1	1070	1187
GGCTGTACTAACCCATGAGA	TRIML1	1054	903
TGAGTCCTCAAGTCAAAGCT	TRIML1	963	913
ACATCACAGAACAGCCGTGT	TRIML2	891	879
AGAACTATGAGATTGAGACA	TRIML2	822	914
CAGCCTCCTAAAGCTCATCG	TRIML2	786	563
CATGGTGTGTGGGATACAAG	TRIML2	578	781
AGTTCGATATTGGGAAACCC	TRIP12	698	785
TCTAAATTGTGGATAGTGAC	TRIP12	759	1059
TGAGCAGCCATTCATAGTCA	TRIP12	1028	556
TTAGATACTCCTCTAAATTG	TRIP12	479	903
AGGCCTACGATCTCTATCCG	TRPC4AP	805	1054
AGTTGGAAGAGTGGTACACA	TRPC4AP	1160	1138
GACACTCAACAAAGTCACTG	TRPC4AP	941	1740
GTACTTGTTACTCAACAACC	TRPC4AP	1536	1619
AGGGTACTGAGAACTTGTTG	TSG101	1611	695
ATCCGCCATACCAGGCAACG	TSG101	704	600
GATTGGGAGGGTATCCGGAT	TSG101	543	627
TAGGGATGGCACAATCAGCG	TSG101	553	611
AATCACGAAATGGCCAACGG	TTC3	567	709
CTGATGCGTATAAAACCCTA	TTC3	670	1000
TATTGAACACTACCCCAGTG	TTC3	896	1162
TGTCAATCACAACAAAACGA	TTC3	1221	1046
AACATTGTAGAACTTGACCA	TULP4	1051	663
CAGGTCACGTCTAATATCTG	TULP4	692	1076
CCTGCGGAGGAACAACCGTG	TULP4	1029	1341
TTCGTGTGGATTCAGTACGA	TULP4	1260	789
ATAGATGCAATGGTGCACAT	UBA3	916	988
CATTCCAGGCAGAATCACCC	UBA3	1044	1097
GTTACGTATAGGCTCACTCA	UBA3	1037	1166
TCGAAATCAGGGTGTGTGAA	UBA3	1223	1044
CACAGTTCCAGACAGAACTC	UBAC1	1062	1131
CAGATAAAGAGGCCATACTG	UBAC1	1019	538
GAAGAGAACATCCAGGACCA	UBAC1	540	664
GTGTTCAATTAGCCACTCCA	UBAC1	582	1076
CAACATAATGGTGTGGAACG	UBE2A	973	462
TCCTCCAGCCGGAGTCAGCG	UBE2A	361	1081
TGGACATACTTCAGAACCGT	UBE2A	1113	424
TTAGAGACAAATCTAACTGT	UBE2A	370	877
CTGAAAACAACATCATGCAG	UBE2B	826	897
CTGGATTTCCAGGTTACAAG	UBE2B	730	1298
TTGGACTCCATCGATTCTGA	UBE2B	1367	613
TTGGATAAAAACCTAACAGT	UBE2B	588	1610
CGGCTCAGCTCCTTTACGGG	UBE2C	1357	354
CTCTCGCTAGAGTTCCCCAG	UBE2C	293	946
GCCCTGCTATCACCCCAACG	UBE2C	836	728
GGGCGTGAGGAACTTCACTG	UBE2C	743	828
CCATAATAGTGGCTTGCCAG	UBE2D1	662	857
CCTGATAGCGCATATCAAGG	UBE2D1	833	811
GGTTTAAAAGGATAATCTGT	UBE2D1	720	1883
GTATTTGTCTCGATATTCTG	UBE2D1	1915	845
AATGACAGTCCCTATCAGGG	UBE2D2	729	897
AGGAATTGAATGATCTGGCA	UBE2D2	782	790
ATTGGCAAGCTACAATAATG	UBE2D2	829	1263
TTGATATTCTACGATCACAG	UBE2D2	1181	518
ACTTACAGGTCCCATAATTG	UBE2D3	522	619
AGAATACACCGCCTTGATAT	UBE2D3	667	927
GGGAAAATACTTGCCTTAGG	UBE2D3	805	1758
TACTTACTATCATCCCCAAC	UBE2D3	1727	966
AATGACAGTCCTTACCAAGG	UBE2D4	896	1319
AGGAGGATCCCTCTGCAAGT	UBE2D4	1132	804
GCATCTGCCTTGATATCCTG	UBE2D4	911	1567
TACTTACAGTCATCACCGAC	UBE2D4	1662	545
ACAGTACCTCTTGGCGCTGG	UBE2E1	796	857
CATTGTAATATTAACAGTCA	UBE2E1	827	1222
CTCACCTGCAATTAGGTGGA	UBE2E1	1122	579
GAATACACCACCCTCATACA	UBE2E1	566	1064
AGTTCAGCCCAAGAAAAAGG	UBE2E2	876	625
CTATCCGTTTAAACCCCCTA	UBE2E2	613	1082
GACAGTCCAAGCACTAGTGG	UBE2E2	1133	674
GAGACAACATTTATGAATGG	UBE2E2	650	1571
ATTTCTTACCTGCAATTAGG	UBE2E3	1577	400
CCTTCATATACAGAACCCGG	UBE2E3	368	1237
TGCAGTGATAGATTCTGGTG	UBE2E3	1288	1180
TTTCACTAACAGAATTCAGA	UBE2E3	1087	712
