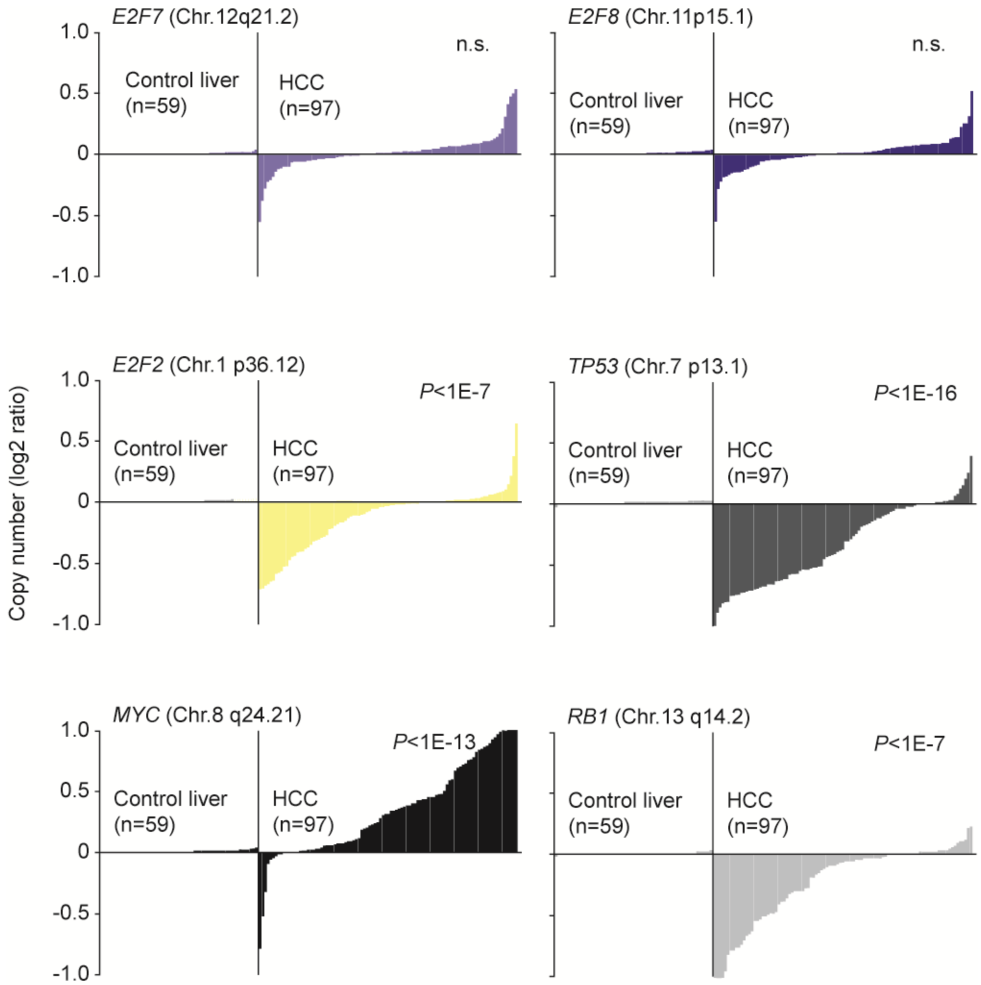
SUPPLEMENTAL METHODS

Deletion of *3a*$^{1KI/1KI}$ in tumors. *Mx1-cre* (1) was utilized to delete the knockin alleles of *E2f1* in adult mice bearing liver tumors. Livers from twelve and a half-month-old *Mx1-cre 3a*$^{1KI/1KI}$ mice were imaged by magnetic resonance imaging (MRI; 11.7 T system, Bruker BioSpin). Mice were then given intraperitoneal injections with poly I-C (Sigma; 10 μg per g of body weight, dissolved in PBS) at 1, 3, 5, 7 and 9 days following the initial MRI. Tumor mice were re-imaged by MRI 24-38 days following the initial MRI. Deletion of the knockin alleles was confirmed by southern blot. Tumor volume was calculated by measuring and summing the tumor area on each MRI section, using ImagJ. The fold growth represents the average of the volume calculated from the axial and coronal views of liver images.

SUPPLEMENTAL REFERENCE

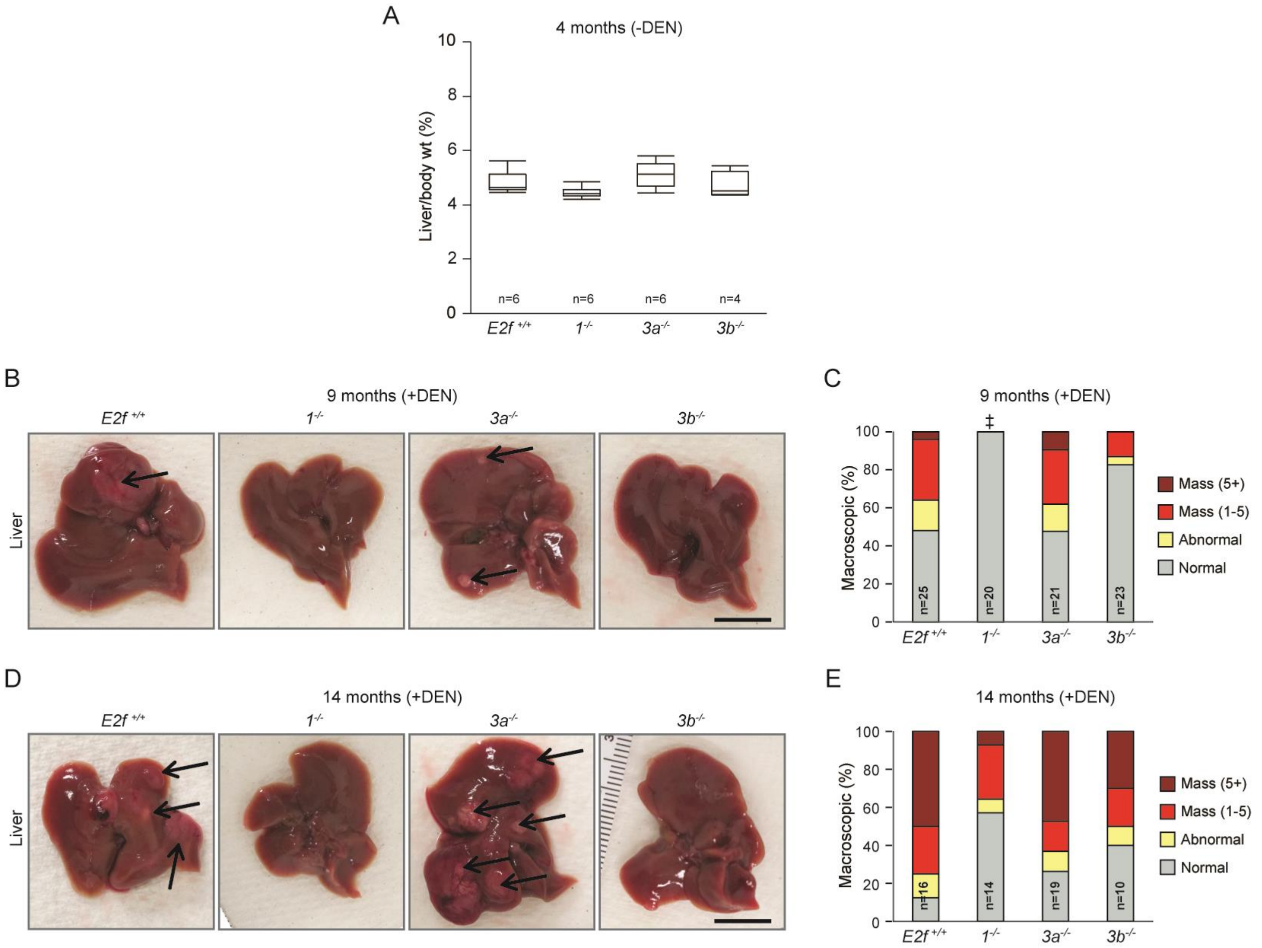
1. Kühn R, Schwenk F, Aguet M, Rajewsky K. Inducible gene targeting in mice. *Science* 1995;269(5229):1427–1429.

Supplemental Figure 1



Alternate view of the box plots illustrating copy number variations in E2F pathway genes in normal and HCC liver samples using the TCGA database, from Figure 1A. Levels of copy number variations are shown on the Y-axis and individual patients on the X-axis. Significance determined by two-sided Student's *t*-test vs. control liver. n.s, not significant.

Supplemental Figure 2



(A) Box plots showing the ratio of liver vs. body weight of 4-month-old wild type (*E2f*$^{+/+}$) and *E2f* knockout male mice. The center lines in the boxes represent the median value. The upper and lower boxes represent the 1st and 3rd quartile and the whiskers represent the highest and lowest value.

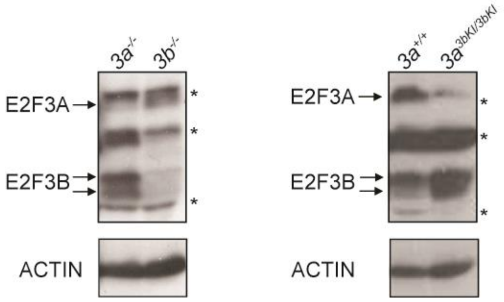
(B) Representative pictures of livers from 9-month-old DEN treated *E2f*$^{+/+}$ and *E2f* knockout male mice. Arrows indicate masses. Scale bars, 1 cm.

(C) Macroscopic evaluation of livers from B. Fisher's exact tests with Bonferroni correction for multiple tests comparing livers with mass vs. livers without masses. ‡, P=0.007 vs. *E2f*

(D) Representative pictures of livers from 14-month-old DEN treated *E2f*$^{+/+}$ and *E2f* knockout male mice. Arrows indicate masses. Scale bars, 1 cm.

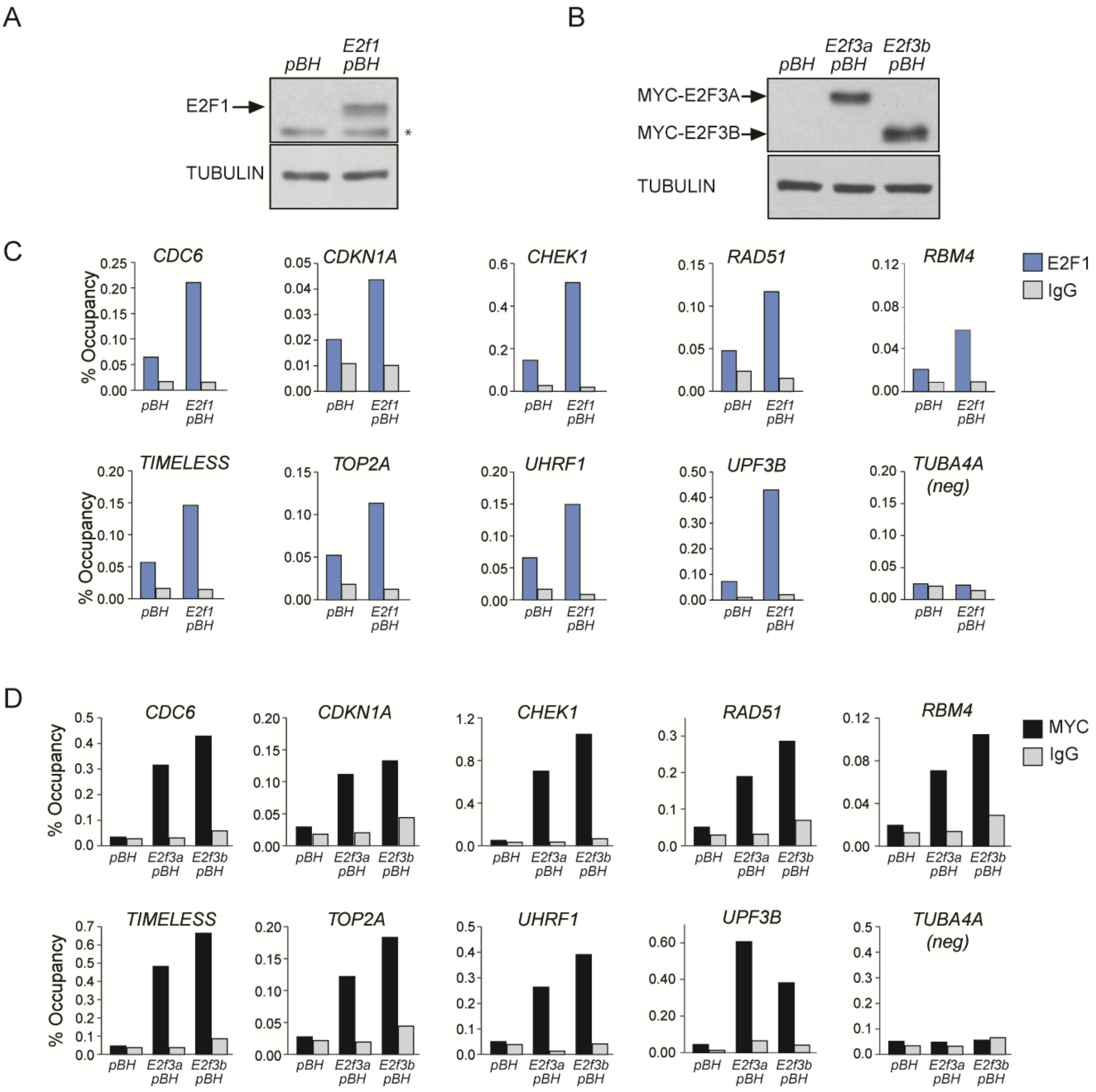
(E) Macroscopic evaluation of livers from D. n, number of mice.

Supplemental Figure 3



Immunoblot showing expected band sizes for E2F3A and E2F3B (left) or elevated E2F3B expression in livers from 1-month-old wild-type ($3a^{+/+}$) $3a^{3bKI/3bKI}$ mice (right). Antibodies against E2F3 were used and bands for E2F3A and E2F3B are indicted with arrows. Nonspecific bands are noted with asterisks. ACTIN or TUBULIN are include as loading controls.

Supplemental Figure 4



Supplemental Figure 4

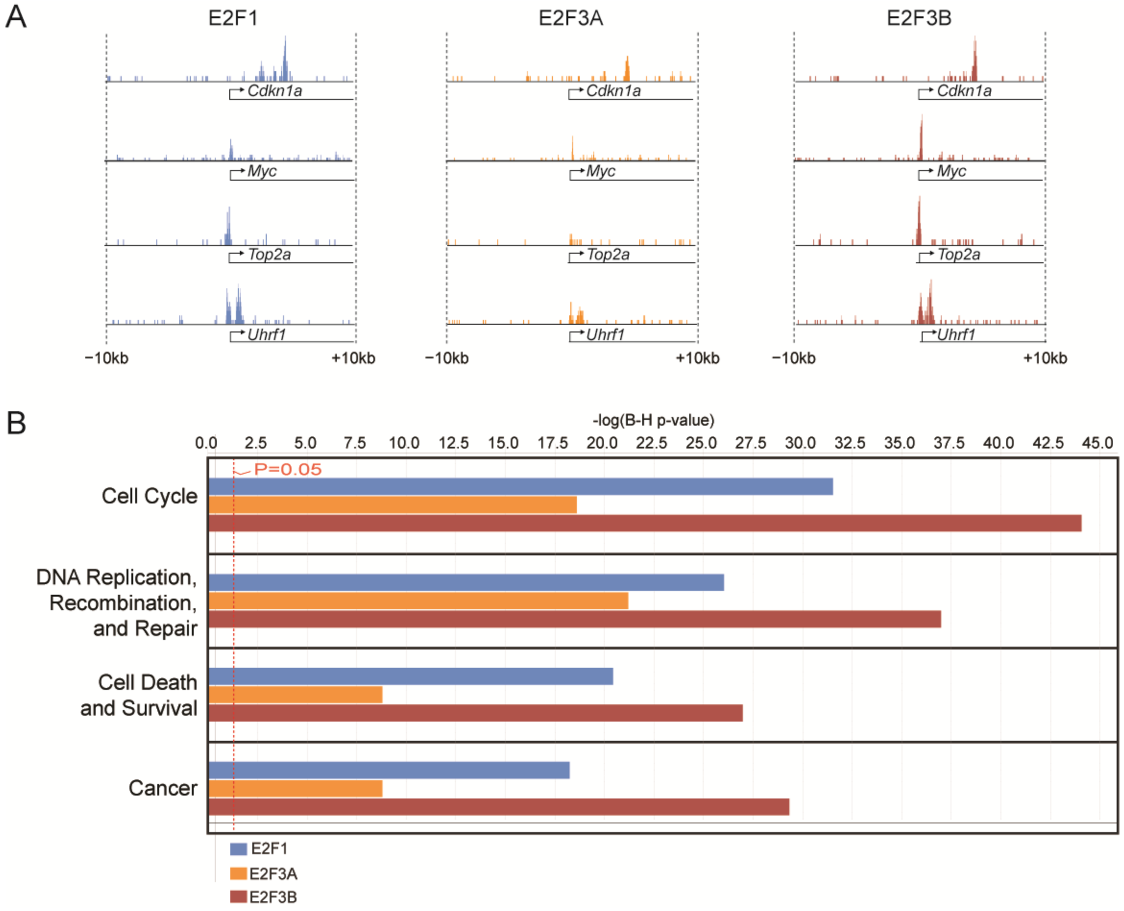
(A) Immunoblot of whole cell extracts from HepG2 cells transduced with the retroviral expression plasmid pBABE-Hygro (pBH) or E2F1 pBH. Antibodies against E2F1 were used to detect the overexpressed protein and TUBULIN was used as a loading control. Nonspecific or endogenous E2F1 band is marked with an asterisk.

(B) Immunoblot of whole cell extracts from HepG2 cells transduced with pBH, E2F3A pBH or E2F3B pBH. Antibodies against the MYC-epitope on E2F3A and E2F3B were used to detect tagged proteins and TUBULIN was used as a loading control.

(C) ChIP-qPCR validation using E2F1 or IgG antibodies in empty vector transduced HepG2 cells (pBH) or HepG2 cells overexpressing E2F1 (E2F1 pBH). Primers were designed to amplify regions with E2F binding as identified by ChIP-seq experiments described in Figure 6. TUBULIN is shown as a negative control.

(D) ChIP-qPCR validation using MYC or IgG antibodies in empty vector transduced HepG2 cells (pBH) or HepG2 cells overexpressing MYC-tagged E2F3A (E2F3A pBH) or E2F3B (E2F3B pBH). Primers were designed to amplify regions with E2F biding as identified by ChIP-seq experiments described in Figure 6. TUBULIN is shown as a negative control.

Supplemental Figure 5

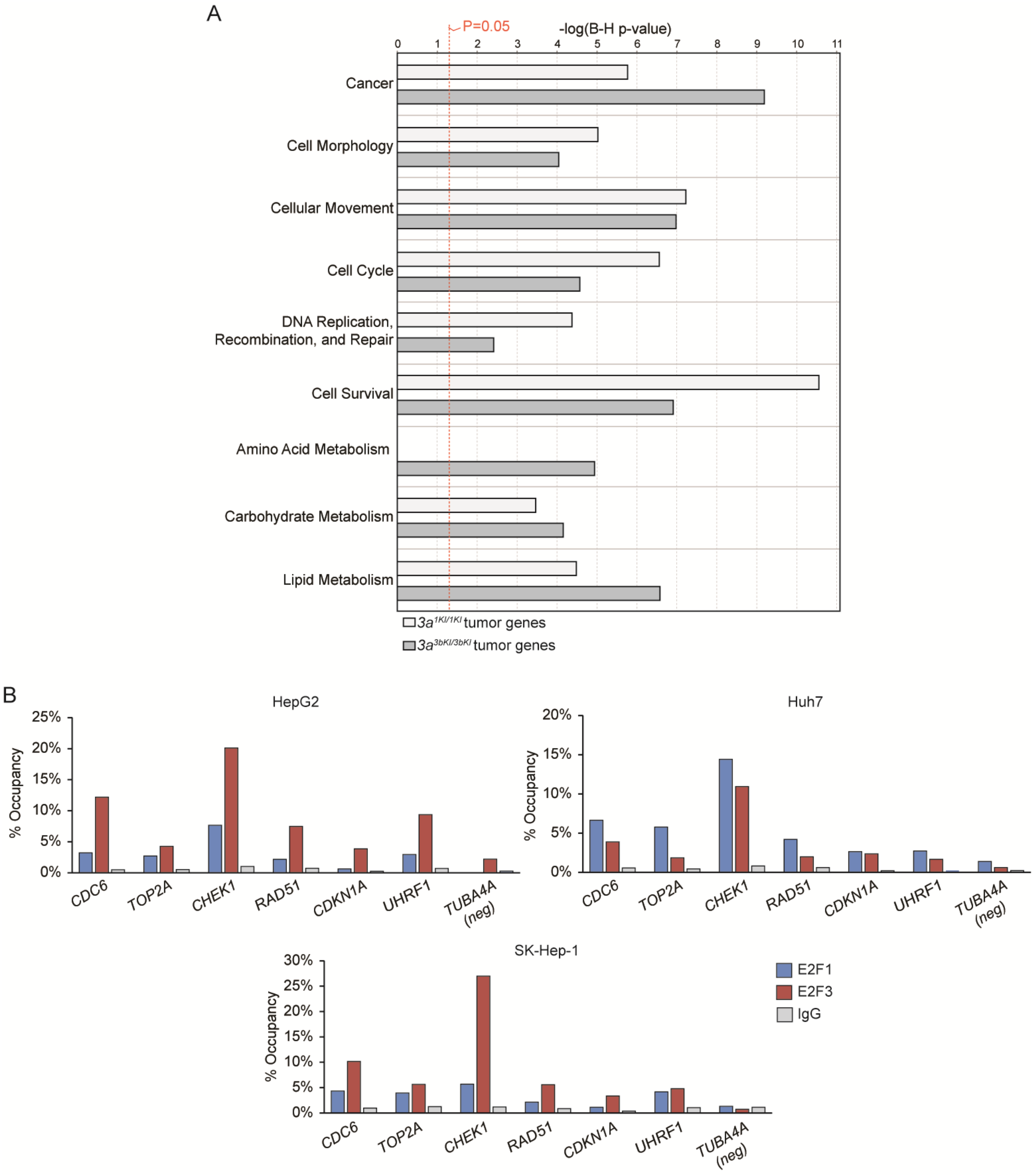


Supplemental Figure 5

(A) Examples of the promoter occupancy of E2Fs on selected gene promoters. All are shown at the same scale.

(B) Gene ontology using Ingenuity pathway analysis (IPA) software depicts the estimated contribution of genes with promoters occupied by E2F1, E2F3A or E2F3B to biological processes. Bars indicate the Benjamini-Hochberg adjusted *P*-value, the threshold of *P*=0.05 is shown.

Supplemental Figure 6

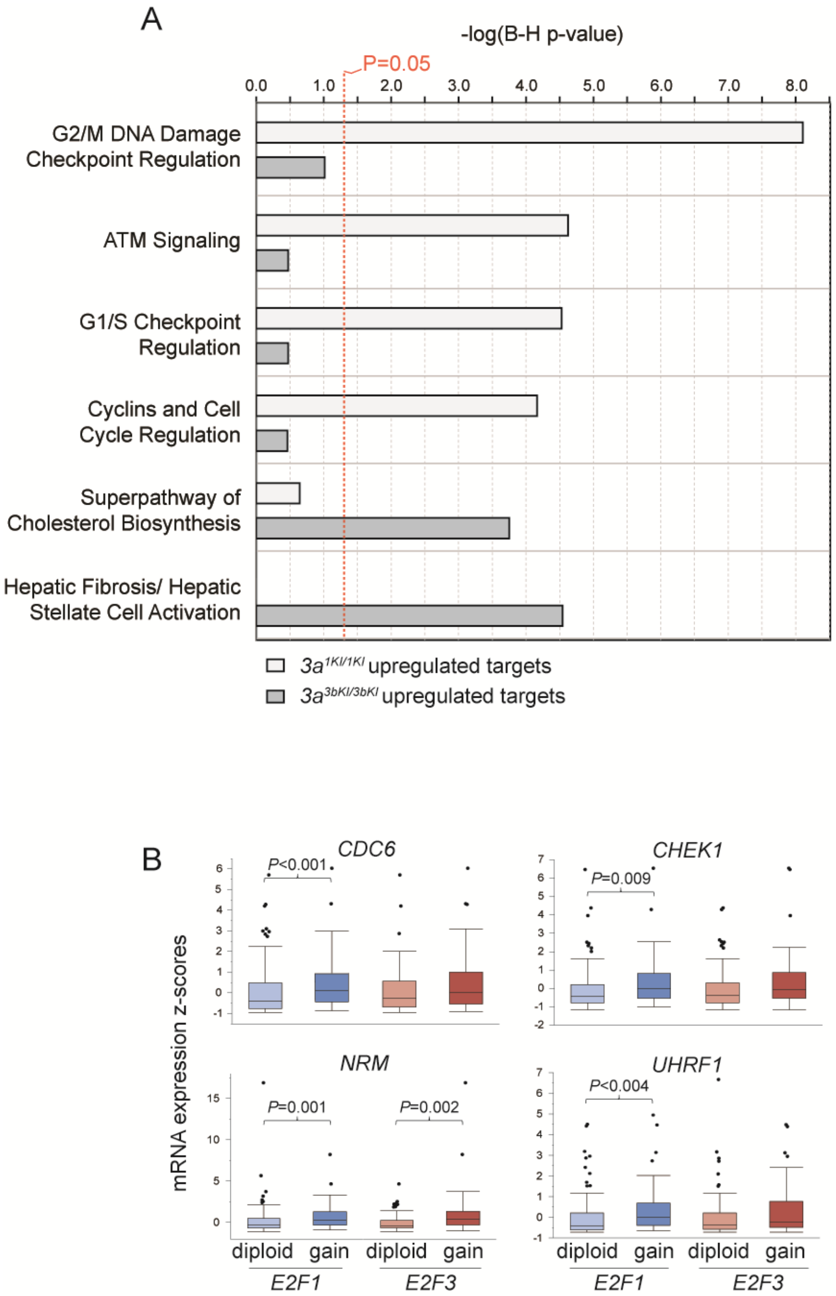


Supplemental Figure 6

(A) Gene ontology using Ingenuity pathway analysis (IPA) software depicts the estimated contribution of genes with altered expression in *3a*$^{1KI/1KI}$ or *3a*$^{3bKI/3bKI}$ liver tumors (fold change ±1.5, $P \leq 0.05$ when compared to *3a*$^{-/-}$ normal liver) to biological processes. Bars indicate the Benjamini-Hochberg adjusted *P*-value, the threshold of $P=0.05$ is shown.

(B) ChIP-qPCR validation using or IgG or antibodies against E2F1 or E2F3 in HepG2 and Huh7 HCC-derived and SK-Hep1 adenocarcinoma-derived cell lines. Occupancy of E2Fs on selected target promoters is shown. A non-promoter region of *TUBA4A* (*TUBA4A neg*) was used as a negative control. Primers were designed to amplify ChIP-seq identified peak regions.

Supplemental Figure 7

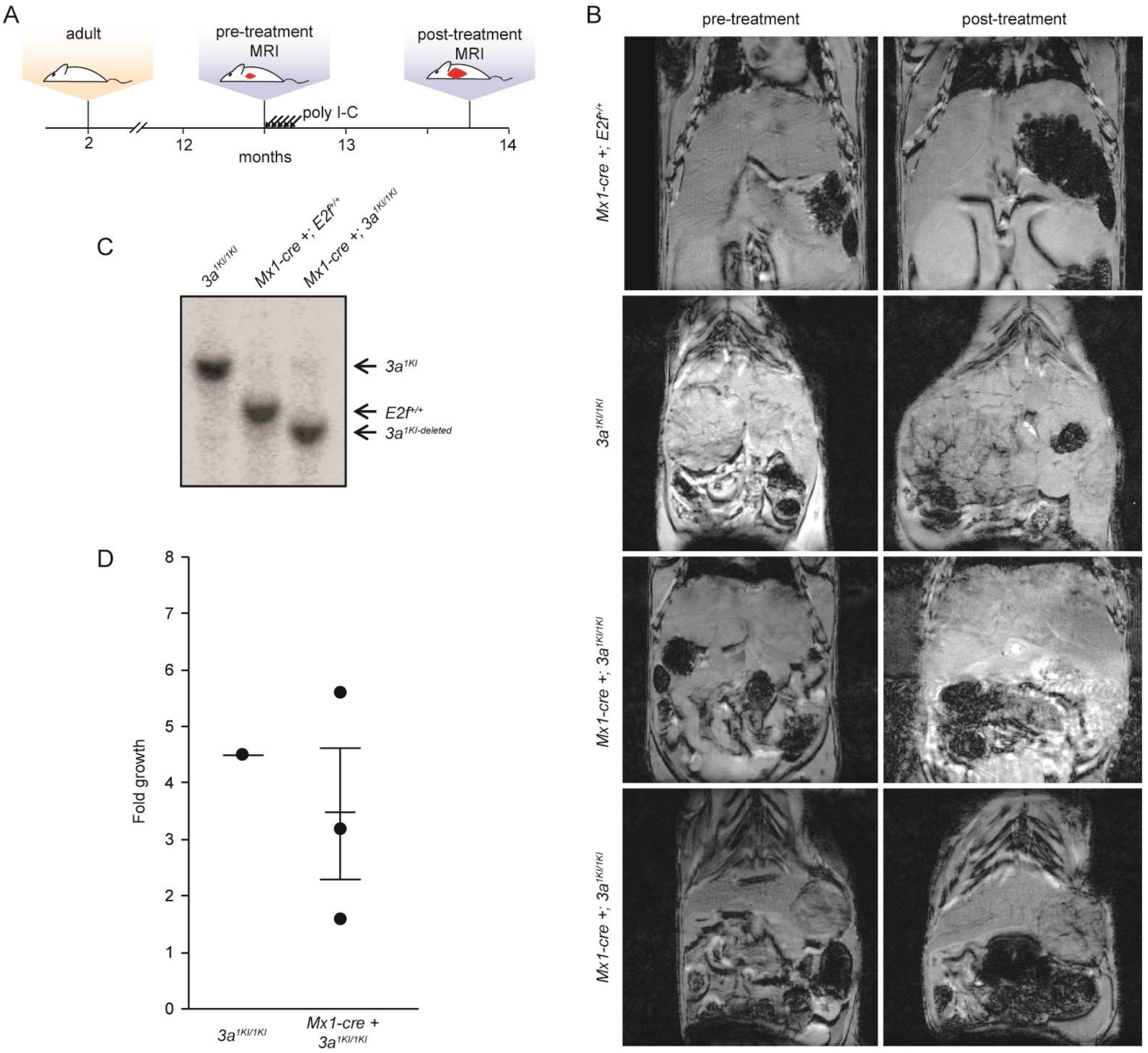


Supplemental Figure 7

(A) Gene ontology using Ingenuity pathway analysis (IPA) software depicts the estimated contribution of *3a*$^{1KI/1KI}$ or *3a*$^{3bKI/3bKI}$ upregulated targets to canonical pathways. Bars indicate the Benjamini-Hochberg adjusted *P*-value, the threshold of *P*=0.05 is shown.

(B) Expression of E2F1 and E2F3B targets in human HCC samples with normal or increased copy numbers of *E2F1* and *E2F3*. *E2F1* diploid, 122 samples; gain, 62 samples. *E2F3* diploid, 102 samples; gain, 80 samples. Wilcoxon rank sum test *P* values are indicated.

Supplemental Figure 8



Supplemental Figure 8

(A) Schematic of experimental design illustrating the relative time points when mice were imaged by MRI and treated with poly I-C. Livers of twelve and a half-month-old-mice were visualized by MRI. The knockin alleles were then deleted in *Mx1-cre* $3a^{1KI/1KI}$ mice by treating with poly I-C (5 injections, 10ug/g). A second MRI was was taken 23-37 days after the start of poly I-C treatment.

(B) Representative MRI images of mice with the indicated genotypes pre- and post-treatment with poly I-C.

(C) Southern blot demonstrating successful deletion of knockin alleles using *Mx1-cre*.

(D) Graph showing the fold growth of tumors in *Mx1-cre* negative (n=1) and positive $3a^{1KI/1KI}$ (n=3) mice. Fold growth was calculated based on the volume of the tumor pre- and post-treatment with poly I-C. Individual values (dots) means (center line) and SEM (bars) are shown.

SUPPLEMENTAL TABLES

Supplemental Table 1: Histopathological grading of hepatocellular carcinomas in DEN treated mice.

Tumor diameter based on the largest carcinoma present, the overall tumor burden, the extent of necrosis, and presence of vascular invasion were all independently graded for hepatocellular carcinomas from DEN treated mice based on the table below. Scores were added together to generate a single pathological score for each animal.

Tumor Diameter: Volume Grade	
Score	**Criteria**
0	No carcinoma present
1	Diameter of the largest carcinoma observed is ≤ one 100x field
2	> one 100x field and < one 40x field
3	> one 40x fields and < one 20x field
4	> one 20x field
Tumor Burden: Multiplicity Grade	
Score	**Criteria**
0	There is no additional carcinoma present that is equal to the diameter of the carcinoma scored above.
1	There are two or more carcinomas present with the same diameter score
Tumor Necrosis	
Score	**Criteria**
0	Necrosis is absent
1	Necrosis is ≤ one 400x field
2	Necrosis is > one 400x field and ≤ one 200x field
3	Necrosis is > one 200x field and ≤ one 100x field
4	Necrosis is > one 100x field and ≤ one 40x field
5	Necrosis is > one 40x field
Vascular Invasion	
Score	**Criteria**
0	Absent
1	Present

Supplemental Table 2. Significant ChIP-seq E2F1 promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Dusp6	NM_026268	chr10	98723587	98724166	-1988
Rab26	NM_177375	chr17	24672416	24672926	-1980
Cirbp	NM_007705	chr10	79628224	79629124	-1911
Col19a1	NM_007733	chr1	24595959	24596407	-1908
Tnfaip3	NM_009397	chr10	18736777	18737453	-1900
Hes1	NM_008235	chr16	30063220	30063878	-1893
9330188P03Rik	NR_102319	chr14	105986564	105987244	-1861
Mir30e	NR_029602	chr4	120446778	120447502	-1839
Rfx4	NM_001024918	chr10	84216717	84217236	-1816
Ugt2a1	NM_053184	chr5	87921423	87921918	-1776
Birc2	NM_007465	chr9	7836600	7837427	-1760
Rarg	NM_001042727	chr15	102078264	102079070	-1737
Pbx3	NM_016768	chr2	34229110	34229423	-1703
Ywhaz	NM_001253807	chr15	36721827	36722876	-1666
Kif14	NM_001287179	chr1	138362508	138363076	-1632
Slc25a18	NM_001081048	chr6	120721945	120722379	-1623
Arpp21	NM_001177623	chr9	112121193	112121657	-1571
Stk40	NM_001145827	chr4	125779381	125779929	-1545
Mir148a	NR_029719	chr6	51220558	51222228	-1485
Egr2	NM_010118	chr10	66998727	66999563	-1471
Hnrnpl	NM_177301	chr7	29594010	29594950	-1428
Prr12	NM_175022	chr7	52309388	52309926	-1407
Kif16b	NM_001081133	chr2	142728244	142728960	-1403
Sfr1	NM_026377	chr19	47804689	47805034	-1384
Gcnt1	NM_173442	chr19	17432255	17432797	-1370
Rrm2	NM_009104	chr12	25391487	25392050	-1350
Zfp516	NM_001177464	chr18	83082539	83082820	-1344
Dusp6	NM_026268	chr10	98724244	98724819	-1333
Hcfc1	NM_008224	chrX	71212642	71213413	-1333
Ier2	NM_010499	chr8	87187723	87188435	-1329
Nr2f2	NM_009697	chr7	77506460	77507080	-1292
Nfatc4	NM_001168346	chr14	56441859	56442853	-1275
Ptma	NM_008972	chr1	88421764	88422330	-1263
Mir331	NR_029764	chr10	93427572	93428162	-1260
Wnk1	NM_198703	chr6	119989509	119990281	-1223
Hivep1	NM_007772	chr13	42145908	42146454	-1208
Bhlhe41	NM_024469	chr6	145814764	145815474	-1180
Maoa	NM_173740	chrX	16195477	16195836	-1167
Fbxw7	NM_001177773	chr3	84617897	84618781	-1159
Trib1	NM_144549	chr15	59478767	59479402	-1124
Large	NM_010687	chr8	75877085	75878019	-1098
Ctdspl	NM_133710	chr9	118834346	118834779	-1091
Hes1	NM_008235	chr16	30063960	30064766	-1079
Irf2bp2	NM_001164598	chr8	129117750	129119047	-1064
Pbx3	NM_016768	chr2	34228169	34229049	-1045
Cdkn2c	NM_007671	chr4	109338559	109339477	-1042
Eno3	NM_001136062	chr11	70469311	70469993	-1025
Memo1	NM_133771	chr17	74694624	74695786	-1003

Supplemental Table 2. Significant ChIP-seq E2F1 promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Lamb2	NM_008483	chr9	108380905	108381514	-983
Hmga1	NM_001166535	chr17	27691772	27693323	-971
Rusc1	NM_001083808	chr3	88894730	88895104	-965
Peli2	NM_033602	chr14	48739325	48739834	-964
Fosl2	NM_008037	chr5	32437472	32438321	-948
Khdrbs1	NR_045036	chr4	129420279	129420702	-945
Usp49	NM_198421	chr17	47766353	47767079	-922
Pi4k2a	NM_145501	chr19	42163728	42164308	-906
Arid1a	NM_001080819	chr4	133310141	133310691	-891
Fbxl19	NM_172748	chr7	134888818	134890002	-878
Mex3b	NM_175366	chr7	90014597	90015343	-872
Rps4x	NM_009094	chrX	99384256	99384885	-862
Fam83b	NM_001045518	chr9	76394177	76394761	-859
Stk11	NM_011492	chr10	79578129	79578716	-858
Gm5129	NR_028426	chr5	30062990	30063652	-846
Bcl11b	NM_021399	chr12	109242309	109242622	-843
Sppl3	NM_029012	chr5	115460323	115461060	-841
Irs2	NM_001081212	chr8	11008925	11009608	-838
G3bp1	NM_013716	chr11	55281855	55282984	-834
Rgs19	NM_001291205	chr2	181427143	181427554	-828
Sox12	NM_011438	chr2	152224409	152224805	-826
Pde10a	NM_001290707	chr17	8718677	8719017	-818
BC005537	NM_024473	chr13	24892314	24893103	-817
Ptprs	NM_001252456	chr17	56602143	56602774	-816
Dennd4b	NM_201407	chr3	90069246	90070003	-811
Gamt	NM_010255	chr10	79724102	79724923	-801
Maz	NM_010772	chr7	134170352	134171232	-800
Plekhh3	NM_146030	chr11	101033239	101033584	-797
Mir1191b	NR_106141	chr10	80879451	80880198	-784
Klf16	NM_078477	chr10	80040111	80041522	-777
Rnf139	NM_175226	chr15	58719652	58720364	-775
Actn1	NM_134156	chr12	81361856	81362377	-760
Efemp2	NM_021474	chr19	5473709	5474179	-745
Spats2	NM_139140	chr15	98956188	98956902	-730
Hivep2	NM_010437	chr10	13685142	13685771	-728
Rprd2	NM_001081293	chr3	95623260	95623935	-723
Sec14l1	NM_001166506	chr11	116975535	116975991	-722
Mex3a	NM_001029890	chr3	88335188	88336007	-719
Mrps30	NM_021556	chr13	119176433	119177117	-717
Camk2n2	NM_028420	chr16	20621636	20622397	-667
Meis2	NM_001159568	chr2	115890972	115891937	-662
Map3k3	NM_011947	chr11	105945043	105946074	-657
Hist1h2be	NM_001290530	chr13	23678171	23678818	-657
Eif3b	NM_133916	chr5	140894172	140895039	-653
Csnk1g2	NM_134002	chr10	80084399	80085346	-652
Atg10	NM_025770	chr13	91363880	91364602	-650
Ndst1	NM_008306	chr18	60873379	60874000	-648
Top1mt	NM_028404	chr15	75509375	75510350	-644

Supplemental Table 2. Significant ChIP-seq E2F1 promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Oxsr1	NM_133985	chr9	119231853	119232513	-639
Hist1h3i	NM_178207	chr13	21875554	21876240	-632
Fzd7	NM_008057	chr1	59538065	59538658	-629
Sdf2l1	NM_022324	chr16	17132923	17133271	-622
Rock2	NM_009072	chr12	16900800	16901527	-620
Spsb4	NM_145134	chr9	96918935	96919850	-620
Slc25a23	NM_025877	chr17	57199663	57200124	-609
Rpl30	NM_001163485	chr15	34373317	34373957	-607
Sp1	NM_013672	chr15	102235491	102236791	-605
Camta1	NM_001081557	chr4	151236146	151236804	-599
Spred1	NM_033524	chr2	116945819	116946606	-594
Zhx1	NM_001042438	chr15	57908022	57909278	-588
Fzr1	NM_019757	chr10	80841420	80841963	-578
Sp4	NM_009239	chr12	119539997	119540977	-575
Taf7	NM_175770	chr18	37804165	37804693	-572
Ubb	NM_011664	chr11	62364211	62364657	-571
H3f3a	NM_008210	chr1	182743828	182744763	-563
Ptp4a2	NM_008974	chr4	129496885	129497437	-561
Pidd1	NM_022654	chr7	148629524	148630102	-560
Gm53	NR_037977	chr11	96112150	96112680	-558
Ubap2	NM_026872	chr4	41222525	41222919	-555
Hnrnpa0	NM_029872	chr13	58230147	58230788	-552
Atn1	NM_007881	chr6	124706719	124707389	-550
Ccne1	NM_007633	chr7	38892587	38893523	-547
Mir210	NR_029793	chr7	148407565	148408307	-545
Sorcs2	NM_030889	chr5	36740729	36741931	-543
Wbp2	NM_016852	chr11	115948229	115949394	-535
Fnip2	NM_001162999	chr3	79371892	79372366	-529
Rnf26	NM_153762	chr9	43921472	43921844	-525
Usp1	NM_146144	chr4	98589469	98590484	-524
Rictor	NM_030168	chr15	6657458	6658271	-516
1190002F15Rik	NR_037956	chr6	134877764	134879426	-514
Pim1	NM_008842	chr17	29626960	29627995	-512
Rfx3	NM_011265	chr19	28085877	28086455	-511
Pgk1	NM_008828	chrX	103381637	103382218	-511
Hmgn5	NM_016710	chrX	106209005	106209452	-511
Fads2	NM_019699	chr19	10176157	10176810	-492
Tcf3	NM_001164147	chr10	79896433	79897343	-491
Cables2	NM_145851	chr2	180008391	180008925	-489
Hdgfrp2	NM_008233	chr17	56217877	56219309	-486
Zfp395	NM_199029	chr14	65976591	65977464	-485
Dleu2	NR_028264	chr14	62301155	62302230	-484
Rnf130	NM_001290750	chr11	49838070	49838631	-482
Pabpc1	NM_008774	chr15	36538652	36539764	-481
Gphn	NM_145965	chr12	79326861	79327461	-480
Slc19a2	NM_001276455	chr1	166178352	166179048	-476
Rbpj	NM_009035	chr5	53980447	53981772	-475
Sorbs3	NM_001271408	chr14	70604580	70605224	-473

Supplemental Table 2. Significant ChIP-seq E2F1 promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Zfp219	NM_001253694	chr14	52639510	52640208	-472
Khsrp	NM_010613	chr17	57170865	57171934	-471
Hsd17b12	NM_019657	chr2	93998195	93998867	-466
Samd4b	NM_175021	chr7	29221439	29221906	-464
Rarg	NM_001042727	chr15	102077100	102077679	-460
Msl2	NM_001100451	chr9	100977782	100978287	-451
Fchsd2	NM_001146010	chr7	108256586	108257091	-450
Smg7	NM_001160256	chr1	154750022	154750416	-444
Rfx2	NM_009056	chr17	56970486	56971258	-442
Btg3	NM_009770	chr16	78377184	78377756	-441
Ran	NM_009391	chr5	129525157	129526029	-437
Xpo1	NM_001035226	chr11	23155161	23156047	-436
Cit	NM_007708	chr5	116294862	116295598	-434
Pes1	NM_022889	chr11	3863248	3863843	-432
Hspa9	NM_010481	chr18	35113960	35114911	-432
Zbed4	NM_181412	chr15	88581423	88582007	-425
Btbd10	NM_133700	chr7	120512906	120513647	-425
Sec11a	NM_019951	chr7	88092436	88093281	-424
Tmem55b	NM_001033271	chr14	51550526	51551362	-421
Brat1	NM_181066	chr5	141180130	141180967	-416
Srsf3	NM_013663	chr17	29168491	29169888	-415
Uvssa	NM_001081101	chr5	33720521	33721340	-414
Sh3bp4	NM_133816	chr1	90966216	90967030	-413
Gtpbp1	NM_013818	chr15	79520372	79521455	-412
Lhx2	NM_010710	chr2	38206154	38206678	-411
Uvrag	NM_178635	chr7	106289884	106290244	-411
Ppp1r7	NM_023200	chr1	95239053	95240568	-411
Adh5	NM_007410	chr3	138105193	138106100	-410
Stim1	NM_009287	chr7	109415618	109416245	-406
Ywhaq	NM_011739	chr12	21423400	21423998	-403
Kpnb1	NM_008379	chr11	97049031	97050180	-401
Odc1	NM_013614	chr12	17550989	17551567	-400
Vcl	NM_009502	chr14	21747753	21748759	-398
Ubtf	NM_011551	chr11	102180490	102181121	-397
Pigv	NM_178698	chr4	133228647	133229264	-395
Rab1	NM_008996	chr11	20100806	20101616	-393
Tbl2	NM_013763	chr5	135624653	135625722	-393
Yy1	NM_009537	chr12	110030979	110031283	-389
Dnajc4	NM_020566	chr19	7066898	7067399	-388
Gkap1	NM_019832	chr13	58375562	58376307	-387
Mrpl34	NM_053162	chr8	73988191	73988694	-382
Rps19	NM_023133	chr7	25668929	25669775	-380
Farp2	NM_145519	chr1	95407857	95408747	-378
Sin3a	NM_001110350	chr9	56923505	56924106	-377
Lrp12	NM_172814	chr15	39775272	39776084	-376
Itfg2	NM_133927	chr6	128374877	128375728	-376
Mtrf1l	NM_175374	chr10	4521836	4522611	-374
Hnrnpf	NM_001166429	chr6	117857193	117857703	-373

Supplemental Table 2. Significant ChIP-seq E2F1 promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Ak1	NM_001198791	chr2	32480294	32480873	-373
Mfsd11	NM_178620	chr11	116714325	116715602	-365
Avpi1	NM_027106	chr19	42203621	42204071	-364
Ap2a1	NM_007458	chr7	52184999	52185447	-364
Cul1	NM_012042	chr6	47403726	47404194	-362
Snhg8	NR_028574	chr3	123211200	123212028	-361
Zfp36l1	NM_007564	chr12	81213674	81215044	-360
Mef2d	NM_133665	chr3	87945624	87946289	-360
Otud4	NM_001256033	chr8	82162853	82163580	-358
Stag1	NM_009282	chr9	100543152	100544216	-357
Myl12a	NM_026064	chr17	71351890	71352565	-356
Trio	NM_001081302	chr15	27955559	27956351	-353
Hoxc9	NM_008272	chr15	102806866	102807356	-351
Asna1	NM_019652	chr8	87549156	87549894	-349
Zkscan5	NM_001167944	chr5	145964766	145965391	-349
D930048N14Rik	NR_027958	chr11	51463834	51464382	-347
Rab40c	NM_139154	chr17	26056765	26057245	-347
Dusp14	NM_019819	chr11	83881923	83882486	-347
Cblb	NM_001033238	chr16	52031126	52031503	-347
Tpst2	NM_009419	chr5	112705120	112705641	-346
Snord1c	NR_028569	chr11	116533178	116533772	-343
Pcbp2	NM_011042	chr15	102300342	102301096	-343
Sec31a	NM_026969	chr5	100845221	100845969	-343
Lcorl	NM_178142	chr5	46248706	46249534	-342
Dcbld2	NM_028523	chr16	58407971	58408640	-342
Cd164	NM_016898	chr10	41238663	41239267	-340
Wtap	NM_175394	chr17	13185395	13186092	-340
Foxp4	NM_001110825	chr17	48061493	48062345	-339
Hnrnpul1	NM_144922	chr7	26539581	26540569	-337
Cercam	NM_207298	chr2	29724480	29724875	-336
Foxn2	NM_180974	chr17	88839343	88840093	-333
Ubqln4	NM_033526	chr3	88356772	88357836	-333
Hexim1	NM_138753	chr11	102976984	102977628	-332
Ipo5	NM_023579	chr14	121309805	121310361	-332
Cox20	NM_025511	chr1	180248494	180249409	-332
Ate1	NM_001136054	chr7	137662934	137663915	-332
Nlk	NM_008702	chr11	78510912	78511601	-331
BC003331	NM_001077237	chr1	152240121	152240906	-330
Zbed3	NM_028106	chr13	96094613	96095110	-330
Pank1	NM_023792	chr19	34952456	34953014	-329
Zfand5	NM_009551	chr19	21346176	21346702	-328
Ulk4	NM_177589	chr9	121186165	121187069	-328
Troap	NM_001162506	chr15	98904756	98905396	-327
Ppp1cb	NM_172707	chr5	32760638	32761392	-327
Klhdc10	NM_029742	chr6	30351215	30351948	-327
Nfix	NM_001081981	chr8	87298272	87298915	-327
Hist1h2af	NM_175661	chr13	23625130	23625776	-326
Vkorc1l1	NM_001001327	chr5	130417308	130418000	-324

Supplemental Table 2. Significant ChIP-seq E2F1 promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Rgl2	NM_009059	chr17	34066290	34066740	-323
Dnajc14	NM_028873	chr10	128241987	128242830	-323
Fam193b	NM_145382	chr13	55672495	55673110	-323
Azin1	NM_018745	chr15	38448964	38449720	-322
Htatsf1	NM_028242	chrX	54305979	54306872	-321
E2f8	NM_001013368	chr7	56136211	56137247	-319
Ing1	NM_011919	chr8	11555248	11556245	-319
Ptma	NM_008972	chr1	88422654	88423331	-318
Akap1	NM_001042541	chr11	88725826	88726607	-318
Zfp46	NM_009557	chr4	135841294	135842040	-316
Stxbp1	NM_001113569	chr2	32702795	32703348	-316
Gls2	NM_001033264	chr10	127631191	127631560	-315
Atxn2l	NM_183020	chr7	133646803	133647455	-314
Cep120	NM_178686	chr18	53904221	53904804	-313
Rnf4	NM_011278	chr5	34678390	34679062	-312
Siva1	NM_001161737	chr12	113882406	113883049	-311
Fam73b	NM_001242407	chr2	30218923	30219960	-311
Pdcd10	NM_019745	chr3	75360877	75361289	-310
Lrr1	NM_001081406	chr12	70269027	70269954	-310
Klf10	NM_001289471	chr15	38229982	38231567	-310
Mlec	NM_175403	chr5	115607967	115609016	-308
Dnajc3	NM_008929	chr14	119336530	119337162	-307
Rab8a	NM_023126	chr8	74684249	74685333	-307
D230025D16Rik	NM_145604	chr8	107748389	107749171	-307
Arhgap35	NM_172739	chr7	17200274	17201021	-307
Pop7	NM_028753	chr5	137943500	137944422	-305
Pja2	NM_144859	chr17	64680969	64682082	-304
Zfp36l2	NM_001001806	chr17	84586904	84588271	-302
Opn3	NM_010098	chr1	177622697	177623429	-301
Eif3l	NM_145139	chr15	78904836	78905868	-300
Ift27	NM_025931	chr15	78004406	78005267	-300
Ptpn21	NM_011877	chr12	99972829	99973476	-299
Rfwd3	NM_146218	chr8	113823861	113824977	-298
Osbpl8	NM_175489	chr10	110601180	110601939	-298
Iws1	NM_173441	chr18	32226696	32227485	-297
D830031N03Rik	NM_001167918	chr4	123088999	123089900	-297
Lgals1	NM_008495	chr15	78756436	78757280	-296
Rbm33	NM_028234	chr5	28643122	28643742	-296
Lrrc20	NM_153542	chr10	60937963	60938606	-296
Slmo2	NM_025531	chr2	174298441	174299030	-295
Ost4	NM_001134692	chr5	31210090	31210819	-295
Mxd3	NM_016662	chr13	55430799	55431969	-294
Mtfr1	NM_026182	chr3	19087554	19088299	-294
Mtf1	NM_008636	chr4	124479196	124479803	-293
Utp3	NM_023054	chr5	88982868	88983561	-293
Smc3	NM_007790	chr19	53674119	53675067	-292
Atf4	NM_009716	chr15	80084732	80085911	-292
Ezh2	NM_007971	chr6	47544888	47545751	-292

Supplemental Table 2. Significant ChIP-seq E2F1 promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Fdft1	NM_010191	chr14	63796552	63797287	-291
Tmem55a	NM_028264	chr4	14790886	14791263	-291
Mcfd2	NM_176808	chr17	87665181	87665970	-290
Afmid	NM_027827	chr11	117686568	117687318	-289
1810026B05Rik	NR_037569	chr7	80703214	80703923	-289
Fzd5	NM_001042659	chr1	64784300	64784920	-287
Nckap5l	NM_001001884	chr15	99288113	99288817	-287
Mir5133	NR_039595	chr9	61970204	61971170	-287
Nap1l1	NM_015781	chr10	110909555	110910367	-286
Hmgn1	NM_008251	chr16	96349108	96350126	-286
Prkce	NM_011104	chr17	86566561	86567120	-284
Kmt2b	NM_029274	chr7	31373819	31374236	-284
Morc2a	NM_001159288	chr11	3549069	3549358	-283
Armc1	NM_028840	chr3	19063118	19063575	-283
Set	NM_001204875	chr2	29921296	29922127	-282
Gna12	NM_010302	chr5	141306416	141306913	-281
Psma1	NM_011965	chr7	121419602	121420214	-279
1700001G11Rik	NR_038077	chr14	66915844	66916643	-279
Srsf4	NM_020587	chr4	131428964	131429585	-279
Cdc34	NM_177613	chr10	79144404	79144918	-278
Fmn1	NM_010230	chr2	113167310	113167918	-278
Hist1h3b	NM_178203	chr13	23843617	23844324	-278
Gan	NM_001081151	chr8	119681556	119681958	-277
1810013L24Rik	NM_001081400	chr16	8829342	8830492	-275
Mcoln1	NM_053177	chr8	3499884	3500602	-275
Cdk19	NM_198164	chr10	40068302	40069375	-275
Slc35b2	NM_028662	chr17	45700491	45701160	-275
Plxna3	NM_008883	chrX	71573753	71574507	-274
Ddx50	NM_053183	chr10	62113762	62114675	-274
Wdtc1	NM_199306	chr4	132895119	132895885	-273
Neurl4	NM_001291118	chr11	69714803	69715287	-272
Cdca7	NM_025866	chr2	72313591	72314415	-272
Ncapd2	NM_146171	chr6	125141496	125142251	-271
Gnaz	NM_010311	chr10	74429511	74429899	-270
Tmco3	NM_172282	chr8	13287373	13288111	-270
Fam83d	NM_027975	chr2	158593094	158594035	-270
Trappc10	NM_001081055	chr10	77707391	77707917	-268
Tomm7	NM_025394	chr5	23349913	23350542	-266
Kpna3	NM_008466	chr14	62058703	62059393	-265
Mapk7	NM_001291035	chr11	61307712	61308348	-263
Drg1	NM_007879	chr11	3166348	3166951	-262
Bicd2	NM_001039179	chr13	49436379	49436932	-262
Rhob	NM_007483	chr12	8506732	8507370	-261
Ebag9	NM_019480	chr15	44450490	44451361	-261
Zcwpw1	NM_001005426	chr5	138228261	138229276	-261
Nup153	NM_175749	chr13	46823263	46823691	-260
Mob3a	NM_172457	chr10	80164330	80165317	-260
Lrrc51	NM_001162973	chr7	109082355	109082902	-259

Supplemental Table 2. Significant ChIP-seq E2F1 promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Pgrmc2	NM_027558	chr3	40886657	40887791	-257
Cdkn2a	NM_009877	chr4	88940273	88941285	-257
Ado	NM_001005419	chr10	67011666	67012249	-256
Hmgcr	NM_008255	chr13	97440792	97441497	-255
Cep95	NM_001166685	chr11	106649672	106650951	-254
Gpr3	NM_008154	chr4	132768413	132768992	-253
Mlxip	NM_133917	chr5	123844062	123845047	-252
Gemin8	NM_146238	chrX	162607796	162608523	-252
Bag6	NM_057171	chr17	35271546	35272197	-251
Lemd2	NM_146075	chr17	27341386	27341878	-250
Nmt2	NM_001290370	chr2	3200708	3201758	-250
Mageb3	NM_008545	chr2	121781371	121782783	-250
2410002F23Rik	NM_025880	chr7	51501369	51502315	-249
Eif2s3x	NM_012010	chrX	91457933	91458543	-249
Ak2	NM_016895	chr4	128669771	128670668	-248
Maged1	NM_019791	chrX	91787448	91787869	-247
Herpud2	NM_020586	chr9	24956199	24956850	-246
Gmeb2	NM_198169	chr2	181022574	181023256	-245
Phf19	NM_028716	chr2	34769357	34770120	-244
Chac1	NM_026929	chr2	119176349	119177118	-244
Dcun1d4	NM_178896	chr5	73881742	73882299	-244
Pcdhgc3	NM_033581	chr18	37965476	37966164	-243
Mgat1	NM_010794	chr11	49057236	49057666	-241
Tra2a	NM_198102	chr6	49213958	49214623	-241
Pcdh9	NM_001271798	chr14	94289717	94290537	-240
Fbxo10	NM_001024142	chr4	45097337	45098092	-240
Ube2n	NM_080560	chr10	94977054	94978058	-239
Metap1d	NM_025633	chr2	71290773	71291537	-239
Fem1c	NM_173423	chr18	46685643	46686082	-239
Kmt2a	NM_001081049	chr9	44689338	44689851	-239
Lsm2	NM_001110101	chr17	35117583	35119537	-238
Ric8b	NM_183172	chr10	84379636	84380604	-237
Farp1	NM_134082	chr14	121434148	121434968	-237
Mbd2	NM_010773	chr18	70727388	70728028	-237
Rps6ka5	NM_153587	chr12	101963101	101963846	-237
Stag3	NM_016964	chr5	138721165	138721835	-236
H2afv	NM_029938	chr11	6344148	6345213	-236
Dscc1	NM_183089	chr15	54921861	54922674	-236
Nmt1	NM_008707	chr11	102889291	102889989	-235
Tnrc6b	NM_177124	chr15	80628176	80629432	-235
Sgcd	NM_011891	chr11	47192585	47193490	-235
Cbfa2t2	NM_009823	chr2	154261839	154262133	-233
Pa2g4	NM_011119	chr10	128002664	128003778	-232
Lin37	NM_001290569	chr7	31344602	31345190	-232
Ilf3	NM_001277321	chr9	21171742	21172422	-232
Hinfp	NM_172162	chr9	44113797	44114173	-232
Lztr1	NM_025808	chr16	17508523	17509140	-232
Gltp	NM_019821	chr5	115140800	115141548	-231

Supplemental Table 2. Significant ChIP-seq E2F1 promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Nsun6	NM_001165943	chr2	14976445	14977012	-231
Kcnab2	NM_010598	chr4	151851565	151852208	-230
Vdac2	NM_011695	chr14	22650026	22651081	-229
Man1c1	NM_207237	chr4	134260216	134260648	-228
Rita1	NM_133908	chr5	121062531	121063119	-228
Taco1	NM_027346	chr11	105926886	105927499	-228
Ano6	NM_001253813	chr15	95620663	95621428	-228
BC004004	NM_030561	chr17	29405006	29406003	-228
Smg5	NM_178246	chr3	88139422	88140487	-227
Ube2s	NM_133777	chr7	4763859	4764476	-227
Snx13	NM_001014973	chr12	35731243	35732028	-225
Sco2	NM_001111288	chr15	89204125	89204819	-224
Mex3c	NM_001039214	chr18	73731800	73732468	-224
Fam168a	NM_178764	chr7	107854524	107855458	-224
Cpsf2	NM_016856	chr12	103213692	103214227	-224
4632415L05Rik	NR_027985	chr3	19794474	19794819	-224
Serbp1	NM_001113564	chr6	67216254	67217243	-224
Mdm1	NM_148922	chr10	117578300	117578938	-223
Shc1	NM_001113331	chr3	89224963	89225675	-223
Scaf4	NM_178923	chr16	90284688	90285095	-223
Katnb1	NM_028805	chr8	97604384	97605372	-222
Alcam	NM_009655	chr16	52453003	52453656	-221
Ndufaf3	NM_023247	chr9	108469576	108470208	-220
Pgp	NM_025954	chr17	24606720	24607675	-220
Ppig	NM_001081086	chr2	69560651	69561198	-220
Pts	NM_011220	chr9	50336609	50337319	-219
Fam214a	NM_001113283	chr9	74800336	74800944	-219
Tmem256	NM_026982	chr11	69651472	69652143	-219
Rad51d	NM_001277939	chr11	82704054	82704633	-219
H2-Ke6	NM_013543	chr17	34164813	34165622	-219
Tiparp	NM_178892	chr3	65331890	65332409	-219
Kbtbd8	NM_001008785	chr6	95067458	95067851	-219
Snip1	NM_175246	chr4	124743393	124744043	-218
Herpud1	NM_022331	chr8	96909724	96910638	-218
Xpnpep3	NM_177310	chr15	81230042	81230757	-218
Mief1	NM_178719	chr15	80063964	80064621	-217
Snrnp27	NM_025665	chr6	86634410	86634989	-216
Stx4a	NM_009294	chr7	134984820	134985391	-216
Trib1	NM_144549	chr15	59479529	59480457	-215
Gna11	NM_010301	chr10	81007516	81008493	-215
Tmtc4	NM_028651	chr14	123382433	123382960	-215
Cstf2t	NM_031249	chr19	31156748	31157483	-215
Rbm15	NM_001045807	chr3	107135860	107136981	-215
N4bp2l2	NM_201369	chr5	151467978	151468823	-215
Rfx1	NM_009055	chr8	86590110	86590929	-215
Mcu	NM_001033259	chr10	59079362	59079944	-214
Hdgf	NM_008231	chr3	87709520	87710538	-213
Ipo4	NM_024267	chr14	56254406	56255047	-213

Supplemental Table 2. Significant ChIP-seq E2F1 promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Cep131	NM_009734	chr11	119948045	119948659	-212
Gm20605	NR_033148	chr5	138069642	138070636	-211
Stx12	NM_133887	chr4	132440220	132440945	-211
Prkdc	NM_011159	chr16	15637261	15638235	-210
Mprip	NM_012027	chr11	59475582	59475991	-210
Arc	NM_018790	chr15	74502939	74503478	-210
Wnt5a	NM_009524	chr14	29317955	29318945	-208
2310057M21Rik	NM_026655	chr7	138506161	138506676	-208
Raly	NM_001139513	chr2	154616260	154617016	-207
Amd1	NM_009665	chr10	40021972	40022427	-207
E2f5	NM_007892	chr3	14578132	14578795	-207
Tmem214	NM_144525	chr5	31171555	31172071	-206
Slc35e1	NM_177766	chr8	75016414	75017022	-206
Mterfd1	NM_025547	chr13	67033765	67034660	-206
Cnot8	NM_026949	chr11	57917057	57917841	-205
Rnf8	NM_021419	chr17	29751134	29752006	-205
Kif13b	NM_001081177	chr14	65270898	65271428	-204
U2af1	NM_024187	chr17	31795487	31796315	-203
Mphosph8	NM_023773	chr14	57286425	57287338	-203
Ccnl1	NM_019937	chr3	65762026	65762671	-203
Zdhhc24	NM_027476	chr19	4878155	4878776	-202
Ddx46	NM_001282055	chr13	55735857	55736459	-201
Rcl1	NM_021525	chr19	29175395	29175934	-200
Papd4	NM_133905	chr13	93962091	93962781	-199
Baz1b	NM_011714	chr5	135662494	135663492	-199
Wwox	NM_019573	chr8	116963012	116963695	-198
Psmd1	NM_027357	chr1	87960601	87961392	-197
Aff1	NM_133919	chr5	104182676	104183291	-197
Rab5c	NM_024456	chr11	100599430	100599848	-196
Tbc1d8b	NM_001081499	chrX	136219121	136219555	-196
Tmx1	NM_028339	chr12	71553512	71554377	-196
Josd1	NM_028792	chr15	79518070	79518923	-196
Tubb4b	NM_146116	chr2	25079996	25080837	-196
Rps27l	NM_026467	chr9	66793293	66794164	-196
Tmub2	NM_028076	chr11	102145745	102146413	-195
Zfp451	NM_001290699	chr1	33871354	33871913	-195
Prdm4	NM_181650	chr10	85379584	85380182	-194
Fam76b	NM_176836	chr9	13631418	13632534	-194
Hspa8	NM_031165	chr9	40608624	40609698	-194
Dtwd2	NM_001170960	chr18	49915191	49915704	-194
Cep55	NM_028293	chr19	38128951	38129691	-193
Prkci	NM_008857	chr3	30894187	30894811	-193
Cep112	NM_029606	chr11	108286079	108286695	-192
Smchd1	NM_028887	chr17	71824295	71825453	-192
Cox5a	NM_007747	chr9	57368519	57369173	-192
Dhx36	NM_028136	chr3	62310886	62311313	-191
Dstn	NM_019771	chr2	143740446	143741306	-190
Ddx27	NM_153065	chr2	166840257	166840987	-190

Supplemental Table 2. Significant ChIP-seq E2F1 promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Por	NM_008898	chr5	136164520	136165269	-189
Cnnm2	NM_001102471	chr19	46835638	46836182	-188
Srd5a1	NM_175283	chr13	69750061	69750994	-188
Hint3	NM_025798	chr10	30338089	30338625	-186
Ncoa5	NM_144892	chr2	164860160	164860766	-185
Zfp622	NM_144523	chr15	25913634	25914237	-185
Btaf1	NM_001080706	chr19	37000029	37000738	-185
Ttc14	NM_025978	chr3	33698513	33699326	-185
Manf	NM_029103	chr9	106793798	106795104	-183
H13	NM_001159551	chr2	152494712	152495315	-183
Prrc2a	NM_001199044	chr17	35301744	35302261	-182
Prmt1	NM_019830	chr7	52241642	52242299	-182
Cstf3	NM_145529	chr2	104429965	104430953	-181
Tmem260	NM_172600	chr14	49065502	49066189	-181
Spink13	NM_001168423	chr18	62900928	62901513	-181
Anp32e	NM_001253758	chr3	95732512	95733485	-181
Phrf1	NM_001081118	chr7	148414153	148414858	-181
Ksr1	NM_013571	chr11	78959781	78960289	-180
Dph3	NR_104305	chr14	32898294	32899008	-180
Fxr2	NM_011814	chr11	69446075	69446511	-179
Ttll5	NM_001081423	chr12	87165264	87166176	-179
Oaz1	NM_008753	chr10	80288841	80289602	-179
Hist1h4d	NM_175654	chr13	23672963	23673620	-179
Pcbp1	NM_011865	chr6	86476078	86476595	-179
Abhd17c	NM_133722	chr7	91300252	91300909	-179
Pias4	NM_021501	chr10	80630335	80630949	-178
Gtpbp2	NM_019581	chr17	46297557	46298047	-178
Ywhah	NM_011738	chr5	33361119	33361453	-178
Vprbp	NM_001015507	chr9	106723603	106724653	-178
Suco	NM_172645	chr1	163806596	163807341	-178
Senp2	NM_029457	chr16	22009185	22009572	-178
Fancg	NM_053081	chr4	43023060	43023639	-178
Matr3	NM_010771	chr18	35721186	35722082	-177
Aurka	NM_001291185	chr2	172195876	172196616	-177
Nxpe3	NM_001134457	chr16	55895246	55895889	-177
Cep152	NM_001081091	chr2	125450603	125451446	-177
Dda1	NM_025600	chr8	73992706	73993125	-177
Aph1c	NM_026674	chr9	66682216	66683161	-177
Obfc1	NM_175360	chr19	47611380	47611990	-176
Fasn	NM_007988	chr11	120685634	120686437	-176
Snhg12	NR_029468	chr4	131864123	131864710	-176
Atad2	NM_027435	chr15	57966122	57967500	-175
Ahcyl1	NM_145542	chr3	107499294	107499986	-175
Poc1a	NM_027354	chr9	106182345	106184087	-175
Eprs	NM_029735	chr1	187186479	187187118	-175
Snrnp70	NM_009224	chr7	52650991	52651390	-175
Zc3h12c	NM_001162921	chr9	51976205	51976574	-175
Rhobtb1	NM_001252637	chr10	68675538	68675996	-174

Supplemental Table 2. Significant ChIP-seq E2F1 promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Fam208b	NM_134063	chr13	3610075	3610979	-174
Wdr90	NM_001163766	chr17	25998220	25999046	-174
Dennd1a	NM_146122	chr2	38142620	38143534	-174
Srsf10	NM_001284196	chr4	135411366	135412256	-174
Ube3a	NM_173010	chr7	66483707	66484183	-174
Phospho1	NM_153104	chr11	95685271	95686008	-174
Macrod1	NM_134147	chr19	7130765	7131402	-174
Uba52	NM_019883	chr8	73034219	73034658	-174
Ccna2	NM_009828	chr3	36470682	36471498	-173
Btbd8	NM_001255991	chr5	107866298	107867386	-173
Dgcr8	NM_033324	chr16	18289108	18289756	-172
Hyls1	NM_029762	chr9	35377383	35378266	-172
Tmpo	NM_001080129	chr10	90633976	90635092	-171
Tdrkh	NM_028307	chr3	94216861	94217277	-170
Hist1h3g	NM_145073	chr13	23626746	23627487	-170
Fgfr3	NM_001163216	chr5	34064498	34065071	-170
Crebl2	NM_177687	chr6	134779765	134780328	-170
Pex3	NM_001164195	chr10	13272797	13273434	-169
Glrx5	NM_028419	chr12	106270450	106271009	-169
Cbfb	NM_001161458	chr8	107694161	107694648	-169
Tcea1	NM_001159750	chr1	4847359	4847853	-168
Ror2	NM_013846	chr13	53381491	53381799	-168
Supt16	NM_033618	chr14	52816603	52817559	-168
Tigd3	NM_198634	chr19	5893957	5894591	-168
Ogt	NM_139144	chrX	98834993	98835449	-168
Mmp16	NM_019724	chr4	17780166	17780755	-168
Supt3	NM_178652	chr17	44913401	44914503	-167
Gins2	NM_178856	chr8	123112809	123113473	-167
BC052040	NM_001145898	chr2	115407009	115407560	-167
Hnrnpf	NM_001166427	chr6	117866793	117867496	-167
Hnrnpll	NM_144802	chr17	80461291	80462255	-166
Slc25a25	NM_146118	chr2	32306823	32307487	-166
Rpa2	NM_011284	chr4	132323727	132324489	-166
Fkbp5	NM_010220	chr17	28623024	28623492	-165
Creb1	NM_133828	chr1	64578948	64579478	-164
Tor1aip2	NM_172843	chr1	157882145	157883113	-164
Nadk2	NM_001286255	chr15	9000476	9001212	-164
Lemd3	NM_001081193	chr10	120416228	120416869	-164
Fbxw2	NM_001164770	chr2	34681592	34682242	-163
Myef2	NM_001162417	chr2	124949216	124949900	-163
Calu	NM_184053	chr6	29297551	29298333	-163
Pelo	NM_134058	chr13	115880215	115880838	-162
Lyrm7	NM_029327	chr11	54673980	54674526	-161
Ppil1	NM_026845	chr17	29400541	29401611	-161
Ddhd2	NM_028102	chr8	26864667	26865157	-161
Taf15	NM_027427	chr11	83286064	83286833	-161
Chaf1b	NM_028083	chr16	93883531	93884438	-161
Taf6	NM_009315	chr5	138628184	138628962	-160

Supplemental Table 2. Significant ChIP-seq E2F1 promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
2310001K24Rik	NR_028122	chr2	163297647	163298594	-160
Casp8ap2	NM_001122978	chr4	32701890	32702685	-160
Nfatc2ip	NM_010900	chr7	133540095	133540724	-160
Nrm	NM_134122	chr17	35997727	35998479	-159
Cpd	NM_007754	chr11	76660422	76660913	-159
Zfp11	NM_172462	chr5	130175607	130176634	-159
Sel1l	NM_011344	chr12	93087300	93088206	-157
Tial1	NM_009383	chr7	135604744	135605622	-157
Mbd3	NM_013595	chr10	79862182	79862576	-156
Itprip	NM_001001738	chr19	47993444	47994444	-156
Slc16a10	NM_001114332	chr10	39861705	39862724	-156
Micall2	NM_174850	chr5	140211964	140212918	-155
Alg12	NM_001142357	chr15	88649455	88650348	-155
Slc2a6	NM_172659	chr2	26883417	26883926	-155
Abcd1	NM_007435	chrX	70961388	70962173	-155
Tango2	NM_138583	chr16	18343828	18344528	-154
Mrpl17	NM_025301	chr7	112959411	112960097	-154
Capzb	NM_001037761	chr4	138748240	138749079	-154
Dlc1	NM_015802	chr8	37676764	37677535	-154
Gtl3	NM_008187	chr8	97958561	97959282	-154
Usp28	NM_175482	chr9	48793025	48793646	-154
Zfp59	NM_011762	chr7	28623226	28623672	-153
Plk1	NM_011121	chr7	129302429	129303165	-153
Kank2	NM_145611	chr9	21602873	21603411	-153
Ptges3	NM_019766	chr10	127495137	127496633	-152
Ccnf	NM_007634	chr17	24388024	24388986	-152
Samd14	NM_146025	chr11	94870749	94871332	-152
Zc3h14	NM_001160107	chr12	99984836	99985215	-152
Nup50	NM_016714	chr15	84753354	84754057	-152
Mir219c	NR_106154	chr17	34161511	34162098	-152
Ap5z1	NM_172725	chr5	142939348	142940117	-152
Upf2	NM_001081132	chr2	5872034	5872692	-151
Scaf1	NM_001008422	chr7	52271519	52272019	-151
Cenpu	NM_027973	chr8	47636998	47637544	-151
Wsb1	NM_019653	chr11	79067919	79068774	-151
Xrcc3	NM_028875	chr12	113051861	113052542	-151
Dis3	NM_028315	chr14	99498751	99499526	-151
Klf5	NM_009769	chr14	99697230	99698287	-151
Gnb2	NM_010312	chr5	137974273	137974940	-151
Cdc25a	NM_007658	chr9	109777401	109778462	-151
Uspl1	NM_001013378	chr5	149995615	149996357	-149
Arid3a	NM_007880	chr10	79389231	79390046	-149
Cluap1	NM_029738	chr16	3908587	3909132	-149
Pcolce	NM_008788	chr5	138052567	138052992	-149
Tra2b	NM_009186	chr16	22265602	22266695	-148
Cpne2	NM_153507	chr8	97056467	97057092	-148
Setd6	NM_001035123	chr8	98239343	98239986	-148
Sept7	NM_009859	chr9	25059525	25060258	-148

Supplemental Table 2. Significant ChIP-seq E2F1 promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Lrfn4	NM_153388	chr19	4615548	4616078	-147
Qrich1	NM_001114119	chr9	108418925	108419615	-147
Hist1h4a	NM_178192	chr13	23852681	23853846	-147
Arl6ip6	NM_022989	chr2	53050537	53051405	-146
Ung	NM_011677	chr5	114580662	114581374	-146
Cyp39a1	NM_001285948	chr17	43803926	43804423	-146
Tex9	NM_009359	chr9	72339573	72340248	-146
Hist1h4c	NM_178208	chr13	23790261	23790681	-145
1810043G02Rik	NM_026431	chr10	77440970	77441529	-145
Cdkn1a	NM_007669	chr17	29230076	29231068	-144
Topbp1	NM_176979	chr9	103207347	103207677	-144
Mdh1	NM_008618	chr11	21471419	21472740	-144
Slc25a37	NM_026331	chr14	69902934	69903671	-144
A630020A06	NR_045740	chr15	3945389	3946401	-143
Gm20753	NR_040630	chr1	108067884	108068601	-143
Ddost	NM_007838	chr4	137860203	137860816	-143
Esyt1	NM_011843	chr10	127962773	127963338	-142
Smc4	NM_133786	chr3	68808305	68809198	-142
Exoc4	NM_009148	chr6	33198549	33199466	-142
Nagk	NM_019542	chr6	83744560	83745257	-142
Cc2d1a	NM_145970	chr8	86671376	86672209	-142
Calr	NM_007591	chr8	87370601	87371340	-142
Usp32	NM_001029934	chr11	84953200	84953992	-140
Tmem43	NM_028766	chr6	91423268	91423940	-140
Iqgap1	NM_016721	chr7	87948102	87948609	-140
Rrs1	NM_021511	chr1	9535133	9535565	-139
Spag5	NM_017407	chr11	78114621	78115285	-139
Rprd1b	NM_001291135	chr2	157853632	157854554	-139
Coq2	NM_027978	chr5	101103212	101103614	-139
Mad1l1	NM_010752	chr5	140797238	140798050	-139
Far1	NM_001285831	chr7	120656898	120657518	-139
Fam122b	NM_001166583	chrX	50622929	50623310	-139
Scamp3	NM_011886	chr3	88981029	88981507	-138
Cpsf6	NM_001013391	chr10	116813713	116814618	-138
Mapk14	NM_011951	chr17	28827697	28828600	-138
Psme3	NM_011192	chr11	101177073	101177782	-137
Zfp7	NM_145916	chr15	76709307	76709830	-137
Cdk5rap2	NM_145990	chr4	70071164	70071909	-137
Diablo	NM_023232	chr5	123973936	123974681	-137
1200014J11Rik	NM_025818	chr11	72860995	72861471	-135
Bard1	NM_007525	chr1	71149400	71149959	-135
Nucks1	NM_001145804	chr1	133806635	133807165	-134
Pigm	NM_026234	chr1	174306205	174306849	-134
Map3k2	NM_011946	chr18	32322422	32322794	-134
Uhrf2	NM_144873	chr19	30104547	30105189	-134
Pdrg1	NM_178939	chr2	152840913	152841591	-134
Zfp689	NM_175163	chr7	134592597	134593013	-134
Fyn	NM_008054	chr10	39089292	39089649	-134

Supplemental Table 2. Significant ChIP-seq E2F1 promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Fam86	NM_027446	chr16	5255869	5256494	-134
Rmi2	NM_001162932	chr16	10834648	10835387	-134
Nfe2l2	NM_010902	chr2	75542515	75543146	-134
Pars2	NM_001285783	chr4	106323003	106324077	-133
Gpbp1l1	NM_029868	chr4	116229754	116230642	-133
Slc7a1	NM_007513	chr5	149211266	149211958	-133
B3gnt2	NM_016888	chr11	22759651	22760082	-133
Trappc6a	NM_025960	chr7	20093603	20094286	-133
Sc5d	NM_172769	chr9	42072198	42072831	-133
Cenpm	NM_001080158	chr15	82074376	82075418	-132
Birc6	NM_007566	chr17	74927127	74927878	-132
Rragc	NM_017475	chr4	123594155	123594932	-132
Nktr	NM_010918	chr9	121627939	121628394	-132
Elmo2	NM_207706	chr2	165151506	165152712	-131
1700012D14Rik	NR_015573	chr7	118266006	118266632	-131
St3gal1	NM_009177	chr15	67008271	67008876	-131
Morn1	NM_001081100	chr4	154460211	154460898	-131
Specc1l	NM_153406	chr10	74674517	74674857	-130
Stom	NM_013515	chr2	35192420	35192896	-130
Hnrnph2	NM_019868	chrX	131135424	131135964	-130
Gm14634	NR_045852	chrX	12338831	12339717	-129
Apoo	NM_026673	chrX	91612065	91612573	-129
Larp4b	NM_172585	chr13	9092748	9093295	-129
Suds3	NM_001122666	chr5	117565813	117566446	-129
Rwdd1	NM_025614	chr10	33739307	33739791	-128
Espl1	NM_001014976	chr15	102125955	102127235	-128
Dnajc30	NM_025362	chr5	135539551	135540343	-128
Arrb2	NM_145429	chr11	70245491	70246416	-128
Vash2	NR_027352	chr1	192803023	192803579	-127
Inpp5k	NM_008916	chr11	75444179	75444609	-127
Nutf2	NM_026532	chr8	108384028	108384784	-127
Ranbp2	NM_011240	chr10	57909057	57909888	-127
Fdxr	NM_007997	chr11	115138131	115138686	-127
Rad21	NM_009009	chr15	51823090	51823773	-127
Ugp2	NM_001290634	chr11	21271165	21271625	-126
Phf23	NM_030064	chr11	69808807	69809475	-126
Gart	NM_010256	chr16	91647050	91647633	-126
Snai2	NM_011415	chr16	14705470	14706182	-125
Cep85	NM_144527	chr4	133742624	133743624	-125
Wdr48	NM_026236	chr9	119803660	119804114	-125
Mms19	NM_028152	chr19	42055351	42056148	-125
Cenpf	NM_001081363	chr1	191511775	191512401	-124
Trim24	NM_001272064	chr6	37820334	37821038	-124
Ticrr	NM_029835	chr7	86804579	86805335	-124
Ltv1	NM_181470	chr10	12912850	12913281	-124
Gpr180	NM_021434	chr14	118535835	118536614	-124
Prpsap1	NM_026364	chr11	116351572	116351992	-123
Mapre1	NM_007896	chr2	153566587	153567211	-123

Supplemental Table 2. Significant ChIP-seq E2F1 promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Zfp280b	NM_177475	chr10	75494817	75495650	-123
Timp2	NM_011594	chr11	118216573	118217120	-123
Myo1c	NM_008659	chr11	75464436	75465341	-122
Pik3c3	NM_181414	chr18	30432284	30432572	-121
Zbtb3	NM_133759	chr19	8876599	8877129	-121
Tbc1d1	NM_019636	chr5	64551083	64551671	-121
Lbr	NM_133815	chr1	183772345	183772958	-121
Wee1	NM_009516	chr7	117264895	117266008	-121
Aamp	NM_001190444	chr1	74330978	74331884	-120
Polg	NM_017462	chr7	86610997	86611559	-120
Tsnaxip1	NM_024445	chr8	108351180	108351866	-120
Rpl10	NM_052835	chrX	71515709	71516359	-120
P4hb	NM_011032	chr11	120434101	120434636	-120
Rpl35a	NM_001130485	chr16	33055938	33056899	-120
Wwtr1	NM_001168281	chr3	57379574	57380327	-120
Klhl21	NM_001033352	chr4	151382609	151383151	-119
Cdca4	NM_028023	chr12	114067430	114068005	-119
Pak4	NM_027470	chr7	29383071	29383570	-119
Gtf2e2	NM_001167921	chr8	34841970	34842563	-119
Suz12	NM_001163018	chr11	79806117	79806861	-118
Cdc6	NM_001025779	chr11	98768801	98769368	-118
Zmiz1	NM_183208	chr14	26278337	26278768	-118
Ezr	NM_009510	chr17	6986774	6987717	-118
Actl6a	NM_019673	chr3	32607006	32607693	-118
Cdc37	NM_016742	chr9	20954175	20954758	-118
9630033F20Rik	NM_177003	chr6	127059453	127059919	-117
Rpgrip1l	NM_173431	chr8	93836773	93837701	-117
Acsl3	NM_001033606	chr1	78653851	78654714	-117
Zfp706	NM_026521	chr15	36937048	36937497	-117
Slc33a1	NM_015728	chr3	63768286	63769255	-117
Naa10	NM_019870	chrX	71167207	71167590	-117
Strip2	NM_001037740	chr6	29866462	29867330	-116
Taok1	NM_144825	chr11	77421137	77421726	-116
Ppp1cc	NM_013636	chr5	122607897	122608446	-116
Dnajc13	NM_001163026	chr9	104164996	104165753	-116
Suv39h2	NM_022724	chr2	3392149	3392595	-115
Rps3a1	NM_016959	chr3	85946373	85947035	-115
Tubg1	NM_134024	chr11	100981061	100981598	-115
Thumpd2	NM_028138	chr17	81464219	81464858	-115
Tctn3	NM_026260	chr19	40686535	40687102	-115
Cdk4	NM_009870	chr10	126499940	126501148	-114
Snord104	NR_030703	chr11	106361743	106362638	-114
Rsrp1	NM_023665	chr4	134479251	134479600	-114
9430015G10Rik	NM_145557	chr4	155483720	155484265	-114
Bbs7	NM_027810	chr3	36512128	36512718	-113
Dnmt1	NM_001199433	chr9	20756810	20757548	-113
Slc25a5	NM_007451	chrX	34335224	34335842	-113
Ppia	NM_008907	chr11	6315477	6316042	-113

Supplemental Table 2. Significant ChIP-seq E2F1 promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Tnfaip8l1	NM_025566	chr17	56301524	56302077	-113
Ccng2	NM_007635	chr5	93696082	93696889	-113
Zfp9	NM_011763	chr6	118429128	118429677	-113
Kif23	NM_024245	chr9	61794264	61795171	-113
Rc3h1	NM_001024952	chr1	162836152	162836707	-112
Ctsd	NM_009983	chr7	149573700	149574071	-112
Morf4l2	NM_001168229	chrX	133275810	133276193	-112
Pdxp	NM_020271	chr15	78744054	78744420	-111
Fam98b	NM_026620	chr2	117074929	117075797	-111
Kif24	NM_024241	chr4	41411639	41412343	-111
Adam10	NM_007399	chr9	70526346	70527048	-110
Rtkn2	NM_001081346	chr10	67441772	67442699	-110
Rad17	NM_001283011	chr13	101420737	101421512	-110
Snd1	NM_019776	chr6	28429920	28430555	-110
Ccdc130	NM_026350	chr8	86794137	86794682	-110
Nupl1	NM_170591	chr14	60869886	60870760	-109
Rad51ap1	NM_009013	chr6	126889101	126890261	-109
Ppp3r1	NM_024459	chr11	17058896	17059487	-109
Nup85	NM_001002929	chr11	115425009	115426288	-109
Gtf2b	NM_145546	chr3	142427890	142428313	-109
Arhgap24	NM_029270	chr5	102910046	102910555	-109
Ttc16	NM_001290564	chr2	32630699	32631233	-108
Pank2	NM_153501	chr2	131087880	131088374	-108
Rps20	NM_026147	chr4	3762411	3763297	-108
Megf9	NM_172694	chr4	70195845	70196293	-108
2700038G22Rik	NR_045042	chr5	23356135	23356477	-108
Mrpl10	NM_026154	chr11	96902479	96903104	-108
Zmynd19	NM_026021	chr2	24805016	24805411	-108
Mbd5	NM_029924	chr2	48804728	48805111	-108
E2f1	NM_007891	chr2	154395235	154396234	-108
Cks1b	NM_016904	chr3	89221989	89222650	-108
Sf3b3	NM_133953	chr8	113370460	113371159	-108
Lca5	NM_029434	chr9	83334530	83335151	-108
Tbccd1	NM_001081368	chr16	22857505	22857991	-107
Rpl3	NM_013762	chr15	79913671	79914212	-107
Pomt2	NM_153415	chr12	88488649	88489265	-106
Adk	NM_001243041	chr14	21894878	21895656	-106
Myh9	NM_022410	chr15	77672044	77673376	-106
Axin1	NM_009733	chr17	26275179	26275869	-106
Prr14l	NM_194340	chr5	33196803	33197165	-106
Polr2a	NM_001291068	chr11	69572044	69572434	-105
9330151L19Rik	NR_033222	chr12	70297922	70298262	-105
Hmgb2	NM_008252	chr8	59989916	59991152	-105
Lnp	NM_027133	chr2	74416600	74417617	-105
Cenpi	NM_145924	chrX	130842289	130842904	-105
Ppwd1	NM_172807	chr13	105018541	105019513	-104
Wdr89	NM_028203	chr12	76770125	76771128	-104
Lrrfip1	NM_008515	chr1	92949296	92950539	-103

Supplemental Table 2. Significant ChIP-seq E2F1 promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Prkca	NM_011101	chr11	108205020	108205587	-103
Nup155	NM_133227	chr15	8058909	8059510	-103
Zfyve1	NM_183154	chr12	84937918	84938477	-102
4930427A07Rik	NM_134041	chr12	114394244	114394815	-102
Fads1	NM_146094	chr19	10256954	10257598	-101
Nup214	NM_172268	chr2	31829382	31830354	-101
Wdr20	NM_027149	chr12	111975818	111976297	-101
Cdca7l	NM_146040	chr12	119081806	119082659	-101
Bub1b	NM_009773	chr2	118423523	118424168	-101
Sfpq	NR_045010	chr4	126698166	126698721	-101
Dnajc8	NM_172400	chr4	132090972	132091774	-100
Fhod1	NM_177699	chr8	107871434	107872504	-100
Hnrnpa2b1	NM_016806	chr6	51419492	51420491	-100
Pelp1	NM_029231	chr11	70223242	70224020	-99
Pdia5	NM_028295	chr16	35490656	35491458	-99
Spc25	NM_025565	chr2	69043912	69044778	-99
Nfyb	NM_010914	chr10	82226773	82227194	-99
Fam64a	NM_144526	chr11	71855563	71856246	-99
Tmem216	NM_001277861	chr19	10629972	10630729	-99
Ehd4	NM_133838	chr2	119980080	119980737	-99
Nup133	NM_172288	chr8	126473009	126473516	-99
Trp53inp2	NM_178111	chr2	155207281	155207705	-98
Sf1	NM_001110791	chr19	6363273	6363910	-98
Pdap1	NM_001033313	chr5	145900746	145901363	-98
Dpy19l4	NM_001081201	chr4	11249048	11249700	-97
Fbxw8	NM_172721	chr5	118605311	118605815	-97
Hps5	NM_001167864	chr7	54051017	54051677	-97
Arf1	NM_007476	chr11	59041595	59042134	-97
Zfr	NM_011767	chr15	12047236	12047781	-97
Frg1	NM_013522	chr8	42502191	42502944	-97
Tmem109	NM_134142	chr19	10956065	10956591	-96
Cdk1	NM_007659	chr10	68815505	68816004	-96
Alg8	NM_199035	chr7	104519506	104520555	-96
H2afx	NM_010436	chr9	44142351	44143053	-95
Glb1	NM_009752	chr9	114309781	114310419	-95
Mpv17l2	NM_183170	chr8	73284535	73285292	-95
Heatr3	NM_172757	chr8	90661426	90661951	-95
Fancm	NM_178912	chr12	66176176	66176820	-94
Sf3b2	NM_030109	chr19	5295039	5296057	-94
Pip5k1a	NM_001293707	chr3	94910716	94911173	-94
Uck2	NM_030724	chr1	169215043	169215657	-93
Eif4a2	NM_001123038	chr16	23106916	23107978	-93
Ifrd2	NM_025903	chr9	107489530	107490380	-93
Zfp574	NM_001168506	chr7	25861896	25862365	-93
Ylpm1	NM_178363	chr12	86336941	86337415	-92
Zfand2a	NM_001159908	chr5	139960316	139960755	-92
Mrpl12	NM_027204	chr11	120345573	120346210	-91
Pafah2	NM_133880	chr4	133951873	133952414	-91

Supplemental Table 2. Significant ChIP-seq E2F1 promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Mkrn2	NM_023290	chr6	115551569	115552160	-91
Stra13	NM_016665	chr11	120574708	120575632	-90
Rfc5	NM_028128	chr5	117838903	117839339	-90
Ccp110	NM_182995	chr7	125855833	125856235	-90
Rpsa	NM_011029	chr9	120036306	120037280	-90
Sec63	NM_153055	chr10	42480953	42481470	-90
Zdhhc12	NM_025428	chr2	29949043	29949444	-90
Sp3	NM_001018042	chr2	72818114	72819069	-90
Ttf2	NM_001013026	chr3	100773361	100773988	-90
Mcm5	NM_008566	chr8	77632770	77633903	-90
Lactb	NM_030717	chr9	66823096	66823663	-90
Ncapg2	NM_133762	chr12	117643453	117644117	-89
Nolc1	NM_053086	chr19	46149832	46150663	-89
Nipsnap3b	NM_025623	chr4	53024401	53025012	-89
Exosc6	NM_028274	chr8	113579934	113580365	-89
1600023N17Rik	NR_073433	chr5	46060570	46061498	-88
Wdr82	NM_029896	chr9	106072864	106073478	-88
Cluh	NM_001081158	chr11	74462673	74463144	-88
Tfrc	NM_011638	chr16	32608594	32609193	-88
Tcf19	NM_001163764	chr17	35653261	35654450	-88
Blvra	NM_026678	chr2	126895832	126896777	-88
Rngtt	NM_011884	chr4	33396847	33397548	-88
Akap11	NM_001164503	chr14	78936373	78937133	-87
Ncoa7	NM_172495	chr10	30522761	30523236	-87
Nedd1	NM_008682	chr10	92184792	92185705	-87
Hnrnpab	NM_010448	chr11	51420226	51420711	-87
Mzf1	NM_001290453	chr7	13640016	13640381	-87
C230052I12Rik	NM_178643	chr7	36181573	36182169	-86
Crkl	NM_001277231	chr16	17451661	17452322	-86
1110020A21Rik	NR_027930	chr17	85356865	85357404	-86
Cds2	NM_138651	chr2	132088358	132089237	-86
Sptssa	NM_134054	chr12	55757268	55758018	-85
Hsp90aa1	NM_010480	chr12	111934335	111935042	-85
Mlf1	NM_010801	chr3	67177624	67178243	-85
Kansl3	NM_172652	chr1	36425843	36426375	-84
B230219D22Rik	NM_181278	chr13	55793921	55794880	-84
Cnpy3	NM_028065	chr17	46888606	46889881	-84
Zc3h18	NM_001029994	chr8	124900263	124900600	-84
Ipo11	NM_029665	chr13	107726819	107727335	-83
Sgol1	NM_028232	chr17	53828315	53829129	-83
Cox8a	NM_007750	chr19	7291792	7292584	-83
Prpf19	NM_134129	chr19	10969452	10969822	-83
Clspn	NM_175554	chr4	126233618	126234662	-83
Rpia	NM_009075	chr6	70741792	70742710	-83
Rad54l	NM_001122959	chr4	115796135	115796617	-82
Nek4	NM_011849	chr14	31764281	31764902	-82
Cdca5	NM_026410	chr19	6084736	6085293	-82
Tmem50b	NM_030018	chr16	91597774	91598236	-81

Supplemental Table 2. Significant ChIP-seq E2F1 promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Zc3h6	NM_178404	chr2	128792751	128793361	-81
Klhl18	NM_177771	chr9	110379052	110379504	-81
3110082I17Rik	NM_028469	chr5	139936302	139936833	-81
Ewsr1	NM_007968	chr11	4998779	4999561	-80
Mrps17	NM_025450	chr5	130221170	130221474	-80
Nap1l4	NM_001285489	chr7	150734852	150735356	-80
Kdm6a	NM_009483	chrX	17739396	17740028	-80
Mapk9	NM_016961	chr11	49659823	49660522	-80
Gchfr	NM_177157	chr2	118993220	118993667	-80
Abhd2	NM_018811	chr7	86417783	86418360	-80
Lpar2	NM_020028	chr8	72346060	72346707	-80
Gtf2h4	NM_010364	chr17	35810483	35810927	-79
2700029M09Rik	NM_028299	chr8	63368869	63369467	-79
Smarcc1	NM_009211	chr9	110034090	110034808	-78
Zfp143	NM_009281	chr7	117204644	117205631	-78
Micu1	NM_001291442	chr10	59164893	59165573	-77
2410006H16Rik	NR_030738	chr11	62415982	62416620	-77
Gfod1	NM_001033399	chr13	43399416	43399818	-77
Gadd45g	NM_011817	chr13	51941601	51942331	-77
Mapk1ip1l	NM_178684	chr14	47917614	47918208	-77
Cdh24	NM_199470	chr14	55260063	55260490	-77
Ltn1	NM_001081068	chr16	87432475	87433378	-77
Plekhf2	NM_175175	chr4	10934483	10935200	-77
Ets1	NM_001038642	chr9	32503138	32503961	-77
Tuba1a	NM_011653	chr15	98783575	98784437	-75
Sssca1	NM_020491	chr19	5731576	5732036	-75
Slc4a1ap	NM_009206	chr5	31828832	31829752	-75
Arf6	NM_007481	chr12	70472768	70473355	-75
Cenpp	NM_025495	chr13	49747936	49748411	-75
Fbxl6	NM_013909	chr15	76368908	76369591	-75
Cers5	NM_028015	chr15	99602786	99603253	-75
Fscn1	NM_007984	chr5	143721741	143722177	-74
Dopey2	NM_027293	chr16	93711796	93712359	-74
Coro1b	NM_011778	chr19	4148419	4148758	-74
Hells	NM_008234	chr19	39005255	39005556	-74
Alms1	NM_145223	chr6	85537255	85537646	-74
Papola	NM_011112	chr12	107022524	107023152	-73
Oip5	NM_001042653	chr2	119444034	119444591	-73
Lpar1	NM_010336	chr4	58566093	58566776	-73
Hat1	NM_026115	chr2	71226693	71227795	-72
St3gal3	NM_009176	chr4	117807391	117807853	-72
Gipc1	NM_018771	chr8	86176121	86176887	-72
Mon2	NM_001163025	chr10	122513312	122513951	-72
Nop56	NM_024193	chr2	130099743	130100408	-72
Rapgef6	NM_001252494	chr11	54335972	54336578	-71
Tpk1	NM_013861	chr6	43615916	43616572	-71
Eif3k	NM_028659	chr7	29766793	29767161	-71
B4galt7	NM_146045	chr13	55701012	55701789	-71

Supplemental Table 2. Significant ChIP-seq E2F1 promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
S1pr2	NM_010333	chr9	20780715	20781898	-71
4933433G15Rik	NR_040719	chr9	75257576	75258263	-71
Snx3	NM_017472	chr10	42221319	42222259	-70
Numb	NR_073563	chr12	85262687	85263219	-70
Ccno	NM_001081062	chr13	113777511	113778367	-70
Fam118a	NM_133750	chr15	84866915	84867927	-70
Stk35	NM_183262	chr2	129625958	129626406	-70
Alg14	NM_024178	chr3	120994419	120994909	-70
Cdc42	NM_009861	chr4	136913570	136913915	-70
Fanca	NM_016925	chr8	125842188	125842901	-70
Them4	NM_029431	chr3	94113706	94114263	-69
Plekha1	NM_133942	chr7	138009098	138009611	-69
Rtn4	NM_194054	chr11	29592414	29593244	-68
Cnot1	NM_001205226	chr8	98330951	98331907	-68
Glyr1	NM_028720	chr16	5049785	5050354	-68
Rint1	NM_177323	chr5	23293160	23293827	-68
Lpcat3	NM_145130	chr6	124612787	124613320	-68
Bambi	NM_026505	chr18	3507562	3508213	-67
Paxip1	NM_018878	chr5	28117884	28118427	-67
Ostf1	NM_017375	chr19	18706136	18706600	-66
Tcerg1	NM_001289526	chr18	42670767	42671382	-66
Zgrf1	NM_197997	chr3	127255878	127256803	-66
Syne3	NM_172500	chr12	106247870	106248296	-65
Ptplb	NM_023587	chr16	35022046	35022836	-65
Mid1ip1	NM_026524	chrX	10293916	10294934	-65
Brca2	NM_009765	chr5	151324681	151325580	-65
Mbd4	NM_010774	chr6	115802924	115803921	-65
Mrps9	NM_023514	chr1	42907719	42908308	-64
Smarcd2	NM_001130187	chr11	106133975	106134722	-64
Ccdc97	NM_028771	chr7	26503924	26504345	-64
Spsb3	NM_001163750	chr17	25023108	25024002	-63
Zfyve19	NM_001164827	chr2	119033857	119034927	-63
Helq	NM_001081107	chr5	101227408	101227954	-63
Fam192a	NM_028221	chr8	97125301	97126075	-63
Stard4	NM_133774	chr18	33373307	33373756	-63
Bub1	NM_009772	chr2	127657244	127658069	-63
Hist1h3c	NM_175653	chr13	23837205	23837697	-62
Pbk	NM_023209	chr14	66424240	66425130	-62
Ppm1g	NM_008014	chr5	31522725	31523233	-62
Prr11	NM_175563	chr11	86921851	86922702	-62
Map1lc3a	NM_025735	chr2	155101800	155102275	-62
Fan1	NM_177893	chr7	71518790	71519293	-62
Dcaf15	NM_172502	chr8	86628505	86628938	-62
Rqcd1	NM_021383	chr1	74551857	74553287	-61
Zfp763	NM_028543	chr17	33170150	33170622	-61
4930465K10Rik	NR_027978	chr18	77952619	77953103	-61
Msmo1	NM_025436	chr8	67212249	67212621	-61
Dock7	NM_026082	chr4	98787505	98787826	-61

Supplemental Table 2. Significant ChIP-seq E2F1 promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
2610002J02Rik	NM_001190445	chr4	154623469	154624558	-61
Sh2b2	NM_018825	chr5	136720569	136721096	-61
4632427E13Rik	NR_015510	chr7	99889599	99890458	-61
Dap3	NM_001164533	chr3	88753978	88754548	-60
Wbscr17	NM_145218	chr5	131782686	131784216	-60
Tex30	NM_029368	chr1	44159000	44159583	-60
1700020I14Rik	NR_015473	chr2	119419460	119420483	-60
Cntln	NM_175275	chr4	84529857	84530448	-60
Gnb2l1	NM_008143	chr11	48613334	48614270	-59
Iscu	NM_025526	chr5	114222500	114223022	-59
D2Wsu81e	NM_172660	chr2	30033872	30034201	-59
Pigu	NM_001004721	chr2	155182940	155183495	-59
Nkiras2	NM_028024	chr11	100484014	100484406	-58
Enpp4	NM_199016	chr17	44242524	44243104	-58
Kif5b	NM_008448	chr18	6241259	6241899	-58
Ssrp1	NM_001136081	chr2	84877062	84878037	-58
Nampt	NM_021524	chr12	33504783	33505501	-57
Clasrp	NM_016680	chr7	20189583	20190163	-57
Rassf1	NM_019713	chr9	107456358	107457355	-57
5430402O13Rik	NR_015581	chr6	50516224	50516946	-56
Pold1	NM_011131	chr7	51803929	51804551	-56
Ints7	NM_178632	chr1	193399018	193400095	-56
Dcaf7	NM_027946	chr11	105897902	105898358	-55
Litaf	NM_019980	chr16	10992934	10993602	-55
Nfkbiz	NM_001159394	chr16	55822017	55822593	-55
Rps3	NM_012052	chr7	106631844	106632702	-55
Ralbp1	NM_001198949	chr17	66234021	66234612	-55
Gid8	NM_001289652	chr2	180444536	180445215	-55
Stard7	NM_139308	chr2	127095580	127096240	-54
Mta2	NM_011842	chr19	9016047	9016664	-54
Cntrl	NM_012018	chr2	34964705	34965210	-54
Fbxo25	NM_025785	chr8	13907482	13908021	-54
Dscr3	NM_007834	chr16	94747745	94748831	-53
Ctnnbl1	NM_025680	chr2	157562894	157563272	-53
Cep68	NM_172260	chr11	20149085	20149872	-53
Hiatl1	NM_133680	chr13	65213998	65214685	-53
9130023H24Rik	NM_177001	chr7	135381212	135381981	-53
Smc2	NM_008017	chr4	52451800	52452336	-52
Mon1a	NM_028369	chr9	107790267	107790547	-52
Rrm2	NM_009104	chr12	25392820	25393313	-52
Bpgm	NM_007563	chr6	34426068	34426539	-52
Cetn4	NM_145825	chr3	37210845	37211991	-51
Sae1	NM_001285892	chr7	16972910	16973680	-51
Slx1b	NM_029420	chr7	133839068	133839626	-51
Syn3	NM_013722	chr10	85961438	85961943	-51
Eif4g1	NM_145941	chr16	20672495	20673046	-51
Paqr4	NM_023824	chr17	23877117	23877576	-51
Top2a	NM_011623	chr11	98885278	98885826	-50

Supplemental Table 2. Significant ChIP-seq E2F1 promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Slc9a1	NM_016981	chr4	132925200	132926072	-50
1810014B01Rik	NR_015572	chr10	86148033	86148410	-50
Abcf1	NM_013854	chr17	36106447	36107040	-50
Ubxn6	NM_024432	chr17	56214267	56214654	-50
Arpc5l	NM_028809	chr2	38863366	38863852	-49
Kdsr	NM_027534	chr1	108656109	108656623	-48
Btg2	NM_007570	chr1	135975587	135975970	-48
Lims1	NM_026148	chr10	57785840	57786491	-48
Ndc80	NM_023294	chr17	71875808	71876679	-48
Tmco1	NM_001039483	chr1	169238334	169239172	-47
Mterfd2	NM_178051	chr1	95202229	95202756	-47
Eml6	NM_146016	chr11	29925868	29926289	-47
Ubxn1	NM_146093	chr19	8945758	8946245	-47
Extl3	NM_018788	chr14	65716747	65717229	-46
Cacul1	NM_001172097	chr19	60656570	60657371	-46
Rfc2	NM_020022	chr5	135058113	135058914	-46
Smim7	NM_172396	chr8	75094678	75095305	-46
Cmc2	NM_026844	chr8	119444883	119445878	-46
Dtymk	NM_001105667	chr1	95698209	95698901	-45
Abhd12	NM_024465	chr2	150730166	150730855	-45
Casp2	NM_007610	chr6	42214636	42215350	-44
Ufsp2	NM_138668	chr8	47060433	47061241	-44
Ttll12	NM_183017	chr15	83425392	83425867	-44
Cdkn2aipnl	NM_029976	chr11	51780819	51781359	-43
Gpatch8	NM_001159492	chr11	102417080	102417948	-43
2900076A07Rik	NR_045299	chr7	88668008	88668776	-43
Fam111a	NM_026640	chr19	12647709	12648234	-43
Eri3	NM_001285901	chr4	117222706	117223065	-43
Peak1	NM_172924	chr9	56265579	56266218	-43
Tmem209	NM_178625	chr6	30459287	30460205	-41
Nsmce1	NM_026330	chr7	132634857	132635335	-41
Mpdu1	NM_011900	chr11	69475835	69476532	-41
Ppp1r16a	NM_033371	chr15	76501812	76502325	-41
Pcbp3	NM_021568	chr10	76424422	76425040	-40
Npm1	NM_001252260	chr11	33063036	33063454	-40
Slc39a13	NM_026721	chr2	90910179	90910843	-40
Mycbp	NM_019660	chr4	123581986	123582444	-40
Msh3	NM_010829	chr13	93124744	93125249	-40
Nubp1	NM_011955	chr16	10411380	10412601	-40
Id1	NM_010495	chr2	152561616	152562277	-40
Magoh	NM_001282737	chr4	107551939	107552700	-40
Arv1	NM_026855	chr8	127245495	127246502	-40
Pim3	NM_145478	chr15	88692272	88692896	-39
Hist2h4	NM_033596	chr3	96067002	96067554	-39
Gps2	NM_019726	chr11	69727314	69727995	-39
Fbxo5	NM_025995	chr10	4540176	4541898	-38
Alkbh7	NM_027372	chr17	57136462	57136984	-38
Ascc3	NM_198007	chr10	50311912	50312961	-38

Supplemental Table 2. Significant ChIP-seq E2F1 promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Dctpp1	NM_023203	chr7	134403767	134404668	-38
Xpo6	NM_028816	chr7	133343725	133344191	-37
Cdk2	NM_016756	chr10	128141876	128142409	-37
Zbtbd6	NM_001034882	chr14	79851422	79851787	-37
Rsl1d1	NM_025546	chr16	11202989	11203852	-37
Atf6b	NM_017406	chr17	34783868	34784239	-37
Gm2a	NM_010299	chr11	54911218	54911683	-36
Mtmr4	NM_133215	chr11	87405067	87406298	-36
Lsm8	NM_133939	chr6	18798182	18799015	-36
Nbeal2	NM_183276	chr9	110556481	110556918	-36
Fam109a	NM_175474	chr5	122298798	122299204	-35
Ppp6r1	NM_172894	chr7	4610295	4610877	-35
Pola2	NM_008893	chr19	5963741	5964738	-35
Fau	NM_001160239	chr19	6057334	6058371	-35
Ccdc134	NM_172428	chr15	81957841	81958793	-34
Vmp1	NM_029478	chr11	86496977	86497736	-34
Sap30bp	NM_020483	chr11	115794729	115795148	-34
Chchd3	NM_025336	chr6	33009956	33010413	-34
Mcmbp	NM_145955	chr7	135883501	135884449	-33
2810417H13Rik	NM_026515	chr9	65737898	65738294	-33
Chchd1	NM_025366	chr14	21521781	21522650	-33
Ncaph	NM_144818	chr2	126959295	126960148	-33
Nsl1	NM_198654	chr1	192886638	192887096	-32
Bsg	NM_001077184	chr10	79166564	79167576	-32
Rbm25	NM_027349	chr12	84972892	84973410	-32
Eef1d	NM_001285434	chr15	75739354	75740256	-32
Hsp90b1	NM_011631	chr10	86167866	86168573	-32
Anapc1	NM_008569	chr2	128512667	128513656	-32
Cep250	NM_001130000	chr2	155781697	155782826	-32
Hk2	NM_013820	chr6	82724066	82724891	-32
Hmbs	NM_013551	chr9	44152173	44152510	-32
Tmem194	NM_001113211	chr10	127113575	127114603	-31
Psmb7	NM_011187	chr2	38499118	38499794	-31
Rgp1	NM_172866	chr4	43591215	43591935	-31
Fh1	NM_010209	chr1	177555516	177556075	-31
Skp2	NM_013787	chr15	9069715	9070764	-31
Pyroxd1	NM_183165	chr6	142293914	142294457	-31
Chtf18	NM_145409	chr17	25863957	25864821	-30
Qsox2	NM_153559	chr2	26092741	26093197	-30
Cops6	NM_012002	chr5	138601947	138602652	-30
4930429F24Rik	NR_040734	chr9	79641031	79641804	-30
Sipa1	NM_001164568	chr19	5663584	5663886	-29
Hnrnpd	NM_007516	chr5	100407578	100408392	-29
2010320M18Rik	NR_029440	chr8	73300405	73301057	-29
Pias1	NM_019663	chr9	62828313	62829115	-29
Ostm1	NM_172416	chr10	42398429	42398956	-29
Adprh	NM_007414	chr16	38452554	38453039	-29
Sbno2	NM_183426	chr10	79564971	79565977	-28

Supplemental Table 2. Significant ChIP-seq E2F1 promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Kif18a	NM_139303	chr2	109120671	109121061	-28
Zbtb5	NM_173399	chr4	45025052	45025570	-28
Nop2	NM_138747	chr6	125081600	125082144	-28
Nr1h2	NM_009473	chr7	51809094	51809630	-28
Racgap1	NM_001253808	chr15	99481916	99482311	-28
Clhc1	NM_001081099	chr4	134066495	134067276	-28
Zfp111	NM_019940	chr7	24992979	24993410	-28
Daxx	NM_001199733	chr17	34046164	34046872	-27
Aifm1	NM_012019	chrX	45866565	45866967	-27
Pold2	NM_008894	chr11	5778020	5778549	-27
Rxrb	NM_001205214	chr17	34168375	34169084	-27
Haus6	NM_173400	chr4	86257634	86258269	-27
Chd4	NM_145979	chr6	125045838	125046469	-27
Ruvbl2	NM_011304	chr7	52689482	52690237	-27
Timm17b	NM_011591	chrX	7476146	7476847	-27
Anapc11	NM_001038230	chr11	120459580	120460058	-26
Atp6v0e	NM_025272	chr17	26813156	26813472	-26
Slc25a16	NM_175194	chr10	62383182	62383528	-25
Ndnl2	NM_023239	chr7	72017704	72018196	-25
Sos1	NM_009231	chr17	80879550	80880083	-25
Cotl1	NM_028071	chr8	122364345	122364660	-25
Pkm	NM_001253883	chr9	59503858	59504441	-25
Golim4	NM_001291069	chr3	75760512	75761276	-24
Wdr83	NM_026399	chr8	87604505	87604831	-24
Serhl	NM_023475	chr15	82930317	82930904	-24
Igf2r	NM_010515	chr17	12962375	12962814	-24
Sp9	NM_001005343	chr2	73109761	73110156	-24
Gja1	NM_010288	chr10	56096871	56097294	-23
Xpot	NM_001081056	chr10	121062973	121063814	-23
Fastkd3	NM_027123	chr13	68720769	68721434	-23
Fra10ac1	NM_001081075	chr19	38298358	38298929	-23
Fam172a	NM_138312	chr13	77847450	77848406	-22
Fdps	NM_134469	chr3	88905478	88906342	-22
Vamp3	NM_009498	chr4	150431775	150432391	-22
Sgol2	NM_199007	chr1	58052315	58053276	-22
Pfas	NM_001159519	chr11	68821600	68822365	-22
Ppif	NM_134084	chr14	26513345	26513922	-22
Gtf2h3	NM_181410	chr5	125028961	125029308	-22
Cnksr3	NM_172546	chr10	3133934	3134630	-21
Rnf217	NM_001146349	chr10	31329318	31329784	-21
Cmss1	NM_025599	chr16	57606582	57607418	-21
Ints8	NM_178112	chr4	11181272	11181580	-21
Chmp2a	NM_026885	chr7	13619846	13620446	-21
Nup205	NM_027513	chr6	35127374	35127815	-21
Prdx4	NM_016764	chrX	151772833	151773199	-20
Tssc4	NM_138631	chr7	150254903	150255602	-20
Dnajb1	NM_018808	chr8	86131399	86132708	-20
Stpg2	NM_198659	chr3	138868549	138869125	-19

Supplemental Table 2. Significant ChIP-seq E2F1 promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Ahdc1	NM_146155	chr4	132567155	132567647	-19
Gatsl2	NM_030719	chr5	134575205	134575991	-19
Kdm3a	NM_173001	chr6	71582451	71582945	-19
Tmpo	NM_001283048	chr10	90632944	90633681	-19
Wapal	NM_001004436	chr14	35486722	35487467	-19
Epb4.1	NM_001128607	chr4	131630979	131631511	-18
Snrnp48	NM_026382	chr13	38296276	38297304	-17
Chaf1a	NM_013733	chr17	56179450	56180192	-17
Zfp568	NM_001167872	chr7	30768640	30769272	-17
Apex2	NM_029943	chrX	147022453	147022963	-17
Snora78	NR_028515	chr17	24856524	24857061	-17
Cebpa	NM_007678	chr7	35904002	35904587	-17
Rad54b	NM_001039556	chr4	11485813	11486287	-16
Gak	NM_001282052	chr5	109058520	109059102	-16
Dennd6b	NM_027081	chr15	89026663	89027176	-16
Nuak2	NM_001195025	chr1	134212408	134212964	-15
Rpl37	NM_026069	chr15	5066198	5066996	-15
Mrps34	NM_023260	chr17	25031752	25032346	-15
Mvb12a	NM_028617	chr8	74066399	74067227	-15
Midn	NM_021565	chr10	79610693	79611346	-15
Rabl6	NM_001024616	chr2	25463585	25464374	-15
Rpa1	NM_001164223	chr11	75161557	75162239	-14
D11Wsu47e	NM_177777	chr11	113545308	113546114	-14
Phgdh	NM_016966	chr3	98143741	98144069	-14
H2afz	NM_016750	chr3	137527158	137527714	-14
Poln	NM_001289803	chr5	34511893	34512483	-14
Brpf1	NM_030178	chr6	113256720	113257512	-14
Ogg1	NM_010957	chr6	113276618	113277292	-14
Hnrnpk	NM_025279	chr13	58503468	58504311	-14
Rnd1	NM_172612	chr15	98507377	98508432	-14
Rbl1	NM_011249	chr2	157029634	157030931	-14
Rfc3	NM_027009	chr5	152453614	152453977	-14
Rad50	NM_009012	chr11	53520340	53521325	-13
Dlst	NM_030225	chr12	86451478	86452061	-13
Cep70	NM_023873	chr9	99143597	99144150	-13
Hmg20b	NM_010440	chr10	80812650	80813715	-12
Hist1h2ad	NM_178188	chr13	23666062	23666413	-12
Wdr91	NM_001013366	chr6	34860677	34861006	-12
Nudt7	NM_001290180	chr8	116657245	116657678	-12
Cnot6	NM_212484	chr11	49525856	49526612	-11
Atad5	NM_001029856	chr11	79902622	79903158	-11
B2m	NM_009735	chr2	121973224	121973598	-11
Wrn	NM_001122822	chr8	34495727	34496291	-11
Snrpf	NM_027246	chr10	93052230	93052595	-11
Msh5	NM_001146215	chr17	35183040	35184315	-11
Pagr1a	NM_030240	chr7	134160374	134161377	-11
Nsun5	NM_145414	chr5	135845356	135846268	-10
Zfp526	NM_175436	chr7	26006172	26006746	-10

Supplemental Table 2. Significant ChIP-seq E2F1 promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Trim59	NM_025863	chr3	68848228	68849117	-10
Cpsf3l	NM_028020	chr4	155243422	155243910	-9
Gm6297	NR_077221	chr4	40669104	40669610	-8
Timm50	NM_025616	chr7	29096823	29097321	-8
Cep57l1	NM_029132	chr10	41528983	41529968	-8
Fam208a	NM_028945	chr14	28241676	28242373	-8
Dnase1l1	NM_027109	chrX	71526799	71527364	-8
Brd8	NM_030147	chr18	34784164	34784882	-7
Bbip1	NM_001195348	chr19	54018911	54019335	-7
Pex11b	NR_027845	chr3	96438816	96439728	-7
F3	NM_010171	chr3	121426180	121426714	-7
Fyttd1	NM_027226	chr16	32877633	32878092	-7
Spdya	NM_029254	chr17	71901199	71901588	-7
Ythdf2	NM_145393	chr4	131767886	131768467	-7
Arhgap33	NM_001289682	chr7	31319590	31320579	-7
Diap3	NM_019670	chr14	87540246	87541606	-6
Rnf219	NM_026047	chr14	104921629	104922147	-6
Tsc2	NM_011647	chr17	24769350	24769804	-6
Nfkbil1	NM_010909	chr17	35372485	35373045	-6
Cdc123	NM_133837	chr2	5765757	5766265	-6
Wdsub1	NM_028118	chr2	59720221	59721115	-6
Gtf3c4	NM_001166033	chr2	28695426	28696343	-6
Irf2bp1	NM_178757	chr7	19589091	19589724	-6
Faf2	NM_178397	chr13	54722756	54723522	-5
Wdr34	NM_001008498	chr2	29903873	29904933	-5
Gtpbp6	NM_145147	chr5	110536950	110537490	-5
Smg9	NM_028047	chr7	25184303	25184979	-5
Tecr	NM_134118	chr8	86118038	86118750	-5
Asxl2	NM_001270988	chr12	3426554	3427149	-5
Rfc4	NM_145480	chr16	23127632	23127981	-5
Dcaf12	NM_026893	chr4	41261693	41262182	-5
Tmem194b	NM_001142647	chr1	52687314	52687774	-4
Cep76	NM_001081073	chr18	67800724	67801262	-4
9430008C03Rik	NR_015463	chr2	158186931	158187565	-4
Cyr61	NM_010516	chr3	145312665	145313239	-4
Mcm6	NM_008567	chr1	130255906	130256565	-4
Amdhd2	NM_172935	chr17	24300482	24300923	-4
Arl4c	NM_177305	chr1	90598412	90599124	-3
Safb	NM_001163300	chr17	56723896	56724906	-3
Ect2	NM_001177625	chr3	27052556	27052999	-3
Prdx2	NM_011563	chr8	87493321	87493766	-3
Gcat	NM_001161712	chr15	78860992	78861610	-2
9230114K14Rik	NR_015537	chr5	52581631	52582203	-2
Polr1c	NM_009085	chr17	46384719	46385270	-2
Toe1	NM_026654	chr4	116479794	116480535	-2
Map4	NM_001205330	chr9	109833807	109834744	-2
Esco2	NM_028039	chr14	66452528	66453084	-1
Fbln1	NM_010180	chr15	85036079	85036793	-1

Supplemental Table 2. Significant ChIP-seq E2F1 promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Gspt1	NM_001130008	chr16	11254010	11254826	-1
Zfp169	NM_001164576	chr13	48608618	48608991	-1
Polh	NM_030715	chr17	46339011	46340136	-1
1700028E10Rik	NR_045700	chr5	152170777	152171720	-1
Hmg20a	NM_025812	chr9	56266272	56267031	-1
Cdan1	NM_026891	chr2	120557004	120557500	0
Scfd2	NM_001114660	chr5	74927502	74928030	0
Htra2	NM_019752	chr6	83004226	83004902	0
Edem1	NM_138677	chr6	108778340	108778928	0
Zfp386	NM_001286214	chr12	117285662	117286207	1
Ranbp1	NM_011239	chr16	18248386	18249185	1
Mthfd1	NM_138745	chr12	77355859	77356579	1
Skiv2l	NM_021337	chr17	34986814	34987480	1
Poli	NM_001289515	chr18	70689668	70690278	1
Ppat	NM_172146	chr5	77379986	77381216	1
Snrnp40	NM_025645	chr4	130037099	130037660	2
Mto1	NM_026658	chr9	78295788	78296247	2
Cct7	NM_007638	chr6	85401127	85401874	3
Huwe1	NM_021523	chrX	148237473	148238180	3
Shmt1	NM_009171	chr11	60624470	60625056	3
Golga1	NM_001290649	chr2	38920728	38921386	3
Zmym6	NM_177462	chr4	126754466	126754792	3
Anapc4	NM_024213	chr5	53225183	53225569	3
Fbxl8	NM_015821	chr8	107788280	107788820	3
Diap2	NM_172493	chrX	126283999	126284561	3
Sarnp	NM_025364	chr10	128258419	128259240	4
Abhd13	NM_026868	chr8	9977284	9978155	4
Dctn6	NM_001293759	chr8	35171481	35172042	4
Asf1b	NM_024184	chr8	86479124	86480067	4
Prim1	NM_008921	chr10	127452019	127452529	4
Pspc1	NM_025682	chr14	57396912	57397384	4
Setdb2	NM_001081024	chr14	60059513	60059905	4
Tmbim6	NM_001171034	chr15	99223167	99223595	4
E4f1	NM_007893	chr17	24591884	24592618	4
Banf1	NM_011793	chr19	5366400	5367342	4
Mitd1	NM_026913	chr1	37947003	37947498	5
Hist1h1c	NM_015786	chr13	23830515	23830844	5
Pole4	NM_025882	chr6	82602493	82603214	5
Gstm1	NM_010358	chr3	107820597	107821173	5
Jade1	NM_001130186	chr3	41368494	41369119	6
Ncbp1	NM_001033201	chr4	46151219	46151556	6
Fancd2	NM_001033244	chr6	113481253	113482108	6
Rbbp4	NM_009030	chr4	129012063	129013150	7
Csrp1	NM_007791	chr1	137625529	137626031	7
Canx	NM_001110500	chr11	50138743	50139591	7
Nans	NM_053179	chr4	46501974	46502440	7
Mtor	NM_020009	chr4	147822365	147823029	7
Ficd	NM_001010825	chr5	114185462	114186132	7

Supplemental Table 2. Significant ChIP-seq E2F1 promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Hjurp	NM_198652	chr1	90173642	90174649	8
Rft1	NM_177815	chr14	31467299	31467836	8
Cuta	NM_026948	chr17	27075861	27077088	8
Cdc5l	NM_152810	chr17	45570218	45571077	8
Itgb3bp	NM_026348	chr4	99495427	99496174	8
Cdkal1	NM_144536	chr13	29947066	29947830	8
Zfp382	NM_001081007	chr7	30906541	30907407	8
Gadd45b	NM_008655	chr10	80392341	80393346	9
Naa60	NM_029090	chr16	3884452	3884801	9
Stard6	NM_001289648	chr18	70631931	70632536	9
Mybl2	NM_008652	chr2	162879873	162880884	9
Nbn	NM_013752	chr4	15884882	15885361	9
Ccdc37	NM_173775	chr6	90378249	90378680	9
Slc17a5	NM_172773	chr9	78435557	78436128	9
Smdt1	NM_026914	chr15	82176111	82176857	9
Ccdc85b	NM_198616	chr19	5457289	5457817	9
Stil	NM_009185	chr4	114672376	114673086	9
Cep41	NM_031998	chr6	30643322	30644022	9
Bag3	NM_013863	chr7	135666863	135667347	9
Xrcc2	NM_020570	chr5	25211375	25211834	10
Sgms1	NM_001168526	chr19	32284994	32285990	10
Eya3	NM_210071	chr4	132194815	132195125	10
Rad18	NM_001167730	chr6	112646242	112647064	10
Anapc13	NM_181394	chr9	102528365	102528905	10
Eif4a3	NM_138669	chr11	119161054	119161637	11
Txndc16	NM_172597	chr14	45838648	45839467	11
Osmr	NM_011019	chr15	6823806	6824797	11
Cep192	NM_027556	chr18	67959471	67960070	11
Pan2	NM_001252327	chr10	127739973	127740830	12
Nr1d1	NM_145434	chr11	98636410	98636947	12
4933427E11Rik	NR_033197	chr15	74538848	74540356	12
Letm1	NM_019694	chr5	34125074	34125606	12
Azi2	NM_001286507	chr9	117949285	117950017	12
A230072C01Rik	NR_027446	chrX	20538993	20539509	12
0610010K14Rik	NM_001177603	chr11	70051018	70051787	13
Rgmb	NM_178615	chr17	15963280	15963793	13
Arhgap19	NM_001163495	chr19	41876161	41876960	13
Zwilch	NM_026507	chr9	64020489	64020960	13
Lin52	NM_173756	chr12	85792254	85792686	13
Ndufv1	NM_133666	chr19	4012250	4013232	13
2410004B18Rik	NM_025555	chr3	145600587	145601429	13
1110008L16Rik	NM_025373	chr12	56403466	56403807	14
Erh	NM_007951	chr12	81744473	81745194	14
Nup188	NM_198304	chr2	30141452	30142479	14
Dut	NM_023595	chr2	125072859	125073668	14
1700123M08Rik	NR_040577	chr4	11893342	11894125	14
Tsfm	NM_025537	chr10	126467593	126468117	14
Smg6	NM_001002764	chr11	74739112	74739662	14

Supplemental Table 2. Significant ChIP-seq E2F1 promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Coro2b	NM_175484	chr9	62384519	62385153	14
Gm10474	NR_033481	chrX	65931230	65931888	14
A430005L14Rik	NM_175287	chr4	153331059	153331660	15
Xrcc1	NM_009532	chr7	25331952	25332413	15
Neil3	NM_146208	chr8	54723939	54724868	15
Med9os	NR_045273	chr11	59761176	59762090	15
Fmnl3	NM_011711	chr15	99200562	99201200	15
Tfg	NM_019678	chr16	56717340	56717754	15
Pola1	NM_008892	chrX	90877142	90877814	15
Sh3bp1	NM_009164	chr15	78729773	78730688	16
Zfp397	NM_027007	chr18	24112997	24113410	16
Depdc1b	NM_178683	chr13	109106095	109106997	16
Pkd1	NM_013630	chr17	24686627	24687193	16
Gpr89	NM_026229	chr3	96708933	96709475	16
1700101E01Rik	NM_001166705	chr2	28910267	28910870	17
Taf12	NM_025579	chr4	131830095	131830516	17
Ndufs2	NM_153064	chr1	173176923	173177527	17
Trim27	NM_009054	chr13	21271449	21272183	17
Cnih1	NM_009919	chr14	47407776	47408252	17
Aasdh	NM_173765	chr5	77334289	77334753	17
Banp	NM_016812	chr8	124474065	124474751	17
4933405D12Rik	NR_046036	chr3	122626772	122627259	18
Wdfy3	NM_172882	chr5	102498702	102499141	18
Cd2bp2	NM_001285905	chr7	134339079	134340066	18
Armc9	NM_027456	chr1	88051115	88051699	18
Pitpnb	NM_019640	chr5	111759414	111760186	18
Dym	NM_027727	chr18	75178215	75178672	19
Pcnxl3	NM_144868	chr19	5688434	5689343	19
Grk4	NM_019497	chr5	35002751	35003340	19
Whsc1l1	NM_001001735	chr8	26712481	26713111	19
Tsga10	NM_207228	chr1	37921502	37922311	20
Clasp1	NM_029709	chr1	120285272	120286035	20
Ppp1r18	NM_175242	chr17	36003218	36003939	20
Aacs	NM_030210	chr5	125955934	125956589	20
Klf13	NM_021366	chr7	71083530	71084031	20
Tmem107	NM_028336	chr11	68883942	68884718	20
Rbfox2	NM_175387	chr15	77136986	77137938	20
Myo9a	NM_173018	chr9	59598534	59599466	20
Atp10a	NM_009728	chr7	65913194	65913989	21
Asnsd1	NM_133728	chr1	53409354	53409794	21
Tmem230	NM_001141971	chr2	132073282	132073722	21
Tmem39b	NM_199305	chr4	129373734	129374386	21
Glmn	NM_133248	chr5	108026305	108026967	21
Zfp930	NM_001013379	chr8	71732714	71733216	21
Snhg6	NR_024067	chr1	9933974	9934379	22
Ncaph2	NM_001271600	chr15	89185619	89186722	22
Mcm8	NM_025676	chr2	132641589	132642206	22
Fam110a	NM_146127	chr2	151805698	151806167	22

Supplemental Table 2. Significant ChIP-seq E2F1 promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Cox18	NM_001033310	chr5	90652728	90653269	22
Myeov2	NR_028108	chr1	94538238	94538766	22
Gtf3a	NM_025652	chr5	147760073	147760435	22
Gm16039	NR_033518	chr6	8208891	8209727	22
Zfp748	NM_001035231	chr13	67653717	67654412	23
Atl2	NM_178050	chr17	80295180	80295699	23
Hnrnpr	NM_001277121	chr4	135866341	135867416	23
Mcph1	NM_173189	chr8	18594793	18595596	23
Kif4	NM_008446	chrX	97821233	97821618	23
Acap2	NM_030138	chr16	31201020	31201579	24
Pskh1	NM_173432	chr8	108424125	108424668	24
Rab11b	NM_008997	chr17	33896986	33897826	24
Tmem138	NM_028411	chr19	10651160	10651964	24
Herc2	NM_010418	chr7	63305245	63305851	24
Gpd1l	NM_175380	chr9	114842713	114843446	25
Taf1	NM_001290729	chrX	98727766	98728429	25
Yeats4	NM_026570	chr10	116661108	116661966	25
Mroh1	NM_175457	chr15	76210663	76211271	25
Spata5	NM_001163511	chr3	37318849	37319603	25
Polr3gl	NM_001293701	chr3	96397750	96398406	25
Zbtb48	NM_133879	chr4	151401482	151402026	25
Nudt21	NM_026623	chr8	96560426	96561400	25
Zfp41	NM_001044718	chr15	75446876	75447401	26
Txnl1	NM_016792	chr18	63851722	63852251	26
Rps11	NM_013725	chr7	52379495	52379970	26
Gas2l3	NM_001284344	chr10	88906154	88907216	26
Triap1	NM_026933	chr5	115791032	115791530	26
Setd8	NM_030241	chr5	124889718	124890210	26
Mast3	NM_199308	chr8	73316003	73316607	26
Hn1	NM_008258	chr11	115375159	115376154	27
Jtb	NM_206924	chr3	90035343	90035746	27
Cant1	NM_001267592	chr11	118280139	118280668	28
1810022K09Rik	NM_001099674	chr3	14610878	14611577	28
Akr1a1	NM_021473	chr4	116323975	116324526	28
Als2	NM_028717	chr1	59293661	59294431	28
Sept2	NM_001159719	chr1	95375331	95375999	28
Stxbp4	NM_011505	chr11	90498981	90499805	28
Zbtb24	NM_001277229	chr10	41169937	41170446	29
Cirbp	NM_007705	chr10	79630054	79631173	29
Ganab	NM_001293621	chr19	8972328	8972821	29
Atp6v1c1	NM_025494	chr15	38591275	38592099	29
C2cd5	NM_001286578	chr6	143048385	143048899	29
Hey2	NM_013904	chr10	30562180	30562937	30
Clk4	NM_007714	chr11	51076412	51076991	30
Invs	NM_010569	chr4	48292317	48293004	30
Pot1a	NM_133931	chr6	25758955	25759436	30
Fanci	NM_145946	chr7	86536896	86537609	30
Txlna	NM_001005506	chr4	129317481	129318555	30

Supplemental Table 2. Significant ChIP-seq E2F1 promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Tipin	NM_025372	chr9	64129165	64129721	30
Ppp2r5d	NM_009358	chr17	46841649	46842190	31
Naa20	NM_026425	chr2	145728805	145729208	31
Rab23	NM_008999	chr1	33776498	33777044	31
Tpm3	NM_001271764	chr3	89883233	89883713	31
Ankle2	NM_027922	chr5	110659747	110660359	31
Serinc1	NM_019760	chr10	57252037	57252568	32
6330408A02Rik	NM_177312	chr7	13863695	13864380	32
Bag4	NM_026121	chr8	26895360	26895937	32
BC020402	NR_033219	chr10	7400777	7401067	33
Nt5dc1	NM_176968	chr10	34137951	34138649	33
Snrpd3	NM_026095	chr10	74980450	74981188	33
Ube2g2	NM_019803	chr10	77084808	77085388	33
Atf7	NM_146065	chr15	102455409	102456227	33
Map1a	NM_032393	chr2	121115152	121115588	33
Klhl32	NM_001163020	chr4	24777802	24778596	33
Athl1	NM_145387	chr7	148127275	148127749	33
Asb1	NM_001039126	chr1	93436860	93437489	34
Opa1	NM_133752	chr16	29579100	29579805	34
Atl3	NM_146091	chr19	7568516	7569405	34
Adal	NM_001290811	chr2	120965968	120966425	34
Idh3b	NM_130884	chr2	130109944	130110361	34
Rps15	NM_009091	chr10	79754710	79755708	34
Atp6v0c-ps2	NR_037854	chr17	24306046	24306564	34
Snx5	NM_001199188	chr2	144096283	144096923	34
Ubfd1	NM_138589	chr7	129210558	129210932	34
1810062O18Rik	NR_033571	chr14	21365176	21365921	35
Gtse1	NM_001168672	chr15	85689751	85690590	35
Dguok	NM_013764	chr6	83456702	83457152	35
Gnb1l	NM_001081682	chr16	18498349	18499332	36
Uap1l1	NM_001033293	chr2	25220891	25221328	36
Kif20b	NM_183046	chr19	34996493	34997273	36
Surf6	NM_009298	chr2	26758049	26758543	36
Idh3g	NM_008323	chrX	71031896	71032502	36
Mcm3	NM_008563	chr1	20809880	20810633	37
Vcpkmt	NM_001033236	chr12	70683528	70684427	37
B3galnt2	NM_178640	chr13	14046787	14047166	37
Pcgf6	NM_027654	chr19	47124925	47125670	37
Palb2	NM_001081238	chr7	129276231	129276614	37
Tarbp2	NM_009319	chr15	102348398	102348921	38
Slc9a3r1	NM_012030	chr11	115024468	115024916	38
Dbr1	NM_031403	chr9	99476060	99476450	38
Dynlrb1	NM_001291108	chr2	155062094	155062670	39
Tbp	NM_013684	chr17	15636462	15637320	40
Faf1	NM_007983	chr4	109348944	109349598	40
Ctnna3	NM_177612	chr10	62892625	62893146	41
Mob1b	NM_026735	chr5	89149611	89150261	41
Ankra2	NM_001271389	chr13	99032572	99033571	42

Supplemental Table 2. Significant ChIP-seq E2F1 promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Gnl3	NM_153547	chr14	31832124	31832425	42
Tab1	NM_025609	chr15	79963251	79963998	42
Rbm39	NM_001291114	chr2	156005659	156006204	42
Pde12	NM_178668	chr14	27488829	27489749	42
Casp7	NM_007611	chr19	56471389	56471931	42
Ccne2	NM_001037134	chr4	11118130	11118948	42
Pias3	NM_146135	chr3	96500077	96500602	43
Wfs1	NM_011716	chr5	37379778	37380577	43
Spice1	NM_144550	chr16	44347141	44347971	43
Ccdc109b	NM_025779	chr3	129672747	129673413	43
Pold3	NM_133692	chr7	107269521	107270411	43
Cldn25	NM_001252451	chr16	58727616	58728515	44
Foxred1	NM_001291449	chr9	35018174	35019016	44
BC068281	NM_001170858	chr12	4849925	4850381	45
Psmc4	NM_011874	chr7	28834651	28835479	45
Mdga1	NM_001081160	chr17	30024513	30025048	46
Eif3a	NM_010123	chr19	60866324	60866775	46
Rps16	NM_013647	chr7	29135482	29136023	46
Stk4	NM_021420	chr2	163899708	163900210	46
Abhd11	NM_001190437	chr5	135484658	135485476	46
Zdhhc7	NM_133967	chr8	122625058	122625592	46
Tfam	NM_009360	chr10	70700493	70700996	47
Aaas	NM_153416	chr15	102180761	102181524	47
Tyw1	NM_178897	chr5	130731259	130731810	47
Gpr19	NM_001167700	chr6	134847648	134848142	47
Brip1	NM_178309	chr11	86014292	86015001	48
Wdr70	NM_001081402	chr15	8048700	8049621	48
Abhd8	NM_022419	chr8	73987146	73987869	48
Mre11a	NM_018736	chr9	14588858	14589537	48
Rmdn3	NM_001033136	chr2	118982515	118982927	48
Pcyox1l	NM_172832	chr18	61867023	61867456	49
Psmd5	NM_080554	chr2	34726148	34726717	49
Cabin1	NM_172549	chr10	75226726	75227378	49
Iqgap3	NM_001033484	chr3	87885745	87886297	49
Polr2j	NM_011293	chr5	136592178	136593040	49
Zbtb45	NM_001024699	chr7	13594822	13595376	49
Sprtn	NM_001111141	chr8	127421479	127422189	49
U2surp	NM_026476	chr9	95411885	95412845	49
Coq6	NM_172582	chr12	85702578	85703355	50
Vps13b	NM_177151	chr15	35300945	35301754	50
2010109A12Rik	NM_029363	chr5	93635297	93635888	50
Mettl25	NM_207522	chr10	105278114	105278656	50
Gm11974	NR_045893	chr11	6428403	6429020	51
Hprt	NM_013556	chrX	50341034	50341575	51
Exosc2	NM_144886	chr2	31525849	31526765	51
Ncln	NM_134009	chr10	80958805	80959306	52
Pip4k2c	NM_054097	chr10	126648357	126648894	52
Zfp672	NM_001256520	chr11	58143397	58144180	52

Supplemental Table 2. Significant ChIP-seq E2F1 promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Ssr1	NM_025965	chr13	38085748	38086265	52
Rad1	NM_001289447	chr15	10415438	10416249	52
Calm2	NM_007589	chr17	87845686	87846759	52
5430416N02Rik	NR_034038	chr5	100858164	100858839	52
Tmem60	NM_177601	chr5	20387966	20388678	52
Tbc1d14	NM_001113364	chr5	36872934	36873504	52
Gm20604	NM_001142939	chr12	103995537	103996396	53
Isy1	NM_133934	chr6	87788278	87789121	53
Tusc3	NM_030254	chr8	40068442	40069503	53
Zfp202	NM_030713	chr9	39999661	40000244	53
Trip13	NM_027182	chr13	74074730	74075591	54
Pck2	NM_028994	chr14	56158676	56159635	54
Ssr3	NM_026155	chr3	65195907	65196934	54
Blm	NM_001042527	chr7	87679656	87680245	54
Qrsl1	NM_001081054	chr10	43621095	43621879	54
2210408I21Rik	NM_001145676	chr13	77274526	77275174	54
Cyb5d2	NM_001024926	chr11	72608740	72609831	55
Ncdn	NM_011986	chr4	126430360	126430875	55
Tgfbr2	NM_029575	chr9	116084229	116084622	55
Hn1l	NM_198937	chr17	25097201	25097823	55
Sf3b4	NM_153053	chr3	95976352	95976702	55
Pcgf2	NM_009545	chr11	97561521	97561988	56
Birc5	NM_001012273	chr11	117710348	117710863	56
Incenp	NM_016692	chr19	9973404	9974529	56
Slc25a11	NM_024211	chr11	70460260	70460707	57
Cdkn3	NM_028222	chr14	47379847	47380696	57
Msh6	NM_010830	chr17	88374029	88374863	57
Ppox	NM_008911	chr1	173210852	173211665	58
Rad9a	NM_011237	chr19	4201283	4201805	58
Fkbp2	NM_008020	chr19	7054611	7055131	58
Dap	NM_146057	chr15	31153785	31154610	59
Ranbp3	NM_001252467	chr17	56812254	56813157	59
Toporsos	NR_045265	chr4	40216273	40217066	59
Eapp	NM_025456	chr12	55796505	55797079	59
Mapk8ip3	NM_001163451	chr17	25073631	25074093	59
Pcdh18	NM_130448	chr3	49560783	49561573	59
Insig1	NM_153526	chr5	28397569	28398451	59
Nfya	NM_001110832	chr17	48548198	48549970	60
Mphosph9	NM_001081323	chr5	124777462	124778378	60
Mcm2	NM_008564	chr6	88848506	88848920	60
Atp5g2	NM_026468	chr15	102501048	102501785	61
Nup62	NM_053074	chr7	52071430	52072269	61
Nav2	NM_175272	chr7	56501330	56501907	61
Zfp90	NM_011764	chr8	108938911	108939686	61
Ppil4	NM_026141	chr10	7512428	7513076	61
Gabpb2	NM_172512	chr3	95021367	95022237	61
Tm9sf2	NM_080556	chr14	122506100	122506629	62
Prkag1	NM_016781	chr15	98661514	98662239	62

Supplemental Table 2. Significant ChIP-seq E2F1 promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Mrpl43	NM_053164	chr19	45080544	45081195	62
Ankle1	NM_172756	chr8	73929731	73930212	62
Ap1s2	NM_001290379	chrX	160346705	160347314	62
Gcc2	NM_027375	chr10	57718025	57718646	63
Mis12	NM_025993	chr11	70832786	70833563	63
Pitrm1	NM_145131	chr13	6547126	6547803	63
Blvrb	NM_144923	chr7	28232836	28233281	63
Eldr	NR_110421	chr11	16850900	16851542	63
Ykt6	NM_019661	chr11	5855464	5856183	64
Gm5464	NM_001034881	chr14	67487302	67488197	64
Bckdk	NM_009739	chr7	135047464	135047835	64
Gm2694	NR_033430	chr8	89996383	89997164	64
Nono	NM_023144	chrX	98624809	98625296	64
Gtf2a1	NM_175335	chr12	92828574	92829150	64
Mmgt1	NM_146234	chrX	53850717	53851345	64
Tob2	NM_020507	chr15	81688365	81689016	65
Wdr25	NM_177602	chr12	110132316	110132776	65
Endov	NM_001164636	chr11	119352313	119353139	66
Chka	NM_001271496	chr19	3851636	3852041	67
Trim28	NM_011588	chr7	13609177	13609956	67
Loh12cr1	NM_026371	chr6	134590749	134591299	67
Glt25d1	NM_146211	chr8	74134809	74135169	67
Med23	NM_027347	chr10	24589564	24590153	68
Hist1h4f	NM_175655	chr13	23643097	23643790	68
Ikbip	NM_027078	chr10	90545578	90546124	68
Secisbp2	NM_029279	chr13	51746834	51747466	68
Rbm6	NM_029169	chr9	107774816	107775346	68
Cd2ap	NM_009847	chr17	43012742	43013865	69
Nfx1	NM_023739	chr4	40917733	40918354	69
Osbpl9	NM_133885	chr4	108874385	108875230	69
Nuf2	NM_023284	chr1	171461288	171461762	69
Gzf1	NM_028986	chr2	148506482	148507366	69
Ccdc57	NM_027745	chr11	120793780	120794451	70
Clpp	NM_017393	chr17	57129384	57130128	70
Mtap	NM_024433	chr4	88782928	88783758	70
Uba2	NM_016682	chr7	34953074	34953880	70
Fignl1	NM_001163359	chr11	11708439	11709348	71
Slc20a1	NM_015747	chr2	129024026	129025131	71
Naglu	NM_013792	chr11	100931192	100931764	71
Cherp	NM_138585	chr8	74998572	74999548	71
Frmd6	NM_028127	chr12	71926375	71926768	72
Pdcd6	NM_011051	chr13	74454448	74454955	72
Epg5	NM_001195633	chr18	78134947	78135606	72
Agpat5	NM_026792	chr8	18845973	18846726	72
Acad8	NM_025862	chr9	26806726	26807396	72
Nfyc	NM_001277095	chr4	120497885	120498659	73
Tsen54	NM_029557	chr11	115675755	115676497	74
Hira	NM_010435	chr16	18876350	18877482	74

Supplemental Table 2. Significant ChIP-seq E2F1 promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Haus4	NM_145462	chr14	55172681	55173564	75
Cyb5r3	NM_029787	chr15	83002208	83002917	75
Dars2	NM_172644	chr1	163000256	163001118	75
Tubb5	NM_011655	chr17	35974876	35975464	75
Lbh	NM_029999	chr17	73267359	73268080	76
Saal1	NM_030233	chr7	53965624	53966265	76
Wrap53	NM_144824	chr11	69392470	69393028	76
Smek1	NM_211355	chr12	102321490	102322180	76
Mrps27	NM_173757	chr13	100114542	100115090	76
Slc25a32	NM_172402	chr15	38943663	38944706	77
Sh3gl1	NM_013664	chr17	56175530	56176435	77
Maml3	NM_001004176	chr3	51908478	51909223	77
Pbdc1	NM_001281871	chrX	102274802	102275539	77
Ipo9	NM_153774	chr1	137326533	137327446	78
Spsb1	NM_029035	chr4	149328720	149329353	78
Lfng	NM_008494	chr5	141083129	141083614	78
Elmod2	NM_178736	chr8	85855756	85856857	78
Ccdc15	NM_001081429	chr9	37155642	37156155	78
Hexdc	NM_001001333	chr11	121065514	121066134	78
Urgcp	NM_001077661	chr11	5662009	5662590	79
Brca1	NM_009764	chr11	101412875	101413503	79
Tecpr2	NM_001289510	chr12	112127204	112127900	79
Poglut1	NM_172380	chr16	38549837	38550535	79
Aldh18a1	NM_019698	chr19	40662595	40663151	79
Slbp	NM_001289724	chr5	33994787	33995499	79
Eny2	NM_175009	chr15	44259097	44260374	80
Ipo8	NM_001081113	chr6	148779360	148780457	80
Dna2	NM_177372	chr10	62409438	62410274	80
Ift140	NM_134126	chr17	25152532	25153688	80
Mat2b	NM_134017	chr11	40505695	40506510	81
Msh2	NM_008628	chr17	88071506	88072447	81
Prpf4	NM_027297	chr4	62069469	62070324	81
Prim2	NM_008922	chr1	33726214	33726900	81
Mfsd5	NM_134100	chr15	102109614	102110320	81
Tubgcp3	NM_198031	chr8	12671649	12672387	81
Aagab	NM_025857	chr9	63450132	63450953	82
Nop58	NM_018868	chr1	59741560	59742303	83
Slc25a10	NM_013770	chr11	120352993	120353473	83
Zfp664	NM_001081750	chr5	125342781	125343533	83
2700094K13Rik	NM_001033166	chr2	84510408	84511153	84
Lrrc40	NM_024194	chr3	157699330	157700127	84
Snapc2	NM_133968	chr8	4252862	4253507	84
Uchl5	NM_001159866	chr1	145624183	145624799	84
Smarcd1	NM_031842	chr15	99532362	99533241	85
Gins4	NM_024240	chr8	24347706	24348403	85
Tmod3	NM_016963	chr9	75406970	75407787	85
Dpp9	NM_172624	chr17	56357942	56358510	85
Lrrcc1	NM_028915	chr3	14533562	14534182	85

Supplemental Table 2. Significant ChIP-seq E2F1 promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Abcf2	NM_001190443	chr5	24082918	24083480	85
Armc8	NM_028768	chr9	99468840	99469624	85
Xrcc5	NM_009533	chr1	72353846	72354313	86
Zswim7	NM_027198	chr11	62094481	62095140	86
Rnaseh2b	NM_026001	chr14	62950603	62951450	86
Appl2	NM_145220	chr10	83110946	83111698	86
Adam17	NM_001291871	chr12	21379067	21379745	86
Dek	NM_025900	chr13	47201063	47201941	86
Pkmyt1	NM_023058	chr17	23863094	23863682	86
9430038I01Rik	NM_029886	chr7	144602029	144602675	86
Ap1g1	NM_009677	chr8	112302326	112302924	86
AA465934	NR_028363	chr11	83104980	83105593	87
Chtop	NM_001293780	chr3	90313031	90313632	88
Cltb	NM_028870	chr13	54712283	54712805	88
Wasl	NM_028459	chr6	24614557	24615255	88
Foxm1	NM_008021	chr6	128312776	128313423	89
Nol9	NM_028727	chr4	151413314	151413734	89
Polr2m	NM_178602	chr9	71333239	71334161	89
Rangap1	NM_001146174	chr15	81559699	81560818	90
Cdc7	NM_001271568	chr5	107392883	107393976	90
Tbc1d22b	NM_198647	chr17	29686491	29687181	90
Ddx39b	NM_019693	chr17	35378271	35379289	90
4930555B11Rik	NR_040633	chr2	57034021	57034641	90
Snrpb	NM_009225	chr2	130004704	130005314	90
Zbtb11	NM_173026	chr16	55973687	55974326	91
Nhp2l1	NM_011482	chr15	81877593	81878279	91
Rtn3	NM_001003934	chr19	7557460	7557918	91
Mrpl46	NM_023331	chr7	85927533	85928233	91
Cyb5b	NM_025558	chr8	109674219	109675083	91
Tardbp	NM_001008546	chr4	148000676	148001349	92
Zfp784	NM_001039532	chr7	4989663	4990247	92
Tor1a	NM_144884	chr2	30822815	30823874	93
Mtf2	NM_013827	chr5	108494497	108495072	93
Serpinb6a	NM_001243192	chr13	34094295	34094843	93
Zfp346	NM_012017	chr13	55206414	55207111	94
Pigp	NM_001159618	chr16	94591725	94592400	94
Ssna1	NM_023464	chr2	25127570	25128117	94
Srrm1	NM_001130477	chr4	134908732	134909336	94
Exo1	NM_012012	chr1	177810636	177811369	95
Nup107	NM_134010	chr10	117229280	117230050	95
Nin	NM_008697	chr12	71212624	71213228	95
Cdca2	NM_175384	chr14	68333030	68334574	95
Ddx23	NM_001080981	chr15	98492836	98493612	95
Orc1	NM_011015	chr4	108251824	108252482	95
Sars	NM_011319	chr3	108247768	108248393	96
Mapk1	NM_011949	chr16	16983206	16983934	96
Fancl	NM_001277273	chr11	26286697	26287662	97
Hnrnpul2	NM_001081196	chr19	8893115	8894858	97

Supplemental Table 2. Significant ChIP-seq E2F1 promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Psmg3	NM_025604	chr5	140302379	140303020	97
Odf2l	NM_025714	chr3	144781321	144781999	97
Mms22l	NM_199467	chr4	24423366	24424044	97
Ptpru	NM_001083119	chr4	131393839	131394350	98
Trnt1	NM_001242358	chr6	106718898	106719559	98
Thoc3	NM_028597	chr13	54569749	54570455	98
Puf60	NM_001164600	chr15	75910887	75911515	98
Ubxn8	NM_178648	chr8	34751954	34752744	98
Xrcc6	NM_010247	chr15	81846575	81847218	99
Rabl3	NM_001042499	chr16	37539737	37540418	99
Rab14	NM_026697	chr2	35056266	35056815	99
Hexa	NM_010421	chr9	59387177	59387967	99
Mns1	NM_008613	chr9	72286106	72286762	99
Yars	NM_134151	chr4	128866847	128867428	100
Chchd5	NM_025395	chr2	128955171	128955901	101
Vkorc1	NM_178600	chr7	135038752	135039306	101
Dnph1	NM_207161	chr17	46633420	46634257	102
Tex10	NM_172304	chr4	48485858	48486525	102
Med28	NM_025895	chr5	45911300	45911837	102
Aimp2	NM_001172146	chr5	144670163	144671048	102
Tbcd	NM_029878	chr11	121313067	121313662	103
Slc29a1	NM_001199116	chr17	45731982	45732853	103
Sars2	NM_023637	chr7	29526764	29527413	103
Ddx19a	NM_007916	chr8	113521176	113522063	103
Mir423	NR_030756	chr11	76891272	76891868	103
Rhebl1	NM_026967	chr15	98711228	98712254	103
Zfp414	NM_026712	chr17	33765728	33766550	103
Cntrob	NM_172560	chr11	69136862	69137679	104
C030039L03Rik	NM_001112731	chr7	28474284	28474639	104
Cox7a2	NM_009945	chr9	79607154	79607957	104
Gins3	NM_030198	chr8	98157231	98157893	104
Pigg	NM_001081234	chr5	108741654	108742441	105
Phf6	NM_027642	chrX	50265244	50265745	105
Mdm2	NM_001288586	chr10	117147377	117148039	105
Mrpl55	NM_026035	chr11	59015790	59016456	105
Rpl10a	NM_011287	chr17	28465335	28465705	105
Pms1	NM_153556	chr1	53353275	53354192	106
Polr2e	NM_025554	chr10	79501847	79502748	106
Dab2	NM_001037905	chr15	6336407	6337298	106
Rbbp6	NM_011247	chr7	130113970	130114395	106
Asb3	NM_023906	chr11	30854292	30854714	106
Lmnb2	NM_010722	chr10	80380557	80381208	107
Mut	NM_008650	chr17	41071343	41072137	107
Mnd1	NM_029797	chr3	83959351	83959849	107
Cdt1	NM_026014	chr8	125091588	125092454	107
D10Wsu102e	NM_026579	chr10	82822753	82823392	108
Wdr76	NM_001290986	chr2	121332286	121332847	109
Tmem2	NM_031997	chr19	21852657	21853219	109

Supplemental Table 2. Significant ChIP-seq E2F1 promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Oser1	NM_025699	chr2	163244688	163245504	109
Wrnip1	NM_030215	chr13	32893546	32894470	110
9130011E15Rik	NM_198296	chr19	46072610	46073124	110
Eefsec	NM_023060	chr6	88396066	88396778	110
Cisd1	NM_134007	chr10	70807050	70807920	111
Csrp2	NM_007792	chr10	110356961	110357723	111
Pno1	NM_025443	chr11	17111166	17111794	111
Smc6	NM_025695	chr12	11272309	11273295	111
Cdc25b	NM_023117	chr2	131012426	131013162	111
Actn4	NM_021895	chr7	29746782	29747592	111
Hnrnph3	NM_001079824	chr10	62486013	62486956	112
Gtf3c2	NM_027901	chr5	31481984	31482823	113
Zfp91Cntf	NR_024093	chr19	12869996	12871000	114
Gne	NM_001190414	chr4	44085148	44085712	114
Phf20	NM_172674	chr2	156021988	156023005	115
Irx5	NM_018826	chr8	94881393	94882224	115
Slc1a5	NM_009201	chr7	17366470	17367148	115
Pofut2	NM_030262	chr10	76721849	76722470	116
Fam173b	NM_026546	chr15	31531489	31532483	116
Idi1	NM_145360	chr13	8884650	8885285	117
Cad	NM_023525	chr5	31357016	31357522	117
Chrac1	NM_053068	chr15	72920673	72921245	118
Polg2	NR_027785	chr11	106640391	106641027	119
Nras	NM_010937	chr3	102862065	102862587	119
Mrpl42	NM_026065	chr10	94964054	94964827	120
Zgpat	NM_001048148	chr2	181099914	181100579	120
Ercc6	NM_001081221	chr14	33326500	33327152	120
Riok2	NM_025934	chr17	17510914	17511917	121
Hirip3	NM_172746	chr7	134005227	134005985	121
Gdi1	NM_010273	chrX	71550172	71550770	121
Gemin4	NM_177367	chr11	76030662	76031241	122
Acat2	NM_009338	chr17	13153128	13153809	122
Fkbp3	NM_013902	chr12	66174477	66175127	122
Ndufaf2	NM_001127346	chr13	108948344	108949048	122
Tmem186	NM_025708	chr16	8637160	8638182	122
Nup35	NM_027091	chr2	80478785	80479397	123
Cbx5	NM_007626	chr15	103045288	103046029	124
Sfxn5	NM_178639	chr6	85282942	85283641	124
Naaa	NM_001163687	chr5	92706707	92707457	124
Med12	NM_021521	chrX	98469250	98469856	124
Scamp4	NM_019575	chr10	80065498	80066003	125
Cox10	NM_178379	chr11	63892525	63893172	125
Cipc	NM_001289430	chr12	88287829	88288400	125
Smc5	NM_001252684	chr19	23347979	23348544	125
4930528A17Rik	NR_028384	chr4	21775010	21775928	125
2510003E04Rik	NM_028197	chr10	62040812	62041345	126
Ajuba	NM_010590	chr14	55196086	55196656	126
Mrto4	NM_001290810	chr4	138908044	138908684	126

Supplemental Table 2. Significant ChIP-seq E2F1 promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Vmn2r29	NR_003555	chr7	7230508	7231238	126
Rad51c	NM_053269	chr11	87217495	87218244	127
Man2c1	NM_028636	chr9	56978406	56979014	127
Socs2	NM_001168655	chr10	94878455	94878980	128
E2f6	NM_033270	chr12	16817518	16818278	128
Trmt2b	NM_172540	chrX	130811124	130811663	129
Fars2	NM_024274	chr13	36209241	36210039	129
Nmral1	NM_001290761	chr16	4718913	4719539	129
Rab31	NM_133685	chr17	66121681	66122243	129
Papss1	NM_011863	chr3	131227416	131228304	129
Rnps1	NM_001080128	chr17	24551243	24552254	130
2500004C02Rik	NR_040318	chr2	153171026	153171805	130
Zfp81	NM_207541	chr17	33495400	33495981	132
5830415F09Rik	NM_029086	chr4	46401835	46402490	132
Ckap2	NM_001004140	chr8	23295881	23296436	132
Enkd1	NM_198299	chr8	108231668	108232203	132
Erp29	NM_026129	chr5	121902166	121902533	133
E2f7	NM_178609	chr10	110182136	110183170	133
Hadhb	NM_145558	chr5	30481563	30482287	133
Naa16	NM_025832	chr14	79789904	79790776	134
Myg1	NM_021713	chr15	102161948	102162598	134
Tfb1m	NM_146074	chr17	3556979	3558177	134
Naa40	NM_027643	chr19	7315254	7315900	134
Neu1	NM_010893	chr17	35068062	35068601	135
Myh10	NM_175260	chr11	68505295	68505809	136
Ing3	NM_023626	chr6	21899434	21900066	136
Fancc	NM_001042673	chr13	63532656	63533175	137
Phactr4	NM_001161797	chr4	131977755	131978691	137
Exog	NM_001172136	chr9	119353794	119354560	137
Nxt1	NM_001110159	chr2	148498114	148498913	138
L3mbtl2	NM_145993	chr15	81494100	81494812	138
Arpp19	NM_021548	chr9	74885312	74886040	138
Eif4h	NM_033561	chr5	135114827	135115290	139
Tmed3	NM_025360	chr9	89599432	89600051	139
Kif15	NM_010620	chr9	122859950	122860723	139
Trim16	NM_053169	chr11	62633534	62634254	140
Gar1	NM_026578	chr3	129533862	129534484	140
Nufip1	NM_013745	chr14	76510546	76511129	141
Rad51	NM_011234	chr2	118938382	118939003	141
Rabep2	NM_030566	chr7	133572133	133572709	141
Cenpj	NM_001014996	chr14	57190059	57191021	142
Dnajb12	NM_019965	chr10	59341808	59343153	143
Mum1	NM_023431	chr10	79689185	79689784	143
Inip	NM_001013577	chr4	59796259	59796908	143
Tpx2	NM_028109	chr2	152673545	152674139	143
Myc	NM_001177353	chr15	61816671	61817407	144
Igf2bp1	NM_009951	chr11	95866779	95867446	145
Emd	NM_007927	chrX	71499905	71500434	145

Supplemental Table 2. Significant ChIP-seq E2F1 promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Cenpa	NM_007681	chr5	30969081	30969757	145
Cep164	NM_001081373	chr9	45636105	45637045	145
Cnot10	NM_153585	chr9	114548863	114549480	146
Sept10	NM_001024910	chr10	58683857	58685039	146
Thrap3	NM_146153	chr4	125879371	125880243	146
Rtfdc1	NM_025542	chr2	172265899	172266548	147
Sdha	NM_023281	chr13	74487261	74487819	147
Cct6a	NM_009838	chr5	130292967	130293789	147
Shcbp1	NM_011369	chr8	4778974	4779798	147
Snrpe	NM_009227	chr1	135506256	135507161	148
Trim37	NM_197987	chr11	86940196	86941252	148
Fadd	NM_010175	chr7	151767724	151768660	148
Usp38	NM_027554	chr8	83538196	83539116	148
Snw1	NM_025507	chr12	88812817	88813382	149
Tpst1	NM_001130476	chr5	130554965	130555810	149
Tkt	NM_009388	chr14	31362016	31362914	149
Pde4dip	NM_178080	chr3	97571484	97572090	149
Sdf2l1	NM_022324	chr16	17131951	17132700	150
Pla2g6	NM_016915	chr15	79158410	79158888	151
Them6	NM_198607	chr15	74551273	74552356	152
Umps	NM_009471	chr16	33966612	33967261	152
Srsf7	NM_146083	chr17	80605760	80607225	152
Vps16	NM_030559	chr2	130249620	130250793	152
Haus8	NM_029621	chr8	73795764	73796909	152
Fam204a	NM_029648	chr19	60302169	60302725	152
Mars	NM_001171582	chr10	126748337	126749040	153
Impa2	NM_053261	chr18	67448586	67449471	153
Cul7	NM_025611	chr17	46787041	46787837	153
1700021K19Rik	NM_172615	chr16	32867804	32868791	154
Mea1	NM_001277310	chr17	46817278	46817831	154
2310022A10Rik	NM_175107	chr7	28338090	28338833	154
Eif3d	NM_018749	chr15	77800408	77801790	154
Recql4	NM_058214	chr15	76540524	76541143	155
Commd1	NM_144514	chr11	22881822	22882433	156
Tmem11	NM_001168507	chr11	60692048	60692719	156
Khnyn	NM_027143	chr14	56503552	56504369	156
Rrp1b	NM_028244	chr17	32172739	32173785	156
Ddx39	NM_197982	chr8	86238768	86239694	156
Zfp560	NM_001004190	chr9	20189058	20189832	156
Orc2	NM_001271526	chr1	58561489	58562102	157
Med18	NM_026039	chr4	132019298	132020059	157
Irak1bp1	NM_001168240	chr9	82723395	82723742	157
Cactin	NM_027381	chr10	80783592	80784416	157
Ifrd1	NM_013562	chr12	40949068	40950168	157
Rmrp	NR_001460	chr4	43505577	43505969	157
2310036O22Rik	NM_026760	chr8	87550534	87551242	157
Rnf168	NM_027355	chr16	32277317	32278091	158
Mcm7	NM_008568	chr5	138612045	138613817	158

Supplemental Table 2. Significant ChIP-seq E2F1 promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Tex264	NM_011573	chr9	106587627	106588349	158
Cuedc2	NM_001164293	chr19	46412633	46413348	159
Ccdc34	NM_026613	chr2	109857779	109858485	159
Gins1	NM_027014	chr2	150735179	150735797	159
Tmem242	NM_027457	chr17	5439819	5440379	160
Mtcp1	NM_001294277	chrX	72661440	72662084	160
Grpel2	NM_021296	chr18	61885516	61886131	161
Rbmxl1	NM_009033	chr8	81032227	81033103	161
Gpx1	NM_008160	chr9	108241123	108242020	162
Lonp1	NM_028782	chr17	56765870	56766456	162
Fnbp4	NM_018828	chr2	90585257	90586120	163
Tinf2	NM_145705	chr14	56300027	56300952	164
Mtch1	NM_019880	chr17	29484370	29484998	164
Tbc1d9	NM_027758	chr8	85689041	85689787	164
Dnajc9	NM_134081	chr14	21207609	21208324	165
E130307A14Rik	NR_038037	chr10	39451163	39452130	166
Ttc33	NM_026213	chr15	5135371	5136081	167
Rab36	NM_029781	chr10	74499840	74500163	169
Mthfd2	NM_008638	chr6	83267084	83267773	169
Foxc1	NM_008592	chr13	31898452	31898914	169
Vars	NM_011690	chr17	35137576	35138464	169
Mtbp	NM_134092	chr15	55388715	55389548	170
Hnrnpm	NM_029804	chr17	33821707	33822757	170
Snrpd1	NM_009226	chr18	10617546	10618381	171
Gas1	NM_008086	chr13	60278352	60279094	172
Zfp213	NM_001033496	chr17	23700530	23701508	173
Tmem170	NM_025781	chr8	114400067	114400735	173
4930483J18Rik	NR_015603	chr15	81021043	81021868	174
Smc1a	NM_019710	chrX	148450674	148451615	175
Palm	NM_001161747	chr10	79256101	79256881	175
Rrp36	NM_144857	chr17	46810809	46811245	176
Bcl2l1	NM_009743	chr2	152656921	152657653	176
Rfc1	NM_011258	chr5	65726311	65727090	177
Rbl2	NM_011250	chr8	93593925	93594338	177
Kxd1	NM_029366	chr8	73046566	73047235	178
Bok	NM_016778	chr1	95582008	95582888	178
Shq1	NM_181590	chr6	100620600	100621344	178
4931428F04Rik	NM_001166394	chr8	107812848	107813648	179
Cops3	NM_011991	chr11	59652723	59653453	180
Net1	NM_019671	chr13	3916952	3917616	181
Dsn1	NM_025853	chr2	156832270	156832988	181
Capza1	NM_009797	chr3	104666911	104667571	181
Arf2	NM_007477	chr11	103828032	103828699	182
Nol7	NM_023554	chr13	43493572	43494280	182
Zfp868	NM_172754	chr8	72148850	72149676	183
Dhx9	NM_007842	chr1	155334151	155335060	184
Nkd2	NM_028186	chr13	73984579	73985207	185
Ttc7	NM_028639	chr17	87682010	87682811	186

Supplemental Table 2. Significant ChIP-seq E2F1 promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Gm5617	NM_001004191	chr9	48303332	48303933	186
Tcp1	NM_013686	chr17	13108951	13109809	186
Kiz	NM_001033298	chr2	146681405	146682216	187
Med21	NM_025315	chr6	146590931	146591642	187
Dck	NM_007832	chr5	89193692	89194759	189
Zfp62	NM_009562	chr11	49016823	49017558	190
Fen1	NM_007999	chr19	10277849	10278635	190
Etaa1	NM_026576	chr11	17853326	17854047	191
Unk	NM_172569	chr11	115891459	115892180	191
Chek1	NM_007691	chr9	36533666	36534431	194
Rab33b	NM_016858	chr3	51287552	51288611	195
Aurkb	NM_011496	chr11	68858987	68859692	196
Nup43	NM_145706	chr10	7387135	7387859	196
Ptpn23	NM_001081043	chr9	110310205	110310828	197
Dxo	NM_001163770	chr17	34973798	34974524	198
Srsf11	NM_001093753	chr3	157694208	157694830	198
Elp6	NM_001081381	chr9	110207526	110208260	198
Acot13	NM_025790	chr13	24922737	24923580	199
Anapc5	NM_001042491	chr5	123270620	123271683	199
Dhps	NM_001039514	chr8	87595456	87596257	202
Rsbn1	NM_172684	chr3	103717816	103718672	202
Dctn4	NM_026302	chr18	60685888	60686266	203
Rasgef1b	NM_145839	chr5	99681478	99682006	203
Gid4	NM_025757	chr11	60230404	60231295	204
Sdf4	NM_011341	chr4	155366957	155367494	204
Ggnbp2	NM_153144	chr11	84683526	84684544	204
Emp2	NM_007929	chr16	10313516	10314196	204
Zc3hav1l	NM_172467	chr6	38248770	38249337	205
Ints3	NM_145540	chr3	90236978	90237726	205
Rrm1	NM_009103	chr7	109589971	109590855	205
Wdyhv1	NM_029734	chr15	57972917	57973478	208
Gapdh	NM_008084	chr6	125115187	125115978	208
Ola1	NM_025942	chr2	73052030	73052560	208
Xrn2	NM_011917	chr2	146838614	146839392	208
3110021A11Rik	NR_030776	chr6	119798171	119798667	209
Cetn3	NM_007684	chr13	81922088	81922911	210
Zfat	NM_198644	chr15	68089465	68090948	211
Srsf1	NM_001078167	chr11	87860530	87861640	211
Sp2	NM_030220	chr11	96838344	96839235	212
Dusp1	NM_013642	chr17	26644373	26646036	212
Cnot7	NM_001271543	chr8	41596514	41597276	212
Nsmce2	NM_026746	chr15	59205614	59206316	213
Kars	NM_001130868	chr8	114534845	114535234	214
Plekhj1	NM_023900	chr10	80260384	80261927	215
Mrm1	NM_145433	chr11	84632388	84633215	215
Slc3a2	NM_001161413	chr19	8797308	8797976	216
Pcnt	NM_008787	chr10	75904868	75906011	217
Sppl2a	NM_023220	chr2	126758521	126758984	218

Supplemental Table 2. Significant ChIP-seq E2F1 promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Raver1	NM_027911	chr9	20895908	20896519	218
Atp5j	NM_016755	chr16	84835366	84835834	218
Fam227a	NM_029407	chr15	79488879	79489454	219
Msra	NM_001253715	chr14	65058983	65060298	222
Ppp6r3	NM_001164159	chr19	3575252	3575798	223
Pole2	NM_011133	chr12	70328535	70329370	224
Ndufaf4	NM_026742	chr4	24825248	24825658	224
Casp3	NM_009810	chr8	47702250	47703487	225
Zdhhc6	NM_025883	chr19	55389924	55390668	225
Znhit2	NM_013859	chr19	6061080	6061783	226
Dlx1	NM_010053	chr2	71367407	71368046	226
Amotl2	NM_019764	chr9	102619574	102621147	228
Kif2c	NM_134471	chr4	116854658	116855342	228
Kansl2	NM_001289439	chr15	98363919	98365021	229
Pcolce2	NM_029620	chr9	95537994	95538557	230
Pmf1	NM_025928	chr3	88213590	88214424	230
Rab27b	NM_030554	chr18	70212563	70213019	231
Poll	NM_020032	chr19	45634541	45635060	232
Ccdc138	NM_001162956	chr10	57960475	57961362	235
Siah2	NM_009174	chr3	58495876	58496273	235
Ptbp1	NM_008956	chr10	79316933	79317889	235
Gm6793	NR_033513	chr2	75496805	75498357	235
Cbx1	NM_007622	chr11	96650249	96651120	236
Arhgap31	NM_020260	chr16	38712708	38713115	236
Pycrl	NM_025412	chr15	75751261	75752242	238
C330006A16Rik	NM_001256521	chr2	25995391	25996184	238
Cep83os	NR_015524	chr10	94150863	94151374	239
Etf1	NM_144866	chr18	35090911	35091924	239
Taok2	NM_001163774	chr7	134027796	134028687	239
Rbm14-rbm4	NM_001290127	chr19	4810858	4811930	239
Ppapdc1b	NM_001293703	chr8	26830382	26831134	239
Fuca2	NM_025799	chr10	13220732	13221413	240
2610015P09Rik	NM_027801	chr16	43889884	43890626	241
Mrpl23	NM_011288	chr7	149718931	149719593	241
Wbp1	NM_016757	chr6	83070919	83071505	242
Eri1	NM_026067	chr8	36557863	36558824	243
Snx1	NM_019727	chr9	65972087	65972809	244
Kdelr3	NM_134090	chr15	79346873	79347290	245
Snn	NM_009223	chr16	11066054	11067215	245
Gm16576	NR_045069	chr15	79572929	79573817	246
Naca	NM_001282976	chr10	127472076	127473219	247
1110038F14Rik	NM_054099	chr15	76778750	76779691	248
Rpusd2	NM_173450	chr2	118860386	118861159	248
Sumo3	NM_019929	chr10	77068930	77069527	251
Helb	NM_080446	chr10	119549345	119550194	251
Prr24	NM_001136270	chr7	16858516	16859060	252
Tom1l1	NM_028011	chr11	90548354	90548969	253
Cdipt	NM_026638	chr7	134119441	134119923	255

Supplemental Table 2. Significant ChIP-seq E2F1 promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Tln1	NM_011602	chr4	43574885	43575512	256
Triobp	NM_001039156	chr15	78778018	78778802	257
Nudc	NM_010948	chr4	133101249	133102119	257
Oxct1	NM_024188	chr15	3976361	3977009	258
Mir7238	NR_106097	chr8	11635079	11635869	261
Nudcd3	NM_173748	chr11	6099896	6100483	264
Ensa	NM_019561	chr3	95428688	95429641	264
Stk3	NM_019635	chr15	35084886	35085706	264
Sfmbt1	NM_001166532	chr14	31528590	31529540	265
Mtx1	NM_001161824	chr3	89017617	89018365	265
Nhlrc2	NM_025811	chr19	56622280	56623752	266
Fancb	NM_001146081	chrX	161418438	161419143	268
Fn1	NM_001276411	chr1	71699159	71699919	268
Gsk3a	NM_001031667	chr7	26022357	26022841	270
E2f3	NM_010093	chr13	30076821	30078497	272
Tsg101	NM_021884	chr7	54174729	54175323	273
Nol12	NM_133800	chr15	78765294	78765978	274
Exosc1	NM_025644	chr19	42007346	42007711	275
Prnd	NM_001278520	chr2	131776765	131777329	275
Stxbp3a	NM_011504	chr3	108642834	108643454	275
Eif4b	NM_145625	chr15	101903951	101905006	276
Cpsf1	NM_001164173	chr15	76437304	76438183	277
Higd1a	NM_019814	chr9	121766584	121767090	280
Zfp367	NM_175494	chr13	64253447	64255003	281
Orc6	NM_019716	chr8	87823305	87824320	283
Tm9sf1	NM_028780	chr14	56261780	56262935	285
Rhof	NM_175092	chr5	123581985	123582720	285
G3bp1	NM_013716	chr11	55283181	55283899	287
Rcc1	NM_001197082	chr4	131900964	131901781	292
Fam178a	NM_001081225	chr19	45005425	45006375	292
Cops5	NM_013715	chr1	10027588	10028303	294
Gtf2ird2	NM_053266	chr5	134659731	134660670	294
Ywhaz	NM_001253805	chr15	36723673	36724321	295
Ccdc91	NM_025911	chr6	147424336	147425040	296
Rps15a	NM_170669	chr7	125259143	125259584	297
Tgfbr3	NM_011578	chr5	107717865	107718764	299
Cep78	NM_198019	chr19	16058908	16059442	303
Tnrc6c	NM_198022	chr11	117515662	117516149	304
Pnn	NM_008891	chr12	60167762	60168655	304
Fbxo7	NM_153195	chr10	85484447	85485507	304
Ubb	NM_011664	chr11	62364911	62365708	305
Wdr4	NM_021322	chr17	31648854	31649396	306
Gm2518	NR_015538	chr19	8848849	8849711	306
Mtss1l	NM_198625	chr8	113245512	113245866	306
Tspan4	NM_053082	chr7	148661143	148661739	307
Rplp0	NM_007475	chr5	116009526	116010043	310
Msl3	NM_010832	chrX	165111201	165111844	311
Cep72	NM_028959	chr13	74198939	74199903	311

Supplemental Table 2. Significant ChIP-seq E2F1 promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
C2cd2	NM_174847	chr16	98143531	98144330	312
Pnrc1	NM_001033225	chr4	33335202	33335695	313
Nek2	NM_010892	chr1	193645275	193646055	314
Mcm9	NM_027830	chr10	53349648	53350203	319
Slc25a22	NM_026646	chr7	148623181	148623721	321
Timeless	NM_001136082	chr10	127668929	127669952	323
Exosc8	NM_001163570	chr3	54538612	54539310	324
Senp1	NM_144851	chr15	97923164	97924184	325
Klf11	NM_178357	chr12	25336227	25336894	326
Matn2	NM_016762	chr15	34236154	34237369	327
Ppp1r15b	NM_133819	chr1	135027697	135028442	328
Dus3l	NM_144858	chr17	56904067	56904936	329
Zfp53	NM_013843	chr17	21625999	21626564	331
Ap2a2	NM_007459	chr7	148748152	148748665	331
Gpank1	NM_001128597	chr17	35258337	35259206	332
Dlgap5	NM_144553	chr14	48037368	48038130	332
Ahctf1	NM_026375	chr1	181733437	181734185	334
Clip2	NM_009990	chr5	135027528	135028407	336
Ctps	NM_016748	chr4	120242154	120242934	336
Ctdsp1	NM_153088	chr1	74437947	74439094	339
Akap8	NM_019774	chr17	32457325	32458187	341
Pcbp2	NM_011042	chr15	102301163	102301646	343
2810403A07Rik	NM_028814	chr3	88489385	88490733	344
Alkbh5	NM_172943	chr11	60351379	60351679	345
Gmfb	NM_022023	chr14	47441280	47441861	346
Klf2	NM_008452	chr8	74842939	74843675	347
Arsb	NM_009712	chr13	94541771	94542192	349
Smarca4	NM_001174079	chr9	21420654	21421269	350
Rccd1	NM_173445	chr7	87468594	87469378	353
Dzip1l	NM_028258	chr9	99530088	99530645	354
Rell1	NM_145923	chr5	64359280	64360262	364
Tbc1d31	NM_001081396	chr15	57743509	57744733	368
Phlda3	NM_013750	chr1	137662738	137663323	370
Ptprm	NM_008984	chr17	67703055	67703801	370
Carhsp1	NM_025821	chr16	8671471	8672277	371
Gtf3c5	NM_001290484	chr2	28438100	28438752	372
Gmnn	NM_020567	chr13	24852969	24853896	373
Gm17762	NR_028378	chr2	17948880	17949616	373
Brd2	NR_037970	chr17	34256007	34256931	375
Higd2a	NM_025933	chr13	54691704	54692234	378
Gm3230	NR_033642	chr2	19578786	19579494	383
Mier1	NM_001286222	chr4	102787139	102787617	384
Tspan4	NM_001252588	chr7	148662422	148662908	387
Hnrnpl	NM_177301	chr7	29595903	29596688	388
Ahcy	NM_016661	chr2	154899387	154900300	389
Bcl7b	NM_009745	chr5	135644316	135644953	394
Tpm2	NM_001277875	chr4	43535488	43536570	396
Tuba1b	NM_011654	chr15	98763948	98764894	399

Supplemental Table 2. Significant ChIP-seq E2F1 promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Shmt2	NM_001252316	chr10	126958574	126959616	404
Ddrgk1	NM_029832	chr2	130489688	130490251	411
Ipp	NM_008389	chr4	116179785	116181342	411
Hook3	NM_207659	chr8	27228947	27229620	412
0610037L13Rik	NM_028754	chr4	107562652	107563182	414
Uhrf1	NM_001111079	chr17	56442385	56443975	421
Anapc15	NM_001291348	chr7	109044748	109045787	424
Eif1	NM_011508	chr11	100181473	100181998	427
Syne2	NM_001005510	chr12	76919246	76920220	429
Lrrc14	NM_145471	chr15	76541282	76541915	430
Snrnp35	NM_029532	chr5	124933222	124933970	433
Nacad	NM_001081652	chr11	6505383	6505861	434
Thada	NM_183021	chr17	84864776	84865435	442
Tacc3	NM_001040435	chr5	34000984	34001496	445
Fam134a	NM_170755	chr1	75139531	75140093	453
Cand1	NM_027994	chr10	118675885	118677425	455
A930005H10Rik	NR_027894	chr3	115590038	115590989	463
Tax1bp3	NM_029564	chr11	72990741	72991356	465
Cbfb	NM_001161458	chr8	107694721	107695357	466
Zfp689	NM_175163	chr7	134591905	134592495	471
Mb21d2	NM_177718	chr16	28929082	28929540	472
Tagln2	NM_178598	chr1	174430636	174431072	478
Pcif1	NM_146129	chr2	164704771	164705923	480
Xiap	NM_009688	chrX	39421112	39421872	480
4932412D23Rik	NR_040521	chr16	42874644	42875781	487
Zfp787	NM_001013012	chr7	6106906	6107260	489
Actn1	NM_134156	chr12	81360629	81361105	490
Rhbdl3	NM_139228	chr11	80114455	80115380	505
Zmym4	NM_001114399	chr4	126644384	126644939	505
Stub1	NM_019719	chr17	25969412	25970181	509
Sin3a	NM_001110350	chr9	56924355	56925037	514
Tapt1	NM_173764	chr5	44617114	44617524	525
Mir6976	NR_105942	chr17	46690139	46690478	529
Casc5	NM_029617	chr2	118873083	118873685	530
Smarcb1	NM_001161853	chr10	75383572	75384083	531
Get4	NM_026269	chr5	139728482	139729137	533
Sumo2	NM_133354	chr11	115396676	115397339	536
Ncapd3	NM_178113	chr9	26837787	26838802	536
Mbd3	NM_013595	chr10	79861264	79862105	539
Rtn4	NM_194051	chr11	29594070	29594564	544
Maf1	NM_001164608	chr15	76181829	76182709	546
4930539J05Rik	NR_030689	chr3	135100785	135101379	546
Prdm11	NM_001177536	chr2	92885547	92885958	548
Dennd4a	NM_001162917	chr9	64659063	64659672	551
Prkar2a	NM_008924	chr9	108594725	108595322	551
Nrf1	NM_001164226	chr6	29998264	29998821	556
Tpm4	NM_001001491	chr8	74659255	74660242	559
Zcchc8	NM_027494	chr5	124169960	124171014	565

Supplemental Table 2. Significant ChIP-seq E2F1 promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
1110007C09Rik	NM_026738	chr13	49310494	49311161	567
Nr1d2	NM_011584	chr14	19070108	19071982	574
Nasp	NM_001081475	chr4	116299172	116299880	575
Rac1	NM_009007	chr5	144287977	144288588	578
Ubr2	NM_001177374	chr17	47146495	47147306	580
Tor1b	NM_133673	chr2	30808873	30809338	586
Agpat1	NM_001163379	chr17	34743173	34743612	588
1810013L24Rik	NM_001081400	chr16	8830558	8831022	598
Laptm4a	NM_008640	chr12	8928325	8929101	601
Rbmx	NR_029425	chrX	54645231	54645988	603
Srsf4	NM_020587	chr4	131429914	131430401	605
Lancl2	NM_133737	chr6	57652592	57653533	615
Map3k11	NM_022012	chr19	5689452	5690061	627
Stk33	NM_054103	chr7	116581786	116582091	628
Pvr	NM_027514	chr7	20505608	20506108	633
Rpl36al	NM_025589	chr12	70284134	70284700	636
Vps26a	NM_001113355	chr10	61948469	61948930	646
Plrg1	NM_016784	chr3	82859855	82860375	656
Mthfsd	NM_172761	chr8	123631375	123631858	662
Tcf7l1	NM_001079822	chr6	72738001	72738741	667
Got2	NM_010325	chr8	98411229	98411955	672
Erp29	NM_026129	chr5	121901529	121902072	682
Brpf3	NM_001081315	chr17	28938436	28939078	687
B3gnt9	NM_178879	chr8	107778030	107778699	688
Tyms	NM_021288	chr5	30399100	30399829	700
Pptc7	NM_177242	chr5	122734818	122735398	702
Phf19	NM_028716	chr2	34768404	34769161	713
Cdh6	NM_007666	chr15	13102061	13103298	714
Unc5b	NM_029770	chr10	60293247	60293980	715
Hist1h2ag	NM_178186	chr13	22133833	22134370	716
Scaf11	NM_028148	chr15	96290276	96290833	719
Stmn1	NM_019641	chr4	134024618	134025296	723
Mthfd1l	NM_001170785	chr10	6372326	6373155	725
Zrsr2	NM_009453	chrX	160395593	160396143	729
Ndrg1	NM_008681	chr15	66800047	66800893	732
Sema4c	NM_001126047	chr1	36614065	36614915	735
Smarce1	NM_020618	chr11	99091234	99091956	735
Gab1	NM_021356	chr8	83403150	83404128	738
Spsb2	NM_013539	chr6	124759284	124760110	739
Slc7a1	NM_007513	chr5	149210438	149211033	744
Hnrnpab	NM_010448	chr11	51419326	51419939	750
Plcg1	NM_021280	chr2	160557507	160558110	764
Snai1	NM_011427	chr2	167364126	167364880	777
Gt(ROSA)26Sor	NR_027010	chr6	113025929	113026991	777
Icam4	NM_023892	chr9	20834351	20834841	780
Thap4	NM_025920	chr1	95650373	95650889	783
Gtf2i	NM_001080748	chr5	134789319	134790359	790
Ccdc170	NM_001195672	chr10	5835586	5836167	792

Supplemental Table 2. Significant ChIP-seq E2F1 promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Hist1h2bn	NM_178201	chr13	21846597	21847000	808
Dhx15	NM_007839	chr5	52580634	52581316	809
Chmp2b	NM_026879	chr16	65561932	65562308	821
Gsr	NM_010344	chr8	34764230	34764835	824
Nmt2	NM_001290370	chr2	3202007	3202608	825
Wdr82	NM_029896	chr9	106073674	106074494	825
Tat	NM_146214	chr8	112514912	112515410	826
Pfn1	NM_011072	chr11	70467051	70467591	830
Dleu2	NR_028264	chr14	62299957	62300801	830
Pacs2	NM_001081170	chr12	114253288	114253868	860
Kitl	NM_013598	chr10	99479034	99479601	861
Fus	NM_139149	chr7	135111672	135112068	878
Zfp422	NM_026057	chr6	116577908	116578315	883
Actb	NM_007393	chr5	143667121	143667889	897
Copg2	NM_017478	chr6	30845513	30846273	900
Eif4a1	NM_144958	chr11	69484628	69485375	923
Zbtb7a	NM_010731	chr10	80599325	80600553	924
Mcm9	NM_027830	chr10	53349065	53349573	925
Cab39l	NM_026908	chr14	60060485	60061005	928
Ska2	NM_025377	chr11	86923370	86924036	941
Rrbp1	NM_024281	chr2	143835668	143836444	942
Hist1h1d	NM_145713	chr13	23647507	23648208	958
Lemd3	NM_001081193	chr10	120415052	120415794	962
Tmsb4x	NM_021278	chrX	163645906	163646437	978
Ttc7	NM_028639	chr17	87682975	87683431	978
Pkd1	NM_013630	chr17	24687664	24688105	991
Pard3	NM_033620	chr8	129588650	129589247	994
Tubb5	NM_011655	chr17	35973866	35974615	1005
Ddx26b	NM_172779	chrX	53708734	53709310	1007
Set	NM_001204875	chr2	29922651	29923388	1027
Sil1	NM_030749	chr18	35657317	35657779	1030
Thoc7	NM_001285780	chr14	14792626	14792955	1036
C030034I22Rik	NR_026848	chr17	69766493	69767162	1042
Sfpq	NR_045010	chr4	126699356	126699822	1045
5430416N02Rik	NR_034038	chr5	100857169	100857837	1050
Nipbl	NM_027707	chr15	8393210	8393610	1052
Sclt1	NM_001081411	chr3	41544959	41545806	1053
Dnmt1	NM_001199433	chr9	20755744	20756273	1058
Jund	NM_010592	chr8	73222241	73223193	1080
Tubb6	NM_026473	chr18	67551153	67551793	1089
Crabp1	NM_013496	chr9	54613302	54614061	1128
Ltbp4	NM_175641	chr7	28121196	28121808	1128
Lmnb1	NM_010721	chr18	56868383	56868812	1132
Hist1h1c	NM_015786	chr13	23831463	23832170	1142
Trp53	NM_001127233	chr11	69394412	69395598	1145
Spred2	NM_033523	chr11	19825071	19826118	1151
Sin3a	NM_001110351	chr9	56920724	56921278	1155
Socs3	NM_007707	chr11	117829300	117829743	1158

Supplemental Table 2. Significant ChIP-seq E2F1 promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
9130011E15Rik	NM_198296	chr19	46071506	46072110	1169
Dlk2	NM_001286013	chr17	46435843	46436280	1186
Bcar1	NM_001198839	chr8	114254554	114255124	1196
Sema5a	NM_009154	chr15	32175598	32176031	1248
Ftx	NR_028381	chrX	100817673	100817989	1261
Senp5	NM_177103	chr16	32001788	32002395	1281
Eml5	NM_001081191	chr12	100138205	100138610	1286
Ube2g1	NM_025985	chr11	72421786	72422320	1291
Hnrnpu	NM_016805	chr1	180266403	180266801	1312
Shisa5	NM_026381	chr9	108958517	108958883	1321
Clip2	NM_009990	chr5	135026678	135027260	1334
Angptl6	NM_145154	chr9	20682311	20683257	1369
Gadd45g	NM_011817	chr13	51942955	51943870	1370
0610009L18Rik	NR_038126	chr11	120211023	120211724	1383
Cdkn1a	NM_007669	chr17	29231157	29233061	1393
Sdc1	NM_011519	chr12	8779385	8779809	1396
Gm17762	NR_028378	chr2	17950019	17950584	1427
Lrp8	NM_001080926	chr4	107475929	107476668	1436
Hnrnpa2b1	NM_016806	chr6	51418124	51418757	1452
Ckap4	NM_175451	chr10	83994760	83995405	1550
Nphp3	NM_028721	chr9	103906189	103906700	1572
Etaa1	NM_026576	chr11	17852022	17852428	1652
Galk1	NM_016905	chr11	115872104	115872619	1671
Rasl10a	NM_145216	chr11	4959603	4960039	1691
Wdr54	NM_023790	chr6	83104486	83104869	1695
Hsd3b3	NM_001161745	chr3	98564433	98564827	1702
Frmd6	NM_028127	chr12	71927924	71928520	1722
Mss51	NM_029104	chr14	21314066	21314697	1741
Ptma	NM_008972	chr1	88424132	88425990	1751
Myc	NM_001177353	chr15	61818333	61818982	1763
Sin3a	NM_001110351	chr9	56921415	56921820	1772
Fam64a	NM_144526	chr11	71857703	71858050	1874
Pou3f2	NM_008899	chr4	22413304	22413965	1878
Ajuba	NM_010590	chr14	55194314	55194891	1895
Gnai2	NM_008138	chr9	107535449	107536089	1903
Ncam1	NM_001113204	chr9	49604902	49605551	1947
Sowahc	NM_172939	chr10	58686305	58686933	1950
Junb	NM_008416	chr8	87499971	87501413	1954
2810002D19Rik	NR_027831	chr2	94248522	94249139	1968
Ing1	NM_011919	chr8	11557747	11558377	1997

