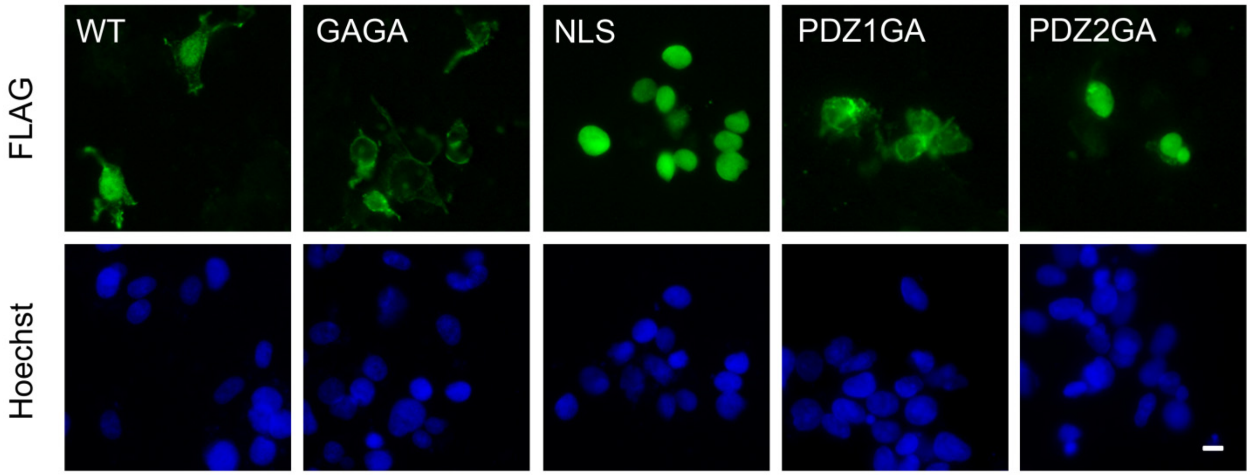
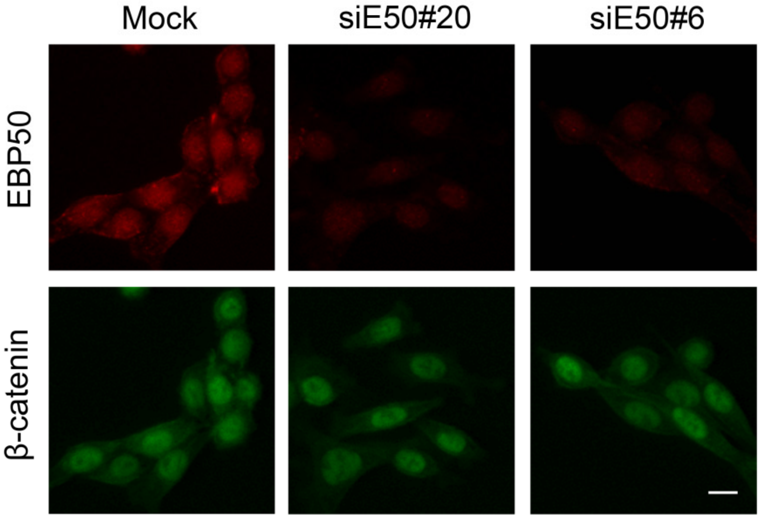
Supplementary Figure 1



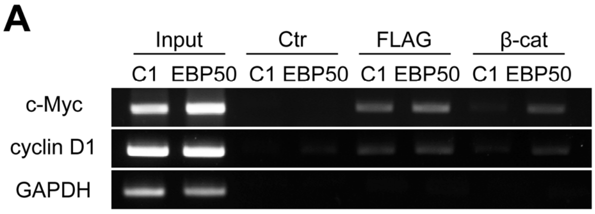
Supplementary Figure 1. HEK293 were transiently transfected with the indicated FLAG-tagged EBP50 plasmids for 6 h and were immunostained with mouse anti-FLAG (M2) antibody (green) and Hoechst 33342 reagent (blue).

Supplementary Figure 2



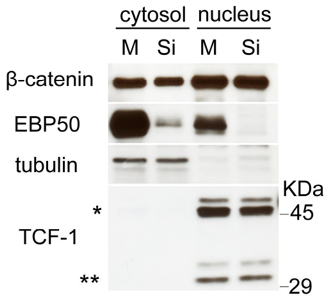
Supplementary Figure 2. Down-regulated EBP50 expression does not affect β-catenin expression in SW480 cells. Two independent EBP50 knockdown SW480 stable clones were processed for double immunofluorescence study using EBP50 (red) and β-catenin (green) antibodies. Scale bars: 10 μm.

Supplementary Figure 3



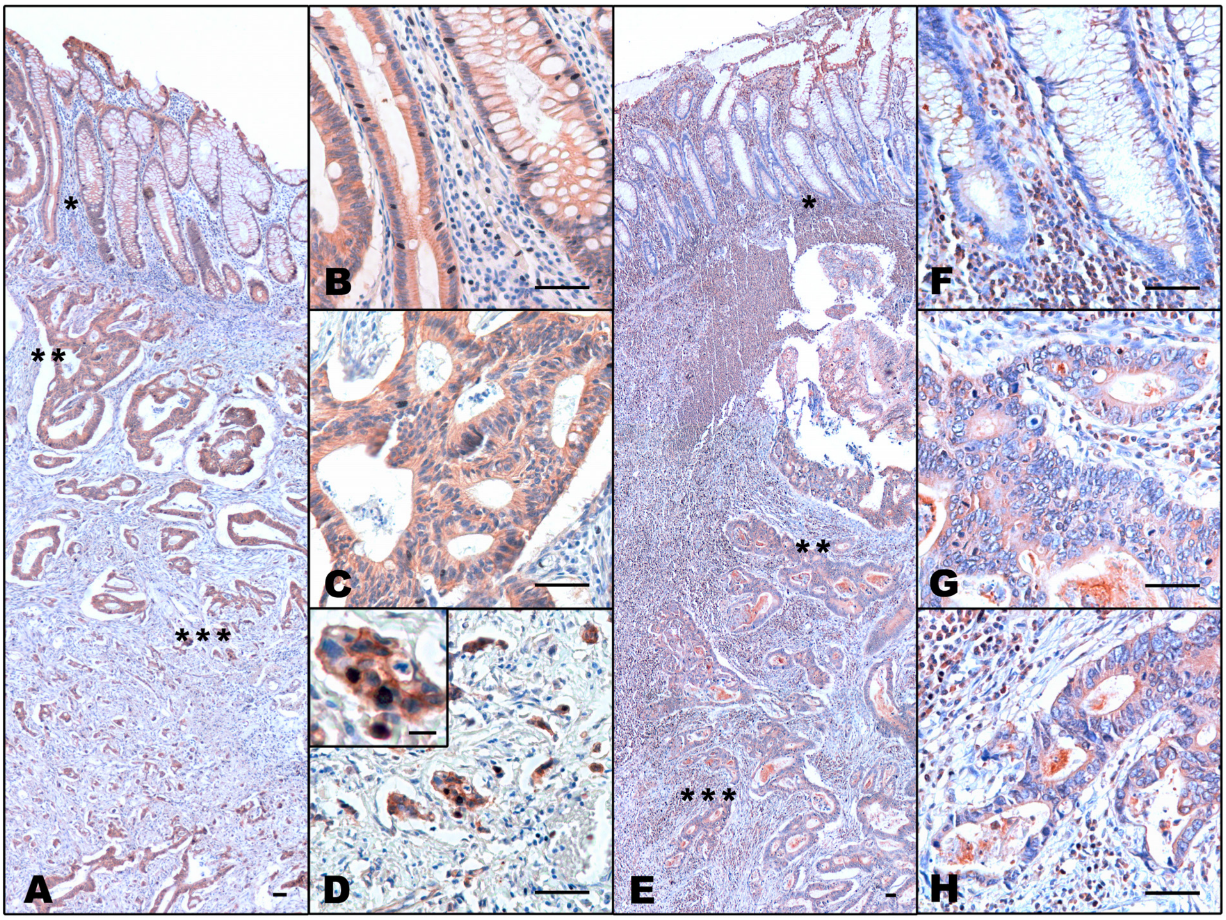
Supplementary Figure 3. SW480 cells stably expressing FLAG-dnTCF-1 were transfected with EGFP-C1 control vector (C1) or EGFP-tagged EBP50 expressing plasmid (E50). Twenty four hours later, the cells were then processed for ChIP assay using affinity purified rabbit anti-FLAG, β-catenin antibody, or a rabbit anti-podocalyxin antibody as a negative control (Ctr). Target c-Myc and cyclin D1 sequences were amplified by PCR.

Supplementary Figure 4



Supplementary Figure 4. Mock (M) and EBP50 knockdown (Si) Colo205 cells were homogenized with Dounce homogenizer (20 strokes with a tight pestle) and centrifuged at 700 g for 5 min to separate cytosol and nuclei. Equal fractions from the cytosolic and nuclear portions were loaded into SDS-PAGE and analyzed by Western blotting analysis for EBP50, β-catenin, and TCF-1. Tubulin serves as a cytosolic marker while TCF-1 itself as a nuclear marker. * and ** indicate full-length and N-terminally truncated TCF-1, respectively.

Supplementary Figure 5



Supplementary Figure 5. **(A)** β-catenin immunostain displayed a similar increasing intensity and nuclear distribution pattern across the tumor to that seen for EBP50 staining shown in the analogous parts shown in Figure 8A. High magnification of areas *, **, and *** labelled in panel A showed β-catenin staining throughout the mucosal **(B)**, submucosal **(C)**, and deeper invasive portions **(D)** of the tumor. These regions are also correspondents of B, C, and D shown in Figure 8. **(E)** A CRC case showed membranous, cytosolic, but not any nuclear EBP50 staining at the invasive front despite the dysmorphic nuclear change. **(F, G, H)** High magnification of areas *, **, and *** labeled in panel E. Please note that there was still no EBP50 nuclear staining in the deeply invasive neoplastic glands in pericolonic soft tissue as shown in panel H. Scale bar, 50 μm for all panels; 10 μm for the insert in panel D.

Supplementary table 1. Chromosome location of 816 EBP50-binding sites sorted by number of TCF motif
* indicates genes in which more than one discrete chromosome location were identified

Gene Symbol	Chromosome Location	Length	number of TCF motif
PORCN*	chrX:48248761-48250134	1373	7
FLJ11184	chr4:164631334-164632821	1487	6
SI	chr3:166282909-166283664	755	6
FUT8	chr14:65204215-65206003	1788	6
ZNF501	chr3:44747094-44747609	515	6
GLS	chr2:191451049-191451529	480	5
STAC	chr3:36394290-36394797	507	5
AOF2/KDM1A	chr1:23291981-23292587	606	5
ARL4A	chr7:12694039-12694858	819	5
MGC52282	chr16:2833797-2835269	1472	5
PPP3R2	chr9:103395353-103396262	909	5
TMEM26	chr10:62886966-62887538	572	5
AKAP5	chr14:64005102-64005456	354	4
C4orf26	chr4:76700625-76701200	575	4
PLSCR4	chr3:147452685-147453200	515	4
APCS	chr1:157819813-157820394	581	4
ASCL4	chr12:106692416-106693003	587	4
chrY:009252280-009252324	chrY:9252232-9253234	1002	4
hsa-mir-125b-1	chr11:121480296-121481146	850	4
IMPG1	chr6:76842309-76843138	829	4
NIPSNAP3A*	chr9:106552041-106552320	279	4
PRDM8	chr4:81321867-81322310	443	4
REG3A	chr2:79242675-79243148	473	4
STARD5	chr15:79408316-79408650	334	4
TAS2R13	chr12:10953157-10953586	429	4
TSPY1*	chrY:9272512-9273574	1062	4
VPS53/HCCS1	chr17:565883-566372	489	4
AMT	chr3:49431397-49433002	1605	4
hsa-mir-190	chr15:60901038-60901462	424	4
PKP2	chr12:32941892-32942439	547	4
PRY2	chrY:23041195-23041991	796	4
RASGRP1	chr15:36645995-36646651	656	4
TRHR	chr8:110169206-110169588	382	4
TRIM46	chr1:153415639-153416250	611	4
VGCNL1	chr13:100868357-100869465	1108	4
CACNA1I	chr22:38294917-38295622	705	4
EIF2C3	chr1:36166658-36167527	869	4
POLR2G	chr11:62288666-62290507	1841	4
TRIM39	chr6:30419283-30419802	519	4
ZNF132-ZNF324B	chr19:63648019-63648559	540	4
YWHAZ	chr8:102035822-102036806	984	4
IL18RAP	chr2:102405848-102406185	337	3
KIAA0913*	chr10:75218356-75218699	343	3
NCAPG	chr4:17425456-17425912	456	3

RANBP3L	chr5:36341631-36342304	673	3
SLC9A11	chr1:171838668-171839333	665	3
UXT	chrX:47400720-47401781	1061	3
ZRANB1	chr10:126661218-126661494	276	3
ACSBG2	chr19:6086156-6086628	472	3
ANP32A	chr15:66902068-66902347	279	3
BIRC3*	chr11:101692463-101692762	299	3
BIRC3*	chr11:101698059-101698296	237	3
chrY:009952039-009952083	chrY:9951991-9952929	938	3
EFEMP1	chr2:56003422-56003859	437	3
ELMO1	chr7:36991993-36992378	385	3
ESR1	chr6:152166503-152167216	713	3
GPR37	chr7:124190104-124190605	501	3
HTR1E	chr6:87699164-87699710	546	3
IRGC	chr19:48912162-48913048	886	3
OPN5	chr6:47853582-47854494	912	3
PRKAR2B	chr7:106467220-106467563	343	3
RDH11*	chr14:67230262-67231134	872	3
TMEM178	chr2:39741634-39742226	592	3
TSPY1*	chrY:9972318-9973242	924	3
C9orf79	chr9:89683167-89683933	766	3
CD97	chr19:14353805-14354825	1020	3
chr7:023492469-023492528	chr7:23492339-23493232	893	3
EFS	chr14:22902908-22903418	510	3
FANK1*	chr10:127572798-127573666	868	3
FCER1A	chr1:157527056-157527493	437	3
GBP7	chr1:89418383-89418680	297	3
LRGUK	chr7:133463272-133463634	362	3
RBMY1F*	chrY:22741869-22742276	407	3
SBNO1	chr12:122400469-122401161	692	3
TMEM161A	chr19:19112981-19114242	1261	3
U89	chr12:6947494-6947953	459	3
BAG4	chr8:38155499-38157065	1566	3
C11orf56-CNGA4	chr11:6212996-6214113	1117	3
chr2:120940376-120940420	chr2:120940340-120940566	226	3
ESAM	chr11:124139223-124139956	733	3
MMP2	chr16:54068928-54069816	888	3
MRTO4	chr1:19452039-19453347	1308	3
OCIAD1	chr4:48526732-48527227	495	3
PCDHGB7	chr5:140777718-140779014	1296	3
TFPT	chr19:59312693-59313828	1135	3
TMEM43	chr3:14142660-14143414	754	3
ADAM18	chr8:39561749-39562003	254	2
C11orf42	chr11:6185259-6185793	534	2
C12orf39	chr12:21571087-21571695	608	2
C15orf23	chr15:38462907-38463285	378	2
C1orf14	chr1:181191388-181191726	338	2
C2orf40	chr2:106044539-106045122	583	2

CASQ2	chr1:116112084-116112569	485	2
CCNJL	chr5:159676534-159676807	273	2
CD79A	chr19:47075192-47075669	477	2
chrX:102716046-102716105	chrX:102715499-102716170	671	2
EVX2-HOXD13	chr2:176662732-176663118	386	2
GABRA6	chr5:161040553-161041031	478	2
GLULD1/ LGSN	chr6:64087799-64088136	337	2
HOXC4	chr12:52734582-52735121	539	2
hsa-mir-409	chr14:100599816-100600310	494	2
LOC728137	chrY:9931732-9932611	879	2
MAB21L2	chr4:151724752-151725025	273	2
NKD2	chr5:1060942-1061233	291	2
OR4D2*	chr17:53601321-53601634	313	2
PECI	chr6:4078672-4078939	267	2
RDH11*	chr14:67231632-67231908	276	2
SCARB2	chr4:77357785-77358911	1126	2
TSPY1*	chrY:9292858-9293765	907	2
USP54	chr10:74981142-74981524	382	2
YEATS4	chr12:68040280-68040602	322	2
ZNF382	chr19:41786098-41786472	374	2
ZNF776	chr19:62950566-62950893	327	2
ADAM23*	chr2:207015394-207015821	427	2
ADRA1A	chr8:26783436-26783669	233	2
AKAP6	chr14:31866691-31867021	330	2
ALS2CR4	chr2:202196160-202196596	436	2
AQP5	chr12:48642812-48643226	414	2
AR	chrX:66679684-66679999	315	2
ARID1A	chr1:26897573-26897743	170	2
ARL6IP1	chr16:18713293-18713623	330	2
ART3	chr4:77214832-77215186	354	2
BBX	chr3:108906854-108907793	939	2
BMP5	chr6:55850702-55850992	290	2
C10orf62	chr10:99334500-99335157	657	2
C11orf11/DAGLA	chr11:61205573-61205991	418	2
C17orf47	chr17:53974344-53974674	330	2
C6orf150-MTO1	chr6:74224461-74225856	1395	2
C8A	chr1:57092283-57092731	448	2
CCL28	chr5:43450369-43452174	1805	2
CDC42EP3	chr2:37755007-37755389	382	2
CDKL1	chr14:49934096-49935365	1269	2
CHAF1A	chr19:4355126-4355610	484	2
CHDH	chr3:53853729-53853971	242	2
COL14A1	chr8:121329622-121330270	648	2
DAAM2	chr6:39869408-39869705	297	2
DBX1	chr11:20143303-20143839	536	2
DUSP28	chr2:241150443-241151022	579	2
ESD	chr13:46269450-46269807	357	2
ESPL1	chr12:51973103-51973802	699	2

FARS2	chr6:5313366-5313795	429	2
FBXL14	chr12:1575192-1575705	513	2
FLJ20701	chr2:229837449-229837775	326	2
FLJ25371	chr4:160177552-160177861	309	2
GABPA	chr21:26029258-26029502	244	2
GAD2	chr10:26543017-26543366	349	2
GPR176	chr15:38000945-38001148	203	2
GTPBP5	chr20:60201576-60201914	338	2
HMG20A	chr15:75535442-75535895	453	2
HRASLS2	chr11:63088073-63088674	601	2
KCNAB3	chr17:7773722-7774317	595	2
LOC346653	chr7:128099269-128099589	320	2
LOC90826	chr4:148825008-148825632	624	2
MBOAT2	chr2:9065606-9065996	390	2
MYBBP1A	chr17:4405472-4406134	662	2
MYC	chr8:128814109-128814494	385	2
MYLK2	chr20:29872807-29873206	399	2
NEXN	chr1:78154871-78155155	284	2
NTSR2	chr2:11726133-11726414	281	2
OR2AG2	chr11:6747053-6747306	253	2
OR51I1	chr11:5418962-5419300	338	2
OR52B6	chr11:5559093-5559449	356	2
PANX3	chr11:123986312-123986775	463	2
PKD2L2	chr5:137251532-137251987	455	2
PRKACA	chr19:14084808-14085157	349	2
RAPH1	chr2:204106323-204106605	282	2
RBMY1A1*	chrY:22476814-22477221	407	2
RBP4-PDE6C	chr10:95354468-95354771	303	2
RFX4	chr12:105601177-105601756	579	2
ROBO2	chr3:77169110-77169447	337	2
SDC2	chr8:97577136-97577459	323	2
SEPHS1	chr10:13428538-13428814	276	2
SLC19A3	chr2:228289412-228290369	957	2
SMARCC2	chr12:54868475-54868846	371	2
SNX17	chr2:27448509-27449040	531	2
STEAP4	chr7:87776471-87776690	219	2
TMEM59	chr1:54290117-54290384	267	2
U32A	chr19:54683045-54683286	241	2
USP5	chr12:6841859-6842133	274	2
ZFAND3	chr6:37893671-37894315	644	2
ZNF416	chr19:62779897-62780330	433	2
ADAM23*	chr2:207017528-207017956	428	2
AQP1	chr7:30918500-30919105	605	2
C1orf181/ZNHIT6	chr1:85950790-85951952	1162	2
CCDC51	chr3:48451485-48451841	356	2
CDK5RAP2	chr9:122382626-122383052	426	2
CGNL1	chr15:55453175-55453409	234	2
COMMD3	chr10:22649018-22649676	658	2

EPB41L5	chr2:120484854-120486295	1441	2
FAM96A-SNX1	chr15:62174270-62174648	378	2
FANK1*	chr10:127571411-127571678	267	2
FGF5*	chr4:81407246-81407681	435	2
GBGT1	chr9:135026870-135027167	297	2
HBII-85-22	chr15:22886367-22886640	273	2
hsa-mir-380	chr14:100560687-100561042	355	2
INCA1	chr17:4833331-4833943	612	2
LOC149134	chr1:245020156-245020893	737	2
MBD2	chr18:50005440-50005746	306	2
MGAT4B	chr5:179164650-179165010	360	2
MICALCL*	chr11:12272294-12272885	591	2
PGAM2	chr7:44072241-44072524	283	2
SECISBP2	chr9:91122377-91123111	734	2
SLC1A7	chr1:53382148-53382654	506	2
PFKM	chr12:46805033-46805171	138	2
MARCH3	chr5:126393185-126393455	270	1
A4GNT	chr3:139332145-139332514	369	1
AIM1	chr6:107064472-107064886	414	1
AKR1C3	chr10:5128288-5128873	585	1
AOC2	chr17:38250627-38250901	274	1
AP3B2	chr15:81180387-81180843	456	1
AP3M2	chr8:42130805-42131441	636	1
ARFGAP1	chr20:61371650-61372427	777	1
BCL2L1	chr20:29771749-29772217	468	1
C15orf39	chr15:73279087-73279719	632	1
C19orf18	chr19:63175473-63176184	711	1
C1orf192	chr1:159602690-159603529	839	1
C21orf88	chr21:39908568-39908834	266	1
C6orf47	chr6:31734241-31734607	366	1
CASC3	chr17:35544911-35545408	497	1
CCDC27	chr1:3659531-3659895	364	1
CCDC42	chr17:8590680-8591244	564	1
CD160-PDZK1	chr1:144430757-144431713	956	1
CEP72	chr5:662348-662738	390	1
chr13:043633831-043633890	chr13:43633575-43633980	405	1
chr5:095212395-095212441	chr5:95212175-95213369	1194	1
chr8:141014651-141014710	chr8:141014611-141014942	331	1
chrY:009232377-009232432	chrY:9232061-9232808	747	1
chrY:009235502-009235546	chrY:9235464-9235764	300	1
chrY:009955587-009955631	chrY:9955466-9955849	383	1
COL12A1	chr6:75975822-75976113	291	1
CSPP1	chr8:68157608-68157902	294	1
CSRP2BP	chr20:18071234-18071633	399	1
DDR2	chr1:160870687-160871041	354	1
DGKZ*	chr11:46306922-46308347	1425	1
DHDDS	chr1:26667174-26667550	376	1
DNAI2	chr17:69779023-69780043	1020	1