AGACAGGGGAAATATGTCTG	UBE2F	701	494
AGCGTCCGACTCGACTCGGA	UBE2F	442	682
AGTAAACTGAAGCGTGACGA	UBE2F	683	1727
TCCCGATGCGTACAACATGG	UBE2F	1960	613
ACAGAAATCTGGCACCCAAA	UBE2G1	583	987
ACTTACTAAAGTGTATCTGG	UBE2G1	886	595
AGAACTCAACAAAAATCCAG	UBE2G1	464	1621
TGACAATGATCTCTACCGAT	UBE2G1	1712	1067
AAATGCAGACTCTCCCATCA	UBE2G2	907	862
GACTTAACGGGTAATCAAGT	UBE2G2	795	546
GTTGGGATGAAACATCTCAC	UBE2G2	601	1003
TTAACACTGAATCCTCCGGA	UBE2G2	841	1209

ACTTACGCTTCATCAATGTT	UBE2H	1263	1199
GCTGCAGCGTCACCATTGAG	UBE2H	1224	1116
GCTTGTATTCTTCTGGTCGG	UBE2H	930	2006
TTAGGATAGGCCAATAACTG	UBE2H	1996	1036
AAGCCCTCCTTACAAATGGG	UBE2I	975	1111
ACATTCGGGTGAAATAATGG	UBE2I	922	1442
ACCCGAATGTGTACCCTTCG	UBE2I	1544	1309
TATTTCCCCACAGACTCCGT	UBE2I	1220	1736
AATGGCACTTCACGGTTAGA	UBE2J1	1705	1073
GCTAATGGTCGATTTGAAGT	UBE2J1	958	1527
TAACACTTACTACTCCACGA	UBE2J1	1610	1451
TTCTCTAGATTACACTCCTG	UBE2J1	1282	701
AATATTCGAAGGGAGGGGCT	UBE2J2	645	1068
AGAATCCTTACCTTCATAAG	UBE2J2	1028	541
ATATGATCACTCCCAACGGG	UBE2J2	420	521
CGGATTTCCACCCGGACACG	UBE2J2	423	1170
ATAGGCTTACAATACCTTAG	UBE2K	1143	616
CCTCCAGACACACCATATGA	UBE2K	574	1248
GCAATGACAATAATACCGTG	UBE2K	1195	1582
TAATATTAGTTCCGTCACAG	UBE2K	1416	580
AAACATCGACGAAAAGGGGC	UBE2L3	554	1279
AAGGCTCCCTTATCATATGG	UBE2L3	1098	1391
GAAAAACTTCCGTAACATCC	UBE2L3	1326	696
TTGAAGAAATCCGCAAATGT	UBE2L3	583	1336
AGCGTGCCACACCAGGACAT	UBE2L6	1529	836
CAAGATCTACCACCCCAACG	UBE2L6	751	607
CCCCATGGATACTCACGGGT	UBE2L6	576	867
GGCTTGAACGGATACTCCGG	UBE2L6	789	970
GCGCAGCTGCGGATCCAGAA	UBE2M	757	1014
TCACCCCAACATTGACCTCG	UBE2M	1060	720
TCCCAGGGCTTCTACAAGAG	UBE2M	566	1129
TGCCTCAACATCCTCAGGTG	UBE2M	1243	575
CCTCAAAGGGGGAATCCTGA	UBE2N	493	999
CTGTTGCCTTCATAGATAAG	UBE2N	1089	1431
TCTGGTTCGGCTTTGATGCC	UBE2N	1309	594
TGGTTCTGCCAGCAAACGCT	UBE2N	538	1289
AATGTAGTCCCCATACATGA	UBE2O	1132	321
CAGAAAAAAACTGCGCCCAG	UBE2O	213	1666
GACTTCGTGGTAGATAAGCG	UBE2O	1580	613
GAGCCTCAAGAACATGACTG	UBE2O	571	680
CGATCACAGAGTTTCAAAGG	UBE2Q1	493	403
CTCGAGTCCATCTTCCACCG	UBE2Q1	432	891
GACCGCATCTCCCCCCACGG	UBE2Q1	765	697
GGAGGTTATAGAGTTTACAC	UBE2Q1	593	886
AGGAAGAAGAGCCTATTAGT	UBE2Q2	780	1280
CCAGCTTCCAACTGACGATG	UBE2Q2	1249	1444
CTAGATCAACCACTACCCAC	UBE2Q2	1460	1106
TCAGAATCCACAAACCATAT	UBE2Q2	980	1126
CGGAGATGAAGCGGTCGCTA	UBE2QL1	925	1372
CTGGTCCAGCGCCTACACCG	UBE2QL1	1200	1656
GAGAACGGCTACGTGCTGGA	UBE2QL1	1488	1171
GAGGTTGAGCAGGATGAACT	UBE2QL1	1220	1082
CATAACTGAAGCATCGACAT	UBE2R2	1251	1347
CGAGTCCGACCTCTACAACT	UBE2R2	1219	1043
CTCTGTGGGTCATCTACAGG	UBE2R2	905	701
GGAATCCTACTCAGAATGTG	UBE2R2	644	1149
AACTCACCAGCAGTACGTGT	UBE2S	1338	824
CAAGATCTTCCACCCGAACG	UBE2S	743	898
CATCAAGGTCTTTCCCAACG	UBE2S	786	784
GAGGGGACCCCATATGCTGG	UBE2S	508	2169
CACCCCCAGGCATCACATGT	UBE2T	2324	1452
CAGCCATGAGCGGGTCATCA	UBE2T	1398	457