Supplemental Table 3. Significant ChIP-seq E2F3A promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Necab3	NM_021546	chr2	154386383	154386737	-1972
Plekha2	NM_031257	chr8	26214051	26214424	-1956
Ftl1	NM_010240	chr7	52717009	52717381	-1940
Tmem194	NM_001113211	chr10	127112086	127112454	-1850
Ywhaz	NM_001253807	chr15	36722149	36722640	-1709
Tomm22	NM_172609	chr15	79499456	79499742	-1698
Fis1	NM_001163243	chr5	137427320	137427583	-1693
Grm8	NM_008174	chr6	28085873	28086225	-1681
Olfr810	NM_146550	chr10	129230095	129230459	-1635
Kif16b	NM_001081133	chr2	142728654	142728955	-1606
Mmp8	NM_008611	chr9	7556718	7556997	-1571
Hcfc1	NM_008224	chrX	71213016	71213510	-1568
Scd2	NM_009128	chr19	44366433	44366790	-1554
Clmp	NM_133733	chr9	40492372	40492713	-1504
Nudt16	NM_029385	chr9	105035507	105035738	-1489
Erbb3	NM_010153	chr10	128027853	128028208	-1475
Ctdsp1	NM_153088	chr1	74436664	74436862	-1419
Rara	NM_009024	chr11	98797364	98797843	-1406
Nfatc4	NM_001168346	chr14	56442043	56442539	-1340
Camk2n2	NM_028420	chr16	20622436	20622741	-1239
Zfp866	NM_177899	chr8	72299842	72300204	-1214
Abcb1b	NM_011075	chr5	8796754	8797217	-1161
Ier2	NM_010499	chr8	87187673	87188088	-1131
Fosl2	NM_008037	chr5	32437521	32437992	-1088
Gm10440	NR_038045	chr5	54740004	54740360	-1048
Pkn3	NM_153805	chr2	29933082	29933450	-1019
Trib1	NM_144549	chr15	59478979	59479433	-1002
Acvr2b	NM_007397	chr9	119310485	119310796	-978
Pbx3	NM_016768	chr2	34228224	34228843	-970
Khdrbs1	NR_045036	chr4	129420421	129420593	-961
Maz	NM_010772	chr7	134170755	134171105	-938
Hivep2	NM_010437	chr10	13685065	13685436	-934
Fam222a	NM_001004180	chr5	115017203	115017485	-915
Spata20	NM_144827	chr11	94347377	94347625	-878
Kcnj16	NM_010604	chr11	110828322	110828620	-875
Mirlet7i	NR_029527	chr10	122423498	122423695	-818
Iqsec2	NM_001005475	chrX	148612598	148612890	-807
Arid1a	NM_001080819	chr4	133310144	133310507	-801
Sox12	NM_011438	chr2	152224319	152224788	-773
Irs2	NM_001081212	chr8	11008985	11009402	-765
Ppp1r9b	NM_172261	chr11	94851628	94851938	-742
Mir1191b	NR_106141	chr10	80879519	80880035	-736
Pds5a	NM_001081321	chr5	66089597	66090035	-722
Dennd4b	NM_201407	chr3	90069551	90069905	-707
Mall	NM_145532	chr2	127556141	127556505	-691
Eif3b	NM_133916	chr5	140894416	140894729	-686
Gng11	NM_025331	chr6	3953143	3953461	-684

Supplemental Table 3. Significant ChIP-seq E2F3A promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Map3k3	NM_011947	chr11	105945346	105945731	-677
Cnot1	NM_001205226	chr8	98331895	98332144	-659
4930577N17Rik	NR_073429	chr3	51079804	51080251	-655
Khsrp	NM_010613	chr17	57171323	57171833	-649
Pfn1	NM_011072	chr11	70468578	70468943	-610
Baz1b	NM_011714	chr5	135662408	135662764	-606
Srsf3	NM_013663	chr17	29168828	29169173	-604
Pidd1	NM_022654	chr7	148629650	148630024	-584
Zfp64	NM_009564	chr2	168781430	168781884	-571
Lce3b	NM_025501	chr3	92736194	92736483	-562
Pop7	NM_028753	chr5	137944026	137944389	-552
Rnf26	NM_153762	chr9	43921511	43921853	-549
Pim1	NM_008842	chr17	29627229	29627673	-538
Gm53	NR_037977	chr11	96112217	96112659	-535
Sash1	NM_175155	chr10	8606223	8606575	-532
Lrif1	NM_001039478	chr3	106487201	106487543	-532
Fchsd2	NM_001146010	chr7	108256592	108256930	-527
Abhd13	NM_026868	chr8	9977001	9977415	-508
Ubap2	NM_026872	chr4	41222431	41222888	-493
Sertad2	NM_001038625	chr11	20531334	20531646	-489
Xpo1	NM_001035226	chr11	23155393	23155714	-487
Zfp36l2	NM_001001806	chr17	84587369	84588153	-475
Usp28	NM_175482	chr9	48792870	48793176	-466
Mir148a	NR_029719	chr6	51220190	51220537	-456
Gphn	NM_145965	chr12	79327037	79327351	-447
Cd3eap	NM_145822	chr7	19945100	19945456	-447
Afmid	NM_027827	chr11	117686650	117686948	-433
Hnrnpa0	NM_029872	chr13	58230243	58230447	-429
Rps19	NM_023133	chr7	25669159	25669447	-429
Stag1	NM_009282	chr9	100543494	100543746	-421
Ric8b	NM_183172	chr10	84379755	84380136	-412
Eef1a1	NM_010106	chr9	78329742	78330077	-380
Gls2	NM_001033264	chr10	127631095	127631534	-376
Raph1	NM_001045513	chr1	60623805	60624157	-373
Ccne1	NM_007633	chr7	38892644	38893110	-369
Slmo2	NM_025531	chr2	174298619	174298999	-368
Zfp219	NM_001253694	chr14	52639376	52640124	-363
Ciart	NM_001033302	chr3	95686339	95686671	-355
Osgepl1	NM_001285839	chr1	53369952	53370275	-354
Otud4	NM_001256033	chr8	82162890	82163553	-353
Mxd3	NM_016662	chr13	55431175	55431695	-345
Gm608	NM_001029889	chr16	44173041	44173292	-343
Fbxo5	NM_025995	chr10	4540287	4541184	-340
Ezh2	NM_007971	chr6	47545037	47545698	-340
Rev1	NM_019570	chr1	38186657	38187027	-336
Smc3	NM_007790	chr19	53674353	53674750	-334
Hmgb2	NM_008252	chr8	59990088	59990539	-326

Supplemental Table 3. Significant ChIP-seq E2F3A promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Klf10	NM_001289471	chr15	38230585	38230994	-325
Ipo5	NM_023579	chr14	121309900	121310287	-322
Rictor	NM_030168	chr15	6657926	6658197	-319
Ccng2	NM_007635	chr5	93696141	93696421	-317
Calm2	NM_007589	chr17	87846482	87846697	-316
Tbl2	NM_013763	chr5	135625088	135625445	-314
Supt16	NM_033618	chr14	52817080	52817370	-312
Zmym6	NM_177462	chr4	126754134	126754499	-310
Foxn2	NM_180974	chr17	88839508	88839977	-309
Ywhaq	NM_011739	chr12	21423457	21423749	-307
Ube2d2a	NM_019912	chr18	35930710	35931112	-301
2310057M21Rik	NM_026655	chr7	138506306	138506717	-301
Zfp609	NM_172536	chr9	65675546	65675788	-297
Rbm33	NM_028234	chr5	28643062	28643801	-297
Hnrnpul1	NM_144922	chr7	26539744	26540317	-293
Lgals1	NM_008495	chr15	78756625	78757103	-290
Cenpb	NM_007682	chr2	131005897	131006172	-288
Lrwd1	NM_027891	chr5	136612064	136612392	-285
Btbd8	NM_001255991	chr5	107866497	107866970	-282
Ptma	NM_008972	chr1	88422727	88423335	-279
Mmp16	NM_019724	chr4	17780217	17780484	-278
Pars2	NM_001285783	chr4	106323180	106323611	-278
Azin1	NM_018745	chr15	38449088	38449505	-277
Lmnb1	NM_010721	chr18	56867046	56867334	-276
Mir199b	NR_029811	chr2	32173509	32173904	-273
Pabpc1	NM_008774	chr15	36538720	36539273	-270
Plekhh3	NM_146030	chr11	101032700	101033058	-264
Ptk7	NM_175168	chr17	46766571	46766857	-262
Hinfp	NM_172162	chr9	44113886	44114139	-260
Tmub2	NM_028076	chr11	102145792	102146240	-258
Aff1	NM_133919	chr5	104182759	104183092	-255
Celf6	NM_175235	chr9	59425706	59426076	-252
Uhrf1	NM_001111080	chr17	56443159	56443812	-250
Cirbp	NM_007705	chr10	79630060	79630621	-245
Psma1	NM_011965	chr7	121419706	121420035	-242
Vav3	NM_146139	chr3	109376504	109376862	-241
Acy1	NM_001276442	chr9	106340631	106340983	-241
Utp3	NM_023054	chr5	88983033	88983501	-240
Plec	NM_201394	chr15	76026158	76026597	-239
Plekha1	NM_133942	chr7	138008989	138009382	-238
Srsf10	NM_001284196	chr4	135411442	135412054	-237
Phf23	NM_030064	chr11	69808753	69809320	-231
Casp2	NM_007610	chr6	42214668	42214947	-230
Rab6a	NM_001163663	chr7	107755723	107756018	-229
E2f8	NM_001013368	chr7	56136467	56136806	-227
Pcbp2	NM_011042	chr15	102300671	102301001	-226
Kpna3	NM_008466	chr14	62058735	62059277	-223

Supplemental Table 3. Significant ChIP-seq E2F3A promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Klf5	NM_009769	chr14	99697540	99697835	-222
Nadk2	NM_001286255	chr15	9000484	9001089	-222
Zfp869	NM_001039965	chr8	72240764	72241278	-221
Maff	NM_010755	chr15	79177692	79178081	-221
Capn7	NM_009796	chr14	32149479	32149903	-218
Srsf4	NM_020587	chr4	131429080	131429590	-218
Dctn1	NM_001198866	chr6	83115495	83115906	-217
Herpud1	NM_022331	chr8	96909969	96910398	-216
Wdr1	NM_011715	chr5	38952911	38953185	-215
Zmynd19	NM_026021	chr2	24804905	24805312	-213
Gltp	NM_019821	chr5	115141042	115141267	-212
Nup50	NM_016714	chr15	84753390	84753903	-211
Gpatch8	NM_001159492	chr11	102417392	102417970	-210
Cdca7	NM_025866	chr2	72313815	72314315	-210
Hspa8	NM_031165	chr9	40608934	40609357	-210
Stt3b	NM_024222	chr9	115219522	115219968	-207
Fam76b	NM_176836	chr9	13631802	13632125	-207
Mllt1	NM_022328	chr17	57074838	57075194	-206
Dgcr8	NM_033324	chr16	18289244	18289682	-203
Myh9	NM_022410	chr15	77672601	77673002	-198
P4hb	NM_011032	chr11	120434341	120434551	-197
Nucks1	NM_001145804	chr1	133806492	133807183	-197
Micu1	NM_001291442	chr10	59164909	59165319	-196
Cstf3	NM_145529	chr2	104430265	104430624	-196
Hist1h4a	NM_178192	chr13	23853025	23853599	-195
Gan	NM_001081151	chr8	119681690	119681988	-195
Ift140	NM_134126	chr17	25152481	25153190	-195
C330013E15Rik	NR_045701	chr15	100445536	100445926	-191
Cbx3	NM_007624	chr6	51420290	51420559	-190
Arid3a	NM_007880	chr10	79389417	79389780	-189
Ift80	NM_026641	chr3	68808288	68809071	-189
Casp8ap2	NM_001122978	chr4	32702085	32702436	-187
Nudt18	NM_153136	chr14	70977298	70977636	-186
Gpr180	NM_021434	chr14	118535990	118536334	-186
Ran	NM_009391	chr5	129525644	129526044	-186
H2afx	NM_010436	chr9	44142402	44142820	-186
Atxn2l	NM_183020	chr7	133646780	133647221	-186
Ppil1	NM_026845	chr17	29400769	29401431	-185
Fam208a	NM_028945	chr14	28241705	28241992	-184
Rbl1	NM_011249	chr2	157030131	157030771	-182
Adss	NM_007422	chr1	179726659	179726981	-181
Birc6	NM_007566	chr17	74927277	74927629	-181
Cep152	NM_001081091	chr2	125450932	125451126	-181
Ap1ar	NM_145964	chr3	127540474	127540706	-181
Mapk1ip1l	NM_178684	chr14	47917619	47917997	-180
Ppp1cc	NM_013636	chr5	122607885	122608336	-177
Vmn2r108	NM_001104570	chr17	20618190	20618559	-176

Supplemental Table 3. Significant ChIP-seq E2F3A promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Dscc1	NM_183089	chr15	54921995	54922416	-174
Gtpbp2	NM_019581	chr17	46297623	46297990	-174
Rcl1	NM_021525	chr19	29175452	29175930	-173
Ndst3	NR_121616	chr3	123393811	123394065	-169
Arhgef40	NM_001145921	chr14	52604185	52604493	-168
Itpr1	NM_010585	chr6	108162834	108163014	-165
Cdc6	NM_001025779	chr11	98768826	98769251	-164
Rps20	NM_026147	chr4	3762720	3763099	-164
Fmnl3	NM_011711	chr15	99200783	99201335	-163
Tssc4	NM_138631	chr7	150254843	150255375	-163
Kif13b	NM_001081177	chr14	65271040	65271371	-162
Ddost	NM_007838	chr4	137860350	137860631	-162
C630043F03Rik	NR_027923	chr4	71861909	71862323	-161
Rfwd3	NM_146218	chr8	113824095	113824469	-161
Cobll1	NM_027225	chr2	65076763	65076922	-161
Ppwd1	NM_172807	chr13	105018881	105019285	-160
Cnot6	NM_212484	chr11	49526200	49526565	-160
Slc35e1	NM_177766	chr8	75016532	75016809	-159
Trappc10	NM_001081055	chr10	77707375	77707712	-158
Nutf2	NM_026532	chr8	108384187	108384565	-157
Chaf1b	NM_028083	chr16	93883677	93884300	-157
Fem1a	NM_010192	chr17	56395896	56396223	-156
Txndc17	NM_026559	chr11	72020742	72021061	-154
Xpot	NM_001081056	chr10	121063383	121063665	-153
Irf2bp1	NM_178757	chr7	19589119	19589402	-153
Hist1h4f	NM_175655	chr13	23643465	23643861	-152
Chaf1a	NM_013733	chr17	56179534	56179838	-152
Dnmt1	NM_001199433	chr9	20756868	20757568	-152
U2af1	NM_024187	chr17	31795668	31796031	-152
Wdr89	NM_028203	chr12	76770491	76770855	-150
Stard4	NM_133774	chr18	33373454	33373784	-150
1810026B05Rik	NR_037569	chr7	80703272	80703585	-149
Slc39a1	NM_013901	chr3	90051803	90052128	-148
Nup85	NM_001002929	chr11	115425287	115425934	-147
Cyp39a1	NM_001285948	chr17	43803966	43804381	-147
Epb4.1l3	NM_013813	chr17	69505815	69506194	-145
Tra2b	NM_009186	chr16	22265939	22266351	-144
Ccnl1	NM_019937	chr3	65762053	65762527	-144
Tef	NM_017376	chr15	81641570	81641829	-144
Piezo1	NM_001037298	chr8	125075196	125075547	-144
Rbbp4	NM_009030	chr4	129012505	129013006	-143
Hist1h3g	NM_145073	chr13	23626868	23627420	-142
Akap11	NM_001164503	chr14	78936623	78936992	-142
Lamtor2	NM_031248	chr3	88356822	88357157	-142
Bard1	NM_007525	chr1	71149520	71149851	-141
Snx18	NM_130796	chr13	114408769	114409054	-141
Zfp706	NM_026521	chr15	36937119	36937474	-141

Supplemental Table 3. Significant ChIP-seq E2F3A promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Ubqln4	NM_033526	chr3	88357366	88357627	-141
Nop56	NM_024193	chr2	130099663	130100351	-140
Zfp382	NM_001081007	chr7	30906657	30906996	-140
Alg8	NM_199035	chr7	104519788	104520185	-140
Ugp2	NM_001290634	chr11	21271282	21271533	-139
Hist1h2af	NM_175661	chr13	23625434	23625847	-139
Trim59	NM_025863	chr3	68848611	68848992	-139
Tmpo	NM_001080129	chr10	90634300	90634702	-138
Ap5z1	NM_172725	chr5	142939544	142939948	-138
Pelp1	NM_029231	chr11	70223529	70223808	-137
Zw10	NM_012039	chr9	48863329	48863768	-137
Ccno	NM_001081062	chr13	113777681	113778066	-136
Dnajc14	NM_028873	chr10	128242444	128242749	-135
Vamp3	NM_009498	chr4	150431993	150432398	-135
Rpa2	NM_011284	chr4	132323936	132324344	-134
3110082I17Rik	NM_028469	chr5	139936445	139936796	-134
Rell1	NM_145923	chr5	64360098	64360438	-133
Mki67	NM_001081117	chr7	142907917	142908470	-133
Ptges3	NM_019766	chr10	127495748	127496062	-132
Tfap4	NM_031182	chr16	4559679	4560023	-132
Pisd-ps2	NR_003519	chr17	3084083	3084545	-132
A630066F11Rik	NR_030698	chr10	7382746	7383330	-130
Slc15a4	NM_133895	chr5	128097751	128098030	-130
Atl2	NM_178050	chr17	80295419	80295761	-128
Psmc4	NM_011874	chr7	28835112	28835364	-128
Map2k7	NM_001164172	chr8	4238371	4238851	-128
Fam111a	NM_026640	chr19	12647694	12648079	-128
Kdm3a	NM_001038695	chr6	71582910	71583164	-127
Smarcd1	NM_031842	chr15	99532355	99532828	-126
Rfc5	NM_028128	chr5	117838944	117839368	-125
Fhod1	NM_177699	chr8	107871666	107872322	-125
Ipo11	NM_029665	chr13	107726988	107727249	-125
Kras	NM_021284	chr6	145198789	145198960	-125
Tor1aip2	NM_172843	chr1	157882498	157882841	-124
Arrb2	NM_145429	chr11	70245815	70246100	-124
Zfp280d	NM_146224	chr9	72122376	72122788	-123
Hist1h2ag	NM_178186	chr13	22134772	22135106	-122
Kif24	NM_024241	chr4	41411817	41412187	-122
Cenpp	NM_025495	chr13	49748049	49748392	-122
Skap2	NM_018773	chr6	51962504	51962832	-121
Msh2	NM_008628	chr17	88071595	88071957	-120
Atad2	NM_027435	chr15	57966325	57967186	-120
Apoo	NM_026673	chrX	91612145	91612516	-118
Commd9	NM_029635	chr2	101726177	101726427	-116
Tmtc4	NM_028651	chr14	123382381	123382814	-116
Nolc1	NM_053086	chr19	46149969	46150472	-116
Nupl1	NM_170591	chr14	60870218	60870440	-115

Supplemental Table 3. Significant ChIP-seq E2F3A promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Srsf3	NM_013663	chr17	29169268	29169710	-115
Smdt1	NM_026914	chr15	82176206	82176520	-112
Mid1ip1	NM_026524	chrX	10294163	10294594	-112
Ado	NM_001005419	chr10	67011665	67011961	-111
Iscu	NM_025526	chr5	114222608	114222810	-111
Brpf3	NM_001081315	chr17	28937770	28938149	-111
Nop58	NM_018868	chr1	59741521	59741958	-110
Ccnf	NM_007634	chr17	24388205	24388720	-110
Mcm6	NM_008567	chr1	130256193	130256488	-109
Larp4b	NM_172585	chr13	9092904	9093180	-108
Mrps17	NM_025450	chr5	130221159	130221429	-108
Wee1	NM_009516	chr7	117265285	117265644	-108
Srsf2	NM_011358	chr11	116714190	116714838	-107
Npat	NM_001081152	chr9	53344851	53345237	-107
Pa2g4	NM_011119	chr10	128002961	128003228	-106
Wwp2	NM_025830	chr8	109960029	109960354	-106
Nap1l1	NM_015781	chr10	110909912	110910373	-105
Msh5	NM_001146215	chr17	35183401	35184142	-105
Spr	NM_011467	chr6	85087672	85088051	-105
Cenpm	NM_001080158	chr15	82074669	82075068	-104
Btf3l4	NM_027453	chr4	108506122	108506458	-102
Sntb2	NM_009229	chr8	109459369	109459725	-102
Kpnb1	NM_008379	chr11	97049155	97049458	-102
Rmi2	NM_001162932	chr16	10834788	10835313	-101
Rrn3	NM_001039521	chr16	13780478	13780904	-100
Rps27l	NM_026467	chr9	66793693	66793955	-100
Ncln	NM_134009	chr10	80959040	80959373	-100
Tmx1	NM_028339	chr12	71553893	71554188	-100
Akip1	NM_020616	chr7	116846997	116847304	-100
Mis18bp1	NM_172578	chr12	66273553	66273777	-99
Khsrp	NM_010613	chr17	57170772	57171284	-99
Elmo2	NM_207706	chr2	165151939	165152215	-99
Zbtbd6	NM_001034882	chr14	79851388	79851697	-99
Rpl3	NM_013762	chr15	79913734	79914132	-98
Prpf19	NM_134129	chr19	10969465	10969780	-98
Megf9	NM_172694	chr4	70195853	70196264	-98
Pitpnb	NM_019640	chr5	111759485	111759885	-97
Suz12	NM_001163018	chr11	79806323	79806699	-96
Gcat	NM_001161712	chr15	78861088	78861326	-96
Hmgb1	NM_010439	chr5	149864537	149864877	-95
Zfp367	NM_175494	chr13	64254412	64254789	-95
Smchd1	NM_028887	chr17	71824596	71824955	-94
Pigm	NM_026234	chr1	174306438	174306699	-93
Naglu	NM_013792	chr11	100931147	100931482	-93
Echs1	NM_053119	chr7	147302202	147302624	-92
Msmo1	NM_025436	chr8	67212234	67212698	-92
Rasl11b	NM_026878	chr5	74591082	74591435	-92

Supplemental Table 3. Significant ChIP-seq E2F3A promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Ncapg2	NM_133762	chr12	117643541	117644026	-91
Gpr137c	NM_027518	chr14	45839090	45839511	-91
Naa16	NM_025832	chr14	79790417	79790712	-91
Crkl	NM_001277231	chr16	17451846	17452127	-91
BC003331	NM_001077237	chr1	152239963	152240584	-90
A430005L14Rik	NM_175287	chr4	153331067	153331444	-90
Brip1	NM_178309	chr11	86014528	86015038	-89
Mef2b	NM_001045484	chr8	72676444	72676730	-89
Nhp2l1	NM_011482	chr15	81877951	81878280	-89
Hnrnpa3	NM_198090	chr2	75496975	75497478	-89
Upf3b	NM_026573	chrX	34650195	34650614	-89
Tcf19	NM_001163764	chr17	35653508	35654204	-88
Ate1	NM_001136054	chr7	137662975	137663386	-88
Cenpi	NM_145924	chrX	130842497	130842730	-88
Ppp1r16a	NM_033371	chr15	76501844	76502200	-87
Fkbp2	NM_001166368	chr19	7054912	7055159	-86
Spc25	NM_025565	chr2	69044107	69044555	-85
4930432K21Rik	NM_001163752	chr8	86671634	86672069	-85
Peak1	NM_172924	chr9	56265843	56266038	-85
Mybl2	NM_008652	chr2	162880005	162880567	-84
Osbpl8	NM_175489	chr10	110601590	110601958	-83
Spg7	NM_153176	chr8	125589168	125589480	-83
Ttll5	NM_001081423	chr12	87165654	87165979	-83
Tex9	NM_009359	chr9	72339581	72340113	-82
Fkbp5	NM_010220	chr17	28623055	28623294	-82
Ufsp2	NM_138668	chr8	47060616	47060983	-82
Polr2m	NM_178602	chr9	71333749	71333992	-82
Aph1a	NM_146104	chr3	95697598	95697927	-81
Mcmbp	NM_145955	chr7	135883927	135884117	-80
Cdc25a	NM_007658	chr9	109777682	109778323	-80
Cdk1	NM_007659	chr10	68815437	68816039	-79
Serf1	NM_011353	chr13	100877774	100878015	-79
Zc3h6	NM_178404	chr2	128792911	128793206	-79
Pnkd	NM_001039509	chr1	74331371	74331687	-78
Cntrl	NM_012018	chr2	34964741	34965125	-78
Phactr4	NM_001161797	chr4	131978307	131978569	-78
Gm20604	NM_001142939	chr12	103995957	103996234	-77
Ost4	NM_001134692	chr5	31210073	31210400	-77
Nktr	NM_010918	chr9	121627992	121628451	-77
Tmem39b	NM_199305	chr4	129374017	129374297	-76
Slc25a25	NM_146118	chr2	32306809	32307320	-76
Mapk7	NM_001291035	chr11	61307629	61308055	-75
Tcp1	NM_013686	chr17	13108858	13109380	-75
Ap1s1	NM_007457	chr5	137521853	137522155	-75
Supt3	NM_178652	chr17	44913891	44914198	-75
Ranbp1	NM_011239	chr16	18248650	18249070	-74
Wwc2	NM_133791	chr8	49075791	49076164	-74

Supplemental Table 3. Significant ChIP-seq E2F3A promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Tmpo	NM_001283048	chr10	90633133	90633601	-73
Pcbd2	NM_028281	chr13	55828534	55828776	-73
Cdkal1	NM_144536	chr13	29947389	29947668	-73
Rbm39	NM_001291114	chr2	156005848	156006243	-73
Ctdspl2	NM_212450	chr2	121781493	121781835	-72
4930427A07Rik	NM_134041	chr12	114394392	114394727	-72
Eif3d	NM_018749	chr15	77801127	77801522	-72
Tpp2	NM_009418	chr1	43990601	43990959	-71
B230219D22Rik	NM_181278	chr13	55794267	55794559	-71
Spdya	NM_029254	chr17	71901235	71901423	-71
Iqgap3	NM_001033484	chr3	87885637	87886165	-71
Tmem106c	NM_201359	chr15	97794412	97794768	-69
Mapk14	NM_011951	chr17	28828005	28828429	-69
Oip5	NM_001042653	chr2	119444109	119444508	-69
Timm50	NM_025616	chr7	29096976	29097289	-69
Snrpe	NM_009227	chr1	135506820	135507028	-68
Tagln2	NM_178598	chr1	174430171	174430446	-68
Pcgf6	NM_027654	chr19	47125242	47125561	-68
Clp1	NM_133840	chr2	84567288	84567695	-68
Hadhb	NM_145558	chr5	30481554	30481897	-67
Acer3	NM_025408	chr7	105457971	105458234	-67
Tnks	NM_175091	chr8	36028619	36029000	-67
1700021F05Rik	NM_026411	chr10	43260662	43261068	-66
BC030867	NM_153544	chr11	102109979	102110279	-66
2700099C18Rik	NR_024720	chr17	95149241	95149505	-66
Pcnt	NM_008787	chr10	75905549	75905894	-66
Ror2	NM_013846	chr13	53381352	53381733	-66
Eefsec	NM_023060	chr6	88396441	88396753	-65
Tbccd1	NM_001081368	chr16	22857613	22857798	-65
Dennd1a	NM_146122	chr2	38142807	38143127	-64
Psmb2	NM_011970	chr4	126354703	126354941	-64
Cdkn1a	NM_007669	chr17	29230550	29230755	-64
Snhg8	NR_028574	chr3	123211011	123211621	-63
Nop2	NM_138747	chr6	125081633	125082041	-63
Dnajb1	NM_018808	chr8	86131783	86132237	-63
Tmco1	NM_001039483	chr1	169238557	169238918	-63
Tsfm	NM_025537	chr10	126467800	126468062	-62
Psap	NM_001146123	chr10	59740172	59740456	-61
Gins3	NM_030198	chr8	98157250	98157544	-61
Zmiz1	NM_183208	chr14	26278486	26278733	-61
Mecp2	NM_010788	chrX	71330931	71331245	-60
Gm11974	NR_045893	chr11	6428685	6428958	-60
1200014J11Rik	NM_025818	chr11	72861139	72861478	-60
Sp2	NM_030220	chr11	96838962	96839159	-60
Rab26os	NR_045289	chr17	24664884	24665387	-60
Dpm2	NM_010073	chr2	32426043	32426592	-60
Timm13	NM_013895	chr10	80363579	80363965	-59

Supplemental Table 3. Significant ChIP-seq E2F3A promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Mcm4	NM_008565	chr16	15637320	15637782	-59
Scaf1	NM_001008422	chr7	52271467	52271887	-59
Rps11	NM_013725	chr7	52379641	52379993	-59
Prim1	NM_008921	chr10	127451966	127452458	-58
Frg1	NM_013522	chr8	42502430	42502628	-58
Elmod2	NM_178736	chr8	85856296	85856588	-58
Cript	NM_019936	chr17	87424646	87425039	-58
Nfx1	NM_001290449	chr4	40917697	40918065	-57
Mmgt1	NM_146234	chrX	53851022	53851280	-56
Rbfox2	NM_175387	chr15	77137313	77137762	-56
Rer1	NM_026395	chr4	154460283	154460637	-55
Tubgcp3	NM_198031	chr8	12672019	12672289	-55
AI314180	NM_172381	chr4	58925527	58925774	-55
Tra2a	NM_198102	chr6	49213989	49214220	-55
Lin52	NM_173756	chr12	85792288	85792518	-54
Uba52	NM_019883	chr8	73034074	73034563	-54
Pigu	NM_001004721	chr2	155183064	155183360	-53
Nfyc	NM_001277095	chr4	120498258	120498538	-53
Hist2h4	NM_033596	chr3	96067093	96067489	-52
Dtl	NM_029766	chr1	193399255	193399672	-52
Msh6	NM_010830	chr17	88374121	88374554	-52
Wdhd1	NM_172598	chr14	47896373	47896790	-51
Ranbp3	NM_001252467	chr17	56812314	56812879	-51
Ppp1r8	NM_146154	chr4	132398978	132399289	-51
Fbxo48	NM_176982	chr11	16851029	16851695	-50
Mrpl12	NM_027204	chr11	120345811	120346055	-49
Prkab2	NM_182997	chr3	97461946	97462224	-49
Mthfd1	NM_138745	chr12	77356063	77356276	-49
Actl6b	NM_031404	chr5	137994552	137994916	-48
Anapc11	NM_001038230	chr11	120459574	120460022	-47
Lyst	NM_010748	chr13	13682436	13682820	-47
Ddx27	NM_153065	chr2	166840582	166840948	-47
Pask	NM_080850	chr1	95239176	95239645	-47
Cnot10	NM_153585	chr9	114549113	114549614	-47
AI413582	NM_001002895	chr17	27702508	27702926	-46
Ccp110	NM_182995	chr7	125855917	125856240	-46
Lsm10	NM_138721	chr4	125773700	125774002	-45
Rangap1	NM_001146174	chr15	81560212	81560573	-45
Dtymk	NM_001105667	chr1	95698303	95698803	-43
Nubp1	NM_011955	chr16	10411767	10412207	-43
Clcc1	NM_145543	chr3	108456647	108456927	-43
Cbx5	NM_001076789	chr15	103070102	103070475	-43
Atg4c	NM_001145967	chr4	98860605	98860984	-43
E2f3	NM_010093	chr13	30077551	30078394	-42
Topbp1	NM_176979	chr9	103207404	103207825	-42
BC049762	NM_177567	chr11	51076361	51076625	-41
Cpsf3l	NM_028020	chr4	155243475	155243793	-41

Supplemental Table 3. Significant ChIP-seq E2F3A promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
1190002N15Rik	NM_001033145	chr9	94438395	94438685	-41
Papd4	NM_133905	chr13	93962089	93962466	-41
Acin1	NM_001085473	chr14	55305590	55306025	-41
Smarcc1	NM_009211	chr9	110034305	110034670	-40
Smc2	NM_008017	chr4	52451783	52452379	-39
Mdm1	NM_148922	chr10	117578611	117578996	-39
Kcnab2	NM_010598	chr4	151851548	151851841	-38
Sh3gl1	NM_013664	chr17	56175878	56176312	-36
Prkci	NM_008857	chr3	30894501	30894811	-36
Mtmr3	NM_028860	chr11	4494726	4494979	-36
Rprd1b	NM_001291135	chr2	157853838	157854555	-36
Srsf1	NM_001078167	chr11	87860629	87861049	-35
Trub2	NM_001290495	chr2	29643105	29643344	-35
Mutyh	NM_133250	chr4	116480159	116480448	-35
Fanca	NM_016925	chr8	125842411	125842607	-34
1700123M08Rik	NR_040577	chr4	11893413	11893960	-34
2410006H16Rik	NR_030738	chr11	62416044	62416648	-32
Smek1	NM_211355	chr12	102321824	102322062	-32
Ltn1	NM_001081068	chr16	87432708	87433056	-32
Sgol1	NM_028232	chr17	53828494	53828848	-32
Bag4	NM_026121	chr8	26895543	26895881	-32
Ptrh2	NM_001098810	chr11	86497265	86497836	-32
Cops4	NM_012001	chr5	100947107	100947484	-32
Mns1	NM_008613	chr9	72286012	72286595	-32
Gadd45b	NM_008655	chr10	80392566	80393042	-31
Rif1	NM_175238	chr2	51928205	51928445	-31
Baz1b	NM_011714	chr5	135662896	135663426	-31
Zfp383	NM_001243908	chr7	30693270	30693740	-30
Crebzf	NM_145151	chr7	97591119	97591401	-30
Vars	NM_011690	chr17	35137629	35138014	-30
Rpusd2	NM_173450	chr2	118860350	118860641	-30
Isy1	NM_133934	chr6	87788623	87788940	-30
Limk2	NM_010718	chr11	3309141	3309397	-29
Acat1	NM_144784	chr9	53418363	53418603	-29
A630020A06	NR_045740	chr15	3945718	3946302	-28
AA465934	NR_028363	chr11	83104984	83105361	-28
Hist1h2ah	NM_175659	chr13	22127443	22127634	-28
Tradd	NM_001033161	chr8	107788398	107788642	-27
Apol7d	NR_040308	chr1	71699664	71700099	-27
Siva1	NM_001161737	chr12	113882847	113883176	-27
Gtse1	NM_001168672	chr15	85689961	85690259	-26
Fadd	NM_010175	chr7	151768247	151768485	-26
Osbpl1a	NM_207530	chr18	13100266	13100483	-26
Gatc	NM_029645	chr5	115791057	115791332	-26
Arhgef1	NM_001130152	chr7	25689194	25689483	-26
Lipt2	NM_026010	chr7	107307595	107307926	-26
Zc3h18	NM_001029994	chr8	124900380	124900599	-26

Supplemental Table 3. Significant ChIP-seq E2F3A promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Mtch1	NM_019880	chr17	29484648	29485097	-25
Ssna1	NM_023464	chr2	25127830	25128091	-24
Med14	NM_001048208	chrX	12338830	12339413	-24
Spag5	NM_017407	chr11	78114957	78115181	-23
Rrm2	NM_009104	chr12	25392881	25393309	-23
Wrap53	NM_144824	chr11	69392706	69392989	-23
Zcwpw1	NM_001005426	chr5	138228846	138229167	-23
Rab11fip1	NM_029423	chr8	28284980	28285298	-22
Cpd	NM_007754	chr11	76660327	76660734	-22
Zfp689	NM_175163	chr7	134592478	134592907	-22
Eif4a2	NM_001123038	chr16	23107354	23107684	-21
Snx27	NM_001082484	chr3	94386547	94386769	-21
Ddx39b	NM_019693	chr17	35378485	35378854	-21
Rad54b	NM_001039556	chr4	11485877	11486214	-21
1600002H07Rik	NM_028056	chr17	24357549	24357916	-20
Nrm	NM_134122	chr17	35998144	35998341	-20
Polg	NM_017462	chr7	86611042	86611313	-20
Rabl3	NM_001042499	chr16	37539780	37540142	-18
Trappc5	NM_025701	chr8	3676301	3676615	-18
Smim8	NM_025471	chr4	34725412	34725793	-18
Fhl2	NM_010212	chr1	43220664	43220980	-17
Cipc	NM_001289432	chr12	88288135	88288415	-17
Mms22l	NM_199467	chr4	24423399	24423783	-17
Ccdc15	NM_001081429	chr9	37155713	37156273	-17
Ankrd32	NM_134071	chr13	77274646	77274843	-17
Hat1	NM_026115	chr2	71227106	71227493	-17
Clspn	NM_175554	chr4	126234017	126234396	-17
Polh	NM_030715	chr17	46339468	46339710	-16
Csrp2	NM_007792	chr10	110356949	110357482	-16
Dnph1	NM_207161	chr17	46633594	46633849	-16
Zfp526	NM_175436	chr7	26006270	26006638	-15
Gins2	NM_178856	chr8	123112909	123113069	-15
Rpsa	NM_011029	chr9	120036676	120037060	-15
Smc6	NM_025695	chr12	11272555	11272798	-15
Tex261	NM_009357	chr6	83725647	83725992	-15
Drosha	NM_026799	chr15	12754298	12754813	-14
Nsl1	NM_198654	chr1	192886740	192887032	-13
Mtrr	NM_172480	chr13	68720814	68721206	-13
Rnf168	NM_027355	chr16	32277188	32277878	-13
Mbd4	NM_010774	chr6	115803168	115803574	-13
Rnf38	NM_175201	chr4	44180235	44180608	-13
Hn1l	NM_198937	chr17	25097302	25097856	-12
Calu	NM_184053	chr6	29297868	29298319	-12
Rad51	NM_011234	chr2	118938327	118938755	-11
Use1	NM_001145780	chr8	73890586	73890884	-11
Pola1	NM_008892	chrX	90877214	90877793	-11
Zfp41	NM_001044718	chr15	75446920	75447286	-10

Supplemental Table 3. Significant ChIP-seq E2F3A promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Tfeb	NM_001161722	chr17	47873815	47874135	-10
Ctnnbl1	NM_025680	chr2	157562982	157563270	-10
6330408A02Rik	NM_177312	chr7	13863848	13864310	-10
Tbc1d15	NM_025706	chr10	114688394	114688719	-9
Tmem194b	NM_001142647	chr1	52687369	52687711	-8
Birc5	NM_001012273	chr11	117710408	117710676	-8
Haus4	NM_145462	chr14	55173076	55173334	-8
Rrm1	NM_009103	chr7	109589952	109590448	-8
Top2a	NM_011623	chr11	98885369	98885650	-8
Hist1h2ad	NM_178188	chr13	23666080	23666403	-8
Usp1	NM_146144	chr4	98590215	98590770	-8
Polr2a	NM_001291068	chr11	69571944	69572338	-7
Adprhl2	NM_133883	chr4	125998734	125999172	-7
Ube2g2	NM_019803	chr10	77084832	77085285	-7
Cntln	NM_175275	chr4	84530024	84530389	-6
Haus6	NM_173400	chr4	86257826	86258035	-6
Cdt1	NM_026014	chr8	125091558	125092259	-6
Ppm1g	NM_008014	chr5	31522644	31523200	-5
Nav2	NM_175272	chr7	56501400	56501706	-5
Nsmce1	NM_026330	chr7	132634950	132635170	-5
Rad51c	NM_053269	chr11	87217764	87218237	-5
Dlgap4	NM_001042488	chr2	156546543	156546848	-5
Ap4m1	NM_021392	chr5	138613061	138613426	-5
Usp39	NM_138592	chr6	72295065	72295280	-5
Mcm3	NM_008563	chr1	20810115	20810479	-4
1700001G17Rik	NR_033199	chr1	33726557	33726771	-4
0610009B22Rik	NM_025319	chr11	51501960	51502318	-4
Nbn	NM_013752	chr4	15884957	15885261	-4
Dis3	NM_028315	chr14	99498818	99499165	-4
Arl6ip6	NM_022989	chr2	53050748	53051481	-3
Shcbp1	NM_011369	chr8	4779405	4779666	-3
Tfrc	NM_011638	chr16	32608773	32609185	-2
Mrpl49	NM_026246	chr19	6057638	6057865	-2
Saal1	NM_030233	chr7	53965891	53966152	-2
BC004004	NM_030561	chr17	29405565	29405897	-1
Mrps18c	NM_026826	chr5	101227558	101227995	-1
Gab1	NM_021356	chr8	83403984	83404771	-1
Dlc1	NM_015802	chr8	37676731	37677258	2
Map1a	NM_032393	chr2	121115136	121115542	2
Dhx9	NM_007842	chr1	155334590	155334983	3
Ercc6l	NM_146235	chrX	99352278	99352575	3
Atl3	NM_146091	chr19	7568742	7569118	3
Rfc3	NM_027009	chr5	152453639	152453919	3
Smpd4	NM_001164610	chr16	17619355	17619544	4
Dnajc5	NM_016775	chr2	181254976	181255409	4
Ppp1r18	NM_175242	chr17	36003392	36003734	4
Txnl1	NM_016792	chr18	63851834	63852182	4

Supplemental Table 3. Significant ChIP-seq E2F3A promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Fsd1l	NM_001195284	chr4	53644218	53644474	4
Brca2	NM_009765	chr5	151325066	151325332	4
Fen1	NM_007999	chr19	10278277	10278578	5
Them4	NM_029431	chr3	94113916	94114200	5
Rabl6	NM_001024616	chr2	25463811	25464108	6
Cdk2	NM_016756	chr10	128141829	128142371	6
Prdm4	NM_181650	chr10	85379550	85379815	7
Ppif	NM_134084	chr14	26513508	26513815	7
Med9	NM_138675	chr11	59761530	59761915	8
Cdc42	NM_009861	chr4	136913498	136913832	8
Lmf2	NM_178919	chr15	89185881	89186280	9
Eif4b	NM_145625	chr15	101904036	101904387	9
Ccdc167	NM_001163741	chr17	29853772	29854133	9
Tubg1	NM_134024	chr11	100981228	100981678	9
Magoh	NM_001282737	chr4	107552223	107552514	10
Rab23	NM_008999	chr1	33776583	33776918	11
Mcm5	NM_008566	chr8	77633154	77633719	11
Cdk4	NM_009870	chr10	126500442	126500896	11
Dxo	NM_001163770	chr17	34973807	34974142	12
Pagr1a	NM_030240	chr7	134160751	134160955	12
Haus8	NM_029621	chr8	73796300	73796652	12
Rpa1	NM_001164223	chr11	75161629	75162114	13
Smc1a	NM_019710	chrX	148450866	148451099	13
Cops3	NM_011991	chr11	59653076	59653434	13
Ppp1r18	NM_001146710	chr17	36002827	36003343	13
Srsf7	NM_146083	chr17	80606434	80606828	13
Cdca5	NM_026410	chr19	6084992	6085226	13
Alms1	NM_145223	chr6	85537300	85537777	15
Polr3c	NM_028925	chr3	96531168	96531524	15
Cdca3	NM_013538	chr6	124780071	124780346	16
Gnl2	NM_145552	chr4	124707153	124707393	16
Inip	NM_001013577	chr4	59796391	59797028	17
Cd2bp2	NM_001285905	chr7	134339307	134339839	17
5830418K08Rik	NM_176976	chr9	15162126	15162302	17
Trip13	NM_027182	chr13	74075092	74075301	18
Pbk	NM_023209	chr14	66424556	66424973	18
Dscr3	NM_007834	chr16	94747990	94748445	18
Depdc1b	NM_178683	chr13	109106367	109106731	19
Commd10	NM_178377	chr18	47118414	47118682	19
Zfp212	NM_001145881	chr6	47870449	47870721	19
Pkm	NM_001253883	chr9	59504055	59504333	20
Stag3	NM_016964	chr5	138721586	138721927	21
4930483J18Rik	NR_015603	chr15	81021125	81021481	21
Cad	NM_023525	chr5	31356990	31357356	21
Spc24	NM_026282	chr9	21564498	21564918	21
Nuf2	NM_023284	chr1	171461432	171461713	22
Shmt1	NM_009171	chr11	60624519	60624968	23

Supplemental Table 3. Significant ChIP-seq E2F3A promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Polr1e	NM_001285800	chr4	45031380	45031625	23
Snai2	NM_011415	chr16	14705854	14706097	25
Ppip5k2	NM_173760	chr1	99666479	99666807	25
Uba2	NM_016682	chr7	34953250	34953794	25
Pafah1b2	NM_008775	chr9	45792775	45793081	25
Recql4	NM_058214	chr15	76540675	76541250	26
Nfxl1	NM_133921	chr5	72950548	72951167	26
Rad51ap1	NM_009013	chr6	126889362	126889731	26
2700029M09Rik	NM_028299	chr8	63369042	63369504	26
Skp2	NM_013787	chr15	9069974	9070391	27
Cav2	NM_016900	chr6	17231059	17231362	27
Mocs1	NM_028464	chr17	49567614	49567816	27
C130036L24Rik	NR_015507	chr1	88256017	88256334	28
Ccdc62	NM_001134767	chr5	124380505	124380944	28
Med23	NM_027347	chr10	24589564	24590074	28
Dnajc8	NM_172400	chr4	132091303	132091699	28
Dbr1	NM_031403	chr9	99476054	99476437	29
Anapc13	NM_181394	chr9	102528469	102528838	29
Fkbp1a	NM_008019	chr2	151368093	151368433	29
Esco2	NM_028039	chr14	66452504	66453046	30
2500004C02Rik	NR_040318	chr2	153171304	153171726	30
Tpk1	NM_013861	chr6	43615944	43616341	31
Gm17769	NR_027377	chr10	76881048	76881254	31
Rbm6	NM_029169	chr9	107774950	107775286	31
Kif15	NM_010620	chr9	122860046	122860412	31
Szt2	NM_198170	chr4	118081671	118082000	32
Uhrf1	NM_001111079	chr17	56442617	56442965	32
Sfpq	NR_045010	chr4	126698388	126698764	32
Ahi1	NM_026203	chr10	20672161	20672608	33
L3mbtl2	NM_145993	chr15	81494162	81494539	33
Zbtb11	NM_173026	chr16	55973762	55974136	33
Rad21	NM_009009	chr15	51823133	51823407	35
Mllt3	NM_027326	chr4	87679106	87679442	36
Snrpb	NM_009225	chr2	130004929	130005196	37
Tmem80	NM_001141950	chr7	148513922	148514207	37
Slc2a1	NM_011400	chr4	118781107	118781665	37
Spcs3	NM_029701	chr8	55615148	55615477	38
Rqcd1	NM_021383	chr1	74552271	74553073	39
Gabpb2	NM_172512	chr3	95021625	95022023	39
4933433G15Rik	NR_040719	chr9	75257841	75258217	39
Rad54l	NM_001122958	chr4	115796075	115796432	40
Mgme1	NM_028984	chr2	144096509	144096850	41
Ehd4	NM_133838	chr2	119980163	119980373	42
Nfkbiz	NM_001159394	chr16	55822041	55822373	43
Slc29a1	NM_001199116	chr17	45732376	45732577	44
H2afz	NM_016750	chr3	137527356	137527631	44
Mis12	NM_025993	chr11	70832946	70833369	46

Supplemental Table 3. Significant ChIP-seq E2F3A promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Nudc	NM_010948	chr4	133101668	133102123	46
Hnrnpa2b1	NM_016806	chr6	51419639	51420054	46
Gm4890	NR_045823	chr8	81818627	81819417	46
Enkd1	NM_198299	chr8	108231855	108232187	46
Dnajc9	NM_134081	chr14	21207974	21208194	47
Mthfd2	NM_008638	chr6	83267429	83267671	47
Dnase2a	NM_010062	chr8	87432353	87432785	47
Tonsl	NM_183091	chr15	76470128	76470492	48
Mdc1	NM_001010833	chr17	35978012	35978968	48
Gpr19	NM_001167700	chr6	134847755	134848032	49
Rfesd	NM_001131069	chr13	76155963	76156256	50
Rpgrip1l	NM_173431	chr8	93836863	93837278	50
Ddx20	NM_017397	chr3	105490247	105490628	51
Ipo9	NM_153774	chr1	137326834	137327198	51
Abcf2	NM_001190443	chr5	24083023	24083443	51
Myg1	NM_021713	chr15	102162033	102162348	52
Primpol	NM_001001184	chr8	47702339	47702662	53
2810417H13Rik	NM_026515	chr9	65737984	65738379	53
Atad5	NM_001029856	chr11	79902816	79903092	53
2310036O22Rik	NM_026760	chr8	87550573	87550995	53
Pde12	NM_178668	chr14	27489142	27489412	54
Gm5617	NM_001004191	chr9	48303393	48303609	54
Tipin	NM_025372	chr9	64129194	64129741	55
Melk	NM_010790	chr4	44313606	44314080	55
Pola2	NM_008893	chr19	5963935	5964364	56
Cherp	NM_138585	chr8	74998801	74999345	58
Brca1	NM_009764	chr11	101413056	101413363	59
A730008H23Rik	NM_172505	chr1	90173816	90174328	59
Nkap	NM_025937	chrX	34666701	34666932	60
Cep250	NM_001130000	chr2	155782134	155782573	61
Ankle1	NM_172756	chr8	73929763	73930178	61
Naa40	NM_027643	chr19	7315541	7315759	61
Med18	NM_026039	chr4	132019534	132020014	61
Scpep1	NM_029023	chr11	88816526	88816861	62
Kif2c	NM_134471	chr4	116854988	116855344	62
Pomt2	NM_153415	chr12	88488625	88488950	64
Ssbp1	NM_001286664	chr6	40421331	40421735	67
Ssrp1	NM_182990	chr2	84877200	84877488	68
Nup155	NM_133227	chr15	8059242	8059519	69
Glt25d1	NM_146211	chr8	74134889	74135094	70
Rnaseh2b	NM_026001	chr14	62950717	62951305	70
E2f1	NM_007891	chr2	154395306	154395808	70
Dek	NM_025900	chr13	47201404	47201631	71
Rassf1	NM_019713	chr9	107456806	107457161	71
Pold3	NM_133692	chr7	107269602	107270274	71
Cox7a2	NM_009945	chr9	79607485	79607686	74
Apitd1	NM_027263	chr4	148511438	148511830	74

Supplemental Table 3. Significant ChIP-seq E2F3A promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Paics	NM_025939	chr5	77380130	77380889	75
Spa17	NM_011449	chr9	37421086	37421373	75
Nudt3	NM_019837	chr17	27760152	27760486	77
Chek1	NM_007691	chr9	36533885	36534442	79
E130307A14Rik	NR_038037	chr10	39451627	39451838	80
Umps	NM_009471	chr16	33966709	33967308	80
Ipp	NM_008389	chr4	116180006	116180461	81
Neil3	NM_146208	chr8	54724183	54724489	82
Rnf219	NM_026047	chr14	104921617	104921980	84
Cotl1	NM_028071	chr8	122364251	122364537	84
Nxf1	NM_001276704	chr19	8831516	8831867	86
Cdc7	NM_001271568	chr5	107393203	107393648	86
Dlx1	NM_010053	chr2	71367361	71367814	87
Sp4	NM_009239	chr12	119539683	119539963	89
Mtbp	NM_134092	chr15	55388703	55389399	89
Cmc1	NM_026442	chr9	118058975	118059472	90
Rfc2	NM_020022	chr5	135058513	135058790	93
Rmi1	NM_028904	chr13	58503877	58504224	94
Gm20554	NR_030701	chr13	72765762	72766071	95
Zfp62	NM_009562	chr11	49016869	49017326	97
Xrcc6	NM_010247	chr15	81846667	81847122	97
Sept10	NM_001024910	chr10	58684205	58684786	99
Cactin	NM_027381	chr10	80783711	80784180	99
Tmed3	NM_025360	chr9	89599597	89599966	99
Tubb5	NM_011655	chr17	35974971	35975320	100
Zdhhc1	NM_175160	chr8	108020505	108020833	100
Cdc5l	NM_152810	chr17	45570417	45570688	103
Ttc32	NM_029321	chr12	9036709	9037101	103
Dlgap5	NM_144553	chr14	48037810	48038146	103
Rfc4	NM_145480	chr16	23127436	23127962	103
Wdr76	NM_001290986	chr2	121332381	121332741	103
5830415F09Rik	NM_029086	chr4	46402001	46402374	107
Myl12a	NM_026064	chr17	71351586	71351942	108
Pmf1	NM_025928	chr3	88213983	88214271	110
Mnd1	NM_029797	chr3	83959407	83959782	113
Tube1	NM_028006	chr10	38853732	38854152	114
Ctc1	NM_001143790	chr11	68829365	68829688	115
Rad54l2	NM_030730	chr9	106691260	106691597	115
Wdyhv1	NM_029734	chr15	57972870	57973342	116
Cdkl2	NM_177270	chr5	92471703	92472198	117
Tmem209	NM_178625	chr6	30459285	30459892	117
Mcm10	NM_027290	chr2	4933529	4933905	119
Dut	NM_023595	chr2	125073196	125073546	121
Mcm8	NM_025676	chr2	132641863	132642134	123
Pim3	NM_145478	chr15	88692497	88692995	123
Nsmce2	NM_026746	chr15	59205696	59206056	124
Aaas	NM_153416	chr15	102180868	102181262	124

Supplemental Table 3. Significant ChIP-seq E2F3A promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Nufip1	NM_013745	chr14	76510624	76511022	126
Snrpc	NM_011432	chr17	27976963	27977351	126
Tardbp	NM_001008546	chr4	148000818	148001130	130
Xylb	NM_001033209	chr9	119266434	119266830	134
Gfer	NM_023040	chr17	24832793	24833130	139
U2surp	NM_026476	chr9	95412059	95412491	139
Eri1	NM_026067	chr8	36557999	36558884	145
Spn-ps	NR_033583	chr15	90728611	90728902	150
Dck	NM_007832	chr5	89194004	89194376	153
Mcm2	NM_008564	chr6	88848417	88848823	153
Sec24b	NM_207209	chr3	129763575	129763766	154
Kxd1	NM_029366	chr8	73046670	73047168	159
Tmem30a	NM_133718	chr9	79640905	79641242	163
Tfb1m	NM_146074	chr17	3557329	3557769	163
Ccdc138	NM_001162956	chr10	57960663	57961036	166
1700028E10Rik	NR_045700	chr5	152171113	152171716	166
Itfg1	NM_028007	chr8	88364482	88364879	167
Ints3	NM_145540	chr3	90237197	90237581	168
Itpa	NM_025922	chr2	130493624	130493869	171
Slbp	NM_001289724	chr5	33994716	33995387	171
Senp1	NM_144851	chr15	97923570	97924086	171
Paxip1	NM_018878	chr5	28117713	28118122	172
Csrp2bp	NM_181417	chr2	144194773	144195114	174
Myh9	NM_022410	chr15	77672253	77672598	179
Cdipt	NM_026638	chr7	134119507	134119708	181
Rsbn1	NM_172684	chr3	103718043	103718404	182
Rtca	NM_025517	chr3	116210729	116211091	182
Arhgap31	NM_020260	chr16	38712785	38713126	192
Gucd1	NM_175133	chr10	74979724	74980022	193
Trim27	NM_009054	chr13	21271827	21272179	204
Acat2	NM_009338	chr17	13153155	13153611	207
Rrp1b	NM_028244	chr17	32173183	32173445	208
Siah2	NM_009174	chr3	58495930	58496270	209
Myc	NM_001177353	chr15	61816956	61817260	213
Mcm6	NM_008567	chr1	130255842	130256190	216
4930451G09Rik	NR_073370	chr16	4964385	4964812	218
Mms19	NM_028152	chr19	42055180	42055620	225
Rab33b	NM_016858	chr3	51287926	51288301	227
Cdca2	NM_001110162	chr14	68333316	68333558	229
Raf1	NM_029780	chr6	115626259	115626585	230
Zscan21	NM_011757	chr5	138558192	138558535	232
Chrac1	NM_053068	chr15	72920903	72921243	232
Oard1	NM_207219	chr17	48549400	48549719	236
Upp1	NM_001159402	chr11	9018654	9018841	239
Lipg	NM_010720	chr18	75120470	75120869	247
Tm9sf1	NM_028780	chr14	56262232	56262551	251
Ptbp1	NM_008956	chr10	79317224	79317630	251

Supplemental Table 3. Significant ChIP-seq E2F3A promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Tead4	NM_011567	chr6	128250388	128250768	252
Timeless	NM_001136082	chr10	127669188	127669568	260
Nol12	NM_133800	chr15	78765399	78765847	261
Actb	NM_007393	chr5	143667983	143668273	274
Get4	NM_026269	chr5	139728430	139728673	275
Zfp628	NM_170759	chr7	4866982	4867207	277
Gar1	NM_026578	chr3	129533868	129534187	286
Bloc1s1	NM_015740	chr10	128360083	128360503	286
Zfat	NM_198644	chr15	68089885	68090372	289
Tcof1	NM_011552	chr18	61008139	61008514	291
Orc6	NM_019716	chr8	87823711	87823934	293
2610015P09Rik	NM_027801	chr16	43890131	43890484	294
Pycrl	NM_025412	chr15	75751529	75751857	296
Unk	NM_172569	chr11	115891686	115892165	297
Slc20a1	NM_015747	chr2	129024636	129024990	305
Ints7	NM_178632	chr1	193399760	193400080	308
Dusp1	NM_013642	chr17	26644842	26645351	320
Plcb1	NM_019677	chr2	134612072	134612369	322
Ibtk	NM_001081282	chr9	85642461	85642774	323
Gtf3c5	NM_001290484	chr2	28438223	28438716	329
Gmnn	NM_020567	chr13	24853208	24853731	336
Anapc5	NM_001042491	chr5	123270852	123271173	338
Pfkm	NM_001163488	chr15	97923231	97923483	338
1700021K19Rik	NM_172615	chr16	32867965	32868258	340
Tuba1b	NM_011654	chr15	98764287	98764670	342
Tacc3	NM_001040435	chr5	34001011	34001275	348
Cln8	NM_012000	chr8	14888749	14889035	357
Tfam	NM_009360	chr10	70700251	70700594	369
Ahcy	NM_016661	chr2	154899749	154899973	371
Lrrc8a	NM_177725	chr2	30093491	30093828	372
Phf20	NM_172674	chr2	156022595	156022922	377
G3bp1	NM_013716	chr11	55283434	55283835	382
Hirip3	NM_172746	chr7	134005682	134006051	382
Zdhhc6	NM_025883	chr19	55390016	55390260	383
Pank2	NM_153501	chr2	131088408	131088828	383
Vps72	NM_009336	chr3	94915253	94915445	386
Ing5	NM_025454	chr1	95700756	95701116	395
1110007C09Rik	NM_026738	chr13	49310843	49311145	400
Tmem17	NM_153596	chr11	22412535	22412848	407
Gm14379	NR_026741	chrX	6953363	6953560	412
Ginm1	NM_145418	chr10	7500118	7500466	422
Tpm4	NM_001001491	chr8	74659418	74659819	429
Brd2	NR_037970	chr17	34256201	34256609	439
Sec62	NM_027016	chr3	30692040	30692449	448
Ubr2	NM_001177374	chr17	47146880	47147169	456
Dus3l	NM_144858	chr17	56904297	56904960	456
Zfp651	NM_001166644	chr9	121669439	121669781	460

Supplemental Table 3. Significant ChIP-seq E2F3A promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Elk4	NM_007923	chr1	133904460	133904826	462
Bcl7b	NM_009745	chr5	135644540	135644869	464
Ddrgk1	NM_029832	chr2	130489723	130490099	469
Klf11	NM_178357	chr12	25336508	25336912	475
Rrm2	NM_009104	chr12	25393472	25393714	475
Cbx5	NM_001076789	chr15	103069487	103070031	487
Gsn	NM_001206368	chr2	35112174	35112557	488
Zfp1	NM_011742	chr8	114167705	114167974	498
Pcna	NM_011045	chr2	132078219	132078580	516
Trmt2a	NM_001080999	chr16	18249351	18249709	555
Arsb	NM_009712	chr13	94542024	94542427	593
Hnrnpl	NM_177301	chr7	29596292	29596730	603
Pacrg	NM_027032	chr17	11032300	11032573	620
Hmgn2	NM_016957	chr4	133523096	133523454	630
Lancl2	NM_133737	chr6	57652930	57653227	631
Tyms	NM_021288	chr5	30399401	30399646	641
Ryr3	NM_177652	chr2	112869637	112869960	689
Epb4.1l4a	NM_013512	chr18	34165984	34166320	707
Gosr1	NM_016810	chr11	76576154	76576515	722
Stmn1	NM_019641	chr4	134024786	134025130	724
Fus	NM_139149	chr7	135111590	135111846	726
Xxylt1	NM_198626	chr16	31080621	31080960	727
Gjc3	NM_080450	chr5	138403313	138403604	728
Mtnr1a	NM_008639	chr8	46155186	46155441	751
Bok	NM_016778	chr1	95582842	95583201	752
Fbxo5	NM_025995	chr10	4541666	4542001	759
Matr3	NM_010771	chr18	35722387	35722770	768
Pck2	NM_028994	chr14	56159738	56160033	784
Dleu2	NR_028264	chr14	62300225	62300588	803
Actb	NM_007393	chr5	143667397	143667801	803
Zyx	NM_001289617	chr6	42300490	42300786	812
Mthfd1l	NM_001170785	chr10	6372305	6372985	820
Vav2	NM_009500	chr2	27281353	27281694	821
Nuak1	NM_001004363	chr10	83902216	83902530	842
Gtf2i	NM_001080748	chr5	134789621	134789883	877
Id3	NM_008321	chr4	135700482	135700749	880
Meox1	NM_010791	chr11	101754571	101754900	932
Mbtps1	NM_019709	chr8	122081508	122081949	932
C030034I22Rik	NR_026848	chr17	69766597	69766878	952
Sstr5	NM_001191008	chr17	25633092	25633467	953
Gabbr1	NM_019439	chr17	37183697	37184050	964
Mcm9	NM_027830	chr10	53348976	53349480	1016
Tubb5	NM_011655	chr17	35973977	35974370	1072
Pmp22	NM_008885	chr11	62946014	62946204	1098
Map4	NM_001205330	chr9	109835251	109835555	1126
Gpt	NM_182805	chr15	76528192	76528523	1165
Trp53	NM_001127233	chr11	69394873	69395205	1179

Supplemental Table 3. Significant ChIP-seq E2F3A promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Tlr7	NM_001290756	chrX	163767152	163767476	1188
Ddx26b	NM_172779	chrX	53709053	53709355	1189
Cnnm3	NM_001039551	chr1	36569827	36570083	1235
Hnrnpu	NM_016805	chr1	180266431	180266872	1263
Tmem253	NM_001033805	chr14	52637675	52638010	1304
Abcc1	NM_008576	chr16	14362859	14363159	1359
Pja1	NM_008853	chrX	96664535	96664865	1373
Map1b	NM_008634	chr13	100285016	100285329	1384
Ptma	NM_008972	chr1	88424447	88425004	1416
Angptl6	NM_145154	chr9	20682543	20682890	1437
0610009L18Rik	NR_038126	chr11	120211297	120211560	1438
Gm17762	NR_028378	chr2	17950153	17950653	1528
Ccdc51	NM_025689	chr9	108986445	108986744	1586
Gdf15	NM_011819	chr8	73153717	73154058	1646
Klhdc10	NM_029742	chr6	30353417	30353774	1688
Olfr1410	NM_146491	chr1	94506015	94506200	1693
9130024F11Rik	NR_024326	chr1	57029802	57030266	1722
Cdkn1a	NM_007669	chr17	29232185	29232734	1744
Ncam1	NM_001113204	chr9	49605194	49605424	1864
Nufip1	NM_013745	chr14	76512436	76512714	1878
Gtpbp2	NM_019581	chr17	46299794	46300104	1969

Supplemental Table 4. Significant ChIP-seq E2F3B promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Ccdc132	NM_001167750	chr6	3446323	3446575	-1943
Rs1	NM_011302	chrX	157203826	157204193	-1935
Smim4	NR_024069	chr14	31943797	31944295	-1931
Necab3	NM_021546	chr2	154386348	154386645	-1909
Arhgap5	NM_009706	chr12	53615036	53615385	-1853
Wisp1	NM_018865	chr15	66720969	66721279	-1830
Slc35e1	NM_177766	chr8	75018191	75018424	-1796
Ywhaz	NM_001253807	chr15	36722197	36722746	-1786
Egr2	NM_010118	chr10	66998663	66999014	-1778
Grm8	NM_008174	chr6	28085899	28086183	-1673
Fam71f1	NM_001289663	chr6	29267310	29267639	-1665
Ccnd1	NM_007631	chr7	152127348	152127639	-1665
Kif14	NM_001287179	chr1	138362628	138362997	-1612
Ssbp4	NM_133772	chr8	73133302	73134234	-1556
Kif16b	NM_001081133	chr2	142728579	142728907	-1544
Cux1	NM_198602	chr5	137044689	137045107	-1539
Mir130a	NR_029544	chr2	84582688	84583008	-1514
Hcfc1	NM_008224	chrX	71212907	71213363	-1440
Cdkn2c	NM_007671	chr4	109339221	109339553	-1411
Igf2bp1	NM_009951	chr11	95868485	95868828	-1400
Wnt5a	NM_001256224	chr14	29323037	29323354	-1395
Rnase4	NM_021472	chr14	51709186	51709532	-1392
Irf2bp2	NM_001164598	chr8	129118429	129118948	-1354
Nfatc4	NM_001168346	chr14	56442027	56442536	-1350
Pde4a	NM_183408	chr9	20968587	20969045	-1341
Zbtb14	NM_009547	chr17	69731863	69732102	-1335
Ptma	NM_008972	chr1	88421769	88422221	-1315
Anks1b	NM_001128086	chr10	89334757	89335119	-1315
Camk2n2	NM_028420	chr16	20622525	20622778	-1302
Fbxw7	NM_001177773	chr3	84618006	84618415	-1288
Hnrnpl	NM_177301	chr7	29594507	29594752	-1279
Rrm2	NM_009104	chr12	25391650	25392053	-1267
Abca7	NM_013850	chr10	79458860	79459326	-1266
Ier2	NM_010499	chr8	87187733	87188287	-1260
Oxtr	NM_001081147	chr6	112440972	112441137	-1254
Wnk1	NM_198703	chr6	119989776	119990022	-1227
Tmem74	NM_175502	chr15	43702564	43703030	-1223
Hecw1	NM_001081348	chr13	14616565	14616861	-1221
Prdm6	NM_001033281	chr18	53622828	53623134	-1218
Scrt1	NM_130893	chr15	76353556	76353989	-1215
Pkn3	NM_153805	chr2	29932899	29933313	-1179
Hes1	NM_008235	chr16	30063982	30064593	-1155
Usp49	NM_198421	chr17	47766363	47766669	-1122
Zdhhc14	NM_146073	chr17	5491300	5491655	-1122
Helb	NM_080446	chr10	119551030	119551251	-1121
Zfp687	NM_030074	chr3	94820053	94820497	-1116
Maoa	NM_173740	chrX	16195549	16195904	-1097
Klhl17	NM_198305	chr4	155609932	155610184	-1093

Supplemental Table 4. Significant ChIP-seq E2F3B promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Pdgfra	NM_011058	chr5	75547024	75547445	-1081
Zdhhc5	NM_144887	chr2	84556284	84556511	-1078
Actrt3	NM_029690	chr3	30499672	30500009	-1050
Zbtb14	NM_009547	chr17	69732176	69732369	-1045
Cnot6l	NM_144910	chr5	96591869	96592212	-1033
Rasgrf1	NM_011245	chr9	89803404	89803755	-1033
9330111N05Rik	NR_015587	chr13	81102133	81102496	-1020
Rusc1	NM_001083808	chr3	88894734	88895166	-998
Trib1	NM_144549	chr15	59478929	59479508	-990
Mir6976	NR_105942	chr17	46691635	46692015	-988
Gm608	NM_001029889	chr16	44172417	44172627	-987
Fam222a	NM_001004180	chr5	115017148	115017411	-980
Ctdspl	NM_133710	chr9	118834471	118834879	-978
Atp13a3	NM_001128094	chr16	30389411	30389768	-975
Toporsos	NR_045265	chr4	40215523	40215777	-961
Rbpj	NM_009035	chr5	53980259	53980987	-961
Kmt2a	NM_001081049	chr9	44690188	44690419	-948
Fndc3b	NM_173182	chr3	27610097	27610493	-935
Mat2b	NM_134017	chr11	40506919	40507306	-930
Khdrbs1	NR_045036	chr4	129420292	129420592	-896
Maz	NM_010772	chr7	134170605	134171163	-892
Capzb	NM_001271406	chr4	138788227	138788588	-890
Itpripl2	NM_001033380	chr7	125636183	125636567	-887
Papd7	NM_198600	chr13	69673364	69673848	-865
Scaf1	NM_001008422	chr7	52272375	52272588	-864
Gmppa	NM_133708	chr1	75431552	75431765	-859
Lphn3	NM_198702	chr5	81449628	81449894	-856
Mir7655	NR_106115	chr2	17978461	17978779	-852
Sox12	NM_011438	chr2	152224484	152224774	-848
Ep300	NM_177821	chr15	81415584	81416011	-846
Lamb2	NM_008483	chr9	108381187	108381508	-845
Arid1a	NM_001080819	chr4	133310160	133310563	-837
Ubtf	NM_001044383	chr11	102179299	102179566	-833
Igfbp6	NM_008344	chr15	101973621	101973948	-832
Pbx3	NM_016768	chr2	34228110	34228674	-828
Gxylt1	NM_001033275	chr15	93106245	93106431	-824
Sox2	NM_011443	chr3	34547862	34548357	-817
Tbcc	NM_178385	chr17	47026561	47026953	-812
Nfib	NM_001113210	chr4	82152313	82152673	-811
Tle3	NM_009389	chr9	61219182	61219551	-806
Fosl2	NM_008037	chr5	32437759	32438321	-804
Camk2n2	NM_028420	chr16	20621805	20622486	-796
Nova1	NM_021361	chr12	47920411	47920701	-795
Usf2	NM_011680	chr7	31742350	31742882	-795
Ccne2	NM_001037134	chr4	11117417	11117995	-791
Ptprs	NM_001252456	chr17	56602273	56602575	-781
Bcl3	NM_033601	chr7	20408719	20409044	-779
Nuak1	NM_001004363	chr10	83903754	83904232	-778

Supplemental Table 4. Significant ChIP-seq E2F3B promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Gse1	NM_198671	chr8	123011851	123012125	-777
Atp2b1	NM_026482	chr10	98376841	98377192	-769
Slk	NM_009289	chr19	47653577	47653905	-767
Slc25a25	NM_146118	chr2	32307614	32307890	-763
Tnfaip3	NM_009397	chr10	18735816	18736133	-760
Ptch1	NM_008957	chr13	63667420	63667752	-759
Pik3r3	NM_181585	chr4	115893577	115893942	-759
Pdzd7	NM_001195265	chr19	45120852	45121183	-757
Slc12a6	NM_133649	chr2	112105595	112105835	-755
Hmga1	NM_001166535	chr17	27692003	27693529	-752
Sp4	NM_009239	chr12	119540418	119540901	-748
Mpnd	NM_026530	chr17	56147686	56148070	-745
Map3k3	NM_011947	chr11	105945324	105945620	-743
Ing1	NM_011919	chr8	11555102	11555553	-738
Mir1191b	NR_106141	chr10	80879439	80880106	-732
Lasp1	NM_010688	chr11	97660090	97660427	-727
Efemp2	NM_021474	chr19	5473820	5474106	-726
Kif13a	NM_010617	chr13	47025612	47025993	-717
Zfpm1	NM_009569	chr8	124805175	124805490	-708
Dennd4b	NM_201407	chr3	90069372	90070085	-707
Mycn	NM_008709	chr12	12949226	12949461	-703
Irs2	NM_001081212	chr8	11008842	11009404	-694
Smarcd3	NM_025891	chr5	24108285	24108733	-690
Kctd20	NM_025888	chr17	29089289	29089663	-684
Smad7	NM_001042660	chr18	75526191	75526484	-681
Lgals1	NM_008495	chr15	78756342	78756606	-680
Tsc22d1	NM_207652	chr14	76814784	76815121	-675
Gpbp1l1	NM_029868	chr4	116229461	116229855	-673
1190002F15Rik	NR_037956	chr6	134878212	134878675	-666
Polr2a	NM_001291068	chr11	69572625	69572973	-665
Hdgfrp2	NM_008233	chr17	56218277	56218555	-663
Hist1h2be	NM_001290530	chr13	23678347	23678647	-659
Sipa1l1	NM_001167983	chr12	83270198	83270492	-657
Meis2	NM_001159568	chr2	115891172	115891728	-657
Pidd1	NM_022654	chr7	148629773	148630036	-652
Ndufa13	NM_023312	chr8	72426983	72427228	-650
Stk11	NM_011492	chr10	79578363	79578907	-645
Hmgb1	NM_010439	chr5	149865104	149865409	-645
Rnd2	NM_009708	chr11	101328801	101329222	-640
Memo1	NM_133771	chr17	74694717	74694966	-640
Slc12a2	NM_009194	chr18	58037534	58037853	-638
Mirlet7i	NR_029527	chr10	122423043	122423786	-636
Sppl3	NM_029012	chr5	115460623	115461171	-635
Pim1	NM_008842	chr17	29627089	29627624	-633
Csnk1g2	NM_134002	chr10	80084695	80085089	-632
Ciart	NM_001033302	chr3	95686546	95687017	-632
Sp1	NM_013672	chr15	102235691	102236539	-631
Dyrk1a	NM_007890	chr16	94790999	94791363	-631

Supplemental Table 4. Significant ChIP-seq E2F3B promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Jag1	NM_013822	chr2	136942682	136943085	-629
Ch25h	NM_009890	chr19	34550093	34550409	-627
Tnrc6b	NM_177124	chr15	80628241	80628593	-622
Mex3a	NM_001029890	chr3	88335460	88335937	-618
Sdccag8	NM_029756	chr1	178744010	178744340	-615
4930577N17Rik	NR_073429	chr3	51079860	51080277	-614
Gm53	NR_037977	chr11	96112107	96112622	-609
Ccdc88a	NM_176841	chr11	29273374	29273755	-607
Ptpn4	NM_019933	chr1	121734084	121734419	-605
Rpl7l1	NM_025433	chr17	46920079	46920337	-604
Xpo1	NM_001035226	chr11	23155199	23155693	-594
Rap2a	NM_029519	chr14	120876938	120877239	-594
Pigg	NM_001081234	chr5	108741166	108741535	-593
Smg7	NM_001160256	chr1	154750227	154750492	-585
Rnf26	NM_153762	chr9	43921569	43921866	-585
Rara	NM_001176528	chr11	98821095	98821308	-583
Fzr1	NM_019757	chr10	80841485	80841901	-579
Actn1	NM_134156	chr12	81361760	81362110	-578
Tiparp	NM_178892	chr3	65331642	65331941	-577
Cit	NM_007708	chr5	116294837	116295348	-572
Spry2	NM_011897	chr14	106296483	106296729	-571
Vgll3	NM_028572	chr16	65815122	65815493	-570
Gli3	NM_008130	chr13	15554704	15555272	-567
Ubap2	NM_026872	chr4	41222399	41223064	-565
Spsb4	NM_145134	chr9	96919001	96919663	-559
Stim1	NM_009287	chr7	109415632	109415934	-554
Usp1	NM_146144	chr4	98589830	98590067	-552
1110038B12Rik	NR_015536	chr17	35089787	35090139	-548
Dixdc1	NM_178118	chr9	50536470	50536801	-548
G3bp1	NM_013716	chr11	55282506	55282922	-539
Tmem170b	NM_001163572	chr13	41700777	41701315	-538
Enthd1	NM_001163189	chr15	80391281	80391590	-537
Srsf3	NM_013663	chr17	29168929	29169207	-536
Lphn1	NM_181039	chr8	86423337	86423596	-530
Btbd10	NM_133700	chr7	120513245	120513514	-528
9130023H24Rik	NM_177001	chr7	135381941	135382183	-518
Cd3eap	NM_145822	chr7	19945181	19945505	-512
Fnip2	NM_001162999	chr3	79371893	79372318	-506
Cox20	NM_025511	chr1	180248532	180249027	-504
H3f3a	NM_008210	chr1	182744078	182744391	-502
Zfp219	NM_001253694	chr14	52639477	52640299	-501
Zbed4	NM_181412	chr15	88581434	88581852	-497
Rnf44	NR_027396	chr13	54795658	54795973	-496
Brat1	NM_181066	chr5	141180192	141180745	-496
E2f3	NM_001289920	chr13	30076548	30076956	-493
Hnrnpa0	NM_029872	chr13	58230248	58230565	-491
Fchsd2	NM_001146010	chr7	108256593	108257002	-491
Klf10	NM_001289471	chr15	38230681	38231223	-487

Supplemental Table 4. Significant ChIP-seq E2F3B promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Mir130a	NR_029544	chr2	84581677	84581964	-487
Agap3	NM_139153	chr5	23957340	23957679	-485
Sh3bp1	NM_009164	chr15	78729593	78729874	-482
Opn3	NM_010098	chr1	177623076	177623410	-481
Mxd3	NM_016662	chr13	55431190	55431941	-476
Phf13	NM_172705	chr4	151370589	151370931	-473
Lrrfip1	NM_008515	chr1	92949354	92949741	-473
Socs1	NM_009896	chr16	10785859	10786341	-472
Cul1	NM_012042	chr6	47403683	47404025	-468
D630045J12Rik	NM_194061	chr6	38204285	38204664	-467
Etv6	NM_007961	chr6	133984929	133985593	-463
Ercc4	NM_015769	chr16	13109213	13109518	-463
Gm14005	NR_028589	chr2	128255380	128255706	-457
Rgl2	NM_009059	chr17	34066144	34066619	-457
Dpagt1	NM_007875	chr9	44134246	44134698	-455
Tle4	NM_011600	chr19	14672717	14673124	-449
Mtrf1l	NM_175374	chr10	4521981	4522319	-447
Tcf3	NM_001164147	chr10	79896531	79897157	-447
Msl2	NM_001100451	chr9	100977801	100978275	-447
Usp34	NM_001190401	chr11	23206262	23206637	-445
Samd1	NM_001081415	chr8	86520940	86521312	-444
Yars2	NM_198246	chr16	16302488	16302743	-442
Emilin1	NM_133918	chr5	31215534	31215899	-442
Sertad2	NM_001038625	chr11	20531349	20531730	-440
Psen1	NM_008943	chr12	85028920	85029231	-437
Hspa2	NM_001002012	chr12	77504495	77504965	-432
Tbx15	NM_009323	chr3	99057090	99057419	-428
Arih1	NM_019927	chr9	59334410	59334804	-427
Msantd2	NM_146222	chr9	37296310	37296649	-426
Ctdnep1	NM_026017	chr11	69794070	69794432	-418
Cmip	NM_001163262	chr8	119780286	119780715	-418
Ipo5	NM_023579	chr14	121309755	121310244	-416
Zfp46	NM_009557	chr4	135841270	135841877	-410
Pop7	NM_028753	chr5	137943696	137944434	-409
Gtpbp1	NM_013818	chr15	79520577	79521258	-408
Igf1r	NM_010513	chr7	75096611	75096863	-405
Bicd2	NM_001039179	chr13	49436234	49436791	-405
Zfp36l2	NM_001001806	chr17	84587069	84588308	-403
Nfkbiz	NM_001159394	chr16	55822504	55822793	-399
Rere	NM_001085492	chr4	149655431	149655821	-398
Rps19	NM_023133	chr7	25669058	25669614	-396
Khk	NM_008439	chr5	31223703	31224040	-396
Ppp1r12a	NM_027892	chr10	107598828	107599294	-394
Ubb	NM_011664	chr11	62364433	62364789	-394
Ube2s	NM_133777	chr7	4764163	4764507	-394
Alkbh5	NM_172943	chr11	60350641	60350945	-391
Gls2	NM_001033264	chr10	127631060	127631539	-391
Nfix	NM_001081981	chr8	87298519	87298793	-389

Supplemental Table 4. Significant ChIP-seq E2F3B promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Atn1	NM_007881	chr6	124706734	124707050	-388
Txndc12	NM_025334	chr4	108506768	108507026	-385
Kpnb1	NM_008379	chr11	97049102	97050077	-385
Sh3bp4	NM_133816	chr1	90966425	90966881	-383
Ppp2r5a	NM_144880	chr1	193221170	193221430	-381
Cdca7l	NM_146040	chr12	119081793	119082115	-379
Eya4	NM_010167	chr10	23069912	23070259	-378
Atp13a3	NM_001128094	chr16	30388873	30389109	-376
Vat1l	NM_173016	chr8	116728929	116729405	-372
Patz1	NM_001253691	chr11	3189920	3190260	-369
Sertad2	NM_021372	chr11	20442674	20443101	-368
Nrg2	NM_001167891	chr18	36357001	36357359	-367
Brd3	NM_001113574	chr2	27331387	27331729	-366
Zfp444	NM_001146024	chr7	6123506	6123990	-366
Phf21a	NM_138755	chr2	92023862	92024088	-363
Fam83d	NM_027975	chr2	158593290	158593652	-363
Otud4	NM_001256033	chr8	82162787	82163638	-362
Ran	NM_009391	chr5	129525477	129525861	-361
Rev1	NM_019570	chr1	38186656	38187075	-360
Fzd5	NM_001042659	chr1	64784481	64784884	-360
Timmdc1	NM_024273	chr16	38522979	38523232	-360
Raph1	NM_001045513	chr1	60623834	60624099	-359
Zfhx2	NM_001039198	chr14	55711132	55711352	-358
Clic4	NM_013885	chr4	134828872	134829190	-357
Neo1	NM_001042752	chr9	58884440	58884766	-356
Smc3	NM_007790	chr19	53674364	53674695	-356
Timm8a1	NM_013898	chrX	131076413	131076630	-355
Incenp	NM_016692	chr19	9974259	9974492	-354
Mef2a	NM_001291196	chr7	74517949	74518238	-351
Efnb2	NM_010111	chr8	8660883	8661359	-349
Wbscr17	NM_145218	chr5	131783513	131783966	-349
Ctnna3	NM_177612	chr10	62892313	62892684	-347
Amigo1	NM_146137	chr3	107988758	107988961	-347
Calm2	NM_007589	chr17	87846441	87846794	-344
Gpr124	NM_054044	chr8	28195825	28196112	-344
Eno1	NM_023119	chr4	149610763	149611163	-342
Klf7	NM_033563	chr1	64168094	64168511	-341
Nipbl	NM_027707	chr15	8394597	8395008	-341
Foxp4	NM_001110825	chr17	48061595	48062242	-339
Rreb1	NR_033615	chr13	37918305	37918579	-338
Cd164	NM_016898	chr10	41238788	41239147	-338
Fbxo5	NM_025995	chr10	4540224	4541253	-337
Ago2	NM_153178	chr15	73015479	73015946	-337
Hexim2	NM_001130516	chr11	102994099	102994534	-336
Atxn7l3	NM_001098837	chr11	102158163	102158389	-334
Rbm15b	NM_175402	chr9	106789500	106789828	-334
Vcl	NM_009502	chr14	21748132	21748510	-333
Lrp12	NM_172814	chr15	39775482	39775788	-333

Supplemental Table 4. Significant ChIP-seq E2F3B promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Zfp946	NM_198003	chr17	22560794	22561009	-333
Cdkn2a	NM_009877	chr4	88940451	88941256	-332
Rfx2	NM_009056	chr17	56970511	56971011	-331
Fam98b	NM_026620	chr2	117074987	117075299	-331
Hdac2	NM_008229	chr10	36693878	36694159	-331
Ilf3	NM_001277322	chr9	21172349	21172945	-328
Set	NM_001204875	chr2	29921500	29921831	-328
Slmo2	NM_025531	chr2	174298569	174298968	-328
Rmi1	NR_031761	chr13	58503141	58503424	-326
Cdk5rap2	NM_145990	chr4	70071623	70071827	-325
Tram2	NM_177409	chr1	21069416	21069843	-325
Vkorc1l1	NM_001001327	chr5	130417363	130417946	-324
Ptp4a1	NM_011200	chr1	31006757	31007087	-323
Suco	NM_172645	chr1	163806884	163807342	-322
Spred1	NM_033524	chr2	116946352	116946618	-321
Fbxo30	NM_027968	chr10	11000604	11001010	-320
BC052040	NM_001145898	chr2	115407022	115407240	-320
Mapkapk2	NM_008551	chr1	132994313	132994558	-317
Rbbp5	NM_172517	chr1	134373493	134373760	-317
Phip	NM_001081216	chr9	82869140	82869683	-317
Tcf7l1	NM_001079822	chr6	72739176	72739531	-316
Tmem55b	NM_001033271	chr14	51550653	51551023	-315
Xpo4	NM_020506	chr14	58283938	58284276	-315
Gphn	NM_145965	chr12	79327019	79327635	-314
Sorbs3	NM_001271408	chr14	70604642	70604844	-314
Rfx1	NM_009055	chr8	86590286	86590554	-314
Rbm33	NM_028234	chr5	28643059	28643771	-313
Yy1	NM_009537	chr12	110030951	110031465	-312
Gm608	NM_001029889	chr16	44173062	44173336	-310
Six5	NM_011383	chr7	19679437	19679727	-310
Usp53	NM_133857	chr3	122687490	122687855	-309
Gm13375	NR_033225	chr2	20890026	20890358	-308
Gatad2a	NM_001286450	chr8	72520437	72520743	-308
Afmid	NM_027827	chr11	117686553	117687296	-308
Snrpd3	NM_026095	chr10	74980278	74980685	-305
2310057M21Rik	NM_026655	chr7	138506342	138506689	-305
Ubtd1	NM_145500	chr19	42055779	42056118	-304
Scaf11	NM_028148	chr15	96291353	96291798	-303
Tead3	NM_011566	chr17	28487812	28488290	-302
Ddx39b	NM_019693	chr17	35378226	35378552	-301
Zfp609	NM_172536	chr9	65675529	65675813	-301
Bcl9l	NM_030256	chr9	44306611	44307224	-301
Slc16a6	NM_001029842	chr11	109335013	109335405	-300
Rictor	NM_030168	chr15	6657908	6658252	-300
Klf13	NM_021366	chr7	71083863	71084336	-300
Abhd17c	NM_133722	chr7	91300566	91300837	-300
D17Wsu92e	NM_001271511	chr17	27957610	27957960	-299
Sap25	NM_001081962	chr5	138082250	138082552	-299

Supplemental Table 4. Significant ChIP-seq E2F3B promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Mlec	NM_175403	chr5	115608221	115608744	-299
A230028O05Rik	NR_040374	chr16	25059239	25059613	-298
Aebp2	NM_001005605	chr6	140571649	140572174	-298
Aff1	NM_133919	chr5	104182789	104182978	-297
Cdk13	NM_001081058	chr13	17897111	17897341	-296
Zfp760	NM_001008501	chr17	21844238	21844585	-296
Rnf41	NM_026259	chr10	127848175	127848578	-295
Nudt8	NM_025529	chr19	4000107	4000462	-295
Nfe2l2	NM_010902	chr2	75542809	75543171	-293
Ric8b	NM_183172	chr10	84379755	84380374	-293
Mllt1	NM_022328	chr17	57074911	57075293	-292
Raly	NM_001139513	chr2	154616331	154616775	-292
Ints6	NM_008715	chr14	63380065	63380413	-291
Lipt1	NM_001037918	chr1	37928602	37928918	-290
Lcorl	NM_178142	chr5	46248766	46249366	-288
Nupl1	NM_170591	chr14	60870186	60870817	-288
Ezh2	NM_007971	chr6	47544995	47545636	-288
Rock2	NM_009072	chr12	16901209	16901785	-286
Commd3	NM_147778	chr2	18593630	18593974	-286
Ccng2	NM_007635	chr5	93696072	93696553	-286
Siah1b	NM_009173	chrX	160513985	160514545	-285
Sik2	NM_178710	chr9	50817271	50817648	-283
Lmnb1	NM_010721	chr18	56867027	56867341	-282
Gm9958	NR_045618	chr5	90795585	90795895	-282
Ctcf	NM_181322	chr8	108159862	108160450	-281
Tsen34	NM_024168	chr7	3645494	3646163	-281
Ptma	NM_008972	chr1	88422678	88423382	-280
Snai2	NM_011415	chr16	14705390	14705952	-280
Smg5	NM_178246	chr3	88139787	88140016	-280
Dctn1	NM_001198866	chr6	83115400	83115876	-279
Uspl1	NM_001013378	chr5	149995736	149995978	-278
Abcc10	NM_170680	chr17	46465031	46465464	-277
Klf6	NM_011803	chr13	5860269	5860647	-276
Nup153	NM_175749	chr13	46823271	46823714	-276
Grpel1	NM_024478	chr5	36807374	36807741	-276
Prkce	NM_011104	chr17	86566647	86567052	-275
Gpc2	NM_172412	chr5	138721080	138721796	-274
Fam214a	NM_001113283	chr9	74800290	74800880	-274
Ube2n	NM_080560	chr10	94977235	94977809	-273
Cd2ap	NM_009847	chr17	43013477	43013813	-273
Hmgb2	NM_008252	chr8	59990056	59990678	-272
Sh2b3	NM_008507	chr5	122286859	122287301	-271
Kmt2b	NM_029274	chr7	31373879	31374147	-269
Cdc34	NM_177613	chr10	79144474	79144867	-269
Nr4a2	NM_001139509	chr2	56976551	56976812	-269
Ube2q1	NM_027315	chr3	89577032	89577491	-269
Mgat1	NM_010794	chr11	49057153	49057696	-268
Phrf1	NM_001081118	chr7	148414266	148414571	-268

Supplemental Table 4. Significant ChIP-seq E2F3B promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Fads2	NM_019699	chr19	10175995	10176522	-267
Ywhaq	NM_011739	chr12	21423247	21423876	-266
Dicer1	NM_148948	chr12	105990256	105990596	-265
Hspa4	NM_008300	chr11	53114118	53114371	-265
Pdik1l	NM_001163794	chr4	133843265	133843598	-265
2410002F23Rik	NM_025880	chr7	51501658	51501995	-265
Sco2	NM_001111288	chr15	89204361	89204663	-264
Nup50	NM_016714	chr15	84753220	84753967	-264
Usp42	NM_029749	chr5	144493279	144493544	-264
Brpf1	NM_030178	chr6	113256709	113257024	-264
Zbtb25	NM_028356	chr12	77470514	77471104	-263
Zbtb12	NM_198886	chr17	35030927	35031553	-263
Pcbp2	NM_011042	chr15	102300591	102301009	-262
B9d1	NM_013717	chr11	61318198	61318625	-262
Rab5c	NM_024456	chr11	100599465	100599944	-262
Cbx8	NM_013926	chr11	118902296	118902679	-262
Dtnb	NM_001162465	chr12	3571904	3572353	-262
Ccdc85c	NM_001159910	chr12	109513685	109514090	-262
Usp32	NM_001029934	chr11	84953571	84953863	-261
Scaf8	NM_134123	chr17	3114242	3115178	-261
Sox4	NM_009238	chr13	29045569	29046051	-260
Phf19	NM_028716	chr2	34769645	34769864	-260
Ppig	NM_001081086	chr2	69560627	69561142	-260
Kat6a	NM_001081149	chr8	23969598	23969903	-260
Ybx2	NM_016875	chr11	69748910	69749372	-259
Psmd1	NM_027357	chr1	87960836	87961035	-258
Map4k4	NM_001252202	chr1	39957317	39957683	-257
Morc2a	NM_001159288	chr11	3549057	3549421	-257
Fam208b	NM_134063	chr13	3610422	3610793	-255
Zmynd19	NM_026021	chr2	24804803	24805330	-255
Amotl2	NM_019764	chr9	102619528	102620230	-254
Nova1	NM_021361	chr12	47919874	47920154	-253
Gxylt1	NM_001033275	chr15	93105596	93105938	-253
Sema3c	NM_013657	chr5	17080180	17080580	-253
Mat2a	NM_145569	chr6	72389518	72390088	-252
Gtpbp3	NM_032544	chr8	74011582	74011916	-252
Trim59	NM_025863	chr3	68848629	68849200	-252
Apoo	NM_026673	chrX	91611934	91612459	-252
Polr3h	NM_030229	chr15	81756749	81757036	-251
Commd7	NM_001195390	chr2	153458666	153458867	-251
Gnaz	NM_010311	chr10	74429586	74429864	-250
Sdk1	NM_177879	chr5	141716834	141717640	-250
Ipo7	NM_181517	chr7	117161498	117161879	-250
Arhgap20	NM_175535	chr9	51573095	51573320	-249
Adam10	NM_007399	chr9	70526357	70526761	-248
Hinfp	NM_172162	chr9	44113827	44114174	-248
Snhg8	NR_028574	chr3	123211190	123211810	-247
Galnt2	NM_139272	chr8	126754876	126755216	-247

Supplemental Table 4. Significant ChIP-seq E2F3B promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Syncrip	NM_019796	chr9	88377330	88377632	-247
Myo9a	NM_173018	chr9	59598503	59598964	-247
Ddit3	NM_001290183	chr10	126727363	126727841	-246
Lrrc58	NM_177093	chr16	37868061	37868417	-246
Smarcd1	NM_031842	chr15	99532283	99532660	-246
Lhx2	NM_010710	chr2	38206397	38206767	-245
Ypel5	NM_027166	chr17	73185635	73185962	-245
Dynll1	NM_019682	chr5	115751007	115751476	-244
Sec61a2	NM_021305	chr2	5816427	5816853	-242
Zmat1	NM_175446	chrX	131543873	131544105	-242
Tmub2	NM_028076	chr11	102145827	102146238	-242
Ndc80	NM_023294	chr17	71876082	71876793	-242
Fam20c	NM_030565	chr5	139230627	139230958	-242
Stag1	NM_009282	chr9	100543368	100544231	-242
Mex3c	NM_001039214	chr18	73731823	73732411	-241
Pds5b	NM_175310	chr5	151475845	151476475	-241
Ets1	NM_001038642	chr9	32503117	32503653	-241
Gps2	NM_019726	chr11	69727229	69727676	-241
Git1	NM_001004144	chr11	77306549	77306796	-241
Slc35b2	NM_028662	chr17	45700713	45701007	-240
Foxo3	NM_019740	chr10	41996648	41996923	-239
Baz1b	NM_011714	chr5	135662427	135663480	-239
Vps13a	NM_173028	chr19	16855530	16855790	-238
Pias3	NM_001165949	chr3	96500603	96500918	-238
Lgals1	NM_008495	chr15	78756669	78757166	-237
Tfcp2	NM_001289603	chr15	100382528	100382820	-236
Atxn1l	NM_001080930	chr8	112261683	112262063	-235
Sept7	NM_009859	chr9	25059577	25060031	-235
Bcl2l11	NM_001284410	chr2	127952899	127953252	-235
Tars	NM_033074	chr15	11329436	11329856	-234
Ing4	NM_133345	chr6	124989387	124989876	-234
Rnf19a	NM_013923	chr15	36212944	36213324	-233
Ssfa2	NM_080558	chr2	79475175	79475522	-233
Tspan17	NM_028841	chr13	54890356	54890710	-232
Pvrl3	NM_021496	chr16	46497044	46497578	-232
Hey2	NM_013904	chr10	30562563	30563075	-231
Tgfbr1	NM_009370	chr4	47365796	47366095	-231
Cstf3	NM_145529	chr2	104430117	104430703	-230
Gabpa	NM_008065	chr16	84834983	84835294	-230
Synj2	NM_001113353	chr17	5940867	5941232	-230
Hnrnpl	NM_177301	chr7	29595366	29595991	-230
Cdc20b	NM_001281487	chr13	113825183	113825531	-229
Arhgap35	NM_172739	chr7	17200283	17200856	-229
Ssbp2	NM_024186	chr13	91600245	91600701	-228
Hnrnpul1	NM_144922	chr7	26539638	26540293	-228
Rplp1	NM_018853	chr9	61762317	61762770	-228
Cbfa2t2	NM_009823	chr2	154261834	154262151	-227
Sh3rf1	NM_021506	chr8	63702475	63703006	-227

Supplemental Table 4. Significant ChIP-seq E2F3B promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Ptk2	NM_007982	chr15	73253681	73254009	-225
Cd47	NM_010581	chr16	49855330	49855753	-225
Ddr1	NM_001198833	chr17	35837626	35837890	-224
Scmh1	NM_013883	chr4	120077522	120077802	-223
Ppp2r5e	NM_012024	chr12	76697191	76697626	-223
Epb4.1	NM_001128606	chr4	131604942	131605487	-223
Pgk1	NM_008828	chrX	103382099	103382332	-223
Acp2	NM_007387	chr2	91042639	91043053	-222
Mtf1	NM_008636	chr4	124479306	124479834	-222
Capzb	NM_001037761	chr4	138748376	138748806	-222
Hexim1	NM_138753	chr11	102977255	102977578	-222
Naa10	NM_019870	chrX	71167285	71167722	-222
Mir199b	NR_029811	chr2	32173506	32174011	-221
Prkaca	NM_008854	chr8	86496545	86496766	-221
Kmt2a	NM_001081049	chr9	44689278	44689875	-221
Tex30	NM_029368	chr1	44159329	44159575	-220
Spop	NM_025287	chr11	95274881	95275471	-220
Ppp1r18	NM_001146710	chr17	36002564	36003140	-220
Nadk2	NM_001286255	chr15	9000513	9001064	-220
Atf2	NM_001284374	chr2	73730723	73731106	-220
Mapk3	NM_011952	chr7	133902765	133903075	-219
Srsf2	NM_011358	chr11	116714312	116714939	-219
1700113A16Rik	NR_045997	chr3	87981802	87982047	-219
Btbd7	NM_172806	chr12	104116670	104116994	-217
Insig1	NM_153526	chr5	28397461	28398007	-217
Fam60a	NM_019643	chr6	148895007	148895332	-217
Tbl2	NM_013763	chr5	135625070	135625658	-216
Sqle	NM_009270	chr15	59146222	59146639	-216
Ubqln4	NM_033526	chr3	88357223	88357620	-216
Cstf2t	NM_031249	chr19	31156896	31157334	-215
Stt3a	NM_008408	chr9	36575142	36575610	-214
Anp32e	NM_001253758	chr3	95732634	95733298	-213
Tomm70a	NM_138599	chr16	57121427	57121800	-213
Plec	NM_201393	chr15	76028649	76029051	-212
Hist1h3g	NM_145073	chr13	23626846	23627303	-212
Pabpc1	NM_008774	chr15	36538625	36539252	-212
Azin1	NM_018745	chr15	38448851	38449612	-212
Gclm	NM_008129	chr3	121948094	121948431	-212
Wdr1	NM_011715	chr5	38952751	38953338	-212
Mast4	NM_175171	chr13	104124507	104125057	-211
Pisd-ps2	NR_003519	chr17	3084011	3084775	-211
Tbx3	NM_198052	chr5	120120429	120120889	-211
Meis1	NM_010789	chr11	18919024	18919339	-211
Ado	NM_001005419	chr10	67011595	67012229	-210
Ccne1	NM_007633	chr7	38892281	38893155	-210
Cdc37	NM_016742	chr9	20954398	20954716	-208
Bag6	NM_057171	chr17	35271652	35272177	-208
Cenpb	NM_007682	chr2	131005857	131006052	-208

Supplemental Table 4. Significant ChIP-seq E2F3B promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Tmem65	NM_175212	chr15	58654963	58655412	-207
Zdhhc12	NM_025428	chr2	29949079	29949641	-206
G3bp2	NM_011816	chr5	92512789	92513142	-206
Fam46b	NM_175307	chr4	133035588	133036096	-205
Fam193a	NM_001243123	chr5	34712133	34712620	-205
Cdkn3	NM_028222	chr14	47379833	47380189	-204
Chaf1a	NM_013733	chr17	56179389	56179879	-204
Tbc1d10a	NM_134023	chr11	4086482	4086781	-204
Arf6	NM_007481	chr12	70472583	70473282	-204
Ccnt1	NM_009833	chr15	98398112	98398427	-204
Rab8a	NM_023126	chr8	74684649	74685140	-204
Nup85	NM_001002929	chr11	115425211	115425897	-203
Herpud1	NM_022331	chr8	96909966	96910427	-203
Plxna3	NM_008883	chrX	71574043	71574360	-203
Cep152	NM_001081091	chr2	125450796	125451304	-202
Ell	NM_007924	chr8	73063102	73063640	-202
Tmcc1	NM_177412	chr6	116143413	116143770	-201
Caprin2	NM_181541	chr6	148844662	148845033	-201
Rcl1	NM_021525	chr19	29175441	29175887	-200
Hspa8	NM_031165	chr9	40608850	40609460	-200
4632415L05Rik	NR_027985	chr3	19794540	19794801	-200
Ncs1	NM_019681	chr2	31101007	31101479	-199
Khsrp	NM_010613	chr17	57170793	57171460	-198
Htatsf1	NM_028242	chrX	54306336	54306761	-198
Eif4ebp2	NM_010124	chr10	60915483	60915742	-197
Gm15941	NR_045283	chr15	37362364	37362865	-197
Kank2	NM_145611	chr9	21602953	21603418	-197
Troap	NM_001162506	chr15	98904885	98905530	-196
Pias4	NM_021501	chr10	80630523	80630795	-195
Mterfd1	NM_025547	chr13	67033985	67034419	-195
Paqr4	NM_023824	chr17	23877251	23877731	-195
Scamp3	NM_011886	chr3	88981071	88981352	-195
Btbd8	NM_001255991	chr5	107866597	107867045	-194
Irs1	NM_010570	chr1	82288039	82288372	-193
Tmem109	NM_134142	chr19	10956181	10956666	-192
Micu1	NM_001291442	chr10	59164878	59165360	-191
Lrig2	NM_001025067	chr3	104315786	104316152	-191
Larp4b	NM_172585	chr13	9092688	9093231	-191
2810408I11Rik	NR_038009	chr1	64737311	64737533	-190
Stx11	NM_029075	chr10	12684078	12684428	-189
Amd1	NM_009665	chr10	40021976	40022388	-189
Siva1	NM_001161737	chr12	113882453	113883245	-189
Ippk	NM_199056	chr13	49516126	49516678	-189
Hbegf	NM_010415	chr18	36675458	36675836	-189
H2afx	NM_010436	chr9	44142362	44142854	-189
Ndufa6	NM_025987	chr15	82184760	82185057	-189
Acn9	NM_001077713	chr6	6905628	6906029	-189
Cep41	NM_031998	chr6	30643745	30643994	-189

Supplemental Table 4. Significant ChIP-seq E2F3B promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Mapk14	NM_011951	chr17	28827717	28828479	-188
Zfp689	NM_175163	chr7	134592652	134593066	-188
Cnot8	NM_026949	chr11	57917305	57917628	-188
Canx	NM_001110500	chr11	50139086	50139636	-187
Upf2	NM_001081132	chr2	5872146	5872508	-187
Oaf	NM_178644	chr9	43047898	43048272	-187
Uap1	NM_133806	chr1	172105039	172105486	-187
Chchd7	NR_104355	chr4	3865668	3866028	-186
Plekha1	NM_133942	chr7	138009078	138009396	-186
Nop58	NM_018868	chr1	59741451	59741876	-186
Rpl18a	NM_029751	chr8	73421427	73421626	-186
Katnal1	NM_153572	chr5	149740141	149740673	-185
Dpy19l1	NM_172920	chr9	24307672	24307864	-185
Cggbp1	NM_178647	chr16	64851594	64851857	-185
Stx4a	NM_009294	chr7	134984952	134985321	-185
Tnrc6c	NM_198022	chr11	117515273	117515563	-184
Ift27	NM_025931	chr15	78004421	78005021	-184
Plcl2	NM_013880	chr17	50648526	50648848	-184
Gna11	NM_010301	chr10	81007809	81008138	-184
Fam208a	NM_028945	chr14	28241574	28242123	-184
H2afv	NM_029938	chr11	6344175	6345081	-183
Col5a1	NM_015734	chr2	27741511	27742011	-183
Supt4a	NM_009296	chr11	87550659	87551108	-183
Gpr116	NM_001081178	chr17	43526088	43526375	-183
Dnajb4	NM_027287	chr3	151873036	151873421	-183
Psma1	NM_011965	chr7	121419661	121419961	-182
Tsc22d1	NM_009366	chr14	76903899	76904370	-182
Cdca7	NM_025866	chr2	72313691	72314496	-182
Ccnl1	NM_019937	chr3	65762101	65762554	-182
Gltp	NM_019821	chr5	115141008	115141240	-181
1810043G02Rik	NM_026431	chr10	77441015	77441413	-180
Oip5	NM_001042653	chr2	119444080	119444760	-180
Ficd	NM_001010825	chr5	114185507	114185713	-180
Tshz3	NM_172298	chr7	37482725	37483188	-180
Armc9	NM_030184	chr1	88050975	88051376	-179
Fdft1	NM_010191	chr14	63796677	63796937	-178
Alg10b	NM_001033441	chr15	90054387	90054739	-178
Tfdp1	NM_001291765	chr8	13338387	13338757	-178
Nucks1	NM_001145804	chr1	133806527	133807186	-178
Khdrbs1	NR_045036	chr4	129419560	129419885	-177
Srsf4	NM_020587	chr4	131429187	131429566	-177
Depdc5	NM_001025426	chr5	33205952	33206435	-176
Tab2	NM_138667	chr10	7675977	7676213	-175
Sgcd	NM_011891	chr11	47192693	47193262	-175
Stx12	NM_133887	chr4	132440283	132440810	-175
Lysmd3	NM_030257	chr13	81796437	81796823	-174
Cacnb2	NM_023116	chr2	14525490	14526027	-174
Avpi1	NM_027106	chr19	42203376	42203934	-173

Supplemental Table 4. Significant ChIP-seq E2F3B promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Gpbp1l1	NM_029868	chr4	116229966	116230350	-173
Cnot6	NM_212484	chr11	49526170	49526621	-173
Mir484	NR_030252	chr16	14159181	14159910	-173
Ptpra	NM_008980	chr2	130275622	130276060	-172
Hnrnpd	NM_007516	chr5	100407884	100408372	-172
1810026B05Rik	NR_037569	chr7	80703275	80703629	-172
Mprip	NM_012027	chr11	59475622	59476027	-172
Pebp1	NM_018858	chr5	117737602	117737885	-172
2210018M11Rik	NM_172280	chr7	105805028	105805470	-171
Nudt3	NM_019837	chr17	27760329	27760804	-171
Gemin8	NM_146238	chrX	162608088	162608393	-171
Slc25a27	NM_028711	chr17	43803918	43804348	-170
Med6	NM_027213	chr12	82695871	82696356	-170
Hist1h4a	NM_178192	chr13	23853016	23853557	-170
Tor1aip2	NM_172843	chr1	157882401	157882847	-169
Rnf126	NM_144528	chr10	79229663	79230067	-169
Slc39a9	NM_026244	chr12	81744770	81745294	-169
Rbm39	NM_001291114	chr2	156005844	156006440	-169
Dhx34	NM_027883	chr7	16807382	16807716	-169
Sgsm2	NM_197943	chr11	74710631	74710867	-168
Nckap5l	NM_001001884	chr15	99288144	99288548	-168
Fyttd1	NM_027226	chr16	32877485	32877919	-167
Polr2h	NM_145632	chr16	20717616	20717847	-167
Slc35e3	NM_029875	chr10	117183416	117183742	-166
Pank3	NM_145962	chr11	35582704	35582956	-166
Ulk4	NM_177589	chr9	121186199	121186711	-166
Ostm1	NM_172416	chr10	42398290	42398821	-166
Isy1	NM_133934	chr6	87788564	87789269	-165
Sertad3	NM_133210	chr7	28258558	28258829	-165
Adipor1	NM_028320	chr1	136311688	136312070	-164
Plekhh3	NM_146030	chr11	101032540	101033018	-164
Prep	NM_011156	chr10	44786670	44787041	-164
Safb2	NM_001029979	chr17	56723783	56724554	-164
Dcaf4	NM_030246	chr12	84861079	84861425	-163
Inf2	NM_198411	chr12	113826587	113827075	-163
Nmt2	NM_001290370	chr2	3201118	3201523	-163
Ift140	NM_134126	chr17	25152614	25153122	-162
Megf9	NM_172694	chr4	70195892	70196354	-162
Ubr4	NM_001160319	chr4	138936197	138936625	-162
Nme2	NM_001077529	chr11	93817094	93817421	-162
Actn1	NM_134156	chr12	81361294	81361741	-161
Capn7	NM_009796	chr14	32149573	32149924	-161
Sh3gl1	NM_013664	chr17	56175955	56176483	-160
Adss	NM_007422	chr1	179726583	179727014	-160
Prkca	NM_011101	chr11	108205200	108205521	-160
Zfyve1	NM_183154	chr12	84938030	84938481	-160
Mtx1	NM_001161824	chr3	89018200	89018631	-160
Phactr4	NM_001161797	chr4	131978258	131978780	-159

Supplemental Table 4. Significant ChIP-seq E2F3B promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Csrp2	NM_007792	chr10	110356814	110357332	-158
Ttll5	NM_001081423	chr12	87165501	87165981	-158
Trerf1	NM_001097623	chr17	47277616	47277848	-158
Hdac1	NM_008228	chr4	129219877	129220217	-158
Nop56	NM_024193	chr2	130099649	130100330	-158
Cltb	NM_028870	chr13	54712583	54712995	-157
C330013E15Rik	NR_045701	chr15	100445484	100445910	-157
Yap1	NM_001171147	chr9	8004536	8004968	-157
Uvssa	NM_001081101	chr5	33720969	33721406	-157
Nfatc2ip	NM_010900	chr7	133540282	133540531	-157
Cdc42bpb	NM_183016	chr12	112615918	112616250	-156
Msh3	NM_010829	chr13	93124857	93125369	-156
Sept11	NM_001009818	chr5	93522058	93522594	-156
Wtap	NM_175394	chr17	13185374	13185745	-156
Kcnab2	NM_010598	chr4	151851552	151852073	-156
Utp3	NM_023054	chr5	88982971	88983732	-156
Chsy1	NM_001081163	chr7	73254050	73254439	-156
Pias1	NM_019663	chr9	62828631	62829050	-156
Fam207a	NM_133998	chr10	76978545	76978879	-155
9130023H24Rik	NM_177001	chr7	135381534	135381864	-155
U2af1	NM_024187	chr17	31795484	31796221	-155
Ncor2	NM_001253904	chr5	125659554	125659921	-155
Prr14l	NM_194340	chr5	33196874	33197190	-154
Kras	NM_021284	chr6	145198745	145199063	-154
Edf1	NM_021519	chr2	25413078	25413453	-154
Acsl1	NM_007981	chr8	47556039	47556444	-154
Fam76b	NM_176836	chr9	13631736	13632297	-154
Cdca4	NM_028023	chr12	114067546	114067958	-153
Agpat4	NM_026644	chr17	12311858	12312134	-153
Ube2k	NM_016786	chr5	65928161	65928531	-153
Slc9a8	NM_148929	chr2	167246851	167247284	-153
Npat	NM_001081152	chr9	53344602	53345395	-153
Smad3	NM_016769	chr9	63605666	63606239	-153
1700012D14Rik	NR_015573	chr7	118266230	118266450	-152
Traf3ip1	NM_028718	chr1	93390860	93391325	-152
Ust	NM_177387	chr10	8238593	8238954	-152
Ptpn21	NM_011877	chr12	99972759	99973252	-152
Dscr3	NM_007834	chr16	94747932	94748840	-151
Scaf1	NM_001008422	chr7	52271573	52271965	-151
Rhou	NM_133955	chr8	126177526	126177828	-151
Gtpbp2	NM_019581	chr17	46297619	46298040	-151
Cers6	NM_172856	chr2	68699317	68699609	-150
4831440E17Rik	NR_030700	chr5	25005304	25005624	-150
Letmd1	NM_134093	chr15	100299164	100299465	-150
Brms1l	NM_001037756	chr12	56936864	56937542	-149
Mamld1	NM_001256048	chrX	68303153	68303410	-149
Wdr19	NM_153391	chr5	65590605	65590967	-148
Xpot	NM_001081056	chr10	121063345	121063691	-147

Supplemental Table 4. Significant ChIP-seq E2F3B promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Pgp	NM_025954	chr17	24607111	24607429	-147
Dazap1	NM_001122604	chr10	79727331	79727846	-147
Phf12	NM_174852	chr11	77796059	77796282	-147
Rrs1	NM_021511	chr1	9535148	9535536	-146
Creb1	NM_133828	chr1	64579090	64579373	-146
Snx18	NM_130796	chr13	114408747	114409086	-146
Metrn	NM_133719	chr17	25934022	25934247	-146
Mmp17	NM_011846	chr5	130089785	130090100	-146
Pcna	NM_011045	chr2	132078831	132079288	-145
Tsn	NM_011650	chr1	120207759	120207945	-144
Slc35e1	NM_177766	chr8	75016479	75016833	-144
Foxn2	NM_180974	chr17	88839593	88840222	-144
Smc4	NM_133786	chr3	68808365	68809134	-144
Hist2h4	NM_033596	chr3	96067073	96067692	-144
Tmem120a	NM_172541	chr5	136220020	136220349	-144
Gm15545	NR_045266	chr7	52241973	52242278	-144
Hnrnpab	NM_010448	chr11	51420342	51420708	-143
Zc3h15	NM_026934	chr2	83484414	83484768	-143
Ehd4	NM_133838	chr2	119980250	119980656	-143
Tbc1d2	NM_198664	chr4	46663018	46663408	-143
Lrrc51	NM_001162973	chr7	109082258	109082768	-143
Ap2b1	NM_001035854	chr11	83115880	83116232	-142
Kif11	NM_010615	chr19	37450566	37450934	-142
Mrfap1	NM_026242	chr5	37187975	37188293	-142
Stard3nl	NM_024270	chr13	19487601	19487922	-142
Ddx23	NM_001080981	chr15	98493241	98493680	-142
Nmt1	NM_008707	chr11	102889555	102889913	-141
Ppwd1	NM_172807	chr13	105018892	105019236	-141
Pars2	NM_001285783	chr4	106323303	106323761	-141
D230025D16Rik	NM_145604	chr8	107748776	107749116	-141
Epg5	NM_001195633	chr18	78134878	78135251	-141
Mtap	NM_024433	chr4	88782919	88783346	-141
Mycbp	NM_019660	chr4	123581935	123582294	-141
Atxn2l	NM_183020	chr7	133646667	133647244	-141
Idh3a	NM_029573	chr9	54433994	54434359	-141
C920006O11Rik	NR_040401	chr9	78023403	78023756	-141
Phf23	NM_030064	chr11	69808939	69809315	-140
Nfyc	NM_001277095	chr4	120498274	120498696	-140
Hist1h2af	NM_175661	chr13	23625454	23625825	-140
Hnrnpa3	NM_198090	chr2	75496788	75497563	-140
Leprot	NM_175036	chr4	101320073	101320422	-140
Morn1	NM_001081100	chr4	154460242	154460849	-140
Gnb2	NM_010312	chr5	137974335	137974856	-140
Aamp	NM_001190444	chr1	74331183	74331717	-139
Klf16	NM_078477	chr10	80039989	80040368	-139
Parp11	NM_181402	chr6	127403387	127403816	-139
Abhd17a	NM_145421	chr10	80052980	80053465	-138
Zfp598	NM_183149	chr17	24806433	24806684	-138

Supplemental Table 4. Significant ChIP-seq E2F3B promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Mir8112	NR_106192	chr6	71221413	71221640	-138
Lemd3	NM_001081193	chr10	120416214	120416830	-137
2500004C02Rik	NR_040318	chr2	153171523	153171841	-137
Ppp1r16a	NM_033371	chr15	76501704	76502241	-137
Runx1	NM_001111023	chr16	92697578	92697841	-137
Arhgef7	NM_017402	chr8	11758013	11758372	-137
Wwp2	NM_025830	chr8	109959988	109960333	-137
0610009B22Rik	NM_025319	chr11	51502089	51502453	-136
Pcnp	NM_001024622	chr16	56029777	56030153	-136
Ubc	NM_019639	chr5	125870280	125870764	-136
Tyw1	NM_001015876	chr5	130732591	130732949	-136
Ints1	NM_026748	chr5	140251589	140251945	-136
Phlpp1	NM_133821	chr1	108068135	108068484	-136
Wdpcp	NM_145425	chr11	21471801	21472494	-136
Hmgn1	NM_008251	chr16	96349199	96349734	-136
Psmc4	NM_011874	chr7	28835051	28835439	-135
Bard1	NM_007525	chr1	71149442	71149917	-135
Tmpo	NM_001080129	chr10	90634244	90634751	-135
Pa2g4	NM_011119	chr10	128002903	128003344	-135
Gpr180	NM_021434	chr14	118536044	118536383	-135
BC031361	NR_033221	chr16	38089242	38089717	-135
Diap1	NM_007858	chr18	38095090	38095307	-135
Bclaf1	NM_153787	chr10	20031914	20032366	-134
Taok1	NM_144825	chr11	77421326	77421574	-134
Obfc1	NM_175360	chr19	47611470	47611816	-134
Mapk1ip1l	NM_178684	chr14	47917666	47918043	-134
Fam111a	NM_026640	chr19	12647676	12648085	-134
Mid1ip1	NM_026524	chrX	10294198	10294515	-134
Sumo1	NM_009460	chr1	59727604	59728016	-133
Gtf2a1	NM_175335	chr12	92828853	92829265	-133
Ap5m1	NM_144535	chr14	49685802	49686270	-133
Arc	NM_018790	chr15	74503001	74503263	-133
Mir3960	NR_039536	chr2	32568451	32568797	-133
Mmp16	NM_019724	chr4	17780328	17780662	-133
Arl4a	NM_007487	chr12	40763878	40764311	-133
Elmo2	NM_207706	chr2	165151884	165152337	-133
E2f8	NM_001013368	chr7	56136267	56136818	-133
BC003331	NM_001077237	chr1	152240109	152240523	-132
Camk2n2	NM_028420	chr16	20621269	20621695	-132
Ugp2	NM_001290634	chr11	21271251	21271549	-131
Ptms	NM_026988	chr6	124867965	124868223	-131
Cebpa	NM_007678	chr7	35904013	35904347	-131
Hist1h4f	NM_175655	chr13	23643475	23643807	-130
Lrr1	NM_001081406	chr12	70269365	70269976	-130
Usp8	NM_019729	chr2	126532825	126533042	-130
Cep250	NM_001130000	chr2	155781824	155782503	-130
Ing1	NM_011919	chr8	11555760	11556111	-130
Prkar2a	NM_008924	chr9	108594183	108594505	-129

Supplemental Table 4. Significant ChIP-seq E2F3B promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Fdps	NM_134469	chr3	88905690	88906343	-129
Srsf10	NM_001284196	chr4	135411600	135412113	-129
Lbr	NM_133815	chr1	183772418	183772900	-128
Harbi1	NM_178724	chr2	91550799	91551157	-128
Ogfr	NM_031373	chr2	180323798	180324168	-128
Nfx1	NM_001290449	chr4	40917649	40917971	-128
Mier2	NM_027422	chr10	79017781	79018144	-128
Atf4	NM_009716	chr15	80085180	80085791	-128
Atl2	NM_178050	chr17	80295297	80295882	-128
Kdm3a	NM_001038695	chr6	71582610	71583465	-128
Ing2	NM_023503	chr8	48760483	48760796	-128
Pld2	NM_008876	chr11	70353397	70353679	-127
Banp	NM_016812	chr8	124473984	124474544	-127
Txn2	NM_019913	chr15	77759295	77759804	-127
A430005L14Rik	NM_175287	chr4	153330926	153331511	-127
Polr2j	NM_011293	chr5	136592205	136592662	-127
Eepd1	NM_026189	chr9	25288872	25289237	-127
Dcp2	NM_027490	chr18	44539900	44540154	-126
Ralgapb	NM_001291138	chr2	158235354	158235570	-126
Lsm14b	NM_177727	chr2	179759317	179759813	-126
Hipk1	NM_010432	chr3	103595135	103595511	-126
Usp30	NM_001033202	chr5	114550051	114550379	-126
Wapal	NM_001004436	chr14	35486757	35487218	-126
Ltn1	NM_001081068	chr16	87432656	87433295	-126
Spcs3	NM_029701	chr8	55615226	55615725	-126
Gnb2l1	NM_008143	chr11	48613554	48613918	-125
Rbm14-rbm4	NM_001290127	chr19	4811593	4811923	-125
Fam129b	NM_146119	chr2	32731266	32731790	-125
Map3k7	NM_172688	chr4	32050767	32051145	-125
Gins2	NM_178856	chr8	123112874	123113324	-125
Polr2m	NM_178602	chr9	71333655	71334173	-125
Snapc2	NM_133968	chr8	4252775	4253178	-125
Ywhae	NM_009536	chr11	75546097	75546431	-124
Slc15a4	NM_133895	chr5	128097667	128098103	-124
Crebzf	NM_145151	chr7	97590936	97591396	-124
Atf6	NM_001081304	chr1	172797878	172798170	-123
Pomt2	NM_153415	chr12	88488834	88489114	-123
Ppp1cc	NM_013636	chr5	122607964	122608364	-123
Hist1h2an	NM_178184	chr13	21879052	21879365	-123
Nup214	NM_172268	chr2	31829524	31830169	-123
Psip1	NM_133948	chr4	83132225	83132722	-123
Mex3b	NM_175366	chr7	90015521	90015918	-123
Mto1	NM_026658	chr9	78295689	78296098	-123
Tbc1d8b	NM_001081499	chrX	136219169	136219654	-123
Ascc2	NM_029291	chr11	4537507	4537840	-122
Adam17	NM_001291871	chr12	21379461	21379766	-122
Cenpj	NM_001014996	chr14	57190634	57190973	-122
Dis3l	NM_172519	chr9	64188176	64188593	-122

Supplemental Table 4. Significant ChIP-seq E2F3B promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Pcdh9	NM_001271798	chr14	94289853	94290163	-121
Tex9	NM_009359	chr9	72339619	72340153	-121
H3f3a	NM_008210	chr1	182743662	182744045	-121
Birc6	NM_007566	chr17	74927144	74927883	-121
Fndc3b	NM_173182	chr3	27609243	27609718	-121
Ankrd10	NR_030781	chr8	11634970	11635341	-121
Tmem164	NM_001199357	chrX	139115654	139115989	-121
Xpnpep3	NM_177310	chr15	81230328	81230666	-120
Pemt	NM_001290012	chr11	59859933	59860286	-120
Farp1	NM_134082	chr14	121434470	121434881	-120
Ppia	NM_008907	chr11	6315548	6315958	-119
Ccnj	NM_172839	chr19	40905514	40905785	-119
Wdr77	NM_027432	chr3	105762190	105762403	-119
Rgp1	NM_172866	chr4	43591349	43591626	-119
Srrm1	NM_001130477	chr4	134908907	134909586	-119
Relt	NM_177073	chr7	108011945	108012144	-119
Tcf12	NM_001253865	chr9	71959554	71959933	-119
Acy1	NM_001276442	chr9	106340492	106340877	-119
Slc16a10	NM_001114332	chr10	39862011	39862343	-118
Dnajc14	NM_028873	chr10	128242405	128242821	-118
Wdr20	NM_027149	chr12	111975896	111976184	-118
Rrp7a	NM_029101	chr15	82953158	82953538	-118
Slc30a9	NM_178651	chr5	67697906	67698248	-118
Zfp628	NM_170759	chr7	4866528	4866872	-118
Tmx1	NM_028339	chr12	71553842	71554203	-118
Wrb	NM_207301	chr16	96366636	96367179	-118
Dusp1	NM_013642	chr17	26645020	26646047	-118
Wwc2	NM_133791	chr8	49075878	49076165	-118
Fam203a	NM_021555	chr15	76199043	76199377	-117
Slc39a13	NM_026721	chr2	90910297	90910879	-117
Zw10	NM_012039	chr9	48863239	48863897	-117
Tfb2m	NM_008249	chr1	181476395	181476632	-117
Rmnd1	NM_025343	chr10	5913819	5914324	-117
Rbl1	NM_011249	chr2	157029967	157030804	-117
Rpgrip1l	NM_173431	chr8	93837073	93837400	-117
Dido1	NM_175551	chr2	180436634	180437210	-116
H2afz	NM_016750	chr3	137527089	137527579	-116
Rpl29	NM_009082	chr9	106331516	106331990	-116
Sptan1	NM_001177667	chr2	29820798	29821129	-116
Xylt1	NM_175645	chr7	124524205	124524548	-116
2410006H16Rik	NR_030738	chr11	62415898	62416628	-115
Sf1	NM_001110791	chr19	6363321	6363827	-115
Scaf4	NM_178923	chr16	90284570	90284997	-115
Txnl1	NM_016792	chr18	63851903	63852350	-115
Rad23b	NM_009011	chr4	55362430	55363167	-115
Arl4c	NM_177305	chr1	90598639	90599118	-114
Frk	NM_010237	chr10	34202912	34203271	-114
Map2k2	NM_023138	chr10	80568348	80568807	-114

Supplemental Table 4. Significant ChIP-seq E2F3B promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Scrib	NM_134089	chr15	75900107	75900438	-114
Zfp318	NM_207671	chr17	46520365	46520836	-114
Cds2	NM_138651	chr2	132088642	132088897	-114
Adrm1	NM_019822	chr2	179905974	179906383	-114
Ost4	NM_001134692	chr5	31210030	31210517	-114
Mboat1	NM_153546	chr13	30228088	30228402	-113
Ddx56	NM_026538	chr11	6167728	6167958	-112
Gemin7	NM_027189	chr7	20158702	20158904	-112
Trib2	NM_144551	chr12	15823438	15823965	-112
Tbc1d24	NM_001163848	chr17	24342394	24342841	-112
Pkn2	NM_178654	chr3	142544890	142545267	-112
Por	NM_008898	chr5	136164829	136165114	-112
Zfp169	NM_001164576	chr13	48608698	48609132	-111
Foxo1	NM_019739	chr3	52071977	52072317	-111
Pitpnb	NM_019640	chr5	111759454	111759888	-111
Casp2	NM_007610	chr6	42214577	42215275	-111
C430049B03Rik	NR_038185	chrX	50410324	50410630	-111
Kdsr	NM_027534	chr1	108656215	108656642	-111
Esyt1	NM_011843	chr10	127962846	127963203	-111
Sept9	NM_001113487	chr11	117127332	117127565	-111
Tnfaip8l1	NM_025566	chr17	56301636	56301969	-111
Wdfy3	NM_172882	chr5	102498876	102499223	-111
Chst2	NM_018763	chr9	95307537	95308060	-111
Col6a3	NM_001243009	chr1	92740487	92740827	-110
Snx3	NM_017472	chr10	42221573	42221925	-110
Rabggtb	NM_001163478	chr3	153575834	153576244	-110
Eya3	NM_210071	chr4	132194678	132195022	-110
Etfa	NM_145615	chr9	55359943	55360375	-110
Ctdsp1	NM_153088	chr1	74437861	74438284	-110
Rangap1	NM_001146174	chr15	81560124	81560791	-110
Cdip1	NM_025670	chr16	4789748	4790339	-110
Atp7b	NM_007511	chr8	23170517	23170792	-110
Fignl1	NM_001163359	chr11	11708769	11709377	-109
Baiap2	NM_001037755	chr11	119804070	119804522	-109
Gstz1	NM_001252555	chr12	88487742	88488268	-109
Ccno	NM_001081062	chr13	113777632	113778168	-109
Kansl2	NM_001289439	chr15	98364585	98365031	-109
Fra10ac1	NM_001081075	chr19	38298583	38298877	-109
Ppm1g	NM_008014	chr5	31522746	31523306	-109
Znrf2	NM_199143	chr6	54766693	54766907	-109
Mcm3	NM_008563	chr1	20810205	20810598	-109
Mapk7	NM_001291035	chr11	61307593	61308158	-109
Cks2	NM_025415	chr13	51740304	51740679	-109
Ldb1	NM_001113408	chr19	46119660	46119957	-109
Hspb11	NM_028394	chr4	106926191	106926668	-109
Slit2	NM_001291227	chr5	48374143	48374426	-109
Luc7l2	NM_001170848	chr6	38501136	38501533	-109
Mtmr14	NM_026849	chr6	113187572	113187883	-109

Supplemental Table 4. Significant ChIP-seq E2F3B promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Erbb2	NM_001003817	chr11	98273491	98273887	-108
Arhgef40	NM_001145921	chr14	52604278	52604520	-108
Mapkapk5	NM_010765	chr5	121995864	121996152	-108
Athl1	NM_145387	chr7	148127199	148127543	-108
Irx5	NM_018826	chr8	94881340	94881832	-108
Mir1941	NR_035462	chr15	101199538	101199811	-108
Ppib	NM_011149	chr9	65907689	65908046	-108
Map2	NM_008632	chr1	66221643	66221947	-107
Zfp706	NM_026521	chr15	36936936	36937590	-107
Slc3a2	NM_008577	chr19	8788316	8788670	-107
Zfp868	NM_001045553	chr8	72148922	72149438	-107
Hist1h3c	NM_175653	chr13	23837384	23837607	-107
Tial1	NM_009383	chr7	135604864	135605401	-107
Cpne2	NM_153507	chr8	97056692	97056949	-107
Dock11	NM_001009947	chrX	33428517	33428922	-107
Zdhhc5	NM_144887	chr2	84555287	84555565	-106
Chac1	NM_026929	chr2	119176683	119177059	-106
Nelfa	NM_011914	chr5	34278791	34279233	-106
Mki67	NM_001081117	chr7	142907880	142908454	-106
Irf1	NM_001159393	chr11	53583197	53583622	-106
Samd4	NM_001037221	chr14	47502326	47502741	-106
Pdcd10	NM_019745	chr3	75360676	75361081	-106
Srm	NM_009272	chr4	147965306	147965725	-106
Mdm2	NM_001288586	chr10	117147746	117148090	-105
Dgkz	NM_138306	chr2	91803676	91803972	-105
Eri3	NM_001285901	chr4	117222671	117222975	-105
Rad9b	NM_144912	chr5	122804086	122804530	-105
Ints10	NM_001293791	chr8	71317547	71317897	-105
Serbp1	NM_001113564	chr6	67216674	67217061	-105
Sgk1	NM_011361	chr10	21714021	21714713	-104
Mtmr4	NM_133215	chr11	87405347	87405881	-104
Maml3	NM_001004176	chr3	51908834	51909228	-104
Ubqln2	NM_018798	chrX	149932502	149932838	-104
Kpna3	NM_008466	chr14	62058558	62059215	-104
Cobll1	NM_027225	chr2	65076571	65077000	-104
Ung	NM_011677	chr5	114580576	114581545	-104
Dnmt1	NM_001199433	chr9	20756720	20757619	-104
Gtf2b	NM_145546	chr3	142427972	142428242	-103
Cpe	NM_013494	chr8	67171770	67172108	-103
Hnrnpll	NM_144802	chr17	80461474	80461945	-103
Orc4	NR_033442	chr2	48804666	48805111	-103
Ddost	NM_007838	chr4	137860364	137860735	-103
Fbxo21	NM_145564	chr5	118426452	118426899	-103
Msmo1	NM_025436	chr8	67212307	67212646	-103
Zc3h6	NM_178404	chr2	128792716	128793354	-102
Adora2b	NM_007413	chr11	62062221	62062546	-102
Prickle1	NM_001033217	chr15	93426247	93426598	-102
Fbxo45	NM_173439	chr16	32247034	32247389	-102

Supplemental Table 4. Significant ChIP-seq E2F3B promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Ephb6	NM_001146351	chr6	41555117	41555640	-102
Cenpt	NM_177150	chr8	108375852	108376165	-102
Peak1	NM_172924	chr9	56265791	56266124	-102
A830080D01Rik	NM_001033472	chrX	155970307	155970688	-102
Matr3	NM_010771	chr18	35721448	35721972	-101
Gcn1l1	NM_172719	chr5	116015010	116015330	-101
Snx8	NM_172277	chr5	140865075	140865527	-101
Pcid2	NM_178708	chr8	13105205	13105681	-101
Ap1g1	NM_009677	chr8	112302296	112302580	-101
Asf1b	NM_024184	chr8	86479168	86479815	-101
Fkbp5	NM_010220	chr17	28623049	28623337	-100
Notch2	NM_010928	chr3	97817186	97817534	-100
Stxbp3a	NM_011504	chr3	108643399	108643639	-100
Pcbp1	NM_011865	chr6	86476110	86476406	-100
Uba52	NM_019883	chr8	73034213	73034517	-100
R3hcc1l	NM_177464	chr19	42593008	42593382	-99
Slc25a5	NM_007451	chrX	34335406	34335688	-99
Psap	NM_001146123	chr10	59740138	59740415	-99
Nos1ap	NM_001109985	chr1	172519928	172520226	-98
Ptrhd1	NM_001204912	chr12	4233774	4234082	-98
Rrn3	NM_001039521	chr16	13780483	13780903	-98
Vprbp	NM_001015507	chr9	106723901	106724515	-98
Mroh1	NM_175457	chr15	76210696	76210993	-98
Metap1	NM_175224	chr3	138152264	138152621	-98
Snx14	NM_172926	chr9	88333705	88334066	-98
Cdk1	NM_007659	chr10	68815479	68816033	-97
Dtnbp1	NM_025772	chr13	45097418	45097704	-97
Zfand2a	NM_001159908	chr5	139960269	139960813	-97
Fam13b	NM_146084	chr18	34666387	34666758	-97
Phf20	NM_172674	chr2	156022065	156022506	-97
Calu	NM_184053	chr6	29297743	29298274	-97
Ppp2cb	NM_017374	chr8	34709844	34710147	-97
Fyn	NM_008054	chr10	39089286	39089730	-96
Tfdp2	NM_001184706	chr9	96096449	96096745	-96
Plec	NM_201394	chr15	76026008	76026461	-96
Gpr3	NM_008154	chr4	132768406	132768685	-96
Ccnc	NM_001290420	chr4	21654664	21654840	-95
Fgfr3	NM_001163215	chr5	34064073	34064481	-95
Pom121	NM_148932	chr5	135870352	135870668	-95
Cops8	NM_133805	chr1	92499770	92500039	-95
4732491K20Rik	NR_045290	chr17	12511449	12511798	-95
Itgb3bp	NM_026348	chr4	99495601	99496204	-95
Nsmce1	NM_026330	chr7	132634875	132635424	-95
Cdk10	NM_194446	chr8	125748475	125748816	-95
Mdm1	NM_148922	chr10	117578553	117578943	-94
Mcm4	NM_008565	chr16	15637103	15638069	-94
Uhrf2	NM_144873	chr19	30104687	30105129	-94
Ccdc91	NM_025911	chr6	147424109	147424487	-94

Supplemental Table 4. Significant ChIP-seq E2F3B promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Whsc1l1	NM_001001735	chr8	26712538	26712828	-94
Ddhd2	NM_028102	chr8	26864528	26865162	-94
Uchl5	NM_001159866	chr1	145624104	145624523	-94
Zc3h18	NM_001029994	chr8	124900174	124900669	-94
Ldha	NM_010699	chr7	54100917	54101243	-93
Fhod1	NM_177699	chr8	107871730	107872194	-93
Ubap2l	NM_001165984	chr3	89856324	89856733	-93
Fbxo10	NM_001024142	chr4	45097408	45097727	-93
Mrps17	NM_025450	chr5	130221174	130221445	-93
Trim24	NM_001272064	chr6	37820445	37820990	-93
Zfp382	NM_001081007	chr7	30906612	30907135	-93
Tssc4	NM_138631	chr7	150254897	150255462	-93
Ash2l	NM_011791	chr8	26951122	26951579	-93
Hmgxb4	NM_178017	chr8	77517358	77517659	-93
Cox8a	NM_007750	chr19	7292018	7292376	-92
Eprs	NM_029735	chr1	187186606	187187157	-92
Mcm3ap	NM_019434	chr10	75931481	75931766	-92
Prkci	NM_008857	chr3	30894310	30894891	-92
Mad1l1	NM_010752	chr5	140797300	140797893	-92
Hdgfrp3	NM_013886	chr7	89079208	89079663	-92
Fasn	NM_007988	chr11	120685723	120686179	-91
Epha7	NM_001290434	chr4	28739985	28740393	-91
Nop2	NM_138747	chr6	125081678	125081940	-91
Eif4a2	NM_001123038	chr16	23107238	23107661	-91
Rps20	NM_026147	chr4	3762679	3762994	-91
Capn2	NM_009794	chr1	184447385	184448021	-90
Inpp5e	NM_033134	chr2	26264682	26264974	-90
Gmeb2	NM_198169	chr2	181022614	181022906	-90
Chd9	NM_177224	chr8	93352523	93352763	-90
4930581F22Rik	NR_029475	chr9	34923972	34924472	-90
Rbm3os	NR_033561	chrX	7722223	7722701	-90
Nt5m	NM_134029	chr11	59661314	59661655	-90
Mycn	NM_008709	chr12	12948529	12948932	-90
Rfwd3	NM_146218	chr8	113823953	113824468	-90
P4hb	NM_011032	chr11	120434119	120434557	-89
Dnajb1	NM_018808	chr8	86131733	86132235	-89
Hbp1	NM_153198	chr12	32635369	32635606	-89
E2f3	NM_010093	chr13	30077768	30078271	-89
Itpr1	NM_010585	chr6	108162821	108163180	-89
Alg12	NM_001142357	chr15	88649493	88650177	-88
1110037F02Rik	NM_001081183	chr4	11412700	11413332	-88
Rassf1	NM_001243748	chr9	107453588	107454006	-88
Ipmk	NM_027184	chr10	70810308	70810597	-88
Wdhd1	NM_172598	chr14	47896379	47896858	-88
Cd2bp2	NM_001285905	chr7	134339567	134339788	-88
Ttll4	NM_001014974	chr1	74708006	74708474	-87
Slc25a29	NM_181328	chr12	110073974	110074370	-87
Fam122a	NM_026520	chr19	24551895	24552205	-87

Supplemental Table 4. Significant ChIP-seq E2F3B promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Mafb	NM_010658	chr2	160192727	160193047	-87
Rdx	NM_009041	chr9	51855803	51856113	-87
Sos1	NM_009231	chr17	80879660	80880097	-87
Mageb3	NM_008545	chr2	121781360	121782467	-87
Map1lc3a	NM_025735	chr2	155101727	155102298	-87
Wee1	NM_009516	chr7	117265258	117265713	-87
Dlc1	NM_015802	chr8	37676882	37677282	-86
Wdr48	NM_026236	chr9	119803795	119804057	-86
Snhg7	NR_024068	chr2	26495725	26495972	-86
Mrpl20	NM_025570	chr4	155177537	155177744	-86
Usp38	NM_027554	chr8	83538674	83539105	-86
Nfyb	NM_010914	chr10	82226750	82227190	-85
Rad50	NM_009012	chr11	53520715	53521095	-85
Top2a	NM_011623	chr11	98885395	98885779	-85
Ifrd1	NM_013562	chr12	40949682	40950038	-85
Scfd1	NM_029825	chr12	52478350	52478612	-85
Ttf1	NM_009442	chr2	28915534	28915860	-85
Iqgap3	NM_001033484	chr3	87885644	87886130	-85
Phlda3	NM_013750	chr1	137662336	137662817	-85
Arl1	NM_025859	chr10	88193840	88194307	-85
Lrrc41	NM_153521	chr4	115747828	115748141	-85
Med23	NM_027347	chr10	24589530	24589884	-84
Cdc6	NM_001025779	chr11	98768833	98769403	-84
Tcf19	NM_001163764	chr17	35653432	35654272	-84
Cbx3	NM_007624	chr6	51420310	51420750	-84
Icosl	NM_015790	chr10	77531807	77532250	-84
Rrm2	NM_009104	chr12	25392816	25393253	-84
Akap11	NM_001164503	chr14	78936503	78936996	-84
Lrrk2	NM_025730	chr15	91503379	91503762	-84
Tctn3	NM_026260	chr19	40686565	40687010	-84
Dpy19l3	NM_178704	chr7	36539420	36539691	-84
Id1	NM_010495	chr2	152561743	152562063	-83
Diap2	NM_172493	chrX	126284073	126284315	-83
1810062O18Rik	NR_033571	chr14	21365259	21365604	-83
Zfpl1	NM_024231	chr19	6084730	6085215	-83
Stard7	NM_139308	chr2	127095623	127096140	-83
Tmem201	NM_001284270	chr4	149111982	149112535	-83
Ift46	NM_023831	chr9	44580864	44581153	-83
Cep131	NM_009734	chr11	119948088	119948356	-82
H2-DMa	NM_010386	chr17	34259462	34259926	-82
Ccna2	NM_009828	chr3	36470670	36471328	-82
Dancr	NR_015531	chr5	74488850	74489200	-82
Cltc	NM_001003908	chr11	86570868	86571281	-82
Igf2r	NM_010515	chr17	12962500	12962805	-82
Cebpg	NM_009884	chr7	35841476	35841855	-82
Mrc2	NM_008626	chr11	105153730	105154026	-81
Rps6ka5	NM_153587	chr12	101963121	101963515	-81
Haus4	NM_145462	chr14	55173082	55173474	-81

Supplemental Table 4. Significant ChIP-seq E2F3B promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Pdxp	NM_020271	chr15	78744120	78744414	-81
Rps10	NM_025963	chr17	27772049	27772485	-81
Ttf2	NM_001013026	chr3	100773493	100773839	-81
AI314180	NM_172381	chr4	58925515	58925839	-81
Jrk	NM_008415	chr15	74539620	74540043	-81
Psmb9	NM_013585	chr17	34324214	34324495	-81
Sgms1	NM_144792	chr19	32462736	32463311	-81
H6pd	NM_173371	chr4	149382983	149383440	-81
Polr2e	NM_025554	chr10	79502196	79502770	-80
1810014B01Rik	NR_015572	chr10	86148060	86148322	-80
Neurl4	NM_001291118	chr11	69715012	69715462	-80
9130401M01Rik	NM_029418	chr15	57865716	57866140	-80
Pskh1	NM_173432	chr8	108424045	108424541	-80
Sf3b3	NM_133953	chr8	113370498	113371066	-80
Cirbp	NM_007705	chr10	79630204	79630807	-80
Pqlc1	NM_001164422	chr18	80452749	80453020	-80
Drap1	NM_001291080	chr19	5424890	5425225	-80
Tra2a	NM_198102	chr6	49213963	49214296	-80
Lsm11	NM_028185	chr11	45758360	45758670	-79
Mir5627	NR_049203	chr12	45311037	45311403	-79
Elf1	NM_007920	chr14	79880582	79881260	-79
Zfp90	NM_011764	chr8	108938891	108939427	-79
Akap1	NM_001042541	chr11	88725734	88726221	-79
Tra2b	NM_009186	chr16	22265788	22266371	-79
Adam9	NM_007404	chr8	26127250	26127693	-79
Bcar1	NM_001198839	chr8	114255935	114256292	-79
Tigd5	NM_178646	chr15	75739917	75740255	-78
Naa15	NM_053089	chr3	51219730	51219988	-78
Rps11	NM_013725	chr7	52379608	52380064	-78
Mum1	NM_023431	chr10	79688912	79689617	-78
Ncapg2	NM_133762	chr12	117643495	117644098	-78
Alms1	NM_145223	chr6	85537219	85537674	-78
Timm50	NM_025616	chr7	29096971	29097312	-78
Lin52	NM_173756	chr12	85792164	85792596	-77
Nr6a1	NM_010264	chr2	38781890	38782224	-77
Zfp664	NM_001081750	chr5	125342739	125343255	-77
Mrps12	NM_011885	chr7	29526686	29527066	-77
Cnot1	NM_001205226	chr8	98331141	98331735	-77
Zbtb24	NM_001277229	chr10	41169926	41170247	-77
D10Wsu102e	NM_026579	chr10	82822647	82823130	-77
Osbpl8	NM_175489	chr10	110601508	110602053	-77
Armc7	NM_177778	chr11	115336780	115337047	-77
Dscc1	NM_183089	chr15	54921770	54922447	-77
Ccdc96	NM_025725	chr5	36826965	36827354	-77
Med14	NM_001048208	chrX	12338760	12339589	-77
Vamp4	NM_016796	chr1	164500712	164501052	-76
Ranbp2	NM_011240	chr10	57909292	57909754	-76
Cdk2	NM_016756	chr10	128141874	128142490	-76

Supplemental Table 4. Significant ChIP-seq E2F3B promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Ccdc134	NM_172428	chr15	81958022	81958528	-76
Pelo	NM_134058	chr13	115880249	115880632	-76
Ahdc1	NM_146155	chr4	132567204	132567485	-76
B330016D10Rik	NR_030695	chr4	141101835	141102166	-76
Fam109a	NM_175474	chr5	122298807	122299114	-76
Cops6	NM_012002	chr5	138602091	138602416	-76
Commd9	NM_029635	chr2	101726199	101726487	-75
Nat10	NM_153126	chr2	103601298	103601664	-75
Ccp110	NM_182995	chr7	125855879	125856219	-75
Nckipsd	NM_030729	chr9	108710407	108710863	-75
Ipo9	NM_153774	chr1	137326909	137327374	-75
Mrps10	NM_001146212	chr17	47505632	47505889	-75
4930577N17Rik	NR_073429	chr3	51080498	51080717	-75
Zfp280d	NM_146224	chr9	72122411	72122850	-75
Nfkbiz	NM_001159394	chr16	55822198	55822450	-74
Efna3	NM_010108	chr3	89126740	89127008	-74
Ap5z1	NM_172725	chr5	142939465	142940155	-74
Suz12	NM_001163018	chr11	79806220	79806847	-74
Ppp1r21	NM_028658	chr17	88929214	88929565	-74
Coro1b	NM_011778	chr19	4148464	4148713	-74
Mtf2	NM_013827	chr5	108494397	108494840	-74
Alg8	NM_199035	chr7	104519927	104520178	-74
Cnot11	NM_028043	chr1	39592395	39592751	-73
Nedd1	NM_008682	chr10	92184980	92185490	-73
Smarcd2	NM_001130187	chr11	106134106	106134610	-73
Eif4a3	NM_138669	chr11	119161251	119161607	-73
Zfyve21	NM_026752	chr12	113051863	113052751	-73
Parp2	NM_009632	chr14	51427385	51427709	-73
Zfp142	NM_029888	chr1	74634190	74635157	-73
Tmpo	NM_001283048	chr10	90633126	90633607	-73
Lrig3	NM_177152	chr10	125402974	125403429	-73
Smpd4	NM_001164610	chr16	17619147	17619600	-73
Frs2	NM_177798	chr10	116585487	116585715	-72
Hist1h3b	NM_178203	chr13	23844021	23844331	-72
Pgrmc2	NM_027558	chr3	40886834	40887244	-72
Dctpp1	NM_023203	chr7	134404113	134404391	-72
Stt3b	NM_024222	chr9	115219283	115219937	-72
Tor1aip1	NM_001160018	chr1	157883555	157883806	-72
Mob3a	NM_172457	chr10	80164341	80164930	-72
BC048403	NM_173022	chr10	121176744	121177097	-72
4930427A07Rik	NM_134041	chr12	114394241	114394878	-72
B4galt7	NM_146045	chr13	55701260	55701539	-72
Sod1	NM_011434	chr16	90220719	90221110	-72
Nelfe	NM_001045864	chr17	34987134	34987393	-72
Casp8ap2	NM_001122978	chr4	32702094	32702657	-72
Smc2	NM_008017	chr4	52451871	52452226	-72
Bod1l	NM_001081422	chr5	42235403	42235846	-72
Rasa3	NM_009025	chr8	13677403	13677912	-72

Supplemental Table 4. Significant ChIP-seq E2F3B promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Rnf7	NM_011279	chr9	96378959	96379210	-72
Atp6ap1	NM_018794	chrX	71542192	71542535	-72
Ercc6l	NM_146235	chrX	99352285	99352716	-72
Npcd	NM_001013362	chr15	79664500	79665166	-71
A930024E05Rik	NR_045820	chr5	123439145	123439437	-71
Mbd4	NM_010774	chr6	115803254	115803604	-71
Ankrd26	NM_001081112	chr6	118512180	118512508	-71
Traip	NM_011634	chr9	107853088	107853356	-71
Agap1	NM_001037136	chr1	91351123	91351506	-71
Marveld1	NM_183195	chr19	42221675	42221940	-71
Prpf3	NM_027541	chr3	95659459	95660032	-71
Cep70	NM_023873	chr9	99143603	99144028	-71
Mcu	NM_001033259	chr10	59079307	59079711	-70
A630020A06	NR_045740	chr15	3945685	3946251	-70
Rab12	NM_024448	chr17	66868994	66869164	-70
Zdhhc24	NM_027476	chr19	4878334	4878860	-70
Sart1	NM_016882	chr19	5388655	5388889	-70
Tmem248	NM_027854	chr5	130697944	130698324	-70
Mutyh	NM_133250	chr4	116480011	116480526	-70
Mepce	NM_144913	chr5	138227825	138228170	-70
Herc2	NM_010418	chr7	63305246	63305663	-70
Dcaf15	NM_172502	chr8	86628564	86628895	-70
Topbp1	NM_176979	chr9	103207320	103207853	-70
Ubald1	NM_145359	chr16	4879784	4880054	-69
Msh2	NM_008628	chr17	88071670	88071984	-69
8030462N17Rik	NM_178670	chr18	77952610	77953024	-69
Rps3a1	NM_016959	chr3	85946368	85946948	-69
Ppp6r1	NM_172894	chr7	4610503	4610737	-69
Nup93	NM_172410	chr8	96738199	96738663	-69
Cenpf	NM_001081363	chr1	191511852	191512213	-69
Pofut1	NM_080463	chr2	153067032	153067365	-69
Cdk5rap2	NM_145990	chr4	70071324	70071613	-69
Acot7	NM_133348	chr4	151551863	151552416	-69
Gde1	NM_019580	chr7	125849197	125849442	-69
Plat	NM_008872	chr8	23867905	23868388	-69
Ttc13	NM_145607	chr8	127245811	127246074	-69
Sbno2	NM_183426	chr10	79565336	79565692	-68
Dis3	NM_028315	chr14	99498856	99499256	-68
Mrpl41	NM_001031808	chr2	24830517	24830853	-68
Zfp661	NM_028141	chr2	127410331	127410629	-68
Dpy19l4	NM_001081201	chr4	11249176	11249514	-68
Rpa2	NM_011284	chr4	132323853	132324559	-68
Rpl13a	NM_009438	chr7	52383939	52384425	-68
Mbd3	NM_013595	chr10	79862116	79862465	-68
Gm11974	NR_045893	chr11	6428687	6428972	-68
Pwwp2a	NM_001164231	chr11	43495262	43495601	-68
Mis12	NM_025993	chr11	70832755	70833334	-68
Ipo11	NM_029665	chr13	107726915	107727208	-68

Supplemental Table 4. Significant ChIP-seq E2F3B promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Rab26os	NR_045289	chr17	24664970	24665285	-68
Hells	NM_008234	chr19	39005256	39005567	-68
Rps27l	NM_026467	chr9	66793656	66794057	-68
Josd1	NM_028792	chr15	79518055	79518681	-67
1600023N17Rik	NR_073433	chr5	46060669	46061357	-67
Opn3	NM_010098	chr1	177622640	177623017	-67
Gm5129	NR_028426	chr5	30062421	30062662	-67
Ssbp1	NM_212468	chr6	40421215	40421478	-67
Hist1h4d	NM_175654	chr13	23673239	23673569	-66
Cdh24	NM_199470	chr14	55260177	55260355	-66
Slc25a32	NM_172402	chr15	38944045	38944609	-66
Msh6	NM_010830	chr17	88373942	88374705	-66
Dpysl3	NM_001291455	chr18	43597808	43598201	-66
Dnaja1	NM_008298	chr4	40669309	40669560	-66
Rnf38	NM_001038993	chr4	44181046	44181393	-66
Map4	NM_001205330	chr9	109833900	109834523	-66
Sbf1	NM_001081030	chr15	89145614	89145998	-65
Lmbr1l	NM_029098	chr15	98748196	98748990	-65
Hsd3b7	NM_133943	chr7	134943936	134944178	-65
Hprt	NM_013556	chrX	50341068	50341310	-65
Rnf187	NM_022423	chr11	58752324	58752619	-65
Hsp90aa1	NM_010480	chr12	111934437	111934900	-65
Hist1h1c	NM_015786	chr13	23830375	23830846	-65
Rab11fip2	NM_001033172	chr19	60019170	60019491	-65
Zbtb43	NM_001025594	chr2	33323992	33324239	-65
Hk2	NM_013820	chr6	82724327	82724696	-65
Iqgap1	NM_016721	chr7	87948096	87948465	-65
Cluh	NM_001081158	chr11	74462699	74463165	-64
Sap30bp	NM_020483	chr11	115794739	115795077	-64
Gpr137c	NM_027518	chr14	45839101	45839553	-64
Hmgb1	NM_010439	chr5	149864453	149864899	-64
Gins4	NM_024240	chr8	24347990	24348416	-64
Zmiz1	NM_183208	chr14	26278383	26278830	-64
Vps28	NM_025842	chr15	76456431	76456608	-64
Fau	NM_001160239	chr19	6057636	6058011	-64
Kif1b	NM_001290995	chr4	148681773	148682036	-64
Cops7a	NM_012003	chr6	124915247	124915708	-64
Pold1	NM_011131	chr7	51804045	51804450	-64
Zdhhc7	NM_133967	chr8	122625305	122625564	-64
Ppp1r7	NM_023200	chr1	95239996	95240320	-63
Pafah1b1	NM_013625	chr11	74537800	74538096	-63
Pum2	NM_030723	chr12	8681259	8681587	-63
Naa16	NM_025832	chr14	79790181	79790893	-63
Rad9a	NM_011237	chr19	4201527	4201803	-63
Babam1	NM_026636	chr8	73920485	73920895	-63
Hmgcr	NM_008255	chr13	97440643	97441262	-63
Litaf	NM_019980	chr16	10993104	10993447	-63
Prpf18	NM_026045	chr2	4573049	4573338	-63

Supplemental Table 4. Significant ChIP-seq E2F3B promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Abl1	NM_009594	chr2	31615267	31615524	-63
Erf	NM_010155	chr7	26035734	26035943	-63
Ncoa7	NM_172495	chr10	30522814	30523134	-62
Irf2bpl	NM_145836	chr12	88225543	88226107	-62
Klf5	NM_009769	chr14	99697583	99698111	-62
Mrpl39	NM_017404	chr16	84735418	84735798	-62
Rbm18	NM_026434	chr2	35992114	35992456	-62
Col16a1	NM_028266	chr4	129724785	129725257	-62
Fbl	NM_007991	chr7	28954581	28954827	-62
Ppap2a	NM_008247	chr13	113590700	113591145	-62
Tigd3	NM_198634	chr19	5893964	5894371	-62
Rchy1	NR_073442	chr5	92391302	92391983	-62
Ate1	NM_001136054	chr7	137662879	137663430	-62
St3gal1	NM_009177	chr15	67008269	67008739	-61
Cntrl	NM_012018	chr2	34964729	34965171	-61
Ireb2	NM_022655	chr9	54711352	54711648	-61
Pitrm1	NM_145131	chr13	6547098	6547585	-61
Spdya	NM_029254	chr17	71901179	71901500	-61
Ube3c	NM_133907	chr5	29895466	29895975	-61
Cand1	NM_027994	chr10	118677000	118677340	-60
Stra13	NM_016665	chr11	120574842	120575438	-60
Arpc5l	NM_028809	chr2	38863324	38863872	-60
Rell1	NM_145923	chr5	64359911	64360479	-60
Pot1a	NM_133931	chr6	25759041	25759529	-60
Enpp4	NM_199016	chr17	44242585	44243046	-60
Tcerg1	NM_001289526	chr18	42670938	42671223	-60
Ncdn	NM_011986	chr4	126430573	126430890	-60
Snx17	NM_153680	chr5	31495376	31495857	-60
Rbpj	NM_009035	chr5	53981381	53981668	-60
Btg2	NM_007570	chr1	135975603	135975977	-59
Tubg1	NM_134024	chr11	100981201	100981569	-59
Mafg	NM_010756	chr11	120494775	120495063	-59
Gtpbp4	NM_027000	chr13	8995096	8995536	-59
Plxnb2	NM_138749	chr15	89011086	89011466	-59
Pex16	NM_145122	chr2	92215147	92215525	-59
Serp1	NM_030685	chr3	58329627	58330101	-59
Grsf1	NM_178700	chr5	89105125	89105383	-59
Zfp383	NM_001243908	chr7	30693333	30693619	-59
Nutf2	NM_026532	chr8	108384096	108384852	-59
Gls	NM_001081081	chr1	52289925	52290342	-59
Rpe	NM_025683	chr1	66747248	66747567	-59
E2f6	NM_033270	chr12	16817563	16817860	-59
Ptpdc1	NM_207232	chr13	48720830	48721169	-59
Them6	NM_198607	chr15	74551396	74551813	-59
Lmln	NM_172823	chr16	33062445	33062650	-59
Srsf7	NM_146083	chr17	80606528	80606877	-59
Bnip2	NM_016787	chr9	69837012	69837415	-59
Tspan15	NM_197996	chr10	61693916	61694130	-58

Supplemental Table 4. Significant ChIP-seq E2F3B promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Ncln	NM_134009	chr10	80958968	80959362	-58
1810021B22Rik	NR_040417	chr15	88906221	88906461	-58
4930549G23Rik	NR_045376	chr18	67959495	67959813	-58
Slc7a5	NM_011404	chr8	124431466	124431820	-58
Hiatl1	NM_133680	chr13	65214128	65214565	-58
Esco2	NM_028039	chr14	66452636	66453089	-58
Rxrb	NM_001205214	chr17	34168556	34168841	-58
Mgst3	NM_025569	chr1	169323824	169324144	-57
Gpx4	NM_008162	chr10	79515888	79516462	-57
Gpatch8	NM_001159492	chr11	102417251	102417805	-57
Snx27	NM_001082484	chr3	94386438	94386950	-57
Cdca7l	NM_146040	chr12	119082156	119082397	-57
Arl14ep	NM_001025102	chr2	106814447	106814772	-57
1700020I14Rik	NR_015473	chr2	119419809	119420140	-57
Gm10069	NR_028593	chr6	128388496	128388939	-57
BC055324	NM_201364	chr1	165924796	165925138	-56
Zfp68	NM_001044747	chr5	139060907	139061145	-56
Ppif	NM_134084	chr14	26513349	26513850	-56
Pole4	NM_025882	chr6	82602764	82603063	-56
Snrnp40	NM_025645	chr4	130037166	130037480	-55
Gm16039	NR_033518	chr6	8209088	8209376	-55
Fam168a	NM_178764	chr7	107854978	107855342	-55
Sesn3	NM_030261	chr9	14080539	14080839	-55
Mbnl3	NM_134163	chrX	48558916	48559210	-55
Bmpr1a	NM_009758	chr14	35315671	35315900	-55
Plec	NM_201389	chr15	76036704	76036905	-55
Supt3	NM_178652	chr17	44913735	44914394	-55
Golga1	NM_001290649	chr2	38920895	38921334	-55
Sf3b4	NM_153053	chr3	95976250	95976585	-55
Asph	NM_001177849	chr4	9596232	9596493	-55
Fam53a	NM_178390	chr5	33972101	33972574	-55
Rps5	NM_009095	chr7	13507438	13507771	-55
Lrrc20	NM_153542	chr10	60938307	60938745	-54
Taf15	NM_027427	chr11	83286309	83286801	-54
Tmem242	NM_027457	chr17	5440077	5440549	-54
Macrod1	NM_134147	chr19	7130979	7131427	-54
Syngr4	NM_021482	chr7	53151993	53152275	-54
Cenpu	NM_027973	chr8	47637052	47637684	-54
Nxt2	NM_001290533	chrX	138663094	138663288	-54
Arl15	NM_172595	chr13	114584442	114584881	-54
Abcf1	NM_013854	chr17	36106629	36106866	-54
Srsf9	NM_025573	chr5	115777018	115777245	-54
Lsm8	NM_133939	chr6	18798402	18798759	-54
Hdac10	NM_199198	chr15	88958933	88959431	-53
Gart	NM_010256	chr16	91647058	91647480	-53
Abcd3	NM_008991	chr3	121518002	121518368	-53
Prpf4	NM_027297	chr4	62069524	62070002	-53
Nap1l1	NM_015781	chr10	110909905	110910484	-53

Supplemental Table 4. Significant ChIP-seq E2F3B promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Rnf144a	NM_001081977	chr12	27099940	27100417	-53
Esco1	NM_001081222	chr18	10610207	10610596	-53
Cnpy4	NM_178612	chr5	138628418	138629001	-53
Xpo6	NM_028816	chr7	133343730	133344217	-53
Cab39l	NM_026908	chr14	60059583	60059947	-52
Cnpy3	NM_028065	chr17	46888977	46889447	-52
Sorbs1	NM_009166	chr19	40588214	40588492	-52
Tpk1	NM_013861	chr6	43615977	43616473	-52
Mcmbp	NM_145955	chr7	135883750	135884238	-52
S1pr2	NM_010333	chr9	20781007	20781569	-52
1190002N15Rik	NM_001033145	chr9	94438399	94438703	-52
Smek1	NM_211355	chr12	102321709	102322216	-52
Zfp81	NM_207541	chr17	33495714	33496033	-52
Spg20	NM_001144988	chr3	54915848	54916107	-52
Larp7	NM_138593	chr3	127256069	127256566	-52
Atrip	NM_172774	chr9	108976513	108976864	-52
Dync1h1	NM_030238	chr12	111839359	111839747	-51
Trpc4ap	NM_001163452	chr2	155518079	155518261	-51
Map2k7	NM_001164172	chr8	4238427	4238949	-51
Cdt1	NM_026014	chr8	125091476	125092250	-51
Lats2	NM_015771	chr14	58364803	58365216	-51
Racgap1	NM_001253808	chr15	99481963	99482310	-51
Crkl	NM_001277231	chr16	17451784	17452269	-51
Cwc22	NM_030560	chr2	77784355	77784570	-51
Acad8	NM_025862	chr9	26807059	26807308	-51
Sugt1	NM_026474	chr14	79987270	79987624	-50
Eny2	NM_175009	chr15	44259243	44259969	-50
Fmnl3	NM_011711	chr15	99200716	99201176	-50
Polh	NM_030715	chr17	46339302	46339944	-50
Zfp704	NM_133218	chr3	9610044	9610224	-50
Smap2	NM_133716	chr4	120689704	120690098	-50
Ccdc18	NM_028481	chr5	108561740	108562024	-50
2810428I15Rik	NM_025577	chr8	73030591	73030783	-50
Zfp319	NM_024467	chr8	97855762	97856036	-50
Rdh10	NM_133832	chr1	16095770	16096055	-50
B230219D22Rik	NM_181278	chr13	55794254	55794615	-50
Tmem260	NM_172600	chr14	49065704	49066249	-50
Atp6v1c1	NM_025494	chr15	38591371	38591846	-50
Cpne8	NM_025815	chr15	90509702	90510033	-50
1110008F13Rik	NM_026124	chr2	156688602	156689013	-50
Sec61a1	NM_016906	chr6	88468656	88469029	-50
Brip1	NM_178309	chr11	86014421	86015065	-49
Diap3	NM_019670	chr14	87540748	87541190	-49
Vps18	NM_172269	chr2	119114272	119114584	-49
Actl6a	NM_019673	chr3	32607175	32607661	-49
Ppil4	NM_026141	chr10	7512357	7512928	-49
Atp5b	NM_016774	chr10	127520204	127520423	-49
Cops3	NM_011991	chr11	59653145	59653488	-49

Supplemental Table 4. Significant ChIP-seq E2F3B promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Ylpm1	NM_178363	chr12	86337093	86337350	-49
Naa60	NM_029090	chr16	3884407	3884732	-49
Snrpd1	NM_009226	chr18	10617545	10617944	-49
Iscu	NM_025526	chr5	114222528	114223015	-49
Ncapd2	NM_146171	chr6	125141374	125141929	-49
Synm	NM_201639	chr7	74904504	74904847	-49
Pcdh18	NM_130448	chr3	49561047	49561523	-48
Prpf38a	NM_172697	chr4	108251893	108252083	-48
Lactb	NM_030717	chr9	66823176	66823500	-48
Thap4	NM_025920	chr1	95651280	95651643	-48
Tmem194	NM_001113211	chr10	127113834	127114311	-48
Chaf1b	NM_028083	chr16	93883731	93884464	-48
Nasp	NM_001081475	chr4	116299865	116300432	-48
Dnajc8	NM_172400	chr4	132091336	132091515	-48
1700003G18Rik	NR_029433	chr7	123236570	123236849	-48
Dis3l	NM_001001295	chr9	64188910	64189311	-48
Armc2	NM_001034858	chr10	41738029	41738439	-47
Clptm1l	NM_146047	chr13	73741239	73741565	-47
Phf13	NM_172705	chr4	151370127	151370541	-47
Tmem38a	NM_144534	chr8	75095837	75096071	-47
Piezo1	NM_001037298	chr8	125074984	125075566	-47
Cpsf3l	NM_028020	chr4	155243476	155243781	-47
Agpat5	NM_026792	chr8	18846034	18846429	-47
Rora	NM_001289916	chr9	69137449	69137752	-47
Mrpl3	NM_053159	chr9	104955325	104955776	-47
Dpy30	NM_001146223	chr17	74715533	74716103	-46
Stard6	NM_029019	chr18	70631917	70632205	-46
Rpl11	NM_025919	chr4	135609196	135609466	-46
Ncam1	NM_001113204	chr9	49607063	49607375	-46
BC030867	NM_153544	chr11	102109978	102110321	-46
Atad2	NM_027435	chr15	57966264	57967099	-46
Myl12a	NM_026064	chr17	71351750	71352085	-46
Hnrnpa2b1	NM_016806	chr6	51419660	51420215	-46
Cnbp	NM_001109746	chr6	87800833	87801456	-46
Ap1s2	NM_001290379	chrX	160346687	160347118	-46
Pcbp3	NM_021568	chr10	76424576	76424896	-45
Trim32	NM_053084	chr4	65265771	65266177	-45
Btf3l4	NM_027453	chr4	108506007	108506459	-45
Cdh11	NM_009866	chr8	105308913	105309197	-45
E2f5	NM_007892	chr3	14578505	14578746	-45
Pdgfa	NM_008808	chr5	139470772	139471129	-45
Gars	NM_180678	chr6	54987821	54988078	-45
Nt5c3	NM_026004	chr6	56873786	56874153	-45
Arpp19	NM_021548	chr9	74885390	74885597	-45
Ube2t	NM_001278115	chr1	136858883	136859311	-44
Mrpl12	NM_027204	chr11	120345814	120346062	-44
March2	NM_145486	chr17	33855535	33855795	-44
Ndufv1	NM_133666	chr19	4012699	4012897	-44

Supplemental Table 4. Significant ChIP-seq E2F3B promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Peo1	NM_153796	chr19	45080913	45081093	-44
Anapc11	NM_001038230	chr11	120459545	120460058	-44
Donson	NM_021720	chr16	91688876	91689155	-44
Atg2a	NM_194348	chr19	6241453	6241794	-44
Fen1	NM_007999	chr19	10278297	10278654	-44
Rexo4	NM_207234	chr2	26819813	26820084	-44
Kntc1	NM_001042421	chr5	124199346	124200035	-44
Ccnt2	NM_028399	chr1	129670503	129670891	-43
Pigm	NM_026234	chr1	174306404	174306832	-43
Eldr	NR_110421	chr11	16851091	16851563	-43
2410089E03Rik	NM_001162906	chr15	8118909	8119215	-43
Zfp41	NM_001044718	chr15	75446833	75447307	-43
Nolc1	NM_053086	chr19	46150060	46150526	-43
Tpm3	NM_001271764	chr3	89883181	89883617	-43
Gtpbp10	NM_153116	chr5	5559422	5559664	-43
Pml	NM_008884	chr9	58097432	58097838	-43
Tle2	NM_019725	chr10	81037826	81038151	-43
Txndc17	NM_026559	chr11	72020865	72021160	-43
Gcat	NM_001161712	chr15	78860978	78861543	-43
Ppp1r18	NM_175242	chr17	36003397	36003636	-43
Mcph1	NM_173189	chr8	18594923	18595336	-43
Tbk1	NM_019786	chr10	121023723	121024059	-42
Pinx1	NM_028228	chr14	64478959	64479253	-42
Slc39a14	NM_001135151	chr14	70751094	70751450	-42
Rab11fip1	NM_029423	chr8	28284957	28285361	-42
Flnb	NM_134080	chr14	8650304	8650553	-42
Supt16	NM_033618	chr14	52816614	52817295	-42
Rpl3	NM_013762	chr15	79913556	79914197	-42
Ccnf	NM_007634	chr17	24388059	24388730	-42
Me2	NM_145494	chr18	73974807	73975366	-42
Nespas	NR_002846	chr2	174120792	174121163	-42
Gtl3	NM_008187	chr8	97958486	97959133	-42
Adk	NM_001243041	chr14	21895041	21895623	-41
Cxcl10	NM_021274	chr5	92777831	92778079	-41
Cox5a	NM_007747	chr9	57368877	57369117	-41
Bop1	NM_013481	chr15	76307566	76307911	-41
Stxbp1	NM_001113569	chr2	32702488	32703105	-41
Soga1	NM_001164663	chr2	156904865	156905216	-41
Ttc14	NM_025978	chr3	33698927	33699200	-41
Srsf11	NM_001093753	chr3	157694659	157694856	-41
Dcaf10	NM_153167	chr4	45354782	45355081	-41
Ube2g2	NM_019803	chr10	77084867	77085183	-40
Arrb2	NM_145429	chr11	70245730	70246352	-40
Cep112	NM_029606	chr11	108286328	108286750	-40
Prmt5	NM_013768	chr14	55136158	55136534	-40
Zfp523	NM_172617	chr17	28314095	28314549	-40
Blm	NM_001042527	chr7	87679838	87680250	-40
Gnl3l	NM_198110	chrX	147451753	147452055	-40

Supplemental Table 4. Significant ChIP-seq E2F3B promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Zfp672	NM_001256520	chr11	58143737	58144022	-40
Nxf1	NM_016813	chr19	8831424	8831681	-40
Mapk9	NM_016961	chr11	49660031	49660395	-39
Eif1ad	NM_027236	chr19	5366432	5367114	-39
Hdgf	NM_008231	chr3	87709840	87710566	-39
Ogfod2	NM_025671	chr5	124562120	124562494	-39
Irf2bp1	NM_178757	chr7	19589132	19589616	-39
Rrm1	NM_009103	chr7	109589879	109590459	-39
Cisd1	NM_134007	chr10	70807516	70807753	-39
Smdt1	NM_026914	chr15	82176275	82176598	-39
Lemd2	NM_146075	chr17	27341238	27341603	-39
Ccdc167	NM_001163741	chr17	29853782	29854217	-39
Mob1b	NM_026735	chr5	89149726	89149987	-39
Smg9	NM_028047	chr7	25184427	25184789	-38
A630066F11Rik	NR_030698	chr10	7382973	7383288	-38
Cox7c	NM_007749	chr13	86186334	86186539	-38
Zfp91Cntf	NR_024093	chr19	12870527	12870772	-38
Tor1a	NM_144884	chr2	30823272	30823677	-38
Bag1	NM_001171739	chr4	40895226	40895501	-38
Ablim2	NM_001177698	chr5	36100314	36100667	-38
Sntb2	NM_009229	chr8	109459429	109459794	-38
Tmem158	NM_001002267	chr9	123169735	123170152	-38
Nde1	NM_001285503	chr16	14163117	14163543	-37
Dzip3	NM_001110017	chr16	48994094	48994428	-37
Gorasp2	NM_027352	chr2	70499342	70499714	-37
Dido1	NM_177852	chr2	180444550	180444930	-37
1200014J11Rik	NM_025818	chr11	72861115	72861548	-37
Ror2	NM_013846	chr13	53381273	53381754	-37
1700037H04Rik	NM_026091	chr2	130985665	130985918	-37
Lxn	NM_016753	chr3	67267784	67267945	-37
B3glct	NM_001081204	chr5	150480682	150480907	-37
Lsm5	NM_025520	chr6	56654637	56654820	-37
Usp47	NM_133758	chr7	119166817	119167148	-37
Lamp1	NM_010684	chr8	13158879	13159316	-37
Rab23	NM_008999	chr1	33776492	33776916	-36
Cnnm3	NM_001039551	chr1	36568494	36568874	-36
Actr2	NM_146243	chr11	20012856	20013122	-36
Flot2	NM_001040403	chr11	77851191	77851621	-36
Rpl23	NM_022891	chr11	97643651	97643925	-36
Nbn	NM_013752	chr4	15884827	15885327	-36
Inip	NM_001013577	chr4	59796587	59796937	-36
Rnf8	NM_021419	chr17	29751464	29752015	-36
Spink10	NM_177829	chr18	62708371	62708686	-36
Hnrnpr	NM_001277121	chr4	135866556	135867085	-36
Gpr19	NM_001167696	chr6	134847700	134848055	-36
Saal1	NM_030233	chr7	53965919	53966192	-36
Hspd1	NM_010477	chr1	55144578	55145042	-35
Gorab	NM_178883	chr1	165333564	165334048	-35

Supplemental Table 4. Significant ChIP-seq E2F3B promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Cradd	NM_009950	chr10	94786545	94786985	-35
Six1	NM_009189	chr12	74147541	74147925	-35
Agpat1	NM_001163379	chr17	34742633	34742907	-35
Znhit6	NM_001081094	chr3	145238870	145239402	-35
Brd9	NM_001024508	chr13	74074998	74075503	-35
Pbk	NM_023209	chr14	66424425	66425000	-35
Tsfm	NM_025537	chr10	126467673	126468133	-34
Wipf2	NM_197940	chr11	98724747	98725007	-34
Gstz1	NM_010363	chr12	88488430	88488814	-34
Mob1a	NM_145571	chr6	83275835	83276161	-34
Mars2	NM_175439	chr1	55293780	55294193	-34
1700016L04Rik	NR_045824	chr10	14425225	14425536	-34
Hmmr	NM_013552	chr11	40546830	40547113	-34
Mtdh	NM_026002	chr15	34012290	34012589	-34
Rbbp4	NM_009030	chr4	129012249	129013044	-34
Mlxip	NM_133917	chr5	123844657	123844888	-34
Rnps1	NM_001080128	chr17	24551259	24551913	-33
Ubr2	NM_001177374	chr17	47147302	47147724	-33
Ddx51	NM_027156	chr5	111082210	111082662	-33
Rhno1	NR_027359	chr6	128312858	128313036	-33
Smim19	NM_001146117	chr8	23587220	23587546	-33
Manf	NM_029103	chr9	106794126	106794476	-33
Rps6ka3	NM_148945	chrX	155693519	155693841	-33
Zswim8	NM_001252081	chr14	21526581	21526900	-33
Ctnnbl1	NM_025680	chr2	157562872	157563335	-33
Dock7	NM_026082	chr4	98787471	98787804	-33
Mafk	NM_010757	chr5	140267263	140267650	-33
Acsl3	NM_001033606	chr1	78654093	78654641	-32
Ptges3	NM_019766	chr10	127495740	127496270	-32
Rcbtb1	NM_027764	chr14	59819753	59820311	-32
Cebpz	NM_001024806	chr17	79336241	79336641	-32
Ankrd10	NM_001281974	chr8	11635576	11636000	-32
Ppp2r3a	NM_001161362	chr9	101153935	101154451	-32
Extl3	NM_018788	chr14	65716789	65717158	-32
Atp5o	NM_138597	chr16	91931742	91932069	-32
Cdan1	NM_026891	chr2	120557078	120557489	-32
Myef2	NM_001162417	chr2	124949288	124949565	-32
Cc2d1b	NM_177045	chr4	108292242	108292815	-32
Cdc16	NM_027276	chr8	13757479	13757836	-32
Zcchc2	NM_001122675	chr1	107886680	107887223	-31
Rif1	NM_175238	chr2	51928195	51928456	-31
Tmem67	NR_110955	chr4	12014993	12015374	-31
Eps15	NM_007943	chr4	108952635	108953062	-31
Rad54l	NM_001122959	chr4	115796196	115796453	-31
Rragb	NM_001004154	chrX	149574286	149574653	-31
Nvl	NM_026171	chr1	183074039	183074595	-30
Cdkl3	NM_001166654	chr11	51817533	51817851	-30
Ankrd32	NM_134071	chr13	77274644	77274872	-30

Supplemental Table 4. Significant ChIP-seq E2F3B promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Alcam	NM_009655	chr16	52452833	52453445	-30
Cdkn2a	NM_001040654	chr4	88927956	88928294	-30
Prmt1	NM_019830	chr7	52241689	52241949	-30
Tmem231	NM_001033321	chr8	114457600	114457840	-30
Vars	NM_011690	chr17	35137631	35138012	-30
Mcm8	NM_025676	chr2	132641623	132642070	-30
Emg1	NM_013536	chr6	124662040	124662409	-30
Plk1	NM_011121	chr7	129302788	129303053	-30
Echs1	NM_053119	chr7	147302205	147302496	-30
Rassf5	NM_018750	chr1	133141602	133141964	-29
E130309D02Rik	NM_172726	chr5	144076919	144077215	-29
Lphn1	NM_181039	chr8	86423818	86424116	-29
5830418K08Rik	NM_176976	chr9	15162087	15162433	-29
Nuf2	NM_023284	chr1	171461417	171461828	-29
Kif13b	NM_001081177	chr14	65271135	65271542	-29
Strn	NM_011500	chr17	79135695	79136160	-29
Emc7	NM_133749	chr2	112295017	112295288	-29
Snrpb	NM_009225	chr2	130004866	130005389	-29
Zranb2	NM_017381	chr3	157197017	157197646	-29
Psmb2	NM_011970	chr4	126354683	126355032	-29
Tmem222	NM_025667	chr4	132833515	132833950	-29
Mcm7	NM_008568	chr5	138612869	138613366	-29
Rad18	NM_001167730	chr6	112646506	112646877	-29
Nfat5	NM_018823	chr8	109817141	109817540	-29
Aurkb	NM_011496	chr11	68859021	68859211	-28
4930452B06Rik	NM_028934	chr14	9498700	9498962	-28
Sgol1	NM_028232	chr17	53828480	53828854	-28
Smchd1	NM_028887	chr17	71824465	71824955	-28
Exosc2	NM_144886	chr2	31526099	31526357	-28
Snrpd2	NM_026943	chr7	19734981	19735335	-28
Fam219b	NM_175273	chr9	57385177	57385435	-28
Adam15	NM_009614	chr3	89153772	89154145	-28
Brca2	NM_009765	chr5	151324920	151325415	-28
Vma21	NM_001081356	chrX	69061955	69062182	-28
Cep78	NM_198019	chr19	16059352	16059658	-27
Kin	NM_025280	chr2	10001949	10002473	-27
Nek6	NM_001159631	chr2	38367202	38367534	-27
Ahcyl1	NM_145542	chr3	107499294	107499690	-27
Rnf38	NM_175201	chr4	44180291	44180581	-27
Cenpc1	NM_007683	chr5	86494520	86494748	-27
Mlh1	NM_026810	chr9	111173970	111174306	-27
Sept2	NM_010891	chr1	95375343	95375742	-27
Ccdc71l	NM_001162903	chr12	33063445	33063808	-27
Nr1d2	NM_011584	chr14	19071347	19071944	-27
Dxo	NM_001163770	chr17	34973682	34974191	-27
Bub1b	NM_009773	chr2	118423669	118424170	-27
Slc20a1	NM_015747	chr2	129024285	129024678	-27
6330408A02Rik	NM_177312	chr7	13863885	13864306	-27

Supplemental Table 4. Significant ChIP-seq E2F3B promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Lipt2	NM_026010	chr7	107307653	107307866	-27
Taf1	NM_001290729	chrX	98727818	98728275	-27
A230046K03Rik	NM_001033375	chr10	83006515	83006803	-26
2310003H01Rik	NM_027980	chr11	120239940	120240230	-26
Aaas	NM_153416	chr15	102180971	102181459	-26
Rbm4	NM_001290125	chr19	4793730	4794122	-26
Adh5	NM_007410	chr3	138105814	138106246	-26
Zcwpw1	NM_001005426	chr5	138228743	138229263	-26
Lsm3	NM_026309	chr6	91465879	91466125	-26
Spc24	NM_026282	chr9	21564617	21564893	-26
Pola1	NM_008892	chrX	90877179	90877859	-26
Tmem220	NM_001291043	chr11	66838465	66838794	-26
Cinp	NM_026048	chr12	112127209	112127550	-26
Ppm1f	NM_176833	chr16	16896378	16896693	-26
Tubb5	NM_011655	chr17	35975119	35975422	-26
Gnpda1	NM_011937	chr18	38498583	38498760	-26
Smim8	NM_025471	chr4	34725405	34725816	-26
Ap1s1	NM_007457	chr5	137521682	137522227	-26
Osr2	NM_054049	chr15	35225663	35226019	-25
Sdf2l1	NM_022324	chr16	17132208	17132792	-25
Zc3h8	NM_020594	chr2	128769622	128769938	-25
Msto1	NM_144898	chr3	88717694	88718098	-25
Chd1l	NM_026539	chr3	97413838	97414436	-25
Tspan3	NM_019793	chr9	56008790	56009012	-25
Epb4.1l2	NM_001199265	chr10	25079370	25079787	-25
Txlna	NM_001005506	chr4	129317830	129318315	-25
Gm4532	NR_030674	chr7	134376483	134376852	-25
Spg7	NM_153176	chr8	125589199	125589566	-25
Rasal2	NM_177644	chr1	159342584	159342914	-24
Tppp	NM_182839	chr13	74146716	74146968	-24
Mrps27	NM_173757	chr13	100114603	100114829	-24
Fam118a	NM_133750	chr15	84867277	84867657	-24
Ubn1	NM_026666	chr16	5049883	5050389	-24
Srsf3	NM_013663	chr17	29169345	29169815	-24
Itgav	NM_008402	chr2	83564362	83564696	-24
Rab2a	NM_021518	chr4	8462589	8462943	-24
Srrd	NM_027323	chr5	112771982	112772184	-24
Tfap4	NM_031182	chr16	4559502	4559983	-24
Olfml3	NM_133859	chr3	103541759	103542134	-24
Cntln	NM_175275	chr4	84529965	84530412	-24
Eif3b	NM_133916	chr5	140895136	140895333	-24
Plagl1	NM_009538	chr10	12810319	12810821	-23
Myo1c	NM_008659	chr11	75464848	75465126	-23
Rreb1	NM_001039188	chr13	37919123	37919353	-23
Matn2	NM_016762	chr15	34236275	34236549	-23
Ddx20	NM_017397	chr3	105490338	105490684	-23
Tmem43	NM_028766	chr6	91423614	91423828	-23
Tmtc3	NM_001110013	chr10	99949665	99950340	-23

Supplemental Table 4. Significant ChIP-seq E2F3B promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Rhebl1	NM_026967	chr15	98711630	98712103	-23
Tcp1	NM_013686	chr17	13108887	13109456	-23
Ppp1cb	NM_172707	chr5	32760970	32761669	-23
Nono	NM_023144	chrX	98624857	98625076	-23
Mthfd1	NM_138745	chr12	77355871	77356521	-22
Myh9	NM_022410	chr15	77672242	77673010	-22
Lpar1	NM_172989	chr4	58566044	58566328	-22
Add1	NM_013457	chr5	34916138	34916542	-22
Coq2	NM_027978	chr5	101103165	101103427	-22
Srpr	NM_026130	chr9	35018552	35018978	-22
Fhl4	NM_010214	chr10	84565102	84565419	-22
Mrpl14	NM_026732	chr17	45823171	45823426	-22
Mrps18c	NM_026826	chr5	101227524	101227987	-22
Eif3g	NM_016876	chr9	20702886	20703223	-22
Hist1h2ag	NM_178186	chr13	22134704	22134972	-21
Amdhd2	NM_172935	chr17	24300546	24300894	-21
Gemin6	NM_026053	chr17	80623720	80623894	-21
Rab33b	NM_016858	chr3	51287664	51288068	-21
Ripk1	NM_009068	chr13	34094604	34094839	-21
E2f1	NM_007891	chr2	154395424	154395871	-21
Tfip11	NM_018783	chr5	112755212	112755523	-21
Rad51ap1	NM_009013	chr6	126889451	126889734	-21
Gemin2	NM_025656	chr12	60114189	60114529	-20
Ifit2	NM_008332	chr19	34624989	34625337	-20
Stk35	NM_183262	chr2	129626096	129626368	-20
Prdx1	NM_011034	chr4	116358050	116358316	-20
Taf12	NM_025579	chr4	131830160	131830378	-20
Pdap1	NM_001033313	chr5	145900725	145901229	-20
Polb	NM_011130	chr8	23763800	23764056	-20
Cab39	NM_133781	chr1	87689838	87690165	-20
Espl1	NM_001014976	chr15	102126510	102126897	-20
Slc35a3	NM_144902	chr3	116415121	116415312	-20
Cyr61	NM_010516	chr3	145312831	145313104	-20
Tma16	NM_025465	chr8	69010234	69010615	-20
Ccdc122	NM_175369	chr14	77436430	77436688	-19
Toporsos	NR_045265	chr4	40216417	40216767	-19
D830031N03Rik	NM_001167918	chr4	123089012	123089332	-19
Klhl17	NM_198305	chr4	155608817	155609151	-19
Fscn1	NM_007984	chr5	143721809	143722219	-19
Ticrr	NM_029835	chr7	86804755	86805369	-19
Ranbp1	NM_011239	chr16	18248495	18249114	-19
Pdia3	NM_007952	chr2	121239345	121239892	-19
Plekhf2	NM_175175	chr4	10934551	10935016	-19
Cdca3	NM_013538	chr6	124780011	124780338	-19
Polr3e	NM_025298	chr7	128061130	128061347	-19
Tceb1	NM_026456	chr1	16646752	16647174	-18
Tanc1	NM_198294	chr2	59449884	59450276	-18
Arl2	NM_019722	chr19	6141022	6141285	-18

Supplemental Table 4. Significant ChIP-seq E2F3B promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Nsl1	NM_198654	chr1	192886689	192887075	-17
Hus1	NM_008316	chr11	8911009	8911303	-17
9330151L19Rik	NR_033222	chr12	70297996	70298364	-17
Mccc2	NM_030026	chr13	100785464	100785756	-17
Smim4	NR_024069	chr14	31941859	31942405	-17
Sema3g	NM_001025379	chr14	32030897	32031185	-17
2700094K13Rik	NM_001033166	chr2	84510735	84511027	-17
Exoc4	NM_009148	chr6	33198884	33199380	-17
Zfp280b	NM_177475	chr10	75495197	75495482	-17
Trim65	NM_178802	chr11	115992289	115992626	-17
Get4	NM_026269	chr5	139728094	139728427	-17
A130010J15Rik	NM_001160360	chr1	194999372	194999920	-16
Naa35	NM_030153	chr13	59686521	59686833	-16
Pigt	NM_133779	chr2	164322870	164323146	-16
Tmem60	NM_177601	chr5	20388130	20388378	-16
Smarcc1	NM_009211	chr9	110034192	110034830	-16
Ppil1	NM_026845	chr17	29400573	29401288	-16
Slc31a2	NM_025286	chr4	61947270	61947623	-16
Recql	NM_001204907	chr6	142335465	142335778	-16
Ppm1m	NM_026447	chr9	106101450	106101707	-16
Alas1	NM_020559	chr9	106150157	106150442	-16
Ptpn23	NM_001081043	chr9	110310555	110310902	-16
Tmco1	NM_001039483	chr1	169238639	169238931	-15
Poc1b	NM_027740	chr10	98569608	98569970	-15
Ghitm	NM_078478	chr14	37948348	37948696	-15
Erp29	NM_026129	chr5	121902278	121902716	-15
Fancb	NM_001146081	chrX	161418265	161418751	-15
Abi2	NM_198127	chr1	60466247	60466648	-15
Gsg2	NM_010353	chr11	72951681	72951938	-15
Stil	NM_009185	chr4	114672346	114673069	-15
Lrwd1	NM_027891	chr5	136611747	136612168	-15
Naf1	NM_001163564	chr8	69383963	69384238	-15
4930432K21Rik	NM_001163752	chr8	86671728	86672115	-15
Prdx4	NM_016764	chrX	151772901	151773120	-15
Tmem194b	NM_001142647	chr1	52687331	52687737	-14
Ing3	NM_023626	chr6	21899482	21899718	-14
Farsa	NM_025648	chr8	87380711	87381029	-14
Ube2d1	NM_145420	chr10	70747762	70748283	-14
AA465934	NR_028363	chr11	83105000	83105373	-14
Xxylt1	NM_198626	chr16	31081319	31081742	-14
Bambi-ps1	NR_027919	chr2	122293367	122293724	-14
Nans	NM_053179	chr4	46501968	46502405	-14
Mapk6	NM_015806	chr9	75257605	75258066	-14
Vamp3	NM_009498	chr4	150431876	150432272	-13
Specc1l	NM_153406	chr10	74674670	74674939	-13
Slc25a10	NM_013770	chr11	120353047	120353228	-13
Tgfbrap1	NM_001013025	chr1	43155318	43155638	-12
Arf1	NM_001130408	chr11	59041496	59041854	-12