DPYSL3	chr5:146815776-146816621	845	1
DPYSL4	chr10:133848370-133848880	510	1
EDAR	chr2:108913514-108914123	609	1
FAM76B	chr11:95159789-95160293	504	1
FBXO42	chr1:16549317-16549761	444	1
FGF5	chr4:81402621-81403077	456	1
FGFR2	chr10:123349173-123349436	263	1
FLJ16331	chr11:64738193-64738642	449	1
FPRL1/ FPR2	chr19:56964124-56964439	315	1
FTH1	chr11:61490234-61490865	631	1
FTMT	chr5:121215923-121216209	286	1
GAB2	chr11:77728586-77728874	288	1
GABRD	chr1:1939628-1940198	570	1
GANAB	chr11:62149824-62150129	305	1
GART-SON	chr21:33836611-33837040	429	1
GATA4	chr8:11600710-11601200	490	1
GGPS1	chr1:233559445-233559811	366	1
GNG10	chr9:113461728-113462036	308	1
GPC4	chrX:132378805-132379038	233	1
GPR119	chrX:129346023-129346269	246	1
GPR39	chr2:132891003-132891343	340	1
HBQ1	chr16:171665-171995	330	1
HGF	chr7:81236660-81236788	128	1
HIST1H4D	chr6:26303340-26303672	332	1
HOXB9	chr17:44059184-44059670	486	1
HS3ST2	chr16:22735429-22735797	368	1
HS3ST3A1	chr17:13447400-13447765	365	1
hsa-mir-325	chrX:76141180-76141453	273	1
INPPL1	chr11:71611331-71611750	419	1
IQCC	chr1:32444888-32445372	484	1
KRTAP13-2*	chr21:30669233-30670145	912	1
LGI4	chr19:40316430-40316718	288	1
LMO4	chr1:87570606-87570942	336	1
LOC387601	chr11:62752592-62753030	438	1
LOC388419-GPR142	chr17:69870085-69870578	493	1
LOC728137	chrY:9935267-9935567	300	1
LOXL3	chr2:74614673-74614956	283	1
LY86	chr6:6534292-6534632	340	1
MAOB	chrX:43624426-43624696	270	1
MAP2K3	chr17:21128847-21129238	391	1
MFSD3	chr8:145706115-145706381	266	1
MGLL	chr3:129023336-129023633	297	1
MTHFD2L	chr4:75237780-75238068	288	1
MYEOV	chr11:68817994-68818273	279	1
MYH8	chr17:10264552-10264787	235	1
NIPSNAP3A*	chr9:106550768-106551089	321	1
NRGN	chr11:124116823-124117129	306	1
NXPH2	chr2:139258962-139259368	406	1

OR13C3	chr9:106338798-106339121	323	1
OR4F15	chr15:100175500-100175991	491	1
OR51I2	chr11:5430474-5430606	132	1
OR52M1	chr11:4522271-4522646	375	1
PAX1	chr20:21630953-21631309	356	1
PAX6	chr11:31787580-31787835	255	1
PCDH9	chr13:66699079-66699376	297	1
PCNT	chr21:46570110-46570607	497	1
PDF	chr16:67926333-67926564	231	1
PEBP4*	chr8:22844096-22844446	350	1
PGRMC2	chr4:129431281-129431420	139	1
PIGR*	chr1:205187253-205187687	434	1
POLG	chr15:87680937-87682248	1311	1
PORCN*	chrX:48254102-48254757	655	1
PTGER2	chr14:51849368-51849662	294	1
PTPRA	chr20:2847597-2848499	902	1
PWP1	chr12:106603483-106603586	103	1
RASGRP2	chr11:64270152-64270475	323	1
RET	chr10:42894118-42894513	395	1
RGS6	chr14:71499188-71499430	242	1
SATB2-FLJ32063	chr2:200040379-200040621	242	1
SCG2	chr2:224176868-224177138	270	1
SHC1	chr1:153206668-153207324	656	1
SLC14A2	chr18:41453330-41453800	470	1
SLC43A3	chr11:56953373-56953657	284	1
SLITRK4	chrX:142552892-142553129	237	1
SMAD1	chr4:146625313-146625460	147	1
SYNPO	chr5:150001423-150001845	422	1
SYT4	chr18:39112010-39112313	303	1
TDRD5	chr1:177829400-177829789	389	1
THBS3	chr1:153431693-153432114	421	1
TIGD2	chr4:90250535-90250643	108	1
TKTL2	chr4:164612568-164612856	288	1
TMEM20	chr10:95640527-95640815	288	1
TNKS2	chr10:93549616-93549929	313	1
TNRC6C	chr17:73557210-73557510	300	1
TRIM59	chr3:161655434-161655536	102	1
TSHB	chr1:115377901-115378244	343	1
UNQ1940	chr7:135084635-135084892	257	1
USH2A	chr1:214665447-214665820	373	1
VPS41	chr7:38875129-38875373	244	1
VSIG9/TIGIT	chr3:115494082-115494426	344	1
WNT5B	chr12:1597850-1598100	250	1
ZBTB39*	chr12:55688059-55688440	381	1
ZFP36	chr19:44586577-44587165	588	1
ZNF678	chr1:225910827-225911191	364	1
ZNF804A	chr2:185173904-185174150	246	1
ABCC5	chr3:185216645-185216981	336	1

ABCG8	chr2:43920316-43920904	588	1
ACCN4	chr2:220086180-220086573	393	1
ACTL6B	chr7:100093208-100093713	505	1
ADAM2	chr8:39814621-39814971	350	1
AMHR2	chr12:52104592-52104810	218	1
APBB3	chr5:139923672-139923937	265	1
ATP2B4	chr1:201864523-201864955	432	1
BIRC4BP	chr17:6596211-6596677	466	1
BMP3	chr4:82172171-82172387	216	1
BRD8	chr5:137541687-137542035	348	1
C10orf92	chr10:134523509-134523891	382	1
C14orf115	chr14:73886543-73887010	467	1
C1orf109	chr1:37928112-37928981	869	1
C1orf32/ ILDR2	chr1:165209642-165209913	271	1
C20orf179/ BANF2	chr20:17628127-17628477	350	1
C20orf28/ SPEF1	chr20:3709617-3709978	361	1
C21orf29	chr21:44942584-44942861	277	1
C3orf26	chr3:101017761-101018711	950	1
C4orf30/ DCAF16	chr4:17421202-17421439	237	1
C9orf116	chr9:137530567-137531087	520	1
CA3	chr8:86539201-86539466	265	1
CACNA2D3	chr3:54130333-54130629	296	1
CAMK2A	chr5:149647876-149648187	311	1
CAV1	chr7:115951653-115951961	308	1
CCDC109B	chr4:110701834-110702148	314	1
CCDC8	chr19:51608195-51608576	381	1
CDKN2D	chr19:10539078-10539574	496	1
ChGn	chr8:19589366-19589601	235	1
chr10:114605087-114605146	chr10:114605029-114605332	303	1
chrX:100630012-100630071	chrX:100629963-100630266	303	1
chrX:151832483-151832527	chrX:151832320-151832556	236	1
chrY:009254152-009254196	chrY:9253850-9254663	813	1
chrY:009256756-009256810	chrY:9256323-9257130	807	1
CMA1	chr14:24046200-24046415	215	1
CXCL11	chr4:77180874-77181202	328	1
DLX5	chr7:96492475-96492881	406	1
DNAH9	chr17:11727162-11727357	195	1
DPF2	chr11:64874034-64874249	215	1
DSC2	chr18:26936148-26936437	289	1
DUOXA2	chr15:43194620-43194934	314	1
DYNLRB1	chr20:32565267-32566443	1176	1
EFS-IL25	chr14:22905006-22905916	910	1
FAM109B	chr22:40803138-40803450	312	1
FGF16	chrX:76592946-76593263	317	1
FLJ39502	chr2:179460150-179460422	272	1
FUBP3	chr9:132446489-132446859	370	1
G0S2	chr1:207916067-207916304	237	1
GDNF	chr5:37869859-37870209	350	1

GIMAP1	chr7:150044426-150044956	530	1
GPR111	chr6:47758197-47758592	395	1
GRM4	chr6:34210894-34211549	655	1
H2AFY2	chr10:71481143-71481477	334	1
HAPLN2	chr1:154852482-154852849	367	1
HAVCR2	chr5:156466452-156466837	385	1
HOP	chr4:57217451-57217762	311	1
HOXD3	chr2:176733762-176734237	475	1
hsa-mir-296	chr20:56828158-56828829	671	1
hsa-mir-331	chr12:94223655-94224075	420	1
HTR4	chr5:148015321-148015737	416	1
ICAM5	chr19:10260682-10260929	247	1
INPP5B	chr1:38187254-38187538	284	1
KRTAP13-3	chr21:30719629-30719979	350	1
KTI12	chr1:52270447-52270938	491	1
L3MBTL4	chr18:6300090-6300607	517	1
LCAP	chrX:152799505-152799865	360	1
LOC253012-CCDC132	chr7:92694358-92694687	329	1
LOC728137	chrY:9296947-9297647	700	1
LOC728137	chrY:9976406-9977106	700	1
MAPT	chr17:41328862-41329197	335	1
MASP2	chr1:11027718-11028184	466	1
MC2R	chr18:13880214-13880542	328	1
MCF2L2	chr3:184626671-184627307	636	1
MEF2D	chr1:154726254-154726638	384	1
MGC13379	chr11:60916846-60917116	270	1
MGC26733	chr2:98228033-98228292	259	1
MLXIPL	chr7:72678946-72679242	296	1
MS4A10	chr11:60307425-60308559	1134	1
MS4A7	chr11:59917920-59918227	307	1
MT1X	chr16:55274943-55275471	528	1
MTDH	chr8:98726883-98727128	245	1
NHLH2	chr1:116182852-116183538	686	1
NPAL2	chr8:99375873-99376112	239	1
NPAS4*	chr11:65940751-65941118	367	1
NPR2	chr9:35784412-35784536	124	1
NRN1	chr6:5953573-5953744	171	1
PA2G4	chr12:54785624-54785910	286	1
PAQR7	chr1:26072173-26072453	280	1
PAX7	chr1:18827637-18828088	451	1
PCP4	chr21:40163182-40163675	493	1
PITX1	chr5:134398494-134398772	278	1
PLXNA1	chr3:128188769-128189114	345	1
PPP4R1L	chr20:56236375-56236640	265	1
PRDM11	chr11:45069895-45070361	466	1
PSMB8	chr6:32916666-32917236	570	1
PSME1*	chr14:23677646-23677754	108	1
RDH16	chr12:55636995-55637363	368	1

RETNLB	chr3:109957672-109958287	615	1
RGAG1	chrX:109582279-109582588	309	1
RNF39	chr6:30149442-30149931	489	1
RRAGB	chrX:55758445-55759286	841	1
SH2D1B	chr1:160647874-160648477	603	1
SHC4	chr15:47044919-47045321	402	1
SHMT2	chr12:55911367-55911782	415	1
SIGIRR	chr11:408013-408331	318	1
SLC28A2	chr15:43332152-43332508	356	1
SLC35F5	chr2:114228998-114229345	347	1
SLC39A11	chr17:68604374-68604872	498	1
SLC6A4	chr17:25571501-25572226	725	1
SMTNL2	chr17:4432730-4433168	438	1
SPATC1	chr8:145159485-145160247	762	1
SPG7	chr16:88151599-88151843	244	1
SPI1	chr11:47356654-47357031	377	1
SRY	chrY:2715394-2715685	291	1
TBX1	chr22:18124821-18125094	273	1
TCL6	chr14:95200830-95201492	662	1
TERF2	chr16:67975371-67975643	272	1
TGIF2	chr20:34631892-34632306	414	1
TP53	chr17:7530676-7530939	263	1
TRPM1	chr15:29182210-29182458	248	1
TSPY1*	chrY:9276601-9277301	700	1
UAP1L1	chr9:139098252-139098685	433	1
UBE1C-ARL6IP5	chr3:69213264-69213580	316	1
WBP11	chr12:14842725-14842984	259	1
WDR90	chr16:654754-655581	827	1
WIPI1	chr17:63965659-63966206	547	1
YIPF3	chr6:43588422-43588842	420	1
YWHAQ	chr2:9690119-9690479	360	1
ZIC4-ZIC1	chr3:148607115-148607757	642	1
ZNF160	chr19:58297559-58298001	442	1
ZNF19	chr16:70080762-70080917	155	1
ZPBP2	chr17:35278251-35278769	518	1
ABI2	chr2:203901882-203902188	306	0
ACOXL	chr2:111269166-111269776	610	0
ACSL5	chr10:114123987-114124563	576	0
ACSL6	chr5:131376810-131377084	274	0
ADAT1	chr16:74212575-74212940	365	0
ADRA1D	chr20:4176208-4176488	280	0
AHDC1	chr1:27746341-27746709	368	0
ALDH1B1	chr9:38383071-38383626	555	0
ALDH1L1	chr3:127382438-127382727	289	0
ALDH4A1	chr1:19103867-19104191	324	0
ANGPT2	chr8:6412368-6412898	530	0
ANXA2	chr15:58470465-58470934	469	0
AP3D1	chr19:2101836-2102176	340	0

APOLD1	chr12:12828941-12829359	418	0
APOM	chr6:31733163-31733472	309	0
ARHGEF17	chr11:72697918-72698619	701	0
ARL6	chr3:98965429-98965782	353	0
ARSB	chr5:78317357-78317474	117	0
BCL2L14	chr12:12116347-12116784	437	0
BMPR1B	chr4:95896326-95896609	283	0
BPIL3	chr20:31081882-31082211	329	0
BSDC1	chr1:32631068-32631512	444	0
BUB3	chr10:124900953-124901356	403	0
C14orf173/ INF2	chr14:104250965-104251393	428	0
C15orf2	chr15:22473457-22473698	241	0
C17orf76	chr17:16333926-16334106	180	0
C1orf38	chr1:28074624-28075188	564	0
C1RL	chr12:7153243-7153753	510	0
C20orf179/ BANF2	chr20:17625384-17625655	271	0
C20orf186	chr20:31131104-31131472	368	0
C22orf15	chr22:22436801-22437151	350	0
C3orf22	chr3:127759125-127759469	344	0
C6orf204	chr6:118993704-118994038	334	0
C8orf79	chr8:12852999-12853282	283	0
C9orf19/ GLIPR2	chr9:36128630-36129074	444	0
CALML4	chr15:66284783-66285215	432	0
CALU	chr7:128167281-128167507	226	0
CAMK1G	chr1:207820029-207820466	437	0
CART1/ ALX1	chr12:84195688-84196028	340	0
CCDC102B	chr18:64655051-64655356	305	0
CCDC117	chr22:27499439-27499770	331	0
CCL27	chr9:34653756-34654112	356	0
CD58	chr1:116913536-116913974	438	0
CD5L	chr1:156080644-156080979	335	0
CD63	chr12:54407747-54408454	707	0
CDH22	chr20:44314782-44315010	228	0
CENTB1/ACAP1	chr17:7191604-7191894	290	0
CENTD2/ARAP1	chr11:72106762-72107013	251	0
chr22:020880519-020880563	chr22:20880442-20880625	183	0
chr9:018815165-018815217	chr9:18814911-18815428	517	0
chr9:129995116-129995160	chr9:129994848-129995333	485	0
CHRNA1	chr2:175337408-175337910	502	0
CHRNE	chr17:4746105-4746457	352	0
chrY:009231390-009231434	chrY:9231170-9231654	484	0
chrY:009233479-009233522	chrY:9233441-9233663	222	0
chrY:009251441-009251499	chrY:9251305-9251941	636	0
chrY:009951247-009951305	chrY:9951198-9951700	502	0
chrY:009953555-009953598	chrY:9953522-9953775	253	0
CHST9	chr18:23019643-23019999	356	0
CHX10/VSX2	chr14:73775141-73775732	591	0
CIDEC-JAGN1	chr3:9903047-9904717	1670	0

CLEC4A	chr12:8165633-8166063	430	0
CLEC4F	chr2:70903953-70904258	305	0
CLIP3	chr19:41199873-41200223	350	0
CLN6	chr15:66311154-66311402	248	0
CNKSR2	chrX:21302820-21303044	224	0
CNTNAP4	chr16:74897750-74898257	507	0
COBRA1	chr9:139270357-139270685	328	0
COLEC12	chr18:491254-491548	294	0
CRMP1	chr4:5948590-5949229	639	0
CRY1	chr12:106011935-106012245	310	0
CSPG4	chr15:73792570-73793130	560	0
CTPS2-SYAP1	chrX:16641814-16642080	266	0
CTTNBP2NL	chr1:112739874-112740131	257	0
CYP19A1	chr15:49416897-49417354	457	0
CYSLTR2	chr13:48179129-48179374	245	0
DCAMKL2/ DCLK2	chr4:151220247-151220782	535	0
DCUN1D3	chr16:20818551-20818811	260	0
DEDD2-ZNF526	chr19:47414073-47414382	309	0
DGKZ*	chr11:46326319-46326657	338	0
DHRS7	chr14:59702105-59702516	411	0
DIP2C	chr10:724149-724401	252	0
DLX1	chr2:172660286-172660524	238	0
DMRTB1	chr1:53699166-53699305	139	0
DNAJA4	chr15:76345797-76346057	260	0
DPYSL2	chr8:26489735-26490054	319	0
DQX1	chr2:74604647-74604922	275	0
EBP	chrX:48264331-48264691	360	0
EIF5	chr14:102865110-102865722	612	0
ELF1	chr13:40455476-40455848	372	0
ELF4	chrX:129047587-129048032	445	0
ELOVL1	chr1:43606685-43606907	222	0
EPHB6	chr7:142272859-142273278	419	0
EPX	chr17:53622391-53622646	255	0
ERAL1	chr17:24211972-24212365	393	0
EXOC4	chr7:132589926-132590188	262	0
F7	chr13:112805222-112805899	677	0
FABP3	chr1:31617520-31617884	364	0
FAM107A	chr3:58540536-58540876	340	0
FAM107B	chr10:14855978-14856487	509	0
FAM129B	chr9:129369644-129370170	526	0
FAM53C	chr5:137710973-137711431	458	0
FBXO32	chr8:124621933-124622167	234	0
FBXW12	chr3:48387459-48388131	672	0
FGF16*	chrX:76591621-76591996	375	0
FLJ10781	chr19:51663252-51663526	274	0
FLJ36748	chr5:148700797-148701679	882	0
FLJ46831	chr10:129427683-129428340	657	0
FRAS1	chr4:79197257-79197641	384	0

FUT4	chr11:93916659-93917006	347	0
GABRB2	chr5:160908695-160909199	504	0
GAL	chr11:68207442-68207730	288	0
GALNTL4	chr11:11601554-11601887	333	0
GATS	chr7:99657109-99657536	427	0
GLCCI1	chr7:7971715-7972005	290	0
GLT1D1	chr12:127903280-127903568	288	0
GMPS	chr3:157072059-157072364	305	0
GPC6	chr13:92677299-92677841	542	0
GPR177/WLS	chr1:68472051-68472492	441	0
GPR21	chr9:124837523-124837777	254	0
GRLF1	chr19:52197686-52198097	411	0
GRPEL1	chr4:7120690-7121063	373	0
GSN	chr9:123103457-123104156	699	0
HBI-115	chr5:76416591-76417182	591	0
HBP1	chr7:106608324-106608655	331	0
HBZ	chr16:138667-139234	567	0
HEXIM1	chr17:40582101-40582400	299	0
HHEX	chr10:94440473-94440706	233	0
HIST1H3H	chr6:27887453-27887809	356	0
HNRPUL2	chr11:62248140-62248456	316	0
HOXB13	chr17:44158717-44158980	263	0
HRK	chr12:115801319-115801587	268	0
HS6ST2	chrX:131923927-131924275	348	0
hsa-let-7b	chr22:44887767-44888118	351	0
hsa-mir-10b	chr2:176719385-176719620	235	0
hsa-mir-138-1	chr3:44127085-44127496	411	0
hsa-mir-217	chr2:56068635-56069196	561	0
hsa-mir-30b	chr8:135882087-135882570	483	0
hsa-mir-32	chr9:110852722-110852971	249	0
hsa-mir-324	chr17:7068862-7069177	315	0
hsa-mir-34a	chr1:9138662-9138777	115	0
hsa-mir-376b	chr14:100576304-100576599	295	0
hsa-mir-9-2	chr5:87997906-87998189	283	0
HSPC171	chr16:65818841-65819162	321	0
HTR1D	chr1:23391237-23391515	278	0
IGSF9	chr1:158182271-158182655	384	0
ISX	chr22:33791648-33792544	896	0
ISY1	chr3:130365124-130365736	612	0
JMJD3/KDM6B	chr17:7696500-7696916	416	0
JPH1	chr8:75401001-75401431	430	0
KCNH7	chr2:163404698-163404998	300	0
KCNJ12	chr17:21258898-21259138	240	0
KCNJ16	chr17:65581955-65582302	347	0
KCNS3	chr2:17920922-17921420	498	0
KCTD12	chr13:76356596-76356885	289	0
KIAA0408	chr6:127838603-127838889	286	0
KIAA0774/MTUS2	chr13:28958071-28958572	501	0