GGAGTGAGAAATCGGATCTG	UBE2T	425	1818
TGGATGACCTGCGAGCTCGT	UBE2T	1877	1760
AATACAGTAGACCCACACAC	UBE2U	1683	848
CTACAGAATTCAGTTTGGCA	UBE2U	648	301
GTTATAAATTTCACAACTGG	UBE2U	253	1111
TAAGTGAAGATATGATGGAA	UBE2U	1039	886
AATGGAGTAAATAGTTCTAA	UBE2V1	787	2377
CCAACAGTCGGAAATTGCGA	UBE2V1	2265	1626
CGTAGCTCGACGCTTACTCT	UBE2V1	1566	2341
TCCAACAGTCGGAAATTGCG	UBE2V1	2255	381
AAGATATGACACTTACAAGG	UBE2V2	366	803
GGCGACGGTACAGTTAGCTG	UBE2V2	728	568
GTTACAAATCTAACTGACGG	UBE2V2	440	1309
TCCAACAAGCGAAAATTACG	UBE2V2	1241	478
ACCAGGTACCTTATATGAAG	UBE2W	483	1182
TAAAGCAAGGCAATTACCTG	UBE2W	1308	1096
TCATTTAAGGTCATTCCAGG	UBE2W	1164	1048
TGACCATTGCTATAAACATG	UBE2W	1015	697
ATTTGACACTCCTTATGAAG	UBE2Z	692	698
CAACGGGCAATAACACAGTG	UBE2Z	695	1085
GGTACAACGAACATTCCTGG	UBE2Z	1030	1081
TGTGTTTACAGTACATGGAC	UBE2Z	1251	820
AAACAAGAAAGGTCCTCGAG	UBE3A	662	822
AAGGAAAACTGATCAGACTG	UBE3A	762	374
ATTAATCTTATAAAGCTCGA	UBE3A	312	967
GAAAGTTAAACAACACACCA	UBE3A	882	1212
AAGAGCTTTAACCCTCCGTG	UBE3B	1055	1120
ACAGCACCATAAGCCACCCG	UBE3B	1105	1061

CCTTCACAGACACTTCAACG	UBE3B	965	1005
GGTGATGTGAGTGACATGCG	UBE3B	1071	807
CATTCAGAAAGGGCTCGTAA	UBE3C	693	960
GTCAGTATCATACATAACAG	UBE3C	897	1105
TAATATCTTCCATGTCAACA	UBE3C	1167	639
TGTTGAAGTCCAGAGACACG	UBE3C	676	755
AAGACCTGAACTATCCCCAG	UBE3D	662	950
AGTAATTTGTAAGCGTTGCA	UBE3D	748	1237
CAACAACAAACTGTAGCCCA	UBE3D	1091	458
CCACTGCCGAGTGAGAACTG	UBE3D	394	815
CCTGTGAAATCCCAAGTACA	UBE4A	712	625
GAAGTAATAAGCGAGCGAAG	UBE4A	565	1572
GATTGGCCCAAATCTTGGTG	UBE4A	1620	1658
TTGGTCAACATAGATCTCTG	UBE4A	1586	590
ACACTCACTCGGGATATGCG	UBE4B	642	1074
GACGCGTGTGAATGCAACGA	UBE4B	1141	387
GCATTACTTAGAGCTCGGAA	UBE4B	326	1051
TCCCAGAGCATGGATATCGA	UBE4B	1117	812
GCGGTATCCCTTGTATCAAG	UBOX5	775	942
GCTTCCATCGCGCCAAAAGG	UBOX5	791	1082
GGCCCCATGTGGCTTCACTG	UBOX5	954	1123
TCAACATAGACCTCACAGCT	UBOX5	1030	1210
AAGACAGTAGTACAATCGTG	UBR1	1252	1402
ATTCTAACTTGTGGACCGAA	UBR1	1531	562
GGAATCTATTAAGAATGATG	UBR1	464	736
TCTTACCCACAATATAGATG	UBR1	809	250
AGAGGGTGTTCTATCAACAT	UBR2	292	1598
GATCCAATTACACGTCAAGT	UBR2	1675	1301
GTGTCATATCTGAAGCCACA	UBR2	1266	982
TCCAGCATAGCTAGTATGCT	UBR2	945	1179
AAAATGGCTGTAGTTAACTG	UBR3	1104	2233
ATGAGACTGGACATACGTCA	UBR3	2365	721
TGTGATAAAAGCCCCCACAT	UBR3	641	1297
TGTTGAAGTCGTGTCCGGTG	UBR3	1432	1257
CTGCCTCAATTACGAAACGT	UBR4	1393	822
GAAGATCTCGATATATGACG	UBR4	826	898
GGAACCGATTGATATAGCGT	UBR4	817	401
GGTGTCAATGAGTTGCAGCG	UBR4	327	708
TTCGGACAGGACGGGATCGA	UBR5	780	1383
TTGATCCTTCAAACTTACGC	UBR5	1475	1124
TTGTTGTCTAAGAACGACGA	UBR5	1091	1784
TTTCTCCCAACAATCACAGT	UBR5	1739	619
AAAAGAACAACGTTTCATGC	UBR7	638	484
AGTCTTCACAGACTACGCAC	UBR7	461	1454
GTTGGTCGACGTCCTTGAGG	UBR7	1558	615
TCAGAACTAGAGCCGGCACA	UBR7	485	1128
AATCGGACTTATTCACGCAG	UCHL1	1097	1136
ACTTCATGAAGCAGACCATT	UCHL1	1117	958