Supplemental Table 4. Significant ChIP-seq E2F3B promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
0610010K14Rik	NM_001177603	chr11	70051250	70051604	-12
Zfp367	NM_175494	chr13	64254216	64254820	-12
Cdc123	NM_133837	chr2	5765869	5766165	-12
Efhd2	NM_025994	chr4	141430662	141431030	-12
Sf3b2	NM_030109	chr19	5295251	5295680	-12
Rap2b	NM_028712	chr3	61168272	61168561	-12
Tob1	NM_009427	chr11	94072591	94072921	-11
Appl1	NM_145221	chr14	27783544	27783950	-11
Psmd2	NM_134101	chr16	20651504	20651922	-11
Med20	NM_020048	chr17	47748306	47748760	-11
Arhgap11a	NM_181416	chr2	113688663	113688993	-11
4930539J05Rik	NR_030689	chr3	135101550	135101728	-11
Cox18	NM_001033310	chr5	90652890	90653172	-11
Wdr61	NM_001025376	chr9	54582263	54582469	-11
Mcm6	NM_008567	chr1	130255917	130256568	-11
Lin9	NM_175186	chr1	182571364	182571543	-11
Adat3	NM_001100606	chr10	80065472	80065755	-11
Gm12359	NR_033551	chr11	98671299	98671526	-11
Sgms1	NM_001168526	chr19	32285254	32285771	-11
Klhl26	NM_178771	chr8	73000726	73000977	-11
Tfrc	NM_011638	chr16	32608767	32609175	-10
Elac1	NM_053255	chr18	73913971	73914313	-10
Haus6	NM_173400	chr4	86257830	86258040	-10
Ppp1r8	NM_146154	chr4	132398959	132399227	-10
Crtap	NM_019922	chr9	114299679	114299999	-10
Dna2	NM_177372	chr10	62409591	62409942	-10
Heatr5a	NM_177171	chr12	53072139	53072494	-10
Pvt1	NR_003368	chr15	61869354	61869709	-10
Tob2	NM_020507	chr15	81688599	81688930	-10
Adprh	NM_007414	chr16	38452570	38452985	-10
Cmtr1	NM_028791	chr17	29797397	29797674	-10
Spry1	NM_011896	chr3	37538755	37538968	-10
Zmym1	NM_026670	chr4	126738238	126738531	-10
Snrpg	NM_026506	chr6	86321328	86321719	-10
Aifm1	NM_012019	chrX	45866533	45866964	-10
Spdl1	NM_027411	chr11	34646961	34647341	-9
Mgat4b	NM_145926	chr11	50038697	50038957	-9
Osbpl1a	NM_207530	chr18	13100232	13100484	-9
Wdr89	NM_028203	chr12	76770239	76770824	-9
Dab2	NM_001037905	chr15	6336536	6336941	-9
Usp1	NM_146144	chr4	98590204	98590779	-9
Ddx55	NM_001190795	chr5	125002620	125003107	-9
4933426M11Rik	NM_178682	chr12	81891280	81891740	-8
F2r	NM_010169	chr13	96388031	96388759	-8
Metap1d	NM_025633	chr2	71291196	71291576	-8
Ywhah	NM_011738	chr5	33361208	33361704	-8
Slc7a1	NM_007513	chr5	149211257	149211717	-8
Pih1d1	NM_029406	chr7	52409524	52409804	-8

Supplemental Table 4. Significant ChIP-seq E2F3B promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
2300009A05Rik	NM_027090	chr9	63246892	63247224	-8
Cenpi	NM_145924	chrX	130842489	130842897	-8
Cap1	NM_007598	chr4	122562940	122563321	-8
Qrsl1	NM_001081054	chr10	43621337	43621759	-7
Nkapl	NM_025719	chr13	21560164	21560588	-7
Vgf	NM_001039385	chr5	137505974	137506340	-7
Pgls	NM_025396	chr8	74115765	74116385	-7
6430548M08Rik	NM_001163761	chr8	122637950	122638138	-7
Csrp1	NM_007791	chr1	137625636	137625897	-7
Lmnb2	NM_010722	chr10	80380762	80381229	-7
Ttll12	NM_183017	chr15	83425481	83425704	-7
Vps37c	NM_181403	chr19	10763116	10763479	-7
Epha2	NM_010139	chr4	140856947	140857310	-7
Nup62-il4i1	NM_001171024	chr7	52071521	52071944	-7
Natd1	NM_025294	chr11	60727159	60727439	-6
Fut8	NM_001252614	chr12	78338951	78339217	-6
Pqlc2	NM_145384	chr4	138866361	138866879	-6
Rpsa	NM_011029	chr9	120036662	120037092	-6
Trmt2b	NM_172540	chrX	130811357	130811699	-6
Pam	NM_013626	chr1	99992039	99992388	-6
Bsg	NM_001077184	chr10	79166928	79167265	-6
Igsf8	NM_080419	chr1	174242310	174242754	-5
Tube1	NM_028006	chr10	38853651	38853995	-5
Fam58b	NM_197989	chr11	78565090	78565380	-5
Tbccd1	NM_001081368	chr16	22857455	22857837	-5
Ctdp1	NM_026295	chr18	80666321	80666499	-5
Psmc3	NM_008948	chr2	90893995	90894339	-5
Msantd3	NM_001145924	chr4	48552765	48553129	-5
Picalm	NM_001252523	chr7	97278598	97278874	-5
Prkcdbp	NM_028444	chr7	112630510	112630920	-5
Abtb2	NM_178890	chr2	103406338	103406585	-5
Exog	NM_001172136	chr9	119353873	119354198	-5
Pan2	NM_001252327	chr10	127740186	127740586	-4
Npm1	NM_001252260	chr11	33063004	33063414	-4
Pfkp	NM_019703	chr13	6647905	6648135	-4
Cbx5	NM_007626	chr15	103045659	103045913	-4
Vti1a	NM_001293686	chr19	55390363	55390721	-4
Polr3k	NM_025901	chr2	181598947	181599173	-4
Zfp111	NM_019940	chr7	24993068	24993274	-4
Zdhhc3	NM_026917	chr9	123022161	123022491	-4
Asnsd1	NM_133728	chr1	53409469	53409728	-4
A730008H23Rik	NM_172505	chr1	90173841	90174428	-4
Psmd6	NM_025550	chr14	14953262	14953579	-4
Tfb1m	NM_146074	chr17	3557305	3558126	-4
Gmps	NM_001033300	chr3	63779918	63780203	-4
Agbl3	NM_001289656	chr6	34730203	34730652	-4
Zbtbd6	NM_001034882	chr14	79851432	79851844	-3
Eif2ak2	NM_011163	chr17	79281667	79282161	-3

Supplemental Table 4. Significant ChIP-seq E2F3B promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Lrrc57	NM_025657	chr2	120434829	120435277	-3
Gtse1	NM_001168672	chr15	85689976	85690291	-3
Mybl2	NM_008652	chr2	162880010	162880725	-3
C2cd3	NM_001017985	chr7	107520487	107520992	-3
Shcbp1	NM_011369	chr8	4779383	4779688	-3
Gm2a	NM_010299	chr11	54911317	54911651	-2
Klhdc2	NM_027117	chr12	70397490	70397840	-2
Rpl36	NM_018730	chr17	56752677	56752953	-2
Commd10	NM_178377	chr18	47118349	47118705	-2
Map1a	NM_032393	chr2	121115152	121115518	-2
Fam192a	NM_028221	chr8	97125328	97125926	-2
Slc7a6	NM_178798	chr8	108692613	108692931	-2
Pde6d	NM_008801	chr1	88478907	88479246	-2
Cyb561a3	NM_201351	chr19	10651404	10651885	-2
Cept1	NM_133869	chr3	106350573	106350868	-2
Ptpn13	NM_011204	chr5	103854022	103854395	-2
Vrk3	NM_133945	chr7	52003761	52004232	-2
Timp1	NM_011593	chrX	20447120	20447459	-2
E2f7	NM_178609	chr10	110182254	110182784	-1
Wrap53	NM_144824	chr11	69392652	69393000	-1
Crlf3	NM_018776	chr11	79894237	79894749	-1
Zfp622	NM_144523	chr15	25913935	25914303	-1
B230319C09Rik	NR_028382	chr6	83391456	83392038	-1
Fadd	NM_010175	chr7	151768187	151768495	-1
Gadd45g	NM_011817	chr13	51941841	51942244	-1
Snhg9	NR_027900	chr17	24856646	24857173	-1
Cav2	NM_016900	chr6	17231019	17231348	-1
Gins3	NM_030198	chr8	98157251	98157664	-1
Sh3bp1	NM_009164	chr15	78730033	78730397	0
Prim2	NM_008922	chr1	33726378	33726897	1
Cep83os	NR_015524	chr10	94151274	94151439	1
Cntrob	NM_172560	chr11	69137145	69137602	1
Wdr45b	NM_025793	chr11	121215571	121215948	1
Pigp	NM_001159620	chr16	94591778	94592093	1
Stom	NM_013515	chr2	35192401	35192654	1
Alg14	NM_024178	chr3	120994605	120994864	1
C2cd5	NM_001286578	chr6	143048571	143048770	1
Actn4	NM_021895	chr7	29747107	29747488	1
Plekhh2	NM_177606	chr17	84911081	84911389	1
Pmpca	NM_173180	chr2	26244750	26244986	1
2810403A07Rik	NM_028814	chr3	88489589	88489843	1
Clcc1	NM_145543	chr3	108456561	108457101	1
Pus1	NM_001025562	chr5	111209495	111209769	1
Mns1	NM_008613	chr9	72286127	72286545	1
Eif4e2	NM_023314	chr1	89110359	89110620	2
Hist1h2ah	NM_175659	chr13	22127399	22127620	2
Tarbp2	NM_009319	chr15	102348286	102348961	2
Mapk1	NM_011949	chr16	16983223	16983728	2

Supplemental Table 4. Significant ChIP-seq E2F3B promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Rcan1	NM_001081549	chr16	92466198	92466625	2
Ranbp3	NM_001252467	chr17	56812291	56813006	2
Pigf	NM_008838	chr17	87424515	87424962	2
Kiz	NM_001033298	chr2	146681514	146681737	2
Intu	NM_175515	chr3	40439569	40439810	2
Asxl2	NM_001270988	chr12	3426563	3427153	2
Gm9776	NR_045619	chr13	95128679	95129071	2
Pde12	NM_178668	chr14	27489073	27489585	2
Map7d1	NM_001145970	chr4	125933399	125933721	2
Taf10	NM_020024	chr7	112892701	112892997	2
Blmh	NM_178645	chr11	76758974	76759345	3
Slc25a1	NM_153150	chr16	17928073	17928544	3
Chtf18	NM_145409	chr17	25864037	25864676	3
Ints3	NM_145540	chr3	90237320	90237789	3
Abcf2	NM_001190443	chr5	24083083	24083480	3
Rfc5	NM_028128	chr5	117838766	117839291	3
Herc1	NM_145617	chr9	66198040	66198477	3
Smad5	NM_008541	chr13	56804168	56804578	3
Brd3	NM_001113574	chr2	27331084	27331294	3
Psmb7	NM_011187	chr2	38499206	38499638	3
Kbtbd8	NM_001008785	chr6	95067562	95068190	3
Ankle1	NM_172756	chr8	73929705	73930121	3
Nkap	NM_025937	chrX	34666650	34666870	3
Med12	NM_021521	chrX	98469272	98469592	3
Abl2	NM_009595	chr1	158488787	158489054	4
Shmt1	NM_009171	chr11	60624517	60625008	4
Rabl6	NM_001024616	chr2	25463792	25464131	4
Cd99l2	NM_138309	chrX	68745801	68746238	4
Ecd	NM_027475	chr14	21167181	21167495	4
Ssna1	NM_023464	chr2	25127681	25128185	4
Abca2	NM_007379	chr2	25284017	25284377	4
Ampd2	NM_028779	chr3	107889486	107889672	4
Rnaseh2a	NM_027187	chr8	87489712	87490098	4
Hmg20b	NM_001163165	chr10	80812888	80813443	5
Prps1l3	NM_001037746	chr12	58331193	58331612	5
Fancm	NM_178912	chr12	66176450	66176743	5
Nfkbil1	NM_010909	chr17	35372495	35373014	5
Grem1	NM_011824	chr2	113598643	113598956	5
Fsd1l	NM_001195284	chr4	53644198	53644495	5
Ormdl1	NM_145517	chr1	53353722	53354164	5
Kctd5	NM_027008	chr17	24210146	24210746	5
Naa40	NM_027643	chr19	7315399	7316013	5
Fam69b	NM_019833	chr2	26483887	26484075	5
Ythdf3	NM_001145919	chr3	16083000	16083374	5
Mphosph8	NM_023773	chr14	57286888	57287291	6
Csnk2b	NM_009975	chr17	35258184	35258587	6
Cep76	NM_001081073	chr18	67800860	67801107	6
Camk2d	NM_001025438	chr3	126299732	126300015	6

Supplemental Table 4. Significant ChIP-seq E2F3B promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Rps16	NM_013647	chr7	29135546	29135879	6
Mir6236	NR_105744	chr9	110183645	110183946	6
1700021F05Rik	NM_026411	chr10	43260478	43261108	6
D15Ertd621e	NM_145959	chr15	58246807	58247249	6
Aldh7a1	NM_001127338	chr18	56732409	56732763	6
Med9os	NR_045273	chr11	59761484	59761799	7
Atpaf2	NM_145427	chr11	60230307	60230880	7
Atad2b	NM_001099628	chr12	4923966	4924363	7
Secisbp2	NM_029279	chr13	51746894	51747283	7
Terf2	NM_009353	chr8	109620274	109620601	7
Dbr1	NM_031403	chr9	99476061	99476386	7
Smc6	NM_025695	chr12	11272509	11272887	7
Xrcc5	NM_009533	chr1	72353873	72354130	8
Rhoj	NM_023275	chr12	76409168	76409445	8
Flywch1	NM_153791	chr17	23908364	23908735	8
Osbpl6	NM_001290733	chr2	76244378	76244765	8
Ppip5k2	NM_173760	chr1	99666533	99666787	8
Itsn2	NM_001198968	chr12	4599656	4599986	8
B3galnt2	NM_178640	chr13	14046699	14047197	8
Tubgcp6	NM_001163319	chr15	88953437	88953705	8
1700123M08Rik	NR_040577	chr4	11893399	11894057	8
Ano6	NM_001253813	chr15	95621132	95621431	9
Cks1b	NM_016904	chr3	89222049	89222358	9
Alg6	NM_001081264	chr4	99382120	99382537	9
Faf1	NM_007983	chr4	109349014	109349465	9
Hsph1	NM_013559	chr5	150438668	150439093	9
Apol7d	NR_040308	chr1	71699578	71700256	9
4930563E22Rik	NM_001163728	chr11	72028524	72028772	9
Gpaa1	NM_010331	chr15	76161362	76162102	9
Clpp	NM_017393	chr17	57129502	57129888	9
Tnfaip8	NM_001177759	chr18	50138908	50139270	9
Qsox2	NM_153559	chr2	26092638	26093222	9
Rpl35	NM_025592	chr2	38860472	38860810	9
Phtf1os	NR_030676	chr3	103771971	103772487	9
Pradc1	NR_028081	chr6	85401710	85402198	9
Fut10	NM_001286425	chr8	32297608	32298014	9
Sppl2b	NM_175195	chr10	80317849	80318208	10
Vrk1	NM_011705	chr12	107248308	107248655	10
Dnph1	NM_207161	chr17	46633551	46633942	10
Itprip	NM_001001738	chr19	47993504	47994053	10
Gab1	NM_021356	chr8	83404178	83404557	10
Prim1	NM_008921	chr10	127452032	127452528	10
Npc2	NM_023409	chr12	86113763	86114339	10
Ap5s1	NM_001291031	chr2	131035945	131036265	10
Zfp821	NM_001167946	chr8	112229311	112229599	10
Vash2	NR_027352	chr1	192802978	192803349	11
Hnrnpm	NM_029804	chr17	33822188	33822595	11
Rusc2	NM_001037709	chr4	43394697	43395030	11

Supplemental Table 4. Significant ChIP-seq E2F3B promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Tyms	NM_021288	chr5	30400025	30400282	11
Fam188b	NM_001142781	chr6	55153256	55153517	11
Ddx50	NM_053183	chr10	62113742	62114126	11
Mcm10	NM_027290	chr2	4933518	4934132	11
Rprd1b	NM_001291135	chr2	157853956	157854530	11
Nav2	NM_175272	chr7	56501323	56501815	11
Palb2	NM_001081238	chr7	129276336	129276560	11
Zfp560	NM_001004190	chr9	20189384	20189796	11
Msantd2	NM_146222	chr9	37296775	37297057	11
Faim	NM_001122851	chr9	98886611	98886993	11
Nme6	NM_018757	chr9	109735072	109735564	11
Ccdc57	NM_027745	chr11	120793935	120794412	12
Tango2	NM_138583	chr16	18343798	18344227	12
Slc6a17	NM_172271	chr3	107320841	107321006	12
Pms2	NM_008886	chr5	144670599	144671162	12
Prdx2	NM_011563	chr8	87493429	87493686	12
Cenpn	NM_028131	chr8	119445315	119445986	12
Gtf2f2	NM_026816	chr14	76410476	76410842	12
Dgcr8	NM_033324	chr16	18288819	18289677	12
Loh12cr1	NM_026371	chr6	134590845	134591093	12
Mcm5	NM_008566	chr8	77633121	77633755	12
Rfesd	NM_001131069	chr13	76156013	76156280	13
Smc3	NM_007790	chr19	53674809	53674987	13
Zbtb49	NM_029162	chr5	38611525	38611781	13
Polg	NM_017462	chr7	86610901	86611389	13
Frg1	NM_013522	chr8	42502280	42502636	13
Fanca	NM_016925	chr8	125842299	125842625	13
Slc12a7	NM_011390	chr13	73900995	73901320	14
Slc35a5	NM_028756	chr16	45158606	45158937	14
Rfc3	NM_027009	chr5	152453612	152453925	14
9430015G10Rik	NM_145557	chr4	155483818	155484422	14
Msn	NM_010833	chrX	93291223	93291571	14
Endov	NM_001164636	chr11	119352464	119352885	15
Pcbd2	NM_028281	chr13	55828566	55828919	15
Nrm	NM_134122	chr17	35997998	35998555	15
Tdp1	NM_028354	chr12	101122601	101122877	15
Kif20b	NM_183046	chr19	34996736	34996988	15
Yif1b	NM_001110201	chr7	30023178	30023534	15
Tomm20	NM_024214	chr8	129469662	129469948	15
Rbfox2	NM_175387	chr15	77137134	77137799	16
Mrpl40	NM_010922	chr16	18876308	18877119	16
Polq	NM_029977	chr16	37011663	37012110	16
Trappc5	NM_025701	chr8	3676317	3676666	16
Zfp62	NM_009562	chr11	49016831	49017203	16
Bora	NM_175265	chr14	99445423	99445799	16
Zfp568	NM_001167872	chr7	30768885	30769093	16
Tubgcp2	NM_001286011	chr7	147222100	147222364	16
Bok	NM_016778	chr1	95582111	95582462	17

Supplemental Table 4. Significant ChIP-seq E2F3B promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Rnf217	NM_001146349	chr10	31329366	31329661	17
Aars2	NM_198608	chr17	45643653	45643958	17
Trpt1	NM_153597	chr19	7070516	7070757	17
Mir5122	NR_039582	chr4	132925497	132925916	17
Arpc1b	NM_023142	chr5	145875024	145875257	17
Sertad1	NM_018820	chr7	28271826	28272149	17
Smad6	NM_008542	chr9	63869617	63870080	17
Tmem64	NM_181401	chr4	15192811	15193155	17
Plekhg2	NM_001290542	chr7	29157340	29157986	17
Coq10b	NM_001039710	chr1	55109472	55109789	18
Tmem107	NM_028336	chr11	68884025	68884630	18
Cpd	NM_007754	chr11	76660352	76660631	18
Puf60	NM_133691	chr15	75911041	75911674	18
4930483J18Rik	NR_015603	chr15	81021152	81021447	18
Mesdc1	NM_030705	chr7	91032628	91033037	18
Mrm1	NM_145433	chr11	84632775	84633221	18
Fkbp3	NM_013902	chr12	66174568	66175244	18
Spata13	NM_001033272	chr14	61253344	61253822	18
Itsn1	NM_010587	chr16	91729397	91729869	18
Atg16l1	NM_029846	chr1	89652434	89652773	19
Pask	NM_080850	chr1	95239018	95239673	19
Rad51c	NM_053269	chr11	87217671	87218284	19
Cbwd1	NM_146097	chr19	25035895	25036278	19
Kirrel	NM_001170985	chr3	86978515	86978784	19
4833439L19Rik	NM_001252648	chr13	54666594	54666852	19
Fbxo42	NM_172518	chr4	140703662	140704048	19
Eif4g1	NM_145941	chr16	20672664	20673017	20
Tbc1d5	NM_028162	chr17	51318363	51318950	20
Psmf1	NM_212446	chr2	151566871	151567146	20
Mmab	NM_029956	chr5	114893717	114894314	20
Mitf	NM_001113198	chr6	97756892	97757249	20
Dhx9	NM_007842	chr1	155334557	155334981	20
1810032O08Rik	NR_027821	chr11	116532836	116533150	20
Itpr3	NM_080553	chr17	27194094	27194442	20
Kif23	NM_024245	chr9	61794360	61794810	20
Nup155	NM_133227	chr15	8059005	8059660	21
1700007L15Rik	NR_045709	chr16	33380666	33380935	21
Map6	NM_001043355	chr7	106416627	106417124	21
2700029M09Rik	NM_028299	chr8	63368945	63369590	21
Ppp3r1	NM_024459	chr11	17059201	17059441	21
Srsf1	NM_001078167	chr11	87860666	87861124	21
Spsb3	NM_001163750	chr17	25023440	25023838	21
Gt(ROSA)26Sor	NR_027010	chr6	113027023	113027409	21
Ccnb2	NM_007630	chr9	70269174	70269504	21
4930429F24Rik	NR_040734	chr9	79641295	79641641	21
Ttc21a	NM_028735	chr9	119846551	119846937	21
Kif15	NM_010620	chr9	122859995	122860443	21
Kif2c	NM_134471	chr4	116855045	116855368	22

Supplemental Table 4. Significant ChIP-seq E2F3B promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Slc25a40	NM_178766	chr5	8422623	8423094	22
Gfod2	NM_027469	chr8	108282315	108282654	22
Rpl19	NM_009078	chr11	97888090	97888428	22
Pex12	NM_134025	chr11	83112314	83112597	23
Dync1li2	NM_001013380	chr8	106966802	106967045	23
Exosc6	NM_028274	chr8	113580042	113580479	23
Pold2	NM_008894	chr11	5777998	5778472	23
Hint1	NM_008248	chr11	54679782	54680142	23
Pfas	NM_001159519	chr11	68821747	68822129	23
Cpsf1	NM_001164173	chr15	76437737	76438257	23
Mrpl17	NM_025301	chr7	112959344	112959810	23
Abce1	NM_015751	chr8	82235461	82235769	23
Cct2	NM_007636	chr10	116500557	116501134	24
Ect2	NM_001177625	chr3	27052632	27052871	24
Rfc1	NM_011258	chr5	65726650	65727057	24
Esyt2	NM_028731	chr12	117519172	117520264	24
Nhp2l1	NM_011482	chr15	81877824	81878182	24
5430402O13Rik	NR_015581	chr6	50516463	50516867	24
Als2	NM_028717	chr1	59293900	59294199	25
Tdp2	NM_019551	chr13	24923424	24923679	25
AI413582	NM_001002895	chr17	27702407	27702886	25
Psmd5	NM_080554	chr2	34726232	34726681	25
Alad	NM_001276446	chr4	62180742	62181093	25
Nup205	NM_027513	chr6	35127512	35127767	25
Man2c1	NM_028636	chr9	56978453	56978762	25
Depdc1a	NM_001172092	chr3	159158216	159158626	25
Chka	NM_001271496	chr19	3851531	3852064	26
Cactin	NM_027381	chr10	80783658	80784088	26
Wasl	NM_028459	chr6	24614791	24615145	26
Dguok	NM_013764	chr6	83456783	83457089	26
2310036O22Rik	NM_026760	chr8	87550613	87550901	26
Wasf1	NM_031877	chr10	40603194	40603537	27
Bbip1	NM_001195348	chr19	54018911	54019268	27
Eif2b1	NM_145371	chr5	125028868	125029209	27
Zfp414	NM_026712	chr17	33765777	33766349	27
Ncaph	NM_144818	chr2	126959348	126959976	27
Itpripl1	NM_001163527	chr2	126969081	126969249	27
Atg16l2	NM_001111111	chr7	108450406	108450742	27
Rrp8	NM_025897	chr7	112884844	112885296	27
Bckdk	NM_009739	chr7	135047422	135047804	27
1700030K09Rik	NM_028170	chr8	74967634	74967976	27
Cep57	NM_026665	chr9	13631383	13631663	27
Ascc3	NM_198007	chr10	50312226	50312777	28
Atad5	NM_001029856	chr11	79902789	79903068	28
Ube2z	NM_172300	chr11	95926449	95926850	28
6030458C11Rik	NM_029998	chr15	12754144	12754623	28
C030006K11Rik	NM_145472	chr15	76554069	76554424	28
Sac3d1	NM_133678	chr19	6118413	6118702	28

Supplemental Table 4. Significant ChIP-seq E2F3B promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Paxip1	NM_018878	chr5	28117907	28118216	28
Nup133	NM_172288	chr8	126472977	126473296	28
Birc5	NM_001012273	chr11	117710453	117710703	28
Stxbp6	NM_144552	chr12	46175264	46175618	28
Tipin	NM_025372	chr9	64129238	64129644	28
Mon2	NM_001163025	chr10	122513367	122513696	29
C1d	NM_020558	chr11	17157452	17157845	29
Myo19	NM_025414	chr11	84693561	84693938	29
Map4k5	NM_201519	chr12	70993977	70994264	29
March5	NM_027314	chr19	37281929	37282196	29
Slc35c1	NM_211358	chr2	92299808	92300035	29
Fkbp1a	NM_008019	chr2	151368025	151368500	29
Smpdl3b	NM_133888	chr4	132312911	132313202	29
Cbln1	NM_019626	chr8	89996193	89996730	29
Ubxn4	NM_026390	chr1	130140530	130141042	29
Ndufaf2	NM_001127346	chr13	108948587	108948991	29
Use1	NM_001145780	chr8	73890679	73890871	29
4931428F04Rik	NM_001166394	chr8	107813163	107813633	29
Ahi1	NM_026203	chr10	20672161	20672602	30
Tbpl1	NM_011603	chr10	22451047	22451398	30
Rab10	NM_016676	chr12	3309728	3310149	30
Gm20604	NM_001142939	chr12	103995642	103996337	30
Cenpe	NM_173762	chr3	134875427	134875684	30
Tubgcp3	NM_198031	chr8	12671814	12672325	30
Zfp39	NM_011758	chr11	58717541	58717851	30
Micall1	NM_177461	chr15	78939221	78939663	30
Tab1	NM_025609	chr15	79963381	79963845	30
Rad51	NM_011234	chr2	118938441	118938723	30
Impa1	NM_018864	chr3	10331277	10331539	30
Cyp51	NM_020010	chr5	4104314	4105018	30
Prpf4b	NM_013830	chr13	34967216	34967569	31
Ythdf2	NM_145393	chr4	131767919	131768360	31
Klhl21	NM_001033352	chr4	151382780	151383279	31
Ahsa1	NM_146036	chr12	88607563	88607853	31
Morc3	NM_001045529	chr16	93832217	93832575	31
Atp10a	NM_009728	chr7	65913376	65913828	31
Plxdc1	NM_001163608	chr11	97847499	97847956	32
Dusp11	NM_028099	chr6	85911478	85911779	32
Ttk	NM_009445	chr9	83728163	83728490	32
Zc3h12c	NM_001162921	chr9	51975904	51976462	32
Cyb5r3	NM_029787	chr15	83002371	83002838	33
Pigu	NM_001004721	chr2	155182936	155183317	33
BC029722	NR_015528	chr2	155644711	155645100	33
Usp19	NM_001168373	chr9	108392854	108393223	33
Polr2a	NM_001291068	chr11	69571882	69572320	33
Wsb1	NM_019653	chr11	79067930	79068396	33
Stambpl1	NM_029682	chr19	34266650	34266934	33
Bcl2l1	NM_009743	chr2	152657300	152657560	33

Supplemental Table 4. Significant ChIP-seq E2F3B promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Ehd2	NM_153068	chr7	16552691	16553009	33
Vps4a	NM_126165	chr8	109555074	109555442	33
Sp2	NM_030220	chr11	96838573	96839362	34
Slc29a1	NM_001199116	chr17	45732267	45732706	34
Atl3	NM_146091	chr19	7568793	7569128	34
Hk1	NM_001146100	chr10	61802850	61803418	34
Sart3	NM_016926	chr5	114221459	114221787	34
Gapdh	NM_008084	chr6	125115608	125115904	34
Fhl2	NM_010212	chr1	43220565	43220976	35
Frmd6	NM_028127	chr12	71926373	71926696	35
Fam173b	NM_026546	chr15	31531710	31532099	35
Rfc4	NM_145480	chr16	23127502	23128033	35
Ntng1	NM_030699	chr3	109946215	109946494	35
Kif24	NM_024241	chr4	41411630	41412061	35
Snrnp48	NM_026382	chr13	38296643	38297041	35
Thoc3	NM_028597	chr13	54570002	54570328	35
Pigq	NM_011822	chr17	26078687	26079109	35
Scfd2	NM_001114660	chr5	74927538	74927924	35
Nagk	NM_019542	chr6	83744843	83745327	35
Hist1h2ad	NM_178188	chr13	23666139	23666430	36
Pgs1	NM_133757	chr11	117848046	117848366	36
Eif4b	NM_145625	chr15	101903955	101904523	36
Arhgap31	NM_020260	chr16	38712823	38713399	36
Kif18a	NM_139303	chr2	109120688	109121172	36
Gtf3c2	NM_027901	chr5	31482223	31482737	36
Mad2l1	NM_019499	chr6	66485272	66485722	36
Slc7a6os	NM_001007567	chr8	108734595	108734997	36
Eif3a	NM_010123	chr19	60866276	60866841	37
Nelfcd	NM_020580	chr2	174241182	174241499	37
Adprhl2	NM_133883	chr4	125998630	125999189	37
Pafah1b2	NM_008775	chr9	45792698	45793135	37
Med22	NM_001033908	chr2	26765945	26766303	37
Ada	NM_001272052	chr2	163575716	163576158	37
Cdc42	NM_009861	chr4	136913464	136913808	37
Med28	NM_025895	chr5	45911345	45911663	37
Agfg2	NM_178162	chr5	138125622	138125992	37
Hccs	NM_008222	chrX	165758015	165758459	37
Mitd1	NM_026913	chr1	37947053	37947382	38
Tm9sf2	NM_080556	chr14	122506071	122506610	38
Msh5	NM_001146215	chr17	35183266	35183993	38
Mdc1	NM_001010833	chr17	35978029	35978930	38
Sipa1	NM_001164568	chr19	5663474	5663863	38
Tpd52l2	NM_001291204	chr2	181231678	181232089	38
Gpsm2	NM_029522	chr3	108524961	108525396	38
Stmn1	NM_019641	chr4	134024134	134024409	38
Gm20554	NR_030701	chr13	72765823	72766123	38
Mnd1	NM_029797	chr3	83959536	83959802	38
Ndufa5	NM_026614	chr6	24477544	24477752	38

Supplemental Table 4. Significant ChIP-seq E2F3B promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Csgalnact1	NM_172753	chr8	71258783	71259229	38
Cyp20a1	NM_030013	chr1	60400043	60400464	39
Xrcc4	NM_028012	chr13	90228948	90229399	39
Atp5g3	NM_175015	chr2	73749135	73749488	39
Kansl3	NM_172652	chr1	36425829	36426143	39
Dnajc9	NM_134081	chr14	21207898	21208285	40
Tef	NM_153484	chr15	81632958	81633325	40
Lonp1	NM_028782	chr17	56766095	56766476	40
Gabpb1	NM_001271469	chr2	126501138	126501437	40
Zfp11	NM_172462	chr5	130175755	130176090	40
Rnf121	NM_029211	chr7	109213407	109213804	40
Tfg	NM_019678	chr16	56717346	56717698	40
Atp2c1	NM_001253834	chr9	105397235	105397609	40
Psmd3	NM_009439	chr11	98543729	98544086	41
5830415F09Rik	NM_029086	chr4	46401928	46402579	41
Iqck	NM_001081446	chr7	125999150	125999507	41
Adpgk	NM_028121	chr9	59139206	59139631	41
Gm10474	NR_033481	chrX	65931367	65931698	41
Pdia6	NM_027959	chr12	17273261	17273621	41
Copg2	NM_017478	chr6	30846525	30846979	41
Zfp9	NM_011763	chr6	118429116	118429382	41
Pxylp1	NM_153420	chr9	96789680	96790022	41
Rpl14	NM_025974	chr9	120480439	120480909	41
Wdr6	NM_031392	chr9	108480568	108481349	42
Sh3pxd2a	NM_008018	chr19	47538705	47539011	42
Mtrr	NM_172480	chr13	68720611	68721298	43
Mrpl28	NM_024227	chr17	26260198	26260781	43
Emc8	NM_010926	chr8	123191714	123192223	43
Kiss1r	NM_053244	chr10	79379599	79379917	43
Ttbk2	NM_080788	chr2	120676095	120676456	44
Mcm2	NM_008564	chr6	88848490	88848969	44
Slc41a3	NM_027868	chr6	90554788	90555045	44
Uba2	NM_016682	chr7	34953308	34953699	44
Ddx28	NM_028038	chr8	108535182	108535501	44
Mrps9	NM_023514	chr1	42908037	42908205	44
Cherp	NM_138585	chr8	74998660	74999514	44
Cnot10	NM_153585	chr9	114548985	114549561	44
Gabpb2	NM_172512	chr3	95021460	95022177	45
Steap2	NM_001285471	chr5	5693859	5694228	45
Serhl	NM_023475	chr15	82930454	82930904	45
Znhit2	NM_013859	chr19	6061097	6061405	45
Htra2	NM_019752	chr6	83004264	83004774	45
Bhlhe40	NM_011498	chr6	108610580	108610754	45
Palld	NM_001293774	chr8	64069745	64070095	45
Neo1	NM_001042752	chr9	58883997	58884407	45
Srxn1	NM_029688	chr2	151931026	151931583	46
Acat1	NM_144784	chr9	53418186	53418631	46
Nup107	NM_134010	chr10	117229541	117229887	46

Supplemental Table 4. Significant ChIP-seq E2F3B promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Etaa1	NM_026576	chr11	17853633	17854029	46
Kif20a	NM_009004	chr18	34784397	34784873	46
Rfc2	NM_020022	chr5	135058456	135058754	46
Fancd2	NM_001033244	chr6	113481513	113481929	46
Psen2	NM_001128605	chr1	182186180	182186587	47
Wdr81	NM_138950	chr11	75268033	75268310	47
Zfat	NM_198644	chr15	68089934	68090807	47
Golim4	NM_001291069	chr3	75760664	75760983	47
Aagab	NM_025857	chr9	63450272	63450743	47
Sptssa	NM_134054	chr12	55757264	55757758	47
Phf1	NM_009343	chr17	27069886	27070350	47
Rce1	NM_023131	chr19	4625349	4625789	47
Dclre1a	NM_018831	chr19	56622458	56622870	47
Lnp	NM_027133	chr2	74416741	74417173	47
Usp10	NM_009462	chr8	122434580	122435016	47
Lrch1	NM_001033439	chr14	75347447	75347824	48
Ptprs	NM_001252456	chr17	56601348	56601843	48
Ganab	NM_001293621	chr19	8972379	8972808	48
Eef1g	NM_026007	chr19	9041343	9041812	48
Arap1	NM_001040111	chr7	108496467	108496792	48
Cnksr3	NM_172546	chr10	3134085	3134617	48
Wdr90	NM_001163766	chr17	25998243	25998579	48
Dym	NM_027727	chr18	75178299	75178647	48
Apbb1ip	NM_019456	chr2	22629752	22630036	48
Tmem165	NM_011626	chr5	76612786	76613118	48
Rmnd5a	NM_024288	chr6	71390446	71390718	48
Pkmyt1	NM_023058	chr17	23863114	23863587	49
5730508B09Rik	NM_027482	chr3	127599063	127599320	49
Mms22l	NM_199467	chr4	24423448	24423865	49
Rps15	NM_009091	chr10	79754967	79755481	49
Tbp	NM_013684	chr17	15636703	15637097	49
Hps5	NM_001167864	chr7	54050908	54051494	49
Mtmr2	NM_023858	chr9	13553498	13553848	49
Polr1b	NM_009086	chr2	128926636	128926925	50
Haus5	NM_027999	chr7	31449765	31450160	50
Ulk2	NM_013881	chr11	61668341	61668745	50
Dcakd	NM_026551	chr11	102878266	102878554	50
Erlin2	NM_153592	chr8	28134119	28134521	50
2010320M18Rik	NR_029440	chr8	73300675	73300945	50
Guk1	NM_008193	chr11	59005222	59005583	51
Ccdc34	NM_026613	chr2	109857828	109858219	51
Atf6b	NM_017406	chr17	34784017	34784266	52
Rpia	NM_009075	chr6	70741773	70742459	52
Rps3	NM_012052	chr7	106632051	106632281	52
Eral1	NM_022313	chr11	77893699	77893964	53
Taf3	NM_027748	chr2	9970020	9970345	53
Cad	NM_023525	chr5	31357079	31357330	53
Timm17a	NM_011590	chr1	137210098	137210422	53

Supplemental Table 4. Significant ChIP-seq E2F3B promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Sipa1l1	NM_001167983	chr12	83270876	83271234	53
Ppp2r5c	NM_012023	chr12	111723872	111724130	53
Mut	NM_008650	chr17	41071301	41072071	53
Zwilch	NM_026507	chr9	64020464	64020903	54
Cldn25	NM_001252451	chr16	58727933	58728219	54
Pcgf1	NM_197992	chr6	83028254	83028620	54
Nipa2	NM_001256133	chr7	63217624	63217992	54
Sec63	NM_153055	chr10	42481119	42481592	55
Mettl25	NM_207522	chr10	105278107	105278654	55
Casp7	NM_007611	chr19	56471486	56471859	55
Prkab1	NM_031869	chr5	116474116	116474647	55
Incenp	NM_016692	chr19	9973763	9974171	55
Fzd1	NM_021457	chr5	4757964	4758356	55
Fancl	NM_001277273	chr11	26286955	26287322	56
Mpdu1	NM_011900	chr11	69475832	69476343	56
Spag5	NM_017407	chr11	78114938	78115357	56
Atg10	NM_025770	chr13	91363359	91363712	56
Wdr34	NM_001008498	chr2	29904084	29904601	56
Rad23a	NM_001297606	chr8	87364313	87364702	56
Pkm	NM_001253883	chr9	59504062	59504397	56
Abracl	NM_028440	chr10	17742638	17743364	56
2700046G09Rik	NR_033198	chr19	32463609	32463913	56
Usp39	NM_138592	chr6	72294906	72295318	56
Scap	NM_001001144	chr9	110235733	110236097	56
Nab2	NM_008668	chr10	127103508	127103895	57
Ep400	NM_029337	chr5	111199432	111199925	57
Appl2	NM_145220	chr10	83111198	83111503	58
Timp2	NM_011594	chr11	118216426	118216907	58
Rnaseh1	NM_011275	chr12	29334421	29334626	58
Ddx46	NM_001282055	chr13	55736193	55736640	58
Zfp451	NM_001290699	chr1	33871212	33871550	58
Ciz1	NM_001252536	chr2	32218399	32218775	58
2610002J02Rik	NM_001190445	chr4	154623895	154624369	58
Zscan22	NM_001290440	chr7	13483029	13483401	58
Mfhas1	NM_001081279	chr8	36650676	36651142	58
Rbm6	NM_029169	chr9	107774819	107775363	58
Ttc32	NM_029321	chr12	9036663	9037058	59
2610020C07Rik	NR_038156	chr16	11203356	11203711	59
Ptprm	NM_008984	chr17	67703589	67703890	59
Kdelr2	NM_025841	chr5	144165317	144165796	59
Mthfd2	NM_008638	chr6	83267372	83267705	59
Gemin4	NM_177367	chr11	76030743	76031285	59
Fgfr1	NM_001079908	chr8	26629124	26629454	59
Atxn7l3b	NM_001033474	chr10	112365749	112366294	60
Ankrd54	NM_144849	chr15	78892917	78893540	60
Cenpw	NM_001109747	chr10	29920042	29920528	60
Tmem206	NM_025864	chr1	193149771	193150036	61
Ctgf	NM_010217	chr10	24315082	24315533	61

Supplemental Table 4. Significant ChIP-seq E2F3B promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Scarb2	NM_007644	chr5	92934385	92934760	61
Mtch1	NM_019880	chr17	29484618	29484956	61
Tle1	NM_011599	chr4	71861706	71862024	61
Atp5j2	NM_020582	chr5	145952202	145952596	61
Hmbs	NM_013551	chr9	44152027	44152471	61
Cstf2	NM_133196	chrX	130593615	130593935	61
Zfp275	NM_001160229	chrX	70587833	70588208	62
Kif5b	NM_008448	chr18	6241252	6241666	62
Spc25	NM_025565	chr2	69043887	69044481	62
Apitd1	NM_027263	chr4	148511349	148511943	62
1700028E10Rik	NR_045700	chr5	152170856	152171766	62
Ccdc15	NM_001081429	chr9	37155707	37156121	62
Hace1	NM_172473	chr10	45297545	45297848	63
Atr	NM_019864	chr9	95757828	95758327	63
Rpa1	NM_001164223	chr11	75161453	75162189	63
Glod4	NM_026029	chr11	76056902	76057372	63
1700086O06Rik	NR_027904	chr18	38410002	38410308	63
Xrcc6	NM_010247	chr15	81846619	81847104	64
Prpf19	NM_134129	chr19	10969500	10970067	64
D3Ertd751e	NM_027271	chr3	41546313	41546892	64
Unc5b	NM_029770	chr10	60294104	60294424	64
Stat6	NM_009284	chr10	127079969	127080241	64
Polr3h	NM_030229	chr15	81756451	81756705	64
Kdm4c	NM_144787	chr4	73897649	73898043	64
Ak2	NM_016895	chr4	128670187	128670875	64
Spg21	NM_138584	chr9	65308667	65308947	64
Ctnna3	NM_177612	chr10	62892773	62893046	65
Asb3	NM_023906	chr11	30854271	30854652	65
Ppp6r3	NM_001164159	chr19	3575391	3575976	65
Pcif1	NM_146129	chr2	164704748	164705115	65
Vwa1	NM_147776	chr4	155148434	155148775	65
Rplp0	NM_007475	chr5	116009346	116009733	65
Arl2bp	NM_024191	chr8	97190386	97190741	65
1600002H07Rik	NM_028056	chr17	24357365	24357931	65
Fam83d	NM_027975	chr2	158593762	158594036	65
Gnb1l	NM_001081682	chr16	18498681	18499060	66
Lsm10	NM_138721	chr4	125773733	125774190	66
Cbfb	NM_001161458	chr8	107694454	107694823	66
Elmsan1	NM_001163502	chr12	85534736	85535060	66
Gm12942	NM_001099319	chr4	126803205	126803500	67
Zfp574	NM_175477	chr7	25862097	25862565	67
Med26	NM_027485	chr8	75071916	75072366	67
Pole	NM_011132	chr5	110715096	110715713	68
Ccdc124	NM_026964	chr8	73397015	73397626	68
Agpat6	NM_018743	chr8	24318744	24318968	68
Trip4	NM_001170907	chr9	65732734	65733088	68
Eaf1	NM_028932	chr14	32308164	32308501	69
Fbln1	NM_010180	chr15	85036315	85036696	69

Supplemental Table 4. Significant ChIP-seq E2F3B promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Chp1	NM_019769	chr2	119373316	119373705	69
Eefsec	NM_023060	chr6	88396139	88396788	69
Rtcb	NM_145422	chr10	85420290	85420646	69
Urgcp	NM_178623	chr11	5640934	5641284	69
Hdac2	NM_008229	chr10	36694238	36694599	70
Ndufaf5	NM_027093	chr2	139996222	139996679	70
Eef2	NM_007907	chr10	80639199	80639691	70
Spag7	NM_172561	chr11	70482733	70482961	70
Rmi1	NM_028904	chr13	58503683	58504371	70
Tonsl	NM_183091	chr15	76470011	76470565	70
Pknox1	NM_016670	chr17	31701614	31701961	71
Slc29a2	NM_007854	chr19	5023970	5024181	71
Snx5	NM_001199188	chr2	144096281	144096852	71
Enkd1	NM_198299	chr8	108231794	108232199	71
Nedd4	NM_010890	chr9	72509998	72510449	71
Mtag2	NR_027802	chr7	52622472	52622874	71
Ppcdc	NM_176831	chr9	57287700	57287998	71
Ska1	NM_001164355	chr18	74367295	74367504	72
Gm5617	NM_001004191	chr9	48303269	48303768	72
Mrpl42	NM_026065	chr10	94964245	94964731	72
Brca1	NM_009764	chr11	101413061	101413331	72
Khnyn	NM_027143	chr14	56503701	56504053	72
Gins1	NM_027014	chr2	150735174	150735628	72
Myc	NM_001177353	chr15	61816774	61817161	73
Tbcc	NM_178385	chr17	47027431	47027852	73
Apip	NM_019735	chr2	102913546	102914261	73
Thrap3	NM_146153	chr4	125879453	125880308	73
Pdp2	NM_001024606	chr8	107115139	107115740	73
Dars2	NM_172644	chr1	163000520	163000858	73
Galc	NM_008079	chr12	99497314	99497632	73
Tcof1	NM_011552	chr18	61008340	61008748	73
Mastl	NM_025979	chr2	23011263	23011677	73
Col4a1	NM_009931	chr8	11312497	11313007	73
H2afy	NM_001159515	chr13	56236673	56237000	74
Gm5464	NM_001034881	chr14	67487401	67488118	74
Scarb1	NM_001205082	chr5	125821185	125821594	74
Xrcc1	NM_009532	chr7	25331977	25332506	74
Tnpo1	NM_178716	chr13	99696096	99696432	74
Skp2	NM_013787	chr15	9069798	9070472	74
Gm1673	NM_001033458	chr5	34326025	34326367	74
Ruvbl2	NM_011304	chr7	52689457	52690061	74
Rad51b	NM_001252562	chr12	80398221	80398602	75
Ighmbp2	NM_009212	chr19	3282792	3283077	75
Dstn	NM_019771	chr2	143740958	143741324	75
Ift74	NM_026319	chr4	94281101	94281411	75
Pbdc1	NM_001281871	chrX	102274847	102275491	75
Mmaa	NM_133823	chr8	81818309	81819248	76
Ddx19a	NM_007916	chr8	113521436	113521857	76

Supplemental Table 4. Significant ChIP-seq E2F3B promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Net1	NM_019671	chr13	3917156	3917622	76
Nudc	NM_010948	chr4	133101551	133102179	76
Paics	NM_025939	chr5	77380068	77380954	76
2810417H13Rik	NM_026515	chr9	65737971	65738439	76
Rnaseh2b	NM_026001	chr14	62950686	62951349	77
Zfp213	NM_001033496	chr17	23700973	23701258	77
Vdac1	NM_011694	chr11	52174576	52174811	78
Pcyox1l	NM_172832	chr18	61867038	61867383	78
Pcnxl3	NM_144868	chr19	5688476	5689183	78
Anxa11	NM_013469	chr14	26661573	26661863	78
Dpm3	NM_026767	chr3	89070259	89070661	78
Msl2	NM_001100451	chr9	100978379	100978747	78
Myg1	NM_021713	chr15	102161914	102162522	79
Capza1	NM_009797	chr3	104667145	104667541	79
Cdc25a	NM_007658	chr9	109777709	109778613	79
Agps	NM_172666	chr2	75670126	75670499	80
Melk	NM_010790	chr4	44313648	44314087	80
Tmem80	NM_001141950	chr7	148513979	148514237	80
Cotl1	NM_028071	chr8	122364199	122364597	80
Msra	NM_001253715	chr14	65059639	65059924	81
Cdc7	NM_001271568	chr5	107393179	107393662	81
Ptbp1	NM_008956	chr10	79316918	79317596	81
Rprd2	NM_001081293	chr3	95622602	95622986	81
Gtf2e2	NM_026584	chr8	34842404	34842834	81
Dlgap5	NM_144553	chr14	48037716	48038282	82
Kat5	NM_001199247	chr19	5609834	5610188	82
Pdk1	NM_172665	chr2	71711020	71711704	82
Rab11a	NM_017382	chr9	64585328	64585632	82
Foxo3	NM_019740	chr10	41996315	41996614	83
Odf2l	NM_025714	chr3	144781345	144781946	83
E130307A14Rik	NR_038037	chr10	39451485	39451973	83
Cenph	NM_021886	chr13	101545616	101545924	83
Rpl10a	NM_011287	chr17	28465279	28465717	83
Tmem209	NM_178625	chr6	30459357	30459887	83
Psmc3ip	NM_008949	chr11	100956527	100956802	84
5430416N02Rik	NR_034038	chr5	100858142	100858797	84
Cmc1	NM_026442	chr9	118059052	118059407	84
1700056E22Rik	NM_028516	chr1	185857695	185857889	84
Lcmt2	NM_177846	chr2	120966026	120966672	84
Mccc1	NM_023644	chr3	35899343	35899686	85
Atg5	NM_053069	chr10	43988111	43988385	85
Rmi2	NM_001162932	chr16	10835010	10835462	85
Morf4l1	NM_001039147	chr9	90009468	90009676	85
Wdfy1	NM_001111279	chr1	79758113	79758401	86
4930467K11Rik	NR_045353	chr10	57205876	57206268	86
Nsmce2	NM_026746	chr15	59205568	59206108	86
Prkag1	NM_016781	chr15	98661623	98662081	86
Rabepk	NM_145522	chr2	34655134	34655556	86

Supplemental Table 4. Significant ChIP-seq E2F3B promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Rbm15	NM_001045807	chr3	107135936	107136304	86
Cyld	NM_001276279	chr8	91220815	91221209	86
Pola2	NM_008893	chr19	5963877	5964360	87
Eef1a1	NM_010106	chr9	78329279	78329608	87
Sgol2	NM_199007	chr1	58052701	58053107	87
Slc38a10	NM_001164800	chr11	120012412	120012742	87
Cbx5	NM_001076789	chr15	103069578	103070740	87
Etohd2	NR_015349	chr13	59871241	59871586	88
Rnf219	NM_026047	chr14	104921553	104922036	88
Pfdn5	NM_027044	chr15	102156439	102156828	88
Man1a2	NM_010763	chr3	100489177	100489438	88
Rmrp	NR_001460	chr4	43505588	43506096	88
Lyplal1	NM_146106	chr1	187940924	187941275	89
Nxt1	NM_001110159	chr2	148498213	148498716	89
Zcchc6	NM_153538	chr13	59924225	59924611	89
Ncaph2	NM_001271600	chr15	89186073	89186403	89
Anapc15	NM_001291348	chr7	109044511	109045355	89
Ckap2	NM_001004140	chr8	23295984	23296418	89
Gnpat	NM_010322	chr8	127386783	127387259	89
Cpm	NM_027468	chr10	117066451	117066838	90
Lars	NM_134137	chr18	42421485	42421784	90
Vps16	NM_030559	chr2	130249944	130250345	90
Kxd1	NM_029366	chr8	73046642	73047334	90
Pir	NM_027153	chrX	160707322	160707582	90
Tusc3	NM_030254	chr8	40068803	40069218	91
Tmem11	NM_001168507	chr11	60692214	60692682	91
Pole2	NM_011133	chr12	70328866	70329304	91
Cdkn2aipnl	NM_029976	chr11	51781043	51781404	92
Gnl3	NM_153547	chr14	31832023	31832426	92
Clhc1	NM_001081099	chr4	134066811	134067198	92
Tmed3	NM_025360	chr9	89599557	89600020	92
Gyk	NM_212444	chrX	83021857	83022274	92
4833418N02Rik	NR_015506	chr17	87681862	87682260	92
Vdac3	NM_011696	chr8	23703959	23704425	92
Raver1	NM_027911	chr9	20896043	20896635	92
Sin3a	NM_001110350	chr9	56924094	56924454	92
Pex2	NM_001163305	chr3	5575864	5576445	93
Minpp1	NM_010799	chr19	32560268	32560434	93
Mtx2	NM_016804	chr2	74663757	74664165	93
Abhd13	NM_026868	chr8	9977643	9977975	93
Recql4	NM_058214	chr15	76540594	76541195	94
Smc5	NM_001252684	chr19	23348086	23348499	94
Rasl11a	NM_026864	chr5	147656523	147656956	94
Rbm4b	NM_025717	chr19	4756397	4756839	94
U2surp	NM_026476	chr9	95412035	95412605	94
Socs3	NM_007707	chr11	117830386	117830782	95
Tm9sf1	NM_028780	chr14	56262280	56262814	95
Kmt2c	NM_001081383	chr5	25004397	25004612	96

Supplemental Table 4. Significant ChIP-seq E2F3B promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Zfp507	NM_177739	chr7	36587729	36588094	96
Pagr1a	NM_030240	chr7	134160573	134160966	96
C130036L24Rik	NR_015507	chr1	88255988	88256500	96
Rtel1	NM_001166665	chr2	181054359	181054689	96
Arfrp1	NM_001165995	chr2	181099809	181100215	96
Slc2a1	NM_011400	chr4	118781279	118781611	96
Fam212a	NM_026597	chr9	107887959	107888341	96
Cnih1	NM_009919	chr14	47407724	47408145	97
Cdipt	NM_026638	chr7	134119360	134119687	97
Sdha	NM_023281	chr13	74487404	74487776	97
Elmod2	NM_178736	chr8	85855934	85856640	97
Asf1a	NM_025541	chr10	53316692	53317035	98
Tmod3	NM_016963	chr9	75407146	75407584	98
2410002F23Rik	NM_025880	chr7	51502056	51502323	99
4930405A21Rik	NR_040505	chr2	156546415	156546675	99
Dars	NM_177445	chr1	130313694	130314091	100
Katnbl1	NM_024254	chr2	112219267	112219666	100
Zdhhc1	NM_175160	chr8	108020437	108020902	100
Smc1a	NM_019710	chrX	148450782	148451357	100
BC004004	NM_030561	chr17	29405663	29406001	100
Spty2d1	NM_175318	chr7	54263551	54263814	101
Tex264	NM_011573	chr9	106587889	106588202	101
Arl6ip6	NM_022989	chr2	53050950	53051486	101
Haus8	NM_029621	chr8	73796075	73796699	101
B930003M22Rik	NR_037588	chr17	10512633	10513137	102
Gm10941	NR_026944	chr10	76721693	76722036	103
Txnrd1	NM_001042514	chr10	82322991	82323384	103
Chrac1	NM_053068	chr15	72920621	72921266	103
Dut	NM_023595	chr2	125072954	125073752	103
Ddi2	NM_001017966	chr4	141278955	141279505	103
Orc5	NM_011959	chr5	22055869	22056221	103
Scaf11	NM_028148	chr15	96291000	96291339	104
Hn1l	NM_198937	chr17	25097172	25097755	104
Pim3	NM_145478	chr15	88692446	88693008	104
Gne	NM_001190414	chr4	44085215	44085665	104
Vps37b	NM_177876	chr5	124481905	124482423	104
Primpol	NM_001001184	chr8	47702211	47702687	104
Bend6	NM_177235	chr1	33964181	33964540	105
Zfp524	NM_025324	chr7	4967014	4967413	105
Zfp354a	NM_009329	chr11	50872712	50873014	105
Rcn1	NM_009037	chr2	105239265	105239475	105
Rpl31	NM_001252219	chr1	39424651	39424951	106
Dtymk	NM_001105667	chr1	95698127	95698681	106
Tgs1	NM_054089	chr4	3501971	3502291	106
Ddx39b	NM_019693	chr17	35378568	35379025	107
Rmdn3	NM_001033136	chr2	118982380	118982945	107
Sord	NM_146126	chr2	122060511	122060851	107
Dlc1	NM_001194941	chr8	37795852	37796148	107

Supplemental Table 4. Significant ChIP-seq E2F3B promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Panx1	NM_019482	chr9	14849632	14849996	107
Tmem14c	NM_025387	chr13	41111574	41111878	108
Gm5475	NR_040351	chr15	100253576	100253886	108
Dtl	NM_029766	chr1	193398867	193399740	109
Mettl1	NM_010792	chr10	126478872	126479319	109
Spice1	NM_144550	chr16	44347273	44347970	109
Elmo1	NM_080288	chr13	20182330	20182638	109
Dap3	NM_001164533	chr3	88753875	88754313	109
Mars	NM_001171582	chr10	126748566	126748897	110
Tfeb	NM_001161722	chr17	47873928	47874261	110
Dis3l2	NM_153530	chr1	88600190	88600786	110
Bag5	NM_027404	chr12	112951202	112951510	110
Tgfbr2	NM_029575	chr9	116084057	116084683	110
Tex30	NM_029368	chr1	44158942	44159301	111
Fam172a	NM_138312	chr13	77847847	77848274	111
Ppfibp1	NM_026221	chr6	146836932	146837319	111
Tnpo2	NM_001122843	chr8	87560986	87561367	111
Ccne2	NM_009830	chr4	11118842	11119090	111
Rragc	NM_017475	chr4	123594542	123595030	111
Tsen15	NM_025677	chr1	154233494	154233905	112
Nmral1	NM_001290761	chr16	4718994	4719493	112
Wdr76	NM_001290986	chr2	121332324	121332815	112
Cox7a2	NM_009945	chr9	79607361	79607734	112
Rbm3	NM_016809	chrX	7722728	7723059	112
Daxx	NM_001199733	chr17	34046387	34046928	113
Gm3230	NR_033642	chr2	19579178	19579643	113
Aarsd1	NM_144829	chr11	101278415	101278851	113
Dek	NM_025900	chr13	47201067	47201882	114
Atpaf1	NM_181040	chr4	115457327	115457738	115
Slbp	NM_001289724	chr5	33994698	33995517	115
Wdr47	NM_181400	chr3	108394122	108394498	115
Fus	NM_139149	chr7	135110886	135111329	116
Rbmxl1	NM_009033	chr8	81032465	81032956	116
Triobp	NM_001039156	chr15	78778026	78778514	117
Zbtb5	NM_173399	chr4	45025019	45025313	117
Zwint	NM_001293683	chr10	72117498	72117923	118
Gspt1	NM_001130008	chr16	11253911	11254687	118
Ssrp1	NM_182990	chr2	84877146	84877642	118
Ipp	NM_008389	chr4	116180103	116180440	119
Zfp398	NM_027477	chr6	47785543	47786012	119
Exo1	NM_012012	chr1	177810821	177811233	119
Frmd4a	NM_001177844	chr2	4480809	4481027	119
Lrrfip1	NM_008515	chr1	92949920	92950359	120
Rrp1	NM_010925	chr10	77875511	77875824	120
Cgnl1	NM_026599	chr9	71619052	71619524	120
Rpl22	NM_001277114	chr4	151699694	151700216	121
Raf1	NM_029780	chr6	115626351	115626709	122
Afg3l1	NM_054070	chr8	126001685	126002081	122

Supplemental Table 4. Significant ChIP-seq E2F3B promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Lims1	NM_026148	chr10	57786116	57786555	123
Nup188	NM_198304	chr2	30141831	30142318	123
Slc3a2	NM_001161413	chr19	8797463	8798007	123
Irs2	NM_001081212	chr8	11008108	11008503	124
Timm13	NM_013895	chr10	80363208	80363970	124
Cul7	NM_025611	chr17	46787266	46787554	124
Dctn4	NM_026302	chr18	60685776	60686220	124
Umps	NM_009471	chr16	33966715	33967212	125
Lsm2	NM_001110101	chr17	35118686	35119159	125
Ccdc85b	NM_198616	chr19	5457287	5457588	125
Gmfb	NM_022023	chr14	47441611	47441971	125
Zfp869	NM_001039965	chr8	72240265	72241085	125
Impa2	NM_053261	chr18	67448785	67449218	126
Fads1	NM_146094	chr19	10257290	10257716	126
Tnfrsf12a	NM_013749	chr17	23814012	23814565	127
Setx	NM_198033	chr2	28980413	28980862	127
F3	NM_010171	chr3	121426425	121426736	127
Rad21	NM_009009	chr15	51822977	51823379	127
Ets2	NM_011809	chr16	95923904	95924377	128
Rab1b	NM_029576	chr19	5106717	5107018	128
Rabep2	NM_030566	chr7	133572174	133572643	129
Sass6	NM_028349	chr3	116297740	116298268	129
Ano8	NM_001164679	chr8	74009614	74010058	129
Dhps	NM_001039514	chr8	87595386	87596182	129
Fam178a	NM_001081225	chr19	45005314	45006161	130
Mrpl4	NM_023167	chr9	20807128	20807491	130
Rsbn1	NM_172684	chr3	103718058	103718286	130
Mir1938	NR_035459	chr12	40949036	40949497	131
Bid	NM_007544	chr6	120866530	120866883	131
Zfp644	NM_026856	chr5	107125417	107126017	131
Snrpe	NM_009227	chr1	135506397	135507051	132
Tmx4	NM_029148	chr2	134469439	134470009	132
Arnt	NM_009709	chr3	95238225	95238661	132
Anapc5	NM_001042491	chr5	123270790	123271646	132
Crem	NM_001110851	chr18	3337309	3337598	133
Ctc1	NM_001143790	chr11	68829390	68829700	133
Immt	NM_001253689	chr6	71781112	71781780	133
Alx1	NM_172553	chr10	102491072	102491477	136
Tax1bp3	NM_029564	chr11	72990547	72990892	136
Bub1	NM_009772	chr2	127657219	127657698	136
Noxo1	NM_027988	chr17	24833198	24833430	136
Tardbp	NM_001008546	chr4	148000662	148001274	136
Tpst1	NM_001130476	chr5	130554998	130555753	137
Zfx	NM_011768	chrX	91368462	91368753	138
Specc1	NM_001281818	chr11	61770217	61770590	140
Zfp521	NM_145492	chr18	14130895	14131308	140
Rnf4	NM_011278	chr5	34678760	34679598	141
Fancc	NM_001042673	chr13	63532715	63533106	142

Supplemental Table 4. Significant ChIP-seq E2F3B promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Prkab2	NM_182997	chr3	97462096	97462455	142
Wrnip1	NM_030215	chr13	32893783	32894299	143
Mark2	NM_001080389	chr19	7416030	7416382	143
Zfp748	NM_001035231	chr13	67653687	67654200	144
Chek1	NM_007691	chr9	36533867	36534330	144
Bcl7a	NM_029850	chr5	123794392	123794810	145
Lsm4	NM_015816	chr8	73196932	73197617	146
Ewsr1	NM_007968	chr11	4998736	4999151	147
H1f0	NM_008197	chr15	78858502	78859073	147
Siah2	NM_009174	chr3	58495952	58496371	148
Chd3os	NR_027827	chr11	69154243	69154593	148
Ubxn8	NM_178648	chr8	34752075	34752522	149
Lyst	NM_010748	chr13	13682730	13682919	150
Pak1ip1	NM_026550	chr13	41096349	41096706	150
Pdlim1	NM_016861	chr19	40345790	40346121	150
Nol7	NM_023554	chr13	43493603	43494185	150
Oard1	NM_207219	chr17	48548852	48550096	150
Yars	NM_134151	chr4	128866890	128867487	151
Cipc	NM_001289430	chr12	88287888	88288395	152
Mtbp	NM_134092	chr15	55388791	55389439	153
Poldip3	NM_178627	chr15	82979360	82979864	153
Senp1	NM_144851	chr15	97923589	97924103	153
Ndufa11	NM_027244	chr17	56857133	56857543	154
Prr5l	NM_001083810	chr2	101637502	101637916	154
Dhodh	NM_020046	chr8	112132137	112132699	154
Slc25a25	NM_146118	chr2	32306653	32307011	157
Gpd1l	NM_175380	chr9	114842695	114843196	159
Gtf2ird2	NM_053266	chr5	134659698	134660436	160
Sae1	NM_001285892	chr7	16972827	16973340	161
Gsr	NM_010344	chr8	34763697	34764043	161
Xylb	NM_001033209	chr9	119266466	119266852	161
Dlx1	NM_010053	chr2	71367543	71367782	162
Bcas2	NM_026602	chr3	102975589	102976000	162
Galnt9	NM_198306	chr5	110973382	110973688	162
Wdr4	NM_021322	chr17	31648977	31649560	163
Phlda1	NM_009344	chr10	110943241	110943767	163
Actb	NM_007393	chr5	143668017	143668461	163
Zc3h7b	NM_001081016	chr15	81575281	81575600	164
Rnf168	NM_027355	chr16	32277373	32278047	164
Evc	NM_021292	chr5	37727759	37728151	164
Zbtb45	NM_001024699	chr7	13594852	13595116	164
Pkd1	NM_013630	chr17	24686848	24687271	166
Trim39	NM_178281	chr17	36407834	36408589	166
Erlin1	NM_145502	chr19	44143867	44144152	166
Ankrd42	NM_028665	chr7	99785323	99785648	166
Ilkap	NM_023343	chr1	93295013	93295373	166
Slc22a15	NM_001039371	chr3	101727970	101728447	167
Zfp948	NM_001002008	chr17	21704021	21704331	167

Supplemental Table 4. Significant ChIP-seq E2F3B promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Luzp1	NM_024452	chr4	136025596	136026088	167
Aco1	NM_007386	chr4	40090354	40090575	168
Hexb	NM_010422	chr13	97967913	97968372	169
Daglb	NM_144915	chr5	144225299	144225758	169
Timeless	NM_001136082	chr10	127669116	127669458	169
Cenpm	NM_178269	chr15	82074761	82075253	169
Ankrd46	NM_175134	chr15	36426008	36426743	170
Tnfaip8	NM_134131	chr18	50212966	50213243	170
Hnrnpdl	NM_016690	chr5	100467886	100468253	171
Cbx1	NM_007622	chr11	96650251	96650989	171
Kpna1	NM_008465	chr16	35983418	35983821	172
Cdk4	NM_009870	chr10	126500513	126501147	172
Rpl22l1	NM_026517	chr3	28704397	28704811	172
Suv39h1	NM_011514	chrX	7651508	7651918	172
Ddx11	NM_001003919	chr17	66472859	66473204	173
Uap1l1	NM_001033293	chr2	25220871	25221072	174
Pank2	NM_153501	chr2	131087988	131088830	174
Prex2	NM_029525	chr1	10983532	10983907	175
Zbtb44	NM_172765	chr9	30838173	30838632	175
Ube2i	NM_001177609	chr17	25410271	25411094	176
Neil3	NM_146208	chr8	54723986	54724499	176
Hint2	NM_026871	chr4	43668960	43669320	176
Ran	NM_009391	chr5	129525986	129526426	176
Atf7	NM_146065	chr15	102455300	102456049	177
Plekhg5	NR_104381	chr4	151460934	151461361	177
Srrt	NM_031405	chr5	137748463	137748986	177
Eri1	NM_026067	chr8	36558065	36558751	178
Iqce	NM_028833	chr5	141177956	141178347	180
Tmem186	NM_025708	chr16	8637381	8637842	182
Invs	NM_010569	chr4	48292515	48293112	183
Lrrfip1	NM_001111312	chr1	92895336	92895636	183
Srebf2	NM_033218	chr15	81977680	81978082	183
Tbl1x	NM_020601	chrX	74756572	74756924	183
4930529M08Rik	NM_175280	chr2	145760531	145760875	184
Atp5g2	NM_026468	chr15	102500965	102501620	185
Mrpl23	NM_011288	chr7	149719087	149719324	185
Rqcd1	NM_021383	chr1	74552042	74553594	185
Pank4	NM_172990	chr4	154338262	154338591	186
LOC101056149	NR_105041	chr13	34744806	34745155	190
Eif4h	NM_033561	chr5	135114685	135115330	190
Rhbdd3	NM_001290491	chr11	4999194	4999736	190
Ppp1r15b	NM_133819	chr1	135027775	135028090	191
Wdyhv1	NM_029734	chr15	57973073	57973288	191
Mir1199	NR_035431	chr8	86535172	86535506	192
Pold3	NM_133692	chr7	107269491	107270142	193
Bak1	NM_007523	chr17	27165196	27165553	196
Kdelr3	NM_134090	chr15	79346891	79347176	197
Med18	NM_026039	chr4	132019311	132019966	197

Supplemental Table 4. Significant ChIP-seq E2F3B promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Rpain	NM_001252415	chr11	70783715	70784081	197
Poc1a	NM_027354	chr9	106183415	106183764	199
Hat1	NM_026115	chr2	71227189	71227843	200
Irak1bp1	NM_001168240	chr9	82723347	82723877	200
Cdc5l	NM_152810	chr17	45570189	45570718	202
Smarcad1	NM_007958	chr6	64992687	64993037	202
Clspn	NM_175554	chr4	126234050	126234801	203
Trim27	NM_009054	chr13	21271711	21272296	205
Ccdc101	NM_029339	chr7	133792805	133793248	205
Chmp6	NM_001085498	chr11	119775168	119775489	206
Jkamp	NM_024205	chr12	73186891	73187170	206
Yod1	NM_178691	chr1	132613895	132614323	206
Vps52	NM_172620	chr17	34092897	34093168	207
Sfmbt1	NM_001166532	chr14	31528771	31529247	209
Slc44a2	NM_001199186	chr9	21125163	21125579	209
Sept10	NM_001024910	chr10	58684085	58684684	210
Fam84b	NM_001162926	chr15	60656187	60656662	210
Ska2	NM_025377	chr11	86922858	86923086	210
Scyl3	NM_028776	chr1	165860011	165860200	211
Csf1	NM_007778	chr3	107562990	107563360	211
Eif3d	NM_018749	chr15	77800823	77801260	212
Exosc10	NM_016699	chr4	147932472	147933021	212
Ercc6l2	NM_023507	chr13	63916669	63917039	213
Fntb	NM_145927	chr12	77938457	77938876	214
Cpox	NM_007757	chr16	58670321	58670749	215
Dck	NM_007832	chr5	89193958	89194547	216
Glt25d1	NM_146211	chr8	74134953	74135323	216
Nup153	NM_175749	chr13	46822748	46823250	218
Endod1	NM_028013	chr9	14185304	14185630	218
Gnb5	NM_138719	chr9	75161909	75162276	219
Iars2	NM_198653	chr1	187152912	187153208	219
Csrp2bp	NM_181417	chr2	144194846	144195133	220
Retsat	NM_026159	chr6	72548665	72549016	220
Pgap2	NM_001291358	chr7	109358914	109359222	220
Dvl2	NM_007888	chr11	69814159	69814536	221
Cep162	NM_199316	chr9	87149996	87150295	221
Ccdc138	NM_001162956	chr10	57960744	57961066	221
Zcchc3	NM_175126	chr2	152240274	152240839	223
Gpbp1	NM_001122963	chr13	112279845	112280205	223
Lrrc8a	NM_177725	chr2	30093347	30093676	224
Mina	NM_025910	chr16	59471536	59472114	225
Trim33	NM_001079830	chr3	103083277	103083605	226
Pmf1	NM_025928	chr3	88213715	88214304	228
Zfp184	NM_183014	chr13	22037039	22037341	228
Ppia	NM_008907	chr11	6315974	6316228	229
Cutc	NM_001113562	chr19	43827517	43827965	229
Xntrpc	NR_104582	chr7	109213958	109214509	230
Sumo3	NM_019929	chr10	77069002	77069416	231

Supplemental Table 4. Significant ChIP-seq E2F3B promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Unk	NM_172569	chr11	115891592	115892131	233
Rassf1	NM_019713	chr9	107456967	107457325	233
Eif2s1	NM_026114	chr12	79963099	79963487	235
Cdca2	NM_001110162	chr14	68333328	68333534	235
Snrpa1	NM_021336	chr7	73205294	73205618	235
Slc25a38	NM_144793	chr9	120019591	120019912	236
Pcnt	NM_008787	chr10	75904987	75905852	237
Cops5	NM_013715	chr1	10027800	10028201	239
Pdss1	NM_019501	chr2	22751146	22751413	239
Yeats4	NM_026570	chr10	116661061	116661585	239
Arf2	NM_007477	chr11	103828255	103828595	241
Dnajc10	NM_024181	chr2	80155727	80155999	241
4930509E16Rik	NR_045735	chr9	72379296	72379548	242
Cdca4	NM_028023	chr12	114067170	114067542	243
Epdr1	NM_134065	chr13	19711323	19711585	244
Papd4	NM_133905	chr13	93961672	93962314	244
Akap8	NM_019774	chr17	32457578	32458125	246
Sppl2a	NM_023220	chr2	126758594	126758854	246
Glra1	NM_020492	chr11	55421324	55421579	248
Mir7672	NR_106132	chr14	27488654	27489037	248
Pycrl	NM_025412	chr15	75751567	75751913	249
Fam98b	NM_026620	chr2	117075611	117075835	249
Nup54	NM_183392	chr5	92863649	92864301	249
Rccd1	NM_173445	chr7	87468902	87469275	251
Slc25a22	NM_026646	chr7	148623348	148623695	251
Rrp1b	NM_028244	chr17	32173091	32173624	252
Anapc13	NM_181394	chr9	102528504	102529249	252
Gar1	NM_026578	chr3	129533847	129534275	252
Fam92a	NM_026558	chr4	12098675	12099142	253
Satb1	NM_001163632	chr17	51972234	51972485	255
Gm17762	NR_028378	chr2	17948980	17949279	255
Wbscr17	NM_145218	chr5	131782835	131783435	256
Rhot2	NM_145999	chr17	25981410	25981665	258
Clasp1	NM_029709	chr1	120285759	120286025	258
Zfp598	NM_183149	chr17	24806796	24807113	259
Myo9a	NM_173018	chr9	59599030	59599448	259
Ccdc155	NM_201374	chr7	52459826	52460176	260
Zc3hav1	NM_028421	chr6	38304114	38304566	262
Hmgxb4	NM_178017	chr8	77517776	77517951	263
Lmna	NM_019390	chr3	88296686	88297253	264
H3f3b	NM_008211	chr11	115885416	115885688	265
Rint1	NM_177323	chr5	23293712	23293940	265
Zfp319	NM_024467	chr8	97855408	97855760	265
Ttll9	NM_001083618	chr2	152788365	152788609	267
Tmem74b	NM_001160363	chr2	151527830	151528192	268
Fastk	NM_023229	chr5	23950619	23950949	268
Gtf2a2	NM_001039519	chr9	69860331	69860914	269
Eif6	NM_010579	chr2	155652274	155652508	269

Supplemental Table 4. Significant ChIP-seq E2F3B promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Tmem243	NM_001081029	chr5	9100849	9101167	272
Gm17296	NM_001159907	chr8	128998577	128998802	275
Naca	NM_001282976	chr10	127472447	127472906	276
Plekhj1	NM_023900	chr10	80260562	80261626	276
Gstt4	NM_029472	chr10	75284829	75285190	278
Srsf9	NM_025573	chr5	115777344	115777583	279
Txn1	NM_011660	chr4	57968729	57969272	282
Gmnn	NM_020567	chr13	24853147	24853898	283
Ptpn2	NM_008977	chr18	67883872	67884111	283
Orc6	NM_019716	chr8	87823642	87823984	283
Ccar2	NM_146055	chr14	70553133	70553493	284
Ss18l1	NM_178750	chr2	179777288	179777654	284
Ndc1	NM_028355	chr4	107040563	107040786	287
Atp1a1	NM_144900	chr3	101408182	101408500	288
Fam134a	NM_170755	chr1	75139414	75139884	290
Tpm2	NM_001277875	chr4	43535650	43536619	291
Fdxacb1	NM_198675	chr9	50576498	50576769	292
2500004C02Rik	NR_040318	chr2	153171043	153171458	295
Alkbh5	NM_172943	chr11	60351310	60351650	296
Serpinb6a	NM_001243192	chr13	34094208	34094524	296
Slc36a4	NM_172289	chr9	15514255	15514764	298
Cmtm3	NM_024217	chr8	106864562	106865020	298
Lysmd2	NM_027309	chr9	75473672	75474002	299
Hivep2	NM_010437	chr10	13686301	13686667	300
Rab33b	NM_016858	chr3	51288084	51288290	300
Ing5	NM_025454	chr1	95700647	95701039	302
Clk2	NM_007712	chr3	88968866	88969190	302
Bola1	NM_026975	chr3	96001008	96001404	302
Grk5	NM_018869	chr19	60965733	60966178	305
Wdr63	NM_172864	chr3	145770505	145770883	305
Fxn	NM_008044	chr19	24354530	24355009	306
Polr1c	NM_009085	chr17	46384547	46384817	311
Fbxl4	NM_172988	chr4	22284844	22285159	313
Csnk1d	NM_139059	chr11	120852167	120852491	317
Camk1d	NM_177343	chr2	5635254	5635726	317
Tbc1d4	NM_001081278	chr14	102007869	102008308	319
Ints7	NM_178632	chr1	193399800	193400062	319
Vps72	NM_009336	chr3	94915169	94915397	320
Cep83os	NR_015524	chr10	94150869	94151203	321
Tln1	NM_011602	chr4	43574993	43575273	321
Zfp248	NM_028335	chr6	118405038	118405362	323
Zhx3	NM_177263	chr2	160698308	160698495	324
Ahctf1	NM_026375	chr1	181733596	181734046	324
Lbr	NM_133815	chr1	183772022	183772384	328
Ahcy	NM_016661	chr2	154899754	154900052	329
Gcfc2	NM_177884	chr6	81873813	81874170	330
Plod3	NM_011962	chr5	137463030	137463408	331
Pomgnt2	NM_153540	chr9	121904571	121905053	331

Supplemental Table 4. Significant ChIP-seq E2F3B promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Gtf3c5	NM_001290484	chr2	28438177	28438756	332
Tpm4	NM_001001491	chr8	74659248	74659795	332
Brd2	NR_037970	chr17	34256042	34256982	332
Ing3	NM_023626	chr6	21899813	21900079	332
Sec62	NM_027016	chr3	30691977	30692283	333
Pgm2	NM_028132	chr4	99602196	99602582	334
Chpf	NM_001001565	chr1	75475465	75475956	335
Nudt5	NM_016918	chr2	5766257	5766574	337
Sys1	NM_025575	chr2	164286581	164287033	337
Chst3	NM_016803	chr10	59681421	59681918	338
Raly	NM_001139513	chr2	154617006	154617360	338
Fasn	NM_007988	chr11	120685339	120685704	339
Foxm1	NM_008021	chr6	128313221	128313479	339
Ngf	NM_013609	chr3	102274002	102274360	340
Gm8773	NR_033499	chr5	5573949	5574332	343
Nme2	NM_001077529	chr11	93816627	93816877	344
Tenc1	NM_153533	chr15	101933622	101933903	345
Cops4	NM_012001	chr5	100947544	100947801	346
Sec24a	NM_175255	chr11	51569869	51570108	347
Tubb4b	NM_146116	chr2	25079701	25080044	349
Adar	NM_001146296	chr3	89534816	89535161	350
B3glct	NM_001081204	chr5	150481035	150481326	350
Exosc8	NM_001163570	chr3	54538615	54539250	353
Pyurf	NM_025574	chr6	57641589	57641848	353
Poc1b	NM_027740	chr10	98570006	98570311	355
Rcc1	NM_001197082	chr4	131901200	131901418	355
Cep97	NM_028815	chr16	55934486	55934723	356
Ube4b	NM_022022	chr4	148800224	148800543	356
Ctps	NM_016748	chr4	120242215	120242833	356
Get4	NM_026269	chr5	139728467	139728803	358
Zfp191	NM_021559	chr18	24178751	24179074	359
Rhbdf1	NM_001291818	chr11	32121739	32122127	359
Hdlbp	NM_133808	chr1	95374872	95375177	360
Cfl1	NM_007687	chr19	5490639	5490990	361
Spidr	NM_146068	chr16	16146408	16146753	363
Sapcd2	NM_001081085	chr2	25227816	25228017	363
Lrrc75b	NM_198860	chr10	75022452	75022969	364
Matn2	NM_016762	chr15	34236648	34236949	364
Klhdc2	NM_027117	chr12	70397849	70398215	365
Stip1	NM_016737	chr19	7113955	7114345	365
Tacc3	NM_001040435	chr5	34000982	34001342	367
Klf11	NM_178357	chr12	25336400	25336806	368
Zfp91Cntf	NR_024093	chr19	12870006	12870482	368
Mcm9	NM_027830	chr10	53349630	53350116	371
Nsmce4a	NM_001162855	chr7	137690311	137690735	371
Cers6	NM_172856	chr2	68699817	68700152	372
Pfkm	NM_001163488	chr15	97923274	97923508	372
Lhfpl2	NM_172589	chr13	94827939	94828310	375

Supplemental Table 4. Significant ChIP-seq E2F3B promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Tead4	NM_011567	chr6	128250257	128250650	377
Nhlrc2	NM_025811	chr19	56622893	56623363	378
Eif4e2	NM_001039169	chr1	89110796	89110990	380
Tfam	NM_009360	chr10	70700269	70700552	381
Mier1	NM_001286222	chr4	102787177	102787574	382
Gas2	NM_008087	chr7	59134706	59135085	382
Tuba1b	NM_011654	chr15	98764196	98764674	385
Fbxo9	NM_023605	chr9	77955875	77956278	386
Bnip1	NM_172149	chr17	26918250	26918575	390
Mrpl34	NM_053162	chr8	73988993	73989434	390
Trmt10a	NM_175389	chr3	137806744	137807043	393
Prmt3	NM_133740	chr7	57033965	57034276	394
E2f3	NM_010093	chr13	30077319	30077752	396
Mepce	NM_144913	chr5	138227357	138227708	396
Seh1l	NM_001039088	chr18	67934737	67935116	398
Msl3	NM_010832	chrX	165111217	165111654	398
Ncl	NM_010880	chr1	88255423	88255832	402
Zfp787	NM_001013012	chr7	6106990	6107351	402
Shmt2	NM_001252316	chr10	126958788	126959405	403
1200014J11Rik	NM_025818	chr11	72861568	72861974	403
Oxsr1	NM_133985	chr9	119230947	119231328	407
Zfp180	NM_001045486	chr7	24867111	24867533	407
Brd2	NM_001204973	chr17	34258852	34259435	408
Vamp3	NM_009498	chr4	150431555	150431752	408
Ibtk	NM_001081282	chr9	85642408	85642657	408
Zmym4	NM_001114399	chr4	126644586	126644927	410
Mettl9	NM_021554	chr7	128178142	128178597	412
Actr1a	NM_016860	chr19	46469644	46469975	415
Pbx3	NM_016768	chr2	34226965	34227334	415
Fbxo7	NM_153195	chr10	85484855	85485321	415
Pxdn	NM_181395	chr12	30623136	30623494	415
Fam19a2	NM_182807	chr10	122701410	122701683	416
Ddrgk1	NM_029832	chr2	130489776	130490153	416
Ift81	NM_009879	chr5	123063930	123064290	416
Pla2g4a	NM_008869	chr1	151807853	151808132	421
Cep78	NM_198019	chr19	16058828	16059287	421
Bloc1s1	NM_015740	chr10	128360055	128360254	425
Sephs1	NM_175400	chr2	4802733	4803334	425
Pbrm1	NM_001081251	chr14	31832641	31832855	425
Bcl7b	NM_009745	chr5	135644472	135644862	426
Aspscr1	NM_026877	chr11	120534561	120534864	427
Smarcb1	NM_001161853	chr10	75383671	75384185	430
Rac1	NM_009007	chr5	144288297	144288563	430
Ubtf	NM_001044383	chr11	102177937	102178401	431
Hmga2	NM_010441	chr10	119913384	119913730	433
Ndufaf3	NM_023247	chr9	108469092	108469385	434
Dock1	NM_001033420	chr7	141862577	141863029	434
Rbbp8	NM_001081223	chr18	11816135	11816449	435

Supplemental Table 4. Significant ChIP-seq E2F3B promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Slc25a4	NM_007450	chr8	47295746	47296104	437
Zkscan17	NM_001291014	chr11	59319448	59319958	438
4632428C04Rik	NR_033631	chr16	30008916	30009464	438
G730013B05Rik	NR_040379	chr16	50528938	50529166	438
Srsf7	NM_146083	chr17	80605998	80606414	438
Hira	NM_010435	chr16	18877163	18877398	439
2700081O15Rik	NM_175381	chr19	7492451	7492654	439
Sdc1	NM_011519	chr12	8778357	8778926	441
Snapc2	NM_133968	chr8	4253310	4253773	441
Dazap2	NM_011873	chr15	100446343	100446727	443
Homer3	NM_001146153	chr8	72807178	72807504	444
Pik3c2b	NM_001099276	chr1	134942865	134943203	446
Hirip3	NM_172746	chr7	134005774	134006088	446
Bcar1	NM_001198839	chr8	114255421	114255757	446
Sp3os	NR_045269	chr2	72817802	72818079	453
Tor1b	NM_133673	chr2	30808804	30809143	454
Rrm2	NM_009104	chr12	25393387	25393760	456
Uhrf1	NM_001111079	chr17	56442502	56443931	458
Gm15417	NR_040404	chr3	89198468	89198869	458
Sap130	NM_172965	chr18	31794334	31794658	460
Carhsp1	NM_025821	chr16	8671600	8671968	461
Bcl2l1	NM_009743	chr2	152656870	152657132	462
Supt16	NM_033618	chr14	52816276	52816613	469
Brpf3	NM_001081315	chr17	28938361	28938722	472
Zfp651	NM_001166644	chr9	121669428	121669818	473
B230208H11Rik	NR_038028	chr10	12642131	12642767	475
Cirbp	NM_007705	chr10	79630877	79631246	477
Rell1	NM_145923	chr5	64359490	64359827	477
Eif1	NM_011508	chr11	100181596	100181977	478
Ctdspl	NM_133710	chr9	118835956	118836305	478
Pcif1	NM_146129	chr2	164705129	164705562	479
Lzts2	NM_001130526	chr19	45092939	45093271	481
Calm2	NM_007589	chr17	87845657	87845928	482
ChkbCpt1b	NR_004843	chr15	89259786	89259955	487
Etv4	NM_008815	chr11	101646024	101646248	487
Elavl4	NM_001163397	chr4	110023872	110024184	487
Phf20	NM_172674	chr2	156022724	156023017	489
Pmm1	NM_001282040	chr15	81790738	81790999	491
Bcdin3d	NM_029236	chr15	99304495	99304839	493
Stub1	NM_019719	chr17	25969511	25970113	493
Mcm7	NM_008568	chr5	138612460	138612731	494
Med16	NM_001163276	chr10	79371017	79371355	496
Cdkn2aip	NM_172407	chr8	48798538	48799038	496
Gm6793	NR_033513	chr2	75497633	75498067	504
Pcbp2	NM_011042	chr15	102301409	102301724	505
Kansl3	NM_172652	chr1	36425304	36425734	506
Eef1b2	NM_018796	chr1	63223771	63224049	506
Rnf149	NM_001033135	chr1	39633544	39633819	510

Supplemental Table 4. Significant ChIP-seq E2F3B promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
4930539J05Rik	NR_030689	chr3	135100882	135101354	510
Plec	NM_201392	chr15	76029136	76029512	511
Espn	NM_019585	chr4	151502416	151502619	516
Cnih4	NM_030131	chr1	183081408	183081746	516
Tra2b	NM_009186	chr16	22265242	22265728	516
Psip1	NM_133948	chr4	83131642	83132026	517
BC051226	NR_045146	chr17	34045471	34045733	520
Rrm1	NM_009103	chr7	109590588	109590870	521
B3gnt9	NM_178879	chr8	107778399	107778659	523
Srsf4	NM_020587	chr4	131429871	131430283	524
Eed	NM_021876	chr7	97128785	97129135	525
Ino80	NM_026574	chr2	119302657	119303018	527
Meaf6	NM_001290701	chr4	124762763	124763050	530
Midn	NM_021565	chr10	79611416	79611713	531
Pnn	NM_008891	chr12	60168251	60168620	531
Tmem165	NM_011626	chr5	76613219	76613654	533
Fkbp5	NM_010220	chr17	28622374	28622736	538
Ubr5	NM_001081359	chr15	38007890	38008248	539
B3galnt1	NM_020026	chr3	69402190	69402492	540
Eea1	NM_001001932	chr10	95403713	95403961	541
Rbl1	NM_011249	chr2	157029547	157029906	543
Id4	NM_031166	chr13	48357164	48357512	543
A930005H10Rik	NR_027894	chr3	115590309	115590548	548
Hmgn2	NM_016957	chr4	133522964	133523746	550
Rangap1	NM_001146174	chr15	81559672	81559922	551
Smc1a	NM_019710	chrX	148451376	148451668	552
Ktn1	NM_001293635	chr14	48269335	48269740	553
Epc2	NM_172663	chr2	49307406	49307717	557
Suv420h1	NM_001167886	chr19	3767781	3768178	560
Scaf4	NM_178923	chr16	90283943	90284274	561
Hist2h4	NM_033596	chr3	96066494	96066860	562
Wnk1	NM_198703	chr6	119987909	119988311	562
Pcna	NM_011045	chr2	132078051	132078648	566
Ncapd3	NM_178113	chr9	26838155	26838502	570
Pkd1	NM_013630	chr17	24687314	24687615	571
Ctdsp1	NM_153088	chr1	74438429	74439085	575
Gm13375	NR_033225	chr2	20890932	20891219	576
Ggnbp2	NM_153144	chr11	84683377	84683946	578
Msra	NM_001253715	chr14	65059082	65059474	584
Nfx1	NM_023739	chr4	40918418	40918700	584
Ttc39b	NM_027238	chr4	82969356	82969660	584
Ccne2	NM_009830	chr4	11119252	11119627	585
Phf19	NM_028716	chr2	34768778	34769036	588
Mir6976	NR_105942	chr17	46690157	46690339	589
Syne2	NM_001005510	chr12	76919660	76920129	591
Gpank1	NM_001128597	chr17	35258871	35259192	592
Lancl2	NM_133737	chr6	57652937	57653151	596
Pdzrn3	NM_018884	chr6	101327181	101327406	597

Supplemental Table 4. Significant ChIP-seq E2F3B promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Smc3	NM_007790	chr19	53675197	53675767	597
Ttc7	NM_028639	chr17	87682649	87682997	598
Slc7a1	NM_007513	chr5	149210736	149211022	600
Hnrnpl	NM_177301	chr7	29596296	29596722	601
Camkk1	NM_018883	chr11	72832937	72833284	602
Mbd3	NM_013595	chr10	79861458	79861783	603
Tgif2	NM_173396	chr2	156666195	156666494	603
Jade1	NM_001130186	chr3	41369228	41369580	603
Gmps	NM_001033300	chr3	63780533	63780805	605
Tpm3	NM_001271764	chr3	89883873	89884222	606
Top3b	NM_011624	chr16	16871418	16871769	611
Map1s	NM_173013	chr8	73430312	73430656	612
Kat6b	NM_017479	chr14	22319312	22319926	613
Rock2	NM_009072	chr12	16902220	16902582	618
Sbf2	NM_177324	chr7	117757683	117757943	620
Gpc6	NM_001079844	chr14	117324964	117325313	621
Rhoa	NM_016802	chr9	108209059	108209268	629
Smarce1	NM_020618	chr11	99091506	99091871	642
Ap3m1	NM_018829	chr14	21870858	21871184	642
Stim2	NM_001081103	chr5	54390230	54390587	648
Mafg	NM_010756	chr11	120494036	120494386	649
Cnn3	NM_028044	chr3	121129824	121130392	650
Srrm1	NM_001130477	chr4	134908269	134908677	655
Zc3h7a	NM_145931	chr16	11175658	11176001	656
Xiap	NM_009688	chrX	39421177	39422158	656
Spsb2	NM_013539	chr6	124759458	124759771	657
Tmem74b	NM_001160363	chr2	151528226	151528575	658
Dhx15	NM_007839	chr5	52580936	52581315	659
Morf4l1	NM_001039147	chr9	90008793	90009188	667
Laptm4a	NM_008640	chr12	8928637	8928924	669
Ccna2	NM_009828	chr3	36470034	36470458	671
Rrp7a	NM_029101	chr15	82952454	82952663	672
Kitl	NM_013598	chr10	99478953	99479305	672
Stag1	NM_009282	chr9	100544481	100544950	675
Fzd5	NM_001042659	chr1	64783483	64783800	682
Rabl6	NM_001024616	chr2	25463069	25463495	683
B4galt1	NM_022305	chr4	40800647	40801125	683
Snn	NM_009223	chr16	11066904	11067249	687
Luc7l2	NM_001170848	chr6	38501916	38502344	687
Stmn1	NM_019641	chr4	134024732	134025125	695
Mthfd1l	NM_001170785	chr10	6372421	6373117	696
Ankrd12	NM_001025572	chr17	66425554	66425821	698
Pomt1	NM_145145	chr2	32092765	32093042	702
Vav2	NM_009500	chr2	27281487	27281797	702
Ep400	NM_029337	chr5	111198863	111199195	706
Kat2b	NM_020005	chr17	53706889	53707123	711
Tnfrsf12a	NM_013749	chr17	23813474	23813916	720
Tmem245	NM_175518	chr4	56959314	56959840	723

Supplemental Table 4. Significant ChIP-seq E2F3B promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Pogz	NM_001165948	chr3	94642101	94642324	725
Ubc	NM_019639	chr5	125869454	125869863	728
Hnrnpa2b1	NM_016806	chr6	51418951	51419372	731
Celsr3	NM_080437	chr9	108729231	108729536	734
Cebpd	NM_007679	chr16	15887950	15888279	737
Tyms	NM_021288	chr5	30399173	30399677	739
Slc38a1	NM_134086	chr15	96471500	96471803	741
Pprc1	NM_001081214	chr19	46131671	46131878	747
Spred1	NM_033524	chr2	116947417	116947695	750
Pan3	NM_028291	chr5	148242762	148243052	752
Helt	NM_173789	chr8	47379098	47379434	758
Slc6a9	NM_008135	chr4	117508483	117508759	759
Nasp	NM_001081475	chr4	116299020	116299651	766
Fus	NM_139149	chr7	135111632	135111886	767
Fbxo5	NM_025995	chr10	4541582	4542114	773
9930021J03Rik	NM_172836	chr19	29879552	29879890	777
Actb	NM_007393	chr5	143667354	143667890	780
Hnrnpab	NM_010448	chr11	51419432	51419762	785
Zfp623	NM_030199	chr15	75772001	75772336	788
Myo10	NM_019472	chr15	25552991	25553197	790
Phldb2	NM_001252442	chr16	45843528	45843861	796
Rcbtb2	NR_033185	chr14	73543254	73543520	796
Gatad1	NM_026033	chr5	3646960	3647318	796
Fam195b	NM_001033231	chr11	120410088	120410394	799
Atp2a2	NM_009722	chr5	122951203	122951657	803
Lpp	NM_001145952	chr16	24448765	24449200	807
Gapdh	NM_008084	chr6	125114903	125115063	807
Ivns1abp	NM_001039512	chr1	153192315	153192577	819
Zbtb7a	NM_010731	chr10	80599670	80600004	822
Tbc1d9	NM_027758	chr8	85689949	85690203	826
Mir3109	NR_037296	chr9	69305407	69305768	838
Ska2	NM_025377	chr11	86923481	86923729	843
Gt(ROSA)26Sor	NR_027010	chr6	113025897	113026882	848
Azin1	NM_018745	chr15	38448007	38448335	849
4930579G18Rik	NR_038053	chr14	55270059	55270344	855
Ndrg1	NM_008681	chr15	66800066	66800629	855
Kpnb1	NM_008379	chr11	97048174	97048525	856
Mcm7	NM_008568	chr5	138612115	138612350	857
Hist1h2bn	NM_178201	chr13	21846655	21847042	858
Pnrc1	NM_001033225	chr4	33334729	33335075	859
Hnrnpd	NM_007516	chr5	100406910	100407281	861
Dusp22	NM_001037955	chr13	30752624	30752954	862
Acly	NM_001199296	chr11	100388219	100388672	868
Anp32b	NM_130889	chr4	46464757	46464961	871
B3gnt9	NM_178879	chr8	107778034	107778315	878
Phldb1	NM_153537	chr9	44542113	44542692	878
Dennd4a	NM_001162917	chr9	64659530	64659861	879
Lancl2	NM_133737	chr6	57653198	57653458	880

Supplemental Table 4. Significant ChIP-seq E2F3B promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Id3	NM_008321	chr4	135700398	135700836	881
Fam19a2	NM_182807	chr10	122701831	122702194	882
Chd3os	NR_027827	chr11	69155035	69155269	882
Dleu2	NR_028264	chr14	62300074	62300558	893
Pkd2	NM_008861	chr5	104889141	104889602	897
Rrbp1	NM_024281	chr2	143835785	143836417	897
Dnm1	NM_010065	chr2	32207697	32208153	898
Hist1h1c	NM_015786	chr13	23831396	23831762	904
Tubb6	NM_026473	chr18	67551128	67551469	915
Inppl1	NM_001122739	chr7	108985247	108985597	915
2310045N01Rik	NM_001145552	chr8	72664410	72664644	916
Fstl3	NM_031380	chr10	79240731	79241163	929
Wee1	NM_009516	chr7	117266276	117266745	939
Dnmt1	NM_001199433	chr9	20756013	20756231	944
Kdm3b	NM_001081256	chr18	34937524	34937712	957
Lrrc29	NM_177449	chr8	107849027	107849402	961
Ltbp4	NM_175641	chr7	28121558	28121775	964
Mcm9	NM_027830	chr10	53349151	53349409	964
Cand1	NM_027994	chr10	118675899	118676380	971
Eif4ebp1	NM_007918	chr8	28371558	28371984	973
Gsr	NM_010344	chr8	34764460	34764906	974
Tfap4	NM_031182	chr16	4558549	4558927	981
Gtf2i	NM_001080748	chr5	134789456	134789810	996
Myo1d	NM_177390	chr11	80592371	80592675	1003
Eif4a1	NM_144958	chr11	69484655	69485172	1011
Sec31b	NM_001033343	chr19	44619165	44619483	1013
Zbtb2	NM_001033466	chr10	5959325	5959569	1015
Ahnak	NM_001286518	chr19	9064623	9064954	1016
Spry1	NM_011896	chr3	37539765	37540008	1016
Lrch1	NM_001033439	chr14	75346497	75346825	1022
Nuak1	NM_001004363	chr10	83902025	83902357	1024
Ltbp3	NM_008520	chr19	5741705	5742186	1043
Zfpm2	NM_011766	chr15	40487511	40487751	1044
Mnt	NM_010813	chr11	74645340	74645632	1061
Sin3a	NM_001110351	chr9	56920705	56921131	1072
1700123M08Rik	NR_040577	chr4	11894653	11894941	1077
Sft2d3	NM_026006	chr18	32070322	32070635	1078
Arhgef25	NM_001166413	chr10	126625556	126626043	1079
Tubb5	NM_011655	chr17	35973955	35974345	1095
Pde5a	NM_153422	chr3	122432927	122433413	1095
Pmp22	NM_008885	chr11	62945852	62946384	1107
Ttc7	NM_028639	chr17	87683106	87683564	1110
Gas1	NM_008086	chr13	60277635	60277924	1116
Coq10a	NM_001081040	chr10	127805700	127806247	1119
Sfpq	NR_045010	chr4	126699581	126699747	1120
Map1lc3b	NM_026160	chr8	124115376	124115605	1124
Mettl24	NM_177793	chr10	40404077	40404345	1124
Hist1h4h	NM_153173	chr13	23623844	23624236	1128

Supplemental Table 4. Significant ChIP-seq E2F3B promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Aim1	NM_172393	chr10	43723396	43723601	1153
Jund	NM_010592	chr8	73222544	73223036	1153
Lmnb1	NM_010721	chr18	56868504	56868763	1168
Hmgb1	NM_010439	chr5	149863273	149863607	1172
Trp53	NM_001127233	chr11	69394913	69395159	1176
Set	NM_023871	chr2	29918520	29918882	1186
Ncoa2	NM_008678	chr1	13362766	13363184	1188
Ddx26b	NM_172779	chrX	53708984	53709423	1189
Slc1a5	NM_009201	chr7	17367707	17368071	1195
Rai1	NM_009021	chr11	59919550	59919887	1205
Hmga1-rs1	NM_001166477	chr17	27694686	27694923	1208
Hoxb9	NM_008270	chr11	96133623	96134098	1218
Ptn	NM_008973	chr6	36759946	36760338	1218
Wnt5a	NM_009524	chr14	29319763	29320017	1232
Gpc6	NM_001079844	chr14	117325521	117325989	1237
Hnrnpu	NM_016805	chr1	180266495	180266847	1243
Foxh1	NM_007989	chr15	76498991	76499271	1246
Ptprg	NM_008981	chr14	12387127	12387519	1257
Cnppd1	NM_026977	chr1	75137544	75137816	1261
Vcan	NM_001081249	chr13	89880714	89880983	1268
Ftx	NR_028381	chrX	100817704	100817935	1273
Scarf2	NM_153790	chr16	17798477	17798819	1274
Vegfa	NM_001287057	chr17	46167878	46168173	1300
Ckap4	NM_175451	chr10	83995067	83995552	1323
Klf1	NM_010635	chr8	87426996	87427305	1325
Hnrnpd	NM_007516	chr5	100406422	100406836	1327
Prrx1	NM_011127	chr1	165242283	165242600	1339
Pim1	NM_008842	chr17	29629246	29629447	1358
Angptl6	NM_145154	chr9	20682519	20683066	1361
Metap2	NM_019648	chr10	93352465	93352697	1365
Lrp8	NM_001080926	chr4	107476092	107476370	1368
Ptma	NM_008972	chr1	88424235	88425141	1378
Zbtb7a	NM_010731	chr10	80600273	80600556	1400
Mrgbp	NM_028479	chr2	180317280	180317612	1438
Sdc1	NM_011519	chr12	8779445	8779852	1448
9130024F11Rik	NR_024326	chr1	57029492	57030064	1466
5031425E22Rik	NR_040469	chr5	22938515	22938875	1475
Rnf122	NM_175136	chr8	32223627	32223985	1489
Loxl1	NM_010729	chr9	58159358	58159684	1497
Csrnp1	NM_153287	chr9	119892044	119892511	1498
Rnd1	NM_172612	chr15	98506204	98506568	1505
1110001J03Rik	NM_025363	chr6	38486247	38486566	1547
Stk25	NM_021537	chr1	95530631	95530849	1563
Elovl6	NM_130450	chr3	129236686	129237063	1572
0610009L18Rik	NR_038126	chr11	120211335	120211816	1585
Afap1	NM_027373	chr5	36237455	36237686	1604
Cdkn1a	NM_007669	chr17	29232028	29232670	1633
Gm17762	NR_028378	chr2	17950315	17950773	1669

Supplemental Table 4. Significant ChIP-seq E2F3B promoter peaks (+/- 2kb from the TSS)

Gene Symbol	Refseq Transcript ID	Chromosome	Start	End	distance from TSS
Mrgbp	NM_028479	chr2	180317614	180317818	1708
Sin3a	NM_001110351	chr9	56921329	56921782	1710
Myc	NM_001177353	chr15	61818456	61818803	1735
Marcks	NM_008538	chr10	36856704	36857135	1812
Hspg2	NM_008305	chr4	137026426	137026672	1832
Rab17	NM_001159725	chr1	92862229	92862582	1838
2810049E08Rik	NR_036594	chr13	84032498	84032809	1842
Amd2	NM_007444	chr10	40019982	40020283	1859
Ncam1	NM_001113204	chr9	49605136	49605486	1862
Crlf2	NM_001164735	chr5	109985937	109986337	1874
Hes1	NM_008235	chr16	30067251	30067463	1915
Myo1c	NM_001080774	chr11	75467410	75467725	1917
Gnai2	NM_008138	chr9	107535584	107535926	1917
Ppp2cb	NM_017374	chr8	34711806	34712230	1926
Tcf7l2	NM_001142918	chr19	55818054	55818417	1937
Hipk2	NM_010433	chr6	38824154	38824343	1940
Gdnf	NM_010275	chr15	7762819	7763100	1950
Adrb3	NM_013462	chr8	28337936	28338227	1978

Supplemental Table 5. Motifs identified by HOMER (de novo) from E2F1, E2F3A and E2F3B ChIP-seq

	Best Match/Details	% of Targets	% of Background	% of Targets - % of	P-value	Motif
E2F1 promoter	E2F1(E2F)/Hela-E2F1-ChIP-Seq(GSE22478)/Homer(0.901)	40.13%	24.16%	**15.97%**	1.00E-66	
	MF0009.1_TRP(MYB)_class/Jaspar(0.715)	35.49%	24.47%	**11.02%**	1.00E-32	
	E2F4(E2F)/K562-E2F4-ChIP-Seq(GSE31477)/Homer(0.676)	25.75%	15.74%	**10.01%**	1.00E-35	
	NFY(CCAAT)/Promoter/Homer(0.963)	11.37%	3.12%	**8.25%**	1.00E-72	
	POL003.1_GC-box/Jaspar(0.872)	15.72%	7.55%	**8.17%**	1.00E-40	
	PB0008.1_E2F2_1/Jaspar(0.854)	14.01%	8.10%	**5.91%**	1.00E-21	
	ETS(ETS)/Promoter/Homer(0.970)	10.12%	4.62%	**5.50%**	1.00E-28	
	NRF1/Promoter/Homer(0.925)	7.78%	3.48%	**4.30%**	1.00E-22	
	GFY(?)/Promoter/Homer(0.941)	2.59%	0.29%	**2.30%**	1.00E-36	
	MA0093.2_USF1/Jaspar(0.949)	3.05%	1.09%	**1.96%**	1.00E-13	

Supplemental Table 5. Motifs identified by HOMER (de novo) from E2F1, E2F3A and E2F3B ChIP-seq

	ZBTB33(Zf)/GM12878-ZBTB33-ChIP-Seq(GSE32465)/Homer(0.941)	1.76%	0.40%	**1.36%**	1.00E-14	
	PB0199.1_Zfp161_2/Jaspar(0.617)	0.29%	0.00%	**0.29%**	1.00E-12	
E2F1 non-promoter	PH0111.1_Nkx2-2/Jaspar(0.635)	11.55%	2.61%	**8.94%**	1.00E-15	

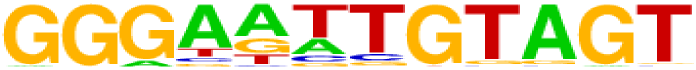
	Best Match/Details	**% of Targets**	**% of Backgro**	**% of Targets -**	**P-value**	**Motif**
E2F3A 0romoter	E2F7(E2F)/Hela-E2F7-ChIP-Seq(GSE32673)/Homer(0.969)	20.81%	3.07%	**17.74%**	#######	
	E2F(E2F)/Cell-Cycle-Exp/Homer(0.612)	37.04%	21.76%	**15.28%**	1.00E-26	
	NFY(CCAAT)/Promoter/Homer(0.957)	17.07%	4.25%	**12.82%**	1.00E-50	
	MA0527.1_ZBTB33/Jaspar(0.725)	23.00%	10.19%	**12.81%**	1.00E-29	
	Sp1(Zf)/Promoter/Homer(0.941)	18.73%	7.98%	**10.75%**	1.00E-25	
	NRF1/Promoter/Homer(0.928)	8.43%	3.13%	**5.30%**	1.00E-14	
	MA0062.2_GABPA/Jaspar(0.883)	6.66%	1.79%	**4.87%**	1.00E-17	

Supplemental Table 5. Motifs identified by HOMER (de novo) from E2F1, E2F3A and E2F3B ChIP-seq

	PB0008.1_E2F2_1/Jaspar(0.765)	6.97%	2.56%	**4.41%**	1.00E-12	
	MA0018.2_CREB1/Jaspar(0.932)	6.35%	1.99%	**4.36%**	1.00E-14	
	GFY(?)/Promoter/Homer(0.977)	4.16%	0.31%	**3.85%**	1.00E-30	
	MA0527.1_ZBTB33/Jaspar(0.593)	0.83%	0.01%	**0.82%**	1.00E-13	
E2F3A non-promoter	PB0203.1_Zfp691_2/Jaspar(0.772)	4.26%	0.15%	**4.11%**	1.00E-12	

	Best Match/Details	**% of Targets**	**% of Background**	**Targets - % of Backgro**	**P-value**	**Motif**
E2F3B promoter	E2F1(E2F)/Hela-E2F1-ChIP-Seq(GSE22478)/Homer(0.950)	21.93%	7.29%	**14.64%**	#######	
	PB0008.1_E2F2_1/Jaspar(0.779)	33.94%	23.00%	**10.94%**	1.00E-47	
	NFY(CCAAT)/Promoter/Homer(0.949)	12.35%	3.48%	**8.87%**	#######	
	Elk1(ETS)/Hela-Elk1-ChIP-Seq(GSE31477)/Homer(0.936)	12.81%	6.30%	**6.51%**	1.00E-43	

Supplemental Table 5. Motifs identified by HOMER (de novo) from E2F1, E2F3A and E2F3B ChIP-seq

	MF0002.1_bZIP_CREB/G-box-like_subclass/Jaspar(0.890)	12.06%	6.11%	**5.95%**	1.00E-38	
	NRF1(NRF)/MCF7-NRF1-ChIP-Seq(Unpublished)/Homer(0.967)	6.97%	3.06%	**3.91%**	1.00E-30	
	Sp1(Zf)/Promoter/Homer(0.834)	5.93%	3.29%	**2.64%**	1.00E-14	
	GFY(?)/Promoter/Homer(0.982)	2.36%	0.32%	**2.04%**	1.00E-41	
	Usf2(HLH)/C2C12-Usf2-ChIP-Seq(GSE36030)/Homer(0.784)	2.99%	1.08%	**1.91%**	1.00E-18	
	GFX(?)/Promoter/Homer(0.951)	1.24%	0.25%	**0.99%**	1.00E-16	
	MA0503.1_Nkx2-5_(var.2)/Jaspar(0.647)	0.89%	0.14%	**0.75%**	1.00E-14	
E2F3B non-promoter	MA0470.1_E2F4/Jaspar(0.930)	16.62%	5.08%	**11.54%**	1.00E-14	
	MA0470.1_E2F4/Jaspar(0.962)	11.71%	1.71%	**10.00%**	1.00E-20	
	Jun-AP1(bZIP)/K562-cJun-ChIP-Seq(GSE31477)/Homer(0.910)	9.54%	1.47%	**8.07%**	1.00E-17	
	AP-1(bZIP)/ThioMac-PU.1-ChIP-Seq(GSE21512)/Homer(0.941)	8.02%	1.43%	**6.59%**	1.00E-12	
	MA0490.1_JUNB/Jaspar(0.960)	6.57%	0.76%	**5.81%**	1.00E-14	

Supplemental Table 6. Liver related IPA functions for E2F1, E2F3A and E2F3B promoter targets

ChIP-se	Category	B-H p-value	Genes
E2F1	Hepatocellular Carcinoma	9.60E-03	NPM1,AXIN1,POLA1,FRMD6,POR,GLB1,ZCCHC8,TSC2,MAP1A,SAFB,HCFC1,ZBTB5,TCF3,RGP1,OGG1,SP4,CNTRL,DAXX,MB21D2,HIST1H2BM,EYA3,ALCAM,ELMO2,ECT2,CCDC138,NDST1,SLC1A5,BAG6,GAK,SMARCA4,FXR2,UGT2A1,TIPARP,KDM6A,PIK3C3,RBMX,VPS13B,C2CD5,ATN1,ZKSCAN5,MTSS1L,SDHA,VPS16,TUBB4B,DHX36,NCBP1,SPSB4,IGF2R,KPNB1,MCM3,BUB1,MTHFD1L,RPL37,TOE1,TFB1M,AP1G1,KANSL2,CDKN2A,KIF23,SOCS3,RAB14,NAV2,MPRIP,YWHAH,PCDH18,TROAP,NUP58,RPGRIP1L,ZC3H14,CTSD,UFSP2,MPHOSPH9,SETD8,COL19A1,STXBP1,SMG6,WEE1,ASNA1,DNA2,AURKA,PHRF1,OSBPL8,KIAA0907,BCL2L1,KIAA0895L,H3F3A/H3F3B,ANKRA2,mir-210,POLL,SF3B4,NAGLU,MAST3,ABCD1,HPS5,STK33,KLF10,RAB23,CLUAP1,DDX27,TEX10,IQGAP1,LSM2,TBC1D1,STPG2,WDTC1,FRA10AC1,NDUFV1,TECPR2,IPO4,HERPUD1,STK3,ALS2,UMPS,MTO1,PPM1G,HTATSF1,CENPI,CKS1B,CAMTA1,ING1,ZDHHC6,MCM6,CCP110,MTBP,CEP120,UBR2,TAPT1,mir-148,MDH1,WBSCR17,GKAP1,HOOK3,PRIM2,SPECC1L,SLC39A13,UBXN6,CNOT1,DNAJB12,HIRA,TIMM17B,MON1A,MBD2,MON2,AP5Z1,MED12,MEX3A,RNF168,SUCO,AAAS,GAMT,EML5,MYO9A,NCLN,RTN4,DNAJC14,ARHGAP35,TMEM50B,NEK2,CANT1,IPO8,SNAI2,CEP78,NCAPD3,SLC4A1AP,GPX1,TRIO,NRF1,AAMP,PITRM1,KANSL3,CORO2B,ATAD5,TYW1,NEIL3,ZBTB3,HK2,RINT1,TICRR,CETN3,RAB33B,CC2D1A,CREB1,RFC2,NUP205,TXNL1,VCL,TCTN3,ZNF25,RGMB,NAP1L4,MCMBP,CEP164,NUP85,CEP152,PDE4DIP,BANP,C2orf44,TIAL1,PLCG1,PLK1,MDM2,CNKSR3,F3,SCAF11,C1orf159,RHOBTB1,NCAPG2,ZNF519,RRM1,GLTP,ZNF546,ATL2,MMS19,DUS3L,CEP192,EML6,WDR25,RBBP6,ZFYVE19,NCAM1,FMNL3,PFN1,FARP1,ARF1,CNNM2,UNC5B,FBXW7,RELL1,FAM208A,KHNYN,TMEM230,FASN,HEXDC,RPRD2,HIST1H3F,C7orf50,P4HB,GJA1,STIL,DCTN4,TRIOBP,USP38,MTA2,BIRC6,ATP10A,MUT,MAPK8IP3,HERC2,NIN,NASP,WHSC1L1,BRAT1,HNRNPUL2,C15orf41,TSNAXIP1,SBNO2,KBTBD8,UVRAG,CDK2,FADS1,KDM3A,BRD2,PA2G4,MRPS30,KIAA0825,ZMIZ1,TRIM24,GTF2B,IFRD1,IPO5,YLPM1,RASSF1,NRAS,TRA2B,COTL1,PANK2,DOCK7,TCF7L1,C19orf68,ZNF382,PIAS3,FAF1,TMEM2,PTPRU,U2SURP,HIVEP1,ZDHHC12,MTRF1L,CBFA2T2,CASP8AP2,C17orf80,MYH10,PRR12,DSN1,PCIF1,FAM208B,CABIN1,ADH5,PAN2,SNRNP48,RCL1,MGAT1,RNGTT,IQGAP3,TP53,ATP5J,TYMS,GNE,ASF1B,ESPL1,PAPD4,APPL2,BLVRA,RRM2,ANO6,SMG5,MDM1,MYO1C,KLF13,TBC1D14,SKP2,HSPA8,FBXW8,ATE1,MORC2,PPOX,TMEM55A,ST3GAL1,MIDN,GTSE1,ANAPC5,PCYOX1L,LTN1,PARD3,NUP188,FKBP2,FBXO10,HNRNPA2B1,ODF2L,CDK4,THOC3,MKRN2,DNAJC13,PRPF4,KIAA0754,RNF130,GAS2L3,LRRFIP1,SLC35B2,THUMPD2,MMS22L,LBR,CDKN3,TMEM209,OGT,TMEM260,TRIM27,FAM227A,ALG8,BTAF1,ZBTB45,NFE2L2,DIS3,RAD21,CCDC57,PRKDC,N4BP2L2,MAPRE1,GNA12,CDH6,LARP4B,MLF1,NCAPD2,SLC29A1,RUBCN,DDX39B,RIC8B,ABCF2,DOPEY2,MBD3,EIF4A1,CDKN1A,VMP1,ZCWPW1,SPICE1,CEP112,PPIL1,WRAP53,FOXRED1,ILF3,MAP3K11,MEGF9,MSH3,GNB2L1,TSFM,AP2A2,KIF16B,NSUN6,MYC,TGFBR2,LEMD3,TNRC6C,AHDC1,PHF20,PACS2,FAM83B,CACTIN,CHTF18,E4F1,PPP1R15B,CLASP1,EIF4B,TXNDC16,HUWE1,NBEAL2,USP28,TEX264,SYNE2,MYEF2,KANK2,KIF4A,ORC6,ENKD1,BRD8,TUSC3,BUB1B,ATAD2,KMT2A,CBLB,PIAS4,TAF1,HNRNPAB,UGP2,MLXIP,XRCC6,SEPT10,SMCHD1,LMNB2,HSP90AA1,MAD1L1,NCKAP5L,FAM83D,PTPN21,RBBP4,B2M,DCBLD2,UBXN1,NMT1,ARID1A,QRICH1,SEC31A,TBC1D8B,UBE2N,FASTKD3,NEURL4,C14orf80,HNRNPK,RAD50,IGF2BP1,MIER1,CDC25B,CCNA2,SHC1,SP3,FANCD2,WDFY3,NET1,DNAJC4,NOP58,CABLES2,ENPP4,MEX3B,MCM9,VARS,LONP1,ARC,POMT2,RFX1,HAUS8,NOP56,AP1S2,XRN2,RALY,CHERP,NMT2,MTHFD1,NFKBIL1,FOXM1,GAN,ATL3,PSME3,HNRNPM,NBN,FAM98B,PSKH1,WDR54,RIOK2,KIF5B,PHF19,ZNF622,EHD4,SMG7,THAP4,MSH6,WNK1,GZF1,FANCI,CENPF,MZF1,GTF3C2,ARV1,GOLIM4,SFPQ,ZNF451,RICTOR,RUSC1,NCOA7,INTS7,MXD3,TTF2,THRAP3,HNRNPUL1,IRS2,OSMR,CEP250,PITPNB,TIMP2,PAPOLA,UPF2,MEX3C,TMEM55B,TOPBP1,COPS5,NUFIP1,SERINC1,FANCC,UBE2S,WDR89,FNBP4,CTPS1,UBQLN4,PLA2G6,NSMCE2,NR1D1,BSG,ZNF202,YARS,E2F1,FBXL6,AHCTF1,RGL2,LRP8,HELB,CYR61,L3MBTL2,CD2BP2,VASH2,ADAM17,FN1,SUV39H2,ALKBH7,CTNNA3,NUP214,RTKN2,TRIB1,YY1,MTOR,POLR2M,PTS,DGCR8,TOP2A,DAP3,EIF3A,E2F5,MCPH1,CFAP77,KIAA0391,PCBP2,SARS,KHSRP,RXRB,POT1,FAM109A,NUP35,AIFM1,SAMD14,FMN1,DCK,CCDC130,ACTB,CENPU,ICAM4,RQCD1,ATXN2L,PCDH9,SIN3A,RAD54B,KIF15,SF3B2,mir-30,RBM6,KIF20B,DENND1A,CENPA,RBPJ,ZFP36L2,USP49,MBD5,ZMYM4,BIRC2,FZR1,SND1,ERCC6,TFG,INSIG1,DIAPH3,MMP16,NR2F2,CDH24,FNIP2,AURKB,UBA2,CCNL1,ROCK2,SRSF1,CPSF6,DPY19L4,SPATA5,NCOA5,POLD3,PMS1,EZH2,PRND,HTRA2,NIPBL,PUF60,BRCA1,RAD51C,ARHGAP24,MRPL43,FARP2,KIF14,RBL2,PDE10A,STK11,ZC3H6,TBP,CCT6A,MARS,TPX2,EPRS,DPP9,GSR,SEL1L,CASC5,ARRB2,TOB2,ZFR,CASP2,PTPRS,GNL3,LTV1,BAZ1B,AK2,PFAS,RFC3,OBFC1,ZBTB7A,TNRC6B,MED23,NFIX,CHD4,GTF3C5,PKM,CUTA,SLC7A1,RAPGEF6,POLI,SIL1,DARS2,STXBP4,GANAB,BCAR1,CENPP,LCA5,NKD2,NFX1,NLK,PCK2,SP1,ADAL,CIT,OXCT1,LTBP4,ZNHIT2,ARSB,BLM,STK40,ACTN1,E2F8,IDH3B,TM9SF1,NACA,BICD2,DCTPP1,MDGA1,FCHSD2,MAPK9,RPS6KA5,USP1,PSMA1,GCC2,HIVEP2,AFF1,ZBTB48,KIF24,PPP6R1,LPAR1,PAQR4,CAD,HMGCR,RTN3,MCM7

Supplemental Table 6. Liver related IPA functions for E2F1, E2F3A and E2F3B promoter targets

ChIP-se	Category	B-H p-value	Genes
E2F1	Liver Hyperplasia/Hyperproliferation	9.60E-03	NPM1,AXIN1,POLA1,FRMD6,POR,GLB1,TSC2,ZCCHC8,MAP1A,SAFB,HCFC1,ZBTB5,TCF3,RGP1,OGG1,SP4,DAXX,CNTRL,MB21D2,HIST1H2BM,EYA3,ALCAM,ELMO2,CCDC138,ECT2,NDST1,SLC1A5,mir-331,BAG6,GAK,SMARCA4,FXR2,TIPARP,UGT2A1,KDM6A,PNRC1,RBMX,PIK3C3,VPS13B,C2CD5,ATN1,ZKSCAN5,MTSS1L,SDHA,VPS16,TUBB4B,DHX36,NCBP1,SPSB4,IGF2R,KPNB1,MCM3,BUB1,MTHFD1L,MSH2,RPL37,TOE1,TFB1M,AP1G1,KANSL2,KIF23,CDKN2A,SOCS3,RAB14,NAV2,MPRIP,YWHAH,PCDH18,TROAP,NUP58,RPGRIP1L,ZC3H14,CTSD,UFSP2,MPHOSPH9,SEC63,SETD8,COL19A1,STXBP1,SMG6,WEE1,ASNA1,DNA2,AURKA,PHRF1,OSBPL8,KIAA0907,BCL2L1,H3F3A/H3F3B,KIAA0895L,ANKRA2,mir-210,POLL,SF3B4,NAGLU,MAST3,ABCD1,HPS5,STK33,KLF10,RAB23,CLUAP1,DDX27,IQGAP1,TEX10,LSM2,TBC1D1,STPG2,WDTC1,FRA10AC1,NDUFV1,TECPR2,IPO4,HERPUD1,STK3,ALS2,UMPS,BIRC5,MTO1,PPM1G,HTATSF1,CENPI,CKS1B,CAMTA1,ING1,ZDHHC6,MCM6,CCP110,MTBP,CEP120,UBR2,TAPT1,RAN,mir-148,MDH1,WBSCR17,GKAP1,HOOK3,PRIM2,SPECC1L,SLC39A13,UBXN6,CNOT1,DNAJB12,HIRA,TIMM17B,MON1A,MBD2,MON2,AP5Z1,MED12,MEX3A,RNF168,SUCO,AAAS,GAMT,EML5,MYO9A,NCLN,RTN4,DNAJC14,ARHGAP35,TMEM50B,NEK2,CANT1,IPO8,SNAI2,CEP78,NCAPD3,SLC4A1AP,GPX1,TRIO,NRF1,AAMP,PITRM1,KANSL3,CORO2B,TYW1,ATAD5,ZBTB3,NEIL3,HK2,RINT1,TICRR,CETN3,CC2D1A,RAB33B,CREB1,RFC2,NUP205,TXNL1,VCL,TCTN3,ZNF25,RGMB,NAP1L4,MCMBP,CEP164,NUP85,CEP152,PDE4DIP,BANP,TRIM28,C2orf44,TIAL1,PLCG1,PLK1,MDM2,CNKSR3,F3,SCAF11,C1orf159,RHOBTB1,NCAPG2,ZNF519,RRM1,GLTP,ZNF546,ATL2,MMS19,DUS3L,CEP192,EML6,WDR25,RBBP6,ZFYVE19,NCAM1,FMNL3,PFN1,FARP1,ARF1,CNNM2,UNC5B,FBXW7,RELL1,FAM208A,KHNYN,TMEM230,STAG1,FASN,HEXDC,RPRD2,HIST1H3F,C7orf50,P4HB,GJA1,STIL,DCTN4,TRIOBP,USP38,MTA2,BIRC6,ATP10A,MUT,MAPK8IP3,HERC2,NIN,NASP,WHSC1L1,BRAT1,HNRNPUL2,C15orf41,TSNAXIP1,SBNO2,KBTBD8,UVRAG,CDK2,FADS1,KDM3A,BRD2,PA2G4,MRPS30,MRE11A,KIAA0825,ZMIZ1,TRIM24,GTF2B,PHGDH,IFRD1,IPO5,YLPM1,RASSF1,NRAS,TRA2B,COTL1,PANK2,DOCK7,TCF7L1,C19orf68,ZNF382,PIAS3,FAF1,RPS4Y1,TMEM2,PTPRU,U2SURP,HIVEP1,ZDHHC12,MTRF1L,CBFA2T2,CASP8AP2,C17orf80,MYH10,PRR12,DSN1,PCIF1,FAM208B,ODC1,CABIN1,ADH5,PAN2,SNRNP48,RCL1,MGAT1,RNGTT,IQGAP3,TP53,ATP5J,TYMS,GNE,ASF1B,ESPL1,PAPD4,APPL2,BLVRA,RRM2,ANO6,SMG5,MDM1,MYO1C,KLF13,TBC1D14,SKP2,HSPA8,FBXW8,ATE1,MORC2,PPOX,TMEM55A,ST3GAL1,MIDN,GTSE1,ANAPC5,PCYOX1L,LTN1,PARD3,NUP188,FKBP2,FANCM,FBXO10,HNRNPA2B1,ODF2L,CDK4,THOC3,MKRN2,DNAJC13,PRPF4,KIAA0754,RNF130,GAS2L3,LRRFIP1,SLC35B2,THUMPD2,MMS22L,LBR,CDKN3,TMEM209,OGT,TMEM260,TRIM27,FAM227A,ALG8,BTAF1,ZBTB45,NFE2L2,DIS3,RAD21,CCDC57,PRKDC,N4BP2L2,MAPRE1,GNA12,POLG,CDH6,MLF1,LARP4B,NCAPD2,SLC29A1,RUBCN,CCNE1,DDX39B,ABCF2,RIC8B,EIF4A1,CDKN1A,MBD3,DOPEY2,ZCWPW1,VMP1,SPICE1,CEP112,PPIL1,WRAP53,FOXRED1,ILF3,MAP3K11,MEGF9,MSH3,GNB2L1,TSFM,AP2A2,KIF16B,NSUN6,MYC,TGFBR2,LEMD3,TNRC6C,AHDC1,PHF20,PACS2,FAM83B,CACTIN,CHTF18,E4F1,PPP1R15B,CLASP1,EIF4B,TXNDC16,HUWE1,NBEAL2,USP28,TEX264,SYNE2,MYEF2,KANK2,KIF4A,ORC6,ENKD1,BUB1B,BRD8,TUSC3,ATAD2,KMT2A,CBLB,HNRNPAB,PIAS4,TAF1,UGP2,MLXIP,XRCC6,SEPT10,SMCHD1,MAD1L1,LMNB2,HSP90AA1,NCKAP5L,FAM83D,PTPN21,RBBP4,B2M,DCBLD2,UBXN1,NMT1,ARID1A,QRICH1,SEC31A,TBC1D8B,UBE2N,FASTKD3,NEURL4,C14orf80,HNRNPK,RAD50,IGF2BP1,MIER1,CDC25B,CCNA2,SHC1,SP3,FANCD2,WDFY3,NET1,DNAJC4,NOP58,CABLES2,ENPP4,MEX3B,MCM9,VARS,LONP1,ARC,POMT2,RFX1,HAUS8,NOP56,AP1S2,XRN2,RALY,CHERP,NMT2,MTHFD1,NFKBIL1,FOXM1,GAN,ATL3,PSME3,NBN,HNRNPM,FAM98B,PSKH1,MAPK14,WDR54,RIOK2,KIF5B,PHF19,ZNF622,EHD4,SMG7,THAP4,MSH6,WNK1,GZF1,FANCI,CENPF,MZF1,GTF3C2,ARV1,GOLIM4,SFPQ,ZNF451,RICTOR,RUSC1,NCOA7,INTS7,MXD3,TTF2,THRAP3,HNRNPUL1,IRS2,OSMR,CEP250,PITPNB,TIMP2,PAPOLA,UPF2,NDRG1,MEX3C,TMEM55B,TOPBP1,COPS5,NUFIP1,SERINC1,FANCC,UBE2S,WDR89,FNBP4,CTPS1,UBQLN4,PLA2G6,NSMCE2,NR1D1,BSG,ZNF202,YARS,E2F1,FBXL6,AHCTF1,RGL2,LRP8,HELB,CYR61,L3MBTL2,CD2BP2,VASH2,ADAM17,FN1,SUV39H2,ALKBH7,CTNNA3,NUP214,RTKN2,TRIB1,YY1,MTOR,POLR2M,PTS,DGCR8,CEBPA,TOP2A,DAP3,EIF3A,E2F5,MCPH1,CFAP77,KIAA0391,PCBP2,SARS,KHSRP,RXRB,POT1,FAM109A,NUP35,AIFM1,SAMD14,FMN1,LETM1,DCK,CCDC130,ACTB,CENPU,ICAM4,RQCD1,ATXN2L,PCDH9,SIN3A,KITLG,RAD54B,KIF15,SF3B2,mir-30,RBM6,KIF20B,DENND1A,CENPA,RBPJ,ZFP36L2,USP49,MBD5,BIRC2,ZMYM4,FZD7,FZR1,SND1,ERCC6,TFG,INSIG1,DIAPH3,MMP16,NR2F2,CDH24,FNIP2,AURKB,UBA2,CCNL1,FGFR3,ROCK2,NCOA5,SRSF1,CPSF6,DPY19L4,SPATA5,POLD3,PMS1,EZH2,PRND,HTRA2,NIPBL,PUF60,BRCA1,RAD51C,ARHGAP24,MRPL43,FARP2,KIF14,RBL2,PDE10A,STK11,ZC3H6,TBP,CCT6A,MARS,TPX2,EPRS,DPP9,GSR,SEL1L,CASC5,ARRB2,TOB2,ZFR,CASP2,PTPRS,GNL3,LTV1,BAZ1B,AK2,PFAS,RFC3,OBFC1,ZBTB7A,TNRC6B,MED23,NFIX,CHD4,GTF3C5,PKM,CUTA,SLC7A1,RAPGEF6,POLI,SIL1,DARS2,STXBP4,GANAB,BCAR1,CENPP,LCA5,NKD2,NFX1,NLK,PCK2,SP1,ADAL,CIT,OXCT1,LTBP4,ZNHIT2,ARSB,BLM,STK40,ACTN1,E2F8,IDH3B,TM9SF1,NACA,BICD2,DCTPP1,MDGA1,MAPK9,FCHSD2,RPS6KA5,USP1,PSMA1,GCC2,HIVEP2,AFF1,ZBTB48,KIF24,PPP6R1,LPAR1,PAQR4,CAD,HMGCR,RTN3,MCM7
E2F1	Liver Proliferation	2.25E-01	SOCS3,MAPK1,ODC1,MYC,TGFBR2,NCOA5,TRIM24,CIT,SMARCB1,CEBPA,ATF4,JUND,OSMR,DLC1,NFE2L2,TIMP2,TP53,SLC20A1,S1PR2,BIRC6,MAPK9,STK3,FOXM1,SKP2,FADD,KITLG,CCNE1,MAPK14,E2F1,CDKN1A,CDK2,LGALS1
E2F1	Liver Hypoplasia	2.43E-01	SLC20A1,TACC3,ARF6,TCEA1,LHX2,TSC2,CDK4,ATF4,CDK2,ARID3A

Supplemental Table 6. Liver related IPA functions for E2F1, E2F3A and E2F3B promoter targets

ChIP-se	Category	B-H p-value	Genes
E2F1	Liver Necrosis/Cell Death	3.29E-01	SOCS3,GADD45B,ATF7,TMBIM6,MYC,STK4,SHC1,NCOA5,MTOR,ARF6,TRIM27,MTF1,CIT,JUND,NFE2L2,TP53,SLC20A1,PAFAH2,CASP3,MAPK9,PLK1,STK3,F3,XIAP,BUB1,FADD,DAXX,BCL2L1,MAPK14,E2F1,CDKN1A,SLC25A5,CASP7,BIRC2
E2F1	Glutathione Depletion In Liver	3.59E-01	GPX1
E2F1	Liver Cirrhosis	3.59E-01	TP53,B2M,ADAM17,FN1,PDE10A,TBC1D9,TXLNA,TUBB,HNRNPK,LBR,FGFR3,mir-30,BSG,VKORC1,mir-210,ADK,FBLN1,TOP2A,HMGCR,NFE2L2,RASSF1,WNT5A
E2F1	Liver Damage	3.59E-01	POLA1,TNFAIP3,TGFBR2,POR,MTOR,TIPARP,STUB1,PPP3R1,ADK,JUND,ARHGAP24,NFE2L2,RASSF1,TP53,PAFAH2,MAPK9,POLD1,CBLB,BCL2L1,mir-30,PPOX,MAPK14,BSG,DUSP1,mir-210,CDKN1A,HPRT1,HMGCR
E2F1	Liver Hematopoiesis	4.02E-01	SOCS3,CBFB,FEN1,TMOD3
E2F1	Liver Inflammation/Hepatitis	4.02E-01	POLA1,PPIA,TNFAIP3,POR,NCOA5,MTOR,WRN,STUB1,PPP3R1,ADK,CEBPA,NFE2L2,RASSF1,TP53,CASP3,MTA2,MAPK9,FANCC,POLD1,XIAP,BCL2L1,mir-30,mir-210,HPRT1,NAGLU,CYR61,HMGCR,CASP7,BIRC2
E2F1	Biliary Hyperplasia	4.74E-01	MYC
E2F1	Liver Congestion	4.74E-01	HEY2
E2F1	Liver Degeneration	4.74E-01	XRCC5
E2F1	Liver Failure	4.74E-01	TP53,ADAM17,DUSP1,TOP2A,CEBPA,MARS
E2F1	Hepatocellular Peroxisome Proliferation	4.74E-01	ABCD1,PEX3,PEX11B
E2F1	Liver Fibrosis	5.01E-01	TP53,MYH10,SOCS3,FN1,S1PR2,MAPK1,LHX2,POLA1,GNB2L1,BAMBI,RPGRIP1L,POLD1,HDGF,TGFBR2,NCOA5,MAPK14,SP1,ADK,CEBPA,NAGLU,NFE2L2,WNT5A,TIMP2,LGALS1
E2F1	Liver Cholestasis	5.57E-01	GJA1,NFE2L2
E2F1	Liver Dysfunction	6.37E-01	FDFT1
E2F1	Liver Steatosis	6.37E-01	KDM3A,ERCC6,INSIG1,POLA1,GNA11,BAG3,FBXW7,POU3F2,RBL1,POR,ID1,NCOA5,MAN2C1,TIPARP,FASN,ADK,FAM73B,ATF4,OSMR,IRS2,KLF2,TP53,MAF1,GPS2,ACOT13,ANGPTL6,MUT,FANCC,POLD1,PSME3,PANK1,DUSP1,CDKN1A,RBPJ,HMGCR,NPHP3
E2F1	Liver Dysplasia	7.50E-01	E2F1

Supplemental Table 6. Liver related IPA functions for E2F1, E2F3A and E2F3B promoter targets

ChIP-se	Category	B-H p-value	Genes
E2F1	Liver Enlargement	1.00E+00	FDFT1,STK11,FADS2,STK3,IGF2R,WNT5A
E2F1	Liver Hepatomegaly	1.00E+00	FDFT1,STK11,FADS2,STK3,IGF2R,WNT5A
E2F3A	Liver Hypoplasia	2.44E-02	SLC20A1,RAF1,TACC3,CDK4,KRAS,MAFF,CDK2,ARID3A
E2F3A	Liver Necrosis/Cell Death	6.53E-02	SLC20A1,TP53,RAF1,GADD45B,FKBP1A,FADD,MYC,TRADD,MAPK14,TRIM27,E2F1,CDKN1A,TLR7
E2F3A	Hepatocellular Carcinoma	9.79E-02	RAF1,PRKAB2,POLA1,KRAS,IFT80,SKAP2,RCL1,MAP1A,IQGAP3,TYMS,TP53,HCFC1,PAPD4,NPAT,GRM8,UPF3B,RRM2,MDM1,SPATA20,SKP2,SP4,ATE1,HSPA8,CNTRL,GTSE1,PDS5A,ANAPC5,LTN1,ELMO2,CCDC138,TRAPPC5,FKBP2,HNRNPA2B1,CDK4,MMS22L,TMEM209,TRIM27,SSTR5,IBTK,TLR7,ALG8,DIS3,RAD21,MTMR3,DROSHA,LARP4B,ING5,SLC29A1,ID3,RUBCN,KPNB1,MCM3,MTHFD1L,DDX39B,ABCF2,RIC8B,CDKN1A,ZCWPW1,PSAP,PPIL1,TFB1M,WRAP53,EEF1A1,NAV2,MEGF9,NUP58,TSFM,RPGRIP1L,PIEZO1,KIF16B,MYC,UFSP2,SMPD4,PHF20,GATC,CACTIN,C17orf53,EIF4B,OSBPL1A,USP28,C3orf58,WEE1,ORC6,ENKD1,ATAD2,OSBPL8,MEF2B,UGP2,XRCC6,SEPT10,SMCHD1,NAGLU,CBX3,RBBP4,ARID1A,VPS72,RAB23,KLF10,DDX27,C14orf80,CSRP2BP,LYST,NOP58,C16orf59,MCM9,VARS,LRRC8A,VAV2,POMT2,HAUS8,ZNF280D,NOP56,CHERP,Scd2,HERPUD1,SNX27,MTHFD1,UMPS,GAN,ATL3,TPP2,PPM1G,NBN,CENPI,VAV3,EHD4,MSH6,ZDHHC6,RER1,MCM6,CCP110,MTBP,UBR2,ZNF628,mir-148,SFPQ,MKI67,RICTOR,RNF38,INTS7,MXD3,RARA,ABCC1,HNRNPUL1,PLCB1,IRS2,CEP250,PITPNB,CNOT1,TOPBP1,NUFIP1,PLEC,MDC1,ITPR1,WDR89,AP5Z1,UBQLN4,MIS18BP1,RNF168,NSMCE2,AAAS,AHI1,E2F1,ACY1,NCLN,DNAJC14,KIAA0368,TBC1D15,CLCC1,L3MBTL2,CD2BP2,SNAI2,MGME1,FKBP1A,ATAD5,XYLB,TRIB1,NEIL3,POLR2M,TCOF1,DGCR8,RAB33B,TOP2A,RFC2,TXNL1,PCBP2,KHSRP,MCMBP,NUP85,CEP152,mir-199,AP4M1,DCK,SEC24B,ACTB,PAICS,RQCD1,IQSEC2,ATXN2L,NCAPG2,RRM1,GLTP,RAD54B,FTL,KIF15,ATL2,RBM6,REV1,MMS19,DENND1A,DUS3L,SEC62,ZFP36L2,COBLL1,NCAM1,OSGEPL1,FMNL3,PFN1,LAMTOR2,MMP16,MAP1B,ZNF609,ZNF91,UBA2,RELL1,CCNL1,FAM208A,USF3,ATG4C,ARHGEF40,SRSF1,POLD3,PTRH2,EZH2,RYR3,CDCA3,BRCA1,RAD51C,C7orf50,P4HB,ZNF212,ZC3H6,BIRC6,MED14,ARRB2,CASP2,MBTPS1,NUAK1,BAZ1B,CDK2,TEX261,RFC3,KDM3A,TEAD4,BRD2,MED23,PA2G4,GTF3C5,PKM,WDHD1,CENPP,ZMIZ1,MCM4,NFX1,PCK2,RRN3,ARSB,IPO5,TM9SF1,E2F8,RASSF1,MAP2K7,MTRR,TRA2B,PANK2,COTL1,let-7,GABBR1,FCHSD2,ERBB3,USP1,PSMA1,HIVEP2,AFF1,C19orf68,ZNF382,CIART,KIF24,U2SURP,SPR,CAD,TONSL,CASP8AP2

Supplemental Table 6. Liver related IPA functions for E2F1, E2F3A and E2F3B promoter targets

ChIP-se	Category	B-H p-value	Genes
E2F3A	Liver Hyperplasia/Hyperproliferation	9.79E-02	RAF1,PRKAB2,POLA1,KRAS,IFT80,SKAP2,RCL1,MAP1A,IQGAP3,TYMS,TP53,HCFC1,PAPD4,SLC2A1,NPAT,GRM8,UPF3B,RRM2,MDM1,SKP2,SPATA20,SP4,ATE1,HSPA8,CNTRL,GTSE1,PDS5A,ANAPC5,LTN1,ELMO2,CCDC138,TRAPPC5,FKBP2,HNRNPA2B1,CDK4,MMS22L,TMEM209,TRIM27,SSTR5,IBTK,TLR7,ALG8,DIS3,RAD21,MTMR3,DROSHA,POLG,LARP4B,ING5,SLC29A1,ID3,RUBCN,KPNB1,MCM3,CCNE1,MTHFD1L,DDX39B,MSH2,ABCF2,RIC8B,CDKN1A,ZCWPW1,PSAP,PPIL1,TFB1M,WRAP53,EEF1A1,NAV2,MEGF9,NUP58,TSFM,RPGRIP1L,PIEZO1,KIF16B,MYC,UFSP2,SMPD4,PHF20,GATC,CACTIN,C17orf53,EIF4B,OSBPL1A,USP28,C3orf58,WEE1,ORC6,ENKD1,ATAD2,OSBPL8,MEF2B,UGP2,XRCC6,SEPT10,SMCHD1,NAGLU,CBX3,RBBP4,ARID1A,VPS72,RAB23,KLF10,DDX27,C14orf80,CSRP2BP,LYST,NOP58,C16orf59,MCM9,VARS,LRRC8A,VAV2,POMT2,HAUS8,ZNF280D,NOP56,CHERP,Scd2,HERPUD1,SNX27,MTHFD1,UMPS,BIRC5,GAN,ATL3,TPP2,PPM1G,NBN,MAPK14,CENPI,VAV3,EHD4,MSH6,ZDHHC6,RER1,MCM6,CCP110,MTBP,UBR2,ZNF628,RAN,mir-148,SFPQ,MKI67,RICTOR,RNF38,INTS7,MXD3,RARA,ABCC1,HNRNPUL1,PLCB1,IRS2,CEP250,PITPNB,CNOT1,TOPBP1,NUFIP1,PLEC,MDC1,ITPR1,WDR89,AP5Z1,UBQLN4,MIS18BP1,RNF168,NSMCE2,AAAS,AHI1,E2F1,ACY1,NCLN,DNAJC14,KIAA0368,TBC1D15,CLCC1,L3MBTL2,CD2BP2,SNAI2,MGME1,FKBP1A,ATAD5,XYLB,TRIB1,NEIL3,POLR2M,TCOF1,DGCR8,RAB33B,TOP2A,RFC2,TXNL1,KHSRP,PCBP2,MCMBP,NUP85,CEP152,mir-199,AP4M1,DCK,SEC24B,ACTB,PAICS,RQCD1,IQSEC2,ATXN2L,NCAPG2,RRM1,GLTP,RAD54B,FTL,KIF15,ATL2,RBM6,REV1,MMS19,DENND1A,DUS3L,SEC62,ZFP36L2,COBLL1,NCAM1,OSGEPL1,FMNL3,PFN1,LAMTOR2,MMP16,MAP1B,ZNF609,ZNF91,UBA2,RELL1,CCNL1,FAM208A,USF3,ATG4C,ARHGEF40,SRSF1,POLD3,PTRH2,STAG1,EZH2,RYR3,CDCA3,BRCA1,RAD51C,C7orf50,P4HB,ZNF212,ZC3H6,BIRC6,MED14,ARRB2,CASP2,MBTPS1,NUAK1,BAZ1B,CDK2,TEX261,RFC3,KDM3A,TEAD4,BRD2,MED23,PA2G4,GTF3C5,PKM,WDHD1,CENPP,ZMIZ1,MCM4,NFX1,PCK2,RRN3,ARSB,IPO5,TM9SF1,E2F8,RASSF1,MAP2K7,MTRR,TRA2B,PANK2,COTL1,let-7,GABBR1,FCHSD2,ERBB3,USP1,PSMA1,HIVEP2,AFF1,C19orf68,ZNF382,CIART,KIF24,U2SURP,SPR,CAD,TONSL,CASP8AP2
E2F3A	Liver Proliferation	9.79E-02	TP53,SLC20A1,RAF1,MAP2K7,BIRC6,GFER,SKP2,MYC,FADD,CCNE1,MAPK14,RARA,E2F1,CDKN1A,DLC1,CDK2,LGALS1
E2F3A	Liver Damage	1.88E-01	TP53,mir-199,Gm21596/Hmgb1,MAPK14,DUSP1,POLA1,CDKN1A,GFER,GABBR1,FKBP1A,RASSF1
E2F3A	Liver Dysplasia	1.88E-01	RARA,E2F1
E2F3A	Biliary Hyperplasia	2.84E-01	MYC
E2F3A	Liver Fibrosis	3.32E-01	TP53,MAPK14,MMP8,POLA1,NAGLU,RPGRIP1L,LGALS1
E2F3A	Liver Steatosis	3.84E-01	UPP1
E2F3A	Liver Hematopoiesis	4.36E-01	KRAS,FEN1
E2F3A	Liver Regeneration	4.87E-01	CCNE1,MAP2K7,GFER,BIRC5,CDK2
E2F3A	Liver Inflammation/Hepatitis	5.52E-01	TP53,mir-199,POLA1,TLR7,GABBR1,NAGLU,FKBP1A,GPT,RASSF1
E2F3A	Liver Hemorrhaging	5.74E-01	DGCR8,FKBP1A
E2F3A	Liver Failure	6.09E-01	TP53,DUSP1,TOP2A
E2F3A	Liver Cirrhosis	1.00E+00	TP53,mir-199,ABCC1,RASSF1

Supplemental Table 6. Liver related IPA functions for E2F1, E2F3A and E2F3B promoter targets

ChIP-se	Category	B-H p-value	Genes
E2F3A	Liver Enlargement	1.00E+00	SSTR5
E2F3A	Liver Hepatomegaly	1.00E+00	SSTR5

Supplemental Table 6. Liver related IPA functions for E2F1, E2F3A and E2F3B promoter targets

ChIP-se	Category	B-H p-value	Genes
E2F3B	Hepatocellular Carcinoma	1.65E-09	GARS,TLE1,FRMD6,TMEM231,POR,TRIM32,GORASP2,PPRC1,ADA,SART3,RELT,TMEM67,ZBTB5,TANC1,DVL2,HIST1H2BM,EYA3,ALCAM,ELMO2,DDIT3,SLC1A5,CDK10,TIPARP,IBTK,RNF19A,ATN1,UBE3C,SLC12A6,SDHA,VPS16,IPO7,ID3,BUB1,KPNB1,MTHFD1L,AP1G1,CDKN2A,EEF1A1,TROAP,INTS1,LHFPL2,MTMR2,PGM1,PTPDC1,PHRF1,DYNC1H1,BCL2L1,KIAA0895L,H3F3A/H3F3B,SEC61A2,CBX3,MCCC2,ZC3H7B,HPS5,RAB23,KLF10,ZBTB2,LSM2,C16orf59,NCS1,ILKAP,IGSF8,FRA10AC1,GALNT9,MEF2A,HERPUD1,FRMD4A,SOD1,SNX27,PPM1G,HTATSF1,CENPI,TFCP2,ING1,MAP4K4,MCM6,ASPSCR1,ZNF628,FAM20C,UBR2,FNDC3B,WBSCR17,RRAGB,PPP1R21,ADIPOR1,RNF38,RASGRF1,TDP2,RAB17,UAP1,CCNT2,PRIM2,SPECC1L,NOVA1,HIRA,PLEC,AGFG2,AP5Z1,TTLL9,MEX3A,SUCO,RNF168,PHLDB1,C11orf30,NCLN,RCBTB1,KIAA0368,ARHGAP35,SNAI2,GALC,NCAPD3,PTPN13,PLAGL1,SPATA13,FKBP1A,DNAJA1,TOR1AIP1,TYW1,NEIL3,HK2,RINT1,TICRR,RFC2,IGF1R,TXNL1,TCTN3,VCL,ZNF25,PSMB9,MCMBP,NUP85,CEP152,STAMBPL1,BANP,PLK1,ACLY,F3,NCAPG2,RRM1,NUDT5,ZNF546,SBF1,ZNF507,TRERF1,COBLL1,NCAM1,FMNL3,ATRIP,FBXW7,DHODH,ZNF91,FAM208A,TBC1D4,ESPN,KHNYN,DZIP3,ZNF717,TFDP2,RPRD2,PANK4,FAM193A,STIL,COL4A1,CLTC,BIRC6,DTNB,ALAD,ATP10A,WHSC1L1,BRAT1,COL6A3,IFT81,SCRIB,C15orf41,RCE1,KBTBD8,FADS1,LRIG3,ZMIZ1,TRIM24,USP47,RPAIN,TMEM220,LRRK2,TCF7L1,PFKP,TSHZ3,ZNF382,FAF1,KIAA1033,TSEN34,PAN3,ZDHHC12,MTRF1L,USP34,RAF1,IQCK,HMMR,RALGAPB,ASCC2,FAM208B,ATP2A2,RNASE4,ADH5,DOCK11,RCL1,CCDC122,CENPE,WDR47,MGAT1,SGSM2,GNE,TYMS,CBX8,ASF1B,PHIP,PAPD4,ESPL1,APPL2,PAM,EEF2,ZBTB43,MDM1,WDR81,ZNF496,ATE1,AGPAT4,PLEKHG2,MORC2,ATXN7L3,MIDN,ST3GAL1,GTSE1,ANAPC5,VPS37B,ZNF644,CENPT,CHD1L,PTPRA,TRAPPC5,INF2,HACE1,FAM188B,ERCC4,FBXO10,PTPN2,ODF2L,HNRNPA2B1,CDK4,KIAA0754,PRPF4,PGS1,LRRFIP1,SDK1,CDKN3,TMEM209,NAA15,TMEM260,ALG8,ASPH,NFE2L2,RAD21,CYP51A1,ESCO1,FBXO21,SLC35A5,CCDC57,ZMYM1,KLHDC2,WIPF2,TUBGCP6,ING5,LARP4B,NCAPD2,SLC29A1,IGHMBP2,ZFPM2,UBR4,DDX39B,ABCF2,EIF4A1,CDKN1A,ZFHX2,PSAP,CEP112,LDHA,PPIL1,ID4,TCF7L2,PSEN1,LRIG2,MEGF9,CAMK1D,MSH3,KIF1B,TSFM,ABCC10,PIEZO1,TGFBR2,MYC,SMPD4,AHDC1,GDE1,SUGT1,CACTIN,EIF4B,CLASP1,SPECC1,TEX264,CCDC18,C3orf58,FSTL3,KANK2,ENDOD1,PSMD6,B3GALNT1,TUSC3,TBL1X,ARIH1,CDC42BPB,TAF1,HNRNPAB,UGP2,XRCC6,SEPT10,SMCHD1,RUSC2,HSP90AA1,MAD1L1,NCKAP5L,SSFA2,FAM83D,RBBP4,DPYSL3,UBE2N,RPS6KA3,DNAJC10,NEURL4,WDR6,VPS4A,IGF2BP1,RAD50,STIM2,CCNA2,LYST,AHNAK,NOP58,MEX3B,ACO1,VARS,CIZ1,LRRC8A,POMT2,HAUS8,RFX1,AP1S2,CHERP,RALY,ZFPL1,NMT2,HSPD1,NFKBIL1,MTHFD1,FAIM,SH3PXD2A,SLK,PHF19,LSM11,PSMD2,C5orf22,SGK1,APIP,ZNF451,SFPQ,KPNA1,RICTOR,RECQL,CHST2,DYNLL1,NCOA7,TTF2,HNRNPUL1,SEC24A,TMEM55B,NAT10,RCBTB2,ITPR1,PLCL2,FANCC,UBQLN4,TERF2,DOCK1,YARS,YTHDF3,CPNE8,IRS1,BHLHE40,E2F1,RGL2,LRP8,HELB,CD2BP2,VASH2,PKD2,SASS6,VCAN,XYLB,BCDIN3D,TRIB1,WDFY1,NCOA2,POLR2M,SLC6A17,DAP3,E2F5,MAP1LC3B,LPP,NCKIPSD,PLOD3,BRMS1L,RAD51B,ATXN2L,PCDH9,SIN3A,KIF15,ABL2,RBM6,HEATR5A,NCOR2,ZFP36L2,USP49,FZR1,ANKS1B,INSIG1,DIAPH3,FNIP2,CCNL1,USF3,DPY19L4,MBNL3,LARS,UBXN4,EZH2,ALG6,DARS,NIPBL,HTRA2,MYO10,PMPCA,RASAL2,FGFR1,LMNA,MARS,GSR,ARRB2,PLEKHH2,ITPRIPL1,PTPRS,PML,PFAS,BCL9L,RFC3,KDM3B,TEAD4,TNRC6B,ZBTB7A,MED23,GTF2F2,MARK2,GANAB,SP1,CIT,RABGGTB,LTBP4,ATG16L2,ZNHIT2,TM9SF1,MAP2K7,CKS2,MRC2,DCTPP1,let-7,RPS6KA5,KIAA2026,KIF24,PPP6R1,PANK3,WRB,PAQR4,TONSL,HMGCR,SLC9A8,DPY19L3,BCL2L11,MCM7,NPM1,mir-130,RPE,POLA1,TAB2,CCNB2,GPSM2,MAP1A,DUSP11,HCFC1,NPAT,TCF3,RGP1,ABCA7,SP4,DAXX,CNTRL,ITPR3,C3orf67,ECT2,CCDC138,FLNB,NRG2,PRDX1,BAG6,CEBPZ,TTK,CDC20B,HEXB,C2CD5,SCFD1,TUBB4B,ZNF521,MAPK6,GREM1,SPSB4,KAT5,IGF2R,MCM3,CSF1,TFB1M,KANSL2,KIF23,SOCS3,NAV2,MPRIP,YWHAH,PCDH18,GNPAT,NUP58,ZFPM1,RPGRIP1L,ECD,PPFIBP1,SOX2,TSEN15,ARHGAP20,EPHA7,OSBPL1A,STXBP1,SESN3,POLR1B,IARS2,WEE1,IFT74,DNA2,H6PD,TXNRD1,OSBPL8,KIAA0907,SF3B4,PBRM1,PVRL3,MCM3AP,RBBP5,IQGAP1,NFAT5,ERBB2,VAV2,NDUFV1,ADAM15,PSMC3IP,TSN,ALS2,UMPS,MTO1,SLC36A4,CKS1B,ZDHHC3,CCP110,RTCB,MTBP,GHITM,MKI67,ARNT,ATP1A1,RARA,MED16,SLC39A13,BAG5,RTEL1,CNOT1,PTPRG,MMAB,MDC1,MON2,ADAR,MED12,ANKRD26,FARSA,ARHGAP5,FUT10,AAAS,MYO9A,AHI1,DNAJC14,ME2,CLCC1,PRICKLE1,SQLE,RREB1,MAP2,CEP78,ARHGEF7,POLQ,TRPT1,PITRM1,AAMP,KANSL3,ANKRD12,EAF1,ATAD5,CDH11,TIGD5,DIS3L2,RAB33B,CREB1,NUP205,ZCCHC6,POLE,PAICS,TIAL1,MDM2,SLIT2,SCMH1,CNKSR3,C1orf159,SCAF11,GLTP,SPIDR,INTS6,GMPS,ATL2,GTPBP3,REV1,H2AFY,UBN1,BTBD7,FARP1,ARF1,PRMT3,GXYLT1,UNC5B,ZNF609,DICER1,RELL1,CAMK2D,ZNF318,SCARB1,FASN,ABLIM2,CDCA3,STX11,HK1,SOX4,P4HB,TRIOBP,DTNBP1,DCTN4,USP38,PREX2,MUT,HERC2,ANKRD10,NASP,CTDP1,LUC7L2,LOXL1,NUAK1,SBNO2,JAG1,CDK2,ARL2,KDM3A,BRD2,SRM,C5orf42,PA2G4,AGAP1,SRRT,WDHD1,KMT2C,GTF2B,FAM13B,IFRD1,NCL,YLPM1,IPO5,ATG16L1,RHBDD3,RASSF1,UBR5,HSPG2,MTRR,TTC13,TRA2B,PANK2,POC1B,COTL1,HSPH1,METTL1,SAP25,DOCK7,C19orf68,CIART,PIAS3,MAP7D1,U2SURP,PLEKHG5,IQCE,NFIB,ADAM9,GRPEL1,CBFA2T2,CENPH,CASP8AP2,PRKAB2,KRAS,PCIF1,TOMM70A,CCND1,PKN2,SNRNP48,PAN2,NEK6,ZNF687,HIPK2,MSTO1,IQGAP3,ALDH7A1,TP53,FBXO9,ZDHHC5,GRM8,TMEM201,RRM2,USP19,ANO6,SMG5,TBK1,MYO1C,KLF13,RBM4,SKP2,ATF2,HSPA8,SCAF8,CLK2,PCYOX1L,KIAA1429,LTN1,SAMD4A,NUP188,TRIM33,GCFC2,PRPF3,THOC3,KIAA1549,GPC2,SLC35B2,MMS22L,HARBI1,LBR,COL16A1,CD47,TRIM27,SORBS1,C1orf112,CSNK2B,ZBTB45,DIS3,TOB1,FRK,PLA2G4A,RIC8B,MBD3,ZCWPW1,SPICE1,SEMA3C,WRAP53,ILF3,RASA3,GNB2L1,PINX1,KNTC1,TBC1D2,KIF16B,LEMD3,TNRC6C,PHF20,

Supplemental Table 6. Liver related IPA functions for E2F1, E2F3A and E2F3B promoter targets

ChIP-se	Category	B-H p-value	Genes
E2F3B	Liver Hyperplasia/Hyperproliferation	1.65E-09	GARS,TLE1,FRMD6,TMEM231,TRIM32,POR,PPRC1,GORASP2,ADA,SART3,RELT,TMEM67,ZBTB5,TANC1,DVL2,HIST1H2BM,EYA3,ALCAM,ELMO2,DDIT3,SLC1A5,CDK10,TIPARP,IBTK,RNF19A,ATN1,UBE3C,SLC12A6,SDHA,VPS16,IPO7,ID3,BUB1,KPNB1,MTHFD1L,AP1G1,CDKN2A,EEF1A1,TROAP,INTS1,LHFPL2,MTMR2,PGM1,PTPDC1,PHRF1,DYNC1H1,BCL2L1,H3F3A/H3F3B,KIAA0895L,SEC61A2,CBX3,MCCC2,ZC3H7B,HPS5,RAB23,KLF10,ZBTB2,LSM2,C16orf59,NCS1,ILKAP,IGSF8,FRA10AC1,GALNT9,MEF2A,HERPUD1,SOD1,SNX27,FRMD4A,PPM1G,HTATSF1,CENPI,TFCP2,ING1,MAP4K4,MCM6,ASPSCR1,ZNF628,FAM20C,UBR2,FNDC3B,WBSCR17,RRAGB,PPP1R21,ADIPOR1,RNF38,RASGRF1,TDP2,RAB17,SPECC1L,UAP1,CCNT2,PRIM2,NOVA1,HIRA,PLEC,AGFG2,AP5Z1,TTLL9,MEX3A,SUCO,RNF168,PHLDB1,C11orf30,NCLN,RCBTB1,KIAA0368,ARHGAP35,SNAI2,GALC,NCAPD3,PTPN13,PLAGL1,SPATA13,FKBP1A,DNAJA1,TOR1AIP1,TYW1,NEIL3,HK2,RINT1,TICRR,RFC2,IGF1R,TXNL1,TCTN3,VCL,ZNF25,PSMB9,MCMBP,NUP85,CEP152,STAMBPL1,BANP,PLK1,ACLY,F3,NCAPG2,RRM1,NUDT5,ZNF546,SBF1,ZNF507,TRERF1,COBLL1,NCAM1,FMNL3,ATRIP,FBXW7,DHODH,ZNF91,FAM208A,TBC1D4,ESPN,KHNYN,DZIP3,ZNF717,TFDP2,RPRD2,PANK4,FAM193A,STIL,COL4A1,CLTC,BIRC6,DTNB,ALAD,ATP10A,WHSC1L1,BRAT1,COL6A3,IFT81,SCRIB,C15orf41,RCE1,KBTBD8,FADS1,LRIG3,ZMIZ1,TRIM24,USP47,RPAIN,TMEM220,LRRK2,TCF7L1,PFKP,TSHZ3,ZNF382,FAF1,KIAA1033,TSEN34,PAN3,ZDHHC12,MTRF1L,USP34,RAF1,IQCK,HMMR,RALGAPB,ASCC2,SLC35C1,FAM208B,ATP2A2,RNASE4,ADH5,DOCK11,RCL1,CCDC122,CENPE,WDR47,MGAT1,SGSM2,GNE,TYMS,CBX8,ASF1B,PHIP,PAPD4,ESPL1,YAP1,APPL2,PAM,EEF2,ZBTB43,MDM1,WDR81,ZNF496,ATE1,AGPAT4,PLEKHG2,MORC2,ATXN7L3,MIDN,ST3GAL1,GTSE1,ANAPC5,VPS37B,ZNF644,CENPT,CHD1L,PTPRA,TRAPPC5,INF2,FANCM,HACE1,FAM188B,ERCC4,FBXO10,PTPN2,HNRNPA2B1,ODF2L,CDK4,KIAA0754,PRPF4,PGS1,LRRFIP1,SDK1,CDKN3,TMEM209,NAA15,TMEM260,ALG8,ASPH,NFE2L2,RAD21,CYP51A1,ESCO1,FBXO21,SLC35A5,CCDC57,ZMYM1,KLHDC2,WIPF2,TUBGCP6,LZTS2,ING5,LARP4B,NCAPD2,SLC29A1,CCNE1,IGHMBP2,ZFPM2,UBR4,DDX39B,ABCF2,EIF4A1,CDKN1A,ZFHX2,PSAP,CEP112,LDHA,PPIL1,ID4,TCF7L2,PSEN1,LRIG2,MEGF9,CAMK1D,MSH3,KIF1B,TSFM,ABCC10,PIEZO1,TGFBR2,MYC,SMPD4,AHDC1,GDE1,SUGT1,CACTIN,EIF4B,CLASP1,SPECC1,TEX264,CCDC18,FSTL3,C3orf58,KANK2,ENDOD1,PSMD6,B3GALNT1,TUSC3,TBL1X,ARIH1,CDC42BPB,HNRNPAB,TAF1,UGP2,XRCC6,ETV4,SEPT10,SMCHD1,MAD1L1,RUSC2,HSP90AA1,NCKAP5L,SSFA2,FAM83D,RBBP4,DPYSL3,UBE2N,RPS6KA3,DNAJC10,NEURL4,WDR6,VPS4A,IGF2BP1,RAD50,STIM2,CCNA2,LYST,AHNAK,TIMP1,NOP58,MEX3B,ACO1,VARS,CIZ1,LRRC8A,POMT2,HAUS8,RFX1,AP1S2,CHERP,RALY,NMT2,ZFPL1,HSPD1,MTHFD1,NFKBIL1,SH3PXD2A,FAIM,SLK,MAPK14,PHF19,LSM11,PSMD2,C5orf22,SGK1,APIP,ZNF451,SFPQ,KPNA1,RICTOR,RECQL,CHST2,VEGFA,NCOA7,DYNLL1,TTF2,HNRNPUL1,SEC24A,TMEM55B,NAT10,RCBTB2,ITPR1,PLCL2,FANCC,UBQLN4,TERF2,DOCK1,YARS,YTHDF3,CPNE8,IRS1,BHLHE40,E2F1,RGL2,LRP8,HELB,CD2BP2,VASH2,PKD2,SASS6,VCAN,XYLB,BCDIN3D,TRIB1,WDFY1,NCOA2,POLR2M,SLC6A17,DAP3,E2F5,MAP1LC3B,LPP,NCKIPSD,PLOD3,BRMS1L,RAD51B,HNRNPDL,ATXN2L,PCDH9,SIN3A,KIF15,ABL2,RBM6,HEATR5A,NCOR2,ZFP36L2,USP49,FZR1,ANKS1B,INSIG1,DIAPH3,FNIP2,CCNL1,USF3,DPY19L4,MBNL3,LARS,UBXN4,EZH2,ALG6,DARS,NIPBL,HTRA2,MYO10,PMPCA,RASAL2,FGFR1,LMNA,MARS,GSR,ARRB2,PLEKHH2,ITPRIPL1,PTPRS,PML,PFAS,BCL9L,RFC3,KDM3B,TEAD4,TNRC6B,ZBTB7A,MED23,GTF2F2,MARK2,ING4,GANAB,SP1,CIT,RABGGTB,LTBP4,ATG16L2,ZNHIT2,TM9SF1,MAP2K7,CKS2,MRC2,DCTPP1,let-7,RPS6KA5,KIAA2026,KIF24,PPP6R1,B4GALT1,PANK3,WRB,PAQR4,TONSL,HMGCR,SLC9A8,DPY19L3,BCL2L11,MCM7,NPM1,mir-130,RPE,POLA1,TAB2,CCNB2,GPSM2,MAP1A,DUSP11,HCFC1,SLC2A1,NPAT,TCF3,RGP1,ABCA7,SP4,DAXX,CNTRL,ITPR3,C3orf67,ECT2,CCDC138,FLNB,NRG2,PRDX1,BAG6,CEBPZ,TTK,PNRC1,CDC20B,HEXB,C2CD5,SCFD1,TUBB4B,ZNF521,MAPK6,GREM1,SPSB4,KAT5,IGF2R,MCM3,MSH2,CSF1,TFB1M,KANSL2,KIF23,SOCS3,NAV2,MPRIP,YWHAH,PCDH18,GNPAT,NUP58,ZFPM1,RPGRIP1L,ECD,PPFIBP1,SOX2,TSEN15,ARHGAP20,SEC63,EPHA7,OSBPL1A,STXBP1,SESN3,HDAC2,POLR1B,IARS2,WEE1,IFT74,DNA2,H6PD,TXNRD1,OSBPL8,KIAA0907,SF3B4,PBRM1,PVRL3,MCM3AP,RBBP5,IQGAP1,NFAT5,ERBB2,VAV2,NDUFV1,ADAM15,PSMC3IP,TSN,ALS2,UMPS,BIRC5,MTO1,SLC36A4,CKS1B,ZDHHC3,CCP110,RTCB,MTBP,RAN,GHITM,MKI67,ARNT,ATP1A1,RARA,MED16,SLC39A13,BAG5,RTEL1,CNOT1,PTPRG,MMAB,MDC1,MON2,ADAR,MED12,ANKRD26,FARSA,ARHGAP5,FUT10,AAAS,MYO9A,AHI1,DNAJC14,ME2,CLCC1,PRICKLE1,SQLE,RREB1,MAP2,CEP78,ARHGEF7,POLQ,TRPT1,PITRM1,AAMP,KANSL3,ANKRD12,EAF1,ATAD5,CDH11,TIGD5,DIS3L2,RAB33B,CREB1,NUP205,ZCCHC6,POLE,PAICS,TIAL1,MDM2,SLIT2,SCMH1,CNKSR3,C1orf159,SCAF11,GLTP,SPIDR,INTS6,GMPS,ATL2,GTPBP3,REV1,H2AFY,UBN1,BTBD7,FARP1,ARF1,PRMT3,GXYLT1,UNC5B,ZNF609,DICER1,RELL1,CAMK2D,ZNF318,SCARB1,STAG1,FASN,ABLIM2,CDCA3,STX11,HK1,SOX4,P4HB,TRIOBP,DTNBP1,DCTN4,USP38,PREX2,MUT,GPAA1,HERC2,ANKRD10,NASP,CTDP1,LUC7L2,LOXL1,NUAK1,SBNO2,JAG1,CDK2,ARL2,KDM3A,BRD2,SRM,C5orf42,PA2G4,AGAP1,SRRT,WDHD1,KMT2C,GTF2B,FAM13B,IFRD1,NCL,YLPM1,IPO5,ATG16L1,RHBDD3,RASSF1,UBR5,HSPG2,MTRR,TTC13,TRA2B,PANK2,POC1B,COTL1,HSPH1,METTL1,SAP25,DOCK7,C19orf68,CIART,PIAS3,MAP7D1,U2SURP,PLEKHG5,IQCE,NFIB,ADAM9,GRPEL1,CBFA2T2,CENPH,CASP8AP2,PRKAB2,KRAS,PCIF1,TOMM70A,CCND1,PKN2,SNRNP48,PAN2,NEK6,ZNF687,HIPK2,MSTO1,ALDH7A1,IQGAP3,FBXO9,TP53,ZDHHC5,GRM8,TMEM201,RRM2,USP19,ANO6,SMG5,TBK1,MYO1C,KLF13,RBM4,ATF2,SKP2,HSPA8,SCAF8,CLK2,PCYOX1L,KIAA1429,LTN1,SAMD4A,NUP188,TRIM33,GCFC2,PRPF3,THOC3,KIAA1549,GPC2,SLC35B2,MMS22L,HA
E2F3B	Liver Hypoplasia	2.10E-03	SLC20A1,MYCN,RAF1,TACC3,LHX2,RDH10,SMAD3,CDK4,KRAS,EIF6,MAFK,MAFG,ARF6,BAG1,KAT6A,ATF4,CDK2

Supplemental Table 6. Liver related IPA functions for E2F1, E2F3A and E2F3B promoter targets

ChIP-se	Category	B-H p-value	Genes
E2F3B	Liver Necrosis/Cell Death	1.47E-02	RAF1,SOCS3,SOCS1,SMAD3,TAF10,DICER1,CCND1,ARNT,GSTZ1,MYC,CXCL10,MTF1,MAPK3,ITGAV,ADA,JUND,TP53,STAT6,HBEGF,TBK1,ADAR,IRF1,ATF2,MNT,DAXX,BCL2L1,E2F1,DDIT3,ATF7,ABL1,FKBP1A,NGF,ARF6,TRIM27,TIMP1,CIT,FOXO3,BID,NCL,NFE2L2,RHBDD3,SLC20A1,MYCN,SLC25A4,MAPK9,PLK1,SOD1,HSPD1,F3,XIAP,BAK1,FAIM,FADD,BUB1,MAPK14,ABL2,CDKN1A,ATR,SLC25A5,BCL2L11,CASP7
E2F3B	Liver Proliferation	2.48E-02	RAF1,SOCS3,CTGF,MAPK1,SMAD3,DICER1,CCND1,ARNT,VEGFA,TGFBR2,MYC,RARA,SMARCB1,ITGAV,ADA,ATF4,SLC7A5,JUND,DLC1,TIMP2,TP53,BIRC6,HBEGF,SKP2,E2F1,PML,CDK2,PTN,TNFRSF12A,TRIM24,TIMP1,CIT,IGF1R,CEBPA,BID,NFE2L2,SLC20A1,MAP2K7,S1PR2,HDAC1,SMAD7,TOB1,MAPK9,FOXM1,KITLG,FADD,CCNE1,MAPK14,CDKN1A,LGALS1
E2F3B	Liver Dysplasia	7.29E-02	RARA,E2F1,PML,CCND1
E2F3B	Liver Hematopoiesis	3.24E-01	SOCS1,SOCS3,KRAS,CBFB,FEN1,TMOD3
E2F3B	Liver Degeneration	3.43E-01	SOCS1,TAB2,TBK1,XRCC5,SRSF10
E2F3B	Liver Fibrosis	3.43E-01	SOCS3,SOCS1,CTGF,DDIT3,LHX2,F2R,MAPK1,SMAD3,POLA1,GNB2L1,RPGRIP1L,POLB,HDGF,CXCL10,VEGFA,TGFBR2,TIMP1,RORA,ADK,CEBPA,ADORA2B,NFE2L2,TIMP2,TP53,S1PR2,FGFR1,SMAD7,TMEM67,POLD1,MAPK14,LGALS1
E2F3B	Liver Cirrhosis	3.91E-01	mir-130,ADAM17,CTGF,F2R,TXLNA,PDE4A,TUBB,ADRB3,LBR,FGFR3,NOTCH2,TIMP1,FBLN1,ADK,ADA,TOP2A,GCLM,NFE2L2,RASSF1,TP53,ATP7B,mir-199,TBC1D9,FGFR1,PTCH1,PCNA,BSG,CSF1,SREBF2,PDE5A,JAG1,HMGCR,WNT5A
E2F3B	Liver Damage	3.91E-01	mir-130,SOCS1,DDIT3,POLA1,TNFAIP3,FKBP1A,DICER1,POLB,POR,CXCL10,TGFBR2,GSTZ1,Gm21596/Hmgb1,SCARB1,TIMP1,STUB1,PPP3R1,ADK,IGF1R,JUND,GPX4,NFE2L2,RASSF1,TP53,STAT6,ATG5,mir-199,RDX,MAPK9,SOD1,POLD1,IRF1,BAK1,BCL2L1,MAPK14,BSG,DUSP1,CSF1,CDKN1A,HPRT1,HMGCR
E2F3B	Liver Inflammation/ Hepatitis	3.91E-01	mir-130,SOCS1,DDIT3,POLA1,PDE4A,PPIA,FKBP1A,TNFAIP3,POLB,GSTZ1,POR,CXCL10,STUB1,TIMP1,PPP3R1,ADK,CEBPA,IGF1R,BID,PEMT,NFE2L2,RASSF1,RHBDD3,TP53,STAT6,mir-199,MAPK9,SOD1,FANCC,POLD1,XIAP,FAIM,BCL2L1,RIPK1,CSF1,PDE5A,HPRT1,CYR61,HMGCR,CASP7
E2F3B	Liver Failure	3.91E-01	TP53,VEGFA,USP8,LARS,ADAM17,TIMP1,DUSP1,TOP2A,CEBPA,MARS,ADRB3,FAIM
E2F3B	Liver Dysfunction	3.91E-01	FDFT1,ATF6
E2F3B	Liver Degradation	3.91E-01	ADAR
E2F3B	Biliary Hyperplasia	5.20E-01	MYC
E2F3B	Liver Congestion	5.20E-01	HEY2
E2F3B	Liver Adhesion	5.20E-01	CTGF,SMAD3
E2F3B	Liver Edema	5.20E-01	VEGFA
E2F3B	Liver Hemorrhaging	5.38E-01	TAB2,DGCR8,BID,FKBP1A,TBK1,FAIM

Supplemental Table 6. Liver related IPA functions for E2F1, E2F3A and E2F3B promoter targets

ChIP-se	Category	B-H p-value	Genes
E2F3B	Liver Regeneration	5.92E-01	SOCS3,CCNE1,MAP2K7,CREM,TOB1,BIRC5,NFE2L2,CDK2,ATF2
E2F3B	Liver Cholestasis	6.11E-01	NFE2L2
E2F3B	Liver Steatosis	6.12E-01	PRKAB1,INSIG1,POLA1,FBXW7,RBL1,CCND1,ARNT,POLB,POR,GSTZ1,RORA,FASN,PRKCDBP,ATF4,IRS2,TP53,GPS2,FSTL3,ANGPTL6,LMNA,HBEGF,FANCC,MUT,PEX2,DUSP1,BHLHE40,IRS1,SSFA2,KDM3A,DDIT3,MARK2,GNA11,PDE4A,ATF6,ID1,MAN2C1,TIPARP,STEAP2,FOXO3,ADK,PEMT,SOD1,POLD1,FOXO1,H2AFY,CDKN1A,PDE5A,RBPJ,HMGCR
E2F3B	Hepatocellular Peroxisome Proliferation	6.69E-01	ABCD3,PEX16
E2F3B	Glutathione Depletion In Liver	7.27E-01	SMAD3

Supplemental Table 7. General IPA functions for E2F1, E2F3A and E2F3B promoter targets

ChIP-seq	Category	B-H p-value	Genes
E2F1	Cell Cycle	6.69E-32	NPM1,POLA1,FRMD6,XRCC2,Ewsr1,AJUBA,SMARCB1,WWOX,TSC2,SENP5,TCERG1,SAFB,AHCY,ETS1,GRK4,HCFC1,CCNE2,RFC1,TCF3,ZBTB5,RAD1,DAXX,RAD18,TINF2,ECT2,FANCA,PIM3,GADD45B,Calm1 (includes others),SMARCA4,DIABLO,RABL6,PELO,RBMX,PIK3C3,ARHGAP19,EXO1,KHDRBS1,GAS1,ARID3A,MCM3,BUB1,KPNB1,ARPP19,MSH2,FBXO5,ACTL6A,CDKN2A,KIF23,SOCS3,YWHAH,RGPD4 (includes others),SMC1A,INTS3,E2F6,AK1,CHMP2A,JUND,ESCO2,SETD8,WEE1,DNA2,RAD54L,AURKA,CDCA2,BCL2L1,DDA1,H3F3A/H3F3B,mir-210,SF3B4,CEP76,RMI2,STK33,KIAA0101,SKA2,BARD1,PIAS1,RNASEH2B,NEDD1,ZNF219,E2F3,PTGES3,LSM2,STUB1,TRIP13,TACC3,LRRC40,RACGAP1,SMARCE1,BIRC5,FANCL,PPM1G,CENPI,E2F7,KLF5,CKS1B,BRCA2,ING1,TUBA1B,CCP110,CEP120,MTBP,PLRG1,DSTN,UBR2,mir-148,RAN,RBL1,XRCC1,CD2AP,CHMP2B,TAOK2,DNMT1,PABPC1,PRR11,HIRA,SEPT7,MTF2,CKAP2,HMGA1,JUNB,CDAN1,CDK19,SGOL1,NEK2,HAUS6,FYN,NCAPD3,CDT1,BTG3,CUL1,GPX1,TRIO,HMGB2,CNTROB,SF3B3,GPR3,RINT1,CETN3,CREB1,RFC2,CEP152,PPIF,BANP,OSBPL9,SPC25,TIAL1,SMC6,PLCG1,MDM2,PLK1,TSG101,CDK1,NCAPG2,RRM1,MUM1,CIRBP,MMS19,CEP192,RBBP6,PRPF19,PFN1,ARF1,VPRBP,FBXW7,YWHAQ,GSPT1,PPP1R7,STAG1,NCAPH,FASN,SNU13,FOSL2,STIL,GJA1,CASP3,NUBP1,BIRC6,RAC1,CDC123,HERC2,PALB2,NASP,Cdc42,SMC2,RPS15A,LFNG,UVRAG,CDK5RAP2,CDK2,PA2G4,GADD45G,SETDB2,MRE11A,DTYMK,UHRF2,TRIM24,POLR2A,NFYA,GMNN,SIPA1,Pvr,CDCA5,IPO5,RASSF1,CALR,NRAS,UHRF1,SNRPB,HAT1,UBE3A,PRMT1,NCAPH2,NR1H2,HMG20B,RPS27L,MIS12,CASP8AP2,MYH10,MAGED1,MYH9,DSN1,SMC5,Ubb,HAUS4,ODC1,C6orf89,STAG3,RUVBL2,IQGAP3,TP53,TYMS,ESPL1,SKP2,HSPA8,ATE1,CCNF,GTSE1,BTG2,NEK4,TFRC,INVS,XRCC5,FANCM,DEK,AKAP8,CDK4,PRPF4,NUF2,MMS22L,KSR1,SPAG5,CDKN3,ARF6,MAP4,DAB2,HJURP,KIF2C,NFE2L2,CDC5L,RAD21,DHX9,PRKDC,PHF6,MAPRE1,GNA12,CUL7,HNRNPD,TDRKH,MLF1,NCAPD2,PES1,CCNE1,TUBA1A,CDKN1A,SPICE1,RAD51AP1,AKAP1,DLGAP5,MAP3K11,MSH3,GNB2L1,RFWD3,BAG3,SMC4,AP2A2,RARG,TGFBR2,MYC,LEMD3,RHOB,RCC1,PIM1,XPO1,FIGNL1,PDCD6,CEP131,MYBL2,CHTF18,E4F1,TAB1,NUCKS1,CLASP1,USP28,NBEAL2,SMC3,PELP1,KANK2,PNN,KIF4A,ORC6,HELLS,BUB1B,KMT2A,CBX1,PIAS4,TAF1,GIPC1,DUSP1,RECQL4,XRCC6,MAD1L1,NDC80,PKMYT1,KLHL21,ACTN4,ARID1A,GTF2I,RAD50,RAD51,CDC25B,CCNA2,SHC1,FANCD2,NET1,RAD17,OPA1,NAMPT,MCM9,RPS3,SUDS3,PRKCA,HAUS8,SLC9A3R1,TUBG1,PRDM4,FOXM1,PSME3,RPA2,NBN,MAPK14,PRKCI,CACUL1,KIF5B,RAD9A,MSH6,ZNF346,CDC34,WNK1,KIF18A,CENPF,PCGF2,CDC7,SFPQ,CDKN2C,HES1,PHACTR4,CHAF1A,INTS7,MXD3,EZR,TARDBP,IRS2,CEP250,ANAPC11,CENPJ,TIMP2,TIPIN,NDRG1,TOPBP1,FANCG,COPS5,SNAI1,RPA1,FANCC,UBE2S,RAD51D,CCNO,NSMCE2,GAB1,H2AFX,E2F1,MBD4,CHKA,AHCTF1,RGL2,MSH5,CLSPN,HELB,MAPK7,CYR61,YEATS4,AZI2,VASH2,FN1,WWTR1,HMGN1,NUP214,CAMK2N2,CHEK1,ID1,YY1,MTOR,BANF1,DAP3,CEBPA,TOP2A,E2F5,PRKCE,STIM1,MCPH1,HEXIM1,POT1,ZWILCH,NUDCD3,LETM1,DCK,CDC6,POLD1,FADD,KITLG,CHCHD3,RAD54B,KIF15,mir-30,SF3B2,NUP153,SPDYA,MCM2,PDXP,KIF20B,CENPA,FEN1,ZFP36L2,HINFP,SEPT2,FZD7,POLH,BIRC2,FZR1,ORC2,MCM8,ERCC6,MAPK1,DIAPH3,AURKB,TUBB,LMNB1,ROCK2,STMN1,SRSF1,WRN,EZH2,HTRA2,BRCA1,RAD51C,CDC25A,KIF14,Ftx,CDC37,RBL2,GPS2,SNRNP27,STK11,RANBP1,TMOD3,SSRP1,FOXC1,TPX2,SRSF3,SEL1L,CASC5,TOB2,CCNG2,RNF4,PKD1,ZFR,CASP2,GNL3,TMPO,Paxip1,JTB,CEP55,RFC3,INCENP,XRCC3,CHD4,MEIS2,NUMB,TAOK1,BCAR1,Tpm2,Ppp1cc,SP1,PMF1/PMF1-BGLAP,CIT,TCP1,ARSB,BLM,E2F8,TAF6,ATG10,PRKAR2A,MAPK9,ING3,USP1,XIAP,GNAI2,NUP62,LGALS1,MCM7

Supplemental Table 7. General IPA functions for E2F1, E2F3A and E2F3B promoter targets

ChIP-seq	**Category**	**B-H p-value**	**Genes**
E2F1	DNA Replication, Recombination, and Repair	2.10E-26	NPM1,POLA1,XRCC2,Ewsr1,SMARCB1,TSC2,SAFB,CCNE2,HCFC1,RFC1,TCF3,OGG1,RAD1,DAXX,EYA3,RAD18,TRIAP1,ECT2,FANCA,BAG6,PPIA,MTCH1,WRNIP1,SMARCA4,DIABLO,PELO,RBMX,ARHGAP19,ATN1,EXO1,HIST2H3D,POLG2,ENDOV,BUB1,MCM3,MSH2,MAZ,FBXO5,CDKN2A,KIF23,SOCS3,SMC1A,INTS3,E2F6,CHMP2A,ESCO2,SETD8,WEE1,DNA2,RAD54L,AURKA,CDCA2,OLA1,BCL2L1,DDA1,H3F3A/H3F3B,GINS1,POLL,CEP76,SF3B4,HIRIP3,POLD2,PPAT,KIAA0101,SKA2,BARD1,RNASEH2B,NEDD1,ZNF219,IQGAP1,E2F3,LSM2,HDGF,TRIP13,TACC3,LRRC40,RACGAP1,SMARCD1,BIRC5,PPM1G,FANCL,CENPI,CKS1B,BRCA2,ING1,MCM6,CCP110,CEP120,MTBP,PLRG1,RAN,mir-148,RBL1,FAN1,XRCC1,CHMP2B,TAOK2,DNMT1,PABPC1,HIRA,HMGA1,RNF168,CDAN1,SGOL1,NEK2,FYN,NCAPD3,CDT1,UVSSA,GPX1,CUL1,NRF1,STRA13,TRIO,HMGB2,CNTROB,EIF4G1,SF3B3,NEIL3,RINT1,CREB1,RFC2,ORC1,DUT,CEP152,TRIM28,SPC25,TIAL1,SMC6,PLCG1,PLK1,MDM2,NAP1L1,TSG101,NCAPG2,CDK1,RRM1,SENP1,MUM1,MMS19,CEP192,RBBP6,WDR48,PFN1,PRPF19,VPRBP,FBXW7,PBK,HIST1H4F,HIST1H4A,HIST1H4C,PPP1R7,STAG1,NCAPH,HIST1H4J,HIST1H3J,AAGAB,SNU13,HIST1H3F,STIL,GJA1,CASP3,POLE2,HIST1H3H,NUBP1,MTA2,RAC1,HERC2,PALB2,NASP,Cdc42,BRAT1,TIMELESS,SMC2,UVRAG,CDK5RAP2,CDK2,BRD2,EXOG,GADD45G,SETDB2,MRE11A,SET,GMNN,CDCA5,IPO5,RASSF1,DNASE1L1,CALR,NRAS,UHRF1,SNRPB,HAT1,PHLDA3,NCAPH2,PRMT1,DSCC1,RPS27L,MIS12,MYH10,RNF8,DSN1,SMC5,SLX1A/SLX1B,ODC1,STAG3,RUVBL2,UNG,TP53,TYMS,ASF1B,ESPL1,PCGF6,RRM2,CDCA4,SKP2,ATE1,HSPA8,SUPT16H,CCNF,BTG2,NEK4,XRCC5,FANCM,DEK,AKAP8,CDK4,SPRTN,PRPF4,BCL11B,NUF2,MMS22L,SPAG5,KSR1,CDKN3,HJURP,KIF2C,RAD21,DHX9,PRKDC,HNRNPU,GNA12,POLG,NCAPD2,SLC29A1,CCNE1,MEF2D,CDKN1A,VMP1,SPICE1,POLA2,UBTF,RAD51AP1,CASP7,DLGAP5,HELQ,MSH3,SLF2,RFWD3,SMC4,MYC,TGFBR2,RCC1,PIM1,FIGNL1,XPO1,CEP131,MYBL2,BRIP1,E4F1,HUWE1,SMC3,USP28,KANK2,KIF4A,ORC6,HELLS,BUB1B,PIAS4,TFAM,DUSP1,RECQL4,XRCC6,NDC80,MAD1L1,PIDD1,ARID1A,UBE2N,HIST2H4B,GTF3A,RAD50,RAD51,CDC25B,CCNA2,SHC1,FANCD2,NET1,RAD17,DNAJB1,MCM9,RPS3,SUDS3,LONP1,C10orf88,PRKCA,XRN2,TUBG1,FOXM1,PSME3,NBN,RPA2,FAM111A,MAPK14,KIF5B,RAD9A,MSH6,KIF18A,FANCI,CENPF,TGFBR3,CDC7,SFPQ,CDKN2C,CHAF1A,INTS7,TARDBP,IRS2,CENPJ,TIMP2,TIPIN,TOPBP1,FANCG,COPS5,SNAI1,RPA1,FANCC,RAD51D,CCNO,PTBP1,NSMCE2,BSG,GAB1,H2AFX,E2F1,MBD4,MSH5,CLSPN,HELB,MAPK7,CYR61,FN1,TCEA1,SUV39H2,ALKBH7,HMGN1,CHEK1,ID1,YY1,MTOR,BANF1,ADK,TOP2A,EIF3A,CEBPA,E2F5,NAA60,MCPH1,POT1,ZWILCH,AIFM1,NUDCD3,DCK,CDC6,POLD1,SIN3A,FADD,KITLG,RAD54B,CHCHD3,SPDYA,SF3B2,mir-30,MCM2,CENPA,ASCC3,FEN1,RBPJ,HINFP,POLH,FZR1,ORC2,MCM8,ERCC6,MAPK1,AURKB,ROCK2,POLD3,WRN,PMS1,EZH2,PRND,NIPBL,INIP,RAD51C,BRCA1,KLF2,CDC25A,Ftx,KIF14,RBL2,STK11,MACROD1,SNRNP27,TBP,SSRP1,TPX2,CCNG2,RNF4,ARRB2,CASP2,BAZ1B,TMPO,Paxip1,INCENP,RFC3,OBFC1,XRCC3,ZBTB7A,CHD4,POLI,STXBP4,TAOK1,BCAR1,Ppp1cc,SP1,PMF1/PMF1-BGLAP,CIT,BLM,S1PR2,MAPK9,USP1,GNAI2,SMARCC1,LGALS1,MCM7

Supplemental Table 7. General IPA functions for E2F1, E2F3A and E2F3B promoter targets