KIAA0892	chr19:19315083-19315424	341	0
KIAA0913*	chr10:75221272-75221834	562	0
KIAA0913*	chr10:75223780-75224064	284	0
KPNA1	chr3:123717182-123717647	465	0
KRT36	chr17:36898423-36898880	457	0
KRTAP13-2*	chr21:30667926-30668040	114	0
LACE1	chr6:108723406-108723635	229	0
LAMB2	chr3:49136450-49136596	146	0
LCE3C	chr1:150839090-150839397	307	0
LDB1	chr10:103869028-103869453	425	0
LIMD2	chr17:59129277-59129583	306	0
LIME1	chr20:61838930-61839236	306	0
LIPC	chr15:56512603-56512746	143	0
LMCD1	chr3:8517305-8517571	266	0
LMNB2	chr19:2406141-2406444	303	0
LMO6/ PRICKLE3	chrX:48929101-48929513	412	0
LOC146325	chr16:548113-548586	473	0
LOC55908	chr19:11207779-11208419	640	0
LOC643905	chr2:240632497-240632722	225	0
LOC728137	chrY:9930777-9931416	639	0
LOC728137	chrY:9933238-9933491	253	0
LRP12	chr8:105669467-105669829	362	0
LYZL4	chr3:42429530-42429640	110	0
MAT2A	chr2:85621713-85622321	608	0
MAZ	chr16:29728829-29729307	478	0
MCART6-CXorf39	chrX:103291210-103291667	457	0
MCRS1	chr12:48244609-48244853	244	0
MEPE	chr4:88967962-88968232	270	0
MGC35308	chr6:166640169-166640514	345	0
MGC61598	chr9:139319446-139319823	377	0
MICALCL*	chr11:12267137-12267422	285	0
MICALCL*	chr11:12268241-12268646	405	0
MMP16	chr8:89410219-89410587	368	0
MTA2	chr11:62124832-62125227	395	0
MTCH2	chr11:47620456-47620766	310	0
MTMR11	chr1:148174395-148175125	730	0
MYADM	chr19:59061678-59062075	397	0
NEFL	chr8:24874720-24875006	286	0
NEUROD4	chr12:53706522-53706804	282	0
NFAM1	chr22:41161665-41162443	778	0
NFATC1	chr18:75253237-75254059	822	0
NKX2-5	chr5:172597459-172597753	294	0
NPAS4*	chr11:65944416-65944768	352	0
NPTXR	chr22:37571280-37571472	192	0
NUDT1	chr7:2249824-2250405	581	0
OIT3	chr10:74322035-74322249	214	0
OLFM3	chr1:102235654-102236022	368	0
OLIG2	chr21:33318732-33318990	258	0

ONECUT1	chr15:50868641-50869119	478	0
OR10A7	chr12:53898824-53899158	334	0
OR1B1	chr9:124431503-124432102	599	0
OR2A5	chr7:143378299-143378526	227	0
OR2AT4	chr11:74478957-74479299	342	0
OR2F1	chr7:143286401-143286723	322	0
OR2T11	chr1:246856593-246856748	155	0
OR4D2*	chr17:53598925-53599180	255	0
OR5BF1	chr1:246579009-246579281	272	0
OR5M3	chr11:55998619-55999341	722	0
OR5V1	chr6:29432128-29432353	225	0
OR6B1	chr7:143332394-143332771	377	0
OR6S1	chr14:20177926-20178216	290	0
OR8B8	chr11:123820676-123821188	512	0
OSBPL5	chr11:3141669-3142089	420	0
PAX9	chr14:36197496-36197848	352	0
PCDHB16	chr5:140542444-140542744	300	0
PEBP4*	chr8:22842184-22842894	710	0
PEPD	chr19:38708467-38708804	337	0
PER2	chr2:238864247-238864550	303	0
PEX10	chr1:2337701-2338163	462	0
PHACTR1	chr6:12828334-12828634	300	0
PHACTR3	chr20:57727134-57727844	710	0
PHIP	chr6:79845456-79845712	256	0
PHLPPL	chr16:70306048-70307096	1048	0
PIGR*	chr1:205185051-205185266	215	0
PIK3AP1	chr10:98381095-98381830	735	0
PIWIL2	chr8:22188638-22188814	176	0
PLK3	chr1:45043537-45043916	379	0
PON3	chr7:94868601-94868857	256	0
PPARG	chr3:12307394-12307708	314	0
PPM1J-FAM19A3	chr1:113064204-113064563	359	0
PPOX	chr1:159403112-159403496	384	0
PPP1CA	chr11:66922959-66923354	395	0
PPP2R3B	chrY:224188-224743	555	0
PREB	chr2:27210002-27210319	317	0
PRPF8	chr17:1501032-1501353	321	0
PSME1*	chr14:23675907-23676180	273	0
PTAFR	chr1:28377462-28377853	391	0
PTF1A	chr10:23522308-23522656	348	0
PTGS1	chr9:124171411-124172108	697	0
QSCN6L1	chr9:138241423-138241762	339	0
RAB11FIP1	chr8:37880639-37880928	289	0
RAI1	chr17:17633670-17633867	197	0
RAXL1/RAX2	chr19:3726037-3726276	239	0
RBM12	chr20:33704136-33704420	284	0
RBM15	chr1:110684724-110685080	356	0
RBMY1A1*	chrY:22453273-22453680	407	0

RBMY1A1*	chrY:22473788-22474194	406	0
RBMY1F*	chrY:22860791-22861010	219	0
REM2	chr14:22422461-22422841	380	0
RETN	chr19:7640668-7641054	386	0
RHOBTB2	chr8:22909270-22909651	381	0
RIOK3	chr18:19287383-19287958	575	0
RLBP1	chr15:87566066-87566535	469	0
RPL12	chr9:129248910-129249476	566	0
RPS6KL1	chr14:74457965-74458464	499	0
RSBN1L	chr7:77164612-77164868	256	0
RSPO1	chr1:37872595-37872931	336	0
RSPO3	chr6:127482898-127483157	259	0
RYR1	chr19:43616537-43616776	239	0
S100A5	chr1:151780520-151780728	208	0
SALL2	chr14:21062667-21062916	249	0
SAMD7	chr3:171113745-171114016	271	0
SCAND1-C20orf152	chr20:34015146-34015395	249	0
SCN10A	chr3:38814325-38814753	428	0
SCN3B	chr11:123027985-123028400	415	0
SCN4B	chr11:117532224-117532476	252	0
SCUBE3	chr6:35285339-35285902	563	0
SDCBP	chr8:59627644-59627982	338	0
SEPN1	chr1:25997796-25998197	401	0
SERPINE2	chr2:224615472-224615750	278	0
SERTAD2	chr2:64737799-64738050	251	0
SH2B3	chr12:110325381-110325945	564	0
SIX2	chr2:45088538-45088896	358	0
SLC17A1	chr6:25939813-25940281	468	0
SLC25A13	chr7:95787757-95788013	256	0
SLC44A5	chr1:75851407-75851825	418	0
SLC5A6	chr2:27289374-27289679	305	0
SLC6A18	chr5:1278921-1279202	281	0
SLC6A19*	chr5:1253195-1253678	483	0
SLC6A19*	chr5:1256160-1256412	252	0
SLC8A3	chr14:69702855-69703149	294	0
SLITRK1	chr13:83356452-83356772	320	0
SNRPB2	chr20:16656613-16657052	439	0
SNX16	chr8:82916335-82916684	349	0
SNX19	chr11:130292412-130292895	483	0
SPOCK2	chr10:73518191-73518398	207	0
SPPL2B	chr19:2283126-2283227	101	0
SPTBN5	chr15:39973957-39974308	351	0
SRF	chr6:43244221-43244751	530	0
SSH1	chr12:107774368-107774680	312	0
ST3GAL4	chr11:125783513-125783967	454	0
ST6GALNAC5	chr1:77107674-77107968	294	0
ST8SIA5	chr18:42589224-42589673	449	0
STEAP2	chr7:89680425-89680732	307	0

STK11	chr19:1157428-1157685	257	0
STK4	chr20:43028719-43029087	368	0
STOML3	chr13:38462640-38462805	165	0
SULT2B1	chr19:53770475-53771201	726	0
SYMPK	chr19:51010844-51011119	275	0
SYT3	chr19:55832483-55832798	315	0
TAP1	chr6:32924348-32924833	485	0
TAS2R16	chr7:122424495-122425048	553	0
TBX15	chr1:119338116-119338242	126	0
TCF2/HNF1B	chr17:33180715-33181386	671	0
TCF21	chr6:134253096-134253367	271	0
TENC1	chr12:51732437-51732627	190	0
TGFBI	chr5:135393929-135394119	190	0
TGM7	chr15:41381751-41381968	217	0
THPO-CHRD	chr3:185578764-185579059	295	0
TJP2	chr9:70980968-70981311	343	0
TLE3	chr15:68178886-68179024	138	0
TMEM113/ WDR82	chr3:52272452-52272661	209	0
TMEM5	chr12:62459856-62460120	264	0
TNFRSF6B	chr20:61797206-61797513	307	0
TNFRSF8	chr1:12047062-12047395	333	0
TNPO3	chr7:128482044-128482356	312	0
TNRC5/ CNPY3	chr6:43005362-43005588	226	0
TRIM47	chr17:71384556-71384827	271	0
TSPY1*	chrY:9271585-9272221	636	0
TSPY1*	chrY:9291956-9292568	612	0
TSPY1*	chrY:9971455-9972028	573	0
TSPY1*	chrY:9294392-9294680	288	0
TSPY1*	chrY:9973851-9974114	263	0
TSPY1*	chrY:9974393-9974746	353	0
TSPY2*	chrY:6175503-6176027	524	0
TSPY2*	chrY:6171161-6171493	332	0
UBXD1/UBXN6	chr19:4407312-4407634	322	0
USP52/PAN2	chr12:55013432-55013755	323	0
VAMP5	chr2:85671309-85671756	447	0
VASH2	chr1:211191708-211191969	261	0
VAX1	chr10:118885229-118885493	264	0
VIP	chr6:153111031-153111191	160	0
WIPF1	chr2:175168636-175168929	293	0
XAB1/ GPN1	chr2:27707545-27708146	601	0
XPO5	chr6:43651125-43651634	509	0
ZBED1	chrY:2429383-2429656	273	0
ZBTB39*	chr12:55685946-55686166	220	0
ZDHHC17	chr12:75682918-75683188	270	0
ZGPAT	chr20:61835313-61835570	257	0
ZNF174	chr16:3392045-3392580	535	0
ZNF197	chr3:44638870-44639219	349	0
ZNF454	chr5:178297077-178297344	267	0

ZNF533	chr2:180435791-180436036	245	0
ZNF7	chr8:146024089-146024643	554	0
ZNF721	chr4:484493-484769	276	0
ZSCAN1	chr19:63238217-63238640	423	0

Supplementary table 2. Fifty seven most significant EBP50 bound genomic regions with potential TCF/LEF motif highlighted in yellow and TEAD1 motif in cyan.

1	**MTMR11**	TAGAACAGAGCCTAGAACAAGGCCTGGCACATAGCAGGCACTAACTATGTATCGAATAAGTAAATTTGAAAAGGGGTAACAGGGTCAAGGAAACAGAAGGAATGTCAAGGTCCAGCTCTCAGCCAGCTCTAGAGGCTGTCAGGGAGGACAGCGAGCCTCAGGCAGACGTACTTCGAGCCACGAGAGGAACACAGGGGTATCTTTGGTGAGGGCATGAAACAAGATTGGCGTAGGATGAAATTTGGAAGTCTTTGGAGAGTGATAGGGCATTATTACCTGGGAGGCATCTGGAGGCCAGGCAACTGCTAGGCTGACGACTCCTGGGCTCCGGCATCCTATTTTCCTGGACAGACTTTGGTCCAGAGGGTTGAGGGGGGTCTAGAGTTAACCCCTAGGCTCCCCAACTCCCCAGAGGCAGCTGCCTGTAGAGGCCTACACTCACACTCTCGGGGGAAACTGAGATCAGTGTCTGTGGGGAGCTCCAGACCTAACAGGGCTGGTAAACAGTAAAGGGAGGGGCTGGTTAATGGATAATGAGACAACGAACTTGAGACTGAGAAAGACGGACCAGGCTCCATCAGCAGAAGCTGATAGACAGACACACCCTCCTCCTCCTCCTCTAGAGCCTTTGCTTCCCCCTTTTATCTCCACCTCATCCCCGTTCTCACCCTCTTGCCGACACCCCCCAAATTCCTTCTCCTTACCCCCATCTCTGGCTCCTCCTTCTGGGG
2	**TRIM46**	GTGTGCATTCACTCACTGAACAAATATTTATTGAGCACCTATGTGCATGGTGCTATTCTAGGTGTTGGAGATACAGCAGTAAACAAGATGGACAAGGTTAATTATTAACTACCAGGCAAAGATTAATTGGCATCATTATTACTGTTATTACCATATATCCCAATGAGAGAGATGAAGGGAGGTGCAATGCTGGTGAAATGGGCACCGCCCGGAGACTGCAGGAAAGGCTCTTTGATGCCAGTATGTACCACCAGGTGGCACTGTGGAGCACCACCAGCGGATGTCTCCACTCCCATCTTGCCAGTGGAGGAGGGCACCAAACTGCTGTAGTGGTAGCATAGCACCCTTACCCACACCATTGTCTGACCATCACATTGTTCTTTGTGTCCCTAGGGCCTTATGTGCCCAGACCACAAGGAAGAGGTGACCCACTACTGCAAGACATGCCAACGCCTGGTATGTCAACTCTGCCGGGTGCGGCGCACCCACAGCGGGCACAAGATCACACCAGTGCTCAGTGCCTACCAGGCCCTCAAGGTAAGGACCCCCCTTATCCAACCCTAGTGCTAACTCACACTCTTACCCTCTTGCACCTCCTCCCAACTGCTGGCT
3	**LOC149134**	TGAAAGGCTGTGGCCACCAGGGAGGGGAGAGGGCTGCTGGGAAGCTGGCAGGGGCCCCAGGGTTGGCAGATTGGGGAGGAAGAGGCAGCGATGTTTGCAAGATGCTGTTCAACCCCTCTCAGTGACAGGCTCTTAGAAAAATCTAAAATGGCACAAAATGTTAGAGCTGGAAGGGACCTTGGAGAACACCTAGTTCAGCCCTCCTTGTTTTCCAGGTGAGGTCAGAGGAGTGAAGTGACTTGCCCAAGACCACACAGTGAGTCAGGAGCAGGCCTGTCCCTCCAGCAGTGGTGCCATGTTGTCCCCAAGCCATGGTGGCAGAGGAGCTGGTGTGAACGCCCCATCCTGCCACGTCTGTGATGTGGGCACCTCACATGACTGTCCCCTCCCAGCTCTTGGGGGGGACCTAGGACATTCTGTGAGCCTGCAGGAAAGTTTACCAAATGCTGCAGCTTTGTCCTGGTGGTGATGGGCACCCCGTTAACGGCAACCTTGCATTTGCTATGTGGAGTGACCGTCACTTTACCGTCGGCATTTGTGAAGGAAGCGTGTTTATCTGAAATTCTAAGAAGATGAGAGTCAAAGACACCCAGCAAACGGCGGTTTCCGTGAGCAGGTAGGCTGACCTTTCTCATGTGCACAGGAGGGAAGGTCTACAGCTGCGGAGGATGGCAGGTGGCATCTCGGGGCCTCCTGTGTGCTGTGGCCCATGATGCATGGGGACAGCAGCGGGCGCAG
4	**XAB1**	AAAGGATGGAAGCTGATTGTGGGAGAGGTAGGTGATCAGAAATACTATTTCAGCTTGAGATTTTAGTTTTCTTACCATCTCCCCAGATGGCAGGCTGTTGTAATTAAAGAGCAGAGAGTATGATAGGATAACTGACAGCTACCTGGGTCCCACAAGGTAGTATTTTGCCTTGGAGGATCATCTGTTGGTCACCACCTCTTTAGACTGGGAAACTCAGAAATGAGTGAGTTTAGTTGGATTAACTCTTAGTAAATTGCTGTATGAAATGTGTACTCTCTCCGTAGGCAAGTCTAAGTAGGAAGACTAATCATAATCAGCAGATTGCTTGGTTTATTTATGAGGATCAGAGCCGGAGGTGTTATACAGGTGGCCTTAATGACCAATGCCAGTGGGCTGTCACTGCCTGATGCACCTGTATTACATTTTGGTCACTTTGCTTTCTTCATTTTGCCTGACCACTCCTTAAATCAAATGAGTGAGCCAGACCTTGATAATGACTGTTTCCCTGTGTGGTTAAGTTTGTATGGTAGTCAAGGATTAGGTTGCCAGTATCCATTAATGGAACACTAATTTCATAATGCCGTTTGTGTGAATGATAGCCT
5	**EFEMP1**	ATCCATTTCAAAGGGGACGGTGCATTTCCTGCCCCCCAGTCCCACACCCCGGGGGATGGAGGTGGGGCTGCAAAACTCTGTTCTCTAGAACGTTAAGGCTTTCCCAGTATACTCACCTTGAGCTAGCAGAGTTCCTTGCACAGCACAGCAAAAATACCTGTGAGCCAATATGAATTGCCTTGGCCTCAAGCTTTTTATTTTTTAAACAAAATAACAAAACAAAACTCGGAGAGCAATCTTCCAGTTCTAGTAGAATACTAGACCTTCTCACATGTCTCAGAGCTTCTCACATCCCCCAGCACAAACTCTCAAAGTGGCATTTCCACGCCTTTCTCTGCGCACAGCTTTGTTTAAAAGTCCCAGGTTGTGTGGAGGGGCAGCCCAAAGCGACTGATTCTCTTTTGTCTTATCAGTCTGGGTCCCCGACACGCTACCTTC

6	**ZNF501**	GTATTAGACAGGAAACCAGGTTCCTGCCTTTGAATACAGTGTTCTTTGCATTAGGAGGGTTCTTGAAACCTTTCCCTTATGAAGAGTCCTTAACATCTTACAGCAGATACTCCTTACACAAAGGCAATCCTCTTGTTATTTTCGAGAAATTCCCCCAATTCTAATTGTAGGAGGATAACTGACAGGAAGTTTCCCTGCTGTTGATTCAGCCCGTTCTTAACAAGACCCATTCACCTCACGGCTAGCTCATTTAGTACTTTTCAAATAAATGAATAAACAGATTCAATCAAAGATGGACTGGAAGGGCTTGATTTGAGGTTTTTGCTCTTTTCCCATCTGTATATAGAATCAAAGCTTTGTAGAATGTTGATATTACAAGAAGCTTTAAATATTATCTAGCTTTTCAATTTCATTTAACAAATAAGAAATGGATGAGACTGAGTGACCTGTGTTAGGTCATTGAACAAATTGGTGGCAGAGCTGAGACTAGAATCCACACCTCTTGACTGAGTCCAT
7	**CCDC51**	GTACGTGGGGCACACCCACGATGTGCTGCATGGCAAACCCAGGGCTGCGCCCCATCATCCTGAGATCTGTGAGGGGGACGCCAGACAGGTCAGCTCACAGCTGAGAAAGGCTGGACATAAGTCAGTTTTGAGGCCTAGGGACAGTTCTGAACAGACTAATCCCCACTCAAATCATCTAAACTGAGCACCACCCTGTTGGGCCCAGAGACTGTGGCCCCTGTGGCAAGAGGATGGTCAGGCTCTCCTCTGGGTGCTCTTGGACAATGGAACACAGTTGGGGACGAGCCTCTAGGATGCCATACCTTCCAGTGCCCGCCACCATGCCACACAAAGCGGACCCTTCCCTGCTACCCACTT
8	**RETNLB**	GGGAGTTTCAGTTTTCTTCGATTTGTGATAAATTCACCTCTCTGTTGGCCCCTACCCATCAAAACAGAGGAATAGATTGGAAAGAGAAATGAAGTATGTGATCATTATGGGACAATGGAGGAGAGGAAGGGCTGAGAAACAGGGGCATGAAGTGAAGGGGTGAAAGGAAGAGGCAGAAGCCCAAGATCCCCCAGTAGCATCCTTCAGGGAAACAAGAATGGGCAAGGGGTCTCTGGGAACCAAGAGTCATGACTCAGCCCCAGGGTGCCAGGGTGATACAGACCTGACATGGGGGAAGACGTAGGTGCAGGGAGATGGACAGGGGAGGATACAGGGCATCGTAGTCGCCATTCCCTCTCAGGGAGTTACTCACCAGCAGGGCAGGAGGACGGTCTGCCTTGGCTTTTGACACTAGCACACGAGAGCTTCTTGCTTATAGGAGAGGGACTGTACTCTGAGTAGGAAAGAAGAAAGGGTACATCCCATGAGCTATCCTCCCCATAATCCCCTTATCCCCTTCCAAATTGTCTTCTACCTTGGAGGTGACACTGTGTCCAGAATCAGCCTACTCATCAGCTTTTAAGGTTAGTTTCCTCATTTTTAAAGCAGAAGTAAT
9	**ZIC4-ZIC1**	CCACTTGATAACTTCTACAACCCACAACTTTTTTTTTTCTCACATTCACTCTTACCCTGTATATTTGGATGTGTTTCCTAAAAATACCCTCTTGTCAACGTCCCCGTTGGATTTTCCACGGACTGGAGAGGAGAAGACTGACTTTTCTTTTTTGAAGAATTATTTTCCCTCTCCCCCTCCCAACAGCTACCCTTCCCCCCTTAGGTCCCCTCCCTTGTTGTGTGTGTGTGTGTGCGCCCGCGTGTGTTTCCTGAAAGGCGGGCGAGGTGGGTTCAATATCTGTTCTCCCTAGTGAGAGGAATACAGCCTCTAGAGAAAACTTCTCCATACAGATGAGGTTTTCTAAACTCCAGGGGAAGCAGGATCCAACTTCCCCTTGTAGGTAAAAAGACTTAGTGCCTCCGATATATCTTTTTTTTTTCCAACCAAGTGTACAATAATTTTTAAAGATACCTCGGCCCTTTCTTTACCTCCACTCCTCATTCCATTCCACTCAAAGTTGGTGGGAAATGCTGGGCTGCTAGACTCAGACTTGTTGATGGGAACAGAACAATTAATTTTTTTTCCGAATTTATATTTCCCGGCACAAGCACAAATGCTCAGCCAGGTCCCTTCAGGCACCGGGAAATCATCCCGGATACCC
10	**OCIAD1**	TGGGGTGTATTTCAGGGAAGGCATCACAAAGGTGGTGATGTAAAAGCAGAATTTTGAAATATCGTTAGAATTGACAAAGCAGGGAGTAGAGTTGTACTGGGGAAACAGTGCACAGAGAACACTGAGGGCAAAGACCTCCAGGCTGTTTCTTGTTAGTGAACCCTGAAATAGAAGAAAGTGACGCTCAAAAGGCACAGGCACCACCAGGCCATGATGGGCCTTATATTCGGTGCATGACTGGAGCTATCAAAAGACTCCAAGGAAGGAAACACAGCGTTGGATTCGTTTCACGTGACTGTCTCCCTTAAGTATGTCTTCGGGAGAATAAATGTTAAATGATAAAGTGGCAAAGGGGCTCAGAAAGAGATGAGAAACCTGAGAGGCTTTGAGGGGTTGACAAATAGTAGGACTGGATTTGCCCACTGTTTAGTCACTAATAACTTGCAGTACATGGCACTAATAAATACTTCAGGAAGGAATGTATGAAAATGAGTAA
11	**SCARB2**	ATGCAGATGTCTGTGCCGTGCGTCTTGTCCAGCCTGCAGAACCATGAGCCAAATAAACCTCTTTTCACTACCCAATCTCAGGTATTGTTATAGCAACACAAACAGACAAGGGCGGAAAATGAGGAGACTGATGCTGTGGCAAGGAGATACGGTGATCTCTCTATACCTAAAATCAGAAGACTTTATCTGAGAAGAACAAGTACACTTAATGAATGATTGCTGGTGCCTGTTGAAATTATGCAATCATTCGGGACTTAGAAAAAGAGCTTTCTTCACAGACTCTAAGGGCTATCGAGGGGAAGCAAGAGGGCTCTTTGGGCTCTACCTTAAATTTAGAATGTTGATACTATACTCAAATGAGTTTAATGATGTAGTCATTGTATACTTTTATGTTCAAAGTGTTAATGTGTTAAATATAAACATTTAAAATACACCACAGGCCGGGCCAGGTGGCTCATGCCTGTAATCCCAGCATTTTGGGAAGCCAAGGCAGGAGAATCACTTGATCCCAGGAGTTTGAATGGAAATGGCCCTAGGCCTTGCCTACTTTGGGACAGGTCAGGCTCCAAGATACTTCTA