CGCCCTACCTGGGCCGTGAG	UCHL1	843	934
CGCCGGCCAGTGGCGCTTCG	UCHL1	907	1168
AAGCGCGCCCACCTCGGGAT	UCHL3	952	839
AATCAGTCCAATTGTTCCAC	UCHL3	869	914
GGATCCTGAACTCCTTAGCA	UCHL3	752	814
GGTCTCATGAGTAACTCGGA	UCHL3	619	1509
AAGTACACAACAGTTTCGCC	UCHL5	1419	1578
ATGATTGGATCAGTGCAGTA	UCHL5	1462	456
CAAAAAATATCGTGTCAAGT	UCHL5	403	1126
GTTACTGAACTGTACCCACC	UCHL5	1084	774
AGGGACTAAAGGAGCCACGA	UEVLD	651	865
CACTTACCCTGATACATCAC	UEVLD	1018	868
TGCCTCTGCTCATTCCAAGG	UEVLD	900	1556
TTCTCTATCATCATCTGATG	UEVLD	1644	404
CCGGTGCTGAAGACTAACGC	UFC1	388	1096
GTTGTGGGTGCAGCGACTGA	UFC1	876	1051
TGACAACGATTGGTTCCGAC	UFC1	1152	718
TGTCAAACTCATATTTCAGG	UFC1	656	1077
CGACATAAAGCACGTATCCG	UFL1	1061	1601
GAATCTCAATCATCCCACAC	UFL1	1668	736
GTTAATAGCGGACGCTTACG	UFL1	618	871
TCTTAATAAAACTTATCTCG	UFL1	722	1141
CCATACCCTCTTCGACTACG	UHRF1	1241	1491
GCGGGAACTCTACGCCAACG	UHRF1	1205	1464
TCAGACAAGTCCTCCACCCA	UHRF1	1450	1362
TCGTCCTCACAGCGGGACTG	UHRF1	1556	1007
AATCTTCTCTGACAGGACCG	UHRF2	880	602
ACAGTCTGAATTAGACGTAG	UHRF2	541	477
CTAAAGTAAAGAAAGCTCCG	UHRF2	374	1659
TTTCCCACCACATACACGAC	UHRF2	1861	550
ACAGGCGGCGCAACCCCCGG	UNKL	409	1044
ACTTGGAGCAGTACACGTCG	UNKL	1140	1159
ATCCACGAGACAGACGCACG	UNKL	1405	792
GTGGAGTTACCTTGCCACCG	UNKL	735	640
AGAAATACCTCATCCGAAAG	USP1	597	1515
GATAACACAACTAATGGTTG	USP1	1430	619
GGCGACTGCTTAACACACTG	USP1	586	944
GGTATTAAGGACGCGTTGCT	USP1	886	1002
ACTGACCAAAATCAGCCCCG	USP10	899	449
AGGGCTTAGAATCATGAAAG	USP10	380	1059
ATCATGGGTGTTGACGTACA	USP10	1200	1016
CCAGTGTCGTTGCAACCCCG	USP10	1099	873

GGGCTCAAGAGAGGACATCG	USP11	847	678
GGTCTCCATGATGATCAACT	USP11	581	1225
GTGGGCGAGAACGTCCACTG	USP11	1236	1268
TGATAGGCAGTGGAACACTG	USP11	1357	873
CAGCACACCAGACCCAACGT	USP12	966	879
CCAAAATAGTGCTCATTGAC	USP12	883	898
CTTGTGATGAACTTCTTAGG	USP12	793	1084
TTGCGTATAAGAGTCAACCT	USP12	1166	1008
ACAAAGGCCTTAAACATGCG	USP13	1061	612
CCTGAAAAGACATGTGCGAG	USP13	602	775
CTGGAGCATTACAGAGACAT	USP13	736	1087
GAAAGTCCGCTACACGGAGA	USP13	950	1241
AACTAGATGGAGTTACCATG	USP14	1351	1625
AGCTGAGCCTTGAATACCAT	USP14	1728	720
GGTGAAAGGAGGAACGCTAA	USP14	653	1398
TTTAATGTTCCTAGGTATGC	USP14	1392	1081
AAGGTGTTCCTTAAGTGACT	USP15	1054	1259
ATTTCACAGAATATTCGCTA	USP15	1125	869
CCAAGTTACTTAGGCCACAG	USP15	847	642
TCTAACTAAGTAAACTTCCA	USP15	605	348
AAGGAAAGATTCATGAACCA	USP16	294	882
CCTTGCCAAATAACCGTGAA	USP16	808	1304
TGGCTCATGGCTAAAGTAAG	USP16	1281	765
TTAAGACACAGCCAAACTGA	USP16	719	1931
GAAGTCACCACTCTCATCTG	USP17L2	1816	2408
GACATGACCAGGACTGTGGA	USP17L2	2518	1486
GGATGACATGACCAGGACTG	USP17L2	1547	2412
TGACATGACCAGGACTGTGG	USP17L2	2520	1177
CCTCGTTCCAGTCGACATGG	USP17L26	1245	551
GACAGAAGTGATGCTAGAGG	USP17L26	484	1089
GACGACTCACTCTACTTGAG	USP17L26	971	927
GCATAGAGGACATAGACGAG	USP17L26	868	1570
CAGATACAGACTGTGTGGTG	USP19	1500	828