ChIP-seq	Category	B-H p-value	Genes
E2F1	Cellular Assembly and Organization	9.12E-22	NPM1,KIF13B,AXIN1,POLA1,NUP133,PALM,XRCC2,GLB1,AJUBA,SMARCB1,TSC2,MAP1A,SAFB,ETS1,GRK4,HCFC1,CRKL,NUP107,SP4,DAXX,RAD18,TINF2,NPHP3,ECT2,BAG6,GNA11,GAK,HEXA,NUAK2,SMARCA4,PELO,PIK3C3,ARHGAP19,ATN1,EXO1,HIST2H3D,POLG2,BBIP1,BUB1,KPNB1,TMEM107,FBXO5,AP1G1,CDKN2A,KIF23,MPRIP,LHX2,YWHAH,MICALL2,RPGRIP1L,SMC1A,INTS3,CTSD,CHMP2A,ESCO2,SMG6,WEE1,DNA2,CEP68,RAD54L,AURKA,CDCA2,PTPRM,OLA1,BCL2L1,H3F3A/H3F3B,CEP76,COMMD1,NAGLU,HIRIP3,MAST3,ABCD1,DZIP1L,HPS5,RND1,KIZ,KIAA0101,RAB23,SKA2,BARD1,NEDD1,CSRP1,CLUAP1,IQGAP1,PTGES3,HDGF,TRIP13,TACC3,IPO4,RACGAP1,SMARCE1,NFATC4,BIRC5,ALS2,KLF5,BRCA2,ING1,CCP110,RAB5C,CEP120,MTBP,DSTN,RAN,PCDHGC3,POU3F2,Cyb5r3,RBL1,HOOK3,CD2AP,CHMP2B,CBFB,SPECC1L,TAOK2,RFX3,DNMT1,SEPT7,YWHAZ,SLC17A5,CKAP2,JUNB,ZMYM6,RAB31,DCTN6,RNF168,CDAN1,RTN4,SGOL1,NEK2,HAUS6,FYN,NCAPD3,CDT1,BTG3,LEMD2,CUL1,TMEM11,EMP2,TSGA10,NRF1,TRIO,HMGB2,CNTROB,AKAP11,RINT1,CC2D1A,CREB1,VCL,TCTN3,RGMB,NUP85,CEP164,MCMBP,CEP152,PDE4DIP,SPC25,SMC6,PLK1,MDM2,F3,TSG101,NCAPG2,CDK1,SENP1,CEP72,ATL2,MUM1,MMS19,CEP192,NCAM1,CLUH,FMNL3,PFN1,FARP1,ARF1,Wasl,UNC5B,MNS1,FBXW7,HIST1H4F,HIST1H4A,HIST1H4C,PPP1R7,STAG1,FASN,NCAPH,MID1IP1,HIST1H3J,HIST1H4J,HIST1H3F,Nolc1,GJA1,STIL,CASP3,HIST1H3H,NUBP1,MTA2,RAC1,MAPK8IP3,RALBP1,PALB2,NASP,Cdc42,ERP29,SMC2,UVRAG,CDK5RAP2,CDK2,KDM3A,BRD2,SETDB2,TMEM216,MRE11A,IPO9,GMNN,PHGDH,CDCA5,SORBS3,IFRD1,RASSF1,CALR,PAK4,NRAS,UHRF1,PANK2,SURF6,DOCK7,UBE3A,PRMT1,NCAPH2,SYNE3,MIS12,MYH10,RNF8,MYH9,SCLT1,DSN1,SMC5,Ubb,HAUS4,C21orf2,STK35,SLC9A1,Tmsb4x (includes others),Diap2,MRPL10,STAG3,RUVBL2,TP53,ASF1B,TUBGCP3,ESPL1,PCGF6,APPL2,SEMA5A,TPM3,MDM1,SKP2,HSPA8,FBXW8,CCNF,FSCN1,BTG2,GAPDH,PARD3,XRCC5,STRIP2,FANCM,DEK,PEX3,PLXNA3,CDK4,DNAJC13,CKAP4,BCL11B,NUF2,GAS2L3,MMS22L,LBR,KSR1,SPAG5,B4GALT7,ARF6,MAP4,TRIM27,TP53INP2,ALMS1,DAB2,HJURP,KIF2C,RAD21,DHX9,PRKDC,MAPRE1,GNA12,CUL7,TDRKH,NCAPD2,LAMB2,PES1,CCNE1,CDKN1A,DOPEY2,SH2B2,SPICE1,PLEKHA1,CEP41,AKAP1,MAOA,DLGAP5,NCDN,RFWD3,SMC4,TIMM50,PEX11B,BAG3,TLN1,TGFBR2,MYC,IFT140,STK4,LEMD3,RHOB,RCC1,PIM1,PACS2,XPO1,CEP131,CLASP1,SMC3,SYNE2,KANK2,KIF4A,ORC6,HELLS,RBFOX2,BUB1B,SLC3A2,PIP5K1A,RFX4,CBX1,TFAM,PIAS4,MATN2,XRCC6,MAD1L1,NDC80,LMNB2,HSP90AA1,Gm15807/Hmgn5,INPP5K,ACTN4,RBBP4,TMEM138,ARID1A,UBE2N,HIST2H4B,RAD50,HNRNPK,CDC25B,RAD51,CCNA2,SHC1,FANCD2,NET1,OPA1,TOR1B,RPS3,SUDS3,MCM9,LONP1,ARC,PRKCA,ARHGAP33,CAPZB,HAUS8,SLC9A3R1,TUBG1,EMD,CANX,FOXM1,ATL3,GAN,RPA2,NBN,PRKCI,MAPK14,RAD9A,KIF5B,EHD4,CEP70,KIF18A,CENPF,TOR1A,CDC7,SFPQ,PHACTR4,RICTOR,CHAF1A,EZR,TARDBP,CEP250,CENPJ,MEX3C,NDRG1,FANCG,RPA1,FANCC,RAD51D,CCNO,NR1D1,GAB1,BSG,H2AFX,E2F1,HPRT1,LRP8,CYR61,FN1,SUV39H2,WWTR1,HMGN1,CHEK1,ID1,YY1,MTOR,ACAP2,CEBPA,TOP2A,NAA60,PRKCE,MAP1LC3A,MCPH1,TBCD,FAM109A,POT1,AIFM1,RPS19,FMN1,NUDCD3,LETM1,ACTB,CDC6,TOR1AIP2,KITLG,CHCHD3,ZNF516,MCM2,KIF20B,CENPA,ADAM10,SEPT2,ZMYM4,FZR1,MCM8,ERCC6,PTPN23,MAPK1,DIAPH3,TUBB,AURKB,LMNB1,STMN1,ROCK2,WRN,LPAR2,NIPBL,HTRA2,INIP,BRCA1,ARHGAP24,DLC1,KLF2,FARP2,SSNA1,Ftx,KIF14,RBL2,NUP155,ULK4,STK11,RAB8A,RANBP1,TMOD3,SSRP1,FOXC1,BAG4,TPX2,RNF4,CCNG2,PKD1,CORO1B,SNX1,BAZ1B,KATNB1,INCENP,OBFC1,GDI1,XRCC3,NFIX,CHD4,Pcnt,COX10,PKM,NUMB,RAPGEF6,TAOK1,BCAR1,ROR2,SP1,PMF1/PMF1-BGLAP,CIT,ARSB,RHOF,BLM,ACTN1,S1PR2,MAPK9,GCC2,XIAP,GNAI2,KIF24,LPAR1,DYM,PJA2,NUP62,RTN3,WNT5A

Supplemental Table 7. General IPA functions for E2F1, E2F3A and E2F3B promoter targets

ChIP-seq	Category	B-H p-value	Genes
E2F1	Gene Expression	1.13E-21	RNF139,NPM1,AXIN1,POLA1,GSK3A,POR,EIF3B,AJUBA,TSC2,SMARCB1,WWOX,TCERG1,SAFB,SARNP,ETS1,HCFC1,NKIRAS2,RANBP3,RFC1,ZBTB5,TCF3,OGG1,SP4,DAXX,TRIAP1,ECT2,EIF3K,PRDX4,PPIA,SMARCA4,TIPARP,KDM6A,RBMX,ATN1,GTF2H3,KHDRBS1,DHX36,NCBP1,ARID3A,NR1D2,MSH2,MAZ,WBP2,RPL37,TFB1M,CDKN2A,SOCS3,LHX2,YWHAH,SFMBT1,ZFP36L1,CBX5,E2F6,MATR3,JUND,SETD8,RAD54L,BAMBI,LZTR1,PHRF1,CAND1,H3F3A/H3F3B,POLR2E,FOXP4,LITAF,KLF10,PIAS1,RNASEH2B,ZNF219,ZNF226,E2F3,IQGAP1,PDCD10,PTGES3,HDGF,TOM1L1,STUB1,WDTC1,TRIP13,GTF3C4,SMARCE1,NFATC4,BIRC5,HTATSF1,E2F7,KLF5,BRCA2,BRPF1,ING1,UBR2,GTF2E2,POU3F2,RBL1,EEF1D,CTDSP1,SNIP1,CBFB,RFX3,DNMT1,CNOT1,HIRA,YWHAZ,MTF2,CKAP2,JUNB,MBD2,HMGA1,MED12,EAPP,ARHGAP35,FYN,SNAI2,GSTM5,BTG3,CUL1,GPX1,POLR2J,STRA13,NRF1,HMGB2,EIF4G1,H2AFZ,RNPS1,CC2D1A,CREB1,TRIM16,HMG20A,PSPC1,RGMB,BANP,SUZ12,TRIM28,PLCG1,TIAL1,PLK1,MDM2,NAP1L1,TRIM37,TSG101,CDK1,SENP1,MORF4L2,CCDC85B,MMS19,RBBP6,NCAM1,PFN1,Klf16,VPRBP,FBXW7,YWHAQ,MID1IP1,FOSL2,MCM5,GJA1,HSPA9,MTA2,RAC1,RALBP1,Cdc42,WHSC1L1,ERP29,TIMELESS,SBNO2,CDK2,CDK5RAP2,CREBL2,KDM3A,BRD2,PA2G4,GADD45G,MRE11A,ZMIZ1,SET,ZFP90,GTF2B,TRIM24,POLR2A,NFYA,GMNN,PHGDH,SORBS3,IFRD1,YLPM1,DHX15,RASSF1,CALR,DAP,MYCBP,NRAS,Bhlhe41,UHRF1,TCF7L1,UBE3A,ZNF382,PIAS3,FAF1,RPS4Y1,PTPRU,NR1H2,HIVEP1,RPS27L,CBFA2T2,EIF3L,LANCL2,RNF8,MAGED1,SLC9A1,ODC1,CABIN1,Tmsb4x (includes others),EGR2,Diap2,MPHOSPH8,FBLN1,ETF1,ATF4,RUVBL2,TARBP2,IQGAP3,MAP3K2,TP53,APPL2,PCGF6,KLF13,CDCA4,NDNL2,HSPA8,EIF4H,CNOT7,SUPT16H,MRPL17,BTG2,BBS7,NEK4,GAPDH,SUMO2,HIST1H1D,PARD3,Zfp568,RBM39,XRCC5,DEK,HNRNPA2B1,CTDSPL,BCL11B,MED28,HOXC9,LRRFIP1,RITA1,OGT,IRF2BP1,TRIM27,TP53INP2,SOS1,DAB2,JADE1,BTAF1,CDC5L,NFE2L2,RAD21,DHX9,PRKDC,HNRNPU,N4BP2L2,PPP2R5D,GNA12,MRPL12,POLG,MLF1,HNRNPD,ST3GAL3,Zfp53,CCNE1,GTF2H4,MEF2D,MBD3,CDKN1A,TCF19,LBH,UBTF,MAP3K3,ILF3,MAP3K11,GNB2L1,NFATC2IP,RARG,AP2A2,MYC,TGFBR2,LEMD3,STK4,ZHX1,RHOB,PIM1,EIF3D,PPP3R1,XPO1,MYBL2,BRIP1,E4F1,KLF11,TAB1,ITGB3BP,EIF4B,SMC3,NBEAL2,PELP1,GABPB2,KANK2,ZNF706,HELLS,RBFOX2,BRD8,ATAD2,KMT2A,RFX4,GMEB2,HNRNPAB,TAF1,CBX1,PIAS4,TFAM,MLXIP,DUSP1,XRCC6,MAD1L1,Gm15807/Hmgn5,FZD5,ACTN4,INPP5K,ZGPAT,ARID1A,UBE2N,GTF2I,ABCF1,TAF7,GTF3A,GTF2A1,IGF2BP1,HNRNPK,MIER1,CDC25B,CCNA2,SHC1,SP3,NAMPT,DNAJB1,SUDS3,RPS3,PRKCA,TAF12,SLC20A1,ENY2,RFX1,RPRD1B,DRG1,TUBG1,PRDM4,SENP2,FOXM1,PSME3,NBN,PRKCI,MAPK14,PHF19,RAD9A,SNAPC2,SLC19A2,WFS1,GZF1,CENPF,MZF1,PCGF2,GTF3C2,TGFBR3,SOX12,CDKN2C,SFPQ,HES1,RICTOR,CHAF1A,NCOA7,MXD3,ZNF367,THRAP3,MTF1,EZR,TARDBP,MED21,Zfp748,HEY2,CENPJ,TOPBP1,COPS5,SNAI1,NUFIP1,RPA1,PTBP1,GAB1,NR1D1,ZNF202,H2AFX,E2F1,GNB2,AHCTF1,LRP8,HELB,MAPK7,CYR61,L3MBTL2,HIST1H1C,AZI2,FN1,TCEA1,ATF7,WWTR1,SUV39H2,HMGN1,ZNF143,SP2,SGMS1,SLBP,WTAP,ID1,MTOR,YY1,DHPS,DAP3,TOP2A,E2F5,CEBPA,SOCS2,PRKCE,HEXIM1,RXRB,SARS,GLMN,RQCD1,DLX1,SIN3A,KITLG,FADD,CHCHD3,ZNF516,mir-30,LIMS1,NOP2,Rbmxl1,RBPJ,SUPT3H,ZFP36L2,HINFP,FZD7,TAF15,BIRC2,SND1,ORC2,ERCC6,MAPK1,TFG,NR2F2,FNIP2,AURKB,LOC102724828/MRPL23,ROCK2,FGFR3,NCOA5,WRN,LPAR2,ASXL2,EZH2,UCHL5,SIAH2,NIPBL,PUF60,BRCA1,CIPC,KLF2,SFR1,RBL2,NONO,GPS2,STK11,TBP,EIF2S3,SNW1,FOXC1,SSRP1,Scaf1,EPRS,RNF4,ARRB2,PKD1,LCORL,EIF4A3,NFYC,TMPO,TAGLN2,ZBTB7A,NFIX,MED23,CHD4,PKM,MEIS2,TNFAIP3,PRKAG1,ROR2,NFX1,NLK,ZBED3,SP1,PMF1/PMF1-BGLAP,MAML3,ATF6B,RBM15,BLM,NFYB,E2F8,NACA,TAF6,RPL30,MAPK9,RPS6KA5,NFKBIZ,XIAP,HIVEP2,AFF1,ZBTB48,PBX3,LPAR1,NUP62,SMARCC1,WNT5A,LGALS1,MCM7

Supplemental Table 7. General IPA functions for E2F1, E2F3A and E2F3B promoter targets

ChIP-seq	Category	B-H p-value	Genes
E2F1	Cellular Growth and Proliferation	7.40E-21	RNF139,NPM1,AXIN1,POLA1,PALM,FRMD6,GSK3A,POR,XRCC2,EIF3B,GLB1,AJUBA,TSC2,SMARCB1,WWOX,SAFB,AHCY,ETS1,RGS19,CCNE2,PEAK1,NKIRAS2,CRKL,RFC1,ZBTB5,TCF3,OGG1,DAXX,RAD18,ALCAM,TINF2,ELMO2,ECT2,FANCA,PIM3,GADD45B,mir-331,BAG6,PRDX4,GNA11,GAK,PPIA,MTCH1,SMARCA4,FXR2,DIABLO,RABL6,PELO,KDM6A,PIK3C3,KHDRBS1,GAS1,TUBB4B,IGF2R,ARID3A,MCM3,BUB1,MSH2,MAZ,WBP2,TOE1,ACTL6A,KIF23,CDKN2A,SOCS3,MPRIP,MICALL2,ZFP36L1,RSL1D1,RPGRIP1L,RGPD4 (includes others),SMC1A,CD164,E2F6,CTSD,JUND,SETD8,WEE1,BAMBI,AURKA,PTPRM,CDCA2,BCL2L1,H3F3A/H3F3B,mir-210,POLL,PPAT,ALG14,SUMO3,LITAF,RND1,KIAA0101,KLF10,PIAS1,BARD1,RNASEH2B,CSRP1,GPHN,IQGAP1,E2F3,PDCD10,SEMA4C,PTGES3,TOM1L1,HDGF,STUB1,NDUFV1,TACC3,RACGAP1,SMARCE1,NFATC4,G3BP1,STK3,ALS2,BIRC5,PPM1G,FANCL,E2F7,KLF5,CKS1B,BRCA2,BRPF1,ING1,SLC25A5,EFEMP2,HNRNPL,CEP120,MTBP,mir-148,RAN,POU3F2,RBL1,EEF1D,HIST1H2AB,XRCC1,CD2AP,PTP4A2,URGCP,SNIP1,CBFB,DNMT1,GET4,Irx5,ANGPTL6,YWHAZ,MTF2,MBD2,HMGA1,JUNB,SSR1,SH3GL1,EAPP,RTN4,CDK19,NEK2,FYN,SNAI2,BTG3,CDT1,B3GNT2,LEMD2,EMP2,CUL1,GPX1,POLR2J,STRA13,NRF1,TRIO,HMGB2,EIF4G1,SF3B3,H2AFZ,GPR3,NEIL3,HK2,CREB1,TXNL1,VCL,FKBP5,ORC1,WSB1,PPIF,SUZ12,HDGFRP2,TRIM28,USPL1,TIAL1,PLCG1,MDM2,PLK1,NAP1L1,SCAF11,COPS3,TSG101,F3,DUSP14,CDK1,RRM1,SENP1,CCDC85B,CIRBP,GCAT,RBBP6,NCAM1,WDR48,PRPF19,PFN1,VPRBP,ARF1,Wasl,UNC5B,FBXW7,AMD1,PBK,YWHAQ,STAG1,FASN,AAGAB,FOSL2,MCM5,STIL,GJA1,CASP3,HSPA9,NUBP1,MTA2,RAC1,BIRC6,CDC123,NDUFAF2,MAT2B,RALBP1,CMC2,HERC2,Cdc42,NASP,BRAT1,TIMELESS,RPS15A,UVRAG,CDK2,FADS1,KDM3A,SH3BP4,SPRED1,PA2G4,GADD45G,TXLNA,MRE11A,DTYMK,ZMIZ1,SET,UHRF2,GTF2B,TRIM24,NFYA,GMNN,SIPA1,OAZ1,Pvr,CDCA5,GTPBP1,DHX15,RASSF1,EXOSC2,CALR,DAP,PAK4,MYCBP,NRAS,Bhlhe41,UHRF1,HAT1,SURF6,DOCK7,UBE3A,MTAP,PRMT1,PIAS3,TMEM2,NR1H2,PTPRU,Sf1,MYH10,MAGED1,MYH9,SCLT1,RASL10A,DNAJC3,SLC9A1,ODC1,C6orf89,RCL1,Tmsb4x (includes others),EGR2,FBLN1,COPS6,ATF4,RUVBL2,MGAT1,MAP3K2,GNE,TYMS,TP53,PDIA5,ESPL1,APPL2,SEMA5A,RRM2,TPM3,SCAMP4,KLF13,CDCA4,SKP2,HSPA8,NDNL2,FBXW8,MICU1,EIF4H,CNOT7,CCNF,FSCN1,BTG2,FADS2,ANAPC5,GAPDH,HIST1H1D,TFRC,SUMO2,ATP6V0E1,XRCC5,PRDX2,PLXNA3,HNRNPA2B1,CDK4,CTDSPL,BCL11B,HOXC9,MED28,LRRFIP1,LBR,KSR1,CDKN3,OGT,B4GALT7,ARF6,TRIM27,ALMS1,SOS1,DAB2,KIF2C,NFE2L2,RAD21,DHX9,PRKDC,PHF6,MEMO1,HNRNPU,GNA12,MAPRE1,CUL7,POLG,HNRNPD,SLC29A1,LAMB2,PES1,CCNE1,TUBA1A,AIMP2,MEF2D,SH2B2,MBD3,EIF4A1,CDKN1A,CCT7,VMP1,SHMT1,TCF19,PLEKHA1,MSRA,UBTF,MAP3K3,PPIL1,CASP7,MAOA,DLGAP5,ILF3,NCDN,MAP3K11,MSH3,GNB2L1,TLN1,NUDC,RARG,MYC,TGFBR2,LEMD3,STK4,FDFT1,SAE1,RHOB,PIM1,PPP3R1,FAM83B,FIGNL1,PDCD6,CEP131,MYBL2,CNOT6,BRIP1,E4F1,KLF11,EIF4B,HUWE1,PGK1,HNRNPF,USP28,SMC3,PELP1,GABPB2,KANK2,PNN,RBFOX2,HELLS,BUB1B,SNX3,TUSC3,ATAD2,KMT2A,SLC3A2,CBLB,PIP5K1A,HNRNPAB,TFAM,CBX1,GCNT1,GIPC1,DUSP1,RC3H1,RECQL4,CDCA7L,XRCC6,LMNB2,HSP90AA1,MAD1L1,FZD5,SYN3,INPP5K,FAM83D,ACTN4,PIDD1,RBBP4,RPSA,B2M,DCBLD2,ZGPAT,ARID1A,UBE2N,GTF2I,MCFD2,TAF7,RAD50,IGF2BP1,HNRNPK,MIER1,CDCA7,CDC25B,TRA2A,RAD51,CCNA2,SHC1,SP3,FANCD2,NET1,NOP58,RAD17,OPA1,NAMPT,STX4,DNAJB1,MCM9,LONP1,PRKCA,ARHGAP33,SLC20A1,NDUFAF4,SDC1,RFX1,SLC9A3R1,RPRD1B,XRN2,CHERP,PRDM4,EMD,SENP2,CNOT8,MTHFD1,FOXM1,PSME3,HNRNPM,NBN,PDAP1,CISD1,MAPK14,PRKCI,CACUL1,RAD9A,EHD4,WNK1,KIF18A,CENPF,MZF1,PCGF2,ARV1,TGFBR3,CDC7,SFPQ,CDKN2C,ZNF451,ERI1,HES1,RICTOR,NEU1,RUSC1,MXD3,THRAP3,EZR,TARDBP,HADHB,KARS,OSMR,IRS2,HEY2,APEX2,CENPJ,THEM4,TIMP2,HNRNPA0,TIPIN,NDRG1,TOPBP1,COPS5,SNAI1,RPA1,FANCC,CTPS1,C9orf69,CCNO,PLA2G6,PTBP1,NR1D1,VKORC1,RFC4,GAB1,BSG,YARS,H2AFX,E2F1,CHKA,HPRT1,RGL2,CLSPN,MAPK7,CYR61,YEATS4,CAPZA1,VASH2,ADAM17,FN1,DUSP6,WWTR1,ZNF143,HMGN1,NUP214,RTKN2,CAMK2N2,SP2,TAX1BP3,SGMS1,CHEK1,WTAP,TRIB1,ID1,YY1,MTOR,DHPS,ADK,DGCR8,TOP2A,DAP3,E2F5,EIF3A,CEBPA,NAA60,PRKCE,SOCS2,STIM1,MCPH1,HNRNPH2,HEXIM1,RXRB,POT1,GLMN,AIFM1,RPS19,NUDCD3,DCK,ACTB,CDC6,SIN3A,FADD,KITLG,KIF15,SF3B2,SPDYA,mir-30,MCM2,RBM6,LIMS1,KIF20B,NOP2,ASCC3,CENPA,ADAM10,RBPJ,FEN1,DNPH1,ZFP36L2,SCAMP3,FZD7,POLH,BIRC2,FZR1,SND1,MCM8,OSTF1,ERCC6,TFG,MAPK1,INSIG1,NR2F2,TUBB,AURKB,LMNB1,ROCK2,FGFR3,STMN1,NCOA5,SRSF1,SIVA1,WRN,LPAR2,EZH2,DLST,BRCA1,ARHGAP24,KLF2,DLC1,Fus,CDC25A,ATP5G2,KIF14,CDC37,RBL2,GPS2,CCDC134,STK11,TBP,PSMC4,RAB8A,RANBP1,SNW1,FOXC1,BAG4,TPX2,SRSF3,SEL1L,TOP1MT,ARRB2,TOB2,RNF4,CCNG2,CORO1B,PKD1,CASP2,SNX1,PTPRS,EXTL3,GNL3,AK2,TMPO,Paxip1,JTB,YTHDF2,CMC4,TAGLN2,RFC3,XRCC3,ZBTB7A,NFIX,CHD4,PKM,NUMB,PPP1CB,TNFAIP3,STXBP4,NAA10,Tpm2,BCAR1,ROR2,HSP90B1,HNRNPR,SP1,PCK2,MANF,MAML3,TCP1,LTBP4,RBM15,BLM,ACTN1,E2F8,NACA,NDUFAF3,TAF6,S1PR2,ATG10,PRKAR2A,MAPK9,RPS6KA5,USP1,FDXR,XIAP,AFF1,ZBTB48,GNAI2,EXOC4,PBX3,LPAR1,PJA2,NUP62,PAQR4,HMGCR,SHMT2,MCM7,LGALS1,WNT5A

Supplemental Table 7. General IPA functions for E2F1, E2F3A and E2F3B promoter targets

ChIP-seq	Category	B-H p-value	Genes
E2F1	Cell Death and Survival	8.21E-21	NPM1,AXIN1,GSK3A,FRMD6,POR,XRCC2,Ewsr1,EIF3B,TSC2,SMARCB1,WWOX,VAMP3,TCERG1,SAFB,ETS1,GRK4,CRKL,RFC1,TCF3,OGG1,RAD1,DAXX,EYA3,RAD18,ALCAM,TRIAP1,ECT2,NDST1,FANCA,PIM3,Calm1 (includes others),GADD45B,mir-331,PRDX4,BAG6,GNA11,PPIA,MTCH1,NUAK2,SMARCA4,DIABLO,RABL6,PIK3C3,EXO1,ATN1,SDHA,KHDRBS1,GAS1,IGF2R,BUB1,KPNB1,TMEM107,MSH2,FBXO5,RPL37,TFB1M,AP1G1,ACTL6A,CDKN2A,SOCS3,MPRIP,PCDH18,YWHAH,LHX2,ZFP36L1,NUP58,RSL1D1,CBX5,SMC1A,RGPD4 (includes others),INTS3,CTSD,CD164,E2F6,AK1,CHMP2A,MPHOSPH9,COQ6,SNRPD1,SNN,JUND,WDR4,SETD8,STXBP1,WEE1,ASNA1,BAMBI,RAD54L,AURKA,PTPRM,CDCA2,BCL2L1,GINS1,POLL,mir-210,NAGLU,SLC25A10,PPAT,ABCD1,KIAA0101,KLF10,BARD1,PIAS1,GPHN,IQGAP1,TEX10,E2F3,PDCD10,PTGES3,HDGF,STUB1,WBP1,TACC3,RACGAP1,ALKBH5,SMARCE1,HERPUD1,SMARCD1,NFATC4,STK3,ALS2,BIRC5,PPM1G,FANCL,TMEM109,TUBB6,CENPI,E2F7,KLF5,BRCA2,ING1,SLC25A5,RPLP0,CCP110,MTBP,PLRG1,UBR2,RAN,mir-148,PCDHGC3,MDH1,Cyb5r3,RBL1,EEF1D,XRCC1,CD2AP,PTP4A2,CBFB,TAOK2,DNMT1,YWHAZ,SLC17A5,CKAP2,HMGA1,JUNB,RTN4,ARHGAP35,CDK19,NEK2,FYN,SNAI2,GSTM5,BTG3,CDT1,GPX1,EMP2,CUL1,BOK,NRF1,HMGB2,EIF4G1,SF3B3,MCOLN1,STOM,HK2,RNPS1,RINT1,CC2D1A,CREB1,NUP205,VCL,FKBP5,NSMCE1,WSB1,RGMB,DUT,SUZ12,PPIF,TRIM28,SPC25,TIAL1,PLCG1,MDM2,PLK1,F3,C1orf159,TSG101,DUSP14,NCAPG2,CDK1,RRM1,SENP1,CTNNBL1,CIRBP,GPR180,RBBP6,NCAM1,WDR48,PFN1,PRPF19,VPRBP,UNC5B,FBXW7,PBK,YWHAQ,STAG1,FASN,ITPRIP,SLC25A23,FOSL2,BCKDK,P4HB,STIL,GJA1,CASP3,DDX19A,HSPA9,BIRC6,RAC1,MTA2,RALBP1,PALB2,Cdc42,BRAT1,HNRNPUL2,TBCCD1,CDK2,CREBL2,KDM3A,BRD2,EXOG,PA2G4,GADD45G,HIGD1A,MRE11A,MRPS30,DTYMK,SET,TRIM24,MAN2C1,UHRF2,POLR2A,NFYA,GMNN,ZNF280B,OAZ1,Pvr,IFRD1,RASSF1,DNASE1L1,CALR,PAK4,DAP,NRAS,UHRF1,HAT1,PHLDA3,AVPI1,TCF7L1,UBE3A,PRMT1,FAF1,PIAS3,NR1H2,CASP8AP2,LANCL2,RNF8,MAGED1,MYH9,RASL10A,DNAJC3,TMBIM6,SLC9A1,ODC1,SLX1A/SLX1B,CABIN1,ADH5,EGR2,HIGD2A,CERS5,FBLN1,ATF4,RUVBL2,UNG,MAP3K2,GNE,SHISA5,TYMS,TP53,ESPL1,BLVRA,RRM2,OPN3,TPM3,ANO6,KLF13,SKP2,NDNL2,HSPA8,ST3GAL1,BTG2,NEK4,INVS,TFRC,GAPDH,RPL10,PARD3,XRCC5,PRDX2,FANCM,DEK,FBXO10,AKAP8,Dleu2,CDK4,CTDSPL,TMEM214,TNFAIP8L1,RNF130,BCL11B,MED28,NUF2,MMS22L,THUMPD2,KSR1,SPAG5,CDKN3,OGT,ARF6,MAP4,TRIM27,ALMS1,ZFAND5,DAB2,DIS3,NFE2L2,RAD21,DHX9,PRKDC,DENND4A,HNRNPU,GNA12,CUL7,CDH6,TPK1,ST3GAL3,SLC29A1,LAMB2,SDF2L1,CCNE1,TUBA1A,MEF2D,EIF4A1,CDKN1A,CCT7,UBTF,MAP3K3,SGCD,CASP7,MAOA,AKAP1,ILF3,MAP3K11,MSH3,GNB2L1,TIMM50,PEX11B,BAG3,RARG,AP2A2,TGFBR2,MYC,FDFT1,STK4,RHOB,PIM1,PPP3R1,PACS2,FIGNL1,XPO1,PDCD6,MYBL2,CHTF18,BRIP1,E4F1,PPP1R15B,KLF11,ITGB3BP,CLASP1,EIF4B,HUWE1,SMC3,EBAG9,PELP1,KANK2,SAP30BP,HELLS,C9orf114,BUB1B,ATAD2,KMT2A,SLC3A2,CBLB,PIAS4,TFAM,DUSP1,GCNT1,CDCA7L,XRCC6,SORCS2,MAD1L1,PKMYT1,NDC80,HSP90AA1,INPP5K,ACTN4,PIDD1,RBBP4,RPSA,B2M,MOB3A,ARID1A,UBE2N,MCFD2,RAD50,HNRNPK,IGF2BP1,CDC25B,RAD51,SHC1,CCNA2,SP3,FANCD2,NET1,NOP58,RAD17,CABLES2,OPA1,NAMPT,DNAJB1,SUDS3,MCM9,RPS3,LONP1,GMFB,C10orf88,PRKCA,ARC,NDUFAF4,SLC20A1,SDC1,HAUS8,EMD,CANX,SENP2,FOXM1,PSME3,NBN,MAPK14,PRKCI,IRF2BP2,RAD9A,SLC33A1,ZNF622,EHD4,COX5A,MSH6,ZNF346,CDC34,SLC19A2,WFS1,KIF18A,CENPF,MZF1,PCGF2,TGFBR3,COX8A,CDC7,SFPQ,CDKN2C,HES1,RICTOR,FANCB,MXD3,MTF1,EZR,MED21,SHQ1,TARDBP,HNRNPUL1,IRS2,KMT2B,CENPJ,TIMP2,UPF2,NDRG1,TOPBP1,FANCG,COPS5,SNAI1,PDRG1,RPA1,FANCC,UBE2S,RAD51D,PLA2G6,PI4K2A,VKORC1,NR1D1,GAB1,BSG,YARS,H2AFX,E2F1,MBD4,TMX1,GNB2,AHCTF1,CHKA,MSH5,HPRT1,CLSPN,LRP8,HELB,MAPK7,FH,CYR61,YEATS4,AZI2,HIST1H1C,VASH2,ADAM17,FN1,ATF7,DUSP6,HMGN1,CAMK2N2,SGMS1,CHEK1,WTAP,ID1,TRIB1,MTOR,YY1,BANF1,DCAF7,ADK,DGCR8,EIF3A,TOP2A,DAP3,CEBPA,PRKCE,SOCS2,MAP1LC3A,MCPH1,STIM1,HEXIM1,RXRB,PCBP2,POT1,AIFM1,EPG5,RPS19,NUDCD3,LETM1,DCK,TBC1D9,ACTB,CDC6,DLX1,MCU,SIN3A,FADD,KITLG,RAD54B,SPDYA,mir-30,MCM2,LIMS1,ASCC3,CENPA,FEN1,RBPJ,ZFP36L2,GLS2,BIRC2,POLH,FZR1,SND1,ORC2,MCM8,ERCC6,PTPN23,MAPK1,INSIG1,FNIP2,TUBB,AURKB,LMNB1,VDAC2,STMN1,ROCK2,FGFR3,SRSF1,NCOA5,SIVA1,WRN,LPAR2,EZH2,DLST,PRND,HTRA2,SIAH2,NAA16,INIP,PUF60,BRCA1,RAD51C,KLF2,DLC1,SFR1,CDC25A,KIF14,RBL2,CDC37,PAFAH2,GPS2,STK11,TBP,PSMC4,SNW1,CCT6A,RANBP1,TMOD3,SSRP1,BAG4,TPX2,DPP9,GSR,SEL1L,CASC5,RNF4,ARRB2,PKD1,ZFR,EIF4A3,CASP2,GNL3,Paxip1,KATNB1,INCENP,TAGLN2,XRCC3,ZBTB7A,NFIX,CHD4,Pcnt,PKM,NUMB,SLC7A1,PPP1CB,TNFAIP3,POLI,TAOK1,BCAR1,PRKAG1,ROR2,HSP90B1,NLK,Ppp1cc,SP1,PCK2,MANF,CIT,TCP1,C11orf31,ARSB,BLM,STK40,E2F8,TAF6,S1PR2,ATG10,MAPK9,RPS6KA5,ING3,PSMA1,NFKBIZ,XIAP,FDXR,FAU,AFF1,FDPS,GNAI2,PBX3,LPAR1,NUP62,SMARCC1,HMGCR,SHMT2,MCM7,LGALS1,WNT5A

Supplemental Table 7. General IPA functions for E2F1, E2F3A and E2F3B promoter targets

ChIP-seq	Category	B-H p-value	Genes
E2F1	RNA Post-Transcriptional Modification	1.06E-18	HNRNPL,NPM1,PCBP1,AHCYL1,PLRG1,SFPQ,RPL35A,RCL1,INTS7,THRAP3,TARDBP,HNRNPUL1,TCERG1,SAFB,RNGTT,PABPC1,HNRNPA0,PAPOLA,HCFC1,NUFIP1,Srrm1,PTBP1,WDR83,CPSF3L,SRSF4,RBM39,HNRNPA2B1,PRPF4,SF3B3,SRSF10,WTAP,ZRSR2,SCAF4,RNPS1,RBMX,KHSRP,SARS,CDC5L,DIS3,SNRNP40,RPS19,HNRNPU,KHDRBS1,NCBP1,SRSF11,HNRNPD,MAGOH,SCAF11,PES1,CLK4,SF3B2,RPS16,DDX39B,RBM6,Rbmxl1,USP49,CSTF3,INTS8,CDKN2A,PRPF19,INTS3,SRSF1,CPSF6,TSEN54,SNRPD1,HNRNPF,NONO,PPIG,PNN,SNRPF,TBP,SNW1,RBFOX2,PHRF1,Scaf1,SRSF3,SRSF7,SF3B4,DDX39A,IWS1,BARD1,CPSF1,RRP36,HNRNPK,TRA2A,POLR2A,CSTF2T,FARS2,NOP58,GEMIN4,TRNT1,DBR1,EXOSC2,TRA2B,NOP56,XRN2,ALKBH5,HNRNPM,RPS15,NUDT21,SNRNP70,HNRNPH3

Supplemental Table 7. General IPA functions for E2F1, E2F3A and E2F3B promoter targets

ChIP-seq	Category	B-H p-value	Genes
E2F1	Cancer	1.28E-18	RNF139,C1orf52,AJUBA,GLB1,WWOX,ZCCHC8,SMARCB1,SENP5,ETS1,RFC1,HIST1H2BM,EYA3,ALCAM,TMEM43,ELMO2,RTFDC1,PIM3,SLC1A5,RABL6,RBMX,PCNXL3,EXO1,ZKSCAN5,MTSS1L,CDS2,KPNB1,WBP2,TOE1,AP1G1,PIGU,IDI1,FBXO25,ZFP36L1,E2F6,SNRPD1,SMG6,CEP68,KCNAB2,PHRF1,NAGLU,ALDH18A1,POLD2,FAM134A,DZIP1L,STK33,NEDD1,CLUAP1,DENND6B,DDX27,GPHN,SEC14L1,HDGF,TBC1D1,STPG2,WDTC1,WBP1,FRA10AC1,TRIP13,TACC3,HERPUD1,TUBB6,CAMTA1,ING1,BRPF1,HNRNPL,MCM6,ZFP62,TAPT1,UBR2,ZNF436,POU3F2,PCDHGC3,GKAP1,XRCC1,ZFP41,ZNF395,HIST1H2AJ,CBFB,TTLL5,DNMT1,PABPC1,GET4,TMEM39B,HIRA,CNOT10,AP5Z1,MEX3A,RNF168,NCLN,ABHD8,SGOL1,HAUS6,CANT1,CPSF2,NCAPD3,CDT1,LEMD2,EMP2,GPX1,CUL1,TSGA10,TRIO,GPR3,HK2,RINT1,RNPS1,TICRR,RFC2,TXNL1,VCL,TCTN3,NCBP3,FKBP5,ORC1,ZNF526,CEP152,BANP,USPL1,SMC6,TSG101,COPS3,TRIM37,RHOBTB1,NCAPG2,RRM1,ZNF546,SENP1,CEP72,C8orf33,MUM1,NIPSNAP3A,KDELR3,DUS3L,NCAM1,PNO1,RPUSD2,FAM208A,YWHAQ,SSR3,TMEM230,KHNYN,PPP1R7,SLC25A23,RPRD2,GOLGA1,BIRC6,ATP10A,CDC123,MAT2B,NDUFAF2,NIN,BRAT1,C15orf41,KBTBD8,FADS1,IWS1,MRE11A,MAN2C1,POLR2A,DSCR3,FBXL19,SURF6,TCF7L1,FAF1,PTPRU,HMG20B,THOC7,SYNE3,TTC7A,MTRF1L,H2AFV,TEX9,C17orf80,DDHD2,WDR90,PCBP1,WDR20,DLK2,ZFYVE1,SKIV2L,ZC3H12C,ZNF689,COPS6,TUBGCP3,APPL2,FAM118A,SCAMP4,ATE1,MORC2,PPOX,GTSE1,ANAPC5,RPL10,CEP95,FRG1,ANKLE1,STRIP2,FKBP2,FANCM,DEK,AP2A1,FBXO7,ARL4C,HNRNPA2B1,ODF2L,CDK4,CTDSPL,SPRTN,KIAA0754,MED28,BCL11B,NUF2,THUMPD2,TMEM209,CDKN3,ZRSR2,OGT,GINS2,MAP4,PRR14L,DCUN1D4,FAM227A,TP53INP2,FAM73B,SOS1,ALG8,CDC5L,RAD21,DENND4A,N4BP2L2,YKT6,NOL9,CDH6,LARP4B,RCCD1,LAMB2,ABCF2,GTF2H4,MEF2D,EIF4A1,C6orf62,MSRA,UBTF,PPIL1,FOXN2,MEGF9,HELQ,RARG,TGFBR2,MYC,AHDC1,RHOB,PPP3R1,AMOTL2,PACS2,FIGNL1,CNOT6,KLF11,EIF4B,USP28,TEX264,KANK2,SAP30BP,FAM64A,BLVRB,DDOST,RBFOX2,CMSS1,BTBD8,BRD8,WDYHV1,RFX4,PIP5K1A,GMEB2,USP32,GIPC1,XRCC6,RAB26,CDCA7L,SEPT10,SORCS2,NDC80,HSP90AA1,MAD1L1,NCKAP5L,SYN3,FZD5,ACTN4,RBBP4,QRICH1,NEURL4,SPTSSA,TRA2A,DNAJC4,FYTTD1,NOP58,MEX3B,ACAD8,STX4,RPS3,VARS,BTBD10,ARHGAP33,POMT2,RFX1,HAUS8,MORN1,DRG1,CANX,NMT2,NFKBIL1,PSME3,SPINK13,CCDC34,FAM111A,MAPK14,RIOK2,RAD9A,RAB36,ARPP21,HNRNPH3,ZNF451,CDKN2C,ERI1,PHACTR4,FANCB,ZNF367,MTF1,HNRNPUL1,EEFSEC,HEY2,KMT2B,TMEM55B,FANCG,GPATCH8,PDRG1,FANCC,ZNF414,RFC4,PI4K2A,ZNF202,E2F1,MSH5,HELB,YEATS4,AZI2,RTKN2,SGMS1,TRIB1,IFRD2,POLR2M,E2F5,ABHD2,PRKCE,NAA60,TBCD,ZWILCH,SAMD14,EPG5,TOR1AIP2,ATXN2L,PCDH9,RPIA,POLD1,WDR76,KIF15,mir-30,RBM6,FEN1,DNPH1,USP49,POLH,OSTF1,INSIG1,DPY19L4,EZH2,PRND,CPNE2,RBL2,PSMC4,RANBP1,TMOD3,DPP9,GSR,ABHD17C,PTPRS,C1orf27,PFAS,TMPO,GDI1,MEIS2,NUP50,TAOK1,GANAB,RSRP1,CENPP,ADAL,PMF1/PMF1-BGLAP,CIT,OXCT1,LTBP4,ARSB,RHOF,S1PR2,ATG10,MDGA1,ANAPC13,GNAI2,KIF24,GFOD1,DYM,SNRNP70,PAQR4,SMARCC1,LRR1,ACAT2,POLA1,NUP133,SMARCD2,EIF4A2,GSK3A,SECISBP2,Ewsr1,EIF3B,MAP1A,SAFB,FAM172A,AHCY,SARNP,GRK4,HCFC1,RGS19,NKTR,MSMO1,TAT,RGP1,GART,RAD1,DAXX,CNTRL,MB21D2,COX18,ECT2,NDST1,CCDC138,FANCA,HERPUD2,EIF3K,IRAK1BP1,BAG6,GNA11,SERHL2,MTCH1,SMARCA4,FXR2,C16orf72,PNRC1,C2CD5,HIST2H3D,FKBP3,KPNA3,GAS1,POLG2,DHX36,NCBP1,VPS26A,IGF2R,RPS16,CHAC1,COX7A2,FBXO5,TFB1M,RAB14,NAV2,MPRIP,YWHAH,LHX2,MICALL2,NUP58,RGPD4 (includes others),SMC1A,CTSD,CHMP2A,SETD8,COL19A1,STXBP1,WEE1,ASNA1,BAMBI,AURKA,HEATR3,CDCA2,PTPRM,DYNLRB1,OSBPL8,KIAA0907,CAND1,HIRIP3,SLC25A10,FOXP4,ABCD1,ALG14,LITAF,RND1,DDX26B,KIAA0101,BARD1,ZNF219,SPSB3,IQGAP1,SEMA4C,ZFAND2A,BCL7B,NAA40,NDUFV1,GTF3C4,RACGAP1,SMARCD1,NFATC4,BIRC5,MTO1,UMPS,ALS2,FANCL,KLF5,C19orf47,ZDHHC6,CERCAM,DEPDC1B,MTBP,PLRG1,DSTN,RAN,GTF2E2,Cyb5r3,RBL1,RPS11,EEF1D,HIST1H2AB,PLPP5,CD2AP,MPV17L2,SNIP1,CNOT1,DNAJB12,SNX13,ANGPTL6,SEPT7,YWHAZ,CKAP2,MTF2,MON2,MBD2,JUNB,MED12,RAB31,LARGE,UBE2G2,AAAS,MYO9A,CDAN1,DNAJC14,RTN4,CPSF3L,CDK19,NEK2,FYN,PRRC2A,KLHL18,CEP78,GSTM5,BTG3,B3GNT2,NRF1,STRA13,HMGB2,KANSL3,AAMP,C9orf89,EIF4G1,CORO2B,SF3B3,ATAD5,AKAP11,STOM,CETN3,RAB33B,CC2D1A,CREB1,HMG20A,NUP205,GNB1L,DTWD2,SUZ12,OSBPL9,SPC25,C2orf44,TIAL1,PLCG1,MDM2,MAGEB1,SCAF11,CDK1,NHLRC2,GLTP,CCDC85B,ATL2,CTNNBL1,CHRAC1,SLC25A11,CIRBP,MMS19,SAAL1,WDR48,FARP1,ARF1,VPRBP,UNC5B,CNNM2,SPRED2,TTLL12,FASN,HEXDC,TMUB2,HIST1H3J,FOSL2,TSPAN4,HIST1H3F,MCM5,GJA1,P4HB,TRIOBP,CASP3,ACOT13,POLE2,HIST1H3H,NUBP1,MUT,HYLS1,STARD4,Cdc42,TIMELESS,RFX2,TSNAXIP1,CDK2,CREBL2,BRD2,SH3BP4,EXOG,PA2G4,GADD45G,TMEM216,SET,IPO9,CSTF2T,GMNN,TTC16,PHGDH,TRNT1,OAZ1,CDCA5,SORBS3,GTPBP1,IFRD1,GOT2,IPO5,DHX15,EXOSC2,DNASE1L1,PAK4,MYCBP,SNRPB,TRA2B,UHRF1,PANK2,COTL1,DOCK7,RFC5,MTAP,PPP1R16A,SAMD4B,NR1H2,U2SURP,Sf1,RAVER1,CBFA2T2,HIST1H2AM,LANCL2,CASP8AP2,PRR12,CAB39L,SMC5,STK35,SNRNP48,MMGT1,MTHFD2,TARBP2,IQGAP3,SERBP1,C10orf76,ANO6,TPM3,GINS3,TBC1D14,HSPA8,TPST1,GALK1,BTG2,PCYOX1L,SRSF4,TSSC4,NUP188,PRDX2,CYP39A1,THADA,RNF130,HOXC9,GAS2L3,IRF2BP1,SLC16A10,RHBDL3,PRDM11,ST3GAL3,PES1,CLK4,TUBA1A,RIC8B,DOPEY2,VMP1,ZCWPW1,TCF19,SHMT1,SGCD,NUTF2,AKAP1,WRAP53,FOXRED1,DLGAP5,ILF3,CCDC15,PRELID3B,SLF2,STARD7,AP2A2,CLPP,KIF16B,BPGM,RFT

Supplemental Table 7. General IPA functions for E2F1, E2F3A and E2F3B promoter targets

ChIP-seq	Category	B-H p-value	Genes
E2F1	Organismal Injury and Abnormalities	1.28E-18	RNF139,C1orf52,AJUBA,GLB1,WWOX,ZCCHC8,SMARCB1,SENP5,ETS1,RFC1,HIST1H2BM,EYA3,ALCAM,TMEM43,ELMO2,RTFDC1,PIM3,SLC1A5,RABL6,RBMX,PCNXL3,EXO1,ZKSCAN5,MTSS1L,CDS2,KPNB1,WBP2,TOE1,AP1G1,PIGU,IDI1,FBXO25,ZFP36L1,E2F6,SNRPD1,SMG6,CEP68,KCNAB2,PHRF1,NAGLU,ALDH18A1,POLD2,FAM134A,DZIP1L,STK33,NEDD1,CLUAP1,DENND6B,DDX27,GPHN,SEC14L1,HDGF,TBC1D1,STPG2,WDTC1,WBP1,FRA10AC1,TRIP13,TACC3,HERPUD1,TUBB6,CAMTA1,ING1,BRPF1,HNRNPL,MCM6,ZFP62,TAPT1,UBR2,ZNF436,POU3F2,PCDHGC3,GKAP1,XRCC1,ZFP41,ZNF395,HIST1H2AJ,CBFB,TTLL5,DNMT1,PABPC1,GET4,TMEM39B,HIRA,CNOT10,AP5Z1,MEX3A,RNF168,NCLN,ABHD8,SGOL1,HAUS6,CANT1,CPSF2,NCAPD3,CDT1,LEMD2,EMP2,GPX1,CUL1,POLR2J,TSGA10,TRIO,GPR3,HK2,RINT1,RNPS1,TICRR,RFC2,TXNL1,VCL,TCTN3,NCBP3,FKBP5,ORC1,ZNF526,CEP152,BANP,USPL1,SMC6,TSG101,COPS3,TRIM37,RHOBTB1,NCAPG2,RRM1,ZNF546,SENP1,CEP72,C8orf33,MUM1,NIPSNAP3A,KDELR3,DUS3L,NCAM1,PNO1,RPUSD2,FAM208A,YWHAQ,SSR3,TMEM230,KHNYN,PPP1R7,SLC25A23,RPRD2,GOLGA1,BIRC6,ATP10A,CDC123,MAT2B,NDUFAF2,NIN,BRAT1,C15orf41,KBTBD8,FADS1,IWS1,MRE11A,MAN2C1,POLR2A,DSCR3,FBXL19,SURF6,TCF7L1,FAF1,PTPRU,HMG20B,THOC7,SYNE3,TTC7A,MTRF1L,H2AFV,TEX9,C17orf80,DDHD2,WDR90,PCBP1,WDR20,DLK2,ZFYVE1,SKIV2L,ZC3H12C,ZNF689,COPS6,TUBGCP3,APPL2,FAM118A,SCAMP4,ATE1,MORC2,PPOX,GTSE1,ANAPC5,RPL10,CEP95,FRG1,ANKLE1,STRIP2,FKBP2,FANCM,DEK,AP2A1,FBXO7,ARL4C,HNRNPA2B1,ODF2L,CDK4,CTDSPL,SPRTN,KIAA0754,MED28,BCL11B,NUF2,THUMPD2,TMEM209,CDKN3,ZRSR2,OGT,GINS2,MAP4,PRR14L,DCUN1D4,FAM227A,TP53INP2,FAM73B,SOS1,ALG8,CDC5L,RAD21,DENND4A,N4BP2L2,YKT6,NOL9,CDH6,LARP4B,RCCD1,LAMB2,ABCF2,GTF2H4,MEF2D,EIF4A1,C6orf62,MSRA,UBTF,PPIL1,FOXN2,MEGF9,HELQ,KXD1,RARG,TGFBR2,MYC,AHDC1,RHOB,PPP3R1,AMOTL2,PACS2,FIGNL1,CNOT6,KLF11,EIF4B,USP28,TEX264,KANK2,SAP30BP,FAM64A,BLVRB,DDOST,RBFOX2,CMSS1,BTBD8,BRD8,WDYHV1,RFX4,PIP5K1A,GMEB2,USP32,GIPC1,XRCC6,RAB26,CDCA7L,SEPT10,SORCS2,NDC80,HSP90AA1,MAD1L1,NCKAP5L,SYN3,FZD5,ACTN4,RBBP4,QRICH1,NEURL4,SPTSSA,TRA2A,DNAJC4,FYTTD1,NOP58,MEX3B,ACAD8,STX4,RPS3,VARS,BTBD10,ARHGAP33,POMT2,RFX1,HAUS8,MORN1,DRG1,CANX,NMT2,NFKBIL1,PSME3,SPINK13,CCDC34,FAM111A,MAPK14,RIOK2,RAD9A,RAB36,ARPP21,HNRNPH3,ZNF451,CDKN2C,ERI1,PHACTR4,FANCB,ZNF367,MTF1,HNRNPUL1,EEFSEC,HEY2,KMT2B,TMEM55B,FANCG,GPATCH8,PDRG1,FANCC,ZNF414,RFC4,PI4K2A,ZNF202,E2F1,MSH5,HELB,YEATS4,AZI2,RTKN2,SGMS1,TRIB1,IFRD2,POLR2M,E2F5,ABHD2,PRKCE,NAA60,TBCD,ZWILCH,SAMD14,EPG5,TOR1AIP2,ATXN2L,PCDH9,RPIA,POLD1,WDR76,KIF15,mir-30,RBM6,FEN1,DNPH1,USP49,POLH,OSTF1,INSIG1,DPY19L4,EZH2,PRND,CPNE2,RBL2,PSMC4,RANBP1,TMOD3,DPP9,GSR,ABHD17C,PTPRS,C1orf27,PFAS,TMPO,GDI1,MEIS2,NUP50,TAOK1,GANAB,RSRP1,CENPP,ADAL,PMF1/PMF1-BGLAP,CIT,OXCT1,LTBP4,ARSB,RHOF,S1PR2,ATG10,MDGA1,ANAPC13,GNAI2,KIF24,GFOD1,DYM,SNRNP70,PAQR4,SMARCC1,LRR1,ACAT2,POLA1,NUP133,SMARCD2,EIF4A2,GSK3A,SECISBP2,Ewsr1,EIF3B,MAP1A,SAFB,FAM172A,AHCY,SARNP,GRK4,HCFC1,RGS19,NKTR,MSMO1,TAT,RGP1,GART,RAD1,DAXX,CNTRL,MB21D2,COX18,ECT2,NDST1,CCDC138,FANCA,HERPUD2,EIF3K,IRAK1BP1,BAG6,GNA11,SERHL2,MTCH1,SMARCA4,FXR2,C16orf72,PNRC1,C2CD5,HIST2H3D,FKBP3,KPNA3,GAS1,POLG2,DHX36,NCBP1,VPS26A,IGF2R,RPS16,CHAC1,COX7A2,FBXO5,TFB1M,ACTL6A,RAB14,NAV2,MPRIP,YWHAH,LHX2,MICALL2,NUP58,RGPD4 (includes others),SMC1A,CD164,CTSD,CHMP2A,SETD8,COL19A1,STXBP1,WEE1,ASNA1,BAMBI,AURKA,HEATR3,CDCA2,PTPRM,DYNLRB1,OSBPL8,KIAA0907,CAND1,HIRIP3,SLC25A10,FOXP4,ABCD1,ALG14,LITAF,RND1,DDX26B,KIAA0101,BARD1,ZNF219,SPSB3,IQGAP1,SEMA4C,ZFAND2A,BCL7B,NAA40,NDUFV1,GTF3C4,RACGAP1,SMARCD1,NFATC4,BIRC5,MTO1,UMPS,ALS2,FANCL,KLF5,C19orf47,ZDHHC6,CERCAM,DEPDC1B,MTBP,PLRG1,DSTN,RAN,GTF2E2,Cyb5r3,RBL1,RPS11,EEF1D,HIST1H2AB,PLPP5,CD2AP,MPV17L2,SNIP1,CNOT1,DNAJB12,SNX13,ANGPTL6,SEPT7,YWHAZ,CKAP2,MTF2,EXOSC8,MON2,MBD2,JUNB,MED12,RAB31,LARGE,UBE2G2,AAAS,MYO9A,CDAN1,DNAJC14,RTN4,CPSF3L,CDK19,NEK2,FYN,PRRC2A,KLHL18,CEP78,GSTM5,BTG3,B3GNT2,NRF1,STRA13,HMGB2,KANSL3,AAMP,C9orf89,EIF4G1,CORO2B,SF3B3,ATAD5,AKAP11,STOM,CETN3,RAB33B,CC2D1A,CREB1,HMG20A,NUP205,GNB1L,DTWD2,SUZ12,OSBPL9,SPC25,C2orf44,TIAL1,PLCG1,MDM2,MAGEB1,SCAF11,CDK1,NHLRC2,GLTP,CCDC85B,ATL2,CTNNBL1,CHRAC1,SLC25A11,CIRBP,MMS19,SAAL1,WDR48,FARP1,ARF1,VPRBP,MNS1,UNC5B,CNNM2,SPRED2,TTLL12,FASN,HEXDC,TMUB2,HIST1H3J,FOSL2,TSPAN4,HIST1H3F,MCM5,GJA1,P4HB,TRIOBP,CASP3,ACOT13,POLE2,HIST1H3H,NUBP1,MUT,HYLS1,STARD4,Cdc42,TIMELESS,RFX2,TSNAXIP1,CDK2,CREBL2,BRD2,SH3BP4,EXOG,PA2G4,GADD45G,TMEM216,SET,IPO9,CSTF2T,GMNN,TTC16,PHGDH,TRNT1,OAZ1,CDCA5,SORBS3,GTPBP1,IFRD1,GOT2,IPO5,DHX15,EXOSC2,DNASE1L1,PAK4,MYCBP,SNRPB,TRA2B,UHRF1,PANK2,COTL1,DOCK7,RFC5,MTAP,PPP1R16A,SAMD4B,NR1H2,U2SURP,Sf1,RAVER1,CBFA2T2,HIST1H2AM,LANCL2,CASP8AP2,PRR12,CAB39L,SMC5,STK35,SNRNP48,MMGT1,MTHFD2,TARBP2,IQGAP3,SERBP1,C10orf76,ANO6,TPM3,GINS3,TBC1D14,HSPA8,TPST1,GALK1,BTG2,PCYOX1L,SRSF4,TSSC4,NUP188,PRDX2,CYP39A1,THADA,RNF130,HOXC9,GAS2L3,IRF2BP1,SLC16A10,RHBDL3,PRDM11,ST3GAL3,PES1,CLK4,TUBA1A,RIC8B,DOPEY2,VMP1,ZCWPW1,TCF19,SHMT1,SGCD,NUTF2,AKAP1,WRAP53,FOXRED1,DLGAP5,ILF3,CCDC15,PRELID3B,SLF2,STARD7,AP2A2,

Supplemental Table 7. General IPA functions for E2F1, E2F3A and E2F3B promoter targets

ChIP-seq	Category	B-H p-value	Genes
E2F1	Gastrointestinal Disease	2.85E-15	RNF139,C1orf52,AJUBA,GLB1,SMARCB1,WWOX,ZCCHC8,ETS1,RFC1,HIST1H2BM,EYA3,ALCAM,ELMO2,RTFDC1,PIM3,SLC1A5,RABL6,RBMX,PCNXL3,EXO1,ZKSCAN5,MTSS1L,CDS2,KPNB1,TOE1,AP1G1,PIGU,IDI1,FBXO25,ZFP36L1,E2F6,SNRPD1,SMG6,CEP68,PHRF1,NAGLU,ALDH18A1,FAM134A,POLD2,DZIP1L,STK33,NEDD1,CLUAP1,DENND6B,DDX27,SEC14L1,HDGF,TBC1D1,STPG2,WDTC1,WBP1,TRIP13,FRA10AC1,TACC3,HERPUD1,TUBB6,CAMTA1,ING1,BRPF1,HNRNPL,MCM6,ZFP62,TAPT1,UBR2,POU3F2,PCDHGC3,GKAP1,XRCC1,ZNF395,CBFB,TTLL5,DNMT1,GET4,PABPC1,TMEM39B,HIRA,CNOT10,AP5Z1,MEX3A,RNF168,NCLN,ABHD8,SGOL1,HAUS6,CANT1,CPSF2,NCAPD3,LEMD2,GPX1,CUL1,TSGA10,TRIO,GPR3,HK2,RINT1,TICRR,RFC2,TXNL1,VCL,TCTN3,FKBP5,ORC1,CEP152,BANP,USPL1,SMC6,TRIM37,COPS3,TSG101,NCAPG2,RHOBTB1,RRM1,ZNF546,SENP1,CEP72,C8orf33,MUM1,KDELR3,DUS3L,NCAM1,RPUSD2,FAM208A,PPP1R7,TMEM230,KHNYN,SLC25A23,RPRD2,GOLGA1,BIRC6,ATP10A,CDC123,NIN,BRAT1,C15orf41,KBTBD8,FADS1,MRE11A,MAN2C1,FBXL19,TCF7L1,FAF1,PTPRU,HMG20B,THOC7,SYNE3,MTRF1L,H2AFV,C17orf80,WDR90,PCBP1,WDR20,SKIV2L,DLK2,ZC3H12C,TUBGCP3,APPL2,SCAMP4,ATE1,MORC2,PPOX,GTSE1,ANAPC5,RPL10,CEP95,ANKLE1,FRG1,STRIP2,FKBP2,FANCM,DEK,AP2A1,FBXO7,ODF2L,HNRNPA2B1,CDK4,SPRTN,KIAA0754,BCL11B,NUF2,THUMPD2,TMEM209,CDKN3,GINS2,OGT,MAP4,DCUN1D4,PRR14L,FAM227A,TP53INP2,FAM73B,SOS1,ALG8,CDC5L,RAD21,DENND4A,YKT6,N4BP2L2,NOL9,CDH6,LARP4B,RCCD1,LAMB2,ABCF2,MEF2D,EIF4A1,MSRA,UBTF,PPIL1,MEGF9,HELQ,RARG,MYC,TGFBR2,RHOB,AHDC1,AMOTL2,PACS2,FIGNL1,KLF11,EIF4B,USP28,TEX264,KANK2,SAP30BP,FAM64A,BLVRB,DDOST,CMSS1,BTBD8,BRD8,RFX4,PIP5K1A,GMEB2,GIPC1,RAB26,CDCA7L,XRCC6,SEPT10,MAD1L1,HSP90AA1,NCKAP5L,SYN3,FZD5,RBBP4,QRICH1,NEURL4,TRA2A,FYTTD1,DNAJC4,NOP58,MEX3B,ACAD8,VARS,BTBD10,ARHGAP33,POMT2,MORN1,HAUS8,RFX1,DRG1,CANX,NMT2,NFKBIL1,PSME3,CCDC34,FAM111A,MAPK14,RIOK2,RAD9A,ARPP21,HNRNPH3,ZNF451,CDKN2C,ERI1,PHACTR4,FANCB,ZNF367,MTF1,EEFSEC,HNRNPUL1,KMT2B,TMEM55B,FANCG,GPATCH8,PDRG1,ZNF414,FANCC,PI4K2A,RFC4,ZNF202,E2F1,MSH5,HELB,YEATS4,AZI2,RTKN2,SGMS1,TRIB1,IFRD2,POLR2M,E2F5,ABHD2,PRKCE,NAA60,TBCD,ZWILCH,EPG5,SAMD14,TOR1AIP2,ATXN2L,PCDH9,POLD1,WDR76,KIF15,mir-30,RBM6,FEN1,USP49,POLH,OSTF1,INSIG1,DPY19L4,EZH2,PRND,CPNE2,RBL2,RANBP1,TMOD3,DPP9,ABHD17C,GSR,PTPRS,C1orf27,PFAS,TMPO,GDI1,MEIS2,TAOK1,GANAB,RSRP1,CENPP,ADAL,CIT,OXCT1,LTBP4,ARSB,RHOF,S1PR2,ATG10,MDGA1,GNAI2,KIF24,GFOD1,DYM,SNRNP70,PAQR4,SMARCC1,LRR1,ACAT2,POLA1,NUP133,GSK3A,EIF4A2,SECISBP2,EIF3B,MAP1A,SAFB,FAM172A,SARNP,AHCY,GRK4,HCFC1,RGS19,NKTR,TAT,RGP1,GART,RAD1,CNTRL,DAXX,MB21D2,COX18,NDST1,CCDC138,ECT2,FANCA,HERPUD2,EIF3K,IRAK1BP1,BAG6,GNA11,MTCH1,SMARCA4,FXR2,C16orf72,PNRC1,C2CD5,KPNA3,DHX36,NCBP1,VPS26A,IGF2R,CHAC1,COX7A2,FBXO5,TFB1M,NAV2,RAB14,MPRIP,LHX2,YWHAH,MICALL2,NUP58,SMC1A,RGPD4 (includes others),CTSD,SETD8,COL19A1,STXBP1,WEE1,ASNA1,AURKA,HEATR3,PTPRM,CDCA2,OSBPL8,KIAA0907,HIRIP3,SLC25A10,FOXP4,ABCD1,DDX26B,KIAA0101,BARD1,ZNF219,IQGAP1,SEMA4C,ZFAND2A,BCL7B,NAA40,NDUFV1,GTF3C4,NFATC4,MTO1,BIRC5,UMPS,ALS2,FANCL,KLF5,C19orf47,ZDHHC6,MTBP,PLRG1,DSTN,RAN,GTF2E2,RBL1,EEF1D,CD2AP,MPV17L2,SNIP1,CNOT1,DNAJB12,SNX13,ANGPTL6,YWHAZ,CKAP2,MTF2,JUNB,MON2,MBD2,MED12,RAB31,UBE2G2,LARGE,AAAS,MYO9A,CDAN1,DNAJC14,CPSF3L,RTN4,CDK19,NEK2,PRRC2A,FYN,CEP78,GSTM5,BTG3,B3GNT2,NRF1,STRA13,HMGB2,KANSL3,AAMP,C9orf89,EIF4G1,CORO2B,SF3B3,ATAD5,AKAP11,STOM,CETN3,RAB33B,CC2D1A,CREB1,HMG20A,NUP205,GNB1L,SUZ12,OSBPL9,SPC25,C2orf44,PLCG1,TIAL1,MDM2,MAGEB1,SCAF11,CDK1,NHLRC2,GLTP,CHRAC1,CTNNBL1,ATL2,CIRBP,MMS19,SAAL1,WDR48,FARP1,VPRBP,ARF1,UNC5B,CNNM2,SPRED2,TTLL12,FASN,HEXDC,HIST1H3J,TMUB2,FOSL2,TSPAN4,HIST1H3F,MCM5,GJA1,P4HB,TRIOBP,CASP3,ACOT13,POLE2,NUBP1,HYLS1,MUT,TIMELESS,RFX2,TSNAXIP1,CDK2,BRD2,SH3BP4,EXOG,PA2G4,SET,IPO9,CSTF2T,GMNN,TRNT1,PHGDH,TTC16,OAZ1,CDCA5,SORBS3,GTPBP1,IFRD1,IPO5,PAK4,MYCBP,TRA2B,SNRPB,UHRF1,PANK2,COTL1,DOCK7,RFC5,MTAP,PPP1R16A,U2SURP,RAVER1,CBFA2T2,HIST1H2AM,CASP8AP2,PRR12,CAB39L,SMC5,STK35,SNRNP48,MMGT1,TARBP2,IQGAP3,SERBP1,C10orf76,ANO6,GINS3,TBC1D14,HSPA8,TPST1,PCYOX1L,TSSC4,NUP188,THADA,RNF130,HOXC9,GAS2L3,IRF2BP1,SLC16A10,RHBDL3,ST3GAL3,PES1,CLK4,TUBA1A,RIC8B,DOPEY2,VMP1,ZCWPW1,TCF19,SHMT1,AKAP1,WRAP53,DLGAP5,FOXRED1,ILF3,CCDC15,SLF2,STARD7,CLPP,AP2A2,KIF16B,NSUN6,IFT140,LEMD3,FDFT1,TNRC6C,PHF20,MITD1,MRPL46,NUCKS1,LACTB,TXNDC16,PGK1,NBEAL2,SYNE2,MYEF2,ZNF706,CLIP2,C9orf114,CBLB,CBX1,MLXIP,SRSF7,RNF219,SP9,PTPN21,DCBLD2,UBXN1,ZGPAT,SEC31A,ARID1A,TBC1D8B,TMEM60,ABCF1,FASTKD3,C14orf80,HNRNPK,MIER1,CDCA7,CDC25B,SHC1,POLR1C,FAM110A,WDFY3,RAD17,ENPP4,CABLES2,NAMPT,DNAJB1,MCM9,ARC,CAPZB,NMRAL1,PRDM4,ATL3,HNRNPM,WDR91,PSKH1,IRF2BP2,C2CD2,KIF5B,EHD4,ZNF622,THAP4,MSH6,QRSL1,CEP70,WNK1,GZF1,CENPF,MZF1,ARV1,TGFBR3,PCOLCE,CHAF1A,ZNF7,NEU1,RUSC1,EZR,TARDBP,KARS,CEP250,ANAPC11,TIMP2,CENPJ,PAPOLA,ARL6IP6,NDRG1,TOPBP1,RABL3,COPS5,NUFIP1,SNAI1,FNBP4,CTPS1,CRABP1,PTBP1,CCDC170,NSMCE2,TMX1,MBD4,AHCTF1,CHKA,HPRT1,CLSPN,MAPK7,SRD5A1,ALKBH7,CTNNA3,NUP214,XPOT,ID1,YY1,SLC2A6,DGCR8,CEBPA,MCPH1,MAP1LC3A,KIAA0391,HNRNPH2,KHSRP,RXRB,PCBP2,FAM109A,AIFM1,FMN1,DCK,DDX50,TBC1D9,ACTB,GINS4,

Supplemental Table 7. General IPA functions for E2F1, E2F3A and E2F3B promoter targets

ChIP-seq	Category	B-H p-value	Genes
E2F1	Organismal Survival	7.20E-15	NPM1,AXIN1,SECISBP2,POR,XRCC2,WWOX,SMARCB1,TSC2,SAFB,ETS1,AFMID,CCNE2,CRKL,TCF3,OGG1,SP4,DAXX,TINF2,RMRP,NDST1,ECT2,BAG6,GNA11,GAK,PPIA,HEXA,NUAK2,SMARCA4,PELO,TIPARP,KDM6A,ATN1,EXO1,KHDRBS1,POLG2,BBIP1,GAS1,DHX36,VPS26A,IGF2R,ARID3A,BUB1,TMEM107,MSH2,FBXO5,TFB1M,AP1G1,ACTL6A,CDKN2A,SOCS3,LHX2,ZFP36L1,RPGRIP1L,SC5D,RGPD4 (includes others),CTSD,E2F6,ESCO2,SETD8,COL19A1,STXBP1,ASNA1,DNA2,RAD54L,GNAZ,KCNAB2,AURKA,BCL2L1,H3F3A/H3F3B,GINS1,POLL,COMMD1,NAGLU,FOXP4,PIAS1,BARD1,CLUAP1,GPHN,PDCD10,E2F3,PTGES3,STUB1,TACC3,NFATC4,STK3,BIRC5,FANCL,KLF5,E2F7,CKS1B,BRCA2,ING1,EFEMP2,PLRG1,UBR2,RAN,POU3F2,PCDHGC3,RBL1,XRCC1,CD2AP,CBFB,RFX3,DNMT1,HMBS,SNX13,ANGPTL6,HIRA,MTF2,MED12,RAB31,SH3GL1,GAMT,RTN4,ARHGAP35,CDK19,FYN,SNAI2,GPX1,CUL1,NRF1,TRIO,H2AFZ,MCOLN1,HK2,RINT1,CC2D1A,CREB1,VCL,PDE4DIP,SUZ12,PPIF,TRIM28,PLCG1,TIAL1,MDM2,COPS3,F3,TSG101,CDK1,NCAPG2,SENP1,MORF4L2,RBBP6,NCAM1,PNO1,PRPF19,PFN1,VPRBP,Wasl,MNS1,FBXW7,AMD1,SPRED2,FASN,FOSL2,STIL,GJA1,CASP3,PPIG,NUBP1,MTA2,RHEBL1,BIRC6,RAC1,SLC25A37,MUT,MAPK8IP3,PALB2,Cdc42,NASP,TIMELESS,LFNG,SBNO2,CDK2,ZFAT,BRD2,SPRED1,ZMIZ1,POLR2A,NFYA,GMNN,PHGDH,RASSF1,CALR,PAK4,NRAS,UHRF1,TRA2B,HAT1,TCF7L1,MTAP,UBE3A,PRMT1,NR1H2,CBFA2T2,MYH10,MYH9,DNAJC3,SLC9A1,CABIN1,ADH5,EGR2,Tmsb4x (includes others),FBLN1,MTHFD2,ATF4,MGAT1,TARBP2,UNG,TP53,GNE,ESPL1,SEMA5A,TPM3,ATE1,FBXW8,CCNF,FSCN1,FADS2,TFRC,HIST1H1D,PARD3,XRCC5,FANCM,CDK4,BCL11B,CDKN3,ARF6,TRIM27,SOS1,DAB2,NFE2L2,DHX9,PRKDC,GNA12,CUL7,POLG,HNRNPD,LAMB2,PES1,CCNE1,MEF2D,EIF4A1,MBD3,CDKN1A,MSRA,SGCD,MAP3K3,CASP7,ILF3,MSH3,PEX11B,BAG3,TLN1,RARG,MYC,TGFBR2,FDFT1,STK4,LEMD3,EIF3D,PPP3R1,MYBL2,CHTF18,BRIP1,E4F1,PPP1R15B,TAB1,HUWE1,SYNE2,PNN,HELLS,C9orf114,BUB1B,KMT2A,SLC3A2,CBLB,RFX4,PIP5K1A,HNRNPAB,PIAS4,TFAM,DUSP1,RC3H1,XRCC6,RECQL4,MAD1L1,LMNB2,HSP90AA1,NDC80,FZD5,ACTN4,RPSA,B2M,ARID1A,UBE2N,GTF2I,TAF7,HNRNPK,IGF2BP1,RAD50,RAD51,CCNA2,SHC1,FANCD2,RAD17,DNAJB1,STX4,SUDS3,PRKCA,ARC,SLC20A1,POMT2,SDC1,CAPZB,SLC9A3R1,TUBG1,CANX,FOXM1,GAN,NBN,MAPK14,PRKCI,KIF5B,RAD9A,EHD4,MSH6,SLC19A2,MZF1,PCGF2,TGFBR3,TOR1A,CDC7,CDKN2C,ERI1,HES1,RICTOR,CHAF1A,MTF1,MED21,TARDBP,IRS2,HEY2,CENPJ,KMT2B,PITPNB,THEM4,TIMP2,UPF2,NDRG1,TOPBP1,FANCG,TKT,COPS5,SNAI1,RAD51D,CRABP1,PTBP1,PLA2G6,BSG,GAB1,VKORC1,H2AFX,E2F1,CHKA,AHCTF1,HPRT1,LRP8,MAPK7,CYR61,FH,HIST1H1C,ADAM17,FN1,TCEA1,ATF7,CTNNA3,HMGN1,SP2,SGMS1,SRSF10,CHEK1,ID1,MTOR,YY1,PTS,ADK,DGCR8,TOP2A,CEBPA,E2F5,MCPH1,STIM1,HEXIM1,KHSRP,RXRB,POT1,AIFM1,RPS19,Anp32e,ACTB,CENPU,DLX1,GINS4,POLD1,SIN3A,FADD,KITLG,RAD54B,MCM2,LIMS1,ADAM10,FEN1,RBPJ,ZFP36L2,MBD5,BIRC2,FZR1,ERCC6,MAPK1,INSIG1,MMP16,DIAPH3,NR2F2,AURKB,LMNB1,FGFR3,ROCK2,SRSF1,NCOA5,SIVA1,WRN,EZH2,SIAH2,HTRA2,RAD51C,BRCA1,DLC1,KLF2,Fus,CDC25A,RBL2,ULK4,STK11,PSMC4,TBP,RAB8A,TMOD3,SSRP1,SRSF3,PANK1,ARRB2,ZFR,PKD1,CASP2,SNX1,CNPY3,PTPRS,GNL3,EXTL3,Paxip1,INCENP,ZBTB7A,NFIX,MED23,PKM,NUMB,SLC7A1,TNFAIP3,BCAR1,ROR2,HSP90B1,SP1,CIT,MAML3,ATF6B,RBM15,DPH3,BLM,STK40,E2F8,SLC25A25,S1PR2,MAPK9,RPS6KA5,USP1,NFKBIZ,XIAP,AFF1,GNAI2,PBX3,LPAR1,NUP62,SMARCC1,HMGCR,SHMT2,WNT5A
E2F1	Embryonic Development	1.38E-14	NPM1,AXIN1,XRCC2,GLB1,AJUBA,SMARCB1,TSC2,MTHFD2,MGAT1,TP53,ETS1,CCNE2,ESPL1,TPM3,ATE1,DAXX,CCNF,BTG2,RAD18,TFRC,HIST1H1D,ECT2,XRCC5,CDK4,SMARCA4,KSR1,OGT,PELO,KDM6A,PIK3C3,ARHGAP19,SOS1,DAB2,NFE2L2,GAS1,POLG2,GNA12,CUL7,POLG,IGF2R,ARID3A,PES1,CCNE1,MTHFD1L,MSH2,CDKN1A,SHMT1,FBXO5,TFB1M,AP1G1,CDKN2A,SOCS3,LHX2,ZFP36L1,TLN1,RPGRIP1L,RARG,MYC,TGFBR2,STK4,TNRC6C,PIM1,PPP3R1,MYBL2,E4F1,PPP1R15B,ESCO2,SETD8,PNN,RAD54L,AURKA,C9orf114,KMT2A,BCL2L1,PIP5K1A,GINS1,RC3H1,COMMD1,LMNB2,FZD5,RPSA,NMT1,ARID1A,RAB23,CLUAP1,PDCD10,RAD50,SEMA4C,TOM1L1,RAD51,SHC1,SP3,RAD17,OPA1,DNAJB1,ARC,POMT2,TACC3,TUBG1,NFATC4,STK3,FOXM1,MTHFD1,BIRC5,NBN,MAPK14,SLC33A1,RAD9A,KIF5B,E2F7,KLF5,BRCA2,BRPF1,MZF1,PCGF2,PLRG1,UBR2,CDC7,CDKN2C,PHACTR4,HES1,RBL1,RICTOR,XRCC1,CHAF1A,MXD3,PTP4A2,MED21,IRS2,CBFB,HEY2,DNMT1,TIMP2,CENPJ,CNOT1,Irx5,NDRG1,TOPBP1,SNX13,ANGPTL6,TKT,COPS5,SNAI1,HIRA,MTF2,JUNB,HMGA1,MED12,GAB1,BSG,H2AFX,ARHGAP35,MAPK7,FYN,HIST1H1C,FN1,ATF7,TCEA1,WWTR1,SUV39H2,CUL1,HMGN1,NRF1,SP2,CHEK1,ID1,NEIL3,YY1,MTOR,HK2,RINT1,TRIM16,MCPH1,VCL,AIFM1,GLMN,RPS19,SUZ12,CENPU,PLCG1,TIAL1,MDM2,PLK1,F3,TSG101,COPS3,CDK1,KITLG,FADD,mir-30,MORF4L2,LIMS1,KIF20B,ADAM10,RBPJ,FEN1,ZFP36L2,RBBP6,NCAM1,PNO1,PFN1,PRPF19,MAPK1,DIAPH3,Wasl,FBXW7,AURKB,AMD1,LMNB1,FGFR3,ROCK2,WRN,EZH2,FASN,BRCA1,KLF2,DLC1,CDC25A,GJA1,RBL2,STIL,CASP3,STK11,TBP,BIRC6,PSMC4,RAC1,MAPK8IP3,FOXC1,SEL1L,SRSF3,PALB2,Cdc42,NASP,TIMELESS,PKD1,SNX1,LFNG,GNL3,Paxip1,CDK2,ZFAT,NUMB,ZMIZ1,ROR2,TRIM24,HSP90B1,NFYA,SP1,GMNN,PHGDH,MAML3,DPH3,BLM,E2F8,PAK4,S1PR2,NRAS,TRA2B,UHRF1,MAPK9,USP1,TCF7L1,LPAR1,LGALS1,WNT5A

Supplemental Table 7. General IPA functions for E2F1, E2F3A and E2F3B promoter targets

ChIP-seq	Category	B-H p-value	Genes
E2F1	Developmental Disorder	2.07E-13	RPL35A,POR,SKIV2L,XRCC2,EGR2,FBLN1,TSC2,WWOX,ATF4,MGAT1,TP53,GNE,TYMS,ETS1,CCNE2,ESPL1,CRKL,TPM3,TCF3,FBXW8,DAXX,CCNF,TFRC,HIST1H1D,TMEM43,RMRP,PARD3,ECT2,NDST1,FANCA,XRCC5,PIM3,AKAP8,mir-331,BAG6,CDK4,HEXA,HOXC9,NUAK2,SMARCA4,LBR,B4GALT7,PELO,KDM6A,PIK3C3,SOS1,DAB2,B3GALNT2,NFE2L2,RAD21,PHF6,HNRNPU,POLG2,GAS1,CUL7,POLG,HNRNPD,VPS26A,IGF2R,LAMB2,PES1,CCNE1,MTHFD1L,TUBA1A,TMEM107,CDKN1A,FBXO5,MSRA,POC1A,SGCD,AP1G1,CASP7,LHX2,ZFP36L1,RPGRIP1L,RARG,SC5D,SMC1A,MYC,TGFBR2,IFT140,FDFT1,E2F6,STK4,LEMD3,UFSP2,PIM1,MATR3,BRIP1,PPP1R15B,CLASP1,ESCO2,SETD8,HUWE1,SMC3,SYNE2,PNN,ORC6,DNA2,LZTR1,C9orf114,AURKA,KMT2A,BCL2L1,RFX4,H3F3A/H3F3B,RC3H1,RECQL4,mir-210,SMCHD1,COMMD1,SF3B4,LMNB2,ACTN4,RPSA,RAB23,E2F3,IGF2BP1,PTGES3,RAD51,POLR1C,FANCD2,DNAJB1,LONP1,ARC,SLC20A1,POMT2,TACC3,TUBG1,CANX,EMD,NFATC4,STK3,MTHFD1,BIRC5,PSME3,ALS2,FANCL,NBN,MAPK14,PRKCI,FAM111A,KIF5B,SLC33A1,KLF5,E2F7,BRCA2,FANCI,PLRG1,CEP120,PCGF2,TGFBR3,UBR2,mir-148,POU3F2,HES1,RBL1,CHAF1A,XRCC1,FANCB,CD2AP,MED21,SNIP1,CBFB,SPECC1L,SLC39A13,HEY2,RFX3,APEX2,CENPJ,KMT2B,CSRP2,FANCG,TKT,COPS5,SNAI1,HIRA,EXOSC8,FANCC,RAD51D,MED12,CRABP1,LARGE,SH3GL1,BSG,H2AFX,ARHGAP35,MAPK7,CANT1,HIST1H1C,SNAI2,FN1,ATF7,CDT1,GPX1,SP2,TAX1BP3,CHEK1,SRSF10,TRIB1,MCOLN1,ID1,MTOR,YY1,HK2,PTS,RAB33B,E2F5,CEBPA,MCPH1,STIM1,VCL,TCTN3,TBCD,RXRB,ORC1,EPG5,RPS19,FMN1,CEP152,SUZ12,ACTB,CDC6,CENPU,TIAL1,PLCG1,DLX1,MDM2,F3,COPS3,POLD1,FADD,mir-30,LIMS1,ADAM10,FEN1,RBPJ,RBBP6,MBD5,FZR1,PFN1,PRPF19,ERCC6,MAPK1,INSIG1,Wasl,MMP16,TMCO1,NR2F2,FBXW7,TUBB,LMNB1,FGFR3,TSEN54,FASN,EZH2,NIPBL,FOSL2,RAD51C,BRCA1,KLF2,CDC25A,RBL2,P4HB,STIL,GJA1,WDR34,CASP3,STK11,RAC1,PSMC4,BIRC6,RANBP1,MUT,FOXC1,SRSF3,PALB2,CASC5,NIN,NASP,PKD1,EIF4A3,CNPY3,PTPRS,SNX1,GNL3,LFNG,Paxip1,KATNB1,CDK5RAP2,MED23,NFIX,NUMB,PIGV,BCAR1,ROR2,HSP90B1,POLR2A,GMNN,PHGDH,DPH3,BLM,E2F8,RASSF1,CALR,PAK4,NRAS,TAF6,UHRF1,SNRPB,MAPK9,UBE3A,MTAP,GNAI2,PBX3,LPAR1,DYM,SMARCC1,WNT5A

Supplemental Table 7. General IPA functions for E2F1, E2F3A and E2F3B promoter targets

ChIP-seq	Category	B-H p-value	Genes
E2F1	Cellular Development	9.94E-13	NPM1,AXIN1,PALM,FRMD6,GSK3A,POR,XRCC2,Ewsr1,EIF3B,AJUBA,TSC2,SMARCB1,WWOX,SAFB,AHCY,RRAGC,ETS1,NKTR,RGS19,CCNE2,PEAK1,CRKL,RFC1,TCF3,SP4,DAXX,ALCAM,NDST1,ECT2,FANCA,PIM3,GADD45B,SLC1A5,mir-331,BAG6,PRDX4,GNA11,GAK,PPIA,SMARCA4,FXR2,DIABLO,RABL6,TIPARP,KDM6A,RBMX,PIK3C3,ARHGAP19,ATN1,KHDRBS1,GAS1,IGF2R,ARID3A,BUB1,AGPAT5,MSH2,WBP2,CDKN2A,SOCS3,LHX2,ZFP36L1,RSL1D1,CBX5,SMC1A,CD164,CTSD,JUND,ESCO2,GNAZ,KCNAB2,AURKA,PTPRM,CDCA2,OSBPL8,CAND1,BCL2L1,H3F3A/H3F3B,mir-210,POLL,SF3B4,PPAT,SUMO3,RND1,KIAA0101,RAB23,KLF10,PIAS1,BARD1,RNASEH2B,CSRP1,NUDT7,IQGAP1,E2F3,PDCD10,ZBTB24,SEMA4C,PTGES3,TOM1L1,HDGF,STUB1,TACC3,RACGAP1,SMARCE1,NFATC4,STK3,BIRC5,RPS15,E2F7,KLF5,CKS1B,BRCA2,BRPF1,ING1,HNRNPL,ZNF784,MTBP,UBR2,mir-148,RAN,POU3F2,RBL1,RPS11,EEF1D,CTDSP1,CHMP2B,SNIP1,CBFB,DNMT1,GET4,CNOT1,HIRA,YWHAZ,MTF2,MBD2,HMGA1,JUNB,MED12,SH3GL1,SUCO,RTN4,NEK2,FYN,SNAI2,CDT1,BTG3,LEMD2,GPX1,CUL1,STRA13,TRIO,HMGB2,EIF4G1,H2AFZ,NEIL3,HK2,CREB1,TRIM16,HMG20A,VCL,FKBP5,WSB1,PPIF,SUZ12,OSBPL9,HDGFRP2,TRIM28,PLCG1,MDM2,PLK1,NAP1L1,COPS3,TSG101,F3,CDK1,RRM1,SENP1,CCDC85B,CIRBP,GCAT,RBBP6,NCAM1,WDR48,PRPF19,PFN1,FARP1,VPRBP,ARF1,Wasl,UNC5B,FBXW7,SPRED2,AMD1,PBK,YWHAQ,HIST1H4F,HIST1H4A,HIST1H4C,STAG1,FASN,HIST1H4J,AAGAB,FOSL2,CYB5D2,GJA1,CASP3,NUBP1,MTA2,RAC1,BIRC6,NDUFAF2,MAT2B,MAPK8IP3,CMC2,OSTM1,HERC2,Cdc42,NASP,LFNG,SBNO2,CDK5RAP2,CDK2,CREBL2,ZFAT,SPRED1,DDX39A,PA2G4,GADD45G,ZMIZ1,SET,UHRF2,TRIM24,NFYA,SETD6,GMNN,SIPA1,PHGDH,OAZ1,Pvr,CDCA5,IFRD1,RASSF1,CALR,PAK4,MYCBP,NRAS,Bhlhe41,UHRF1,HAT1,DOCK7,TCF7L1,UBE3A,MTAP,NCAPH2,C19orf68,PRMT1,FAF1,PIAS3,TMEM2,NR1H2,PTPRU,HMG20B,TTC7A,CBFA2T2,MAGED1,RASL10A,SLC9A1,ODC1,ADH5,DLK2,Tmsb4x (includes others),EGR2,FBLN1,COPS6,ATF4,GNE,TYMS,TP53,PAPD4,ESPL1,SEMA5A,RRM2,TPM3,KLF13,CDCA4,SKP2,NDNL2,FBXW8,MICU1,EIF4H,CCNF,FSCN1,BTG2,GAPDH,HIST1H1D,TFRC,SUMO2,SRSF4,SPPL2A,XRCC5,PRDX2,DEK,HNRNPA2B1,CDK4,CTDSPL,DNAJC13,BCL11B,MED28,KSR1,CDKN3,OGT,B4GALT7,ARF6,TRIM27,ALMS1,TP53INP2,SOS1,DAB2,KIF2C,NFE2L2,RAD21,DHX9,PRKDC,PHF6,MEMO1,HNRNPU,N4BP2L2,GNA12,MAPRE1,CUL7,MLF1,LAMB2,CCNE1,TUBA1A,MEF2D,SH2B2,EIF4A1,CDKN1A,VMP1,SHMT1,LBH,UBTF,PPIL1,CASP7,DLGAP5,ILF3,MAP3K11,MSH3,GNB2L1,PEX11B,TLN1,RARG,MYC,TGFBR2,LEMD3,STK4,FDFT1,TNRC6C,RHOB,PIM1,AMOTL2,XPO1,FIGNL1,MYBL2,E4F1,TAB1,EIF4B,HUWE1,PGK1,USP28,SMC3,PELP1,IER2,HELLS,BRD8,ATAD2,KMT2A,SLC3A2,CBLB,PIP5K1A,TFAM,CBX1,GCNT1,DUSP1,RC3H1,RECQL4,XRCC6,LMNB2,HSP90AA1,MAD1L1,FZD5,INPP5K,ACTN4,B2M,DCBLD2,NMT1,ZGPAT,ARID1A,GTF2I,HIST2H4B,TAF7,IGF2BP1,HNRNPK,CDCA7,CDC25B,TRA2A,RAD51,CCNA2,SHC1,SP3,FANCD2,NET1,NOP58,OPA1,NAMPT,MCM9,LONP1,PRKCA,ARHGAP33,NDUFAF4,SDC1,CAPZB,RFX1,SLC9A3R1,RPRD1B,AP1S2,EMD,SENP2,FOXM1,PSME3,NBN,CISD1,MAPK14,PRKCI,PHF19,KIF5B,RAD9A,ARPP21,WNK1,CENPF,MZF1,PCGF2,TGFBR3,SFPQ,CDKN2C,ZNF451,HES1,RICTOR,MXD3,THRAP3,EZR,TARDBP,IRS2,HEY2,KMT2B,THEM4,TIMP2,MEX3C,NDRG1,TOPBP1,COPS5,SNAI1,RPA1,FANCC,PLA2G6,PTBP1,NR1D1,VKORC1,RFC4,GAB1,BSG,E2F1,AHCTF1,CHKA,RGL2,LRP8,MAPK7,CYR61,YEATS4,AZI2,VASH2,ADAM17,FN1,TCEA1,SUV39H2,DUSP6,WWTR1,HMGN1,RTKN2,CAMK2N2,SP2,SGMS1,CHEK1,TRIB1,ID1,YY1,MTOR,ADK,DGCR8,TOP2A,E2F5,EIF3A,CEBPA,SOCS2,PRKCE,MCPH1,STIM1,HNRNPH2,HEXIM1,SARS,RXRB,POT1,AIFM1,GLMN,RPS19,NUDCD3,DCK,ACTB,CDC6,RQCD1,DLX1,SIN3A,FADD,KITLG,ZNF516,mir-30,MCM2,LIMS1,KIF20B,ASCC3,CENPA,ADAM10,RBPJ,FEN1,ZFP36L2,HINFP,FZD7,POLH,BIRC2,FZR1,SND1,MCM8,ERCC6,TFG,MAPK1,INSIG1,TUBB,AURKB,LMNB1,ROCK2,FGFR3,STMN1,SRSF1,WRN,LPAR2,ASXL2,EZH2,NIPBL,SIAH2,BRCA1,KLF2,DLC1,FARP2,CDC25A,CDC37,RBL2,GPS2,STK11,ERH,RAB8A,SNW1,KIAA1715,FOXC1,TPX2,SRSF3,SEL1L,TOP1MT,TOB2,RNF4,CCNG2,PKD1,CASP2,EXTL3,GNL3,TAGLN2,RFC3,ZBTB7A,NFIX,PKM,MEIS2,NUMB,TNFAIP3,NAA10,BCAR1,ROR2,HSP90B1,NLK,Ppp1cc,SP1,PCK2,CIT,TCP1,RBM15,LTBP4,BLM,E2F8,NDUFAF3,TAF6,S1PR2,ATG10,MDGA1,MAPK9,RPS6KA5,USP1,RRS1,FDXR,XIAP,HIVEP2,AFF1,GNAI2,EXOC4,PBX3,LPAR1,PAQR4,HMGCR,MCM7,LGALS1,WNT5A

Supplemental Table 7. General IPA functions for E2F1, E2F3A and E2F3B promoter targets

ChIP-seq	Category	B-H p-value	Genes
E2F1	Connective Tissue Development and Function	1.16E-12	NPM1,AXIN1,FRMD6,ODC1,XRCC2,Ewsr1,EGR2,EIF3B,SMARCB1,FBLN1,TSC2,ATF4,SAFB,UNG,AHCY,TP53,CCNE2,ESPL1,TPM3,RFC1,KLF13,TCF3,OGG1,SKP2,CNOT7,CCNF,BTG2,RAD18,TFRC,FANCA,XRCC5,PRDX2,PIM3,GADD45B,PRDX4,GAK,CDK4,SMARCA4,KSR1,OGT,B4GALT7,MAP4,PIK3C3,SOS1,NFE2L2,EXO1,DHX9,PRKDC,KHDRBS1,GAS1,GNA12,CUL7,IGF2R,ARID3A,BUB1,CCNE1,MSH2,CDKN1A,SH2B2,SHMT1,UBTF,PPIL1,CASP7,ACTL6A,CDKN2A,SOCS3,MAP3K11,LHX2,GNB2L1,MYC,TGFBR2,E2F6,CTSD,AK1,RHOB,PIM1,JUND,MYBL2,E4F1,PPP1R15B,TAB1,PGK1,SMC3,PELP1,HELLS,AURKA,BUB1B,KMT2A,SLC3A2,BCL2L1,DUSP1,RECQL4,XRCC6,POLL,MAD1L1,Gm15807/Hmgn5,PPAT,ARID1A,KIAA0101,GTF2I,PIAS1,RNASEH2B,E2F3,PTGES3,RAD50,HDGF,SHC1,CCNA2,FANCD2,STUB1,NOP58,MCM9,PRKCA,SLC20A1,EMD,FOXM1,BIRC5,PSME3,NBN,MAPK14,RAD9A,E2F7,KLF5,CKS1B,ZNF346,BRCA2,SLC19A2,BRPF1,ING1,WNK1,PCGF2,MTBP,PLRG1,CDC7,CDKN2C,SFPQ,RBL1,RICTOR,EEF1D,CBFB,IRS2,APEX2,NDRG1,COPS5,FANCG,CKAP2,HMGA1,JUNB,FANCC,SH3GL1,GAB1,E2F1,MBD4,FYN,FN1,BTG3,HMGN1,CUL1,SP2,CHEK1,ID1,YY1,CREB1,E2F5,EIF3A,CEBPA,PRKCE,VCL,POT1,RPS19,DCK,PPIF,SUZ12,ACTB,HDGFRP2,CDC6,PLCG1,MDM2,TSG101,SIN3A,RRM1,KITLG,FADD,SENP1,CIRBP,KIF20B,CENPA,FEN1,ZFP36L2,POLH,FZR1,MCM8,ERCC6,PRPF19,MAPK1,TFG,VPRBP,DIAPH3,Wasl,FBXW7,LMNB1,AMD1,STMN1,FGFR3,SRSF1,WRN,LPAR2,STAG1,FASN,EZH2,BRCA1,FOSL2,KLF2,CDC25A,GJA1,RBL2,PAFAH2,CASP3,STK11,RAC1,TMOD3,SSRP1,FOXC1,TOP1MT,TOB2,Cdc42,PKD1,GNL3,TMPO,CDK2,PA2G4,GADD45G,SLC7A1,BCAR1,PRKAG1,ZMIZ1,TRIM24,NFYA,SIPA1,Pvr,CDCA5,BLM,RASSF1,PAK4,S1PR2,NRAS,TAF6,HAT1,MAPK9,PRMT1,GNAI2,LPAR1,SHMT2,WNT5A
E2F1	Cellular Movement	5.81E-11	MYH10,NPM1,CCP110,MYH9,DSTN,TGFBR3,mir-148,SLC9A1,CD2AP,EZR,IRS2,CENPJ,ETS1,TP53,SNAI1,SEPT7,CKAP2,MBD2,PTBP1,BSG,FSCN1,AHCTF1,NEK2,ECT2,SNAI2,FN1,DUSP6,WWTR1,TRIO,CNTROB,ID1,ARF6,MTOR,YY1,PIK3C3,EIF3A,TOP2A,PRKCE,HEXIM1,MAPRE1,CDC6,PLCG1,PLK1,MDM2,FADD,PDXP,KIF20B,CDKN1A,WBP2,SEPT2,KIF23,ILF3,PFN1,MAPK1,DIAPH3,CBX5,AURKB,TGFBR2,MYC,STMN1,RHOB,PIM1,EZH2,BRCA1,ARHGAP24,TAB1,SETD8,KIF14,CASP3,STK11,KIF4A,RAC1,BIRC6,RBFOX2,AURKA,FOXC1,SSRP1,BCL2L1,Cdc42,GIPC1,HSP90AA1,ACTN4,KLHL21,JTB,UVRAG,CEP55,INCENP,IQGAP1,PTGES3,CDC25B,CCNA2,NET1,CIT,NAMPT,STX4,SUDS3,RASSF1,PRKCA,CALR,PAK4,SLC9A3R1,RACGAP1,BIRC5,XIAP,PRMT1,GNAI2,FAF1,BRCA2
E2F1	Cellular Function and Maintenance	6.93E-11	NPM1,MYH10,RNF8,KIF13B,MYH9,SCLT1,AXIN1,POLA1,NUP133,Ubb,HAUS4,PALM,C21orf2,STK35,SLC9A1,XRCC2,Diap2,Tmsb4x (includes others),GLB1,AJUBA,MAP1A,SAFB,TP53,ETS1,GRK4,TUBGCP3,ESPL1,APPL2,CRKL,SEMA5A,TPM3,OGG1,SP4,FBXW8,DAXX,CCNF,FSCN1,BTG2,RAD18,GAPDH,TINF2,PARD3,NPHP3,ECT2,XRCC5,STRIP2,FANCM,DEK,PEX3,PLXNA3,GAK,CDK4,HEXA,DNAJC13,CKAP4,BCL11B,NUAK2,GAS2L3,SPAG5,ARF6,MAP4,TRIM27,PELO,ALMS1,PIK3C3,KIF2C,RAD21,PRKDC,BBIP1,GNA12,MAPRE1,CUL7,KPNB1,LAMB2,PES1,TMEM107,CDKN1A,SH2B2,DOPEY2,FBXO5,CEP41,AP1G1,MAOA,KIF23,CDKN2A,DLGAP5,MPRIP,NCDN,YWHAH,LHX2,MICALL2,SMC4,BAG3,PEX11B,TIMM50,RPGRIP1L,TLN1,SMC1A,MYC,IFT140,LEMD3,RHOB,RCC1,CHMP2A,XPO1,CEP131,CLASP1,SMG6,SYNE2,WEE1,KIF4A,DNA2,CEP68,RAD54L,RBFOX2,AURKA,PTPRM,SLC3A2,PIP5K1A,RFX4,H3F3A/H3F3B,MATN2,XRCC6,NAGLU,LMNB2,NDC80,HSP90AA1,ACTN4,MAST3,RBBP4,ABCD1,DZIP1L,TMEM138,ARID1A,RND1,KIZ,KIAA0101,UBE2N,RAB23,NEDD1,CSRP1,CLUAP1,IQGAP1,PTGES3,RAD50,HNRNPK,HDGF,RAD51,CDC25B,SHC1,NET1,OPA1,TOR1B,RPS3,LONP1,ARC,PRKCA,ARHGAP33,TACC3,HAUS8,CAPZB,SLC9A3R1,RACGAP1,TUBG1,SMARCE1,EMD,CANX,NFATC4,FOXM1,ATL3,ALS2,GAN,BIRC5,NBN,RPA2,MAPK14,PRKCI,RAD9A,KIF5B,KLF5,BRCA2,CEP70,KIF18A,CENPF,CCP110,RAB5C,CEP120,MTBP,TOR1A,RAN,SFPQ,POU3F2,PHACTR4,RBL1,RICTOR,CHAF1A,HOOK3,CD2AP,CHMP2B,EZR,SPECC1L,CEP250,TAOK2,RFX3,CENPJ,NDRG1,FANCG,SEPT7,SLC17A5,RPA1,CKAP2,FANCC,RAD51D,ZMYM6,RAB31,DCTN6,CCNO,RNF168,BSG,GAB1,H2AFX,CDAN1,RTN4,HPRT1,LRP8,CYR61,NEK2,HAUS6,FYN,FN1,TCEA1,BTG3,SUV39H2,WWTR1,LEMD2,HMGN1,EMP2,TMEM11,TSGA10,TRIO,NRF1,HMGB2,AKAP11,CHEK1,ID1,MTOR,YY1,CREB1,CC2D1A,ACAP2,CEBPA,PRKCE,TBCD,VCL,TCTN3,POT1,FAM109A,RGMB,FMN1,RPS19,CEP152,NUP85,CEP164,PDE4DIP,ACTB,SPC25,TOR1AIP2,PLK1,TSG101,F3,CDK1,KITLG,CHCHD3,CEP72,ATL2,MUM1,KIF20B,ADAM10,CEP192,SEPT2,NCAM1,ZMYM4,CLUH,FMNL3,MCM8,PRPF19,ERCC6,PFN1,MAPK1,PTPN23,FARP1,ARF1,DIAPH3,Wasl,MNS1,UNC5B,TUBB,ROCK2,STMN1,WRN,EZH2,FASN,MID1IP1,HTRA2,BRCA1,KLF2,ARHGAP24,Nolc1,DLC1,SFR1,FARP2,Ftx,RBL2,GJA1,STIL,NUP155,CASP3,STK11,ULK4,NUBP1,RAC1,RAB8A,RANBP1,TMOD3,MAPK8IP3,SSRP1,RALBP1,BAG4,TPX2,PALB2,RNF4,Cdc42,PKD1,SMC2,CORO1B,SNX1,UVRAG,CDK2,KATNB1,CDK5RAP2,KDM3A,OBFC1,GDI1,XRCC3,NFIX,CHD4,Pcnt,COX10,PKM,NUMB,RAPGEF6,TMEM216,MRE11A,TAOK1,BCAR1,ROR2,SP1,CIT,PHGDH,ARSB,RHOF,IFRD1,BLM,ACTN1,RASSF1,CALR,PAK4,S1PR2,MAPK9,DOCK7,GCC2,UBE3A,PRMT1,KIF24,LPAR1,SYNE3,DYM,PJA2,RTN3,WNT5A
E2F1	Cellular Compromise	1.42E-10	NPM1,MCM8,ARID1A,SMARCD2,SMARCA4,SLX1A/SLX1B,MYC,SET,PIM1,SMARCB1,MCPH1,BRCA1,BLM,MCM9,RAD51C,BRIP1,POT1,CDC25A,TP53,PRKDC,NRAS,COPS5,FANCG,TUBG1,SMARCE1,SMARCD1,MDM2,HMGA1,FANCC,USP1,NBN,PALB2,MSH2,SUPT16H,RECQL4,H2AFX,CDKN1A,SMARCC1,FANCA,XRCC5,POLH

Supplemental Table 7. General IPA functions for E2F1, E2F3A and E2F3B promoter targets

ChIP-seq	Category	B-H p-value	Genes
E2F1	Post-Translational Modification	3.46E-10	RNF139,RNF8,GCHFR,AXIN1,UBR2,TGFBR3,HES1,CHAF1A,SCO2,RUSC1,CD2AP,AJUBA,MED21,VAMP3,CBFB,ANAPC11,TP53,HCFC1,NUP107,FANCC,HMGA1,MED12,SKP2,NDNL2,FBXW8,DAXX,RNF168,CCNF,NCLN,AHCTF1,COX18,FBXL6,PHF23,SUMO2,HPRT1,LTN1,PARD3,FANCA,CAPZA1,FYN,FBXO7,WWTR1,UVSSA,CUL1,STRA13,SPRTN,SF3B3,OGT,MTOR,TRIM27,CHAF1B,PRKCE,HJURP,NUP205,HEXIM1,NSMCE1,PCBP2,NFE2L2,AIFM1,GLMN,KPNA3,FMN1,TRIM28,CUL7,PLK1,MDM2,TRIM37,TSG101,CDK1,NUP153,AIMP2,NCAM1,BIRC2,CDKN2A,FOXRED1,PRPF19,FBXO25,SLF2,Wasl,RFWD3,FNIP2,FBXW7,FGFR3,FBXW2,SAE1,SIAH2,TSPAN4,BRCA1,HUWE1,BIRC6,PSMC4,KMT2A,EPRS,HERC2,CAND1,PIP5K1A,RNF4,ARRB2,UBE2G1,RC3H1,COMMD1,KLHL21,Paxip1,UBXN1,MED23,UBE2N,COX10,PIAS1,TNFAIP3,UHRF2,TRIM24,STUB1,GMNN,STX4,RPS3,NDUFAF3,RASSF1,NDUFAF4,MED18,CAPZB,SLC9A3R1,UHRF1,MAPK9,HERPUD1,SENP2,UBE3A,GAN,FANCL,XIAP,FAF1,PJA2,CDC34,WFS1,FANCI,TRIM59

Supplemental Table 7. General IPA functions for E2F1, E2F3A and E2F3B promoter targets

ChIP-seq	Category	B-H p-value	Genes
E2F1	Reproductive System Disease	7.82E-10	RNF139,PPWD1,FRMD6,POR,XRCC2,AJUBA,TSC2,ZCCHC8,WWOX,SENP5,ETS1,CCNE2,PEAK1,NUP107,RANBP3,HIST1H2BM,ALCAM,NPHP3,ELMO2,PRDX4,DIABLO,RABL6,TIPARP,KDM6A,RBMX,ARHGAP19,VPS13B,ATN1,EXO1,SDHA,VPS16,CDS2,BUB1,WBP2,AP1G1,CDKN2A,HSD3B1,RSL1D1,E2F6,JUND,SMG6,CEP68,RAD54L,KCNAB2,PHRF1,BCL2L1,H3F3A/H3F3B,DZIP1L,ETAA1,KLF10,RAB23,PIAS1,RNASEH2B,CLUAP1,GPHN,SEC14L1,STPG2,TRIP13,TECPR2,LRRC40,ALKBH5,STK3,HTATSF1,RPS15,TUBB6,CENPI,E2F7,CAMTA1,ING1,SLC25A5,RPLP0,HNRNPL,MCM6,TUBA1B,CEP120,UBR2,TAPT1,PCDHGC3,ZNF436,XRCC1,HOOK3,HIST1H2AJ,ZGRF1,CBFB,SPECC1L,PRIM2,DNMT1,PABPC1,HMGA1,ZMYM6,SH3GL1,SUCO,EML5,NCLN,ARHGAP35,HAUS6,CANT1,CPSF2,SNAI2,CDT1,GPX1,TRIO,TYW1,GPR3,NEIL3,SCAF4,RINT1,TICRR,TXNL1,VCL,FKBP5,ZNF25,NSMCE1,NAP1L4,DUT,CEP152,PDE4DIP,USPL1,PLK1,TRIM37,TSG101,F3,RRM1,SENP1,ZNF546,MUM1,WDR25,ZFYVE19,NCAM1,CLUH,TMCO1,PYROXD1,FBXW7,TIGD3,TMEM242,FAM208A,YWHAQ,TMEM230,PPP1R7,PGP,MSL2,GOLGA1,STIL,BIRC6,ATP10A,MAT2B,RALBP1,NIN,PALB2,WHSC1L1,BRAT1,KBTBD8,UVRAG,CDK5RAP2,HIGD1A,SETDB2,IWS1,MRE11A,ZMIZ1,KIAA0825,MRPS27,ZFP90,TRIM24,POLR2A,ZNF664,UBE3A,C1orf174,NCAPH2,ZNF382,PTPRU,DSCC1,HIVEP1,ZDHHC12,SLC25A32,TRIM59,TEX9,DDHD2,SCFD2,MYH9,WDR90,PCBP1,PPIL4,FAM208B,ODC1,ZFYVE1,ZC3H12C,MPHOSPH8,HIGD2A,FBLN1,GNE,TYMS,ASF1B,TUBGCP3,ESPL1,FAM118A,APPL2,BLVRA,MORC2,AACS,TFRC,ANKLE1,FRG1,RBM39,NOL7,FBXO10,PLXNA3,PEX3,ARL4C,HN1,HNRNPA2B1,ODF2L,CDK4,CTDSPL,DNAJC13,KIAA0754,TECR,NUF2,CDKN3,ZRSR2,OGT,MAP4,PRR14L,SOS1,LAPTM4A,DAB2,CDC5L,NFE2L2,RAD21,RSBN1,DHX9,PHF6,DENND4A,HNRNPU,N4BP2L2,YKT6,MAPRE1,FUCA2,GNA12,RUBCN,LAMB2,CCNE1,ABCF2,GTF2H4,EIF4A1,CDKN1A,FOXN2,MAOA,HELQ,MEGF9,MSH3,TSFM,TLN1,RARG,MYC,TGFBR2,STK4,RHOB,AMOTL2,FAM83B,XPO1,FIGNL1,PDCD6,CNOT6,TMCO3,KLF11,CLASP1,EIF4B,SMC3,USP28,DDX23,PNN,KIF4A,RBFOX2,TUSC3,BRD8,WDYHV1,PIP5K1A,TAF1,UGP2,USP32,GIPC1,MATN2,SEPT10,SORCS2,HSP90AA1,MAD1L1,NCKAP5L,SYN3,FAM83D,ACTN4,RBBP4,B2M,UBE2N,DENND4B,CFAP100,IGF2BP1,RAD50,RAD51,TRA2A,CCNA2,AKR1A1,SP3,DNAJC4,FYTTD1,ACAD8,NDUFS2,RPS3,VARS,PRKCA,SLC20A1,POMT2,SDC1,HAUS8,AP1S2,XRN2,RALY,GAN,PSME3,RPA2,PRKCI,RIOK2,PHF19,SLC33A1,SPATS2,ZNF451,SFPQ,CDKN2C,RICTOR,FANCB,NCOA7,ZNF367,MTF1,HNRNPUL1,HADHB,HEY2,THEM4,KMT2B,OTUD4,TMEM55B,FANCG,PSMD5,FANCC,RAD51D,RFC4,PI4K2A,E2F1,MSH5,LRP8,HELB,YEATS4,SUV39H2,WWTR1,RTKN2,CAMK2N2,TAX1BP3,CHEK1,TRIB1,MTOR,ADK,PRKCE,SOCS2,TBCD,ZWILCH,EPG5,RPS19,ICAM4,POLD1,PCDH9,RPIA,SIN3A,KIF15,mir-30,SPDYA,MCM2,CENPA,ADAM10,FEN1,ZFP36L2,SCAMP3,USP49,FZD7,FZR1,DIAPH3,FNIP2,CCNL1,STMN1,C19orf43,EZH2,PRND,SIAH2,HTRA2,NIPBL,RBL2,WDR34,PSMC4,RANBP1,MARS,DPP9,GSR,PANK1,TOP1MT,ARRB2,LCORL,mir-423,C1orf27,NFYC,PFAS,TMPO,RFC3,TAGLN2,TNRC6B,ZBTB7A,MED23,NUMB,MEIS2,RAPGEF6,NUP50,TAOK1,Ppp1cc,ENSA,CIT,OXCT1,LTBP4,RBM15,ARSB,S1PR2,RPS6KA5,ANAPC13,GNAI2,PPP6R1,DYM,SNRNP70,NUP62,PAQR4,HMGCR,SHMT2,MCM7,WNT5A,LGALS1,NPM1,AXIN1,POLA1,NUP133,SMARCD2,EIF4A2,GSK3A,Ewsr1,EIF3B,MAP1A,TCERG1,SAFB,GRK4,HCFC1,NKTR,RGS19,RGP1,OGG1,GART,RAD1,DAXX,CNTRL,MB21D2,ECT2,CCDC138,NDST1,FANCA,EIF3K,GADD45B,BAG6,GNA11,SERHL2,SMARCA4,UGT2A1,PNRC1,C2CD5,KPNA3,TUBB4B,GAS1,IGF2R,ARID3A,MSH2,MAZ,FBXO5,KANSL2,KIF23,NAV2,SOCS3,MPRIP,YWHAH,PCDH18,MICALL2,RPGRIP1L,SMC1A,ZC3H14,RGPD4 (includes others),INTS3,CTSD,UFSP2,CHMP2A,SETD8,COL19A1,POLE4,STXBP1,MAN1C1,WEE1,BAMBI,AURKA,PTPRM,DYNLRB1,OSBPL8,OLA1,CAND1,GINS1,mir-210,CEP76,PPAT,ABCD1,LITAF,KIAA0101,BARD1,E2F3,IQGAP1,SEMA4C,GTPBP2,FARS2,RACGAP1,NFATC4,ALS2,BIRC5,MTO1,FANCL,C19orf47,CKS1B,BRCA2,CERCAM,CCP110,DEPDC1B,PLRG1,DSTN,mir-148,Cyb5r3,RBL1,MDH1,HIST1H2AB,EEF1D,PLPP5,SLC39A13,TAOK2,PYCRL,CNOT1,YWHAZ,HINT3,MTF2,JUNB,MON2,MED12,RAB31,UBE2G2,GAMT,AAAS,MYO9A,RTN4,CDK19,NEK2,BRPF3,FYN,GSTM5,BTG3,TMEM11,NRF1,PITRM1,EIF4G1,SF3B3,CORO2B,AKAP11,MCOLN1,STOM,CETN3,TRIM16,NUP205,CEP164,SUZ12,PPIF,SPC25,PLCG1,MDM2,SCAF11,CDK1,NHLRC2,GLTP,CIRBP,EML6,RBBP6,LRFN4,PFN1,FARP1,VPRBP,MNS1,SPRED2,AMD1,GSPT1,STAG1,TTLL12,FASN,HEXDC,TMUB2,FOSL2,TSPAN4,HIST1H3F,MCM5,GJA1,P4HB,ACSL3,TRIOBP,CASP3,ACOT13,POLE2,PPIG,USP38,NUBP1,HYLS1,MAPK8IP3,HERC2,Cdc42,NASP,SBNO2,TSNAXIP1,CDK2,LRRC14,KDM3A,ZFAT,SH3BP4,DDX39A,MRPS30,TMEM216,ANAPC1,SPSB1,IPO9,PRIM1,NFYA,CSTF2T,GMNN,ZNF280B,TRNT1,OAZ1,GOT2,IFRD1,YLPM1,IPO5,RASSF1,EXOSC2,DNASE1L1,NRAS,UHRF1,TRA2B,PHLDA3,AVPI1,DOCK7,RFC5,PRMT1,PIAS3,NR1H2,Sf1,HIST1H2AM,MYH10,MAGED1,CAB39L,SCLT1,SMC5,HAUS4,CABIN1,EGR2,MTHFD2,ATF4,TARBP2,MAP3K2,TP53,SEMA5A,RRM2,TPM3,SMG5,ANO6,IKBIP,MYO1C,TBC1D14,SKP2,CNOT7,FSCN1,SUPT16H,CCNF,BTG2,NEK4,GAPDH,LTN1,ZNF780A,PARD3,XRCC5,NUP188,THADA,RNF130,KSR1,NOL12,KIF2C,DIS3,Rrbp1,PRKDC,CUL7,POLG,TDRKH,TUBA1A,RIC8B,DOPEY2,MBD3,VMP1,WRAP53,ILF3,MAP3K11,CCDC15,SMC4,STARD7,KIF16B,IFT140,LEMD3,FDFT1,TNRC6C,FBXW2,PIM1,MYBL2,CHTF18,BRIP1,MRPL34,LACTB,HUWE1,TXNDC16,PGK1,NBEAL2,HNRNPF,PELP1,SYNE2,IER2,GM2A,IPO11,BUB1B,ATAD2,SLC3A2,CBX1,DUSP1,LMNB2,ARID1A,TBC1D8B,GTF2I,ABCF1,FASTKD3,GTF3A,GTF2A1,MIER1,CDCA7,CDC25B,POLR1C,FANCD2,WDF

Supplemental Table 7. General IPA functions for E2F1, E2F3A and E2F3B promoter targets

ChIP-seq	Category	B-H p-value	Genes
E2F1	Cell Morphology	7.82E-10	NPM1,MYH10,RNF8,MCM8,PRPF19,MYH9,MNS1,TOR1A,RAN,LMNB1,CHAF1A,Tmsb4x (includes others),RCC1,CHMP2A,EZH2,EZR,TAOK2,BRCA1,SFR1,DNMT1,ETS1,TP53,SYNE2,ESPL1,SEPT7,DNA2,YWHAZ,RAC1,ORC6,RAD54L,RPA1,HELLS,TMOD3,AURKA,OGG1,PALB2,RNF4,RNF168,H3F3A/H3F3B,SMC2,XRCC6,H2AFX,RAD18,ECT2,XRCC5,FANCM,DEK,FN1,TCEA1,CHD4,UBE2N,HMGN1,NEDD1,TAOK1,IQGAP1,RAD50,CHEK1,RAD51,MAP4,NET1,GMNN,SIPA1,CEBPA,MCPH1,TOR1B,BLM,MCM9,EXO1,RASSF1,AIFM1,PRKDC,NUDCD3,TACC3,NRAS,GNA12,RACGAP1,CUL7,TUBG1,EMD,PLK1,TDRKH,FOXM1,BIRC5,TSG101,CDK1,NCAPG2,NBN,BUB1,RAD9A,CDKN1A,FBXO5,BRCA2
E2F1	Hematological Disease	8.51E-10	NPM1,PPWD1,POLA1,NUP133,POR,XRCC2,GLB1,TSC2,SMARCB1,WWOX,MAP1A,ETS1,NKTR,RANBP3,MSMO1,TCF3,OGG1,GART,TINF2,PSMD1,FANCA,HERPUD2,GADD45B,mir-331,CPD,PPIA,NUAK2,SMARCA4,DIABLO,KDM6A,PIK3C3,RBMX,PNRC1,PCNXL3,VPS13B,EXO1,ATN1,FKBP3,VPS16,TUBB4B,BUB1,KPNB1,MTHFD1L,RPS16,MSH2,RPL37,ACTL6A,CDKN2A,NAV2,MPRIP,LHX2,ZFP36L1,SMC1A,RGPD4 (includes others),E2F6,AK1,COQ6,POLE4,WEE1,CEP68,DNA2,RAD54L,AURKA,PTPRM,CDCA2,BCL2L1,KIAA0895L,mir-210,PPAT,HPS5,PIAS1,BARD1,DDX27,GPHN,PDCD10,IQGAP1,E2F3,LSM2,TBC1D1,STUB1,STPG2,NFATC4,G3BP1,ALS2,BIRC5,FANCL,TMEM109,BRCA2,CAMTA1,ING1,RPLP0,MCM6,TUBA1B,GLRX5,mir-148,RAN,ZNF436,RPS11,XRCC1,ZNF395,MPV17L2,ZGRF1,CBFB,PRIM2,TAOK2,DNMT1,PABPC1,PYCRL,UBXN6,YWHAZ,JUNB,HMGA1,MED12,SH3GL1,MTMR4,GAMT,CDAN1,ARHGAP35,FYN,SNAI2,UVSSA,GPX1,EMP2,CUL1,NRF1,PITRM1,EIF4G1,STOM,HK2,RINT1,VCL,NCBP3,ZNF526,CEP164,PDE4DIP,SUZ12,TRIM28,USPL1,PLCG1,MDM2,PLK1,NAP1L1,F3,CDK1,RHOBTB1,RRM1,SENP1,MUM1,NIPSNAP3A,KDELR3,GPR180,CEP192,NCAM1,WDR48,PFN1,CNNM2,FBXW7,FAM208A,STAG1,FASN,GOLGA1,MCM5,CASP3,POLE2,RAC1,BIRC6,SLC25A37,CDC123,ATP10A,MUT,PALB2,WHSC1L1,Cdc42,C15orf41,RPS15A,LFNG,CDK5RAP2,CDK2,BRD2,GADD45G,TXLNA,MRE11A,ANAPC1,ZMIZ1,GTF2B,PRIM1,SIPA1,TRNT1,IPO5,DHX15,RASSF1,CNTLN,CALR,NRAS,SNRPB,TPST2,HAT1,SURF6,TCF7L1,UBE3A,ALG12,HIVEP1,PAPSS1,SLC25A32,LANCL2,MYH10,SCFD2,MAGED1,MYH9,WDR90,SMC5,RPL35A,FAM208B,ODC1,EGR2,ZC3H12C,ATF4,MGAT1,TARBP2,UNG,MAP3K2,TP53,TYMS,ESPL1,SEMA5A,RRM2,PPTC7,MDM1,KLF13,ZNF169,SKP2,CCNF,BTG2,NEK4,INVS,TFRC,GAPDH,RPL10,SRSF4,PARD3,FRG1,XRCC5,PRDX2,DEK,AKAP8,CCDC97,CDK4,BCL11B,MMS22L,KSR1,ZRSR2,ARF6,TMEM260,HJURP,SNRPD3,KIF2C,NFE2L2,DIS3,RAD21,PRKDC,PHF6,CUL7,MLF1,TUBA1A,CDKN1A,SH2B2,CCT7,SHMT1,CEP112,CSTF3,CASP7,NUTF2,FOXRED1,MSH3,GNB2L1,BAG3,RARG,AP2A2,KIF16B,MYC,TGFBR2,FDFT1,TNRC6C,RHOB,EIF3D,RCC1,PIM1,PPP3R1,FAM83B,XPO1,CACTIN,BRIP1,E4F1,HUWE1,SMC3,NBEAL2,SYNE2,DDX23,PNN,SH3BP1,HELLS,BUB1B,KMT2A,CBLB,TAF1,XRCC6,RECQL4,CDCA7L,MAD1L1,NDC80,RPSA,RBBP4,B2M,ARID1A,DENND4B,GTF2I,RAD50,RAD51,CCNA2,SHC1,POLR1C,FANCD2,LONP1,PRKCA,SLC20A1,SDC1,NMRAL1,TUBG1,FAR1,MTHFD1,FOXM1,PSME3,NBN,WDR91,MAPK14,PRKCI,RIOK2,C2CD2,SLC33A1,RAD9A,MSH6,SLC19A2,CDC34,FANCI,KIF18A,CEP85,CENPF,MZF1,TGFBR3,CDKN2C,HES1,ABHD11,CHAF1A,FANCB,MXD3,THRAP3,EZR,HADHB,EEFSEC,OSMR,HEY2,SARS2,TIMP2,CENPJ,UPF2,NDRG1,FANCG,NUFIP1,RPA1,FANCC,CTPS1,H2AFX,E2F1,AHCTF1,HPRT1,LRP8,HELB,CYR61,L3MBTL2,HIST1H1C,ADAM17,FN1,TCEA1,ATF7,CTNNA3,NUP214,CHEK1,ID1,TRIB1,MTOR,ADK,TOP2A,CEBPA,HSD17B12,STIM1,HEXIM1,RXRB,POT1,RPS19,FMN1,DCK,ACTB,PCDH9,POLD1,KITLG,FADD,RAD54B,mir-30,KIF20B,ADAM10,FEN1,ZFP36L2,FZD7,CLTB,AURKB,TUBB,VDAC2,STMN1,ROCK2,FGFR3,SRSF1,WRN,RPS20,EZH2,NIPBL,RAD51C,PPP6R3,BRCA1,KLF2,DLC1,ARHGAP24,CDC25A,RBL2,NONO,RPL3,STK11,ULK4,TBP,CCT6A,RANBP1,TMOD3,MARS,TPX2,GSR,ANAPC4,CASP2,SNX1,GNL3,CEP55,GDI1,XRCC3,NFIX,CHD4,COX10,NUMB,SLC7A1,POLI,TNFAIP3,RAPGEF6,TAOK1,PRKAG1,LCA5,ROR2,SP1,PMF1/PMF1-BGLAP,MAML3,ATF6B,RBM15,BLM,ANKLE2,E2F8,S1PR2,MAPK9,USP1,GCC2,XIAP,FDPS,EXOC4,PBX3,SNRNP70,ARHGAP31,CAD,SMARCC1,HMGCR,SHMT2,WNT5A,LGALS1

Supplemental Table 7. General IPA functions for E2F1, E2F3A and E2F3B promoter targets

ChIP-seq	Category	B-H p-value	Genes
E2F1	Immunological Disease	8.51E-10	NPM1,MAGED1,PPWD1,POLA1,ODC1,POR,XRCC2,EGR2,SMARCB1,WWOX,TSC2,TARBP2,UNG,MAP3K2,TYMS,ETS1,TP53,ESPL1,SEMA5A,RRM2,RANBP3,KLF13,TCF3,OGG1,SKP2,GART,CCNF,BTG2,NEK4,GAPDH,PSMD1,FRG1,XRCC5,GADD45B,AKAP8,mir-331,CCDC97,CDK4,BCL11B,NUAK2,SMARCA4,KSR1,DIABLO,PNRC1,PCNXL3,KIF2C,DIS3,NFE2L2,EXO1,ATN1,FKBP3,PRKDC,KHDRBS1,TUBB4B,KPNB1,MTHFD1L,TUBA1A,MSH2,CDKN1A,CCT7,CEP112,CSTF3,NUTF2,CASP7,CDKN2A,FOXRED1,MSH3,RARG,MYC,FDFT1,RCC1,PIM1,PPP3R1,XPO1,POLE4,DNA2,RAD54L,AURKA,BUB1B,CDCA2,BCL2L1,TAF1,XRCC6,RECQL4,CDCA7L,mir-210,HSP90AA1,NDC80,MAD1L1,PPAT,B2M,ARID1A,GTF2I,IQGAP1,RAD50,LSM2,POLR1C,CCNA2,STUB1,LONP1,PRKCA,SDC1,TUBG1,G3BP1,PSME3,BIRC5,NBN,TMEM109,PRKCI,RIOK2,SLC33A1,RAD9A,MSH6,BRCA2,CDC34,ING1,MZF1,mir-148,RAN,CDKN2C,CHAF1A,MXD3,OSMR,PRIM2,SARS2,TIMP2,PABPC1,PYCRL,YWHAZ,RPA1,JUNB,HMGA1,MED12,H2AFX,E2F1,HPRT1,HELB,CYR61,HIST1H1C,FYN,FN1,CUL1,EMP2,CHEK1,ID1,MTOR,RINT1,CEBPA,TOP2A,STIM1,RXRB,POT1,DCK,PLCG1,MDM2,NAP1L1,POLD1,CDK1,RRM1,FADD,RAD54B,mir-30,MUM1,FEN1,NCAM1,FBXW7,AURKB,TUBB,VDAC2,FGFR3,ROCK2,STMN1,FASN,EZH2,NIPBL,BRCA1,PPP6R3,MCM5,RBL2,NONO,CASP3,POLE2,STK11,RAC1,BIRC6,CDC123,RANBP1,TPX2,GSR,Cdc42,CASP2,SNX1,LFNG,CDK2,BRD2,GADD45G,TXLNA,TNFAIP3,POLI,MRE11A,TAOK1,ROR2,HSP90B1,GTF2B,PRIM1,PMF1/PMF1-BGLAP,BLM,IPO5,ANKLE2,RASSF1,S1PR2,NRAS,TPST2,SNRPB,HAT1,MAPK9,TCF7L1,UBE3A,XIAP,FDPS,EXOC4,CAD,SMARCC1,HMGCR,SHMT2,LANCL2,LGALS1,WNT5A
E2F1	Tissue Morphology	1.23E-09	NPM1,MYH9,AXIN1,ODC1,POR,XRCC2,TSC2,TP53,CCNE2,KLF13,DAXX,CCNF,TFRC,HIST1H1D,NDST1,ECT2,PRDX2,PIM3,BAG6,GNA11,CDK4,HOXC9,SMARCA4,PELO,KDM6A,PIK3C3,SOS1,DAB2,NFE2L2,DHX9,GAS1,IGF2R,ARID3A,PES1,CCNE1,MTHFD1L,MSH2,CDKN1A,FBXO5,SHMT1,CDKN2A,SOCS3,LHX2,ZFP36L1,KXD1,TLN1,RPGRIP1L,RARG,MYC,TGFBR2,STK4,PIM1,PPP3R1,MYBL2,PPP1R15B,NBEAL2,AURKA,BCL2L1,GINS1,RC3H1,COMMD1,NAGLU,FZD5,Gm15807/Hmgn5,ARID1A,RAB23,CLUAP1,SEMA4C,RAD51,SHC1,FANCD2,RAD17,OPA1,ARC,SLC20A1,POMT2,NFATC4,FOXM1,STK3,MTHFD1,BIRC5,NBN,PRKCI,MAPK14,RAD9A,E2F7,KLF5,BRCA2,SLC19A2,BRPF1,PCGF2,UBR2,SOX12,CDKN2C,POU3F2,HES1,PHACTR4,RBL1,XRCC1,CBFB,HEY2,APEX2,DNMT1,CENPJ,KMT2B,TIMP2,Irx5,SNX13,COPS5,ANGPTL6,SNAI1,HIRA,FANCC,RAD51D,MED12,GAB1,E2F1,AHCTF1,ARHGAP35,LRP8,MAPK7,HIST1H1C,ADAM17,FN1,H2AFZ,ID1,MTOR,CEBPA,PRKCE,MCPH1,VCL,RXRB,GLMN,RPS19,DCK,SUZ12,TRIM28,CENPU,PLCG1,MDM2,COPS3,F3,TSG101,KITLG,SENP1,LIMS1,KIF20B,ADAM10,FEN1,ZFP36L2,FZR1,PFN1,MAPK1,Wasl,MMP16,DIAPH3,NR2F2,FBXW7,ROCK2,WRN,EZH2,BRCA1,KLF2,DLC1,CDC25A,RBL2,STIL,CASP3,STK11,RAC1,BIRC6,TMOD3,MAPK8IP3,PALB2,ARRB2,Cdc42,SNX1,LFNG,TMPO,Paxip1,CDK2,INCENP,ZFAT,RAB27B,NUMB,SLC7A1,ZMIZ1,PRKAG1,ROR2,HSP90B1,GMNN,SIPA1,MAML3,RBM15,BLM,E2F8,PAK4,NRAS,S1PR2,TRA2B,UHRF1,HAT1,MAPK9,TCF7L1,NR1H2,SMARCC1,WNT5A
E2F1	Tissue Development	1.79E-09	NPM1,MYH10,MYH9,FRMD6,SLC9A1,XRCC2,Diap2,Tmsb4x (includes others),GLB1,SMARCB1,FBLN1,TSC2,MAP1A,ATF4,SAFB,TP53,ESPL1,TPM3,MDM1,SKP2,CNOT7,CCNF,PRDX4,GNA11,HNRNPA2B1,CDK4,BCL11B,SMARCA4,KSR1,OGT,B4GALT7,ARF6,KDM6A,ALMS1,PIK3C3,SOS1,ARHGAP19,DAB2,KIF2C,NFE2L2,PRKDC,KHDRBS1,MAPRE1,GNA12,ARID3A,BUB1,CCNE1,MTHFD1L,CDKN1A,FBXO5,SHMT1,AKAP1,CDKN2A,SOCS3,DLGAP5,MPRIP,LHX2,MICALL2,RPGRIP1L,RARG,MYC,TGFBR2,CTSD,STK4,RHOB,FIGNL1,JUND,MYBL2,CLASP1,PGK1,HUWE1,SMC3,KANK2,WEE1,AURKA,KMT2A,SLC3A2,BCL2L1,PIP5K1A,DUSP1,RC3H1,POLL,INPP5K,PPAT,RBBP4,RND1,ARID1A,KLF10,RAB23,RNASEH2B,CLUAP1,PTGES3,SEMA4C,HDGF,TOM1L1,CDC25B,CCNA2,FANCD2,NET1,OPA1,RPS3,MCM9,PRKCA,TACC3,CAPZB,SMARCE1,EMD,FOXM1,MTHFD1,PSME3,BIRC5,PPM1G,NBN,PRKCI,MAPK14,KLF5,BRCA2,BRPF1,CENPF,PCGF2,DSTN,CDKN2C,PHACTR4,Cyb5r3,RICTOR,RBL1,SNIP1,CBFB,CENPJ,TIMP2,Irx5,NDRG1,JUNB,FANCC,HMGA1,MED12,PLA2G6,GAB1,E2F1,ARHGAP35,CYR61,FYN,FN1,SNAI2,SUV39H2,HMGN1,SP2,AKAP11,ID1,MTOR,YY1,CREB1,CEBPA,TRIM16,PRKCE,TBCD,VCL,GLMN,FMN1,ACTB,HDGFRP2,CDC6,MDM2,PLK1,TSG101,SIN3A,CDK1,RRM1,FADD,KITLG,CIRBP,KIF20B,FEN1,RBPJ,FZR1,MCM8,ERCC6,PFN1,TFG,MAPK1,ARF1,Wasl,DIAPH3,FBXW7,TUBB,AURKB,LMNB1,STMN1,FGFR3,ROCK2,WRN,LPAR2,STAG1,EZH2,FASN,BRCA1,FOSL2,KLF2,DLC1,SSNA1,GJA1,RBL2,STIL,CASP3,STK11,RAC1,TMOD3,FOXC1,BAG4,TOP1MT,Cdc42,CCNG2,GNL3,CDK2,PA2G4,GADD45G,STXBP4,BCAR1,ZMIZ1,TRIM24,NFYA,GMNN,SORBS3,BLM,RASSF1,PAK4,S1PR2,NRAS,UHRF1,HAT1,MAPK9,GNAI2,LPAR1,WNT5A,LGALS1

Supplemental Table 7. General IPA functions for E2F1, E2F3A and E2F3B promoter targets

ChIP-seq	Category	B-H p-value	Genes
E2F1	Organismal Development	7.87E-09	MYH10,NPM1,DNAJC3,ODC1,ADH5,POR,XRCC2,RCL1,Tmsb4x (includes others),GLB1,AJUBA,SMARCB1,TSC2,MGAT1,TARBP2,TP53,CCNE2,ESPL1,KLF13,ATE1,DAXX,CCNF,SUMO2,TFRC,ECT2,XRCC5,PRDX2,NOL7,PIM3,CDK4,SMARCA4,KSR1,PELO,KDM6A,PIK3C3,ARHGAP19,SOS1,DAB2,NFE2L2,PRKDC,GAS1,GNA12,MAPRE1,CUL7,IGF2R,ARID3A,LAMB2,PES1,CCNE1,MTHFD1L,MSH2,EIF4A1,CDKN1A,FBXO5,SHMT1,PLEKHA1,MAOA,CDKN2A,SOCS3,LHX2,GNB2L1,ZFP36L1,KXD1,TLN1,RPGRIP1L,RARG,RGPD4 (includes others),TGFBR2,MYC,FDFT1,CTSD,STK4,TNRC6C,PIM1,JUND,MYBL2,TAB1,PPP1R15B,NBEAL2,AURKA,KMT2A,BCL2L1,PIP5K1A,GINS1,RC3H1,LMNB2,HSP90AA1,Gm15807/Hmgn5,ALG14,NMT1,ARID1A,IDH3G,RAB23,CLUAP1,E2F3,PDCD10,RAD50,IGF2BP1,SEMA4C,TOM1L1,RAD51,SHC1,SP3,FANCD2,OPA1,ARC,PRKCA,WDTC1,SLC20A1,POMT2,CAPZB,TUBG1,EMD,NFATC4,STK3,FOXM1,MTHFD1,PSME3,BIRC5,NBN,MAPK14,RAD9A,KIF5B,SLC33A1,KLF5,E2F7,BRCA2,BRPF1,SLC19A2,SLC25A5,MZF1,PCGF2,ARV1,UBR2,TGFBR3,CDC7,RAN,mir-148,CDKN2C,HES1,PHACTR4,RBL1,XRCC1,CHAF1A,MXD3,PTP4A2,TARDBP,KARS,IRS2,CBFB,HEY2,APEX2,DNMT1,CENPJ,TIMP2,CNOT1,Irx5,TOPBP1,SNX13,CSRP2,COPS5,TKT,HIRA,SNAI1,MTF2,JUNB,HMGA1,FANCC,MED12,GAB1,YARS,E2F1,AHCTF1,ARHGAP35,MAPK7,FYN,ADAM17,FN1,ATF7,SUV39H2,WWTR1,CUL1,CTNNA3,HMGN1,NRF1,SP2,H2AFZ,SRSF10,CHEK1,ID1,NEIL3,MTOR,YY1,RINT1,PTS,CREB1,TRIM16,SOCS2,PRKCE,MCPH1,STIM1,HEXIM1,VCL,PCBP2,AIFM1,GLMN,RPS19,SUZ12,DCK,TIAL1,PLCG1,MDM2,PLK1,F3,COPS3,TSG101,CDK1,FADD,KITLG,SENP1,mir-30,LIMS1,KIF20B,FEN1,RBPJ,ZFP36L2,RBBP6,NCAM1,WDR48,FZR1,PNO1,PRPF19,ERCC6,PFN1,MAPK1,Wasl,DIAPH3,FBXW7,AURKB,LMNB1,AMD1,FGFR3,ROCK2,WRN,EZH2,MID1IP1,FOSL2,BRCA1,DLC1,KLF2,CDC25A,GJA1,RBL2,STIL,CASP3,STK11,TBP,PSMC4,RAC1,BIRC6,RANBP1,TMOD3,MAPK8IP3,FOXC1,SEL1L,PALB2,NASP,Cdc42,TIMELESS,CASP2,SNX1,LFNG,GNL3,TMPO,Paxip1,CDK2,INCENP,ZFAT,Pcnt,RAB27B,NUMB,PPP1CB,SLC7A1,BCAR1,PRKAG1,TRIM24,HSP90B1,SP1,NFYA,GMNN,CIT,SIPA1,RBM15,BLM,STK40,DHX15,E2F8,SLC25A25,CALR,PAK4,S1PR2,NRAS,TPST2,UHRF1,MAPK9,USP1,TCF7L1,LPAR1,SMARCC1,LGALS1,WNT5A
E2F1	Connective Tissue Disorders	1.19E-08	AXIN1,SLC9A1,CABIN1,SKIV2L,POR,XRCC2,EGR2,EIF3B,WWOX,SMARCB1,TSC2,ATF4,UNG,TYMS,ETS1,TP53,CRKL,SKP2,DAXX,RPL10,NDST1,GADD45B,AKAP8,BAG6,CDK4,TNFAIP8L1,HOXC9,NUAK2,SMARCA4,KSR1,DIABLO,MAP4,KDM6A,SOS1,NFE2L2,ATN1,PRKDC,DENND4A,KHDRBS1,GAS1,CUL7,VPS26A,IGF2R,BUB1,MTHFD1L,CCNE1,TMEM107,MSH2,CDKN1A,RPL37,POC1A,CASP7,CDKN2A,RPGRIP1L,RARG,SC5D,RGPD4 (includes others),MYC,TGFBR2,CTSD,STK4,RHOB,PIM1,SNN,JUND,MYBL2,CLASP1,ESCO2,SMC3,ORC6,DNA2,LZTR1,KMT2A,BCL2L1,TFAM,DUSP1,XRCC6,RECQL4,MAD1L1,LMNB2,SF3B4,PIDD1,ARID1A,RAB23,PIAS1,POLR1C,FANCD2,STUB1,CABLES2,OPA1,GMFB,PRKCA,TACC3,EMD,SENP2,NFATC4,MTHFD1,BIRC5,NBN,FAM111A,MAPK14,COX5A,BRCA2,ZNF346,PCGF2,PLRG1,TGFBR3,CDKN2C,HES1,RBL1,MTF1,SNIP1,SPECC1L,DNMT1,CENPJ,FANCG,COPS5,SNAI1,YWHAZ,RAD51D,MED12,GAB1,MBD4,E2F1,GNB2,RTN4,ARHGAP35,CYR61,FYN,SNAI2,FN1,GSTM5,CDT1,GPX1,EMP2,BOK,CHEK1,ID1,MTOR,YY1,CREB1,TOP2A,MCPH1,TCTN3,NSMCE1,AIFM1,ORC1,EPG5,CEP152,ACTB,CDC6,DLX1,PLCG1,MDM2,POLD1,C1orf159,TSG101,CDK1,FADD,SENP1,RBPJ,BIRC2,ERCC6,MAPK1,VPRBP,INSIG1,TMCO1,MMP16,UNC5B,LMNB1,STMN1,FGFR3,SIVA1,WRN,LPAR2,ITPRIP,HTRA2,BRCA1,KLF2,P4HB,RBL2,STIL,CASP3,BIRC6,RAC1,RALBP1,CASC5,PALB2,NIN,ARRB2,PKD1,CASP2,EIF4A3,SNX1,PTPRS,LFNG,GNL3,CDK5RAP2,CREBL2,TNFAIP3,ROR2,PHGDH,OAZ1,Pvr,BLM,CALR,NRAS,SNRPB,MAPK9,RPS6KA5,GNAI2,FAF1,NR1H2,PBX3,LPAR1,SMARCC1,WNT5A,CASP8AP2
E2F1	Molecular Transport	1.75E-08	CDKN2A,NPM1,AHCYL1,DDX39A,NUP133,HNRNPA2B1,RAN,THOC3,XPOT,NUP214,SLBP,RGPD4 (includes others),RITA1,EGR2,FYTTD1,XPO1,SARNP,UPF2,CALR,SMG6,NUP155,KHDRBS1,HSPA9,NCBP1,ALKBH5,NUP107,SMG5,NXT1,SRSF3,PKD1,DDX39B,THOC7,SRSF7,SMG7,NUTF2,XPO6
E2F1	RNA Trafficking	4.21E-08	DDX39A,NUP133,HNRNPA2B1,RAN,THOC3,XPOT,NUP214,SLBP,RGPD4 (includes others),FYTTD1,XPO1,SARNP,UPF2,SMG6,NUP155,KHDRBS1,NCBP1,ALKBH5,NUP107,SMG5,NXT1,SRSF3,DDX39B,THOC7,SRSF7,SMG7
E2F1	Cellular Response to Therapeutics	1.22E-07	CDKN2A,HIST1H1C,MCM8,ERCC6,GPX1,HMGN1,RAD50,RAD51,SHC1,XRCC2,MXD3,WRN,MTF1,CC2D1A,MCPH1,MYBL2,STIM1,BRCA1,MCM9,APEX2,NFE2L2,UNG,TP53,PRKDC,PAFAH2,PPIF,CASP3,RAD54L,HELLS,FANCC,RAD51D,XIAP,NBN,RAD54B,MSH2,XRCC6,CDKN1A,BRCA2,FEN1,SLC25A10,ING1,Paxip1,XRCC5,PRDX2,POLH

Supplemental Table 7. General IPA functions for E2F1, E2F3A and E2F3B promoter targets

ChIP-seq	Category	B-H p-value	Genes
E2F1	Renal and Urological Disease	1.50E-07	RNF139,RNF8,PCBP1,SMARCD2,EIF4A2,FAM208B,SECISBP2,ODC1,POR,SNRNP48,MPHOSPH8,GLB1,AJUBA,SMARCB1,TSC2,TCERG1,SARNP,TP53,GNE,TYMS,PAPD4,SEMA5A,RRM2,RANBP3,ZBTB5,OGG1,ZC3H18,GART,SP4,BTG2,HIST1H1D,PSMD1,ZNF780A,FRG1,STRIP2,PRDX2,SSSCA1,FBXO7,AKAP8,BAG6,GNA11,ESYT1,CDK4,CTDSPL,MFSD5,SMARCA4,TMEM209,UGT2A1,PELO,POFUT2,KDM6A,BTAF1,NFE2L2,RAD21,HIST2H3D,PHF6,POLG2,TUBB4B,CDH6,POLG,SLC29A1,TUBA1A,DOPEY2,MBD3,CDKN1A,C6orf62,CDKN2A,KIF23,DLGAP5,NAV2,ILF3,CCDC15,PCDH18,HELQ,TROAP,ZFP36L1,TSFM,TLN1,RARG,BPGM,RGPD4 (includes others),SMC1A,MYC,TGFBR2,FDFT1,RHOB,UFSP2,CACTIN,SMC3,POLE4,SYNE2,ZNF706,BLVRB,RBFOX2,AURKA,BUB1B,KMT2A,KIAA0907,BCL2L1,TAF1,UGP2,mir-210,CEP76,HSP90AA1,SYN3,ABCD1,B2M,ARID1A,TBC1D8B,FASTKD3,GPHN,SPSB3,E2F3,HNRNPK,POLR1C,WDFY3,FANCD2,TBC1D1,TUBG1,PRDM4,SMARCD1,NMT2,BIRC5,MAPK14,KLF5,SMG7,BRCA2,CDC34,SLC25A5,CENPF,PLRG1,GTF3C2,TOR1A,CDKN2C,RBL1,ABHD11,THRAP3,HADHB,CBFB,IRS2,RFX3,KMT2B,TIMP2,PABPC1,OTUD4,SNX13,CCDC91,SH3GL1,EAPP,RNF168,PI4K2A,BSG,E2F1,ZNF672,DNAJC14,ARHGAP35,MAPK7,HELB,CDK19,CYR61,FH,SGOL1,CANT1,BRPF3,HIST1H1C,ADAM17,KLHL18,FN1,ATF7,BTG3,SUV39H2,DUSP6,CUL1,GPX1,XPOT,NUP214,HMGB2,PITRM1,ATAD5,TYW1,SGMS1,TRIB1,YY1,MTOR,RNPS1,TICRR,TOP2A,CEBPA,TRIM16,PRKCE,VCL,KHSRP,PDE4DIP,ACTB,MDM2,PLK1,ATXN2L,ZBTB11,SIN3A,ZNF519,CCDC109B,RRM1,KIF15,ZNF516,NUP153,MCM2,KIF20B,NOP2,CEP192,ZFP36L2,ZFYVE19,NAGK,MAPK1,NR2F2,FBXW7,TUBB,AURKB,FGFR3,GSPT1,TMEM230,ASXL2,EZH2,DLST,HEXDC,NIPBL,SIAH2,HTRA2,PUF60,BRCA1,RAD51C,DLC1,SSNA1,ACSL3,NONO,TRIOBP,NUP155,CASP3,POLE2,STK11,NUBP1,TBP,NDUFAF2,RALBP1,PANK1,ANAPC4,NASP,PKD1,CASP2,KBTBD8,CDK2,CDK5RAP2,KDM3A,ZFAT,PKM,POLI,MRE11A,TMEM216,RSRP1,C12orf45,UHRF2,HSP90B1,PCK2,ADAL,GEMIN4,GMNN,DSCR3,BLM,YLPM1,IDH3B,RASSF1,CALR,NRAS,TPST2,PHLDA3,NFKBIZ,FDPS,PIAS3,GFOD1,PPP6R1,LPAR1,NUP62,SMARCC1,HMGCR
E2F1	Protein Synthesis	2.06E-06	RNF139,NPM1,RNF8,GCHFR,MYH9,PCBP1,AXIN1,GSK3A,EIF4A2,ODC1,SCO2,EIF3B,AJUBA,TSC2,ETF1,VAMP3,ATF4,TARBP2,TP53,HCFC1,RGS19,ESPL1,NUP107,TCF3,SKP2,HSPA8,CNOT7,EIF4H,MRPL17,BTG2,COX18,GAPDH,PARD3,FANCA,SPPL2A,EIF3K,FBXO7,BAG6,CDK4,OGT,TRIM27,TIPARP,RBMX,TP53INP2,HJURP,GTF2H3,DHX9,STX12,KPNA3,KHDRBS1,MRPL12,NCBP1,LARP4B,HNRNPD,DDX39B,EIF4A1,RPL37,CASP7,CDKN2A,FOXRED1,SOCS3,ILF3,SLF2,GNB2L1,ZFP36L1,BAG3,TSFM,MYC,STK4,CTSD,FBXW2,TOMM7,UFSP2,EIF3D,PIM1,XPO1,EIF4B,STXBP1,AURKA,SNX3,KMT2A,CBLB,BCL2L1,PIP5K1A,GIPC1,EDEM1,NAGLU,FAM83D,PPAT,UBXN1,UBE2N,RAB23,ABCF1,PDCD10,HNRNPK,IGF2BP1,STUB1,STX4,RPS3,LONP1,PRKCA,NDUFAF4,SDC1,CAPZB,SLC9A3R1,HERPUD1,CANX,SENP2,CNOT8,STK3,PSME3,PPM1G,QRSL1,WFS1,HNRNPL,TGFBR3,UBR2,HES1,RBL1,CHAF1A,PCOLCE,CD2AP,DNMT1,TIMP2,PABPC1,CNOT1,COPS5,SERINC1,HMGA1,FANCC,JUNB,UBE2G2,PTBP1,RNF168,NCLN,AHCTF1,FBXL6,ZSWIM7,CAPZA1,FYN,ADAM17,FN1,PITRM1,EIF4G1,SF3B3,H2AFZ,MTOR,DHPS,CHAF1B,CREB1,EIF3A,SOCS2,NUP205,SARS,AIFM1,FMN1,AZIN1,BANP,MDM2,PLK1,TSG101,TRIM37,CDK1,FADD,SENP1,NUP153,CIRBP,ADAM10,NCAM1,FZR1,PFN1,MAPK1,Wasl,DIAPH3,MMP16,FNIP2,FBXW7,LOC102724828/MRPL23,RPS20,HTRA2,SIAH2,NAA16,TSPAN4,KLF2,Fus,GJA1,CDC37,CASP3,PSMC4,EIF2S3,MARS,EPRS,SEL1L,ARRB2,Cdc42,CASP2,UBE2G1,EIF4A3,SNX1,RPS15A,CREBL2,TNRC6B,COX10,TNFAIP3,SLC7A1,STXBP4,HSP90B1,UHRF2,TRIM24,IPO9,ZBED3,NLK,SP1,GMNN,OAZ1,LTBP4,NACA,RASSF1,NDUFAF3,CALR,NRAS,RPL30,NXT1,UBE3A,XIAP,FAF1,RPS4Y1,NR1H2,RPS27L,SNRNP70,EIF3L,WNT5A
E2F1	Hereditary Disorder	2.38E-06	CDKN2A,MYH10,MYH9,RPL35A,SMC1A,TGFBR2,XRCC2,FANCB,TSC2,SMARCB1,NIPBL,SEC63,BRIP1,RAD51C,BRCA1,TP53,SMC3,CCNE2,STK11,FANCG,LZTR1,FANCC,RAD51D,KMT2A,PALB2,E2F1,FH,FANCA,SPRED1,BARD1,GPX1,CDK4,MRE11A,PDCD10,RAD50,RAD51,MTOR,FANCD2,SOS1,BLM,RAD21,PRKCA,GLMN,SDHA,RPS19,NRAS,TAF6,PLCG1,FANCL,NBN,CCNE1,MSH2,MSH6,BRCA2,FANCI
E2F1	Neurological Disease	1.44E-05	NPM1,AXIN1,POLA1,CDKN2C,HES1,POR,XRCC2,EGR2,AJUBA,TSC2,SMARCB1,IRS2,CENPJ,KMT2B,TYMS,PABPC1,TP53,CSRP2,RRM2,EXOSC8,MBD2,GART,RAD1,LARGE,CCNF,E2F1,BTG2,ARHGAP35,ALCAM,TINF2,NDST1,FRG1,ECT2,XRCC5,HIST1H1C,FN1,CDT1,BAG6,ARL4C,HNRNPA2B1,GNA11,CDK4,TRIO,NUAK2,SMARCA4,CDKN3,YY1,MTOR,KDM6A,E2F5,TOP2A,MCPH1,B3GALNT2,POT1,RAD21,ORC1,EPG5,PHF6,CEP152,GAS1,CDC6,MDM2,VPS26A,POLD1,SIN3A,RRM1,MTHFD1L,CLK4,TUBA1A,mir-30,SF3B2,MSH2,CDKN1A,MAZ,RBPJ,CASP7,NCAM1,CDKN2A,FOXRED1,ERCC6,LHX2,CLTB,FBXW7,RPGRIP1L,TUBB,LMNB1,SMC1A,FGFR3,TGFBR2,MYC,E2F6,PIM1,TSEN54,EZH2,BRCA1,KLF2,CLASP1,SMC3,STIL,CASP3,DNA2,ORC6,RAC1,TUSC3,FOXC1,GSR,BCL2L1,NIN,PALB2,CASC5,TOP1MT,RFX4,TAF1,H3F3A/H3F3B,CDCA7L,CASP2,PTPRS,SNX1,LMNB2,MAST3,CDK5RAP2,KATNB1,NFIX,ARID1A,PA2G4,KIAA0101,PKM,MRE11A,TAOK1,ROR2,PHGDH,ACTN1,RASSF1,POMT2,CALR,NRAS,RFX1,SLC9A3R1,TUBG1,MAPK9,FOXM1,BIRC5,NBN,FAM111A,LPAR1,CAMTA1,ZNF346,BRCA2,SMARCC1,CBFA2T2

Supplemental Table 7. General IPA functions for E2F1, E2F3A and E2F3B promoter targets

ChIP-seq	Category	B-H p-value	Genes
E2F1	Endocrine System Disorders	1.49E-05	MYH10,MYH9,EIF4A2,HAUS4,ODC1,CABIN1,POR,ZC3H12C,EGR2,ZCCHC8,WWOX,MTHFD2,SAFB,TP53,GNE,TYMS,CCNE2,HCFC1,SEMA5A,RRM2,TPM3,OGG1,GART,SUPT16H,GAPDH,ALCAM,LTN1,ECT2,RBM39,FANCA,XRCC5,FBXO10,PRDX4,ARL4C,BAG6,HN1,HNRNPA2B1,ODF2L,CDK4,CTDSPL,RNF130,SMARCA4,CDKN3,RABL6,PRR14L,TIPARP,UGT2A1,KDM6A,LAPTM4A,DAB2,RAD21,PHF6,PRKDC,N4BP2L2,TUBB4B,FUCA2,CUL7,TDRKH,IGF2R,CDS2,RUBCN,TUBA1A,MSH2,ABCF2,MAZ,CDKN1A,WBP2,FOXN2,WRAP53,CDKN2A,NAV2,MAP3K11,MICALL2,SMC4,RSL1D1,STARD7,KIF16B,SMC1A,MYC,TGFBR2,LEMD3,CHMP2A,FAM83B,XPO1,MYBL2,CNOT6,BRIP1,CLASP1,NBEAL2,SMC3,POLE4,SMG6,DDX23,GM2A,TUSC3,ATAD2,PHRF1,DYNLRB1,OSBPL8,OLA1,CAND1,BCL2L1,GINS1,TAF1,GIPC1,DUSP1,mir-210,HSP90AA1,NCKAP5L,ABCD1,B2M,ARID1A,KIAA0101,GTF2I,BARD1,RNASEH2B,CLUAP1,FASTKD3,CFAP100,GTF2A1,E2F3,SEMA4C,IGF2BP1,RAD50,TRA2A,POLR1C,AKR1A1,FANCD2,VARS,RACGAP1,TUBG1,EMD,FOXM1,ALS2,BIRC5,GAN,FANCL,NBN,HNRNPM,PDAP1,PRKCI,RIOK2,COX5A,C19orf47,MSH6,BRCA2,CAMTA1,SLC19A2,WNK1,WFS1,KIF18A,CERCAM,CEP85,CEP120,DSTN,CDKN2C,ZNF436,HIST1H2AB,EEF1D,IRS2,PRIM2,SLC39A13,TAOK2,DNMT1,KMT2B,PAPOLA,PYCRL,OTUD4,FANCC,HMGA1,JUNB,RAD51D,MED12,SH3GL1,PTBP1,EML5,MYO9A,H2AFX,NCLN,E2F1,RTN4,ARHGAP35,LRP8,CDK19,CYR61,HAUS6,HIST1H1C,ADAM17,FN1,GSTM5,ALKBH7,ZNF143,NRF1,CAMK2N2,EIF4G1,CORO2B,TYW1,CHEK1,STOM,MTOR,SCAF4,RINT1,TOP2A,MCPH1,NUP205,TBCD,AIFM1,GLMN,CEP152,LETM1,MVB12A,MDM2,TSG101,F3,SIN3A,CDK1,RRM1,KITLG,RAD54B,ZNF546,ADAM10,EML6,USP49,ZFYVE19,NCAM1,LRFN4,CLUH,FZR1,ORC2,MCM8,MAPK1,FARP1,VPRBP,PYROXD1,FBXW7,TIGD3,TUBB,AURKB,STMN1,FGFR3,LPAR2,STAG1,EZH2,PGP,HTRA2,TSPAN4,BRCA1,HIST1H3F,FARP2,PDE10A,POLE2,STK11,ULK4,TBP,CCT6A,MAT2B,MAPK8IP3,SSRP1,RALBP1,TPX2,HERC2,SRSF3,TOP1MT,PALB2,PKD1,LCORL,CASP2,SBNO2,CDK2,LRRC14,TNRC6B,DDX39A,IWS1,CUTA,PKM,RAPGEF6,NUP50,MRE11A,KIAA0825,TRIM24,HSP90B1,PRIM1,PCK2,ZNF280B,LTBP4,RBM15,GOT2,STK40,YLPM1,E2F8,BICD2,S1PR2,NRAS,TRA2B,DOCK7,HIVEP2,FDPS,GNAI2,NR1H2,HIVEP1,NUP62,Sf1,CAD,RTN3,HIST1H2AM,SHMT2
E2F1	Infectious Diseases	1.70E-05	NPM1,POLA1,NUP133,MTX1,POR,MRPL10,SMARCB1,ETF1,VAMP3,ATF4,SENP5,RUVBL2,SAFB,MGAT1,FAM172A,TP53,TYMS,PGRMC2,RRM2,NUP107,TAT,TCF3,RGP1,DAXX,CNOT7,FSCN1,SUPT16H,BTG2,SUMO2,TFRC,GAPDH,NPHP3,ATP6V0E1,PRDX2,ERI3,DEK,AP2A1,BAG6,ARL4C,GAK,CDK4,PPIA,MKRN2,MED28,TECR,OGT,ARF6,MAP4,PIK3C3,PNRC1,SNRPD3,RAD21,DHX9,HNRNPU,VPS16,KHDRBS1,TUBB4B,POLG,SERPINB6,ST3GAL3,IGF2R,KPNB1,MND1,RPS16,TUBA1A,MSH2,POLA2,MSRA,CDKN2A,SDF4,SOCS3,ILF3,MAP3K11,PCDH18,AMDHD2,KXD1,RSL1D1,GLYR1,RARG,RGPD4 (includes others),TGFBR2,MYC,CD164,SAE1,RHOB,RAB11B,CHMP2A,PPP3R1,XPO1,MITD1,SNN,PPP1R15B,HUWE1,HNRNPF,NBEAL2,STXBP1,DDX23,MYEF2,GABPB2,GM2A,SAP30BP,DDOST,CEP68,CBLB,BCL2L1,PIP5K1A,H3F3A/H3F3B,DUSP1,OXSR1,EDEM1,mir-210,HSP90AA1,PKMYT1,RPSA,B2M,ALG14,NMT1,ZGPAT,RND1,ARID1A,GTF2I,GTF2A1,PTGES3,IGF2BP1,HNRNPK,SEC14L1,CCNA2,DNAJB1,LONP1,PRKCA,SLC20A1,WDTC1,SDC1,SLC9A3R1,NOP56,RNF26,RACGAP1,TUBG1,G3BP1,UMPS,HNRNPM,HTATSF1,MAPK14,PRKCI,WNK1,RAB5C,AHCYL1,SOX12,RAN,mir-148,SFPQ,TM9SF2,ZNF436,HES1,CHAF1A,INTS7,CHMP2B,MED21,KARS,IRS2,TIMP2,PYCRL,TIPIN,TKT,FANCG,COPS5,HIRA,TIMM17B,HMGA1,MON2,SSR1,RAB31,UBQLN4,RPL10A,LARGE,SHCBP1,BSG,GAB1,WDR83,AHCTF1,CANT1,HIST1H1C,FYN,FN1,SRD5A1,POLR2J,NUP214,NRF1,NEIL3,YY1,MTOR,RNPS1,ADK,RAB33B,DGCR8,CREB1,TOP2A,EIF3A,SOCS2,MAP1LC3A,NUP205,RXRB,KHSRP,PCBP2,NUDCD3,NUP85,SUZ12,DDX50,ACTB,PLCG1,GINS4,PLK1,MVB12A,MDM2,F3,POLD1,TSG101,FADD,SF3B2,mir-30,NUP153,ADAM10,RBPJ,CLUH,FAM76B,MAPK1,ARF1,VPRBP,Wasl,CLTB,TUBB,LOC102724828/MRPL23,PBK,SSR3,SRSF1,WRN,LPAR2,RPS20,ASXL2,FASN,EZH2,DLST,IMPA2,MID1IP1,SNU13,BRCA1,KLF2,NUP155,CASP3,CCDC134,RPL3,SNRNP27,SNRPF,HSPA9,RAC1,PSMC4,RAB8A,RANBP1,SNW1,NDUFAF2,SSRP1,PANK1,PKD1,CASP2,EIF4A3,TMPO,UVRAG,KATNB1,CDK2,TAGLN2,SH3BP4,MRE11A,NUP50,TAOK1,GANAB,NAA10,BCAR1,HSP90B1,POLR2A,ADAL,CIT,Pvr,DHX15,ACTN1,NDUFAF3,RASSF1,BICD2,PCOLCE2,PSMA1,NFKBIZ,XIAP,C1orf174,FAU,FDPS,RPS4Y1,PTPRU,SNRNP70,NUP62,CAD,HMGCR,RTN3,EIF3L,LGALS1

Supplemental Table 7. General IPA functions for E2F1, E2F3A and E2F3B promoter targets

ChIP-seq	Category	B-H p-value	Genes
E2F1	Skeletal and Muscular Disorders	1.86E-05	CEP120,PCGF2,TGFBR3,mir-148,HES1,POR,SKIV2L,XRCC2,FBLN1,SNIP1,CBFB,SPECC1L,SLC39A13,CENPJ,TP53,GNE,TYMS,CSRP2,CRKL,SNAI1,TPM3,MED12,CRABP1,LARGE,ARHGAP35,TMEM43,RMRP,NDST1,CANT1,SNAI2,AKAP8,mir-331,CDT1,BAG6,HEXA,HOXC9,NUAK2,TAX1BP3,SMARCA4,LBR,B4GALT7,YY1,KDM6A,RAB33B,SOS1,DAB2,STIM1,MCPH1,B3GALNT2,TBCD,TCTN3,ORC1,EPG5,FMN1,CEP152,HNRNPU,GAS1,ACTB,CDC6,DLX1,MDM2,VPS26A,IGF2R,POLD1,MTHFD1L,mir-30,TMEM107,CDKN1A,ADAM10,RBPJ,SGCD,POC1A,CASP7,INSIG1,MMP16,TMCO1,RPGRIP1L,RARG,LMNB1,SC5D,IFT140,FGFR3,TGFBR2,LEMD3,UFSP2,MATR3,BRCA1,KLF2,CLASP1,ESCO2,SMC3,GJA1,P4HB,STIL,WDR34,SYNE2,CASP3,DNA2,ORC6,LZTR1,KMT2A,BCL2L1,NIN,PALB2,CASC5,PKD1,EIF4A3,RECQL4,mir-210,SMCHD1,PTPRS,SNX1,SF3B4,LMNB2,LFNG,CDK5RAP2,NFIX,RAB23,PIGV,POLR1C,ROR2,HSP90B1,PHGDH,LONP1,RASSF1,POMT2,CALR,TACC3,NRAS,SNRPB,EMD,CANX,MAPK9,MTHFD1,ALS2,MTAP,NBN,GNAI2,FAM111A,LPAR1,PBX3,DYM,BRCA2,SMARCC1,WNT5A
E2F1	Cardiovascular Disease	2.32E-05	NPM1,GLRX5,MYH9,TGFBR3,CDKN2C,RPL35A,RICTOR,POR,FANCB,WWOX,SMARCB1,TSC2,ATF4,CBFB,MGAT1,DNMT1,TYMS,TP53,FANCG,RRM2,FANCC,TCF3,OGG1,LARGE,DAXX,CDAN1,E2F1,TFRC,ALCAM,TINF2,HELB,FH,FANCA,PRDX2,FANCM,FN1,SNAI2,TCEA1,ATF7,GSTM5,HMGN1,GPX1,CDK4,SMARCA4,STOM,ARF6,RINT1,KDM6A,PIK3C3,PNRC1,ADK,TOP2A,RXRB,NFE2L2,DIS3,RAD21,GLMN,SDHA,PRKDC,RPS19,TUBB4B,TRIM28,PLCG1,PLK1,MDM2,IGF2R,CDK1,RRM1,FADD,KITLG,BUB1,SENP1,CCNE1,TUBA1A,MSH2,CDKN1A,ZFP36L2,ACTL6A,BIRC2,CDKN2A,ERCC6,LHX2,MAPK1,HELQ,ZFP36L1,TUBB,RARG,TGFBR2,MYC,E2F6,AK1,PMS1,WRN,PIM1,STAG1,PPP3R1,EZH2,BRCA1,BRIP1,RAD51C,KLF2,DLC1,SMC3,STIL,POLE4,POLE2,STK11,RAC1,SLC25A37,TMOD3,MUT,AURKA,BUB1B,KMT2A,GSR,CASC5,PALB2,BCL2L1,Cdc42,RECQL4,C15orf41,MAD1L1,HSP90AA1,CDK2,FOXP4,SEC31A,SLC7A1,TNFAIP3,PDCD10,PRKAG1,TRIM24,SP3,FANCD2,SIPA1,TRNT1,BLM,SLC20A1,NRAS,TUBG1,NFATC4,NFKBIZ,IPP,FANCL,NBN,AFF1,MAPK14,LPAR1,MSH6,BRCA2,SLC19A2,FANCI
E2F1	Cell Signaling	3.34E-05	NPM1,GCHFR,AXIN1,TGFBR3,DNAJC3,HES1,PHACTR4,CHAF1A,SCO2,CD2AP,AJUBA,TSC2,VAMP3,TAOK2,TARBP2,MAP3K2,IQGAP3,TP53,HCFC1,NUP107,RFC1,FANCC,HMGA1,HSPA8,DAXX,GAB1,NCLN,AHCTF1,COX18,LRP8,PARD3,CYR61,FANCA,PRDX2,CAPZA1,GADD45B,Calm1 (includes others),FBXO7,WWTR1,BOK,MTCH1,PITRM1,SF3B3,DIABLO,TRIB1,TRIM27,CHAF1B,CEBPA,DAB2,NUP205,HJURP,HEXIM1,AIFM1,KPNA3,FMN1,AZIN1,PLK1,MDM2,F3,CDK1,SENP1,NUP153,CDKN1A,MAP3K3,NCAM1,CDKN2A,FOXRED1,MAP3K11,ERCC6,MAPK1,ARF1,Wasl,SLF2,MMP16,NR2F2,GNB2L1,FNIP2,UBA2,MYC,SAE1,LPAR2,PDCD6,TSPAN4,DLC1,CASP3,CYB5B,MAPK8IP3,KMT2A,EPRS,PIP5K1A,ERP29,NAGLU,INPP5K,PIDD1,JTB,GADD45G,COX10,TNFAIP3,TAF7,IQGAP1,PRKAG1,CDC25B,SHC1,GMNN,STX4,GMFB,PRKCA,NDUFAF3,NDUFAF4,DAP,S1PR2,CAPZB,GTF3C4,SLC9A3R1,AVPI1,MAPK9,ALS2,GNAI2,FAF1,CACUL1,LPAR1,RPS27L,CASP8AP2,WNT5A
E2F1	Hematological System Development and Function	3.94E-05	CDKN2A,FZR1,NPM1,SOCS3,LHX2,Wasl,DIAPH3,ZFP36L1,FBXW7,KXD1,TGFBR2,MYC,STK4,TNRC6C,PIM1,CBFB,MYBL2,KLF2,APEX2,PPP1R15B,TIMP2,TP53,NBEAL2,RBL2,STK11,BIRC6,RAC1,TMOD3,FANCC,KLF13,KMT2A,BCL2L1,E2F1,TFRC,LFNG,Gm15807/Hmgn5,TMPO,CDK2,PRDX2,ZFAT,PIM3,RAB27B,CDK4,SLC7A1,SMARCA4,PRKAG1,ID1,NFYA,SIPA1,PRKCE,RBM15,BLM,NFE2L2,SLC20A1,RPS19,NRAS,DCK,PLCG1,MDM2,STK3,IGF2R,BIRC5,ARID3A,KITLG,SENP1,MAPK14,MSH2,FEN1,SLC19A2,ZFP36L2

Supplemental Table 7. General IPA functions for E2F1, E2F3A and E2F3B promoter targets

ChIP-seq	Category	B-H p-value	Genes
E2F1	Respiratory Disease	4.28E-05	NPM1,MAGED1,MYH9,PCBP1,NUP133,EIF4A2,STK35,ODC1,POR,AJUBA,CERS5,TSC2,WWOX,COPS6,TARBP2,TP53,TYMS,SERBP1,RRM2,OGG1,GART,SKP2,MB21D2,ALCAM,ECT2,PRDX2,GADD45B,PRDX4,GNA11,ODF2L,CDK4,PPIA,MED28,ARF6,MAP4,PRR14L,KDM6A,NFE2L2,ATN1,RAD21,DHX9,PHF6,GAS1,TUBB4B,GNA12,TPK1,SLC29A1,BUB1,CLK4,TUBA1A,MSH2,AIMP2,CDKN1A,EIF4A1,CDKN2A,PRELID3B,GNB2L1,RARG,SMC1A,RGPD4 (includes others),MYC,TGFBR2,CTSD,FDFT1,RCC1,MLEC,PDCD6,HUWE1,SMC3,POLE4,SYNE2,MYEF2,TMTC4,DNA2,HELLS,AURKA,BUB1B,CDCA2,KIAA0907,BCL2L1,TFAM,TAF1,mir-210,MAD1L1,HSP90AA1,B2M,QRICH1,ARID1A,CCNA2,FANCD2,RALY,TUBG1,G3BP1,FOXM1,BIRC5,FANCL,NBN,MAPK14,PRKCI,SLC33A1,PHF19,KLF5,MSH6,CKS1B,BRCA2,WNK1,CCP110,CDKN2C,HES1,RBL1,RPS11,XRCC1,EZR,OSMR,CBFB,PRIM2,DNMT1,KMT2B,PABPC1,DNAJB12,NDRG1,COPS5,YWHAZ,AP5Z1,RFC4,E2F1,ARHGAP35,CYR61,YEATS4,HIST1H1C,ADAM17,FN1,BTG3,DUSP6,GPX1,ID1,MTOR,HK2,SCAF4,RINT1,DGCR8,TOP2A,CEBPA,EIF3A,PRKCE,MAP1LC3A,TBCD,RXRB,LETM1,DCK,CDC6,TIAL1,MDM2,PLK1,F3,SCAF11,C1orf159,TSG101,CDK1,SIN3A,RRM1,FADD,mir-30,MCM2,CTNNBL1,DNPH1,ZFP36L2,MBD5,TAF15,NCAM1,FZR1,SND1,PRPF19,ERCC6,MMP16,FBXW7,TUBB,AURKB,STMN1,FGFR3,DPY19L4,SRSF1,STAG1,ASXL2,EZH2,FASN,HEXDC,BRCA1,P4HB,RBL2,CASP3,POLE2,STK11,RAC1,TBP,ATP10A,TPX2,HERC2,TOP1MT,ARRB2,AK2,TNRC6B,IWS1,PKM,MRE11A,TAOK1,ANAPC1,HSP90B1,POLR2A,CDCA5,NACA,RASSF1,NRAS,PPP4R3A,MTAP,XIAP,FDPS,PTPRU,SHMT2,WNT5A,LGALS1
E2F1	Hematopoiesis	5.49E-05	CDKN2A,FZR1,SOCS3,NPM1,LHX2,DIAPH3,ZFP36L1,FBXW7,TGFBR2,MYC,STK4,TNRC6C,PIM1,MYBL2,CBFB,KLF2,APEX2,PPP1R15B,TP53,RBL2,BIRC6,RAC1,TMOD3,FANCC,KLF13,KMT2A,BCL2L1,TFRC,LFNG,Gm15807/Hmgn5,TMPO,CDK2,PRDX2,ZFAT,PIM3,CDK4,SLC7A1,PRKAG1,ID1,NFYA,SIPA1,PRKCE,NFE2L2,SLC20A1,RPS19,NRAS,DCK,PLCG1,MDM2,STK3,IGF2R,BIRC5,ARID3A,KITLG,SENP1,MAPK14,MSH2,FEN1,SLC19A2,ZFP36L2
E2F1	RNA Damage and Repair	1.07E-04	UPF2,SMG6,NCBP1,SMG5,HNRNPD,MAGOH,CNOT8,GSPT1,SMG9,RNPS1,EIF4A3,SMG7,TOE1
E2F1	Reproductive System Development and Function	1.20E-04	MCM8,UBR2,Ubb,GPR3,CDC25B,Ewsr1,Ppp1cc,FANCD2,MCPH1,STIM1,CHTF18,BRCA1,RAD51C,EXO1,TP53,TRIP13,CCNE2,TDRKH,AURKA,BUB1B,FANCL,BUB1,PALB2,BRCA2,MSH5,LFNG,KIF18A,CDK2,FANCA,AKAP1
E2F1	Protein Degradation	3.08E-04	RNF8,MYH9,AXIN1,UBR2,ODC1,PCOLCE,TIMP2,TP53,RGS19,HCFC1,ESPL1,JUNB,TCF3,SKP2,UBE2G2,HSPA8,RNF168,FBXL6,GAPDH,ZSWIM7,SPPL2A,FYN,ADAM17,FBXO7,BAG6,PITRM1,SF3B3,OGT,MTOR,TIPARP,RBMX,TP53INP2,CREB1,SOCS2,STX12,BANP,AZIN1,PLK1,MDM2,TSG101,TRIM37,FADD,SENP1,ADAM10,CASP7,CDKN2A,FZR1,SOCS3,PFN1,MMP16,DIAPH3,BAG3,FBXW7,STK4,CTSD,FBXW2,TOMM7,UFSP2,XPO1,SIAH2,HTRA2,NAA16,STXBP1,CDC37,GJA1,CASP3,PSMC4,AURKA,SNX3,SEL1L,CBLB,BCL2L1,Cdc42,GIPC1,EDEM1,UBE2G1,CASP2,SNX1,NAGLU,FAM83D,CREBL2,UBXN1,RAB23,UBE2N,COX10,TNFAIP3,STXBP4,PDCD10,HSP90B1,UHRF2,IPO9,TRIM24,NLK,ZBED3,SP1,STUB1,OAZ1,LTBP4,LONP1,RASSF1,NACA,CALR,SDC1,HERPUD1,CANX,SENP2,STK3,PSME3,UBE3A,FAF1,NR1H2,QRSL1,WFS1,WNT5A
E2F1	Cell-To-Cell Signaling and Interaction	5.70E-04	TP53,CDKN2A,POLA1,GNA12,BIRC5,XRCC1,MYC,CTSD,BCL2L1,MTOR,MSH2,mir-210,CDKN1A,TOP2A,GAPDH
E2F1	Inflammatory Response	5.70E-04	TP53,CDKN2A,POLA1,GNA12,BIRC5,XRCC1,MYC,CTSD,BCL2L1,MTOR,MSH2,mir-210,CDKN1A,TOP2A,GAPDH
E2F1	Dermatological Diseases and Conditions	8.27E-04	TGFBR2,TP53,WRN,NRAS,CDKN1A,MAPK9,PRKCE,ODC1

Supplemental Table 7. General IPA functions for E2F1, E2F3A and E2F3B promoter targets

ChIP-seq	Category	B-H p-value	Genes
E2F1	Cardiovascular System Development and Function	8.45E-04	MYH10,PCGF2,TGFBR3,UBR2,CDKN2C,RICTOR,CABIN1,POR,CD2AP,Tmsb4x (includes others),FBLN1,CBFB,HEY2,MGAT1,TP53,ETS1,CCNE2,CSRP2,SNX13,SEMA5A,CRKL,HIRA,HMGA1,ATE1,GAB1,CCNF,TFRC,HIST1H1D,MAPK7,PARD3,PRDX2,HIST1H1C,ADAM17,PIM3,FN1,CTNNA3,CDK4,SRSF10,ID1,CC2D1A,CREB1,VCL,HEXIM1,RXRB,NFE2L2,DLX1,IGF2R,F3,ARID3A,FADD,RAD54B,CCNE1,CDKN1A,ADAM10,RBPJ,GPR180,SGCD,TFB1M,CASP7,BIRC2,MAPK1,LHX2,Wasl,ZFP36L1,NR2F2,FBXW7,RPGRIP1L,RARG,MYC,TGFBR2,STK4,PIM1,PPP3R1,SIAH2,HTRA2,DLC1,KLF2,TAB1,PPP1R15B,NBEAL2,GJA1,RBL2,CASP3,STK11,BIRC6,RAC1,RAD54L,MAPK8IP3,PALB2,BCL2L1,Cdc42,PKD1,COMMD1,LFNG,FZD5,ACTN4,CDK2,FOXP4,DCBLD2,NUMB,SLC7A1,PDCD10,BCAR1,ZMIZ1,PRKAG1,SHC1,HSP90B1,NLK,RAD17,MAML3,DPH3,ARSB,BLM,E2F8,PRKCA,CALR,PAK4,CAPZB,NRAS,S1PR2,EMD,MAPK9,TCF7L1,NFATC4,STK3,FOXM1,XIAP,NR1H2,MAPK14,EHD4,KLF5,E2F7,EFEMP2

Supplemental Table 7. General IPA functions for E2F1, E2F3A and E2F3B promoter targets

ChIP-seq	Category	B-H p-value	Genes
E2F1	Hepatic System Disease	9.76E-04	NPM1,AXIN1,POLA1,FRMD6,POR,GLB1,ZCCHC8,SMARCB1,TSC2,MAP1A,SAFB,HCFC1,TCF3,ZBTB5,RGP1,OGG1,SP4,DAXX,CNTRL,HIST1H2BM,MB21D2,EYA3,ALCAM,ELMO2,ECT2,CCDC138,NDST1,SLC1A5,mir-331,BAG6,GAK,SMARCA4,FXR2,TIPARP,UGT2A1,KDM6A,PNRC1,RBMX,PIK3C3,VPS13B,C2CD5,ATN1,SDHA,MTSS1L,ZKSCAN5,VPS16,TUBB4B,DHX36,NCBP1,SPSB4,IGF2R,KPNB1,MCM3,BUB1,MTHFD1L,RPL37,TOE1,TFB1M,AP1G1,KANSL2,KIF23,CDKN2A,RAB14,SOCS3,NAV2,MPRIP,YWHAH,PCDH18,TROAP,NUP58,RPGRIP1L,ZC3H14,CTSD,UFSP2,MPHOSPH9,SETD8,COL19A1,STXBP1,POLE4,SMG6,WEE1,ASNA1,DNA2,AURKA,PHRF1,OSBPL8,KIAA0907,BCL2L1,H3F3A/H3F3B,KIAA0895L,ANKRA2,POLL,mir-210,NAGLU,SF3B4,MAST3,ABCD1,HPS5,STK33,KLF10,RAB23,CLUAP1,DDX27,IQGAP1,TEX10,LSM2,TBC1D1,STPG2,WDTC1,FRA10AC1,NDUFV1,TECPR2,IPO4,HERPUD1,STK3,ALS2,UMPS,BIRC5,MTO1,PPM1G,HTATSF1,CENPI,CKS1B,BRCA2,CAMTA1,ING1,ZDHHC6,RPLP0,MCM6,CCP110,MTBP,CEP120,UBR2,TAPT1,RAN,mir-148,MDH1,WBSCR17,GKAP1,HOOK3,PRIM2,SPECC1L,SLC39A13,PABPC1,UBXN6,CNOT1,DNAJB12,HIRA,TIMM17B,MON1A,MBD2,MON2,JUNB,AP5Z1,MED12,MEX3A,RNF168,SUCO,AAAS,GAMT,EML5,MYO9A,NCLN,RTN4,DNAJC14,ARHGAP35,TMEM50B,NEK2,CANT1,IPO8,SNAI2,CEP78,NCAPD3,SLC4A1AP,GPX1,TRIO,NRF1,AAMP,PITRM1,KANSL3,CORO2B,TYW1,ATAD5,AKAP11,ZBTB3,NEIL3,HK2,RINT1,TICRR,CETN3,CREB1,CC2D1A,RAB33B,RFC2,TXNL1,NUP205,TCTN3,VCL,ZNF25,RGMB,NAP1L4,MCMBP,CEP164,NUP85,CEP152,PDE4DIP,BANP,TRIM28,C2orf44,TIAL1,PLCG1,PLK1,MDM2,CNKSR3,F3,SCAF11,C1orf159,RHOBTB1,NCAPG2,ZNF519,RRM1,GLTP,ZNF546,ATL2,MMS19,DUS3L,CEP192,EML6,WDR25,RBBP6,ZFYVE19,NCAM1,FMNL3,PFN1,FARP1,ARF1,CNNM2,UNC5B,FBXW7,RELL1,FAM208A,KHNYN,TMEM230,FASN,HEXDC,RPRD2,HIST1H3F,C7orf50,P4HB,GJA1,STIL,DCTN4,TRIOBP,POLE2,USP38,MTA2,BIRC6,ATP10A,MUT,MAPK8IP3,HERC2,NIN,NASP,WHSC1L1,BRAT1,HNRNPUL2,C15orf41,TSNAXIP1,SBNO2,KBTBD8,UVRAG,CDK2,FADS1,KDM3A,BRD2,PA2G4,MRPS30,MRE11A,KIAA0825,ZMIZ1,TRIM24,GTF2B,PHGDH,IFRD1,IPO5,YLPM1,RASSF1,NRAS,TRA2B,COTL1,PANK2,DOCK7,TCF7L1,C19orf68,ZNF382,PIAS3,FAF1,RPS4Y1,TMEM2,PTPRU,U2SURP,HIVEP1,ZDHHC12,MTRF1L,CBFA2T2,CASP8AP2,C17orf80,MYH10,PRR12,DSN1,PCIF1,FAM208B,CABIN1,ADH5,PAN2,SNRNP48,RCL1,MGAT1,RNGTT,IQGAP3,TP53,ATP5J,TYMS,GNE,ASF1B,ESPL1,PAPD4,APPL2,BLVRA,RRM2,ANO6,SMG5,MDM1,MYO1C,KLF13,TBC1D14,SKP2,HSPA8,FBXW8,ATE1,MORC2,PPOX,TMEM55A,ST3GAL1,MIDN,GTSE1,ANAPC5,PCYOX1L,LTN1,PARD3,WDR70,NUP188,FKBP2,FBXO10,HNRNPA2B1,ODF2L,CDK4,THOC3,MKRN2,DNAJC13,PRPF4,KIAA0754,RNF130,GAS2L3,LRRFIP1,SLC35B2,THUMPD2,MMS22L,LBR,CDKN3,TMEM209,OGT,TMEM260,TRIM27,FAM227A,ALG8,BTAF1,ZBTB45,NFE2L2,DIS3,RAD21,CCDC57,PRKDC,N4BP2L2,GNA12,MAPRE1,CDH6,POLG,MLF1,LARP4B,NCAPD2,SLC29A1,RUBCN,CCNE1,DDX39B,ABCF2,RIC8B,EIF4A1,CDKN1A,MBD3,DOPEY2,ZCWPW1,VMP1,SPICE1,CEP112,PPIL1,MAOA,WRAP53,FOXRED1,ILF3,MAP3K11,MEGF9,MSH3,GNB2L1,TSFM,AP2A2,KIF16B,NSUN6,MYC,TGFBR2,LEMD3,TNRC6C,AHDC1,PHF20,PACS2,FAM83B,CACTIN,CHTF18,E4F1,PPP1R15B,CLASP1,EIF4B,PGK1,TXNDC16,HUWE1,NBEAL2,USP28,TEX264,SYNE2,MYEF2,KANK2,KIF4A,CLIP2,ORC6,ENKD1,BUB1B,BRD8,TUSC3,ATAD2,KMT2A,CBLB,HNRNPAB,PIAS4,TAF1,UGP2,MLXIP,XRCC6,SEPT10,SMCHD1,MAD1L1,LMNB2,HSP90AA1,NCKAP5L,FAM83D,PTPN21,RBBP4,B2M,DCBLD2,UBXN1,NMT1,ARID1A,QRICH1,SEC31A,TBC1D8B,UBE2N,FASTKD3,NEURL4,C14orf80,HNRNPK,RAD50,IGF2BP1,MIER1,CDC25B,CCNA2,SHC1,SP3,FANCD2,WDFY3,NET1,DNAJC4,NOP58,CABLES2,ENPP4,MEX3B,MCM9,VARS,LONP1,ARC,POMT2,RFX1,HAUS8,NOP56,AP1S2,XRN2,RALY,CHERP,NMT2,FOXM1,MTHFD1,NFKBIL1,GAN,ATL3,PSME3,NBN,HNRNPM,FAM98B,PSKH1,MAPK14,WDR54,RIOK2,KIF5B,PHF19,ZNF622,EHD4,SMG7,THAP4,MSH6,WNK1,GZF1,FANCI,CENPF,MZF1,GTF3C2,ARV1,GOLIM4,SFPQ,ZNF451,RICTOR,RUSC1,NCOA7,INTS7,MXD3,TTF2,THRAP3,HNRNPUL1,IRS2,OSMR,CEP250,PITPNB,TIMP2,PAPOLA,UPF2,NDRG1,MEX3C,TMEM55B,TOPBP1,COPS5,NUFIP1,SERINC1,FANCC,UBE2S,WDR89,FNBP4,CTPS1,UBQLN4,PLA2G6,NSMCE2,NR1D1,BSG,ZNF202,YARS,E2F1,FBXL6,AHCTF1,RGL2,LRP8,HELB,CYR61,L3MBTL2,CD2BP2,VASH2,ADAM17,FN1,SUV39H2,ALKBH7,CTNNA3,NUP214,RTKN2,TRIB1,YY1,MTOR,POLR2M,PTS,DGCR8,TOP2A,DAP3,EIF3A,E2F5,MCPH1,CFAP77,KIAA0391,PCBP2,SARS,KHSRP,RXRB,POT1,FAM109A,NUP35,AIFM1,SAMD14,FMN1,LETM1,DCK,CCDC130,ACTB,CENPU,ICAM4,RQCD1,ATXN2L,PCDH9,SIN3A,RAD54B,KIF15,SF3B2,mir-30,RBM6,KIF20B,DENND1A,CENPA,RBPJ,ZFP36L2,USP49,MBD5,BIRC2,ZMYM4,FZD7,FZR1,SND1,ERCC6,TFG,INSIG1,DIAPH3,MMP16,NR2F2,CDH24,FNIP2,AURKB,UBA2,CCNL1,FGFR3,ROCK2,NCOA5,SRSF1,CPSF6,DPY19L4,SPATA5,POLD3,PMS1,EZH2,PRND,HTRA2,NIPBL,PUF60,BRCA1,RAD51C,ARHGAP24,MRPL43,FARP2,KIF14,RBL2,PDE10A,STK11,ZC3H6,TBP,CCT6A,MARS,TPX2,EPRS,DPP9,GSR,SEL1L,CASC5,ARRB2,TOB2,ZFR,CASP2,PTPRS,GNL3,LTV1,BAZ1B,AK2,PFAS,RFC3,OBFC1,ZBTB7A,TNRC6B,MED23,NFIX,CHD4,GTF3C5,PKM,CUTA,SLC7A1,RAPGEF6,POLI,SIL1,DARS2,STXBP4,GANAB,BCAR1,CENPP,LCA5,NKD2,NFX1,NLK,PCK2,SP1,ADAL,CIT,OXCT1,LTBP4,ZNHIT2,ARSB,BLM,STK40,ACTN1,E2F8,IDH3B,TM9SF1,NACA,BICD2,DCTPP1,MDGA1,MAPK9,FCHSD2,RPS6KA5,USP1,PSMA1,GCC2,HIVEP2,AFF1,ZBTB48,KIF24,PPP6R1,LPAR1,PAQR4,CAD,HMGCR,RTN3,MCM7
E2F1	Organ Morphology	9.94E-04	CDKN2A,MYH10,MCM8,MAPK1,UBR2,TGFBR3,POR,Tmsb4x (includes others),SAFB,HEY2,TAB1,RBL2,CCNE2,CSRP2,HMGA1,FANCC,ATE1,BCL2L1,E2F1,MAPK7,CDK2,ADAM17,FN1,GTF2I,PRDX4,CTNNA3,CDK4,RAPGEF6,PDCD10,E2F3,BCAR1,SRSF10,SHC1,HSP90B1,MCPH1,HEXIM1,VCL,PRKCA,CALR,PAK4,CAPZB,EMD,TDRKH,NFATC4,FOXM1,IGF2R,ARID3A,FADD,NR1H2,CDKN1A,RBPJ,KIF18A

Supplemental Table 7. General IPA functions for E2F1, E2F3A and E2F3B promoter targets

ChIP-seq	Category	B-H p-value	Genes
E2F1	Skeletal and Muscular System Development and Function	9.94E-04	MYH10,ADAM17,FN1,MAPK1,TGFBR3,UBR2,CTNNA3,CDK4,PDCD10,BCAR1,SRSF10,POR,SHC1,HSP90B1,Tmsb4x (includes others),VCL,HEY2,HEXIM1,TAB1,PRKCA,CALR,RBL2,PAK4,CAPZB,CSRP2,EMD,NFATC4,HMGA1,FOXM1,IGF2R,ARID3A,FADD,ATE1,BCL2L1,CDKN1A,RBPJ,MAPK7,CDK2
E2F1	Nucleic Acid Metabolism	1.01E-03	TYMS,DUT,ADK,RRM2,SHMT1,DTYMK,RRM1
E2F1	Small Molecule Biochemistry	1.01E-03	TYMS,DUT,ADK,RRM2,SHMT1,DTYMK,RRM1
E2F1	Protein Trafficking	2.00E-03	CDKN2A,CALR,EGR2,PKD1,AHCYL1,HSPA9,RAN,XPO1,NUP214,NXT1,NUTF2,XPO6
E2F1	Hair and Skin Development and Function	2.00E-03	CDKN2A,FYN,FN1,SUV39H2,FBXW7,RBL1,AURKB,SMARCA4,TOM1L1,ROCK2,MYC,STK4,ID1,SOS1,ARHGAP19,TRIM16,CDC25A,TP53,PAK4,RBL2,CASP3,MAPK9,PLK1,JUNB,FOXM1,TSG101,CDK1,CCNE1,PIP5K1A,CCNG2,MAPK14,GAB1,KLF5,CDKN1A,E2F1,RBPJ,CDK2
E2F1	Hepatic System Development and Function	2.00E-03	TP53,CDKN1A,E2F1,E2F7,E2F8
E2F1	Organ Development	2.03E-03	CDKN2A,FYN,FN1,SUV39H2,FBXW7,RBL1,AURKB,SMARCA4,TOM1L1,MYC,ROCK2,ID1,STK4,SOS1,ARHGAP19,TRIM16,TP53,PAK4,RBL2,CASP3,MAPK9,PLK1,JUNB,FOXM1,TSG101,CDK1,CCNE1,PIP5K1A,MAPK14,GAB1,KLF5,CDKN1A,RBPJ,CDK2
E2F3A	DNA Replication, Recombination, and Repair	1.42E-21	SNTB2,RAF1,RMI1,TIMM13,POLA1,AP1AR,KRAS,STAG3,TP53,TYMS,HCFC1,PCGF6,RRM2,SKP2,HSPA8,ATE1,CCNF,SUPT16H,PDS5A,FANCA,DEK,CDK4,MTCH1,NUF2,MMS22L,SPAG5,KIF2C,RAD21,DHX9,HNRNPU,MECP2,POLG,ING5,ID3,SLC29A1,MCM3,CCNE1,MSH2,NUDT16,CDKN1A,MAZ,FBXO5,POLA2,RAD51AP1,DLGAP5,RFWD3,SMC1A,ZW10,MYC,INTS3,Gm21596/Hmgb1,PIM1,XPO1,MYBL2,BRIP1,ESCO2,SMC3,USP28,WEE1,ORC6,RAD54L,CDCA2,TFAM,DUSP1,RECQL4,XRCC6,HIRIP3,PIDD1,RMI2,ARID1A,KIAA0101,BARD1,RNASEH2B,ZNF219,E2F3,RAD51,DNAJB1,MCM9,C10orf88,LRWD1,TRIP13,TACC3,TUBG1,SMARCD1,BIRC5,TPP2,PPM1G,RPA2,NBN,FAM111A,MAPK14,VAV3,MSH6,BRCA2,MCM6,CCP110,MTBP,CDC7,RAN,mir-148,GFER,SFPQ,RBL1,CHAF1A,ACIN1,INTS7,RARA,TARDBP,IRS2,DNMT1,PABPC1,TIPIN,TOPBP1,MDC1,RPA1,TFAP4,CCNO,PTBP1,PCNA,RNF168,SSBP1,NSMCE2,GAB1,H2AFX,E2F1,MBD4,MSH5,CLSPN,MAPK7,SGOL1,CTC1,MGME1,CDT1,HMGB2,CHEK1,NEIL3,RIF1,DGCR8,TOP2A,RFC2,MCM10,CEP152,DUT,mir-199,DCK,CDC6,SPC25,SMC6,NAP1L1,NCAPG2,CDK1,RRM1,FADD,RAD54B,SENP1,SPDYA,MCM2,REV1,MUTYH,MMS19,FEN1,HINFP,POLH,MCM8,PFN1,PRPF19,MELK,PBK,POLD3,STAG1,EZH2,INIP,SNU13,RAD51C,BRCA1,CDC25A,APITD1/APITD1-CORT,DNASE2,NUBP1,SSRP1,Cdc42,CCNG2,ARRB2,TIMELESS,SMC2,CASP2,BAZ1B,TMPO,Paxip1,CDK2,RFC3,PRIMPOL,WDHD1,MCM4,Ppp1cc,GMNN,PMF1/PMF1-BGLAP,CDCA5,IPO5,RASSF1,DTL,MAP2K7,MTRR,SNRPB,UHRF1,HAT1,let-7,ERBB3,USP1,ITPA,DSCC1,RPS27L,MIS12,TONSL,SMARCC1,LGALS1