		AAAGTCTTGGCTTTCTTCTTATTGAAGGTGATCTATAAAATGTACCATCACACCCTAGTGATTTGACATATGTTATTCCTAAATGTTTGTGGGGCATCCTAAATCCTGAGCAATACAGCCTCCATAAGAAAAAATTACTCTCTCCTCCCTCCTCCCCTACCCATCATTCCAAAGTTCTTACATTACAGAACTGCTTTATGCAGATAGGCTTACATATCCCAGAGGAGAGCTCATATACCATTTATATTATATCACATGCACCTGTGCCAGGCCACAGGGACTCTCTGTGAAGTTACCCATGTCCCTGTCTACCGCCTCCTCCGATCAAGAAGACCTCATGGCTTCCTCATTATCATCTTTGCACCCCCAACTAGGGGAATCTTTTCCAGTTTGTTTTGGTTTGGTTTGGTTTTTATTTTGTTTGGGGTTATGGAAAATGAGAATTCCCCTCTTCAAATTCTTATTTTCCTTTTTGTTCCCCTAATAATGCAGACTTATTGAAACACGGAACTAGGAGGAGATATCCTATTCACCTTTTTCTCTTCCC
12	**PCDHGB7**	GATTCCGGAGGAGCTGGCCAAGGGCTCGGTGGTGGGGAACCTCGCTAAGGATCTAGGGCTTAGTGTCCTGGATGTGTCGGCTCGCGAGCTGCGAGTGAGCGCGGAGAAGCTGCACTTCAGCGTAGACGCGCAGAGCGGGGACTTACTTGTGAAGGACCGAATAGACCGTGAGCAAATATGCAAAGAGAGAAGAAGATGTGAGTTGCAATTGGAAGCTGTGGTGGAAAATCCTTTAAATATTTTTCATGTCATTGTGGTGATTGAGGATGTTAATGACCACGCCCCTCAATTCCGGAAAGATGAAATAAACTTAGAAATCAGTGAATCCGTCAGCCTGGGGATGGGAACAATTCTTGAGTCTGCAGAAGATCCTGATATTAGTATGAATTCGCTGAGCAAATACCAACTAAGTCCTAACGAGTATTTCTCATTGGTGGAGAAAGACAATCCTGATGGTGGCAAATATCCAGAATTAGTATTGCAGAAGACTCTGGACCGAGAAACGCAGAGCGCTCACCACTTGGTACTGACCGCCTTAGATGGTGGGGACCCTCCCCGAAGCGGTACTGCTCAGATAAGAATCCTGGTAATAGATGCCAATGACAACCCCCCAGTGTTCAGCCAGGACGTGTACAGGGTTAGCCTTCGGGAAGACGTGCCTCCAGGCACCTCCATCCTGAGAGTGAAGGCCACTGACCAGGACGAGGGCATCAACTCAGAGATCACTTATTCCTTCTTTGGTGTGGCTGACAAAGCTCAGCACGTGTTCTCTCTGGATTACACTACAGGAAACATTCTAACTCAGCAGCCTTTGGATTTTGAAGAAGTAGAAAGATATACGATAAACATAGAAGCAAAAGACCGAGGATCTCTCTCAACACGGTGTAAAGTAATTGTAGAAGTTGTAGACGAAAACGACAACAGCCCAGAAATAATCATCACGTCACTCTCTGATCAGATTATGGAGGATTCCCCTCCAGGAGTGGTTGTTGCCCTCTTCAAAACACGGGACCAAGACTCAGGGGAAAATGGGGAAGTCAGGTGTAGCTTAAGTAGAGGTGTTCCATTTAAGATTCATTCTTCTTCTAATAATTACTACAAGCTAGTAACAGATGAGGCCCTGGATCGGGAGCAGACCCCAGAGTACAACGTCACCATCGCAGCCACAGACAGGGGCAAGCCTCCGTTATCCTCCAGCAAAACCATAACCCTGCACATTACTGACGTCAATGACAACGCGCCGGTTTTCGGACAGTCAGCCTACCTGGTCCACGTGCCAGAAAACAACCAGCCGGGT
13	**HTR4**	GCCAAGTTTTTGTCTCAACATCTCTCAGCCATTTCCACCTGTTAGTTCTTTCCTTGGTGTGTATGTCTTGAATATGTATTTATCTCATATCCCCTATGAAAAATTTAAAAGGAGAGGAGCTGTAGATTGTTTCTTTAATGACAATAAGATCTAAACTTGAATTTGCCACTACTCCCCTTCCCTAAACCAAACACCTCACTTAAATAAAGCCATTATCCTCACTCATGGATGCTCAGAGCCTGAATCATCTTTGACACCTCCACCTCTGTTCCCCTTCTCCCCACTTTCTACTCAAACATTTGCCAGTTCCTGGGGACTCTATTTCCACTCTGTCATTTGCATCTGTCCCTTCCTTCTTATTTCCACTGGGCCTAATTTTATATATATGTATGTATGTATGTGTATATATATATATAT
14	**TAP1**	ATTTAGGATGGCAGAATTGCAGTTGGGGCCAGTGGAATACAGGGAGTGGTAGGTTGTACCTGTAGCACTAAGACATCTGGGCGGTTTGGGTAGGCAAAGGAGACATCTTGGAACTGGACAAGGCCCTCCAAGTGTAAGGGAGTCAACAGACCACTGGGTGGGCAGCGAGGGGTGCGGTCCAGGTACTCAAATATTTTCTCTGAGGAGCCCACAGCCTTCTGTACTCTGGGGTAGATGGAGAGCAGTACCTAGAGGGAGGTAAGAATAGTGAAAGTGAGGTAGTCTGCTTGCCAGCATTATGTGAAGCAAGAAGGGTAAAGAATGGAAGGACATCACACAGATGGTGCTGGGCCAGAGGAAGGAATCACACTGGGGAGTGAAGGTGGAGGGACCTCACCTCCACAGCCTGGGTGAACTGCATCTGGTAGAGAACAAATGTGACAAGGTTCCCACTGCTTACAGCCCCACTGGTCACCAGCTGCCCAC
15	**OPN5**	AATAAGCTGTTATGAGAACAGTCTTAGGAAGATTTATTCATGGTCCAAAAGACCATTGATTAGCAGATGTGAGAGCAGTGGAGTATATTTTATGGCTTAAAGGATTATGCTAACATGAATAATCACATACAACTTACTCCAAGAAGTTTCATTTATATCTTTCACAGAATCATAAATTCAGCAGAAATTTTGACAAGTCATTTAGTTTCTCCTCCACTTTTAAACAGGATACTTTCCTCCAACCCCCATATGTTGTTTCCCAAGCAATAGTGCCATGAAATATTGTGCAAGAAAGGCAAGCTTCCATGGTTACAAAATTCGACAAACTGATCCTCTTGGAAATAATATCATAGACCCTGGAAGTTGTACCCAGACTACAGTACCTAAAGAATAGCTACAATACAAAATACAACAATAACAATATACAAAAAATAAAAAATAAGTACATAAGAGATTCAGATATGCAGCTGATTGGGAACCATTGGTTTGATCATAGGATGCCATCCCAGGGAACTGGGGGATGTGGTGTTGAGGGCCCTGACCACCTGGGAAGGTAGATAGGACAGCATCTATCTACTATGGGCG

		GTAGGCAATCTTCAAATACAGGAGGTAAAAGAGGGAAGGAATCGACAAATGACTATTTTATTTACACAATGAGGTAATTCAGGCACATTCAATACTGAAAAAGAAACTCTCTAAAACATATCTCTGAACAAATTCAGTCATGACTATGTGTTGCATTTATTATTTTAAGTAGTACAGTTAGTGTTCTGCAAAAATATTTATGATGGTTGCATTGCTATAGCCTGTTTTCAGCAAAAAGTATAATTCTGTATCAATGATGAAATAGCACCTCAACAAAATAATGATAATGATCCCATACTATGCACTGGTACCTCTAATTTCTTTATGA
16	**ESR1**	GAGGCCGTTAGGACAGGTAAGGTAATGGGTCTCAAAGGGAGTGGCCGAAATGCAATGGAAAAAGAGAGATTGTAAAGCTAGAAGGCTTAGGAATTGCCTCTTGATTAGGTGTGGAAGGCAAGGGAAAATCAGCCCTCGAAGAAGACAGTGAGATTTTAATCTGGGTGGCTGGAGAGACAGTGATGCTGGGCACAGACACGGGGAAGTTGAGAGGAACACCATGTTTGAGAATGGTGACTCATATTTGAACAAGCCTGCAATGCCCAGCAGACCGCTGGAAAAGTGGGGCTGGAGACACATTCAACGGAGGAGCCAGATCAATCTTTACCCTTCTTCACCTGAGAGAGCCAGTAAGTCACGGCTGGAACGTGTGTGTCCAGCAGGAGAGGGTAGGGAGGGAAGCCAAGAGAGCTGGGAGCCCGAGTGAAGTTTTTGCCAAAGGCAGAAGAGGAAAGTCGGCGTAGCACAGTATACTTTCCCACCCATGCTCACCAAGCCCAGGGACAAGGCTCACCAAGATGAGTTTGGAAGAGAATGCTGGAGAGAAAGTGGTTAAGAAAACTGCCTTTACTGAACTTCTTGGGCTAACTTTGATTGTAAGTCTCTGAACAATCAAAGCCTGTGAGGAGACAGCTAACCTTCTTATTCTTCCTATGTCAATAGTGAACAATTGCAGATCCCCTTTCCTTTCCTTCTCCTTTCCCCTGTTCCTCT
17	**PRKAR2B**	GTACGTAAAACTGAGGCTGATGATCACAGTCAGCCTTGGGCAAGAACAGGCCCTGTATCCTCTCAATTGCCTCCTTTTTTTTCCTTGAGTGGGTATATATTTCTTGCACTCCAGAGACTTGATCAGGAAACACCTTAACTATTGACAGGAAATGCTGCATGATTGATTGGTCATAGTTATTATTCTGTACTGCTTGCCCAAGCCATTGACTTTGTTTTTTTGGCAGTTACATATAAGCAAGTTGATGGGTCTGTTTAATTTCCTGGTGTGAAAACAAATTTGATAGCACTCTTTTCATTTCAATGCTGAGCTCTCAGAGTTCATTTGCCATTGCTTCCAGTCTG
18	**ADAM2**	TGGGAAAGCCCTTATTCTACGTGGATTTTGGGTGGGGAAGGCGGCAATGTCGGGGATGAGCTTGGAATTGCTGAGTTGGAAACCCCTCAGGAAAGCATCCTCCCAGGGATGTCAATGTAACTTGGAGGCAAAGGGAGAGTAGCGCTGAGGGTCCCAAAAGGCCAGAGGAGGGGTTTTTCTGCTTACTACTGTCCATCCGCAGCCCGCCGAGCCCGCTGAGCAGAAACAAGACGCGCCACATGGCTTGAAGTCCTGGGTCCCAGCCGGAATAATGGCAGTTGGTGGTTACAGGGCAGTTGGAAGCGCGAGATGACGCCCCGGCCACGCAGCCTGGAAGAGGTAGGCGGCTGG
19	**SECISBP2**	CTGTTTTGCTGACATTTTCTGTTCCTTAAATCCACTTGCACTTTCCTCCAAGCCTTTGAGTGAGAGGAAAGTTCCTCCTCCATCTATTGAAATCCACTCTGCATTCTTCCCTGTACTTTTGGTCAACCTCCTATCCCTGCCGCACTTTATACATTTCTCTCAATATTTAACGAATTTGCTCTGTGTAGAACTTTTTTTTTCTCGTGAAAATTATACTATTCCATCTCTTGACCATATCTTAGCACTTTTTTTAATTTTTGAAAGAAACCGAGCGATTTTTAAATTATTTTCTGTGGCTACTTCCAAACTTAAGGTTTCTGGAAATTTAGGATACCATCAAGAGTCTTGTAGGCTTTCCAGGTTTGTAGGACCTACAGGGTATGCAATTCCTGTAAGTCACCAATCTTGGGGAAATTTTAGGGAAATGCAGTGGCGGGGGTGAGAGTAATCTCGGCCTCCTCAGTTTCCTTATTAGTAAATCTTTCTCTTCAGGTGACTGCTCAAAGGTCACCTCAGCGAGAGGCCTTTCCAGACTACCCCATCCCGTCCTAACGCTAGACTCGTGAGGCCCAGGGGAGAAAAGTAAATCACGGCCTAACTCTTGTTTATAGTCGCTACTGCCTTGGTGGAGACTATCTCCGATATCCCAGCACTAAAAGGCAGATCCAAGACTCCCGCAAGCTACGGTGGGTCCCCAGCCCAGAGGACTCCTGGGGGTCCCCATTTTCCGCAAGC
20	**PPP3R2**	ACAGGCTCCGGCTCACCCAATGGTGGAGATCTGTTAGTGTGTGAGGACTTCTGCACTGAATGTTCCACTAGGGAAAAGGCTTCCTGGAATGAGAGAGCTCTCAGTTTCTCTTCTAGGCCTCAGATCTGATTTTCAAAATCAGCATAGCTGGTGTAGCTAGCATCCACCTCTGCTGTGGAGACACAATTGTCAGTCTCTGCATCTGTGAGCAACAGACATAATGCCACTTTGGCATCCTAGGGAGATTCCACTGCAGCCTGACTCTACTGCCTCTCCTCCGTAGGACAACTAACTAAATGTCTCATTGTCTCCACCTGGGGGTAGGGACCAGTGTCGGAGGTGAGAGCACTTTCTGGGAGAACACTTTGCTTGCCCTATTTAGCTGGAGGTCCCCTTCATTGAAATTAATGCTGGTGTGGGCTGCCAACCCTGGAAACCCACTGCTAATGAGGATGATGGCTGAGCTGGGCACTTAGTCCAGGCTTAGCATTTCCTATAAGAGCCCTGAAGCTAGTTTCTGTTCAGGAGCTGGAGCAACAAGTCAGGAGGAGGCCAAATGAACTCCTACCCCTCAAACATGCACAGCGATTTCTGGATGCATTGTGGGGAATGGGGCTGCAATCTGCCGAAGGAAAAGATGGGATTCTGTCCCCTAAGAAAAGTGATTACGAGATGCCCAGCAAAGACAAATATATTTGTCCCTGTTGCTACAATAGGAAGTTAACAATCTGGCAAGATATCTGAACACAAGCAAATGAAAACAGTTCACCTAACACCCATGCAAATTATAAATTTCCTCCCATATACAAAATGATGAG

		AAATAACAGCAAAAATGTATACTTTCTTATTTTTGAACTTTTAAAGTTCTAGTTTGGTCTTTGAATCAAAACAAAGTAAAAGATGTTTATAA
21	**GAD2**	CTGAGGAAGGGCCTTCCAAAGCGGCCGCCTTCCCTTCCCATTCACTGGCTGCCTCCTTTGTGAACTAATGACTGTAATTATTACCTCCCAGAGCTCTTTTGTTATCTCCAACCCCAAGCCCCGGAGAGGGGGAATGGGCTCTTTAGTGAAATGAAAGTCATTACAAAGCAAATTACCGTCTAGGGAGGGACAGCCTTCAGGAAAGACAAATCAGATCTCCATCTGCATCTGAAGTAGGGTGTGTTTAAATAAAAAATGTAAATATCACCATTAGATCCAAAGTACTCCAGAGCTGTGGGATTTAATGGAGTTTAAACGGTAGCACTTGAAGCCATTGCTTTACCAAAAAG
22	**SIGIRR**	ACAGCCAGGATGGGGGCACGGCAGGATCTGGCGCCCAGAAGTCAGAGGGAGGCCCAGGAAATTTGCGCCAGTTTTCCTGCCTTGTGGCTGCCTGAGGAGCCCTCACTCCCAGTTCTGTGGGTGCCCAGGGTCACCCAGAGTTCAAGTCAGGGCTGTGCCAAGCCTGAGAGCCCCCACAAAGACGGAGCAGGCGGAATAGGGTGGCAGCTCACAGCCCTGAACATACAGGGGATTCCTGCGGCCCCACATGGGCACAGCCTTCTCACAGCACCCCTCAACACGCACAGCGGTGGGCTTGTGGGAGGTGCTGGTGGTGGCA
23	**C11orf42**	GTCTTATTTGTGTAGGATCCTTGACACCAAAGGAGCAGTTAGTGTGAGATTCTGATGTCATGCTTGGTGCCTCTGATTTCATGGTCATGGGGCAAAGCATTGCATCCAAAAATGTCAACCCACCAGTGTTCTGCTCTCTCCCTGGAAACGCAACTGGTCCTTCTCAGAGCCCCACCCAAAAGGAAGTGTTTTCCAGTGAAGCAAAGGAGAAGGAATGATGGGAAACTGTCCCATGCAGACCACAAAAGAACATCAGTTATTCCTTCAGCCAGGTGACAAGACAGTAGTCTACAAGCTACCTCAGCTTATCCAAGGTGCAGATGCAACTCCATAGTTAGCTACCTTCCTCTTATGCTAGGAGGCAGTACTTCCAAAACAGCTTTGTAGAAAAAGCAGATCAGCCTTAAGGAGCCACTGGTGAATTCTACCAGAAGGCCAACAAAGAGGGCAATGCCATCAGTAGGGGCATAGATGTGCGAAATTTGGTCCTGGAGGTAGGGAGTAGAGTACAGCACTGTAAGCACTGGGCTCAAAT
24	**C11orf11**	CACCATCTATCTGTAGTCACGGGGTCCTGCCTTCTCCCTGGGTTGATGGGTTCACTCCAGGGTATCTGGGAGTTGCCTCTCTTCTTTGATGCTGGGGAGCCTTTGGGTCCAGAGGATTGGATCGATTGGGGTATGCTTGAAAGATGATTCTGCAGCCACTGGGAATCTGCTGGGGCCACCGGGACTCCCACCCCCAGGCTTAAATTCCTTTCCAAGGGCTCTGTCTGTCCTCTCTGCTTAGCTCCTATGTTAAAACCCCTCCATCTGCGCTGAGATTGTGTTTGCTCTCACCAGTCCTTTGGGAAGCTTTGGGTGAAGGTCTCACTCAGCATCACCTAGTGCCTTACTTTACAGAGAAGCAATTTGCAGCTCCTCCTAGAGAAGTCTTACAGTGTAGGGGAAATCTTCAGTTCTTTGTG
25	**HRASLS2**	GAGATTCATGCCTCCAAATTGGGAATGATGGTTGCCGGGACAGGCAAACATTTCCACCAACCTCAAACCCCATGGCCCTAGAAAAATCGTATTATTGGAGGCACATTCCTCTACCCTGGAAACAGAGTGAGCCTGCTTGGACAGCAGTATAGAAACCACTCCCCTTTCTGCCTCTCACCCACAGTTCAGAAACACTCATTCCACACCAAATGGAAACCAAAACCCAGTACTGGGTGTGTAGAGGTTGCTTCTTTGAGGCACCTGCATGCTTATCTCACCCAAGCTCCAAATAAGTATCTCTTCTGTCATCTACATATAGTTGTCCGGTCCTGAGCAAACTGGACAGGAAGGGGTGGGTGGGGCTGGGGGGAGCTGAGCATCCTCACTGTGGGGCATGGGGGCGAGGACCAATAACTTACCCTCTTCAGGCTATAAACAAACAAACAAACAAAGAGCTTTAGTGTGGGGATGCAGATGGACTGGAGCCAGAACTGGAAAACTCTTTGGGAGCCACAGCAGTTCTGCATGACCAGCTACTCCCTCAGCTCACGTGGTCATGTGGTCTTGCTCCCATGGAGACGGCCTCTCTCAGCACCTCCACT
26	**OR2AT4**	TACTATGCAGCTGCTCACACTCTTATTAAGTTTCTTTCTTGTATGCCTTGACTAGTGGTTCTTTCTGACTCCATTTAAGCTAGGTGTCTGGACTTCTGCTCCTGTATTGGATATAATAGACCATGATAGCCCAACACTTTCACTGCAATGATTAGGGAAACCTGGATAAATTACACAAATCACATTTTTAAACAAATTGAGGAATATGGGTGCCATAAGGATGAGATGAAGGCAAACTCCAATGGGTGGGGACCCTCCAAAGTTAACTAATAATCACCAGCTCTTTTGTTCTCTGGGAATATTTGATTTGGGGACCATGATGTGGCTTAGACTTGGACCAGGC
27	**OR8B8**	ACATACCTCAGAGCTTGCTCCTCTGCCACATGTGGAATGTATTTTAGTCACTGCTCAGAAACAAGATGCCTCAAGTGTAACTCTTATACCTAGAAATCTGCCACTCCCTCAGTGATTATGAGAAACCTCAATCCTTGCTCTCATTCCCACTGTAGTCAACTCACAATTTAAGAAAATAAGTCATTATTACAAGCATGAAATGAGTCCCACAGGAAAGGTGCTCCTTAGGGCACAGAAAGCAAGACTCCGGCTTCATTAAAAGTTGACTTTTCTCTGGGAGCCTTAGAGGATTCCTGTTTGGATGGTAGAACAACCAAGAAAAGTTCTTC