CCTCTAGCAACTGAGCGAGG	USP19	705	983
GCAGAGGAGCGTATCAGATG	USP19	1053	1220
TCATCGTGGACCTATTTCAG	USP19	1158	739
ATAGCTACCGGATAGACCCC	USP2	643	939
CAATGCACACACAGCCCTCG	USP2	969	1167
CATTGGCCGCTACACGCTGT	USP2	1229	789
CTGAGACCCGACATCACTGG	USP2	736	1407
CCTTTCTTGAGCACGTACGA	USP20	1431	627
CTCACCCTTTAACTCATCAG	USP20	649	1018
GGACTCAGATTCGAGTGACA	USP20	922	1141
GTAACACCACAGTCGGAACG	USP20	1153	1149
AAGACAGCTCGGAATCGAGT	USP21	1168	935
AGGACCGGGCGGATATCATG	USP21	890	784
CACCTTGAAATCAACCGCCG	USP21	623	1356
GAGGCAGAGGTCGTAACATG	USP21	1346	970
ACCTGGTGTGGACCCACGCG	USP22	925	750
AGCCGAAGAAGACACAGTAG	USP22	793	1467
GCCATTGATCTGATGTACGG	USP22	1413	1017
GGACATCTCACAGACCAGAC	USP22	1010	582
AGACACGGACAACTGTCGGT	USP24	536	1484
TCAAGTGCTGTTCACAAGTG	USP24	1468	1699
TCACAGCATGTGTTAGAGTG	USP24	1685	863
TTATGAGAGGAGTCAATCAG	USP24	933	952
ACAAAATCTCTCAAATCCGG	USP25	754	1173
GAGACTGAAAGATTACCTCA	USP25	1101	650
GGCACCAAGGCACATAACGG	USP25	685	1575
TGTGATGGTATGGAACCACT	USP25	1820	1362
ACTGAATGAGTGCACTCCAA	USP26	1303	1305
ATAGTGACGGTTACACAAAG	USP26	1438	380
GAAGCCTAAAAGTGAATTTG	USP26	339	447
GGACAGAGTTCATCAAAACG	USP26	402	1101
ACCCCAATCCCAATGACTGG	USP28	997	677
AGAACTGCATGCAAGCGATA	USP28	577	679
AGAAGTGGAAGCCCTATCTG	USP28	563	832
ATACTTCACCGAGTGATCGG	USP28	738	1664
ACTCACTCAAGGTGTCCCAT	USP29	1824	797
TCATCTCCACAAATGCATGT	USP29	1033	1398
TGGTTCAACGGGTAGAACCA	USP29	1501	1004
TTACAGTTGGTATTGAATGA	USP29	1060	980
CCCATTCCTTAACTCCACGG	USP3	1037	881
CTACACTTGGAACTTCAGGG	USP3	684	637
GTGGTTAATGACACCAAGCT	USP3	612	956
GTTGTCACGGCTATATTCGG	USP3	906	480
AAGAACTGGGGAGTTATAGG	USP30	393	1092
ATCAGTACATACCCATGTGG	USP30	1121	1053
TCAAACAAATGTGTGACCCG	USP30	900	865
TGTGTGTGACAACTGTACAA	USP30	870	1589
CAAACCTGAATGCAAACCGT	USP31	1539	1473
GACTTATTACCTGATCAGTG	USP31	1274	946
GGCAACGCCAGGCATCATCG	USP31	935	1067
TGTCATCGAAGCAGTACCAG	USP31	1181	512
AATGGAAAGAATGCTCCACG	USP32	505	766
CTGTAGTATTCACGTAACTG	USP32	804	1321
GAATGCACATGACACCACAA	USP32	1467	748
TGCTGAAACCCATTAAACCT	USP32	614	1100
CATTGGCCAAAGCTACCTCG	USP32P3	1081	824
CTCCAGTGAGATACTCCACG	USP32P3	782	673

GCTATGTGCCTTCTACTCAG	USP32P3	649	728
TCCAGCTATGGGAAAAACCG	USP32P3	632	1450
ACTGTAAATCCAACATTTCG	USP33	1331	658
ATAACACCATACTCGAAGAG	USP33	663	1063
ATAGTCAAAGCAGGATCATG	USP33	1127	799
GGAGGGCTTGCCGATAAACG	USP33	765	1218
GTCTTGTATCACACGAACTG	USP34	1282	675
TCATATACCACGATTAACAG	USP34	710	988
TTACAAACGCATGGAACCAG	USP34	1005	1015
TTGTATCTTTGGGTGCACCA	USP34	1060	1341
AGAACTCGGCGAAGACGTCG	USP35	1197	1176
CATCCATGAGCTCCAATGGG	USP35	897	1498
CTGCTGTACCCCATCGTCCG	USP35	1364	1731
GGACCTCCATGTTCCCAATG	USP35	1506	1608
AACTTACTTAGCACACATGT	USP36	1966	631
CACTCCAAAACGCCGCCAAG	USP36	449	1335
GAGCACACGTATGAGAGCTG	USP36	1357	723
GATCTGGAATCACACTCGGG	USP36	552	941
AATGTGGTGCTTCGACCCAG	USP37	954	692