Supplemental Table 7. General IPA functions for E2F1, E2F3A and E2F3B promoter targets

ChIP-seq	Category	B-H p-value	Genes
E2F3A	Cell Cycle	5.46E-19	RAF1,RMI1,TIMM13,MYH9,PRKAB2,POLA1,HAUS4,KRAS,C6orf89,FHL2,STAG3,AHCY,IQGAP3,TP53,TYMS,HCFC1,NPAT,SKP2,HSPA8,ATE1,CCNF,GTSE1,PDS5A,TFRC,FANCA,DEK,PIM3,GADD45B,Calm1 (includes others),GDF15,CDK4,NUF2,MMS22L,SPAG5,RABL6,MAP4,SSTR5,KIF2C,CDC5L,RAD21,DHX9,MECP2,KHDRBS1,ING5,ID3,ARID3A,MCM3,KPNB1,CCNE1,MSH2,NUDT16,CDKN1A,PSAP,FBXO5,RAD51AP1,DLGAP5,SRSF2,RFWD3,SMC1A,INTS3,ZW10,MYC,PIM1,MLLT3,XPO1,MYBL2,NUCKS1,ESCO2,USP28,SMC3,PELP1,WEE1,ORC6,RAD54L,CDCA2,DUSP1,RECQL4,XRCC6,RMI2,ARID1A,KIAA0101,GTF2I,BARD1,RNASEH2B,ZNF219,E2F3,PTGES3,RAD51,CSRP2BP,MCM9,LRWD1,VAV2,TRIP13,TACC3,HAUS8,TUBG1,PRDM4,SMARCD1,BIRC5,TPP2,PPM1G,NBN,RPA2,MAPK14,PRKCI,CENPI,VAV3,KLF5,MSH6,DCTN1,BRCA2,TUBA1B,CCP110,MTBP,UBR2,mir-148,CDC7,RAN,SFPQ,PHACTR4,MKI67,RBL1,CHAF1A,ACIN1,INTS7,MXD3,RARA,TARDBP,PLCB1,IRS2,CEP250,ANAPC11,DNMT1,PABPC1,TIPIN,TOPBP1,CENPB,MDC1,RPA1,TFAP4,CCNO,PCNA,NSMCE2,GAB1,H2AFX,MBD4,E2F1,MSH5,CLSPN,MAPK7,SGOL1,HAUS6,CTC1,CDT1,FKBP1A,HMGB2,CAMK2N2,CHEK1,TRADD,TNKS,TOP2A,RFC2,MCM10,CEP152,mir-199,PPIF,DCK,CDC6,SPC25,SMC6,CDK1,NCAPG2,RRM1,FADD,FIS1,RAD54B,KIF15,CDKL2,SPDYA,MCM2,REV1,CIRBP,MMS19,FEN1,ZFP36L2,HINFP,POLH,MCM8,PFN1,PRPF19,LIMK2,MELK,TUBB,LMNB1,YWHAQ,STMN1,SRSF1,STAG1,EZH2,SNU13,BRCA1,RAD51C,FOSL2,CDC25A,NUBP1,BIRC6,RANBP1,SSRP1,SRSF3,CCNG2,Cdc42,SMC2,TUBE1,CASP2,NUAK1,TMPO,Paxip1,CDK2,RFC3,PRIMPOL,PA2G4,WDHD1,DTYMK,MCM4,POLR2A,Ppp1cc,PPP1R9B,GMNN,PMF1/PMF1-BGLAP,TCP1,CDCA5,ARSB,IPO5,E2F8,DTL,RASSF1,MAP2K7,UHRF1,SNRPB,HAT1,let-7,ERBB3,USP1,ITPA,RPS27L,SMARCC1,TONSL,MIS12,CASP8AP2,LGALS1
E2F3A	Organismal Survival	1.30E-10	RAF1,MYH9,PRKAB2,KRAS,MTHFD2,AFMID,TP53,SLC2A1,CRKL,MAFF,SP4,ATE1,CCNF,APH1A,PDS5A,TFRC,GDF15,CDK4,TRIM27,MMP8,TLR7,DHX9,Mocs1,KHDRBS1,MECP2,POLG,ID3,ARID3A,CCNE1,MSH2,CDKN1A,PSAP,FBXO5,TFB1M,MAP3K3,NDST3,SRSF2,RPGRIP1L,MYC,Gm21596/Hmgb1,EIF3D,MLLT3,MYBL2,BRIP1,ESCO2,RAD54L,MEOX1,KCNAB2,PFKM,DNAJC5,TFAM,DUSP1,XRCC6,RECQL4,NAGLU,RPSA,TFEB,ARID1A,GTF2I,BARD1,GPHN,E2F3,PTGES3,RAD51,DNAJB1,LRRC8A,WDR1,SLC20A1,POMT2,TACC3,TUBG1,Scd2,SNX27,NFATC4,BIRC5,GAN,TPP2,NBN,PRKCI,MAPK14,VAV3,EHD4,KLF5,MSH6,DCTN1,BRCA2,ACTL6B,UBR2,CDC7,RAN,ERI1,MKI67,RBL1,RICTOR,CHAF1A,RARA,ABCC1,TARDBP,PLCB1,IRS2,DNMT1,PITPNB,THEM4,TOPBP1,CENPB,ANGPTL6,PLEC,TFAP4,ITPR1,SH3GL1,PTBP1,PCNA,GAB1,AHI1,H2AFX,E2F1,MAPK7,CTC1,SNAI2,FKBP1A,ACVR2B,H2AFZ,SP2,CHEK1,SRSF10,TNKS,RIF1,TCOF1,DGCR8,TOP2A,MCM10,KHSRP,RPS19,SUZ12,PPIF,PPP1R8,ACTB,DLX1,COPS3,CDK1,NCAPG2,FADD,SENP1,RAD54B,MCM2,REV1,MUTYH,FEN1,ZFP36L2,NCAM1,PFN1,PRPF19,LAMTOR2,MMP16,MAP1B,MNS1,LMNB1,SRSF1,SIVA1,PTRH2,EZH2,SIAH2,BRCA1,RAD51C,FOSL2,DLC1,Fus,CDC25A,DNASE2,NUBP1,PSMC4,BIRC6,GSN,Abcb1b,SSRP1,WWP2,SRSF3,Cdc42,ARRB2,TIMELESS,MBTPS1,USE1,CASP2,Paxip1,CDK2,TEAD4,ZFAT,BRD2,MED23,PKM,ZMIZ1,ROR2,POLR2A,GMNN,RRN3,E2F8,DTL,RASSF1,SLC25A25,MAP2K7,TRA2B,UHRF1,HAT1,GABBR1,ERBB3,USP1,NFKBIZ,MLLT1,AFF1,ITPA,PBX3,SPR,SMARCC1
E2F3A	Embryonic Development	1.30E-10	RAF1,UBR2,CDC7,KRAS,PHACTR4,RBL1,RICTOR,CHAF1A,MXD3,RARA,TARDBP,MTHFD2,IRS2,DNMT1,TP53,SLC2A1,TOPBP1,ANGPTL6,ATE1,PCNA,CCNF,APH1A,E2F1,MSH5,MAPK7,PIM3,CDK4,ACVR2B,SP2,CHEK1,NEIL3,TNKS,TCOF1,MCM10,DHX9,PTK7,STT3B,RPS19,SUZ12,SEC24B,PPP1R8,POLG,ING5,ID3,COPS3,NCAPG2,ARID3A,FADD,MTHFD1L,CCNE1,SPDYA,MSH2,CDKN1A,SHMT1,FBXO5,FEN1,TFB1M,NCAM1,DLGAP5,PFN1,PRPF19,MAP1B,RPGRIP1L,LMNB1,MYC,PIM1,EZH2,MYBL2,BRCA1,DLC1,ESCO2,PSMC4,MEOX1,SRSF3,Cdc42,TIMELESS,Paxip1,CDK2,RPSA,TEAD4,ZFAT,ARID1A,RAB23,E2F3,ZMIZ1,RAD51,ROR2,Ppp1cc,GMNN,RRN3,DNAJB1,LRWD1,E2F8,RASSF1,DTL,POMT2,TACC3,UHRF1,TRA2B,TUBG1,ERBB3,USP1,NFATC4,MTHFD1,BIRC5,TPP2,NBN,AFF1,MAPK14,KLF5,DCTN1,BRCA2,LGALS1
E2F3A	Developmental Disorder	1.30E-10	RAF1,PRPF19,PFN1,LAMTOR2,MMP16,UBR2,MAP1B,KRAS,RBL1,CHAF1A,SMC1A,MYC,Gm21596/Hmgb1,PIM1,EZH2,RARA,BRCA1,FOSL2,CDC25A,ESCO2,TP53,SMC3,DNASE2,SLC2A1,PSMC4,BIRC6,ORC6,RANBP1,MAFF,SRSF3,SH3GL1,PCNA,DNAJC5,RECQL4,H2AFX,PDS5A,TFRC,MAPK7,Paxip1,CDK2,RPSA,TEAD4,PIM3,MED23,SNAI2,CDT1,CDK4,ACVR2B,E2F3,SP2,PTGES3,CHEK1,SRSF10,RAD51,TRIB1,POLR2A,GMNN,TCOF1,RRN3,MCM10,DNAJB1,RAD21,E2F8,DTL,SLC20A1,POMT2,RPS19,TACC3,SUZ12,MECP2,UHRF1,TUBG1,CDC6,POLG,SNX27,NFATC4,BIRC5,COPS3,ARID3A,NBN,FADD,CCNE1,PRKCI,MAPK14,ITPA,KLF5,CDKN1A,FBXO5,BRCA2,FEN1,SPR
E2F3A	RNA Post-Transcriptional Modification	1.94E-10	HNRNPL,SRSF2,PRPF19,SFPQ,DDX20,ACIN1,INTS3,SRSF1,INTS7,RCL1,TARDBP,HNRNPUL1,PLCB1,HNRNPA0,PABPC1,HCFC1,NUFIP1,RBFOX2,Scaf1,SRSF3,PTBP1,SRSF7,CPSF3L,SRSF4,RBM39,HNRNPA2B1,BARD1,WDHD1,USP39,SRSF10,TRA2A,POLR2A,CLP1,NOP58,DBR1,KHSRP,CDC5L,DIS3,RPS19,HNRNPU,MECP2,TRA2B,KHDRBS1,PPP1R8,NOP56,MAGOH,DDX39B,RBM6,CSTF3

Supplemental Table 7. General IPA functions for E2F1, E2F3A and E2F3B promoter targets

ChIP-seq	Category	B-H p-value	Genes
E2F3A	Cellular Growth and Proliferation	2.28E-09	RAF1,RMI1,MYH9,POLA1,KRAS,IFT80,SKAP2,C6orf89,RCL1,FHL2,EIF3B,SCPEP1,AHCY,TYMS,TP53,PEAK1,SLC2A1,CRKL,RRM2,MAFF,SKP2,HSPA8,MICU1,ACER3,CCNF,ANAPC5,TFRC,ZYX,ELMO2,FANCA,PIM3,GADD45B,HNRNPA2B1,GDF15,CDK4,MTCH1,RABL6,TRIM27,MMP8,ALMS1,SSTR5,TLR7,KIF2C,RAD21,DHX9,STT3B,SERTAD2,HNRNPU,KHDRBS1,MECP2,DROSHA,POLG,ING5,SLC29A1,ID3,ARID3A,MCM3,CCNE1,MSH2,NUDT16,MAZ,CDKN1A,PSAP,TCF19,SHMT1,PLEKHA1,MAP3K3,PPIL1,EEF1A1,DLGAP5,SRSF2,RPGRIP1L,NUDC,SMC1A,MYC,Gm21596/Hmgb1,PIM1,MLLT3,MYBL2,CNOT6,BRIP1,KLF11,EIF4B,SMC3,USP28,OSBPL1A,PELP1,GABPB2,WEE1,RBFOX2,CDCA2,ATAD2,TFAM,DUSP1,RECQL4,XRCC6,PIDD1,RPSA,RBBP4,ARID1A,KIAA0101,KLF10,GTF2I,BARD1,RNASEH2B,GPHN,E2F3,PTGES3,CDCA7,RAD51,TRA2A,NOP58,DNAJB1,MCM9,LRRC8A,SLC20A1,VAV2,TACC3,RPRD1B,CHERP,UPP1,PRDM4,NFATC4,G3BP1,MTHFD1,ZSCAN21,BIRC5,PPM1G,TPP2,NBN,PMP22,PRKCI,MAPK14,EHD4,VAV3,KLF5,BRCA2,PLEKHA2,HNRNPL,MTBP,GFER,KCNJ16,CDC7,mir-148,RAN,SFPQ,ERI1,ARHGEF1,DDX20,MKI67,RAPH1,RBL1,RICTOR,HIST1H2AB,ACIN1,MXD3,ABCC1,RARA,TARDBP,HADHB,IRS2,DNMT1,THEM4,GET4,HNRNPA0,TIPIN,TOPBP1,ANGPTL6,CENPB,PLEC,YWHAZ,RPA1,TFAP4,ITPR1,SH3GL1,CCNO,PTBP1,PCNA,SSBP1,RFC4,GAB1,PSMB2,H2AFX,E2F1,CLSPN,MAPK7,CTC1,SNAI2,CDT1,FKBP1A,HMGB2,CAMK2N2,SP2,H2AFZ,CHEK1,TRADD,TRIB1,NEIL3,TNKS,TCOF1,DGCR8,TOP2A,LIPG,TXNL1,MCM10,FKBP5,RPS19,mir-199,DCK,SUZ12,PPIF,PPP1R8,ACTB,CDC6,NAP1L1,COPS3,CDK1,RRM1,FADD,FIS1,SENP1,KIF15,FTL,SPDYA,MCM2,RBM6,CIRBP,NOP2,FEN1,GCAT,DNPH1,ZFP36L2,NCAM1,POLH,MCM8,PRPF19,PFN1,CAV2,LAMTOR2,MAP1B,MELK,TUBB,PBK,LMNB1,YWHAQ,STMN1,SRSF1,STAG1,EZH2,FOSL2,BRCA1,DLC1,Fus,CDC25A,MCM5,NUBP1,PSMC4,BIRC6,RANBP1,Abcb1b,GSN,BAG4,WWP2,SRSF3,ARRB2,CCNG2,Cdc42,TIMELESS,CASP2,NUAK1,TMPO,Paxip1,ELK4,CDK2,TAGLN2,RFC3,KDM3A,TEAD4,COPS4,PA2G4,PKM,AKIP1,DTYMK,MCM4,ZMIZ1,ROR2,PPP1R9B,PCK2,GMNN,RRN3,TCP1,CDCA5,E2F8,DTL,RASSF1,MAP2K7,UHRF1,HAT1,let-7,GABBR1,ERBB3,USP1,MLLT1,AFF1,PBX3,ACAT1,LGALS1
E2F3A	Cell Death and Survival	3.55E-09	RAF1,MYH9,PRKAB2,KRAS,FHL2,EIF3B,SPA17,VAMP3,TYMS,TP53,SLC2A1,CRKL,RRM2,SKP2,HSPA8,APH1A,ZYX,TFRC,FANCA,DEK,PIM3,Calm1 (includes others),GADD45B,Dleu2,GDF15,CDK4,MTCH1,NUF2,MMS22L,SPAG5,RABL6,MAP4,TRIM27,ALMS1,MMP8,TLR7,DIS3,RAD21,DHX9,HNRNPU,MECP2,KHDRBS1,DROSHA,TPK1,ING5,SLC29A1,ID3,PACRG,KPNB1,CCNE1,MSH2,CDKN1A,FBXO5,PSAP,MAP3K3,TFB1M,EEF1A1,SRSF2,TIMM50,NUP58,PIEZO1,CBX5,SMC1A,INTS3,MYC,Gm21596/Hmgb1,SMPD4,PIM1,MLLT3,XPO1,MYBL2,BRIP1,KLF11,EIF4B,SMC3,PELP1,WEE1,RAD54L,CDCA2,ATAD2,PFKM,TFAM,DNAJC5,DUSP1,XRCC6,NAGLU,PIDD1,RPSA,RBBP4,TFEB,ARID1A,KIAA0101,KLF10,BARD1,GPHN,E2F3,PTGES3,RAD51,CLP1,NOP58,DNAJB1,MCM9,LRRC8A,C10orf88,SLC20A1,VAV2,TACC3,HAUS8,HERPUD1,SMARCD1,NFATC4,BIRC5,PPM1G,TPP2,NBN,PMP22,PRKCI,MAPK14,CENPI,VAV3,EHD4,KLF5,MSH6,BRCA2,DCTN1,CCP110,MTBP,UBR2,mir-148,CDC7,RAN,GFER,SFPQ,ARHGEF1,DDX20,MKI67,RICTOR,RBL1,ACIN1,MXD3,ABCC1,RARA,TARDBP,HNRNPUL1,PLCB1,IRS2,DNMT1,TOPBP1,CENPB,YWHAZ,PLEC,MDC1,RPA1,SPG7,TFAP4,ITPR1,PCNA,GAB1,AHI1,H2AFX,MBD4,E2F1,TMX1,TBC1D15,MSH5,CLSPN,MAPK7,SNAI2,CDT1,FKBP1A,BOK,HMGB2,ACVR2B,CAMK2N2,CHEK1,TRIB1,TRADD,TNKS,TCOF1,DGCR8,TOP2A,MCM10,FKBP5,PCBP2,NSMCE1,RPS19,DUT,mir-199,PPIF,SUZ12,DCK,PPP1R8,ACTB,SPC25,CDC6,DLX1,NCAPG2,CDK1,RRM1,FADD,RAD54B,FIS1,SENP1,SPDYA,MCM2,CTNNBL1,REV1,CIRBP,MUTYH,GPR180,FEN1,ZFP36L2,GLS2,POLH,NCAM1,MCM8,PRPF19,PFN1,CLN8,LAMTOR2,MAP1B,MELK,LIMK2,ZNF91,TUBB,PBK,LMNB1,YWHAQ,STMN1,SRSF1,SIVA1,PTRH2,STAG1,EZH2,RYR3,SIAH2,NAA16,INIP,BRCA1,FOSL2,RAD51C,DLC1,CDC25A,P4HB,PJA1,DNASE2,BIRC6,PSMC4,RANBP1,Abcb1b,GSN,SSRP1,MED14,BAG4,WWP2,Cdc42,ARRB2,USE1,CASP2,MBTPS1,NUAK1,TBCCD1,Paxip1,CDK2,TEX261,TAGLN2,KDM3A,PAFAH1B2,BRD2,PA2G4,Pcnt,PKM,DTYMK,ROR2,Ppp1cc,POLR2A,PCK2,PPP1R9B,GMNN,RRN3,TCP1,ARSB,E2F8,RASSF1,DTL,MAP2K7,UHRF1,HAT1,let-7,GABBR1,GPT,ERBB3,PSMA1,NFKBIZ,AFF1,PBX3,ACAT1,SPR,TONSL,SMARCC1,CASP8AP2,LANCL2,LGALS1

Supplemental Table 7. General IPA functions for E2F1, E2F3A and E2F3B promoter targets

ChIP-seq	Category	B-H p-value	Genes
E2F3A	Cancer	3.55E-09	TIMM13,C6orf203,PPWD1,SKAP2,AFMID,PEAK1,CRKL,RANBP3,MRPL49,ELMO2,PIM3,RABL6,IBTK,MTMR3,POLR1E,ID3,KPNB1,MTHFD1L,EEF1A1,ZFP1,PIGU,CBX5,MATR3,ESCO2,RAD54L,KCNAB2,NAGLU,CBX3,TFEB,FEM1A,ELMOD2,KLF10,RAB23,RNASEH2B,GPHN,DDX27,C16orf59,TRIP13,TACC3,RNF26,Scd2,HERPUD1,SNX27,PPM1G,CENPI,ACTL6B,RER1,HNRNPL,MCM6,TUBA1B,ZFP62,ZNF628,UBR2,RNF38,CTDSP1,ZFP41,GJC3,HIST1H2AJ,PNKD,TTLL5,DNMT1,LMF2,C19orf57,TMEM39B,GET4,MALL,PABPC1,CENPB,COMMD9,PLEC,CNOT10,ZMYM6,AP5Z1,SH3GL1,RNF168,FAM222A,NCLN,KIAA0368,HAUS6,SGOL1,SNAI2,MGME1,CDT1,BOK,FKBP1A,H2AFZ,TNKS,NEIL3,RIF1,RFC2,TXNL1,FKBP5,NSMCE1,NCBP3,PKN3,MCMBP,DUT,RRP1B,NUP85,CEP152,ZNF526,AP4M1,SMC6,COPS3,NCAPG2,RRM1,ADSS,SENP1,DUS3L,GPR180,COBLL1,NCAM1,FMNL3,PRPF19,MRPS17,TMCO1,ZNF91,PBK,RPUSD2,YWHAQ,FAM208A,FSD1L,BIRC6,GSN,SMC2,ZMIZ1,GNG11,POLR2A,DSCR3,CNTLN,ZNF383,C1orf174,MLLT1,ZNF382,DSCC1,RPS27L,TRMT2A,TRIM59,TEX9,RAF1,MYH9,MTNR1A,IFT80,NKAP,C6orf89,RCL1,ZNF689,STAG3,TYMS,TUBGCP3,PAPD4,DNAJC9,GINM1,MDM1,SPATA20,ATE1,APH1A,GTSE1,ANAPC5,TFRC,ZYX,ZDHHC1,FRG1,ANKLE1,RBM39,TRAPPC5,FKBP2,DEK,HNRNPA2B1,GDF15,CRIPT,CDK4,CCDC191,NUF2,TMEM209,GINS2,MAP4,ALG8,CDC5L,RAD21,DHX9,RSBN1,SERTAD2,HNRNPU,MECP2,TPK1,ING5,LARP4B,SLC29A1,RUBCN,CCNE1,DDX39B,NUDT16,ABCF2,CDKN1A,PSAP,BTF3L4,PPIL1,FOXN2,MEGF9,RFWD3,TIMM50,TSFM,PIEZO1,MYC,ZW10,SMPD4,GATC,XPO1,CACTIN,CNOT6,KLF11,EIF4B,POLR3C,SMC3,USP28,LIPT2,C3orf58,TMTC4,DDOST,MEOX1,RBFOX2,BTBD8,WDYHV1,DNAJC5,UGP2,XRCC6,RECQL4,SEPT10,SMCHD1,RBBP4,DENND4B,GPR19,TRA2A,RAD51,LYST,NOP58,VARS,LRRC8A,CNNM3,LRWD1,WDR1,SLC20A1,MED18,POMT2,HAUS8,CHERP,UPP1,MTHFD1,GAN,RPA2,TBL2,PRKCI,FAM111A,MAPK14,VAV3,KCNJ16,SFPQ,ARHGEF1,ERI1,PHACTR4,RICTOR,ACIN1,ZNF367,ABCC1,EEFSEC,HNRNPUL1,HADHB,THEM4,OTUD4,CSRP2,GPATCH8,RPA1,ITPR1,UBQLN4,MIS18BP1,PCNA,RFC4,PSMB2,E2F1,TBC1D15,MSH5,CD2BP2,C12orf10,CAMK2N2,SP2,CHEK1,XYLB,TRIB1,POLR2M,MCM10,LIPG,PTK7,RPS19,TOR1AIP2,ATXN2L,WDR76,FTL,KIF15,SPDYA,MCM2,RBM6,UNK,FEN1,DNPH1,ZFP36L2,GLS2,POLH,XXYLT1,MELK,TMEM30A,CCNL1,STMN1,USF3,ATG4C,C19orf43,EZH2,SIAH2,CIPC,ADPRHL2,RTCA,SSNA1,NUP155,ZNF212,RPL3,PSMC4,RANBP1,ARRB2,UBE2D2,C1orf27,NFYC,TMPO,TEX261,TAGLN2,RFC3,TEAD4,PAFAH1B2,MED23,NUP50,CENPP,PMF1/PMF1-BGLAP,C4orf27,ARSB,TM9SF1,DTL,SLC25A25,MAP2K7,DLGAP4,let-7,PPP4R3A,ANAPC13,KIF24,ZFP64,ITPA,ARHGAP31,SPR,TONSL,SMARCC1,LGALS1,SNTB2,KIF13B,ACAT2,POLA1,EIF4A2,EIF3B,GNL2,MAP1A,AHCY,HCFC1,NKTR,SLC2A1,NPAT,CD3EAP,UPF3B,MSMO1,SP4,CNTRL,ACER3,CCDC138,FANCA,GADD45B,DPM2,CPD,MTCH1,KPNA3,KHDRBS1,DROSHA,PASK,ARID3A,MCM3,MSH2,MAZ,COX7A2,FBXO5,TFB1M,NAV2,NUP58,RPGRIP1L,SMC1A,INTS3,UFSP2,MLLT3,OSBPL1A,WEE1,CDCA2,OSBPL8,HIRIP3,TEF,DDX26B,KIAA0101,BARD1,ZNF219,E2F3,BCL7B,GTPBP2,VAV2,NAA40,SMARCD1,NFATC4,G3BP1,BIRC5,UMPS,KLF5,BRCA2,ZDHHC6,CCP110,DEPDC1B,MTBP,RAN,mir-148,DDX20,MKI67,SLC15A4,RBL1,HIST1H2AB,RPS11,RARA,PYCRL,CNOT1,ANGPTL6,YWHAZ,MDC1,SPG7,UBE2G2,SSBP1,AAAS,AHI1,CPSF3L,DNAJC14,CLCC1,BRPF3,HMGB2,C9orf89,ATAD5,AKAP11,RAB33B,PPIF,SUZ12,SEC24B,SPC25,PAICS,NAP1L1,IQSEC2,CDK1,GLTP,CHRAC1,ATL2,CTNNBL1,CALU,REV1,CIRBP,MMS19,SAAL1,OSGEPL1,CCDC62,PFN1,LAMTOR2,MAP1B,PPP1R18,ZNF609,RELL1,PTRH2,STAG1,RAB11FIP1,RYR3,TMUB2,CDCA3,HIST1H3J,FOSL2,C7orf50,MCM5,P4HB,NUBP1,STARD4,Cdc42,TIMELESS,CDIPT,USE1,NUAK1,TBCCD1,SLC35E1,CDK2,KDM3A,ZFAT,COPS4,BRD2,RASL11B,TMEM17,PA2G4,NUDT3,WDHD1,IPO9,PRIM1,GMNN,CDCA5,IPO5,RASSF1,MTRR,TRA2B,UHRF1,SNRPB,PANK2,COTL1,HAT1,ERBB3,RFC5,PPP1R16A,C19orf68,CIART,U2SURP,ACAT1,MIS12,HIST1H2AM,CASP8AP2,LANCL2,RMI1,PRKAB2,CLMP,HAUS4,KRAS,MMGT1,FHL2,SPA17,MTHFD2,SCPEP1,IQGAP3,TP53,PCGF6,GRM8,RRM2,ADO,GINS3,ZC3H18,SKP2,HSPA8,TOMM22,SUPT16H,CCNF,PDS5A,CCDC51,TSSC4,SRSF4,CAPN7,LTN1,CYP39A1,GUCD1,CCDC167,WWC2,MMS22L,SPAG5,ZMYND19,IRF2BP1,TRIM27,RAD54L2,MMP8,SSTR5,RANGAP1,NOL12,TLR7,KIF2C,DIS3,STT3B,ECHS1,MRPL12,POLG,NXF1,GPR137C,CTDSPL2,RIC8B,TMEM106C,ZCWPW1,TCF19,SHMT1,PLEKHA1,RAD51AP1,CSTF3,PPIP5K2,NUTF2,WRAP53,DLGAP5,NDST3,SRSF2,CCDC15,PRELID3B,KIF16B,IFT140,PIM1,EIF3D,PHF20,MYBL2,C17orf53,BRIP1,NUCKS1,PELP1,ZNF706,IER2,SNX18,IPO11,ORC6,MED9,ENKD1,ATAD2,PFKM,MEF2B,SASH1,OR6C70,TFAM,DUSP1,SRSF7,RNF219,RPSA,ARID1A,VPS72,GTF2I,C14orf80,CDCA7,CSRP2BP,CLP1,DBR1,DNAJB1,MCM9,ZNF280D,NOP56,TUBG1,PRDM4,ZSCAN21,ATL3,TPP2,NBN,PMP22,EHD4,MSH6,DCTN1,CDC7,RAPH1,CHAF1A,INTS7,MXD3,TARDBP,PLCB1,IRS2,CEP250,ANAPC11,CREBZF,PITPNB,NFXL1,HNRNPA0,TIPIN,SMIM8,ARL6IP6,TOPBP1,RABL3,NUFIP1,TFAP4,WDR89,AP1S1,PTBP1,CCNO,NSMCE2,GAB1,H2AFX,TMX1,MBD4,ACY1,CLSPN,MAPK7,L3MBTL2,CTC1,XPOT,ACVR2B,SLBP,TRADD,TCOF1,CHAF1B,DGCR8,TOP2A,KHSRP,PCBP2,mir-199,DCK,ACTB,CDC6,RQCD1,ZBTB11,FADD,FIS1,RAD54B,CDKL2,TRAPPC10,MUTYH,NOP2,DENND1A,SEC62,SUPT3H,HINFP,MCM8,SZT2,MMP16,C5orf24,LIMK2,TUBB,UBA2,LMNB1,SRSF1,ARHGEF40,POLD3,RPS20,DNAJC8,NAA16,BRCA1,RAD51C,DLC1,CDC25A,PJA1,DNASE2,ZC3H6,SSRP1,MED14,BAG4,WWP2,SRSF3,CCNG2,TUBE1,MBTPS1,CASP2,BAZ1B,PLEKHH3,ELK4,GTF3C5,PKM,NSL1,MCM4,NFX1,ROR2,PCK2,RRN3,TCP1,E2F8,GABBR1,GPT,FCH

Supplemental Table 7. General IPA functions for E2F1, E2F3A and E2F3B promoter targets

ChIP-seq	Category	B-H p-value	Genes
E2F3A	Organismal Injury and Abnormalities	3.55E-09	TIMM13,C6orf203,PPWD1,SKAP2,AFMID,PEAK1,CRKL,RANBP3,MAFF,MRPL49,LCE3C,ELMO2,PIM3,RABL6,IBTK,MTMR3,POLR1E,ID3,KPNB1,MTHFD1L,EEF1A1,ZFP1,PIGU,CBX5,MATR3,ESCO2,RAD54L,KCNAB2,NAGLU,CBX3,FEM1A,ELMOD2,KLF10,RAB23,RNASEH2B,GPHN,DDX27,C16orf59,TRIP13,TACC3,RNF26,Scd2,HERPUD1,SNX27,PPM1G,CENPI,ACTL6B,RER1,HNRNPL,MCM6,TUBA1B,ZFP62,ZNF628,UBR2,RNF38,CTDSP1,ZFP41,GJC3,HIST1H2AJ,PNKD,TTLL5,DNMT1,LMF2,C19orf57,TMEM39B,GET4,MALL,PABPC1,CENPB,COMMD9,PLEC,CNOT10,ZMYM6,AP5Z1,SH3GL1,RNF168,FAM222A,NCLN,KIAA0368,HAUS6,SGOL1,SNAI2,MGME1,CDT1,BOK,FKBP1A,H2AFZ,TNKS,NEIL3,RIF1,RFC2,TXNL1,FKBP5,NSMCE1,NCBP3,PKN3,MCMBP,DUT,RRP1B,NUP85,CEP152,ZNF526,AP4M1,SMC6,COPS3,NCAPG2,RRM1,ADSS,SENP1,DUS3L,GPR180,COBLL1,NCAM1,FMNL3,PRPF19,MRPS17,TMCO1,ZNF91,PBK,RPUSD2,YWHAQ,FAM208A,FSD1L,MID1IP1,BIRC6,GSN,SMC2,ZMIZ1,GNG11,POLR2A,DSCR3,CNTLN,ZNF383,C1orf174,MLLT1,ZNF382,DSCC1,RPS27L,TRMT2A,TRIM59,TEX9,RAF1,MYH9,MTNR1A,IFT80,NKAP,C6orf89,RCL1,ZNF689,STAG3,TYMS,TUBGCP3,PAPD4,DNAJC9,GINM1,MDM1,SPATA20,ATE1,APH1A,GTSE1,ANAPC5,TFRC,ZYX,ZDHHC1,FRG1,ANKLE1,RBM39,TRAPPC5,FKBP2,DEK,HNRNPA2B1,GDF15,CRIPT,CDK4,CCDC191,NUF2,TMEM209,GINS2,MAP4,ALG8,CDC5L,RAD21,DHX9,RSBN1,SERTAD2,HNRNPU,MECP2,TPK1,ING5,LARP4B,SLC29A1,RUBCN,CCNE1,DDX39B,NUDT16,ABCF2,CDKN1A,PSAP,BTF3L4,PPIL1,FOXN2,MEGF9,RFWD3,TIMM50,TSFM,KXD1,PIEZO1,MYC,ZW10,SMPD4,GATC,XPO1,CACTIN,CNOT6,KLF11,EIF4B,POLR3C,SMC3,USP28,LIPT2,C3orf58,TMTC4,DDOST,MEOX1,RBFOX2,BTBD8,WDYHV1,DNAJC5,UGP2,XRCC6,RECQL4,SEPT10,SMCHD1,RBBP4,DENND4B,GPR19,TRA2A,RAD51,LYST,NOP58,VARS,LRRC8A,CNNM3,LRWD1,WDR1,SLC20A1,MED18,POMT2,HAUS8,CHERP,UPP1,MTHFD1,GAN,RPA2,TBL2,PRKCI,FAM111A,MAPK14,VAV3,KCNJ16,SFPQ,ARHGEF1,ERI1,PHACTR4,RICTOR,ACIN1,ZNF367,ABCC1,EEFSEC,HNRNPUL1,HADHB,THEM4,OTUD4,CSRP2,GPATCH8,RPA1,ITPR1,UBQLN4,MIS18BP1,PCNA,RFC4,PSMB2,E2F1,TBC1D15,MSH5,CD2BP2,C12orf10,CAMK2N2,SP2,CHEK1,XYLB,TRIB1,POLR2M,MCM10,LIPG,PTK7,RPS19,TOR1AIP2,ATXN2L,WDR76,FTL,KIF15,SPDYA,MCM2,RBM6,UNK,FEN1,DNPH1,ZFP36L2,GLS2,POLH,XXYLT1,MELK,TMEM30A,CCNL1,STMN1,USF3,ATG4C,C19orf43,EZH2,SIAH2,CIPC,ADPRHL2,RTCA,SSNA1,NUP155,ZNF212,RPL3,PSMC4,RANBP1,ARRB2,UBE2D2,C1orf27,NFYC,TMPO,TEX261,TAGLN2,RFC3,TEAD4,PAFAH1B2,MED23,NUP50,CENPP,PMF1/PMF1-BGLAP,C4orf27,ARSB,TM9SF1,DTL,SLC25A25,MAP2K7,DLGAP4,let-7,PPP4R3A,ANAPC13,KIF24,ZFP64,ITPA,ARHGAP31,SPR,TONSL,SMARCC1,LGALS1,SNTB2,KIF13B,ACAT2,POLA1,EIF4A2,EIF3B,GNL2,MAP1A,AHCY,HCFC1,NKTR,SLC2A1,NPAT,CD3EAP,UPF3B,MSMO1,SP4,CNTRL,ACER3,CCDC138,FANCA,GADD45B,DPM2,CPD,MTCH1,KPNA3,KHDRBS1,DROSHA,PASK,ARID3A,MCM3,MSH2,MAZ,COX7A2,FBXO5,TFB1M,NAV2,NUP58,RPGRIP1L,SMC1A,INTS3,UFSP2,MLLT3,OSBPL1A,WEE1,CDCA2,OSBPL8,HIRIP3,TEF,DDX26B,KIAA0101,BARD1,ZNF219,E2F3,PTGES3,BCL7B,GTPBP2,VAV2,NAA40,SMARCD1,NFATC4,G3BP1,BIRC5,UMPS,KLF5,BRCA2,ZDHHC6,CCP110,DEPDC1B,MTBP,RAN,mir-148,DDX20,MKI67,SLC15A4,RBL1,HIST1H2AB,RPS11,RARA,PYCRL,CNOT1,ANGPTL6,YWHAZ,MDC1,SPG7,UBE2G2,SSBP1,AAAS,AHI1,CPSF3L,DNAJC14,CLCC1,BRPF3,HMGB2,C9orf89,ATAD5,AKAP11,RAB33B,PPIF,SUZ12,SEC24B,SPC25,PAICS,NAP1L1,IQSEC2,CDK1,GLTP,CHRAC1,ATL2,CTNNBL1,CALU,REV1,CIRBP,MMS19,SAAL1,OSGEPL1,CCDC62,PFN1,LAMTOR2,MAP1B,PPP1R18,ZNF609,RELL1,PTRH2,STAG1,RAB11FIP1,RYR3,TMUB2,CDCA3,HIST1H3J,FOSL2,C7orf50,MCM5,P4HB,NUBP1,STARD4,Cdc42,TIMELESS,CDIPT,USE1,NUAK1,TBCCD1,SLC35E1,CDK2,KDM3A,ZFAT,COPS4,BRD2,RASL11B,TMEM17,PA2G4,NUDT3,WDHD1,IPO9,PRIM1,GMNN,CDCA5,IPO5,RASSF1,MTRR,TRA2B,UHRF1,SNRPB,PANK2,COTL1,HAT1,ERBB3,RFC5,PPP1R16A,C19orf68,CIART,U2SURP,ACAT1,MIS12,HIST1H2AM,CASP8AP2,LANCL2,RMI1,PRKAB2,CLMP,HAUS4,KRAS,MMGT1,FHL2,SPA17,MTHFD2,SCPEP1,IQGAP3,TP53,PCGF6,GRM8,RRM2,ADO,GINS3,ZC3H18,SKP2,HSPA8,TOMM22,SUPT16H,CCNF,PDS5A,CCDC51,TSSC4,SRSF4,CAPN7,LTN1,CYP39A1,GUCD1,CCDC167,WWC2,MMS22L,SPAG5,NECAB3,ZMYND19,IRF2BP1,TRIM27,RAD54L2,MMP8,SSTR5,RANGAP1,NOL12,TLR7,KIF2C,DIS3,STT3B,ECHS1,MRPL12,POLG,NXF1,GPR137C,CTDSPL2,RIC8B,TMEM106C,ZCWPW1,TCF19,SHMT1,PLEKHA1,RAD51AP1,CSTF3,PPIP5K2,NUTF2,WRAP53,DLGAP5,NDST3,SRSF2,CCDC15,PRELID3B,KIF16B,IFT140,PIM1,EIF3D,PHF20,MYBL2,C17orf53,BRIP1,NUCKS1,PELP1,ZNF706,IER2,SNX18,IPO11,ORC6,MED9,ENKD1,ATAD2,PFKM,MEF2B,SASH1,OR6C70,TFAM,DUSP1,SRSF7,RNF219,RPSA,ARID1A,VPS72,GTF2I,C14orf80,CDCA7,CSRP2BP,CLP1,DBR1,DNAJB1,MCM9,ZNF280D,NOP56,TUBG1,PRDM4,ZSCAN21,ATL3,TPP2,NBN,PMP22,EHD4,MSH6,DCTN1,CDC7,RAPH1,CHAF1A,INTS7,MXD3,TARDBP,PLCB1,IRS2,CEP250,ANAPC11,CREBZF,PITPNB,NFXL1,HNRNPA0,TIPIN,SMIM8,ARL6IP6,TOPBP1,RABL3,NUFIP1,TFAP4,WDR89,AP1S1,PTBP1,CCNO,NSMCE2,GAB1,H2AFX,TMX1,MBD4,ACY1,CLSPN,MAPK7,L3MBTL2,CTC1,XPOT,ACVR2B,SLBP,TRADD,TCOF1,CHAF1B,DGCR8,TOP2A,KHSRP,PCBP2,mir-199,DCK,ACTB,CDC6,RQCD1,ZBTB11,FADD,FIS1,RAD54B,CDKL2,TRAPPC10,MUTYH,NOP2,DENND1A,SEC62,SUPT3H,HINFP,MCM8,SZT2,MMP16,C5orf24,LIMK2,TUBB,UBA2,LMNB1,SRSF1,ARHGEF40,POLD3,RPS20,DNAJC8,NAA16,BRCA1,RAD51C,DLC1,CDC25A,PJA1,DNASE2,ZC3H6,SSRP1,MED14,BAG4,WWP2,SRSF3,CCNG2,TUBE1,MBTPS1,CASP2,BAZ1B,PLEKHH3,ELK4,GTF3C5,PKM,NSL1,MCM4,NFX1,ROR2,PCK2,RRN3,TCP1,E2F8,GABBR1,GPT,FCH

Supplemental Table 7. General IPA functions for E2F1, E2F3A and E2F3B promoter targets

ChIP-seq	Category	B-H p-value	Genes
E2F3A	Reproductive System Disease	3.55E-09	RAF1,MCM6,TUBA1B,CCP110,MYH9,C6orf203,POLA1,mir-148,SFPQ,KRAS,EIF4A2,MKI67,DDX20,ZNF367,FHL2,EIF3B,ABCC1,RARA,TARDBP,MTHFD2,HNRNPUL1,IRS2,CEP250,THEM4,HNRNPA0,TP53,TYMS,NFXL1,OTUD4,SMIM8,TOPBP1,PLEC,YWHAZ,RRM2,ITPR1,SKP2,UBE2G2,SH3GL1,PTBP1,PCNA,RFC4,APH1A,H2AFX,E2F1,ZYX,MAPK7,HAUS6,FRG1,ANKLE1,RBM39,GADD45B,CDT1,GDF15,CDK4,FKBP1A,CAMK2N2,CHEK1,TRIB1,NEIL3,MAP4,RABL6,MMP8,NOL12,TOP2A,TLR7,MCM10,KIF2C,KHSRP,FKBP5,CDC5L,RAD21,RPS19,mir-199,CEP152,CDC6,POLG,CDK1,RRM1,FADD,FIS1,RAD54B,CCNE1,MCM2,MSH2,MAZ,CDKN1A,TMEM106C,FBXO5,FEN1,ZFP36L2,NCAM1,FOXN2,EEF1A1,PFN1,SZT2,TMCO1,MMP16,MELK,TUBB,UBA2,CCNL1,SMC1A,YWHAQ,STMN1,MYC,PIM1,EZH2,RAB11FIP1,RYR3,XPO1,MYBL2,SIAH2,FOSL2,BRIP1,BRCA1,DLC1,KLF11,EIF4B,CDC25A,SMC3,USP28,P4HB,PELP1,IER2,WEE1,SNX18,RAD54L,RANBP1,GSN,SSRP1,BAG4,PFKM,WWP2,Cdc42,DUSP1,TUBE1,CASP2,NFYC,CBX3,CDK2,RFC3,TAGLN2,PAFAH1B2,MED23,ARID1A,KIAA0101,DENND4B,KLF10,PKM,BARD1,RNASEH2B,NUP50,E2F3,MCM4,CDCA7,TRA2A,RAD51,POLR2A,PRIM1,PCK2,GMNN,TCP1,VARS,E2F8,WDR1,RASSF1,VAV2,UHRF1,TRA2B,UPP1,TUBG1,let-7,ERBB3,NFATC4,RFC5,ANAPC13,ATL3,BIRC5,NBN,PRKCI,VAV3,DSCC1,MSH6,BRCA2,CAD,LGALS1
E2F3A	Gene Expression	1.27E-08	RAF1,POLA1,KRAS,NKAP,FHL2,EIF3B,IQGAP3,TP53,HCFC1,PCGF6,CD3EAP,NPAT,UPF3B,RANBP3,MAFF,SP4,HSPA8,SUPT16H,RBM39,DEK,HNRNPA2B1,WWC2,IRF2BP1,TRIM27,RAD54L2,IBTK,CDC5L,RAD21,DHX9,SERTAD2,HNRNPU,MECP2,KHDRBS1,DROSHA,MRPL12,ING5,NXF1,ID3,ARID3A,CCNE1,MSH2,CDKN1A,MAZ,TCF19,MAP3K3,TFB1M,SRSF2,CBX5,MYC,Gm21596/Hmgb1,EIF3D,PIM1,MATR3,XPO1,MYBL2,BRIP1,KLF11,POLR3C,EIF4B,OSBPL1A,PELP1,Hmgn2 (includes others),ZNF706,GABPB2,MEOX1,RBFOX2,ATAD2,MEF2B,TFAM,DUSP1,XRCC6,PCBD2,CBX3,TEF,TFEB,ARID1A,VPS72,KLF10,GTF2I,RNASEH2B,ZNF219,E2F3,PTGES3,DNAJB1,LRWD1,SLC20A1,VAV2,TRIP13,RPRD1B,TUBG1,Scd2,PRDM4,NFATC4,ZSCAN21,BIRC5,PRKCI,MAPK14,VAV3,KLF5,BRCA2,PLEKHA2,UBR2,ZNF628,SOX12,SFPQ,DDX20,RBL1,CHAF1A,ZNF367,CTDSP1,MXD3,RARA,TARDBP,PLCB1,DNMT1,CREBZF,CNOT1,TOPBP1,NUFIP1,YWHAZ,TFAP4,PTBP1,PCNA,GAB1,PSMB2,AHI1,H2AFX,E2F1,MAPK7,SNAI2,FKBP1A,HMGB2,ACVR2B,H2AFZ,SP2,SLBP,TRADD,TNKS,TOP2A,SUZ12,PPP1R8,DLX1,NAP1L1,CDK1,FADD,SENP1,NOP2,MMS19,SUPT3H,ZFP36L2,HINFP,NCAM1,CCDC62,PFN1,MELK,ZNF91,YWHAQ,PTRH2,EZH2,MID1IP1,SIAH2,CIPC,FOSL2,BRCA1,MCM5,GSN,SSRP1,Scaf1,MED14,WWP2,ARRB2,Cdc42,TIMELESS,NFYC,TMPO,ELK4,CDK2,TAGLN2,KDM3A,PRIMPOL,TEAD4,BRD2,MED23,PA2G4,PKM,ZMIZ1,NFX1,ROR2,POLR2A,GMNN,PMF1/PMF1-BGLAP,RRN3,E2F8,MAP2K7,UHRF1,let-7,NFKBIZ,MLLT1,AFF1,HIVEP2,ZNF382,CIART,PBX3,RPS27L,SMARCC1,LGALS1,LANCL2

Supplemental Table 7. General IPA functions for E2F1, E2F3A and E2F3B promoter targets

ChIP-seq	Category	B-H p-value	Genes
E2F3A	Gastrointestinal Disease	2.05E-08	SNTB2,KIF13B,ACAT2,POLA1,PPWD1,EIF4A2,SKAP2,EIF3B,GNL2,MAP1A,AHCY,NKTR,HCFC1,PEAK1,SLC2A1,NPAT,UPF3B,RANBP3,MAFF,SP4,CNTRL,MRPL49,ACER3,ELMO2,CCDC138,FANCA,PIM3,DPM2,MTCH1,RABL6,IBTK,MTMR3,KPNA3,KHDRBS1,PASK,DROSHA,POLR1E,ID3,ARID3A,MCM3,KPNB1,MTHFD1L,MSH2,MAZ,COX7A2,FBXO5,TFB1M,NAV2,EEF1A1,ZFP1,PIGU,NUP58,RPGRIP1L,CBX5,SMC1A,INTS3,UFSP2,MATR3,MLLT3,ESCO2,OSBPL1A,WEE1,RAD54L,CDCA2,OSBPL8,NAGLU,HIRIP3,CBX3,TEF,DDX26B,FEM1A,ELMOD2,KIAA0101,KLF10,RAB23,BARD1,RNASEH2B,ZNF219,DDX27,E2F3,BCL7B,GTPBP2,C16orf59,VAV2,NAA40,TRIP13,TACC3,RNF26,Scd2,HERPUD1,NFATC4,SNX27,G3BP1,BIRC5,UMPS,PPM1G,CENPI,KLF5,BRCA2,ACTL6B,ZDHHC6,RER1,HNRNPL,MCM6,CCP110,ZFP62,MTBP,UBR2,ZNF628,RAN,mir-148,DDX20,MKI67,SLC15A4,RBL1,RNF38,CTDSP1,RARA,PNKD,TTLL5,DNMT1,LMF2,TMEM39B,GET4,PYCRL,MALL,PABPC1,CNOT1,CENPB,ANGPTL6,COMMD9,PLEC,YWHAZ,MDC1,SPG7,CNOT10,AP5Z1,UBE2G2,RNF168,AAAS,FAM222A,AHI1,NCLN,CPSF3L,DNAJC14,KIAA0368,SGOL1,HAUS6,CLCC1,BRPF3,SNAI2,MGME1,BOK,FKBP1A,HMGB2,C9orf89,ATAD5,AKAP11,NEIL3,TNKS,RIF1,RAB33B,RFC2,TXNL1,NSMCE1,FKBP5,PKN3,RRP1B,NUP85,CEP152,MCMBP,AP4M1,SUZ12,SEC24B,SPC25,SMC6,PAICS,IQSEC2,NAP1L1,COPS3,NCAPG2,CDK1,RRM1,GLTP,ADSS,SENP1,ATL2,CHRAC1,CTNNBL1,REV1,CIRBP,MMS19,DUS3L,SAAL1,GPR180,COBLL1,NCAM1,OSGEPL1,CCDC62,FMNL3,PFN1,LAMTOR2,MRPS17,TMCO1,MAP1B,PPP1R18,ZNF609,ZNF91,RPUSD2,PBK,RELL1,FAM208A,PTRH2,STAG1,RYR3,CDCA3,TMUB2,HIST1H3J,FOSL2,C7orf50,MCM5,P4HB,NUBP1,BIRC6,GSN,SMC2,TIMELESS,CDIPT,USE1,NUAK1,TBCCD1,SLC35E1,CDK2,KDM3A,COPS4,ZFAT,BRD2,RASL11B,TMEM17,PA2G4,NUDT3,WDHD1,ZMIZ1,IPO9,GMNN,CDCA5,IPO5,RASSF1,CNTLN,MTRR,SNRPB,TRA2B,UHRF1,ZNF383,COTL1,PANK2,HAT1,ERBB3,RFC5,PPP1R16A,C19orf68,MLLT1,ZNF382,CIART,U2SURP,RPS27L,DSCC1,ACAT1,MIS12,TRMT2A,HIST1H2AM,TRIM59,CASP8AP2,RAF1,MYH9,PRKAB2,MTNR1A,CLMP,HAUS4,IFT80,KRAS,NKAP,C6orf89,MMGT1,RCL1,STAG3,IQGAP3,TYMS,TP53,TUBGCP3,PAPD4,PCGF6,GRM8,RRM2,GINM1,ADO,MDM1,GINS3,SPATA20,SKP2,ZC3H18,ATE1,HSPA8,TOMM22,SUPT16H,CCNF,PDS5A,GTSE1,ANAPC5,ZYX,TFRC,CCDC51,TSSC4,ZDHHC1,CAPN7,LTN1,FRG1,ANKLE1,RBM39,TRAPPC5,FKBP2,DEK,GUCD1,HNRNPA2B1,GDF15,CDK4,CCDC191,WWC2,NUF2,MMS22L,SPAG5,TMEM209,GINS2,ZMYND19,MAP4,TRIM27,IRF2BP1,RAD54L2,MMP8,RANGAP1,SSTR5,TLR7,ALG8,KIF2C,CDC5L,DIS3,RAD21,DHX9,RSBN1,STT3B,SERTAD2,HNRNPU,ECHS1,MECP2,MRPL12,POLG,ING5,LARP4B,TPK1,NXF1,SLC29A1,GPR137C,RUBCN,CCNE1,DDX39B,ABCF2,NUDT16,RIC8B,CDKN1A,ZCWPW1,TCF19,PSAP,SHMT1,BTF3L4,PPIL1,CSTF3,RAD51AP1,PPIP5K2,WRAP53,NDST3,DLGAP5,CCDC15,MEGF9,RFWD3,TIMM50,TSFM,PIEZO1,KIF16B,IFT140,MYC,SMPD4,PIM1,PHF20,GATC,XPO1,MYBL2,CACTIN,C17orf53,BRIP1,KLF11,NUCKS1,EIF4B,USP28,SMC3,PELP1,LIPT2,C3orf58,ZNF706,SNX18,TMTC4,IPO11,ORC6,DDOST,MEOX1,ENKD1,BTBD8,ATAD2,PFKM,MEF2B,SASH1,TFAM,UGP2,DUSP1,SRSF7,RECQL4,XRCC6,SEPT10,RNF219,SMCHD1,RBBP4,ARID1A,VPS72,DENND4B,C14orf80,GPR19,CDCA7,TRA2A,RAD51,CSRP2BP,LYST,CLP1,NOP58,DNAJB1,VARS,MCM9,CNNM3,LRRC8A,LRWD1,WDR1,MED18,SLC20A1,POMT2,HAUS8,ZNF280D,NOP56,CHERP,TUBG1,PRDM4,ZSCAN21,MTHFD1,ATL3,GAN,TPP2,RPA2,NBN,TBL2,PMP22,MAPK14,FAM111A,PRKCI,VAV3,EHD4,MSH6,DCTN1,CDC7,KCNJ16,SFPQ,ARHGEF1,ERI1,PHACTR4,RAPH1,RICTOR,CHAF1A,ACIN1,INTS7,ZNF367,MXD3,ABCC1,TARDBP,HNRNPUL1,EEFSEC,PLCB1,IRS2,CEP250,ANAPC11,PITPNB,CREBZF,TIPIN,ARL6IP6,TOPBP1,CSRP2,RABL3,GPATCH8,NUFIP1,RPA1,ITPR1,WDR89,UBQLN4,AP1S1,PTBP1,MIS18BP1,PCNA,NSMCE2,RFC4,GAB1,H2AFX,TMX1,ACY1,MBD4,E2F1,MSH5,TBC1D15,CLSPN,MAPK7,L3MBTL2,CTC1,CD2BP2,C12orf10,XPOT,ACVR2B,SP2,SLBP,CHEK1,XYLB,TRADD,TRIB1,POLR2M,TCOF1,DGCR8,TOP2A,LIPG,MCM10,PCBP2,KHSRP,PTK7,RPS19,mir-199,DCK,ACTB,CDC6,RQCD1,TOR1AIP2,ATXN2L,FIS1,RAD54B,WDR76,FTL,KIF15,SPDYA,CDKL2,MCM2,RBM6,TRAPPC10,NOP2,MUTYH,DENND1A,UNK,SEC62,FEN1,SUPT3H,ZFP36L2,GLS2,HINFP,POLH,MCM8,SZT2,MMP16,XXYLT1,MELK,LIMK2,TUBB,UBA2,LMNB1,CCNL1,STMN1,USF3,SRSF1,ATG4C,ARHGEF40,POLD3,DNAJC8,EZH2,SIAH2,NAA16,CIPC,RAD51C,ADPRHL2,BRCA1,DLC1,RTCA,CDC25A,NUP155,DNASE2,PJA1,ZNF212,ZC3H6,RANBP1,SSRP1,MED14,BAG4,WWP2,UBE2D2,ARRB2,CCNG2,TUBE1,CASP2,MBTPS1,C1orf27,NFYC,BAZ1B,PLEKHH3,TMPO,TEX261,ELK4,RFC3,TAGLN2,TEAD4,MED23,GTF3C5,PKM,MCM4,CENPP,NFX1,ROR2,PCK2,RRN3,C4orf27,TCP1,ARSB,E2F8,TM9SF1,DTL,SLC25A25,MAP2K7,DLGAP4,let-7,FCHSD2,GABBR1,GPT,PSMA1,USP1,NFKBIZ,IPP,AFF1,HIVEP2,KIF24,ZFP64,ARHGAP31,SPR,CAD,TONSL,SMARCC1,LGALS1
E2F3A	Cellular Compromise	2.60E-08	TP53,MCM8,TUBG1,KRAS,USP1,NBN,MYC,CCNE1,Gm21596/Hmgb1,MSH2,PIM1,RECQL4,H2AFX,CDKN1A,BRIP1,RAD51C,MCM9,BRCA1,FANCA,CDK2,POLH,CDC25A,RASSF1

Supplemental Table 7. General IPA functions for E2F1, E2F3A and E2F3B promoter targets

ChIP-seq	Category	B-H p-value	Genes
E2F3A	Cellular Assembly and Organization	2.80E-08	RAF1,CCP110,MYH9,POLA1,CDC7,RAN,SFPQ,KRAS,HAUS4,DDX20,RBL1,CHAF1A,STAG3,TARDBP,DNMT1,TP53,TUBGCP3,HCFC1,PCGF6,RPA1,TFAP4,SPG7,SKP2,RNF168,H2AFX,CCNF,PDS5A,E2F1,SGOL1,HAUS6,DEK,CTC1,CDT1,CRIPT,CDK4,FKBP1A,NUF2,USP39,MMS22L,SPAG5,CHEK1,TNKS,MAP4,RIF1,TOP2A,KIF2C,RAD21,DHX9,RPS19,CEP152,MCMBP,MECP2,PPP1R8,SPC25,CDC6,SMC6,TOR1AIP2,NCAPG2,CDK1,FIS1,SENP1,CCNE1,DDX39B,ATL2,NUDT16,CDKN1A,MMS19,FBXO5,PLEKHA1,DLGAP5,MCM8,PRPF19,CLN8,CAV2,RFWD3,TIMM50,MELK,LIMK2,TUBB,LMNB1,SMC1A,MYC,ZW10,INTS3,STMN1,PIM1,STAG1,XPO1,INIP,BRCA1,Nolc1,ESCO2,SMC3,NUP155,NUBP1,ORC6,RAD54L,RANBP1,GSN,CDCA2,SSRP1,CCNG2,Cdc42,SMC2,XRCC6,MBTPS1,USE1,NAGLU,HIRIP3,BAZ1B,TMPO,CBX3,CDK2,RBBP4,KDM3A,TFEB,ARID1A,Pcnt,KIAA0101,BARD1,WDHD1,MCM4,PTGES3,RAD51,LYST,PPP1R9B,GMNN,RRN3,PMF1/PMF1-BGLAP,CDCA5,ARSB,MCM9,LRWD1,RASSF1,TRIP13,TACC3,HAUS8,UHRF1,TUBG1,ATL3,BIRC5,TPP2,NBN,RPA2,PRKCI,MAPK14,ITPA,DCTN1,BRCA2,TONSL,MIS12,RAB6A
E2F3A	Cellular Development	1.99E-07	RAF1,RMI1,MTBP,RAN,mir-148,SFPQ,ARHGEF1,KRAS,MKI67,RICTOR,RBL1,ACIN1,FHL2,EIF3B,RARA,TARDBP,IRS2,AHCY,THEM4,TP53,TYMS,PEAK1,SLC2A1,TOPBP1,CRKL,CENPB,YWHAZ,RRM2,ITPR1,SKP2,SH3GL1,PTBP1,MICU1,PCNA,SSBP1,GAB1,RFC4,CCNF,E2F1,TFRC,MAPK7,FANCA,PIM3,CTC1,GADD45B,CDT1,GDF15,HNRNPA2B1,CDK4,CAMK2N2,H2AFZ,SP2,CHEK1,TRADD,RABL6,TNKS,MMP8,SSTR5,DGCR8,KIF2C,FKBP5,RAD21,DHX9,STT3B,mir-199,KHDRBS1,PPIF,SUZ12,ACTB,DROSHA,CDC6,POLG,ID3,COPS3,CDK1,RRM1,ARID3A,FADD,SENP1,FTL,CCNE1,SPDYA,MCM2,CIRBP,CDKN1A,SHMT1,GCAT,FEN1,PPIL1,POLH,NCAM1,SRSF2,DLGAP5,EEF1A1,MCM8,PRPF19,PFN1,CAV2,MAP1B,MELK,TUBB,LMNB1,PBK,SMC1A,STMN1,MYC,YWHAQ,SRSF1,PIM1,STAG1,EZH2,MLLT3,MYBL2,BRCA1,FOSL2,DLC1,CDC25A,EIF4B,SMC3,PELP1,NUBP1,BIRC6,ATAD2,CDCA2,SRSF3,Cdc42,CCNG2,DUSP1,RECQL4,CASP2,XRCC6,CDK2,ELK4,RFC3,TAGLN2,TEAD4,COPS4,ARID1A,PA2G4,KIAA0101,GTF2I,KLF10,BARD1,PKM,RNASEH2B,E2F3,PTGES3,ZMIZ1,TRA2A,RAD51,PCK2,PPP1R9B,GMNN,NOP58,TCP1,CDCA5,MCM9,E2F8,RASSF1,DTL,MAP2K7,UHRF1,RPRD1B,HAT1,let-7,ERBB3,NFATC4,BIRC5,TPP2,NBN,AFF1,PMP22,MAPK14,PRKCI,PBX3,VAV3,KLF5,ACAT1,BRCA2,LGALS1
E2F3A	Cellular Function and Maintenance	2.17E-07	RAF1,MCM8,CCP110,PRPF19,POLA1,RAN,SFPQ,RBL1,SMC1A,CHAF1A,STMN1,MYC,Gm21596/Hmgb1,EZH2,XPO1,BRIP1,BRCA1,Nolc1,TP53,TUBGCP3,NUP155,NUBP1,RAD54L,RANBP1,RPA1,SSRP1,RNF168,PCNA,SMC2,H2AFX,XRCC6,CCNF,E2F1,CDK2,KDM3A,DEK,CTC1,ARID1A,Pcnt,CDK4,WDHD1,PTGES3,CHEK1,SPAG5,RAD51,MAP4,TNKS,RIF1,RRN3,RAD21,LRWD1,RPS19,TACC3,CEP152,HAUS8,TUBG1,SPC25,BIRC5,TPP2,RPA2,NBN,MSH2,ITPA,REV1,NUDT16,CDKN1A,BRCA2,DCTN1
E2F3A	Cell Morphology	2.17E-07	DEK,MCM8,PRPF19,RAN,LMNB1,CHAF1A,CHEK1,RAD51,MAP4,RIF1,Gm21596/Hmgb1,EZH2,GMNN,MCM9,BRCA1,DNMT1,RASSF1,TP53,TACC3,TUBG1,ORC6,RAD54L,TFAP4,RPA1,CDK1,NCAPG2,SKP2,NBN,RNF168,PCNA,SMC2,REV1,XRCC6,H2AFX,CDKN1A,BRCA2,FBXO5,TMPO,RBBP4
E2F3A	Hematological Disease	4.30E-06	MCM6,TUBA1B,RAF1,MYH9,MTNR1A,PPWD1,POLA1,RAN,mir-148,KRAS,MKI67,RPS11,CHAF1A,MXD3,ABCC1,RARA,HADHB,EEFSEC,PNKD,MAP1A,DNMT1,C19orf57,LMF2,PYCRL,TP53,TYMS,PABPC1,NKTR,NPAT,NUFIP1,RRM2,YWHAZ,MSMO1,MDC1,RANBP3,RPA1,ITPR1,MDM1,SKP2,SH3GL1,PCNA,PSMB2,AHI1,H2AFX,CCNF,APH1A,PDS5A,E2F1,SRSF4,FRG1,FANCA,L3MBTL2,DEK,SNAI2,GADD45B,CRIPT,CPD,DPM2,GDF15,CDK4,FKBP1A,MMS22L,CHEK1,TRIB1,TNKS,RIF1,TOP2A,TLR7,NCBP3,KIF2C,DIS3,RAD21,MTMR3,RPS19,mir-199,ZNF526,SUZ12,DCK,SEC24B,ACTB,PASK,NAP1L1,ID3,CDK1,RRM1,KPNB1,FADD,RAD54B,MTHFD1L,MSH2,REV1,MUTYH,CDKN1A,SHMT1,GPR180,FEN1,ZFP36L2,CSTF3,NUTF2,NCAM1,EEF1A1,NAV2,SRSF2,ZNF609,MELK,TMEM30A,TUBB,ZNF91,KIF16B,SMC1A,FAM208A,MYC,STMN1,SRSF1,Gm21596/Hmgb1,RPS20,STAG1,EIF3D,PIM1,EZH2,MLLT3,XPO1,CACTIN,BRCA1,DLC1,CDC25A,MCM5,OSBPL1A,SMC3,ZNF212,RPL3,WEE1,SNX18,BIRC6,RAD54L,RANBP1,GSN,CDCA2,MEF2B,Cdc42,TUBE1,XRCC6,CASP2,RECQL4,CDK2,RBBP4,RPSA,BRD2,ARID1A,DENND4B,GTF2I,BARD1,GPHN,DDX27,E2F3,ZMIZ1,RAD51,ROR2,PRIM1,PMF1/PMF1-BGLAP,IPO5,LRRC8A,E2F8,CNTLN,RASSF1,SLC20A1,SNRPB,HAT1,TUBG1,let-7,GABBR1,USP1,MTHFD1,G3BP1,BIRC5,TPP2,MLLT1,NBN,PRKCI,PBX3,MSH6,ARHGAP31,BRCA2,SMARCC1,CAD,LANCL2,LGALS1

Supplemental Table 7. General IPA functions for E2F1, E2F3A and E2F3B promoter targets

ChIP-seq	Category	B-H p-value	Genes
E2F3A	Immunological Disease	4.30E-06	RAF1,PPWD1,POLA1,mir-148,RAN,KRAS,MKI67,CHAF1A,MXD3,RARA,DNMT1,LMF2,TP53,TYMS,PABPC1,PYCRL,NPAT,RRM2,YWHAZ,MDC1,RANBP3,RPA1,SKP2,PCNA,AHI1,PSMB2,H2AFX,CCNF,APH1A,E2F1,FRG1,DEK,GADD45B,GDF15,CDK4,FKBP1A,CHEK1,SSTR5,TOP2A,TLR7,KIF2C,DIS3,RAD21,MTMR3,SUZ12,DCK,KHDRBS1,NAP1L1,ID3,CDK1,RRM1,KPNB1,FADD,RAD54B,MTHFD1L,MSH2,MUTYH,CDKN1A,FEN1,CSTF3,NUTF2,NCAM1,SRSF2,TUBB,TMEM30A,ZNF91,SMC1A,MYC,STMN1,SRSF1,Gm21596/Hmgb1,PIM1,EZH2,XPO1,BRCA1,DLC1,MCM5,RPL3,BIRC6,RAD54L,RANBP1,GSN,CDCA2,MEF2B,Cdc42,TUBE1,XRCC6,CASP2,RECQL4,CDK2,BRD2,ARID1A,GTF2I,ZMIZ1,RAD51,ROR2,PRIM1,PMF1/PMF1-BGLAP,IPO5,LRRC8A,RASSF1,SNRPB,HAT1,TUBG1,let-7,GABBR1,G3BP1,BIRC5,NBN,PRKCI,MSH6,BRCA2,SMARCC1,CAD,LANCL2,LGALS1
E2F3A	Connective Tissue Development and Function	4.54E-06	SRSF2,RAF1,MCM8,PRPF19,MTBP,CDC7,SFPQ,KRAS,ARHGEF1,RBL1,RICTOR,LMNB1,MYC,STMN1,SRSF1,EIF3B,STAG1,EZH2,RARA,MYBL2,FOSL2,BRCA1,AHCY,CDC25A,TP53,SMC3,PELP1,SSRP1,SKP2,SH3GL1,Cdc42,GAB1,DUSP1,XRCC6,RECQL4,CCNF,MBD4,E2F1,TFRC,FANCA,CDK2,PIM3,CTC1,ARID1A,GADD45B,PA2G4,KIAA0101,GTF2I,CDK4,RNASEH2B,E2F3,SP2,ZMIZ1,PTGES3,CHEK1,TRADD,MAP4,NOP58,CDCA5,MCM9,DHX9,RASSF1,MAP2K7,MECP2,KHDRBS1,PPIF,SUZ12,HAT1,ACTB,CDC6,let-7,ERBB3,ID3,TPP2,ARID3A,NBN,FADD,CCNE1,MAPK14,MSH2,REV1,CIRBP,KLF5,CDKN1A,ACAT1,SHMT1,BRCA2,FEN1,PPIL1
E2F3A	Infectious Diseases	6.78E-05	RAF1,RMI1,POLA1,SOX12,mir-148,RAN,SFPQ,KRAS,SLC15A4,CHAF1A,INTS7,RARA,VAMP3,IRS2,PYCRL,TYMS,TP53,TIPIN,SLC2A1,UPF3B,RRM2,TFAP4,SPG7,UBQLN4,AP1S1,LCE3C,SHCBP1,GAB1,SUPT16H,ZYX,TFRC,CCDC51,LRIF1,DEK,CDK4,FKBP1A,USP39,TRADD,NECAB3,NEIL3,MAP4,RAB33B,DGCR8,TLR7,TOP2A,KHSRP,PCBP2,RAD21,DHX9,mir-199,NUP85,HNRNPU,SUZ12,KHDRBS1,PPP1R8,DROSHA,ACTB,POLR1E,POLG,NXF1,FADD,MND1,KPNB1,FTL,MSH2,POLA2,SPCS3,EEF1A1,SRSF2,FAM76B,CAV2,KXD1,LIMK2,TUBB,PBK,MYC,SRSF1,RPS20,EZH2,RAB11FIP1,XPO1,MID1IP1,SNU13,BRCA1,NUP155,RPL3,GABPB2,DDOST,PSMC4,RANBP1,SSRP1,MED14,WWP2,PFKM,DUSP1,TUBE1,USE1,MBTPS1,CASP2,TMPO,CDK2,TAGLN2,RPSA,ARID1A,NUDT3,GTF2I,NUP50,PTGES3,POLR2A,DNAJB1,RASSF1,SLC20A1,DLGAP4,NOP56,RNF26,TUBG1,let-7,GPT,GABBR1,PSMA1,G3BP1,NFKBIZ,UMPS,C1orf174,PRKCI,MAPK14,CAD,ACTL6B,RAB6A,LGALS1
E2F3A	Connective Tissue Disorders	7.79E-05	SRSF2,EEF1A1,RAF1,MELK,KRAS,RBL1,STMN1,MYC,SIVA1,PTRH2,EIF3B,PIM1,RARA,ABCC1,MYBL2,BRCA1,DNMT1,TP53,P4HB,YWHAZ,BIRC6,ITPR1,GSN,SKP2,ARRB2,TFAM,GAB1,DUSP1,XRCC6,MBTPS1,CASP2,USE1,MBD4,E2F1,PIDD1,SNAI2,ARID1A,GADD45B,CDK4,BOK,CHEK1,TRADD,MAP4,TOP2A,NSMCE1,MAP2K7,KHDRBS1,ACTB,GABBR1,NFATC4,BIRC5,CDK1,TPP2,NBN,FADD,SENP1,CCNE1,MAPK14,MSH2,CDKN1A,BRCA2,CASP8AP2
E2F3A	Cellular Response to Therapeutics	1.09E-04	TP53,MCM8,PPIF,RAD54L,KRAS,Abcb1b,NBN,RAD51,RAD54B,PCNA,MXD3,MSH2,ABCC1,XRCC6,CDKN1A,BRCA2,FEN1,MYBL2,BRCA1,MCM9,Paxip1,POLH
E2F3A	Nucleic Acid Metabolism	1.20E-04	TYMS,ADSS,DUT,DCK,RRM2,SHMT1,DTYMK,UMPS,RRM1
E2F3A	Small Molecule Biochemistry	1.20E-04	TYMS,ADSS,DUT,DCK,RRM2,SHMT1,DTYMK,UMPS,RRM1
E2F3A	Tissue Development	1.73E-04	RAF1,MCM8,PFN1,KRAS,RPGRIP1L,PHACTR4,RBL1,LMNB1,MYC,STAG1,EZH2,RARA,MYBL2,FOSL2,BRCA1,DLC1,TP53,WEE1,SKP2,Cdc42,DUSP1,CCNF,E2F1,CDK2,CTC1,ARID1A,PA2G4,RAB23,CDK4,RNASEH2B,SP2,ZMIZ1,PTGES3,GMNN,TCOF1,MCM10,MCM9,PTK7,UHRF1,HAT1,SEC24B,ACTB,CDC6,MTHFD1,BIRC5,ID3,NCAPG2,PPM1G,ARID3A,NBN,FADD,CCNE1,MTHFD1L,MAPK14,CIRBP,CDKN1A,SHMT1,BRCA2,FEN1
E2F3A	Organismal Development	1.73E-04	RAF1,RMI1,UBR2,mir-148,RAN,CDC7,KRAS,PHACTR4,RBL1,CHAF1A,RCL1,MXD3,RARA,ABCC1,TARDBP,IRS2,DNMT1,TP53,TOPBP1,CRKL,MAFF,ATE1,CCNF,APH1A,E2F1,TFRC,MAPK7,CTC1,CDK4,ACVR2B,H2AFZ,SP2,CHEK1,NEIL3,TNKS,TCOF1,MCM10,PCBP2,PTK7,mir-199,SEC24B,ING5,ID3,COPS3,NCAPG2,CDK1,MTHFD1L,CCNE1,CDKN1A,SHMT1,FBXO5,FEN1,PLEKHA1,NCAM1,PRPF19,PFN1,MAP1B,RPGRIP1L,LMNB1,MYC,EZH2,MID1IP1,MYBL2,BRCA1,FOSL2,DLC1,CDC25A,ESCO2,OSBPL1A,BIRC6,PSMC4,RANBP1,GSN,Abcb1b,SRSF3,Cdc42,TIMELESS,CASP2,Paxip1,TEAD4,ARID1A,Pcnt,RAB23,E2F3,RAD51,ROR2,Ppp1cc,GMNN,ARSB,LRRC8A,E2F8,SLC25A25,POMT2,UHRF1,TUBG1,GABBR1,ERBB3,SNX27,USP1,MTHFD1,NBN,MAPK14,KLF5,DCTN1,BRCA2,SMARCC1,LGALS1

Supplemental Table 7. General IPA functions for E2F1, E2F3A and E2F3B promoter targets

ChIP-seq	Category	B-H p-value	Genes
E2F3A	Tissue Morphology	1.89E-04	NDST3,PFN1,MYH9,LAMTOR2,UBR2,MMP16,SOX12,KRAS,RPGRIP1L,PHACTR4,RBL1,MYC,PTRH2,EZH2,RARA,MYBL2,BRCA1,DLC1,CDC25A,TP53,ANGPTL6,BIRC6,MEOX1,Cdc42,ARRB2,GAB1,CCNF,APH1A,TFRC,NAGLU,MAPK7,Paxip1,ZFAT,ARID1A,RAB23,ACVR2B,H2AFZ,ZMIZ1,RAD51,ROR2,GMNN,TCOF1,MCM10,E2F8,PTK7,DHX9,SLC20A1,POMT2,UHRF1,SUZ12,TRA2B,SEC24B,HAT1,PPP1R8,ERBB3,NFATC4,MTHFD1,COPS3,ARID3A,NBN,SENP1,MTHFD1L,CCNE1,PRKCI,MAPK14,KLF5,SHMT1,FBXO5,BRCA2,SMARCC1
E2F3A	Hereditary Disorder	2.11E-04	TP53,MYH9,BARD1,CDK4,FKBP1A,NBN,RAD51,PCNA,CCNE1,MSH2,MUTYH,ABCC1,E2F1,MSH6,BRCA2,BRCA1,BRIP1,RAD51C
E2F3A	Respiratory Disease	2.21E-04	RAF1,EEF1A1,CCP110,PRPF19,MYH9,MTNR1A,PRELID3B,MMP16,KCNJ16,KRAS,EIF4A2,MKI67,RBL1,TUBB,RPS11,SMC1A,STMN1,MYC,SRSF1,STAG1,EZH2,RARA,MLLT3,BRCA1,DNMT1,TYMS,TP53,PABPC1,SMC3,P4HB,GRM8,TMTC4,RRM2,YWHAZ,TFAP4,ITPR1,GSN,CDCA2,AP5Z1,SKP2,PFKM,ARRB2,PCNA,TFAM,RFC4,TUBE1,MBTPS1,E2F1,ZYX,ARID1A,GADD45B,PKM,CDK4,MAP4,POLR2A,MMP8,DGCR8,TOP2A,CDCA5,RAD21,RASSF1,DHX9,DCK,DROSHA,CDC6,TUBG1,let-7,GABBR1,TPK1,ERBB3,PPP4R3A,G3BP1,SLC29A1,BIRC5,CDK1,NBN,RRM1,FADD,FTL,MAPK14,PRKCI,MCM2,CTNNBL1,MSH2,MUTYH,KLF5,CDKN1A,MSH6,BRCA2,DNPH1,ZFP36L2,NCAM1,LGALS1
E2F3A	Molecular Transport	8.61E-04	NUP155,KHDRBS1,HNRNPA2B1,RAN,XPOT,Hnrnpa3,NXF1,SLBP,SRSF3,KPNB1,DDX39B,SRSF7,XPO1,NUTF2
E2F3A	RNA Trafficking	8.61E-04	SRSF3,NUP155,KHDRBS1,DDX39B,SRSF7,HNRNPA2B1,RAN,XPO1,XPOT,Hnrnpa3,NXF1,SLBP
E2F3A	Renal and Urological System Development and Function	1.10E-03	TP53,STT3B,TEAD4,DLGAP5,CAV2,POLG,SFPQ,KRAS,BIRC5,TPP2,AFF1,SKP2,PMP22,MAPK14,SPDYA,NOP58,KLF5,CDKN1A,E2F1,CDCA5,DLC1,RASSF1
E2F3A	Cardiovascular Disease	1.50E-03	RAF1,CTC1,MYH9,CDK4,KRAS,MKI67,TUBB,RICTOR,MYC,TNKS,STAG1,RARA,EZH2,MLLT3,TOP2A,BRIP1,BRCA1,DLC1,DIS3,DNMT1,RAD21,TP53,SMC3,TUBG1,RRM2,ERBB3,NFKBIZ,IPP,CDK1,AFF1,RRM1,CCNE1,ITPA,MSH2,TUBE1,MUTYH,RECQL4,E2F1,CDKN1A,MSH6,BRCA2,CDK2,FANCA
E2F3A	Hair and Skin Development and Function	1.53E-03	RAF1,SNAI2,KLF10,CDK4,FKBP1A,KRAS,MKI67,RBL1,LMNB1,ZMIZ1,STMN1,MYC,TNKS,BRCA1,TP53,VAV2,MECP2,CRKL,ANGPTL6,BIRC6,NFKBIZ,TPP2,ARID3A,ATE1,CCNG2,MAPK14,VAV3,KLF5,E2F1,CDKN1A,NAGLU,TFRC,MAPK7,ZFP36L2,CDK2
E2F3A	Hepatic System Development and Function	1.53E-03	TP53,CDKN1A,E2F1,E2F8
E2F3A	Tumor Morphology	1.64E-03	RAF1,PIM3,SNAI2,KLF10,GDF15,BOK,KRAS,CHEK1,MYC,TRIB1,TRADD,FHL2,EZH2,RARA,TLR7,BRCA1,RASSF1,TP53,CDC6,TFAP4,ITPR1,BIRC5,CDK1,FADD,MCM2,CASP2,CDKN1A,E2F1,MAPK7,CDK2,LGALS1
E2F3A	Protein Synthesis	2.35E-03	HNRNPL,EEF1A1,MYH9,PFN1,CLN8,UBR2,MMP16,TSFM,EIF4A2,ARHGEF1,KRAS,RBL1,MYC,ATG4C,RPS20,UFSP2,EIF3B,EIF3D,PIM1,RARA,XPO1,SIAH2,NAA16,Fus,DNMT1,EIF4B,TP53,PABPC1,CNOT1,HCFC1,PJA1,UPF3B,PSMC4,GSN,SKP2,HSPA8,UBE2G2,PTBP1,UBE2D2,Cdc42,RNF168,ARRB2,CASP2,APH1A,USE1,MBTPS1,ACY1,KIAA0368,NAGLU,CAPN7,RAB23,DPM2,CDK4,FKBP1A,AKIP1,H2AFZ,NECAB3,IPO9,MMP8,RASSF1,DTL,DHX9,STT3B,AZIN1,KHDRBS1,PASK,DROSHA,MRPL12,let-7,HERPUD1,LARP4B,NXF1,PPM1G,TPP2,FADD,SENP1,CDKL2,DDX39B,CIRBP,NUDT16,RPS27L

Supplemental Table 7. General IPA functions for E2F1, E2F3A and E2F3B promoter targets

ChIP-seq	Category	B-H p-value	Genes
E2F3A	Skeletal and Muscular System Development and Function	2.35E-03	TP53,mir-199,CRKL,CDK4,E2F3,BIRC5,ID3,SKP2,ROR2,MAPK14,PIM1,KLF5,E2F1,ARSB
E2F3A	Renal and Urological Disease	3.32E-03	RAF1,ARID1A,PKM,BOK,EIF4A2,MELK,KRAS,SMC1A,STMN1,MYC,RAD51,YWHAQ,TRIM27,EZH2,ABCC1,TOP2A,PLCB1,BRCA1,RAD21,RASSF1,TP53,SMC3,MAP2K7,ERBB3,ITPR1,GSN,SSRP1,BIRC5,BAG4,CDK1,FADD,Cdc42,PMP22,MAPK14,DUSP1,CASP2,KLF5,TMX1,CDKN1A,TFRC,BRCA2,MSH5,CDK2
E2F3A	Post-Translational Modification	4.13E-03	PRPF19,MED23,UBR2,RFWD3,FKBP1A,RNF38,TNKS,SIAH2,BRCA1,PCBP2,ANAPC11,NSMCE1,APITD1/APITD1-CORT,RASSF1,DTL,MED18,UHRF1,BIRC6,PSMC4,HERPUD1,GAN,TPP2,SKP2,WWP2,SASH1,UBE2D2,RNF168,ARRB2,CCNF,PHF23,LTN1,Paxip1,TRIM59
E2F3A	Reproductive System Development and Function	4.31E-03	TP53,TRIP13,MCM8,Ppp1cc,UBR2,MSH5,BRCA2,BRCA1,RAD51C,CDK2,FANCA
E2F3A	Cardiovascular System Development and Function	4.31E-03	mir-199,E2F1,CDK4,E2F3,BIRC5,SKP2
E2F3A	RNA Damage and Repair	4.35E-03	PPP1R8,DXO,NUDT16,let-7,RNASEH2B,RBFOX2,ZFP36L2,KHSRP,DIS3
E2F3A	Organ Development	4.65E-03	SNAI2,KLF10,CDK4,KRAS,MKI67,RBL1,LMNB1,MYC,STMN1,BRCA1,VAV2,TP53,MECP2,ANGPTL6,NFKBIZ,ID3,TPP2,SKP2,CCNG2,MAPK14,VAV3,CDKN1A,E2F1,KLF5,NAGLU,CDK2
E2F3A	Neurological Disease	4.75E-03	HNRNPL,RAF1,POLA1,KRAS,MKI67,RAPH1,ACIN1,RNF38,RARA,ABCC1,TARDBP,PLCB1,IRS2,TYMS,PABPC1,TP53,OTUD4,CSRP2,RRM2,PLEC,YWHAZ,HSPA8,E2F1,ACY1,MAPK7,FRG1,TRAPPC5,SNAI2,HNRNPA2B1,GDF15,CDK4,FKBP1A,HMGB2,H2AFZ,TMEM209,MAP4,TOP2A,PCBP2,RAD21,PTK7,MECP2,ID3,CDK1,RRM1,FADD,MSH2,CDKN1A,MAZ,SAAL1,NCAM1,CCDC15,MAP1B,NUP58,LIMK2,ZNF91,TUBB,SMC1A,YWHAQ,USF3,MYC,PIM1,EZH2,MLLT3,RYR3,MYBL2,BRCA1,CDC25A,SMC3,GSN,DUSP1,TUBE1,CASP2,CDK2,ARID1A,FEM1A,PA2G4,KIAA0101,DENND4B,PKM,E2F3,LYST,TCP1,RASSF1,UHRF1,CHERP,TUBG1,GPT,FCHSD2,NFATC4,BIRC5,NBN,MAPK14,FAM111A,VAV3,EHD4,MSH6,BRCA2
E2F3A	Endocrine System Disorders	5.54E-03	EIF4A2,KRAS,DDX20,MKI67,TUBB,SMC1A,MYC,RYR3,MTHFD2,BRCA1,BRIP1,NFXL1,TYMS,TP53,OTUD4,SMC3,SMIM8,RRM2,SSRP1,SH3GL1,PTBP1,TUBE1,H2AFX,CASP2,E2F1,HAUS6,CDK2,ARID1A,KIAA0101,BARD1,GDF15,PKM,RNASEH2B,CDK4,NUP50,CAMK2N2,E2F3,CHEK1,TRA2A,RABL6,PCK2,TOP2A,VARS,RAD21,E2F8,CEP152,mir-199,TUBG1,ERBB3,BIRC5,CDK1,NBN,RRM1,RAD54B,PRKCI,MSH2,VAV3,CDKN1A,MSH6,BRCA2,CAD,FOXN2,NCAM1
E2F3A	Protein Trafficking	6.29E-03	KPNB1,RAN,NUTF2
E2F3A	Hepatic System Disease	7.34E-03	SLC20A1,TP53,TYMS,PABPC1,RAF1,TACC3,ARID1A,PKM,RRM2,CDK4,ERBB3,WWC2,KRAS,BIRC5,MAFF,RRM1,AKAP11,ARID3A,CCNE1,ACY1,TOP2A,BRCA2,BRCA1,CDK2

Supplemental Table 7. General IPA functions for E2F1, E2F3A and E2F3B promoter targets

ChIP-seq	Category	B-H p-value	Genes
E2F3B	Cell Cycle	1.96E-44	mir-130,NPM1,TIMM13,TGFBR1,CTCF,PRKAB1,POLA1,CCNB2,SMARCD2,SSBP2,FRMD6,GPSM2,TRIM32,Ewsr1,GORASP2,PRKCDBP,SMARCB1,TCERG1,MOB1A,AHCY,CENPW,ETS1,HCFC1,CCNE2,NPAT,RFC1,TMEM67,TCF3,ZBTB5,MASTL,DAXX,KAT6A,RAD18,PRKACA,ECT2,FANCA,MORC3,KIF20A,PIM3,NRG2,Calm1 (includes others),DDIT3,PRDX1,TTK,CDK10,SYNM,RABL6,NOTCH2,PELO,EXO1,EP400,KHDRBS1,GAS1,MAPK6,KAT5,ID3,BAK1,MCM3,BUB1,KPNB1,MAD2L1,ARPP19,MSH2,CSF1,FBXO5,ACTL6A,KIF23,CDKN2A,SOCS3,YWHAH,SEPT9,SMAD3,RNF7,RGPD4 (includes others),SMC1A,SOX2,INTS3,USP8,E2F6,CEP57,MAPK3,JUND,ZWINT,GPX4,ING2,ESCO2,HDAC2,WEE1,DNA2,MAPKAPK5,RAD54L,NDC1,CDCA2,DYNC1H1,BCL2L1,H3F3A/H3F3B,SF3B4,CEP76,UBE2I,PBRM1,PEBP1,RMI2,KIAA0101,SKA2,BARD1,PIAS1,NEDD1,RNASEH2B,ZNF219,EIF2S1,E2F3,PTGES3,LSM2,STUB1,ILKAP,ERBB2,PDK1,VAV2,TACC3,RACGAP1,SMARCE1,PSMC3IP,SMARCD1,SOD1,TSN,SERTAD1,BIRC5,MORF4L1,PPM1G,CENPI,E2F7,KLF5,TFCP2,CKS1B,BRCA2,TSC22D1,BORA,ING1,TUBA1B,DDX11,CCP110,MTBP,DSTN,SUV39H1,RAN,HBP1,MKI67,RBL1,EIF6,ARNT,XRCC1,POLB,CD2AP,RASGRF1,RARA,TDP2,CCNT2,FRS2,DNMT1,PABPC1,TFDP1,CENPB,HIRA,SEPT7,MDC1,HBEGF,CKAP2,MTF2,GRK5,HMGA1,Anp32b,MNT,RERE,CDAN1,CREM,ME2,SAC3D1,SGOL1,HAUS6,FYN,NCAPD3,CDT1,PLAGL1,CUL1,PTN,FKBP1A,HMGB2,CNTROB,SF3B3,XRCC4,EIF4EBP1,KAT2B,RINT1,CREB1,DIS3L2,RFC2,IGF1R,CEP152,PMS2,PPIF,BANP,POLE,SPC25,SUPT4H1,TIAL1,SMC6,PLK1,MDM2,ACLY,SCMH1,CDK1,NCAPG2,RRM1,SPIDR,REV1,CIRBP,MUM1,CAMKK1,UBN1,CAP1,BABAM1,PRPF19,ARF1,VPRBP,ATRIP,FBXW7,DICER1,METAP2,YWHAQ,GSPT1,CAMK2D,STAG1,PPP1R7,NCAPH,FASN,SNU13,TFDP2,FOSL2,SOX4,STIL,CLTC,BIRC6,RAC1,CCDC155,CDC123,SMARCD3,HERC2,PALB2,Cdc42,NASP,SMC2,RHOA,SH2B3,SCRIB,NUAK1,SPTAN1,CYLD,CDK2,CDK5RAP2,ZBTB49,CCNC,PA2G4,GADD45G,CENPC,DTYMK,NGF,WDHD1,RAD9B,UHRF2,TRIM24,POLR2A,PPP1R12A,HAUS5,GMNN,SIPA1,GTPBP4,MAPKAPK2,IPO5,RPAIN,RASSF1,UBR5,UHRF1,SNRPB,HAT1,PHF13,NCAPH2,PRMT1,HMG20B,RPS27L,MIS12,CENPH,CASP8AP2,MSN,RAF1,RMI1,RNF8,MYH9,PRKAB2,SMC5,HAUS4,RBM3,KRAS,CCND1,C6orf89,PKN2,BOP1,FHL2,KIF13A,CENPE,NEK6,ADORA2B,RUVBL2,KLF1,CDC16,HIPK2,IQGAP3,TYMS,TP53,ATG5,PHIP,ESPL1,YAP1,EEF2,CSNK1D,PTP4A1,SKP2,ATF2,HSPA8,ATE1,DYNC1LI2,CCNF,SUPT16H,BTG2,GTSE1,TFRC,INVS,CENPT,CHD1L,PTPRA,XRCC5,INF2,FANCM,DEK,TRIM33,AKAP8,PTPN2,CDK4,PDS5B,CEBPD,PRPF4,PSEN2,SEPT11,NUF2,MMS22L,SPAG5,CDKN3,MAP4,ARF6,DAB2,DDX28,CSNK2B,KIF2C,NFE2L2,CDC5L,ESCO1,RAD21,DHX9,TUBGCP6,CUL7,LZTS2,HNRNPD,ING5,VDAC3,NCAPD2,IGHMBP2,CCNE1,NR4A2,CDKN1A,PSAP,SPICE1,RAD51AP1,ID4,TCF7L2,PSEN1,DLGAP5,SRSF2,MSH3,KLF6,GNB2L1,PARP2,RFWD3,SMC4,KNTC1,SART1,TCEB1,SKA1,CRLF3,CEBPG,TGFBR2,ZW10,MYC,LEMD3,MAP2K2,RCC1,PIM1,FIGNL1,XPO1,MYBL2,SUGT1,CEP131,TAB1,SNRPA1,NUCKS1,CLASP1,TOP3B,SMC3,YWHAE,KANK2,MYO19,PNN,ORC6,HELLS,BUB1B,KMT2A,ERCC6L,PPP2CB,CBX1,TAF1,PIAS4,TRIM39,DUSP1,RECQL4,XRCC6,PKMYT1,DIXDC1,NDC80,MAD1L1,CAPN2,KLHL21,ACTN4,SUV420H1,RBBP4,RUNX1,ARID1A,GTF2I,RPS6KA3,WDR6,ETV6,VPS4A,MLH1,RAD50,RAD51,CCNA2,DIAPH1,CSRP2BP,AHNAK,FANCD2,SPDL1,TIMP1,BMPR1A,NET1,FOXO3,SNRPD2,CIZ1,RPS3,MCM9,LRWD1,PRKCA,HAUS8,TUBG1,RPL23,FOXM1,GIT1,RPA2,NBN,IVNS1ABP,PRKCI,MAPK14,FOXO1,KIF5B,RAD9A,MSH6,DCTN1,ATR,CDC34,WNK1,DPY30,KIF18A,CENPF,SOCS1,ITSN1,SGK1,DNAJB4,CDC7,CDKN2C,SFPQ,HES1,PHACTR4,KPNA1,Rpl29 (includes others),CHAF1A,RECQL,CXCL10,VEGFA,INTS7,MXD3,TARDBP,MAP1S,IRS2,TXN,CEP250,ANAPC11,LSM4,TIMP2,CENPJ,STAT6,CDK13,TIPIN,NDRG1,CFL1,TOPBP1,MITF,COPS5,PTCH1,TFAP4,RPA1,UBE2S,FANCC,IRF1,TERF2,CCNO,PCNA,NSMCE2,PATZ1,INO80,GAB1,PPP2R3A,BHLHE40,H2AFX,IRS1,E2F1,MBD4,CHKA,AHCTF1,RGL2,MSH5,RAB11A,CLSPN,MAPK7,HELB,CYR61,YEATS4,VASH2,CTC1,PKD2,HMGN1,NUP214,RCHY1,FNTB,CAMK2N2,SASS6,VCAN,EP300,CHEK1,ID1,YY1,HUS1,DAP3,PDGFRA,E2F5,RHOU,TOP2A,CEBPA,PRKCE,BID,MAP1LC3B,MCM10,MCPH1,HEXIM1,RASSF5,POT1,ZWILCH,MYCN,VPS18,mir-199,DCK,TBX3,CDC6,RAD51B,POLD1,PPP2R5A,KITLG,FADD,DGKZ,KIF15,SF3B2,NUP153,SPDYA,MCM2,PDXP,NDE1,KIF20B,SPRY2,PRMT5,TBPL1,FEN1,NCOR2,MAFB,ZFP36L2,PAFAH1B1,HINFP,SEPT2,DYRK1A,SMARCAD1,POLH,RPL11,FZR1,MCM8,EPS15,MAPK1,DIAPH3,MELK,TAF10,MEPCE,TUBB,AURKB,LATS2,LMNB1,PTK2,STMN1,ROCK2,SRSF1,EZH2,ITGAV,DARS,HTRA2,BRCA1,RAD51C,CDC25A,KIF14,Ftx,CDC37,GPS2,FGFR1,STK11,LMNA,RANBP1,TMOD3,SSRP1,SRSF3,CCNT1,TOB2,RNF4,CCNG2,PKD1,TUBE1,CASP2,LIN9,GNL3,BAZ1B,MTDH,PML,TMPO,Paxip1,KIF11,RFC3,INCENP,PRIMPOL,GDNF,MEIS2,ABL1,Spg20,RBBP8,Ttf1,TAOK1,ING4,BCAR1,Tpm2,MCM4,TNFRSF12A,SP1,PMF1/PMF1-BGLAP,CIT,TCP1,ERF,BLM,E2F8,DTL,MAP2K7,CKS2,ATG10,COPS7A,HDAC1,let-7,SMAD7,PRKAR2A,MAPK9,BCL3,ING3,USP1,XIAP,GNAI2,DNM1,UBQLN2,RIPK1,B4GALT1,SATB1,TONSL,EIF2AK2,SMARCC1,UBC,BCL2L11,GSG2,LGALS1,MCM7

Supplemental Table 7. General IPA functions for E2F1, E2F3A and E2F3B promoter targets

ChIP-seq	Category	B-H p-value	Genes
E2F3B	Gene Expression	1.70E-41	TGFBR1,TLE1,POR,SMARCB1,ADA,SART3,ETS1,RANBP3,RFC1,ZBTB5,DVL2,DDIT3,BEND6,PRDX4,PPIA,NOTCH2,TIPARP,IBTK,ATN1,LSM14B,ID3,NR1D2,PIR,CDKN2A,SMAD3,CBX5,E2F6,MAPK3,MATR3,JUND,ING2,Hmgn2 (includes others),MAPKAPK5,RAD54L,PHRF1,H3F3A/H3F3B,POLR2E,CBX3,TFEB,KLF10,PIAS1,RNASEH2B,PDCD10,EIF2S1,HDGF,TARBP1,SIX1,LARP7,MEF2A,SOD1,BRD3,HTATSF1,TFCP2,E2F7,TSC22D1,ING1,BRPF1,MAP4K4,CTGF,UBR2,ZNF628,ADIPOR1,RASGRF1,CTDSP1,TDP2,CBFB,CCNT2,UAP1,HIPK1,DNMT1,SPTY2D1,TFDP1,HIRA,ZC3HAV1,SYNCRIP,HBEGF,HMGA1,SPOP,ARHGAP35,SNAI2,Mamld1,PLAGL1,CUL1,POLR2J,FKBP1A,CCAR2,FZD1,H2AFZ,MAFG,GTF2A2,RNPS1,IGF1R,PPM1F,RPS5,EED,BANP,SUPT4H1,PLK1,SENP1,RNF187,TRERF1,NCAM1,METAP1,FBXW7,ZNF91,YWHAQ,ETS2,MID1IP1,TFDP2,PUS1,SMARCD3,WHSC1L1,CDK5RAP2,ZBTB49,NGF,ZMIZ1,NELFE,ZFP90,HINT1,TRIM24,POLR2A,USP47,RPAIN,ATP2C1,TCF7L1,MLLT1,TSHZ3,ZNF382,FAF1,RPS27L,RAF1,RNF8,NKAP,KLF7,GATAD2A,Diap2,MPHOSPH8,FBLN1,TGIF2,KLF1,CBX8,PHIP,PAM,YAP1,APPL2,CDCA4,ZNF496,PLEKHG2,PEX2,ATXN7L3,MRPL17,Meis1,RBM39,DEK,WDR61,HNRNPA2B1,CEBPD,CTDSPL,DUSP22,MED28,LRRFIP1,SLC31A2,NAA15,IRF2BPL,SOS1,DAB2,ASPH,NFE2L2,CDC5L,RAD21,DHX9,SERTAD2,HNRNPU,KLHDC2,MED20,ING5,IGHMBP2,CCNE1,ZFPM2,GPBP1,CAPRIN2,CDKN1A,EIF2B1,UBTF,MAP3K3,ID4,TCF7L2,PSEN1,CAMK1D,NME2,NFATC2IP,ATXN1L,CRLF3,CEBPG,TGFBR2,MYC,Gm21596/Hmgb1,PPP3R1,XPO1,Hmga2,WDR77,KLF11,EIF4B,SMC3,FSTL3,YWHAE,KANK2,GABPB2,HELLS,RBFOX2,TBL1X,TAF1,HNRNPAB,GMEB2,ETV4,XRCC6,MAD1L1,FZD5,H1F0,ACTN4,Rplp1 (includes others),COMMD7,UBE2N,RPS6KA3,IGF2BP1,ETV6,CCNA2,DIAPH1,BMPR1A,TIMP1,Zfp68,RPS3,ACO1,LRWD1,PRKCA,SLC20A1,TAF12,RFX1,RPL23,SS18L1,PRKCI,MAPK14,FOXO1,PHF19,RAD9A,SNAPC2,TEAD3,SGK1,SOX12,CDKN2C,SFPQ,RICTOR,Rpl29 (includes others),VEGFA,CXCL10,NCOA7,ZNF367,IPMK,MTF1,PCID2,HEY2,MITF,RPA1,IRF1,TERF2,PCNA,INO80,PATZ1,PSMB2,BHLHE40,E2F1,LRP8,HELB,SCAP,PKD2,SP2,SGMS1,EP300,WTAP,TGFBRAP1,DHPS,NCOA2,PRRX1,E2F5,DAP3,PRKCE,DLX1,MAFK,NELFA,SIN3A,PVT1,PRMT5,GABPA,NCOR2,ZFP36L2,ASH2L,FNIP2,MELK,LOC102724828/MRPL23,PTK2,EZH2,DARS,NIPBL,SIAH2,CIPC,GPS2,FGFR1,LMNA,ELF1,ARRB2,FLOT2,LCORL,NFYC,MAP4K5,PML,MTDH,TMPO,BCL9L,CNBP,PRIMPOL,TEAD4,DRAP1,GABPB1,PKNOX1,ZBTB7A,MED23,PDGFA,GTF2F2,MEIS2,ING4,SP1,PMF1/PMF1-BGLAP,ATF6B,RBM15,PHF21A,NFYB,MAP2K7,Nedd4,let-7,SMAD7,BCL3,RPS6KA5,ENO1,TONSL,SMARCC1,MCM7,WNT5A,LGALS1,mir-130,NPM1,CTCF,PRKAB1,POLA1,TAB2,SSBP2,EIF3B,TCERG1,HCFC1,CD3EAP,NPAT,TCF3,SP4,DAXX,POLR3H,KAT6A,PRKACA,ECT2,CPE,EIF4EBP2,PRDX1,CEBPZ,HEXB,ZNF398,KHDRBS1,GREM1,KAT5,BAK1,MSH2,CSF1,MAZ,TFB1M,SOCS3,LHX2,YWHAH,SFMBT1,CCT2,HDAC10,ZFPM1,ECD,SOX2,OSBPL1A,POLR1B,HDAC2,IFT74,RDX,POLR2H,PFDN5,EIF4E2,TXNRD1,CAND1,AEBP2,RAI1,UBE2I,FOXP4,TEF,PEBP1,PBRM1,LITAF,ZNF219,ZNF226,INPPL1,E2F3,IQGAP1,PTGES3,NFAT5,STUB1,ZNF24,ERBB2,VAV2,KDM4C,SMARCE1,CSRNP1,PSMC3IP,MED26,NFATC4,SERTAD1,BIRC5,SERTAD3,KLF5,BRCA2,F2R,SUV39H1,ZNF76,GTF2E2,HBP1,DDX20,RBL1,ARNT,POLB,RARA,MED16,CNOT1,YWHAZ,MTF2,CKAP2,SCRT1,MED12,PHF12,MNT,AHI1,CREM,HEXIM2,PRICKLE1,C1D,FYN,RREB1,OSR2,STRA13,HMGB2,EIF4G1,MRPL39,EIF4EBP1,KAT2B,CREB1,SUZ12,ELL,TIAL1,MDM2,SLIT2,NAP1L1,CDK1,CCDC85B,H2AFY,UBN1,HOXB9,2700046G09Rik,NAB2,Klf16,VPRBP,DICER1,CAMK2D,RPL19,ABLIM2,FOSL2,SOX4,MCM5,DTNBP1,RAC1,SIX5,Cdc42,ERP29,TIMELESS,SH2B3,RHOA,PDLIM1,SBNO2,JAG1,CDK2,KDM3A,BRD2,PA2G4,SRRT,GADD45G,TLE2,CGGBP1,Cux1,SET,GTF2B,PPP1R12A,GMNN,SORBS3,NCL,MAPKAPK2,IFRD1,YLPM1,DHX15,RASSF1,UBR5,MYCBP,UHRF1,HSPH1,EDF1,CIART,PIAS3,TFB2M,NFIB,CBFA2T2,PSMC3,LANCL2,MSN,KRAS,RBM3,CCND1,PKN2,EGR2,FHL2,RBM4B,SUMO1,NEK6,ATF4,RUVBL2,HIPK2,TARBP2,IQGAP3,TP53,TBK1,KLF13,RBM4,ATF2,HSPA8,SCAF8,EIF4H,SUPT16H,BTG2,GAPDH,SAMD4A,XRCC5,Zfp568,RAP2A,GCFC2,USF2,PSEN2,WWC2,ALX1,VRK1,APPL1,CD47,ZC3H8,IRF2BP1,TRIM27,JADE1,MRPL12,POLG,TOB1,HNRNPD,NXF1,FRK,Kat6b,NR4A2,MBD3,TCF19,SRSF2,ILF3,GNB2L1,KLF6,SART1,TCEB1,HSPA4,LEMD3,MAP2K2,EIF3D,PIM1,MYBL2,BRIP1,ITGB3BP,TAB1,SBF2,ZNF706,SIK2,ATAD2,KMT2A,PIAS4,CBX1,TFAM,MLXIP,DUSP1,DIXDC1,PCBD2,HELT,ELMO1,RUNX1,ARID1A,VPS72,PPIB,GTF2I,ABCF1,ATF6,SMAD5,GTF2A1,MLH1,MIER1,LDB1,FOXO3,DNAJB1,PRDM6,ENY2,ZNF354A,RRP8,RPRD1B,TUBG1,CHP1,SMAD6,SAP130,FOXM1,ZHX3,NBN,IVNS1ABP,RCAN1,TLE4,CENPF,SOCS1,NR6A1,ABCA2,ITSN1,GTF3C2,HES1,CHAF1A,MXD3,THRAP3,BAG1,TARDBP,ZBTB14,Zfp748,TXN,CREBZF,CENPJ,STAT6,ACTR2,CFL1,FOXH1,TOPBP1,COPS5,PTCH1,TFAP4,PTBP1,GAB1,H2AFX,AHCTF1,GNB2,MRPL41,MAPK7,SLC44A2,CYR61,HIST1H1C,DEPDC1,ATF7,PDIA3,HMGN1,SETX,TRIP4,RCHY1,SLBP,ID1,YY1,SEC61A1,CEBPA,TOP2A,BID,TAF3,HEXIM1,RXRB,MYCN,TBX3,PPP1R8,C10orf2,CC2D1B,AGO2,RQCD1,PPP2R5A,YBX2,FADD,EIF3G,KITLG,SLC30A9,LIMS1,SREBF2,SPRY2,NOP2,Rbmxl1,TBPL1,SUPT3H,RBPJ,MAFB,IREB2,HINFP,TAF15,DYRK1A,TFG,MAPK1,MEPCE,TAF10,AURKB,FGFR3,ROCK2,ASXL2,RORA,NEO1,UCHL5,PUF60,BRCA1,NONO,STK11,mir-3960,TBP,SSRP1,Scaf1,MED14,WWP2,EPRS,CCNT1,RNF4,PKD1,EIF4A3,TLE3,MRPL3,RPL13A,NFIX,GDNF,PICALM,PKM,RBBP8,ABL1,TNFAIP3,Ttf1,BCLAF1,PRKAG1,TCF12,NFX1,ROR2,GLI3,RRN3,MAML3,BLM,ERF,E2F8,NACA,HDAC1,MAPK9,NFKBIZ,MED6,PSIP1,NDUFA13,XIAP,AFF1,HIVEP2,DNM1,RIPK1,

Supplemental Table 7. General IPA functions for E2F1, E2F3A and E2F3B promoter targets

ChIP-seq	Category	B-H p-value	Genes
E2F3B	Organismal Survival	1.36E-40	NPM1,CTCF,TGFBR1,PRKAB1,SLC6A9,TAB2,CCNB2,SSBP2,ELAVL4,SECISBP2,POR,PPRC1,PRKCDBP,SMARCB1,ADA,PLXNB2,FBL,ETS1,AFMID,CCNE2,SLC2A1,PIGF,CRKL,TCF3,MASTL,DCLRE1A,SP4,DAXX,DVL2,KAT6A,ITPR3,PRKACA,CELSR3,CPOX,RMRP,ECT2,FLNB,NRG2,PRDX1,BAG6,GNA11,PPIA,NOTCH2,TIPARP,PELO,HEXB,ATN1,EXO1,EP400,KHDRBS1,BBIP1,GAS1,GREM1,KAT5,IGF2R,ID3,BAK1,BUB1,MAD2L1,TMEM107,MSH2,CSF1,FBXO5,TFB1M,AP1G1,ACTL6A,CDKN2A,SOCS3,LHX2,SMAD3,GNPAT,ZFPM1,RPGRIP1L,ECD,INTS1,RGPD4 (includes others),USP8,E2F6,MAPK3,MTMR2,GPX4,ESCO2,STXBP1,HDAC2,DNA2,MAPKAPK5,RAD54L,GNAZ,KCNAB2,EIF4E2,TXNRD1,DYNC1H1,BCL2L1,GINS1,H3F3A/H3F3B,RAI1,FOXP4,UBE2I,TFEB,PIAS1,PVRL3,MCM3AP,BARD1,INPPL1,GPHN,E2F3,EIF2S1,PDCD10,CLIC4,PTGES3,SIX1,NFAT5,STUB1,LARP7,ZNF24,ERBB2,TACC3,ADAM15,MEF2A,CSRNP1,SNX27,NFATC4,SOD1,SERTAD1,BIRC5,MORF4L1,FANCL,E2F7,KLF5,CKS1B,BRCA2,ING1,EFEMP2,MAP4K4,DDX11,CTGF,F2R,UBR2,FAM20C,FNDC3B,MKI67,RBL1,EIF6,POLB,XRCC1,RAD23A,ARNT,ATP1A1,CD2AP,RARA,ZFX,CBFB,HIPK1,FRS2,HMBS,RTEL1,DNMT1,NOVA1,TFDP1,CENPB,ANGPTL6,HIRA,PLEC,HBEGF,MTF2,ADAR,MED12,Anp32b,SH3GL1,MNT,ARHGAP5,AHI1,CREM,ARHGAP35,B9D1,FYN,SNAI2,MAP2,PLAGL1,CUL1,FKBP1A,CRLF2,ATP6AP1,H2AFZ,XRCC4,MAFG,HK2,KAT2B,RIF1,RINT1,CREB1,IGF1R,VCL,PMS2,BLMH,SUZ12,PPIF,ELL,TIAL1,MDM2,SLIT2,ACLY,F3,COPS3,SRXN1,CDK1,NCAPG2,SENP1,REV1,SBF1,H2AFY,CAP1,NCAM1,NAB2,PRPF19,VTI1A,VPRBP,Wasl,MNS1,IPPK,FBXW7,DICER1,AMD1,HSD3B7,METAP2,TBC1D4,SCARB1,ETS2,FASN,Map3k7,Dazap1,FOSL2,SOX4,STIL,COL4A1,PPIG,BIRC6,RAC1,RHEBL1,MUT,PALB2,NASP,Cdc42,TIMELESS,RHOA,USE1,SCRIB,INTU,CYLD,SBNO2,RCE1,JAG1,CDK2,BRD2,ZFAT,SPRED1,Nespas,SRRT,NGF,KMT2C,RAD9B,ZMIZ1,SCARB2,Cux1,POLR2A,PPP1R12A,FXN,GMNN,MAPKAPK2,ATG16L1,RHBDD3,RASSF1,HSPG2,UHRF1,TRA2B,HAT1,ATP2C1,LRRK2,TCF7L1,MTAP,PRMT1,MLLT1,TSHZ3,NFIB,ADAM9,PSMC3,CBFA2T2,MSN,RAF1,TRAIP,MYH9,PRKAB2,RDH10,TMEM38A,KRAS,SLC35C1,CCND1,ATP2A2,ADH5,KLF7,GATAD2A,EGR2,CENPE,FBLN1,MTHFD2,ATF4,ADORA2B,KLF1,MGAT1,HIPK2,UNG,TARBP2,GNE,TP53,ATG5,ESPL1,PAM,YAP1,UBE2Q1,CSNK1D,TPM3,TBK1,MAN1A2,DDR1,ATF2,Marcks,ATE1,PEX2,CCNF,FSCN1,FADS2,TFRC,XRCC5,FANCM,TRIM33,PTPN2,USF2,CEBPD,CDK4,PDS5B,PSEN2,COPS8,ALX1,CDKN3,KISS1R,CD47,ARF6,TRIM27,SOS1,ATP5J2,DAB2,ASPH,CSNK2B,NFE2L2,POMGNT2,CYP51A1,DHX9,ATP7B,SPRY1,CUL7,POLG,HNRNPD,VDAC3,TGS1,LAMB2,CCNE1,ZFPM2,NR4A2,UBR4,EIF4A1,MBD3,CDKN1A,PSAP,MSRA,SGCD,MAP3K3,TCF7L2,CASP7,PSEN1,SRSF2,LRIG2,ILF3,MSH3,RASA3,ATP2B1,KIF1B,PARP2,KLF6,ABCC10,PINX1,TLN1,RNASEH1,ATXN1L,CRLF3,CEBPG,MYC,TGFBR2,FDFT1,LEMD3,Gm21596/Hmgb1,EIF3D,PPP3R1,WDPCP,MYBL2,GCLM,CHTF18,WDR77,BRIP1,TAB1,PPP1R15B,ULK2,TOP3B,SYNE2,UBE4B,YWHAE,PNN,WASF1,HELLS,POFUT1,BUB1B,B3GALNT1,KMT2A,PFKM,SLC3A2,HNRNPAB,TFAM,PIAS4,DUSP1,XRCC6,RECQL4,MAD1L1,NDC80,HSP90AA1,LMNB2,CAPN2,FZD5,H1F0,ACTN4,SUV420H1,RPSA,RHBDF1,RUNX1,ARID1A,PPIB,UBE2N,GTF2I,ATF6,SMAD5,VPS4A,ETV6,RAD50,IGF2BP1,MLH1,ARFRP1,STIM2,RAD51,CCNA2,FANCD2,HLA-DMA,TIMP1,BMPR1A,LDB1,FOXO3,DNAJB1,STX4,EYA4,LRRC8A,PRDM6,RAD23B,WDR1,ARC,PRKCA,SLC20A1,POMT2,SDC1,CAPZB,SLC12A2,TUBG1,CANX,FOXM1,GIT1,FAIM,SH3PXD2A,NBN,IVNS1ABP,RCAN1,SS18L1,MAPK14,PRKCI,FOXO1,KIF5B,RAD9A,EHD4,MSH6,DCTN1,ATR,NR6A1,SOCS1,ABCA2,ITSN1,DNAJB4,TOR1A,CDC7,CDKN2C,ERI1,HES1,KPNA1,RICTOR,Rpl29 (includes others),CHAF1A,GSTZ1,CXCL10,VEGFA,IPMK,BAG1,MTF1,TARDBP,IRS2,TXN,HEY2,CENPJ,KMT2B,PITPNB,TIMP2,UPF2,STAT6,IMPA1,CFL1,NDRG1,TOPBP1,FOXH1,MITF,COPS5,PTCH1,TFAP4,ITPR1,IRF1,TERF2,DOCK1,PTBP1,PCNA,PATZ1,BSG,GAB1,H2AFX,STIP1,E2F1,AHCTF1,CHKA,HPRT1,RAB11A,LRP8,MAPK7,CYR61,IFIT2,HIST1H1C,CTC1,ADAM17,ATF7,PDIA3,PKD2,CTNNA3,HMGN1,FNTB,SP2,VCAN,SGMS1,CHEK1,EP300,SRSF10,COL5A1,EFNB2,ID1,YY1,NCOA2,TCOF1,PRRX1,HUS1,ADK,DGCR8,TOP2A,LAMP1,E2F5,PDGFRA,CEBPA,BID,MCM10,MAP1LC3B,CACNB2,MCPH1,STIM1,RASSF5,HEXIM1,KHSRP,RXRB,POT1,PLOD3,PLAT,AIFM1,POGZ,RPS19,MYCN,Anp32e,C10orf2,PPP1R8,TBX3,INPP5E,ACTB,CENPU,DPAGT1,AGO2,DLX1,RAD51B,GINS4,MAFK,POLD1,SIN3A,FADD,KITLG,ABL2,MCM2,LIMS1,SREBF2,MUTYH,SPRY2,ADD1,PRMT5,ADAM10,GABPA,FEN1,RBPJ,NCOR2,MAFB,IREB2,PAFAH1B1,ZFP36L2,VPS52,DYRK1A,FZR1,PALLD,MAPK1,INSIG1,DIAPH3,MMP16,GNB5,TAF10,LATS2,AURKB,LMNB1,PTK2,FGFR3,SRSF1,SIVA1,SERP1,RORA,EZH2,ITGAV,SLC7A5,HTRA2,SIAH2,RAD51C,BRCA1,FBXO45,DLC1,CDC25A,STK11,FGFR1,ULK4,PSMC4,TBP,LMNA,RAB8A,TMOD3,SSRP1,WWP2,SRSF3,ARRB2,PKD1,CASP2,LIN9,CNPY3,PTPRS,POMT1,GNL3,EXTL3,VDAC1,PML,MTDH,Paxip1,INCENP,TEAD4,DRAP1,GABPB1,PKNOX1,ZBTB7A,MED23,NFIX,GDNF,PICALM,PDGFA,MARK2,PKM,RBBP8,ABL1,TNFAIP3,SLC7A1,ING4,BCLAF1,BCAR1,TCF12,FUT8,ROR2,SP1,RRN3,CIT,MAML3,ATF6B,RBM15,ERF,BLM,CTDNEP1,PHF21A,E2F8,DTL,SLC25A25,MAP2K7,CKS2,S1PR2,Nedd4,HDAC1,EFNA3,SMAD7,MAPK9,RPS6KA5,BCL3,USP1,NFKBIZ,NDUFA13,XIAP,AFF1,GNAI2,DNM1,RIPK1,PBX3,B4GALT1,LPAR1,SATB1,PANK3,SMARCC1,EIF2AK2,VGF,UBC,HMGCR,SHMT2,BCL2L11,WNT5A

Supplemental Table 7. General IPA functions for E2F1, E2F3A and E2F3B promoter targets

ChIP-seq	Category	B-H p-value	Genes
E2F3B	Cellular Growth and Proliferation	3.23E-38	TGFBR1,TLE1,FRMD6,ELAVL4,POR,TRIM32,CRADD,PPRC1,SMARCB1,ADA,SART3,ETS1,CCNE2,PEAK1,RELT,CRKL,RFC1,ZBTB5,DCLRE1A,DVL2,RAD18,ALCAM,ELMO2,MORC3,PIM3,DDIT3,PRDX4,PPIA,CDK10,SYNM,RABL6,NOTCH2,TIPARP,PELO,SLC12A6,IPO7,ID3,BUB1,MAD2L1,CDKN2A,EEF1A1,SMAD3,SMAP2,E2F6,CEP57,MAPK3,MTMR2,JUND,ING2,DYNC1H1,PIK3R3,BCL2L1,H3F3A/H3F3B,SUMO3,KLF10,PIAS1,RNASEH2B,PDE4A,CSRP1,GPHN,CLIC4,PDCD10,HDGF,SIX1,LARP7,ILKAP,PDK1,LASP1,TACC3,MEF2A,ALKBH5,SOD1,MORF4L1,PPM1G,TFCP2,E2F7,TSC22D1,ING1,BRPF1,SLC25A5,MAP4K4,EFEMP2,HNRNPL,ASPSCR1,AGPS,CTGF,UBR2,FNDC3B,RRAGB,ADIPOR1,XRCC1,RASGRF1,URGCP,ZFX,RAB17,CBFB,TTLL5,HIPK1,FRS2,DNMT1,GET4,RND2,PIK3C2B,Irx5,TFDP1,CENPB,PLEC,HBEGF,GRK5,HMGA1,Anp32b,SH3GL1,SAC3D1,SNAI2,CDT1,PTPN13,PLAGL1,LEMD2,PTN,CUL1,POLR2J,FKBP1A,CCAR2,FZD1,DNAJA1,H2AFZ,MAFG,GPR3,NEIL3,HK2,IGF1R,DAGLB,TXNL1,VCL,FKBP5,EED,OXTR,PSMB9,DDX56,USPL1,PLK1,ACLY,COPS3,F3,RRM1,SENP1,SBF1,RNF187,CAMKK1,GCAT,NCAM1,ARL2BP,PRPF19,CAV2,FBXW7,PBK,HSD3B7,YWHAQ,ETS2,TRIB2,Map3k7,AAGAB,Dazap1,TBC1D24,STIL,COL4A1,PSMF1,CLTC,BIRC6,DTNB,RHOJ,CDC123,MAT2B,NDUFAF2,SMARCD3,BRAT1,COL6A3,SCRIB,INTU,RCE1,HDGFRP3,FADS1,ZBTB49,NGF,DTYMK,ZMIZ1,NELFE,HINT1,TRIM24,FXN,USP47,RPAIN,SLC25A4,LRRK2,PFKP,NCAPH2,MLLT1,TTC7A,RAF1,RNF8,TRAIP,MYH9,RDH10,MAP6,HMMR,NKAP,C6orf89,RCL1,KLF7,FBLN1,COPS6,TGIF2,KLF1,MGAT1,TYMS,GNE,CBX8,ATG5,PHIP,ESPL1,YAP1,APPL2,CDCA4,PEX2,FADS2,ANAPC5,TFRC,Meis1,PTPRA,PLXNA3,PTPN2,HNRNPA2B1,EEF1B2,PDS5B,CEBPD,CDK4,CTDSPL,DUSP22,SEPT11,MED28,COPS8,SDK1,LRRFIP1,CDKN3,SOS1,DAB2,ASPH,NFE2L2,PEMT,RAD21,DHX9,SERTAD2,HNRNPU,SPRY1,LZTS2,ING5,SLC29A1,LAMB2,CCNE1,ZFPM2,CAPRIN2,CDKN1A,EIF4A1,EIF2B1,PSAP,MSRA,LDHA,UBTF,PPIL1,MAP3K3,TCF7L2,CASP7,ID4,PSEN1,MAOA,RPL22,NCDN,CAMK1D,MSH3,NME2,PIEZO1,ABCC10,TLN1,NUDC,CRLF3,TGFBR2,MYC,Gm21596/Hmgb1,SAE1,PPP3R1,Hmga2,FIGNL1,SUGT1,CEP131,CNOT6,WDR77,RNF41,KLF11,EIF4B,SMC3,FSTL3,GABPB2,KANK2,PNN,RBFOX2,HELLS,TUSC3,SNX3,ARIH1,NT5C3A,CDC42BPB,HNRNPAB,MATN2,XRCC6,CDCA7L,TXN2,ETV4,RECQL4,HSP90AA1,MAD1L1,FZD5,ACTN4,FAM83D,SUV420H1,PIDD1,RBBP4,ABI2,DPYSL3,UBE2N,RPS6KA3,WDR6,IGF2BP1,ETV6,RAD50,STIM2,RAD51,TRA2A,CCNA2,DIAPH1,AHNAK,TIMP1,BMPR1A,HLA-DMA,NOP58,STX4,CIZ1,LRRC8A,PRKCA,SLC20A1,RFX1,SDC1,SLC12A2,CHERP,HSPD1,MTHFD1,CNOT8,SH3PXD2A,FAIM,SLK,SS18L1,MAPK14,PRKCI,FOXO1,RAD9A,PSMD2,AMIGO1,SGK1,CDKN2C,SFPQ,ZNF451,ERI1,RICTOR,Rpl29 (includes others),RS1,RECQL,VEGFA,CXCL10,DYNLL1,IPMK,CSTF2,HEY2,KIN,MITF,CNOT6L,RPA1,FANCC,ITPR1,PLCL2,IRF1,GEMIN2,TERF2,DOCK1,PCNA,PATZ1,INO80,RFC4,YARS,PSMB2,IRS1,BHLHE40,E2F1,MSH5,RGL2,LRP8,YEATS4,PHLPP1,CAPZA1,VASH2,PKD2,CAMK2N2,FNTB,SP2,VCAN,SGMS1,TAX1BP3,EP300,CHEK1,WTAP,TRIB1,DHPS,NCOA2,USP42,PRRX1,ADK,LAMP1,DAP3,E2F5,NAA60,PRKCE,MCM10,PLOD3,PLAT,RPS19,DLX1,RAD51B,CINP,MAFK,SIN3A,DGKZ,KIF15,SPDYA,ABL2,MCM2,RBM6,UNK,ADAM10,PRMT5,KCTD5,GABPA,FEN1,DNPH1,NCOR2,ZFP36L2,SCAMP3,ASH2L,POLH,FZR1,EPS15,VPS28,INSIG1,DIAPH3,PAK1IP1,MELK,STMN1,PTK2,EZH2,HTRA2,ARHGEF25,FBXO45,MYO10,ATP5G2,GPS2,FGFR1,PSMC4,RAB8A,LMNA,RANBP1,TMOD3,ELF1,GSR,ARRB2,FLOT2,CORO1B,PTPRS,TMPO,MTDH,PML,PHF1,YTHDF2,CNBP,RFC3,PAFAH1B2,TEAD4,KDM3B,PKNOX1,ZBTB7A,PDGFA,MARK2,ING4,FUT8,Ppp1cc,HNRNPR,SP1,CIT,MANF,MICALL1,LTBP4,RBM15,DTL,TIMM8A,MAP2K7,CKS2,S1PR2,Nedd4,ATG10,C2CD3,SMAD7,let-7,BCL3,RPS6KA5,GNAI2,ENO1,B4GALT1,SLC25A27,PAQR4,SMARCC1,UBC,VGF,HMGCR,SHMT2,BCL2L11,MCM7,WNT5A,LGALS1,mir-130,NPM1,KIF13B,TPD52L2,CTCF,PRKAB1,POLA1,TAB2,CCNB2,SECISBP2,Ewsr1,EIF3B,PRKCDBP,PLXNB2,MOB1A,AHCY,SLC2A1,PIGF,STK25,TCF3,SP4,DAXX,ITPR3,PRKACA,ECT2,FANCA,KIF20A,FLNB,NRG2,EIF4EBP2,PRDX1,BAG6,GNA11,MTCH1,TTK,HEXB,EP400,KHDRBS1,TUBB4B,GAS1,ZNF521,MAPK6,GREM1,KAT5,IGF2R,BAK1,MCM3,MSH2,CSF1,SLC29A2,MAZ,ACTL6A,KIF23,SOCS3,MPRIP,YWHAH,LHX2,SEPT9,SFMBT1,CCT2,GNPAT,ZFPM1,HDAC10,RNF7,RPGRIP1L,ECD,RGPD4 (includes others),SMC1A,SOX2,USP8,CD164,ANXA11,ERAL1,GPX4,EPHA7,OSBPL1A,HDAC2,WEE1,IFT74,RDX,POLR2H,PFDN5,CYP20A1,NDC1,PTPRM,CDCA2,TXNRD1,UBE2I,PBRM1,PEBP1,ALG14,LITAF,RND1,KIAA0101,CHSY1,BARD1,INPPL1,E2F3,IQGAP1,PTGES3,NFAT5,STUB1,ZNF24,ERBB2,VAV2,NDUFV1,KDM4C,ADAM15,RACGAP1,SMARCE1,NFATC4,G3BP1,TSN,SERTAD1,ALS2,BIRC5,FANCL,SERTAD3,KLF5,CKS1B,BRCA2,F2R,MTBP,SUV39H1,RAN,DDX20,MKI67,HBP1,RBL1,EIF6,HIST1H2AB,POLB,ARNT,RAD23A,CD2AP,AHSA1,RARA,MGAT4B,LEPROT,AFAP1,PTPRG,ANGPTL6,YWHAZ,MTF2,ADAR,MED12,CMIP,ARHGAP5,MNT,FUT10,SSBP1,RERE,AHI1,CREM,FYN,OSR2,MAP2,ARHGEF7,TTLL4,STRA13,HMGB2,NAA35,CRLF2,EIF4G1,SF3B3,XRCC4,CDH11,EIF4EBP1,KAT2B,DIS3L2,CREB1,WSB1,PMS2,SUZ12,PPIF,HDGFRP2,ELL,TIAL1,MDM2,SLIT2,NAP1L1,SCMH1,SCAF11,CBLN1,CDK1,CCDC85B,IMMT,RNF144A,GTPBP3,CIRBP,H2AFY,HOXB9,WDR48,NAB2,STRN,FARP1,VTI1A,ARF1,VPRBP,Wasl,MNS1,UNC5B,DICER1,AMD1,METAP2,CAMK2D,SCARB1,STAG1,FASN,FOSL2,MCM5,SOX4,HK1,DTNBP1,RAC1,PREX2,CCDC155,SIX5,PREP,HERC2,VRK3,Cdc42,NASP,TIMELESS,RHOA,SH2B3,LOXL1,NUAK1,CYLD,SPTAN1,JAG1,CDK2,KDM3A,BRD2,ZFAT,SRM,COPS4,SH3BP4,SPRED1,PA2G4,SRRT,GADD45G,TXLNA,KMT2C,Cux1,SET,UHRF2,GTF2B,PPP1R12A,CSTF2T,GMN

Supplemental Table 7. General IPA functions for E2F1, E2F3A and E2F3B promoter targets

ChIP-seq	Category	B-H p-value	Genes
E2F3B	DNA Replication, Recombination, and Repair	2.36E-37	mir-130,NPM1,TIMM13,CTCF,POLA1,SMARCD2,CCNB2,GPSM2,Ewsr1,SMARCB1,ADA,CENPW,FBL,HCFC1,CCNE2,RFC1,TMEM67,TCF3,MASTL,DCLRE1A,DAXX,REXO4,EYA3,PRKACA,RAD18,ECT2,FANCA,NRG2,DDIT3,PRDX1,BAG6,PPIA,MTCH1,TTK,CDK10,WRNIP1,PELO,ATN1,EXO1,GREM1,KAT5,ID3,BAK1,ENDOV,BUB1,MCM3,MAD2L1,MSH2,CSF1,MAZ,FBXO5,ACTL6A,CDKN2A,KIF23,SOCS3,SMAD3,TDP1,SMC1A,INTS3,E2F6,CEP57,MAPK3,GPX4,ZWINT,ING2,ESCO2,HDAC2,WEE1,DNA2,RAD54L,NDC1,CDCA2,PIK3R3,BCL2L1,GINS1,SF3B4,CEP76,HIRIP3,POLD2,UBE2I,PEBP1,PBRM1,KIAA0101,SKA2,BARD1,MCM3AP,RNASEH2B,NEDD1,ZNF219,INPPL1,RBBP5,IQGAP1,E2F3,LSM2,HDGF,SIX1,NFAT5,ERBB2,TACC3,RACGAP1,SMARCE1,PSMC3IP,SMARCD1,SOD1,TSN,SERTAD1,BIRC5,PPM1G,MORF4L1,FANCL,CENPI,CKS1B,BRCA2,ING1,MCM6,CCP110,F2R,MTBP,SUV39H1,RAN,RBL1,RAD23A,XRCC1,POLB,RASGRF1,RARA,TDP2,HIPK1,DNMT1,RTEL1,PABPC1,TFDP1,HIRA,HBEGF,MDC1,HMGA1,RNASEH2A,RNF168,SSBP1,RERE,CDAN1,CREM,SAC3D1,SGOL1,FYN,NCAPD3,CDT1,UVSSA,PTN,CUL1,POLQ,STRA13,CNTROB,HMGB2,EIF4G1,DNAJA1,SF3B3,XRCC4,NEIL3,RIF1,KAT2B,CREB1,RFC2,IGF1R,CEP152,DUT,PMS2,BANP,SPC25,POLE,SUPT4H1,TIAL1,SMC6,MDM2,PLK1,NAP1L1,SCMH1,NCAPG2,CDK1,RRM1,SPIDR,MUM1,REV1,BABAM1,WDR48,PRPF19,VPRBP,ATRIP,FBXW7,DICER1,PBK,STAG1,PPP1R7,NCAPH,BOD1L1,SNU13,AAGAB,SOX4,STIL,POLE2,RAC1,CCDC155,SMARCD3,HERC2,PALB2,NASP,Cdc42,BRAT1,TIMELESS,SMC2,RHOA,CDK2,CDK5RAP2,EXOG,GADD45G,CENPC,NGF,WDHD1,SET,Pgap2,GMNN,USP47,GTPBP4,MAPKAPK2,NCL,IPO5,RPAIN,RASSF1,UBR5,UHRF1,SNRPB,HAT1,PHF13,PHLDA3,NCAPH2,PRMT1,CDKN2AIP,NT5M,DSCC1,RPS27L,MIS12,CENPH,RAF1,RMI1,MINPP1,RNF8,SMC5,KRAS,CCND1,CDIP1,PKN2,CENPE,SUMO1,NEK6,ADORA2B,RUVBL2,KLF1,HIPK2,UNG,CBX8,TYMS,TP53,ATG5,PHIP,ESPL1,YAP1,RRM2,CSNK1D,CDCA4,ATF2,SKP2,HSPA8,ATE1,CCNF,SUPT16H,BTG2,CENPT,CHD1L,PTPRA,XRCC5,FANCM,DEK,TRIM33,ERCC4,CDK4,PRPF4,NUF2,MMS22L,SPAG5,CDKN3,CD47,KIF2C,ESCO1,RAD21,DHX9,HNRNPU,TUBGCP6,POLG,ING5,VDAC3,NCAPD2,SLC29A1,CCNE1,IGHMBP2,NR4A2,CDKN1A,SPICE1,POLA2,RAD51AP1,CASP7,PSEN1,DLGAP5,MSH3,VPS13A,SLF2,PARP2,RFWD3,SMC4,KNTC1,SART1,RNASEH1,SKA1,CEBPG,TGFBR2,MYC,ZW10,Gm21596/Hmgb1,RCC1,PIM1,FIGNL1,XPO1,MYBL2,CEP131,BRIP1,SNRPA1,TOP3B,SMC3,YWHAE,KANK2,ORC6,HELLS,BUB1B,ERCC6L,PIAS4,TFAM,DUSP1,RECQL4,XRCC6,NDC80,MAD1L1,CAPN2,SUV420H1,PIDD1,RBBP4,RUNX1,TNFAIP8,ARID1A,PPIB,UBE2N,ETV6,RAD50,MLH1,RAD51,CCNA2,FANCD2,NET1,FOXO3,SNRPD2,DNAJB1,CIZ1,MCM9,RPS3,LONP1,C10orf88,LRWD1,RAD23B,PRKCA,TUBG1,FOXM1,NBN,RPA2,FAM111A,MAPK14,FOXO1,KIF5B,RAD9A,MSH6,ATR,KIF18A,CENPF,SGK1,CDC7,CDKN2C,SFPQ,KPNA1,CHAF1A,RECQL,CXCL10,VEGFA,DYNLL1,INTS7,IPMK,TARDBP,IRS2,KIN,LSM4,TIMP2,CENPJ,STAT6,TIPIN,TOPBP1,MITF,COPS5,RPA1,TFAP4,FANCC,IRF1,TERF2,PTBP1,CCNO,PCNA,NSMCE2,INO80,BSG,GAB1,IRS1,H2AFX,E2F1,MBD4,ORC5,MSH5,CLSPN,MAPK7,HELB,CYR61,CTC1,PDIA3,HMGN1,ASF1A,SETX,SASS6,EP300,CHEK1,ID1,YY1,NCOA2,ADK,HUS1,E2F5,CEBPA,TOP2A,EIF3A,PDGFRA,BID,MCPH1,MCM10,POT1,ZWILCH,AIFM1,POGZ,mir-199,ADRM1,DCK,C10orf2,CDC6,RAD51B,POLD1,PPP2R5A,SIN3A,FADD,KITLG,DGKZ,SLC30A9,SF3B2,SPDYA,MCM2,NDE1,MUTYH,ASCC3,FEN1,RBPJ,PAFAH1B1,HINFP,ASH2L,POLH,SMARCAD1,FZR1,MCM8,VPS28,MAPK1,MELK,MEPCE,LATS2,AURKB,PTK2,ROCK2,POLD3,EZH2,NIPBL,INIP,RAD51C,BRCA1,FBXO45,CDC25A,APITD1/APITD1-CORT,IGFBP6,Ftx,KIF14,FGFR1,MACROD1,STK11,LMNA,SSRP1,ARRB2,RNF4,CCNG2,CASP2,BAZ1B,TMPO,PHF1,PML,Paxip1,ORC4,KIF11,INCENP,RFC3,PRIMPOL,OBFC1,ZBTB7A,GDNF,PDGFA,RBBP8,ABL1,Ttf1,ING4,TAOK1,BCLAF1,BCAR1,MCM4,CCDC88A,Ppp1cc,SP1,PMF1/PMF1-BGLAP,CIT,BLM,DTL,S1PR2,CKS2,COPS7A,HDAC1,let-7,SMAD7,MAPK9,BCL3,USP1,UBE2T,GNAI2,ENO1,SATB1,EIF2AK2,SMARCC1,TONSL,LGALS1,MCM7

Supplemental Table 7. General IPA functions for E2F1, E2F3A and E2F3B promoter targets

ChIP-seq	Category	B-H p-value	Genes
E2F3B	Cancer	1.05E-29	TGFBR1,GARS,CRADD,SMARCB1,MARCH2,ADA,SART3,ETS1,SRPR,RFC1,TMEM67,HIST1H2BM,EYA3,ALCAM,TMEM43,ELMO2,CPOX,PIM3,DDIT3,SLC1A5,NOTCH2,PTPN4,RABL6,BNIP1,IBTK,PCNXL3,RNF19A,GPC6,EXO1,SLC12A6,LSM14B,CSGALNACT1,CDS2,KPNB1,MAD2L1,PLXDC1,AP1G1,PIGU,GMPPA,SMAD3,DEPDC5,SMAP2,E2F6,CEP57,SNRPD1,MTMR2,ZWINT,ING2,KCNAB2,PTPDC1,PHRF1,DYNC1H1,PIK3R3,YPEL5,SEC61A2,AGBL3,POLD2,FAM134A,MCCC2,ZC3H7B,FLYWCH1,GFOD2,NEDD1,ZBTB2,GPHN,CLIC4,C20orf24,HDGF,ILKAP,IGSF8,PDK1,LASP1,FRA10AC1,TACC3,MEF2A,HERPUD1,SNX27,UBE2D1,FAM122A,BRD3,TUBB6,PAPD7,ING1,BRPF1,HNRNPL,RAP2B,MCM6,AGPS,CTGF,ZFP62,MRPL20,UBR2,FAM20C,ZNF436,HOMER3,PPP1R21,ADIPOR1,XRCC1,RNF38,ZFP41,SLC22A15,HIST1H2AJ,ZFX,RAB17,TDP2,CBFB,CCNT2,TTLL5,HIPK1,FRS2,DNMT1,C19orf57,PABPC1,GET4,PIK3C2B,NOVA1,TFDP1,HIRA,PLEC,ZC3HAV1,HBEGF,GRK5,CNOT10,AGFG2,AP5Z1,MEX3A,SPOP,PHLDB1,RNF168,FAM222A,C11orf30,NCLN,RMND1,KIAA0368,SGOL1,HAUS6,TMEM158,R3HCC1L,GALC,NCAPD3,CDT1,PTPN13,PLAGL1,LEMD2,CUL1,SPATA13,CENPN,FKBP1A,CCAR2,FZD1,DNAJA1,H2AFZ,TOR1AIP1,ATP6AP1,GPR3,HK2,RINT1,RNPS1,TICRR,RFC2,TXNL1,PPM1F,VCL,TCTN3,NCBP3,TTC39B,FKBP5,OXTR,PSMB9,PKN3,CEP152,STAMBPL1,BLMH,BANP,DDX56,USPL1,SMC6,COPS3,NCAPG2,RRM1,ADSS,ZNF546,SENP1,SBF1,MUM1,CAMKK1,KDELR3,ZNF507,TRERF1,ARL14EP,COBLL1,NCAM1,IPPK,TMEM74B,HSD3B7,FAM208A,YWHAQ,NAF1,KHNYN,PPP1R7,TRIB2,DDI2,RPRD2,GOLGA1,TBC1D24,COL4A1,PSMF1,CLTC,BIRC6,DTNB,ALAD,CDC123,ATP10A,NDUFAF2,MAT2B,BRAT1,COL6A3,C15orf41,INTU,KBTBD8,FADS1,CCNC,ZBTB49,NGF,RAD9B,NELFE,PDP2,HINT1,MAN2C1,POLR2A,FXN,USP47,DSCR3,RPAIN,SLC25A4,PFKP,TCF7L1,TSHZ3,FAF1,HMG20B,TTC7A,MTRF1L,H2AFV,TEX9,DDHD2,NIPA2,WDR90,PCBP1,RALGAPB,WDR20,SLC35C1,ZFYVE1,ZC3H12C,ZNF689,CENPE,COPS6,EHD2,ATP5G3,CERS6,TUBGCP3,APPL2,YAP1,FAM118A,EEF2,C4orf32,MAN1A2,WDR81,ATE1,SYNJ2,PLEKHG2,MORC2,OGFOD2,DYNC1LI2,GTSE1,ANAPC5,ZC3H7A,ZDHHC1,FAM19A2,FRG1,ANKLE1,TMEM64,TRAPPC5,FAM188B,FANCM,DEK,FBXO7,CEP97,ARL4C,HNRNPA2B1,ODF2L,RHOT2,CDK4,CEBPD,PDS5B,CTDSPL,KIAA0754,MED28,SEPT11,NUF2,SDK1,CDKN3,TMEM209,NAA15,GINS2,MAP4,PRR14L,SOS1,ATPAF1,ALG8,CDC5L,PEMT,ESCO1,RAD21,SLC35A5,ZMYM1,DENND4A,WIPF2,SPRY1,OLFML3,LARP4B,RCCD1,LAMB2,IGHMBP2,PRPF18,UBR4,ABCF2,ATP13A3,ZSWIM8,EIF4A1,ZFHX2,BTF3L4,MSRA,UBTF,PPIL1,ID4,FOXN2,TMCC1,LRIG2,PDZD7,MEGF9,KIF1B,SLC41A3,NME2,LMBR1L,CEBPG,LRRC57,MYC,TGFBR2,ZW10,SMPD4,AHDC1,PPP3R1,AMOTL2,FIGNL1,AP5M1,SUGT1,WDR77,DPM3,CNOT6,SNRPA1,KLF11,RNF41,EIF4B,PRPF38A,ARHGAP11A,SPECC1,TEX264,LIPT2,FSTL3,KANK2,SAP30BP,DDOST,PSMD6,RBFOX2,BTBD8,B3GALNT1,WDYHV1,ARIH1,GMEB2,USP32,TXN2,CDCA7L,XRCC6,ETV4,SEPT10,NDC80,RUSC2,MAD1L1,HSP90AA1,SEC31B,NCKAP5L,FZD5,SSFA2,ACTN4,SUV420H1,GEMIN7,MGST3,RBBP4,DPYSL3,NEURL4,SLC39A14,SPTSSA,ETV6,ARFRP1,TRA2A,RABEPK,DIAPH1,LYST,SPAG7,FYTTD1,NOP58,MEX3B,LCMT2,ACAD8,STX4,RPS3,ACO1,VARS,CIZ1,CNNM3,BTBD10,POMT2,HAUS8,RFX1,MORN1,CANX,NMT2,RPL23,NFKBIL1,AMPD2,FAIM,SH3PXD2A,CCDC34,SLK,FAM111A,MAPK14,RAD9A,LSM11,COX8A,ZNF451,CDKN2C,ERI1,PHACTR4,KPNA1,GSTZ1,FANCB,DYNLL1,ZNF367,MTF1,HNRNPUL1,EEFSEC,CSTF2,HEY2,KIN,KMT2B,TMEM55B,MITF,PGLS,GPATCH8,NAT10,FANCC,PLCL2,ZNF414,DONSON,IRF1,DOCK1,PCNA,INO80,RFC4,PSMB2,IRS1,CPNE8,E2F1,GLRA1,MSH5,HELB,YEATS4,SCAP,PKD2,SASS6,VCAN,SGMS1,EP300,XYLB,TRIB1,NCOA2,POLR2M,PRRX1,USP42,SLC6A17,LAMP1,E2F5,PRKCE,NAA60,MCM10,ZWILCH,PLOD3,EPG5,CWC22,TOR1AIP2,MAFK,ATXN2L,POLD1,STXBP6,PCDH9,RPIA,WDR76,KIF15,ABL2,PVT1,RBM6,PRMT5,FEN1,NCOR2,DNPH1,USP49,VPS52,ASH2L,POLH,RPL11,INSIG1,DPY19L4,LARS,UBXN4,EZH2,FBXO45,ADPRHL2,PMPCA,CPNE2,AIM1,RASAL2,FGFR1,PSMC4,LMNA,RANBP1,TMOD3,GSR,ABHD17C,PLEKHH2,PCGF1,PTPRS,C1orf27,PFAS,PHF1,TMPO,PEX12,PAFAH1B2,KDM3B,TEAD4,VWA1,DRAP1,GABPB1,CCDC85C,GTF2F2,SLC25A29,CHPF,MARK2,MEIS2,NUP50,TAOK1,GANAB,PMF1/PMF1-BGLAP,CIT,LTBP4,PHF21A,MAP2K7,S1PR2,MRC2,ATG10,let-7,BCL3,ANAPC13,LRCH1,GNAI2,KIF24,ZNF704,DYM,PANK3,PAQR4,TONSL,SMARCC1,UBC,VGF,LRR1,SNTB2,CAB39,SLC6A9,POLA1,NUP133,SMARCD2,CCNB2,EIF4A2,GPSM2,CNPPD1,SECISBP2,Ewsr1,EIF3B,PRKCDBP,MAP1A,DUSP11,FAM172A,AHCY,FBL,HCFC1,PIGF,CD3EAP,MSMO1,RGP1,GART,DAXX,CNTRL,KAT6A,ITPR3,PRKACA,COX18,CELSR3,C3orf67,ECT2,CCDC138,CPE,FANCA,KIF20A,FLNB,EIF4EBP2,IRAK1BP1,BAG6,GNA11,SERHL2,CEBPZ,MTCH1,PNRC1,HEXB,C2CD5,HIST2H3D,KPNA3,FKBP3,EP400,PMM1,GAS1,PASK,MAPK6,GREM1,IGF2R,BAK1,RPS16,CSF1,SEPHS1,CHAC1,SLC29A2,COX7A2,FBXO5,C12orf66,TFB1M,NAV2,MPRIP,LHX2,YWHAH,CCT2,GNPAT,NUP58,HDAC10,ZFPM1,LIPT1,ECD,PPFIBP1,SMC1A,RGPD4 (includes others),SOX2,TSEN15,ANXA11,ERAL1,EPHA7,OSBPL1A,STXBP1,SESN3,WEE1,IFT74,POLR2H,H6PD,PTPRM,CDCA2,OSBPL8,CAND1,KIAA0907,AEBP2,HIRIP3,SLC25A10,TMEM248,UBE2I,FOXP4,ALG14,INTS10,LITAF,RND1,DDX26B,OSBPL6,KIAA0101,BARD1,CHSY1,PVRL3,MCM3AP,ZNF219,SPSB3,ALAS1,RBBP5,IQGAP1,ZFAND2A,BCL7B,NFAT5,RPL18A,ERBB2,NAA40,VAV2,KDM4C,NDUFV1,AP3M1,IFT46,ADAM15,RACGAP1,CSRNP1,SMARCD1,NFATC4,SERTAD1,SLC7A6OS,TSN,BIRC5,ALS2,UMPS,MTO1,FANCL,SLC36A4,KLF5,ZDHHC3,BORA,DDX11,F2R,MTBP,DSTN,SUV39H1,RAN,ZNF76,GTF2E2,GHITM,DDX20,HBP1,MKI67,EIF6,Cyb5r3,RBL1,HIST1H2AB,RPS11,RAD23A,POLB,ARNT,CXorf23,CD2AP,ATP1A1,AHSA1,RARA,MGAT4B,MED16,BAG5,RTEL1,CNOT1,

Supplemental Table 7. General IPA functions for E2F1, E2F3A and E2F3B promoter targets

ChIP-seq	Category	B-H p-value	Genes
E2F3B	Organismal Injury and Abnormalities	1.05E-29	TGFBR1,GARS,CRADD,SMARCB1,MARCH2,ADA,DAZAP2,SART3,ETS1,SRPR,RFC1,TMEM67,HIST1H2BM,EYA3,ALCAM,TMEM43,ELMO2,CPOX,PIM3,DDIT3,SLC1A5,NOTCH2,PTPN4,RABL6,BNIP1,IBTK,PCNXL3,RNF19A,GPC6,EXO1,SLC12A6,LSM14B,CSGALNACT1,CDS2,KPNB1,MAD2L1,PLXDC1,AP1G1,PIGU,GMPPA,SMAD3,DEPDC5,SMAP2,E2F6,CEP57,SNRPD1,MTMR2,ZWINT,ING2,KCNAB2,PTPDC1,PHRF1,DYNC1H1,PIK3R3,YPEL5,SEC61A2,AGBL3,POLD2,FAM134A,MCCC2,ZC3H7B,FLYWCH1,GFOD2,NEDD1,ZBTB2,GPHN,CLIC4,C20orf24,HDGF,ILKAP,IGSF8,PDK1,LASP1,FRA10AC1,TACC3,MEF2A,HERPUD1,SNX27,UBE2D1,FAM122A,BRD3,TUBB6,PAPD7,ING1,BRPF1,HNRNPL,RAP2B,MCM6,AGPS,CTGF,ZFP62,MRPL20,UBR2,FAM20C,ZNF436,HOMER3,PPP1R21,ADIPOR1,XRCC1,RNF38,ZFP41,SLC22A15,HIST1H2AJ,ZFX,RAB17,TDP2,CBFB,CCNT2,TTLL5,HIPK1,FRS2,DNMT1,C19orf57,PABPC1,GET4,PIK3C2B,NOVA1,TFDP1,HIRA,PLEC,ZC3HAV1,HBEGF,GRK5,CNOT10,AGFG2,AP5Z1,MEX3A,SPOP,PHLDB1,RNF168,FAM222A,C11orf30,NCLN,RMND1,KIAA0368,SGOL1,HAUS6,TMEM158,R3HCC1L,GALC,NCAPD3,CDT1,PTPN13,PLAGL1,LEMD2,CUL1,POLR2J,SPATA13,CENPN,FKBP1A,CCAR2,FZD1,DNAJA1,H2AFZ,TOR1AIP1,ATP6AP1,GPR3,HK2,RINT1,RNPS1,TICRR,RFC2,TXNL1,PPM1F,VCL,TCTN3,NCBP3,TTC39B,FKBP5,OXTR,PSMB9,PKN3,CEP152,STAMBPL1,BLMH,BANP,DDX56,USPL1,SMC6,COPS3,NCAPG2,RRM1,ADSS,ZNF546,SENP1,SBF1,MUM1,CAMKK1,KDELR3,ZNF507,TRERF1,ARL14EP,COBLL1,NCAM1,IPPK,TMEM74B,HSD3B7,FAM208A,YWHAQ,NAF1,KHNYN,PPP1R7,TRIB2,DDI2,RPRD2,GOLGA1,TBC1D24,COL4A1,PSMF1,CLTC,BIRC6,DTNB,ALAD,CDC123,ATP10A,NDUFAF2,MAT2B,BRAT1,COL6A3,C15orf41,INTU,KBTBD8,FADS1,CCNC,ZBTB49,NGF,RAD9B,NELFE,PDP2,HINT1,MAN2C1,POLR2A,FXN,USP47,DSCR3,RPAIN,SLC25A4,MRPS12,PFKP,TCF7L1,TSHZ3,FAF1,HMG20B,TTC7A,MTRF1L,H2AFV,TEX9,DDHD2,NIPA2,WDR90,PCBP1,RALGAPB,WDR20,SLC35C1,ZFYVE1,ZC3H12C,ZNF689,CENPE,COPS6,EHD2,ATP5G3,CERS6,TUBGCP3,APPL2,YAP1,FAM118A,EEF2,C4orf32,MAN1A2,WDR81,ATE1,SYNJ2,PLEKHG2,MORC2,OGFOD2,DYNC1LI2,GTSE1,ANAPC5,ZC3H7A,ZDHHC1,FAM19A2,FRG1,ANKLE1,TMEM64,TRAPPC5,FAM188B,FANCM,DEK,FBXO7,CEP97,ARL4C,HNRNPA2B1,ODF2L,RHOT2,CDK4,CEBPD,PDS5B,CTDSPL,KIAA0754,MED28,SEPT11,NUF2,SDK1,CDKN3,TMEM209,NAA15,GINS2,MAP4,PRR14L,SOS1,ATPAF1,ALG8,CDC5L,PEMT,ESCO1,RAD21,SLC35A5,ZMYM1,DENND4A,WIPF2,SPRY1,OLFML3,LARP4B,RCCD1,LAMB2,IGHMBP2,PRPF18,UBR4,ABCF2,ATP13A3,ZSWIM8,EIF4A1,ZFHX2,BTF3L4,MSRA,UBTF,PPIL1,ID4,FOXN2,TMCC1,LRIG2,PDZD7,MEGF9,KIF1B,SLC41A3,NME2,KXD1,LMBR1L,CEBPG,LRRC57,MYC,TGFBR2,ZW10,SMPD4,AHDC1,PPP3R1,AMOTL2,FIGNL1,AP5M1,SUGT1,WDR77,DPM3,CNOT6,SNRPA1,KLF11,RNF41,EIF4B,PRPF38A,ARHGAP11A,SPECC1,TEX264,LIPT2,FSTL3,KANK2,SAP30BP,DDOST,PSMD6,RBFOX2,BTBD8,B3GALNT1,WDYHV1,ARIH1,GMEB2,USP32,TXN2,CDCA7L,XRCC6,ETV4,SEPT10,NDC80,RUSC2,MAD1L1,HSP90AA1,SEC31B,NCKAP5L,FZD5,SSFA2,ACTN4,SUV420H1,GEMIN7,MGST3,RBBP4,DPYSL3,NEURL4,SLC39A14,SPTSSA,ETV6,ARFRP1,TRA2A,RABEPK,DIAPH1,LYST,SPAG7,FYTTD1,NOP58,MEX3B,LCMT2,ACAD8,STX4,RPS3,ACO1,VARS,CIZ1,CNNM3,GMFB,BTBD10,POMT2,HAUS8,RFX1,MORN1,CANX,NMT2,RPL23,NFKBIL1,AMPD2,FAIM,SH3PXD2A,CCDC34,SLK,FAM111A,MAPK14,RAD9A,LSM11,COX8A,ZNF451,CDKN2C,ERI1,PHACTR4,KPNA1,GSTZ1,FANCB,DYNLL1,ZNF367,MTF1,HNRNPUL1,EEFSEC,CSTF2,HEY2,KIN,KMT2B,TMEM55B,MITF,PGLS,GPATCH8,NAT10,FANCC,PLCL2,ZNF414,DONSON,IRF1,DOCK1,PCNA,INO80,RFC4,PSMB2,IRS1,CPNE8,E2F1,GLRA1,MSH5,HELB,YEATS4,SCAP,PKD2,SASS6,VCAN,SGMS1,EP300,XYLB,TRIB1,NCOA2,POLR2M,PRRX1,USP42,SLC6A17,LAMP1,E2F5,PRKCE,NAA60,MCM10,ZWILCH,PLOD3,EPG5,CWC22,TOR1AIP2,MAFK,ATXN2L,POLD1,STXBP6,PCDH9,RPIA,WDR76,KIF15,ABL2,PVT1,RBM6,PRMT5,FEN1,NCOR2,DNPH1,USP49,VPS52,ASH2L,POLH,RPL11,INSIG1,DPY19L4,LARS,UBXN4,EZH2,FBXO45,ADPRHL2,PMPCA,CPNE2,AIM1,RASAL2,FGFR1,PSMC4,LMNA,RANBP1,TMOD3,GSR,ABHD17C,PLEKHH2,PCGF1,PTPRS,C1orf27,PFAS,PHF1,TMPO,PEX12,PAFAH1B2,KDM3B,TEAD4,VWA1,DRAP1,GABPB1,CCDC85C,GTF2F2,SLC25A29,CHPF,MARK2,MEIS2,NUP50,TAOK1,GANAB,PMF1/PMF1-BGLAP,CIT,LTBP4,PHF21A,MAP2K7,S1PR2,MRC2,ATG10,let-7,BCL3,ANAPC13,LRCH1,GNAI2,KIF24,ZNF704,DYM,PANK3,PAQR4,TONSL,SMARCC1,UBC,VGF,LRR1,SNTB2,CAB39,SLC6A9,POLA1,NUP133,SMARCD2,CCNB2,EIF4A2,GPSM2,CNPPD1,SECISBP2,Ewsr1,EIF3B,PRKCDBP,MAP1A,DUSP11,FAM172A,AHCY,FBL,HCFC1,PIGF,CD3EAP,MSMO1,RGP1,GART,DAXX,CNTRL,KAT6A,ITPR3,PRKACA,COX18,CELSR3,C3orf67,ECT2,CCDC138,CPE,FANCA,KIF20A,FLNB,IRAK1BP1,BAG6,GNA11,SERHL2,CEBPZ,MTCH1,PNRC1,HEXB,C2CD5,HIST2H3D,KPNA3,FKBP3,EP400,PMM1,GAS1,PASK,MAPK6,GREM1,IGF2R,BAK1,RPS16,CSF1,SEPHS1,CHAC1,SLC29A2,COX7A2,FBXO5,C12orf66,TFB1M,NAV2,MPRIP,LHX2,YWHAH,CCT2,GNPAT,NUP58,HDAC10,ZFPM1,LIPT1,ECD,PPFIBP1,SMC1A,RGPD4 (includes others),SOX2,CD164,TSEN15,ANXA11,ERAL1,EPHA7,OSBPL1A,STXBP1,SESN3,WEE1,IFT74,POLR2H,H6PD,PTPRM,CDCA2,OSBPL8,CAND1,KIAA0907,AEBP2,HIRIP3,SLC25A10,TMEM248,UBE2I,FOXP4,ALG14,INTS10,LITAF,RND1,DDX26B,OSBPL6,KIAA0101,BARD1,CHSY1,PVRL3,MCM3AP,ZNF219,SPSB3,ALAS1,RBBP5,IQGAP1,ZFAND2A,BCL7B,NFAT5,RPL18A,STUB1,ERBB2,NAA40,VAV2,KDM4C,NDUFV1,AP3M1,IFT46,ADAM15,RACGAP1,CSRNP1,SMARCD1,NFATC4,SERTAD1,SLC7A6OS,TSN,BIRC5,ALS2,UMPS,MTO1,FANCL,SLC36A4,KLF5,ZDHHC3,BORA,DDX11,F2R,MTBP,DSTN,SUV39H1,RAN,ZNF76,GTF2E2,GHITM,DDX20,HBP1,MKI67,EIF6,Cyb5r3,RBL1,HIST1H2AB,RPS11,RAD23A,POLB,ARNT,CXorf23,CD2AP,ATP1A1,AHSA1,RARA,MGAT4B,MED16,BAG5,R

Supplemental Table 7. General IPA functions for E2F1, E2F3A and E2F3B promoter targets

ChIP-seq	Category	B-H p-value	Genes
E2F3B	Gastrointestinal Disease	9.89E-28	TGFBR1,GARS,CRADD,MARCH2,SMARCB1,ADA,SART3,ETS1,SRPR,RFC1,TMEM67,HIST1H2BM,EYA3,ALCAM,CPOX,ELMO2,PIM3,DDIT3,SLC1A5,RABL6,PTPN4,NOTCH2,BNIP1,IBTK,PCNXL3,GPC6,RNF19A,EXO1,SLC12A6,LSM14B,CDS2,KPNB1,MAD2L1,PLXDC1,AP1G1,PIGU,GMPPA,SMAD3,DEPDC5,SMAP2,E2F6,CEP57,SNRPD1,MTMR2,ZWINT,ING2,PTPDC1,PHRF1,DYNC1H1,PIK3R3,YPEL5,SEC61A2,AGBL3,FAM134A,POLD2,MCCC2,ZC3H7B,FLYWCH1,GFOD2,NEDD1,ZBTB2,HDGF,IGSF8,ILKAP,PDK1,LASP1,FRA10AC1,TACC3,MEF2A,HERPUD1,SNX27,BRD3,TUBB6,PAPD7,ING1,BRPF1,HNRNPL,MCM6,ZFP62,CTGF,MRPL20,FAM20C,UBR2,HOMER3,PPP1R21,ADIPOR1,XRCC1,RNF38,SLC22A15,ZFX,RAB17,TDP2,CBFB,CCNT2,TTLL5,HIPK1,DNMT1,GET4,PABPC1,PIK3C2B,NOVA1,TFDP1,HIRA,ZC3HAV1,PLEC,HBEGF,CNOT10,GRK5,AGFG2,AP5Z1,MEX3A,SPOP,RNF168,PHLDB1,FAM222A,C11orf30,NCLN,RMND1,KIAA0368,SGOL1,HAUS6,TMEM158,R3HCC1L,GALC,NCAPD3,PTPN13,PLAGL1,LEMD2,CUL1,SPATA13,CENPN,FKBP1A,CCAR2,FZD1,DNAJA1,TOR1AIP1,ATP6AP1,GPR3,HK2,RINT1,TICRR,RFC2,PPM1F,TXNL1,TCTN3,VCL,TTC39B,FKBP5,OXTR,PSMB9,PKN3,CEP152,STAMBPL1,BLMH,BANP,DDX56,USPL1,SMC6,COPS3,NCAPG2,RRM1,ADSS,ZNF546,SENP1,MUM1,SBF1,CAMKK1,KDELR3,ZNF507,ARL14EP,TRERF1,NCAM1,COBLL1,IPPK,TMEM74B,HSD3B7,FAM208A,PPP1R7,KHNYN,TRIB2,DDI2,RPRD2,GOLGA1,TBC1D24,COL4A1,PSMF1,CLTC,BIRC6,DTNB,ALAD,ATP10A,CDC123,BRAT1,COL6A3,C15orf41,INTU,KBTBD8,FADS1,ZBTB49,RAD9B,PDP2,HINT1,MAN2C1,USP47,RPAIN,SLC25A4,TCF7L1,PFKP,TSHZ3,FAF1,HMG20B,H2AFV,MTRF1L,NIPA2,WDR90,PCBP1,RALGAPB,WDR20,SLC35C1,ZC3H12C,CENPE,EHD2,ATP5G3,TUBGCP3,APPL2,YAP1,EEF2,C4orf32,MAN1A2,WDR81,SYNJ2,ATE1,PLEKHG2,MORC2,DYNC1LI2,GTSE1,ANAPC5,ZC3H7A,ZDHHC1,FAM19A2,FRG1,ANKLE1,TMEM64,TRAPPC5,FAM188B,FANCM,DEK,FBXO7,CEP97,ODF2L,RHOT2,HNRNPA2B1,PDS5B,CDK4,CEBPD,KIAA0754,SEPT11,NUF2,SDK1,TMEM209,NAA15,CDKN3,GINS2,MAP4,PRR14L,SOS1,ATPAF1,ALG8,CDC5L,RAD21,ESCO1,SLC35A5,ZMYM1,DENND4A,WIPF2,SPRY1,OLFML3,LARP4B,RCCD1,LAMB2,IGHMBP2,PRPF18,UBR4,ATP13A3,ABCF2,ZSWIM8,EIF4A1,ZFHX2,BTF3L4,MSRA,UBTF,PPIL1,ID4,TMCC1,LRIG2,PDZD7,MEGF9,KIF1B,SLC41A3,NME2,MYC,TGFBR2,SMPD4,AHDC1,AMOTL2,FIGNL1,SUGT1,DPM3,KLF11,RNF41,PRPF38A,EIF4B,SPECC1,TEX264,LIPT2,FSTL3,KANK2,SAP30BP,DDOST,PSMD6,BTBD8,B3GALNT1,ARIH1,GMEB2,CDCA7L,XRCC6,ETV4,SEPT10,RUSC2,HSP90AA1,MAD1L1,SEC31B,NCKAP5L,FZD5,SSFA2,SUV420H1,MGST3,RBBP4,DPYSL3,NEURL4,SLC39A14,ETV6,TRA2A,DIAPH1,LYST,SPAG7,FYTTD1,NOP58,MEX3B,ACAD8,LCMT2,ACO1,VARS,CIZ1,CNNM3,BTBD10,POMT2,MORN1,HAUS8,RFX1,CANX,RPL23,NMT2,NFKBIL1,AMPD2,CCDC34,FAIM,SH3PXD2A,SLK,MAPK14,FAM111A,RAD9A,LSM11,ZNF451,CDKN2C,ERI1,PHACTR4,KPNA1,FANCB,DYNLL1,ZNF367,MTF1,EEFSEC,HNRNPUL1,CSTF2,KIN,KMT2B,TMEM55B,MITF,PGLS,GPATCH8,NAT10,FANCC,ZNF414,PLCL2,DONSON,IRF1,DOCK1,PCNA,INO80,RFC4,IRS1,CPNE8,GLRA1,E2F1,MSH5,HELB,YEATS4,SCAP,PKD2,SASS6,SGMS1,VCAN,EP300,XYLB,TRIB1,NCOA2,POLR2M,USP42,PRRX1,SLC6A17,E2F5,PRKCE,NAA60,MCM10,ZWILCH,PLOD3,EPG5,CWC22,TOR1AIP2,ATXN2L,PCDH9,STXBP6,POLD1,WDR76,KIF15,ABL2,RBM6,PRMT5,FEN1,NCOR2,USP49,VPS52,ASH2L,POLH,INSIG1,DPY19L4,LARS,UBXN4,EZH2,FBXO45,ADPRHL2,PMPCA,CPNE2,AIM1,RASAL2,FGFR1,LMNA,RANBP1,TMOD3,GSR,ABHD17C,PLEKHH2,PCGF1,PTPRS,C1orf27,PFAS,PHF1,TMPO,PEX12,TEAD4,KDM3B,VWA1,DRAP1,GABPB1,CCDC85C,SLC25A29,GTF2F2,CHPF,MARK2,MEIS2,TAOK1,GANAB,CIT,LTBP4,PHF21A,MAP2K7,S1PR2,ATG10,MRC2,let-7,LRCH1,GNAI2,KIF24,ZNF704,DYM,PANK3,PAQR4,SMARCC1,TONSL,VGF,UBC,LRR1,SNTB2,CAB39,POLA1,NUP133,CCNB2,EIF4A2,GPSM2,SECISBP2,EIF3B,PRKCDBP,DUSP11,MAP1A,FAM172A,AHCY,HCFC1,RGP1,GART,DAXX,CNTRL,KAT6A,ITPR3,PRKACA,COX18,CELSR3,C3orf67,CCDC138,ECT2,CPE,FANCA,KIF20A,FLNB,IRAK1BP1,BAG6,GNA11,CEBPZ,MTCH1,PNRC1,HEXB,C2CD5,KPNA3,EP400,PMM1,PASK,MAPK6,GREM1,IGF2R,BAK1,CSF1,SEPHS1,CHAC1,COX7A2,FBXO5,C12orf66,TFB1M,NAV2,MPRIP,LHX2,YWHAH,GNPAT,CCT2,NUP58,ZFPM1,HDAC10,LIPT1,ECD,PPFIBP1,RGPD4 (includes others),SMC1A,SOX2,TSEN15,ANXA11,ERAL1,EPHA7,OSBPL1A,STXBP1,SESN3,WEE1,IFT74,H6PD,CDCA2,PTPRM,OSBPL8,KIAA0907,HIRIP3,SLC25A10,TMEM248,FOXP4,INTS10,DDX26B,OSBPL6,KIAA0101,BARD1,CHSY1,PVRL3,MCM3AP,ZNF219,RBBP5,ALAS1,IQGAP1,ZFAND2A,NFAT5,BCL7B,RPL18A,ERBB2,VAV2,NAA40,KDM4C,NDUFV1,AP3M1,ADAM15,IFT46,NFATC4,SERTAD1,TSN,SLC7A6OS,ALS2,UMPS,MTO1,BIRC5,FANCL,SLC36A4,KLF5,ZDHHC3,BORA,DDX11,F2R,MTBP,DSTN,SUV39H1,RAN,GHITM,GTF2E2,DDX20,MKI67,HBP1,RBL1,POLB,RAD23A,ARNT,CXorf23,ATP1A1,CD2AP,AHSA1,RARA,MGAT4B,MED16,BAG5,RTEL1,CNOT1,PTPRG,ANGPTL6,C1orf74,YWHAZ,SPG7,MTF2,CKAP2,MON2,SCRT1,ADAR,MED12,PHF12,FARSA,UBE2G2,ARHGAP5,MNT,PWWP2A,AAAS,MYO9A,CDAN1,DNAJC14,CPSF3L,TFIP11,CLCC1,SQLE,FYN,OSR2,MAP2,CEP78,USP53,CRTAP,ARHGEF7,TTLL4,POLQ,STRA13,HMGB2,BRD9,NAA35,KANSL3,AAMP,CRLF2,MRPL39,EIF4G1,EAF1,SF3B3,ATAD5,CDH11,TIGD5,EIF4EBP1,AKAP11,STOM,KAT2B,CREB1,RAB33B,MYO1D,NUP205,XPO4,GNB1L,PMS2,SUZ12,KHK,ELL,SPC25,POLE,PAICS,TIAL1,MDM2,MAGEB1,SCAF11,NHLRC2,CDK1,GLTP,SPIDR,INTS6,CTNNBL1,CHRAC1,ATL2,CIRBP,REV1,H2AFY,ZNF184,UBN1,SAAL1,CAP1,HOXB9,BTBD7,NAB2,WDR48,FARP1,ARF1,VPRBP,PRMT3,UNC5B,PIGQ,ZNF609,DICER1,CAMK2D,SCARB1,TTLL12,FASN,CDCA3,HIST1H3J,TMUB2,ABLIM2,FOSL2,STX11,SOX4,MCM5,HK1,P4HB,TRIOBP,POLE2,XYLT1,CCDC155,MUT,SIX5,GPAA1,PREP,CTDP1,TIMELESS,RHOA,NUAK1,RFX2,JAG1,CDK2,ARL2,GAS2,TMX4,SRM,BRD2,COPS4,SH3BP4,C5orf42,ZBTB25,EXOG,PA2G4,AGAP1,NUDT3,TLE2,ZNF180,WD

Supplemental Table 7. General IPA functions for E2F1, E2F3A and E2F3B promoter targets

ChIP-seq	Category	B-H p-value	Genes
E2F3B	Cell Death and Survival	2.39E-27	TGFBR1,FRMD6,ELAVL4,POR,TRIM32,CRADD,SMARCB1,ADA,ETS1,CRKL,RFC1,DCLRE1A,DVL2,EYA3,RAD18,ALCAM,CPOX,PIM3,Calm1 (includes others),DDIT3,PRDX4,PPIA,SYNM,NOTCH2,RABL6,BNIP1,RNF19A,EXO1,ATN1,SLC12A6,SDHA,PPM1M,ID3,BUB1,KPNB1,MAD2L1,AP1G1,CDKN2A,EEF1A1,SMAD3,CBX5,INTS1,E2F6,MAPK3,SNRPD1,SNN,JUND,MTMR2,ING2,RAD54L,DYNC1H1,BCL2L1,TFEB,KLF10,PIAS1,PDE4A,GPHN,PDCD10,CLIC4,EIF2S1,HDGF,SIX1,NCS1,ILKAP,PDK1,TACC3,ALKBH5,MEF2A,HERPUD1,SOD1,PPM1G,TMEM109,TUBB6,CENPI,TFCP2,E2F7,TSC22D1,ING1,SLC25A5,MAP4K4,RPLP0,AGPS,CTGF,UBR2,ADIPOR1,XRCC1,ZFX,TDP2,CBFB,HIPK1,FRS2,DNMT1,NOVA1,TFDP1,CENPB,PLEC,HBEGF,GRK5,HMGA1,Anp32b,ARHGAP35,TMEM158,SNAI2,CDT1,PTPN13,PLAGL1,CUL1,PTN,BOK,FKBP1A,CCAR2,DNAJA1,ATP6AP1,MAFG,HK2,RNPS1,RINT1,IGF1R,PPM1F,VCL,NSMCE1,FKBP5,DUT,PLK1,ACLY,SRXN1,F3,NCAPG2,RRM1,SENP1,SBF1,CAMKK1,GPR180,NCAM1,PRPF19,IPPK,FBXW7,DHODH,ZNF91,PBK,YWHAQ,ETS2,TRIB2,Map3k7,TFDP2,STIL,COL4A1,ACP2,BIRC6,RHOJ,SMARCD3,PALB2,BRAT1,SCRIB,CCNC,DTYMK,NGF,RAD9B,HINT1,MAN2C1,TRIM24,POLR2A,FXN,USP47,SLC25A4,ATP2C1,LRRK2,TCF7L1,TSHZ3,FAF1,SLC25A38,RAF1,RNF8,TRAIP,MYH9,RDH10,HMMR,PANX1,ATP2A2,ADH5,EMG1,KLF7,GATAD2A,NUP93,CENPE,FBLN1,KLF1,CERS6,TYMS,GNE,ATG5,PHIP,ESPL1,YAP1,EEF2,OPN3,WDR81,PLEKHG2,TNPO2,ST3GAL1,TFRC,Meis1,PTPRA,ABCE1,FANCM,ERCC4,DEK,FBXO10,PTPN2,AKAP8,Dleu2,CDK4,CEBPD,CTDSPL,DUSP22,TNFAIP8L1,MED28,NUF2,CDKN3,NAA15,MAP4,UBE2K,DAB2,NFE2L2,ESCO1,RAD21,DHX9,DENND4A,HNRNPU,SPRY1,TUBGCP6,LZTS2,TPK1,ING5,SLC29A1,LAMB2,SDF2L1,CCNE1,ZFPM2,UBR4,CAPRIN2,EIF4A1,CDKN1A,EIF2B1,PSAP,UBTF,LDHA,MAP3K3,ID4,TCF7L2,CASP7,PSEN1,MAOA,CAMK1D,KIF1B,MSH3,VPS13A,TIMM50,NME2,ABCC10,PIEZO1,RNASEH1,SKA1,CEBPG,MYC,TGFBR2,Gm21596/Hmgb1,SMPD4,PPP3R1,XPO1,FIGNL1,DPM3,SNRPA1,KLF11,EIF4B,CLASP1,SMC3,SPECC1,FSTL3,YWHAE,KANK2,SAP30BP,SLC12A7,PSMD6,HELLS,NT5C3A,CDCA7L,TXN2,XRCC6,NDC80,HSP90AA1,PKMYT1,MAD1L1,ACTN4,PIDD1,RBBP4,DPYSL3,UBE2N,RPS6KA3,RAD50,ETV6,IGF2BP1,STIM2,RAD51,CCNA2,HLA-DMA,BMPR1A,TIMP1,NOP58,RPS3,LRRC8A,GMFB,PRKCA,SLC20A1,HAUS8,SDC1,SLC12A2,CANX,HSPD1,FAIM,SH3PXD2A,SLK,MAPK14,PRKCI,FOXO1,RAD9A,PSMD2,SH3RF1,SGK1,COX8A,APIP,CDKN2C,SFPQ,RICTOR,RECQL,GSTZ1,CXCL10,VEGFA,FANCB,DYNLL1,IPMK,MTF1,HNRNPUL1,PCID2,KMT2B,MITF,RPA1,FANCC,ITPR1,GEMIN2,IRF1,TERF2,DOCK1,PCNA,YARS,IRS1,BHLHE40,E2F1,HSPB11,MSH5,LRP8,HELB,YEATS4,PHLPP1,Nos1ap,SCAP,VASH2,ASF1A,CAMK2N2,SGMS1,VCAN,CHEK1,EP300,WTAP,TRIB1,NCOA2,ADK,DAP3,LAMP1,PRKCE,MCM10,MAP1LC3B,PLAT,EPG5,RPS19,TOMM20,DLX1,MCU,MAFK,SIN3A,CHMP6,SPDYA,MCM2,ABL2,PRMT5,FEN1,NCOR2,ZFP36L2,GLS2,POLH,FZR1,ANKS1B,PTPN23,VPS28,INSIG1,FNIP2,MELK,STMN1,PTK2,EZH2,SIAH2,HTRA2,GPS2,FGFR1,PSMC4,LMNA,RANBP1,TMOD3,GSR,ARRB2,FLOT2,MTDH,PML,PHF1,PAFAH1B2,GABPB1,ZBTB7A,PDGFA,GTF2F2,Pcnt,MARK2,TAOK1,ING4,Ppp1cc,SP1,MANF,CIT,RABGGTB,DTL,MAP2K7,S1PR2,ATG10,SMAD7,let-7,RPS6KA5,BCL3,FAU,GNAI2,ENO1,B4GALT1,SLC25A27,TONSL,SMARCC1,VGF,HMGCR,UBC,SHMT2,BCL2L11,WNT5A,LGALS1,MCM7,NPM1,mir-130,CTCF,PRKAB1,TAB2,Ewsr1,EIF3B,PRKCDBP,VAMP3,TCERG1,MOB1A,FBL,SLC2A1,STK25,TCF3,DAXX,ITPR3,PRKACA,ECT2,FANCA,FLNB,NRG2,PRDX1,BAG6,GNA11,MTCH1,TTK,HEXB,EP400,KHDRBS1,GAS1,GREM1,KAT5,IGF2R,BAK1,TMEM107,MSH2,CSF1,SLC29A2,FBXO5,TFB1M,ACTL6A,SOCS3,MPRIP,PCDH18,SEPT9,YWHAH,LHX2,CCT2,NUP58,RNF7,SMC1A,RGPD4 (includes others),SOX2,INTS3,USP8,CD164,ANXA11,GPX4,WDR4,EPHA7,STXBP1,HDAC2,WEE1,IFT74,RDX,H6PD,PFDN5,PTPRM,CDCA2,TXNRD1,GINS1,SLC25A10,UBE2I,PEBP1,KIAA0101,BARD1,CHSY1,INPPL1,IQGAP1,E2F3,PTGES3,NFAT5,STUB1,ERBB2,VAV2,ADAM15,RACGAP1,SMARCE1,CSRNP1,SMARCD1,NFATC4,ALS2,BIRC5,FANCL,KLF5,BRCA2,DDX11,CCP110,MTBP,F2R,SUV39H1,RAN,DDX20,MKI67,Cyb5r3,RBL1,EIF6,POLB,ARNT,CD2AP,ATP1A1,AHSA1,RARA,LEPROT,AFAP1,BAG5,PTPRG,YWHAZ,MDC1,SPG7,CKAP2,ADAR,RNASEH2A,CMIP,MNT,AHI1,CREM,FYN,ARHGEF7,NAA35,HMGB2,EIF4G1,SF3B3,XRCC4,CDH11,EIF4EBP1,STOM,KAT2B,CREB1,NUP205,WSB1,PMS2,SUZ12,PPIF,KHK,SPC25,ELL,TIAL1,MDM2,SLIT2,C1orf159,CDK1,SPIDR,CTNNBL1,IMMT,REV1,CIRBP,ZNF184,HOXB9,WDR48,VTI1A,VPRBP,UNC5B,DICER1,METAP2,CAMK2D,SCARB1,STAG1,FASN,ITPRIP,FOSL2,BCKDK,STX11,SOX4,HK1,P4HB,CNOT11,DDX19A,RAC1,PREP,Cdc42,RHOA,USE1,NUAK1,TBCCD1,CYLD,JAG1,CDK2,KDM3A,GAS2,BRD2,EXOG,PA2G4,SRRT,GADD45G,SCARB2,SET,UHRF2,Pgap2,GMNN,ZNF280B,IFRD1,NCL,MAPKAPK2,ATG16L1,RHBDD3,RASSF1,HSPG2,UHRF1,HAT1,PHLDA3,HSPH1,GLS,AVPI1,PRMT1,PIAS3,NT5M,ACAT1,NFIB,PSMC3,LANCL2,MSN,CASP8AP2,MINPP1,PRKAB2,KRAS,RBM3,CCND1,CDIP1,PKN2,EGR2,FHL2,RBM4B,SUMO1,NEK6,ATF4,RUVBL2,ADORA2B,HIPK2,UNG,PIGT,FBXO9,TP53,UBE2Q1,RRM2,ANO6,TPM3,TBK1,KLF13,DDR1,ATF2,SKP2,HSPA8,CLK2,BTG2,INVS,GAPDH,XRCC5,PRDX2,TRIM33,PSEN2,MMS22L,SPAG5,APPL1,ARF6,CD47,ZC3H8,TRIM27,ALMS1,DIS3,ATP7B,CUL7,HSPA2,PLA2G4A,NR4A2,SGCD,AKAP1,SRSF2,ILF3,ATP2B1,GNB2L1,PARP2,KLF6,POLR3E,TCEB1,HSPA4,FDFT1,MAP2K2,PIM1,MYBL2,CHTF18,GCLM,BRIP1,ULK2,PPP1R15B,SCYL3,ITGB3BP,BCAS2,UBE4B,DIDO1,WASF1,BUB1B,ATAD2,KMT2A,SLC3A2,PFKM,PIAS4,TFAM,TRIM39,DUSP1,AGAP3,CAPN2,ELMO1,CDKL3,RPSA,RUNX1,TNFAIP8,MOB3A,ARID1A,PPIB,ATF6,SMA

Supplemental Table 7. General IPA functions for E2F1, E2F3A and E2F3B promoter targets

ChIP-seq	Category	B-H p-value	Genes
E2F3B	Cellular Development	5.01E-24	TGFBR1,TLE1,FRMD6,ELAVL4,POR,TRIM32,SMARCB1,ADA,RRAGC,ETS1,CCNE2,PEAK1,CRKL,RFC1,TMEM67,ZBTB5,DVL2,ALCAM,ELMO2,MORC3,PIM3,DDIT3,BEND6,SLC1A5,PRDX4,PPIA,SYNM,RABL6,NOTCH2,TIPARP,ATN1,SLC12A6,IPO7,ID3,BUB1,PIR,CDKN2A,EEF1A1,SMAD3,CBX5,MAPK3,JUND,ESCO2,KCNAB2,GNAZ,PIK3R3,DYNC1H1,BCL2L1,H3F3A/H3F3B,CBX3,SUMO3,KLF10,RAB23,PIAS1,RNASEH2B,PDE4A,CSRP1,GPHN,CLIC4,PDCD10,ZBTB24,HDGF,SIX1,ILKAP,TACC3,MEF2A,SOD1,MORF4L1,RPS15,E2F7,TSC22D1,ING1,BRPF1,SLC25A5,MAP4K4,EFEMP2,HNRNPL,ASPSCR1,CTGF,FAM20C,UBR2,FNDC3B,RRAGB,RASGRF1,CTDSP1,RAB17,CBFB,CCNT2,HIPK1,FRS2,DNMT1,RND2,GET4,PIK3C2B,Irx5,TFDP1,CENPB,HIRA,HBEGF,SYNCRIP,GRK5,HMGA1,SH3GL1,SUCO,SNAI2,CDT1,PTPN13,LEMD2,PLAGL1,PTN,CUL1,FZD1,ATP6AP1,H2AFZ,MAFG,GPR3,NEIL3,HK2,IGF1R,DAGLB,VCL,FKBP5,EED,OXTR,BANP,PLK1,ACLY,COPS3,F3,RRM1,SENP1,SBF1,RNF187,GCAT,NCAM1,ARL2BP,PRPF19,CAV2,TBX15,FBXW7,PBK,YWHAQ,ETS2,TRIB2,Map3k7,AAGAB,TBC1D24,COL4A1,CLTC,BIRC6,RHOJ,NDUFAF2,MAT2B,SMARCD3,COL6A3,INTU,RCE1,HDGFRP3,CDK5RAP2,NGF,ZMIZ1,NELFE,HINT1,TRIM24,FXN,USP47,ATP2C1,ANKRD54,LRRK2,TMEM14C,TCF7L1,PFKP,NCAPH2,TSHZ3,MLLT1,FAF1,SLC25A38,HMG20B,TTC7A,RAF1,TRAIP,MYH9,PCBP1,RDH10,HMMR,PANX1,ATP2A2,NKAP,ADH5,KLF7,FBLN1,COPS6,TGIF2,KLF1,TYMS,GNE,ATG5,PHIP,PAPD4,ESPL1,PAM,YAP1,EEF2,CDCA4,PEX2,TFRC,Meis1,TMEM64,PTPRA,SPPL2A,DEK,PLXNA3,PTPN2,WDR61,HNRNPA2B1,EEF1B2,PDS5B,CEBPD,CDK4,CTDSPL,SEPT11,MED28,COPS8,SDK1,CDKN3,SOS1,DAB2,NFE2L2,PEMT,RAD21,DHX9,HNRNPU,SPRY1,LZTS2,LAMB2,CCNE1,ZFPM2,CDKN1A,EIF4A1,EIF2B1,PSAP,LDHA,UBTF,PPIL1,MAP3K3,TCF7L2,CASP7,ID4,PSEN1,MAOA,RPL22,NCDN,MSH3,NME2,TLN1,ABCC10,MYC,TGFBR2,Gm21596/Hmgb1,AMOTL2,PPP3R1,FIGNL1,Hmga2,XPO1,SUGT1,RNF41,EIF4B,SMC3,FSTL3,PNN,HELLS,SNX3,TUSC3,TBL1X,ARIH1,NT5C3A,HNRNPAB,XRCC6,ETV4,RECQL4,HSP90AA1,MAD1L1,FZD5,ACTN4,FAM83D,SUV420H1,DPYSL3,RPS6KA3,IGF2BP1,ETV6,STIM2,RAD51,TRA2A,CCNA2,DIAPH1,AHNAK,HLA-DMA,TIMP1,BMPR1A,NOP58,CIZ1,LRRC8A,PRKCA,SDC1,RFX1,AP1S2,SLC12A2,HSPD1,SH3PXD2A,FAIM,PRKCI,MAPK14,FOXO1,PHF19,RAD9A,SGK1,ZNF451,SFPQ,CDKN2C,RICTOR,Rpl29 (includes others),RECQL,VEGFA,CXCL10,DYNLL1,CSTF2,PCID2,HEY2,KIN,KMT2B,MITF,CNOT6L,RPA1,PLCL2,FANCC,ITPR1,IRF1,GEMIN2,TERF2,DOCK1,PCNA,PATZ1,RFC4,BHLHE40,IRS1,E2F1,RGL2,LRP8,YEATS4,PHLPP1,VASH2,ASF1A,CAMK2N2,FNTB,SP2,VCAN,SGMS1,TAX1BP3,EP300,CHEK1,TRIB1,ADK,LAMP1,E2F5,PRKCE,LPP,PLAT,RPS19,DLX1,CINP,MAFK,SIN3A,SPDYA,ABL2,MCM2,PRMT5,KCTD5,ADAM10,GABPA,FEN1,NCOR2,ZFP36L2,NPC2,POLH,FZR1,EPS15,VPS28,INSIG1,MELK,STMN1,PTK2,MBNL3,EZH2,NIPBL,SIAH2,ARHGEF25,MYO10,GPS2,FGFR1,RAB8A,LMNA,ELF1,CORO1B,PTPRS,MTDH,PML,PHF1,RFC3,TEAD4,KDM3B,PKNOX1,ZBTB7A,PDGFA,MARK2,MEIS2,TMEM120A,ING4,FUT8,Ppp1cc,SP1,VGLL3,CIT,MANF,RBM15,LTBP4,NFYB,DTL,MAP2K7,S1PR2,CKS2,MRC2,ATG10,Nedd4,SMAD7,let-7,RPS6KA5,BCL3,GNAI2,ENO1,SLC25A27,PAQR4,UBC,HMGCR,VGF,BCL2L11,MCM7,WNT5A,LGALS1,NPM1,mir-130,CTCF,TAB2,CCNB2,SSBP2,GPSM2,Ewsr1,EIF3B,PLXNB2,AHCY,FBL,SLC2A1,PIGF,TCF3,SP4,DAXX,KAT6A,PRKACA,ECT2,FANCA,KIF20A,FLNB,NRG2,EIF4EBP2,BAG6,GNA11,EP400,KHDRBS1,GAS1,ZNF521,MAPK6,GREM1,KAT5,IGF2R,BAK1,AGPAT5,MSH2,CSF1,KIF23,SOCS3,MPRIP,SEPT9,LHX2,RNF7,ZFPM1,RPGRIP1L,SMC1A,SOX2,USP8,CD164,ERAL1,HDAC2,PFDN5,CDCA2,PTPRM,TXNRD1,OSBPL8,CAND1,SF3B4,UBE2I,PBRM1,PEBP1,LITAF,RND1,KIAA0101,BARD1,IQGAP1,E2F3,PTGES3,STUB1,ERBB2,KDM4C,ADAM15,RACGAP1,SMARCE1,NFATC4,SERTAD1,TSN,SLC7A6OS,BIRC5,ALS2,KLF5,CKS1B,BRCA2,F2R,MTBP,SUV39H1,RAN,HBP1,MKI67,RBL1,EIF6,RPS11,RAD23A,ARNT,POLB,AHSA1,RARA,AFAP1,CNOT1,PTPRG,YWHAZ,MTF2,ADAR,MED12,ANKRD26,CMIP,MNT,ARHGAP5,SSBP1,CREM,ME2,FYN,OSR2,MAP2,ARHGEF7,TTLL4,STRA13,HMGB2,NAA35,CRLF2,EIF4G1,CDH11,XRCC4,EIF4EBP1,KAT2B,CREB1,WSB1,PMS2,SUZ12,PPIF,HDGFRP2,ELL,MDM2,NAP1L1,SLIT2,CBLN1,CDK1,CCDC85B,RNF144A,IMMT,H2AFY,CIRBP,UBN1,HOXB9,BTBD7,NAB2,WDR48,FARP1,VTI1A,VPRBP,ARF1,Wasl,UNC5B,DICER1,AMD1,HIST1H4A,HIST1H4C,CAMK2D,SCARB1,STAG1,FASN,HIST1H4I,HIST1H4J,FOSL2,HK1,SOX4,DTNBP1,RAC1,OSTM1,HERC2,PREP,NASP,Cdc42,SH2B3,RHOA,NUAK1,SBNO2,CYLD,SPTAN1,JAG1,CDK2,TMTC3,ZFAT,COPS4,SRM,SPRED1,PA2G4,GADD45G,TXLNA,KMT2C,Cux1,SET,UHRF2,PPP1R12A,GMNN,SIPA1,GTPBP4,IFRD1,NCL,MAPKAPK2,RASSF1,EMILIN1,HSPG2,OGFR,MYCBP,UHRF1,HAT1,GLS,DOCK7,MTAP,EDF1,C19orf68,PRMT1,PIAS3,ACAT1,NFIB,CBFA2T2,ADAM9,RMI1,MINPP1,RBM3,KRAS,CCND1,ADRB3,PKN2,EGR2,BOP1,FHL2,KIF13A,SUMO1,BAIAP2,ATF4,ADORA2B,CDC16,HIPK2,PIGT,FBXO9,TP53,CSNK1D,RRM2,USP19,TPM3,KLF13,PTP4A1,RBM4,DDR1,SKP2,ATF2,MICU1,EIF4H,CCNF,FSCN1,BTG2,GAPDH,SRSF4,XRCC5,PRDX2,RAP2A,PRPF3,GALNT2,GPC2,PSEN2,ALX1,KISS1R,B4GALT7,ARF6,CD47,TRIM27,ALMS1,CSNK2B,KIF2C,STT3B,MEMO1,CUL7,POLG,TOB1,HSPA2,FRK,PLA2G4A,NR4A2,SHMT1,DLGAP5,SRSF2,ILF3,RASA3,PARP2,GNB2L1,KLF6,POLR3E,SART1,LEMD3,FDFT1,HSPA4,TNRC6C,MAP2K2,PIM1,MYBL2,TAB1,ULK2,PGK1,UBE4B,IER2,DIDO1,POFUT1,ATAD2,KMT2A,SLC3A2,METRN,TFAM,CBX1,ATP5B,TRIM39,DUSP1,LMNB2,DIXDC1,HELT,ELMO1,EEA1,TNFAIP8,RUNX1,NMT1,ARID1A,GTF2I,HIST2H4B,ATF6,SMAD5,MLH1,CDCA7,MIER1,FANCD2,NET1,LDB1,