		TGGATGTATGTCATTTTAAAGCCTGTTGCCATGGAAACTACTCTTCAAAATCCTCTCAACTGGGGCTTTACTAAAGTCTTGTTGCCTGAGGAGCAGATGAAGCCCAAGCAGGAAGCAGTGTAGGAAGAACTATTCTTAACTCTGTTCCTTTTGTTGCAGAACTGCCCTCCTTCCAAAACTTGGA
28	**ESAM**	TGTAGCCTCAACATTCATTCCCTGTAGCTAACTTTTCCTTCAGAATTCAGATCCCAAATGACTTGTGACATGGGAAGTAAAGCTGCAACCAATGATTTGTAGTCAGTGAATGTCTCCATGTGACACAGGGGCAGTCTCTTCAAGATTCTTTGACCGTAAAGAATTGTCCTCACTGTCTCCTGTCTCCTATTTCAGCTATTTCTTTCTTCTGACCCTGAGGGCAGTCAAGTCGTAGAAGTTAGCAGAGCAGCTCCATTACTTTGTGAAAGTTTTCACCAAGATGCATTTTAGGGTGGACTGCTCTCCACCCTGGTGTAAATCATGAATGCTGACACAGATGATCTATGTGCGACCTGGGAACTGCTTACATAAACGTGTGCAAGAGCTAGTTCATAGTTTCATATGTTAGAGACTTGCAGGTCATTAGTGTTTCTTCCAATCACATCTCATGTTAGATTCCGAAAGTAATTCCTAATATTTACCTTTACATTTGAATATACTTTCTCTGTCCCCCTTGAATCAGTTATAAGGCTTCATTAAGGTCTAAATATTCCATTTCTTATTTTCGGCAGTGCTCATAGTTATCTGACATCCTGCTATCTTCTTTTCTAGACTGTTCTGGCCAAAGAGACTGGAGATCCAGTATCAGCAAGCTACTTTCTTGGTAAACCTCCATTTCCCAATGCTCATCTTTGTCCTCTACCCCCACCCATCCCAAGGCAAATGATGAAAAC
29	**PKP2**	AGAGATCCACGGAGAGGGCCTCCAACTTTCAATCGAATCTTCCACAACTTGTATTTATCGTGCTATTAATTATGTTTCACCGCAGTTGACTACTGAGAACTTGAGAGCTAAGCTCAACAGAAAGGATCCTTGACCTTAAAGTTTACAACCAAAGCCACTTGTCCTGATTTGCCTCTTTGGACTTAAGAGGCAGAAAGAAAAACATGTATCCCTGGTATTAAGATAATATTCCCTTTGATTGCTTGGGTTTGTATGTTCACTTTCCCTCAAATCACTCAATTGCTGCAAAACCCCACTTACTCAAGTCTGAAGTGTTTGGAGAACGCAGCTTCCCTCGTCTTTGTTTTCCTACCCACACCCTTCTGCCTTTAGACACACACTGAATGCTTAGACACACAATGCACAGGTATATGGCCTCCCTTTTTACATGAGCGTCCAGGGAGTGAAGAGGAAACCAAAGGACTGAAAGCGTGGACAACAGAGTAGTGACAGTTCCGCCACCCTTTGTCAGCAGGCCACATGGCTAAGTGGGAGCCATATGGATGTGA
30	**ESPL1**	GCCTCTCTTGTGCCCCATTTTCCTCCTATCCTAGTTAGTTCCCTGGCATGCCTGGACCATTAACCCTTAGCTCCCTTCTGTTCTTCTCTTGTAACCAAGGGCCAAAGGAGTTTCTCATTGGTTCAATCCTCTCCACTCACCCACCCCCACCACCAATGGTGTTTTCCTATGTATTCTGTTTTAGAGCCCTTACTTTGTATTTCCTCCTTTTCTTTTCCCAGCCCCTTGTTTCTGGGTAATCTCTGGGATGTGACTGACCGCGACATTGACCGCTACACGGAAGCTCTGCTGCAAGGCTGGCTTGGAGCAGGCCCAGGGGCCCCCCTTCTCTACTATGTAAACCAGGCCCGCCAAGCTCCCCGACTCAAGTATCTTATTGGGGCTGCACCTATAGCCTATGGCTTGCCTGTCTCTCTGCGGTAACCCCATGGAGCTGTCTTATTGATGCTAGAAGCCTCATAACTGTTCTACCTCCAAGGTTAGATTTAATCCTTAGGATAACTCTTTTAAAGTGATTTTCCCCAGTGTTTTATATGAAACATTTCCTTTTGATTTAACCTCAGTATAATAAAGATACATCATTTAAACCCTGTTTTGCGTAGTTTATCTGAGAACATTTAAAGACACGGCATGACTGCCCCCTTCCTACTATGTGGTACTGTAAGCTGACAGGAACAGGTTACAGCAGATCAAGTTTGAG
31	**SHMT2**	TTCTGAGAATGCTGCCTCTGGCTTTGCCCCAGGCCTGGTGCTGAGTGAATGGAGCTTTCTGCAGGGAGTACTCCCGCTTTCAGCTCTGGCTCTGGCAGGGAGGGACTGTGGGAGTCCAGGGGAAGGGGCTCAATACCTTCTGACATTGCCCCCCACCACCCCAGAACTTCTGCAGCCGAGCTGCGCTGGAGGCCCTGGGGTCCTGTCTGAACAACAAGTACTCGGAGGGTTATCCTGGCAAGAGGTGAGGGCTGGAGGGCAGTGTCAGGGATGGTGCTCCCAGTGGGGGAACCCACCTGTACCTTCCCAGTGTTCATTGAGGAGTGAACTTCCCAGTCCTTTGCTGATGGTTGAGAGTCCTTTCTCTGTGCCCTCATTACCCCTCTCCCACGGCAGATACTATGGGGGAGCAGAGG
32	**ASCL4**	CTCGCCCCGGGTCTTCCTTGACTTGACACATTTTATAACCGCAAGAGAGCAGTTTTTCCTTTGATGAGGCTAAGACCCCAGAAATGAAAGAGCAAGTTTAAGTTTGCAAACACTCTAAAAGCTCCTTCCATTAGACCTGGTCGCGGGAAACCACAAAGGACAGTCAAGTGATTTTCAAGGAGAAAGCCTCTGGTCCACTTTCCCTCCGCCGCCAGATCTGCAGGTTCCTGGGAGGAGCTCTTCTCAAATCCTGAAGATTGCTAGGCTCTTGGCGAACGACTCATCTCTTGAAGACCTAGAGTGGTGGATTACAGGCATTGAAAAGCTTTTGGTGGCTTTGGAAGATGACTCTGGTGTGAGCTCACCTTTCCAGGCTGGGGGACCAGGCAGAGGAACCCCCTTTGTTATCTTCTGAAAGAAGATCAGTGGGGAAGACGGGGTTTGAAGTGTGGATTAGGAGATCCTACGTCTTTGCCTACCACCTCTGCCTAAATCATAAAAAGATCGAGGAGTGCAATGAACTTCAGGAATCATGCACCGTTTCCCTGAAGCCTGTCCAGGAACCTAACTTCTGGACCCAGAAACTTC

33	**KIAA0774**	CGGGGGAAGCGGGGGCCTGTGTTTTTACAGTGTGCCATGGCCTAAGTGACACCTGTAATGGAGCAGAAAGAAAAGATATTTCCTTTTTTAAACCAGTGATTTATTTTTCCAACAGATTGAAAGGTTTTGGACAAAGATTCCATGAAAACCTCCTATAAACAGGAATTGGACAATTAAATACTGTTGTAATCAGCCTTTCTCCTGGTGGGTTCATAGCTCTGAGCTTCAAGTAAATACGGTTTGATCAAGAATGGCCTTTAAATGGGAGTGAGCCATTGTGCACCACGTCCGTTCTCACACTGCGATGCAGCTTTCCTAATGCCATGGGTCTGCTGTAGGTTTTGCTCAGTGATATTTGTTTTAGTGGATGAAGTTCTCATTTACCATAAGAGAGAGAAGTCAGGATAATTGTTTGATGAAATTATAGTATGCAGAATGGGAAACCACCCTTTTTTAAAACAAATATATCCTCACGTGTCAACTTCACAGTCAGGCTTCCTTT
34	**ESD**	CGTGGGCGCCCCCTCCAACTCCTGCCTTCGCCCGCGTTTCTGCTCTGTGTGGTTACTAGGACCAACGAGGAGGGCGTTAGGTTAGTCCCTGTCACCTTGTCGGGGATCAGTCTGCTGTGCGTGCTCAGACTCTTCCCAGAGCCAGCAGCAAGAACCCGAGGCATTAATAAACTTGAGATGTAGCTTCGCTTAACTCGTGCAGAGGGTTTCCGTGTCACTTATGTAGAAACTAGGGCCTAATTTCAACTCCCTCAACTCCTCTGTCCCAAGACTATCCACGTCACCTACTTGGTAGCTTGAGTTAAACAAGAAACCTTTGAAATCTCCAGTGGCCGACACGCAGTGGGAACTCCATCAG
35	**CHX10**	AATACATATTAGTCGAATGAATTGGGTGGAAGAATCAAGTCCTCCCATGAAAGTTGGGCATGCTTCATGCTTACTCTAGGAAGAGGTTTGGATGTCCATGGTTGTTCTCCAAAAGTAATCATCACTGTTCCTCTTTCCCACCAGGGACCCCTCTTTCTGACCCATTTATCATTCATTCATTGGGCCAATATGTGTTGAGTAGCTCTTCCGAACTAGGCATTATACCTTGTGCTGGGGAAGCAAACTTTCCCTACCCCTACATCACCCTCTGCACACCTTGGCCTGATCTTTTCCCAGCTTACCACCACACACACTGCCCCAGCACTTACCTCTCCCTTGTTCAACCGTTTACACAGAGGTGCCATATTCAGGCCGCCCTGATGCTGCCAACCTGCATAGGAGTTGAGGGAAGGAGGTCTCCCAGTCTCTCACCTCTGCCCTTAGCCCATCCTTCCACCTGACCTCAGGGACCTGTCCCTGCCAGAATCTGCCCAGAGCCCCAAGCCACTCTGCCTCCCGGAACAGCCCTGAACCTGAACCTGGTTGTCTCACTTCGGCCCCTGGGGTCCCTGCCCATGGGCATCCTGCAGAG
36	**OR4F15**	GTTAGGTGGCTCATGTGACTGGCTGAAATCATATCCATTGATAAGAAATCATAGTGAAAAGTATTTAAAGATGACCTTATATCTCACCCAAATAGAACATCCTGGGAAGGATCAAATAGGAAATATTCATGTAACACAAAAGCAGAGGAGAGCTAGGTCTAAGGATGGAATTAATTTAGTAGTAGTAGTTTTGAAAACCATAATGCCAAATAGCAGCCAGCTGACCCCTCTAAGTGGAAGTCCAGGGTGCATGTGATGAGGGTTATTTGGCTGTGTAAGATGTTAATATGATAGTTATTTTCATGGCTGGAGGCTTTCTTTCTTGAACATGAATACTTGCCTAGGTAATTCTTTCTCATTTTCTTTCTTCCTTCAGGTAAGTAACATGAAAACTGATCTTGGAGTCTGAGGCAATGAATGGAATGAATCACTCTGTGGTATCAGAATTTGTATTCATGGGACTCACCAACTCACGGGAGATTCAGCTTCTAC
37	**SLC6A4**	TTTTCCCCACTGCTCTGCTCTCCCCCAGGTTCCCATCTTCATGCCTACAGTCAGCTACTATTTTTTATAATCTACAAGTTAACTACTTGAGAGGCTTTAGGGGTACAAGGAACAAGATAGGGCCTCTGGCCTCAAAAATCTAACATCCCAGGAGGAGATAGGAGGGCCAGCCATGCGTGGTTTGAGGTTGGTATTAATGTCATGCTGTGGATCTAATCCAGCTTAAATTCTGCCCAGACTGGTAATTAAGATTTAGGACTTAACGCTGATGCCCTTCTCTGACCTCACACAGGTCCAAAGGATCAGAAGCATCTGGGACTCTGAAGCCACCTCCAAATTTTCCCTTACGCAGGCCTACCCTCGTGGACTCTTCCCAGCAGAACTTGCCAGCAGGAGTGAAGGGACTCAGCACAGGGCTGACGGCCATTCCCTCACTTCTGGCTGGGGGAGGACAGAGCCTGGAGAATGCAGGATGAGAAGGAGGCCCTTCAATAAATGGAGCGCTAATGATGCTGGAGATCTGTGAGGTCAGGTTTGGGAGGGCTTCACCCAGCTTCACAACCCGGAGAGCCTCAGACACGCTGTCTTCAGCTTTTGGCTTGCTGGAGATTTGACTTTTTTTTTTTTTTTTTTTTTTTGAGACAGAGTCTCGCTCTGTCGCCTAGGCTGGAGTGCAGTGGTGCCATCTCGGCTCACTGCAACCTCCACCTCCCAGGTTCAAGTGAT
38	**RIOK3**	TCTCTGCCTTCATTCCCGAATGGATCTGGTAGGAGTGGCATCGCCTGAGCCCGGGACGGCAGCGGCCTGGGGACCCAGCAAGGTAAGTGGCAGACGAGACTGGAGTACTAGCCTTGGTCACACGGGCTGGATCTCTCGGAAAGCTCGGAGAGGGCGGCTTCGTGGGCGATTCGGGAAGTTCTGGGGCGGGACCCCGCGGACCTCGGCAAGGGGGCACTGGCCGCGGGGGTGCCGGGATGGGGATGGAGGGAGCGGAAAGAGGGGCGGAGGGCGGCTGGATCTCCCAAAGGCCACCTTGAGTGGTTAGGGCTCTCTATTTCTTCAGCGTACTTTCTGTATCACCGTAGCATGTATTTGAGCAGGACTGGCTTACACACCCTGATGATACTGGAGGGGAAACAAGCACGATCTTGTTTTTCACTGGCCAAGTGAGTCAGCCGAATACACAGCTAGCCAGACAGAAAGTTGGTTTAGGAAGCTGTTTACTTAATTTGATAAGTGTGGTTATCCCAGTTTGGAAATGTCTTGTTTTTGAAGCAGTAAAAGATAAAACCCAGGCG

		CACCCTCCTCCCTCGA
39	**ST8SIA5**	ATACCTGATGTATCCACCTCACCCAAAGGATGAGAAGAGGGCTGTTTCGTTATGGGGAAGTTTAGAGAAGAAGGTGGGATGCTTACTTAGCTAGAGAGACATTTATTTTCCTATCAACCTAGGGGAGGGGCGGTGAGAGTAGGGAGACACTAGCAGCAAACTAAAAAACAGCCCAGCAGCTAGGAGAGAGGGCTCTTGCCAAGAGAGGCTCTGATATGGGTGTATCCTAGAGCAAGAACCTCCCCTAATCTCTCAAACCAGGCGGAGGAACCCCAAGTGTTTCCTTAAGCCAGCAGAGCCGGCAGAAGGAAGTGGCTGGCATTTCAGTGTATCTTCTGCAAATAGAGAGGCTGAGGCTGTGCCCGAATTGAATTTCTGAGTGACACCTCCTACTGCTCTTTCTCTTGGAGTTTAACCGTGGATTGGGGTGGAGTAGGGGGAGAGCCCAAC
40	**NFATC1**	GTTGGGGCTGCAGGGAGCCCTGTTCATGCCGCTGCACTCCAGCCTGCAAGACAGAGCAGAAAAAAAGAATCAGGATCCTGGGCAGAGGGAGGAGAGGGGACCGGGGTCCAGCAAGCACTTGGGGATTGACTGAATGGCGTTGGGGAGAGATGACTCCAAAGTCCTGGAGTGGGTGAGAATGACTGCGAGTGGCTTTTAGGTGGGGAGGTTCCTGCCTGGCCACTCCGGGAGGGGACGTGGGGCTGAAGGGTATCAGGTGCCGTGCTGAGCAGTTTGGCCTTGATCCTAATGCCCTGGACACACGTCTAGGGTAGGAAAGTTGACTGATCCATTGGTGATCTGAGTTTTTAGACATGGTGGTAGTCCATGAGGTGGGTGTTCATGCTAAGAGTTTAGACAGGGAAACCTATGAAGCCCTTAGCAACCCTCCAGGGAAGGGGCGTGGTTAAAGAGATGTTTCATAAGTAACAGCATGGTATAGAAACTCTGAACCCCAAATGTATGGGTCCTCAGGAACACCCCAGACTTTAGAAGGAAAGTCAGAAGGTGCTGACACGGGTGTATAACTAAAGGGAAATCCTTCTTTCTCAGCTCCAACCATGGCTGTGAGGTTCATTCACACTGACTTAAAAAAAAAAAATCTCAGTTTACTTAAAAGTAAATAGCTTTTTCTATAATTCTGGTTTGCTAATTTAATCCTAGTCTCCAGACCCTGGCTAAATAAATGCCCATTTCTCCAGATGGTCTCAAGAGTCTCTGGACATCGTGGGGGCCCTTCCCTGTTGGTTGGAAGGTGCCTCAGGAAGAAGGGGGTGGATTCTGAG
41	**CD97**	AGCAGCAGGGGCAGCCCCCAGAGACCCCAGTTCTTGCTCCCCGCAGACCTGGCTGGGGCTCAGCTGCGGATCGAAGGGACTTTGCCTGGTTCTGGGTTTGAATTTGATTTTTGTTGTGACTTCCTGGGACTCCCTTTCCCGCCCCACCCAAGGTGACTGTAACGGTTATCAGGGTAGCTCGTTGCCTAAGCAACGGGGCAACAAAGAGAGTGAAGAAATGACATTTGGGGCAAAAACCAGAACTTCCTGGACCACAGGGACACAGCTTCCCTGGGCCAGCCCCAAGTGGCAGGTGTCAGCTCAGCACCCCGCCTTGGCTTGAGAGTGAGAGACAAGAGCCCACCTTGGGTTTCTTGGGGGCACACTTGTTGGGGGCAGTTGCCAAGACCTGGCTTCCCAAGGGTTCCACGCCCTGGCTGTCTGTGTCACCAGGGCCAAGTCAGAGAGCCTCTGCGCCTCACTTTTCTCATCTATAAAATGGAGCACAACCCGTCTCCGTCTTAGATTGTTTTAAGGGATGAGTGAGTTAGGACACAAACTATTCCTGGTTCACAGTAAGAATTAGGTAAACAGCATTTTAAAAGTGTTGGCTGGGCACAGTGGCTCACACCTGCAATCCCAGCACTTTGAGAGGCCGAGGCAGGTGGATCTCTTGAGCCCAGGGACTGGAGACTAGCCTGGGCAACACATCGAGACGTTGTCTCTACCAAAAACAAATTTTTTTTTTTTTTTTGAGACAAAGTCTCGCTCTTGTCGCTCAGGCTGGAGTGCAATGGTGCAATCTCGGCTCACTGCAACCTCCGCCTCCTGGGTTCAAGCGATTCTCCTGCCTCGCCCCCATCCACCCCGAGTAGCTGGGATTATAGGTGCCTGCCACCATGCCCGGCTAGTTTTTTGTTTTAGTTTTTGTGTTTGTATTTTTAGTAGAGACGGGGTTTCACCATGATGGCCAGGCTGGTCTCAAACTCCTGACCTCAGGTGATTCACCCGCCTCCGCCTCCCAAAGTGCTGGGATTACAG
42	**TMEM161A**	TTGCTTGCACCCATGAGATCAAGGCTGCAGAGAGCTATGATTGCACCACCGCAGTACAGCCTGGGCAATAGGGCAAGACACTGCCTCAAAAATAAAAAAATAGGCCAGGCGCAGTGGCTCATGCCTGTAATCCCAACATTTTGGGAGGCTGAGGTGGGAGGATCACTTGAGGTCAGGAGTTTGAAACCAGCCTGGCCAACATGGTGAAACCCCATCTCTACTGAAAATACAAAAATTAGCCGGGTGTGGTGGCAGTCGCCTGTAATCCGAGCTATTTGGGAAGGACGAGAATCGTTTGAACCCGGGAGGCAGAAGCTGCAGTGAGCCGAGATCCCGCCACTGCACTCCAGCCTGGGCAACAGAGTGAGACTTTGTCTCAGAACAAAAAAACAAAAAAAAAAACCCAATAATAATAAAAACAAAATTAGGCCAGGAGCGGTGGCTCACACCTGTAATCCCAGCACTTTGGGAGACCGAGGTGGGTGGATTACCTGAGGTCAGGAGTTTGAGACCAGCCTTGCCAACATAGTGAAACCCCGTCTCCACTAAAGATACAAAAAATTAGCTGAGCATGGTGGCACATGCCTGTAGTCCCAGCTACTCAGGAGGCTGAGGCAGGAGAATCGCTTGAACCTGGGAGGCAGAGGCTGCAGTGAGCCGAGATCGTGCCATTGCACTCCAGCCTGCATGACAGAGCGAGACTCTCTCTCAAAACAAAAAACAAAAACAAAACAAAATAATAAAAATAAGTAAGTAGAAAAGAAAAAGAAAAAAGACCTGAGTCTGGGTTGGGTGAGCGAAATCTCTAGCCGCACTTGGACACTCTGCAGAGGCTTCAAGTTCACCCCATCCAAGTCTCATTCCCTACAAGCTTCCACAGCACAGAGGA