AGGGTTGCTAGAAAATCGGT	USP37	614	1064
ATTCTTGTGAGAAGTGTGGT	USP37	1088	1667
TGCTTAAACAAGGTATCCCA	USP37	1657	804
GAAAACTATGCAAATCACGG	USP38	710	345
GAAGCCTCAAAGAATATCCG	USP38	268	714
GAGACCCCTCGTACAAGTGA	USP38	694	1037
TCATCACCCAGTATACAAGA	USP38	898	1054
CAGCTGGGACATGTACAATG	USP4	1125	1285
CTACCTACTTTGAACATGCG	USP4	1245	973
GTGATAGCACTAGCACCTGT	USP4	900	1003
GTGTGATTGACGCAGGTACG	USP4	1097	884
ATAGATGAGGTCATGACCGG	USP40	908	992
GAAAACAGCATGGACCACTG	USP40	1001	600
GCTTGAGATTAATCCGGAGA	USP40	469	964
TCGAGCTAATCCAAGATATG	USP40	886	1456
AAAGCCCCTGAAGACACTGG	USP41	1020	581
CCAGGCACAGGGGATCCATG	USP41	623	1288
CTTCATCCGGATCATATACA	USP41	1185	690
GCATCATGTTGGACAAACAG	USP41	689	895
AAATATCTGACAAACAAGAG	USP42	851	910
AGTCATTCATTTGATACCAG	USP42	835	777
CCCCGCCGCCGAATCCCTGG	USP42	700	1151
GGACGCAAAGGGGATGATCG	USP42	1214	822
CACACCACTGACCTGTACAG	USP43	841	1274
CACCTGTTTCATGAACGCGG	USP43	1221	1454
CTGCAAGGTGGGCATTACAC	USP43	1501	897
GAACTGAAAACATTCATCCA	USP43	780	1524
TATCACTGCACAACTCGTAG	USP44	1576	1684
TATTGGCCTTCGTTTAACTG	USP44	1696	836
TGGTTTGAACAATCACCCAT	USP44	902	944
TTGTTGGGCGTAACCACGAA	USP44	1058	1289
AATGAATGGATCTTTCACCG	USP45	1092	735
ACAGATGAAATACAGAAGGG	USP45	617	1185
GACGTGACTCAGAATTCATG	USP45	1116	952
GGGCTGTTCAGATCCAGTAG	USP45	842	529
AGTTCATATACCTTAGACAG	USP46	510	997
CTTTGATAACTACATGCAGC	USP46	906	1378
TGGCAACATGAACGAACCTG	USP46	1358	1376
TGTATGCCAACACATTCTCC	USP46	1587	1761
AATTGAGCGCAATACATGCA	USP47	1727	1501
CAATGATCAACATGTCAGCA	USP47	1735	1233
CCATAAATGAGAGTCTGCAA	USP47	985	659
CTTGGCTGGACCCATAAGGT	USP47	541	1184
AGACTGTGGATCTTTCACGT	USP48	1272	805
GCTTAGACTCTCTGCCACAC	USP48	805	1499
TACTACACATTCCTTACACA	USP48	1505	1110
TGAGATGCGTAAGCAAAGTG	USP48	1212	978
AGCAGCCGTGCACTCTTGCG	USP49	1029	386
CGTGCTCAATGATAACCCAG	USP49	364	1400
CTGCCTCAAGTGCTCCCACG	USP49	1401	1345
GGACCACATGACTCGGAAGA	USP49	1221	961
ATAGACATGAACCAGCGGAT	USP5	851	1168
ATCCTGGGTAGGGTCCGTCG	USP5	1017	803
GAGTCTACTTGCACCTCCGG	USP5	662	674
GGAGAAGTTTGAATTAGACG	USP5	510	583
AGGGAGCATTCATATTTGGA	USP50	526	1123
CATCAGCCTCCTTAACTGGA	USP50	1062	1350
CCTATCTGATGACAGACATG	USP50	1610	2186
TGATTCAGTACCACTACTCC	USP50	2188	1403
CACAGACCAGACACAAGCTG	USP51	1397	916
TCCCACTCCAAACGAAACGC	USP51	965	1277
TGGTGACCTAGACGGGTCGG	USP51	1371	1352
TTGATGAGAAACATCTGTTG	USP51	1365	579
AAATCAGTATTCGAAAAGCA	USP54	554	953
AAGGTTTACCTAAAGCACCA	USP54	877	2256
ACTGACCACAGACTCATGGT	USP54	2328	734
GGAAGTGAATTCTCATCAGG	USP54	611	1749
AAAGTACAACTCTCAGTGAG	USP6	1491	696
GAAAAACGAGATGCCCATGG	USP6	600	1029
TATACTCCGAATAGGCCAGG	USP6	969	1196
TTAGTGCAGGAACTCTGGAG	USP6	1062	1181

ACCATACCCAAATTATTCCG	USP7	963	560
AGATGTATGATCCCAAAACG	USP7	606	901
GGCAACCTTTCAGTTCACTG	USP7	808	1382
GTGTACATGATGCCAACCGA	USP7	1416	578
ATGAAGGAGCCATTTCCGGT	USP8	492	1774