Supplemental Table 7. General IPA functions for E2F1, E2F3A and E2F3B promoter targets

ChIP-seq	Category	B-H p-value	Genes
E2F3B	Connective Tissue Development and Function	5.01E-24	RAF1,NPM1,TRAIP,MINPP1,TGFBR1,HMMR,RBM3,KRAS,FRMD6,CCND1,TRIM32,Ewsr1,BOP1,EGR2,EIF3B,SUMO1,SMARCB1,FBLN1,ATF4,HIPK2,UNG,AHCY,TP53,ATG5,ESPL1,SLC2A1,YAP1,TMEM201,TPM3,RFC1,KLF13,TCF3,SKP2,PEX2,KAT6A,CCNF,BTG2,RAD18,PRKACA,TFRC,PTPRA,XRCC5,FANCA,PRDX2,MORC3,RAP2A,FLNB,PIM3,DDIT3,PTPN2,PRDX1,SNX17,PRDX4,CEBPD,CDK4,B4GALT7,APPL1,MAP4,CD47,SOS1,CSNK2B,NFE2L2,DHX9,SLC12A6,ATP7B,EP400,SPRY1,KHDRBS1,GAS1,CUL7,MAPK6,TOB1,LZTS2,KAT5,IGF2R,ID3,BAK1,BUB1,CCNE1,MSH2,CSF1,CDKN1A,SHMT1,UBTF,PPIL1,CASP7,ACTL6A,PSEN1,CDKN2A,SOCS3,LHX2,SMAD3,PARP2,GNB2L1,KLF6,ABCC10,TGFBR2,MYC,E2F6,USP8,Gm21596/Hmgb1,PIM1,MAPK3,MYBL2,JUND,PPP1R15B,TAB1,PGK1,SMC3,SYNE2,HDAC2,DIDO1,PFDN5,HELLS,BUB1B,KMT2A,PFKM,SLC3A2,BCL2L1,DUSP1,RECQL4,XRCC6,MAD1L1,SUV420H1,PBRM1,RUNX1,TNFAIP8,ARID1A,KIAA0101,GTF2I,PIAS1,RPS6KA3,RNASEH2B,SMAD5,E2F3,ETV6,MLH1,PTGES3,RAD50,HDGF,CCNA2,SIX1,AHNAK,FANCD2,STUB1,TIMP1,NOP58,STEAP2,FOXO3,ERBB2,CIZ1,MCM9,PRKCA,SLC20A1,SOD1,TSN,SERTAD1,FOXM1,BIRC5,MORF4L1,NBN,IVNS1ABP,MAPK14,FOXO1,RAD9A,TFCP2,KLF5,E2F7,CKS1B,BRCA2,TSC22D1,ATR,WISP1,BRPF1,ING1,WNK1,DPY30,SOCS1,ASPSCR1,CTGF,F2R,MTBP,ITSN1,SUV39H1,CDC7,CDKN2C,SFPQ,FNDC3B,RBL1,EIF6,RICTOR,Rpl29 (includes others),RECQL,POLB,VEGFA,CXCL10,RASGRF1,RARA,CSTF2,CBFB,IRS2,TXN,FRS2,TIMP2,TFDP1,NDRG1,MITF,COPS5,PLEC,CNOT6L,HBEGF,CKAP2,GRK5,FANCC,HMGA1,IRF1,TERF2,MNT,SH3GL1,PATZ1,GAB1,IRS1,STIP1,MBD4,E2F1,ME2,ARHGAP35,SAC3D1,CYR61,FYN,CTC1,ARHGEF7,TTLL4,CUL1,HMGN1,SETX,RCHY1,FNTB,SP2,VCAN,XRCC4,CHEK1,EP300,ID1,YY1,CREB1,E2F5,EIF3A,CEBPA,RHOU,PDGFRA,IGF1R,BID,PRKCE,RASSF5,VCL,LPP,POT1,PLAT,RPS19,MYCN,PMS2,DCK,SUZ12,PPIF,TBX3,HDGFRP2,ACTB,CDC6,MDM2,MAFK,SIN3A,KITLG,FADD,DGKZ,SENP1,ABL2,REV1,SBF1,CIRBP,KIF20B,SPRY2,RNF187,ADD1,TBPL1,FEN1,IREB2,ZFP36L2,DYRK1A,POLH,FZR1,MCM8,PRPF19,PALLD,TFG,MAPK1,VPRBP,DIAPH3,Wasl,FBXW7,DICER1,LATS2,AMD1,LMNB1,FGFR3,STMN1,PTK2,SRSF1,SCARB1,STAG1,FASN,EZH2,FOSL2,BRCA1,STX11,CDC25A,STK11,FGFR1,CLTC,RAC1,LMNA,TMOD3,SSRP1,TOB2,Cdc42,PKD1,SH2B3,RHOA,LIN9,GNL3,RCE1,TMPO,VDAC1,JAG1,PML,CDK2,GDNF,PA2G4,PICALM,GADD45G,PDGFA,ABL1,SLC7A1,NGF,BCAR1,KMT2C,PRKAG1,ZMIZ1,TRIM24,HINT1,SIPA1,GTPBP4,ERF,MAPKAPK2,BLM,RASSF1,MAP2K7,CKS2,S1PR2,HAT1,MRC2,HDAC1,let-7,SMAD7,MAPK9,PRMT1,GNAI2,RIPK1,B4GALT1,LPAR1,ACAT1,EIF2AK2,SHMT2,WNT5A

Supplemental Table 7. General IPA functions for E2F1, E2F3A and E2F3B promoter targets

ChIP-seq	Category	B-H p-value	Genes
E2F3B	Cellular Assembly and Organization	7.18E-24	NPM1,KIF13B,TGFBR1,CTCF,RAB2A,POLA1,NUP133,SMARCD2,CCNB2,ELAVL4,GPSM2,TMEM231,GORASP2,SMARCB1,PRKCDBP,MAP1A,PLXNB2,CENPW,ETS1,HCFC1,CRKL,STK25,NUP107,TMEM67,DCLRE1A,SP4,DAXX,DVL2,KAT6A,RAD18,PRKACA,CELSR3,ELMO2,ECT2,FLNB,EIF4EBP2,BAG6,GNA11,TTK,SYNM,PELO,BNIP1,HEXB,RNF19A,ATN1,EXO1,BBIP1,GREM1,KAT5,BUB1,KPNB1,MAD2L1,TMEM107,CSF1,FBXO5,AP1G1,ACTL6A,CDKN2A,KIF23,SOCS3,EEF1A1,MPRIP,YWHAH,LHX2,SEPT9,SMAD3,RPGRIP1L,SMC1A,USP8,CEP57,TPPP,MAPK3,ARHGAP20,ZWINT,GPX4,ESCO2,EPHA7,HDAC2,WEE1,IFT74,DNA2,RDX,RAD54L,MAPKAPK5,Afg3l1,NDC1,CDCA2,PTPDC1,PTPRM,TXNRD1,BCL2L1,H3F3A/H3F3B,CEP76,HIRIP3,CBX3,UBE2I,PBRM1,HPS5,TFEB,RND1,KIZ,KIAA0101,RAB23,SKA2,BARD1,PVRL3,PDE4A,NEDD1,CSRP1,INPPL1,GPHN,IQGAP1,PHLDB2,PTGES3,HDGF,STUB1,ERBB2,LASP1,VAV2,TACC3,IFT46,RACGAP1,SMARCE1,MEF2A,SMARCD1,NFATC4,SOD1,SERTAD1,BIRC5,ALS2,MORF4L1,KLF5,PAPD7,BRCA2,BORA,ING1,SLC25A5,DDX11,CCP110,CTGF,RAB5C,F2R,MTBP,DSTN,SUV39H1,RAN,HBP1,Cyb5r3,RBL1,CD2AP,RASGRF1,RARA,TDP2,RAB17,CBFB,AFAP1,SPECC1L,BAG5,RTEL1,DNMT1,RND2,TFDP1,SEPT7,YWHAZ,PLEC,SPG7,GRK5,CKAP2,ARHGAP5,RNF168,PHLDB1,SSBP1,AHI1,RERE,CDAN1,SGOL1,SAC3D1,HAUS6,B9D1,FYN,MAP2,NCAPD3,CDT1,ARHGEF7,LEMD2,CUL1,PTN,TMEM11,SPATA13,FKBP1A,CNTROB,HMGB2,TOR1AIP1,CDH11,AKAP11,EIF4EBP1,GPR3,KAT2B,RIF1,CREB1,IGF1R,PPM1F,PARP11,TCTN3,VCL,FKBP5,MCMBP,PMS2,CEP152,NUP85,SPC25,SUPT4H1,SMC6,PLK1,MDM2,SLIT2,SCMH1,F3,NCAPG2,CDK1,SENP1,ATL2,MUM1,CAP1,CLUH,NCAM1,FMNL3,STRN,VTI1A,FARP1,CAV2,ARF1,Wasl,MNS1,UNC5B,FBXW7,DICER1,NAF1,ESPN,STAG1,PPP1R7,FASN,NCAPH,MID1IP1,Nolc1,PANK4,TBC1D24,STIL,DTNBP1,TRAF3IP1,ACP2,CLTC,RAC1,PREX2,RHOJ,SMARCD3,PALB2,Cdc42,ERP29,SMC2,IFT81,USE1,RHOA,NUAK1,INTU,HDGFRP3,CYLD,SPTAN1,JAG1,CDK5RAP2,CDK2,KDM3A,ARL2,C5orf42,CENPC,NGF,WDHD1,SET,Cux1,IPO9,PPP1R12A,FXN,HAUS5,GMNN,USP47,SORBS3,MAPKAPK2,IFRD1,ATG16L1,RASSF1,UHRF1,ATP2C1,POC1B,PANK2,PHF13,LRRK2,DOCK7,PRMT1,NCAPH2,KIAA1033,NFIB,MIS12,CENPH,MSN,RAF1,RNF8,MYH9,MAP6,Ubb,SMC5,HAUS4,KRAS,C21orf2,STK35,ATP2A2,CCND1,ADRB3,PKN2,KLF7,FHL2,Diap2,BOP1,CENPE,SUMO1,BAIAP2,EHD2,NEK6,RUVBL2,KLF1,HIPK2,MSTO1,TP53,TUBGCP3,ATG5,PHIP,ESPL1,APPL2,PAM,CSNK1D,TPM3,TBK1,DDR1,SKP2,HSPA8,PEX2,DYNC1LI2,FSCN1,CCNF,BTG2,GAPDH,CENPT,CHD1L,PTPRA,XRCC5,HACE1,FANCM,RAP2A,ERCC4,DEK,PLXNA3,CDK4,PDS5B,PSEN2,CKAP4,SEPT11,NUF2,SDK1,MMS22L,LBR,SPAG5,CEP162,KISS1R,B4GALT7,CD47,ARF6,MAP4,TRIM27,SORBS1,ALMS1,DAB2,KIF2C,ESCO1,RAD21,DHX9,TUBGCP6,CUL7,VDAC3,NCAPD2,FRK,LAMB2,CCNE1,CAPRIN2,CDKN1A,EIF2B1,PSAP,SPICE1,PLEKHA1,CEP41,MAOA,KLHL17,PSEN1,AKAP1,DLGAP5,NCDN,CAMK1D,ATP2B1,POLR3E,RFWD3,TIMM50,SMC4,TLN1,PINX1,SKA1,CEBPG,IFT140,TGFBR2,MYC,ZW10,LEMD3,Gm21596/Hmgb1,MAP2K2,RCC1,WDPCP,ARL1,XPO1,CEP131,ULK2,CLASP1,TOP3B,SMC3,SYNE2,UBE4B,KANK2,ORC6,RBFOX2,WASF1,HELLS,BUB1B,SNX3,SLC3A2,METRN,CDC42BPB,CBX1,TFAM,PIAS4,MATN2,ETV4,XRCC6,MAD1L1,LMNB2,DIXDC1,HSP90AA1,NDC80,CAPN2,ACTN4,SUV420H1,ELMO1,EEA1,CDKL3,RBBP4,ABI2,ARID1A,DPYSL3,UBE2N,RPS6KA3,ATF6,SMAD5,VPS4A,MLH1,RAD50,STIM2,RAD51,CCNA2,DIAPH1,LYST,FANCD2,BMPR1A,TIMP1,NET1,FOXO3,TOR1B,RPS3,MCM9,LONP1,LRWD1,PRKCA,ARC,WDR1,HAUS8,CAPZB,KIRREL,APBB1IP,SLC12A2,CHP1,TUBG1,CANX,TUBGCP2,FOXM1,GIT1,ATL3,FAIM,SH3PXD2A,RPA2,NBN,SLK,PMP22,SS18L1,MAPK14,PRKCI,RAD9A,KIF5B,EHD4,AMIGO1,DCTN1,ATR,CEP70,KIF18A,CENPF,PLD2,ITSN1,SGK1,TOR1A,CDC7,SFPQ,PHACTR4,KPNA1,RAPH1,RICTOR,CHAF1A,RECQL,CXCL10,VEGFA,RUSC1,DYNLL1,PEX16,BAG1,TARDBP,MAP1S,TXN,CEP250,CENPJ,STAT6,ACTR2,NDRG1,CFL1,RPA1,ITPR1,FANCC,GEMIN2,IRF1,MRPL14,TERF2,POM121/POM121C,CCNO,DOCK1,INO80,BSG,GAB1,H2AFX,STIP1,E2F1,RAB11A,HPRT1,LRP8,MAPK7,SEH1L,CYR61,EPHA2,ADAM17,CTC1,PDIA3,HMGN1,SASS6,VCAN,CHEK1,EP300,COL5A1,EFNB2,ID1,YY1,SEC61A1,PDGFRA,RHOU,CEBPA,LAMP1,TOP2A,BID,PRKCE,MAP1LC3A,MCPH1,RASSF5,FAM109A,NCKIPSD,POT1,PLOD3,POGZ,PLAT,AIFM1,MYCN,RPS19,VPS18,HERC1,ACTB,CDC6,TOR1AIP2,MAFK,PPP2R5A,KITLG,BNIP2,CHMP6,ABL2,NDE1,KIF20B,SPRY2,ADAM10,ARAP1,ADD1,PAFAH1B1,ASH2L,SEPT2,WDR19,VAMP4,DYRK1A,ZMYM4,SMARCAD1,FZR1,MCM8,EPS15,PALLD,PTPN23,MAPK1,DIAPH3,MELK,TUBB,AURKB,LATS2,LMNB1,FGFR3,ROCK2,PTK2,STMN1,SERP1,TTBK2,NVL,ITGAV,NEO1,NIPBL,HTRA2,ARHGEF25,BRCA1,MYO10,DLC1,Ftx,KIF14,NUP155,ULK4,FGFR1,STK11,RAB10,RAB8A,LMNA,RANBP1,TMOD3,SSRP1,SIPA1L1,RNF4,CCNG2,PKD1,CORO1B,PTPRS,EXTL3,BAZ1B,PEX12,KIF11,INCENP,OBFC1,NFIX,GDNF,PDGFA,PICALM,Pcnt,PKM,MARK2,Spg20,ABL1,Ttf1,TAOK1,BCAR1,MCM4,TNFRSF12A,FUT8,EPHB6,NTNG1,ROR2,CCDC88A,SP1,RRN3,PMF1/PMF1-BGLAP,CIT,MICALL1,BLM,CTDNEP1,ACTN1,ABCD3,S1PR2,Nedd4,C2CD3,HDAC1,EFNA3,MAPK9,XIAP,DNM1,GNAI2,KIF24,UBQLN2,EXOC4,LPAR1,SATB1,DYM,SMARCC1,TONSL,HMGCR,VGF,GSG2,LGALS1,WNT5A

Supplemental Table 7. General IPA functions for E2F1, E2F3A and E2F3B promoter targets

ChIP-seq	Category	B-H p-value	Genes
E2F3B	Embryonic Development	3.48E-21	NPM1,TGFBR1,CTCF,Ap2b1,TAB2,CCNB2,POR,ADA,PLXNB2,ETS1,CCNE2,SLC2A1,CRKL,TMEM67,TCF3,DAXX,CNTRL,DVL2,KAT6A,RAD18,PRKACA,CELSR3,ECT2,FANCA,NRG2,SNX17,BAG6,GNA11,NOTCH2,PELO,TIPARP,EP400,GAS1,GREM1,KAT5,IGF2R,ID3,MAD2L1,TMEM107,MSH2,CSF1,FBXO5,TFB1M,AP1G1,CDKN2A,SOCS3,SMAD3,ZFPM1,RPGRIP1L,INTS1,SOX2,USP8,MAPK3,MATR3,GPX4,SEC63,ESCO2,HDAC2,IFT74,TXNRD1,BCL2L1,GINS1,RAI1,FOXP4,PBRM1,PDCD10,HDGF,SIX1,NFAT5,ERBB2,TACC3,PSMC3IP,NFATC4,SOD1,BIRC5,MORF4L1,FANCL,E2F7,KLF5,BRCA2,TSC22D1,DDX11,CTGF,F2R,UBR2,EIF6,RBL1,XRCC1,ARNT,POLB,RARA,ZFX,CBFB,HIPK1,FRS2,RTEL1,DNMT1,TFDP1,ANGPTL6,HIRA,PLEC,HBEGF,HMGA1,ADAR,MED12,MNT,ARHGAP5,AHI1,ARHGAP35,PRICKLE1,FYN,OSR2,LEMD2,ARHGEF7,CUL1,PTN,FKBP1A,FZD1,XRCC4,CDH11,NEIL3,HK2,RINT1,CREB1,DAGLB,IGF1R,VCL,EED,OXTR,SUZ12,TIAL1,MDM2,SLIT2,COPS3,F3,NCAPG2,HOXB9,NCAM1,PRPF19,CAV2,Wasl,FBXW7,DICER1,AMD1,METAP2,CAMK2D,SCARB1,ETS2,FASN,Map3k7,FOSL2,SOX4,STIL,DTNBP1,BIRC6,RAC1,SMARCD3,PALB2,NASP,Cdc42,TIMELESS,RHOA,SH2B3,LOXL1,INTU,CYLD,JAG1,CDK2,TMTC3,ZFAT,C5orf42,SRRT,GADD45G,NGF,RAD9B,ZMIZ1,Cux1,FXN,GMNN,NCL,RASSF1,RHBDD3,HSPG2,UHRF1,TRA2B,ATP2C1,HAT1,LRRK2,TCF7L1,TSHZ3,NFIB,PSMC3,RAF1,TRAIP,RDH10,FAM212A,Ubb,KRAS,SLC35C1,CCND1,ATP2A2,GATAD2A,EGR2,CENPE,FBLN1,MTHFD2,TGIF2,ATF4,KLF1,MGAT1,HIPK2,TP53,ESPL1,UBE2Q1,YAP1,TPM3,MAN1A2,DDR1,RBM4,ATF2,SKP2,ATE1,CCNF,BTG2,FADS2,TFRC,INVS,PRDX2,TRIM33,USF2,CDK4,CEBPD,PDS5B,PSEN2,COPS8,KISS1R,ARF6,DAB2,CSNK2B,NFE2L2,CYP51A1,DHX9,ATP7B,SPRY1,CUL7,POLG,LZTS2,ING5,TGS1,Kat6b,CCNE1,ZFPM2,UBR4,CDKN1A,PSAP,SEMA3C,PLEKHA1,CASP7,TCF7L2,ID4,PSEN1,RPL22,PARP2,KLF6,TLN1,PINX1,RNASEH1,ATXN1L,CEBPG,IFT140,TGFBR2,MYC,FDFT1,TNRC6C,Gm21596/Hmgb1,MAP2K2,PIM1,PPP3R1,WDPCP,Hmga2,PPP1R15B,TAB1,TOP3B,PNN,POFUT1,KMT2A,TFAM,DUSP1,TXN2,XRCC6,MAD1L1,LMNB2,CAPN2,FZD5,SUV420H1,RPSA,RUNX1,ARID1A,SMAD5,ETV6,RAD50,IGF2BP1,MLH1,RAD51,CCNA2,BMPR1A,TIMP1,LDB1,FOXO3,DNAJB1,MCM9,LRRC8A,ARC,WDR1,PRKCA,SLC20A1,POMT2,TUBG1,SMAD6,MTHFD1,FOXM1,GIT1,NBN,PMP22,PSKH1,MAPK14,FOXO1,KIF5B,RAD9A,EHD4,DCTN1,NR6A1,SOCS1,SOX12,CDC7,CDKN2C,HES1,KPNA1,RICTOR,CHAF1A,VEGFA,CXCL10,GSTZ1,MXD3,IPMK,ZBTB14,PCID2,IRS2,TXN,HEY2,KMT2B,CENPJ,TIMP2,UPF2,STAT6,CFL1,TOPBP1,FOXH1,COPS5,PTCH1,FANCC,IRF1,PCNA,BSG,GAB1,STIP1,IRS1,HSPB11,MAPK7,CYR61,EPHA2,HIST1H1C,ADAM17,CTC1,ATF7,PKD2,SP2,VCAN,CHEK1,EP300,COL5A1,EFNB2,ID1,YY1,NCOA2,PRRX1,TCOF1,HUS1,PDGFRA,CEBPA,BID,MCPH1,MCM10,HEXIM1,RXRB,NCKIPSD,PLOD3,AIFM1,LUZP1,PLAT,RPS19,MYCN,mir-199,ADRM1,DCK,PPP1R8,C10orf2,TBX3,CENPU,AGO2,RQCD1,RAD51B,GINS4,FADD,KITLG,YBX2,ABL2,NDE1,LIMS1,SPRY2,ADAM10,GABPA,RBPJ,FEN1,NCOR2,MAFB,ZFP36L2,PAFAH1B1,DYRK1A,MCM8,PALLD,MAPK1,DIAPH3,TAF10,LATS2,LMNB1,PTK2,FGFR3,ASXL2,TTBK2,EZH2,ITGAV,NIPBL,BRCA1,DLC1,CDC25A,STK11,FGFR1,TBP,PSMC4,RANBP1,TMOD3,SRSF3,ARRB2,PKD1,PTPRS,POMT1,GNL3,Paxip1,RPL13A,TEAD4,NFIX,GDNF,PICALM,PDGFA,PKM,RBBP8,ABL1,BCLAF1,BCAR1,TCF12,FUT8,ROR2,SP1,GLI3,RRN3,MAML3,RBM15,BLM,ERF,E2F8,DTL,NACA,MAP2K7,S1PR2,HDAC1,C2CD3,SMAD7,let-7,MAPK9,BCL3,USP1,NDUFA13,XIAP,LPAR1,PBX3,B4GALT1,SATB1,VGF,UBC,BCL2L11,LGALS1,WNT5A
E2F3B	RNA Post-Transcriptional Modification	2.11E-19	HNRNPL,NPM1,SRSF9,AHCYL1,PCBP1,SFPQ,RBM3,DDX20,ELAVL4,INTS7,RCL1,BOP1,THRAP3,PRPF4B,TARDBP,HNRNPUL1,TCERG1,CSTF2,DUSP11,LSM3,KIN,GRSF1,LSM4,SART3,HNRNPA0,PABPC1,FBL,HCFC1,CDK13,NOVA1,SYNCRIP,RBM4,GEMIN2,Srrm1,PTBP1,SCAF8,CLK2,CPSF3L,SRSF4,RBM39,GCFC2,PRPF3,HNRNPA2B1,CCAR2,PRPF4,SETX,USP39,SF3B3,SRSF10,WTAP,SCAF4,RNPS1,CMTR1,KHSRP,CDC5L,DIS3,SNRNP40,RPS19,HNRNPU,KHDRBS1,PPP1R8,DDX56,SRSF11,AGO2,HNRNPD,SCAF11,PRPF18,IGHMBP2,INTS6,RPS16,SF3B2,DDX39B,RBM6,Rbmxl1,CSTF3,USP49,DYRK1A,RPL11,CDKN2A,SRSF2,PRPF19,GEMIN6,DICER1,INTS1,INTS3,MBNL3,SRSF1,SNRPD1,BCAS2,NONO,PPIG,PNN,TBP,RBFOX2,PHRF1,Scaf1,SRSF3,CTDP1,SRSF7,RBM15B,SF3B4,GEMIN7,INTS10,BARD1,CPSF1,WDHD1,TRA2A,RPL14,POLR2A,AHNAK,CSTF2T,NOP58,GEMIN4,DBR1,SNRPD2,EXOSC2,TRA2B,NOP56,ALKBH5,HNRNPM,IVNS1ABP,RPS15,FASTK,LSM5

Supplemental Table 7. General IPA functions for E2F1, E2F3A and E2F3B promoter targets

ChIP-seq	Category	B-H p-value	Genes
E2F3B	Developmental Disorder	2.99E-19	mir-130,TGFBR1,SSBP2,TMEM231,IFT27,TRIM32,POR,PLXNB2,ETS1,CCNE2,SLC2A1,STK25,CRKL,TMEM67,TCF3,DAXX,DVL2,KAT6A,ITPR3,PRKACA,TMEM43,RMRP,ECT2,FANCA,FLNB,PIM3,BAG6,GNA11,NOTCH2,PELO,HEXB,GPC6,SLC12A6,BBIP1,GAS1,CSGALNACT1,KAT5,ID3,IGF2R,MTHFD1L,TMEM107,CSF1,FBXO5,POC1A,AP1G1,LHX2,SMAD3,GNPAT,RPGRIP1L,INTS1,SMC1A,E2F6,USP8,MATR3,GPX4,ESCO2,EPHA7,DNA2,H6PD,TXNRD1,BCL2L1,H3F3A/H3F3B,SCARF2,RAI1,SF3B4,PBRM1,KIAA0101,RAB23,CHSY1,INPPL1,E2F3,PTGES3,SIX1,NFAT5,STUB1,LARP7,ERBB2,TACC3,PSMC3IP,SOD1,NFATC4,SNX27,BIRC5,ALS2,FANCL,KLF5,E2F7,BRCA2,MAP4K4,AGPS,DDX11,CTGF,F2R,FAM20C,UBR2,EIF6,RBL1,XRCC1,ARNT,POLB,CD2AP,RASGRF1,RARA,CBFB,SLC39A13,SPECC1L,HIPK1,FRS2,DNMT1,TFDP1,CENPB,SLC35A3,HIRA,PLEC,HBEGF,EXOSC8,ADAR,MED12,Anp32b,MNT,SH3GL1,RERE,AHI1,ARHGAP35,B9D1,FYN,OSR2,SNAI2,CDT1,CRTAP,CUL1,FKBP1A,CRLF2,DNAJA1,CDH11,XRCC4,MAFG,HK2,KAT2B,RAB33B,IGF1R,TCTN3,VCL,CEP152,SUZ12,POLE,SDCCAG8,TIAL1,MDM2,ACLY,F3,COPS3,REV1,CAP1,HOXB9,PRPF19,VTI1A,CAV2,TMCO1,Wasl,TBX15,FBXW7,DICER1,DHODH,HSD3B7,METAP2,ETS2,FASN,Map3k7,Dazap1,FOSL2,SOX4,TBC1D24,P4HB,STIL,COL4A1,XYLT1,RAC1,BIRC6,SIX5,MUT,PALB2,NASP,CTDP1,COL6A3,LOXL1,SCRIB,INTU,JAG1,CDK2,CDK5RAP2,C5orf42,NGF,KMT2C,RAD9B,Cux1,POLR2A,GMNN,EMILIN1,RASSF1,HSPG2,MTRR,UHRF1,SNRPB,ATP2C1,MTAP,TSEN34,NFIB,PSMC3,RAF1,TRAIP,RDH10,KRAS,SLC35C1,ATP2A2,CCND1,ADRB3,EMG1,EGR2,SUMO1,FBLN1,GORAB,ATF4,HIPK2,MGAT1,PIGT,GNE,TYMS,TP53,ESPL1,UBE2Q1,YAP1,TPM3,DDR1,Marcks,ATF2,PEX2,CCNF,FADS2,TFRC,Meis1,XRCC5,PDE6D,ERCC4,TRIM33,AKAP8,PTPN2,CDK4,PDS5B,PSEN2,COPS8,ALX1,LBR,VRK1,KISS1R,B4GALT7,ARF6,SOS1,DAB2,B3GALNT2,ASPH,CSNK2B,POMGNT2,NFE2L2,RAD21,CYP51A1,ATP7B,HNRNPU,TUBGCP6,CUL7,POLG,HNRNPD,VDAC3,LAMB2,CCNE1,ZFPM2,CDKN1A,MSRA,CEP41,SGCD,TCF7L2,CASP7,PSEN1,LRIG2,ABCC10,ATXN1L,CLPP,IFT140,TGFBR2,MYC,LEMD3,FDFT1,Gm21596/Hmgb1,MAP2K2,PIM1,WDPCP,BRIP1,TAB1,PPP1R15B,CLASP1,SMC3,SYNE2,YWHAE,PNN,ORC6,HELLS,POFUT1,KMT2A,PFKM,XRCC6,RECQL4,SMCHD1,LMNB2,CAPN2,ACTN4,RHBDF1,RPSA,RUNX1,RPS6KA3,SMAD5,SLC39A14,ETV6,IGF2BP1,ARFRP1,STIM2,RAD51,POLR1C,DIAPH1,AHNAK,FANCD2,BMPR1A,DNAJB1,MCM9,LONP1,RAD23B,ARC,SLC20A1,POMT2,SLC12A2,TUBG1,CANX,FOXM1,MTHFD1,AMPD2,NBN,LTBP3,FAM111A,MAPK14,PRKCI,KIF5B,ATR,NR6A1,SOCS1,ITSN1,FAM58A,SOX12,HES1,Rpl29 (includes others),CHAF1A,VEGFA,FANCB,PEX16,IPMK,BAG1,HEY2,CENPJ,KMT2B,STAT6,IMPA1,CFL1,FOXH1,MITF,CSRP2,COPS5,PTCH1,FANCC,PCNA,PATZ1,BSG,H2AFX,IRS1,E2F1,GLRA1,MAPK7,HIST1H1C,ADAM17,SCAP,ATF7,SP2,TAX1BP3,CHEK1,EP300,SRSF10,COL5A1,ID1,TRIB1,EFNB2,YY1,NCOA2,PRRX1,TCOF1,DGCR8,HUS1,E2F5,PDGFRA,LAMP1,CHST3,CEBPA,MCM10,MCPH1,STIM1,HEXIM1,RASSF5,RXRB,PLOD3,PLAT,EPG5,RPS19,MYCN,mir-199,DCK,C10orf2,INPP5E,ACTB,CDC6,CENPU,DPAGT1,DLX1,AGO2,RAD51B,MAFK,HNRNPDL,POLD1,KITLG,FADD,LIMS1,NDE1,SPRY2,ADAM10,FEN1,RBPJ,MAFB,PAFAH1B1,WDR19,DYRK1A,FZR1,PALLD,MAPK1,INSIG1,MMP16,TAF10,TUBB,LATS2,LMNB1,FGFR3,PTK2,EZH2,ITGAV,NIPBL,BRCA1,RAD51C,CDC25A,KIF14,WDR34,FGFR1,STK11,PSMC4,LMNA,RANBP1,SRSF3,ARRB2,PKD1,EIF4A3,LIN9,PTPRS,CNPY3,POMT1,GNL3,VDAC1,ORC4,Paxip1,CNBP,PEX12,KIF11,KDELR2,TEAD4,PKNOX1,NFIX,MED23,PDGFA,PICALM,MARK2,ABL1,RBBP8,NAA10,BCLAF1,BCAR1,TCF12,EVC,FUT8,ROR2,GLI3,RRN3,LTBP4,BLM,ERF,E2F8,DTL,ABCD3,Nedd4,C2CD3,MTMR14,SMAD7,let-7,MAPK9,RPS6KA5,BCL3,AFF1,GNAI2,EXOC4,B4GALT1,PBX3,LPAR1,CNN3,SATB1,DYM,ARHGAP31,PDE5A,SMARCC1,WNT5A

Supplemental Table 7. General IPA functions for E2F1, E2F3A and E2F3B promoter targets

ChIP-seq	Category	B-H p-value	Genes
E2F3B	Infectious Diseases	4.59E-18	NPM1,mir-130,TGFBR1,RAB2A,POLA1,NUP133,POR,SMARCB1,MARCH2,VAMP3,ADA,DAZAP2,FAM172A,SART3,FBL,SLC2A1,NUP107,TCF3,RGP1,DAXX,PDSS1,KAT6A,PRKACA,EIF4EBP2,ARPC1B,DDIT3,PRDX1,BAG6,PPIA,PNRC1,UBE3C,SCFD1,LSM14B,VPS16,KHDRBS1,PMM1,TUBB4B,RPS10,DDX55,SERPINB6,IGF2R,BAK1,KPNB1,RPS16,MSH2,CSF1,CDKN2A,EEF1A1,SOCS3,PCDH18,SMAD3,CCT2,DEPDC5,RGPD4 (includes others),CD164,TPPP,SNN,STXBP1,HDAC2,PGM1,POLR2H,BCL2L1,AEBP2,H3F3A/H3F3B,ALG14,ZC3H7B,RND1,OSBPL6,PDE4A,ZBTB2,CLIC4,EIF2S1,PTGES3,C20orf24,TARBP1,NUP54,AP3M1,RACGAP1,RNF26,MED26,G3BP1,UMPS,HTATSF1,TFCP2,MAP4K4,RAB5C,F2R,RAN,ZNF436,SLC15A4,RRAGB,RAD23A,POLB,RARA,MED16,UAP1,HIPK1,FRS2,PYCRL,RND2,HIRA,ZC3HAV1,GRK5,SPG7,MON2,HMGA1,ADAR,PHF12,RPL10A,SHCBP1,FYN,RREB1,GALC,POLR2J,FKBP1A,TRPT1,DNAJA1,ATP6AP1,EIF4EBP1,NEIL3,RNPS1,RAB33B,CREB1,IGF1R,PARP11,NUP205,RPS5,PSMB9,NUP85,SUZ12,DDX56,MDM2,PLK1,SLIT2,F3,INTS6,RNF144A,TRERF1,CLUH,FAM76B,CAV2,ARF1,VPRBP,PRMT3,Wasl,DICER1,PBK,SCARB1,ETS2,RAB11FIP1,FASN,MID1IP1,SNU13,TFDP2,STX11,SOX4,TRAF3IP1,CLTC,RAC1,NDUFAF2,CTDP1,USE1,RHOA,SH2B3,SPTAN1,CDK2,SH3BP4,SRRT,NUDT3,NGF,SCARB2,POLR2A,NCL,DHX15,RASSF1,UBR5,ATP2C1,C4orf33,MRPS12,C1orf174,STT3A,PSMC3,RAF1,RMI1,KRAS,PANX1,TOMM70A,MTX1,PKN2,GATAD2A,SUMO1,ATF4,RUVBL2,LSM3,MGAT1,TP53,TYMS,ATG5,PGRMC2,RRM2,TBK1,SYNJ2,RAB1B,FSCN1,SUPT16H,BTG2,TFRC,GAPDH,ABCE1,PRDX2,ERI3,DEK,ARL4C,CDK4,CEBPD,UBE2Z,PSEN2,MED28,USP39,HARBI1,NECAB3,MAP4,CD47,ARF6,SNRPD3,CSNK2B,FBXO21,CYP51A1,RAD21,DHX9,G3BP2,KLHDC2,HNRNPU,MED20,POLG,NXF1,MND1,IGHMBP2,POLA2,MSRA,CH25H,SRSF2,ILF3,CAMK1D,AMDHD2,KXD1,TCEB1,MYC,TGFBR2,HSPA4,SAE1,MAP2K2,PPP3R1,XPO1,MITD1,SNRPA1,PPP1R15B,RNF41,TOP3B,PRPF38A,SBF2,DDX23,MYEF2,GABPB2,GM2A,SAP30BP,DDOST,PSMD6,PFKM,CDC42BPB,ATP5B,DUSP1,OXSR1,NDUFA6,HSP90AA1,RUSC2,PKMYT1,SUV420H1,RPSA,EEA1,RUNX1,NMT1,ARID1A,PPIB,GTF2I,RPS6KA3,GTF2A1,MLH1,VPS4A,IGF2BP1,RABEPK,CCNA2,DIAPH1,TIMP1,ITSN2,DNAJB1,LONP1,PRKCA,SLC20A1,ZNF354A,SDC1,APBB1IP,NOP56,TUBG1,HSPD1,HNRNPM,MAPK14,PRKCI,PSMD2,TEAD3,ATR,WNK1,ACSL1,SOCS1,PLD2,AHCYL1,SGK1,SOX12,EXOSC10,SFPQ,TM9SF2,HES1,CHAF1A,VEGFA,CXCL10,INTS7,ZBTB14,IRS2,TXN,TIMP2,ACTR2,STAT6,TIPIN,COPS5,TFAP4,GEMIN2,IRF1,UBQLN4,AP1S1,TERF2,BSG,GAB1,STIP1,AHCTF1,RAB11A,IFIT2,EPHA2,HIST1H1C,PDIA3,NUP214,ASF1A,EP300,COL5A1,EFNB2,YY1,RPL35,ADK,DGCR8,TOP2A,PDGFRA,EIF3A,MAP1LC3B,MAP1LC3A,RXRB,DCP2,KHSRP,PCBP2,PLOD3,PLAT,VPS18,mir-199,INPP5E,PPP1R8,DDX50,ACTB,AGO2,GINS4,HNRNPDL,MAFK,POLD1,FADD,EIF3G,BNIP2,CHMP6,SF3B2,NUP153,PDIA6,PVT1,SREBF2,NDE1,SPRY2,ADAM10,RBPJ,PPP2R5E,NCOR2,DYRK1A,SPCS3,EPS15,VPS28,MAPK1,CLTB,TUBB,LOC102724828/MRPL23,SRSF1,LARS,RPS20,ASXL2,EZH2,ITGAV,STARD3NL,IMPA2,BRCA1,NUP155,CCDC134,RPL3,FGFR1,PSMC4,LMNA,RAB8A,RANBP1,SSRP1,MED14,WWP2,CCNT1,FLOT2,PCGF1,PKD1,TUBE1,CASP2,EIF4A3,TMPO,PML,KIF11,RPL13A,GABPB1,PICALM,MARK2,ABL1,NUP50,TAOK1,GANAB,NAA10,BCLAF1,BCAR1,EPHB6,TBC1D10A,CIT,MICALL1,ATG16L2,ACTN1,NDUFAF3,TIMM8A,BICD2,HDAC1,let-7,BCL3,PSMA1,NFKBIZ,MED6,PSIP1,XIAP,FAU,DNM1,FDPS,PDE5A,PANK3,MAT2A,EIF2AK2,CAD,HMGCR,BCL2L11,LGALS1

Supplemental Table 7. General IPA functions for E2F1, E2F3A and E2F3B promoter targets

ChIP-seq	Category	B-H p-value	Genes
E2F3B	Connective Tissue Disorders	8.35E-17	RAF1,TGFBR1,RDH10,KRAS,CCND1,POR,EMG1,EGR2,EIF3B,CRADD,SUMO1,SMARCB1,ATF4,PLXNB2,HIPK2,UNG,TYMS,TP53,ETS1,ATG5,YAP1,CRKL,STK25,TBK1,SKP2,ATF2,Marcks,DAXX,DVL2,PEX2,KAT6A,PRKACA,ABCE1,AKAP8,DDIT3,BAG6,CDK4,PDS5B,PSEN2,TNFAIP8L1,ALX1,MAP4,SOS1,UBE2K,ASPH,NFE2L2,CYP51A1,ATN1,DENND4A,EP400,KHDRBS1,GAS1,TUBGCP6,CUL7,LZTS2,IGF2R,BAK1,BUB1,PLA2G4A,MTHFD1L,CCNE1,TMEM107,NR4A2,MSH2,CSF1,CDKN1A,POC1A,TCF7L2,CASP7,PSEN1,CDKN2A,SRSF2,EEF1A1,SMAD3,PARP2,RPGRIP1L,RGPD4 (includes others),TGFBR2,MYC,MAP2K2,PIM1,WDPCP,MAPK3,SNN,MYBL2,JUND,GPX4,DPM3,ESCO2,CLASP1,SMC3,ORC6,DNA2,PSMD6,KMT2A,BCL2L1,TFAM,DUSP1,RECQL4,XRCC6,SF3B4,LMNB2,MAD1L1,PIDD1,RUNX1,TNFAIP8,ARID1A,RAB23,PIAS1,PDE4A,ATF6,SMAD5,EIF2S1,CLIC4,MLH1,POLR1C,SIX1,NFAT5,FANCD2,BMPR1A,STUB1,TIMP1,LARP7,FOXO3,ERBB2,EYA4,RAD23B,GMFB,PRKCA,TACC3,HSPD1,NFATC4,SOD1,MTHFD1,BIRC5,NBN,IVNS1ABP,SLK,FAM111A,MAPK14,FOXO1,COX5A,BRCA2,ATR,F2R,ITSN1,FAM58A,FAM20C,CDKN2C,HES1,RBL1,EIF6,POLB,RECQL,ARNT,VEGFA,MTF1,RARA,MAP1S,SPECC1L,TXN,HIPK1,DNMT1,CENPJ,IMPA1,CFL1,TFDP1,MITF,FOXH1,COPS5,PTCH1,YWHAZ,HBEGF,ITPR1,MED12,IRF1,Anp32b,MNT,PATZ1,GAB1,GLRA1,E2F1,MBD4,GNB2,ARHGAP35,CYR61,FYN,SCAP,OSR2,SNAI2,CDT1,PDIA3,PTN,FKBP1A,BOK,CHEK1,EIF4EBP1,EP300,ID1,EFNB2,YY1,TCOF1,PRRX1,CREB1,LAMP1,PDGFRA,TOP2A,IGF1R,BID,MCPH1,MAP1LC3B,TCTN3,RASSF5,NSMCE1,AIFM1,EPG5,MYCN,CEP152,PMS2,INPP5E,ACTB,POLE,CDC6,DLX1,MDM2,POLD1,C1orf159,CDK1,FADD,SENP1,ABL2,NDE1,SPRY2,HOXB9,RBPJ,DYRK1A,PALLD,VPS28,MAPK1,INSIG1,VPRBP,TMCO1,MMP16,UNC5B,MELK,DHODH,DICER1,LMNB1,FGFR3,PTK2,STMN1,SIVA1,ETS2,ITPRIP,ITGAV,Map3k7,HTRA2,BRCA1,SOX4,P4HB,STIL,FGFR1,BIRC6,RAC1,LMNA,PALB2,ARRB2,CTDP1,PKD1,EIF4A3,USE1,CASP2,RHOA,PTPRS,INTU,GNL3,NSMCE4A,CYLD,PML,ORC4,KIF11,CDK5RAP2,C5orf42,CCNC,PDGFA,ABL1,RBBP8,TNFAIP3,NGF,TCF12,ROR2,HINT1,GLI3,ERF,BLM,HSPG2,MAP2K7,MTRR,SNRPB,ATP2C1,GLS,C2CD3,MAPK9,RPS6KA5,GNAI2,FAF1,ENO1,RIPK1,PBX3,LPAR1,SMARCC1,EIF2AK2,BCL2L11,WNT5A,CASP8AP2
E2F3B	Skeletal and Muscular Disorders	8.35E-17	mir-130,RAF1,TGFBR1,PRKAB2,PRKAB1,RDH10,GARS,RBM3,KRAS,ADRB3,TRIM32,POR,EMG1,EGR2,SUMO1,FBLN1,GORAB,PLXNB2,HIPK2,GNE,TYMS,ETS1,TP53,YAP1,STK25,CRKL,TPM3,Marcks,DAXX,PEX2,DVL2,KAT6A,PRKACA,GAPDH,TMEM43,RMRP,FLNB,DDIT3,AKAP8,BAG6,PDS5B,ALX1,LBR,B4GALT7,NOTCH2,SOS1,DAB2,HEXB,B3GALNT2,ASPH,POMGNT2,GPC6,CYP51A1,HNRNPU,TUBGCP6,GAS1,IGF2R,MTHFD1L,TMEM107,CDKN1A,SGCD,POC1A,TCF7L2,CASP7,PSEN1,MAOA,EEF1A1,SOCS3,KIF1B,SMAD3,GNPAT,RPGRIP1L,IFT140,MYC,TGFBR2,LEMD3,MAP2K2,PIM1,WDPCP,MATR3,JUND,GPX4,CLASP1,ESCO2,SMC3,SYNE2,UBE4B,FSTL3,HDAC2,ORC6,DNA2,H6PD,KMT2A,PFKM,DYNC1H1,BCL2L1,SCARF2,RECQL4,SMCHD1,SF3B4,LMNB2,RPSA,RAB23,CHSY1,RPS6KA3,INPPL1,ATF6,SMAD5,E2F3,POLR1C,SIX1,AHNAK,HLA-DMA,STUB1,TIMP1,BMPR1A,LARP7,FOXO3,ERBB2,LONP1,RAD23B,POMT2,TACC3,CANX,HSPD1,MTHFD1,BIRC5,ALS2,NBN,IVNS1ABP,SLK,PMP22,LTBP3,FAM111A,MAPK14,FOXO1,KLF5,BRCA2,ATR,WISP1,AGPS,PLD2,CTGF,F2R,FAM20C,FAM58A,APIP,HES1,MKI67,VEGFA,BAG1,CBFB,SLC39A13,SPECC1L,HIPK1,TIMP2,CENPJ,IMPA1,TFDP1,CFL1,CSRP2,FOXH1,MITF,SLC35A3,PTCH1,PLEC,HBEGF,MED12,IRF1,Anp32b,TERF2,MNT,PATZ1,GLRA1,E2F1,CREM,ARHGAP35,CYR61,B9D1,SCAP,OSR2,SNAI2,CDT1,CRTAP,PTN,FKBP1A,CAMK2N2,TAX1BP3,EP300,COL5A1,WTAP,ID1,YY1,HK2,TCOF1,PRRX1,RAB33B,DGCR8,CHST3,IGF1R,PDGFRA,LAMP1,BID,STIM1,MCPH1,CACNB2,TCTN3,PLAT,EPG5,MYCN,mir-199,CEP152,PPIF,INPP5E,ACTB,CDC6,POLE,DPAGT1,DLX1,MDM2,HNRNPDL,ACLY,POLD1,KITLG,FADD,BNIP2,NDE1,LIMS1,SPRY2,ADAM10,HOXB9,CAP1,RBPJ,WDR19,DYRK1A,PALLD,CAV2,MAPK1,INSIG1,MMP16,TMCO1,TBX15,DICER1,DHODH,LMNB1,FGFR3,CAMK2D,ETS2,ITGAV,Map3k7,BRCA1,HK1,SOX4,P4HB,STIL,COL4A1,WDR34,XYLT1,FGFR1,RAC1,LMNA,CCNT1,PALB2,ARRB2,COL6A3,PKD1,CTDP1,EIF4A3,RHOA,LOXL1,PTPRS,POMT1,INTU,JAG1,ORC4,KDELR2,CDK2,KIF11,CDK5RAP2,NFIX,C5orf42,PDGFA,RBBP8,TNFAIP3,BCLAF1,NGF,TCF12,ROR2,Ppp1cc,GLI3,SP1,MANF,ERF,MAPKAPK2,NCL,ATG16L1,EMILIN1,RASSF1,HSPG2,BICD2,MTRR,SNRPB,ATP2C1,MTMR14,C2CD3,let-7,MAPK9,MTAP,XIAP,GNAI2,PBX3,LPAR1,CNN3,DYM,PDE5A,SMARCC1,BCL2L11,WNT5A

Supplemental Table 7. General IPA functions for E2F1, E2F3A and E2F3B promoter targets

ChIP-seq	Category	B-H p-value	Genes
E2F3B	Tissue Morphology	1.45E-16	NPM1,TRAIP,MYH9,TGFBR1,RDH10,KRAS,CCND1,POR,GATAD2A,PPRC1,PLXNB2,TP53,CCNE2,PAM,YAP1,KLF13,Marcks,DAXX,DVL2,PEX2,CCNF,KAT6A,PRKACA,TFRC,CELSR3,ECT2,PRDX2,TRIM33,PIM3,PTPN2,PRDX1,BAG6,GNA11,CDK4,PSEN2,ALX1,CD47,PELO,SOS1,DAB2,CSNK2B,NFE2L2,DHX9,EP400,SPRY1,GAS1,LZTS2,IGF2R,TGS1,MAD2L1,CCNE1,MSH2,UBR4,FBXO5,PSEN1,CDKN2A,SOCS3,LHX2,SMAD3,KLF6,KXD1,ZFPM1,ABCC10,TLN1,RPGRIP1L,TGFBR2,MYC,PIM1,MAPK3,PPP3R1,MYBL2,PPP1R15B,DIDO1,POFUT1,TXNRD1,PFKM,BCL2L1,GINS1,FZD5,H1F0,UBE2I,RUNX1,ARID1A,RPS6KA3,SMAD5,ETV6,ARFRP1,RAD51,BMPR1A,LDB1,FOXO3,PRDM6,RAD23B,ARC,SLC20A1,POMT2,SOD1,NFATC4,BIRC5,NBN,PRKCI,MAPK14,FOXO1,RAD9A,E2F7,KLF5,BRCA2,MAP4K4,NR6A1,DDX11,CTGF,F2R,UBR2,SOX12,HES1,RBL1,ARNT,XRCC1,VEGFA,IPMK,RARA,ZFX,CBFB,TXN,HEY2,FRS2,RTEL1,TIMP2,KMT2B,CENPJ,CFL1,TFDP1,FOXH1,ANGPTL6,COPS5,HIRA,FANCC,ADAR,MNT,PATZ1,GAB1,E2F1,AHCTF1,ARHGAP35,LRP8,MAPK7,SAC3D1,B9D1,HIST1H1C,ADAM17,PKD2,H2AFZ,EP300,COL5A1,ID1,EFNB2,PRRX1,TCOF1,HUS1,PDGFRA,PRKCE,MCM10,MCPH1,VCL,RXRB,PLOD3,RPS19,MYCN,DCK,SUZ12,PPP1R8,TBX3,CENPU,AGO2,MDM2,SLIT2,MAFK,F3,COPS3,KITLG,SENP1,ABL2,NDE1,LIMS1,ADD1,ADAM10,HOXB9,FEN1,IREB2,ZFP36L2,PAFAH1B1,FZR1,MAPK1,DIAPH3,Wasl,MMP16,FBXW7,TAF10,LATS2,METAP2,PTK2,SCARB1,ETS2,EZH2,ITGAV,Map3k7,BRCA1,FBXO45,DLC1,STX11,CDC25A,SOX4,STK11,FGFR1,RAC1,BIRC6,TMOD3,PALB2,Cdc42,ARRB2,SH2B3,SCRIB,POMT1,INTU,CYLD,TMPO,JAG1,Paxip1,CDK2,INCENP,ZFAT,GDNF,PICALM,ABL1,SLC7A1,BCLAF1,PRKAG1,ZMIZ1,ROR2,FXN,GMNN,SIPA1,MAML3,RBM15,BLM,ERF,CTDNEP1,E2F8,S1PR2,UHRF1,TRA2B,HAT1,ATP2C1,SMAD7,TCF7L1,NDUFA13,B4GALT1,EIF2AK2,SMARCC1,WNT5A

Supplemental Table 7. General IPA functions for E2F1, E2F3A and E2F3B promoter targets

ChIP-seq	Category	B-H p-value	Genes
E2F3B	Reproductive System Disease	2.45E-15	TGFBR1,C6orf203,PPWD1,TLE1,FRMD6,POR,PPRC1,SART3,ETS1,CCNE2,PEAK1,NUP107,RANBP3,TMEM67,MASTL,DCLRE1A,HIST1H2BM,ALCAM,ELMO2,CPOX,SNX17,SYNM,NOTCH2,RABL6,PTPN4,TIPARP,ATN1,EXO1,SLC12A6,UBE3C,SDHA,LSM14B,VPS16,CSGALNACT1,ID3,CDS2,BUB1,AP1G1,CDKN2A,EEF1A1,SMAD3,DEPDC5,SMAP2,CEP57,MAPK3,JUND,ZWINT,ZSCAN22,PGM1,RAD54L,KCNAB2,PTPDC1,PHRF1,PIK3R3,DYNC1H1,BCL2L1,YPEL5,H3F3A/H3F3B,SEC61A2,CBX3,MCCC2,ETAA1,ZC3H7B,KLF10,RAB23,PIAS1,RNASEH2B,GPHN,CLIC4,EIF2S1,MARVELD1,TARBP1,SIX1,NUP54,LARP7,ARL15,IGSF8,ILKAP,LASP1,MEF2A,SOD1,SNX27,FRMD4A,FAM122A,HTATSF1,RPS15,TUBB6,CENPI,E2F7,TSC22D1,ING1,SLC25A5,RPLP0,RAP2B,HNRNPL,TUBA1B,MCM6,AGPS,ASPSCR1,CTGF,FAM20C,ZNF436,FNDC3B,XRCC1,SLC22A15,HIST1H2AJ,ZFX,TDP2,CBFB,UAP1,PRIM2,SPECC1L,CCNT2,HIPK1,DNMT1,C19orf57,PABPC1,PIK3C2B,TTC21A,TFDP1,ZC3HAV1,PLEC,HBEGF,GRK5,HMGA1,SPOP,SH3GL1,SUCO,FAM222A,C11orf30,NCLN,RCBTB1,RMND1,ARHGAP35,HAUS6,R3HCC1L,SNAI2,GALC,CDT1,PLAGL1,PTN,CENPN,FKBP1A,FZD1,DNAJA1,ATP6AP1,TYW1,GPR3,NEIL3,SCAF4,RIF1,RINT1,TICRR,IGF1R,TXNL1,VCL,FKBP5,ZNF25,NSMCE1,TTC39B,EED,PSMB9,CEP152,DUT,BLMH,USPL1,PLK1,F3,RRM1,ZNF546,SENP1,MUM1,ZNF507,TRERF1,COBLL1,NCAM1,CLUH,TMCO1,METAP1,TBX15,FBXW7,TIGD3,DHODH,ZNF91,TMEM242,YWHAQ,FAM208A,TBC1D4,NAF1,ETS2,DZIP3,PPP1R7,FSD1L,ZNF717,TRIB2,PGP,MSL2,PANK4,GOLGA1,STIL,COL4A1,BIRC6,RHOJ,ATP10A,MAT2B,SMARCD3,ZBTB44,PALB2,SORD,WHSC1L1,LRRC41,BRAT1,COL6A3,SCRIB,HDGFRP3,KBTBD8,CDK5RAP2,ZNHIT6,ATAD2B,NGF,ZMIZ1,NELFE,MRPS27,ZFP90,TRIM24,POLR2A,C19orf44,SLC25A4,ATP2C1,ZNF664,LRRK2,PFKP,MARCH5,C1orf174,NCAPH2,TSHZ3,ZNF382,KIAA1033,PAN3,ZDHHC12,DSCC1,SLC25A32,USP34,TRIM59,TEX9,SCFD2,NIPA2,RAF1,DDHD2,TRAIP,WDR90,MYH9,PCBP1,RDH10,IQCK,MAP6,HMMR,PPIL4,RALGAPB,SLC35C1,FAM208B,RNASE4,ZFYVE1,DOCK11,ZC3H12C,MPHOSPH8,CCDC122,NUP93,CENPE,FBLN1,CD99L2,TGIF2,GNE,TYMS,CBX8,TUBGCP3,ASF1B,PHIP,ESPL1,SOGA1,APPL2,YAP1,FAM118A,EEF2,ZNF496,AGPAT4,PLEKHG2,TNPO2,PEX2,MORC2,TFRC,ZNF644,PTPRA,FRG1,ANKLE1,ABCE1,RBM39,INF2,FAM188B,NOL7,PLXNA3,FBXO10,ARL4C,HNRNPA2B1,ODF2L,RHOT2,EEF1B2,CDK4,PDS5B,CEBPD,CTDSPL,KIAA0754,PGS1,NUF2,SDK1,NAA15,CDKN3,MAP4,PRR14L,SOS1,ATP5J2,LAPTM4A,DAB2,PEMT,CDC5L,NFE2L2,CYP51A1,RAD21,RSBN1,DHX9,DENND4A,HNRNPU,SPRY1,MED20,TUBGCP6,LZTS2,ING5,LAMB2,PRPF18,CCNE1,ZFPM2,UBR4,CAPRIN2,ABCF2,CDKN1A,EIF4A1,WDR63,MAOA,FOXN2,RPL22,MEGF9,MSH3,VPS13A,NME2,TSFM,TLN1,LMBR1L,LRRC57,ZW10,MYC,TGFBR2,KCTD20,AMOTL2,WDPCP,ZNF598,FIGNL1,XPO1,SUGT1,CNOT6,KLF11,CLASP1,EIF4B,ARHGAP11A,SPECC1,SMC3,CCDC18,YWHAE,C3orf58,DDX23,FSTL3,PNN,TNPO1,SLC12A7,RBFOX2,PSMD3,WDYHV1,B3GALNT1,TUSC3,TBL1X,TAF1,UGP2,USP32,MATN2,ETV4,SEPT10,RUSC2,HSP90AA1,MAD1L1,NCKAP5L,ACTN4,SSFA2,FAM83D,SUV420H1,RBBP4,ABI2,UBE2N,COMMD7,DENND4B,DCAF4,RPS6KA3,SLC39A14,RAD50,IGF2BP1,STIM2,TRA2A,RAD51,CCNA2,RABEPK,DIAPH1,LYST,AHNAK,SPAG7,FYTTD1,BMPR1A,TIMP1,ACAD8,IDH3A,ACO1,VARS,RPS3,LRRC8A,PRKCA,WDR1,SLC20A1,POMT2,HAUS8,SDC1,APBB1IP,ETFA,AP1S2,SLC12A2,RALY,HSPD1,AMPD2,RPA2,SH3PXD2A,PRKCI,FOXO1,PHF19,PSMD2,LSM11,TEAD3,SGK1,APIP,CDKN2C,ZNF451,SFPQ,RICTOR,KPNA1,CHST2,CXCL10,VEGFA,NCOA7,ZNF367,MTF1,HNRNPUL1,CSTF2,HEY2,KMT2B,OTUD4,TMEM55B,PSMD5,RCBTB2,ITPR1,IRF1,ERCC6L2,DOCK1,PCNA,RFC4,CPNE8,BHLHE40,IRS1,GLRA1,E2F1,MSH5,LRP8,HELB,SEH1L,YEATS4,PKD2,CAMK2N2,VCAN,TAX1BP3,EP300,CHEK1,XYLB,TGFBRAP1,TRIB1,NCOA2,ADK,PRKCE,MCM10,MAP1LC3B,LPP,ZWILCH,LUZP1,PLAT,EPG5,RPS19,CWC22,RAD51B,STXBP6,PCDH9,RPIA,POLD1,SIN3A,KIF15,SPDYA,ABL2,MCM2,ADAM10,FEN1,HEATR5A,NCOR2,SCAMP3,ZFP36L2,USP49,ASH2L,RPL11,FZR1,ANKS1B,DIAPH3,PAK1IP1,XXYLT1,FNIP2,MELK,CCNL1,USF3,PTK2,STMN1,C19orf43,EZH2,NVL,NIPBL,HTRA2,SIAH2,ZNF623,MYO10,AIM1,RASAL2,WDR34,FGFR1,PSMC4,LMNA,RANBP1,MARS,ELF1,GSR,ARRB2,PLEKHH2,LCORL,RRP7A,C1orf27,NFYC,MAP4K5,TMPO,MTDH,PFAS,PHF1,RFC3,DRAP1,TEAD4,KDM3B,PAFAH1B2,ZBTB7A,TNRC6B,MED23,PDGFA,MEIS2,NUP50,ING4,TAOK1,FUT8,VGLL3,CIT,RABGGTB,MICALL1,MCCC1,RBM15,LTBP4,S1PR2,C2CD3,let-7,RPS6KA5,KIAA2026,ANAPC13,GNAI2,ENO1,PPP6R1,DYM,PAQR4,HMGCR,SHMT2,BCL2L11,MCM7,GSG2,LGALS1,WNT5A,NPM1,mir-130,TPD52L2,CTCF,RPE,PRKAB1,POLA1,NUP133,SMARCD2,CCNB2,EIF4A2,TSPAN15,Ewsr1,EIF3B,TCERG1,MAP1A,MOB1A,FBL,HCFC1,SLC2A1,STK25,RGP1,GART,CNTRL,DAXX,ITPR3,CELSR3,C3orf67,CCDC138,ECT2,CPE,FANCA,KIF20A,FLNB,PRDX1,BAG6,GNA11,CEBPZ,SERHL2,VAT1L,TTK,PNRC1,C2CD5,SCFD1,KPNA3,EP400,TUBB4B,GAS1,PASK,MAPK6,IGF2R,BAK1,MSH2,CSF1,SEPHS1,MAZ,FBXO5,KANSL2,KIF23,SOCS3,NAV2,MPRIP,PCDH18,YWHAH,SEPT9,CCT2,RNF7,RPGRIP1L,ZDHHC14,SMC1A,RGPD4 (includes others),INTS3,SOX2,USP8,TSEN15,ANXA11,ARHGAP20,ERAL1,EPHA7,OSBPL1A,STXBP1,POLE4,SESN3,HDAC2,POLR1B,WEE1,RDX,H6PD,PTPRM,TXNRD1,OSBPL8,CAND1,GINS1,RBM15B,RAI1,CEP76,PBRM1,LITAF,OSBPL6,KIAA0101,MCM3AP,BARD1,ALAS1,RBBP5,IQGAP1,E2F3,PHLDB2,NFAT5,GTPBP2,ZNF24,ERBB2,VAV2,ADAM15,RACGAP1,PSMC3IP,MED26,NFATC4,MTO1,BIRC5,ALS2,FANCL,SLC36A4,CKS1B,ZDHHC3,BRCA2,CCP110,DDX11,F2R,DSTN,GHITM,MKI67,DDX20,HBP1,RBL1,Cyb5r3,HIST1H2AB,ARNT,POLB,RARA,MGAT4B,AFAP1,SLC39A13,RTEL1,PYCRL,CNOT1,PTPRG,YWHAZ,MDC1,MTF2,

Supplemental Table 7. General IPA functions for E2F1, E2F3A and E2F3B promoter targets

ChIP-seq	Category	B-H p-value	Genes
E2F3B	Organismal Development	2.85E-15	TGFBR1,TLE1,POR,SMARCB1,ADA,ETS1,CCNE2,CRKL,TMEM67,DVL2,RAD18,ALCAM,PIM3,DDIT3,SNX17,PRDX4,PPIA,NOTCH2,TIPARP,PELO,EXO1,ATN1,SLC12A6,CSGALNACT1,ID3,POC1A,AP1G1,CDKN2A,SMAD3,INTS1,SMAP2,CEP57,MAPK3,MATR3,JUND,MTMR2,ING2,MAPKAPK5,KCNAB2,GNAZ,BCL2L1,TFEB,PIAS1,PDCD10,CLIC4,HDGF,SIX1,LARP7,LASP1,TACC3,MEF2A,ALKBH5,SOD1,SNX27,MORF4L1,E2F7,TFCP2,TSC22D1,ING1,BRPF1,SLC25A5,CTGF,FAM20C,UBR2,XRCC1,RASGRF1,ZFX,CBFB,SPECC1L,TTLL5,HIPK1,FRS2,DNMT1,PIK3C2B,Irx5,TFDP1,CENPB,HIRA,PLEC,ZC3HAV1,HBEGF,HMGA1,Anp32b,SH3GL1,ARHGAP35,SAC3D1,SNAI2,LEMD2,PTN,CUL1,FKBP1A,FZD1,DNAJA1,H2AFZ,MAFG,GPR3,NEIL3,HK2,RINT1,IGF1R,DAGLB,VCL,TCTN3,EED,OXTR,BLMH,F3,COPS3,SENP1,SBF1,CAMKK1,NCAM1,PRPF19,CAV2,FBXW7,ETS2,Map3k7,MID1IP1,Dazap1,STIL,COL4A1,BIRC6,RHOJ,SMARCD3,PALB2,SCRIB,INTU,RCE1,Nespas,LRIG3,NGF,ZMIZ1,RAD9B,HINT1,MAN2C1,POLR2A,FXN,SLC25A4,LRRK2,TCF7L1,TSHZ3,RAF1,TRAIP,RNF8,MYH9,RDH10,FAM212A,SLC35C1,ATP2A2,ADH5,RCL1,GATAD2A,FBLN1,TGIF2,KLF1,MGAT1,GNE,ATG5,PHIP,ESPL1,YAP1,MAN1A2,Marcks,ATE1,PEX2,FADS2,TFRC,Meis1,SPPL2A,FANCM,NOL7,AKAP8,PTPN2,PDS5B,CDK4,CEBPD,SDK1,SOS1,DAB2,ASPH,NFE2L2,PEMT,CYP51A1,SPRY1,LZTS2,ING5,SLC29A1,LAMB2,CCNE1,ZFPM2,UBR4,CDKN1A,EIF4A1,PSAP,MSRA,LDHA,MAP3K3,TCF7L2,CASP7,ID4,PSEN1,MAOA,LRIG2,RPL22,KIF1B,KXD1,TLN1,ABCC10,RNASEH1,ATXN1L,CEBPG,MYC,TGFBR2,Gm21596/Hmgb1,WDPCP,PPP3R1,Hmga2,CEP131,YWHAE,FSTL3,SLC12A7,HELLS,TXN2,XRCC6,RECQL4,MAD1L1,HSP90AA1,FZD5,SSFA2,ACTN4,H1F0,SUV420H1,RPS6KA3,SLC39A14,ETV6,IGF2BP1,RAD50,RAD51,CCNA2,DIAPH1,AHNAK,HLA-DMA,BMPR1A,TIMP1,LRRC8A,PRKCA,WDR1,SLC20A1,POMT2,SLC12A2,AP1S2,CANX,HSPD1,MTHFD1,AMPD2,SS18L1,MAPK14,FOXO1,RAD9A,SOX12,CDKN2C,ERI1,KPNA1,RICTOR,Rpl29 (includes others),CXCL10,GSTZ1,VEGFA,FANCB,DYNLL1,MTF1,PCID2,HEY2,KMT2B,MITF,CSRP2,ITPR1,FANCC,IRF1,DOCK1,PCNA,PATZ1,YARS,BHLHE40,IRS1,E2F1,HSPB11,MSH5,LRP8,VASH2,PKD2,SP2,VCAN,SGMS1,EP300,SRSF10,CHEK1,WTAP,TRIB1,NCOA2,PRRX1,USP42,LAMP1,PRKCE,MCM10,NCKIPSD,PLOD3,LUZP1,PLAT,RPS19,DLX1,RAD51B,MAFK,POLD1,ABL2,ADAM10,GABPA,FEN1,NCOR2,ZFP36L2,FZR1,EPS15,VPS28,INSIG1,DIAPH3,GNB5,PTK2,EZH2,NIPBL,HTRA2,FBXO45,FGFR1,PSMC4,LMNA,RAB8A,RANBP1,TMOD3,GSR,ARRB2,PTPRS,TMPO,PML,MTDH,TEAD4,PAFAH1B2,PKNOX1,PDGFA,Pcnt,MARK2,ING4,FUT8,Ppp1cc,SP1,CIT,RBM15,SLC25A25,TIMM8A,MAP2K7,S1PR2,Nedd4,C2CD3,SMAD7,let-7,BCL3,GNAI2,B4GALT1,SMARCC1,VGF,UBC,BCL2L11,WNT5A,LGALS1,mir-130,NPM1,CTCF,PRKAB1,SLC6A9,Ap2b1,TAB2,CCNB2,SSBP2,PRKCDBP,PLXNB2,PIGF,TCF3,ABCA7,SP4,CNTRL,DAXX,KAT6A,ITPR3,PRKACA,CELSR3,ECT2,FANCA,CPE,FLNB,NRG2,PRDX1,BAG6,GNA11,HEXB,EP400,KHDRBS1,GAS1,GREM1,IGF2R,BAK1,TMEM107,MSH2,CSF1,FBXO5,TFB1M,SOCS3,LHX2,SEPT9,SFMBT1,GNPAT,ZFPM1,RPGRIP1L,RGPD4 (includes others),SOX2,USP8,GPX4,SEC63,OSBPL1A,HDAC2,IFT74,RDX,H6PD,POLR2H,EIF4E2,NDC1,PTPRM,TXNRD1,GINS1,RAI1,FOXP4,UBE2I,PBRM1,PEBP1,ALG14,RND1,INPPL1,E2F3,IQGAP1,PTGES3,NFAT5,STUB1,ZNF24,ERBB2,VAV2,ADAM15,PSMC3IP,NFATC4,BIRC5,FANCL,KLF5,CKS1B,BRCA2,DDX11,F2R,RTCB,RAN,DDX20,EIF6,RBL1,POLB,ARNT,CD2AP,RARA,RTEL1,YWHAZ,SPG7,ADAR,MED12,ANKRD26,CMIP,ARHGAP5,MNT,AAAS,AHI1,RERE,CREM,PRICKLE1,B9D1,FYN,MAP2,OSR2,ARHGEF7,HMGB2,CDH11,EIF4EBP1,CREB1,POLE,TIAL1,MDM2,SLIT2,SCMH1,CDK1,REV1,GTPBP3,HOXB9,WDR48,NAB2,VTI1A,PRMT3,Wasl,MNS1,UNC5B,DICER1,AMD1,METAP2,CAMK2D,SCARB1,FASN,FOSL2,STX11,SOX4,DTNBP1,RAC1,CCDC155,MUT,SIX5,HERC2,Cdc42,NASP,CTDP1,TIMELESS,RHOA,SH2B3,LOXL1,SBNO2,CYLD,JAG1,CDK2,TMTC3,KDM3A,BRD2,ZFAT,SPRED1,C5orf42,GADD45G,SRRT,KMT2C,SCARB2,Cux1,CSTF2T,GMNN,SIPA1,IFRD1,MAPKAPK2,NCL,DHX15,RASSF1,RHBDD3,HSPG2,TRA2B,UHRF1,HAT1,PANK2,EDF1,PLEKHG5,NFIB,ADAM9,CBFA2T2,PSMC3,RMI1,PRKAB2,TMEM38A,Ubb,KRAS,CCND1,ADRB3,EGR2,FHL2,SUMO1,MTHFD2,ATF4,ADORA2B,HIPK2,UNG,TARBP2,TP53,KLF13,DDR1,RBM4,ATF2,SKP2,TPST1,CCNF,FSCN1,BTG2,INVS,KIAA1429,XRCC5,PRDX2,TRIM33,USF2,PSEN2,ALX1,KISS1R,ARF6,CD47,TRIM27,ALMS1,CSNK2B,POMGNT2,ATP7B,CUL7,HNRNPD,TGS1,HSPA2,PLA2G4A,SEMA3C,PLEKHA1,SGCD,ILF3,RASA3,KLF6,PARP2,GNB2L1,IFT140,FDFT1,HSPA4,LEMD3,TNRC6C,MAP2K2,PIM1,MYBL2,CHTF18,GCLM,TAB1,PPP1R15B,TOP3B,PGK1,UBE4B,DIDO1,WASF1,POFUT1,KMT2A,PFKM,TFAM,ATP5B,DUSP1,LMNB2,CAPN2,HELT,RHBDF1,RPSA,RUNX1,ARID1A,PPIB,GTF2I,SMAD5,MLH1,FANCD2,LDB1,FOXO3,EYA4,MCM9,ARL4A,RAD23B,PRDM6,ARC,KIRREL,CAPZB,TUBG1,SMAD6,FOXM1,GIT1,NBN,RCAN1,LTBP3,PMP22,PSKH1,KIF5B,EHD4,DCTN1,WNK1,KIF18A,SOCS1,NR6A1,ABCA2,ITSN1,CDC7,HES1,CHAF1A,MXD3,THRAP3,ZBTB14,TARDBP,MAP1S,IRS2,TXN,ICOSLG/LOC102723996,CENPJ,TIMP2,UPF2,STAT6,MEX3C,CFL1,NDRG1,FOXH1,TOPBP1,COPS5,PTCH1,GAB1,BSG,STIP1,H2AFX,AHCTF1,MAPK7,CYR61,EPHA2,HIST1H1C,ADAM17,CTC1,ATF7,CTNNA3,COL5A1,EFNB2,ID1,YY1,TCOF1,HUS1,DGCR8,CEBPA,CHST3,PDGFRA,BID,MCPH1,STIM1,HEXIM1,RASSF5,RXRB,PCBP2,AIFM1,MYCN,mir-199,ADRM1,DCK,INPP5E,PPP1R8,TBX3,AGO2,ROCD1,KATNAL1,KITLG,FADD,YBX2,NUP153,SREBF2,LIMS1,NDE1,SPRY2,ADD1,TBPL1,RBPJ,MAFB,IREB2
E2F3B	Cellular Compromise	1.26E-14	KIF23,CDKN2A,NPM1,MCM8,DIAPH3,SUV39H1,PARP2,KRAS,AURKB,LATS2,RECQL,POLB,MYC,CD2AP,DYNLL1,Gm21596/Hmgb1,PIM1,BRCA1,BRIP1,RAD51C,RTEL1,CDC25A,TP53,ATG5,KIF14,HCFC1,COPS5,SEPT7,LMNA,FANCC,TERF2,PALB2,DAXX,RECQL4,H2AFX,ECT2,FANCA,XRCC5,CDK2,RUNX1,ERCC4,PTPN2,SEPT11,XRCC4,SIX1,HUS1,MCPH1,BLM,MCM9,POT1,E2F8,RASSF1,LZTS2,MAPK9,MDM2,SOD1,USP1,NBN,KPNB1,MAD2L1,SPIDR,CCNE1,MSH2,PDXP,CSF1,CDKN1A,BRCA2,POLH

Supplemental Table 7. General IPA functions for E2F1, E2F3A and E2F3B promoter targets

ChIP-seq	Category	B-H p-value	Genes
E2F3B	Tissue Development	1.74E-13	TGFBR1,FRMD6,ELAVL4,POR,SMARCB1,ADA,ETS1,CCNE2,CRKL,TMEM67,DVL2,RAD18,ELMO2,MORC3,DDIT3,SNX17,SLC1A5,PRDX4,PPIA,NOTCH2,TIPARP,ID3,BUB1,MAD2L1,CDKN2A,SMAD3,INTS1,SMAP2,CEP57,MAPK3,MATR3,JUND,MTMR2,ING2,BCL2L1,H3F3A/H3F3B,KLF10,RAB23,PIAS1,PDE4A,RNASEH2B,CSRP1,GPHN,CLIC4,HDGF,SIX1,PDK1,TACC3,ALKBH5,MEF2A,SOD1,MORF4L1,PPM1G,RPS15,BRPF1,SLC25A5,MAP4K4,HNRNPL,CTGF,UBR2,FAM20C,FNDC3B,RASGRF1,ZFX,RAB17,CBFB,CCDC124,CCNT2,TTLL5,HIPK1,FRS2,DNMT1,RND2,GET4,PIK3C2B,Irx5,HIRA,PLEC,HBEGF,SYNCRIP,GRK5,HMGA1,SUCO,SNAI2,PLAGL1,LEMD2,PTN,FKBP1A,FZD1,DNAJA1,ATP6AP1,MAFG,GPR3,NEIL3,DAGLB,IGF1R,VCL,FKBP5,EED,OXTR,PSMB9,PLK1,F3,NCAPG2,RRM1,SBF1,NCAM1,PRPF19,CAV2,TBX15,FBXW7,ETS2,TRIB2,Map3k7,Dazap1,TBC1D24,STIL,COL4A1,CLTC,SMARCD3,PALB2,INTU,RCE1,HDGFRP3,NGF,ZMIZ1,HINT1,TRIM24,USP47,ANKRD54,LRRK2,TMEM14C,TSHZ3,NCAPH2,FAF1,SLC25A38,TTC7A,RAF1,RNF8,MYH9,RDH10,MAP6,HMMR,FAM212A,SLC35C1,ATP2A2,NKAP,KLF7,CENPE,FBLN1,KLF1,MGAT1,ATG5,ESPL1,YAP1,MAN1A2,ATE1,PEX2,FADS2,TFRC,Meis1,PTPRA,TMEM64,PLXNA3,PTPN2,HNRNPA2B1,CDK4,CEBPD,COPS8,SEPT11,SDK1,DAB2,NFE2L2,CYP51A1,DHX9,HNRNPU,LAMB2,CCNE1,ZFPM2,CAPRIN2,CDKN1A,EIF2B1,PSAP,ID4,TCF7L2,CASP7,MAOA,PSEN1,RPL22,NCDN,CAMK1D,PIEZO1,ATXN1L,CEBPG,TGFBR2,MYC,Gm21596/Hmgb1,PPP3R1,FIGNL1,Hmga2,CEP131,SMC3,FSTL3,RBFOX2,SNX3,TBL1X,MATN2,ETV4,TXN2,XRCC6,MAD1L1,HSP90AA1,FZD5,SUV420H1,ABI2,DPYSL3,UBE2N,RPS6KA3,ETV6,STIM2,CCNA2,DIAPH1,TIMP1,BMPR1A,HLA-DMA,LRRC8A,PRKCA,WDR1,SLC12A2,AP1S2,HSPD1,MTHFD1,FAIM,SH3PXD2A,SS18L1,MAPK14,PRKCI,FOXO1,AMIGO1,SGK1,SOX12,CDKN2C,RICTOR,Rpl29 (includes others),RECQL,RS1,CXCL10,VEGFA,DYNLL1,HEY2,KIN,MITF,RPA1,PLCL2,FANCC,ITPR1,GEMIN2,IRF1,DOCK1,PATZ1,IRS1,BHLHE40,E2F1,HSPB11,MSH5,LRP8,PHLPP1,VASH2,PKD2,ASF1A,FNTB,SP2,VCAN,CHEK1,EP300,WTAP,NCOA2,USP42,ADK,LAMP1,PRKCE,MCM10,NCKIPSD,PLOD3,LUZP1,PLAT,RPS19,DLX1,MAFK,SIN3A,DGKZ,ABL2,UNK,ADAM10,GABPA,FEN1,NCOR2,ZFP36L2,FZR1,INSIG1,DIAPH3,PTK2,STMN1,EZH2,NIPBL,HTRA2,ARHGEF25,FBXO45,MYO10,FGFR1,LMNA,RAB8A,RANBP1,TMOD3,GSR,ARRB2,CORO1B,PTPRS,PML,PAFAH1B2,TEAD4,PKNOX1,ZBTB7A,PDGFA,MARK2,TMEM120A,FUT8,Ppp1cc,SP1,VGLL3,MANF,CIT,MICALL1,RBM15,MAP2K7,S1PR2,Nedd4,MRC2,C2CD3,SMAD7,let-7,BCL3,GNAI2,B4GALT1,SLC25A27,SMARCC1,HMGCR,VGF,BCL2L11,WNT5A,LGALS1,NPM1,KIF13B,CTCF,Ap2b1,TAB2,SECISBP2,Ewsr1,PLXNB2,FBL,STK25,TCF3,SP4,CNTRL,KAT6A,PRKACA,CELSR3,ECT2,FLNB,NRG2,EIF4EBP2,BAG6,GNA11,HEXB,EP400,KHDRBS1,GAS1,ZNF521,GREM1,IGF2R,TMEM107,MSH2,CSF1,KIF23,SOCS3,MPRIP,SEPT9,LHX2,YWHAH,SFMBT1,GNPAT,RNF7,ZFPM1,RPGRIP1L,SOX2,USP8,GPX4,EPHA7,HDAC2,WEE1,IFT74,RDX,PTPRM,NDC1,TXNRD1,OSBPL8,GINS1,SF3B4,FOXP4,PBRM1,PEBP1,RND1,KIAA0101,CHSY1,IQGAP1,E2F3,PTGES3,NFAT5,STUB1,ERBB2,VAV2,ADAM15,SMARCE1,NFATC4,SERTAD1,BIRC5,ALS2,FANCL,KLF5,BRCA2,F2R,MKI67,DDX20,RBL1,RPS11,ARNT,POLB,RARA,LEPROT,RTEL1,YWHAZ,ADAR,MED12,ANKRD26,ARHGAP5,MNT,AHI1,RERE,CREM,PRICKLE1,FYN,OSR2,MAP2,ARHGEF7,HMGB2,XRCC4,CDH11,EIF4EBP1,CREB1,PMS2,HDGFRP2,TIAL1,MDM2,SLIT2,SCMH1,CDK1,CBLN1,CCDC85B,CIRBP,NAB2,WDR48,STRN,VTI1A,FARP1,VPRBP,Wasl,MNS1,DICER1,METAP2,CAMK2D,SCARB1,STAG1,FASN,FOSL2,SOX4,DTNBP1,RAC1,CCDC155,PREX2,SIX5,OSTM1,HERC2,Cdc42,TIMELESS,RHOA,SH2B3,LOXL1,NUAK1,SBNO2,CYLD,JAG1,CDK2,KDM3A,TMTC3,ZFAT,BRD2,SPRED1,C5orf42,PA2G4,GADD45G,KMT2C,SET,Cux1,CSTF2T,GMNN,GTPBP4,MAPKAPK2,RASSF1,HSPG2,HAT1,PANK2,DOCK7,EDF1,PRMT1,PIAS3,NFIB,MSN,Ubb,KRAS,RBM3,CCND1,ADRB3,EGR2,FHL2,BAIAP2,ATF4,ADORA2B,HIPK2,TARBP2,TP53,FBXO9,CSNK1D,TPM3,KLF13,DDR1,ATF2,SKP2,CCNF,BTG2,KIAA1429,XRCC5,PRDX2,RAP2A,PSEN2,ALX1,KISS1R,B4GALT7,CD47,ARF6,TRIM27,ALMS1,CSNK2B,CUL7,TOB1,FRK,HSPA2,PLA2G4A,NR4A2,SEMA3C,PLEKHA1,RASA3,POLR3E,GNB2L1,PARP2,SART1,IFT140,FDFT1,HSPA4,MAP2K2,PIM1,MYBL2,CHTF18,PDZRN3,TAB1,ULK2,TOP3B,PGK1,UBE4B,POFUT1,KMT2A,SLC3A2,METRN,TFAM,ATP5B,DUSP1,DIXDC1,LMNB2,ELMO1,EEA1,CDKL3,RUNX1,TNFAIP8,ARID1A,ATF6,SMAD5,MLH1,FANCD2,LDB1,FOXO3,MCM9,ARL4A,LONP1,RAD23B,CAPZB,SMAD6,FOXM1,GIT1,ZHX3,NBN,RCAN1,LTBP3,PMP22,PSKH1,EHD4,ATR,WISP1,WNK1,SOCS1,NR6A1,PLD2,ITSN1,TOR1A,HES1,RAPH1,RUSC1,MXD3,THRAP3,BAG1,TARDBP,ZBTB14,MAP1S,IRS2,TXN,CEP250,ICOSLG/LOC102723996,TIMP2,CENPJ,STAT6,CDK13,CFL1,NDRG1,MEX3C,FOXH1,PTCH1,TFAP4,GAB1,BSG,STIP1,H2AFX,AHCTF1,RAB11A,HPRT1,MAPK7,CYR61,EPHA2,HIST1H1C,ADAM17,CTC1,ATF7,PDIA3,HMGN1,COL5A1,EFNB2,ID1,YY1,TCOF1,HUS1,CEBPA,PDGFRA,BID,STIM1,CACNB2,HEXIM1,RXRB,MYCN,mir-199,ADRM1,DCK,TBX3,ACTB,HERC1,CDC6,RQCD1,AGO2,GINS4,KATNAL1,KITLG,FADD,YBX2,NUP153,NDE1,LIMS1,SPRY2,KIF20B,ADD1,TBPL1,RBPJ,MAFB,PAFAH1B1,SEPT2,DYRK1A,MCM8,PALLD,MAPK1,TFG,LMNB1,ROCK2,FGFR3,TTBK2,ASXL2,RORA,ITGAV,BRCA1,RAD51C,DLC1,Fus,IGFBP6,STK11,mir-3960,RAB10,KIAA1715,SIPA1L1,CCNG2,TOB2,PKD1,LIN9,GNL3,EXTL3,Paxip1,RPL13A,NFIX,GDNF,PICALM,PKM,ABL1,TNFAIP3,BCLAF1,BCAR1,PRKAG1,T

Supplemental Table 7. General IPA functions for E2F1, E2F3A and E2F3B promoter targets

ChIP-seq	Category	B-H p-value	Genes
E2F3B	Cellular Function and Maintenance	2.59E-13	mir-130,NPM1,KIF13B,TGFBR1,CTCF,RAB2A,POLA1,NUP133,ELAVL4,TMEM231,GPSM2,GORASP2,PRKCDBP,MAP1A,PLXNB2,CENPW,ETS1,CRKL,STK25,TMEM67,SP4,DAXX,DVL2,PRKACA,RAD18,CELSR3,ECT2,FLNB,DDIT3,EIF4EBP2,BAG6,TTK,SYNM,PELO,BNIP1,HEXB,RNF19A,BBIP1,KAT5,KPNB1,MAD2L1,TMEM107,CSF1,FBXO5,AP1G1,KIF23,CDKN2A,EEF1A1,MPRIP,SEPT9,LHX2,YWHAH,SMAD3,RNF7,HDAC10,RPGRIP1L,SMC1A,SOX2,USP8,CEP57,TPPP,MAPK3,ARHGAP20,GPX4,EPHA7,HDAC2,WEE1,IFT74,RDX,DNA2,RAD54L,MAPKAPK5,Afg3l1,PTPRM,PTPDC1,TXNRD1,BCL2L1,H3F3A/H3F3B,SF3B4,UBE2I,PBRM1,TFEB,RND1,KIZ,KIAA0101,RAB23,PVRL3,NEDD1,CSRP1,INPPL1,EIF2S1,IQGAP1,LRRC29,ZBTB24,PHLDB2,PTGES3,HDGF,STUB1,ERBB2,PDK1,LASP1,VAV2,TACC3,IFT46,RACGAP1,MEF2A,SMARCE1,SOD1,NFATC4,ALS2,BIRC5,KLF5,BRCA2,BORA,CCP110,CTGF,RAB5C,F2R,MTBP,SUV39H1,RAN,HBP1,RBL1,POLB,RASGRF1,CD2AP,RAB17,AFAP1,SPECC1L,BAG5,RTEL1,RND2,SEPT7,PLEC,HBEGF,CKAP2,GRK5,SPG7,ARHGAP5,PHLDB1,RNF168,RERE,AHI1,CDAN1,HAUS6,SAC3D1,B9D1,FYN,MAP2,ARHGEF7,LEMD2,TMEM11,PTN,SPATA13,FKBP1A,HMGB2,EIF4G1,ATP6AP1,SF3B3,AKAP11,EIF4EBP1,RIF1,CREB1,IGF1R,PARP11,TCTN3,VCL,PMS2,CEP152,NUP85,SPC25,USPL1,MDM2,USP30,PLK1,SLIT2,ACLY,F3,CDK1,ATG2A,ATL2,REV1,RAB12,MUM1,CAP1,CLUH,NCAM1,FMNL3,STRN,PRPF19,CAV2,FARP1,ARF1,Wasl,UNC5B,MNS1,DICER1,YWHAQ,TBC1D4,NAF1,SCARB1,ESPN,FASN,Map3k7,MID1IP1,PANK4,Nolc1,TBC1D24,STIL,DTNBP1,ACP2,TRAF3IP1,CLTC,BIRC6,RAC1,PREX2,RHOJ,OSTM1,PALB2,Cdc42,SMC2,USE1,RHOA,IFT81,NUAK1,INTU,SPTAN1,CYLD,HDGFRP3,CDK2,CDK5RAP2,ARL2,KDM3A,SH3BP4,C5orf42,NGF,WDHD1,SCARB2,Cux1,PPP1R12A,HAUS5,FXN,IFRD1,MAPKAPK2,ATG16L1,RASSF1,HSPG2,POC1B,ATP2C1,LRRK2,DOCK7,PRMT1,KIAA1033,PAN3,NFIB,CENPH,MSN,RAF1,RNF8,MYH9,MAP6,RALGAPB,Ubb,HAUS4,KRAS,C21orf2,STK35,CCND1,NKAP,PKN2,KLF7,FHL2,Diap2,CENPE,SUMO1,EHD2,BAIAP2,NEK6,ATF4,RUVBL2,KLF1,MSTO1,SGSM2,TP53,ATG5,TUBGCP3,PHIP,ESPL1,SOGA1,PAM,APPL2,CSNK1D,USP19,TPM3,TBK1,DDR1,PEX2,DYNC1LI2,CCNF,FSCN1,BTG2,GAPDH,CENPT,CHD1L,TBC1D5,XRCC5,FANCM,HACE1,TRIM33,DEK,ERCC4,RAP2A,PLXNA3,FBXO7,CDK4,CKAP4,PSEN2,SEPT11,NUF2,SDK1,SPAG5,CEP162,ARF6,CD47,MAP4,TRIM27,SORBS1,ALMS1,DAB2,KIF2C,NFE2L2,CDC5L,RAD21,TUBGCP6,CUL7,POLG,LAMB2,PLA2G4A,NR4A2,UBR4,CAPRIN2,CDKN1A,EIF2B1,CEP41,KLHL17,MAOA,PSEN1,DLGAP5,NCDN,CAMK1D,ATP2B1,GNB2L1,TIMM50,SMC4,PINX1,TLN1,SART1,MYC,ZW10,IFT140,LEMD3,Gm21596/Hmgb1,MAP2K2,RCC1,WDPCP,ARL1,XPO1,CEP131,ULK2,CLASP1,SYNE2,UBE4B,SIK2,RBFOX2,WASF1,SLC3A2,METRN,CDC42BPB,MATN2,XRCC6,ETV4,HSP90AA1,NDC80,DIXDC1,LMNB2,CAPN2,ACTN4,ELMO1,RBBP4,CDKL3,ABI2,ARID1A,DPYSL3,UBE2N,RPS6KA3,ATF6,SMAD5,WDR6,RAD50,VPS4A,STIM2,RAD51,DIAPH1,LYST,WDFY3,NET1,FOXO3,TOR1B,RPS3,LONP1,LRWD1,WDR1,ARC,PRKCA,KIRREL,HAUS8,CAPZB,APBB1IP,CHP1,TUBG1,CANX,PTRHD1,TUBGCP2,FOXM1,GIT1,ATL3,RPA2,NBN,SLK,CISD1,PMP22,SS18L1,PRKCI,MAPK14,FOXO1,RAD9A,KIF5B,COX5A,AMIGO1,DCTN1,CEP70,KIF18A,CENPF,PLD2,ITSN1,SGK1,TOR1A,SFPQ,PHACTR4,KPNA1,RAPH1,RICTOR,CHAF1A,CXCL10,VEGFA,DYNLL1,PEX16,USP10,MAP1S,CEP250,CENPJ,ACTR2,CFL1,NDRG1,MITF,RPA1,ITPR1,FANCC,TERF2,POM121/POM121C,CCNO,DOCK1,PCNA,BSG,GAB1,H2AFX,STIP1,E2F1,RAB11A,HPRT1,LRP8,SEH1L,CYR61,EPHA2,CTC1,PDIA3,HMGN1,SASS6,EP300,CHEK1,EFNB2,ID1,YY1,SEC61A1,LAMP1,PDGFRA,RHOU,CEBPA,PRKCE,NAA60,MAP1LC3A,STIM1,MAP1LC3B,RASSF5,NCKIPSD,FAM109A,POT1,PLAT,EPG5,RPS19,VPS18,TBC1D9,HERC1,ACTB,TOR1AIP2,FADD,KITLG,BNIP2,CHMP6,ABL2,NDE1,KIF20B,ADAM10,ARAP1,ADD1,PAFAH1B1,SEPT2,WDR19,VAMP4,DYRK1A,ZMYM4,MCM8,PALLD,EPS15,PTPN23,MAPK1,DIAPH3,TUBB,LATS2,PTK2,STMN1,ROCK2,TTBK2,EZH2,ITGAV,NEO1,HTRA2,ARHGEF25,BRCA1,MYO10,DLC1,Ftx,NUP155,ULK4,FGFR1,STK11,RAB10,LMNA,RAB8A,RANBP1,TMOD3,SSRP1,SIPA1L1,SRSF3,CCNT1,RNF4,PCGF1,PKD1,CORO1B,CASP2,MTDH,PML,KIF11,PEX12,PAFAH1B2,OBFC1,NFIX,GDNF,PDGFA,PICALM,Pcnt,MARK2,PKM,ABL1,RBBP8,TAOK1,BCAR1,TNFRSF12A,FUT8,EPHB6,TBC1D10A,NTNG1,ROR2,CCDC88A,SP1,RRN3,CIT,MICALL1,BLM,CTDNEP1,ACTN1,ABCD3,S1PR2,ATG10,Nedd4,HDAC1,C2CD3,EFNA3,MAPK9,HIVEP2,DNM1,KIF24,RIPK1,UBQLN2,LPAR1,SATB1,DYM,EIF2AK2,VGF,BCL2L11,WNT5A

Supplemental Table 7. General IPA functions for E2F1, E2F3A and E2F3B promoter targets

ChIP-seq	Category	B-H p-value	Genes
E2F3B	Cell Morphology	1.44E-11	SNTB2,mir-130,NPM1,KIF13B,TGFBR1,SLC6A9,PRKAB1,TAB2,ELAVL4,TMEM231,SMARCB1,ADA,PLXNB2,ETS1,HCFC1,STK25,CRKL,TMEM67,TCF3,SP4,DCLRE1A,DAXX,DVL2,KAT6A,ITPR3,PRKACA,RAD18,CELSR3,ELMO2,ECT2,PIM3,DDIT3,EIF4EBP2,PRDX1,BAG6,GNA11,SYNM,HEXB,EXO1,SLC12A6,FKBP3,EP400,BBIP1,GAS1,KAT5,IGF2R,ID3,BAK1,KPNB1,BUB1,MAD2L1,TMEM107,CSF1,MAZ,FBXO5,CDKN2A,KIF23,EEF1A1,SOCS3,MPRIP,YWHAH,SEPT9,SMAD3,GNPAT,HDAC10,ZFPM1,RNF7,RPGRIP1L,SOX2,MAPK3,GPX4,ING2,EPHA7,HDAC2,WEE1,IFT74,DNA2,RDX,H6PD,RAD54L,PTPDC1,PTPRM,TXNRD1,BCL2L1,H3F3A/H3F3B,PBRM1,PEBP1,TFEB,RND1,KIAA0101,RAB23,KLF10,PVRL3,CHSY1,PDE4A,NEDD1,CSRP1,GPHN,EIF2S1,IQGAP1,E2F3,LRRC29,CLIC4,PHLDB2,ZBTB24,SIX1,STUB1,ZNF24,ERBB2,PDK1,LASP1,VAV2,TACC3,IFT46,ADAM15,RACGAP1,MEF2A,SMARCE1,PSMC3IP,SOD1,NFATC4,ALS2,BIRC5,MORF4L1,KLF5,E2F7,BRCA2,SLC25A5,CTGF,MTBP,F2R,DSTN,RAN,HBP1,RBL1,EIF6,POLB,ARNT,CD2AP,RASGRF1,RARA,RAB17,TDP2,CBFB,DNMT1,RND2,Irx5,SEPT7,PLEC,COMMD9,YWHAZ,SYNCRIP,HBEGF,GRK5,SPG7,HMGA1,ADAR,CMIP,ARHGAP5,SH3GL1,RNF168,RERE,AHI1,CREM,SAC3D1,B9D1,FYN,MAP2,SNAI2,PTPN13,ARHGEF7,PLAGL1,PTN,SPATA13,FKBP1A,HMGB2,EIF4G1,DNAJA1,H2AFZ,ATP6AP1,TOR1AIP1,CDH11,EIF4EBP1,GPR3,RIF1,HK2,CREB1,IGF1R,PPM1F,TCTN3,VCL,FKBP5,PSMB9,NUP85,PMS2,PPIF,USPL1,USP30,MDM2,PLK1,SLIT2,ACLY,F3,CDK1,NCAPG2,ATG2A,SENP1,REV1,RAB12,SBF1,CIRBP,CAMKK1,CAP1,NCAM1,NAB2,STRN,PRPF19,FARP1,VTI1A,CAV2,ARF1,Wasl,MNS1,FBXW7,DICER1,AMD1,YWHAQ,NAF1,CAMK2D,TBC1D4,ESPN,SCARB1,ETS2,FASN,TRIB2,Map3k7,FOSL2,SOX4,TBC1D24,STIL,DTNBP1,TRAF3IP1,ACP2,CLTC,BIRC6,RAC1,PREX2,MUT,SIX5,OSTM1,PALB2,Cdc42,SMC2,IFT81,RHOA,SH2B3,NUAK1,INTU,HDGFRP3,CYLD,SBNO2,CDK2,KDM3A,SH3BP4,C5orf42,NGF,SCARB2,Cux1,SET,MAN2C1,CSTF2T,GMNN,MAPKAPK2,ATG16L1,RASSF1,RHBDD3,EMILIN1,HSPG2,SLC25A4,POC1B,ATP2C1,LRRK2,DOCK7,PRMT1,NFIB,CBFA2T2,MSN,DDHD2,RAF1,RNF8,MYH9,PRKAB2,MAP6,Ubb,RALGAPB,TMEM38A,KRAS,C21orf2,CCND1,ATP2A2,ADRB3,ZFYVE1,KLF7,Diap2,SUMO1,BAIAP2,FBLN1,NEK6,ATF4,RUVBL2,KLF1,MGAT1,ATP5G3,SGSM2,IQGAP3,TP53,GNE,CERS6,ATG5,ESPL1,APPL2,SOGA1,PAM,YAP1,CSNK1D,USP19,TPM3,ANO6,TBK1,KLF13,DDR1,ATF2,SKP2,ATE1,PLEKHG2,PEX2,FSCN1,BTG2,FADS2,TFRC,CHD1L,TBC1D5,PTPRA,XRCC5,PRDX2,FANCM,RAP2A,TRIM33,DEK,PLXNA3,FBXO7,PTPN2,PDS5B,CDK4,CEBPD,PSEN2,KIAA1549,SEPT11,SDK1,CEP162,KISS1R,ARF6,MAP4,CD47,SORBS1,ALMS1,SOS1,CSNK2B,CDC5L,POMGNT2,NFE2L2,PEMT,RAD21,CUL7,POLG,LZTS2,TOB1,VDAC3,FRK,LAMB2,PLA2G4A,CCNE1,NR4A2,UBR4,CAPRIN2,CDKN1A,EIF2B1,PSAP,CEP41,TCF7L2,PSEN1,ILF3,NCDN,CAMK1D,POLR3E,PARP2,TLN1,NFATC2IP,RNASEH1,TBC1D2,IFT140,MYC,TGFBR2,HSPA4,Gm21596/Hmgb1,MAP2K2,RCC1,PIM1,WDPCP,ARL1,XPO1,Hmga2,MYBL2,GCLM,CHTF18,ULK2,TAB1,PPP1R15B,SYNE2,UBE4B,FSTL3,SIK2,GM2A,DIDO1,ORC6,SLC12A7,RBFOX2,WASF1,HELLS,POFUT1,SNX3,KMT2A,PFKM,METRN,PPP2CB,CDC42BPB,HNRNPAB,TFAM,MATN2,DUSP1,ETV4,TXN2,XRCC6,DIXDC1,HSP90AA1,CAPN2,ACTN4,SSFA2,ELMO1,CDKL3,EEA1,RPSA,RBBP4,RHBDF1,ABI2,PPIB,DPYSL3,UBE2N,RPS6KA3,ATF6,SMAD5,SLC39A14,WDR6,RAD50,STIM2,RAD51,CCNA2,DIAPH1,LYST,WDFY3,FANCD2,TIMP1,NET1,HLA-DMA,BMPR1A,LDB1,FOXO3,TOR1B,MCM9,LRRC8A,RAD23B,PRKCA,KIRREL,CAPZB,SLC12A2,TUBG1,PTRHD1,FOXM1,AMPD2,GIT1,FAIM,NBN,CISD1,RCAN1,SS18L1,PMP22,PRKCI,MAPK14,FOXO1,RAD9A,KIF5B,EHD4,AMIGO1,COX5A,DPY30,PLD2,ABCA2,ITSN1,SGK1,TOR1A,ZNF451,CDKN2C,HES1,RAPH1,RICTOR,CHAF1A,RECQL,VEGFA,CXCL10,GSTZ1,RUSC1,FANCB,DYNLL1,BAG1,TARDBP,USP10,MAP1S,IRS2,CEP250,TXN,HEY2,CENPJ,STAT6,ACTR2,NDRG1,CFL1,CSRP2,MITF,RPA1,ITPR1,FANCC,IRF1,TERF2,CCNO,PTBP1,DOCK1,PCNA,BSG,GAB1,STIP1,H2AFX,BHLHE40,IRS1,E2F1,HPRT1,RAB11A,MSH5,LRP8,MAPK7,CYR61,IFIT2,EPHA2,PHLPP1,ADAM17,ATF7,PDIA3,HMGN1,CTNNA3,VCAN,SGMS1,CHEK1,EP300,COL5A1,EFNB2,ID1,TRIB1,NCOA2,PRRX1,RHOU,PDGFRA,DAP3,CEBPA,LAMP1,BID,PRKCE,MAP1LC3A,MAP1LC3B,MCPH1,POLDIP3,STIM1,HEXIM1,RXRB,NCKIPSD,PLOD3,PLAT,AIFM1,EPG5,MYCN,VPS18,DCK,TBC1D9,INPP5E,ACTB,HERC1,DPAGT1,MAFK,FADD,KITLG,YBX2,DGKZ,KIF15,ABL2,PDXP,SREBF2,NDE1,LIMS1,KIF20B,SPRY2,ADD1,ARAP1,ADAM10,TBPL1,GABPA,FEN1,MAFB,IREB2,PAFAH1B1,SEPT2,WDR19,DYRK1A,PHLDA1,MCM8,PALLD,EPS15,PTPN23,MAPK1,INSIG1,DIAPH3,MMP16,TAF10,AURKB,LATS2,LMNB1,STMN1,PTK2,ROCK2,FGFR3,SRSF1,TTBK2,RORA,EZH2,NEO1,HTRA2,ARHGEF25,BRCA1,FBXO45,MYO10,KIF14,ULK4,FGFR1,STK11,RAB10,TBP,RAB8A,LMNA,RANBP1,TMOD3,SIPA1L1,CCNT1,RNF4,ARRB2,FLOT2,PCGF1,CORO1B,PKD1,CASP2,LIN9,PTPRS,EXTL3,MTDH,PML,TEAD4,PAFAH1B2,NFIX,GDNF,PICALM,PDGFA,PKM,MARK2,RBBP8,Spg20,ABL1,SLC7A1,BCAR1,PRKAG1,TNFRSF12A,FUT8,EPHB6,NTNG1,TBC1D10A,ROR2,CCDC88A,Ppp1cc,CIT,MICALL1,BLM,CTDNEP1,E2F8,MAP2K7,S1PR2,ATG10,Nedd4,C2CD3,HDAC1,MTMR14,MAPK9,BCL3,USP1,NFKBIZ,HIVEP2,AFF1,DNM1,KIF24,UBQLN2,RIPK1,EXOC4,B4GALT1,LPAR1,EIF2AK2,VGF,HMGCR,BCL2L11,WNT5A,LGALS1

Supplemental Table 7. General IPA functions for E2F1, E2F3A and E2F3B promoter targets

ChIP-seq	Category	B-H p-value	Genes
E2F3B	Neurological Disease	3.12E-11	NPM1,CTCF,PRKAB1,POLA1,GARS,ELAVL4,POR,SMARCB1,ADA,TCERG1,PLXNB2,SLC2A1,ABCA7,GART,DAXX,DVL2,PRKACA,ALCAM,ECT2,DDIT3,BAG6,GNA11,NOTCH2,PCNXL3,RNF19A,ATN1,SLC12A6,SDHA,EP400,GAS1,TUBB4B,ID3,BAK1,BUB1,MAD2L1,MTHFD1L,MSH2,CSF1,MAZ,TFB1M,CDKN2A,MPRIP,SEPT9,LHX2,YWHAH,TROAP,SMAD3,NUP58,RPGRIP1L,TDP1,SMC1A,RGPD4 (includes others),SOX2,E2F6,MTMR2,EPHA7,STXBP1,HDAC2,DNA2,DYNC1H1,BCL2L1,H3F3A/H3F3B,SLC25A10,MCCC2,PBRM1,LITAF,KIAA0101,PDE4A,E2F3,PDCD10,HDGF,SIX1,NCS1,ERBB2,PDK1,KDM4C,MEF2A,SMARCE1,HERPUD1,SOD1,NFATC4,ALS2,BIRC5,BRCA2,MAP4K4,HNRNPL,CTGF,F2R,FAM20C,MKI67,ARNT,POLB,RNF38,CXorf23,RARA,ZFX,MGAT4B,HIPK1,BAG5,DNMT1,PABPC1,PIK3C2B,NOVA1,TFDP1,YWHAZ,PLEC,HBEGF,SPG7,GRK5,EXOSC8,MON2,AP5Z1,MED12,ARHGAP5,AHI1,RERE,CREM,ARHGAP35,TMEM158,FYN,RREB1,GALC,SNAI2,CDT1,PLAGL1,PTN,POLQ,FKBP1A,BOK,HMGB2,EIF4G1,H2AFZ,XRCC4,HK2,CREB1,IGF1R,MYO1D,CEP152,PMS2,PPIF,ELL,MDM2,SLIT2,CDK1,RRM1,SBF1,SAAL1,NCAM1,WDR48,NAB2,VTI1A,UNC5B,FBXW7,PIGQ,DICER1,ZNF91,YWHAQ,ETS2,ITPRIP,ZNF717,BCKDK,HK1,SOX4,P4HB,STIL,COL4A1,TRIOBP,MARS2,RAC1,ALAD,PREP,PALB2,Cdc42,RHOA,SCRIB,INTU,JAG1,CDK2,CDK5RAP2,PA2G4,NGF,KMT2C,SET,UHRF2,ZNF280B,RASSF1,HSPG2,MTRR,UHRF1,ATP2C1,HSPH1,LRRK2,TSHZ3,SLC25A38,PLEKHG5,TSEN34,NFIB,RAVER1,ADAM9,CBFA2T2,DDHD2,RAF1,KRAS,ASCC2,PANX1,CCND1,ATP2A2,EMG1,DOCK11,KLF7,EGR2,SUMO1,NEK6,ATF4,HIPK2,UNG,PIGT,TP53,CBX8,FBXO9,TYMS,ATG5,YAP1,RRM2,TBK1,ATF2,Marcks,SYNJ2,HSPA8,PEX2,CCNF,BTG2,CLK2,GAPDH,FRG1,XRCC5,TRAPPC5,INF2,PRDX2,HACE1,TRIM33,FBXO7,ARL4C,HNRNPA2B1,PDS5B,CDK4,PSEN2,ALX1,KISS1R,VRK1,TMEM209,CDKN3,MAP4,UBE2K,B3GALNT2,POMGNT2,NFE2L2,RAD21,CYP51A1,TUBGCP6,POLG,HSPA2,PLA2G4A,IGHMBP2,NR4A2,CDKN1A,PSAP,LDHA,CASP7,TCF7L2,MAOA,PSEN1,LRIG2,RPL22,CCDC15,KIF1B,KLF6,ABCC10,TLN1,KNTC1,TGFBR2,MYC,PIM1,MYBL2,GCLM,ULK2,TAB1,CLASP1,SMC3,SBF2,YWHAE,TNPO1,ORC6,TUSC3,TAF1,ATP5B,DUSP1,XRCC6,CDCA7L,ETV4,AGAP3,LMNB2,ELMO1,RUNX1,ARID1A,DPYSL3,DENND4B,DCAF4,RPS6KA3,SMAD5,ETV6,MLH1,LYST,BMPR1A,TIMP1,LDB1,FOXO3,EYA4,RPS3,CIZ1,PRKCA,POMT2,RFX1,SPG21,SLC12A2,TUBG1,CHERP,SAP130,HSPD1,MTHFD1,FOXM1,ATL3,AMPD2,NBN,FAIM,SH3PXD2A,RCAN1,PMP22,MAPK14,PRKCI,FAM111A,FOXO1,EHD4,MSH6,DCTN1,SH3RF1,ATR,CDC34,WNK1,CENPF,SOCS1,ABCA2,ITSN1,SGK1,CDKN2C,HES1,RAPH1,VEGFA,MXD3,FAM91A1,BAG1,TARDBP,IRS2,CENPJ,KMT2B,UPF2,OTUD4,NDRG1,CFL1,FOXH1,CSRP2,PTCH1,ITPR1,TERF2,DOCK1,PATZ1,YARS,STIP1,E2F1,ACY1,HPRT1,MAPK7,EPHA2,Nos1ap,HIST1H1C,SCAP,PDIA3,HMGN1,SETX,EP300,CHEK1,EFNB2,YY1,TCOF1,PRRX1,E2F5,TOP2A,PDGFRA,BID,PRKCE,MCPH1,RASSF5,PCBP2,POT1,PLAT,AIFM1,EPG5,MYCN,C10orf2,INPP5E,HERC1,CDC6,DLX1,POLD1,SIN3A,FADD,KITLG,SF3B2,LIMS1,NDE1,PVT1,SPRY2,MUTYH,PRMT5,RBPJ,PAFAH1B1,PCBP3,DYRK1A,PALLD,TFG,MAPK1,DIAPH3,CLTB,TUBB,LMNB1,ROCK2,FGFR3,USF3,SIVA1,EZH2,ERLIN2,ITGAV,HTRA2,BRCA1,CDC25A,KIF14,FGFR1,TBP,LMNA,GSR,FLOT2,PKD1,TUBE1,CASP2,LIN9,PTPRS,POMT1,PML,ORC4,KIF11,NFIX,GDNF,PDGFA,GTF2F2,PKM,RBBP8,ABL1,TAOK1,ING4,EPHB6,ROR2,GLI3,SP1,MAML3,TCP1,ERF,CTDNEP1,ACTN1,MAP2K7,CKS2,HDAC1,EFNA3,FCHSD2,MAPK9,RPS6KA5,XIAP,RIPK1,LPAR1,SLC25A27,SMARCC1,VGF,BCL2L11,LGALS1,WNT5A

Supplemental Table 7. General IPA functions for E2F1, E2F3A and E2F3B promoter targets

ChIP-seq	Category	B-H p-value	Genes
E2F3B	Post-Translational Modification	3.67E-10	RAF1,RNF8,TRAIP,TGFBR1,PRKAB2,PRKAB1,KRAS,CCND1,TRIM32,SCO2,PKN2,NUP93,SUMO1,MARCH2,FBLN1,NEK6,VAMP3,PLXNB2,HIPK2,IQGAP3,FBXO9,TP53,ATG5,HCFC1,PHIP,PEAK1,SLC2A1,STK25,CSNK1D,NUP107,TBK1,DDR1,SKP2,HSPA8,DAXX,DVL2,CCNF,ST3GAL1,TRPC4AP,CLK2,PHF23,COX18,PRKACA,CELSR3,LTN1,PTPRA,FANCA,MORC3,PCNP,HACE1,TRIM33,RAP2A,PIM3,PTPN2,FBXO7,PRDX1,GNA11,CDK4,CTDSPL,GALNT2,PPIA,UBE2Z,PSEN2,CDK10,VRK1,CD47,TRIM27,IBTK,UBE2K,DAB2,CSNK2B,NFE2L2,UBE3C,KPNA3,MED20,PASK,CUL7,MAPK6,FRK,HSPA2,CCNE1,CSF1,CDKN1A,PSAP,MAP3K3,PSEN1,CDKN2A,SOCS3,ILF3,MPRIP,SMAD3,SLF2,GNB2L1,NME2,RFWD3,TCEB1,TGFBR2,ZW10,HSPA4,USP8,Gm21596/Hmgb1,KCTD20,SAE1,MAP2K2,PIM1,MAPK3,CACTIN,PDZRN3,ULK2,RNF41,EPHA7,UBE4B,CSNK1G2,SIK2,WEE1,RDX,MAPKAPK5,NDC1,KMT2A,SLC3A2,ARIH1,CAND1,CDC42BPB,TAF1,DUSP1,OXSR1,PKMYT1,KLHL21,UBE2I,PEBP1,UBE2N,BARD1,PIAS1,DNAJC10,SMAD5,EIF2S1,PRR5L,IQGAP1,ETV6,RAD51,BMPR1A,STUB1,HLA-DMA,ERBB2,STX4,PDK1,RPS3,GMFB,PRKCA,BTBD10,MED18,KIRREL,CAPZB,CHP1,HERPUD1,TUBGCP2,BIRC5,UBE2D1,FANCL,SLK,PSKH1,MAPK14,PRKCI,ATR,CDC34,WNK1,MAP4K4,SOCS1,CTGF,F2R,SGK1,FAM20C,UBR2,CDKN2C,HES1,RICTOR,CHAF1A,VEGFA,RNF38,RUSC1,DYNLL1,CD2AP,CTDSP1,BAG1,RARA,TARDBP,CBFB,HIPK1,BAG5,ANAPC11,MOB1B,NDUFAF5,CFL1,MITF,GRK5,TFAP4,HMGA1,FANCC,MED12,DOCK1,RNF168,BSG,IRS1,NCLN,AHCTF1,HPRT1,CLSPN,MAPK7,CYR61,PRICKLE1,PHLPP1,CAPZA1,FYN,ADAM17,PDIA3,UVSSA,PTN,CUL1,FKBP1A,STRA13,FZD1,RCHY1,DNAJA1,SF3B3,EP300,AKAP11,CHEK1,EIF4EBP1,EFNB2,CHAF1B,CREB1,HUS1,IGF1R,PDGFRA,PRKCE,NUP205,HEXIM1,RASSF5,PCBP2,NSMCE1,SLC7A6,AIFM1,JKAMP,PLK1,MDM2,SLIT2,CDK1,KITLG,DGKZ,SPIDR,NUP153,ABL2,CAMKK1,RNF187,ADAM10,ADD1,DYRK1A,NCAM1,PRPF19,MAPK1,VPS28,PRMT3,Wasl,FNIP2,FBXW7,MELK,DICER1,LATS2,AURKB,PBK,ROCK2,PTK2,FGFR3,CAMK2D,SCARB1,TTBK2,DZIP3,EZH2,Map3k7,DARS,SIAH2,BCKDK,FBXO45,BRCA1,APITD1/APITD1-CORT,HK1,SOX4,TRAF3IP1,STK11,FGFR1,RAC1,PSMC4,BIRC6,DGUOK,ELF1,WWP2,EPRS,CCNT1,HERC2,Cdc42,ARRB2,RNF4,BRAT1,ERP29,PKD1,PTPRS,NUAK1,MAP4K5,PML,Paxip1,CDK2,MED23,CCNC,PICALM,MARK2,ABL1,TNFAIP3,TAOK1,NGF,PRKAG1,EPHB6,CCDC88A,TRIM24,UHRF2,GMNN,GTPBP4,MAPKAPK2,DTL,RASSF1,NDUFAF3,UBR5,MAP2K7,UHRF1,Nedd4,SMAD7,RNF126,MAPK9,LRRK2,RPS6KA5,MED6,MARCH5,UBE2T,XIAP,FAF1,RIPK1,FASTK,EIF2AK2,TRIM59,WNT5A,LGALS1,GSG2,MCM7

Supplemental Table 7. General IPA functions for E2F1, E2F3A and E2F3B promoter targets

ChIP-seq	Category	B-H p-value	Genes
E2F3B	Hepatic System Disease	5.28E-10	GARS,TLE1,FRMD6,TMEM231,TRIM32,POR,PPRC1,GORASP2,SMARCB1,ADA,SART3,RELT,TMEM67,ZBTB5,TANC1,HIST1H2BM,DVL2,EYA3,ALCAM,ELMO2,DDIT3,SLC1A5,CDK10,TIPARP,IBTK,RNF19A,ATN1,SLC12A6,UBE3C,SDHA,VPS16,IPO7,ID3,KPNB1,BUB1,MTHFD1L,AP1G1,CDKN2A,EEF1A1,TROAP,INTS1,LHFPL2,MTMR2,PGM1,PTPDC1,PHRF1,DYNC1H1,BCL2L1,KIAA0895L,H3F3A/H3F3B,SEC61A2,CBX3,MCCC2,ZC3H7B,HPS5,RAB23,KLF10,ZBTB2,LSM2,C16orf59,NCS1,ILKAP,IGSF8,FRA10AC1,GALNT9,MEF2A,HERPUD1,SOD1,SNX27,FRMD4A,PPM1G,HTATSF1,CENPI,TFCP2,ING1,MAP4K4,RPLP0,MCM6,ASPSCR1,UBR2,FAM20C,ZNF628,FNDC3B,RRAGB,WBSCR17,ADIPOR1,PPP1R21,RNF38,RASGRF1,RAB17,TDP2,PRIM2,CCNT2,UAP1,SPECC1L,PABPC1,NOVA1,HIRA,PLEC,AGFG2,AP5Z1,TTLL9,MEX3A,SUCO,RNF168,PHLDB1,C11orf30,NCLN,RCBTB1,KIAA0368,ARHGAP35,SNAI2,GALC,NCAPD3,PTPN13,PLAGL1,SPATA13,FKBP1A,DNAJA1,TOR1AIP1,TYW1,NEIL3,HK2,RINT1,TICRR,RFC2,IGF1R,TXNL1,TCTN3,VCL,ZNF25,PSMB9,MCMBP,NUP85,CEP152,STAMBPL1,BANP,PLK1,ACLY,F3,NCAPG2,RRM1,NUDT5,ZNF546,SBF1,ZNF507,TRERF1,COBLL1,NCAM1,FMNL3,ATRIP,FBXW7,DHODH,ZNF91,FAM208A,TBC1D4,ESPN,KHNYN,DZIP3,ZNF717,TFDP2,RPRD2,PANK4,FAM193A,STIL,COL4A1,CLTC,BIRC6,DTNB,ATP10A,ALAD,WHSC1L1,BRAT1,COL6A3,IFT81,SCRIB,C15orf41,RCE1,KBTBD8,FADS1,LRIG3,ZMIZ1,TRIM24,USP47,RPAIN,TMEM220,LRRK2,PFKP,TCF7L1,TSHZ3,ZNF382,FAF1,KIAA1033,TSEN34,PAN3,ZDHHC12,MTRF1L,USP34,RAF1,IQCK,HMMR,RALGAPB,ASCC2,SLC35C1,FAM208B,ATP2A2,RNASE4,ADH5,DOCK11,RCL1,CCDC122,CENPE,WDR47,MGAT1,SGSM2,GNE,TYMS,CBX8,ASF1B,PHIP,PAPD4,ESPL1,YAP1,APPL2,PAM,EEF2,ZBTB43,MDM1,WDR81,ZNF496,ATE1,AGPAT4,PLEKHG2,MORC2,ATXN7L3,MIDN,ST3GAL1,GTSE1,ANAPC5,VPS37B,ZNF644,CENPT,CHD1L,PTPRA,TRAPPC5,INF2,FANCM,HACE1,FAM188B,ERCC4,FBXO10,PTPN2,HNRNPA2B1,ODF2L,CDK4,KIAA0754,PRPF4,PGS1,LRRFIP1,SDK1,CDKN3,TMEM209,NAA15,TMEM260,ALG8,ASPH,NFE2L2,RAD21,CYP51A1,ESCO1,FBXO21,SLC35A5,CCDC57,ZMYM1,KLHDC2,WIPF2,TUBGCP6,LZTS2,ING5,LARP4B,NCAPD2,SLC29A1,IGHMBP2,CCNE1,ZFPM2,UBR4,DDX39B,ABCF2,EIF4A1,CDKN1A,ZFHX2,PSAP,CEP112,LDHA,PPIL1,ID4,TCF7L2,MAOA,PSEN1,LRIG2,MEGF9,CAMK1D,MSH3,KIF1B,TSFM,ABCC10,PIEZO1,MYC,TGFBR2,SMPD4,AHDC1,GDE1,SUGT1,CACTIN,EIF4B,CLASP1,SPECC1,TEX264,CCDC18,FSTL3,C3orf58,KANK2,ENDOD1,PSMD6,B3GALNT1,TUSC3,TBL1X,ARIH1,CDC42BPB,HNRNPAB,TAF1,UGP2,XRCC6,ETV4,SEPT10,SMCHD1,MAD1L1,RUSC2,HSP90AA1,NCKAP5L,SSFA2,FAM83D,RBBP4,DPYSL3,UBE2N,RPS6KA3,DNAJC10,NEURL4,WDR6,VPS4A,IGF2BP1,RAD50,STIM2,CCNA2,LYST,AHNAK,TIMP1,NOP58,MEX3B,ACO1,VARS,CIZ1,LRRC8A,POMT2,RFX1,HAUS8,AP1S2,CHERP,RALY,ZFPL1,NMT2,HSPD1,NFKBIL1,MTHFD1,FAIM,SH3PXD2A,SLK,MAPK14,PHF19,PSMD2,LSM11,C5orf22,SGK1,APIP,SFPQ,ZNF451,RICTOR,KPNA1,RECQL,CHST2,VEGFA,NCOA7,DYNLL1,TTF2,HNRNPUL1,SEC24A,TMEM55B,NAT10,RCBTB2,ITPR1,PLCL2,FANCC,UBQLN4,TERF2,DOCK1,YARS,YTHDF3,CPNE8,IRS1,BHLHE40,E2F1,RGL2,LRP8,HELB,CD2BP2,VASH2,PKD2,SASS6,VCAN,XYLB,BCDIN3D,TRIB1,WDFY1,NCOA2,POLR2M,SLC6A17,DAP3,E2F5,MAP1LC3B,LPP,NCKIPSD,PLOD3,BRMS1L,RAD51B,HNRNPDL,ATXN2L,PCDH9,SIN3A,KIF15,ABL2,RBM6,HEATR5A,NCOR2,ZFP36L2,USP49,FZR1,ANKS1B,INSIG1,DIAPH3,FNIP2,CCNL1,USF3,DPY19L4,MBNL3,LARS,UBXN4,EZH2,ALG6,DARS,NIPBL,HTRA2,MYO10,PMPCA,RASAL2,FGFR1,LMNA,MARS,GSR,ARRB2,PLEKHH2,ITPRIPL1,PTPRS,MAP4K5,PFAS,PML,BCL9L,RFC3,KDM3B,TEAD4,TNRC6B,ZBTB7A,MED23,GTF2F2,MARK2,ING4,GANAB,SP1,CIT,RABGGTB,LTBP4,ATG16L2,ZNHIT2,TM9SF1,MAP2K7,CKS2,MRC2,DCTPP1,let-7,RPS6KA5,KIAA2026,KIF24,PPP6R1,B4GALT1,PANK3,WRB,PAQR4,TONSL,HMGCR,SLC9A8,DPY19L3,BCL2L11,MCM7,NPM1,mir-130,RPE,POLA1,TAB2,CCNB2,GPSM2,MAP1A,DUSP11,HCFC1,SLC2A1,NPAT,TCF3,RGP1,ABCA7,SP4,DAXX,CNTRL,ITPR3,C3orf67,ECT2,CCDC138,FLNB,NRG2,PRDX1,BAG6,CEBPZ,TTK,PNRC1,CDC20B,HEXB,C2CD5,SCFD1,TUBB4B,ZNF521,MAPK6,GREM1,SPSB4,KAT5,IGF2R,MCM3,MSH2,CSF1,TFB1M,KANSL2,KIF23,NAV2,SOCS3,MPRIP,YWHAH,PCDH18,GNPAT,NUP58,ZFPM1,RPGRIP1L,ECD,PPFIBP1,SOX2,TSEN15,ARHGAP20,SEC63,EPHA7,OSBPL1A,STXBP1,POLE4,SESN3,HDAC2,POLR1B,IARS2,WEE1,IFT74,DNA2,H6PD,TXNRD1,OSBPL8,KIAA0907,SF3B4,PBRM1,PVRL3,MCM3AP,RBBP5,IQGAP1,NFAT5,ERBB2,VAV2,NDUFV1,ADAM15,PSMC3IP,TSN,ALS2,UMPS,BIRC5,MTO1,SLC36A4,CKS1B,ZDHHC3,BRCA2,CCP110,RTCB,MTBP,RAN,GHITM,MKI67,ARNT,ATP1A1,RARA,MED16,SLC39A13,BAG5,RTEL1,CNOT1,PTPRG,MMAB,MDC1,MON2,ADAR,MED12,ANKRD26,FARSA,ARHGAP5,FUT10,AAAS,MYO9A,AHI1,DNAJC14,ME2,CLCC1,PRICKLE1,SQLE,RREB1,MAP2,CEP78,ARHGEF7,POLQ,TRPT1,PITRM1,AAMP,KANSL3,ANKRD12,EAF1,ATAD5,CDH11,TIGD5,AKAP11,DIS3L2,RAB33B,CREB1,NUP205,ZCCHC6,POLE,PAICS,TIAL1,MDM2,SLIT2,SCMH1,CNKSR3,C1orf159,SCAF11,GLTP,SPIDR,INTS6,GMPS,ATL2,GTPBP3,REV1,H2AFY,UBN1,BTBD7,FARP1,ARF1,PRMT3,GXYLT1,UNC5B,ZNF609,DICER1,RELL1,CAMK2D,ZNF318,SCARB1,STAG1,FASN,ABLIM2,CDCA3,STX11,HK1,SOX4,P4HB,TRIOBP,DTNBP1,DCTN4,POLE2,USP38,PREX2,MUT,GPAA1,HERC2,ANKRD10,NASP,CTDP1,LUC7L2,LOXL1,NUAK1,SBNO2,JAG1,CDK2,ARL2,KDM3A,BRD2,SRM,C5orf42,PA2G4,AGAP1,SRRT,WDHD1,KMT2C,GTF2B,FAM13B,IFRD1,NCL,YLPM1,IPO5,ATG16L1,RHBDD3,RASSF1,UBR5,HSPG2,MTRR,TTC13,TRA2B,PANK2,POC1B,COTL1,HSPH1,METTL1,SAP25,DOCK7,C19orf68,CIART,PIAS3,MAP7D1,U2SURP,PLEKHG5,IQCE,NFIB,ADAM9,GRPEL1,CBFA2T2,CENPH,CASP8AP2,PRKAB2,PCIF1,KRAS,TOMM70A,CCND1,PKN2,SNRNP48,PAN2,NEK6,ZNF687,HIPK2,MSTO1,IQGAP3,ALDH7A1,TP53,FBX

Supplemental Table 7. General IPA functions for E2F1, E2F3A and E2F3B promoter targets

ChIP-seq	Category	B-H p-value	Genes
E2F3B	Protein Synthesis	5.83E-10	RAF1,NPM1,RNF8,TGFBR1,MYH9,PCBP1,RBM3,KRAS,EIF4A2,ELAVL4,CCND1,SCO2,TRIM32,EIF3B,NUP93,RBM4B,SUMO1,NEK6,VAMP3,ATF4,HIPK2,TARBP2,TP53,HCFC1,ESPL1,SLC2A1,PAM,EEF2,CSNK1D,NUP107,USP19,TBK1,MAN1A2,TCF3,RBM4,SKP2,HSPA8,EIF4H,MRPL17,BTG2,TRPC4AP,PRKACA,COX18,GAPDH,CAPN7,SAMD4A,FANCA,SPPL2A,MORC3,EIF4EBP2,FBXO7,PTPN2,DDIT3,BAG6,CDK4,PSEN2,FBXL4,NAA15,NECAB3,TRIM27,TIPARP,UBE2K,HEXB,ASPH,DHX9,KPNA3,STT3B,STX12,KHDRBS1,PASK,MRPL12,TOB1,LARP4B,HNRNPD,NXF1,BAK1,MAD2L1,ZFPM2,DDX39B,CSF1,EIF4A1,EIF2B1,CASP7,PSEN1,CDKN2A,EEF1A1,SOCS3,ILF3,SLF2,SMAD3,GNB2L1,TSFM,TGFBR2,MYC,ZW10,EIF3D,PIM1,MAPK3,XPO1,SUGT1,DPM3,EIF4B,STXBP1,UBE4B,HDAC2,CSNK1G2,RDX,MAPKAPK5,SNX3,EIF4E2,TBL1X,NDC1,KMT2A,ARIH1,BCL2L1,TAF1,AGBL3,AGAP3,CAPN2,RNF149,FAM83D,UBE2I,Rplp1 (includes others),PPIB,RAB23,UBE2N,ABCF1,INPPL1,ATF6,PDCD10,EIF2S1,VPS4A,IGF2BP1,DIAPH1,STUB1,HLA-DMA,FOXO3,ERBB2,STX4,PDK1,ACO1,RPS3,LONP1,PRKCA,SDC1,CAPZB,IFT46,ADAM15,CHP1,MEF2A,HERPUD1,CANX,RPL23,HSPD1,SOD1,CNOT8,TUBGCP2,UBE2D1,AMPD2,PPM1G,MAPK14,FOXO1,PSMD2,QRSL1,ATR,HNRNPL,SOCS1,SGK1,UBR2,HES1,RICTOR,EIF6,RBL1,Rpl29 (includes others),RAD23A,CHAF1A,VEGFA,CD2AP,BAG1,RARA,DNMT1,TIMP2,PABPC1,CNOT1,STAT6,NDUFAF5,MITF,COPS5,SYNCRIP,TFAP4,HMGA1,FANCC,UBE2G2,PTBP1,DOCK1,RNF168,PPP2R3A,STIP1,IRS1,ACY1,NCLN,AHCTF1,KIAA0368,MRPL41,CLSPN,MAPK7,PHLPP1,CAPZA1,FYN,ADAM17,PDIA3,CRTAP,FKBP1A,CCAR2,PITRM1,MRPL39,EIF4G1,H2AFZ,SF3B3,EP300,EIF4EBP1,SPPL2B,DHPS,NCOA2,CHAF1B,CREB1,EIF3A,LAMP1,PRKCE,POLDIP3,NUP205,RPS5,SLC7A6,PLAT,AIFM1,ADRM1,BANP,AZIN1,AGO2,PLK1,MDM2,CDK1,FADD,EIF3G,YBX2,SENP1,SPIDR,NUP153,CIRBP,ADAM10,ADD1,IREB2,DYRK1A,NCAM1,FZR1,MAPK1,VPS28,MMP16,DIAPH3,Wasl,METAP1,FNIP2,FBXW7,PIGQ,DICER1,PBK,LOC102724828/MRPL23,METAP2,CAMK2D,SERP1,UBXN4,RPS20,TTBK2,RPL19,DARS,SIAH2,HTRA2,NAA16,PMPCA,Fus,HK1,SOX4,CDC37,TRAF3IP1,PSMF1,PSMC4,MARS,EPRS,PREP,Cdc42,ARRB2,FLOT2,PKD1,CASP2,USE1,EIF4A3,RCE1,MRPL3,PML,CDK2,RPL13A,CNBP,TNRC6B,PICALM,TNFAIP3,SLC7A1,TBC1D10A,IPO9,UHRF2,TRIM24,SP1,GMNN,LTBP4,GTPBP4,MAPKAPK2,NCL,RASSF1,RHBDD3,DTL,NACA,NDUFAF3,UBR5,HSPG2,Nedd4,HDAC1,C2CD3,SMAD7,let-7,LRRK2,BCL3,NXT1,NDUFA13,XIAP,CDKN2AIP,FAF1,RPS27L,EIF2AK2,UBC,ADAM9,WNT5A
E2F3B	Respiratory Disease	2.13E-09	mir-130,NPM1,RAF1,MYH9,TGFBR1,CTCF,PCBP1,NUP133,SSBP2,CCNB2,EIF4A2,KRAS,STK35,CCND1,POR,COPS6,NEK6,HIPK2,TARBP2,TP53,SERBP1,TYMS,PHIP,GRM8,RRM2,DDR1,DCLRE1A,SKP2,GART,ITPR3,ALCAM,ECT2,PRDX2,HACE1,DDIT3,PRDX1,PRDX4,GNA11,ODF2L,CDK4,EEF1B2,PPIA,PSEN2,MED28,KISS1R,MAP4,NOTCH2,ARF6,PRR14L,IRF2BPL,GPC6,NFE2L2,RAD21,ATN1,SLC12A6,DHX9,EP400,GAS1,TUBB4B,LZTS2,TPK1,SLC29A1,BUB1,PLA2G4A,MAD2L1,NR4A2,MSH2,CSF1,EIF4A1,SLC29A2,CDKN1A,LDHA,CDKN2A,EEF1A1,RPL22,CBWD1,PRELID3B,SMAD3,GNPAT,GNB2L1,PINX1,RGPD4 (includes others),SMC1A,MYC,TGFBR2,SOX2,FDFT1,RCC1,MLEC,SMC3,POLE4,SYNE2,YWHAE,MYEF2,HDAC2,DNA2,HELLS,BUB1B,CDCA2,PFKM,KIAA0907,BCL2L1,TFAM,TAF1,SEC61A2,MAD1L1,HSP90AA1,RUNX1,PBRM1,ARID1A,PDE4A,EIF2S1,MLH1,TARBP1,CCNA2,FANCD2,AHNAK,TIMP1,FOXO3,ERBB2,CIZ1,ADAM15,TUBG1,RALY,HSPD1,FOXM1,G3BP1,BIRC5,FANCL,NBN,RNF44,MAPK14,PRKCI,PHF19,KLF5,MSH6,CKS1B,PAPD7,BRCA2,ATR,WNK1,MAP4K4,DDX11,CCP110,DNAJB4,CDKN2C,HES1,MKI67,RBL1,ADIPOR1,RPS11,XRCC1,VEGFA,RARA,TDP2,CBFB,PRIM2,DNMT1,KMT2B,PABPC1,STAT6,NDRG1,COPS5,C1orf74,YWHAZ,TFAP4,ITPR1,AGFG2,AP5Z1,IRF1,SPOP,ARHGAP5,PCNA,RFC4,E2F1,ARHGAP35,CYR61,YEATS4,HIST1H1C,ADAM17,PDIA3,PTN,POLQ,FNTB,EIF4EBP1,EP300,ID1,HK2,SCAF4,NCOA2,RINT1,DGCR8,TOP2A,CEBPA,IGF1R,PDGFRA,EIF3A,PRKCE,MAP1LC3A,CACNB2,RASSF5,RXRB,MMP17,PSMB9,mir-199,DCK,TBX3,CDC6,POLE,AGO2,TIAL1,MDM2,PLK1,SLIT2,ACLY,C1orf159,F3,SCAF11,SIN3A,CDK1,CBLN1,RRM1,FADD,MCM2,CTNNBL1,H2AFY,MUTYH,UBN1,MAFB,TRERF1,DNPH1,ZFP36L2,NCAM1,TAF15,FZR1,NAB2,PHLDA1,PRPF19,MMP16,FBXW7,DICER1,TUBB,AURKB,STMN1,PTK2,FGFR3,DPY19L4,SRSF1,STAG1,ASXL2,FASN,EZH2,ZNF717,ITGAV,SLC7A5,BRCA1,AIM1,SOX4,IGFBP6,P4HB,LMLN,POLE2,FGFR1,STK11,TBP,RAC1,ATP10A,HERC2,ARRB2,TUBE1,SCRIB,MAP4K5,MTDH,AK2,BCL9L,KIF11,SRM,TNRC6B,PKM,MARK2,ABL1,RBBP8,TAOK1,ING4,KMT2C,PDP2,FUT8,EPHB6,POLR2A,RABGGTB,NCL,RASSF1,NACA,CKS2,GLS,HDAC1,let-7,LRRK2,PPP4R3A,PFKP,MTAP,XIAP,TSHZ3,FDPS,ENO1,ADAM9,BCL2L11,SHMT2,MSN,LGALS1,WNT5A

Supplemental Table 7. General IPA functions for E2F1, E2F3A and E2F3B promoter targets

ChIP-seq	Category	B-H p-value	Genes
E2F3B	Cellular Movement	2.17E-09	mir-130,RAF1,NPM1,MYH9,TGFBR1,RALGAPB,KRAS,FRMD6,CCND1,PKN2,FHL2,KIF13A,NEK6,FBLN1,HIPK2,AHCY,ETS1,TP53,YAP1,SLC2A1,STK25,CRKL,TMEM201,RRM2,ZFYVE21,TCF3,PTP4A1,MASTL,DDR1,SKP2,DVL2,FSCN1,PRKACA,ALCAM,ECT2,PTPRA,INF2,KIF20A,RAP2A,FLNB,PTPN2,SNX17,HNRNPA2B1,GALNT2,SEPT11,ALX1,NAA15,KISS1R,APPL1,ARF6,NOTCH2,SOS1,DAB2,NFE2L2,SLC12A6,LZTS2,FRK,NR4A2,CSF1,CDKN1A,LDHA,ID4,KIF23,CDKN2A,ILF3,SEPT9,SMAD3,KLF6,GNB2L1,NME2,HDAC10,CBX5,SOX2,TGFBR2,MYC,Gm21596/Hmgb1,MAP2K2,PIM1,JUND,TAB1,SYNE2,HDAC2,DIDO1,RBFOX2,BCL2L1,CDC42BPB,HNRNPAB,ETV4,HSP90AA1,CAPN2,KLHL21,ACTN4,ELMO1,RPSA,PEBP1,TNFAIP8,RPS6KA3,IQGAP1,PTGES3,IGF2BP1,ETV6,HDGF,CCNA2,DIAPH1,NFAT5,AHNAK,NET1,TIMP1,FOXO3,ZNF24,STX4,ERBB2,LASP1,PRKCA,SDC1,ADAM15,RPRD1B,RACGAP1,SLC12A2,FOXM1,BIRC5,GIT1,IVNS1ABP,MAPK14,PRKCI,FOXO1,RAD9A,BRCA2,WISP1,WNK1,MAP4K4,SOCS1,CCP110,PLD2,CTGF,F2R,DSTN,DNAJB4,FNDC3B,HBP1,RICTOR,CXCL10,VEGFA,CD2AP,RASGRF1,IRS2,FRS2,CENPJ,TIMP2,CFL1,NDRG1,MITF,CENPB,SEPT7,PLEC,HBEGF,CKAP2,TFAP4,HMGA1,PTBP1,DOCK1,GAB1,RFC4,BSG,BHLHE40,AHCTF1,RAB11A,ARHGAP35,MAPK7,CYR61,IFIT2,EPHA2,FYN,ADAM17,SNAI2,ARHGEF7,FKBP1A,CNTROB,CDH11,VCAN,ID1,YY1,PRRX1,TOP2A,PDGFRA,E2F5,IGF1R,EIF3A,PRKCE,PPM1F,VCL,HEXIM1,LPP,PLOD3,PLAT,MYCN,mir-199,DCK,PPIF,SUZ12,TBX3,ACTB,CDC6,AGO2,PLK1,MDM2,SLIT2,F3,CDK1,RRM1,FADD,KITLG,SENP1,ABL2,PDXP,KIF20B,SPRY2,CAP1,HOXB9,BTBD7,PAFAH1B1,SEPT2,EPS15,PALLD,PTPN23,MAPK1,MMP16,DIAPH3,UNC5B,DICER1,AURKB,LATS2,AMD1,YWHAQ,PTK2,STMN1,SERP1,RORA,ETS2,EZH2,RAB11FIP1,ITGAV,BRCA1,DLC1,SOX4,KIF14,STK11,FGFR1,BIRC6,RAC1,LMNA,SSRP1,Cdc42,RHOA,SCRIB,NUAK1,PDLIM1,MTDH,PML,INCENP,ZBTB7A,GDNF,PA2G4,PDGFA,PICALM,PKM,Spg20,ABL1,NGF,BCAR1,TCF12,FUT8,EPHB6,CCDC88A,SP1,CIT,MAPKAPK2,RASSF1,MRC2,HDAC1,let-7,SMAD7,PRKAR2A,HDLBP,XIAP,PRMT1,DNM1,GNAI2,FAF1,LPAR1,SATB1,ACAT1,EIF2AK2,ADAM9,MSN,WNT5A,LGALS1
E2F3B	Cardiovascular Disease	2.69E-09	RAF1,NPM1,MYH9,SSBP2,KRAS,CCND1,ADRB3,POR,SMARCB1,ATF4,KLF1,MGAT1,PIGT,TP53,TYMS,SLC2A1,RRM2,TCF3,DDR1,ATF2,DAXX,ALCAM,TFRC,CPOX,FANCA,PRDX2,FANCM,ERCC4,FLNB,TRIM33,DDIT3,PTPN2,PRDX1,CDK4,KIAA1549,NOTCH2,CD47,ARF6,PNRC1,DIS3,NFE2L2,RAD21,SLC12A6,SDHA,EP400,TUBB4B,RPS10,IGF2R,BAK1,BUB1,CCNE1,MSH2,CDKN1A,PLXDC1,ACTL6A,CDKN2A,LHX2,KIF1B,SMAD3,ZFPM1,PINX1,PIEZO1,DEPDC5,CEBPG,TGFBR2,MYC,E2F6,Gm21596/Hmgb1,MAP2K2,PIM1,PPP3R1,BRIP1,EPHA7,SMC3,POLE4,HDAC2,DIDO1,SLC12A7,BUB1B,KMT2A,TXNRD1,BCL2L1,NT5C3A,ETV4,RECQL4,MAD1L1,HSP90AA1,FOXP4,RUNX1,PBRM1,PDCD10,MLH1,ETV6,ARFRP1,DIAPH1,NFAT5,FANCD2,BMPR1A,FOXO3,ERBB2,SLC20A1,TUBG1,SOD1,NFATC4,FANCL,NBN,MAPK14,MSH6,BRCA2,ATR,SGK1,CDKN2C,MKI67,RICTOR,ARNT,VEGFA,FANCB,RARA,CBFB,DNMT1,PIK3C2B,TFDP1,PTCH1,FANCC,IRF1,CDAN1,E2F1,HELB,CTC1,SNAI2,ATF7,PTPN13,HMGN1,CRLF2,EP300,STOM,RINT1,ADK,IGF1R,PDGFRA,TOP2A,CACNB2,RXRB,EED,MYCN,RPS19,PMS2,POLE,MDM2,PLK1,SLIT2,CDK1,RRM1,KITLG,FADD,SENP1,ABL2,GMPS,MUTYH,ADD1,ZFP36L2,IREB2,RPL11,MAPK1,DICER1,TUBB,PTK2,SCARB1,STAG1,EZH2,BRCA1,RAD51C,DLC1,HK1,STIL,POLE2,STK11,FGFR1,RAC1,PREX2,TMOD3,MUT,GSR,PALB2,Cdc42,TUBE1,SH2B3,C15orf41,CYLD,SPTAN1,JAG1,PML,CDK2,PKNOX1,PICALM,ABL1,SLC7A1,TNFAIP3,KMT2C,PRKAG1,TRIM24,GLI3,SIPA1,ERF,BLM,MTRR,HDAC1,NFKBIZ,IPP,AFF1,SLC25A38,YARS2,LPAR1,PDE5A,MSN

Supplemental Table 7. General IPA functions for E2F1, E2F3A and E2F3B promoter targets

ChIP-seq	Category	B-H p-value	Genes
E2F3B	Hematological Disease	6.59E-09	NPM1,mir-130,CTCF,TGFBR1,POLA1,PPWD1,NUP133,SSBP2,POR,PPRC1,SMARCB1,ADA,MAP1A,ETS1,SLC2A1,NPAT,RANBP3,MSMO1,TCF3,ABCA7,MASTL,GART,DCLRE1A,DVL2,KAT6A,PSMD1,CPOX,FANCA,PRDX1,CPD,PPIA,NOTCH2,PNRC1,PCNXL3,GPC6,ATN1,EXO1,SLC12A6,UBE3C,FKBP3,SCFD1,EP400,VPS16,TUBB4B,PASK,RPS10,IPO7,KAT5,ID3,BAK1,BUB1,KPNB1,MTHFD1L,RPS16,MSH2,SLC29A2,ACTL6A,CDKN2A,EEF1A1,NAV2,MPRIP,LHX2,ZFPM1,HDAC10,SMC1A,RGPD4 (includes others),SMAP2,E2F6,USP8,CEP57,ANXA11,MTMR2,ING2,OSBPL1A,POLE4,POLR1B,HDAC2,WEE1,PGM1,DNA2,POLR2H,H6PD,RAD54L,PTPRM,CDCA2,TXNRD1,DYNC1H1,BCL2L1,KIAA0895L,UBE2I,PBRM1,HPS5,PIAS1,CHSY1,BARD1,PDE4A,ZBTB2,GPHN,ALAS1,E2F3,PDCD10,IQGAP1,LSM2,TARBP1,NFAT5,STUB1,ILKAP,ERBB2,GALNT9,MEF2A,PSMC3IP,NFATC4,SOD1,G3BP1,ALS2,UBE2D1,BIRC5,FANCL,BRD3,TMEM109,BRCA2,ING1,MAP4K4,RPLP0,TUBA1B,MCM6,DDX11,RAN,ZNF436,HBP1,MKI67,RPS11,XRCC1,RAD23A,ARNT,POLB,RASGRF1,RARA,TDP2,CBFB,PRIM2,DNMT1,C19orf57,RND2,PYCRL,PABPC1,TTC21A,TFDP1,ZC3HAV1,YWHAZ,RPL7L1,MDC1,HMGA1,MED12,ANKRD26,CMIP,SH3GL1,MNT,MTMR4,AHI1,CDAN1,FBXO30,ARHGAP35,PRICKLE1,FYN,SNAI2,UVSSA,POLQ,CUL1,CENPN,FKBP1A,CRLF2,PITRM1,EIF4G1,XRCC4,EIF4EBP1,STOM,HK2,RIF1,RINT1,IGF1R,VCL,NCBP3,EED,PSMB9,PMS2,BLMH,SUZ12,POLE,USPL1,PLK1,MDM2,NAP1L1,F3,CDK1,RRM1,SENP1,IMMT,REV1,MUM1,UBN1,KDELR3,GPR180,TRERF1,NCAM1,WDR48,STRN,FBXW7,ZNF609,ZNF91,FAM208A,NAF1,SCARB1,STAG1,ETS2,FASN,PANK4,GOLGA1,STX11,SOX4,HK1,MCM5,COL4A1,PSMF1,POLE2,BIRC6,RAC1,PREX2,DTNB,ATP10A,CDC123,MUT,PREP,PALB2,WHSC1L1,Cdc42,COL6A3,LUC7L2,SH2B3,RHOA,C15orf41,CYLD,JAG1,CDK5RAP2,CDK2,GAS2,BRD2,ZBTB49,GADD45G,TXLNA,LRIG3,KMT2C,ZMIZ1,GTF2B,PRIM1,USP47,SIPA1,IPO5,DHX15,CNTLN,RASSF1,HSPG2,UBR5,TMEM220,MTRR,SNRPB,HAT1,LRRK2,TCF7L1,TSHZ3,MLLT1,ALG12,SLC25A38,YARS2,IQCE,SLC25A32,USP34,ADAM9,LANCL2,SCFD2,RAF1,WDR90,MYH9,RDH10,SMC5,KRAS,FAM208B,CCND1,ZC3H12C,EGR2,CENPE,NEK6,ATF4,LSM3,KLF1,HIPK2,MGAT1,TARBP2,UNG,PIGT,TP53,TYMS,FBXO9,ATG5,PHIP,ESPL1,RRM2,MDM1,KLF13,ZNF169,DDR1,RBM4,ATF2,SKP2,PLEKHG2,CCNF,TRPC4AP,BTG2,INVS,TFRC,GAPDH,SRSF4,Meis1,FRG1,XRCC5,PRDX2,HACE1,GCFC2,DEK,ERCC4,PTPN2,AKAP8,EEF1B2,CDK4,KIAA1549,PSEN2,MMS22L,COL16A1,ARF6,CD47,ZC3H8,TMEM260,SNRPD3,KIF2C,NFE2L2,DIS3,RAD21,CYP51A1,CUL7,ZFPM2,UBR4,CAPRIN2,CDKN1A,SHMT1,CEP112,LDHA,CSTF3,TCF7L2,ID4,NUTF2,CASP7,PSEN1,SRSF2,CBWD1,KIF1B,SLC38A10,MSH3,VPS13A,GNB2L1,PARP2,POLR3E,PIEZO1,PINX1,TCEB1,KIF16B,TBC1D2,TGFBR2,MYC,FDFT1,TNRC6C,Gm21596/Hmgb1,EIF3D,PIM1,RCC1,PPP3R1,PXDN,XPO1,Hmga2,CACTIN,BRIP1,PDZRN3,SMC3,SYNE2,DDX23,YWHAE,SH3BP1,PNN,SNX18,DIDO1,SLC12A7,HELLS,BUB1B,KMT2A,ARIH1,NT5C3A,GSE1,TAF1,XRCC6,RECQL4,CDCA7L,MAD1L1,NDC80,CAPN2,SSFA2,ELMO1,RPSA,RBBP4,CDKL3,RUNX1,ARID1A,DENND4B,GTF2I,DCAF4,SLC39A14,RAD50,ETV6,MLH1,RAD51,CCNA2,POLR1C,DIAPH1,FANCD2,TIMP1,STEAP2,LDB1,FOXO3,LRRC8A,LONP1,PRKCA,SLC20A1,ZNF354A,SDC1,NMRAL1,SLC12A2,TUBG1,SMAD6,ZFPL1,RPL23,HSPD1,MTHFD1,FOXM1,GIT1,FAIM,NBN,PRKCI,MAPK14,CHD9,FOXO1,RAD9A,PSMD2,MSH6,ATR,CDC34,KIF18A,CENPF,SOCS1,PLD2,ITSN1,SGK1,CDKN2C,HES1,CHAF1A,VEGFA,CXCL10,FANCB,IPMK,MXD3,THRAP3,EEFSEC,USP10,HEY2,CENPJ,TIMP2,UPF2,STAT6,CDK13,CFL1,NDRG1,PTCH1,RCBTB2,RPA1,ITPR1,PLCL2,FANCC,FAM129B,CTPS1,GEMIN2,IRF1,DOCK1,PCNA,PATZ1,PSMB2,STIP1,H2AFX,E2F1,AHCTF1,ORC5,HPRT1,LRP8,HELB,SLC44A2,CYR61,IFIT2,EPHA2,DDX51,HIST1H1C,ADAM17,ATF7,PDIA3,CTNNA3,NUP214,SETX,FNTB,VCAN,EP300,CHEK1,TRIB1,ID1,RPL35,NCOA2,ADK,RHOU,LAMP1,TOP2A,PDGFRA,CEBPA,BID,STIM1,HEXIM1,RASSF5,LPP,RXRB,POT1,RPS19,MYCN,mir-199,DCK,ACTB,HERC1,PCDH9,POLD1,STXBP6,KITLG,FADD,ABL2,PDIA6,KIF20B,MUTYH,ADAM10,ADD1,PRMT5,FEN1,NCOR2,IREB2,ZFP36L2,RPL11,CLTB,MELK,TUBB,AURKB,ROCK2,STMN1,FGFR3,SRSF1,RPS20,UBXN4,EZH2,SMPDL3B,NIPBL,RAD51C,BRCA1,PPP6R3,DLC1,CDC25A,NONO,RPL3,ULK4,FGFR1,STK11,TBP,RANBP1,TMOD3,MARS,SIPA1L1,ELF1,GSR,TUBE1,CASP2,ITPRIPL1,GNL3,NSMCE4A,PML,RPL13A,KIF11,PKNOX1,NFIX,GDNF,PICALM,CHPF,ABL1,RBBP8,SLC7A1,TNFAIP3,TAOK1,BCLAF1,PRKAG1,TBC1D10A,ROR2,SP1,PMF1/PMF1-BGLAP,MAML3,ATF6B,RBM15,BLM,ERF,E2F8,S1PR2,HDAC1,SMAD7,let-7,MAPK9,BCL3,USP1,PSIP1,XIAP,FDPS,RIPK1,PBX3,EXOC4,SATB1,ARHGAP31,PDE5A,EIF2AK2,SMARCC1,CAD,HMGCR,BCL2L11,SHMT2,LGALS1,WNT5A

Supplemental Table 7. General IPA functions for E2F1, E2F3A and E2F3B promoter targets

ChIP-seq	Category	B-H p-value	Genes
E2F3B	Immunological Disease	6.59E-09	mir-130,NPM1,RAF1,RDH10,HMMR,POLA1,PPWD1,SSBP2,KRAS,CCND1,POR,EGR2,PPRC1,SMARCB1,NEK6,ADA,TARBP2,UNG,FBXO9,ETS1,TP53,TYMS,ESPL1,YAP1,NPAT,RRM2,RANBP3,KLF13,TCF3,DDR1,RBM4,ABCA7,DCLRE1A,GART,SKP2,PLEKHG2,KAT6A,CCNF,BTG2,GAPDH,PSMD1,FRG1,XRCC5,HACE1,PTPN2,AKAP8,PRDX1,CDK4,NOTCH2,ZC3H8,PNRC1,PCNXL3,KIF2C,DIS3,NFE2L2,ATN1,EXO1,CYP51A1,FKBP3,KHDRBS1,TUBB4B,LZTS2,IPO7,ID3,BAK1,KPNB1,MTHFD1L,MSH2,CDKN1A,SLC29A2,CEP112,CSTF3,CASP7,NUTF2,CDKN2A,SRSF2,MSH3,VPS13A,POLR3E,HDAC10,PINX1,TCEB1,MYC,FDFT1,USP8,Gm21596/Hmgb1,ANXA11,RCC1,PIM1,PPP3R1,PXDN,XPO1,Hmga2,PDZRN3,ING2,POLE4,YWHAE,HDAC2,DNA2,H6PD,RAD54L,BUB1B,CDCA2,KMT2A,TXNRD1,BCL2L1,TAF1,XRCC6,RECQL4,CDCA7L,HSP90AA1,NDC80,MAD1L1,ELMO1,RUNX1,ARID1A,GTF2I,ALAS1,IQGAP1,RAD50,LSM2,ETV6,MLH1,RAD51,POLR1C,CCNA2,DIAPH1,NFAT5,TIMP1,STUB1,LDB1,FOXO3,ERBB2,LRRC8A,LONP1,PRKCA,SDC1,TUBG1,MEF2A,RPL23,G3BP1,GIT1,BIRC5,FAIM,NBN,TMEM109,PRKCI,FOXO1,RAD9A,PSMD2,MSH6,BRCA2,CDC34,ING1,MAP4K4,SOCS1,SGK1,RAN,CDKN2C,MKI67,POLB,CHAF1A,CXCL10,VEGFA,RASGRF1,MXD3,RARA,USP10,PRIM2,DNMT1,TIMP2,RND2,PABPC1,PYCRL,STAT6,TFDP1,YWHAZ,MDC1,RPA1,HMGA1,MED12,IRF1,GEMIN2,CMIP,MNT,PCNA,PATZ1,PSMB2,H2AFX,STIP1,E2F1,ORC5,HPRT1,HELB,SLC44A2,IFIT2,CYR61,EPHA2,DDX51,FYN,HIST1H1C,CUL1,NUP214,FKBP1A,CRLF2,XRCC4,EIF4EBP1,EP300,CHEK1,ID1,RPL35,RINT1,RHOU,CEBPA,PDGFRA,LAMP1,TOP2A,BID,STIM1,RASSF5,RXRB,POT1,EED,PSMB9,PMS2,SUZ12,DCK,POLE,MDM2,SLIT2,NAP1L1,F3,POLD1,STXBP6,CDK1,RRM1,FADD,PDIA6,MUM1,MUTYH,PRMT5,FEN1,NCOR2,NCAM1,STRN,FBXW7,TUBB,AURKB,ZNF91,FGFR3,STMN1,ROCK2,SCARB1,ETS2,EZH2,FASN,NIPBL,PPP6R3,BRCA1,DLC1,STX11,MCM5,COL4A1,NONO,POLE2,STK11,FGFR1,RAC1,BIRC6,RANBP1,CDC123,GSR,Cdc42,TUBE1,RHOA,CASP2,SH2B3,CYLD,PML,KIF11,CDK2,BRD2,GADD45G,TXLNA,RBBP8,ABL1,TNFAIP3,LRIG3,TAOK1,BCLAF1,KMT2C,ZMIZ1,ROR2,GTF2B,PRIM1,PMF1/PMF1-BGLAP,BLM,IPO5,RASSF1,UBR5,S1PR2,SNRPB,HAT1,HDAC1,let-7,SMAD7,MAPK9,BCL3,TCF7L1,PSIP1,XIAP,FDPS,RIPK1,EXOC4,SATB1,PDE5A,CAD,SMARCC1,HMGCR,ADAM9,SHMT2,BCL2L11,LANCL2,WNT5A,LGALS1

Supplemental Table 7. General IPA functions for E2F1, E2F3A and E2F3B promoter targets

ChIP-seq	Category	B-H p-value	Genes
E2F3B	Renal and Urological Disease	3.48E-08	CTCF,SLC6A9,SMARCD2,EIF4A2,SECISBP2,TRIM32,POR,SMARCB1,TCERG1,RANBP3,ZBTB5,TCF3,ABCA7,SP4,DCLRE1A,GART,DAXX,PDSS1,PSMD1,DDIT3,BAG6,CEBPZ,NOTCH2,PELO,ATN1,UBE3C,HIST2H3D,EP400,TUBB4B,PASK,KAT5,CSF1,CDKN2A,KIF23,NAV2,PCDH18,TROAP,SMAD3,INTS1,SMC1A,RGPD4 (includes others),E2F6,LHFPL2,POLE4,IFT74,KIAA0907,BCL2L1,AEBP2,CEP76,MCCC2,PBRM1,PIAS1,ALAS1,GPHN,SPSB3,E2F3,NFAT5,STUB1,ERBB2,SMARCD1,SOD1,BIRC5,KLF5,BRCA2,ZDHHC3,TSC22D1,SLC25A5,DDX11,CTGF,MKI67,RBL1,CD2AP,ATP1A1,CBFB,PABPC1,PIK3C2B,CENPB,DPY19L1,COQ10A,CCDC91,SH3GL1,ARHGAP5,SPOP,RNF168,RERE,CREM,DNAJC14,ARHGAP35,SGOL1,TMEM158,BRPF3,RREB1,ARHGEF7,CUL1,POLQ,CENPN,FKBP1A,BOK,HMGB2,PITRM1,ANKRD12,ATP6AP1,ATAD5,TYW1,HK2,RNPS1,TICRR,DIS3L2,IGF1R,VCL,ZCCHC6,PSMB9,POLE,PLK1,MDM2,SLIT2,SCMH1,SRXN1,F3,CDK1,RRM1,H2AFY,SBF1,CAP1,GXYLT1,UNC5B,IPPK,FBXW7,ZNF91,METAP2,YWHAQ,GSPT1,ETS2,STX11,HK1,ACSL3,TRIOBP,TRAF3IP1,POLE2,RAC1,PREX2,ALAD,NDUFAF2,GPAA1,PREP,NASP,Cdc42,COL6A3,IFT81,RHOA,SCRIB,KBTBD8,CDK5RAP2,CDK2,KDM3A,ZFAT,AGAP1,SRRT,LRIG3,KMT2C,UHRF2,GMNN,DSCR3,YLPM1,EMILIN1,RASSF1,HSPG2,LXN,UBR5,POC1B,PHLDA3,GLS,LRRK2,GUK1,TSHZ3,PIAS3,SLC25A38,ACAT1,TFB2M,USP34,CENPH,RAF1,RNF8,PCBP1,KRAS,FAM208B,CCND1,ADRB3,PKN2,SNRNP48,MPHOSPH8,CENPE,ZNF687,HIPK2,MSTO1,PIGT,ALDH7A1,TP53,TYMS,GNE,ATG5,PAPD4,YAP1,RRM2,ZC3H18,SYNJ2,OGFOD2,BTG2,TFRC,GAPDH,ZDHHC1,FRG1,PRDX2,TRIM33,AKAP8,FBXO7,ESYT1,EEF1B2,CDK4,CTDSPL,KIAA1549,PSEN2,TMEM209,CGNL1,TRIM27,ATP5J2,NFE2L2,RAD21,CYP51A1,SLC35A5,TUBGCP6,POLG,LZTS2,SLC29A1,PLA2G4A,ATP13A3,CDKN1A,MBD3,PSAP,LDHA,CASP7,KLHL17,PSEN1,DLGAP5,SRSF2,RPL22,ILF3,CCDC15,KIF1B,ATP2B1,SLC41A3,VPS13A,KLF6,TSFM,TLN1,TCEB1,TGFBR2,MYC,FDFT1,PPP3R1,AP5M1,CACTIN,DPM3,SMC3,BCAS2,CCDC18,SYNE2,MAST4,ZNF706,DIDO1,HELLS,RBFOX2,BUB1B,KMT2A,ARIH1,TAF1,TRIM39,UGP2,DUSP1,NDUFA6,SEC31B,HSP90AA1,RUNX1,ARID1A,LETMD1,TBC1D8B,RPS6KA3,DNAJC10,ATF6,RAD51,POLR1C,RPL14,LYST,AHNAK,FANCD2,WDFY3,TIMP1,FOXO3,GMFB,PRKCA,TUBG1,NMT2,ZHX3,SLK,PMP22,LTBP3,MAPK14,FOXO1,CHD9,PSMD2,ZNF622,SMG7,ATR,CDC34,CENPF,GTF3C2,TOR1A,CDKN2C,GSTZ1,VEGFA,THRAP3,BAG1,SEC24A,MAP1S,IRS2,TIMP2,KMT2B,OTUD4,MITF,PTCH1,ITPR1,IRF1,POM121/POM121C,PCNA,BSG,BHLHE40,IRS1,ZNF672,E2F1,TMX1,GNB2,MSH5,MAPK7,HELB,CYR61,PHLPP1,HIST1H1C,ADAM17,CTC1,ATF7,PKD2,XPOT,NUP214,SGMS1,EP300,XYLB,TRIB1,PDGFRA,CEBPA,TOP2A,DAP3,PRKCE,BID,MAP1LC3A,RASSF5,KHSRP,PLAT,MYCN,mir-199,C10orf2,TBX3,ACTB,ATXN2L,SIN3A,FADD,SLC30A9,KIF15,CHMP6,NUP153,MCM2,SREBF2,KIF20B,NOP2,NCOR2,MAFB,ZFP36L2,SMARCAD1,NAGK,PALLD,MAPK1,MELK,TUBB,AURKB,LATS2,FGFR3,PTK2,STMN1,ASXL2,EZH2,ERLIN2,ITGAV,NEO1,SIAH2,NIPBL,HTRA2,PUF60,RAD51C,BRCA1,DLC1,AIM1,SSNA1,NONO,NUP155,LMLN,STK11,FGFR1,TBP,SSRP1,MED14,SIPA1L1,WWP2,PKD1,TUBE1,CASP2,RRP7A,VDAC1,KIF11,PKM,ABL1,BCLAF1,ACOT7,C12orf45,TCF12,EPHB6,NTNG1,GEMIN4,RRN3,BLM,MAP2K7,C2CD3,SMAD7,NFKBIZ,PSIP1,XIAP,FDPS,PPP6R1,RIPK1,LPAR1,SMARCC1,EIF2AK2,VGF,HMGCR,BCL2L11
E2F3B	Tumor Morphology	4.06E-08	SOCS1,NPM1,RAF1,TGFBR1,F2R,PRKAB1,SGK1,HMMR,TLE1,KRAS,MKI67,HES1,CCND1,VEGFA,FHL2,BAG1,RARA,USP10,TXN,HIPK2,AHCY,TIMP2,TP53,ETS1,NDRG1,MITF,PTCH1,HBEGF,TFAP4,ITPR1,IRF1,SKP2,ATF2,DAXX,DVL2,BSG,IRS1,BTG2,CREM,E2F1,EYA3,MAPK7,CYR61,EPHA2,PTPRA,XRCC5,PHLPP1,PIM3,SNAI2,DDIT3,PTPN13,PLAGL1,CUL1,PTN,CDK4,BOK,TAX1BP3,VCAN,CDH11,EIF4EBP1,CHEK1,EP300,KISS1R,ID1,TRIB1,YY1,CD47,DGCR8,PDGFRA,IGF1R,PRKCE,BID,NFE2L2,PLAT,AIFM1,ATP7B,MYCN,CDC6,LZTS2,GREM1,PLK1,MDM2,ACLY,ID3,F3,CDK1,FADD,KITLG,MAD2L1,CCNE1,NR4A2,MCM2,CSF1,SPRY2,CDKN1A,ADAM10,EIF2B1,HOXB9,NCOR2,LDHA,TCF7L2,CDKN2A,EEF1A1,PHLDA1,SOCS3,TFG,MAPK1,SMAD3,GNB2L1,DICER1,FGFR3,STMN1,SOX2,MYC,TGFBR2,SRSF1,PIM1,TTBK2,EZH2,FASN,ITGAV,SUGT1,MYBL2,BRCA1,HDAC2,FGFR1,RAC1,TUSC3,BUB1B,KMT2A,SLC3A2,PREP,SRSF3,BCL2L1,CBX1,DUSP1,CASP2,RHOA,NUAK1,ACTN4,PML,JAG1,CDK2,RUNX1,BRD2,LITAF,ZBTB7A,GDNF,TXLNA,KLF10,PDE4A,ABL1,NGF,RAD50,MIER1,HDGF,NELFE,RAD51,SIX1,SP1,TIMP1,FOXO3,ERBB2,PRKCA,NDUFAF3,RASSF1,HSPG2,GLS,HDAC1,MAPK9,LRRK2,USP1,SOD1,FOXM1,BIRC5,XIAP,MLLT1,RCAN1,ENO1,PRKCI,MAPK14,LPAR1,FOXO1,ZNF622,TSC22D1,EIF2AK2,HMGCR,EFEMP2,BCL2L11,WNT5A,LGALS1

Supplemental Table 7. General IPA functions for E2F1, E2F3A and E2F3B promoter targets

ChIP-seq	Category	B-H p-value	Genes
E2F3B	Cardiovascular System Development and Function	6.89E-08	mir-130,RAF1,CTCF,MYH9,TGFBR1,PRKAB1,PRKAB2,RDH10,Ap2b1,TAB2,TMEM38A,KRAS,ATP2A2,CCND1,POR,FHL2,GATAD2A,FBLN1,ADA,ADORA2B,KLF1,HIPK2,MGAT1,TP53,ETS1,CCNE2,PAM,YAP1,PIGF,CRKL,TMEM67,DDR1,SKP2,ATF2,ATE1,CNTRL,DVL2,CCNF,KAT6A,ALCAM,KIAA1429,TFRC,Meis1,ECT2,PRDX2,FLNB,PIM3,NRG2,DDIT3,SNX17,PRDX1,GNA11,PDS5B,CDK4,PPIA,PSEN2,NOTCH2,TIPARP,DAB2,NFE2L2,CYP51A1,EP400,GAS1,CUL7,GREM1,ID3,IGF2R,BAK1,PLA2G4A,CCNE1,ZFPM2,CSF1,CDKN1A,PSAP,SEMA3C,LDHA,MAP3K3,SGCD,TFB1M,TCF7L2,CASP7,PSEN1,CDKN2A,SOCS3,SEPT9,LHX2,RASA3,SMAD3,KLF6,ZFPM1,RPGRIP1L,IFT140,MYC,TGFBR2,LEMD3,USP8,Gm21596/Hmgb1,MAP2K2,PIM1,PPP3R1,MATR3,GCLM,PPP1R15B,TAB1,PGK1,UBE4B,HDAC2,YWHAE,IFT74,DIDO1,RDX,MAPKAPK5,RAD54L,POFUT1,PTPRM,KMT2A,PFKM,BCL2L1,TFAM,ATP5B,DUSP1,TXN2,FZD5,CAPN2,ACTN4,RPSA,RHBDF1,FOXP4,RUNX1,PBRM1,TFEB,RND1,ARID1A,GTF2I,SMAD5,CLIC4,PDCD10,ETV6,CCNA2,NFAT5,TIMP1,BMPR1A,LDB1,ZNF24,FOXO3,ERBB2,RAD23B,PRDM6,LASP1,WDR1,PRKCA,VAV2,CAPZB,ADAM15,AP1S2,SMAD6,MEF2A,HSPD1,SOD1,SNX27,NFATC4,MTHFD1,FOXM1,BIRC5,MORF4L1,RCAN1,PSKH1,MAPK14,FOXO1,EHD4,TFCP2,E2F7,KLF5,BRPF1,WNK1,EFEMP2,NR6A1,CTGF,F2R,UBR2,CDKN2C,HES1,RICTOR,ARNT,CXCL10,VEGFA,CD2AP,THRAP3,RARA,ZBTB14,MAP1S,TDP2,CBFB,HEY2,HIPK1,FRS2,TIMP2,PIK3C2B,NDRG1,CSRP2,FOXH1,HIRA,PTCH1,YWHAZ,PLEC,HBEGF,HMGA1,MED12,DOCK1,PATZ1,BSG,GAB1,YARS,AHI1,H2AFX,IRS1,STIP1,E2F1,HSPB11,LRP8,MAPK7,CYR61,PRICKLE1,EPHA2,B9D1,HIST1H1C,VASH2,ADAM17,SNAI2,ATF7,LEMD2,PKD2,PTN,CTNNA3,FKBP1A,HMGB2,FZD1,VCAN,SRSF10,EP300,WTAP,COL5A1,ID1,EFNB2,YY1,PRRX1,DGCR8,IGF1R,PDGFRA,PRKCE,STIM1,MCPH1,VCL,HEXIM1,RXRB,NCKIPSD,PLOD3,PLAT,LUZP1,MYCN,mir-199,TBX3,AGO2,DLX1,MDM2,SLIT2,F3,KITLG,FADD,ABL2,LIMS1,SPRY2,ADAM10,ADD1,RBPJ,GPR180,NCOR2,IREB2,DYRK1A,NAB2,CAV2,MAPK1,DIAPH3,Wasl,UNC5B,FBXW7,DICER1,LATS2,METAP2,FGFR3,ROCK2,PTK2,CAMK2D,SCARB1,RORA,ASXL2,ITGAV,Map3k7,NIPBL,SIAH2,HTRA2,BRCA1,DLC1,SOX4,STIL,COL4A1,DTNBP1,STK11,FGFR1,BIRC6,RAC1,LMNA,RHOJ,SMARCD3,Cdc42,PKD1,RHOA,INTU,CYLD,MTDH,PML,JAG1,Paxip1,CDK2,TEAD4,SPRED1,PKNOX1,C5orf42,GDNF,PDGFA,PKM,MARK2,ABL1,TNFAIP3,SLC7A1,ING4,NGF,BCLAF1,BCAR1,PRKAG1,ZMIZ1,TNFRSF12A,ROR2,GLI3,MAML3,RBM15,NCL,MAPKAPK2,BLM,E2F8,RASSF1,NACA,HSPG2,MAP2K7,S1PR2,TRA2B,Nedd4,C2CD3,MTMR14,let-7,SMAD7,MAPK9,TCF7L1,EDF1,XIAP,B4GALT1,PLEKHG5,ADAM9,LGALS1,WNT5A
E2F3B	Organ Development	6.89E-08	TGFBR1,RDH10,Ap2b1,TAB2,KRAS,SLC35C1,ATP2A2,CCND1,POR,FBLN1,ADA,TP53,YAP1,CRKL,MAN1A2,TMEM67,ATF2,ATE1,CNTRL,DVL2,KAT6A,CELSR3,SNX17,BAG6,GNA11,CDK4,PSEN2,NOTCH2,NFE2L2,CYP51A1,GAS1,GREM1,ID3,IGF2R,ZFPM2,CDKN1A,SEMA3C,CASP7,PSEN1,SMAD3,ZFPM1,RPGRIP1L,ATXN1L,CEBPG,IFT140,TGFBR2,MYC,SOX2,USP8,Gm21596/Hmgb1,MAP2K2,PPP3R1,MAPK3,MATR3,TAB1,TOP3B,HDAC2,IFT74,POFUT1,TFAM,DUSP1,TXN2,LMNB2,SUV420H1,FOXP4,PBRM1,ARID1A,SMAD5,CCNA2,NFAT5,BMPR1A,LDB1,FOXO3,ERBB2,PRKCA,WDR1,SMAD6,NFATC4,FOXM1,MTHFD1,GIT1,MORF4L1,MAPK14,PSKH1,FOXO1,CTGF,UBR2,HES1,POLB,CXCL10,VEGFA,RARA,ZBTB14,HEY2,FRS2,STAT6,FOXH1,HIRA,PTCH1,PLEC,HBEGF,MED12,GAB1,AHI1,STIP1,HSPB11,MAPK7,CYR61,PRICKLE1,ADAM17,ATF7,PKD2,LEMD2,FKBP1A,FZD1,VCAN,CDH11,EP300,COL5A1,ID1,NCOA2,CREB1,PDGFRA,CEBPA,BID,HEXIM1,VCL,RXRB,NCKIPSD,PLOD3,LUZP1,MYCN,mir-199,TBX3,RQCD1,MDM2,KITLG,FADD,LIMS1,SPRY2,FEN1,RBPJ,NCOR2,DYRK1A,MAPK1,CAV2,DIAPH3,FBXW7,DICER1,LMNB1,PTK2,FGFR3,CAMK2D,ASXL2,Map3k7,NIPBL,BRCA1,DLC1,SOX4,STIL,DTNBP1,FGFR1,SMARCD3,Cdc42,ARRB2,PKD1,TIMELESS,RHOA,LOXL1,PTPRS,INTU,CYLD,JAG1,Paxip1,CDK2,RPL13A,TMTC3,C5orf42,PDGFA,ABL1,BCLAF1,BCAR1,ZMIZ1,FUT8,ROR2,Cux1,GLI3,SP1,MAML3,RBM15,NACA,RASSF1,HSPG2,MAP2K7,S1PR2,HAT1,C2CD3,SMAD7,MAPK9,LRRK2,TSHZ3,B4GALT1,NFIB,WNT5A
E2F3B	Hereditary Disorder	7.22E-08	DDHD2,TGFBR1,MYH9,GARS,CCND1,VEGFA,FANCB,EGR2,TARDBP,SMARCB1,DNMT1,TP53,CCNE2,CFL1,NDRG1,TFDP1,CSRP2,MITF,PTCH1,TBK1,SPG7,FANCC,AP5Z1,PCNA,YARS,E2F1,TMEM43,FANCA,INF2,ERCC4,GALC,FBXO7,DDIT3,CDK4,FKBP1A,SETX,EIF4G1,TAX1BP3,EIF4EBP1,COL5A1,DIS3L2,SOS1,DAB2,AIFM1,SLC12A6,SDHA,PMS2,C10orf2,POLG,HNRNPDL,ACLY,CCNE1,IGHMBP2,NR4A2,MSH2,SBF1,MUTYH,CAP1,PSAP,PSEN1,CDKN2A,PALLD,CAV2,TFG,SEPT9,KIF1B,DIAPH3,PARP2,TDP1,TGFBR2,ERLIN2,MTMR2,HTRA2,TFDP2,BRCA1,RAD51C,BRIP1,SEC63,HK1,SYNE2,COL4A1,SBF2,STK11,MARS2,LMNA,TXNRD1,DYNC1H1,BCL2L1,PALB2,FLOT2,COL6A3,LOXL1,CYLD,JAG1,KDELR2,RUNX1,LITAF,SPRED1,GDNF,CCNC,BARD1,RBBP8,NGF,PDCD10,RAD50,MLH1,RAD51,AHNAK,FANCD2,BMPR1A,BLM,EMILIN1,RASSF1,PRKCA,BICD2,SPG21,MTMR14,LRRK2,HSPD1,SOD1,ALS2,ATL3,FANCL,NBN,LTBP3,PMP22,CNN3,PLEKHG5,MSH6,BRCA2,DCTN1,ATR,WNK1

Supplemental Table 7. General IPA functions for E2F1, E2F3A and E2F3B promoter targets

ChIP-seq	Category	B-H p-value	Genes
E2F3B	Cellular Response to Therapeutics	1.79E-07	CDKN2A,MCM8,PARP2,KRAS,POLB,MXD3,CRADD,MTF1,MYBL2,GCLM,HIPK2,BRCA1,HIPK1,UNG,TP53,STAT6,RAD54L,HELLS,FANCC,TERF2,PCNA,XRCC6,SLC25A10,SUV420H1,Paxip1,XRCC5,PRDX2,HIST1H1C,PRDX1,HMGN1,RCHY1,XRCC4,RAD9B,RAD50,STIM2,RAD51,HINT1,HUS1,MCPH1,STIM1,ERBB2,MCM9,NFE2L2,PPIF,XIAP,BAK1,NBN,MSH2,CDKN1A,BRCA2,FEN1,ING1,EIF2AK2,POLH
E2F3B	Nervous System Development and Function	2.85E-07	RAF1,PLD2,MYH9,SGK1,CDKN2C,KRAS,ELAVL4,RBL1,RAPH1,CCND1,VEGFA,RUSC1,KLF7,RASGRF1,MXD3,BAG1,BAIAP2,TARDBP,RAB17,PLXNB2,TXN,FRS2,RND2,GET4,TP53,Irx5,CFL1,PTCH1,CSNK1D,YWHAZ,GRK5,GEMIN2,DDR1,ARHGAP5,DOCK1,DVL2,GAB1,E2F1,PRKACA,RAB11A,MAPK7,ELMO2,EPHA2,PTPRA,ADAM17,MAP2,PLXNA3,PDIA3,PLAGL1,ARHGEF7,PTN,CDK4,VCAN,EIF4EBP1,EP300,GPR3,EFNB2,ID1,CD47,ARF6,TCOF1,CREB1,IGF1R,DAGLB,STIM1,VCL,FKBP5,PLAT,MYCN,SLIT2,MAFK,FRK,ID3,CDK1,KITLG,NDE1,CSF1,SPRY2,CDKN1A,ADAM10,PSAP,PAFAH1B1,ID4,DYRK1A,NCAM1,MAOA,PSEN1,FZR1,KIF23,SOCS3,PALLD,NCDN,MPRIP,MAPK1,SEPT9,VTI1A,POLR3E,RPGRIP1L,TGFBR2,ROCK2,SOX2,FGFR3,Gm21596/Hmgb1,MAPK3,ARHGEF25,MYO10,TBC1D24,UBE4B,FGFR1,RAC1,SNX3,PTPRM,SMARCD3,Cdc42,CORO1B,RHOA,ETV4,PTPRS,DIXDC1,EXTL3,HDGFRP3,JAG1,CDK2,EEA1,RND1,NFIX,GDNF,DPYSL3,MARK2,ABL1,PDE4A,CSRP1,GPHN,IQGAP1,NGF,E2F3,TNFRSF12A,SET,SIX1,GLI3,STUB1,BMPR1A,MANF,USP47,MAML3,ERBB2,PRKCA,S1PR2,Nedd4,SLC12A2,LRRK2,MAPK9,SOD1,NFATC4,ALS2,NBN,FAIM,EXOC4,LPAR1,FOXO1,SLC25A5,VGF,HMGCR,WNT5A,LGALS1
E2F3B	Renal and Urological System Development and Function	3.56E-07	CDKN2A,DLGAP5,SOCS3,CTCF,CAV2,UNC5B,KLF6,SFPQ,KRAS,FGFR3,HSPA4,SUMO1,CSTF2,DLC1,ULK2,TP53,ATG5,TFDP1,YAP1,PNN,PTCH1,LMNA,ZBTB5,PTP4A1,KMT2A,SKP2,PKD1,RHOA,E2F1,CHKA,HSP90AA1,VDAC1,TEAD4,TTLL4,PIAS1,MED28,Tpm2,EIF4EBP1,NOP58,STEAP2,FOXO3,CEBPA,ERBB2,NCL,PEMT,RASSF1,OXTR,STT3B,POLG,PLK1,HSPD1,BIRC5,AFF1,PMP22,SPDYA,MAPK14,CSF1,KLF5,CDKN1A,WISP1
E2F3B	Molecular Transport	4.70E-07	CENPF,CDKN2A,NPM1,ASPSCR1,MYH9,EPS15,YWHAH,AHCYL1,ARF1,KIF1B,SNX8,RAB2A,RAN,NME2,NUP58,KRAS,KPNA1,TOMM70A,IFT27,CEP57,PEX16,EGR2,KIF13A,SUMO1,XPO1,TP53,PHIP,NUP155,CFL1,TNPO1,CLTC,RAB10,CSNK1D,RAB8A,SNX3,ADAR,WWP2,HSPA8,TNPO2,ERP29,PKD1,RHOA,COX18,RAB11A,AGAP3,PML,ECT2,PRICKLE1,XPO6,KDELR2,PICALM,PDIA3,MCM3AP,FAM53A,NUP214,PSEN2,DNAJA1,TGFBRAP1,IPO9,ARF6,NUP54,Pgap2,GLI3,HLA-DMA,STEAP2,RANGAP1,IPO5,RPAIN,HSPG2,SCFD1,VPS18,VPS16,IFT46,CHP1,TOB1,BCL3,IPO7,SOD1,SNX27,NXT1,IGF2R,DNM1,KPNB1,MAPK14,EXOC4,NDE1,RAB12,CAP1,POLA2,DCTN1,ING1,SCAMP3,Arf2,NUTF2,AP1G1,PSEN1
E2F3B	Protein Trafficking	4.70E-07	CENPF,CDKN2A,NPM1,ASPSCR1,MYH9,EPS15,YWHAH,AHCYL1,ARF1,KIF1B,SNX8,RAB2A,RAN,NME2,NUP58,KRAS,KPNA1,TOMM70A,IFT27,CEP57,PEX16,EGR2,KIF13A,SUMO1,XPO1,TP53,PHIP,NUP155,CFL1,TNPO1,CLTC,RAB10,CSNK1D,RAB8A,SNX3,ADAR,WWP2,HSPA8,TNPO2,ERP29,PKD1,RHOA,COX18,RAB11A,AGAP3,PML,ECT2,PRICKLE1,XPO6,KDELR2,PICALM,PDIA3,MCM3AP,FAM53A,NUP214,PSEN2,DNAJA1,TGFBRAP1,IPO9,ARF6,NUP54,Pgap2,GLI3,HLA-DMA,STEAP2,RANGAP1,IPO5,RPAIN,HSPG2,SCFD1,VPS18,VPS16,IFT46,CHP1,TOB1,BCL3,IPO7,SOD1,SNX27,NXT1,IGF2R,DNM1,KPNB1,MAPK14,EXOC4,NDE1,RAB12,CAP1,POLA2,DCTN1,ING1,SCAMP3,Arf2,NUTF2,AP1G1,PSEN1
E2F3B	Hematological System Development and Function	3.40E-06	NPM1,RAF1,TGFBR1,CTCF,KRAS,CCND1,VEGFA,RARA,BAIAP2,ADA,ATF4,CBFB,KLF1,TIMP2,TP53,PAPD4,EEF2,FANCC,HMGA1,KLF13,TCF3,ADAR,IRF1,DOCK1,PATZ1,BSG,KAT6A,E2F1,BTG2,TFRC,SRSF4,Meis1,SAC3D1,PRDX2,FYN,DEK,PIM3,PTPN2,PRDX1,ARHGEF7,CDK4,CEBPD,PSEN2,HMGB2,XRCC4,MAFG,ID1,CD47,YY1,HUS1,PDGFRA,CEBPA,TOP2A,PRKCE,NFE2L2,RPS19,DCK,MDM2,MAFK,IGF2R,SIN3A,KITLG,FADD,SENP1,AGPAT5,ZFPM2,MSH2,CSF1,CDKN1A,ADD1,GABPA,FEN1,MAFB,IREB2,ZFP36L2,PSEN1,FZR1,CDKN2A,SOCS3,PALLD,LHX2,MAPK1,SMAD3,DIAPH3,Wasl,KLF6,FBXW7,KXD1,ZFPM1,ABCC10,TGFBR2,MYC,TNRC6C,HIST1H4A,HIST1H4C,SCARB1,PIM1,MAPK3,HIST1H4I,MYBL2,HIST1H4J,PPP1R15B,STX11,ESCO2,SOX4,FSTL3,STK11,DIDO1,BIRC6,RAC1,TMOD3,POFUT1,KCNAB2,KMT2A,PFKM,BCL2L1,Cdc42,SH2B3,MAD1L1,CYLD,TMPO,PML,JAG1,CDK2,UBE2I,RUNX1,ZFAT,PICALM,HIST2H4B,ABL1,SLC7A1,SMAD5,PRKAG1,ZBTB24,ETV6,TNFRSF12A,SP1,GLI3,TIMP1,LDB1,FOXO3,SIPA1,RBM15,BLM,LRRC8A,LONP1,PRKCA,SLC20A1,SOD1,DOCK7,RRS1,SLC7A6OS,BIRC5,PRMT1,C19orf68,MLLT1,MAPK14,B4GALT1,SATB1,EIF2AK2,UBC

Supplemental Table 7. General IPA functions for E2F1, E2F3A and E2F3B promoter targets

ChIP-seq	Category	B-H p-value	Genes
E2F3B	Reproductive System Development and Function	4.49E-06	RAF1,RNF8,TGFBR1,RDH10,Ubb,CCND1,ADA,ATF4,TARBP2,TP53,CCNE2,YAP1,DDR1,SKP2,CCNF,RAD18,FADS2,FANCA,PRDX4,BAG6,USF2,CDK4,CEBPD,KISS1R,NOTCH2,TRIM27,TIPARP,ALMS1,HEXB,ATP7B,CUL7,HSPA2,BAK1,ZFPM2,MSH2,CSF1,PLEKHA1,ID4,CDKN2A,SOCS3,SFMBT1,KLF6,TGFBR2,SMAP2,SOX2,HSPA4,CEP57,Hmga2,JUND,CEP131,MTMR2,CHTF18,GPX4,ING2,FSTL3,HELLS,NDC1,BCL2L1,FZD5,PBRM1,PEBP1,TFEB,SMAD5,MLH1,FANCD2,TIMP1,LDB1,FOXO3,ERBB2,MCM9,ARL4A,LRRC8A,RAD23B,SLC12A2,ALKBH5,PSMC3IP,SOD1,FANCL,NBN,MAPK14,EHD4,E2F7,BRCA2,BRPF1,KIF18A,SOCS1,NR6A1,CTGF,F2R,RTCB,UBR2,CDKN2C,DDX20,KPNA1,ARNT,VEGFA,DYNLL1,RARA,ZFX,IRS2,TTLL5,KMT2B,STAT6,HIRA,PTCH1,HMGA1,FANCC,ARHGAP5,PCNA,PATZ1,BSG,GAB1,H2AFX,IRS1,CREM,MSH5,LRP8,FYN,SNAI2,PKD2,PTN,HMGB2,DNAJA1,GPR3,ID1,YY1,NCOA2,USP42,CREB1,CEBPA,IGF1R,PDGFRA,LAMP1,HEXIM1,RXRB,OXTR,ADRM1,TBX3,TIAL1,KATNAL1,SLIT2,SCMH1,YBX2,KITLG,NUP153,SBF1,TBPL1,HOXB9,RBPJ,PAFAH1B1,WDR19,WDR48,MCM8,MAPK1,MNS1,DICER1,PTK2,SCARB1,EZH2,FASN,ITGAV,NIPBL,Dazap1,RAD51C,BRCA1,CDC25A,STK11,BIRC6,CCDC155,RANBP1,SIX5,HERC2,GSR,TOB2,PKD1,SCRIB,CDK2,KDM3A,PAFAH1B2,BRD2,GDNF,PDGFA,GADD45G,ABL1,NGF,PRKAG1,Ppp1cc,SP1,GLI3,CSTF2T,CIT,TCP1,ERF,CTDNEP1,E2F8,PANK2,let-7,XIAP,B4GALT1,VGF,BCL2L11,WNT5A
E2F3B	Organ Morphology	7.31E-06	NR6A1,F2R,UBR2,TMEM38A,CDKN2C,KRAS,CCND1,ATP2A2,VEGFA,POR,CD2AP,RARA,MAP1S,HEY2,TP53,Irx5,CSRP2,FOXH1,CRKL,PTCH1,HIRA,PLEC,HBEGF,ITPR1,HMGA1,ATF2,Marcks,ARHGAP5,ATE1,DOCK1,PEX2,DVL2,PATZ1,AHI1,FSCN1,KAT6A,E2F1,BTG2,LRP8,MAPK7,FYN,HIST1H1C,ADAM17,MAP2,CTNNA3,PDS5B,CDK4,FKBP1A,PSEN2,SRSF10,EP300,ID1,EFNB2,IGF1R,MCPH1,VCL,HEXIM1,RXRB,CYP51A1,AIFM1,SLC12A6,MYCN,KHDRBS1,AGO2,ID3,IGF2R,F3,BAK1,FADD,PLA2G4A,ZFPM2,ABL2,NDE1,CDKN1A,ADAM10,RBPJ,NCOR2,PAFAH1B1,TFB1M,SGCD,CASP7,NCAM1,DYRK1A,PSEN1,VTI1A,LHX2,MAPK1,KIF1B,Wasl,RPGRIP1L,DICER1,LATS2,LMNB1,MYC,TGFBR2,PTK2,SERP1,SCARB1,PPP3R1,ITGAV,HTRA2,FBXO45,TAB1,SOX4,IGFBP6,UBE4B,HDAC2,YWHAE,FGFR1,LMNA,WASF1,POFUT1,EIF4E2,PFKM,BCL2L1,PTPRS,LMNB2,CAPN2,JAG1,CDK2,RHBDF1,FOXP4,GDNF,PDGFA,ABL1,E2F3,PDCD10,BCAR1,ZMIZ1,ETV6,NFAT5,GLI3,BMPR1A,LDB1,FOXO3,MAML3,ERBB2,PRDM6,LASP1,PRKCA,VAV2,HSPG2,CAPZB,ADAM15,MTMR14,SMAD7,MEF2A,MAPK9,NFATC4,SNX27,TCF7L1,FOXM1,MORF4L1,XIAP,RCAN1,PLEKHG5,ADAM9
E2F3B	Hematopoiesis	8.64E-06	NPM1,RAF1,TGFBR1,CTCF,KRAS,CCND1,VEGFA,RARA,BAIAP2,ADA,ATF4,CBFB,KLF1,TP53,PAPD4,EEF2,FANCC,HMGA1,KLF13,TCF3,ADAR,IRF1,DOCK1,PATZ1,BSG,KAT6A,E2F1,BTG2,TFRC,SRSF4,Meis1,SAC3D1,PRDX2,FYN,DEK,PIM3,PTPN2,PRDX1,ARHGEF7,CDK4,CEBPD,PSEN2,HMGB2,XRCC4,MAFG,ID1,CD47,YY1,HUS1,PDGFRA,CEBPA,TOP2A,PRKCE,NFE2L2,RPS19,DCK,MDM2,MAFK,IGF2R,SIN3A,KITLG,FADD,SENP1,AGPAT5,ZFPM2,MSH2,CSF1,CDKN1A,ADD1,GABPA,FEN1,MAFB,IREB2,ZFP36L2,PSEN1,FZR1,CDKN2A,SOCS3,PALLD,LHX2,MAPK1,SMAD3,DIAPH3,KLF6,FBXW7,ZFPM1,ABCC10,TGFBR2,MYC,TNRC6C,HIST1H4A,HIST1H4C,SCARB1,PIM1,MAPK3,HIST1H4I,MYBL2,HIST1H4J,PPP1R15B,STX11,ESCO2,SOX4,FSTL3,STK11,DIDO1,BIRC6,RAC1,TMOD3,POFUT1,KCNAB2,KMT2A,PFKM,BCL2L1,Cdc42,SH2B3,MAD1L1,TMPO,PML,JAG1,CDK2,UBE2I,RUNX1,ZFAT,PICALM,HIST2H4B,ABL1,SLC7A1,SMAD5,PRKAG1,ZBTB24,ETV6,TNFRSF12A,SP1,GLI3,TIMP1,LDB1,SIPA1,FOXO3,RBM15,LRRC8A,LONP1,PRKCA,SLC20A1,SOD1,DOCK7,RRS1,SLC7A6OS,BIRC5,PRMT1,C19orf68,MLLT1,MAPK14,B4GALT1,SATB1,EIF2AK2,UBC
E2F3B	Respiratory System Development and Function	1.26E-05	CTGF,TGFBR1,RDH10,KRAS,HES1,SLC35C1,CCND1,POLB,VEGFA,RARA,FBLN1,ADA,HEY2,FRS2,STAT6,PTCH1,HBEGF,MAN1A2,ATF2,HSPB11,CELSR3,NOL7,ADAM17,BAG6,PSEN2,CDH11,EP300,ID1,NCOA2,CREB1,CEBPA,PDGFRA,BID,NFE2L2,PLOD3,MYCN,GAS1,RQCD1,GREM1,IGF2R,ZFPM2,SPRY2,CDKN1A,FEN1,PSEN1,LHX2,MAPK1,CAV2,FBXW7,RPGRIP1L,DICER1,ATXN1L,LMNB1,CEBPG,TGFBR2,SOX2,FGFR3,Gm21596/Hmgb1,MAP2K2,PPP3R1,WDPCP,MAPK3,TAB1,TOP3B,SOX4,FGFR1,ARRB2,TIMELESS,PKD1,DUSP1,LOXL1,PTPRS,LMNB2,CYLD,SUV420H1,RPL13A,TMTC3,PDGFA,BCLAF1,FUT8,ROR2,Cux1,SIX1,SP1,GLI3,BMPR1A,HAT1,LRRK2,MAPK9,FOXM1,GIT1,MORF4L1,TSHZ3,MAPK14,B4GALT1,FOXO1,NFIB,WNT5A
E2F3B	Cell Signaling	1.58E-05	RAF1,TGFBR1,MAPK1,SGK1,Wasl,SLF2,FNIP2,HES1,RICTOR,PBK,CHAF1A,TGFBR2,VEGFA,SCO2,ZW10,CD2AP,CAMK2D,NUP93,TTBK2,SUMO1,MAPK3,NEK6,VAMP3,DARS,HIPK2,HK1,TP53,NDUFAF5,HCFC1,TRAF3IP1,SLC2A1,CSNK1G2,MITF,CSNK1D,RDX,NUP107,TBK1,TFAP4,HMGA1,FANCC,NDC1,KMT2A,EPRS,DOCK1,TAF1,PKD1,NCLN,PRKACA,COX18,AHCTF1,CLSPN,MAPK7,PML,CDK2,FANCA,MORC3,CAPZA1,PICALM,PSEN2,NGF,SF3B3,EIF4EBP1,TRIM27,HLA-DMA,CHAF1B,GMNN,PRKCE,NUP205,STX4,PDK1,MAPKAPK2,SLC7A6,PRKCA,NDUFAF3,AIFM1,KPNA3,CAPZB,LRRK2,PLK1,MDM2,TUBGCP2,CDK1,FAF1,SPIDR,MAPK14,NUP153,ADD1,ATR,MAP4K4,DYRK1A,NCAM1