		TGAAATGGGAGCTTCCAGTCACCCACGGCACGCTCTTCCCTTCACCTCCACCTCCGAGCCGTTCTGGAGTCCTGGTGGGTTTGCCTCCACGCACACACAGAGAGTGATCATTCCAGGGGGCACTGCCTCCCCTCAGCTCCCAATGCCCCCTGCCACGGGAGCCTGGGGAGGGGCTTTTACACACTTTGATCATGCCATATCCCTATCCTGGAAACTGGGGCCCCAAAGCCCCCACCTCACTGGGGATGAGGGTGGCGAAGATGACGTAGGACAAACCTTAGCTGGGGTCTGGGGTGCAGATGGCATCCTATACTCCGCCGTATAAACAAGTGCCCCCTCCGGGTTCTGTCACTTATATACTTTGTCCAGTCTC
43	**PEPD**	ATCCAATTATCGACATTCAATATAAGAAATAAAGTTCTGAAATGGTTTTCTTCAGCACATGCAGAGTGAGCCGACCAGGTTGGGCAGGTGATAATTACTTTTATTTCTTACGAGTGGGTATCACCGCGGAGTGGCTAGAAGCTTCACCTTTTATTGCCTTCACCTTTTATTACATTTCCCACGTTGTGCAGGGCTATTCATTGGTAATTTTATTATCCCATATCAAGATCTTGATTAAAAAAAAGGATGAAATTTCTAATTTCAAAAGATATGAGTGCAAAGTCCCAGAGTAGGAGGATTTGGTCCTATACCTTGTGACCTGAAGAGTAACCCTCCAG
44	**TFPT**	AGGTGATCTCTGGAGTTTTGCAGCTGGGTTTCCATACCTAGTTTGTTTCAAGATTAGCCCCTGCGGCGAGGCGCGGTGGCTTACGCCTGTAATCCCAACAGTTTGGGAGGCCAAGGTGGGTCGCTCACTTGAGGTCAAGAGTTCAAGACCAGCCTGGCTTACATAGTGAAACCTTGACTCTACAAAAAAAAAAAAAAAAAATTAGCTGGGCATGGTGGCAGGTGCCTGTAGTCCCAGCTACTCAGGAGGCTGAGGCAGGAGAATCGCTTGAACCCAGGAGGTGGAGGTTGCAAGTGAGCCAAGACTGCGCCACTGCACTCCAACCTGGGTGTCAGAGCCAGACTCCATCTTTAAAAAATAAATAAATAAAGATTAGCCCCTGGAACTTCTAAGTAAGCACATAGATAAGCCAGCAGTGCAAGACAGTATCTAGTGGGAAAGGAGGGAAACAAAGAATTTCAAAGTATGTTTTCAAGGCTAAAGGCAAGAAAGGAATAAGAAAGTTTGCAAATGCATTTGGAATCTACACCACTTGGTTCCAGTAAGTCTTAGCAAGGTGGCGGTCATAGGGGTGTGCTGCGTCTTGCACAGGTCGGAGCTGGAGACTCGCCAGTGAACAAAACAAACTAAAGCACCTGTTGTCGTGGAGCCTGCATGCTAGTGGGGTTGATAAAGAAGGACCAGGGTCTTCTGGGGGAGAATCATCGCTCAGTAATAAGGAGGGACTTTGTCGGGGCAAGTTTTTAGGGAACGCTGCTGTCCCTCCCCAGGCCTCGGGATGTCTCTGGCAGATGAGCTCTTAGCTGATCTCGAAGAGGCAGCAGAAGAGGAGGAAGGAGGAAGCTATGGGGAGGAAGAAGAGGAGCCAGCGATCGAGGATGTGCAGGAGGAGACACAGCTGGATCTTTCCGGGGATTCAGTCAAGACCATCGCCAAGCTATGGGATAGTAAGATGGTAAGAGGACAAGAGGTGTTCCTAGCAGGGGGCTCTAGACAGAATCTCCCAGAAGGGGGTGATACAGGCTTCTTTTTGAAGAGTGCTGGATTCTGACTGTCTTCTCCTTTCCTACAGTTTGCTGAGATTATGATGAAGATTGAGGAGTATATCAGCAAGCAAGCCAAAGCTTCAGAAGGTG
45	**SNRPB2**	AGCTATTCGATCCTTATCATTCCCTTCCTGTACTGTTCTCAATAACTGGCTTCTCAAATCGTTCAGGAAACCACTGAGAATCATTAACGGGTTATTGGAATGCCCAGAGTGACTGCCCAAGGACAGGAAAATGCACTGGCTCTTTTTAGAAGAACCTGGAAAAGTGCATGCAGACCATTGCGGCTGAGTTGGCAATGGATGATTTCCTTCTCACAGTGTAATGTACAATAGCTGTAATTTAATTGTTAATAGAACACAACATGCAGTCTGTCTTCAGGCCTCTGTGTTTCTTGTGGTATTTTCTTCCCAGGTTGGAGTGTTTTTGTATAATCACATCTTATTCTCTTTTAACAGTTATCAACTCTTGGCTAGATCCCCTTATACAATACAGAGTATAGTTTATTCTCAGTAGTGTAGCCATCCTCATTATTATCAAACAG
46	**PPP2R3B**	GGCGGGAGGGAGACCTCGCCAACGGGAGGCGGGAGGGAGACCTCGCCAACGGGAGGCGGGAGGGAGACCTCGCCAACGGGAGGCGGGAGTGAGACCTCGCCAACGGGAGGCGGGAGTGAGACCTCGCCAACGGGAGGCGGGAGTGAGACCTCGCCAACGGGAGGCGGGAGTGAGACCTCGCCAACGGGAGGCGGGAGTGAGACCTCGCCAACGGGAGGCGGGAGGGAGACCTCGCCAACGGGAGGCGGGAGTGAGACCTCAGCAACGGGAGGCGGGAGTGAGACCTCACCAAGGAGACGCGGGAGTGAGACCTCAGCAACGGGAGGGGGGGAGGGAGACCTCACCAAGGAGACGCGGGAGTGAGACCTCAGCAACGGGAGGCGGTAGGGAGACCTCACCAAGGAGACGCGGGAGTGAGACCTCAGCAACGGGAGGCGGGAGGGAGACCTCACCAAGGAGAGGCGGGAGGGAGACCTCAGCAACGGGAGGCGGGAGGGAGACCTCAGCAACGGGAGGCGGGAGGGAGACCTCAGCAACGGGAGGCGGGAGGGAGACG
47	**chrY:009232377-009232432**	CAATTCCCCAGAGACCAAGGAATGACCAGCTAGGTCCTTTCCCATGATGCCCCACGGCAAACACCACCTCCGAACTCGTGCCAAAACCCAGGCAGTCATGTTCAGCCAAACAGCTGAATAAGCTCAGGTAGGAGGTGTACTGCCTGCAGCTGGAGGCTTAACCTTCGTGAACCCAGAACCGCTGGACTGCAGTGGAATGAGACACCCTGTAGCCTGCAGGGAGAGGAGTCAGGAAGGTT

		CATGCCAGTTCCACCCTCCCACACACCAGCTCTCCTACCATGCTGGGAGGCATTCCTTACCGAGGATGCCAACACAGTGCTCCTTCATGATGATTTCACTGTGGAAATAAAGGTTGGGATGAAAGGAAATCATCCTGCCACCGGTAACCGGGATGGCTGTGTTCCTCCACCTGCCGGATCAAGGAGAAAGAGGATGGATTCAATGGGACCATCTCAACTAGCTGGGCTGAGGTGGCCTACTTGCTGTAGTGAGCCATGAGTTTCCCTTTCCCAGCTCTGCCACTGAGACGACCCTGGTCCCAGGGGGACCTCAAACTGACTCAGACACTGGACTCCTCCCACAGACCCAGGCTCCCCAGCCTGACCTGCAAATCCATCACGTAGCAAAGCAGGACTTCCGCATGCTTTCTGACCCACGCCGACATCTCGTGTGCCAAACAATCTACCTCTGCGCAAGAACTCTCCAGAGGATTGGGTGGGCAAGCCTCGTGACGCCTTGCAATTTCGCA
48	**chrY:009251441-009251499**	AAATGATCATAAAAACTGGCAGGAGTAGACGAATAGAAATGCATCTTAAAACTTGCTAAACCCTTCAAGTCTCCCATAAGAATTGTAATGGAAAATGGATCGGTCGGCAGCTTTTTCCATACAATTATGAACAAATTATATTTCTTCATACATAGATTTGTTTTTTCAATATTCTAAGGAATTAACTTTTATATTAATAGTAGGTGATGTAAGAAAGCAGGCCTTTATCAAGATAACTGACACTGGATGTCCATACCATTACTCAGGTGGGCCTTAATTCCCAGCCGGGTTCCCTCCCTGGACACACACTGAAGGTCCCCAGCCATTTGGCAATCTCTTCACATTCCCAGCCCTGGAGGTAGCCCTAAAATACATGTACCTGAAGAAAATAAAACATTGCCTCACACTGGAGCCCAGTGTGGTCCTCCAGATTCCGTGTGAGGTGGACTAACTTATATGGGAAGGCAGGGCAGCGGGAGTGAGGATGGCAGAGAGGATTACACATGTCAAGGCAGCCGGGGTCATGGAAACAAAACATGACTGGCCTGGGAGAAACACTGTGAAAGGACACAGACCTAGGTGGGCCTCAGGTGGACATCCTCATGGAGAAAAAGGGGGCCCTGGTTGATCTCAAAAT
49	**chrY:009252280-009252324**	CAGCCCTAGGCTGCTCGCCTGGCCTCCTCTCTGTTCCGCCTCTAGGGCTGACCCTCTCTCCATGGGATAGAACTGCAATGGATTGAGCCATAGGCCCTGGCTGATGATCTAGGGGACTGCAGAAGTGGGTCCAGGACAGTTCAGGTGACAGTTCAAAGCCAATTCCCCAGAGACCAAGGAATGACCAGCTAGGTCCTTTCCCATGATGCCCCACGGCGAACCCCACCTCAGCAATCCTGCCAAAACCCGGGCAGTCATGTTCAGCCAAACAGCTGAATGAGCTCAGGTAGGAGGTGTACTGCCTGCAGCTGGAGGCTTGACCTTCGTGATCCCAGAACCGCTGGACTGCAGTGGAATGAGACACCCTGTAGCCTGCAGGGAGAGGAGTCAGGAAGGTTCATGCCAGTCCCACCCTCCCACACACCAGCTCCCCTACCATGCTGGGAGGCATTCCTTACCGAGGATGCCAACACAGTGCTCCTTCATGATGATTTCACTGTGGAAATAAAGGTTGGGATGAAAGGAAATCATCCTGCCACCGGTAACCGGGATGGCTGAGTTCCTCCACCTGCCGGATCAAGGAGAAAGAGGATGGATTCAATGGGACCATCTCAACTAGCTGGGCTGAGGTGGCCTACTAGCTGTAGTGAACCATGAGTTTCCCCTTCCCAGCTCTCCCACTGAGACAACCCTGGTCCCCAGGGGGACCTCAAACTGACTCAGACACTGGACTCCTCCCACAGACCCAGGCTCCCCAGCCTGACCTGCAAATCCATCACGTAGCAAAGCAGGACTTCCGCATGCTTTCCGACCCACGCCGACATCTCGGGTGTGCCAAACAATCTACCTCTGCGCAAGAACTCTCCAGAGGATTGGGTGGGCAAGCCTCGTGACGCCTTGCAATTTCGCAAGAACACAGACAATGTGGAACAGGGCCATCTCCCAGACATTTGGCCAGTCACCCTTCATTGTTGGCCCTCTATCTCTGTCTGGCGAGGAGGCA
50	**TSPY1**	AAATGATCATAAAAACTGGCAGGAGTAGACGAATAGAAATGCATCTTAAAACTTGCTAAACCCTTCAAGTCTCCCATAAGAATTGTAATGGAAAATGGATCGGTCGGCAGCTTTTTCCATACAATTATGAACAAATTATATTTCTTCATACATAGATTTGTTTTTTCAATATTCTAAGGAATTAACTTTTATATTAATAGTAGGTGATGTAAGAAAGCAGGCCTTTATCAAGATAACTGACACTGGATGTCCATACCATTACTCAGGTGGGCCTTAATTCCCAGCCGGGTTCCCTCCCTGGACACACACTGAAGGTCCCCAGCCATTTGGCAATCTCTTCACATTCCCAGCCCTGGAGGTAGCCCTAAAATACATGTACCTGAAGAAAATAAAACATTGCCTCACACTGGAGCCCAGTGTGGTCCTCCAGATTCCGTGTGAGGTGGACTAACTTATATGGGAAGGCAGGGCAGCGGGAGTGAGGATGGCAGAGAGGATTACACATGTCAAGGCAGCCGGGGTCATGGAAACAAAACATGACTGGCCTGGGAGAAACACTGTGAAAGGACACAGACCTAGGTGGGCCTCAGGTGGACATCCTCGTGGAGAAAAAGGGGGCCCTGGTTGATCTCAAAAT
51	**TSPY1**	CAGCCCTAGGCTGCTCGCCTGGCCTCCTCTCTGTTCCGCCTCTAGGGCTGACCCTCTCTCCATGGGATAGAACTGCAATGGATTGAGCCATAGGCCCTGGCTGATGATCTAGGGGACTGCAGAAGTGGGTCCAGGACAGTTCAGGTGACAGTTCAAAGCCAATTCCCCAGAGACCAAGGAATGACCAGCTAGGTCCTTTCCCATGATGCCCCACGGCGAACCCCACCTCAGCAATCCTGCCAAAACCCGGGCAGTCATGTTCAGCCAAACAGCTGAATGAGCTCAGGTAGGAGGTGTACTGCCTGCAGCTGGAGGCTTGACCTTCGTGATCCCAGAACCGCTGGACTGCAGTGGAATGAGACACCCTGTAGCCTGCAGGGAGAGGAGTCAGGAAGGTTCATGCCAGTCCCACCCTCCCACACACCAGCTCCCCTACCATGCTGGGAGGCATTCCTTACCGAGGATGCCAACACAGTGCT

		CCTTCATGATGATTTCACTGTGGAAATAAAGGTTGGGATGAAAGGAAATCATCCTGCCACCGGTAACCGGGATGGCTGAGTTCCTCCACCTGCCGGATCAAGGAGAAAGAGGATGGATTCAATGGGACCATCTCAACTAGCCGGGCTGAGGTGGCCTACTAGCTGTAGTGAACCATGAGTTTCCCCTTCCCAGCTCTCCCACTGAGACAACCCTGGTCCCCAGGGGGACCTCAAACTGACTCAGACACTGGACTCCTCCCACAGACCCAGGCTCCCCAGCCTGACCTGCAAATCCATCACGTAGCAAAGCAGGACTTCCGCATGCTTTCCGACCCACGCCGACATCTCGTGTGCCAAACAATCTACCTCTGCGCAAGAACTCTCCAGAGGATTGGGTGGGCAAGCCTCGTGACGCCTTGCAATTTCGCAAGAACACAGACAATGTGGAACAGGGCCATCTCCCAGACATTTGGCCAGTCACCCTTCATTGTTGGCCCTCTATCTCTGTCTGGCGAGGAGGCAACGCCACAACTGTGGTGGTTTTTGGAGTGGGTGGACCCCGGCCAAGACGGCCTGGGCTGACC
52	**TSPY1**	TAGACGAATAGAAATGCATCTTAAAACTTGCCGAACACTTCAAGTCTCCCATAAGAATTGTAATGGAAAATGGATCAGTCGGCAGTTTTTTCCATACAATTATGAACAAATTATATTTCTTCATACATAGATTTGTTTTTTCAATATTCTAAGGAATTAACTTTTATATTAATAGTAGGTGATGTAAGAAAGCAGGCCTTTATCAAGATAACTGACACTGGATGTCCATACCATTACTCAGGTGGGCCTTAATTCCCAGCCAGGTTCCCTCCCTGGACACACACTGAAGGTCCCCAGCCATTTGGCAATCTCTTCACATTCCCAGCCCTGGAGGTAGCCCTAAAATACATGTACCTGAAGAAAATAAAACATTGCCTCACACTGGAGCCCAGTGTGGTCCTCCAGATTCCGTGTGAGGTGGACTAACTTATATGGGAAGGCAGGGCAGCGGGAGTGAGGATGGCAGAGAGGATTACACATGTCAAGGCAGCCGGGGTCATGGAAACAAAACATGACTGGCCTGGGAGAAACACTGTGAAAGGACATACACCTAGGTGGGCCTCAGGTGGACATCCTCGTGGAGAAAAAGGGGGCCCTGGTTGATCTCAAAATG
53	**TSPY1**	CAGCCCTAGGCTGCTCGCCTGGCCTCCTCTCTGTTCCGCCTCTAGGGCTGACCCTCTCTCCATGGGATAGAACTGCAATGGATTGAGCCATAGGCCCTGGCTGATGATCTAGGGGACTGCAGAAGTGGGTCCAGGACAGTTCAGGTGACAGTTCAAAGCCAATTCCCCAGAGACCAAGGAATGACCAGCTAGGTCCTTTCCCATGATGCCCCACGGCGAACCCCACCTCAGCAATCCTGCCAAAACCCGGGCAGTCATGTTCAGCCAAACAGCTGAATGAGCTCAGGTAGGAGGTGTACTGCCTGCAGCTGGAGGCTTGACCTTCGTGATCCCAGAACCGCTGGACTGCAGTGGAATGAGACACCCTGTAGCCTGCAGGGAGAGGAGTCAGGAAGGTTCATGCCAGTCCCACCCTCCCACACACCAGCTCCCCTACCATGCTGGGAGGCATTCCTTACCGAGGATGCCAACACAGTGCTCCTTCATGATGATTTCACTGTGGAAATAAAGGTTGGGATGAAAGGAAATCATCCTGCCACCGGTAACCGGGATGGCTGAGTTCCTCCACCTGCCGGATCAAGGAGAAAGAGGATGGATTCAATGGGACCATCTCAACTAGCCGGGCTGAGGTGGCCTACTAGCTGTAGTGAACCATGAGTTTCCCCTTCCCAGCTCTCCCACTGAGACAACCCTGGTCCCCAGGGGGACCTCAAACTGACTCAGACACTGGACTCCTCCCACAGACCCAGGCTCCCCAGCCTGACCTGCAAATCCATCACGTAGCAAAGCAGGACTTCCGCATGCTTTCCGACCCACGCCGACATCTCGTGTGCCAAACAATCTACCTCTGCGCAAGAACTCTCCAGAGGATTGGGTGGGCAAGCCTCGTGACGCCTTGCAATTTCGCA
54	**LOC728137**	AAATGATCATAAAAACTGGCAGGAGTAGACGAATAGAAATGCATCTTAAAACTTGCTAAACCCTTCAAGTCTCCCATAAGAATTGTAATGGAAAATGGATCGGTCGGCAGCTTTTTCCATACAATTATGAACAAATTATATTTCTTCATACATAGATTTGTTTTTTCAATATTCTAAGGAATTAACTTTTATATTAATAGTAGGTGATGTAAGAAAGCAGGCCTTTATCAAGATAACTGACACTGGATGTCCATACCATTACTCAGGTGGGCCTTAATTCCCAGCCGGGTTCCCTCCCTGGACACACACTGAAGGTCCCCAGCCATTTGGCAATCTCTTCACATTCCCAGCCCTGGAGGTAGCCCTAAAATACATGTACCTGAAGAAAATAAAACATTGCCTCACACTGGAGCCCAGTGTGGTCCTCCAGATTCCGTGTGAGGTGGACTAACTTATATGGGAAGGCAGGGCAGCGGGAGTGAGGATGGCAGAGAGGATTACACATGTCAAGGCAGCCGGGGTCATGGAAACAAAACATGACTGGCCTGGGAGAAACACTATGAAAGGACATACACCTAGGTGGGCCTTAGGTGGACATCCTCGTGGAGAAAAAGGGGGCCCTGGTTGATCTCAAAATGAG
55	**LOC728137**	CTCTGTTCCGCCTCTAGGGCTGACCCTCTCTCCATGGGATAGAACTGCAATGGATTGAGCCATAGGCCCTGGGTGATGATCTAGGTGACTGCAGAAGTGGGTCCAGGACAGTTCAGGTGACAGTTCAAAGCCAATTCCCCAGAGACCAAGGAATGACCAGCTAGGTCCTTTCCCATGATGCCCCACGGCGAACCCCACCTCAGCAATCCTGCCAAAACCCGGGCAGTCATGTTCAGCCAAACAGCTGAATGAGCTCAGGTAGGAGGTGTACTGCCTGCAGCTGGAGGCTTGACCTTCGTGATCCCAGAACCGCTGGACTGCAGTGGAATGAGACACCCTGTAGCCTGCAGGGAGAGGAGTCAGGAAGGTTCATGCCAGTCCCACCCTCCCACACACCAGCTCCCCTACCATGCTGGGAGGCATTCCTTACCGAGGATGCCAACACAGTGCTCCTTCATGATGATTTCACTGTGGAAATAAAG