CCCACGACGCCAGAATGAAG	USP8	1643	998
TAGTATAAAGAATGTTCCAC	USP8	949	586
TGAAGTCCGGAAAAAAACTTG	USP8	454	818
CAAAAGAGAGGTGTTTACCG	USP9X	759	870
GCCCACCCAAAGGATTCGTG	USP9X	808	1306
TCATACTATACTCATCGACA	USP9X	1244	537
TCATGGCGATAAAACACATG	USP9X	619	1073
CAAGACGGCGTATCAACTCA	USP9Y	1100	1153
GTGGTATTCCAAGTTAATGG	USP9Y	1026	1538
TAACAATACTCATCGCCTAG	USP9Y	1647	949
TGTTAGGTATAGAACTTGGG	USP9Y	922	1036
AGGAGGAATCTATATTCTGG	USPL1	877	1713
CCTAATGTGCATCTAAGCTG	USPL1	1637	928
GATGCTACTGGTCTTATACA	USPL1	804	714
GTCCTGTGAAAGAGTACGAG	USPL1	659	976
CAGTCTGATGCAATATAGTG	VCPIP1	1053	996
CCTTTCGCACAGATGTGCCA	VCPIP1	983	816
GTGTAGCACTACGTCCGGGT	VCPIP1	736	1055
TGAAGACTTAAGGGTAACCA	VCPIP1	939	1491
CCCGTATGGCTCAACTTCGA	VHL	1445	686
CGCCGCATCCACAGCTACCG	VHL	612	1261
GAGATGCAGGGACACACGAT	VHL	1521	767
GCGATTGCAGAAGATGACCT	VHL	670	783
CCAAAGAGTATTGTCGAGAG	VPS18	671	1143
GGCAAATGAGCCCAACCACG	VPS18	1119	1313
TAACAAAGCTACGCCCATCA	VPS18	1340	1042
TGGGTCAAGACGATGGCTAG	VPS18	1137	1101
AACTGGATCTCACGAAATGT	VPS41	1158	2181
ATTGGGCACACATTATGGCA	VPS41	2385	757
CGAAGACTTATATCATCCCG	VPS41	706	1495
GAGACTATGACATAGCAGCA	VPS41	1519	939
AGTTGTGGAAATAGAATACG	WDR12	875	1948
ATGACCTCTACAGCAGTGTA	WDR12	1957	1110
CTGAGGAAACTGCCTCCATG	WDR12	1105	808
TACTAAAGGACAAAAATGGT	WDR12	1002	1190
CAGCCTGAATGTCAATAACG	WDR26	1080	829
CCTCTTACCACAATAGCATG	WDR26	861	1296
GACATCCTGACTCTTGCATG	WDR26	1289	1226
GAGAGTCTGTAAACGCCGTG	WDR26	1017	419
AGGGAATATCCGATGTAGCC	WDR5	410	716
GAACTTCACAAAAGACACGG	WDR5	640	787
TCTGAGTGGCGGATGACGAA	WDR5	739	1270
TTCAGTTTGACGAAAGCGTG	WDR5	1370	738
ACTAATGGTTTCTCCATGTG	WDR53	665	319
AGGACACACGCGGTTCCAAG	WDR53	344	1256
TATCCAGTCCACATGACACC	WDR53	1255	627
TGCCTGAATGCAAGTAAAGA	WDR53	517	1170
CCTACCTGATGACACGAGTG	WDR59	1305	564
GCAAATCCGGAATGTCAATG	WDR59	528	912
GGCTCCCACTGTATAAACGA	WDR59	691	960
GTGGTCACCCGCGCAAACGT	WDR59	946	693
AGAATCTGGGATGCTGCATC	WDR5B	715	1091
CTCATCGGCCAATCAGAGCA	WDR5B	1064	1490
GATAGGCTAATCATAATTTG	WDR5B	1432	757
TGAGACTGTAAAAATATGGG	WDR5B	648	2270
AAGTCCATAGATGCAGGACC	WDR61	2223	1040
CCTGTTGAAGGCGTGATGAG	WDR61	1081	925
CTGGCCACAGGAACTCATGT	WDR61	926	1266
GAATATTCTTTGGACACGAG	WDR61	1153	533
CGGGATTGTCACCCTACGAA	WDR76	483	762
TAAAGGATTTCTGCACACAT	WDR76	600	1674
TCATCTGCTACTAATGTCGG	WDR76	1581	2467
TGATGGCACGTTACGCTGTG	WDR76	2950	1144
AGGGCCTCATGCATCTGCAG	WDR82	1143	1004
GTACAGTAAGAAATATGGTG	WDR82	856	496
TACAGCTCTAACAAAATAGA	WDR82	383	769
TTTCAGCCCCAACGGCGAGA	WDR82	728	950
AATATAAAAGTACACTGAGT	WDSUB1	848	758
ATGTGGTGATTTAACAGTGT	WDSUB1	844	567
GATGCCAAAATATGTCCTGA	WDSUB1	525	1062
GCAGTGATGGAACAGCCTAG	WDSUB1	1080	846
ACAGAGCTACTAGTCAACAT	WDTC1	967	782
AGAGAACAGCAAACACTCGG	WDTC1	671	1475
ATGTCATAGAGCCTCACGAA	WDTC1	1275	1192
TCACTGACCCCTTTATCCGG	WDTC1	973	1145