Supplemental Table 7. General IPA functions for E2F1, E2F3A and E2F3B promoter targets

ChIP-seq	Category	B-H p-value	Genes
E2F3B	Hair and Skin Development and Function	1.96E-05	NPM1,RAF1,CTCF,TAB2,KRAS,CCND1,POLB,BOP1,SUMO1,CSTF2,CBFB,MGAT1,TP53,TFDP1,YAP1,CRKL,PTCH1,TBK1,ZBTB5,PTP4A1,ATF2,ATE1,KAT6A,FSCN1,E2F1,CHKA,TFRC,MAPK7,CYR61,PTN,PDS5B,CDK4,FKBP1A,MED28,EIF4EBP1,CREB1,IGF1R,CEBPA,DAB2,PEMT,OXTR,STT3B,POLG,PLK1,MDM2,F3,ZFPM2,SPDYA,ABL2,CDKN1A,ZFP36L2,ID4,CDKN2A,SOCS3,DLGAP5,LHX2,SMAD3,UNC5B,KLF6,FBXW7,ZFPM1,PINX1,LATS2,FGFR3,TGFBR2,MYC,HSPA4,EZH2,ITGAV,FBXO45,DLC1,PPP1R15B,FGFR1,PNN,RAC1,BIRC6,KMT2A,PKD1,TRIM39,RHOA,HSP90AA1,VDAC1,CDK2,TEAD4,PDCD10,IGF2BP1,ETV6,ZMIZ1,SP1,FOXO3,ERBB2,BLM,PRDM6,RASSF1,SMAD7,MAPK9,BIRC5,MORF4L1,AFF1,GNAI2,PRKCI,MAPK14,BRCA2,WNT5A
E2F3B	Endocrine System Disorders	6.04E-05	TPD52L2,CTCF,TGFBR1,PRKAB1,CCNB2,EIF4A2,POR,FBL,HCFC1,GART,DCLRE1A,ALCAM,CPOX,ECT2,FANCA,CPE,SNX17,BAG6,CEBPZ,SYNM,RABL6,NOTCH2,TIPARP,SLC12A6,EP400,TUBB4B,PASK,IGF2R,CDS2,MSH2,MAZ,CDKN2A,NAV2,RNF7,DEPDC5,ZDHHC14,SMC1A,OSBPL1A,POLE4,HDAC2,POLR1B,RDX,PHRF1,TXNRD1,OSBPL8,CAND1,BCL2L1,GINS1,RAI1,PBRM1,ZC3H7B,KIAA0101,BARD1,RNASEH2B,E2F3,CLIC4,MARVELD1,PHLDB2,TARBP1,NFAT5,ERBB2,LASP1,RACGAP1,MED26,BIRC5,ALS2,FANCL,ZDHHC3,BRCA2,RAP2B,ASPSCR1,CTGF,F2R,DSTN,FAM20C,ZNF436,MKI67,FNDC3B,DDX20,HIST1H2AB,MGAT4B,TDP2,SLC39A13,PRIM2,DNMT1,PYCRL,PIK3C2B,TTC21A,PTPRG,TFDP1,MDC1,HBEGF,HMGA1,MED12,SPOP,SH3GL1,MYO9A,NCLN,ARHGAP35,HAUS6,TFIP11,PLAGL1,POLQ,EIF4G1,DNAJA1,TYW1,EIF4EBP1,STOM,SCAF4,KAT2B,RINT1,IGF1R,NUP205,CEP152,BLMH,ELL,POLE,MDM2,SLIT2,F3,CDK1,RRM1,ZNF546,REV1,H2AFY,TRERF1,CLUH,NCAM1,FARP1,VPRBP,FBXW7,TIGD3,DICER1,TBC1D4,ZNF318,STAG1,DZIP3,ETS2,PGP,ABLIM2,PANK4,HK1,COL4A1,POLE2,MAT2B,HERC2,PALB2,COL6A3,CTDP1,LOXL1,SCRIB,HDGFRP3,SBNO2,CDK2,TMTC3,KMT2C,TRIM24,PRIM1,ZNF280B,GTPBP4,MAPKAPK2,YLPM1,UBR5,TRA2B,LRRK2,DOCK7,TSHZ3,CIART,Sf1,USP34,HIST1H2AM,NIPA2,MYH9,MAP6,HMMR,HAUS4,KRAS,DOCK11,ZC3H12C,EGR2,CENPE,MTHFD2,TGIF2,ADORA2B,RNF121,TP53,TYMS,GNE,RRM2,TPM3,DDR1,TNPO2,SUPT16H,GAPDH,LTN1,RBM39,XRCC5,FAM188B,FBXO10,ARL4C,ODF2L,HNRNPA2B1,PDS5B,CDK4,CTDSPL,SLC25A40,CDKN3,KISS1R,CD47,PRR14L,SORBS1,DAB2,LAPTM4A,RAD21,MED20,CUL7,ING5,HSPA2,ZFPM2,ABCF2,CDKN1A,SEMA3C,FOXN2,WRAP53,FAM60A,VPS13A,KLF6,PARP2,SMC4,PINX1,STARD7,SART1,KIF16B,MYC,TGFBR2,ZW10,LEMD3,WDPCP,XPO1,MYBL2,BRIP1,PDZRN3,CNOT6,CLASP1,TOP3B,SMC3,DDX23,SIK2,SNX18,GM2A,TNPO1,DIDO1,SLC12A7,WASF1,TUSC3,ATAD2,TBL1X,TAF1,DUSP1,ETV4,HSP90AA1,NCKAP5L,RNF149,RUNX1,ARID1A,GTF2A1,IGF2BP1,MLH1,RAD50,TRA2A,RABEPK,POLR1C,DIAPH1,LYST,SPAG7,FANCD2,TIMP1,FOXO3,VARS,ZNF354A,TUBG1,FOXM1,AMPD2,NBN,HNRNPM,PDAP1,PMP22,LTBP3,PRKCI,MSH6,COX5A,TEAD3,WISP1,ATR,WNK1,APIP,CDKN2C,RAPH1,KPNA1,VEGFA,CXCL10,PRPF4B,CSTF2,IRS2,KMT2B,OTUD4,ACTR2,SMIM8,RCBTB2,PTBP1,POM121/POM121C,H2AFX,E2F1,LRP8,CYR61,EPHA2,TMEM74,HIST1H1C,ADAM17,PDIA3,PKD2,CAMK2N2,VCAN,CHEK1,EP300,COL5A1,TGFBRAP1,EFNB2,HECW1,TOP2A,PDGFRA,POLDIP3,LUZP1,AIFM1,mir-199,VPS18,CWC22,TBX3,SIN3A,KITLG,MUTYH,ADAM10,NCOR2,USP49,WDR19,SMARCAD1,FZR1,PHLDA1,MCM8,MAPK1,AURKB,TUBB,STMN1,PTK2,USF3,FGFR3,ARHGEF40,RORA,EZH2,ERLIN2,HTRA2,BRCA1,MYO10,ULK4,FGFR1,STK11,TBP,LMNA,SSRP1,WWP2,SRSF3,PKD1,LCORL,TUBE1,CASP2,NSMCE4A,MTDH,KDM3B,TNRC6B,GDNF,PKM,ABL1,NUP50,BCLAF1,EPHB6,EVC,CCDC88A,RABGGTB,LTBP4,RBM15,MCCC1,E2F8,S1PR2,BICD2,C2CD3,HDAC1,let-7,PSIP1,HIVEP2,GNAI2,FDPS,ENO1,UBQLN2,CAD,BCL2L11,SHMT2

Supplemental Table 8. Significant differently expressed genes in 1KI HCC samples

Affymetrix ID	Gene Symbol	Description	Transcript ID (Array Design)	3aKO avg signal log2 (n=5)	1KI Avg Signal log2 (n=5)	Fold Change (linear)	ANOVA p-value
1416645_a_at	Afp	alpha fetoprotein	Mm.80.1	3.7	8.7	**31.0**	0.001
1448194_a_at	H19	H19, imprinted maternally expressed transcript; microRNA 675	Mm.14802.1	4.2	8.4	**17.5**	0.001
1436879_x_at	Afp	alpha fetoprotein	Mm.80.5	2.8	6.7	**15.1**	0.006
1423140_at	Lipa	lysosomal acid lipase A	Mm.181935.1	6.1	9.7	**12.1**	0.027
1416646_at	Afp	alpha fetoprotein	Mm.80.1	5.7	8.9	**9.4**	0.010
1424649_a_at	Tspan8	tetraspanin 8	Mm.22270.1	4.2	7.4	**9.0**	0.020
1419314_at	Tinag	tubulointerstitial nephritis antigen	Mm.23199.1	3.6	6.5	**7.7**	0.003
1417507_at	Cyb561	cytochrome b-561	Mm.154456.1	5.4	8.1	**6.7**	0.008
1418457_at	Cxcl14	chemokine (C-X-C motif) ligand 14	Mm.30211.1	3.9	6.6	**6.7**	0.000
1453473_a_at	Dynlt1a	dynein light chain Tctex-type 1A; dynein light chain Tctex-type 1B; dynein light chain Tctex-type 1C; dynein light chain Tctex-type 1F	Mm.1948.3	7.4	10.1	**6.6**	0.000
1460550_at	Mtmr11	myotubularin related protein 11	Mm.24379.1	4.7	7.5	**6.5**	0.003
1424638_at	Cdkn1a	cyclin-dependent kinase inhibitor 1A (P21)	Mm.34446.2	7.1	9.8	**6.3**	0.000
1428116_a_at	Dynlt1a	dynein light chain Tctex-type 1A; dynein light chain Tctex-type 1B; dynein light chain Tctex-type 1C; dynein light chain Tctex-type 1F	Mm.1948.2	8.1	10.8	**6.2**	0.000
1452905_at	Meg3	maternally expressed 3	Mm.41602.1	5.5	8.1	**5.8**	0.018
1418191_at	Usp18	ubiquitin specific peptidase 18	Mm.27498.1	6.6	9.1	**5.7**	0.001
1421679_a_at	Cdkn1a	cyclin-dependent kinase inhibitor 1A (P21)	Mm.34446.1	7.1	9.6	**5.7**	0.000
1436713_s_at	Meg3	maternally expressed 3	Mm.200506.1	3.0	5.4	**5.4**	0.022
1438752_at	A230058F20Rik	RIKEN cDNA A230058F20 gene	Mm.74679.1	3.4	5.8	**5.4**	0.000
1443509_at			Mm.214915.1	3.7	6.1	**5.2**	0.010
1415822_at	Scd2	stearoyl-Coenzyme A desaturase 2	Mm.193096.1	6.4	8.7	**4.9**	0.036
1441946_at	Itih5	inter-alpha (globulin) inhibitor H5	Mm.77620.1	4.8	7.1	**4.9**	0.028
1417821_at	D17H6S56E-5	DNA segment, Chr 17, human D6S56E 5	Mm.22506.1	4.8	7.1	**4.9**	0.020
1448754_at	Rbp1	retinol binding protein 1, cellular	Mm.2450.1	9.1	11.3	**4.7**	0.002
1416930_at	Ly6d	lymphocyte antigen 6 complex, locus D	Mm.878.1	6.2	8.4	**4.7**	0.013
1452183_a_at	Meg3	maternally expressed 3	Mm.154560.1	7.1	9.3	**4.6**	0.039
1451780_at	Blnk	B cell linker	Mm.9749.1	6.9	9.1	**4.5**	0.020
1423555_a_at	Ifi44	interferon-induced protein 44	Mm.30756.1	5.4	7.6	**4.4**	0.004
1419195_at	Wfdc15b	WAP four-disulfide core domain 15B	Mm.10859.1	6.0	8.2	**4.4**	0.009
1424775_at	Oas1a	2'-5' oligoadenylate synthetase 1A	Mm.14301.1	7.5	9.6	**4.4**	0.000
1424339_at	Oasl1	2'-5' oligoadenylate synthetase-like 1	Mm.95479.1	6.3	8.4	**4.3**	0.001
1448595_a_at	Bex1	brain expressed gene 1	Mm.14768.1	3.0	5.1	**4.2**	0.027
1449254_at	Spp1	secreted phosphoprotein 1	Mm.321.1	9.0	11.1	**4.1**	0.003
1418171_at	Tceal8	transcription elongation factor A (SII)-like 8	Mm.182094.1	7.2	9.2	**3.9**	0.005

Supplemental Table 8. Significant differently expressed genes in 1KI HCC samples

Affymetrix ID	Gene Symbol	Description	Transcript ID (Array Design)	3aKO avg signal log2 (n=5)	1KI Avg Signal log2 (n=5)	Fold Change (linear)	ANOVA p-value
1434728_at	Gria3	glutamate receptor, ionotropic, AMPA3 (alpha 3)	Mm.32184.1	3.6	5.6	**3.9**	0.001
1441388_at			Mm.65393.1	3.4	5.3	**3.7**	0.041
1417409_at	Jun	jun proto-oncogene	Mm.482.1	7.4	9.2	**3.7**	0.000
1445328_at	Col4a4	collagen, type IV, alpha 4	Mm.40253.1	4.0	5.9	**3.6**	0.030
1417244_a_at	Irf7	interferon regulatory factor 7	Mm.3233.1	7.9	9.7	**3.6**	0.005
1427878_at	Cystm1	cysteine-rich transmembrane module containing 1	Mm.27841.1	7.8	9.6	**3.6**	0.013
1449145_a_at	Cav1	caveolin 1, caveolae protein	Mm.28278.1	6.0	7.9	**3.5**	0.021
1449002_at	Phlda3	pleckstrin homology-like domain, family A, member 3	Mm.34346.1	6.9	8.7	**3.5**	0.000
1460406_at	Pls1	plastin 1 (I-isoform)	Mm.11869.1	6.8	8.6	**3.5**	0.017
1434292_at	Snhg11	small nucleolar RNA host gene 11	Mm.200806.1	3.1	4.9	**3.4**	0.011
1418930_at	Cxcl10	chemokine (C-X-C motif) ligand 10	Mm.877.1	6.5	8.2	**3.4**	0.016
1450245_at	Slc10a2	solute carrier family 10, member 2	Mm.3500.1	4.6	6.4	**3.3**	0.006
1429159_at	Itih5	inter-alpha (globulin) inhibitor H5	Mm.2935.1	6.2	7.9	**3.3**	0.017
1455144_s_at	Arhgap44	Rho GTPase activating protein 44	Mm.18455.1	4.7	6.4	**3.2**	0.015
1417822_at	D17H6S56E-5	DNA segment, Chr 17, human D6S56E 5	Mm.22506.1	6.4	8.1	**3.2**	0.026
1431056_a_at	Lpl	lipoprotein lipase	Mm.1514.2	6.9	8.6	**3.2**	0.013
1427514_at	LOC624295	uncharacterized LOC624295	Mm.156929.1	5.0	6.7	**3.2**	0.000
1444139_at	Ddit4l	DNA-damage-inducible transcript 4-like	Mm.205420.1	5.0	6.7	**3.1**	0.004
1452956_a_at	Ifi27l1	interferon, alpha-inducible protein 27	Mm.2121.1	10.5	12.1	**3.1**	0.000
1417323_at	Psrc1	proline/serine-rich coiled-coil 1	Mm.23776.1	3.8	5.4	**3.0**	0.001
1417370_at	Tff3	trefoil factor 3, intestinal	Mm.4641.1	5.9	7.5	**3.0**	0.025
1450783_at	Ifit1	interferon-induced protein with tetratricopeptide repeats 1	Mm.6718.1	6.9	8.6	**3.0**	0.003
1448261_at	Cdh1	cadherin 1	Mm.35605.1	6.6	8.2	**3.0**	0.024
1459333_at			Mm.17671.1	4.9	6.4	**3.0**	0.013
1433575_at	Sox4	SRY (sex determining region Y)-box 4	Mm.18789.2	6.3	7.9	**3.0**	0.005
1418320_at	Prss8	protease, serine 8 (prostasin)	Mm.5875.1	5.5	7.1	**3.0**	0.023
1450531_at	H2-Bl	histocompatibility 2, blastocyst	Mm.34289.1	5.8	7.4	**3.0**	0.013
1429734_at	4632434I11Rik	DNA damage-induced apoptosis suppressor	Mm.26468.1	5.0	6.6	**2.9**	0.010
1424594_at	Samd4	sterile alpha motif domain containing 4	Mm.20973.2	6.5	8.0	**2.9**	0.003
1449133_at	Sprr1a	small proline-rich protein 1A	Mm.625.1	5.2	6.7	**2.9**	0.041
1425120_x_at	Ifi27l2b	interferon, alpha-inducible protein 27 like 2B	Mm.46348.1	7.6	9.1	**2.9**	0.003
1437308_s_at	F2r	coagulation factor II (thrombin) receptor	Mm.24816.2	8.7	10.2	**2.9**	0.022
1456226_x_at	Ddr1	discoidin domain receptor family, member 1	Mm.5021.4	3.5	5.0	**2.8**	0.007
1436755_at	Itih5	inter-alpha (globulin) inhibitor H5	Mm.38459.1	4.0	5.5	**2.8**	0.048

Supplemental Table 8. Significant differently expressed genes in 1KI HCC samples

Affymetrix ID	Gene Symbol	Description	Transcript ID (Array Design)	3aKO avg signal log2 (n=5)	1KI Avg Signal log2 (n=5)	Fold Change (linear)	ANOVA p-value
1456981_at	Tmc7	transmembrane channel-like gene family 7	Mm.33000.1	5.1	6.6	**2.8**	0.007
1451828_a_at	Acsl4	acyl-CoA synthetase long-chain family member 4	Mm.143689.2	7.5	9.0	**2.8**	0.013
1454904_at	Mtm1	X-linked myotubular myopathy gene 1	Mm.30502.2	6.6	8.0	**2.8**	0.006
1415904_at	Lpl	lipoprotein lipase	Mm.1514.1	8.7	10.2	**2.7**	0.019
1446368_at	9130221J18 Rik	RIKEN cDNA 9130221J18 gene	Mm.37328.1	6.3	7.7	**2.7**	0.033
1428671_at	2200002D01 Rik	RIKEN cDNA 2200002D01 gene	Mm.46332.1	7.8	9.2	**2.7**	0.013
1426628_at	Tmem184c	transmembrane protein 184C	Mm.85137.1	7.7	9.1	**2.7**	0.000
1419658_at	C920025E04 Rik	RIKEN cDNA C920025E04 gene; histocompatibility 2, T region locus 23; h-2 class I histocompatibility antigen, D-37 alpha chain-like	Mm.35016.1	5.2	6.6	**2.7**	0.042
1454757_s_at	Ifi27l1	interferon, alpha-inducible protein 27	Mm.2121.2	10.3	11.7	**2.7**	0.000
1450852_s_at	F2r	coagulation factor II (thrombin) receptor	Mm.24816.1	6.7	8.1	**2.6**	0.021
1423556_at	Akr1b7	aldo-keto reductase family 1, member B7	Mm.14460.1	5.1	6.5	**2.6**	0.037
1426278_at	Ifi27l2a	interferon, alpha-inducible protein 27 like 2A	Mm.46382.1	6.5	7.9	**2.6**	0.002
1431708_a_at	Tia1	cytotoxic granule-associated RNA binding protein 1	Mm.156851.2	3.7	5.1	**2.6**	0.012
1442049_at			Mm.44860.1	9.5	10.9	**2.6**	0.030
1415823_at	Scd2	stearoyl-Coenzyme A desaturase 2	Mm.193096.1	6.1	7.5	**2.6**	0.035
1440250_at	Col4a4	collagen, type IV, alpha 4	Mm.107258.1	4.0	5.4	**2.5**	0.020
1415810_at	Uhrf1	ubiquitin-like, containing PHD and RING finger domains, 1	Mm.42196.1	4.6	5.9	**2.5**	0.017

Supplemental Table 8. Significant differently expressed genes in 1KI HCC samples

Affymetrix ID	Gene Symbol	Description	Transcript ID (Array Design)	3aKO avg signal log2 (n=5)	1KI Avg Signal log2 (n=5)	Fold Change (linear)	ANOVA p-value
1452731_x_at	Gm10340	predicted gene 10340; predicted pseudogene 8348; predicted gene, 16525; predicted gene 2897; alpha-takusan pseudogene; predicted gene 3005; predicted gene 3095; predicted gene 3115; predicted gene 3164; predicted gene 3173; predicted gene 3239; predicted gene 3252; predicted gene 3264; predicted gene 3317; predicted gene 3373; predicted gene 3383; predicted gene, 3488; predicted gene 3500; predicted gene 3558; predicted gene 3636; predicted gene 3642; predicted gene 3667; predicted gene 3696; predicted gene 3739; predicted gene 5796; alpha takusan-like; uncharacterized LOC102638110	Mm.204.1	2.9	4.2	**2.5**	0.039
1417389_at	Gpc1	glypican 1	Mm.24193.1	5.9	7.2	**2.5**	0.012
1452951_at	2410089E03 Rik	RIKEN cDNA 2410089E03 gene	Mm.74311.1	6.5	7.8	**2.5**	0.040
1438824_at	Slc20a1	solute carrier family 20, member 1	Mm.16757.3	5.3	6.6	**2.5**	0.024
1451538_at	Sox9	SRY (sex determining region Y)-box 9	Mm.46607.1	5.7	7.0	**2.5**	0.026
1428626_at	Lysmd2	LysM, putative peptidoglycan-binding, domain containing 2	Mm.19119.1	5.6	6.9	**2.5**	0.041
1427883_a_at	Col3a1	collagen, type III, alpha 1	Mm.147387.1	8.2	9.5	**2.5**	0.007
1424950_at	Sox9	SRY (sex determining region Y)-box 9	Mm.46607.1	4.5	5.8	**2.4**	0.023
1434278_at	Mtm1	X-linked myotubular myopathy gene 1	Mm.30502.2	6.9	8.2	**2.4**	0.005
1453196_a_at	Oasl2	2'-5' oligoadenylate synthetase-like 2	Mm.27162.2	5.1	6.4	**2.4**	0.005
1419157_at	Sox4	SRY (sex determining region Y)-box 4	Mm.18789.1	4.7	6.0	**2.4**	0.021
1452260_at	Cidec	cell death-inducing DFFA-like effector c	Mm.10026.1	4.3	5.5	**2.4**	0.035
1428640_at	Hsf2bp	heat shock transcription factor 2 binding protein	Mm.75856.1	6.8	8.0	**2.3**	0.013
1426434_at	Tmem43	transmembrane protein 43	Mm.38801.1	7.5	8.7	**2.3**	0.001
1431176_at	Chmp4c	charged multivesicular body protein 4C	Mm.24595.1	5.6	6.8	**2.3**	0.029
1418355_at	Nucb2	nucleobindin 2	Mm.9901.1	6.0	7.2	**2.3**	0.039
1434582_at	Erc2	ELKS/RAB6-interacting/CAST family member 2	Mm.32667.1	4.8	6.0	**2.3**	0.018
1449153_at	Mmp12	matrix metallopeptidase 12	Mm.2055.1	4.4	5.6	**2.3**	0.002
1420827_a_at	Ccng1	cyclin G1	Mm.2103.1	8.5	9.7	**2.3**	0.015

Supplemental Table 8. Significant differently expressed genes in 1KI HCC samples

Affymetrix ID	Gene Symbol	Description	Transcript ID (Array Design)	3aKO avg signal log2 (n=5)	1KI Avg Signal log2 (n=5)	Fold Change (linear)	ANOVA p-value
1431591_s_at	Gm9706	predicted gene 9706; ISG15 ubiquitin-like modifier	Mm.204646.1	6.5	7.7	**2.3**	0.009
1452227_at	Sel1l3	sel-1 suppressor of lin-12-like 3 (C. elegans)	Mm.24656.1	6.2	7.3	**2.3**	0.010
1416658_at	Frzb	frizzled-related protein	Mm.3246.1	4.1	5.3	**2.3**	0.001
1434241_at	Wdr67	TBC1 domain family, member 31	Mm.31972.1	7.3	8.5	**2.3**	0.033
1448152_at	Igf2	insulin-like growth factor 2	Mm.3862.1	6.0	7.1	**2.3**	0.001
1448694_at	Jun	jun proto-oncogene	Mm.482.1	7.1	8.2	**2.3**	0.002
1416529_at	Emp1	epithelial membrane protein 1	Mm.30024.1	4.9	6.1	**2.3**	0.030
1417960_at	Cpeb1	cytoplasmic polyadenylation element binding protein 1	Mm.22062.1	4.9	6.0	**2.2**	0.004
1460351_at	Gm12854	predicted gene 12854; predicted gene 5068; S100 calcium binding protein A11 (calgizzarin)	Mm.175848.1	8.2	9.4	**2.2**	0.035
1416076_at	Ccnb1	cyclin B1; predicted gene 5593	Mm.22569.1	3.7	4.9	**2.2**	0.031
1439380_x_at	Meg3	maternally expressed 3	Mm.154560.3	7.5	8.6	**2.2**	0.028
1448380_at	Lgals3bp	lectin, galactoside-binding, soluble, 3 binding protein	Mm.3152.1	9.5	10.7	**2.2**	0.003
1425868_at	Hist2h2bb	histone cluster 2, H2bb	Mm.214641.1	5.5	6.6	**2.2**	0.028
1418334_at	Dbf4	DBF4 homolog (S. cerevisiae)	Mm.22430.1	4.7	5.8	**2.2**	0.009
1438724_at	Osbpl3	oxysterol binding protein-like 3	Mm.44153.1	5.6	6.7	**2.2**	0.047
1454254_s_at	1600029D21Rik	placenta expressed transcript 1	Mm.195522.1	4.6	5.8	**2.2**	0.024
1418911_s_at	Acsl4	acyl-CoA synthetase long-chain family member 4	Mm.143689.1	8.2	9.4	**2.2**	0.028
1449975_a_at	Park2	Parkinson disease (autosomal recessive, juvenile) 2, parkin	Mm.42046.1	5.7	6.8	**2.2**	0.001
1450017_at	Ccng1	cyclin G1	Mm.2103.1	8.1	9.2	**2.2**	0.011
1418580_at	Rtp4	receptor transporter protein 4	Mm.180157.1	8.5	9.6	**2.2**	0.012
1438009_at	Hist1h2ab	histone cluster 1, H2ab; histone cluster 1, H2ac; histone cluster 1, H2ad; histone cluster 1, H2ae; histone cluster 1, H2ag; histone cluster 1, H2ah; histone cluster 1, H2ai; histone cluster 1, H2an; histone cluster 1, H2ao; histone cluster 1, H2ap	Mm.14767.2	8.0	9.1	**2.2**	0.004
1438665_at	Smpd3	sphingomyelin phosphodiesterase 3, neutral	Mm.23298.1	4.2	5.3	**2.2**	0.049
1416492_at	Ccne1	cyclin E1	Mm.16110.1	5.9	7.0	**2.2**	0.022
1418293_at	Ifit2	interferon-induced protein with tetratricopeptide repeats 2	Mm.2036.1	4.9	6.0	**2.2**	0.015
1418655_at	B4galnt1	beta-1,4-N-acetyl-galactosaminyl transferase 1	Mm.1853.1	4.6	5.7	**2.2**	0.044
1423669_at	Col1a1	collagen, type I, alpha 1	Mm.22621.1	6.0	7.1	**2.2**	0.033
1443698_at	Xaf1	XIAP associated factor 1	Mm.149240.1	7.9	9.0	**2.2**	0.008
1455162_at	Ttc39a	tetratricopeptide repeat domain 39A	Mm.23454.1	6.5	7.6	**2.2**	0.000

Supplemental Table 8. Significant differently expressed genes in 1KI HCC samples

Affymetrix ID	Gene Symbol	Description	Transcript ID (Array Design)	3aKO avg signal log2 (n=5)	1KI Avg Signal log2 (n=5)	Fold Change (linear)	ANOVA p-value
1424245_at	Ces2c	carboxylesterase 2C; carboxylesterase 2D, pseudogene	Mm.28191.1	8.9	10.0	**2.1**	0.003
1433531_at	Acsl4	acyl-CoA synthetase long-chain family member 4	Mm.12166.1	8.3	9.4	**2.1**	0.023
1451751_at	Ddit4l	DNA-damage-inducible transcript 4-like	Mm.195809.1	5.1	6.2	**2.1**	0.001
1415993_at	Sqle	squalene epoxidase	Mm.22663.1	11.0	12.0	**2.1**	0.022
1420647_a_at	Krt8	keratin 8	Mm.6800.1	10.9	12.0	**2.1**	0.005
1424626_at	2010003K11 Rik	RIKEN cDNA 2010003K11 gene	Mm.22966.1	7.7	8.8	**2.1**	0.025
1448314_at	Cdk1	cyclin-dependent kinase 1	Mm.4761.1	6.9	7.9	**2.1**	0.023
1440085_at	Eda2r	ectodysplasin A2 receptor	Mm.189270.1	4.1	5.2	**2.1**	0.038
1415698_at	Golm1	golgi membrane protein 1	Mm.171335.1	6.4	7.4	**2.1**	0.022
1450016_at	Ccng1	cyclin G1	Mm.2103.1	9.0	10.1	**2.1**	0.007
1419091_a_at	Anxa2	annexin A2	Mm.584.1	8.5	9.6	**2.1**	0.030
1425913_a_at	Spats2l	spermatogenesis associated, serine-rich 2-like	Mm.27691.2	4.9	6.0	**2.1**	0.001
1441793_at			Mm.117140.1	7.3	8.4	**2.1**	0.032
1451749_at	Irak4	interleukin-1 receptor-associated kinase 4	Mm.159942.2	6.0	7.1	**2.1**	0.009
1451777_at	Ddx60	DEAD (Asp-Glu-Ala-Asp) box polypeptide 60	Mm.33332.1	5.2	6.3	**2.1**	0.031
1453304_s_at	Ly6e	lymphocyte antigen 6 complex, locus E	Mm.204648.1	12.0	13.1	**2.1**	0.001
1420563_at	Gria3	glutamate receptor, ionotropic, AMPA3 (alpha 3)	Mm.42021.1	5.1	6.2	**2.1**	0.000
1435819_at			Mm.99958.1	6.2	7.2	**2.1**	0.007
1436356_at	Samd4	sterile alpha motif domain containing 4	Mm.40604.1	6.0	7.0	**2.1**	0.008
1441137_at	Bicc1	bicaudal C homolog 1 (Drosophila)	Mm.179033.1	4.8	5.8	**2.1**	0.007
1449221_a_at	Rrbp1	ribosome binding protein 1	Mm.13705.1	10.8	11.9	**2.1**	0.013
1423691_x_at	Krt8	keratin 8	Mm.6800.2	10.8	11.8	**2.0**	0.007
1423933_a_at	1600029D21 Rik	placenta expressed transcript 1	Mm.29959.1	5.9	6.9	**2.0**	0.022
1437162_at			Mm.116993.1	6.0	7.0	**2.0**	0.001
1438779_at	Col4a3	collagen, type IV, alpha 3	Mm.113295.1	3.4	4.4	**2.0**	0.041
1434089_at	Synpo	synaptopodin	Mm.27313.1	5.6	6.7	**2.0**	0.002
1417965_at	Plekha1	pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 1	Mm.25248.1	6.8	7.8	**2.0**	0.017
1423484_at	Bicc1	bicaudal C homolog 1 (Drosophila)	Mm.46051.1	6.2	7.2	**2.0**	0.006
1435853_at	Cyp2d12	cytochrome P450, family 2, subfamily d, polypeptide 12	Mm.104363.3	5.0	6.0	**2.0**	0.023
1449025_at	Ifit3	interferon-induced protein with tetratricopeptide repeats 3	Mm.951.1	6.8	7.9	**2.0**	0.018
1415849_s_at	Stmn1	stathmin 1	Mm.28479.1	7.5	8.5	**2.0**	0.049

Supplemental Table 8. Significant differently expressed genes in 1KI HCC samples

Affymetrix ID	Gene Symbol	Description	Transcript ID (Array Design)	3aKO avg signal log2 (n=5)	1KI Avg Signal log2 (n=5)	Fold Change (linear)	ANOVA p-value
1417267_s_at	Fkbp11	FK506 binding protein 11	Mm.30729.1	7.2	8.2	**2.0**	0.029
1424246_a_at	Tes	testis derived transcript	Mm.88645.1	5.5	6.4	**2.0**	0.030
1427167_at	Armcx4	armadillo repeat containing, X-linked 4	Mm.31961.1	4.1	5.1	**2.0**	0.007
1437609_at	Ube2u	ubiquitin-conjugating enzyme E2U (putative)	Mm.87383.1	3.9	4.9	**2.0**	0.013
1425567_a_at	Anxa5	annexin A5	Mm.1620.2	9.2	10.2	**2.0**	0.030
1455431_at	Slc5a1	solute carrier family 5 (sodium/glucose cotransporter), member 1	Mm.25237.2	2.9	3.9	**2.0**	0.010
1415798_at	Ddr1	discoidin domain receptor family, member 1	Mm.5021.1	5.0	6.0	**2.0**	0.042
1416803_at	Fkbp7	FK506 binding protein 7	Mm.24720.1	5.9	6.9	**2.0**	0.012
1460603_at	Samd9l	sterile alpha motif domain containing 9-like	Mm.196013.1	7.7	8.7	**2.0**	0.013
1422587_at	Tmem45a	transmembrane protein 45a	Mm.4992.1	5.8	6.8	**2.0**	0.018
1423904_a_at	Pvr	poliovirus receptor	Mm.134436.1	5.6	6.6	**2.0**	0.029
1449191_at	Wfdc12	WAP four-disulfide core domain 12	Mm.6433.1	5.8	6.7	**2.0**	0.008
1452899_at	Rian	RNA imprinted and accumulated in nucleus	Mm.23086.2	4.3	5.3	**2.0**	0.049
1416698_a_at	Cks1b	CDC28 protein kinase 1b	Mm.3049.1	9.4	10.4	**2.0**	0.015
1419057_at	Slc5a1	solute carrier family 5 (sodium/glucose cotransporter), member 1	Mm.25237.1	4.9	5.8	**2.0**	0.011
1422160_at	H2-T24	histocompatibility 2, T region locus 24	Mm.14573.1	4.7	5.7	**2.0**	0.030
1426276_at	Ifih1	interferon induced with helicase C domain 1	Mm.21551.1	8.9	9.8	**2.0**	0.002
1435989_x_at	Krt8	keratin 8	Mm.6800.3	10.6	11.5	**2.0**	0.007
1454694_a_at	Top2a	topoisomerase (DNA) II alpha	Mm.4237.3	4.7	5.7	**2.0**	0.047
1428066_at	Ccdc120	coiled-coil domain containing 120	Mm.59673.1	4.4	5.4	**1.9**	0.030
1429139_at	Otud7b	OTU domain containing 7B	Mm.3050.1	7.0	8.0	**1.9**	0.005
1434891_at	Ptgfrn	prostaglandin F2 receptor negative regulator	Mm.24807.1	5.6	6.6	**1.9**	0.031
1440862_at			Mm.153468.1	4.9	5.9	**1.9**	0.000
1441081_a_at	1110038B12 Rik	RIKEN cDNA 1110038B12 gene	Mm.28895.3	8.8	9.8	**1.9**	0.050
1450646_at	Cyp51	cytochrome P450, family 51	Mm.140158.1	10.2	11.1	**1.9**	0.004
1450857_a_at	Col1a2	collagen, type I, alpha 2	Mm.4482.1	8.4	9.3	**1.9**	0.006
1422684_a_at	Exoc4	exocyst complex component 4	Mm.6925.1	8.0	8.9	**1.9**	0.011
1423110_at	Col1a2	collagen, type I, alpha 2	Mm.4482.1	5.4	6.4	**1.9**	0.047
1417541_at	Hells	helicase, lymphoid specific	Mm.57223.1	4.0	4.9	**1.9**	0.026
1418189_s_at	Malat1	metastasis associated lung adenocarcinoma transcript 1 (non-coding RNA)	Mm.218611.1	7.2	8.1	**1.9**	0.001
1418714_at	Dusp8	dual specificity phosphatase 8	Mm.39725.1	4.7	5.7	**1.9**	0.010
1419398_a_at	Reep5	receptor accessory protein 5	Mm.21251.1	8.1	9.1	**1.9**	0.012

Supplemental Table 8. Significant differently expressed genes in 1KI HCC samples

Affymetrix ID	Gene Symbol	Description	Transcript ID (Array Design)	3aKO avg signal log2 (n=5)	1KI Avg Signal log2 (n=5)	Fold Change (linear)	ANOVA p-value
1421670_a_at	Irak4	interleukin-1 receptor-associated kinase 4	Mm.159942.1	3.5	4.4	**1.9**	0.010
1444326_at			Mm.168098.1	6.2	7.1	**1.9**	0.019
1448393_at	Cldn7	claudin 7	Mm.42189.1	4.9	5.9	**1.9**	0.006
1416689_at	Tuft1	tuftelin 1	Mm.10214.1	6.7	7.7	**1.9**	0.028
1452954_at	Ube2c	ubiquitin-conjugating enzyme E2C	Mm.89830.1	5.8	6.8	**1.9**	0.040
1457356_at			Mm.80556.1	5.7	6.6	**1.9**	0.013
1428387_at	Acsl3	acyl-CoA synthetase long-chain family member 3	Mm.27944.1	4.6	5.5	**1.9**	0.049
1438635_x_at	B930041F14Rik	RIKEN cDNA B930041F14 gene	Mm.132095.1	5.8	6.8	**1.9**	0.002
1416250_at	Btg2	B cell translocation gene 2, anti-proliferative	Mm.903.1	8.0	8.9	**1.9**	0.018
1417019_a_at	Cdc6	cell division cycle 6	Mm.20912.1	3.4	4.4	**1.9**	0.002
1417116_at	Slc6a8	solute carrier family 6 (neurotransmitter transporter, creatine), member 8	Mm.41401.1	6.3	7.3	**1.9**	0.018
1422685_at	Exoc4	exocyst complex component 4	Mm.6925.1	6.4	7.3	**1.9**	0.013
1427020_at	Scara3	scavenger receptor class A, member 3	Mm.44135.1	5.2	6.1	**1.9**	0.037
1433446_at	Hmgcs1	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1	Mm.61526.4	11.3	12.2	**1.9**	0.028
1440912_at	Rnf39	ring finger protein 39	Mm.105324.1	6.6	7.5	**1.9**	0.034
1443941_at	Ccdc149	coiled-coil domain containing 149	Mm.86468.1	4.9	5.9	**1.9**	0.021
1424921_at	Bst2	bone marrow stromal cell antigen 2	Mm.143755.2	10.5	11.4	**1.9**	0.000
1431192_at	Sorbs2	sorbin and SH3 domain containing 2	Mm.32247.1	4.8	5.7	**1.9**	0.004
1444438_at	Cib3	calcium and integrin binding family member 3	Mm.211247.1	5.3	6.2	**1.9**	0.013
1419853_a_at	P2rx7	purinergic receptor P2X, ligand-gated ion channel, 7	Mm.31661.2	5.0	5.9	**1.8**	0.043
1426123_a_at	Rrbp1	ribosome binding protein 1	Mm.13705.8	9.3	10.2	**1.8**	0.031
1431900_a_at	Foxa3	forkhead box A3	Mm.42260.2	9.6	10.5	**1.8**	0.017
1441811_x_at	Tmem176a	transmembrane protein 176A	Mm.200272.1	10.8	11.7	**1.8**	0.017
1456482_at	Pik3r3	phosphatidylinositol 3 kinase, regulatory subunit, polypeptide 3 (p55)	Mm.94590.1	5.2	6.1	**1.8**	0.002
1418281_at	Rad51	RAD51 homolog	Mm.231.1	3.8	4.7	**1.8**	0.038
1448259_at	Fstl1	follistatin-like 1	Mm.22763.1	5.8	6.6	**1.8**	0.005
1438118_x_at	Vim	vimentin	Mm.7.4	5.8	6.6	**1.8**	0.022
1442439_at	W91776	expressed sequence W91776	Mm.34265.1	4.6	5.5	**1.8**	0.019
1420965_a_at	Enc1	ectodermal-neural cortex 1	Mm.30502.1	6.8	7.6	**1.8**	0.008
1423909_at	Tmem176a	transmembrane protein 176A	Mm.27061.1	11.9	12.7	**1.8**	0.011
1427473_at	Gstm3	glutathione S-transferase, mu 3	Mm.37199.1	9.0	9.8	**1.8**	0.041
1432579_at	Rsph3a	radial spoke 3A homolog (Chlamydomonas)	Mm.159766.1	5.2	6.0	**1.8**	0.001
1433914_at	Lipo1	lipase, member O1	Mm.30678.1	3.6	4.4	**1.8**	0.025
1449353_at	Zmat3	zinc finger matrin type 3	Mm.35705.1	7.2	8.1	**1.8**	0.000

Supplemental Table 8. Significant differently expressed genes in 1KI HCC samples

Affymetrix ID	Gene Symbol	Description	Transcript ID (Array Design)	3aKO avg signal log2 (n=5)	1KI Avg Signal log2 (n=5)	Fold Change (linear)	ANOVA p-value
1450295_s_at	Pvr	poliovirus receptor	Mm.8071.1	4.3	5.1	**1.8**	0.022
1416543_at	Nfe2l2	nuclear factor, erythroid derived 2, like 2	Mm.1025.1	10.2	11.1	**1.8**	0.009
1437992_x_at	Gja1	gap junction protein, alpha 1	Mm.4504.3	7.1	7.9	**1.8**	0.004
1438001_x_at	Reep5	receptor accessory protein 5	Mm.21251.3	7.8	8.7	**1.8**	0.009
1440166_x_at	Htr1d	5-hydroxytryptamine (serotonin) receptor 1D	Mm.40573.1	3.7	4.6	**1.8**	0.003
1458179_at			Mm.130940.1	3.8	4.7	**1.8**	0.009
1416802_a_at	Cdca5	cell division cycle associated 5	Mm.23526.1	4.5	5.4	**1.8**	0.027
1423319_at	Hhex	hematopoietically expressed homeobox	Mm.33896.1	10.0	10.8	**1.8**	0.045
1427474_s_at	Gstm3	glutathione S-transferase, mu 3	Mm.37199.1	11.4	12.3	**1.8**	0.025
1445966_at			Mm.182814.1	5.4	6.3	**1.8**	0.013
1448205_at	Ccnb1	cyclin B1; predicted gene 5593	Mm.22569.1	4.0	4.8	**1.8**	0.044
1448272_at	Btg2	B cell translocation gene 2, anti-proliferative	Mm.903.1	7.2	8.0	**1.8**	0.023
1460416_s_at	Csprs	component of Sp100-rs; predicted pseudogene 15433; predicted gene 2666; predicted pseudogene 7609; uncharacterized LOC100041903; uncharacterized LOC100503923; component of Sp100-rs-like	Mm.99965.1	6.7	7.5	**1.8**	0.020
1416664_at	Cdc20	cell division cycle 20	Mm.29931.1	5.7	6.5	**1.8**	0.030
1422534_at	Cyp51	cytochrome P450, family 51	Mm.140158.1	6.2	7.0	**1.8**	0.017
1433985_at	Abi2	abl-interactor 2	Mm.40762.1	5.2	6.1	**1.8**	0.047
1446730_at			Mm.212815.1	3.9	4.7	**1.8**	0.026
1458296_at			Mm.202183.1	5.1	5.9	**1.8**	0.002
1458525_at			Mm.167985.1	5.9	6.7	**1.8**	0.039
1415811_at	Uhrf1	ubiquitin-like, containing PHD and RING finger domains, 1	Mm.42196.1	4.4	5.2	**1.8**	0.027
1424942_a_at	Myc	myelocytomatosis oncogene	Mm.2444.2	6.8	7.6	**1.8**	0.013
1436539_at	Clmn	calmin	Mm.22921.1	6.4	7.2	**1.8**	0.030
1415800_at	Gja1	gap junction protein, alpha 1	Mm.4504.1	5.2	6.0	**1.8**	0.003
1419156_at	Sox4	SRY (sex determining region Y)-box 4	Mm.18789.1	4.9	5.7	**1.8**	0.017
1422437_at	Col5a2	collagen, type V, alpha 2	Mm.10299.1	5.9	6.7	**1.8**	0.023
1422686_s_at	Exoc4	exocyst complex component 4	Mm.6925.1	7.2	8.0	**1.8**	0.008
1427683_at	Egr2	early growth response 2	Mm.1353.2	3.2	4.0	**1.8**	0.009
1436029_at	Bicc1	bicaudal C homolog 1 (Drosophila)	Mm.25695.2	6.8	7.6	**1.8**	0.009
1439787_at	P2rx7	purinergic receptor P2X, ligand-gated ion channel, 7	Mm.31661.1	6.5	7.3	**1.8**	0.047
1441145_at	Phf21a	PHD finger protein 21A	Mm.173646.1	5.0	5.8	**1.8**	0.004
1444424_at			Mm.218393.1	4.0	4.9	**1.8**	0.005
1455439_a_at	Lgals1	lectin, galactose binding, soluble 1	Mm.43831.3	8.1	8.9	**1.8**	0.009
1460378_a_at	Tes	testis derived transcript	Mm.88645.2	5.9	6.7	**1.8**	0.040
1460521_a_at	Nabp1	nucleic acid binding protein 1	Mm.196290.2	5.8	6.6	**1.8**	0.043

Supplemental Table 8. Significant differently expressed genes in 1KI HCC samples

Affymetrix ID	Gene Symbol	Description	Transcript ID (Array Design)	3aKO avg signal log2 (n=5)	1KI Avg Signal log2 (n=5)	Fold Change (linear)	ANOVA p-value
1415919_at	Npdc1	neural proliferation, differentiation and control 1	Mm.1131.1	6.9	7.7	**1.8**	0.015
1416067_at	Ifrd1	interferon-related developmental regulator 1	Mm.168.1	7.7	8.5	**1.8**	0.005
1416953_at	Ctgf	connective tissue growth factor	Mm.1810.1	7.5	8.3	**1.8**	0.003
1435110_at	Unc5b	unc-5 homolog B (C. elegans)	Mm.4580.2	6.7	7.5	**1.8**	0.044
1438945_x_at	Gja1	gap junction protein, alpha 1	Mm.4504.5	4.5	5.3	**1.8**	0.033
1449297_at	Casp12	caspase 12	Mm.42163.1	4.6	5.4	**1.8**	0.047
1455980_a_at	Gas2l3	growth arrest-specific 2 like 3	Mm.11982.1	4.3	5.1	**1.8**	0.010
1417911_at	Ccna2	cyclin A2	Mm.4189.1	5.2	6.0	**1.7**	0.035
1435655_at	Rpl12	ribosomal protein L12	Mm.70127.3	6.5	7.3	**1.7**	0.003
1435948_at	Tmem181a	transmembrane protein 181A; transmembrane protein 181B, pseudogene; transmembrane protein 181C, pseudogene	Mm.39489.1	5.8	6.6	**1.7**	0.029
1460259_s_at	Clca1	chloride channel calcium activated 1; chloride channel calcium activated 2	Mm.20897.1	6.4	7.2	**1.7**	0.004
1435437_at	Setd7	SET domain containing (lysine methyltransferase) 7	Mm.39291.1	7.3	8.0	**1.7**	0.012
1439377_x_at	Cdc20	cell division cycle 20	Mm.29931.4	5.4	6.2	**1.7**	0.048
1448211_at	Atp6v0e2	ATPase, H+ transporting, lysosomal V0 subunit E2	Mm.30214.1	6.5	7.3	**1.7**	0.002
1448441_at	Cks1b	CDC28 protein kinase 1b	Mm.3049.1	8.4	9.2	**1.7**	0.018
1416431_at	Tubb6	tubulin, beta 6 class V	Mm.181860.1	7.7	8.4	**1.7**	0.016
1416927_at	Trp53inp1	transformation related protein 53 inducible nuclear protein 1	Mm.28708.1	7.4	8.2	**1.7**	0.005
1418949_at	Gdf15	growth differentiation factor 15	Mm.31325.1	7.4	8.2	**1.7**	0.016
1448182_a_at	Cd24a	CD24a antigen	Mm.6417.1	6.1	6.9	**1.7**	0.024
1456139_at	Airn	antisense Igf2r RNA	Mm.138484.1	6.3	7.1	**1.7**	0.014
1419573_a_at	Lgals1	lectin, galactose binding, soluble 1	Mm.43831.1	8.4	9.2	**1.7**	0.010
1424022_at	Osgin1	oxidative stress induced growth inhibitor 1	Mm.34045.1	10.4	11.2	**1.7**	0.036
1424511_at	Aurka	aurora kinase A	Mm.11738.1	4.8	5.5	**1.7**	0.006
1425349_a_at	Myef2	myelin basic protein expression factor 2, repressor	Mm.18535.1	4.8	5.5	**1.7**	0.038
1451335_at	Plac8	placenta-specific 8	Mm.34609.1	8.3	9.0	**1.7**	0.029
1452197_at	Smc4	structural maintenance of chromosomes 4	Mm.206841.1	7.7	8.4	**1.7**	0.004
1454301_at	2900073C17Rik	RIKEN cDNA 2900073C17 gene	Mm.158924.1	5.1	5.8	**1.7**	0.002
1416926_at	Trp53inp1	transformation related protein 53 inducible nuclear protein 1	Mm.28708.1	9.4	10.1	**1.7**	0.009
1438434_at	Arhgap11a	Rho GTPase activating protein 11A	Mm.45753.1	5.3	6.1	**1.7**	0.009
1459098_at			Mm.173922.1	5.6	6.3	**1.7**	0.000
1433643_at	Cacna2d1	calcium channel, voltage-dependent, alpha2/delta subunit 1	Mm.25672.1	4.9	5.7	**1.7**	0.001
1439489_at	Ffar4	free fatty acid receptor 4	Mm.35288.1	4.5	5.3	**1.7**	0.035

Supplemental Table 8. Significant differently expressed genes in 1KI HCC samples

Affymetrix ID	Gene Symbol	Description	Transcript ID (Array Design)	3aKO avg signal log2 (n=5)	1KI Avg Signal log2 (n=5)	Fold Change (linear)	ANOVA p-value
1449483_at	Polk	polymerase (DNA directed), kappa	Mm.89926.1	6.7	7.4	**1.7**	0.002
1457619_at	Ces2b	carboxyesterase 2B	Mm.117410.1	3.3	4.1	**1.7**	0.020
1424278_a_at	Birc5	baculoviral IAP repeat-containing 5	Mm.8552.2	4.4	5.2	**1.7**	0.044
1426381_at	Pprc1	peroxisome proliferative activated receptor, gamma, coactivator-related 1	Mm.2415.1	7.0	7.8	**1.7**	0.042
1427718_a_at	Mdm2	transformed mouse 3T3 cell double minute 2	Mm.22670.2	8.2	8.9	**1.7**	0.000
1456292_a_at	Vim	vimentin	Mm.7.4	5.7	6.5	**1.7**	0.033
1460732_a_at	Ppl	periplakin	Mm.10225.1	7.0	7.8	**1.7**	0.036
1430172_a_at	Cyp4f16	cytochrome P450, family 4, subfamily f, polypeptide 16; cytochrome P450, family 4, subfamily f, polypeptide 37	Mm.30504.2	6.3	7.1	**1.7**	0.044
1460243_at	Sptlc2	serine palmitoyltransferase, long chain base subunit 2	Mm.565.1	7.7	8.5	**1.7**	0.029
1416342_at	Tnc	tenascin C	Mm.980.1	4.6	5.4	**1.7**	0.010
1417327_at	Cav2	caveolin 2	Mm.31915.1	7.1	7.9	**1.7**	0.040
1418004_a_at	Tmem176b	transmembrane protein 176B	Mm.28385.1	11.9	12.7	**1.7**	0.018
1425398_at	Hist1h2bf	histone cluster 1, H2bf; histone cluster 1, H2bj; histone cluster 1, H2bl; histone cluster 1, H2bn; histone cluster 1, H2bq; histone cluster 1 H2br	Mm.21579.2	3.2	4.0	**1.7**	0.011
1425911_a_at	Fgfr1	fibroblast growth factor receptor 1	Mm.3157.3	5.2	5.9	**1.7**	0.015
1450020_at	Cx3cr1	chemokine (C-X3-C motif) receptor 1	Mm.44065.1	5.1	5.8	**1.7**	0.028
1451122_at	Idi1	isopentenyl-diphosphate delta isomerase	Mm.29847.1	11.7	12.5	**1.7**	0.015
1417837_at	Phlda2	pleckstrin homology-like domain, family A, member 2	Mm.23697.1	5.6	6.4	**1.7**	0.020
1419070_at	Cys1	cystin 1	Mm.52265.1	7.1	7.9	**1.7**	0.002
1426806_at	Nabp1	nucleic acid binding protein 1	Mm.196290.1	7.2	7.9	**1.7**	0.029
1434748_at	Ckap2	cytoskeleton associated protein 2	Mm.22448.1	5.6	6.3	**1.7**	0.010
1451224_at	Scamp5	secretory carrier membrane protein 5	Mm.102278.2	7.1	7.9	**1.7**	0.008
1423957_at	Aen	apoptosis enhancing nuclease	Mm.34109.2	8.5	9.2	**1.6**	0.027
1426774_at	Parp12	poly (ADP-ribose) polymerase family, member 12	Mm.29894.1	8.8	9.5	**1.6**	0.019
1426817_at	Mki67	antigen identified by monoclonal antibody Ki 67	Mm.4078.1	5.0	5.7	**1.6**	0.033
1443095_at			Mm.127026.1	4.1	4.8	**1.6**	0.033
1448682_at	Dynll1	dynein light chain LC8-type 1	Mm.29908.1	9.9	10.6	**1.6**	0.039
1417817_a_at	Wwtr1	WW domain containing transcription regulator 1	Mm.28060.1	7.0	7.7	**1.6**	0.030
1419089_at	Timp3	tissue inhibitor of metalloproteinase 3	Mm.4871.1	7.4	8.1	**1.6**	0.006
1430201_at	9130017K11 Rik	RIKEN cDNA 9130017K11 gene	Mm.158885.1	3.7	4.4	**1.6**	0.008
1459632_at			Mm.217722.1	5.0	5.6	**1.6**	0.008

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1416579_a_at	Epcam	epithelial cell adhesion molecule	Mm.4259.1	6.0	6.7	**1.6**	0.012
1418260_at	Hunk	hormonally upregulated Neu-associated kinase	Mm.25120.1	6.7	7.3	**1.6**	0.017
1418456_a_at	Cxcl14	chemokine (C-X-C motif) ligand 14	Mm.30211.1	6.4	7.1	**1.6**	0.002
1419518_at	Tuba8	tubulin, alpha 8	Mm.32884.1	5.7	6.4	**1.6**	0.034
1419943_s_at	Ccnb1	cyclin B1; predicted gene 5593	Mm.195316.1	5.3	5.9	**1.6**	0.023
1424880_at	Trib1	tribbles homolog 1 (Drosophila)	Mm.40298.1	8.4	9.1	**1.6**	0.049
1427005_at	Plk2	polo-like kinase 2	Mm.380.1	7.9	8.6	**1.6**	0.003
1427386_at	Arhgef16	Rho guanine nucleotide exchange factor (GEF) 16	Mm.38481.1	6.0	6.7	**1.6**	0.019
1435353_a_at	Pisd-ps1	phosphatidylserine decarboxylase, pseudogene 1; phosphatidylserine decarboxylase, pseudogene 3	Mm.30245.3	9.2	9.9	**1.6**	0.006
1450061_at	Enc1	ectodermal-neural cortex 1	Mm.30502.1	6.6	7.3	**1.6**	0.004
1419088_at	Timp3	tissue inhibitor of metalloproteinase 3	Mm.4871.1	6.3	6.9	**1.6**	0.003
1421063_s_at	Snrpn	small nuclear ribonucleoprotein N; SNRPN upstream reading frame	Mm.195990.1	7.1	7.8	**1.6**	0.019
1422018_at	Hivep2	human immunodeficiency virus type I enhancer binding protein 2	Mm.42157.1	5.6	6.3	**1.6**	0.023
1422140_at	Gm7609	component of Sp100-rs; predicted gene 2666; predicted pseudogene 7609; uncharacterized LOC100041903; uncharacterized LOC100503923	Mm.207045.1	6.4	7.0	**1.6**	0.011
1428209_at	Bex4	brain expressed gene 4	Mm.14768.2	3.1	3.8	**1.6**	0.019
1429204_at	Camk2n2	calcium/calmodulin-dependent protein kinase II inhibitor 2	Mm.31199.1	5.8	6.5	**1.6**	0.021
1429233_at	Sept11	septin 11	Mm.27384.1	8.2	8.9	**1.6**	0.001
1441129_at			Mm.207515.1	4.0	4.7	**1.6**	0.000
1448568_a_at	Slc20a1	solute carrier family 20, member 1	Mm.16757.1	9.3	10.0	**1.6**	0.013
1449024_a_at	Hexa	hexosaminidase A	Mm.2284.1	9.4	10.1	**1.6**	0.043
1452242_at	Cep55	centrosomal protein 55	Mm.9916.1	3.6	4.3	**1.6**	0.047
1415834_at	Dusp6	dual specificity phosphatase 6	Mm.1791.1	9.6	10.3	**1.6**	0.037
1418711_at	Pdgfa	platelet derived growth factor, alpha	Mm.2675.1	6.7	7.4	**1.6**	0.003
1418943_at	B230120H23Rik	sterile alpha motif and leucine zipper containing kinase AZK	Mm.33127.1	6.3	6.9	**1.6**	0.020
1423605_a_at	Mdm2	transformed mouse 3T3 cell double minute 2	Mm.22670.1	8.9	9.5	**1.6**	0.000
1424394_at	Selm	selenoprotein M	Mm.34046.1	5.9	6.5	**1.6**	0.041
1427884_at	Col3a1	collagen, type III, alpha 1	Mm.147387.1	4.3	5.0	**1.6**	0.045
1428146_s_at	Acaa2	acetyl-Coenzyme A acyltransferase 2 (mitochondrial 3-oxoacyl-Coenzyme A thiolase)	Mm.142498.1	12.1	12.8	**1.6**	0.011
1436847_s_at	Cdca8	cell division cycle associated 8	Mm.28038.2	5.9	6.5	**1.6**	0.010
1438408_at	Sowahb	sosondowah ankyrin repeat domain family member B	Mm.76746.1	7.3	8.0	**1.6**	0.050
1445144_at			Mm.173903.1	6.9	7.5	**1.6**	0.005

Supplemental Table 8. Significant differently expressed genes in 1KI HCC samples

Affymetrix ID	Gene Symbol	Description	Transcript ID (Array Design)	3aKO avg signal log2 (n=5)	1KI Avg Signal log2 (n=5)	Fold Change (linear)	ANOVA p-value
1450342_at	Bmp8b	bone morphogenetic protein 8b	Mm.30413.1	3.8	4.4	**1.6**	0.023
1450843_a_at	Serpinh1	serine (or cysteine) peptidase inhibitor, clade H, member 1	Mm.22708.1	6.4	7.0	**1.6**	0.013
1450986_at	Nop58	NOP58 ribonucleoprotein	Mm.10303.1	7.7	8.3	**1.6**	0.020
1460583_at	Golt1b	golgi transport 1 homolog B (S. cerevisiae)	Mm.80325.1	3.6	4.3	**1.6**	0.040
1415890_at	Papss1	3'-phosphoadenosine 5'-phosphosulfate synthase 1	Mm.18161.1	8.4	9.0	**1.6**	0.047
1415935_at	Smoc2	SPARC related modular calcium binding 2	Mm.30162.1	5.8	6.5	**1.6**	0.004
1417450_a_at	Tacc3	transforming, acidic coiled-coil containing protein 3	Mm.27836.1	4.4	5.1	**1.6**	0.045
1424050_s_at	Fgfr1	fibroblast growth factor receptor 1	Mm.3157.2	5.8	6.4	**1.6**	0.022
1427137_at	Ces2e	carboxylesterase 2E	Mm.218630.1	9.7	10.4	**1.6**	0.032
1429234_s_at	Sept11	septin 11	Mm.27384.1	8.2	8.9	**1.6**	0.000
1434240_at	4632434I11Rik	DNA damage-induced apoptosis suppressor	Mm.26468.2	3.0	3.6	**1.6**	0.009
1436362_x_at	2700079J08Rik	RIKEN cDNA 2700079J08 gene	Mm.220953.2	8.3	8.9	**1.6**	0.019
1437469_at	Zfp750	zinc finger protein 750	Mm.11395.1	7.0	7.6	**1.6**	0.007
1440916_at	2510049J12Rik	makorin, ring finger protein 2, opposite strand	Mm.133694.1	8.5	9.2	**1.6**	0.003
1460677_at	Spats2	spermatogenesis associated, serine-rich 2	Mm.21619.1	7.7	8.4	**1.6**	0.018
1416299_at	Shcbp1	Shc SH2-domain binding protein 1	Mm.37801.1	4.0	4.6	**1.6**	0.046
1423905_at	Pvr	poliovirus receptor	Mm.134436.1	5.5	6.2	**1.6**	0.030
1424030_at	Grhl1	grainyhead-like 1 (Drosophila)	Mm.25552.1	5.0	5.7	**1.6**	0.048
1428260_at	Atl1	atlastin GTPase 1	Mm.26381.1	4.4	5.1	**1.6**	0.042
1433857_at	Fat1	FAT tumor suppressor homolog 1 (Drosophila)	Mm.27365.1	9.8	10.4	**1.6**	0.009
1440139_at			Mm.174301.1	3.4	4.1	**1.6**	0.002
1444728_at			Mm.207868.1	5.5	6.2	**1.6**	0.021
1451928_a_at	Rad18	RAD18 homolog (S. cerevisiae)	Mm.103812.2	4.7	5.4	**1.6**	0.011
1415828_a_at	Serp1	stress-associated endoplasmic reticulum protein 1	Mm.29702.1	11.7	12.3	**1.6**	0.002
1416665_at	Coq7	demethyl-Q 7	Mm.20634.1	8.8	9.5	**1.6**	0.014
1417818_at	Wwtr1	WW domain containing transcription regulator 1	Mm.28060.1	8.0	8.7	**1.6**	0.018
1426208_x_at	Plagl1	pleiomorphic adenoma gene-like 1	Mm.220978.3	6.7	7.3	**1.6**	0.021

Supplemental Table 8. Significant differently expressed genes in 1KI HCC samples

Affymetrix ID	Gene Symbol	Description	Transcript ID (Array Design)	3aKO avg signal log2 (n=5)	1KI Avg Signal log2 (n=5)	Fold Change (linear)	ANOVA p-value
1431658_at	Hist1h4a	histone cluster 1, H4a; histone cluster 1, H4b; histone cluster 1, H4c; histone cluster 1, H4d; histone cluster 1, H4f; histone cluster 1, H4h; histone cluster 1, H4i; histone cluster 1, H4j; histone cluster 1, H4k; histone cluster 1, H4m; histone cluster 1, H4n; histone cluster 2, H4; histone cluster 4, H4	Mm.53269.1	3.3	3.9	**1.6**	0.002
1432885_at	4632432E15Rik	RIKEN cDNA 4632432E15 gene	Mm.195692.1	4.3	5.0	**1.6**	0.043
1433536_at	Lrp11	low density lipoprotein receptor-related protein 11	Mm.206759.1	5.8	6.4	**1.6**	0.003
1433770_at	Dpysl2	dihydropyrimidinase-like 2	Mm.34656.1	8.6	9.2	**1.6**	0.008
1436660_at	Rrbp1	ribosome binding protein 1	Mm.190511.1	6.4	7.1	**1.6**	0.011
1438973_x_at	Gja1	gap junction protein, alpha 1	Mm.4504.6	5.0	5.6	**1.6**	0.003
1443086_at	Alcam	activated leukocyte cell adhesion molecule	Mm.216113.1	7.8	8.4	**1.6**	0.016
1453852_at	Ddx50	DEAD (Asp-Glu-Ala-Asp) box polypeptide 50	Mm.96287.1	5.6	6.3	**1.6**	0.014
1456927_at	Mast2	microtubule associated serine/threonine kinase 2	Mm.87251.1	4.1	4.8	**1.6**	0.001
1416222_at	Nsdhl	NAD(P) dependent steroid dehydrogenase-like	Mm.38792.1	11.4	12.0	**1.6**	0.032
1422006_at	Eif2ak2	eukaryotic translation initiation factor 2-alpha kinase 2	Mm.807.1	6.3	7.0	**1.6**	0.002
1425113_x_at			Mm.172352.1	9.1	9.7	**1.6**	0.033
1434789_at	Depdc1b	DEP domain containing 1B	Mm.32318.1	4.9	5.6	**1.6**	0.035
1436038_a_at	Pigp	phosphatidylinositol glycan anchor biosynthesis, class P	Mm.39490.4	8.4	9.1	**1.6**	0.027
1440975_at	Mxra7	matrix-remodelling associated 7	Mm.44857.1	5.1	5.8	**1.6**	0.012
1446258_at	9530067D14Rik	Riken cDNA 9530067D14 gene	Mm.215385.1	6.7	7.3	**1.6**	0.004
1446720_at			Mm.182621.1	6.0	6.6	**1.6**	0.021
1448627_s_at	Pbk	PDZ binding kinase	Mm.24337.1	4.6	5.3	**1.6**	0.014
1450247_a_at	Scamp5	secretory carrier membrane protein 5	Mm.102278.1	7.0	7.6	**1.6**	0.007
1453714_a_at	Shroom3	shroom family member 3	Mm.46014.3	5.4	6.1	**1.6**	0.034
1455390_at	Alkbh6	alkB, alkylation repair homolog 6 (E. coli)	Mm.40726.1	7.6	8.2	**1.6**	0.012
1416554_at	Pdlim1	PDZ and LIM domain 1 (elfin)	Mm.5567.1	10.1	10.7	**1.5**	0.003
1430623_s_at	Nabp1	nucleic acid binding protein 1	Mm.219618.1	7.6	8.2	**1.5**	0.018
1439433_a_at	Slc35a2	solute carrier family 35 (UDP-galactose transporter), member A2	Mm.214976.5	6.1	6.7	**1.5**	0.020
1441372_at	5930405F01Rik	RIKEN cDNA 5930405F01 gene	Mm.207507.1	4.5	5.1	**1.5**	0.000
1441797_at			Mm.215957.1	5.0	5.6	**1.5**	0.019
1441910_x_at	Ccne1	cyclin E1	Mm.128432.1	6.5	7.1	**1.5**	0.003

Supplemental Table 8. Significant differently expressed genes in 1KI HCC samples

Affymetrix ID	Gene Symbol	Description	Transcript ID (Array Design)	3aKO avg signal log2 (n=5)	1KI Avg Signal log2 (n=5)	Fold Change (linear)	ANOVA p-value
1449187_at	Pdgfa	platelet derived growth factor, alpha	Mm.2675.1	6.9	7.6	**1.5**	0.009
1451526_at	Arhgap12	Rho GTPase activating protein 12	Mm.22834.1	6.2	6.8	**1.5**	0.023
1455548_at	Dlgap4	discs, large homolog-associated protein 4 (Drosophila)	Mm.41192.1	6.5	7.1	**1.5**	0.012
1455987_at	Sec61a1	Sec61 alpha 1 subunit (S. cerevisiae)	Mm.28375.3	6.4	7.0	**1.5**	0.024
1416837_at	Bax	BCL2-associated X protein	Mm.19904.1	8.5	9.2	**1.5**	0.002
1420768_a_at	Dhx58	DEXH (Asp-Glu-X-His) box polypeptide 58	Mm.170797.1	4.3	4.9	**1.5**	0.001
1422779_at	Smpd3	sphingomyelin phosphodiesterase 3, neutral	Mm.143806.1	4.4	5.1	**1.5**	0.043
1434975_x_at	Pisd-ps3	phosphatidylserine decarboxylase, pseudogene 3	Mm.30245.2	9.7	10.3	**1.5**	0.019
1438668_x_at	Atxn2l	ataxin 2-like	Mm.22653.1	8.0	8.6	**1.5**	0.027
1439093_at	Hspa4l	heat shock protein 4 like	Mm.155691.1	6.5	7.1	**1.5**	0.015
1449110_at	Rhob	ras homolog gene family, member B	Mm.687.1	9.6	10.2	**1.5**	0.003
1449117_at	Jund	jun D proto-oncogene	Mm.1175.1	9.3	9.9	**1.5**	0.002
1451310_a_at	Ctsl	cathepsin L	Mm.930.2	12.2	12.8	**1.5**	0.009
1419493_a_at	Tpd52	tumor protein D52	Mm.2777.1	8.4	9.0	**1.5**	0.036
1420704_at	Csf2ra	colony stimulating factor 2 receptor, alpha, low-affinity (granulocyte-macrophage)	Mm.156264.1	4.7	5.3	**1.5**	0.022
1423648_at	Pdia6	protein disulfide isomerase associated 6	Mm.182959.1	11.2	11.8	**1.5**	0.009
1426376_at	Reep5	receptor accessory protein 5	Mm.21251.2	7.1	7.7	**1.5**	0.019
1428228_at	Pgm3	phosphoglucomutase 3	Mm.20245.1	7.4	8.0	**1.5**	0.031
1434564_at	E2f3	E2F transcription factor 3	Mm.86324.1	6.8	7.4	**1.5**	0.001
1436473_at	Zfp248	zinc finger protein 248	Mm.68415.1	2.6	3.2	**1.5**	0.016
1449334_at	Timp3	tissue inhibitor of metalloproteinase 3	Mm.4871.1	7.3	7.9	**1.5**	0.002
1450677_at	Chek1	checkpoint kinase 1	Mm.16753.1	3.3	3.9	**1.5**	0.029
1452214_at	Skil	SKI-like	Mm.23176.1	8.5	9.1	**1.5**	0.019
1452217_at	Ahnak	AHNAK nucleoprotein (desmoyokin)	Mm.203866.1	6.9	7.5	**1.5**	0.003
1453434_at	1110019D14Rik	RIKEN cDNA 1110019D14 gene	Mm.54132.1	3.9	4.5	**1.5**	0.003
1456693_at	Gm20213	predicted gene, 20213	Mm.54297.1	3.4	4.0	**1.5**	0.043
1456733_x_at	Serpinh1	serine (or cysteine) peptidase inhibitor, clade H, member 1	Mm.22708.4	6.6	7.2	**1.5**	0.010
1460121_at	9630010G10Rik	RIKEN cDNA 9630010G10 gene	Mm.89324.1	5.4	6.0	**1.5**	0.010
1460698_a_at	Sec11c	SEC11 homolog C (S. cerevisiae)	Mm.27800.1	9.1	9.7	**1.5**	0.013
1416199_at	Kifc3	kinesin family member C3	Mm.22513.1	7.7	8.3	**1.5**	0.019
1418591_at	Dnaja4	DnaJ (Hsp40) homolog, subfamily A, member 4	Mm.52319.1	6.6	7.1	**1.5**	0.026
1423721_at	Tpm1	tropomyosin 1, alpha	Mm.121878.2	8.7	9.3	**1.5**	0.034
1423804_a_at	Idi1	isopentenyl-diphosphate delta isomerase	Mm.29847.1	9.2	9.8	**1.5**	0.037
1424289_at	Osgin2	oxidative stress induced growth inhibitor family member 2	Mm.46455.1	5.5	6.1	**1.5**	0.043

Supplemental Table 8. Significant differently expressed genes in 1KI HCC samples

Affymetrix ID	Gene Symbol	Description	Transcript ID (Array Design)	3aKO avg signal log2 (n=5)	1KI Avg Signal log2 (n=5)	Fold Change (linear)	ANOVA p-value
1427869_at	Ighm	immunoglobulin heavy constant mu	Mm.196085.1	4.3	4.9	**1.5**	0.049
1439041_at	Slc39a10	solute carrier family 39 (zinc transporter), member 10	Mm.215090.1	5.2	5.8	**1.5**	0.021
1442368_at	Kctd12b	potassium channel tetramerisation domain containing 12b	Mm.211646.1	3.5	4.1	**1.5**	0.044
1445606_a_at	2900009J06Rik	RIKEN cDNA 2900009J06 gene	Mm.25735.1	5.8	6.4	**1.5**	0.037
1447640_s_at	Pbx3	pre B cell leukemia homeobox 3	Mm.137604.1	5.4	6.0	**1.5**	0.026
1451431_a_at	Dbndd2	dysbindin (dystrobrevin binding protein 1) domain containing 2	Mm.195525.1	8.4	9.0	**1.5**	0.043
1417184_s_at	Hbb-b1	hemoglobin, beta adult major chain; hemoglobin, beta adult minor chain; hemoglobin, beta adult s chain; hemoglobin, beta adult t chain	Mm.206691.1	14.1	13.5	**-1.5**	0.040
1417898_a_at	Gzma	granzyme A	Mm.15510.1	6.5	5.9	**-1.5**	0.016
1425057_at	Pbld1	phenazine biosynthesis-like protein domain containing 1	Mm.104960.1	11.4	10.9	**-1.5**	0.016
1425597_a_at	Qk	quaking	Mm.2655.3	5.8	5.2	**-1.5**	0.001
1425851_a_at	Amigo1	adhesion molecule with Ig like domain 1	Mm.153435.1	6.6	6.0	**-1.5**	0.005
1438349_at	Zfp229	zinc finger protein 229	Mm.28736.1	5.0	4.4	**-1.5**	0.009
1448825_at	Pdk2	pyruvate dehydrogenase kinase, isoenzyme 2	Mm.29768.1	9.8	9.2	**-1.5**	0.016
1449579_at	Sh3yl1	Sh3 domain YSC-like 1	Mm.218624.1	8.5	7.9	**-1.5**	0.032
1455506_at	Slc25a34	solute carrier family 25, member 34	Mm.101716.1	7.2	6.6	**-1.5**	0.011
1421825_at	Bace1	beta-site APP cleaving enzyme 1	Mm.24044.1	6.8	6.2	**-1.5**	0.018
1426876_at	Pm20d1	peptidase M20 domain containing 1	Mm.23844.1	11.3	10.7	**-1.5**	0.042
1428926_at	Fbxo31	F-box protein 31	Mm.41330.1	8.6	8.0	**-1.5**	0.005
1432509_at	5033430I15Rik	RIKEN cDNA 5033430I15 gene	Mm.44949.1	5.4	4.8	**-1.5**	0.030
1436332_at	Hspb6	heat shock protein, alpha-crystallin-related, B6	Mm.34885.1	8.2	7.6	**-1.5**	0.026
1437590_at	Pyroxd2	pyridine nucleotide-disulphide oxidoreductase domain 2	Mm.212966.1	7.8	7.2	**-1.5**	0.010
1447750_x_at	Pih1d1	PIH1 domain containing 1	Mm.82139.1	8.1	7.5	**-1.5**	0.002
1448938_at	Rpa3	replication protein A3	Mm.29073.1	8.3	7.7	**-1.5**	0.013
1451543_at	Fbxo21	F-box protein 21	Mm.216305.1	8.5	7.9	**-1.5**	0.037
1418996_a_at	Lyrm5	LYR motif containing 5	Mm.46847.1	11.1	10.5	**-1.5**	0.011
1426850_a_at	Map2k6	mitogen-activated protein kinase kinase 6	Mm.14487.2	7.7	7.1	**-1.5**	0.044
1428562_at	Mir22hg	Mir22 host gene (non-protein coding)	Mm.41393.1	8.9	8.2	**-1.5**	0.010
1431011_at	Dlst	dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex)	Mm.28365.2	8.2	7.5	**-1.5**	0.003
1436109_at	AI317395	expressed sequence AI317395	Mm.220844.1	9.7	9.1	**-1.5**	0.045

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Affymetrix ID	Gene Symbol	Description	Transcript ID (Array Design)	3aKO avg signal log2 (n=5)	1KI Avg Signal log2 (n=5)	Fold Change (linear)	ANOVA p-value
1437473_at	Maf	avian musculoaponeurotic fibrosarcoma (v-maf) AS42 oncogene homolog	Mm.18453.1	7.9	7.3	**-1.5**	0.046
1444143_at			Mm.117589.1	5.8	5.2	**-1.5**	0.006
1446861_at	Gns	glucosamine (N-acetyl)-6-sulfatase	Mm.209847.1	7.2	6.6	**-1.5**	0.001
1449186_at	Bag4	BCL2-associated athanogene 4	Mm.27102.1	8.8	8.2	**-1.5**	0.043
1458295_at	BC038331	cDNA sequence BC038331	Mm.78325.1	6.6	6.0	**-1.5**	0.002
1460216_at	Acads	acyl-Coenzyme A dehydrogenase, short chain	Mm.18759.1	11.1	10.5	**-1.5**	0.006
1416631_at	Ap4b1	adaptor-related protein complex AP-4, beta 1	Mm.29234.1	7.8	7.2	**-1.5**	0.007
1424399_at	Uck1	uridine-cytidine kinase 1	Mm.2559.1	9.4	8.8	**-1.5**	0.042
1434742_s_at	Aifm3	apoptosis-inducing factor, mitochondrion-associated 3	Mm.40038.2	7.0	6.4	**-1.5**	0.027
1439831_at		predicted gene 4951	Mm.100018.1	10.8	10.2	**-1.5**	0.003
1448930_at	3010026O09 Rik	RIKEN cDNA 3010026O09 gene	Mm.41784.1	6.9	6.3	**-1.5**	0.003
1449443_at	Decr1	2,4-dienoyl CoA reductase 1, mitochondrial	Mm.24395.1	9.5	8.9	**-1.5**	0.033
1451627_a_at	Slc1a2	solute carrier family 1 (glial high affinity glutamate transporter), member 2	Mm.2861.2	9.3	8.7	**-1.5**	0.039
1452416_at	Il6ra	interleukin 6 receptor, alpha	Mm.2856.2	9.3	8.7	**-1.5**	0.020
1453961_a_at	Mospd3	motile sperm domain containing 3	Mm.41355.2	7.4	6.8	**-1.5**	0.037
1457279_at	Gm17586	predicted gene, 17586	Mm.139237.1	6.5	5.9	**-1.5**	0.003
1458395_at	B930054O08	uncharacterized protein B930054O08	Mm.33144.1	7.6	7.0	**-1.5**	0.020
1416772_at	Cpt2	carnitine palmitoyltransferase 2	Mm.29499.1	11.7	11.0	**-1.6**	0.027
1423871_at	Tmem63a	transmembrane protein 63a	Mm.185518.1	8.6	8.0	**-1.6**	0.009
1427082_at	Sdr42e1	short chain dehydrogenase/reductase family 42E, member 1	Mm.23630.1	11.5	10.9	**-1.6**	0.048
1427100_at	Metrn	meteorin, glial cell differentiation regulator	Mm.41925.1	7.6	7.0	**-1.6**	0.022
1427957_at	Adtrp	androgen dependent TFPI regulating protein	Mm.25195.1	11.7	11.1	**-1.6**	0.045
1428290_at	Mipep	mitochondrial intermediate peptidase	Mm.38407.1	9.6	9.0	**-1.6**	0.023
1433705_at	Zfp213	zinc finger protein 213	Mm.6929.1	7.3	6.7	**-1.6**	0.029
1436187_at	1110054M08 Rik	RIKEN cDNA 1110054M08 gene	Mm.205997.1	9.2	8.6	**-1.6**	0.014
1441033_at	Tmtc2	transmembrane and tetratricopeptide repeat containing 2	Mm.25225.1	5.6	4.9	**-1.6**	0.024
1441342_at	Dpp4	dipeptidylpeptidase 4	Mm.189904.1	7.9	7.2	**-1.6**	0.028
1444178_at	Gm9895	predicted gene 9895	Mm.103412.1	6.8	6.2	**-1.6**	0.000
1444531_at			Mm.40499.1	7.3	6.6	**-1.6**	0.008
1447811_s_at	Amigo1	adhesion molecule with Ig like domain 1	Mm.44915.2	6.4	5.8	**-1.6**	0.005

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Affymetrix ID	Gene Symbol	Description	Transcript ID (Array Design)	3aKO avg signal log2 (n=5)	1KI Avg Signal log2 (n=5)	Fold Change (linear)	ANOVA p-value
1450816_at	Polg2	polymerase (DNA directed), gamma 2, accessory subunit	Mm.859.1	8.4	7.8	**-1.6**	0.003
1460659_at			Mm.200447.2	6.7	6.1	**-1.6**	0.003
1419747_at	Asgr2	asialoglycoprotein receptor 2	Mm.1357.1	10.1	9.4	**-1.6**	0.003
1434065_at	Cwf19l1	CWF19-like 1, cell cycle control (S. pombe)	Mm.36543.1	9.3	8.6	**-1.6**	0.007
1441765_at		pantothenate kinase 1	Mm.209969.1	8.4	7.8	**-1.6**	0.025
1444805_at			Mm.182876.1	4.3	3.6	**-1.6**	0.005
1457991_at			Mm.161241.1	6.3	5.6	**-1.6**	0.026
1460159_at	Mysm1	myb-like, SWIRM and MPN domains 1	Mm.208868.1	5.1	4.4	**-1.6**	0.003
1418238_at	Ivd	isovaleryl coenzyme A dehydrogenase	Mm.6635.1	11.1	10.4	**-1.6**	0.022
1420549_at	Gbp2b	guanylate binding protein 2b	Mm.250.1	6.5	5.9	**-1.6**	0.033
1441926_x_at	Tmie	transmembrane inner ear	Mm.153982.1	6.8	6.2	**-1.6**	0.019
1446742_at			Mm.209315.1	4.2	3.6	**-1.6**	0.047
1451405_at	Pcca	propionyl-Coenzyme A carboxylase, alpha polypeptide	Mm.23876.1	11.3	10.6	**-1.6**	0.030
1451782_a_at	Slc29a1	solute carrier family 29 (nucleoside transporters), member 1	Mm.29744.3	11.2	10.6	**-1.6**	0.049
1455502_at	Madd	MAP-kinase activating death domain	Mm.36410.1	8.4	7.7	**-1.6**	0.021
1415944_at	Sdc1	syndecan 1	Mm.2580.1	10.6	9.9	**-1.6**	0.043
1416739_a_at	Brap	BRCA1 associated protein	Mm.153372.1	8.4	7.7	**-1.6**	0.023
1425033_at	Slc17a2	solute carrier family 17 (sodium phosphate), member 2	Mm.24030.1	11.8	11.1	**-1.6**	0.035
1438327_at	Zfp385b	zinc finger protein 385B	Mm.87653.2	6.3	5.6	**-1.6**	0.032
1438689_at	Zfp784	zinc finger protein 784	Mm.45078.2	6.8	6.1	**-1.6**	0.019
1439144_at	Cwf19l1	CWF19-like 1, cell cycle control (S. pombe)	Mm.93826.1	7.4	6.7	**-1.6**	0.009
1440845_at	Tmem243	uncharacterized LOC102633802; transmembrane protein 243, mitochondrial	Mm.216118.2	4.9	4.2	**-1.6**	0.005
1442436_at	Fn3k	fructosamine 3 kinase	Mm.38358.1	5.7	5.0	**-1.6**	0.009
1444195_at			Mm.37916.1	7.1	6.4	**-1.6**	0.010
1450725_s_at	Car14	carbonic anhydrase 14	Mm.34556.1	9.8	9.1	**-1.6**	0.030
1453586_at	Entpd1	ectonucleoside triphosphate diphosphohydrolase 1	Mm.45585.1	5.8	5.1	**-1.6**	0.037
1425362_at	Agfg2	ArfGAP with FG repeats 2	Mm.35097.1	7.6	7.0	**-1.6**	0.016
1438082_at	Tmem206	transmembrane protein 206	Mm.205569.2	6.7	6.0	**-1.6**	0.026
1438313_at			Mm.124117.1	4.2	3.5	**-1.6**	0.014
1439821_at	Lrp2bp	Lrp2 binding protein	Mm.115430.1	5.6	4.9	**-1.6**	0.012
1442258_at	Lonp2	lon peptidase 2, peroxisomal	Mm.178192.1	8.2	7.5	**-1.6**	0.044
1423488_at	Mmd	monocyte to macrophage differentiation-associated	Mm.38791.1	12.0	11.3	**-1.6**	0.035
1425088_at	Scnn1a	sodium channel, nonvoltage-gated 1 alpha	Mm.144114.1	8.4	7.7	**-1.6**	0.024

Supplemental Table 8. Significant differently expressed genes in 1KI HCC samples

Affymetrix ID	Gene Symbol	Description	Transcript ID (Array Design)	3aKO avg signal log2 (n=5)	1KI Avg Signal log2 (n=5)	Fold Change (linear)	ANOVA p-value
1431189_a_at	Fahd2a	fumarylacetoacetate hydrolase domain containing 2A	Mm.180782.2	7.6	6.9	**-1.6**	0.018
1449534_at	Sycp3	synaptonemal complex protein 3	Mm.148209.1	4.0	3.3	**-1.6**	0.023
1460373_a_at	Setd4	SET domain containing 4	Mm.981.1	7.6	6.9	**-1.6**	0.024
1416187_s_at	Pnrc2	proline-rich nuclear receptor coactivator 2	Mm.29159.1	7.7	7.0	**-1.6**	0.009
1416987_at	Elp4	elongation protein 4 homolog (S. cerevisiae)	Mm.33870.1	5.5	4.8	**-1.6**	0.015
1418311_at	Fn3k	fructosamine 3 kinase	Mm.32787.1	7.9	7.2	**-1.6**	0.030
1439175_at			Mm.184021.1	6.9	6.3	**-1.6**	0.022
1444622_at			Mm.202462.1	5.8	5.2	**-1.6**	0.039
1447372_at	Aldh16a1	aldehyde dehydrogenase 16 family, member A1	Mm.212548.1	8.7	8.0	**-1.6**	0.018
1447380_at	Amdhd1	amidohydrolase domain containing 1	Mm.214299.1	8.1	7.4	**-1.6**	0.005
1448756_at	S100a9	S100 calcium binding protein A9 (calgranulin B)	Mm.2128.1	7.1	6.4	**-1.6**	0.012
1419687_at	Macrod1	MACRO domain containing 1	Mm.38346.1	10.1	9.4	**-1.6**	0.021
1428978_at	2900009J20Rik		Mm.82240.1	6.6	5.9	**-1.6**	0.004
1429692_s_at	Gch1	GTP cyclohydrolase 1	Mm.41683.2	9.8	9.1	**-1.6**	0.023
1432492_a_at	Haao	3-hydroxyanthranilate 3,4-dioxygenase	Mm.30100.2	12.9	12.2	**-1.6**	0.019
1441878_s_at	Oxld1	oxidoreductase like domain containing 1	Mm.136392.1	8.6	7.9	**-1.6**	0.002
1451523_a_at	Mif4gd	MIF4G domain containing	Mm.24635.1	9.2	8.5	**-1.6**	0.033
1457363_at	Gm17753	predicted gene, 17753	Mm.211685.1	8.4	7.7	**-1.6**	0.030
1457883_at	Pm20d2	peptidase M20 domain containing 2	Mm.212481.1	5.8	5.1	**-1.6**	0.018
1460336_at	Ppargc1a	peroxisome proliferative activated receptor, gamma, coactivator 1 alpha	Mm.10707.1	7.4	6.7	**-1.6**	0.043
1419997_at			Mm.195273.1	6.1	5.4	**-1.6**	0.046
1417639_at	Slc22a4	solute carrier family 22 (organic cation transporter), member 4	Mm.42185.1	5.0	4.3	**-1.6**	0.003
1422526_at	Acsl1	acyl-CoA synthetase long-chain family member 1	Mm.28962.1	12.1	11.4	**-1.6**	0.042
1424029_at	Tspyl4	TSPY-like 4	Mm.21485.1	7.0	6.3	**-1.6**	0.048
1434293_at	Hectd3	HECT domain containing 3	Mm.220986.1	7.5	6.8	**-1.6**	0.002
1425177_at	Shmt1	serine hydroxymethyltransferase 1 (soluble)	Mm.3379.2	11.5	10.8	**-1.7**	0.040
1427370_at	Amdhd1	amidohydrolase domain containing 1	Mm.80810.1	10.8	10.1	**-1.7**	0.003
1435551_at	Fhod3	formin homology 2 domain containing 3	Mm.28387.1	5.0	4.3	**-1.7**	0.007
1449310_at	Ptger2	prostaglandin E receptor 2 (subtype EP2)	Mm.4630.1	4.5	3.8	**-1.7**	0.028
1451512_s_at	Hibch	3-hydroxyisobutyryl-Coenzyme A hydrolase	Mm.25250.1	10.2	9.5	**-1.7**	0.022
1438775_at			Mm.32269.1	5.3	4.6	**-1.7**	0.010
1441285_at	Pdp2		Mm.151162.1	8.3	7.6	**-1.7**	0.006

Supplemental Table 8. Significant differently expressed genes in 1KI HCC samples

Affymetrix ID	Gene Symbol	Description	Transcript ID (Array Design)	3aKO avg signal log2 (n=5)	1KI Avg Signal log2 (n=5)	Fold Change (linear)	ANOVA p-value
1452005_at	Dlat	dihydrolipoamide S-acetyltransferase (E2 component of pyruvate dehydrogenase complex)	Mm.38786.1	7.4	6.6	**-1.7**	0.009
1455095_at	Hist2h2be	histone cluster 2, H2be	Mm.5220.1	5.5	4.8	**-1.7**	0.002
1427974_s_at	Cacna1d	calcium channel, voltage-dependent, L type, alpha 1D subunit	Mm.9772.1	6.2	5.5	**-1.7**	0.005
1431381_at	3110005L24 Rik	RIKEN cDNA 3110005L24 gene	Mm.158940.1	5.7	5.0	**-1.7**	0.013
1441242_at			Mm.133119.1	7.0	6.3	**-1.7**	0.048
1449403_at	Pde9a	phosphodiesterase 9A	Mm.10812.1	8.2	7.4	**-1.7**	0.027
1457110_at	Pank1	pantothenate kinase 1	Mm.129337.1	7.0	6.2	**-1.7**	0.002
1460061_at			Mm.74137.1	6.0	5.2	**-1.7**	0.016
1417212_at	Fam195a	family with sequence similarity 195, member A	Mm.34532.1	10.2	9.4	**-1.7**	0.010
1435682_at	Lars2	leucyl-tRNA synthetase, mitochondrial	Mm.27719.1	7.7	7.0	**-1.7**	0.002
1448034_at	Inca1	inhibitor of CDK, cyclin A1 interacting protein 1	Mm.2295.1	9.3	8.6	**-1.7**	0.013
1452828_at	Fbxo21	F-box protein 21	Mm.21912.1	10.1	9.3	**-1.7**	0.032
1453081_at	2410022M11 Rik	RIKEN cDNA 2410022M11 gene	Mm.218553.1	8.0	7.3	**-1.7**	0.001
1416142_at	Rps6	ribosomal protein S6	Mm.1139.1	8.7	7.9	**-1.7**	0.028
1417208_at	Amacr	alpha-methylacyl-CoA racemase	Mm.2787.1	11.1	10.4	**-1.7**	0.012
1436317_at	Pgap1	post-GPI attachment to proteins 1	Mm.103539.1	7.5	6.8	**-1.7**	0.023
1452914_at	N4bp2l1	NEDD4 binding protein 2-like 1	Mm.220888.1	9.3	8.5	**-1.7**	0.028
1455792_x_at	Ndn	necdin	Mm.7089.3	4.6	3.8	**-1.7**	0.012
1423731_at	Aldh16a1	aldehyde dehydrogenase 16 family, member A1	Mm.200969.1	10.3	9.5	**-1.7**	0.008
1425343_at	Hdhd3	haloacid dehalogenase-like hydrolase domain containing 3	Mm.41506.1	9.8	9.0	**-1.7**	0.048
1427373_at	Amigo1	adhesion molecule with Ig like domain 1	Mm.153435.2	6.2	5.5	**-1.7**	0.003
1443458_at	D630033O11 Rik	RIKEN cDNA D630033O11 gene	Mm.135745.1	7.9	7.2	**-1.7**	0.027
1423554_at	Ggcx	gamma-glutamyl carboxylase	Mm.19937.1	9.6	8.8	**-1.7**	0.032
1450488_at	Ccl24	chemokine (C-C motif) ligand 24	Mm.31505.1	7.2	6.4	**-1.7**	0.024
1452757_s_at	Hba-a1	hemoglobin alpha, adult chain 1; hemoglobin alpha, adult chain 2	Mm.30266.3	13.6	12.8	**-1.7**	0.004
1426847_at	Sirt4	sirtuin 4	Mm.104731.1	7.7	7.0	**-1.7**	0.002
1443056_at			Mm.167541.1	7.5	6.7	**-1.7**	0.038
1445235_at			Mm.120444.1	5.4	4.7	**-1.7**	0.002
1449817_at	Abcb11	ATP-binding cassette, sub-family B (MDR/TAP), member 11	Mm.26728.1	12.1	11.3	**-1.7**	0.028
1460673_at	Fpgs	folylpolyglutamyl synthetase	Mm.3830.1	10.8	10.0	**-1.7**	0.017
1418833_at	Agxt	alanine-glyoxylate aminotransferase	Mm.7457.1	12.4	11.6	**-1.7**	0.020
1430450_at	Atp5sl	ATP5S-like	Mm.159956.1	5.0	4.2	**-1.7**	0.016

Supplemental Table 8. Significant differently expressed genes in 1KI HCC samples

Affymetrix ID	Gene Symbol	Description	Transcript ID (Array Design)	3aKO avg signal log2 (n=5)	1KI Avg Signal log2 (n=5)	Fold Change (linear)	ANOVA p-value
1437751_at	Ppargc1a	peroxisome proliferative activated receptor, gamma, coactivator 1 alpha	Mm.10707.2	6.5	5.7	**-1.7**	0.016
1445676_at			Mm.156700.1	5.9	5.1	**-1.7**	0.031
1451156_s_at	Vldlr	very low density lipoprotein receptor	Mm.4141.2	5.5	4.7	**-1.7**	0.009
1418472_at	Aspa	aspartoacylase	Mm.20317.1	8.5	7.7	**-1.8**	0.029
1422178_a_at	Rab17	RAB17, member RAS oncogene family	Mm.38889.1	9.3	8.5	**-1.8**	0.004
1454995_at	Ddah1	dimethylarginine dimethylaminohydrolase 1	Mm.119073.1	10.8	10.0	**-1.8**	0.000
1431833_a_at	Hmgcs2	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2	Mm.10633.2	12.5	11.7	**-1.8**	0.016
1431930_x_at	Crls1	cardiolipin synthase 1	Mm.37972.3	9.8	9.0	**-1.8**	0.026
1433734_at	Slc13a4	solute carrier family 13 (sodium/sulfate symporters), member 4	Mm.23666.1	6.5	5.6	**-1.8**	0.009
1455826_a_at	Bace1	beta-site APP cleaving enzyme 1	Mm.24044.2	7.3	6.5	**-1.8**	0.003
1425312_s_at	Cpsf4l	cleavage and polyadenylation specific factor 4-like	Mm.195521.1	7.2	6.4	**-1.8**	0.026
1447157_at	4930480K23 Rik	RIKEN cDNA 4930480K23 gene	Mm.141422.1	4.2	3.4	**-1.8**	0.009
1455400_at	Ddah1	dimethylarginine dimethylaminohydrolase 1	Mm.33757.1	10.7	9.9	**-1.8**	0.001
1452107_s_at	Npnt	nephronectin	Mm.205021.4	3.7	2.9	**-1.8**	0.048
1423878_at	Gypc	glycophorin C	Mm.38774.1	8.2	7.4	**-1.8**	0.027
1447854_s_at	Hist2h2be	histone cluster 2, H2be	Mm.200193.1	5.0	4.2	**-1.8**	0.018
1451579_at	BC024139	cDNA sequence BC024139	Mm.205253.1	6.7	5.9	**-1.8**	0.001
1457227_at	Gm11266	predicted gene 11266	Mm.41666.1	5.8	4.9	**-1.8**	0.019
1429339_a_at	Acad10	acyl-Coenzyme A dehydrogenase family, member 10	Mm.24273.2	8.6	7.8	**-1.8**	0.034
1439024_at	Bag4	BCL2-associated athanogene 4	Mm.35264.1	9.3	8.5	**-1.8**	0.007
1440624_at			Mm.214662.1	5.7	4.9	**-1.8**	0.011
1449568_at	Klb	klotho beta	Mm.45274.1	9.7	8.9	**-1.8**	0.003
1450242_at	Tlr5	toll-like receptor 5	Mm.116894.1	6.5	5.7	**-1.8**	0.023
1416049_at	Gldc	glycine decarboxylase	Mm.27953.1	10.7	9.9	**-1.8**	0.019
1429899_at	5730414N17 Rik	RIKEN cDNA 5730414N17 gene	Mm.112365.1	7.4	6.5	**-1.8**	0.041
1437424_at	Syde2	synapse defective 1, Rho GTPase, homolog 2 (C. elegans)	Mm.24692.1	7.8	6.9	**-1.8**	0.017
1457284_at			Mm.45553.1	5.5	4.7	**-1.8**	0.018
1438238_at	2010315B03 Rik	RIKEN cDNA 2010315B03 gene	Mm.86344.1	8.2	7.3	**-1.8**	0.010
1429299_at	Ddah1	dimethylarginine dimethylaminohydrolase 1	Mm.30203.1	9.7	8.8	**-1.8**	0.001
1434987_at	Aldh2	aldehyde dehydrogenase 2, mitochondrial	Mm.2621.2	8.9	8.0	**-1.8**	0.035
1451527_at	Pcolce2	procollagen C-endopeptidase enhancer 2	Mm.46016.1	6.5	5.6	**-1.8**	0.018

Supplemental Table 8. Significant differently expressed genes in 1KI HCC samples

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1428338_at	Spata2l	spermatogenesis associated 2-like	Mm.41459.1	8.5	7.6	**-1.9**	0.008
1434817_s_at	Rprd2	regulation of nuclear pre-mRNA domain containing 2	Mm.26257.1	7.3	6.4	**-1.9**	0.027
1418857_at	Slc13a2	solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 2	Mm.57258.1	6.5	5.6	**-1.9**	0.000
1418739_at	Sgk2	serum/glucocorticoid regulated kinase 2	Mm.26462.1	10.4	9.5	**-1.9**	0.024
1441413_at			Mm.215325.1	9.1	8.2	**-1.9**	0.049
1444589_at	Gm4944	predicted gene 4944	Mm.31829.1	5.9	5.0	**-1.9**	0.001
1417784_at	Als2	amyotrophic lateral sclerosis 2 (juvenile)	Mm.30114.1	6.0	5.1	**-1.9**	0.009
1420541_at	Rdh16	retinol dehydrogenase 16	Mm.100276.1	9.4	8.5	**-1.9**	0.036
1455281_at	Wdr33	WD repeat domain 33	Mm.32512.3	6.1	5.2	**-1.9**	0.005
1435292_at	Tbc1d4	TBC1 domain family, member 4	Mm.27439.1	6.0	5.1	**-1.9**	0.004
1418649_at	Egln3	egl-9 family hypoxia-inducible factor 3	Mm.33484.1	8.4	7.4	**-1.9**	0.013
1439331_at	4932439E07 Rik	RIKEN cDNA 4932439E07 gene	Mm.43978.1	6.2	5.3	**-1.9**	0.007
1443908_at	Gm19696	predicted gene, 19696	Mm.215578.1	8.4	7.4	**-1.9**	0.014
1456395_at	Ppargc1a	peroxisome proliferative activated receptor, gamma, coactivator 1 alpha	Mm.10707.3	7.2	6.3	**-1.9**	0.013
1442169_at	Vldlr	very low density lipoprotein receptor	Mm.202246.1	7.0	6.0	**-1.9**	0.017
1457791_at	B830008H07 Rik	RIKEN cDNA B830008H07 gene	Mm.37292.1	9.8	8.8	**-1.9**	0.016
1426243_at	Cth	cystathionase (cystathionine gamma-lyase)	Mm.28301.1	12.1	11.1	**-2.0**	0.004
1440965_at	Pigl	phosphatidylinositol glycan anchor biosynthesis, class L	Mm.37323.1	8.2	7.2	**-2.0**	0.003
1453547_at	1810046K07 Rik	RIKEN cDNA 1810046K07 gene	Mm.75315.1	7.2	6.3	**-2.0**	0.007
1423495_at	Decr2	2-4-dienoyl-Coenzyme A reductase 2, peroxisomal	Mm.35760.1	11.8	10.8	**-2.0**	0.000
1432181_s_at	Sco2	SCO cytochrome oxidase deficient homolog 2 (yeast)	Mm.219419.2	10.8	9.8	**-2.0**	0.023
1431199_at	Ggnbp1	gametogenetin binding protein 1	Mm.105357.1	7.9	6.9	**-2.0**	0.002
1458658_at			Mm.139088.1	5.1	4.1	**-2.0**	0.000
1436931_at	Rfx4	regulatory factor X, 4 (influences HLA class II expression)	Mm.32654.1	6.4	5.4	**-2.0**	0.034
1452375_at	Aldh4a1	aldehyde dehydrogenase 4 family, member A1	Mm.218879.1	12.2	11.2	**-2.0**	0.016
1432562_at	1110006G14 Rik	SRY (sex determining region Y)-box 6, opposite strand	Mm.158213.1	6.1	5.1	**-2.0**	0.002
1430410_at	1810019N24 Rik	RIKEN cDNA 1810019N24 gene	Mm.158236.1	5.0	4.0	**-2.0**	0.001
1443921_at	Ranbp3l	RAN binding protein 3-like	Mm.209787.1	5.8	4.8	**-2.1**	0.013
1454402_at	Zfp942	zinc finger protein 942	Mm.219772.1	3.7	2.6	**-2.1**	0.010

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1449001_at	Ivd	isovaleryl coenzyme A dehydrogenase	Mm.6635.1	10.2	9.2	**-2.1**	0.045
1453692_at	4930581F22Rik	RIKEN cDNA 4930581F22 gene	Mm.160157.1	7.6	6.6	**-2.1**	0.000
1435349_at	Nrp2	neuropilin 2	Mm.37629.1	8.5	7.4	**-2.1**	0.008
1421758_at	Nat1	N-acetyl transferase 1	Mm.14125.1	7.3	6.2	**-2.1**	0.014
1426389_at	Camk1d	calcium/calmodulin-dependent protein kinase ID	Mm.26888.1	8.2	7.2	**-2.1**	0.050
1450271_at	Ptk6	PTK6 protein tyrosine kinase 6	Mm.4497.1	4.4	3.3	**-2.1**	0.014
1431648_at	Meiob	meiosis specific with OB domains	Mm.52592.1	8.6	7.5	**-2.1**	0.005
1417130_s_at	Angptl4	angiopoietin-like 4	Mm.196189.1	9.9	8.8	**-2.1**	0.010
1435893_at	Vldlr	very low density lipoprotein receptor	Mm.32795.1	7.2	6.1	**-2.1**	0.037
1460258_at	Lect1	leukocyte cell derived chemotaxin 1	Mm.46561.1	7.7	6.6	**-2.1**	0.025
1417714_x_at	Hba-a1	hemoglobin alpha, adult chain 1; hemoglobin alpha, adult chain 2	Mm.196110.1	13.5	12.4	**-2.1**	0.005
1417976_at	Ada	adenosine deaminase	Mm.388.1	6.6	5.5	**-2.2**	0.008
1432916_at	5730407I07Rik	RIKEN cDNA 5730407I07 gene	Mm.158393.1	5.5	4.4	**-2.2**	0.002
1455100_at	Akr1d1	aldo-keto reductase family 1, member D1	Mm.77361.2	9.4	8.3	**-2.2**	0.042
1417066_at	Adck3	aarF domain containing kinase 3	Mm.28337.1	11.3	10.2	**-2.2**	0.009
1427480_at	Leap2	liver-expressed antimicrobial peptide 2	Mm.24283.1	11.4	10.3	**-2.2**	0.019
1450069_a_at	Celf2	CUGBP, Elav-like family member 2	Mm.27880.1	7.6	6.5	**-2.2**	0.007
1420385_at	Gna14	guanine nucleotide binding protein, alpha 14	Mm.22322.1	6.5	5.4	**-2.2**	0.042
1425409_at	Chrna2	cholinergic receptor, nicotinic, alpha polypeptide 2 (neuronal)	Mm.57350.1	5.9	4.8	**-2.2**	0.006
1435645_at	Mmd	monocyte to macrophage differentiation-associated	Mm.139683.1	8.9	7.8	**-2.2**	0.027
1431803_at	Cyp2d13	cytochrome P450, family 2, subfamily d, polypeptide 13	Mm.46933.2	10.3	9.2	**-2.2**	0.035
1435514_at	Lztfl1	leucine zipper transcription factor-like 1	Mm.39928.2	4.5	3.4	**-2.3**	0.002
1452823_at	Gstk1	glutathione S-transferase kappa 1	Mm.27395.1	12.5	11.3	**-2.3**	0.018
1439934_at	Slc30a10	solute carrier family 30, member 10	Mm.187893.1	9.1	7.9	**-2.3**	0.038
1417067_s_at	Adck3	aarF domain containing kinase 3	Mm.28337.1	7.1	5.9	**-2.3**	0.001
1423895_a_at	Celf2	CUGBP, Elav-like family member 2	Mm.27880.2	8.7	7.5	**-2.3**	0.010
1426664_x_at	Slc45a3	solute carrier family 45, member 3	Mm.200307.1	8.5	7.3	**-2.3**	0.023
1460318_at	Csrp3	cysteine and glycine-rich protein 3	Mm.17235.1	9.5	8.3	**-2.3**	0.017
1425771_at	Akr1d1	aldo-keto reductase family 1, member D1	Mm.77361.1	11.6	10.4	**-2.4**	0.036
1417280_at	Slc17a1	solute carrier family 17 (sodium phosphate), member 1	Mm.2656.1	8.7	7.5	**-2.4**	0.000
1453287_at	Ankrd33b	ankyrin repeat domain 33B	Mm.27619.1	7.9	6.7	**-2.4**	0.007
1428832_at	1600002H07Rik	RIKEN cDNA 1600002H07 gene	Mm.23881.1	8.9	7.6	**-2.4**	0.017

Supplemental Table 8. Significant differently expressed genes in 1KI HCC samples

Affymetrix ID	Gene Symbol	Description	Transcript ID (Array Design)	3aKO avg signal log2 (n=5)	1KI Avg Signal log2 (n=5)	Fold Change (linear)	ANOVA p-value
1436867_at	Srl	sarcalumenin	Mm.35811.1	6.0	4.8	**-2.4**	0.027
1451373_at	Ugt3a1	UDP glycosyltransferases 3 family, polypeptide A1	Mm.201628.1	10.8	9.6	**-2.4**	0.002
1438258_at	Vldlr	very low density lipoprotein receptor	Mm.38836.1	7.2	6.0	**-2.4**	0.014
1421183_at	Tex12	testis expressed gene 12	Mm.78133.1	6.7	5.4	**-2.4**	0.015
1427410_at	Dleu2	deleted in lymphocytic leukemia, 2	Mm.25679.1	8.3	7.0	**-2.5**	0.045
1419906_at	Hpgd	hydroxyprostaglandin dehydrogenase 15 (NAD)	Mm.199536.1	8.9	7.6	**-2.5**	0.019
1425246_at	0610008F07 Rik	hepatic nuclear factor 4 alpha, opposite strand	Mm.46190.1	7.5	6.2	**-2.5**	0.001
1429809_at	Tmtc2	transmembrane and tetratricopeptide repeat containing 2	Mm.37266.1	6.7	5.4	**-2.5**	0.011
1426663_s_at	Slc45a3	solute carrier family 45, member 3	Mm.200307.1	8.9	7.6	**-2.5**	0.019
1438975_x_at	Zdhhc14	zinc finger, DHHC domain containing 14	Mm.22338.7	7.1	5.8	**-2.5**	0.002
1438751_at	Slc30a10	solute carrier family 30, member 10	Mm.62038.1	8.6	7.3	**-2.6**	0.046
1435872_at			Mm.2322.3	8.5	7.0	**-2.7**	0.005
1449298_a_at	Pde1a	phosphodiesterase 1A, calmodulin-dependent	Mm.40678.1	6.7	5.2	**-2.7**	0.010
1421430_at	Rad51b	RAD51 homolog B	Mm.25289.1	8.8	7.3	**-2.8**	0.010
1424715_at	Retsat	retinol saturase (all trans retinol 13,14 reductase)	Mm.27506.1	12.8	11.3	**-2.8**	0.011
1437614_x_at	Zdhhc14	zinc finger, DHHC domain containing 14	Mm.22338.2	7.2	5.7	**-2.9**	0.003
1424493_s_at	Ugt3a1	UDP glycosyltransferases 3 family, polypeptide A1	Mm.201628.1	10.5	9.0	**-2.9**	0.001
1417355_at	Peg3	paternally expressed 3	Mm.7952.1	8.4	6.9	**-3.0**	0.037
1451154_a_at	Celf2	CUGBP, Elav-like family member 2	Mm.27880.2	8.1	6.5	**-3.0**	0.006
1455786_at	Zfp820	zinc finger protein 820	Mm.42298.1	5.5	3.9	**-3.0**	0.033
1420405_at	Slco1a4	solute carrier organic anion transporter family, member 1a4	Mm.101645.1	10.6	8.9	**-3.1**	0.044
1428636_at	Steap2	six transmembrane epithelial antigen of prostate 2	Mm.41944.1	6.0	4.3	**-3.2**	0.001
1427329_a_at	Ighm	immunoglobulin heavy constant mu	Mm.28362.2	8.4	6.7	**-3.3**	0.007
1424716_at	Retsat	retinol saturase (all trans retinol 13,14 reductase)	Mm.27506.1	10.6	8.9	**-3.3**	0.006
1429822_at	4633401B06 Rik	RIKEN cDNA 4633401B06 gene	Mm.178280.1	8.7	6.9	**-3.5**	0.020
1419094_at	Cyp2c37	cytochrome P450, family 2. subfamily c, polypeptide 37	Mm.220317.1	7.0	5.2	**-3.6**	0.047
1440921_at	Nlrp12	NLR family, pyrin domain containing 12	Mm.161578.1	8.8	7.0	**-3.6**	0.037
1423891_at	Gstt3	glutathione S-transferase, theta 3	Mm.25313.1	10.7	8.8	**-3.7**	0.030
1424838_at	Ncmap	noncompact myelin associated protein	Mm.35548.1	8.2	6.3	**-3.8**	0.023
1431817_at	Adh6-ps1	alcohol dehydrogenase 6 (class V), pseudogene 1	Mm.158750.1	5.9	4.0	**-3.8**	0.046

Supplemental Table 8. Significant differently expressed genes in 1KI HCC samples

Affymetrix ID	Gene Symbol	Description	Transcript ID (Array Design)	3aKO avg signal log2 (n=5)	1KI Avg Signal log2 (n=5)	Fold Change (linear)	ANOVA p-value
1458297_s_at	Marco	macrophage receptor with collagenous structure	Mm.200861.1	7.2	5.2	**-3.9**	0.007
1427351_s_at	Ighm	immunoglobulin heavy constant mu	Mm.218842.1	9.8	7.8	**-4.0**	0.004
1418051_at	Ephb6	Eph receptor B6	Mm.1480.1	6.0	4.0	**-4.1**	0.000
1417880_at	G6pc	glucose-6-phosphatase, catalytic	Mm.18064.1	11.1	8.9	**-4.9**	0.023
1437128_a_at	Zfp945	zinc finger protein 945	Mm.33710.2	7.1	4.7	**-5.0**	0.001
1448080_at	Gm2788	predicted gene 2788	Mm.176935.2	10.1	7.3	**-6.9**	0.014
1449498_at	Marco	macrophage receptor with collagenous structure	Mm.1856.1	8.3	5.3	**-7.6**	0.005
1416318_at	Serpinb1a	serine (or cysteine) peptidase inhibitor, clade B, member 1a	Mm.46316.1	9.4	6.4	**-8.0**	0.030
1424853_s_at	Cyp4a10	cytochrome P450, family 4, subfamily a, polypeptide 10; cytochrome P450, family 4, subfamily a, polypeptide 31	Mm.10742.1	13.4	10.1	**-10.1**	0.049

Supplemental Table 9. Significant differently expressed genes in 3bKI HCC samples

Affymetrix ID	Gene Symbol	Description	Transcript ID (Array Design)	3aKO avg signal log2 (n=4)	3bKI Avg Signal log2 (n=5)	Fold Change (linear)	ANOVA p-value
1419669_at	Prtn3	proteinase 3	Mm.2364.1	4.6	8.5	**14.96**	0.01
1460550_at	Mtmr11	myotubularin related protein 11	Mm.24379.1	4.7	7.9	**9.34**	0.00
1416930_at	Ly6d	lymphocyte antigen 6 complex, locus D	Mm.878.1	6.1	9.0	**7.38**	0.00
1436503_at	BC048546	cDNA sequence BC048546	Mm.26869.1	6.6	9.2	**6.12**	0.00
1424649_a_at	Tspan8	tetraspanin 8	Mm.22270.1	3.9	6.4	**5.59**	0.01
1427747_a_at	Lcn2	lipocalin 2	Mm.9537.1	8.3	10.8	**5.54**	0.02
1448377_at	Slpi	secretory leukocyte peptidase inhibitor	Mm.1395.1	8.1	10.6	**5.52**	0.03
1416645_a_at	Afp	alpha fetoprotein	Mm.80.1	3.3	5.8	**5.49**	0.00
1422437_at	Col5a2	collagen, type V, alpha 2	Mm.10299.1	5.6	8.1	**5.48**	0.00
1418457_at	Cxcl14	chemokine (C-X-C motif) ligand 14	Mm.30211.1	3.7	6.1	**5.4**	0.04
1425120_x_at	Ifi27l2b	interferon, alpha-inducible protein 27 like 2B	Mm.46348.1	7.5	9.9	**5.31**	0.00
1416022_at	Fabp5	fatty acid binding protein 5, epidermal	Mm.741.1	9.1	11.6	**5.3**	0.02
1448754_at	Rbp1	retinol binding protein 1, cellular	Mm.2450.1	8.7	11.1	**5.19**	0.00
1417507_at	Cyb561	cytochrome b-561	Mm.154456.1	5.1	7.4	**5.03**	0.04
1456226_x_at	Ddr1	discoidin domain receptor family, member 1	Mm.5021.4	3.1	5.4	**4.95**	0.01
1417370_at	Tff3	trefoil factor 3, intestinal	Mm.4641.1	5.4	7.7	**4.91**	0.03
1417267_s_at	Fkbp11	FK506 binding protein 11	Mm.30729.1	7.0	9.2	**4.85**	0.01
1448595_a_at	Bex1	brain expressed gene 1	Mm.14768.1	3.0	5.3	**4.85**	0.03
1424857_a_at	Trim34a	tripartite motif-containing 34A	Mm.219657.2	4.2	6.4	**4.83**	0.02
1437094_x_at	Dnaic1	dynein, axonemal, intermediate chain 1	Mm.79127.1	5.2	7.5	**4.82**	0.01
1416021_a_at	Fabp5	fatty acid binding protein 5, epidermal	Mm.741.1	10.3	12.6	**4.73**	0.02
1448261_at	Cdh1	cadherin 1	Mm.35605.1	6.3	8.5	**4.71**	0.04
1424638_at	Cdkn1a	cyclin-dependent kinase inhibitor 1A (P21)	Mm.34446.2	7.0	9.2	**4.66**	0.00
1449326_x_at	Saa2	serum amyloid A 2	Mm.200941.1	7.6	9.8	**4.61**	0.04
1431362_a_at	Smoc2	SPARC related modular calcium binding 2	Mm.30162.2	4.1	6.3	**4.57**	0.00
1437093_at	Dnaic1	dynein, axonemal, intermediate chain 1	Mm.79127.1	5.2	7.4	**4.48**	0.01
1415935_at	Smoc2	SPARC related modular calcium binding 2	Mm.30162.1	5.6	7.8	**4.46**	0.00
1448194_a_at	H19	H19, imprinted maternally expressed transcript; microRNA 675	Mm.14802.1	3.6	5.8	**4.38**	0.01
1427220_a_at	Svs5	seminal vesicle secretory protein 5	Mm.140154.2	3.9	6.0	**4.36**	0.00
1424339_at	Oasl1	2'-5' oligoadenylate synthetase-like 1	Mm.95479.1	6.1	8.2	**4.35**	0.00
1418191_at	Usp18	ubiquitin specific peptidase 18	Mm.27498.1	6.3	8.4	**4.21**	0.01
1421679_a_at	Cdkn1a	cyclin-dependent kinase inhibitor 1A (P21)	Mm.34446.1	6.9	8.9	**4.05**	0.00

Supplemental Table 9. Significant differently expressed genes in 3bKI HCC samples

Affymetrix ID	Gene Symbol	Description	Transcript ID (Array Design)	3aKO avg signal log2 (n=4)	3bKI Avg Signal log2 (n=5)	Fold Change (linear)	ANOVA p-value
1459333_at			Mm.17671.1	4.8	6.9	**4.03**	0.00
1460406_at	Pls1	plastin 1 (I-isoform)	Mm.11869.1	6.6	8.6	**3.99**	0.01
1417821_at	D17H6S56E-5	DNA segment, Chr 17, human D6S56E 5	Mm.22506.1	4.7	6.7	**3.95**	0.05
1435665_at	Trim30d	tripartite motif-containing 30D	Mm.33905.1	4.4	6.4	**3.94**	0.04
1419398_a_at	Reep5	receptor accessory protein 5	Mm.21251.1	8.1	10.1	**3.92**	0.00
1423556_at	Akr1b7	aldo-keto reductase family 1, member B7	Mm.14460.1	5.0	7.0	**3.9**	0.03
1435275_at	Cox6b2	cytochrome c oxidase subunit VIb polypeptide 2	Mm.29625.1	5.5	7.4	**3.84**	0.02
1429734_at	4632434I11Rik	DNA damage-induced apoptosis suppressor	Mm.26468.1	4.8	6.7	**3.76**	0.00
1449002_at	Phlda3	pleckstrin homology-like domain, family A, member 3	Mm.34346.1	6.9	8.8	**3.76**	0.03
1454686_at	6430706D22Rik	RIKEN cDNA 6430706D22 gene; RIKEN cDNA A730008H23 gene; Holliday junction recognition protein	Mm.22226.2	6.1	8.1	**3.76**	0.00
1419195_at	Wfdc15b	WAP four-disulfide core domain 15B	Mm.10859.1	5.9	7.8	**3.73**	0.00
1418171_at	Tceal8	transcription elongation factor A (SII)-like 8	Mm.182094.1	7.0	8.9	**3.72**	0.00
1430979_a_at	Prdx2	peroxiredoxin 2	Mm.42948.2	5.7	7.6	**3.69**	0.01
1428116_a_at	Dynlt1a	dynein light chain Tctex-type 1A; dynein light chain Tctex-type 1B; dynein light chain Tctex-type 1C; dynein light chain Tctex-type 1F	Mm.1948.2	7.9	9.8	**3.66**	0.00
1427167_at	Armcx4	armadillo repeat containing, X-linked 4	Mm.31961.1	3.5	5.4	**3.65**	0.02
1415904_at	Lpl	lipoprotein lipase	Mm.1514.1	8.2	10.1	**3.64**	0.01
1448272_at	Btg2	B cell translocation gene 2, anti-proliferative	Mm.903.1	7.1	8.9	**3.62**	0.01
1425385_a_at	Ighg2c	RecName: Full=Ig gamma-2A chain C region secreted form; AltName: Full=B allele;; immunoglobulin heavy constant gamma 2C; immunoglobulin heavy constant mu	Mm.144308.1	4.4	6.2	**3.56**	0.01
1445328_at	Col4a4	collagen, type IV, alpha 4	Mm.40253.1	3.7	5.5	**3.56**	0.01
1433575_at	Sox4	SRY (sex determining region Y)-box 4	Mm.18789.2	6.0	7.8	**3.5**	0.00
1453473_a_at	Dynlt1a	dynein light chain Tctex-type 1A; dynein light chain Tctex-type 1B; dynein light chain Tctex-type 1C; dynein light chain Tctex-type 1F	Mm.1948.3	7.2	9.0	**3.5**	0.00
1419491_at	Defb1	defensin beta 1	Mm.5341.1	4.1	5.9	**3.49**	0.01
1451780_at	Blnk	B cell linker	Mm.9749.1	6.7	8.5	**3.34**	0.00

Supplemental Table 9. Significant differently expressed genes in 3bKI HCC samples

Affymetrix ID	Gene Symbol	Description	Transcript ID (Array Design)	3aKO avg signal log2 (n=4)	3bKI Avg Signal log2 (n=5)	Fold Change (linear)	ANOVA p-value
1451456_at	6430706D22Rik	RIKEN cDNA 6430706D22 gene; RIKEN cDNA A730008H23 gene; Holliday junction recognition protein	Mm.22226.1	3.7	5.4	**3.32**	0.00
1438001_x_at	Reep5	receptor accessory protein 5	Mm.21251.3	7.6	9.3	**3.31**	0.01
1438635_x_at	B930041F14Rik	RIKEN cDNA B930041F14 gene	Mm.132095.1	5.3	7.1	**3.3**	0.00
1416250_at	Btg2	B cell translocation gene 2, anti-proliferative	Mm.903.1	7.8	9.5	**3.21**	0.02
1431788_at	Fabp12	fatty acid binding protein 12	Mm.47052.1	5.1	6.8	**3.19**	0.01
1431056_a_at	Lpl	lipoprotein lipase	Mm.1514.2	6.8	8.5	**3.17**	0.02
1424775_at	Oas1a	2'-5' oligoadenylate synthetase 1A	Mm.14301.1	7.4	9.0	**3.16**	0.01
1438009_at	Hist1h2ab	histone cluster 1, H2ab; histone cluster 1, H2ac; histone cluster 1, H2ad; histone cluster 1, H2ae; histone cluster 1, H2ag; histone cluster 1, H2ah; histone cluster 1, H2ai; histone cluster 1, H2an; histone cluster 1, H2ao; histone cluster 1, H2ap	Mm.14767.2	7.9	9.5	**3.15**	0.05
1416658_at	Frzb	frizzled-related protein	Mm.3246.1	4.0	5.6	**3.12**	0.00
1424626_at	2010003K11Rik	RIKEN cDNA 2010003K11 gene	Mm.22966.1	7.5	9.1	**3.11**	0.00
1450783_at	Ifit1	interferon-induced protein with tetratricopeptide repeats 1	Mm.6718.1	6.3	7.9	**3.07**	0.02
1416808_at	Nid1	nidogen 1	Mm.4691.1	7.6	9.3	**3.05**	0.03
1427883_a_at	Col3a1	collagen, type III, alpha 1	Mm.147387.1	8.1	9.7	**3.05**	0.01
1417409_at	Jun	jun proto-oncogene	Mm.482.1	7.2	8.8	**3.02**	0.00
1418086_at	Ppp1r14a	protein phosphatase 1, regulatory (inhibitor) subunit 14A	Mm.46581.1	5.1	6.7	**3.02**	0.02
1450224_at	Col4a3	collagen, type IV, alpha 3	Mm.8069.1	4.2	5.7	**2.96**	0.01
1437325_x_at	Aldh18a1	aldehyde dehydrogenase 18 family, member A1	Mm.29751.3	3.9	5.5	**2.93**	0.00
1433685_a_at	6430706D22Rik	RIKEN cDNA 6430706D22 gene; RIKEN cDNA A730008H23 gene; Holliday junction recognition protein	Mm.22226.2	7.4	8.9	**2.92**	0.00
1416953_at	Ctgf	connective tissue growth factor	Mm.1810.1	7.2	8.8	**2.91**	0.03
1455439_a_at	Lgals1	lectin, galactose binding, soluble 1	Mm.43831.3	7.9	9.5	**2.88**	0.01
1449254_at	Spp1	secreted phosphoprotein 1	Mm.321.1	8.8	10.3	**2.83**	0.00
1418320_at	Prss8	protease, serine 8 (prostasin)	Mm.5875.1	5.5	7.0	**2.82**	0.01
1429947_a_at	Zbp1	Z-DNA binding protein 1	Mm.116687.2	6.1	7.6	**2.82**	0.04
1452855_at	Ly6k	lymphocyte antigen 6 complex, locus K	Mm.46441.1	4.8	6.3	**2.77**	0.03
1426278_at	Ifi27l2a	interferon, alpha-inducible protein 27 like 2A	Mm.46382.1	6.5	7.9	**2.75**	0.02
1448259_at	Fstl1	follistatin-like 1	Mm.22763.1	5.4	6.8	**2.73**	0.00
1418355_at	Nucb2	nucleobindin 2	Mm.9901.1	5.8	7.3	**2.72**	0.02
1455905_at	2610507B11Rik	RIKEN cDNA 2610507B11 gene	Mm.35854.3	7.8	9.3	**2.72**	0.00

Supplemental Table 9. Significant differently expressed genes in 3bKI HCC samples

Affymetrix ID	Gene Symbol	Description	Transcript ID (Array Design)	3aKO avg signal log2 (n=4)	3bKI Avg Signal log2 (n=5)	Fold Change (linear)	ANOVA p-value
1450407_a_at	Anp32a	acidic (leucine-rich) nuclear phosphoprotein 32 family, member A	Mm.613.1	7.8	9.3	**2.71**	0.00
1438752_at	A230058F20Rik	RIKEN cDNA A230058F20 gene	Mm.74679.1	3.5	4.9	**2.7**	0.00
1415698_at	Golm1	golgi membrane protein 1	Mm.171335.1	6.1	7.6	**2.69**	0.03
1418949_at	Gdf15	growth differentiation factor 15	Mm.31325.1	7.2	8.6	**2.67**	0.01
1434240_at	4632434I11Rik	DNA damage-induced apoptosis suppressor	Mm.26468.2	3.3	4.7	**2.66**	0.00
1417084_at	Eif4ebp2	eukaryotic translation initiation factor 4E binding protein 2	Mm.140186.1	8.9	10.3	**2.64**	0.00
1417496_at	Cp	ceruloplasmin	Mm.13787.1	11.7	13.1	**2.64**	0.00
1449133_at	Sprr1a	small proline-rich protein 1A	Mm.625.1	4.8	6.2	**2.64**	0.01
1419057_at	Slc5a1	solute carrier family 5 (sodium/glucose cotransporter), member 1	Mm.25237.1	4.7	6.1	**2.63**	0.00
1444139_at	Ddit4l	DNA-damage-inducible transcript 4-like	Mm.205420.1	5.0	6.4	**2.63**	0.01
1450530_at	B3galt1	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 1	Mm.57041.1	6.3	7.7	**2.63**	0.01
1455144_s_at	Arhgap44	Rho GTPase activating protein 44	Mm.18455.1	4.5	5.9	**2.63**	0.01
1449153_at	Mmp12	matrix metallopeptidase 12	Mm.2055.1	4.1	5.5	**2.62**	0.00
1419314_at	Tinag	tubulointerstitial nephritis antigen	Mm.23199.1	3.8	5.1	**2.61**	0.00
1415977_at	Isyna1	myo-inositol 1-phosphate synthase A1	Mm.29357.1	7.5	8.9	**2.59**	0.02
1418661_at	Abhd2	abhydrolase domain containing 2	Mm.87337.1	7.1	8.4	**2.57**	0.01
1419573_a_at	Lgals1	lectin, galactose binding, soluble 1	Mm.43831.1	8.2	9.6	**2.56**	0.01
1423630_at	Cygb	cytoglobin	Mm.34598.1	6.5	7.9	**2.56**	0.02
1452035_at	Col4a1	collagen, type IV, alpha 1	Mm.738.1	8.1	9.5	**2.56**	0.01
1416431_at	Tubb6	tubulin, beta 6 class V	Mm.181860.1	7.3	8.7	**2.53**	0.00
1438207_at	Gbf1	golgi-specific brefeldin A-resistance factor 1	Mm.44823.1	7.4	8.7	**2.53**	0.00
1435012_x_at	Cela3b	chymotrypsin-like elastase family, member 3B; predicted gene 13011; uncharacterized LOC102641402	Mm.30780.3	2.5	3.8	**2.52**	0.04
1425567_a_at	Anxa5	annexin A5	Mm.1620.2	9.1	10.4	**2.5**	0.03
1427878_at	Cystm1	cysteine-rich transmembrane module containing 1	Mm.27841.1	7.8	9.1	**2.5**	0.03
1448898_at	Ccl9	chemokine (C-C motif) ligand 9	Mm.2271.1	10.0	11.3	**2.5**	0.04
1451751_at	Ddit4l	DNA-damage-inducible transcript 4-like	Mm.195809.1	4.8	6.1	**2.49**	0.01
1423110_at	Col1a2	collagen, type I, alpha 2	Mm.4482.1	5.0	6.3	**2.48**	0.01
1427386_at	Arhgef16	Rho guanine nucleotide exchange factor (GEF) 16	Mm.38481.1	5.7	7.0	**2.48**	0.00
1417822_at	D17H6S56E-5	DNA segment, Chr 17, human D6S56E 5	Mm.22506.1	6.0	7.3	**2.47**	0.04
1418655_at	B4galnt1	beta-1,4-N-acetyl-galactosaminyl transferase 1	Mm.1853.1	4.6	5.9	**2.46**	0.00

Supplemental Table 9. Significant differently expressed genes in 3bKI HCC samples

Affymetrix ID	Gene Symbol	Description	Transcript ID (Array Design)	3aKO avg signal log2 (n=4)	3bKI Avg Signal log2 (n=5)	Fold Change (linear)	ANOVA p-value
1440250_at	Col4a4	collagen, type IV, alpha 4	Mm.107258.1	3.6	4.9	**2.46**	0.02
1419004_s_at	Bcl2a1a	B cell leukemia/lymphoma 2 related protein A1a; B cell leukemia/lymphoma 2 related protein A1b; B cell leukemia/lymphoma 2 related protein A1d	Mm.196731.1	4.9	6.2	**2.44**	0.01
1426348_at	Col4a1	collagen, type IV, alpha 1	Mm.738.1	7.3	8.5	**2.44**	0.01
1417273_at	Pdk4	pyruvate dehydrogenase kinase, isoenzyme 4	Mm.10283.1	6.0	7.3	**2.43**	0.00
1417268_at	Cd14	CD14 antigen	Mm.3460.1	7.3	8.5	**2.41**	0.02
1418537_at	Isoc2b	isochorismatase domain containing 2b	Mm.41385.1	6.9	8.2	**2.4**	0.01
1419449_a_at	Gnai2	guanine nucleotide binding protein (G protein), alpha inhibiting 2	Mm.196464.1	8.6	9.8	**2.4**	0.00
1421550_a_at	Trim34a	tripartite motif-containing 34A; tripartite motif-containing 34B	Mm.219657.1	5.8	7.1	**2.4**	0.02
1430172_a_at	Cyp4f16	cytochrome P450, family 4, subfamily f, polypeptide 16; cytochrome P450, family 4, subfamily f, polypeptide 37	Mm.30504.2	6.1	7.4	**2.4**	0.01
1437432_a_at	Trim12a	tripartite motif-containing 12A	Mm.26466.3	3.0	4.2	**2.39**	0.03
1417860_a_at	Spon2	spondin 2, extracellular matrix protein	Mm.34694.1	6.4	7.7	**2.38**	0.01
1422587_at	Tmem45a	transmembrane protein 45a	Mm.4992.1	5.4	6.6	**2.37**	0.02
1433833_at	Fndc3b	fibronectin type III domain containing 3B	Mm.200324.1	9.5	10.7	**2.37**	0.03
1426808_at	Lgals3	lectin, galactose binding, soluble 3	Mm.2970.1	7.9	9.2	**2.36**	0.04
1422206_at	B3galt1	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 1	Mm.57041.1	5.9	7.1	**2.35**	0.02
1424140_at	Gale	galactose-4-epimerase, UDP	Mm.20363.1	7.5	8.7	**2.35**	0.01
1429088_at	Lbh	limb-bud and heart	Mm.154109.1	5.8	7.0	**2.35**	0.01
1430190_at	Ccdc30	coiled-coil domain containing 30	Mm.196069.1	3.4	4.7	**2.35**	0.01
1437019_at	Fam25c	family with sequence similarity 25, member C	Mm.27156.1	9.7	11.0	**2.34**	0.04
1448694_at	Jun	jun proto-oncogene	Mm.482.1	6.9	8.1	**2.34**	0.00
1453304_s_at	Ly6e	lymphocyte antigen 6 complex, locus E	Mm.204648.1	11.9	13.1	**2.34**	0.00
1423933_a_at	1600029D21Rik	placenta expressed transcript 1	Mm.29959.1	5.7	6.9	**2.32**	0.00
1428671_at	2200002D01Rik	RIKEN cDNA 2200002D01 gene	Mm.46332.1	7.6	8.8	**2.32**	0.01
1430890_at	Igsf23	immunoglobulin superfamily, member 23	Mm.158322.1	5.1	6.3	**2.32**	0.00
1448152_at	Igf2	insulin-like growth factor 2	Mm.3862.1	5.6	6.8	**2.32**	0.00
1434728_at	Gria3	glutamate receptor, ionotropic, AMPA3 (alpha 3)	Mm.32184.1	2.8	4.0	**2.31**	0.01
1436879_x_at	Afp	alpha fetoprotein	Mm.80.5	2.7	3.9	**2.3**	0.00

Supplemental Table 9. Significant differently expressed genes in 3bKI HCC samples

Affymetrix ID	Gene Symbol	Description	Transcript ID (Array Design)	3aKO avg signal log2 (n=4)	3bKI Avg Signal log2 (n=5)	Fold Change (linear)	ANOVA p-value
1455162_at	Ttc39a	tetratricopeptide repeat domain 39A	Mm.23454.1	6.3	7.5	**2.3**	0.00
1424594_at	Samd4	sterile alpha motif domain containing 4	Mm.20973.2	6.2	7.4	**2.28**	0.01
1438779_at	Col4a3	collagen, type IV, alpha 3	Mm.113295.1	3.6	4.7	**2.28**	0.01
1460351_at	Gm12854	predicted gene 12854; predicted gene 5068; S100 calcium binding protein A11 (calgizzarin)	Mm.175848.1	8.1	9.2	**2.28**	0.01
1436564_at	Rims4	regulating synaptic membrane exocytosis 4	Mm.131617.1	6.7	7.9	**2.27**	0.03
1448433_a_at	Pcolce	procollagen C-endopeptidase enhancer protein	Mm.18808.1	5.9	7.1	**2.27**	0.01
1454254_s_at	1600029D21Rik	placenta expressed transcript 1	Mm.195522.1	4.5	5.7	**2.26**	0.00
1420378_at	Sftpd	surfactant associated protein D	Mm.1321.1	5.6	6.8	**2.25**	0.00
1419091_a_at	Anxa2	annexin A2	Mm.584.1	8.3	9.5	**2.24**	0.00
1419820_at	Pkhd1	polycystic kidney and hepatic disease 1	Mm.198060.1	5.3	6.5	**2.24**	0.02
1449184_at	Pglyrp1	peptidoglycan recognition protein 1	Mm.21855.1	4.5	5.7	**2.24**	0.00
1417178_at	Gipc2	GIPC PDZ domain containing family, member 2	Mm.97.1	5.0	6.2	**2.23**	0.01
1450857_a_at	Col1a2	collagen, type I, alpha 2	Mm.4482.1	8.3	9.4	**2.2**	0.00
1428066_at	Ccdc120	coiled-coil domain containing 120	Mm.59673.1	4.3	5.5	**2.19**	0.00
1423669_at	Col1a1	collagen, type I, alpha 1	Mm.22621.1	5.9	7.0	**2.18**	0.00
1417500_a_at	Tgm2	transglutaminase 2, C polypeptide	Mm.18843.1	10.7	11.8	**2.17**	0.01
1452814_at	Cpne3	copine III	Mm.38390.1	7.6	8.7	**2.16**	0.00
1455431_at	Slc5a1	solute carrier family 5 (sodium/glucose cotransporter), member 1	Mm.25237.2	2.7	3.8	**2.15**	0.00
1417836_at	Gpx7	glutathione peroxidase 7	Mm.20164.1	5.7	6.8	**2.14**	0.01
1449024_a_at	Hexa	hexosaminidase A	Mm.2284.1	9.3	10.4	**2.13**	0.04
1425764_a_at	Bcat2	branched chain aminotransferase 2, mitochondrial	Mm.24210.2	5.8	6.9	**2.12**	0.01
1451431_a_at	Dbndd2	dysbindin (dystrobrevin binding protein 1) domain containing 2	Mm.195525.1	8.3	9.4	**2.12**	0.00
1417936_at	Ccl9	chemokine (C-C motif) ligand 9	Mm.2271.1	10.9	12.0	**2.11**	0.04
1420699_at	Clec7a	C-type lectin domain family 7, member a	Mm.132943.1	7.6	8.7	**2.11**	0.05
1448469_at	Nid1	nidogen 1	Mm.4691.1	6.5	7.6	**2.11**	0.03
1451978_at	Loxl1	lysyl oxidase-like 1	Mm.21049.1	5.3	6.4	**2.11**	0.05
1456981_at	Tmc7	transmembrane channel-like gene family 7	Mm.33000.1	5.0	6.1	**2.11**	0.02
1417389_at	Gpc1	glypican 1	Mm.24193.1	5.7	6.8	**2.1**	0.00
1424927_at	Glipr1	GLI pathogenesis-related 1 (glioma)	Mm.173790.1	6.0	7.0	**2.1**	0.05
1438074_at	Igsf23	immunoglobulin superfamily, member 23	Mm.12097.1	6.1	7.2	**2.09**	0.01
1443941_at	Ccdc149	coiled-coil domain containing 149	Mm.86468.1	4.7	5.7	**2.08**	0.03
1445606_a_at	2900009J06Rik	RIKEN cDNA 2900009J06 gene	Mm.25735.1	5.2	6.3	**2.08**	0.01
1448393_at	Cldn7	claudin 7	Mm.42189.1	4.6	5.7	**2.08**	0.00

Supplemental Table 9. Significant differently expressed genes in 3bKI HCC samples

Affymetrix ID	Gene Symbol	Description	Transcript ID (Array Design)	3aKO avg signal log2 (n=4)	3bKI Avg Signal log2 (n=5)	Fold Change (linear)	ANOVA p-value
1452956_a_at	Ifi27l1	interferon, alpha-inducible protein 27	Mm.2121.1	10.4	11.4	**2.08**	0.00
1448380_at	Lgals3bp	lectin, galactoside-binding, soluble, 3 binding protein	Mm.3152.1	9.3	10.4	**2.07**	0.00
1439341_at	Greb1l	growth regulation by estrogen in breast cancer-like	Mm.183863.1	4.2	5.3	**2.06**	0.01
1449221_a_at	Rrbp1	ribosome binding protein 1	Mm.13705.1	10.6	11.6	**2.06**	0.02
1416072_at	Cd34	CD34 antigen	Mm.29798.1	4.6	5.6	**2.05**	0.03
1419157_at	Sox4	SRY (sex determining region Y)-box 4	Mm.18789.1	4.7	5.7	**2.05**	0.00
1436061_at			Mm.27610.1	3.2	4.3	**2.05**	0.01
1419156_at	Sox4	SRY (sex determining region Y)-box 4	Mm.18789.1	4.4	5.4	**2.04**	0.00
1428640_at	Hsf2bp	heat shock transcription factor 2 binding protein	Mm.75856.1	6.5	7.5	**2.04**	0.01
1435758_at	B4galt6	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 6	Mm.26364.2	5.4	6.4	**2.04**	0.01
1441811_x_at	Tmem176a	transmembrane protein 176A	Mm.200272.1	10.6	11.7	**2.04**	0.00
1443698_at	Xaf1	XIAP associated factor 1	Mm.149240.1	7.6	8.6	**2.04**	0.01
1448663_s_at	Mvd	mevalonate (diphospho) decarboxylase	Mm.28146.1	8.2	9.3	**2.04**	0.04
1428514_at	Cpne3	copine III	Mm.38390.1	7.0	8.0	**2.03**	0.00
1449007_at	Btg3	B cell translocation gene 3; B-cell translocation gene 3 pseudogene	Mm.2823.1	6.1	7.1	**2.03**	0.03
1423357_at	Lipt2	lipoyl(octanoyl) transferase 2 (putative)	Mm.46777.1	6.7	7.7	**2.02**	0.00
1424268_at	Smox	spermine oxidase	Mm.29763.1	5.7	6.7	**2.02**	0.04
1426628_at	Tmem184c	transmembrane protein 184C	Mm.85137.1	7.4	8.4	**2.02**	0.01
1427137_at	Ces2e	carboxylesterase 2E	Mm.218630.1	9.5	10.5	**2.02**	0.02
1460086_at			Mm.152571.1	3.1	4.1	**2.02**	0.00
1423505_at	Tagln	transgelin	Mm.2006.1	7.1	8.1	**2.01**	0.01
1424051_at	Col4a2	collagen, type IV, alpha 2	Mm.181021.1	7.5	8.5	**2.01**	0.01
1431004_at	Loxl2	predicted gene, 21451; lysyl oxidase-like 2	Mm.157089.1	5.1	6.1	**2.01**	0.01
1419059_at	Apcs	serum amyloid P-component	Mm.2165.1	12.8	13.8	**2**	0.03
1419647_a_at	Ier3	immediate early response 3	Mm.25613.1	5.6	6.6	**1.99**	0.02
1435950_at	Hr	hairless	Mm.10225.3	5.1	6.1	**1.99**	0.00
1441137_at	Bicc1	bicaudal C homolog 1 (Drosophila)	Mm.179033.1	4.6	5.6	**1.99**	0.01
1420965_a_at	Enc1	ectodermal-neural cortex 1	Mm.30502.1	6.6	7.6	**1.98**	0.00
1426004_a_at	Tgm2	transglutaminase 2, C polypeptide	Mm.18843.3	9.0	10.0	**1.98**	0.01
1435695_a_at	Ggct	gamma-glutamyl cyclotransferase	Mm.27337.2	7.8	8.8	**1.98**	0.02
1416221_at	Fstl1	follistatin-like 1	Mm.22763.1	5.4	6.4	**1.97**	0.00
1420911_a_at	Mfge8	milk fat globule-EGF factor 8 protein	Mm.1451.1	7.9	8.9	**1.97**	0.00
1421106_at	Jag1	jagged 1	Mm.87380.1	3.7	4.6	**1.97**	0.02
1423484_at	Bicc1	bicaudal C homolog 1 (Drosophila)	Mm.46051.1	6.0	7.0	**1.97**	0.00
1426601_at	Slc37a1	solute carrier family 37 (glycerol-3-phosphate transporter), member 1	Mm.204968.1	6.2	7.2	**1.97**	0.04
1430574_at	Cdkn3	cyclin-dependent kinase inhibitor 3	Mm.27224.1	3.8	4.8	**1.97**	0.05

Supplemental Table 9. Significant differently expressed genes in 3bKI HCC samples

Affymetrix ID	Gene Symbol	Description	Transcript ID (Array Design)	3aKO avg signal log2 (n=4)	3bKI Avg Signal log2 (n=5)	Fold Change (linear)	ANOVA p-value
1431591_s_at	Gm9706	predicted gene 9706; ISG15 ubiquitin-like modifier	Mm.204646.1	6.3	7.3	**1.97**	0.01
1424713_at	Calml4	calmodulin-like 4	Mm.28623.1	5.9	6.9	**1.96**	0.04
1424931_s_at	Iglc1	immunoglobulin lambda constant 1; immunoglobulin lambda variable 1	Mm.780.1	4.2	5.1	**1.96**	0.04
1439407_x_at	Tagln2	transgelin 2	Mm.22632.4	6.5	7.4	**1.96**	0.01
1452227_at	Sel1l3	sel-1 suppressor of lin-12-like 3 (C. elegans)	Mm.24656.1	6.0	6.9	**1.96**	0.03
1420013_s_at	Lss	lanosterol synthase	Mm.195350.1	10.0	11.0	**1.95**	0.02
1456733_x_at	Serpinh1	serine (or cysteine) peptidase inhibitor, clade H, member 1	Mm.22708.4	6.3	7.3	**1.95**	0.05
1420647_a_at	Krt8	keratin 8	Mm.6800.1	10.8	11.8	**1.94**	0.00
1439773_at	Ly6e	lymphocyte antigen 6 complex, locus E	Mm.45974.1	6.7	7.6	**1.94**	0.02
1415993_at	Sqle	squalene epoxidase	Mm.22663.1	10.9	11.9	**1.93**	0.02
1418075_at	St6galnac4	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 4	Mm.27446.1	5.9	6.8	**1.93**	0.03
1418580_at	Rtp4	receptor transporter protein 4	Mm.180157.1	8.5	9.4	**1.93**	0.04
1429570_at	Mlkl	mixed lineage kinase domain-like	Mm.207971.1	7.0	8.0	**1.93**	0.02
1440447_at	Abhd2	abhydrolase domain containing 2	Mm.214741.1	5.5	6.5	**1.93**	0.03
1416529_at	Emp1	epithelial membrane protein 1	Mm.30024.1	4.6	5.6	**1.92**	0.01
1417303_at	Mvd	mevalonate (diphospho) decarboxylase	Mm.28146.1	8.0	9.0	**1.92**	0.04
1449078_at	St3gal6	ST3 beta-galactoside alpha-2,3-sialyltransferase 6	Mm.100109.1	6.1	7.0	**1.92**	0.05
1450625_at	Col5a2	collagen, type V, alpha 2	Mm.10299.1	3.4	4.3	**1.92**	0.00
1453269_at	Unc5b	unc-5 homolog B (C. elegans)	Mm.29888.1	5.2	6.2	**1.92**	0.00
1428209_at	Bex4	brain expressed gene 4	Mm.14768.2	3.2	4.2	**1.91**	0.01
1449106_at	Gpx3	glutathione peroxidase 3	Mm.7156.1	7.2	8.1	**1.91**	0.03
1459589_at	Cryl1	crystallin, lambda 1	Mm.200251.1	6.1	7.0	**1.91**	0.00
1427451_a_at	BC018473	cDNA sequence BC018473	Mm.100084.1	3.8	4.8	**1.9**	0.03
1438716_at	Trim30d	tripartite motif-containing 30D	Mm.3288.3	3.8	4.8	**1.9**	0.05
1448213_at	Anxa1	annexin A1	Mm.14860.1	7.5	8.4	**1.9**	0.04
1452360_a_at	Kdm5a	lysine (K)-specific demethylase 5A	Mm.95879.2	7.1	8.0	**1.9**	0.00
1423909_at	Tmem176a	transmembrane protein 176A	Mm.27061.1	11.7	12.6	**1.89**	0.00
1434758_at	Crispld2	cysteine-rich secretory protein LCCL domain containing 2	Mm.59441.1	5.1	6.0	**1.89**	0.01
1435653_at	Abhd2	abhydrolase domain containing 2	Mm.161353.1	10.3	11.2	**1.89**	0.02
1417501_at	Fbxo6	F-box protein 6	Mm.27445.1	8.6	9.5	**1.88**	0.01
1423691_x_at	Krt8	keratin 8	Mm.6800.2	10.6	11.5	**1.88**	0.00
1429527_a_at	Plscr1	phospholipid scramblase 1	Mm.14627.3	5.7	6.7	**1.88**	0.02
1415919_at	Npdc1	neural proliferation, differentiation and control 1	Mm.1131.1	6.7	7.6	**1.87**	0.00
1426123_a_at	Rrbp1	ribosome binding protein 1	Mm.13705.8	9.3	10.2	**1.87**	0.02
1427665_a_at	Nfic	nuclear factor I/C	Mm.5104.2	6.7	7.6	**1.87**	0.00

Supplemental Table 9. Significant differently expressed genes in 3bKI HCC samples

Affymetrix ID	Gene Symbol	Description	Transcript ID (Array Design)	3aKO avg signal log2 (n=4)	3bKI Avg Signal log2 (n=5)	Fold Change (linear)	ANOVA p-value
1450355_a_at	Capg	capping protein (actin filament), gelsolin-like	Mm.18626.1	6.1	7.0	**1.87**	0.01
1441230_at			Mm.187354.1	6.0	6.9	**1.86**	0.03
1449360_at	Csf2rb2	colony stimulating factor 2 receptor, beta 2, low-affinity (granulocyte-macrophage)	Mm.1940.1	4.7	5.6	**1.86**	0.02
1449363_at	Atf3	activating transcription factor 3	Mm.2706.1	6.2	7.0	**1.86**	0.02
1460302_at	Thbs1	thrombospondin 1	Mm.4159.1	4.2	5.1	**1.86**	0.02
1416342_at	Tnc	tenascin C	Mm.980.1	4.4	5.3	**1.85**	0.00
1417837_at	Phlda2	pleckstrin homology-like domain, family A, member 2	Mm.23697.1	5.3	6.1	**1.85**	0.01
1424754_at	Ms4a7	membrane-spanning 4-domains, subfamily A, member 7	Mm.193094.1	4.9	5.8	**1.85**	0.00
1425810_a_at	Csrp1	cysteine and glycine-rich protein 1	Mm.196484.2	7.0	7.9	**1.85**	0.01
1426805_at	Smarca4	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4	Mm.200406.1	7.0	7.8	**1.85**	0.00
1437708_x_at	Vamp3	vesicle-associated membrane protein 3	Mm.168744.4	6.9	7.8	**1.85**	0.03
1420017_at	Tspan8	tetraspanin 8	Mm.219820.1	5.2	6.0	**1.84**	0.03
1427347_s_at	Tubb2a	tubulin, beta 2A class IIA	Mm.200858.1	9.9	10.8	**1.84**	0.03
1450641_at	Vim	vimentin	Mm.7.1	8.3	9.2	**1.84**	0.03
1450661_x_at	Nfic	nuclear factor I/C	Mm.5104.1	7.4	8.3	**1.84**	0.00
1418069_at	Apoc2	apolipoprotein C-II	Mm.28394.1	12.2	13.1	**1.83**	0.01
1424245_at	Ces2c	carboxylesterase 2C; carboxylesterase 2D, pseudogene	Mm.28191.1	8.7	9.6	**1.83**	0.02
1415961_at	Itm2c	integral membrane protein 2C	Mm.29870.1	9.4	10.3	**1.82**	0.02
1416579_a_at	Epcam	epithelial cell adhesion molecule	Mm.4259.1	5.8	6.7	**1.82**	0.03
1416646_at	Afp	alpha fetoprotein	Mm.80.1	5.5	6.4	**1.82**	0.01
1417290_at	Lrg1	leucine-rich alpha-2-glycoprotein 1	Mm.176946.1	12.8	13.6	**1.82**	0.00
1428936_at	Atp2b1	ATPase, Ca++ transporting, plasma membrane 1	Mm.103450.1	6.8	7.7	**1.82**	0.00
1436722_a_at	Actb	actin, beta	Mm.297.2	12.8	13.7	**1.82**	0.00
1457047_at			Mm.151885.1	4.8	5.6	**1.82**	0.00
1421813_a_at	Psap	prosaposin	Mm.3363.1	11.0	11.9	**1.81**	0.00
1424704_at	Runx2	runt related transcription factor 2	Mm.4509.1	3.2	4.1	**1.81**	0.01
1448281_a_at	Cela2a	chymotrypsin-like elastase family, member 2A	Mm.21925.1	4.5	5.4	**1.81**	0.01
1436029_at	Bicc1	bicaudal C homolog 1 (Drosophila)	Mm.25695.2	6.3	7.1	**1.8**	0.00
1453181_x_at	Plscr1	phospholipid scramblase 1	Mm.14627.3	6.1	7.0	**1.8**	0.02
1418374_at	Fxyd3	FXYD domain-containing ion transport regulator 3	Mm.1662.1	5.8	6.6	**1.79**	0.01
1422916_at	Fgf21	fibroblast growth factor 21	Mm.143736.1	6.5	7.4	**1.79**	0.04
1437633_at	Ankrd11	ankyrin repeat domain 11	Mm.41929.2	7.3	8.1	**1.79**	0.00
1450061_at	Enc1	ectodermal-neural cortex 1	Mm.30502.1	6.4	7.2	**1.79**	0.00

Supplemental Table 9. Significant differently expressed genes in 3bKI HCC samples

Affymetrix ID	Gene Symbol	Description	Transcript ID (Array Design)	3aKO avg signal log2 (n=4)	3bKI Avg Signal log2 (n=5)	Fold Change (linear)	ANOVA p-value
1450541_at	Pvt1	plasmacytoma variant translocation 1	Mm.4608.1	4.8	5.6	**1.79**	0.00
1417392_a_at	Slc7a7	solute carrier family 7 (cationic amino acid transporter, y+ system), member 7	Mm.142455.1	7.4	8.2	**1.78**	0.04
1418004_a_at	Tmem176b	transmembrane protein 176B	Mm.28385.1	11.8	12.6	**1.78**	0.00
1418280_at	Klf6	Kruppel-like factor 6	Mm.196627.1	5.2	6.0	**1.78**	0.02
1450562_at	Ly6f	lymphocyte antigen 6 complex, locus F	Mm.57179.1	4.0	4.8	**1.78**	0.00
1420991_at	Ankrd1	ankyrin repeat domain 1 (cardiac muscle)	Mm.10279.1	3.9	4.7	**1.77**	0.02
1421504_at	Sp4	trans-acting transcription factor 4	Mm.5073.1	5.7	6.6	**1.77**	0.00
1423549_at	Slc1a4	solute carrier family 1 (glutamate/neutral amino acid transporter), member 4	Mm.6379.1	5.9	6.7	**1.77**	0.00
1425182_x_at	Klk1b22	kallikrein 1-related peptidase b22; kallikrein 1-related peptidase b9	Mm.200410.1	6.0	6.8	**1.77**	0.03
1427683_at	Egr2	early growth response 2	Mm.1353.2	3.3	4.2	**1.77**	0.03
1439566_at	Gprin3	GPRIN family member 3	Mm.138080.1	6.6	7.5	**1.77**	0.04
1416103_at	Ywhaz	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide	Mm.3360.1	7.7	8.5	**1.76**	0.02
1416521_at	Sepw1	selenoprotein W, muscle 1	Mm.42829.1	8.8	9.6	**1.76**	0.03
1429159_at	Itih5	inter-alpha (globulin) inhibitor H5	Mm.2935.1	5.9	6.7	**1.76**	0.02
1437277_x_at	Tgm2	transglutaminase 2, C polypeptide	Mm.18843.7	10.8	11.7	**1.76**	0.02
1448169_at	Krt18	keratin 18	Mm.22479.1	11.4	12.2	**1.76**	0.02
1416410_at	Pafah1b3	platelet-activating factor acetylhydrolase, isoform 1b, subunit 3	Mm.597.1	6.1	6.9	**1.75**	0.02
1416443_a_at	Sae1	SUMO1 activating enzyme subunit 1	Mm.29698.1	9.3	10.2	**1.75**	0.00
1418499_a_at	Kcne3	potassium voltage-gated channel, Isk-related subfamily, gene 3	Mm.18733.1	2.8	3.6	**1.75**	0.00
1422912_at	Bmp4	bone morphogenetic protein 4	Mm.6813.1	6.6	7.4	**1.75**	0.03
1426366_at	Ago2	argonaute RISC catalytic subunit 2	Mm.26266.1	7.0	7.8	**1.75**	0.00
1435611_x_at	Cela3b	chymotrypsin-like elastase family, member 3B	Mm.30780.4	5.1	6.0	**1.75**	0.03
1436890_at	Uap1l1	UDP-N-acteylglucosamine pyrophosphorylase 1-like 1	Mm.33797.2	6.9	7.7	**1.75**	0.01
1438133_a_at	Cyr61	cysteine rich protein 61	Mm.1231.2	6.3	7.1	**1.75**	0.00
1418263_at	Ddx25	DEAD (Asp-Glu-Ala-Asp) box polypeptide 25	Mm.45108.1	4.7	5.5	**1.74**	0.00
1434241_at	Wdr67	TBC1 domain family, member 31	Mm.31972.1	7.3	8.1	**1.74**	0.00
1449984_at	Cxcl2	chemokine (C-X-C motif) ligand 2	Mm.4979.1	3.4	4.2	**1.74**	0.03
1460330_at	Anxa3	annexin A3	Mm.7214.1	6.6	7.4	**1.74**	0.04

Supplemental Table 9. Significant differently expressed genes in 3bKI HCC samples

Affymetrix ID	Gene Symbol	Description	Transcript ID (Array Design)	3aKO avg signal log2 (n=4)	3bKI Avg Signal log2 (n=5)	Fold Change (linear)	ANOVA p-value
1416028_a_at	Hn1	hematological and neurological expressed sequence 1	Mm.1775.1	6.9	7.7	**1.73**	0.02
1424131_at	Col6a3	collagen, type VI, alpha 3	Mm.7562.1	6.8	7.6	**1.73**	0.01
1436539_at	Clmn	calmin	Mm.22921.1	6.3	7.1	**1.73**	0.00
1442439_at	W91776	expressed sequence W91776	Mm.34265.1	4.2	5.0	**1.73**	0.03
1444182_at	Igsf23	immunoglobulin superfamily, member 23	Mm.98583.1	4.1	4.8	**1.73**	0.04
1460227_at	Timp1	tissue inhibitor of metalloproteinase 1	Mm.8245.1	4.6	5.4	**1.73**	0.00
1418073_at	Acot9	acyl-CoA thioesterase 9	Mm.23368.1	6.6	7.3	**1.72**	0.04
1430964_at	2310034O05Rik	RIKEN cDNA 2310034O05 gene	Mm.58173.1	3.8	4.6	**1.72**	0.03
1450295_s_at	Pvr	poliovirus receptor	Mm.8071.1	4.0	4.8	**1.72**	0.00
1423418_at	Fdps	farnesyl diphosphate synthetase	Mm.39472.1	12.0	12.8	**1.71**	0.03
1423547_at	Lyz2	lysozyme 2	Mm.45436.1	10.2	11.0	**1.71**	0.01
1423550_at	Slc1a4	solute carrier family 1 (glutamate/neutral amino acid transporter), member 4	Mm.6379.1	6.5	7.3	**1.71**	0.00
1424612_at	Nipal2	NIPA-like domain containing 2	Mm.179043.1	4.6	5.4	**1.71**	0.01
1425603_at	Tmem176a	transmembrane protein 176A	Mm.153276.1	10.5	11.3	**1.71**	0.02
1425811_a_at	Csrp1	cysteine and glycine-rich protein 1	Mm.196484.2	7.6	8.3	**1.71**	0.03
1426964_at	Abracl	ABRA C-terminal like; predicted pseudogene 6314	Mm.28149.1	8.7	9.5	**1.71**	0.04
1434027_at	Rcan3	regulator of calcineurin 3	Mm.11946.2	5.2	6.0	**1.71**	0.02
1435650_at	Hapln4	hyaluronan and proteoglycan link protein 4	Mm.152048.1	7.4	8.2	**1.71**	0.03
1435989_x_at	Krt8	keratin 8	Mm.6800.3	10.5	11.3	**1.71**	0.00
1438322_x_at	Fdft1	farnesyl diphosphate farnesyl transferase 1	Mm.3204.3	10.3	11.1	**1.71**	0.03
1416164_at	Fbln5	fibulin 5	Mm.25347.1	7.0	7.8	**1.7**	0.01
1416498_at	Ppic	peptidylprolyl isomerase C	Mm.4587.1	6.0	6.8	**1.7**	0.04
1416501_at	Pdpk1	3-phosphoinositide dependent protein kinase 1	Mm.10504.1	7.2	8.0	**1.7**	0.00
1416589_at	Sparc	secreted acidic cysteine rich glycoprotein	Mm.35439.1	9.8	10.6	**1.7**	0.05
1428626_at	Lysmd2	LysM, putative peptidoglycan-binding, domain containing 2	Mm.19119.1	5.9	6.7	**1.7**	0.03
1433428_x_at	Tgm2	transglutaminase 2, C polypeptide	Mm.18843.4	10.6	11.4	**1.7**	0.02
1433507_a_at	Gm6750	predicted gene 6750; predicted pseudogene 7931; predicted gene 9525; high mobility group nucleosomal binding domain 2	Mm.911.2	9.2	9.9	**1.7**	0.04
1434089_at	Synpo	synaptopodin	Mm.27313.1	5.2	6.0	**1.7**	0.03
1435936_at	Slc13a5	solute carrier family 13 (sodium-dependent citrate transporter), member 5	Mm.30956.1	6.4	7.2	**1.7**	0.04
1436996_x_at	Lyz1	lysozyme 1	Mm.45436.2	10.8	11.5	**1.7**	0.01
1441042_at	Fgf1	fibroblast growth factor 1	Mm.139120.1	5.8	6.6	**1.7**	0.01

Supplemental Table 9. Significant differently expressed genes in 3bKI HCC samples

Affymetrix ID	Gene Symbol	Description	Transcript ID (Array Design)	3aKO avg signal log2 (n=4)	3bKI Avg Signal log2 (n=5)	Fold Change (linear)	ANOVA p-value
1444774_at	Det1	de-etiolated homolog 1 (Arabidopsis)	Mm.218272.1	5.7	6.4	**1.7**	0.04
1451230_a_at	Wbp5	WW domain binding protein 5	Mm.512.1	9.6	10.4	**1.7**	0.03
1417087_at	Glg1	golgi apparatus protein 1	Mm.488.1	8.2	9.0	**1.69**	0.05
1417399_at	Gas6	growth arrest specific 6	Mm.3982.1	9.0	9.7	**1.69**	0.04
1417971_at	Nrm	nurim (nuclear envelope membrane protein)	Mm.18478.1	4.7	5.4	**1.69**	0.01
1419100_at	Serpina3n	serine (or cysteine) peptidase inhibitor, clade A, member 3N	Mm.22650.1	11.1	11.9	**1.69**	0.00
1419838_s_at	Plk4	polo-like kinase 4	Mm.198533.1	4.0	4.8	**1.69**	0.01
1427002_s_at	Arsg	arylsulfatase G	Mm.41370.1	7.5	8.3	**1.69**	0.02
1429139_at	Otud7b	OTU domain containing 7B	Mm.3050.1	6.8	7.6	**1.69**	0.01
1435902_at	Nudt18	nudix (nucleoside diphosphate linked moiety X)-type motif 18	Mm.34191.1	8.2	8.9	**1.69**	0.01
1439041_at	Slc39a10	solute carrier family 39 (zinc transporter), member 10	Mm.215090.1	4.9	5.6	**1.69**	0.02
1448130_at	Fdft1	farnesyl diphosphate farnesyl transferase 1	Mm.3204.1	10.7	11.5	**1.69**	0.02
1448207_at	Lasp1	LIM and SH3 protein 1	Mm.200673.1	7.4	8.1	**1.69**	0.01
1448710_at	Cxcr4	chemokine (C-X-C motif) receptor 4	Mm.1401.1	3.8	4.6	**1.69**	0.00
1415836_at	Aldh18a1	aldehyde dehydrogenase 18 family, member A1	Mm.29751.1	5.0	5.7	**1.68**	0.00
1415890_at	Papss1	3'-phosphoadenosine 5'-phosphosulfate synthase 1	Mm.18161.1	8.2	9.0	**1.68**	0.00
1416407_at	Pea15a	phosphoprotein enriched in astrocytes 15A	Mm.544.1	7.8	8.6	**1.68**	0.02
1417116_at	Slc6a8	solute carrier family 6 (neurotransmitter transporter, creatine), member 8	Mm.41401.1	6.2	6.9	**1.68**	0.02
1417379_at	Iqgap1	IQ motif containing GTPase activating protein 1	Mm.56685.1	7.6	8.4	**1.68**	0.04
1423141_at	Lipa	lysosomal acid lipase A	Mm.181935.1	9.3	10.1	**1.68**	0.00
1429745_at	DXBay18	DNA segment, Chr X, Baylor 18; predicted gene 14685; predicted pseudogene 5639; predicted gene 5640; predicted gene 5936	Mm.5154.2	3.0	3.7	**1.68**	0.00
1433446_at	Hmgcs1	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1	Mm.61526.4	11.2	12.0	**1.68**	0.01
1435792_at	Csprs	component of Sp100-rs; predicted pseudogene 15433; predicted gene 2666; predicted pseudogene 7609; uncharacterized LOC100041903; uncharacterized LOC100503923	Mm.99965.2	6.8	7.5	**1.68**	0.03
1448229_s_at	Ccnd2	cyclin D2	Mm.3141.1	4.8	5.5	**1.68**	0.01
1417225_at	Arl6ip5	ADP-ribosylation factor-like 6 interacting protein 5	Mm.30009.1	9.3	10.0	**1.67**	0.01

Supplemental Table 9. Significant differently expressed genes in 3bKI HCC samples

Affymetrix ID	Gene Symbol	Description	Transcript ID (Array Design)	3aKO avg signal log2 (n=4)	3bKI Avg Signal log2 (n=5)	Fold Change (linear)	ANOVA p-value
1418517_at	Irx3	Iroquois related homeobox 3	Mm.39039.1	4.8	5.5	**1.67**	0.01
1418711_at	Pdgfa	platelet derived growth factor, alpha	Mm.2675.1	6.6	7.3	**1.67**	0.00
1425911_a_at	Fgfr1	fibroblast growth factor receptor 1	Mm.3157.3	4.6	5.3	**1.67**	0.01
1436902_x_at	Tmsb10	thymosin, beta 10	Mm.3532.5	8.2	8.9	**1.67**	0.03
1448429_at	Gyg	glycogenin	Mm.6375.1	6.6	7.3	**1.67**	0.03
1454757_s_at	Ifi27l1	interferon, alpha-inducible protein 27	Mm.2121.2	10.3	11.0	**1.67**	0.01
1416726_s_at	Ube2s	ubiquitin-conjugating enzyme E2S	Mm.22491.1	9.3	10.1	**1.66**	0.02
1418136_at	Tgfb1i1	transforming growth factor beta 1 induced transcript 1	Mm.3248.1	6.5	7.2	**1.66**	0.00
1418760_at	Rdh11	retinol dehydrogenase 11	Mm.219462.1	9.0	9.7	**1.66**	0.04
1423406_at	Sv2a	synaptic vesicle glycoprotein 2 a	Mm.200365.1	5.6	6.4	**1.66**	0.01
1423584_at	Igfbp7	insulin-like growth factor binding protein 7	Mm.534.1	11.1	11.8	**1.66**	0.00
1426434_at	Tmem43	transmembrane protein 43	Mm.38801.1	7.3	8.0	**1.66**	0.02
1432579_at	Rsph3a	radial spoke 3A homolog (Chlamydomonas)	Mm.159766.1	5.1	5.8	**1.66**	0.00
1437185_s_at	Tmsb10	thymosin, beta 10	Mm.3532.6	10.3	11.0	**1.66**	0.03
1437536_at	Fkrp	fukutin related protein	Mm.39703.1	5.8	6.6	**1.66**	0.00
1439178_at	Adrbk2	adrenergic receptor kinase, beta 2	Mm.153148.1	6.0	6.8	**1.66**	0.04
1447043_at			Mm.127541.1	3.1	3.8	**1.66**	0.00
1453238_s_at	A130040M12Ril	RIKEN cDNA 3930401B19 gene	Mm.196616.1	11.5	12.3	**1.66**	0.04
1456230_at	4933422H20Rik	RIKEN cDNA 4933422H20 gene	Mm.50902.1	5.2	5.9	**1.66**	0.01
1419665_a_at	Nupr1	nuclear protein transcription regulator 1	Mm.18742.1	5.4	6.1	**1.65**	0.03
1421424_a_at	Anpep	alanyl (membrane) aminopeptidase	Mm.4487.1	8.8	9.5	**1.65**	0.01
1424186_at	Ccdc80	coiled-coil domain containing 80	Mm.181074.1	8.2	9.0	**1.65**	0.02
1428705_at	1700007K13Rik	RIKEN cDNA 1700007K13 gene	Mm.46470.1	3.4	4.2	**1.65**	0.01
1429233_at	Sept11	septin 11	Mm.27384.1	8.0	8.7	**1.65**	0.00
1434788_at	Fzd3	frizzled homolog 3 (Drosophila)	Mm.115175.1	3.8	4.5	**1.65**	0.03
1448596_at	Slc6a8	solute carrier family 6 (neurotransmitter transporter, creatine), member 8	Mm.41401.1	5.9	6.7	**1.65**	0.01
1448619_at	Dhcr7	7-dehydrocholesterol reductase	Mm.182149.1	10.1	10.8	**1.65**	0.01
1449187_at	Pdgfa	platelet derived growth factor, alpha	Mm.2675.1	6.8	7.5	**1.65**	0.00
1460259_s_at	Clca1	chloride channel calcium activated 1; chloride channel calcium activated 2	Mm.20897.1	6.2	6.9	**1.65**	0.04
1418929_at	Ift57	intraflagellar transport 57	Mm.31355.1	6.2	7.0	**1.64**	0.02
1426529_a_at	Tagln2	transgelin 2	Mm.22632.1	8.1	8.8	**1.64**	0.00
1426774_at	Parp12	poly (ADP-ribose) polymerase family, member 12	Mm.29894.1	8.6	9.3	**1.64**	0.05
1428420_a_at	Exoc3l4	exocyst complex component 3-like 4	Mm.28857.1	5.5	6.2	**1.64**	0.01
1448333_at	Adprh	ADP-ribosylarginine hydrolase	Mm.20047.1	7.5	8.2	**1.64**	0.02
1448424_at	Frzb	frizzled-related protein	Mm.3246.1	4.0	4.7	**1.64**	0.01
1451680_at	Srxn1	sulfiredoxin 1 homolog (S. cerevisiae)	Mm.181594.1	8.9	9.6	**1.64**	0.00

Supplemental Table 9. Significant differently expressed genes in 3bKI HCC samples

Affymetrix ID	Gene Symbol	Description	Transcript ID (Array Design)	3aKO avg signal log2 (n=4)	3bKI Avg Signal log2 (n=5)	Fold Change (linear)	ANOVA p-value
1455390_at	Alkbh6	alkB, alkylation repair homolog 6 (E. coli)	Mm.40726.1	7.3	8.0	**1.64**	0.01
1455900_x_at	Tgm2	transglutaminase 2, C polypeptide	Mm.18843.6	9.9	10.6	**1.64**	0.02
1415806_at	Plat	plasminogen activator, tissue	Mm.154660.1	4.9	5.6	**1.63**	0.00
1416222_at	Nsdhl	NAD(P) dependent steroid dehydrogenase-like	Mm.38792.1	11.1	11.8	**1.63**	0.01
1418184_at	Cenpm	centromere protein M	Mm.23596.1	7.2	7.9	**1.63**	0.01
1419492_s_at	Defb1	defensin beta 1	Mm.5341.1	5.0	5.7	**1.63**	0.04
1424142_at	Ikbkap	inhibitor of kappa light polypeptide enhancer in B cells, kinase complex-associated protein	Mm.46573.1	6.3	7.0	**1.63**	0.00
1444616_x_at			Mm.29305.1	4.3	5.0	**1.63**	0.00
1447530_at	F8a	factor 8-associated gene A	Mm.165807.1	5.9	6.7	**1.63**	0.00
1448471_a_at	Ctla2a	cytotoxic T lymphocyte-associated protein 2 alpha	Mm.30144.1	4.7	5.4	**1.63**	0.01
1449110_at	Rhob	ras homolog gene family, member B	Mm.687.1	9.4	10.1	**1.63**	0.00
1418719_at	Haus8	4HAUS augmin-like complex, subunit 8	Mm.27355.1	5.5	6.2	**1.62**	0.04
1419256_at	Sptbn1	spectrin beta, non-erythrocytic 1	Mm.123110.1	7.9	8.6	**1.62**	0.00
1429509_at	Lsm12	LSM12 homolog (S. cerevisiae)	Mm.36280.1	6.0	6.7	**1.62**	0.03
1431422_a_at	Dusp14	dual specificity phosphatase 14	Mm.142293.2	5.3	6.0	**1.62**	0.04
1434322_at	Micall2	MICAL-like 2	Mm.89789.1	4.8	5.5	**1.62**	0.02
1439426_x_at	Lyz1	lysozyme 1	Mm.45436.3	9.2	9.9	**1.62**	0.01
1451421_a_at	Rogdi	rogdi homolog (Drosophila)	Mm.27792.2	8.7	9.4	**1.62**	0.04
1416554_at	Pdlim1	PDZ and LIM domain 1 (elfin)	Mm.5567.1	9.8	10.5	**1.61**	0.01
1417472_at	Myh9	myosin, heavy polypeptide 9, non-muscle	Mm.5938.1	9.0	9.7	**1.61**	0.01
1423754_at	Ifitm3	interferon induced transmembrane protein 3	Mm.141021.1	12.6	13.3	**1.61**	0.00
1436785_a_at	Sec14l3	SEC14-like 3 (S. cerevisiae)	Mm.46347.1	6.6	7.3	**1.61**	0.00
1448188_at	Ucp2	uncoupling protein 2 (mitochondrial, proton carrier)	Mm.144413.1	8.8	9.5	**1.61**	0.03
1453351_at	Tbx20	T-box 20	Mm.117009.1	4.1	4.8	**1.61**	0.01
1457687_at	Bcl2	B cell leukemia/lymphoma 2	Mm.86383.1	5.1	5.8	**1.61**	0.03
1418456_a_at	Cxcl14	chemokine (C-X-C motif) ligand 14	Mm.30211.1	5.8	6.5	**1.6**	0.01
1419155_a_at	Sox4	SRY (sex determining region Y)-box 4	Mm.18789.1	6.7	7.3	**1.6**	0.00
1422779_at	Smpd3	sphingomyelin phosphodiesterase 3, neutral	Mm.143806.1	4.1	4.7	**1.6**	0.02
1423642_at	Tubb4b	tubulin, beta 4B class IVB	Mm.21840.1	10.3	11.0	**1.6**	0.00
1424398_at	Dhx36	DEAH (Asp-Glu-Ala-His) box polypeptide 36	Mm.34158.1	8.2	8.9	**1.6**	0.01
1429621_at	Cand2	cullin-associated and neddylation-dissociated 2 (putative)	Mm.46006.1	3.8	4.5	**1.6**	0.01
1429891_at	Capsl	calcyphosine-like	Mm.82143.1	2.5	3.2	**1.6**	0.01
1431062_a_at	Exoc4	exocyst complex component 4	Mm.6925.2	6.7	7.4	**1.6**	0.00

Supplemental Table 9. Significant differently expressed genes in 3bKI HCC samples

Affymetrix ID	Gene Symbol	Description	Transcript ID (Array Design)	3aKO avg signal log2 (n=4)	3bKI Avg Signal log2 (n=5)	Fold Change (linear)	ANOVA p-value
1456796_at	Snai3	snail family zinc finger 3	Mm.22910.1	6.0	6.7	**1.6**	0.02
1420940_x_at	Rgs5	regulator of G-protein signaling 5	Mm.20954.1	6.0	6.7	**1.59**	0.00
1422583_at	Rab3b	RAB3B, member RAS oncogene family	Mm.41580.1	5.2	5.8	**1.59**	0.00
1423904_a_at	Pvr	poliovirus receptor	Mm.134436.1	5.6	6.2	**1.59**	0.00
1428018_a_at	AF251705	cDNA sequence AF251705	Mm.2699.2	6.6	7.3	**1.59**	0.00
1433714_at	Sult4a1	sulfotransferase family 4A, member 1	Mm.29330.1	4.1	4.8	**1.59**	0.03
1437692_x_at	Anxa2	annexin A2	Mm.584.3	4.4	5.0	**1.59**	0.00
1440844_at	Tob1	transducer of ErbB-2.1	Mm.31688.1	7.6	8.3	**1.59**	0.01
1442693_at	Trim5	tripartite motif-containing 5	Mm.34718.1	2.6	3.3	**1.59**	0.01
1448303_at	Gpnmb	glycoprotein (transmembrane) nmb	Mm.23567.1	4.8	5.5	**1.59**	0.04
1455494_at	Col1a1	collagen, type I, alpha 1	Mm.22621.2	4.7	5.3	**1.59**	0.02
1456046_at	Cd93	CD93 antigen	Mm.69004.1	7.4	8.0	**1.59**	0.01
1456110_at	Ankrd11	ankyrin repeat domain 11	Mm.41929.2	7.3	8.0	**1.59**	0.01
1458587_at	2310047D07Rik	RIKEN cDNA 2310047D07 gene	Mm.44573.1	5.5	6.1	**1.59**	0.01
1418350_at	Hbegf	heparin-binding EGF-like growth factor	Mm.4661.1	6.1	6.7	**1.58**	0.04
1420563_at	Gria3	glutamate receptor, ionotropic, AMPA3 (alpha 3)	Mm.42021.1	5.2	5.9	**1.58**	0.00
1424906_at	Pqlc3	PQ loop repeat containing	Mm.5675.1	4.7	5.4	**1.58**	0.01
1434265_s_at	Ank2	ankyrin 2, brain	Mm.41182.1	4.7	5.4	**1.58**	0.03
1440156_s_at	Tox2	TOX high mobility group box family member 2	Mm.40354.1	5.3	6.0	**1.58**	0.03
1449117_at	Jund	jun D proto-oncogene	Mm.1175.1	9.2	9.9	**1.58**	0.00
1450484_a_at	Cmpk2	cytidine monophosphate (UMP-CMP) kinase 2, mitochondrial	Mm.1676.1	5.0	5.7	**1.58**	0.04
1454808_at	Micu2	mitochondrial calcium uptake 2	Mm.26834.1	8.5	9.1	**1.58**	0.01
1458018_at			Mm.207589.1	3.4	4.0	**1.58**	0.01
1416013_at	Pld3	phospholipase D family, member 3	Mm.6483.1	8.5	9.2	**1.57**	0.00
1425398_at	Hist1h2bf	histone cluster 1, H2bf; histone cluster 1, H2bj; histone cluster 1, H2bl; histone cluster 1, H2bn; histone cluster 1, H2bq; histone cluster 1 H2br	Mm.21579.2	3.7	4.3	**1.57**	0.05
1429234_s_at	Sept11	septin 11	Mm.27384.1	8.1	8.8	**1.57**	0.01
1446798_at	Map4k3	mitogen-activated protein kinase kinase kinase kinase 3	Mm.210311.1	3.4	4.0	**1.57**	0.00
1451788_at	F11	coagulation factor XI	Mm.33326.1	9.4	10.0	**1.57**	0.01
1456907_at	Cxcl9	chemokine (C-X-C motif) ligand 9	Mm.119763.1	4.0	4.7	**1.57**	0.04
1459864_at	Gpr146	G protein-coupled receptor 146	Mm.169778.1	4.8	5.4	**1.57**	0.00
1419108_at	Ophn1	oligophrenin 1	Mm.100064.1	4.3	4.9	**1.56**	0.00
1419970_at	Slc35a5	solute carrier family 35, member A5	Mm.195368.1	4.0	4.7	**1.56**	0.01
1422534_at	Cyp51	cytochrome P450, family 51	Mm.140158.1	6.3	6.9	**1.56**	0.02
1426410_at	Pdk3	pyruvate dehydrogenase kinase, isoenzyme 3	Mm.12775.1	5.2	5.9	**1.56**	0.04
1426511_at	Susd2	sushi domain containing 2	Mm.31096.1	5.9	6.6	**1.56**	0.04

Supplemental Table 9. Significant differently expressed genes in 3bKI HCC samples

Affymetrix ID	Gene Symbol	Description	Transcript ID (Array Design)	3aKO avg signal log2 (n=4)	3bKI Avg Signal log2 (n=5)	Fold Change (linear)	ANOVA p-value
1431909_at	Zc3hav1	zinc finger CCCH type, antiviral 1	Mm.195653.1	4.7	5.3	**1.56**	0.00
1449191_at	Wfdc12	WAP four-disulfide core domain 12	Mm.6433.1	5.6	6.3	**1.56**	0.03
1453768_a_at	Fam110a	family with sequence similarity 110, member A	Mm.18228.2	5.8	6.4	**1.56**	0.00
1457356_at			Mm.80556.1	5.4	6.0	**1.56**	0.00
1415798_at	Ddr1	discoidin domain receptor family, member 1	Mm.5021.1	4.8	5.5	**1.55**	0.00
1428497_at	Secisbp2	SECIS binding protein 2	Mm.46606.1	7.3	7.9	**1.55**	0.00
1436058_at	Rsad2	radical S-adenosyl methionine domain containing 2	Mm.27276.1	7.2	7.8	**1.55**	0.04
1437670_x_at	Cd151	CD151 antigen	Mm.30246.4	9.0	9.7	**1.55**	0.00
1438677_at	Pkp4	plakophilin 4	Mm.153748.2	8.3	8.9	**1.55**	0.00
1448883_at	Lgmn	legumain	Mm.17185.1	9.8	10.4	**1.55**	0.01
1452139_at	Slc35c1	solute carrier family 35, member C1	Mm.35136.1	6.6	7.2	**1.55**	0.01
1459766_x_at	Sf1	splicing factor 1	Mm.125450.1	9.7	10.4	**1.55**	0.00
1459788_at	Gpr107	G protein-coupled receptor 107	Mm.162126.1	4.8	5.5	**1.55**	0.00
1417495_x_at	Cp	ceruloplasmin	Mm.13787.1	12.7	13.4	**1.54**	0.01
1428549_at	Ccdc3	coiled-coil domain containing 3	Mm.18797.1	6.5	7.1	**1.54**	0.02
1428864_at	Dusp8	dual specificity phosphatase 8	Mm.39987.1	6.6	7.2	**1.54**	0.00
1433445_x_at	Hmgcs1	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1	Mm.61526.4	11.9	12.5	**1.54**	0.01
1434020_at	Pdap1	PDGFA associated protein 1	Mm.3360.2	8.1	8.7	**1.54**	0.00
1435990_at	Adamts2	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 2	Mm.23038.1	4.7	5.3	**1.54**	0.01
1437188_at	Gabbr1	gamma-aminobutyric acid (GABA) B receptor, 1	Mm.32191.5	3.8	4.4	**1.54**	0.02
1437616_x_at	Zdhhc14	zinc finger, DHHC domain containing 14	Mm.22338.3	6.8	7.4	**1.54**	0.00
1443475_at	Hist1h3i		Mm.39245.1	4.2	4.8	**1.54**	0.01
1448180_a_at	Hn1	hematological and neurological expressed sequence 1	Mm.1775.1	7.7	8.3	**1.54**	0.02
1452964_at	Ttll11	tubulin tyrosine ligase-like family, member 11	Mm.21591.1	5.8	6.4	**1.54**	0.00
1415922_s_at	Marcksl1	MARCKS-like 1	Mm.2769.1	8.3	8.9	**1.53**	0.01
1416686_at	Plod2	procollagen lysine, 2-oxoglutarate 5-dioxygenase 2	Mm.79983.1	3.8	4.5	**1.53**	0.00
1418448_at	Rras	Harvey rat sarcoma oncogene, subgroup R	Mm.257.1	8.9	9.5	**1.53**	0.01
1419416_a_at	Rarg	retinoic acid receptor, gamma	Mm.1273.1	5.8	6.5	**1.53**	0.00
1420293_at	Lpcat1	lysophosphatidylcholine acyltransferase 1	Mm.130349.2	4.0	4.6	**1.53**	0.00
1421027_a_at	Mef2c	myocyte enhancer factor 2C	Mm.24001.1	4.4	5.0	**1.53**	0.01
1424262_at	Aif1l	allograft inflammatory factor 1-like	Mm.24838.1	7.4	8.0	**1.53**	0.00
1430619_a_at	Mvk	mevalonate kinase	Mm.28088.2	7.9	8.5	**1.53**	0.01
1438904_at	Nhsl1	NHS-like 1	Mm.208961.1	8.4	9.0	**1.53**	0.00

Supplemental Table 9. Significant differently expressed genes in 3bKI HCC samples

Affymetrix ID	Gene Symbol	Description	Transcript ID (Array Design)	3aKO avg signal log2 (n=4)	3bKI Avg Signal log2 (n=5)	Fold Change (linear)	ANOVA p-value
1440916_at	2510049J12Rik	makorin, ring finger protein 2, opposite strand	Mm.133694.1	8.4	9.0	**1.53**	0.01
1449271_a_at	Hebp2	heme binding protein 2	Mm.35551.1	4.7	5.3	**1.53**	0.01
1449370_at	Sox4	SRY (sex determining region Y)-box 4	Mm.18789.1	4.4	5.0	**1.53**	0.01
1416916_at	Elf3	E74-like factor 3	Mm.3963.1	5.9	6.5	**1.52**	0.04
1417059_at	Krtcap2	keratinocyte associated protein 2	Mm.177991.1	10.6	11.2	**1.52**	0.00
1422286_a_at	Tgif1	TGFB-induced factor homeobox 1	Mm.8155.1	7.5	8.1	**1.52**	0.00
1423140_at	Lipa	lysosomal acid lipase A	Mm.181935.1	6.2	6.8	**1.52**	0.00
1424684_at	Rab5c	RAB5C, member RAS oncogene family	Mm.29829.1	8.8	9.4	**1.52**	0.01
1428228_at	Pgm3	phosphoglucomutase 3	Mm.20245.1	7.3	7.9	**1.52**	0.03
1430021_a_at	Sae1	SUMO1 activating enzyme subunit 1	Mm.29698.2	8.5	9.1	**1.52**	0.00
1434314_s_at	Rab11fip5	RAB11 family interacting protein 5 (class I)	Mm.28032.1	5.7	6.3	**1.52**	0.00
1435625_at	Entpd7	ectonucleoside triphosphate diphosphohydrolase 7	Mm.24247.1	4.5	5.1	**1.52**	0.04
1436124_at	Pcyt1b	phosphate cytidylyltransferase 1, choline, beta isoform	Mm.44503.1	3.8	4.4	**1.52**	0.04
1437451_at	Ecscr	endothelial cell surface expressed chemotaxis and apoptosis regulator	Mm.46243.1	5.7	6.3	**1.52**	0.01
1449139_at	Ostc	oligosaccharyltransferase complex subunit	Mm.9811.1	10.7	11.3	**1.52**	0.02
1449976_a_at	Gpr35	G protein-coupled receptor 35	Mm.152780.1	4.3	4.9	**1.52**	0.04
1451224_at	Scamp5	secretory carrier membrane protein 5	Mm.102278.2	7.0	7.6	**1.52**	0.04
1452152_at	Clint1	clathrin interactor 1	Mm.24036.1	9.3	9.9	**1.52**	0.00
1454965_at	Fam171b	family with sequence similarity 171, member B	Mm.26101.1	4.2	4.8	**1.52**	0.00
1457171_at			Mm.128801.1	6.0	6.6	**1.52**	0.02
1457455_at	Zfp280d	zinc finger protein 280D	Mm.132512.1	5.2	5.8	**1.52**	0.00
1459729_at	Slc13a5	solute carrier family 13 (sodium-dependent citrate transporter), member 5	Mm.151058.1	4.8	5.4	**1.52**	0.03
1459761_x_at	Cadm2	cell adhesion molecule 2	Mm.117889.1	4.2	4.8	**1.52**	0.01
1460343_at	Neurl1a	neuralized homolog 1A (Drosophila)	Mm.103587.2	3.8	4.4	**1.52**	0.00
1423362_at	Sort1	sortilin 1	Mm.157119.1	7.6	8.2	**1.51**	0.01
1423829_at	Fam49b	family with sequence similarity 49, member B	Mm.22383.1	7.0	7.6	**1.51**	0.03
1437132_x_at	Nedd9	neural precursor cell expressed, developmentally down-regulated gene 9	Mm.8315.2	5.4	6.0	**1.51**	0.04
1446109_at	Wdfy3	WD repeat and FYVE domain containing 3	Mm.209277.1	4.3	4.9	**1.51**	0.00
1447803_x_at	Capg	capping protein (actin filament), gelsolin-like	Mm.70286.1	2.8	3.4	**1.51**	0.01