		GTTGGGATGAAAGGAAATCATCCTGCCACCGGTAACCGGGATGGCTGAGTTCCTCCACCTGCCGGATCAAGGAGAAAGAGGATGGATTCAATGGGACCATCTCAACTAGCCGGGCTGAGGTGGCCTACTAGCTGTAGTGAACCATGAGTTTCCCCTTCCCAGCTCTCCCACTGAGACAACCCTGGTCCCCAGGGGGACCTCAAACTGACTCAGACACTGGACTCCTCCCACAGACCCAGGCTCCCCAGCCTGACCTGCAAATCCATCACGTAGCAAAGCAGGACTTCCGCATGCTTTCCGACCCACGCCGACATCTCGTGTGCCAAACAATCTACCTCTGCGCAAGAACTCTCCAGAGGATTGGGTGGGCAAGCCTCGTGACGCCTTGCAATTTCGCA
56	**chrY:009952039-009952083**	CAGCCCTAGGCTGCTCGCCTGGCCTCCTCTCTGTTCCGCCTCTAGGGCTGACCCTCTCTCCATGGGATAGAACTGCAATGGATTGAGCCATAGGCCCTGGCTGATGATCTAGGGGACTGCAGAAGTGGGTCCAGGACAGTTCAGGTGACAGTTCAAAGCCAATTCCCCAGAGACCAAGGAATGACCAGCTAGGTCCTTTCCCATGATGCCCCATGGCGAACCCCACCTCAGCAATCCTGCCAAAACCCGGGCAGTCATGTTCAGCCAAACAGCTGAATGAGCTCAGGTAGGAGGTGTACTGCCTGCAGCTGGAGGCTTGACCTTCGTGATCCCAGAACCGCTGGACTGCAGTGGAATGAGACACCCTGTAGCCTGCAGGGAGAGGAGTCAGGAAGGTTCATGCCAGTCCCACCCTCCCACACACCAGCTCCCCTACCATGCTGGGAGGCATTCCTTACCGAGGATGCCAACACAGTGCTCCTTCATGATGATTTCACTGTGGAAATAAAGGTTGGGATGAAAGGAAATCATCCTGCCACCGGTAACCGGGATGGCTGAGTTCCTCCACCTGCCGGATCAAGGAGAAAGAGGATGGATTCAATGGGACCATCTCAACTAGCTGGGCTGAGGTGGCCTACTAGCTGTAGTGAACCATGAGTTTCCCCTTCCCAGCTCTCCCACTGAGACAACCCTGGTCCCCAGGGGGACCTCAAACTGACTCAGACACTGGACTCCTCCCACAGACCCAGCTCCCCAGCCTGACCTGCAAATCCATCACGTAGCAAAGCAGGACTTCCGCATGCTTTCCGACCCACGCCGACATCTCGTGTGCCAAACAATCTACCTCTGCGCAAGAACTCTCCAGAGGATTGGGTGGCAAGCCTCGTGACGCCTTGCAATTTCGCAAGAACACAGACAATGTGGAACAGGGCCATCTCC
57	**TSPY1**	CAGCCCTAGGCTGCTCGCCTGGCCTCCTCTCTGTTCCGCCTCTAGGGCTGACCCTCTCTCCATGGGATAGAACTGCAATGGATTGAGCCATAGGCCCTGGCTGATGATCTAGGGGACTGCAGAAGTGGGTCCAGGACAGTTCAGGTGACAGTTCAAAGCCAATTCCCCAGAGACCAAGGAATGACCAGCTAGGTCCTTTCCCATGATGCCCCACGGCGAACCCCACCTCAGCAATCCTGCCAAAACCCGGGCAGTCATGTTCAGCCAAACAGCTGAATGAGCTCAGGTAGGAGGTGTACTGCCTGCAGCTGGAGGCTTGACCTTCGTGATCCCAGAACCGCTGGACTGCAGTGGAATGAGACACCCTGTAGCCTGCAGGGAGAGGAGTCAGGAAGGTTCATGCCAGTCCCACCCTCCCACACACCAGCTCCCCTACCATGCTGGGAGGCATTCCTTACCGAGGATGCCAACACAGTGCTCCTTCATGATGATTTCACTGTGGAAATAAAGGTTGGGATGAAAGGAAATCATCCTGCCACCGGTAACCGGGATGGCTGAGTTCCTCCACCTGCCGGATCAAGGAGAAAGAGGATGGATTCAATGGGACCATCTCAACTAGCCGGGCTGAGGTGGCCTACTAGCTGTAGTGAACCATGAGTTTCCCCTTCCCAGCTCTCCCACTGAGACAACCCTGGTCCCCAGGGGGACCTCAAACTGACTCAGACACTGGACTCCTCCCACAGACCCAGGCTCCCCAGCCTGACCTGCAAATCCATCACGTAGCAAAGCAGGACTTCCGCATGCTTTCCGACCCACGCCGACATCTCGTGTGCCAAACAATCTACCTCTGCGCAAGAACTCTCCAGAGGATTGGGTGGGCAAGCCTCGTGACGCCTTGCAATTTCGCAAGAACACAGACAATGTG

Supplementary Table 3. Univariate Cox regression analysis for disease-specific and overall survival

Variable	**Disease-specific survival**		**Overall survival**	
	Hazard ratio (95% CI)	p	Hazard ratio (95% CI)	p
Nuclear EBP50 (positive *vs* negative)	5.49 (2.59-11.66)	<0.001	6.13 (3.49-10.76)	<0.001
Age	0.99 (0.97-1.02)	0.838	1.02 (0.99-1.04)	0.172
Sex (female *vs* male)	0.75 (0.37-1.52)	0.424	1.06 (0.62-1.80)	0.842
CEA	1.004 (1.001-1.006)	0.007	1.003 (1.001-1.005)	0.011
Tumor stage				
II *vs* I	0.64 (0.16-2.55)	0.524	0.98 (0.38-2.53)	0.963
III *vs* I	1.53 (0.47-4.96)	0.483	1.97 (0.83-4.64)	0.123
IV *vs* I	7.69 (2.49-23.72)	<0.001	4.84 (1.97-11.89)	0.001

Supplementary Table 4. Sequence information of the plasmids used in this study. Start codon and stop codon are highlighted in red. NLS tag is highlighted in yellow.

pcDNA3.1 **-FLAG-EBP50**	1 TAATACGACT CACTATAGGG AGACCCAAGC TGGCTAGCGA TTACGCCAAG CTCGAAATTA 61 ACCCTCACTA AAGGGAACAA AAGCTGGAGC TCCACCGCGG TGGCGGCCGC CACCATGGAT 121 TACAAGGATG ACGACGATAA GGCCCGGGCG GATCCCCCGG GCTGCAGGAA TTCGATATCA 181 AGCTTGCGGG GCGAGATGAG CGCGGACGCG GCCGCGGGGG CGCCCCTGCC CCGGCTCTGC 241 TGTCTGGAGA AGGGCCCGAA CGGCTACGGC TTCCACCTGC ACGGGGAGAA GGGCAAGGTG 301 GGCCAGTTCA TCCGGCTGGT GGAGCCTGGT TCTCCGGCCG AGAAGGCGGG GCTGCTGGCC 361 GGAGACCGGC TGGTGGAGGT GAACGGCGAG AACGTAGAGA AGGAGACCCA CCAGCAGGTG 421 GTGAGCCGCA TCCGCGCCGC GCTCAACGCC GTGCGCCTGC TGGTGGTCGA CCCCGACGCG 481 GACGAGCGGC TGCAGAAGCT GGGCGTCCCG GTGCGGGAGG AGCTGCTGCG CGCCCAGGAC 541 GGGCCCGGGC AGGCCGAGCC GCCGGCCGCC ACCGAGGCGC GGGGGGCTGG CGCCGAAAGT 601 GAGCCGCAGG CCGCCGCGCC GGAGCCGCGC GAAGCCGAGA GGAGCGGTCC GGAGCGGCGT 661 GAGCTCCGGC CTCGGCTCTG CGCCATGAAG AAAGGCGCCA ACGGCTACGG TTTCAACTTG 721 CACAGCGACA AGTCCAAGCC AGGCCAGTTC ATCCGGGCGG TGGACCCAGA CTCACCAGCT 781 GAGGCCTCGG GGCTCCGGGC TCAGGACCGC ATTGTGGAGG TGAATGGGGT CTGCGTGGAG 841 GGCAAGCAGC ATGGGGATGT GGTATCTGCC ATCAAGGCTG GTGGGGACGA GACCAAGCTG 901 CTGGTGGTAG ACAAGGAGAC TGATGAGTTC TTCAAGAAAT GCAAAGTGAT CCCGTCCCAG 961 GAGCACCTGA CTGGTCCCTT GCCTGAGCCC TTTACCAATG GGGAGATCCG GAAGGAGAAC 1021 AGTCGTGAAC CTCTGGCCGA GGTAGCCTCT GAGAGCCCCA GATCAGCCCT GGCAAGATCC 1081 ACCTCCAGTG ATACCAGTGA GGAGCTGAAT TCCCAAGACA GCCCCAGGAA ACAGGACTCC 1141 ACGGCACCCT CGTCTACCTC CTCCTCCTCT GACCCCATCT TGGACTTCAA CATCTCCCTG 1201 GCCATGGCCA GGGAGCGGGC CCACCAGAAG CGCAGCAGCA AGCGGGCCCC GCAGATGGAC 1261 TGGAGCAAGA AAAATGAACT CTTCAGCAAC CTCTGAGCAT CCTCCCACAG GCTCAGATCT 1321 GGATCCCCTC TAGAGTCGAC CTGCAGGCAT GCAAGCTTAT CGATACCGTC GACCTCGAGT 1381 CTAGAGGGCC CGTTTAAACC CGCTGATCAG CCTCGACTGT GCCTTCTA
pcDNA3.1 **-FLAG-EBP50-GAGA**	1 TAATACGACT CACTATAGGG AGACCCAAGC TGGCTAGCGA TTACGCCAAG CTCGAAATTA 61 ACCCTCACTA AAGGGAACAA AAGCTGGAGC TCCACCGCGG TGGCGGCCGC CACCATGGAT 121 TACAAGGATG ACGACGATAA GGCCCGGGCG GATCCCCCGG GCTGCAGGAA TTCGATGGCC 181 GCGGGGGCGC CCCTGCCCCG GCTCTGCTGT CTGGAGAAGG GCCCGAACGG CGCCGGCGCG 241 CACCTGCACG GGGAGAAGGG CAAGGTGGGC CAGTTCATCC GGCTGGTGGA GCCTGGTTCT 301 CCGGCCGAGA AGGCGGGGCT GCTGGCCGGA GACCGGCTGG TGGAGGTGAA CGGCGAGAAC 361 GTAGAGAAGG AGACCCACCA GCAGGTGGTG AGCCGCATCC GCGCCGCGCT CAACGCCGTG 421 CGCCTGCTGG TGGTCGACCC CGACGCGGAC GAGCGGCTGC AGAAGCTGGG CGTCCCGGTG 481 CGGGAGGAGC TGCTGCGCGC CCAGGACGGG CCCGGGCAGG CCGAGCCGCC GGCCGCCACC

	541 GAGGCGCGGG GGGCTGGCGC CGAAAGTGAG CCGCAGGCCG CCGCGCCGGA GCCGCGCGAA 601 GCCGAGAGGA GCGGTCCGGA GCGGCGTGAG CTCCGGCCTC GGCTCTGCGC CATGAAGAAA 661 GGCGCCAACG GCGCCGGCGC GAACTTGCAC AGCGACAAGT CCAAGCCAGG CCAGTTCATC 721 CGGGCGGTGG ACCCAGACTC ACCAGCTGAG GCCTCGGGGC TCCGGGCTCA GGACCGCATT 781 GTGGAGGTGA ATGGGGTCTG CGTGGAGGGC AAGCAGCATG GGGATGTGGT ATCTGCCATC 841 AAGGCTGGTG GGGACGAGAC CAAGCTGCTG GTGGTAGACA AGGAGACTGA TGAGTTCTTC 901 AAGAAATGCA AAGTGATCCC GTCCCAGGAG CACCTGACTG GTCCCTTGCC TGAGCCCTTT 961 ACCAATGGGG AGATCCGGAA GGAGAACAGT CGTGAACCTC TGGCCGAGGT AGCCTCTGAG 1021 AGCCCCAGAT CAGCCCTGGC AAGATCCACC TCCAGTGATA CCAGTGAGGA GCTGAATTCC 1081 CAAGACAGCC CCAGGAAACA GGACTCCACG GCACCCTCGT CTACCTCCTC CTCCTCTGAC 1141 CCCATCTTGG ACTTCAACAT CTCCCTGGCC ATGGCCAGGG AGCGGGCCCA CCAGAAGCGC 1201 AGCAGCAAGC GGGCCCCGCA GATGGACTGG AGCAAGAAAA ATGAACTCTT CAGCAACCTC 1261 TGAGCATCCT CCCACAGGCT CAGATCTGGA TCCCCTCTAG AGTCGACCTG CAGGCATGCA 1321 AGCTTATCGA TACCGTCGAC CTCGAGTCTA GAGGGCCCGT TTAAACCCGC TGATCAGCCT 1381 CGACTGTGCC TTCTA
pcDNA3.1 **-FLAG-EBP50-NLS**	1 TAATACGACT CACTATAGGG AGACCCAAGC TGGCTAGCGA TTACGCCAAG CTCGAAATTA 61 ACCCTCACTA AAGGGAACAA AAGCTGGAGC TCCACCGCGG TGGCGGCCGC CACCATGGAT 121 TACAAGGATG ACGACGATAA GGCCCGGGCG GATCCCCCGG GCTGCAGGAA TTCGATATCA 181 AGCTTGCGGG GCGAGATGAG CGCGGACGCG GCCGCGGGGG CGCCCCTGCC CCGGCTCTGC 241 TGTCTGGAGA AGGGCCCGAA CGGCTACGGC TTCCACCTGC ACGGGGAGAA GGGCAAGGTG 301 GGCCAGTTCA TCCGGCTGGT GGAGCCTGGT TCTCCGGCCG AGAAGGCGGG GCTGCTGGCC 361 GGAGACCGGC TGGTGGAGGT GAACGGCGAG AACGTAGAGA AGGAGACCCA CCAGCAGGTG 421 GTGAGCCGCA TCCGCGCCGC GCTCAACGCC GTGCGCCTGC TGGTGGTCGA CCCCGACGCG 481 GACGAGCGGC TGCAGAAGCT GGGCGTCCCG GTGCGGGAGG AGCTGCTGCG CGCCCAGGAC 541 GGGCCCGGGC AGGCCGAGCC GCCGGCCGCC ACCGAGGCGC GGGGGGCTGG CGCCGAAAGT 601 GAGCCGCAGG CCGCCGCGCC GGAGCCGCGC GAAGCCGAGA GGAGCGGTCC GGAGCGGCGT 661 GAGCTCCGGC CTCGGCTCTG CGCCATGAAG AAAGGCGCCA ACGGCTACGG TTTCAACTTG 721 CACAGCGACA AGTCCAAGCC AGGCCAGTTC ATCCGGGCGG TGGACCCAGA CTCACCAGCT 781 GAGGCCTCGG GGCTCCGGGC TCAGGACCGC ATTGTGGAGG TGAATGGGGT CTGCGTGGAG 841 GGCAAGCAGC ATGGGGATGT GGTATCTGCC ATCAAGGCTG GTGGGGACGA GACCAAGCTG 901 CTGGTGGTAG ACAAGGAGAC TGATGAGTTC TTCAAGAAAT GCAAAGTGAT CCCGTCCCAG 961 GAGCACCTGA CTGGTCCCTT GCCTGAGCCC TTTACCAATG GGGAGATCCG GAAGGAGAAC 1021 AGTCGTGAAC CTCTGGCCGA GGTAGCCTCT GAGAGCCCCA GATCAGCCCT GGCAAGATCC 1081 ACCTCCAGTG ATACCAGTGA GGAGCTGAAT TCCCAAGACA GCCCCAGGAA ACAGGACTCC 1141 ACGGCACCCT CGTCTACCTC CTCCTCCTCT GACCCCATCT TGGACTTCAA CATCTCCCTG 1201 GCCATGGCCA GGGAGCGGGC CCACCAGAAG CGCAGCAGCA AGCGGGCCCC GCAGATGGAC

	1261 TGGAGCAAGA AAAATGAACT CTTCAGCAAC CTCTCTCGAG CTGATCCAAA AAAGAAGAGA 1321 AAGGTAGATC CAAAAAAGAA GAGAAAGGTA GATCCAAAAA AGAAGAGAAA GGTAGGATCC 1381 CCTCTAGAGT CGACCTGCAG GCATGCAAGC TTATCGATAC CGTCGACCTC GAGTCTAGAG 1441 GGCCCGTTTA AACCCGCTGA TCAGCCTCGA CTGTGCCTTC TAGTTGCCAG CCATCTGTTG 1501 TTTGCCCCTC CCCCGTGCCT TCCTTGA
pcDNA3.1 **-FLAG-dnTcf1**	1 TAATACGACT CACTATAGGG AGACCCAAGC TGGCTAGCGA TTACGCCAAG CTCGAAATTA 61 ACCCTCACTA AAGGGAACAA AAGCTGGAGC TCCACCGCGG TGGCGGCCGC CACCATGGAT 121 TACAAGGATG ACGACGATAA GGCCCGGGCG GATCCCCCGG GCTGCAGGAA TTCCAAGCTT 181 TCCGGATCCA TGTACAAAGA GACCGTCTAC TCCGCCTTCA ATCTGCTCAT GCATTACCCA 241 CCCCCCTCGG GAGCAGGGCA GCACCCCCAG CCGCAGCCCC CGCTGCACAA GGCCAATCAG 301 CCCCCCCACG GTGTCCCCCA ACTCTCTCTC TACGAACATT TCAACAGCCC ACATCCCACC 361 CCTGCACCTG CGGACATCAG CCAGAAGCAA GTTCACAGGC CTCTGCAGAC CCCTGACCTC 421 TCTGGCTTCT ACTCCCTGAC CTCAGGCAGC ATGGGGCAGC TCCCCCACAC TGTGAGCTGG 481 TTCACCCACC CATCCTTGAT GCTAGGTTCT GGTGTACCTG GTCACCCAGC AGCCATCCCC 541 CACCCGGCCA TTGTGCCCCC CTCAGGGAAG CAGGAGCTGC AGCCCTTCGA CCGCAACCTG 601 AAGACACAAG CAGAGTCCAA GGCAGAGAAG GAGGCCAAGA AGCCAACCAT CAAGAAGCCC 661 CTCAATGCCT TCATGCTGTA CATGAAGGAG ATGAGAGCCA AGGTCATTGC AGAGTGCACA 721 CTTAAGGAGA GCGCTGCCAT CAACCAGATC CTGGGCCGCA GGTGGCACGC GCTGTCGCGA 781 GAAGAGCAGG CCAAGTACTA TGAGCTGGCC CGCAAGGAGA GGCAGCTGCA CATGCAGCTA 841 TACCCAGGCT GGTCAGCGCG GGACAACTAC GGGAAGAAGA AGAGGCGGTC GAGGGAAAAG 901 CACCAAGAAT CCACCACAGG AGGAAAAAGA AATGCATTCG GTACTTACCC GGAGAAGGCC 961 GCTGCCCCAG CCCCGTTCCT TCCGATGACA GTGCTCTAGA GGGCCCGTTT AAACCCGCTG 1021 ATCAGCCTCG ACTGTGCCTT CTA
pcDNA3.1 **-FLAG-dnTcf1dc**	1 TAATACGACT CACTATAGGG AGACCCAAGC TGGCTAGCGA TTACGCCAAG CTCGAAATTA 61 ACCCTCACTA AAGGGAACAA AAGCTGGAGC TCCACCGCGG TGGCGGCCGC CACCATGGAT 121 TACAAGGATG ACGACGATAA GGCCCGGGCG GATCCCCCGG GCTGCAGGAA TTCCAAGCTT 181 TCCGGATCCA TGTACAAAGA GACCGTCTAC TCCGCCTTCA ATCTGCTCAT GCATTACCCA 241 CCCCCCTCGG GAGCAGGGCA GCACCCCCAG CCGCAGCCCC CGCTGCACAA GGCCAATCAG 301 CCCCCCCACG GTGTCCCCCA ACTCTCTCTC TACGAACATT TCAACAGCCC ACATCCCACC 361 CCTGCACCTG CGGACATCAG CCAGAAGCAA GTTCACAGGC CTCTGCAGAC CCCTGACCTC 421 TCTGGCTTCT ACTCCCTGAC CTCAGGCAGC ATGGGGCAGC TCCCCCACAC TGTGAGCTGG 481 TTCACCCACC CATCCTTGAT GCTAGGTTCT GGTGTACCTG GTCACCCAGC AGCCATCCCC 541 CACCCGGCCA TTGTGCCCCC CTCAGGGAAG CAGGAGCTGC AGCCCTTCGA CCGCAACCTG 601 AAGACACAAG CAGAGTCCAA GGCAGAGAAG GAGGCCAAGA AGCCAACCAT CAAGAAGCCC 661 CTCAATGCCT TCATGCTGTA CATGAAGGAG ATGAGAGCCA AGGTCATTGC AGAGTGCACA 721 CTTAAGGAGA GCGCTGCCAT CAACCAGATC CTGGGCCGCA GGTGGCACGC GCTGTCGCGA