AGTCACAAGCTACCACATCA	WSB1	1172	1055
CAGTCTATAATATGTTCACG	WSB1	1008	576
GCACAGTAAAGCTTGTTCCG	WSB1	527	986
TATGATCTACCAAGTTAAGG	WSB1	967	944
ATCTGGGACCTGAATAAACA	WSB2	925	1118
CACGTTAATTCGGAAGCTAG	WSB2	1129	945
GGGGTCCCACATAATCACAT	WSB2	904	1628
TTGCTACGGGACTCAACGAT	WSB2	1714	1451
ATAATACTCGAACTACCACA	WWP1	1371	1037
CCACAAATTGCTTATGAACG	WWP1	903	935

GTGACAGACGCATTATCAGT	WWP1	987	700
TTACCGAATAGAGGTATCGT	WWP1	742	857
AACGTCTTGAAGAACAATGG	WWP2	772	511
ACTGCGGTCATAAGCACCAG	WWP2	487	618
ATAACACTCGCACGACCCAG	WWP2	563	1302
ATAGTTGCGCACGTACTCCG	WWP2	1478	974
ACCAGAATTTGTAGACTGCG	XIAP	861	870
ATGACAACTAAAGCACCGCA	XIAP	899	737
TCTAGCTTCTTCACTATACA	XIAP	723	1688
TCTGACCAGGCACGATCACA	XIAP	1822	1309
AGTGTGTACTATGTCGTCGA	YOD1	1256	858
GAGGATTCGCTGACCGCCGG	YOD1	629	569
GCGGAGCCGCCACATCGTGT	YOD1	462	2205
TGGTGCTTCTAGTTACGTCA	YOD1	2264	1012
CATCTCGAAGCATTCCAGCG	ZBTB16	923	868
GGTCGAGCTTCCTGATAACG	ZBTB16	815	1245
GTGGACAGTTTGATGACCAT	ZBTB16	1180	898
TCAATACAGCGTCAGCCTTG	ZBTB16	876	1018
AAAGTCGAGAGTCTCTCCGA	ZBTB18	907	1387
ATCTGCCGAATCCCTCACGG	ZBTB18	1265	763
CAAGCAGGAGAGCGAAAGCG	ZBTB18	671	760
TGCAGTCACAAAGAAAACCC	ZBTB18	596	1145
ATGTTCGCAATGTATGAGGA	ZC3HC1	1090	741
CCAGAAACAGAACTTCTCAT	ZC3HC1	606	1349
GGGTGATCCATTAACTGACT	ZC3HC1	1257	1181
TGGTGCCTGAATCTCCTCGG	ZC3HC1	1124	530
AGGCCGAGTATCCCCGCCGG	ZFP91	310	1194
GCACTGTACCATAATCAAGT	ZFP91	1203	475
GCTGCATCTAGACCTAGCCG	ZFP91	509	1048
TCACTGACCTGCAAATAGCG	ZFP91	1055	1331
ACACCTACCGGCAGACTTCG	ZMIZ1	1199	1440
ATACTGCCCCATGTTGACCG	ZMIZ1	1443	744
GTTGGTTACTCCCCAAACCG	ZMIZ1	536	875
TATGGCCGGCCCAACTACCC	ZMIZ1	714	593
CAGGTAGAGTGGCTTGTGCG	ZMIZ2	533	924
CAGTAGGGTTCATGCCAGCG	ZMIZ2	788	1125
CCTTATAATGCAGTCCCGTG	ZMIZ2	1213	1468
CTCCACTGACTTCACGCAAG	ZMIZ2	1458	878
AAATACTAACGGTTTCCCAC	ZNF645	737	689
AGCACAGGATAACGACAGCG	ZNF645	585	1285
TCCACCAGAACAGCACACCA	ZNF645	1274	350
TGAGTGTCAAAGTCAACCAG	ZNF645	366	1474
AGGTGGTTCAGCTCGCATAG	ZNRF1	1502	799
CTCCTGGTAACCATTGCCAT	ZNRF1	782	894
CTGCCACCGAGCTGACCGAG	ZNRF1	956	1494
GTCCGGTAGTGCCCGAAATG	ZNRF1	1443	1772
AACAGCAGCAGCGGCCCGTA	ZNRF2	1579	1098
AGCCCGAGTACGCGCGCGTG	ZNRF2	1081	660
GTAGCAGCGGAGGCGCCAAT	ZNRF2	575	1279
TCCGTACCTCCAAACATGTG	ZNRF2	1393	632
AGCCACTGCACACCGAGCGG	ZNRF3	667	1019
ATGATGTTGTGCCGACAGTG	ZNRF3	1109	1236
CCATCCCAGCCTACCCTACG	ZNRF3	1165	991
CCGCCTCACTGGCACGACAG	ZNRF3	969	814
CGAAGGTGCAGTCGTAGCGG	ZNRF4	659	714
GGAAGACAACTCGAGCTCGG	ZNRF4	725	796
GTTGAGTTGGAATGACCGCG	ZNRF4	713	1189
TGCTCACGAGGTCGTCGGAG	ZNRF4	1211	2102
ACAGTCGACTGTATGCACTT	ZRANB1	2202	935
AGCAAGACAGAGCTCGATGG	ZRANB1	807	824
AGTTCAAATATGTACACATG	ZRANB1	867	937
CAGCAAGCGTACTTCATCTG	ZRANB1	893	731
AGATAAGTGACTTGCTTCGG	ZSWIM2	698	1688
ATTGCTACCATGTACTCACA	ZSWIM2	2000	706
CAGTGGGGCCCATCTCTCGT	ZSWIM2	605	993
CCACACGTTTACATTTCGTG	ZSWIM2	1057	