	781 GAAGAGCAGG CCAAGTACTA TGAGCTGGCC CGCAAGGAGA GGCAGCTGCA CATGCAGCTA 841 TACCCAGGCT GGTCAGCGCG GGACAACTAC GGGAAGAAGA AGAGGCGGTC GAGGGAAAAG 901 CACCAAGAAT CCACCACAGG AGGAAAAAGA AATGCATTCG GTACTTACCC GGAGAAGGCC 961 GCTGCCCCAG CCCCGTTCCT TCCGTAGAAG CTTAGATCTG GATCCCCTCT AGAGGGCCCG 1021 TTTAAACCCG CTGATCAGCC TCGACTGTGC CTTCTA
pcDNA3.1 **-Myc-FLTcf1**	1 TAATACGACT CACTATAGGG AGACCCAAGC TGGCTAGCGT TTAAACTTAA GCTTGGTACC 61 GAGCTCGGAT CCACTAGTCC AGTGTGGTGG AATTCTGCAG ATATCCAGCA CAGTGGCGGC 121 CGCCATGGAG CAGAAACTCA TCTCTGAAGA GGATCTGGCC CGGGCGGATC CCCCGGGCTG 181 CAGGAATTCG ATATCAAGCT TCACGTGCAC CATGCCGCAG CTGGACTCCG GCGGGGGCGG 241 CGCGGGCGGC GGCGACGACC TCGGCGCGCC GGACGAGCTG CTGGCCTTCC AGGATGAAGG 301 CGAGGAGCAG GACGACAAGA GCCGCGACAG CGCCGCCGGT CCCGAGCGCG ACCTGGCCGA 361 GCTCAAGTCG TCGCTCGTGA ACGAGTCCGA GGGCGCGGCC GGCGGCGCAG GGATCCCGGG 421 GGTCCCGGGG GCCGGCGCCG GGGCCCGCGG CGAGGCCGAG GCTCTCGGGC GGGAACACGC 481 TGCGCAGAGA CTCTTCCCGG ACAAACTTCC AGAGCCCCTG GAGGACGGCC TGAAGGCCCC 541 GGAGTGCACC AGCGGCATGT ACAAAGAGAC CGTCTACTCC GCCTTCAATC TGCTCATGCA 601 TTACCCACCC CCCTCGGGAG CAGGGCAGCA CCCCCAGCCG CAGCCCCCGC TGCACAAGGC 661 CAATCAGCCC CCCCACGGTG TCCCCCAACT CTCTCTCTAC GAACATTTCA ACAGCCCACA 721 TCCCACCCCT GCACCTGCGG ACATCAGCCA GAAGCAAGTT CACAGGCCTC TGCAGACCCC 781 TGACCTCTCT GGCTTCTACT CCCTGACCTC AGGCAGCATG GGGCAGCTCC CCCACACTGT 841 GAGCTGGTTC ACCCACCCAT CCTTGATGCT AGGTTCTGGT GTACCTGGTC ACCCAGCAGC 901 CATCCCCCAC CCGGCCATTG TGCCCCCCTC AGGGAAGCAG GAGCTGCAGC CCTTCGACCG 961 CAACCTGAAG ACACAAGCAG AGTCCAAGGC AGAGAAGGAG GCCAAGAAGC CAACCATCAA 1021 GAAGCCCCTC AATGCCTTCA TGCTGTACAT GAAGGAGATG AGAGCCAAGG TCATTGCAGA 1081 GTGCACACTT AAGGAGAGCG CTGCCATCAA CCAGATCCTG GGCCGCAGGT GGCACGCGCT 1141 GTCGCGAGAA GAGCAGGCCA AGTACTATGA GCTGGCCCGC AAGGAGAGGC AGCTGCACAT 1201 GCAGCTATAC CCAGGCTGGT CAGCGCGGGA CAACTACGGG AAGAAGAAGA GGCGGTCGAG 1261 GGAAAAGCAC CAAGAATCCA CCACAGGAGG AAAAAGAAAT GCATTCGGTA CTTACCCGGA 1321 GAAGGCCGCT GCCCCAGCCC CGTTCCTTCC GATGACAGTG CTCTAGAGGG CCCGTTTAAA 1381 CCCGCTGATC AGCCTCGACT GTGCCTTCTA
pcDNA3.1 **-Myc-FLTcf1dc**	1 TAATACGACT CACTATAGGG AGACCCAAGC TGGCTAGCGT TTAAACTTAA GCTTGGTACC 61 GAGCTCGGAT CCACTAGTCC AGTGTGGTGG AATTCTGCAG ATATCCAGCA CAGTGGCGGC 121 CGCCATGGAG CAGAAACTCA TCTCTGAAGA GGATCTGGCC CGGGCGGATC CCCCGGGCTG 181 CAGGAATTCG ATATCAAGCT TCACGTGCAC CATGCCGCAG CTGGACTCCG GCGGGGGCGG 241 CGCGGGCGGC GGCGACGACC TCGGCGCGCC GGACGAGCTG CTGGCCTTCC AGGATGAAGG 301 CGAGGAGCAG GACGACAAGA GCCGCGACAG CGCCGCCGGT CCCGAGCGCG ACCTGGCCGA 361 GCTCAAGTCG TCGCTCGTGA ACGAGTCCGA GGGCGCGGCC GGCGGCGCAG GGATCCCGGG

	421 GGTCCCGGGG GCCGGCGCCG GGGCCCGCGG CGAGGCCGAG GCTCTCGGGC GGGAACACGC 481 TGCGCAGAGA CTCTTCCCGG ACAAACTTCC AGAGCCCCTG GAGGACGGCC TGAAGGCCCC 541 GGAGTGCACC AGCGGCATGT ACAAAGAGAC CGTCTACTCC GCCTTCAATC TGCTCATGCA 601 TTACCCACCC CCCTCGGGAG CAGGGCAGCA CCCCCAGCCG CAGCCCCCGC TGCACAAGGC 661 CAATCAGCCC CCCCACGGTG TCCCCCAACT CTCTCTCTAC GAACATTTCA ACAGCCCACA 721 TCCCACCCCT GCACCTGCGG ACATCAGCCA GAAGCAAGTT CACAGGCCTC TGCAGACCCC 781 TGACCTCTCT GGCTTCTACT CCCTGACCTC AGGCAGCATG GGGCAGCTCC CCCACACTGT 841 GAGCTGGTTC ACCCACCCAT CCTTGATGCT AGGTTCTGGT GTACCTGGTC ACCCAGCAGC 901 CATCCCCCAC CCGGCCATTG TGCCCCCCTC AGGGAAGCAG GAGCTGCAGC CCTTCGACCG 961 CAACCTGAAG ACACAAGCAG AGTCCAAGGC AGAGAAGGAG GCCAAGAAGC CAACCATCAA 1021 GAAGCCCCTC AATGCCTTCA TGCTGTACAT GAAGGAGATG AGAGCCAAGG TCATTGCAGA 1081 GTGCACACTT AAGGAGAGCG CTGCCATCAA CCAGATCCTG GGCCGCAGGT GGCACGCGCT 1141 GTCGCGAGAA GAGCAGGCCA AGTACTATGA GCTGGCCCGC AAGGAGAGGC AGCTGCACAT 1201 GCAGCTATAC CCAGGCTGGT CAGCGCGGGA CAACTACGGG AAGAAGAAGA GGCGGTCGAG 1261 GGAAAAGCAC CAAGAATCCA CCACAGGAGG AAAAAGAAAT GCATTCGGTA CTTACCCGGA 1321 GAAGGCCGCT GCCCCAGCCC CGTTCCTTCC GTAGAAGCTT AGATCTGGAT CCCCTCTAGA 1381 GGGCCCGTTT AAACCCGCTG ATCAGCCTCG ACTGTGCCTT CTA
pET32 **-Trx-His-EBP50**	1 TAATACGACT CACTATAGGG GAATTGTGAG CGGATAACAA TTCCCCTCTA GAAATAATTT 61 TGTTTAACTT TAAGAAGGAG ATATACATAT GAGCGATAAA ATTATTCACC TGACTGACGA 121 CAGTTTTGAC ACGGATGTAC TCAAAGCGGA CGGGGCGATC CTCGTCGATT TCTGGGCAGA 181 GTGGTGCGGT CCGTGCAAAA TGATCGCCCC GATTCTGGAT GAAATCGCTG ACGAATATCA 241 GGGCAAACTG ACCGTTGCAA AACTGAACAT CGATCAAAAC CCTGGCACTG CGCCGAAATA 301 TGGCATCCGT GGTATCCCGA CTCTGCTGCT GTTCAAAAAC GGTGAAGTGG CGGCAACCAA 361 AGTGGGTGCA CTGTCTAAAG GTCAGTTGAA AGAGTTCCTC GACGCTAACC TGGCCGGTTC 421 TGGTTCTGGC CATATGCACC ATCATCATCA TCATTCTTCT GGTCTGGTGC CACGCGGTTC 481 TGGTATGAAA GAAACCGCTG CTGCTAAATT CGAACGCCAG CACATGGACA GCCCAGATCT 541 GGGTACCGAC GACGACGACA AGGCCATGGC TGATATCGGA TCCATGAGCG CGGACGCAGC 601 GGCCGGGGCG CCCCTGCCCC GGCTCTGCTG CCTGGAGAAG GGTCCGAACG GCTACGGCTT 661 CCACCTGCAC GGGGAGAAGG GCAAGTTGGG CCAGTACATC CGGCTGGTGG AGCCCGGCTC 721 GCCGGCCGAG AAGGCGGGGC TGCTGGCGGG GGACCGGCTG GTGGAGGTGA ACGGCGAAAA 781 CGTGGAGAAG GAGACCCACC AGCAGGTGGT GAGCCGCATC CGCGCCGCAC TCAACGCCGT 841 GCGCCTGCTG GTGGTCGACC CCGAGACGGA CGAGCAGCTG CAGAAGCTCG GCGTCCAGGT 901 CCGAGAGGAG CTGCTGCGCG CCCAGGAAGC GCCGGGGCAG GCCGAGCCGC CGGCCGCCGC 961 CGAGGTGCAG GGGGCTGGCA ACGAAAATGA GCCTCGCGAG GCCGACAAGA GCCACCCGGA 1021 GCAGCGCGAG CTTCGGCCTC GGCTCTGTAC CATGAAGAAG GGCCCCAGTG GCTATGGCTT 1081 CAACCTGCAC AGCGACAAGT CCAAGCCAGG CCAGTTCATC CGGTCAGTGG ACCCAGACTC

	1141 CCCGGCTGAG GCTTCAGGGC TCCGGGCCCA GGATCGCATT GTGGAGGTGA ACGGGGTCTG 1201 CATGGAGGGG AAGCAGCATG GGGACGTGGT GTCCGCCATC AGGGCTGGCG GGGACGAGAC 1261 CAAGCTGCTG GTGGTGGACA GGGAAACTGA CGAGTTCTTC AAGAAATGCA GAGTGATCCC 1321 ATCTCAGGAG CACCTGAATG GTCCCCTGCC TGTGCCCTTC ACCAATGGGG AGATACAGAA 1381 GGAGAACAGT CGTGAAGCCC TGGCAGAGGC AGCCTTGGAG AGCCCCAGGC CAGCCCTGGT 1441 GAGATCCGCC TCCAGTGACA CCAGCGAGGA GCTGAATTCC CAAGACAGCC CCCCAAAACA 1501 GGACTCCACA GCGCCCTCGT CTACCTCCTC CTCCGACCCC ATCCTAGACT TCAACATCTC 1561 CCTGGCCATG GCCAAAGAGA GGGCCCACCA GAAACGCAGC AGCAAACGGG CCCCGCAGAT 1621 GGACTGGAGC AAGAAAAACG AACTCTTCAG CAACCTCTGA AAGCTTGCGG CCGCACTCGA 1681 GCACCACCAC CACCACCAC
pET32 **-Trx-His-PDZ1**	1 TAATACGACT CACTATAGGG GAATTGTGAG CGGATAACAA TTCCCCTCTA GAAATAATTT 61 TGTTTAACTT TAAGAAGGAG ATATACATAT GAGCGATAAA ATTATTCACC TGACTGACGA 121 CAGTTTTGAC ACGGATGTAC TCAAAGCGGA CGGGGCGATC CTCGTCGATT TCTGGGCAGA 181 GTGGTGCGGT CCGTGCAAAA TGATCGCCCC GATTCTGGAT GAAATCGCTG ACGAATATCA 241 GGGCAAACTG ACCGTTGCAA AACTGAACAT CGATCAAAAC CCTGGCACTG CGCCGAAATA 301 TGGCATCCGT GGTATCCCGA CTCTGCTGCT GTTCAAAAAC GGTGAAGTGG CGGCAACCAA 361 AGTGGGTGCA CTGTCTAAAG GTCAGTTGAA AGAGTTCCTC GACGCTAACC TGGCCGGTTC 421 TGGTTCTGGC CATATGCACC ATCATCATCA TCATTCTTCT GGTCTGGTGC CACGCGGTTC 481 TGGTATGAAA GAAACCGCTG CTGCTAAATT CGAACGCCAG CACATGGACA GCCCAGATCT 541 GGGTACCGAC GACGACGACA AGGCCATGGC TGATATCGGA TCCATGAGCG CGGACGCAGC 601 GGCCGGGGCG CCCCTGCCCC GGCTCTGCTG CCTGGAGAAG GGTCCGAACG GCTACGGCTT 661 CCACCTGCAC GGGGAGAAGG GCAAGTTGGG CCAGTACATC CGGCTGGTGG AGCCCGGCTC 721 GCCGGCCGAG AAGGCGGGGC TGCTGGCGGG GGACCGGCTG GTGGAGGTGA ACGGCGAAAA 781 CGTGGAGAAG GAGACCCACC AGCAGGTGGT GAGCCGCATC CGCGCCGCAC TCAACGCCGT 841 GCGCCTGCTG GTGGTCGACC CCGAGACGGA CGAGCAGCTG CAGAAGCTCG GCGTCCAGGT 901 CCGAGAGGAG CTGCTGCGCG CCCAGGAAGC GCCGGGGCAG GCCGAGCCGC CGGCCGCCGC 961 CGAGGTGCAG GGGGCTGGCA ACGAAAATGA GCCTCGCGAG GCCGACAAGA GCCACCCGGA 1021 GTGAAAGCTT GCGGCCGCAC TCGAGCACCA CCACCACCAC CAC
pET32 **-Trx-His-PDZ2**	1 TAATACGACT CACTATAGGG GAATTGTGAG CGGATAACAA TTCCCCTCTA GAAATAATTT 61 TGTTTAACTT TAAGAAGGAG ATATACATAT GAGCGATAAA ATTATTCACC TGACTGACGA 121 CAGTTTTGAC ACGGATGTAC TCAAAGCGGA CGGGGCGATC CTCGTCGATT TCTGGGCAGA 181 GTGGTGCGGT CCGTGCAAAA TGATCGCCCC GATTCTGGAT GAAATCGCTG ACGAATATCA 241 GGGCAAACTG ACCGTTGCAA AACTGAACAT CGATCAAAAC CCTGGCACTG CGCCGAAATA 301 TGGCATCCGT GGTATCCCGA CTCTGCTGCT GTTCAAAAAC GGTGAAGTGG CGGCAACCAA 361 AGTGGGTGCA CTGTCTAAAG GTCAGTTGAA AGAGTTCCTC GACGCTAACC TGGCCGGTTC 421 TGGTTCTGGC CATATGCACC ATCATCATCA TCATTCTTCT GGTCTGGTGC CACGCGGTTC

	481 TGGTATGAAA GAAACCGCTG CTGCTAAATT CGAACGCCAG CACATGGACA GCCCAGATCT 541 GGGTACCGAC GACGACGACA AGGCCATGGC TGATATCGGA TCCCAGCGCG AGCTTCGGCC 601 TCGGCTCTGT ACCATGAAGA AGGGCCCCAG TGGCTATGGC TTCAACCTGC ACAGCGACAA 661 GTCCAAGCCA GGCCAGTTCA TCCGGTCAGT GGACCCAGAC TCCCCGGCTG AGGCTTCAGG 721 GCTCCGGGCC CAGGATCGCA TTGTGGAGGT GAACGGGGTC TGCATGGAGG GGAAGCAGCA 781 TGGGGACGTG GTGTCCGCCA TCAGGGCTGG CGGGGACGAG ACCAAGCTGC TGGTGGTGGA 841 CAGGGAAACT GACGAGTTCT TCAAGAAATG CAGAGTGATC CCATCTCAGG AGCACCTGAA 901 TGGTCCCCTG CCTGTGCCCT TCACCAATGG GGAGATACAG AAGGAGAACA GTCGTGAAGC 961 CCTGGCAGAG GCAGCCTTGG AGAGCCCCAG GCCAGCCCTG GTGAGATCCG CCTCCAGTGA 1021 CACCAGCGAG GAGCTGAATT CCCAAGACAG CCCCCCAAAA CAGGACTCCA CAGCGCCCTC 1081 GTCTACCTCC TCCTGAAAGC TTGCGGCCGC ACTCGAGCAC CACCACCACC ACCAC
GST-β-catenin-C’	1 ACGTTATCGA CTGCACGGTG CACCAATGCT TCTGGCGTCA GGCAGCCATC GGAAGCTGTG 61 GTATGGCTGT GCAGGTCGTA AATCACTGCA TAATTCGTGT CGCTCAAGGC GCACTCCCGT 121 TCTGGATAAT GTTTTTTGCG CCGACATCAT AACGGTTCTG GCAAATATTC TGAAATGAGC 181 TGTTGACAAT TAATCATCGG CTCGTATAAT GTGTGGAATT GTGAGCGGAT AACAATTTCA 241 CACAGGAAAC AGTATTCATG TCCCCTATAC TAGGTTATTG GAAAATTAAG GGCCTTGTGC 301 AACCCACTCG ACTTCTTTTG GAATATCTTG AAGAAAAATA TGAAGAGCAT TTGTATGAGC 361 GCGATGAAGG TGATAAATGG CGAAACAAAA AGTTTGAATT GGGTTTGGAG TTTCCCAATC 421 TTCCTTATTA TATTGATGGT GATGTTAAAT TAACACAGTC TATGGCCATC ATACGTTATA 481 TAGCTGACAA GCACAACATG TTGGGTGGTT GTCCAAAAGA GCGTGCAGAG ATTTCAATGC 541 TTGAAGGAGC GGTTTTGGAT ATTAGATACG GTGTTTCGAG AATTGCATAT AGTAAAGACT 601 TTGAAACTCT CAAAGTTGAT TTTCTTAGCA AGCTACCTGA AATGCTGAAA ATGTTCGAAG 661 ATCGTTTATG TCATAAAACA TATTTAAATG GTGATCATGT AACCCATCCT GACTTCATGT 721 TGTATGACGC TCTTGATGTT GTTTTATACA TGGACCCAAT GTGCCTGGAT GCGTTCCCAA 781 AATTAGTTTG TTTTAAAAAA CGTATTGAAG CTATCCCACA AATTGATAAG TACTTGAAAT 841 CCAGCAAGTA TATAGCATGG CCTTTGCAGG GCTGGCAAGC CACGTTTGGT GGTGGCGACC 901 ATCCTCCAAA ATCGGATCTG GTTCCGCGTG GATCCATGGC TACTCAAGCT GACCTGATGG 961 AGTTGGACAT GGCCATGGGT GGAACGCAGC AGCAGTTTGT GGAGGGCGTG CGCATGGAGG 1021 AGATAGTAGA AGGGTGTACT GGAGCTCTCC ACATCCTTGC TCGGGACGTT CACAACCGGA 1081 TTGTAATCCG AGGACTCAAT ACCATTCCAT TGTTTGTGCA GTTGCTTTAT TCTCCCATTG 1141 AAAATATCCA AAGAGTAGCT GCAGGGGTCC TCTGTGAACT TGCTCAGGAC AAGGAGGCTG 1201 CAGAGGCCAT TGAAGCTGAG GGAGCCACAG CTCCCCTGAC AGAGTTACTC CACTCCAGGA 1261 ATGAAGGCGT GGCAACATAC GCAGCTGCTG TCCTATTCCG AATGTCTGAG GACAAGCCAC 1321 AGGATTACAA GAAGCGGCTT TCAGTCGAGC TGACCAGTTC CCTCTTCAGG ACAGAGCCAA 1381 TGGCTTGGAA TGAGACTGCA GATCTTGGAC TGGACATTGG TGCCCAGGGA GAAGCCCTTG 1441 GATATCGCCA GGATGATCCC AGCTACCGTT CTTTTCACTC TGGTGGATAC GGCCAGGATG

	1501 CCTTGGGGAT GGACCCTATG ATGGAGCATG AGATGGGTGG CCACCACCCT GGTGCTGACT 1561 ATCCAGTTGA TGGGCTGCCT GATCTGGGAC ACGCCCAGGA CCTCATGGAT GGGCTGCCCC 1621 CAGGTGATAG CAATCAGCTG GCCTGGTTTG ATACTGACCT GTAAATCGTC CTTTAGGTAA 1681 GAAAGCTGGA AATCGGAATT CCTGTGACTG ACGATCTGCC TCGCGCGTTT CGGTGATGAC 1741 GGTGAAAACC TCTGACACAT GCAGCTCCCG GAGACGGTCA CAGCTTGTCT GTAAGCGGAT

Supplementary Table 5. Synthetic oligonucleotides used in ChIP and RT-PCR assays

ChIP		
c-Myc	forward	GTGAATACACGTTTGCGGGTTAC
	reverse	AGAGACCCTTGTGAAAAAAACCG
MMP2	forward	GAGGTCGCTTTCTTTGCCATCT
	reverse	AGCGACTCCATCTTGAACAGG
EDAR	forward	TGTGCCCCTCCATAAGACTCC
	reverse	GCAGAACATGGTTGGGTGAAGG
FRAS1	forward	CCTGAGCAAGAACTGTGCAACC
	reverse	GCCTCCTTCCTCTCTGCTTTG
cyclin D1	forward	CGCTCCCATTCTCTGCCGG
	reverse	GGGGCTCTTCCTGGGCAGC
BIRC5	forward	GGGGCGCTAGGTGTGGG
	reverse	TTCAAATCTGGCGGTTAATGGC
EDN1	forward	GGCAGAGAGCTGTCCAAGTC
	reverse	CGGGTTCCTCAGATCTCAAA
GAPDH	forward	TAGGCCTTTGCCTGAGCAGTCCGG
	reverse	TTGAGGCCTGAGCTACGTGCGCCC

RT-PCR		
c-Myc	forward	GCGACTCTGAGGAGGAACA
	reverse	TGTCCAACTTGACCCTCTTG
cyclin D1	forward	CGTCCATGCGGAAGATCGT
	reverse	TGGAAATGAACTTCACATCTGTGGC
EBP50	forward	ATCGCATTG TGGAGGTGA
	reverse	TTTGCTGCTGCGTTTCT
GAPDH	forward	CTGATGCCCCCATGTTCGTC
	reverse	CACCCTGTTGCTGTAGCCAAATT