Supplemental Table 9. Significant differently expressed genes in 3bKI HCC samples

Affymetrix ID	Gene Symbol	Description	Transcript ID (Array Design)	3aKO avg signal log2 (n=4)	3bKI Avg Signal log2 (n=5)	Fold Change (linear)	ANOVA p-value
1448534_at	Sirpa	signal-regulatory protein alpha	Mm.1682.1	7.9	8.5	**1.51**	0.05
1450919_at	Mpp1	membrane protein, palmitoylated	Mm.2814.1	9.7	10.3	**1.51**	0.02
1451210_at	Ppap2c	phosphatidic acid phosphatase type 2C	Mm.28873.2	8.7	9.3	**1.51**	0.01
1452124_at	Ank3	ankyrin 3, epithelial	Mm.3526.5	7.5	8.1	**1.51**	0.00
1455393_at	Cp	ceruloplasmin	Mm.13787.2	13.3	13.9	**1.51**	0.02
1455576_at	Rinl	Ras and Rab interactor-like	Mm.74632.1	4.5	5.1	**1.51**	0.00
1455730_at	Dlgap5	discs, large (Drosophila) homolog-associated protein 5	Mm.35569.1	4.8	5.4	**1.51**	0.03
1456310_a_at	2610002J02Rik	RIKEN cDNA 2610002J02 gene	Mm.10374.3	8.0	8.6	**1.51**	0.03
1458818_at	D3Ertd162e	DNA segment, Chr 3, ERATO Doi 162, expressed	Mm.154754.1	4.3	4.9	**1.51**	0.01
1417227_at	Mccc1	methylcrotonoyl-Coenzyme A carboxylase 1 (alpha)	Mm.154589.1	9.8	9.2	**-1.51**	0.01
1417555_at	Atad1	ATPase family, AAA domain containing 1	Mm.27123.1	5.7	5.1	**-1.51**	0.01
1418504_at	Hspa9	heat shock protein 9	Mm.2849.1	11.5	10.9	**-1.51**	0.00
1418586_at	Adcy9	adenylate cyclase 9	Mm.4294.1	9.1	8.5	**-1.51**	0.01
1418640_at	Sirt1	sirtuin 1	Mm.12604.1	6.8	6.2	**-1.51**	0.05
1419918_at	Tmed7	transmembrane emp24 protein transport domain containing 7	Mm.202023.1	9.0	8.4	**-1.51**	0.00
1420339_at	Memo1	mediator of cell motility 1	Mm.28773.1	6.9	6.3	**-1.51**	0.00
1420542_at	Dnajc28	DnaJ (Hsp40) homolog, subfamily C, member 28	Mm.101927.1	6.8	6.2	**-1.51**	0.02
1423044_at	Prosc	proline synthetase co-transcribed	Mm.214583.1	10.4	9.8	**-1.51**	0.01
1423386_at	Psmd9	proteasome (prosome, macropain) 26S subunit, non-ATPase, 9	Mm.30237.1	9.1	8.5	**-1.51**	0.01
1423780_at	Hibadh	3-hydroxyisobutyrate dehydrogenase	Mm.4290.1	12.2	11.6	**-1.51**	0.00
1425206_a_at	Ube3a	ubiquitin protein ligase E3A	Mm.132544.2	6.6	6.0	**-1.51**	0.00
1425331_at	Zfp106	zinc finger protein 106	Mm.27653.2	8.3	7.7	**-1.51**	0.00
1428725_at	Pias2	protein inhibitor of activated STAT 2	Mm.30882.1	7.8	7.2	**-1.51**	0.01
1429351_at	Klhl24	kelch-like 24	Mm.126970.1	7.7	7.1	**-1.51**	0.02
1429537_at	Sfrs18	PNN interacting serine/arginine-rich	Mm.100117.1	7.8	7.2	**-1.51**	0.00
1430458_at	Supt6	suppressor of Ty 6	Mm.159554.1	3.4	2.8	**-1.51**	0.01
1431071_at	Mtx3	metaxin 3	Mm.23391.1	5.3	4.8	**-1.51**	0.01
1433574_at	Cdc37l1	cell division cycle 37-like 1	Mm.73550.2	8.7	8.1	**-1.51**	0.00
1434806_at	Mtx3	metaxin 3	Mm.202301.1	6.1	5.5	**-1.51**	0.02
1435339_at	Kctd15	potassium channel tetramerisation domain containing 15	Mm.34811.1	6.8	6.2	**-1.51**	0.02
1435982_at	Stx12	syntaxin 12	Mm.41266.1	6.9	6.3	**-1.51**	0.01
1436387_at	C330006P03Rik	RIKEN cDNA C330006P03 gene; homer homolog 1 (Drosophila)	Mm.131563.1	5.9	5.3	**-1.51**	0.04
1436590_at	Ppp1r3b	protein phosphatase 1, regulatory (inhibitor) subunit 3B	Mm.24668.1	11.8	11.2	**-1.51**	0.04
1436697_at			Mm.88335.1	6.4	5.8	**-1.51**	0.00

Supplemental Table 9. Significant differently expressed genes in 3bKI HCC samples

Affymetrix ID	Gene Symbol	Description	Transcript ID (Array Design)	3aKO avg signal log2 (n=4)	3bKI Avg Signal log2 (n=5)	Fold Change (linear)	ANOVA p-value
1436844_at	Pura	purine rich element binding protein A	Mm.44643.1	6.7	6.1	**-1.51**	0.00
1437179_at	Rif1	Rap1 interacting factor 1 homolog (yeast)	Mm.12647.1	7.1	6.5	**-1.51**	0.01
1442005_at	AW987390	expressed sequence AW987390	Mm.116907.1	7.9	7.3	**-1.51**	0.01
1443619_at	Tmem30a	transmembrane protein 30A	Mm.218453.1	5.3	4.8	**-1.51**	0.00
1444574_at			Mm.219403.1	4.9	4.3	**-1.51**	0.02
1449012_s_at	Fndc4	fibronectin type III domain containing 4	Mm.40009.1	6.8	6.2	**-1.51**	0.01
1450744_at	Ell2	elongation factor RNA polymerase II 2	Mm.21288.1	9.3	8.8	**-1.51**	0.00
1450776_at	Agpat6	1-acylglycerol-3-phosphate O-acyltransferase 6 (lysophosphatidic acid acyltransferase, zeta)	Mm.200898.1	10.4	9.8	**-1.51**	0.00
1451275_at	Uhrf1bp1l	UHRF1 (ICBP90) binding protein 1-like	Mm.34798.1	9.9	9.3	**-1.51**	0.01
1451378_at	Utp6	UTP6, small subunit (SSU) processome component, homolog (yeast)	Mm.30167.1	7.7	7.1	**-1.51**	0.00
1452573_a_at	Ercc6l2	excision repair cross-complementing rodent repair deficiency, complementation group 6 like 2	Mm.45349.2	6.2	5.6	**-1.51**	0.00
1452780_at	Gtf3c2	general transcription factor IIIC, polypeptide 2, beta	Mm.35779.1	8.6	8.0	**-1.51**	0.00
1453208_at	2700089E24Rik	RIKEN cDNA 2700089E24 gene	Mm.608.1	9.7	9.1	**-1.51**	0.00
1454777_at	Slco2b1	solute carrier organic anion transporter family, member 2b1	Mm.27178.1	10.5	9.9	**-1.51**	0.01
1455092_at	Zfp207	zinc finger protein 207	Mm.12236.3	7.1	6.5	**-1.51**	0.01
1455163_at	Guf1	GUF1 GTPase homolog (S. cerevisiae)	Mm.186774.1	6.5	5.9	**-1.51**	0.00
1455534_s_at	Osbpl11	oxysterol binding protein-like 11	Mm.26564.1	8.7	8.1	**-1.51**	0.00
1455625_at	Taf10	TAF10 RNA polymerase II, TATA box binding protein (TBP)-associated factor	Mm.8131.3	7.0	6.4	**-1.51**	0.00
1455631_at	H13	histocompatibility 13	Mm.26991.4	5.2	4.6	**-1.51**	0.00
1455746_at	Kif13a	kinesin family member 13A	Mm.116937.1	7.7	7.1	**-1.51**	0.00
1456597_at	Heatr3	HEAT repeat containing 3	Mm.36291.2	7.9	7.3	**-1.51**	0.01
1458708_at			Mm.189097.1	8.0	7.4	**-1.51**	0.01
1459887_at			Mm.37791.2	6.4	5.8	**-1.51**	0.00
1460316_at	Acsl1	acyl-CoA synthetase long-chain family member 1	Mm.28962.1	9.4	8.8	**-1.51**	0.00
1460705_at	Rps6kb1	ribosomal protein S6 kinase, polypeptide 1	Mm.34490.1	8.3	7.8	**-1.51**	0.00
1416409_at	Acox1	acyl-Coenzyme A oxidase 1, palmitoyl	Mm.8403.1	12.9	12.3	**-1.52**	0.01

Supplemental Table 9. Significant differently expressed genes in 3bKI HCC samples

Affymetrix ID	Gene Symbol	Description	Transcript ID (Array Design)	3aKO avg signal log2 (n=4)	3bKI Avg Signal log2 (n=5)	Fold Change (linear)	ANOVA p-value
1419931_at	Abcb7	ATP-binding cassette, sub-family B (MDR/TAP), member 7	Mm.198847.1	6.1	5.5	**-1.52**	0.00
1420971_at	Ubr1	ubiquitin protein ligase E3 component n-recognin 1	Mm.10731.1	7.5	6.9	**-1.52**	0.00
1422064_a_at	Zbtb20	zinc finger and BTB domain containing 20	Mm.38250.1	9.6	9.0	**-1.52**	0.01
1422524_at	Abcb6	ATP-binding cassette, sub-family B (MDR/TAP), member 6	Mm.28663.1	9.7	9.1	**-1.52**	0.00
1424540_at	Hipk1	homeodomain interacting protein kinase 1	Mm.20827.2	10.1	9.5	**-1.52**	0.00
1424836_a_at	Clasp2	CLIP associating protein 2	Mm.26780.1	7.6	7.0	**-1.52**	0.04
1425036_a_at	Tnrc6a	trinucleotide repeat containing 6a	Mm.220983.1	8.4	7.8	**-1.52**	0.00
1425540_at	Otc	ornithine transcarbamylase	Mm.2611.2	7.8	7.1	**-1.52**	0.00
1425668_a_at	St3gal4	ST3 beta-galactoside alpha-2,3-sialyltransferase 4	Mm.2793.2	10.1	9.5	**-1.52**	0.02
1426981_at	Pcsk6	proprotein convertase subtilisin/kexin type 6	Mm.32906.1	10.1	9.5	**-1.52**	0.00
1427574_s_at	Sh3d19	SH3 domain protein D19	Mm.207077.1	6.9	6.3	**-1.52**	0.00
1427966_at	Fam105b	OTU deubiquitinase with linear linkage specificity	Mm.100380.1	9.4	8.8	**-1.52**	0.00
1428448_a_at	Gtf3c2	general transcription factor IIIC, polypeptide 2, beta	Mm.35779.1	8.2	7.6	**-1.52**	0.00
1428546_at	Syncrip	synaptotagmin binding, cytoplasmic RNA interacting protein	Mm.196209.1	7.6	7.0	**-1.52**	0.01
1428919_at	Fgfr1op	Fgfr1 oncogene partner	Mm.79782.1	8.4	7.8	**-1.52**	0.00
1430097_at			Mm.96601.1	4.0	3.4	**-1.52**	0.01
1431052_at	Arhgap12	Rho GTPase activating protein 12	Mm.101434.1	5.4	4.8	**-1.52**	0.01
1431068_at	Rmnd5a	required for meiotic nuclear division 5 homolog A (S. cerevisiae)	Mm.69047.1	8.5	7.9	**-1.52**	0.02
1433669_at	Akap8	A kinase (PRKA) anchor protein 8	Mm.200919.1	9.0	8.4	**-1.52**	0.00
1433724_at	D15Ertd621e	DNA segment, Chr 15, ERATO Doi 621, expressed	Mm.3224.1	8.5	7.9	**-1.52**	0.00
1433911_at	Smg6	Smg-6 homolog, nonsense mediated mRNA decay factor (C. elegans)	Mm.27034.1	7.5	6.9	**-1.52**	0.00
1434039_at	Appbp2	amyloid beta precursor protein (cytoplasmic tail) binding protein 2	Mm.86454.1	5.8	5.2	**-1.52**	0.00
1435444_at	Atf6	activating transcription factor 6	Mm.27843.1	8.8	8.2	**-1.52**	0.00
1436666_at			Mm.96522.1	5.0	4.4	**-1.52**	0.00
1437065_at	Zbtb20	zinc finger and BTB domain containing 20	Mm.31375.1	8.0	7.4	**-1.52**	0.04
1438268_at	Rc3h2	ring finger and CCCH-type zinc finger domains 2	Mm.216644.1	6.3	5.7	**-1.52**	0.01
1438807_at	Hnrnpr	heterogeneous nuclear ribonucleoprotein R	Mm.38819.1	6.4	5.8	**-1.52**	0.01
1444259_at	AW495222	expressed sequence AW495222	Mm.40930.1	7.1	6.5	**-1.52**	0.00

Supplemental Table 9. Significant differently expressed genes in 3bKI HCC samples

Affymetrix ID	Gene Symbol	Description	Transcript ID (Array Design)	3aKO avg signal log2 (n=4)	3bKI Avg Signal log2 (n=5)	Fold Change (linear)	ANOVA p-value
1445629_at	Slc35d1	Mus musculus solute carrier family 35 (UDP-glucuronic acid/UDP-N-acetylgalactosamine dual transporter), member D1 (Slc35d1), mRNA.; solute carrier family 35 (UDP-glucuronic acid/UDP-N-acetylgalactosamine dual transporter), member D1	Mm.69097.1	6.0	5.4	**-1.52**	0.01
1446626_at	Tango2	transport and golgi organization 2	Mm.214694.1	6.4	5.8	**-1.52**	0.01
1447944_at	Zkscan1	zinc finger with KRAB and SCAN domains 1	Mm.25477.2	7.6	7.0	**-1.52**	0.00
1449505_at	Kpna1	karyopherin (importin) alpha 1	Mm.6952.1	9.3	8.7	**-1.52**	0.00
1449536_at	Kcnn1	potassium intermediate/small conductance calcium-activated channel, subfamily N, member 1	Mm.32074.1	6.2	5.6	**-1.52**	0.03
1452300_at	Rmdn1	regulator of microtubule dynamics 1	Mm.78312.1	3.8	3.2	**-1.52**	0.01
1452718_at	Ubr5	ubiquitin protein ligase E3 component n-recognin 5	Mm.7361.1	10.3	9.7	**-1.52**	0.00
1452973_at	Ppm1k	protein phosphatase 1K (PP2C domain containing)	Mm.46011.1	10.4	9.8	**-1.52**	0.01
1453017_at	Ankle2	ankyrin repeat and LEM domain containing 2	Mm.103407.1	7.5	6.9	**-1.52**	0.00
1455351_at	U2surp	U2 snRNP-associated SURP domain containing	Mm.27137.1	7.1	6.5	**-1.52**	0.00
1455491_at	Hnrnph3	heterogeneous nuclear ribonucleoprotein H3	Mm.28070.1	7.8	7.2	**-1.52**	0.00
1455759_a_at	Ankhd1	ankyrin repeat and KH domain containing 1; multiple ankyrin repeats single KH domain binding protein 3	Mm.28671.2	6.4	5.8	**-1.52**	0.00
1455805_x_at	Ccdc22	coiled-coil domain containing 22	Mm.182291.3	6.5	5.9	**-1.52**	0.01
1456181_at	Wdr91	WD repeat domain 91	Mm.44185.1	7.7	7.1	**-1.52**	0.00
1456521_at		nuclear receptor subfamily 5, group A, member 2	Mm.24295.1	9.7	9.1	**-1.52**	0.00
1456541_x_at	Atad3a	ATPase family, AAA domain containing 3A	Mm.21881.4	7.9	7.3	**-1.52**	0.03
1458295_at	BC038331	cDNA sequence BC038331	Mm.78325.1	6.5	5.9	**-1.52**	0.01
1459679_s_at	Myo1b	myosin IB	Mm.200345.1	10.1	9.5	**-1.52**	0.00
1460580_at	Pcnx	pecanex homolog (Drosophila)	Mm.22991.1	7.7	7.1	**-1.52**	0.01
1460655_a_at	Ubp1	upstream binding protein 1	Mm.28052.1	7.7	7.1	**-1.52**	0.01
1416042_s_at	Nasp	nuclear autoantigenic sperm protein (histone-binding)	Mm.7516.1	7.6	7.0	**-1.53**	0.01
1417783_at	Als2	amyotrophic lateral sclerosis 2 (juvenile)	Mm.30114.1	10.3	9.7	**-1.53**	0.00
1418607_at	Zkscan14	zinc finger with KRAB and SCAN domains 14	Mm.26782.1	7.3	6.7	**-1.53**	0.01

Supplemental Table 9. Significant differently expressed genes in 3bKI HCC samples

Affymetrix ID	Gene Symbol	Description	Transcript ID (Array Design)	3aKO avg signal log2 (n=4)	3bKI Avg Signal log2 (n=5)	Fold Change (linear)	ANOVA p-value
1419951_at	Lman1	lectin, mannose-binding, 1	Mm.28142.1	7.5	6.9	**-1.53**	0.00
1420142_s_at	Pa2g4	proliferation-associated 2G4	Mm.199839.1	8.7	8.1	**-1.53**	0.00
1420487_at	Nol7	nucleolar protein 7	Mm.142195.1	6.2	5.6	**-1.53**	0.02
1422882_at	Sypl	synaptophysin-like protein	Mm.45146.1	6.7	6.1	**-1.53**	0.00
1426345_at	Prepl	prolyl endopeptidase-like	Mm.18300.2	8.3	7.7	**-1.53**	0.00
1426994_at	Phlpp1	PH domain and leucine rich repeat protein phosphatase 1	Mm.24115.1	8.6	8.0	**-1.53**	0.01
1428467_at	Tardbp	TAR DNA binding protein	Mm.22453.1	7.3	6.7	**-1.53**	0.01
1428941_at	Zmym2	zinc finger, MYM-type 2	Mm.31417.1	5.5	4.9	**-1.53**	0.01
1429121_at	Spopl	speckle-type POZ protein-like	Mm.101788.1	6.2	5.6	**-1.53**	0.01
1429463_at	Prkaa2	protein kinase, AMP-activated, alpha 2 catalytic subunit	Mm.48638.1	9.8	9.1	**-1.53**	0.00
1429504_at	Amy1	amylase 1, salivary; RNA-binding region (RNP1, RRM) containing 3	Mm.181446.1	4.5	3.8	**-1.53**	0.01
1431226_a_at	Fndc4	fibronectin type III domain containing 4	Mm.40009.2	9.1	8.5	**-1.53**	0.01
1433503_at	Ptgr2	prostaglandin reductase 2	Mm.41320.1	9.4	8.8	**-1.53**	0.00
1434391_at	AI503316	expressed sequence AI503316; heterogeneous nuclear ribonucleoprotein U	Mm.28927.2	8.3	7.7	**-1.53**	0.00
1434721_at	Ankle2	ankyrin repeat and LEM domain containing 2	Mm.37551.1	7.9	7.3	**-1.53**	0.00
1435551_at	Fhod3	formin homology 2 domain containing 3	Mm.28387.1	4.8	4.2	**-1.53**	0.02
1435559_at	Myo6	myosin VI	Mm.28931.1	6.8	6.2	**-1.53**	0.02
1435711_at	LOC100503186	expressed sequence AI480526	Mm.32658.1	7.3	6.7	**-1.53**	0.03
1436597_at	Ankhd1	ankyrin repeat and KH domain containing 1	Mm.28671.2	6.3	5.7	**-1.53**	0.00
1436898_at	Sfpq	splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated)	Mm.43213.3	8.1	7.5	**-1.53**	0.01
1437856_at	Ipmk	inositol polyphosphate multikinase	Mm.12055.2	8.5	7.9	**-1.53**	0.00
1438006_at	Gid4	GID complex subunit 4, VID24 homolog (S. cerevisiae)	Mm.29950.3	8.6	8.0	**-1.53**	0.00
1440195_at	Serbp1	serpine1 mRNA binding protein 1	Mm.117943.1	6.6	6.0	**-1.53**	0.00
1440573_at	Gm2590	predicted gene 2590	Mm.209864.1	6.5	5.9	**-1.53**	0.00
1440993_at	AW111846		Mm.36341.1	11.4	10.8	**-1.53**	0.00
1444037_at	Lman1	lectin, mannose-binding, 1	Mm.152817.1	6.5	5.9	**-1.53**	0.01
1448717_at	Gcdh	glutaryl-Coenzyme A dehydrogenase	Mm.2475.1	11.3	10.7	**-1.53**	0.01
1452868_at	Usp24	ubiquitin specific peptidase 24	Mm.148342.1	8.6	7.9	**-1.53**	0.00
1452977_at	Zhx3	zinc fingers and homeoboxes 3	Mm.70619.1	9.0	8.4	**-1.53**	0.00
1455073_at	Cdadc1	cytidine and dCMP deaminase domain containing 1	Mm.203878.1	8.4	7.8	**-1.53**	0.00
1457510_at			Mm.132324.1	5.2	4.6	**-1.53**	0.00
1459874_s_at	Mtmr4	myotubularin related protein 4	Mm.78770.1	8.6	8.0	**-1.53**	0.02
1460244_at	Upb1	ureidopropionase, beta	Mm.25557.1	12.4	11.8	**-1.53**	0.00

Supplemental Table 9. Significant differently expressed genes in 3bKI HCC samples

Affymetrix ID	Gene Symbol	Description	Transcript ID (Array Design)	3aKO avg signal log2 (n=4)	3bKI Avg Signal log2 (n=5)	Fold Change (linear)	ANOVA p-value
1460633_at	Prpf19	PRP19/PSO4 pre-mRNA processing factor 19 homolog (S. cerevisiae)	Mm.29835.1	9.0	8.4	**-1.53**	0.03
1416731_at	Top2b	topoisomerase (DNA) II beta	Mm.4093.1	8.6	7.9	**-1.54**	0.01
1419158_a_at	Hars2	histidyl-tRNA synthetase 2, mitochondrial (putative)	Mm.46741.1	8.6	8.0	**-1.54**	0.00
1419301_at	Fzd4	frizzled homolog 4 (Drosophila)	Mm.68712.1	7.8	7.2	**-1.54**	0.01
1419977_s_at	Esrp2	epithelial splicing regulatory protein 2	Mm.10285.1	6.9	6.3	**-1.54**	0.00
1423169_at	Taf7	TAF7 RNA polymerase II, TATA box binding protein (TBP)-associated factor	Mm.12001.1	5.9	5.2	**-1.54**	0.00
1423411_at	Rbm47	RNA binding motif protein 47	Mm.36863.1	8.0	7.4	**-1.54**	0.00
1424166_at	Msh3	mutS homolog 3 (E. coli)	Mm.116254.2	7.4	6.8	**-1.54**	0.00
1425821_at	Clcn7	chloride channel 7	Mm.190634.1	5.4	4.7	**-1.54**	0.01
1426840_at	Ythdf3	YTH domain family 3	Mm.23834.1	8.7	8.0	**-1.54**	0.00
1426881_at	Ube3c	ubiquitin protein ligase E3C	Mm.28711.1	8.2	7.5	**-1.54**	0.00
1426884_at	Rmnd5a	required for meiotic nuclear division 5 homolog A (S. cerevisiae)	Mm.28474.1	11.1	10.5	**-1.54**	0.00
1427075_s_at	Pcmtd2	protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 2	Mm.29308.1	6.6	6.0	**-1.54**	0.00
1429083_at	Agl	amylo-1,6-glucosidase, 4-alpha-glucanotransferase	Mm.41348.1	8.3	7.7	**-1.54**	0.03
1429094_at	Ddi2	DNA-damage inducible protein 2	Mm.40897.1	9.1	8.5	**-1.54**	0.03
1430130_at	Vwce	von Willebrand factor C and EGF domains	Mm.169261.1	8.8	8.2	**-1.54**	0.03
1430798_x_at	Mrpl15	mitochondrial ribosomal protein L15	Mm.29904.2	7.4	6.8	**-1.54**	0.00
1431792_a_at	Stk11ip	serine/threonine kinase 11 interacting protein	Mm.3463.1	6.3	5.7	**-1.54**	0.00
1432099_a_at	Prodh2	proline dehydrogenase (oxidase) 2	Mm.182309.2	11.3	10.7	**-1.54**	0.00
1433203_at	6030400A10Rik	RIKEN cDNA 6030400A10 gene	Mm.159840.1	7.0	6.4	**-1.54**	0.01
1434842_s_at	Upf3b	UPF3 regulator of nonsense transcripts homolog B (yeast)	Mm.5935.1	8.7	8.1	**-1.54**	0.00
1434970_a_at	Mrpl15	mitochondrial ribosomal protein L15	Mm.29904.4	10.0	9.4	**-1.54**	0.00
1435150_at			Mm.97269.1	4.2	3.6	**-1.54**	0.02
1435574_at			Mm.128892.1	5.0	4.4	**-1.54**	0.03
1437181_at	Peli2	pellino 2	Mm.17370.1	7.4	6.8	**-1.54**	0.02
1437590_at	Pyroxd2	pyridine nucleotide-disulphide oxidoreductase domain 2	Mm.212966.1	7.8	7.1	**-1.54**	0.00
1438637_x_at	Sf3b2	splicing factor 3b, subunit 2	Mm.1668.7	8.7	8.1	**-1.54**	0.00
1438809_at	Atp5c1	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1	Mm.12677.5	7.2	6.5	**-1.54**	0.04
1439144_at	Cwf19l1	CWF19-like 1, cell cycle control (S. pombe)	Mm.93826.1	7.2	6.6	**-1.54**	0.01
1440198_at			Mm.82435.1	3.9	3.2	**-1.54**	0.05

Supplemental Table 9. Significant differently expressed genes in 3bKI HCC samples

Affymetrix ID	Gene Symbol	Description	Transcript ID (Array Design)	3aKO avg signal log2 (n=4)	3bKI Avg Signal log2 (n=5)	Fold Change (linear)	ANOVA p-value
1440260_at	Ccdc58	coiled-coil domain containing 58	Mm.102774.1	5.6	5.0	**-1.54**	0.02
1443355_at			Mm.120898.1	6.1	5.5	**-1.54**	0.04
1444171_at			Mm.213038.1	6.5	5.9	**-1.54**	0.00
1448761_a_at	Copg2	coatomer protein complex, subunit gamma 2	Mm.39896.1	8.0	7.4	**-1.54**	0.00
1449006_at	Gla	galactosidase, alpha	Mm.1114.1	5.3	4.7	**-1.54**	0.01
1449014_at	Lactb	lactamase, beta	Mm.157882.1	9.4	8.8	**-1.54**	0.02
1452262_at	Grpel2	GrpE-like 2, mitochondrial	Mm.12959.1	9.0	8.3	**-1.54**	0.01
1452944_at	Afmid	arylformamidase	Mm.30192.1	11.1	10.5	**-1.54**	0.00
1453216_at	Gpt	glutamic pyruvic transaminase, soluble	Mm.178753.1	8.7	8.0	**-1.54**	0.02
1453277_at	3021401N23Rik	RIKEN cDNA 3021401N23 gene	Mm.149413.1	4.6	4.0	**-1.54**	0.01
1455134_at	Tmem245	transmembrane protein 245	Mm.31787.1	7.8	7.2	**-1.54**	0.01
1455189_at	Trim33	tripartite motif-containing 33	Mm.100128.1	7.0	6.4	**-1.54**	0.00
1455218_at	Ccp110	centriolar coiled coil protein 110	Mm.23279.1	5.9	5.2	**-1.54**	0.01
1455668_at	Whsc1l1	Wolf-Hirschhorn syndrome candidate 1-like 1 (human)	Mm.71065.1	8.2	7.6	**-1.54**	0.01
1456662_at	AA386476	expressed sequence AA386476	Mm.45721.1	4.8	4.1	**-1.54**	0.01
1457287_at			Mm.30907.1	8.7	8.1	**-1.54**	0.00
1457751_at	Rsf1	remodeling and spacing factor 1	Mm.43977.1	6.6	6.0	**-1.54**	0.00
1458585_at			Mm.33549.1	6.1	5.5	**-1.54**	0.00
1415902_at	Aldh7a1	aldehyde dehydrogenase family 7, member A1	Mm.30250.1	6.7	6.1	**-1.55**	0.01
1418996_a_at	Lyrm5	LYR motif containing 5	Mm.46847.1	11.0	10.4	**-1.55**	0.01
1421029_a_at	Hbs1l	Hbs1-like (S. cerevisiae)	Mm.28882.1	9.6	8.9	**-1.55**	0.00
1421035_a_at	Magi3	membrane associated guanylate kinase, WW and PDZ domain containing 3	Mm.149760.1	6.9	6.3	**-1.55**	0.00
1422780_at	Pxmp4	peroxisomal membrane protein 4	Mm.24673.1	10.3	9.7	**-1.55**	0.00
1423170_at	Taf7	TAF7 RNA polymerase II, TATA box binding protein (TBP)-associated factor	Mm.12001.1	6.3	5.6	**-1.55**	0.00
1428382_at	Smarcc2	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 2	Mm.24449.1	8.9	8.3	**-1.55**	0.00
1430863_at	4933411B09Rik	RIKEN cDNA 4933411B09 gene	Mm.67563.1	5.1	4.5	**-1.55**	0.02
1434041_at	Appbp2	amyloid beta precursor protein (cytoplasmic tail) binding protein 2	Mm.86454.1	6.5	5.9	**-1.55**	0.00
1434337_at	Cmtm4	CKLF-like MARVEL transmembrane domain containing 4	Mm.24881.1	10.0	9.3	**-1.55**	0.00
1434486_x_at	Ugp2	UDP-glucose pyrophosphorylase 2	Mm.28877.4	10.8	10.1	**-1.55**	0.00
1434681_at	Txlng	taxilin gamma	Mm.1603.3	8.5	7.9	**-1.55**	0.00
1435664_at	Zfp397	zinc finger protein 397	Mm.46024.1	6.6	6.0	**-1.55**	0.01
1436229_at	Fam126b	family with sequence similarity 126, member B	Mm.94709.1	7.4	6.8	**-1.55**	0.00

Supplemental Table 9. Significant differently expressed genes in 3bKI HCC samples

Affymetrix ID	Gene Symbol	Description	Transcript ID (Array Design)	3aKO avg signal log2 (n=4)	3bKI Avg Signal log2 (n=5)	Fold Change (linear)	ANOVA p-value
1436427_at	Prpf4b	PRP4 pre-mRNA processing factor 4 homolog B (yeast)	Mm.10027.3	8.2	7.6	**-1.55**	0.00
1437067_at	Phtf2	putative homeodomain transcription factor 2	Mm.3028.1	5.9	5.2	**-1.55**	0.01
1437600_at			Mm.129295.1	6.6	6.0	**-1.55**	0.01
1440016_at			Mm.103039.1	4.5	3.8	**-1.55**	0.01
1440027_at	Mon2	MON2 homolog (yeast)	Mm.23191.1	5.8	5.2	**-1.55**	0.00
1440896_at			Mm.133061.1	6.7	6.0	**-1.55**	0.01
1441842_s_at	Zfp707	zinc finger protein 707	Mm.141644.1	6.9	6.3	**-1.55**	0.01
1442911_at			Mm.218423.1	5.0	4.4	**-1.55**	0.01
1443206_at			Mm.182861.1	6.3	5.7	**-1.55**	0.04
1443466_s_at	Polr3b	polymerase (RNA) III (DNA directed) polypeptide B	Mm.200932.1	7.5	6.9	**-1.55**	0.00
1443708_at	BC068281	cDNA sequence BC068281	Mm.214691.1	6.1	5.5	**-1.55**	0.00
1443857_at	Hook3	hook homolog 3 (Drosophila)	Mm.63527.1	6.4	5.7	**-1.55**	0.00
1451848_a_at	Cryz	crystallin, zeta	Mm.3534.2	10.6	9.9	**-1.55**	0.02
1452025_a_at	Zfp2	zinc finger protein 2	Mm.4958.2	4.3	3.7	**-1.55**	0.00
1454735_at	Odf2	outer dense fiber of sperm tails 2	Mm.24261.1	7.9	7.2	**-1.55**	0.00
1454842_a_at	B3galnt2	UDP-GalNAc:betaGlcNAc beta 1,3-galactosaminyltransferase, polypeptide 2	Mm.21686.1	4.7	4.1	**-1.55**	0.01
1454843_at	Prps2	phosphoribosyl pyrophosphate synthetase 2	Mm.30784.1	9.6	9.0	**-1.55**	0.05
1455254_at	4833420G11Rik	GID complex subunit 8 homolog (S. cerevisiae)	Mm.29561.2	9.1	8.5	**-1.55**	0.00
1455435_s_at	Chdh	choline dehydrogenase	Mm.9772.3	10.6	10.0	**-1.55**	0.00
1456386_at		RNA binding motif protein 39	Mm.17307.3	7.1	6.5	**-1.55**	0.01
1456395_at	Ppargc1a	peroxisome proliferative activated receptor, gamma, coactivator 1 alpha	Mm.10707.3	7.1	6.4	**-1.55**	0.04
1456630_x_at	Son	Son DNA binding protein	Mm.46401.3	6.0	5.3	**-1.55**	0.00
1457141_at			Mm.180664.1	7.7	7.1	**-1.55**	0.02
1460325_at	Pum1	pumilio RNA-binding family member 1	Mm.34701.1	8.1	7.5	**-1.55**	0.00
1460577_at	Jmy	junction-mediating and regulatory protein	Mm.73671.1	8.0	7.3	**-1.55**	0.00
1415917_at	Mthfd1	methylenetetrahydrofolate dehydrogenase (NADP+ dependent), methenyltetrahydrofolate cyclohydrolase, formyltetrahydrofolate synthase	Mm.29584.1	11.8	11.1	**-1.56**	0.00
1417754_at	Topors	topoisomerase I binding, arginine/serine-rich	Mm.39006.1	7.9	7.2	**-1.56**	0.00
1422461_at	Atad3a	ATPase family, AAA domain containing 3A	Mm.21881.1	9.0	8.3	**-1.56**	0.00

Supplemental Table 9. Significant differently expressed genes in 3bKI HCC samples

Affymetrix ID	Gene Symbol	Description	Transcript ID (Array Design)	3aKO avg signal log2 (n=4)	3bKI Avg Signal log2 (n=5)	Fold Change (linear)	ANOVA p-value
1423108_at	Slc25a20	solute carrier family 25 (mitochondrial carnitine/acylcarnitine translocase), member 20	Mm.29666.1	11.1	10.5	**-1.56**	0.04
1423995_at	Kif1b	kinesin family member 1B	Mm.42027.1	8.3	7.7	**-1.56**	0.01
1424583_at	Farp2	FERM, RhoGEF and pleckstrin domain protein 2	Mm.192479.1	7.1	6.4	**-1.56**	0.00
1424738_at	Ap5m1	adaptor-related protein complex 5, mu 1 subunit	Mm.87037.1	7.6	7.0	**-1.56**	0.00
1425088_at	Scnn1a	sodium channel, nonvoltage-gated 1 alpha	Mm.144114.1	8.4	7.7	**-1.56**	0.04
1425557_x_at	Tsc22d3	TSC22 domain family, member 3	Mm.22216.3	7.6	7.0	**-1.56**	0.00
1426781_at	Tyw1	tRNA-yW synthesizing protein 1 homolog (S. cerevisiae)	Mm.38464.1	6.7	6.0	**-1.56**	0.03
1426879_at	Trmt1l	tRNA methyltransferase 1 like	Mm.45758.1	8.1	7.5	**-1.56**	0.00
1429040_at	6820431F20Rik	cadherin 11 pseudogene	Mm.1571.1	8.3	7.7	**-1.56**	0.01
1431232_a_at	Mga	MAX gene associated	Mm.87532.2	6.1	5.4	**-1.56**	0.00
1434108_at	Fbxo11	F-box protein 11	Mm.18210.2	7.2	6.6	**-1.56**	0.02
1436303_at	Mllt4	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 4	Mm.35797.1	9.1	8.5	**-1.56**	0.00
1436544_at	Atp10d	ATPase, class V, type 10D	Mm.30781.1	7.0	6.4	**-1.56**	0.05
1437064_at	Ar	androgen receptor	Mm.133787.1	8.4	7.8	**-1.56**	0.01
1438236_at	Nfia	nuclear factor I/A	Mm.31274.2	7.9	7.2	**-1.56**	0.00
1443046_at	Abcd3	ATP-binding cassette, sub-family D (ALD), member 3	Mm.194462.1	5.3	4.6	**-1.56**	0.00
1444021_at	Sqstm1	sequestosome 1	Mm.148901.1	6.2	5.6	**-1.56**	0.00
1444057_at			Mm.156169.1	4.6	3.9	**-1.56**	0.02
1445765_at	9430011C21Rik	RIKEN cDNA 9430011C21 gene	Mm.208023.1	6.6	5.9	**-1.56**	0.01
1445831_at			Mm.173456.1	7.7	7.0	**-1.56**	0.03
1447310_at	Agphd1	hydroxylysine kinase 1	Mm.23202.1	8.1	7.4	**-1.56**	0.04
1447750_x_at	Pih1d1	PIH1 domain containing 1	Mm.82139.1	7.9	7.3	**-1.56**	0.00
1448889_at	Slc38a4	solute carrier family 38, member 4	Mm.180455.1	13.1	12.4	**-1.56**	0.03
1450396_at	Stag2	stromal antigen 2	Mm.24025.1	8.0	7.4	**-1.56**	0.00
1450400_at	Tgs1	trimethylguanosine synthase homolog (S. cerevisiae)	Mm.34104.1	6.9	6.3	**-1.56**	0.00
1452532_x_at	Ceacam1	carcinoembryonic antigen-related cell adhesion molecule 1	Mm.14114.7	9.9	9.3	**-1.56**	0.00
1452986_at	Hgd	homogentisate 1, 2-dioxygenase	Mm.157442.1	13.1	12.4	**-1.56**	0.00
1453332_at	Trappc13	trafficking protein particle complex 13	Mm.76059.1	5.0	4.4	**-1.56**	0.02
1454769_at	Tatdn2	TatD DNase domain containing 2	Mm.73402.1	7.0	6.3	**-1.56**	0.01
1456200_at	Ipmk	inositol polyphosphate multikinase	Mm.12055.2	8.6	7.9	**-1.56**	0.00
1457017_at	Rmdn1	regulator of microtubule dynamics 1	Mm.168010.1	4.2	3.5	**-1.56**	0.00
1457568_at	Hnrnpd	heterogeneous nuclear ribonucleoprotein D	Mm.150231.1	6.1	5.5	**-1.56**	0.01

Supplemental Table 9. Significant differently expressed genes in 3bKI HCC samples

Affymetrix ID	Gene Symbol	Description	Transcript ID (Array Design)	3aKO avg signal log2 (n=4)	3bKI Avg Signal log2 (n=5)	Fold Change (linear)	ANOVA p-value
1416375_at	Ap3m1	adaptor-related protein complex 3, mu 1 subunit	Mm.3256.1	8.4	7.7	**-1.57**	0.02
1418238_at	Ivd	isovaleryl coenzyme A dehydrogenase	Mm.6635.1	10.9	10.3	**-1.57**	0.00
1419288_at	Jam2	junction adhesion molecule 2	Mm.41758.1	7.4	6.7	**-1.57**	0.01
1420059_at	Mtfr1l	mitochondrial fission regulator 1-like	Mm.198745.1	6.7	6.1	**-1.57**	0.00
1420132_s_at	Pttg1ip	pituitary tumor-transforming 1 interacting protein	Mm.199914.1	7.4	6.7	**-1.57**	0.00
1423309_at	Tgoln1	trans-golgi network protein; trans-golgi network protein 2	Mm.141187.1	11.3	10.7	**-1.57**	0.02
1423416_at	Smarcc1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 1	Mm.1050.1	8.0	7.3	**-1.57**	0.00
1423889_at	Gm5617	predicted gene 5617	Mm.220921.2	9.3	8.6	**-1.57**	0.02
1424589_s_at	Rnpc3	RNA-binding region (RNP1, RRM) containing 3	Mm.58104.1	5.8	5.2	**-1.57**	0.00
1428011_a_at	Erbb2ip	Erbb2 interacting protein	Mm.45357.2	8.5	7.9	**-1.57**	0.02
1428267_at	Dhx40	DEAH (Asp-Glu-Ala-His) box polypeptide 40	Mm.2830.1	8.6	7.9	**-1.57**	0.00
1429910_at	March5	membrane-associated ring finger (C3HC4) 5	Mm.33211.1	6.1	5.4	**-1.57**	0.01
1430519_a_at	Cnot7	CCR4-NOT transcription complex, subunit 7	Mm.206770.3	8.6	8.0	**-1.57**	0.01
1434038_at	Dnajc13	DnaJ (Hsp40) homolog, subfamily C, member 13	Mm.26242.1	8.6	8.0	**-1.57**	0.00
1434072_at	Smcr7	mitochondrial elongation factor 2	Mm.61562.1	8.6	7.9	**-1.57**	0.01
1435198_at	Gm5817	predicted gene 5817	Mm.24614.1	6.8	6.1	**-1.57**	0.05
1435805_at	Lin7a	lin-7 homolog A (C. elegans)	Mm.38592.1	9.0	8.4	**-1.57**	0.00
1436244_a_at	Tle2	transducin-like enhancer of split 2, homolog of Drosophila E(spl)	Mm.38608.2	6.9	6.2	**-1.57**	0.00
1436532_at	Dclk3	doublecortin-like kinase 3	Mm.26361.1	7.7	7.0	**-1.57**	0.04
1436740_at	2610005L07Rik	cadherin 11 pseudogene	Mm.27819.1	8.2	7.5	**-1.57**	0.00
1439103_at	Cdc73	cell division cycle 73, Paf1/RNA polymerase II complex component	Mm.221175.1	3.7	3.1	**-1.57**	0.00
1439319_at	Elf1	E74-like factor 1	Mm.131142.1	6.0	5.4	**-1.57**	0.02
1440755_at			Mm.215581.1	5.8	5.1	**-1.57**	0.00
1440856_at	Mapk8	mitogen-activated protein kinase 8	Mm.39724.1	7.6	7.0	**-1.57**	0.00
1446511_at	Msh3	mutS homolog 3 (E. coli)	Mm.215509.1	5.4	4.8	**-1.57**	0.01
1447459_at			Mm.215669.1	3.7	3.1	**-1.57**	0.02
1448825_at	Pdk2	pyruvate dehydrogenase kinase, isoenzyme 2	Mm.29768.1	9.6	9.0	**-1.57**	0.00
1451459_at	Ahctf1	AT hook containing transcription factor 1	Mm.128165.1	9.0	8.3	**-1.57**	0.00
1455079_at	Dcun1d4	DCN1, defective in cullin neddylation 1, domain containing 4 (S. cerevisiae)	Mm.220312.1	8.1	7.5	**-1.57**	0.01

Supplemental Table 9. Significant differently expressed genes in 3bKI HCC samples

Affymetrix ID	Gene Symbol	Description	Transcript ID (Array Design)	3aKO avg signal log2 (n=4)	3bKI Avg Signal log2 (n=5)	Fold Change (linear)	ANOVA p-value
1455584_at	Sdf4	stromal cell derived factor 4	Mm.39710.1	8.2	7.5	**-1.57**	0.00
1455647_at	Ar	androgen receptor	Mm.39005.1	8.2	7.5	**-1.57**	0.01
1456607_at	Vcpip1	valosin containing protein (p97)/p47 complex interacting protein 1	Mm.89906.3	7.2	6.5	**-1.57**	0.02
1457218_at	Strbp	spermatid perinuclear RNA binding protein	Mm.192898.1	8.2	7.6	**-1.57**	0.02
1459994_x_at	Tfr2	transferrin receptor 2	Mm.21757.3	11.9	11.2	**-1.57**	0.01
1416660_at	Eif3a	eukaryotic translation initiation factor 3, subunit A	Mm.2238.1	9.0	8.3	**-1.58**	0.00
1417066_at	Adck3	aarF domain containing kinase 3	Mm.28337.1	11.3	10.6	**-1.58**	0.00
1418444_a_at	Gde1	glycerophosphodiester phosphodiesterase 1	Mm.30126.1	9.6	8.9	**-1.58**	0.01
1418594_a_at	Ncoa1	nuclear receptor coactivator 1	Mm.2028.1	7.5	6.9	**-1.58**	0.02
1418667_at	Trappc13	trafficking protein particle complex 13	Mm.12755.1	8.5	7.8	**-1.58**	0.01
1419101_at	Sin3a	transcriptional regulator, SIN3A (yeast)	Mm.15755.1	7.4	6.7	**-1.58**	0.00
1421018_at	Aaed1	AhpC/TSA antioxidant enzyme domain containing 1	Mm.35724.1	8.3	7.7	**-1.58**	0.00
1421055_at	Lats2	large tumor suppressor 2; exportin 4	Mm.143753.1	7.4	6.7	**-1.58**	0.00
1421220_at	Ankrd17	ankyrin repeat domain 17	Mm.24624.1	6.8	6.1	**-1.58**	0.00
1422560_at	Ddi2	DNA-damage inducible protein 2; regulatory solute carrier protein, family 1, member 1	Mm.17880.1	10.2	9.5	**-1.58**	0.01
1423109_s_at	Slc25a20	solute carrier family 25 (mitochondrial carnitine/acylcarnitine translocase), member 20	Mm.29666.1	10.3	9.6	**-1.58**	0.05
1425114_at	Rbbp6	retinoblastoma binding protein 6	Mm.127823.1	6.9	6.3	**-1.58**	0.01
1425956_a_at	Cdadc1	cytidine and dCMP deaminase domain containing 1	Mm.2046.2	9.4	8.8	**-1.58**	0.00
1426463_at	Gphn	gephyrin	Mm.40282.1	9.7	9.0	**-1.58**	0.01
1428654_at	Swt1	SWT1 RNA endoribonuclease homolog (S. cerevisiae)	Mm.26639.1	7.4	6.8	**-1.58**	0.01
1429427_s_at	Tcf7l2	transcription factor 7 like 2, T cell specific, HMG box	Mm.4269.4	5.5	4.8	**-1.58**	0.02
1429616_at	Zfp91	zinc finger protein 91	Mm.28324.1	4.7	4.0	**-1.58**	0.00
1429649_at	Slc35a3	solute carrier family 35 (UDP-N-acetylglucosamine (UDP-GlcNAc) transporter), member 3	Mm.29250.1	8.3	7.6	**-1.58**	0.01
1431947_at	Ldlr	low density lipoprotein receptor	Mm.3213.2	7.7	7.0	**-1.58**	0.01
1433585_at	Tnpo1	transportin 1	Mm.29005.1	9.1	8.4	**-1.58**	0.02
1434389_at	Sos1	son of sevenless homolog 1 (Drosophila)	Mm.28960.1	8.8	8.1	**-1.58**	0.00
1434401_at	Zcchc2	zinc finger, CCHC domain containing 2	Mm.40627.1	8.7	8.1	**-1.58**	0.00

Supplemental Table 9. Significant differently expressed genes in 3bKI HCC samples

Affymetrix ID	Gene Symbol	Description	Transcript ID (Array Design)	3aKO avg signal log2 (n=4)	3bKI Avg Signal log2 (n=5)	Fold Change (linear)	ANOVA p-value
1434485_a_at	Ugp2	UDP-glucose pyrophosphorylase 2	Mm.28877.4	11.4	10.7	**-1.58**	0.00
1434712_at	Smcr7l	mitochondrial elongation factor 1	Mm.34816.1	8.2	7.5	**-1.58**	0.00
1438221_at	Fam126b	family with sequence similarity 126, member B	Mm.41046.1	8.7	8.1	**-1.58**	0.00
1439175_at			Mm.184021.1	6.7	6.1	**-1.58**	0.01
1439381_x_at	Marveld1	MARVEL (membrane-associating) domain containing 1	Mm.206250.3	10.0	9.3	**-1.58**	0.01
1444178_at	Gm9895	predicted gene 9895	Mm.103412.1	6.7	6.0	**-1.58**	0.00
1448410_at	Ube4b	ubiquitination factor E4B	Mm.21634.1	8.8	8.2	**-1.58**	0.00
1450983_at	Akap8	A kinase (PRKA) anchor protein 8	Mm.27351.1	8.9	8.2	**-1.58**	0.01
1452500_at			Mm.139078.2	5.7	5.0	**-1.58**	0.03
1454987_a_at	H2-Ke6	H2-K region expressed gene 6	Mm.15479.2	9.6	8.9	**-1.58**	0.00
1455151_at	Akap9	A kinase (PRKA) anchor protein (yotiao) 9	Mm.46044.1	5.9	5.2	**-1.58**	0.00
1455521_at	Klf12		Mm.25852.1	7.8	7.1	**-1.58**	0.00
1457936_at	Mapk8	mitogen-activated protein kinase 8	Mm.210096.1	6.0	5.3	**-1.58**	0.01
1459879_at	Marf1	meiosis arrest female 1	Mm.24004.2	7.4	6.7	**-1.58**	0.00
1416610_a_at	Clcn3	chloride channel 3	Mm.28842.1	8.5	7.9	**-1.59**	0.00
1416679_at	Abcd3	ATP-binding cassette, sub-family D (ALD), member 3	Mm.1519.1	12.7	12.0	**-1.59**	0.02
1416772_at	Cpt2	carnitine palmitoyltransferase 2	Mm.29499.1	11.6	10.9	**-1.59**	0.04
1417212_at	Fam195a	family with sequence similarity 195, member A	Mm.34532.1	10.0	9.4	**-1.59**	0.01
1417431_a_at	Sphk2	sphingosine kinase 2	Mm.24222.1	8.7	8.0	**-1.59**	0.04
1419047_at	Pcnx	pecanex homolog (Drosophila)	Mm.86584.1	7.3	6.7	**-1.59**	0.00
1419369_at	Rnf138	ring finger protein 138	Mm.42154.1	6.7	6.0	**-1.59**	0.00
1420948_s_at	Atrx	alpha thalassemia/mental retardation syndrome X-linked homolog (human)	Mm.10141.1	6.5	5.8	**-1.59**	0.00
1422982_at	Ar	androgen receptor	Mm.4470.1	8.3	7.6	**-1.59**	0.01
1423565_at	Paics	phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoribosylaminoimidazole, succinocarboxamide synthetase	Mm.182931.1	12.0	11.4	**-1.59**	0.00
1424544_at	Nrbp2	nuclear receptor binding protein 2	Mm.157125.1	8.7	8.1	**-1.59**	0.00
1424712_at	Ahctf1	AT hook containing transcription factor 1	Mm.128165.1	8.5	7.9	**-1.59**	0.00
1424898_at	Slc10a1	solute carrier family 10 (sodium/bile acid cotransporter family), member 1	Mm.104295.2	13.0	12.3	**-1.59**	0.01
1426461_at	Ugp2	UDP-glucose pyrophosphorylase 2	Mm.28877.2	10.3	9.6	**-1.59**	0.00
1428385_at	March8	membrane-associated ring finger (C3HC4) 8	Mm.27064.1	8.6	7.9	**-1.59**	0.02
1429623_at	Zfp644	zinc finger protein 644	Mm.220900.1	7.7	7.0	**-1.59**	0.00
1429810_at	Rictor	RPTOR independent companion of MTOR, complex 2	Mm.40332.1	6.5	5.8	**-1.59**	0.00

Supplemental Table 9. Significant differently expressed genes in 3bKI HCC samples

Affymetrix ID	Gene Symbol	Description	Transcript ID (Array Design)	3aKO avg signal log2 (n=4)	3bKI Avg Signal log2 (n=5)	Fold Change (linear)	ANOVA p-value
1435800_a_at	Ybx3	Y box protein 3	Mm.193526.3	9.3	8.6	**-1.59**	0.00
1436256_at	Grpel2	GrpE-like 2, mitochondrial	Mm.25786.1	7.7	7.0	**-1.59**	0.00
1436550_at	Fbxo30	F-box protein 30	Mm.44605.1	6.5	5.8	**-1.59**	0.00
1436968_x_at	Klhl24	kelch-like 24	Mm.201175.1	3.4	2.8	**-1.59**	0.00
1437041_at	Sfrs18	PNN interacting serine/arginine-rich	Mm.100117.3	7.5	6.8	**-1.59**	0.00
1439117_at	Clmn	calmin	Mm.82595.1	8.4	7.7	**-1.59**	0.00
1441285_at	Pdp2		Mm.151162.1	8.0	7.3	**-1.59**	0.00
1441963_at	Lzts3	leucine zipper, putative tumor suppressor family member 3	Mm.40621.1	8.7	8.1	**-1.59**	0.00
1442007_at	Zmym5	zinc finger, MYM-type 5	Mm.100820.1	6.8	6.1	**-1.59**	0.00
1442191_at	5033411D12Rik	succinyl-CoA glutarate-CoA transferase	Mm.100005.1	6.3	5.6	**-1.59**	0.01
1442959_at	Birc6	baculoviral IAP repeat-containing 6	Mm.218035.1	4.5	3.9	**-1.59**	0.01
1443962_at	Tfdp2	transcription factor Dp 2	Mm.55109.1	7.3	6.6	**-1.59**	0.01
1444612_at	Ppp2r3a	protein phosphatase 2, regulatory subunit B'', alpha	Mm.169667.1	4.5	3.9	**-1.59**	0.00
1448044_a_at	Gm10658	predicted gene 10658	Mm.35221.2	6.7	6.1	**-1.59**	0.04
1451499_at	Cadps2	Ca2+-dependent activator protein for secretion 2	Mm.41732.1	8.2	7.5	**-1.59**	0.01
1452962_at	Tmem25	transmembrane protein 25	Mm.41409.1	8.3	7.6	**-1.59**	0.01
1460279_a_at	Gtf2i	general transcription factor II I	Mm.22593.1	9.0	8.3	**-1.59**	0.00
1460631_at	Ogt	O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyl transferase)	Mm.206715.2	9.8	9.2	**-1.59**	0.00
1417125_at	Ahcy	S-adenosylhomocysteine hydrolase	Mm.2573.1	13.9	13.2	**-1.6**	0.00
1417854_at	Map2k5	mitogen-activated protein kinase kinase 5	Mm.19947.1	8.5	7.9	**-1.6**	0.00
1419913_at	Strap	serine/threonine kinase receptor associated protein	Mm.199211.1	6.2	5.5	**-1.6**	0.00
1421479_at	Zfp318	zinc finger protein 318	Mm.116965.1	6.5	5.8	**-1.6**	0.01
1422975_at	Mme	membrane metallo endopeptidase	Mm.38931.1	7.4	6.7	**-1.6**	0.03
1424412_at	Ogfrl1	opioid growth factor receptor-like 1	Mm.28013.1	8.3	7.6	**-1.6**	0.04
1424427_at	Tada1	transcriptional adaptor 1	Mm.24671.1	8.0	7.3	**-1.6**	0.00
1427630_x_at	Ceacam1	carcinoembryonic antigen-related cell adhesion molecule 1	Mm.14114.5	10.7	10.0	**-1.6**	0.00
1428021_at	Mccc2	methylcrotonoyl-Coenzyme A carboxylase 2 (beta)	Mm.221067.1	8.2	7.5	**-1.6**	0.00
1429468_at	1110018F16Rik	RIKEN cDNA 1110018F16 gene; DnaJ (Hsp40) homolog, subfamily B, member 14	Mm.40490.1	6.9	6.3	**-1.6**	0.00
1432120_at	Rmdn2	regulator of microtubule dynamics 2	Mm.158495.1	6.3	5.6	**-1.6**	0.02
1432472_a_at	Mccc2	methylcrotonoyl-Coenzyme A carboxylase 2 (beta)	Mm.137327.1	9.1	8.4	**-1.6**	0.00
1433647_s_at	Rhobtb3	Rho-related BTB domain containing 3	Mm.46219.1	8.0	7.3	**-1.6**	0.00
1435000_at	Gspt1	G1 to S phase transition 1	Mm.29255.1	8.9	8.2	**-1.6**	0.01

Supplemental Table 9. Significant differently expressed genes in 3bKI HCC samples

Affymetrix ID	Gene Symbol	Description	Transcript ID (Array Design)	3aKO avg signal log2 (n=4)	3bKI Avg Signal log2 (n=5)	Fold Change (linear)	ANOVA p-value
1436766_at	LOC100861853	LUC7-like 2 (S. cerevisiae)	Mm.24304.2	8.9	8.2	**-1.6**	0.00
1439283_at	Osbpl9	oxysterol binding protein-like 9	Mm.5706.1	6.5	5.8	**-1.6**	0.01
1439443_x_at	Tkt	transketolase	Mm.154387.6	11.7	11.0	**-1.6**	0.02
1440225_at	Gpr116	G protein-coupled receptor 116	Mm.23478.1	6.3	5.6	**-1.6**	0.01
1443901_at	C2cd2	C2 calcium-dependent domain containing 2	Mm.153973.1	8.1	7.4	**-1.6**	0.00
1446433_at	Acbd5	acyl-Coenzyme A binding domain containing 5	Mm.215977.1	7.6	6.9	**-1.6**	0.02
1449534_at	Sycp3	synaptonemal complex protein 3	Mm.148209.1	3.4	2.7	**-1.6**	0.02
1452252_at	Utp20	UTP20, small subunit (SSU) processome component, homolog (yeast)	Mm.29631.1	8.3	7.6	**-1.6**	0.01
1452292_at	Ap2b1	adaptor-related protein complex 2, beta 1 subunit	Mm.39053.1	9.4	8.7	**-1.6**	0.00
1452619_a_at	Agbl3	ATP/GTP binding protein-like 3	Mm.154155.1	5.6	4.9	**-1.6**	0.00
1455605_at	Rufy3	RUN and FYVE domain containing 3	Mm.37819.3	8.5	7.8	**-1.6**	0.00
1455826_a_at	Bace1	beta-site APP cleaving enzyme 1	Mm.24044.2	7.1	6.4	**-1.6**	0.00
1456754_at	Zfyve20	zinc finger, FYVE domain containing 20	Mm.218383.1	6.8	6.1	**-1.6**	0.00
1458305_at	Tmtc3	transmembrane and tetratricopeptide repeat containing 3	Mm.213462.1	3.7	3.0	**-1.6**	0.03
1418472_at	Aspa	aspartoacylase	Mm.20317.1	8.6	7.9	**-1.61**	0.02
1418491_a_at	Pus3	pseudouridine synthase 3	Mm.89425.1	5.7	5.0	**-1.61**	0.00
1418495_at	Zc3h8	zinc finger CCCH type containing 8	Mm.11675.1	6.9	6.2	**-1.61**	0.02
1419191_at	Hipk3	homeodomain interacting protein kinase 3	Mm.20333.1	7.2	6.5	**-1.61**	0.00
1419866_s_at	Atxn2	ataxin 2	Mm.199057.1	9.1	8.4	**-1.61**	0.01
1424121_at	Commd1	COMM domain containing 1	Mm.29542.1	7.6	6.9	**-1.61**	0.01
1425401_at	Cpsf4l	cleavage and polyadenylation specific factor 4-like	Mm.190626.1	5.4	4.7	**-1.61**	0.00
1430942_at	8430437O03Rik	RIKEN cDNA 8430437O03 gene	Mm.158722.1	6.6	5.9	**-1.61**	0.00
1431328_at	Ppp1cb	protein phosphatase 1, catalytic subunit, beta isoform	Mm.4572.2	6.3	5.6	**-1.61**	0.00
1433734_at	Slc13a4	solute carrier family 13 (sodium/sulfate symporters), member 4	Mm.23666.1	6.1	5.4	**-1.61**	0.02
1434243_s_at	Tomm70a	translocase of outer mitochondrial membrane 70 homolog A (yeast)	Mm.21473.2	7.4	6.7	**-1.61**	0.00
1435537_at	Ptprd	protein tyrosine phosphatase, receptor type, D	Mm.41736.2	9.2	8.6	**-1.61**	0.02
1436332_at	Hspb6	heat shock protein, alpha-crystallin-related, B6	Mm.34885.1	8.0	7.3	**-1.61**	0.03
1436618_at	Sfxn5	sideroflexin 5	Mm.41018.1	7.9	7.2	**-1.61**	0.00
1438721_a_at	Irf3	interferon regulatory factor 3	Mm.3960.4	5.8	5.2	**-1.61**	0.01
1441947_x_at	Sik3	SIK family kinase 3	Mm.125629.1	7.9	7.2	**-1.61**	0.00
1442892_at			Mm.139122.1	5.8	5.1	**-1.61**	0.04

Supplemental Table 9. Significant differently expressed genes in 3bKI HCC samples

Affymetrix ID	Gene Symbol	Description	Transcript ID (Array Design)	3aKO avg signal log2 (n=4)	3bKI Avg Signal log2 (n=5)	Fold Change (linear)	ANOVA p-value
1448155_at	Pdcd6ip	programmed cell death 6 interacting protein	Mm.29816.1	9.3	8.7	**-1.61**	0.00
1450376_at	Mxi1	Max interacting protein 1	Mm.2154.1	8.7	8.0	**-1.61**	0.01
1453287_at	Ankrd33b	ankyrin repeat domain 33B	Mm.27619.1	7.8	7.1	**-1.61**	0.01
1455222_a_at	Ubp1	upstream binding protein 1	Mm.28052.3	9.7	9.0	**-1.61**	0.00
1455329_at		cell division cycle 37-like 1	Mm.31013.1	6.2	5.5	**-1.61**	0.00
1457110_at	Pank1	pantothenate kinase 1	Mm.129337.1	6.9	6.2	**-1.61**	0.02
1459030_at	Bbox1	butyrobetaine (gamma), 2-oxoglutarate dioxygenase 1 (gamma-butyrobetaine hydroxylase)	Mm.40249.1	9.3	8.6	**-1.61**	0.02
1417531_at	Cyp2j5	cytochrome P450, family 2, subfamily j, polypeptide 5	Mm.12838.1	12.6	11.9	**-1.62**	0.00
1417850_at	Rb1	retinoblastoma 1	Mm.304.1	6.4	5.8	**-1.62**	0.02
1418474_at	Emc9	ER membrane protein complex subunit 9	Mm.40667.1	10.0	9.3	**-1.62**	0.00
1422857_at	Trip4	thyroid hormone receptor interactor 4	Mm.27462.1	8.2	7.5	**-1.62**	0.02
1424035_at	Rora	RAR-related orphan receptor alpha	Mm.8858.2	6.5	5.8	**-1.62**	0.01
1426850_a_at	Map2k6	mitogen-activated protein kinase kinase 6	Mm.14487.2	7.8	7.1	**-1.62**	0.02
1428085_at	1110057K04Rik	RIKEN cDNA 1110057K04 gene	Mm.25608.1	9.2	8.5	**-1.62**	0.00
1428280_at	Fip1l1	FIP1 like 1 (S. cerevisiae)	Mm.24084.2	8.2	7.5	**-1.62**	0.00
1429988_at	Zfp235	zinc finger protein 235	Mm.70963.1	5.6	4.9	**-1.62**	0.02
1431189_a_at	Fahd2a	fumarylacetoacetate hydrolase domain containing 2A	Mm.180782.2	7.4	6.7	**-1.62**	0.01
1435274_at	Spopl	speckle-type POZ protein-like	Mm.49884.1	6.2	5.5	**-1.62**	0.04
1435591_at	AI426330	expressed sequence AI426330	Mm.33776.1	5.9	5.2	**-1.62**	0.00
1435626_a_at	Herpud1	homocysteine-inducible, endoplasmic reticulum stress-inducible, ubiquitin-like domain member 1	Mm.29151.2	12.3	11.6	**-1.62**	0.01
1436189_at	Nqo2	NAD(P)H dehydrogenase, quinone 2	Mm.99453.1	7.7	7.0	**-1.62**	0.01
1436219_at	Fam210a	family with sequence similarity 210, member A	Mm.34672.1	7.4	6.7	**-1.62**	0.02
1437570_at	AI503301	expressed sequence AI503301; LUC7-like 3 (S. cerevisiae)	Mm.31113.1	5.6	4.9	**-1.62**	0.01
1438816_at	Ahctf1	AT hook containing transcription factor 1	Mm.126099.1	6.1	5.4	**-1.62**	0.01
1440886_at	Cdc37l1	cell division cycle 37-like 1	Mm.170751.1	7.0	6.3	**-1.62**	0.00
1442916_at			Mm.125754.1	6.2	5.5	**-1.62**	0.01
1443196_at		ring finger protein 217	Mm.209415.1	6.1	5.4	**-1.62**	0.01
1447121_at			Mm.54150.1	7.7	7.0	**-1.62**	0.03
1448973_at	Sult1d1	sulfotransferase family 1D, member 1	Mm.6824.1	10.9	10.2	**-1.62**	0.04
1449620_s_at	Adcy9	adenylate cyclase 9	Mm.201803.1	7.7	7.0	**-1.62**	0.00

Supplemental Table 9. Significant differently expressed genes in 3bKI HCC samples

Affymetrix ID	Gene Symbol	Description	Transcript ID (Array Design)	3aKO avg signal log2 (n=4)	3bKI Avg Signal log2 (n=5)	Fold Change (linear)	ANOVA p-value
1454663_at	Eif5	eukaryotic translation initiation factor 5	Mm.196515.1	9.9	9.2	**-1.62**	0.00
1456371_a_at	Shroom1	shroom family member 1	Mm.202216.3	7.9	7.2	**-1.62**	0.00
1457020_at			Mm.131196.1	6.6	5.9	**-1.62**	0.01
1457883_at	Pm20d2	peptidase M20 domain containing 2	Mm.212481.1	5.5	4.8	**-1.62**	0.00
1424400_a_at	Aldh1l1	aldehyde dehydrogenase 1 family, member L1	Mm.30035.1	13.5	12.7	**-1.63**	0.00
1424826_s_at	Mtss1	metastasis suppressor 1	Mm.220818.1	10.6	9.9	**-1.63**	0.01
1425596_at	AI317395	expressed sequence AI317395	Mm.26536.1	8.4	7.7	**-1.63**	0.01
1426325_at	Kif1c	kinesin family member 1C	Mm.90223.1	6.2	5.5	**-1.63**	0.00
1428231_at	Cpsf6	cleavage and polyadenylation specific factor 6	Mm.34851.1	9.0	8.3	**-1.63**	0.00
1429264_at	Fam120aos	family with sequence similarity 120A, opposite strand	Mm.33215.1	8.1	7.4	**-1.63**	0.00
1429530_a_at	Smpd4	sphingomyelin phosphodiesterase 4	Mm.34659.2	4.3	3.6	**-1.63**	0.00
1434036_at	Mtss1	metastasis suppressor 1	Mm.196718.3	11.4	10.7	**-1.63**	0.02
1434273_at	Fam174b	family with sequence similarity 174, member B	Mm.4143.2	8.0	7.3	**-1.63**	0.02
1434529_x_at	Chfr	checkpoint with forkhead and ring finger domains	Mm.30264.2	7.1	6.4	**-1.63**	0.00
1434807_s_at	Mtx3	metaxin 3	Mm.202301.1	7.2	6.5	**-1.63**	0.01
1437481_at	Trmt61b	tRNA methyltransferase 61B	Mm.75202.2	6.9	6.2	**-1.63**	0.00
1442141_at	BC028454		Mm.88727.1	6.9	6.2	**-1.63**	0.00
1445341_at		ragulator complex protein LAMTOR4-like	Mm.182701.1	3.9	3.2	**-1.63**	0.01
1446074_at	Marc1	mitochondrial amidoxime reducing component 1	Mm.212414.1	10.1	9.4	**-1.63**	0.02
1451281_at	Zscan12	zinc finger and SCAN domain containing 12	Mm.24124.1	5.8	5.1	**-1.63**	0.00
1454375_at	5730458M16Rik	RIKEN cDNA 5730458M16 gene	Mm.158121.1	5.2	4.5	**-1.63**	0.01
1454647_at	Acad11	acyl-Coenzyme A dehydrogenase family, member 11	Mm.41274.4	12.5	11.8	**-1.63**	0.03
1417070_at	Cyp4v3	cytochrome P450, family 4, subfamily v, polypeptide 3	Mm.1554.1	10.8	10.1	**-1.64**	0.02
1417208_at	Amacr	alpha-methylacyl-CoA racemase	Mm.2787.1	11.0	10.3	**-1.64**	0.00
1419975_at	Scp2	sterol carrier protein 2, liver	Mm.206843.1	7.1	6.4	**-1.64**	0.01
1422990_at	Met	met proto-oncogene	Mm.86844.1	8.3	7.6	**-1.64**	0.00
1423878_at	Gypc	glycophorin C	Mm.38774.1	8.0	7.3	**-1.64**	0.05
1425280_at	Leng1	leukocyte receptor cluster (LRC) member 1	Mm.175032.1	6.8	6.0	**-1.64**	0.01
1427171_at	Rlf	rearranged L-myc fusion sequence	Mm.68846.1	7.1	6.4	**-1.64**	0.00
1427425_at	Slc25a51	solute carrier family 25, member 51	Mm.154573.1	8.8	8.1	**-1.64**	0.01
1428978_at	2900009J20Rik		Mm.82240.1	6.3	5.6	**-1.64**	0.00
1429784_at	Mapk1ip1l	mitogen-activated protein kinase 1 interacting protein 1-like	Mm.111185.1	6.8	6.1	**-1.64**	0.01
1432562_at	1110006G14Rik	SRY (sex determining region Y)-box 6, opposite strand	Mm.158213.1	5.7	5.0	**-1.64**	0.00

Supplemental Table 9. Significant differently expressed genes in 3bKI HCC samples

Affymetrix ID	Gene Symbol	Description	Transcript ID (Array Design)	3aKO avg signal log2 (n=4)	3bKI Avg Signal log2 (n=5)	Fold Change (linear)	ANOVA p-value
1433618_at	C330006A16Rik	RIKEN cDNA C330006A16 gene	Mm.27954.1	8.7	7.9	**-1.64**	0.00
1434099_at	Ppargc1a	peroxisome proliferative activated receptor, gamma, coactivator 1 alpha	Mm.35687.3	4.6	3.9	**-1.64**	0.02
1435391_at	Rbm33	RNA binding motif protein 33	Mm.89914.1	8.3	7.6	**-1.64**	0.00
1437668_at	Ccrl1	atypical chemokine receptor 4	Mm.29762.2	6.3	5.6	**-1.64**	0.01
1437751_at	Ppargc1a	peroxisome proliferative activated receptor, gamma, coactivator 1 alpha	Mm.10707.2	6.6	5.8	**-1.64**	0.02
1438178_x_at	Atad3a	ATPase family, AAA domain containing 3A	Mm.21881.3	9.5	8.8	**-1.64**	0.01
1439290_at			Mm.218143.1	5.1	4.4	**-1.64**	0.01
1446342_at	2310001H17Rik	RIKEN cDNA 2310001H17 gene	Mm.213246.1	6.2	5.5	**-1.64**	0.02
1448181_at	Klf15	Kruppel-like factor 15	Mm.41389.1	11.2	10.5	**-1.64**	0.02
1448418_s_at	Dcaf11	DDB1 and CUL4 associated factor 11	Mm.11535.1	12.5	11.8	**-1.64**	0.00
1450068_at	Baz1b	bromodomain adjacent to zinc finger domain, 1B	Mm.40331.1	6.7	6.0	**-1.64**	0.01
1453140_at	Zfp871	zinc finger protein 871	Mm.38813.1	8.8	8.1	**-1.64**	0.01
1456430_at	Ttc14	tetratricopeptide repeat domain 14	Mm.6148.1	6.7	6.0	**-1.64**	0.00
1457756_at	Zkscan8	zinc finger with KRAB and SCAN domains 8	Mm.151515.1	5.4	4.7	**-1.64**	0.00
1457791_at	B830008H07Rik	RIKEN cDNA B830008H07 gene	Mm.37292.1	9.6	8.9	**-1.64**	0.02
1458314_at			Mm.101872.1	5.0	4.3	**-1.64**	0.01
1458618_at			Mm.218563.1	5.8	5.1	**-1.64**	0.00
1460132_at			Mm.150378.1	6.7	5.9	**-1.64**	0.00
1460448_s_at	Ttc14	tetratricopeptide repeat domain 14	Mm.87673.1	6.2	5.4	**-1.64**	0.00
1415950_a_at	Pebp1	phosphatidylethanolamine binding protein 1	Mm.195898.1	12.7	12.0	**-1.65**	0.02
1419068_at	Rabgef1	RAB guanine nucleotide exchange factor (GEF) 1	Mm.101118.1	7.4	6.7	**-1.65**	0.00
1419173_at	Acy1	aminoacylase 1	Mm.7165.1	9.7	9.0	**-1.65**	0.00
1419811_at	Adcy9	adenylate cyclase 9	Mm.201803.1	7.7	7.0	**-1.65**	0.00
1421478_a_at	Zfp318	zinc finger protein 318	Mm.116965.1	7.1	6.3	**-1.65**	0.01
1424952_at	Ociad1	OCIA domain containing 1	Mm.24272.2	6.6	5.9	**-1.65**	0.00
1429320_at	Cdkn2aip	CDKN2A interacting protein	Mm.53963.1	5.9	5.2	**-1.65**	0.00
1434778_at	Wapal	wings apart-like homolog (Drosophila)	Mm.28257.1	8.2	7.5	**-1.65**	0.00
1435397_at	Zbtb44	zinc finger and BTB domain containing 44	Mm.86401.1	8.4	7.7	**-1.65**	0.02
1437926_at	Xpnpep3	X-prolyl aminopeptidase (aminopeptidase P) 3, putative	Mm.42492.1	8.5	7.7	**-1.65**	0.00
1438695_at	C230091D08Rik	RIKEN cDNA C230091D08 gene	Mm.132544.4	7.7	6.9	**-1.65**	0.00
1438842_at	Mtch2	mitochondrial carrier homolog 2 (C. elegans)	Mm.28023.5	5.7	4.9	**-1.65**	0.00
1447693_s_at	Neo1	neogenin	Mm.132212.1	7.4	6.7	**-1.65**	0.00
1448760_at	Zfp68	zinc finger protein 68	Mm.27575.1	6.4	5.7	**-1.65**	0.03

Supplemental Table 9. Significant differently expressed genes in 3bKI HCC samples

Affymetrix ID	Gene Symbol	Description	Transcript ID (Array Design)	3aKO avg signal log2 (n=4)	3bKI Avg Signal log2 (n=5)	Fold Change (linear)	ANOVA p-value
1449186_at	Bag4	BCL2-associated athanogene 4	Mm.27102.1	8.6	7.9	**-1.65**	0.01
1450097_s_at	Gna12	guanine nucleotide binding protein, alpha 12	Mm.140610.1	9.2	8.5	**-1.65**	0.01
1450715_at	Cyp1a2	cytochrome P450, family 1, subfamily a, polypeptide 2	Mm.15537.1	12.7	12.0	**-1.65**	0.02
1451559_a_at	Dhrs4	dehydrogenase/reductase (SDR family) member 4	Mm.27427.2	11.4	10.7	**-1.65**	0.04
1452122_at	AI314180	expressed sequence AI314180	Mm.27829.1	8.9	8.2	**-1.65**	0.00
1453156_s_at	Ptgr2	prostaglandin reductase 2	Mm.195974.2	8.2	7.5	**-1.65**	0.00
1455261_at	Luc7l	Luc7 homolog (S. cerevisiae)-like	Mm.25619.1	7.6	6.9	**-1.65**	0.00
1456791_at	Zfp800	zinc finger protein 800	Mm.30860.1	6.5	5.8	**-1.65**	0.01
1457027_at	Dhtkd1	dehydrogenase E1 and transketolase domain containing 1	Mm.128121.1	10.3	9.6	**-1.65**	0.01
1457227_at	Gm11266	predicted gene 11266	Mm.41666.1	5.4	4.6	**-1.65**	0.02
1415716_a_at	Gm9846	ribosomal protein S27; ribosomal protein S27, retrogene	Mm.29911.1	11.9	11.2	**-1.66**	0.00
1418473_at	Cutc	cutC copper transporter homolog (E.coli)	Mm.20257.1	8.7	8.0	**-1.66**	0.00
1421054_at	Xpo4	exportin 4	Mm.143753.1	6.4	5.7	**-1.66**	0.00
1425057_at	Pbld1	phenazine biosynthesis-like protein domain containing 1	Mm.104960.1	11.3	10.6	**-1.66**	0.02
1426061_x_at			Mm.212861.1	7.2	6.4	**-1.66**	0.00
1427322_at	Brwd1	bromodomain and WD repeat domain containing 1	Mm.131039.2	7.4	6.6	**-1.66**	0.00
1428768_at	Pan3	PAN3 polyA specific ribonuclease subunit homolog (S. cerevisiae)	Mm.79960.1	8.1	7.3	**-1.66**	0.00
1429966_at	3110057O12Rik	RIKEN cDNA 3110057O12 gene	Mm.34725.1	5.3	4.5	**-1.66**	0.01
1434978_at	Fam210a	family with sequence similarity 210, member A	Mm.171701.1	8.6	7.8	**-1.66**	0.00
1435483_x_at	Slc25a32	solute carrier family 25, member 32	Mm.17875.2	5.2	4.5	**-1.66**	0.01
1436543_at	Gtpbp10	GTP-binding protein 10 (putative)	Mm.86921.2	7.7	6.9	**-1.66**	0.00
1440936_at	Serac1	serine active site containing 1	Mm.5548.1	6.4	5.6	**-1.66**	0.01
1444531_at			Mm.40499.1	7.0	6.3	**-1.66**	0.01
1444599_at	Herc4	hect domain and RLD 4	Mm.183744.1	6.0	5.3	**-1.66**	0.00
1455407_at	Zfp236	zinc finger protein 236	Mm.127095.1	6.6	5.8	**-1.66**	0.00
1456019_at	Cwf19l2	CWF19-like 2, cell cycle control (S. pombe)	Mm.72009.1	7.1	6.4	**-1.66**	0.00
1421990_at	Syt1	synaptotagmin I	Mm.5101.1	7.0	6.3	**-1.67**	0.01
1423249_at	Nktr	natural killer tumor recognition sequence	Mm.23964.1	7.8	7.1	**-1.67**	0.00
1429778_at	Optn	optineurin	Mm.116942.1	9.2	8.4	**-1.67**	0.01
1433527_at	Ireb2	iron responsive element binding protein 2	Mm.163230.1	9.4	8.7	**-1.67**	0.00
1433664_at	Ube2q2	ubiquitin-conjugating enzyme E2Q (putative) 2	Mm.24729.1	7.3	6.6	**-1.67**	0.01
1433694_at	Pde3b	phosphodiesterase 3B, cGMP-inhibited	Mm.39980.1	10.3	9.5	**-1.67**	0.01

Supplemental Table 9. Significant differently expressed genes in 3bKI HCC samples

Affymetrix ID	Gene Symbol	Description	Transcript ID (Array Design)	3aKO avg signal log2 (n=4)	3bKI Avg Signal log2 (n=5)	Fold Change (linear)	ANOVA p-value
1433782_at	Cldn12	claudin 12	Mm.40132.1	9.1	8.4	**-1.67**	0.00
1434454_at	Adcy9	adenylate cyclase 9	Mm.43948.1	7.6	6.8	**-1.67**	0.01
1437950_at	Fam149a	family with sequence similarity 149, member A	Mm.213405.1	6.2	5.5	**-1.67**	0.03
1441026_at	Parp4	poly (ADP-ribose) polymerase family, member 4	Mm.213013.1	4.9	4.2	**-1.67**	0.01
1441141_at			Mm.100257.1	5.6	4.8	**-1.67**	0.02
1443695_at	Habp2	hyaluronic acid binding protein 2	Mm.202667.1	7.3	6.5	**-1.67**	0.00
1446504_at			Mm.207949.1	3.8	3.1	**-1.67**	0.02
1448661_at	Plcb3	phospholipase C, beta 3	Mm.6888.1	7.4	6.7	**-1.67**	0.00
1449628_s_at	Stard7	START domain containing 7	Mm.219882.1	11.4	10.7	**-1.67**	0.00
1454840_at	Mccc2	methylcrotonoyl-Coenzyme A carboxylase 2 (beta)	Mm.137327.2	10.1	9.4	**-1.67**	0.00
1454935_at	Fitm2	fat storage-inducing transmembrane protein 2	Mm.28554.1	9.1	8.4	**-1.67**	0.01
1454975_at	Zfc3h1	zinc finger, C3H1-type containing	Mm.38383.1	8.6	7.9	**-1.67**	0.00
1455740_at	Hnrnpa1	heterogeneous nuclear ribonucleoprotein A1	Mm.27927.6	4.8	4.1	**-1.67**	0.00
1456506_at	Prpf38b	PRP38 pre-mRNA processing factor 38 (yeast) domain containing B	Mm.139225.1	5.0	4.2	**-1.67**	0.00
1460189_at	Dcaf11	DDB1 and CUL4 associated factor 11	Mm.11535.1	12.5	11.8	**-1.67**	0.00
1460368_at	Mpp4	membrane protein, palmitoylated 4 (MAGUK p55 subfamily member 4)	Mm.101838.1	5.4	4.7	**-1.67**	0.01
1418565_at	Serbp1	serpine1 mRNA binding protein 1	Mm.18700.1	6.4	5.7	**-1.68**	0.00
1418715_at	Pank1	pantothenate kinase 1	Mm.24742.1	11.3	10.6	**-1.68**	0.02
1419102_at	Sin3a	transcriptional regulator, SIN3A (yeast)	Mm.15755.1	7.0	6.2	**-1.68**	0.00
1419915_at	Nus1	nuclear undecaprenyl pyrophosphate synthase 1 homolog (S. cerevisiae)	Mm.199964.1	6.3	5.5	**-1.68**	0.00
1428162_at	Lrif1	ligand dependent nuclear receptor interacting factor 1	Mm.32150.1	6.0	5.2	**-1.68**	0.03
1430991_at	1810014B01Rik	RIKEN cDNA 1810014B01 gene	Mm.46783.2	8.9	8.1	**-1.68**	0.00
1432355_at	2210039B01Rik	RIKEN cDNA 2210039B01 gene	Mm.219773.1	6.7	6.0	**-1.68**	0.01
1433713_at	Gcn1l1	GCN1 general control of amino-acid synthesis 1-like 1 (yeast); predicted gene 13123	Mm.45024.1	7.8	7.1	**-1.68**	0.00
1434870_at	2810004N23Rik	RIKEN cDNA 2810004N23 gene	Mm.33233.1	7.6	6.9	**-1.68**	0.00
1435925_at	Git2	G protein-coupled receptor kinase-interactor 2	Mm.22844.1	7.4	6.7	**-1.68**	0.00
1436363_a_at	Nfix	nuclear factor I/X	Mm.9394.3	10.6	9.8	**-1.68**	0.00
1439696_at	Nr2c2	nuclear receptor subfamily 2, group C, member 2	Mm.132673.1	4.9	4.1	**-1.68**	0.00
1442381_at			Mm.162073.1	6.2	5.4	**-1.68**	0.00
1447527_at			Mm.99929.1	6.0	5.3	**-1.68**	0.02
1448426_at	Sardh	sarcosine dehydrogenase	Mm.141020.1	11.2	10.4	**-1.68**	0.01

Supplemental Table 9. Significant differently expressed genes in 3bKI HCC samples

Affymetrix ID	Gene Symbol	Description	Transcript ID (Array Design)	3aKO avg signal log2 (n=4)	3bKI Avg Signal log2 (n=5)	Fold Change (linear)	ANOVA p-value
1449481_at	Slc25a13	solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 13	Mm.24513.1	12.1	11.3	**-1.68**	0.01
1449817_at	Abcb11	ATP-binding cassette, sub-family B (MDR/TAP), member 11	Mm.26728.1	12.1	11.4	**-1.68**	0.00
1450051_at	Atrx	alpha thalassemia/mental retardation syndrome X-linked homolog (human)	Mm.10141.1	7.3	6.5	**-1.68**	0.01
1454980_at	Pdpr	Mus musculus non-coding RNA, oocyte_piRNA216, complete sequence.	Mm.28350.1	8.6	7.9	**-1.68**	0.01
1455095_at	Hist2h2be	histone cluster 2, H2be	Mm.5220.1	5.3	4.6	**-1.68**	0.02
1457899_at	Kalrn	kalirin, RhoGEF kinase	Mm.28453.1	6.1	5.3	**-1.68**	0.00
1417969_at	Fbxo31	F-box protein 31	Mm.24829.1	8.5	7.8	**-1.69**	0.00
1418412_at	Tpd52l1	tumor protein D52-like 1	Mm.7821.1	7.2	6.4	**-1.69**	0.00
1427677_a_at	Sox6	SRY (sex determining region Y)-box 6	Mm.4656.3	7.2	6.4	**-1.69**	0.01
1428894_at	1300018J18Rik	selenoprotein O	Mm.44763.1	10.3	9.5	**-1.69**	0.00
1429773_at	Dnajc22	DnaJ (Hsp40) homolog, subfamily C, member 22	Mm.30544.1	10.5	9.7	**-1.69**	0.00
1450254_at	Tert	telomerase reverse transcriptase	Mm.10109.1	6.9	6.2	**-1.69**	0.05
1456941_at	Tert	telomerase reverse transcriptase	Mm.38000.1	6.7	6.0	**-1.69**	0.05
1457302_at		Mus musculus, clone IMAGE:5367487, mRNA.; predicted gene, 17491	Mm.34024.1	8.4	7.7	**-1.69**	0.00
1416991_at	Mto1	mitochondrial translation optimization 1 homolog (S. cerevisiae)	Mm.23781.1	8.5	7.7	**-1.7**	0.00
1417422_at	Gnmt	glycine N-methyltransferase	Mm.29395.1	14.3	13.5	**-1.7**	0.01
1418152_at	Hmgn5	high-mobility group nucleosome binding domain 5	Mm.20450.1	9.7	9.0	**-1.7**	0.00
1420379_at	Slco1a1	solute carrier organic anion transporter family, member 1a1	Mm.103665.1	12.5	11.7	**-1.7**	0.04
1420630_at	8430419L09Rik	RIKEN cDNA 8430419L09 gene	Mm.34182.1	8.4	7.7	**-1.7**	0.00
1421346_a_at	Slc6a6	solute carrier family 6 (neurotransmitter transporter, taurine), member 6	Mm.200518.1	9.7	8.9	**-1.7**	0.03
1424401_at	Aldh1l1	aldehyde dehydrogenase 1 family, member L1	Mm.30035.1	7.9	7.1	**-1.7**	0.03
1426460_a_at	Ugp2	UDP-glucose pyrophosphorylase 2	Mm.28877.2	9.9	9.1	**-1.7**	0.00
1428010_at	Timm9	translocase of inner mitochondrial membrane 9	Mm.158852.1	4.9	4.2	**-1.7**	0.05
1434674_at	Lyst		Mm.1423.3	8.1	7.3	**-1.7**	0.00
1440146_at	Vps13a	vacuolar protein sorting 13A (yeast)	Mm.213679.1	5.0	4.2	**-1.7**	0.01
1443471_at	Zbtb20	zinc finger and BTB domain containing 20	Mm.213242.1	6.8	6.0	**-1.7**	0.05
1445379_at			Mm.35406.1	7.5	6.8	**-1.7**	0.01

Supplemental Table 9. Significant differently expressed genes in 3bKI HCC samples

Affymetrix ID	Gene Symbol	Description	Transcript ID (Array Design)	3aKO avg signal log2 (n=4)	3bKI Avg Signal log2 (n=5)	Fold Change (linear)	ANOVA p-value
1448400_a_at	Smarcd2	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 2	Mm.21772.1	10.6	9.8	**-1.7**	0.00
1449954_at	Hyal1	hyaluronoglucosaminidase 1; N-acetyltransferase 6	Mm.10305.1	9.3	8.5	**-1.7**	0.01
1455008_at	Gna12	guanine nucleotide binding protein, alpha 12	Mm.200500.1	9.5	8.7	**-1.7**	0.00
1455728_at	Pten	phosphatase and tensin homolog	Mm.220979.1	9.4	8.7	**-1.7**	0.00
1416418_at	Gabarapl1	gamma-aminobutyric acid (GABA) A receptor-associated protein-like 1	Mm.14638.1	11.6	10.8	**-1.71**	0.01
1420982_at	Rbm39	RNA binding motif protein 39	Mm.17307.1	7.6	6.8	**-1.71**	0.00
1423062_at	Igfbp3	insulin-like growth factor binding protein 3	Mm.29254.1	7.9	7.1	**-1.71**	0.02
1428562_at	Mir22hg	Mir22 host gene (non-protein coding)	Mm.41393.1	8.7	7.9	**-1.71**	0.01
1431012_a_at	Eci2	enoyl-Coenzyme A delta isomerase 2	Mm.28883.2	11.5	10.7	**-1.71**	0.01
1431829_a_at	Rgl3	ral guanine nucleotide dissociation stimulator-like 3	Mm.110594.2	8.8	8.0	**-1.71**	0.00
1433068_at	6330582A15Rik	RIKEN cDNA 6330582A15 gene	Mm.215199.1	7.3	6.5	**-1.71**	0.00
1434394_at	N4bp2	NEDD4 binding protein 2	Mm.33936.1	9.3	8.5	**-1.71**	0.00
1437669_x_at	Ccrl1	atypical chemokine receptor 4	Mm.29762.2	5.9	5.1	**-1.71**	0.03
1438397_a_at	Rbm39	RNA binding motif protein 39	Mm.17307.3	7.7	6.9	**-1.71**	0.00
1439074_a_at	Son	Son DNA binding protein	Mm.46401.3	7.3	6.5	**-1.71**	0.00
1441685_at	Prosc	proline synthetase co-transcribed	Mm.101801.1	5.3	4.5	**-1.71**	0.00
1445657_at	AW111846	expressed sequence AW111846	Mm.36341.2	8.4	7.6	**-1.71**	0.00
1451221_at	BC018507	interactor of little elongation complex ELL subunit 1	Mm.139738.1	6.8	6.0	**-1.71**	0.00
1451271_a_at	Acat1	acetyl-Coenzyme A acetyltransferase 1	Mm.219649.1	11.6	10.8	**-1.71**	0.04
1452375_at	Aldh4a1	aldehyde dehydrogenase 4 family, member A1	Mm.218879.1	12.1	11.4	**-1.71**	0.00
1455696_a_at	Prpf4b	PRP4 pre-mRNA processing factor 4 homolog B (yeast)	Mm.10027.3	7.3	6.5	**-1.71**	0.01
1423883_at	Acsl1	acyl-CoA synthetase long-chain family member 1	Mm.220964.1	12.9	12.1	**-1.72**	0.00
1427957_at	Adtrp	androgen dependent TFPI regulating protein	Mm.25195.1	11.6	10.8	**-1.72**	0.01
1428805_at	Slc35e3	solute carrier family 35, member E3	Mm.26071.1	8.4	7.6	**-1.72**	0.03
1429538_a_at	Sfrs18	PNN interacting serine/arginine-rich	Mm.100117.1	8.1	7.3	**-1.72**	0.01
1436318_at	Tardbp	TAR DNA binding protein	Mm.220359.1	7.4	6.6	**-1.72**	0.00
1439167_at	Pecr	peroxisomal trans-2-enoyl-CoA reductase	Mm.29988.2	6.8	6.0	**-1.72**	0.01
1441718_at			Mm.125543.1	5.9	5.1	**-1.72**	0.01
1442615_at			Mm.130736.1	6.5	5.7	**-1.72**	0.00

Supplemental Table 9. Significant differently expressed genes in 3bKI HCC samples

Affymetrix ID	Gene Symbol	Description	Transcript ID (Array Design)	3aKO avg signal log2 (n=4)	3bKI Avg Signal log2 (n=5)	Fold Change (linear)	ANOVA p-value
1452110_at	Mtrr	5-methyltetrahydrofolate-homocysteine methyltransferase reductase	Mm.205514.1	7.6	6.8	**-1.72**	0.00
1457034_at	D14Abb1e	family with sequence similarity 208, member A	Mm.216841.1	6.9	6.1	**-1.72**	0.00
1457682_at	Arhgap42	Rho GTPase activating protein 42	Mm.80648.1	9.5	8.7	**-1.72**	0.00
1418179_at	Atg3	autophagy related 3	Mm.41775.1	6.3	5.5	**-1.73**	0.00
1423086_at	Npc1	Niemann-Pick type C1	Mm.3484.1	9.6	8.8	**-1.73**	0.01
1424353_at	Lrpprc	leucine-rich PPR-motif containing	Mm.180895.1	10.2	9.4	**-1.73**	0.00
1427711_a_at	Ceacam1	carcinoembryonic antigen-related cell adhesion molecule 1	Mm.14114.6	8.5	7.7	**-1.73**	0.00
1428681_at	Gm608	predicted gene 608	Mm.21200.1	8.6	7.8	**-1.73**	0.00
1428908_at	Rbm25	RNA binding motif protein 25	Mm.46005.1	6.8	6.0	**-1.73**	0.01
1434293_at	Hectd3	HECT domain containing 3	Mm.220986.1	7.3	6.5	**-1.73**	0.01
1434311_at	Cnot6l	CCR4-NOT transcription complex, subunit 6-like	Mm.28374.2	8.1	7.3	**-1.73**	0.00
1438391_x_at	Hsd17b10	hydroxysteroid (17-beta) dehydrogenase 10	Mm.6994.2	9.0	8.2	**-1.73**	0.01
1449118_at	Dbt	dihydrolipoamide branched chain transacylase E2	Mm.3636.1	10.0	9.2	**-1.73**	0.00
1455878_at	Dancr	differentiation antagonizing non-protein coding RNA	Mm.46547.1	7.3	6.5	**-1.73**	0.00
1455958_s_at	Pptc7	PTC7 protein phosphatase homolog (S. cerevisiae)	Mm.200168.1	9.1	8.3	**-1.73**	0.00
1457673_at	2610005L07Rik	cadherin 11 pseudogene	Mm.80617.1	6.4	5.6	**-1.73**	0.00
1419037_at	Csnk2a1	casein kinase 2, alpha 1 polypeptide	Mm.23692.1	9.5	8.7	**-1.74**	0.00
1424886_at	Ptprd	protein tyrosine phosphatase, receptor type, D	Mm.89191.1	10.5	9.7	**-1.74**	0.00
1426060_at			Mm.212861.1	7.3	6.5	**-1.74**	0.00
1429052_at	Ptprd	protein tyrosine phosphatase, receptor type, D	Mm.41736.1	10.7	9.9	**-1.74**	0.01
1434642_at	Hsd17b11	hydroxysteroid (17-beta) dehydrogenase 11	Mm.1187.2	12.7	11.9	**-1.74**	0.02
1436966_at	Peli2	pellino 2	Mm.51196.1	7.1	6.3	**-1.74**	0.00
1446143_at			Mm.208356.1	5.7	4.9	**-1.74**	0.00
1455255_at	4833420G11Rik	GID complex subunit 8 homolog (S. cerevisiae)	Mm.29561.2	7.6	6.8	**-1.74**	0.00
1458962_at	Tmed5	transmembrane emp24 protein transport domain containing 5	Mm.33047.1	5.3	4.5	**-1.74**	0.01
1459398_at	Peli1	pellino 1	Mm.209921.1	3.6	2.8	**-1.74**	0.00
1415826_at	Atp6v1h	ATPase, H+ transporting, lysosomal V1 subunit H	Mm.27082.1	8.9	8.1	**-1.75**	0.00
1416631_at	Ap4b1	adaptor-related protein complex AP-4, beta 1	Mm.29234.1	7.7	6.9	**-1.75**	0.00
1422868_s_at	Gda	guanine deaminase	Mm.45054.1	6.5	5.7	**-1.75**	0.03

Supplemental Table 9. Significant differently expressed genes in 3bKI HCC samples

Affymetrix ID	Gene Symbol	Description	Transcript ID (Array Design)	3aKO avg signal log2 (n=4)	3bKI Avg Signal log2 (n=5)	Fold Change (linear)	ANOVA p-value
1423495_at	Decr2	2-4-dienoyl-Coenzyme A reductase 2, peroxisomal	Mm.35760.1	11.7	10.9	**-1.75**	0.04
1423564_a_at	Paics	phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoribosylaminoimidazole, succinocarboxamide synthetase	Mm.182931.1	11.5	10.7	**-1.75**	0.00
1426008_a_at	Slc7a2	solute carrier family 7 (cationic amino acid transporter, y+ system), member 2	Mm.4676.2	9.3	8.5	**-1.75**	0.03
1433781_a_at	Cldn12	claudin 12	Mm.40132.1	9.6	8.8	**-1.75**	0.00
1435075_at	Tmem106b	transmembrane protein 106B	Mm.27742.1	9.0	8.2	**-1.75**	0.00
1437424_at	Syde2	synapse defective 1, Rho GTPase, homolog 2 (C. elegans)	Mm.24692.1	7.8	7.0	**-1.75**	0.01
1438081_at	Mcc	mutated in colorectal cancers	Mm.210479.1	6.6	5.8	**-1.75**	0.01
1438418_at	Ap5m1	adaptor-related protein complex 5, mu 1 subunit	Mm.87037.2	7.6	6.8	**-1.75**	0.02
1441733_s_at	Nup153	nucleoporin 153	Mm.219831.1	5.5	4.7	**-1.75**	0.00
1443579_s_at	Deptor	DEP domain containing MTOR-interacting protein	Mm.220905.1	9.1	8.3	**-1.75**	0.00
1443628_at			Mm.44833.1	6.0	5.2	**-1.75**	0.00
1445928_at	March6	membrane-associated ring finger (C3HC4) 6	Mm.173425.1	6.9	6.1	**-1.75**	0.01
1450090_at	Zfp101	zinc finger protein 101	Mm.4417.1	7.0	6.2	**-1.75**	0.00
1460468_s_at	Dnajc22	DnaJ (Hsp40) homolog, subfamily C, member 22	Mm.30544.1	10.8	10.0	**-1.75**	0.00
1425034_at	Slc17a2	solute carrier family 17 (sodium phosphate), member 2	Mm.24030.1	8.9	8.1	**-1.76**	0.01
1428904_at	Ammecr1l	AMME chromosomal region gene 1-like	Mm.86513.1	9.4	8.5	**-1.76**	0.00
1434280_at		Mus musculus 8 days embryo whole body cDNA, RIKEN full-length enriched library, clone:5730463B09 product:unclassifiable, full insert sequence.	Mm.30502.2	5.5	4.7	**-1.76**	0.02
1434393_at	Usp34	ubiquitin specific peptidase 34	Mm.13148.1	7.6	6.8	**-1.76**	0.00
1434742_s_at	Aifm3	apoptosis-inducing factor, mitochondrion-associated 3	Mm.40038.2	7.0	6.1	**-1.76**	0.01
1438649_x_at	Pebp1	phosphatidylethanolamine binding protein 1	Mm.195898.6	13.3	12.5	**-1.76**	0.05
1443323_at	Trmt13	tRNA methyltransferase 13	Mm.138136.1	3.6	2.8	**-1.76**	0.02
1446193_at			Mm.207675.1	3.8	3.0	**-1.76**	0.01
1449844_at	Slco1a1	solute carrier organic anion transporter family, member 1a1	Mm.103665.1	11.7	10.9	**-1.76**	0.05

Supplemental Table 9. Significant differently expressed genes in 3bKI HCC samples

Affymetrix ID	Gene Symbol	Description	Transcript ID (Array Design)	3aKO avg signal log2 (n=4)	3bKI Avg Signal log2 (n=5)	Fold Change (linear)	ANOVA p-value
1453065_at	Aldh5a1	aldhehyde dehydrogenase family 5, subfamily A1	Mm.100159.1	9.8	9.0	**-1.76**	0.00
1453783_at	Pura	purine rich element binding protein A	Mm.214568.1	5.6	4.7	**-1.76**	0.00
1455446_x_at	Acadsb	acyl-Coenzyme A dehydrogenase, short/branched chain	Mm.28430.3	10.6	9.8	**-1.76**	0.00
1458235_at			Mm.214663.1	6.0	5.2	**-1.76**	0.00
1418279_a_at	Akap1	A kinase (PRKA) anchor protein 1	Mm.2969.1	9.2	8.4	**-1.77**	0.00
1427342_at	Fastkd1	FAST kinase domains 1	Mm.221029.1	8.7	7.9	**-1.77**	0.00
1428926_at	Fbxo31	F-box protein 31	Mm.41330.1	8.4	7.6	**-1.77**	0.00
1431109_at	Prr16	proline rich 16	Mm.63546.1	8.8	7.9	**-1.77**	0.00
1431199_at	Ggnbp1	gametogenetin binding protein 1	Mm.105357.1	7.6	6.8	**-1.77**	0.00
1434628_a_at	Rhpn2	rhophilin, Rho GTPase binding protein 2	Mm.35465.4	7.2	6.4	**-1.77**	0.00
1434766_at	Prkaa2	protein kinase, AMP-activated, alpha 2 catalytic subunit	Mm.10344.1	9.2	8.4	**-1.77**	0.00
1437410_at	Aldh2	aldehyde dehydrogenase 2, mitochondrial	Mm.132896.1	9.9	9.1	**-1.77**	0.04
1440883_at	Usp6nl	USP6 N-terminal like	Mm.86484.1	7.5	6.7	**-1.77**	0.00
1441242_at			Mm.133119.1	6.8	6.0	**-1.77**	0.02
1449337_at	Tdo2	tryptophan 2,3-dioxygenase	Mm.21545.1	11.7	10.9	**-1.77**	0.00
1452416_at	Il6ra	interleukin 6 receptor, alpha	Mm.2856.2	9.1	8.3	**-1.77**	0.01
1416775_at	Atp5sl	ATP5S-like	Mm.24062.1	8.1	7.3	**-1.78**	0.00
1425688_a_at	Dpys	dihydropyrimidinase	Mm.30994.2	11.7	10.9	**-1.78**	0.02
1426896_at	Zfp191	zinc finger protein 191	Mm.153618.1	6.5	5.6	**-1.78**	0.00
1428338_at	Spata2l	spermatogenesis associated 2-like	Mm.41459.1	8.3	7.5	**-1.78**	0.01
1428592_s_at	Usp38	ubiquitin specific peptidase 38	Mm.200389.1	6.8	6.0	**-1.78**	0.00
1434408_at	Atxn3	ataxin 3	Mm.30782.1	6.2	5.4	**-1.78**	0.00
1437128_a_at	Zfp945	zinc finger protein 945	Mm.33710.2	7.0	6.1	**-1.78**	0.00
1441204_at	A130019P10Rik	RIKEN cDNA A130019P10 gene	Mm.207398.1	6.0	5.2	**-1.78**	0.00
1442470_at			Mm.172615.1	5.2	4.4	**-1.78**	0.00
1443305_at	Gm3134	predicted gene 3134	Mm.212496.1	4.1	3.3	**-1.78**	0.02
1455091_at	Ppp2r3a	protein phosphatase 2, regulatory subunit B'', alpha	Mm.28416.1	6.5	5.7	**-1.78**	0.00
1457486_at			Mm.218159.1	8.7	7.8	**-1.78**	0.02
1417042_at	Slc37a4	solute carrier family 37 (glucose-6-phosphate transporter), member 4	Mm.30087.1	11.7	10.9	**-1.79**	0.01
1429057_at	Naa16	N(alpha)-acetyltransferase 16, NatA auxiliary subunit	Mm.24425.1	7.4	6.6	**-1.79**	0.00
1429332_at	4632427E13Rik	RIKEN cDNA 4632427E13 gene	Mm.45354.1	6.0	5.2	**-1.79**	0.00
1437354_at	C230091D08Rik	RIKEN cDNA C230091D08 gene	Mm.132544.3	7.7	6.8	**-1.79**	0.00
1439795_at	Gpr64	G protein-coupled receptor 64	Mm.31520.1	4.6	3.8	**-1.79**	0.04
1442525_at	Ccdc47	coiled-coil domain containing 47	Mm.101379.1	5.6	4.7	**-1.79**	0.00
1443872_at			Mm.41941.1	7.0	6.2	**-1.79**	0.00
1448385_at	Slc15a4	solute carrier family 15, member 4	Mm.28506.1	9.2	8.3	**-1.79**	0.01
1453385_at	Xiap	X-linked inhibitor of apoptosis	Mm.57689.1	5.1	4.3	**-1.79**	0.01

Supplemental Table 9. Significant differently expressed genes in 3bKI HCC samples

Affymetrix ID	Gene Symbol	Description	Transcript ID (Array Design)	3aKO avg signal log2 (n=4)	3bKI Avg Signal log2 (n=5)	Fold Change (linear)	ANOVA p-value
1456611_at	Fam13a	family with sequence similarity 13, member A	Mm.28813.1	8.3	7.4	**-1.79**	0.01
1457367_at			Mm.128883.1	6.5	5.7	**-1.79**	0.00
1457672_at	Chd9	chromodomain helicase DNA binding protein 9	Mm.100615.1	7.5	6.6	**-1.79**	0.00
1416193_at	Car1	carbonic anhydrase 1	Mm.3471.1	6.8	5.9	**-1.8**	0.02
1417600_at	Slc15a2	solute carrier family 15 (H+/peptide transporter), member 2	Mm.63479.1	8.1	7.2	**-1.8**	0.03
1418311_at	Fn3k	fructosamine 3 kinase	Mm.32787.1	7.8	6.9	**-1.8**	0.00
1420043_s_at	Thoc1	THO complex 1	Mm.202015.1	4.6	3.7	**-1.8**	0.01
1427480_at	Leap2	liver-expressed antimicrobial peptide 2	Mm.24283.1	11.3	10.5	**-1.8**	0.02
1433407_at	Mcm10	minichromosome maintenance deficient 10 (S. cerevisiae)	Mm.23828.1	6.3	5.4	**-1.8**	0.02
1433986_at	Smim13	small integral membrane protein 13	Mm.38578.1	9.0	8.2	**-1.8**	0.00
1438050_x_at	Gm9222	predicted gene 9222	Mm.212712.4	5.9	5.1	**-1.8**	0.00
1439988_at	Mrpl15	mitochondrial ribosomal protein L15	Mm.172125.1	7.3	6.4	**-1.8**	0.00
1451006_at	Xdh	xanthine dehydrogenase	Mm.11223.1	9.1	8.2	**-1.8**	0.04
1457175_at			Mm.100049.1	6.3	5.4	**-1.8**	0.00
1458099_at			Mm.214692.1	7.8	6.9	**-1.8**	0.02
1420451_at	Asic5	acid-sensing (proton-gated) ion channel family member 5	Mm.88839.1	6.2	5.4	**-1.81**	0.00
1421704_a_at	Pik3c2g	phosphatidylinositol 3-kinase, C2 domain containing, gamma polypeptide	Mm.10301.1	8.0	7.2	**-1.81**	0.00
1426706_s_at	Xylb	xylulokinase homolog (H. influenzae)	Mm.27002.1	10.1	9.2	**-1.81**	0.01
1428410_at	Naa50	N(alpha)-acetyltransferase 50, NatE catalytic subunit	Mm.28064.1	8.1	7.3	**-1.81**	0.00
1430220_at	4833420G17Rik	RIKEN cDNA 4833420G17 gene	Mm.170194.1	6.0	5.2	**-1.81**	0.00
1435462_at	Plcxd2	phosphatidylinositol-specific phospholipase C, X domain containing 2	Mm.41360.1	10.3	9.5	**-1.81**	0.01
1435470_at	1810015C11Rik	uncharacterized LOC101056118	Mm.102063.1	8.0	7.1	**-1.81**	0.01
1437791_s_at	Eml5	echinoderm microtubule associated protein like 5	Mm.25549.4	5.5	4.7	**-1.81**	0.00
1438279_at	Dpp4	dipeptidylpeptidase 4	Mm.132862.1	7.2	6.3	**-1.81**	0.00
1443049_at	Tmem19	transmembrane protein 19	Mm.215567.1	7.2	6.4	**-1.81**	0.03
1449214_a_at	Opa1	optic atrophy 1	Mm.31402.1	9.0	8.1	**-1.81**	0.00
1451762_a_at	Kif1b	kinesin family member 1B	Mm.42027.3	7.5	6.7	**-1.81**	0.02
1416419_s_at	Gabarapl1	gamma-aminobutyric acid (GABA) A receptor-associated protein-like 1	Mm.14638.1	12.8	12.0	**-1.82**	0.01
1416730_at	Rcl1	RNA terminal phosphate cyclase-like 1	Mm.28630.1	11.0	10.1	**-1.82**	0.00
1417067_s_at	Adck3	aarF domain containing kinase 3	Mm.28337.1	6.9	6.0	**-1.82**	0.00
1417280_at	Slc17a1	solute carrier family 17 (sodium phosphate), member 1	Mm.2656.1	8.6	7.8	**-1.82**	0.00

Supplemental Table 9. Significant differently expressed genes in 3bKI HCC samples

Affymetrix ID	Gene Symbol	Description	Transcript ID (Array Design)	3aKO avg signal log2 (n=4)	3bKI Avg Signal log2 (n=5)	Fold Change (linear)	ANOVA p-value
1419245_at	Rab14	RAB14, member RAS oncogene family	Mm.58771.1	5.5	4.6	**-1.82**	0.00
1420951_a_at	Son	Son DNA binding protein	Mm.46401.1	7.1	6.3	**-1.82**	0.00
1428651_at	Klhl24	kelch-like 24	Mm.181757.1	9.1	8.2	**-1.82**	0.00
1434977_at	Fam210a	family with sequence similarity 210, member A	Mm.171701.1	7.9	7.0	**-1.82**	0.00
1438450_at	Lin7a	lin-7 homolog A (C. elegans)	Mm.141274.1	7.7	6.9	**-1.82**	0.00
1441283_at		cyclin Y	Mm.37824.1	4.6	3.7	**-1.82**	0.00
1442815_at			Mm.33686.1	6.8	5.9	**-1.82**	0.00
1448185_at	Herpud1	homocysteine-inducible, endoplasmic reticulum stress-inducible, ubiquitin-like domain member 1	Mm.29151.1	12.1	11.2	**-1.82**	0.00
1449886_a_at	Timm9	translocase of inner mitochondrial membrane 9	Mm.28996.1	6.2	5.3	**-1.82**	0.03
1450816_at	Polg2	polymerase (DNA directed), gamma 2, accessory subunit	Mm.859.1	8.3	7.4	**-1.82**	0.00
1452831_s_at	Ppat	phosphoribosyl pyrophosphate amidotransferase	Mm.27743.1	7.8	6.9	**-1.82**	0.02
1453840_at	Pabpc1	poly(A) binding protein, cytoplasmic 1	Mm.2642.2	5.9	5.0	**-1.82**	0.00
1457999_at	Rmdn1	regulator of microtubule dynamics 1	Mm.168010.2	7.9	7.1	**-1.82**	0.00
1458913_at	4831440E17Rik	RIKEN cDNA 4831440E17 gene	Mm.156689.1	4.8	3.9	**-1.82**	0.00
1440658_at	Ammecr1l	AMME chromosomal region gene 1-like	Mm.138551.1	6.2	5.3	**-1.83**	0.01
1447854_s_at	Hist2h2be	histone cluster 2, H2be	Mm.200193.1	4.5	3.7	**-1.83**	0.02
1459957_at			Mm.102973.1	6.7	5.8	**-1.83**	0.00
1419093_at	Tdo2	tryptophan 2,3-dioxygenase	Mm.21545.1	13.3	12.4	**-1.84**	0.00
1419367_at	Decr1	2,4-dienoyl CoA reductase 1, mitochondrial	Mm.24395.1	12.2	11.3	**-1.84**	0.04
1424744_at	Sds	serine dehydratase	Mm.28685.1	11.7	10.9	**-1.84**	0.01
1434480_at	Pdpr	pyruvate dehydrogenase phosphatase regulatory subunit	Mm.28350.1	7.6	6.7	**-1.84**	0.00
1435452_at	Slc35g1	solute carrier family 35, member G1	Mm.123755.1	8.9	8.1	**-1.84**	0.00
1446990_at	Nfia	nuclear factor I/A	Mm.103170.1	8.4	7.6	**-1.84**	0.00
1421026_at	Gna12	guanine nucleotide binding protein, alpha 12	Mm.140610.1	8.3	7.5	**-1.85**	0.01
1422648_at	Slc7a2	solute carrier family 7 (cationic amino acid transporter, y+ system), member 2	Mm.4676.1	9.2	8.4	**-1.85**	0.01
1425033_at	Slc17a2	solute carrier family 17 (sodium phosphate), member 2	Mm.24030.1	11.6	10.7	**-1.85**	0.01
1431174_at	A930036K24Rik		Mm.134224.1	8.6	7.7	**-1.85**	0.02
1435334_at	Ttc7	tetratricopeptide repeat domain 7	Mm.77396.2	8.9	8.0	**-1.85**	0.00
1441988_at	Ppm1k	protein phosphatase 1K (PP2C domain containing)	Mm.216238.1	8.9	8.0	**-1.85**	0.01
1442169_at	Vldlr	very low density lipoprotein receptor	Mm.202246.1	6.4	5.5	**-1.85**	0.02

Supplemental Table 9. Significant differently expressed genes in 3bKI HCC samples

Affymetrix ID	Gene Symbol	Description	Transcript ID (Array Design)	3aKO avg signal log2 (n=4)	3bKI Avg Signal log2 (n=5)	Fold Change (linear)	ANOVA p-value
1444458_at			Mm.80567.1	7.4	6.5	**-1.85**	0.00
1420118_s_at			Mm.221024.1	7.3	6.4	**-1.86**	0.00
1433545_s_at	Acad11	acyl-Coenzyme A dehydrogenase family, member 11	Mm.41274.4	11.9	11.0	**-1.86**	0.01
1439079_a_at	Erbb2ip	Erbb2 interacting protein	Mm.27107.3	7.0	6.1	**-1.86**	0.00
1440899_at	Fmo5	flavin containing monooxygenase 5	Mm.89547.1	9.9	9.0	**-1.86**	0.02
1447811_s_at	Amigo1	adhesion molecule with Ig like domain 1	Mm.44915.2	6.2	5.3	**-1.86**	0.00
1454801_at	Ankrd28		Mm.7463.1	8.1	7.2	**-1.86**	0.00
1455381_at	Marf1	meiosis arrest female 1	Mm.85442.1	8.3	7.4	**-1.86**	0.00
1425559_a_at	Acsm3	acyl-CoA synthetase medium-chain family member 3	Mm.9821.2	9.9	9.0	**-1.87**	0.01
1430410_at	1810019N24Rik	RIKEN cDNA 1810019N24 gene	Mm.158236.1	5.0	4.1	**-1.87**	0.00
1441022_at	Arih1	ariadne ubiquitin-conjugating enzyme E2 binding protein homolog 1 (Drosophila)	Mm.126328.1	6.0	5.1	**-1.87**	0.00
1444080_at	Nav2	neuron navigator 2	Mm.101203.1	6.3	5.4	**-1.87**	0.00
1449292_at	Rb1cc1	RB1-inducible coiled-coil 1	Mm.141567.1	5.8	4.9	**-1.87**	0.00
1449668_s_at	Fnip1	folliculin interacting protein 1	Mm.203784.1	7.9	7.0	**-1.87**	0.01
1450896_at	Arhgap5		Mm.35059.1	5.6	4.7	**-1.87**	0.00
1458491_at	Zfp949	zinc finger protein 949	Mm.101162.1	7.0	6.1	**-1.87**	0.00
1459463_at			Mm.207860.1	4.3	3.4	**-1.87**	0.01
1436326_at	Rora	RAR-related orphan receptor alpha	Mm.88712.1	8.0	7.1	**-1.88**	0.01
1439024_at	Bag4	BCL2-associated athanogene 4	Mm.35264.1	9.2	8.3	**-1.88**	0.01
1443949_at			Mm.24932.1	6.9	6.0	**-1.88**	0.01
1455961_at		membrane metallo endopeptidase	Mm.13052.2	8.0	7.1	**-1.88**	0.00
1457458_at	Zc3h4	zinc finger CCCH-type containing 4	Mm.164114.1	5.5	4.6	**-1.88**	0.01
1429299_at	Ddah1	dimethylarginine dimethylaminohydrolase 1	Mm.30203.1	9.5	8.6	**-1.89**	0.03
1429899_at	5730414N17Rik	RIKEN cDNA 5730414N17 gene	Mm.112365.1	7.3	6.4	**-1.89**	0.01
1434100_x_at	Ppargc1a	peroxisome proliferative activated receptor, gamma, coactivator 1 alpha	Mm.35687.3	5.2	4.2	**-1.89**	0.00
1434515_at	Ncoa1	nuclear receptor coactivator 1	Mm.2028.3	8.1	7.2	**-1.89**	0.01
1435836_at	Pdk1	pyruvate dehydrogenase kinase, isoenzyme 1	Mm.137538.1	8.6	7.7	**-1.89**	0.01
1438271_at	Lpp	LIM domain containing preferred translocation partner in lipoma	Mm.196783.1	8.2	7.3	**-1.89**	0.00
1455014_at	Gm20300	predicted gene, 20300	Mm.86217.1	8.9	7.9	**-1.89**	0.00
1459917_at	Ggnbp2	gametogenetin binding protein 2	Mm.25583.1	7.1	6.2	**-1.89**	0.00
1418138_at	Sult1d1	sulfotransferase family 1D, member 1	Mm.6824.1	9.6	8.6	**-1.9**	0.04
1451360_at	Ergic2	ERGIC and golgi 2	Mm.22179.1	5.9	4.9	**-1.9**	0.00
1455146_at	Strbp	spermatid perinuclear RNA binding protein	Mm.40554.1	6.0	5.1	**-1.9**	0.01
1416739_a_at	Brap	BRCA1 associated protein	Mm.153372.1	8.1	7.2	**-1.91**	0.01
1425362_at	Agfg2	ArfGAP with FG repeats 2	Mm.35097.1	7.4	6.5	**-1.91**	0.00

Supplemental Table 9. Significant differently expressed genes in 3bKI HCC samples

Affymetrix ID	Gene Symbol	Description	Transcript ID (Array Design)	3aKO avg signal log2 (n=4)	3bKI Avg Signal log2 (n=5)	Fold Change (linear)	ANOVA p-value
1428414_at	Ccny	cyclin Y	Mm.41707.1	3.8	2.9	**-1.91**	0.00
1424585_at	Ranbp10	RAN binding protein 10	Mm.4206.1	8.9	8.0	**-1.92**	0.05
1427037_at	Eif4g1	eukaryotic translation initiation factor 4, gamma 1	Mm.219670.1	9.2	8.2	**-1.92**	0.00
1429096_at	2810455D13Rik	RIKEN cDNA 2810455D13 gene	Mm.64974.1	5.6	4.6	**-1.92**	0.00
1433784_at	Zfp871	zinc finger protein 871	Mm.22459.1	9.5	8.6	**-1.92**	0.00
1433819_s_at	Agpat3	1-acylglycerol-3-phosphate O-acyltransferase 3	Mm.86311.1	8.8	7.9	**-1.92**	0.02
1435691_at	Agphd1	hydroxylysine kinase 1	Mm.123952.1	10.0	9.1	**-1.92**	0.02
1456533_at	Dpy19l1	dpy-19-like 1 (C. elegans)	Mm.191939.1	8.0	7.0	**-1.92**	0.01
1458125_at			Mm.217603.1	6.4	5.5	**-1.92**	0.00
1458134_at			Mm.212355.1	7.1	6.1	**-1.92**	0.00
1460256_at	Car3	carbonic anhydrase 3	Mm.300.1	14.0	13.0	**-1.92**	0.02
1421040_a_at	Gsta2	glutathione S-transferase, alpha 2 (Yc2)	Mm.197422.1	9.9	9.0	**-1.93**	0.05
1424858_at	L2hgdh	L-2-hydroxyglutarate dehydrogenase	Mm.103362.1	9.3	8.4	**-1.93**	0.00
1427191_at	Npr2	natriuretic peptide receptor 2	Mm.103477.1	10.0	9.0	**-1.93**	0.02
1427798_x_at			Mm.214467.1	5.6	4.7	**-1.93**	0.03
1429166_s_at	Clmn	calmin	Mm.38859.1	8.4	7.5	**-1.93**	0.00
1435781_at	Cand1	cullin associated and neddylation disassociated 1	Mm.66300.1	6.7	5.7	**-1.93**	0.00
1441547_at			Mm.89160.1	7.0	6.1	**-1.93**	0.02
1452333_at	Smarca2	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2	Mm.12184.2	8.5	7.5	**-1.93**	0.00
1453186_at	Sfrs18	PNN interacting serine/arginine-rich	Mm.100117.1	7.2	6.3	**-1.93**	0.01
1453319_at	Ccar1	cell division cycle and apoptosis regulator 1	Mm.196371.1	3.7	2.7	**-1.93**	0.00
1424584_a_at	Ranbp10	RAN binding protein 10	Mm.4206.1	10.1	9.1	**-1.94**	0.04
1453692_at	4930581F22Rik	RIKEN cDNA 4930581F22 gene	Mm.160157.1	7.5	6.5	**-1.94**	0.00
1455770_at	Tdo2	tryptophan 2,3-dioxygenase	Mm.30146.1	11.1	10.1	**-1.94**	0.00
1438244_at	Nfib	nuclear factor I/B	Mm.4025.4	7.0	6.1	**-1.95**	0.00
1439590_at	Xkr8	X Kell blood group precursor related family member 8 homolog	Mm.44558.1	5.9	4.9	**-1.95**	0.01
1456822_at	Rad23b	RAD23b homolog (S. cerevisiae)	Mm.210247.1	5.2	4.2	**-1.95**	0.01
1431175_at	1810019D21Rik	RIKEN cDNA 1810019D21 gene	Mm.183003.1	9.6	8.6	**-1.96**	0.00
1433855_at	Abat	4-aminobutyrate aminotransferase	Mm.1348.2	11.8	10.9	**-1.96**	0.00
1434133_s_at	Dcaf8	DDB1 and CUL4 associated factor 8	Mm.196080.1	8.1	7.1	**-1.96**	0.00
1416383_a_at	Pcx	pyruvate carboxylase	Mm.1845.1	12.0	11.0	**-1.97**	0.00
1423963_at	Wdr26	WD repeat domain 26	Mm.21126.1	7.3	6.4	**-1.97**	0.00
1435074_at	Tmem106b	transmembrane protein 106B	Mm.27742.1	12.1	11.1	**-1.97**	0.00
1440799_s_at	Farp2	FERM, RhoGEF and pleckstrin domain protein 2	Mm.200915.1	7.3	6.4	**-1.97**	0.00
1452914_at	N4bp2l1	NEDD4 binding protein 2-like 1	Mm.220888.1	9.3	8.3	**-1.97**	0.02

Supplemental Table 9. Significant differently expressed genes in 3bKI HCC samples

Affymetrix ID	Gene Symbol	Description	Transcript ID (Array Design)	3aKO avg signal log2 (n=4)	3bKI Avg Signal log2 (n=5)	Fold Change (linear)	ANOVA p-value
1455901_at	Chpt1	choline phosphotransferase 1	Mm.21754.4	7.5	6.5	**-1.97**	0.03
1459302_at	A030007N12Rik	RIKEN cDNA A030007N12 gene	Mm.207475.1	4.5	3.5	**-1.97**	0.00
1416178_a_at	Plekhb1	pleckstrin homology domain containing, family B (evectins) member 1	Mm.26633.1	9.6	8.6	**-1.98**	0.02
1418013_at	Cml1	camello-like 1	Mm.13036.1	11.2	10.2	**-1.98**	0.02
1421456_at	P2ry1	purinergic receptor P2Y, G-protein coupled 1	Mm.3556.1	7.1	6.1	**-1.98**	0.00
1427945_at	Dpyd	dihydropyrimidine dehydrogenase	Mm.27907.1	10.1	9.1	**-1.98**	0.01
1439331_at	4932439E07Rik	RIKEN cDNA 4932439E07 gene	Mm.43978.1	6.1	5.1	**-1.98**	0.01
1446675_at	Adk	adenosine kinase	Mm.221040.1	7.5	6.5	**-1.98**	0.00
1449316_at	Cyp4f15	cytochrome P450, family 4, subfamily f, polypeptide 15	Mm.26539.1	11.3	10.3	**-1.98**	0.00
1449462_at	Pbld2	phenazine biosynthesis-like protein domain containing 2	Mm.24795.1	10.2	9.2	**-1.98**	0.01
1457279_at	Gm17586	predicted gene, 17586	Mm.139237.1	6.2	5.2	**-1.98**	0.01
1418519_at	Aadat	aminoadipate aminotransferase	Mm.35020.1	11.1	10.1	**-1.99**	0.02
1419924_at	Fnip1	folliculin interacting protein 1	Mm.203784.1	6.5	5.5	**-1.99**	0.01
1420772_a_at	Tsc22d3	TSC22 domain family, member 3	Mm.22216.1	9.7	8.7	**-1.99**	0.01
1428111_at	Slc38a4	solute carrier family 38, member 4	Mm.22260.1	11.4	10.4	**-1.99**	0.00
1442593_at			Mm.103073.1	7.2	6.2	**-1.99**	0.00
1443516_at	Atxn2	ataxin 2	Mm.152851.1	7.4	6.4	**-1.99**	0.00
1418649_at	Egln3	egl-9 family hypoxia-inducible factor 3	Mm.33484.1	8.1	7.1	**-2**	0.03
1424973_at	Cyp3a25	cytochrome P450, family 3, subfamily a, polypeptide 25	Mm.26993.1	13.2	12.2	**-2**	0.01
1427410_at	Dleu2	deleted in lymphocytic leukemia, 2	Mm.25679.1	8.0	7.0	**-2**	0.04
1443075_at			Mm.218689.1	4.7	3.7	**-2**	0.01
1431032_at	Agl	amylo-1,6-glucosidase, 4-alpha-glucanotransferase	Mm.17221.1	8.7	7.7	**-2.01**	0.00
1432916_at	5730407I07Rik	RIKEN cDNA 5730407I07 gene	Mm.158393.1	5.3	4.3	**-2.01**	0.00
1452989_at	2900009J20Rik		Mm.82240.1	6.9	5.9	**-2.01**	0.00
1435292_at	Tbc1d4	TBC1 domain family, member 4	Mm.27439.1	6.0	5.0	**-2.02**	0.00
1443056_at			Mm.167541.1	7.2	6.2	**-2.02**	0.00
1428981_at	2810007J24Rik	RIKEN cDNA 2810007J24 gene	Mm.30070.1	12.8	11.8	**-2.03**	0.00
1439483_at	AI506816	expressed sequence AI506816	Mm.5399.1	7.4	6.4	**-2.03**	0.00
1440965_at	Pigl	phosphatidylinositol glycan anchor biosynthesis, class L	Mm.37323.1	8.0	6.9	**-2.03**	0.02
1435163_at	Zfp871	zinc finger protein 871	Mm.27433.1	7.7	6.7	**-2.04**	0.00
1447018_at	Gm12971	predicted gene 12971	Mm.182794.1	6.1	5.0	**-2.04**	0.00
1452828_at	Fbxo21	F-box protein 21	Mm.21912.1	10.0	9.0	**-2.04**	0.02
1454033_at	Pdilt	protein disulfide isomerase-like, testis expressed	Mm.84631.1	5.7	4.7	**-2.04**	0.03
1455418_at			Mm.138292.1	8.4	7.4	**-2.04**	0.00
1456599_at	Nxt2	nuclear transport factor 2-like export factor 2	Mm.41899.1	6.8	5.8	**-2.04**	0.01
1457817_at			Mm.86731.1	3.8	2.8	**-2.04**	0.00

Supplemental Table 9. Significant differently expressed genes in 3bKI HCC samples

Affymetrix ID	Gene Symbol	Description	Transcript ID (Array Design)	3aKO avg signal log2 (n=4)	3bKI Avg Signal log2 (n=5)	Fold Change (linear)	ANOVA p-value
1416946_a_at	Acaa1a	acetyl-Coenzyme A acyltransferase 1A; acetyl-Coenzyme A acyltransferase 1B	Mm.205266.1	12.2	11.2	**-2.05**	0.03
1419407_at	Hc	hemolytic complement	Mm.2168.1	12.0	11.0	**-2.05**	0.02
1425281_a_at	Tsc22d3	TSC22 domain family, member 3	Mm.22216.2	9.4	8.4	**-2.05**	0.01
1430177_at	Ube2b	ubiquitin-conjugating enzyme E2B	Mm.158142.1	6.6	5.5	**-2.05**	0.00
1443353_at			Mm.207472.1	7.2	6.2	**-2.05**	0.00
1445574_at			Mm.25466.1	7.1	6.1	**-2.05**	0.00
1449040_a_at	Sephs2	selenophosphate synthetase 2	Mm.20294.1	12.4	11.4	**-2.05**	0.00
1454617_at	Arrdc3	arrestin domain containing 3	Mm.34385.1	9.8	8.8	**-2.05**	0.04
1457732_at			Mm.36913.1	4.9	3.8	**-2.05**	0.00
1425981_a_at	Rbl2	retinoblastoma-like 2	Mm.28027.2	9.0	7.9	**-2.06**	0.00
1426782_at	Gpr125	G protein-coupled receptor 125	Mm.18062.1	9.3	8.3	**-2.06**	0.00
1431033_x_at	Agl	amylo-1,6-glucosidase, 4-alpha-glucanotransferase	Mm.17221.1	8.7	7.6	**-2.06**	0.00
1443923_at	Akap13	A kinase (PRKA) anchor protein 13	Mm.142922.1	7.0	6.0	**-2.06**	0.00
1420656_at	Abcg8	ATP-binding cassette, sub-family G (WHITE), member 8	Mm.26581.1	9.6	8.5	**-2.07**	0.03
1424451_at	Acaa1b	acetyl-Coenzyme A acyltransferase 1B	Mm.205266.2	13.9	12.8	**-2.07**	0.02
1436276_at			Mm.102310.1	6.4	5.3	**-2.07**	0.00
1445676_at			Mm.156700.1	5.6	4.6	**-2.07**	0.01
1449375_at	Ces2a	carboxylesterase 2A	Mm.212983.1	12.3	11.2	**-2.07**	0.02
1456257_at	Fam126b	family with sequence similarity 126, member B	Mm.26272.1	8.0	7.0	**-2.07**	0.00
1416947_s_at	Acaa1a	acetyl-Coenzyme A acyltransferase 1A; acetyl-Coenzyme A acyltransferase 1B	Mm.205266.1	13.9	12.8	**-2.08**	0.01
1441789_at			Mm.164973.1	4.1	3.0	**-2.08**	0.00
1443137_at			Mm.187830.1	4.8	3.7	**-2.08**	0.02
1457263_at			Mm.27508.1	12.3	11.2	**-2.08**	0.00
1427411_s_at	Dleu2	deleted in lymphocytic leukemia, 2	Mm.25679.1	7.1	6.1	**-2.1**	0.05
1435333_at	Ndufaf4	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, assembly factor 4	Mm.28983.2	8.8	7.8	**-2.1**	0.01
1444622_at			Mm.202462.1	5.8	4.7	**-2.1**	0.03
1452889_at	Lhpp	phospholysine phosphohistidine inorganic pyrophosphate phosphatase	Mm.18775.1	10.0	8.9	**-2.1**	0.03
1416738_at	Brap	BRCA1 associated protein	Mm.153372.1	9.8	8.7	**-2.11**	0.01
1429510_at	2810410L24Rik	RIKEN cDNA 2810410L24 gene	Mm.51309.1	6.6	5.5	**-2.11**	0.01
1433944_at	Hectd2	HECT domain containing 2	Mm.61107.1	3.9	2.9	**-2.11**	0.02
1434390_at	AI503316	expressed sequence AI503316; heterogeneous nuclear ribonucleoprotein U	Mm.28927.2	8.0	6.9	**-2.11**	0.00
1455918_at	Adrb3	adrenergic receptor, beta 3	Mm.212992.1	5.8	4.7	**-2.11**	0.02
1442349_at	Agphd1	hydroxylysine kinase 1	Mm.216628.1	7.5	6.4	**-2.12**	0.01

Supplemental Table 9. Significant differently expressed genes in 3bKI HCC samples

Affymetrix ID	Gene Symbol	Description	Transcript ID (Array Design)	3aKO avg signal log2 (n=4)	3bKI Avg Signal log2 (n=5)	Fold Change (linear)	ANOVA p-value
1459274_at	Gpr135	G protein-coupled receptor 135	Mm.214523.1	5.0	3.9	**-2.12**	0.04
1459804_at	Crebbp	CREB binding protein	Mm.132238.1	5.3	4.3	**-2.12**	0.00
1421041_s_at	Gm3776	predicted gene 3776; glutathione S-transferase, alpha 1 (Ya); glutathione S-transferase, alpha 2 (Yc2)	Mm.197422.1	9.8	8.7	**-2.13**	0.04
1417532_at	Cyp2j5	cytochrome P450, family 2, subfamily j, polypeptide 5	Mm.12838.1	10.3	9.2	**-2.14**	0.00
1419687_at	Macrod1	MACRO domain containing 1	Mm.38346.1	10.0	8.9	**-2.14**	0.00
1425631_at	Ppp1r3c	protein phosphatase 1, regulatory (inhibitor) subunit 3C	Mm.24724.1	8.4	7.3	**-2.14**	0.01
1427177_at	Fyco1	FYVE and coiled-coil domain containing 1	Mm.204793.1	8.7	7.6	**-2.14**	0.00
1427982_s_at	Syne2	spectrin repeat containing, nuclear envelope 2	Mm.26652.1	6.8	5.7	**-2.14**	0.00
1422135_at	Zfp146	zinc finger protein OZF-like	Mm.42054.1	5.5	4.4	**-2.15**	0.00
1445065_at			Mm.217125.1	6.3	5.2	**-2.15**	0.00
1426243_at	Cth	cystathionase (cystathionine gamma-lyase)	Mm.28301.1	11.9	10.8	**-2.16**	0.01
1427974_s_at	Cacna1d	calcium channel, voltage-dependent, L type, alpha 1D subunit	Mm.9772.1	6.0	4.9	**-2.16**	0.00
1438130_at	Taf15	TAF15 RNA polymerase II, TATA box binding protein (TBP)-associated factor	Mm.144060.1	5.8	4.7	**-2.16**	0.00
1451156_s_at	Vldlr	very low density lipoprotein receptor	Mm.4141.2	5.4	4.3	**-2.16**	0.01
1451373_at	Ugt3a1	UDP glycosyltransferases 3 family, polypeptide A1	Mm.201628.1	10.7	9.6	**-2.16**	0.01
1434906_at	0610005C13Rik	RIKEN cDNA 0610005C13 gene	Mm.200459.1	11.3	10.2	**-2.17**	0.00
1458208_s_at	Mccc1	methylcrotonoyl-Coenzyme A carboxylase 1 (alpha)	Mm.211374.1	6.1	5.0	**-2.17**	0.02
1418146_a_at	Rbl2	retinoblastoma-like 2	Mm.28027.1	8.2	7.1	**-2.18**	0.00
1450643_s_at	Acsl1	acyl-CoA synthetase long-chain family member 1	Mm.28962.1	12.4	11.2	**-2.18**	0.00
1447227_at			Mm.89658.1	7.8	6.6	**-2.2**	0.03
1419946_s_at	Rab2a	RAB2A, member RAS oncogene family	Mm.206835.1	6.3	5.2	**-2.21**	0.00
1436317_at	Pgap1	post-GPI attachment to proteins 1	Mm.103539.1	7.4	6.3	**-2.21**	0.00
1430893_at	Mup10	major urinary protein 10	Mm.196051.1	12.2	11.1	**-2.22**	0.03
1431805_a_at	Rhpn2	rhophilin, Rho GTPase binding protein 2	Mm.35465.1	6.5	5.3	**-2.22**	0.00
1443053_at			Mm.136244.1	5.0	3.9	**-2.22**	0.02
1448499_a_at	Ephx2	epoxide hydrolase 2, cytoplasmic	Mm.15295.1	12.5	11.3	**-2.22**	0.03
1453487_at	Dhdh	dihydrodiol dehydrogenase (dimeric)	Mm.34208.1	8.8	7.7	**-2.22**	0.00
1421183_at	Tex12	testis expressed gene 12	Mm.78133.1	6.5	5.4	**-2.24**	0.00
1424182_at	Acat1	acetyl-Coenzyme A acetyltransferase 1	Mm.219649.1	10.4	9.2	**-2.25**	0.03

Supplemental Table 9. Significant differently expressed genes in 3bKI HCC samples

Affymetrix ID	Gene Symbol	Description	Transcript ID (Array Design)	3aKO avg signal log2 (n=4)	3bKI Avg Signal log2 (n=5)	Fold Change (linear)	ANOVA p-value
1424493_s_at	Ugt3a1	UDP glycosyltransferases 3 family, polypeptide A1	Mm.201628.1	10.3	9.2	**-2.25**	0.01
1424657_at	Taok1	TAO kinase 1	Mm.24585.1	9.1	8.0	**-2.25**	0.00
1438596_at	1500017E21Rik	RIKEN cDNA 1500017E21 gene	Mm.61107.2	4.0	2.9	**-2.25**	0.02
1422565_s_at	Nfic	nuclear factor I/C	Mm.5104.1	7.0	5.8	**-2.27**	0.00
1433691_at	Ppp1r3c	protein phosphatase 1, regulatory (inhibitor) subunit 3C	Mm.24724.2	10.7	9.5	**-2.28**	0.01
1435446_a_at	Chpt1	choline phosphotransferase 1	Mm.21754.3	10.6	9.4	**-2.28**	0.02
1419510_at	Ces1e	carboxylesterase 1E	Mm.63490.1	10.2	9.0	**-2.29**	0.03
1419906_at	Hpgd	hydroxyprostaglandin dehydrogenase 15 (NAD)	Mm.199536.1	8.8	7.6	**-2.3**	0.02
1436555_at	Slc7a2	solute carrier family 7 (cationic amino acid transporter, y+ system), member 2	Mm.16796.1	11.6	10.4	**-2.3**	0.00
1418051_at	Ephb6	Eph receptor B6	Mm.1480.1	5.6	4.4	**-2.31**	0.00
1448491_at	Ech1	enoyl coenzyme A hydratase 1, peroxisomal	Mm.2112.1	12.7	11.5	**-2.31**	0.03
1449298_a_at	Pde1a	phosphodiesterase 1A, calmodulin-dependent	Mm.40678.1	6.6	5.3	**-2.31**	0.03
1418697_at	Inmt	indolethylamine N-methyltransferase	Mm.299.1	12.8	11.5	**-2.33**	0.02
1422526_at	Acsl1	acyl-CoA synthetase long-chain family member 1	Mm.28962.1	12.0	10.8	**-2.33**	0.00
1435349_at	Nrp2	neuropilin 2	Mm.37629.1	8.4	7.1	**-2.33**	0.00
1441498_at			Mm.102808.1	7.0	5.8	**-2.34**	0.00
1445188_at			Mm.173907.1	3.4	2.2	**-2.34**	0.00
1458007_at	Myo1b	myosin IB	Mm.93416.1	4.9	3.6	**-2.35**	0.00
1427285_s_at	Malat1	metastasis associated lung adenocarcinoma transcript 1 (non-coding RNA)	Mm.220932.1	8.1	6.9	**-2.37**	0.00
1457284_at			Mm.45553.1	5.0	3.7	**-2.37**	0.00
1428832_at	1600002H07Rik	RIKEN cDNA 1600002H07 gene	Mm.23881.1	8.7	7.5	**-2.38**	0.03
1446742_at			Mm.209315.1	4.0	2.8	**-2.38**	0.00
1417629_at	Prodh	proline dehydrogenase	Mm.28456.1	11.2	9.9	**-2.39**	0.02
1457554_at	Apob	apolipoprotein B	Mm.214778.1	11.5	10.3	**-2.39**	0.00
1427371_at	Abca8a	ATP-binding cassette, sub-family A (ABC1), member 8a	Mm.138955.1	10.9	9.6	**-2.41**	0.00
1446797_at	A330075M08Ril	RIKEN cDNA A330075M08 gene	Mm.210056.1	4.6	3.3	**-2.41**	0.00
1455454_at	Akr1c19	aldo-keto reductase family 1, member C19	Mm.22832.1	8.5	7.2	**-2.42**	0.01
1428636_at	Steap2	six transmembrane epithelial antigen of prostate 2	Mm.41944.1	6.1	4.9	**-2.43**	0.00
1434465_x_at	Vldlr	very low density lipoprotein receptor	Mm.4141.3	8.1	6.8	**-2.43**	0.03
1439920_at			Mm.174409.1	5.6	4.4	**-2.44**	0.00
1445506_at	Abhd15	abhydrolase domain containing 15	Mm.122731.1	4.5	3.3	**-2.45**	0.00
1457150_at	AI428301	expressed sequence AI428301	Mm.31702.1	5.6	4.3	**-2.45**	0.00

Supplemental Table 9. Significant differently expressed genes in 3bKI HCC samples

Affymetrix ID	Gene Symbol	Description	Transcript ID (Array Design)	3aKO avg signal log2 (n=4)	3bKI Avg Signal log2 (n=5)	Fold Change (linear)	ANOVA p-value
1457262_at	Smg1	SMG1 homolog, phosphatidylinositol 3-kinase-related kinase (C. elegans)	Mm.110251.1	7.2	5.9	**-2.45**	0.00
1431916_at	Hsd3b3	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 3	Mm.158717.1	9.6	8.3	**-2.46**	0.02
1449001_at	Ivd	isovaleryl coenzyme A dehydrogenase	Mm.6635.1	10.1	8.8	**-2.47**	0.00
1419144_at	Cd163	CD163 antigen	Mm.30679.1	6.4	5.0	**-2.48**	0.02
1424608_a_at	Bzw2	basic leucine zipper and W2 domains 2; predicted gene 4354; predicted gene 5589	Mm.182434.2	8.6	7.2	**-2.51**	0.02
1440351_at			Mm.102770.1	6.2	4.9	**-2.51**	0.00
1455457_at	Cyp2c54	cytochrome P450, family 2, subfamily c, polypeptide 54	Mm.220317.2	12.2	10.8	**-2.51**	0.04
1426146_a_at	Chpt1	choline phosphotransferase 1	Mm.21754.1	9.8	8.5	**-2.52**	0.02
1431833_a_at	Hmgcs2	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2	Mm.10633.2	12.4	11.1	**-2.53**	0.03
1452913_at	Pcp4l1	Purkinje cell protein 4-like 1	Mm.28040.1	7.7	6.3	**-2.53**	0.01
1455267_at	Esrrg	estrogen-related receptor gamma	Mm.23206.1	7.1	5.8	**-2.55**	0.05
1435870_at	Chpt1	choline phosphotransferase 1	Mm.148209.2	8.1	6.8	**-2.57**	0.01
1428663_at	Sgms2	sphingomyelin synthase 2	Mm.35676.1	9.2	7.8	**-2.59**	0.01
1457915_at	Mettl20	methyltransferase like 20	Mm.66631.1	7.1	5.7	**-2.61**	0.02
1455593_at	Apob	apolipoprotein B	Mm.29123.1	13.1	11.7	**-2.64**	0.00
1423867_at	Serpina3k	serine (or cysteine) peptidase inhibitor, clade A, member 3K	Mm.196242.1	11.4	10.0	**-2.65**	0.00
1440624_at			Mm.214662.1	5.6	4.2	**-2.71**	0.00
1456048_at	Cpeb3	cytoplasmic polyadenylation element binding protein 3	Mm.203968.4	6.8	5.4	**-2.72**	0.00
1421212_at	Abcc6	ATP-binding cassette, sub-family C (CFTR/MRP), member 6	Mm.63514.1	10.2	8.7	**-2.75**	0.00
1456120_at	Secisbp2l	SECIS binding protein 2-like	Mm.183116.2	7.9	6.4	**-2.78**	0.00
1450703_at	Slc7a2	solute carrier family 7 (cationic amino acid transporter, y+ system), member 2	Mm.4676.1	7.8	6.3	**-2.81**	0.00
1437798_at	6720422M22Rik	RIKEN cDNA 6720422M22 gene	Mm.23277.1	4.9	3.4	**-2.89**	0.04
1453220_at	Nxpe2	neurexophilin and PC-esterase domain family, member 2	Mm.31626.1	7.4	5.9	**-2.9**	0.03
1438258_at	Vldlr	very low density lipoprotein receptor	Mm.38836.1	7.1	5.6	**-2.91**	0.01
1427202_at	Mettl20	methyltransferase like 20	Mm.1043.1	9.4	7.8	**-2.92**	0.01
1431817_at	Adh6-ps1	alcohol dehydrogenase 6 (class V), pseudogene 1	Mm.158750.1	5.2	3.7	**-2.94**	0.02
1429809_at	Tmtc2	transmembrane and tetratricopeptide repeat containing 2	Mm.37266.1	6.5	4.9	**-2.96**	0.00
1452569_at	Slco1b2	solute carrier organic anion transporter family, member 1b2	Mm.24074.2	7.3	5.7	**-3.03**	0.00
1435893_at	Vldlr	very low density lipoprotein receptor	Mm.32795.1	7.0	5.4	**-3.08**	0.01

Supplemental Table 9. Significant differently expressed genes in 3bKI HCC samples

Affymetrix ID	Gene Symbol	Description	Transcript ID (Array Design)	3aKO avg signal log2 (n=4)	3bKI Avg Signal log2 (n=5)	Fold Change (linear)	ANOVA p-value
1457156_at	Trhde	TRH-degrading enzyme	Mm.131457.1	4.4	2.8	**-3.12**	0.03
1428988_at	Abcc3	ATP-binding cassette, sub-family C (CFTR/MRP), member 3	Mm.23942.1	10.4	8.7	**-3.14**	0.01
1427797_s_at	Ctse	cathepsin E	Mm.214467.1	9.4	7.7	**-3.15**	0.01
1416147_at	Hspa4	heat shock protein 4	Mm.1032.1	8.2	6.6	**-3.17**	0.00
1424159_at	Fam134c	family with sequence similarity 134, member C	Mm.33881.1	9.2	7.4	**-3.34**	0.00
1444552_at			Mm.218148.1	6.7	4.9	**-3.47**	0.00
1417900_a_at	Vldlr	very low density lipoprotein receptor	Mm.4141.1	7.6	5.7	**-3.64**	0.02
1429822_at	4633401B06Rik	RIKEN cDNA 4633401B06 gene	Mm.178280.1	8.2	6.3	**-3.66**	0.03
1416452_at	Oat	ornithine aminotransferase	Mm.13694.1	13.5	11.6	**-3.81**	0.01
1444691_at	Prkd3	protein kinase D3	Mm.211715.1	6.2	4.3	**-3.82**	0.01
1441430_at			Mm.44625.1	7.3	5.3	**-3.83**	0.00
1437213_at	Nudt21	nudix (nucleoside diphosphate linked moiety X)-type motif 21	Mm.35006.2	7.7	5.7	**-3.87**	0.00
1451787_at	Cyp2b10	cytochrome P450, family 2, subfamily b, polypeptide 10	Mm.14177.1	8.9	6.9	**-3.9**	0.01
1424715_at	Retsat	retinol saturase (all trans retinol 13,14 reductase)	Mm.27506.1	12.7	10.6	**-4.1**	0.02
1455966_s_at	Nudt21	nudix (nucleoside diphosphate linked moiety X)-type motif 21	Mm.35006.2	8.6	6.5	**-4.31**	0.00
1460258_at	Lect1	leukocyte cell derived chemotaxin 1	Mm.46561.1	7.5	5.2	**-4.77**	0.00
1424716_at	Retsat	retinol saturase (all trans retinol 13,14 reductase)	Mm.27506.1	10.5	8.3	**-4.8**	0.03
1459253_at	1700023H06Rik	RIKEN cDNA 1700023H06 gene	Mm.103191.1	6.7	4.5	**-4.85**	0.02
1428223_at	Mfsd2a	major facilitator superfamily domain containing 2A	Mm.38305.1	9.9	7.6	**-4.87**	0.04
1449065_at	Acot1	acyl-CoA thioesterase 1	Mm.1978.1	8.0	5.6	**-5.11**	0.04
1431406_at	Agxt2l1	ethanolamine phosphate phospholyase	Mm.219551.1	6.3	3.9	**-5.27**	0.01
1452730_at	Rps4y2	ribosomal protein S4-like	Mm.3572.1	7.9	5.3	**-5.83**	0.05
1452975_at	Agxt2l1	ethanolamine phosphate phospholyase	Mm.29125.1	10.9	8.3	**-5.9**	0.00
1453588_at	Car3	carbonic anhydrase 3	Mm.160284.1	6.0	3.0	**-7.97**	0.03
1425645_s_at	Cyp2b10	cytochrome P450, family 2, subfamily b, polypeptide 10	Mm.14177.1	9.0	5.9	**-8.72**	0.00
1422257_s_at	Cyp2b10	cytochrome P450, family 2, subfamily b, polypeptide 10	Mm.218749.1	8.6	5.3	**-9.85**	0.00
1460606_at	Hsd17b13	hydroxysteroid (17-beta) dehydrogenase 13	Mm.220914.1	10.1	6.7	**-10.58**	0.04
1430584_s_at	Car3	carbonic anhydrase 3	Mm.160284.1	10.8	7.1	**-12.58**	0.02

Supplemental Table 10. General IPA functions for genes altered in 1KI or 3bKI tumors

Category	Group	B-H p-value	Genes
Cancer	1KI tumor genes	1.72E-06	DUSP8,HDHD3,SEL1L3,LZTFL1,PPRC1,ADA,IFIT3,ANXA2,RPS6,HIBCH,RAD18,ALCAM,TSPYL4,TMEM43,UBE2C,SERPINB1,SETD7,ANKRD33B,HIST2H2BF,BEX4,LY6E,OTUD7B,OAS1,POLG2,Clca3a1/Clca3a2,SPATS2L,DDX60,SOX9,CTH,CSRP3,IDI1,CLDN7,CX3CR1,ZDHHC14,HMGCS2,ABCB11,JUND,TMEM45A,ELP4,MARCO,PBLD,H19,AURKA,AGXT,PIK3R3,IGF2,RPA3,GNS,E2F3,SIRT4,ARHGAP44,TNC,ALDH2,LEAP2,C16orf59,IGHM,HSPB6,HSPA4L,TIMP3,TACC3,PSRC1,N4BP2L1,Scd2,ZNF213,ALS2,BIRC5,TUBB6,CKS1B,MALAT1,DEPDC1B,CTGF,ZNF784,QKI,F2R,MKI67,HBA1/HBA2,CTSV,CCNG1,SLC5A1,RAB17,ACAD10,GSTK1,UGT3A1,SLC22A4,PGM3,CIB3,CKAP2,AGFG2,PLS1,FAHD2B,AKR1D1,PTGER2,FAM195A,LRP2BP,COL3A1,SQLE,HLA-A,PLAGL1,OXLD1,GNA14,JUN,CSF2RA,MTM1,SORBS2,SLC17A1,SMPD3,GBP3,BRAP,Casp12,MDM2,Cyp2c54 (includes others),Meg3,CDK1,SCAMP5,PTK6,CELF2,AMDHD1,IRAK4,TFF3,FAT1,UNC5B,PBK,SH3YL1,TBC1D4,SETD4,GPC1,FPGS,RPRD2,GZMA,SOX4,SLC6A8,ACSL3,GJA1,RPL12,AFP,TES,TMEM176A,ITIH5,CACNA2D1,Hbb-b2,PDLIM1,SYDE2,CYP4A11,FOXA3,HLA-E,SLC45A3,LYRM5,Ifi27l2a/Ifi27l2b,ERC2,BLNK,C5orf42,IFIT1B,SLC17A2,NAT2,KLB,ACAA2,Cyp2d13,ANGPTL4,UBE2U,EGLN3,CDCA5,IFRD1,MMP12,DBF4,COL5A2,UHRF1,SLC30A10,PHLDA3,PCOLCE2,BAX,IFI44,TSPAN8,EMP1,COL1A1,SDR42E1,PAPSS1,SLC1A2,NUCB2,TINAG,GLDC,PLET1,OSBPL3,FHOD3,DPYSL2,SPRR1A,EDA2R,SRL,IFIH1,ATP5SL,MADD,EGR2,PRSS8,CAV1,GOLT1B,ARHGAP12,AMACR,TP53INP1,CDCA8,MOSPD3,PYROXD2,ATL1,MTMR11,SLC13A4,GYPC,GGCX,OSGIN2,VLDLR,SMOC2,NDN,DDR1,AEN,CDH1,C5orf45,BTG2,UCK1,HHEX,CHRNA2,ALDH16A1,SAMD4A,NPDC1,RNF39,PHLDA2,OSGIN1,PGAP1,COL4A3,GDF15,FKBP7,SLC39A10,HTR1D,SEPT11,GAS2L3,PTGFRN,MYSM1,BICC1,NFE2L2,CYP51A1,FBXO21,DHX58,Rrbp1,NSDHL,CACNA1D,ENTPD1,NRP2,SPATA2L,VIM,SLC29A1,MFN1,CCNE1,SELM,SERPINH1,CDKN1A,XAF1,CHMP4C,SHMT1,PLEKHA1,PPARGC1A,DBNDD2,CAMK1D,SMC4,PARP12,SYNPO,ZNF248,RBP1,MYC,SHROOM3,B4GALNT1,RHOB,TMTC2,LECT1,CCDC149,CXCL14,LPL,LRP11,ARHGAP11A,MYEF2,TIA1,IL6R,BACE1,HELLS,SGK2,CYB561,CCNB1,IRF7,RFX4,ARHGEF16,CPT2,EPCAM,PDK2,TMEM176B,MAST2,ABI2,TMEM206,FRZB,AP4B1,CDC20,PDE1A,TMEM63A,RAD51,CCNA2,AHNAK,TMC7,STEAP2,NOP58,ADCK3,DECR2,SLC20A1,DPP4,SDC1,ADTRP,RANBP3L,PPL,SLC13A2,LARS2,KIFC3,PCCA,SCARA3,DLAT,LGALS3BP,AMIGO1,SPATS2,SKIL,IVD,ACSL1,GRIA3,MAF,NCMAP,CXCL10,SCNN1A,DYNLL1,SPTLC2,DDAH1,RDH16,PITPNB,FFAR4,INCA1,PEG3,TPD52,LONP2,SAMD9L,ZNF385B,RSPH3,ZAK,IFIT2,ENC1,MAP2K6,ALDH4A1,DECR1,CA14,WWTR1,DUSP6,CWF19L1,SYCP3,CAMK2N2,ARMCX4,OASL,CHEK1,LIPA,TRIB1,FSTL1,SEC61A1,TUBA8,ANXA5,CLMN,TOP2A,ACSL4,PARK2,PLAC8,DDX50,CDC6,RAD51B,ATXN2L,RETSAT,ASPA,GOLM1,KRT8,S100A9,PDIA6,HECTD3,PM20D1,COL4A4,TMEM184C,DYNLT1,C11orf86,NPNT,STMN1,ZNF750,DLST,POLK,ASGR2,GCH1,TMIE,SPP1,FGFR1,MACROD1,CCDC120,WDR33,BAG4,ACADS,PANK1,TTC39A,CEP55,AIFM3,PDGFA,EPHB6,COL1A2,HIST1H2BH,ZMAT3,SLC10A2,PLK2,HPGD,PHF21A,HMGCS1,KIAA1919,ATP6V0E2,DLGAP4,MIPEP,PDE9A,GRHL1,HUNK,HIVEP2,PBX3,EXOC4,TLR5,NLRP12,G6PC,EIF2AK2,P2RX7,LGALS1

Supplemental Table 10. General IPA functions for genes altered in 1KI or 3bKI tumors

Category	Group	B-H p-value	Genes
Cancer	3bKI tumor genes	6.48E-10	DUSP8,LRG1,CP,MPP4,AFMID,PRR16,ANXA2,CD300C,TMEM43,ACOT9,SLC10A1,ANKRD33B,TRHDE,ARRDC3,BEX4,LY6E,UBE3C,UTP20,CALML4,PRPF38B,MARCKSL1,HSD3B1,EPHX2,RGL3,CLDN7,F11,SV2A,TMED7,ABCB11,HOMER1,JUND,TMEM45A,CEACAM1,PBLD,SMG6,LCN2,HARS2,INMT,GUF1,FAAP20,IGF2,BRWD1,AGBL3,ALDH18A1,MLKL,MCCC2,RAB11FIP5,MRPL15,GPHN,MARVELD1,GID4,C16orf59,FXYD3,ZFC3H1,PDK1,LASP1,Slco1a1,HERPUD1,MPP1,TUBB6,SPARC,MEF2C,MALAT1,SIK3,CTGF,DDX25,ANKRD17,TAPT1,FNDC3B,TRIM6-TRIM34,UPB1,ABCC6,DNAJC28,LENG1,HOOK3,ZBTB20,LSS,DHDH,KLF12,HIPK1,ANKHD1/ANKHD1-EIF4EBP3,PABPC1,UGT3A1,PGM3,RRAS,ZNF236,ADRBK2,ZC3HAV1,HBEGF,SYNCRIP,AGFG2,PLS1,FAHD2B,IFITM3,ACAD11,EML5,UBR1,FBXO30,KIAA0368,RCAN3,COL3A1,SUSD2,RBM47,SERAC1,NQO2,ST6GALNAC4,PPM1K,TYW1,TOP2B,CADM2,RIF1,CELA2A,THOC1,SMPD3,XKR8,SLC25A13,BRAP,GPRIN3,B4GALT6,SOX6,NFIA,PLCXD2,PRPF19,FAM234B,DNAI1,NAA50,CCDC47,SLC15A2,ZFP2,FAM208A,TBC1D4,FAM49B,DHTKD1,DDI2,TFDP2,SLC6A8,MFSD2A,SEC14L3,COL4A1,BIRC6,AFP,SECISBP2L,GPR146,ZBTB44,MAP4K3,WHSC1L1,COL6A3,ATP6V1H,SYDE2,LYRM5,CRYZ,SLC17A2,ZNF394,DCAF8,ARHGAP42,RNPC3,THBS1,MARCH8,CYGB,KLHL24,HYAL1,PLEKHB1,HERC4,MARCH5,UBE3A,PPP1R3B,EMP1,COL1A1,PDILT,PAN3,TTC7A,PAPSS1,SLC25A32,PLET1,USP34,FHOD3,PIAS2,MYH9,ABAT,CYP4V2,SLC35C1,ZMYM5,RCL1,PLK4,ATP5SL,SNAI3,ANKRD28,MTX3,APCS,PRSS8,RNF217,CELA3B,ZKSCAN1,SLCO2B1,GREB1L,AMACR,PLD3,MTSS1,SPOPL,LHPP,MTMR11,CLASP2,SMOC2,HR,GPX7,SCP2,ZNF644,SQSTM1,BCL2A1,RBM39,MAGI3,KIAA0430,OGFRL1,PTTG1IP,HSD17B10,NOL7,NPDC1,AKAP8,HN1,GPR35,GDF15,HSD17B11,GPR107,SLC39A10,DNAJC13,MFGE8,SEPT11,CDKN3,OGT,DCUN1D4,ABCB7,BICC1,SOS1,OCIAD1,PDCD6IP,CYP51A1,FBXO21,ICE1,SLC35A5,OPTN,NRP2,ERBB2IP,GNA12,SLC6A6,SPATA2L,VIM,TMEM25,LDLR,RMDN2,SERPINH1,CDKN1A,PSAP,CTSE,ST3GAL4,TCF7L2,BZW2,JMY,ARL6IP5,KIF1B,MSH3,VPS13A,JAM2,ZNF397,CD163,RBP1,RARG,GPNMB,CXCL3,GPX3,B4GALNT1,ADGRF5,SAE1,CYP1A2,SMPD4,RHOB,RUNX2,TMTC2,CCDC149,GDE1,CXCL14,LPL,FGFR1OP,NUPR1,AP5M1,MXI1,GLA,ATF3,LIPT2,TNPO1,BACE1,C5,ARIH1,NXPE2,ATP5C1,NPC1,RLF,UGP2,CCNY,SLC7A7,PECR,UHRF1BP1L,ZNF707,PDK2,TMEM176B,ELL2,AADAT,SLC1A4,AP4B1,FRZB,PUM1,TERT,PDE1A,NHSL1,LYST,RGS5,TIMP1,ADCK3,GNMT,FAM171B,DPP4,HAUS8,ADTRP,ST3GAL6,ACADSB,MTHFD1,LOC102724788/PRODH,HABP2,AMIGO1,DBT,HNRNPH3,PAFAH1B3,SFPQ,KPNA1,RICTOR,ADAMTS2,ATXN2,ZNF235,IPMK,SMARCC2,PELI2,WAPL,ERGIC2,IER3,KIAA0100,ERCC6L2,AKAP13,ANKRD11,RSPH3,YTHDF3,MS4A7,ENC1,ATAD1,PHLPP1,ALDH4A1,TPD52L1,OASL,NIPAL2,XYLB,CA3,LIPA,MYO1B,ANXA5,ADK,ABHD2,MCM10,LPP,PLAT,RSF1,ACOX1,MAPK8,PIK3C2G,SIN3A,RABGEF1,ASPA,GOLM1,PVT1,HECTD3,PELI1,CHFR,PEA15,COL4A4,RUFY3,MVD,CSNK2A1,ZBP1,TMEM184C,TMEM30A,DYNLT1,USF3,TMED5,CPSF6,KCNN1,FBXO11,CHPT1,CLCN3,DEPTOR,RPS6KB1,RBL2,SPP1,CDC37L1,FGFR1,MACROD1,IFT57,CD93,GPAT4,SEPW1,ELF1,PANK1,GYG1,SDS,MAP2K5,TAGLN2,PDGFA,TAOK1,TGIF1,BCL2,ROGDI,MCCC1,L2HGDH,CPNE3,ESRP2,VWCE,CCDC58,STRAP,GNAI2,LPCAT1,TANGO2,SMARCC1,C1orf131,SWT1,LGALS1,GAS6,MLLT4,SMARCD2,SEL1L3,SECISBP2,ESRRG,ELF3,BCAT2,SYPL1,AHCY,SON,NKTR,ACAA1,UPF3B,SP4,CDC73,CSF2RB,PRTN3,CD34,DPYS,EIF4EBP2,ANPEP,SMARCA4,FABP5,OTUD7B,PLOD2,OAS1,UCP2,TUBB4B,POLG2,Clca3a1/Clca3a2,DHX36,PARP4,GIT2,CTH,SDF4,NAV2,RAB14,MICALL2,HGD,HMGCS2,ZDHHC14,PTEN,FNDC4,H19,RIMS4,HEATR3,CAND1,ADCY9,TMEM19,SLC7A2,CCDC80,PPAT,PEBP1,ZFP91,SFTPD,PC,SLC13A5,IQGAP1,STK11IP,ALDH2,ARHGAP44,TNC,DHCR7,OTC,LEAP2,ZNF24,IGHM,HSPB6,AP3M1,N4BP2L1,MTO1,PDK3,ALS2,POLR3B,ZC3H4,ITM2C,CCP110,BMP4,HSD17B13,CMTM4,GTPBP10,SLC15A4,LGMN,IRX3,SLC5A1,PRKD3,UBE2Q2,ACBD5,DPY19L1,YWHAZ,C5orf34,MON2,LMAN1,SPON2,ARHGAP5,OPHN1,MTMR4,AMMECR1L,KRT18,AGPAT3,FAM195A,SQLE,BTG3,PPP1R3C,PSMD9,MVK,FAM174B,LIN7A,EIF4G1,LYZ,JUN,PDE3B,GID8,SLC17A1,XPO4,PURA,OSBPL9,C2orf44,PAICS,MARCH6,Cyp2c54 (includes others),SCAMP5,FGF21,TBX20,CLEC7A,GALE,ANXA3,UAP1L1,NEURL1,ATAD3A,RBBP6,TFF3,RMDN1,FZD3,HECTD2,UNC5B,SLPI,B3GALT1,PXMP4,NID1,GSPT1,PCYT1B,ZSCAN12,ZNF318,GPC1,RC3H2,HIST1H3F,MYO6,SOX4,CMPK2,USP38,HSPA9,NASP,TMEM176A,LUC7L2,ITIH5,LOXL1,NCOA1,PDLIM1,CD14,CLCN7,JAG1,CLINT1,Ifi27l2a/Ifi27l2b,BLNK,TMTC3,PA2G4,TLE2,IFIT1B,USP6NL,FMO5,SLC38A4,EGLN3,Pvr,MMP12,FAM149A,PLSCR1,UBR5,COL5A2,MTRR,PHLDA3,GGCT,FNIP1,ACSM3,TSPAN8,Anp32a,CDKN2AIP,PGLYRP1,FZD4,U2SURP,HM13,ACAT1,NUCB2,Sf1,NFIB,IKBKAP,TINAG,FYCO1,TOPORS,PLPP2,ABCG8,ZNF800,CCDC22,SPRR1A,XDH,GSTA5,SLC35E3,SERPINA3,TOMM70A,ADRB3,RB1,HAPLN4,EGR2,KIF13A,Ly6a (includes others),ARHGAP12,DNAJC22,ALDH7A1,SERBP1,PYROXD2,PROSC,RHOBTB3,SLC13A4,ARSG,PPTC7,GYPC,VLDLR,RNF138,DDR1,MET,CDH1,GIPC2,SULT4A1,CNOT7,BTG2,DHX40,CYP2B6,SAMD4A,ENTPD7,PRDX2,ANK3,TRIM33,CYP4F8,PHLDA2,PGAP1,COL4A3,MCC,IGFBP7,GLIPR1,TGM2,AMN1,ISYNA1,AR,CHDH,LDAH,OSBPL11,HJURP,ALDH5A1,Rrbp1,MEMO1,NSDHL,CACNA1D,TOB1,PDPR,AGL,TGS1,PCNX,GALM,GLG1,TRMT1L,X

Supplemental Table 10. General IPA functions for genes altered in 1KI or 3bKI tumors

Category	Group	B-H p-value	Genes
Cell Morphology	1KI tumor genes	9.46E-06	DPYSL2,CTGF,F2R,HBA1/HBA2,SRL,Akr1b7,CXCL10,DYNLL1,MADD,DDAH1,CAV1,ADA,RAB17,GSTK1,FFAR4,ATL1,CIDEC,ANXA2,TPD52,VLDLR,NDN,PLS1,DDR1,CDH1,Bmp8b,BTG2,RAD18,PTGER2,HHEX,IFIT2,ENC1,UBE2C,COL3A1,MAP2K6,HLA-A,WWTR1,COL4A3,PLAGL1,GDF15,HEXA,SYCP3,SEPT11,CHEK1,LIPA,TRIB1,FSTL1,PTGFRN,JUN,CLMN,MTM1,PARK2,NFE2L2,CACNA1D,NRP2,POLG2,Cd24a,VIM,MDM2,Meg3,CDK1,MFN1,KRT8,SERPINH1,CDKN1A,SOX9,CSRP3,PPARGC1A,CAMK1D,CAV2,FAT1,Tpm1,SYNPO,CX3CR1,DYNLT1,PNRC2,RBP1,STMN1,MYC,B4GALNT1,TBC1D4,RHOB,LPL,CXCL14,ABCB11,MARCO,SOX4,GJA1,SPP1,FGFR1,IL6R,BACE1,HELLS,AURKA,METRN,RFX4,IGF2,Hbb-b2,EPCAM,TMEM176B,ERC2,BLNK,ABI2,C5orf42,CDC20,PDGFA,E2F3,EPHB6,CCNA2,TNC,ANGPTL4,COQ7,IGHM,EGLN3,DPP4,TIMP3,COL5A2,TACC3,FBXO31,Scd2,BAX,BIRC5,ALS2,HIVEP2,COL1A1,AMIGO1,SKIL,P2RX7,LGALS1
Cell Morphology	3bKI tumor genes	9.05E-05	PIAS2,MYH9,GAS6,MLLT4,CP,ADRB3,RB1,PLK4,SNAI3,Tmsb4x (includes others),Ly6a (includes others),MPP4,MTSS1,ARSG,ANXA2,CLASP2,VLDLR,DDR1,SP4,MET,CDH1,CNOT7,SCP2,BTG2,CD34,PRDX2,ANK3,KLF15,EIF4EBP2,COL4A3,GDF15,HEXA,SEPT11,IGFBP7,ANPEP,SMARCA4,OGT,AR,SOS1,PDCD6IP,CACNA1D,NRP2,OPTN,POLG2,ERBB2IP,GNA12,SLC6A6,VIM,TOB1,AGL,MARCKSL1,LDLR,SERPINH1,CDKN1A,PSAP,ST3GAL4,TCF7L2,PPARGC1A,LGALS3,GDA,JMY,EPHX2,MICALL2,JAM2,PDPK1,SYNPO,ODF2,RARG,RBP1,TSC22D3,PTEN,F11,SV2A,HSPA4,B4GALNT1,CYP1A2,ADGRF5,UBE2B,RHOB,LECT1,RUNX2,FGFR1OP,LPL,CXCL14,ABCB11,MXI1,GLA,ATF3,SYNE2,UBE4B,LCN2,IL6R,RIMS4,BACE1,NR2C2,CAPG,C5,IGF2,ANKRD1,SIRT1,IGFBP3,CCNY,EPCAM,TMEM176B,SIRPA,CD151,PEBP1,AADAT,SFTPD,TERT,CSRP1,ATF6,CADPS2,GPHN,IQGAP1,TNC,TGFB1I1,LYST,ZNF24,PRKAA2,OPA1,IGHM,LASP1,RAD23B,DPP4,FBXO31,ST3GAL6,PKHD1,ALS2,MPP1,FGF1,AMIGO1,SPARC,PAFAH1B3,SIK3,CTGF,BMP4,DDX25,RICTOR,ADAMTS2,Akr1b7,PCOLCE,ATXN2,HOOK3,LGMN,DDAH1,TARDBP,PRKD3,KALRN,Ank2,OAT,CREBBP,YWHAZ,HBEGF,SYNCRIP,IER3,PLS1,ARHGAP5,OPHN1,AKAP13,CCND2,KRT18,CYR61,ENC1,KDM5A,PHLPP1,COL3A1,SPTBN1,MAP2K6,BTG3,SYCP3,TOP2B,PKP4,FSTL1,LIPA,JUN,PDE3B,ANXA5,CLMN,RB1CC1,SORT1,PURA,PLAT,ACTB,ACOX1,MAPK8,RABGEF1,FGF21,KRT8,NFIA,CHFR,PEA15,NEURL1,IREB2,RUFY3,NEDD9,CSNK2A1,FAM234B,TAF10,DYNLT1,NID1,PCYT1B,TBC1D4,RORA,NEO1,CLCN3,FARP2,PDK4,MYO6,DEPTOR,SOX4,MFSD2A,RPS6KB1,RBL2,SPP1,TMEM106B,FGFR1,IFT57,GPAT4,NCOA1,CLCN7,MAP2K5,BLNK,NFIX,PDGFA,TAOK1,TGIF1,CPEB3,BCL2,EPHB6,THBS1,ANXA1,EGLN3,PLSCR1,COL5A2,CXCR4,HYAL1,SGMS2,GABBR1,UBE3A,COL1A1,Ptprd,NFIB,LGALS1
Cellular Movement	1KI tumor genes	5.98E-08	MALAT1,DPYSL2,CTGF,F2R,CTSV,SCNN1A,CXCL10,EGR2,ADA,CAV1,TP53INP1,FFAR4,ANXA2,VLDLR,PLS1,DDR1,NDN,CDH1,ZAK,BTG2,ALCAM,PTGER2,HHEX,IFIT2,COL3A1,LY6D,MAP2K6,SERPINB1,PHLDA2,HLA-A,OSGIN1,DUSP6,WWTR1,COL4A3,GDF15,SEPT11,TRIB1,FSTL1,LIPA,JUN,MYSM1,CSF2RA,ANXA5,ACSL4,PARK2,NFE2L2,ENTPD1,NRP2,Cd24a,VIM,MDM2,CDK1,KRT8,S100A9,SERPINH1,CDKN1A,PTK6,SOX9,IRAK4,TFF3,CAMK1D,FAT1,UNC5B,Tpm1,CLDN7,CX3CR1,RBP1,PBK,MYC,STMN1,SERP1,RHOB,CXCL14,JUND,GPC1,MARCO,SOX4,GJA1,SPP1,FGFR1,IL6R,AFP,AURKA,BAG4,IGF2,IRF7,ARHGEF16,PDLIM1,EPCAM,TMEM176B,PDGFA,CCL24,E2F3,EPHB6,ALDH2,TNC,CCNA2,ANGPTL4,AHNAK,HPGD,IGHM,EGLN3,Pvr,MMP12,DBF4,TIMP3,DPP4,SDC1,PCOLCE2,BAX,BIRC5,TSPAN8,COL1A1,TLR5,NLRP12,LGALS3BP,SLC1A2,NUCB2,G6PC,EIF2AK2,SKIL,CPEB1,PLET1,P2RX7,LGALS1,GRIA3

Supplemental Table 10. General IPA functions for genes altered in 1KI or 3bKI tumors

Category	Group	B-H p-value	Genes
Cellular Movement	3bKI tumor genes	1.05E-07	MYH9,GAS6,XDH,MLLT4,SERPINA3,Cxcl9,ADRB3,RB1,ANKRD28,ELF3,Tmsb4x (includes others),EGR2,APCS,Ly6a (includes others),AHCY,MTSS1,ANXA2,CLASP2,VLDLR,DDR1,MET,CSF2RB,CDH1,PRTN3,BTG2,SQSTM1,CD34,PRDX2,ANK3,WDR26,PHLDA2,KCNE3,COL4A3,GDF15,MFGE8,SEPT11,ANPEP,SMARCA4,CDKN3,TGM2,ARRDC3,AR,CHDH,SOS1,FABP5,UCP2,NRP2,GNA12,VIM,GIT2,MARCKSL1,LDLR,SERPINH1,CDKN1A,TAGLN,CTSE,ST3GAL4,TCF7L2,LGALS3,JMY,KLF6,JAM2,PDPK1,CLDN7,RBP1,TSC22D3,PTEN,CXCL3,CYP1A2,ADGRF5,RHOB,RUNX2,FKRP,CXCL14,FGFR1OP,JUND,CEACAM1,SYNE2,ATF3,IL6R,LCN2,PCSK6,NR2C2,CAPG,C5,NPC1,IGF2,ARHGEF16,SIRT1,IGFBP3,EPCAM,PLCB3,P2RY1,TMEM176B,SIRPA,CD151,PEBP1,SFTPD,TERT,CADPS2,IQGAP1,ALDH2,TNC,TGFB1I1,LYST,TIMP1,SAA1,ZNF24,PRKAA2,IGHM,PDK1,LASP1,DPP4,ST3GAL6,ECSCR,MPP1,FGF1,HABP2,LGALS3BP,SPARC,MEF2C,GRIA3,MALAT1,CTGF,BMP4,APOB,FNDC3B,RICTOR,SCNN1A,LGMN,SMG1,FBLN5,KALRN,RRAS,TKT,YWHAZ,HBEGF,IER3,PLS1,SPON2,ARHGAP5,IFITM3,CYR61,KDM5A,COL3A1,LY6D,MME,MAP2K6,KLK3,NQO2,TPD52L1,GBF1,COL4A2,TOP2B,CA3,FSTL1,LIPA,LYZ,MYO1B,JUN,ANXA5,EIF3A,ABHD2,SORT1,LPP,PLAT,NFIC,ACTB,ATG3,PIK3C2G,MAPK8,AGO2,RABGEF1,TBX20,CLEC7A,KRT8,NFIA,CHFR,PELI1,ANXA3,NEURL1,NEDD9,RUFY3,KIF1C,CSNK2A1,TFF3,FZD3,DNAI1,SPHK2,UNC5B,SLPI,NUS1,TMEM30A,MTCH2,RORA,NEO1,GPC1,CLCN3,SOX4,MYO6,DEPTOR,RPS6KB1,SPP1,COL4A1,FGFR1,CD93,AFP,BAG4,PPIC,SLC37A4,NCOA1,PDLIM1,CD14,JAG1,MAP2K5,TAGLN2,NFIX,PA2G4,PDGFA,IRF3,LOXL2,BCL2,EPHB6,THBS1,ANXA1,HPGD,EGLN3,CYGB,ACKR4,Pvr,MMP12,CPNE3,ESRP2,CXCR4,HYAL1,CCAR1,XIAP,TSPAN8,Ccl9,GNAI2,PGLYRP1,COL1A1,FZD4,ACAT1,NUCB2,IKBKAP,PLET1,LGALS1
Cell Cycle	1KI tumor genes	2.76E-07	QKI,SYNPO,DDIAS,MKI67,CXCL10,MYC,STMN1,CCNG1,MADD,RHOB,CXCL14,CAV1,GPC1,POLK,AMACR,TP53INP1,GJA1,CDCA8,SPP1,H19,FGFR1,IL6R,ANXA2,CKAP2,HELLS,AURKA,CCNB1,RPS6,IRF7,CDH1,IGF2,RPA3,ZAK,BTG2,RAD18,EPCAM,PDK2,CEP55,UBE2C,BLNK,MAP2K6,CDC20,OSGIN1,PLAGL1,GDF15,SYCP3,SEPT11,CAMK2N2,E2F3,CHEK1,RAD51,TNC,CCNA2,JUN,AHNAK,PLK2,HPGD,TOP2A,IGHM,Pvr,CDCA5,PARK2,PLAC8,NFE2L2,DBF4,DPP4,TACC3,FBXO31,UHRF1,BRAP,CDC6,NABP1,MDM2,BAX,BIRC5,CDK1,EMP1,COL1A1,CCNE1,KRT8,CDKN1A,CKS1B,SOX9,CTH,SKIL,EIF2AK2,IRAK4,LGALS1
Cell Cycle	3bKI tumor genes	2.70E-05	BMP4,PIAS2,ANKRD17,GAS6,SFPQ,DDIAS,ESRRG,RB1,PLK4,TARDBP,Ly6a (includes others),ZBTB20,VCPIP1,PRKD3,AMACR,WAPL,SON,CREBBP,HBEGF,ANXA2,IER3,UBE2S,MET,CDH1,CCND2,PPP2R3A,BTG2,KRT18,CYR61,BCL2A1,KDM5A,MAP2K6,TRIM33,AKAP8,KLK3,BTG3,GDF15,TPD52L1,SYCP3,GBF1,IGFBP7,GLIPR1,SMARCA4,TOP2B,CDKN3,AR,JUN,RB1CC1,MCM10,THOC1,PURA,OSBPL9,BRAP,GNA12,MAPK8,NUP153,KRT8,SF3B2,CHFR,CDKN1A,PEA15,PSAP,NR5A2,CTH,NEDD9,RBBP6,TCF7L2,KIF1C,DLGAP5,CSNK2A1,PRPF19,LGALS3,JMY,SPHK2,KLF6,TAF10,RARG,MTCH2,PTEN,GSPT1,RHOB,RUNX2,CXCL14,NUPR1,GPC1,TFDP2,CEACAM1,MXI1,RPS6KB1,RBL2,ATF3,H19,SPP1,ZMYM2,FGFR1,IL6R,BIRC6,C5,FAAP20,NASP,IGF2,SMARCA2,SIRT1,IGFBP3,EPCAM,CCNY,PEBP1,BLNK,PA2G4,GTF2I,PUM1,TERT,TAOK1,TGIF1,BCL2,TNC,THBS1,TIMP1,HPGD,PRKAA2,IGHM,Pvr,PDK1,PLSCR1,UBR5,DPP4,HAUS8,ATRX,HYAL1,UBE3A,XIAP,FGF1,Anp32a,EMP1,COL1A1,LOC102724788/PRODH,SPARC,PLPP2,TXLNG,LGALS1
DNA Replication, Recombination, and Repair	1KI tumor genes	4.21E-05	TFF3,F2R,MAF,DDIAS,PBK,CXCL10,CCNG1,MYC,ADA,CAV1,ELP4,POLK,GZMA,GJA1,SPP1,H19,TIA1,FGFR1,MACROD1,HELLS,AURKA,SMOC2,CCNB1,AEN,PIK3R3,RPS6,IGF2,RPA3,IRF7,ZAK,BTG2,RAD18,Airn,CDC20,PDGFA,SETD7,E2F3,SIRT4,CHEK1,RAD51,TNC,ALDH2,CCNA2,ZMAT3,JUN,PLK2,TOP2A,DBF4,TACC3,FBXO31,ENTPD1,UHRF1,POLG2,PHLDA3,CDC6,NABP1,MDM2,BAX,SLC29A1,Meg3,BIRC5,CDK1,CCNE1,KRT8,CDKN1A,CHMP4C,CKS1B,CTH,TINAG,EIF2AK2,LGALS1,PPARGC1A
DNA Replication, Recombination, and Repair	3bKI tumor genes	3.85E-03	PEBP1,LGALS3,APOB,BMP4,PDGFA,TFR2,TERT,IRF3,IQGAP1,SMARCA4,PTEN,TNC,RB1,AR,JUN,RUNX2,ADK,CEACAM1,RPS6KB1,RBL2,SPP1,ATF3,FBLN5,POLG2,FGFR1,GNA12,MAPK8,HBEGF,SMOC2,FGF1,GNAI2,MET,AKAP13,IGF2,CCND2,LDLR,Hnrnpa1,CDKN1A,NCOA1,IGFBP3,SPARC,IKBKAP,CTH,CYR61,PPAT,MAP2K5,LGALS1

Supplemental Table 10. General IPA functions for genes altered in 1KI or 3bKI tumors

Category	Group	B-H p-value	Genes
Cell Survival	1KI tumor genes	2.78E-11	SPRR1A,DDIAS,EDA2R,IFIH1,EGR2,MADD,PRSS8,ADA,CAV1,AMACR,IFIT3,TP53INP1,CIDEC,ANXA2,DDR1,NDN,AEN,RPS6,CDH1,BTG2,RAD18,ALCAM,HHEX,UBE2C,USP18,OSGIN1,PHLDA2,COL4A3,GDF15,Dleu2,SLC39A10,MYSM1,OTUD7B,NFE2L2,DHX58,OAS1,CACNA1D,ENTPD1,Clca3a1/Clca3a2,VIM,SLC29A1,MFN1,CCNE1,SERPINH1,CDKN1A,XAF1,SOX9,CTH,PPARGC1A,CAMK1D,CX3CR1,CLDN7,RBP1,MYC,B4GALNT1,RHOB,JUND,TIA1,IL6R,BACE1,HELLS,AURKA,FN3K,CCNB1,IRF7,IGF2,EPCAM,CDC20,FRZB,CCL24,E2F3,SIRT4,RAD51,CCNA2,ALDH2,TNC,NOP58,ADCK3,IGHM,HSPB6,SLC20A1,DPP4,TIMP3,TACC3,FBXO31,SDC1,BIRC5,ALS2,KIFC3,TUBB6,LGALS3BP,SKIL,GRIA3,MALAT1,CTGF,F2R,QKI,MAF,MIF4GD,HBA1/HBA2,MKI67,CXCL10,CCNG1,CTSV,DYNLL1,SPTLC2,FFAR4,CKAP2,PEG3,TPD52,PLS1,ZNF385B,Bmp8b,ZAK,PTGER2,IFIT2,ENC1,MAP2K6,DECR1,HLA-A,DUSP6,PLAGL1,SYCP3,CAMK2N2,CHEK1,FSTL1,TRIB1,LIPA,JUN,CSF2RA,ANXA5,MTM1,TOP2A,ACSL4,SORBS2,PARK2,PLAC8,SMPD3,CDC6,Cd24a,NABP1,Casp12,MDM2,Meg3,CDK1,KRT8,S100A9,PTK6,IRAK4,TFF3,FAT1,UNC5B,PBK,NPNT,STMN1,SERP1,DLST,GPC1,FPGS,POLK,GZMA,SOX4,SLC6A8,GCH1,GJA1,SPP1,FGFR1,AFP,BAG4,Hbb-b2,HLA-E,BLNK,AIFM3,PDGFA,KLB,EPHB6,ZMAT3,ANGPTL4,PLK2,HPGD,EGLN3,Pvr,IFRD1,UHRF1,PDE9A,SLC30A10,PHLDA3,BAX,HUNK,EMP1,COL1A1,PBX3,SLC1A2,G6PC,TINAG,EIF2AK2,CPEB1,P2RX7,LGALS1
Cell Survival	3bKI tumor genes	1.23E-07	MYH9,PIAS2,GAS6,XDH,SPRR1A,SERPINA3,DDIAS,CP,Cxcl9,RB1,PLK4,ELF3,EGR2,APCS,PRSS8,VAMP3,AMACR,SON,ANXA2,GPX7,DDR1,MET,CDC73,CSF2RB,CDH1,SCP2,PRTN3,BTG2,SQSTM1,CYP2B6,BCL2A1,PRDX2,HSD17B10,ANK3,TRIM33,USP18,WDR26,AKAP8,PHLDA2,COL4A3,GDF15,Dleu2,SLC39A10,MFGE8,IGFBP7,ANPEP,GLIPR1,SMARCA4,TGM2,CDKN3,OGT,AR,ZC3H8,ABCB7,NAT8B,PDCD6IP,OTUD7B,OAS1,CACNA1D,UCP2,OPTN,GNA12,Clca3a1/Clca3a2,PARP4,SLC6A6,VIM,LDLR,SERPINH1,CDKN1A,XAF1,PSAP,CTH,CTSE,ABCC3,TCF7L2,PPARGC1A,AKAP1,ABCB6,LGALS3,GDA,JMY,MSH3,KIF1B,ARL6IP5,ATP2B1,EPHX2,VPS13A,KLF6,PDPK1,CLDN7,RBP1,RARG,TSC22D3,PTEN,F11,CXCL3,FDFT1,HSPA4,B4GALNT1,SUPT6H,RHOB,UBE2B,SMPD4,RUNX2,FGFR1OP,NUPR1,HOMER1,JUND,HEBP2,MXI1,CEACAM1,ATF3,ZMYM2,UBE4B,PCSK6,IL6R,LCN2,NR2C2,BACE1,FN3K,FAAP20,C5,NPC1,IGF2,ANKRD1,SIRT1,IGFBP3,EPCAM,CCDC80,PPAT,SIRPA,MLKL,CD151,PEBP1,SFTPD,FRZB,PUM1,TERT,CADPS2,ATF6,GPHN,IQGAP1,TNC,ALDH2,DHCR7,TGFB1I1,RGS5,TIMP1,SAA1,ADCK3,PRKAA2,OPA1,IGHM,GNMT,PDK1,RAD23B,HSPB6,NDUFAF4,DPP4,FBXO31,HAUS8,ATRX,HERPUD1,PKHD1,ALS2,ECSCR,FGF1,LOC102724788/PRODH,TUBB6,LGALS3BP,SPARC,MEF2C,GRIA3,PAFAH1B3,MALAT1,CCP110,DDX25,DPYD,BMP4,APOB,CTGF,TFR2,SFPQ,RICTOR,ABCC6,ATXN2,ALDH1L1,IPMK,LGMN,TARDBP,ZBTB20,SMARCC2,SMG1,HIPK1,PRKD3,WAPL,RRAS,CREBBP,YWHAZ,HBEGF,UBE2S,IER3,PLS1,AKAP13,CCND2,PPP2R3A,AHCTF1,KRT18,CYR61,ENC1,PHLPP1,SPTBN1,MAP2K6,MME,DECR1,KLK3,BTG3,NQO2,MVK,TPD52L1,SYCP3,COL4A2,EIF4G1,TOP2B,FSTL1,LIPA,CA3,LYZ,JUN,ANXA5,ADK,CELA2A,EIF3A,RB1CC1,SORT1,MCM10,THOC1,PURA,SMPD3,PLAT,RSF1,NFIC,ACTB,ATG3,MAPK8,AGO2,SRXN1,DUSP14,SIN3A,RABGEF1,FGF21,TBX20,KRT8,SOX6,CHFR,PEA15,NR5A2,NEURL1,ATAD3A,IREB2,NEDD9,RBBP6,KIF1C,TFF3,CSNK2A1,PRPF19,ATXN3,FZD3,SPHK2,UNC5B,SLPI,TAF10,CCDC47,Defb1,NEO1,TFDP2,GPC1,NAA16,CLCN3,SLCO1B3,PDK4,MYO6,SOX4,DEPTOR,RPS6KB1,SLC6A8,RBL2,SPP1,COL4A1,FGFR1,IFT57,HSPA9,BIRC6,AFP,BAG4,SMOX,SMARCA2,SLC37A4,NCOA1,CD14,CLCN7,Nrbp2,JAG1,MAP2K5,TAGLN2,BLNK,AIFM3,NFIX,PA2G4,PDGFA,PPP1CB,IRF3,TAOK1,LOXL2,BCL2,EPHB6,TNRC6A,THBS1,MARCH8,ANXA1,HPGD,EGLN3,Pvr,PLSCR1,HIPK3,CXCR4,PHLDA3,HYAL1,GPT,CCAR1,GABBR1,YBX3,SGMS2,UBE3A,XIAP,FNIP1,Ccl9,GNAI2,EMP1,FDPS,COL1A1,PGLYRP1,ACAT1,IKBKAP,NFIB,SMARCC1,TINAG,TOPORS,LGALS1
Amino Acid Metabolism	3bKI tumor genes	1.14E-05	ABAT,GTPBP10,HGD,UPB1,BCAT2,RUNX2,DDAH1,HOMER1,SLCO1B3,PDK4,AFMID,SLC6A8,TDO2,OAT,C5,MET,PANK1,HIBADH,SLC7A2,SIRT1,NCOA1,SLC7A7,ALDH18A1,SDS,PPAT,MCCC2,AADAT,BCL2,OTC,PRKAA2,GNMT,SMPD3,ALDH5A1,Slco1a1,SLC25A13,MTRR,SLC6A6,ATG3,MAPK8,GPT,MTHFD1,ASPA,FGF1,SARDH,LDLR,LOC102724788/PRODH,DBT,SLC25A32,CTH,IVD
Carbohydrate Metabolism	1KI tumor genes	3.44E-04	DECR1,CTGF,F2R,PLAGL1,GDF15,HEXA,RBP1,KLB,Akr1b7,MYC,FSTL1,MADD,TBC1D4,CSF2RA,SLC5A1,ANXA5,LPL,CXCL14,ADA,CAV1,MTM1,ABCB11,EGLN3,PARK2,DPP4,TP53INP1,SPP1,FFAR4,CIDEC,BACE1,BAX,Slco1a4,PANK1,IGF2,PCCA,SLC1A2,NUCB2,G6PC,EIF2AK2,PDK2,CTH,ACSL1,PPARGC1A

Supplemental Table 10. General IPA functions for genes altered in 1KI or 3bKI tumors

Category	Group	B-H p-value	Genes
Carbohydrate Metabolism	3bKI tumor genes	7.02E-05	SIK3,BMP4,CTGF,CP,ADRB3,Akr1b7,ATXN2,ESRRG,BCAT2,SLC5A1,ZBTB20,DHDH,PRKD3,UGT3A1,Ank2,PGM3,SLC35A3,ADRBK2,TKT,CREBBP,HBEGF,MET,CSF2RB,PRPS2,CNOT7,SCP2,SQSTM1,PRDX2,KLF15,MAP2K6,DECR1,SLC10A1,GPR35,PPP1R3C,PGAP1,GDF15,HEXA,XYLB,OGT,FSTL1,PDE3B,ANXA5,FABP5,SORT1,B3GALNT2,ALDH5A1,PLAT,STX12,SLC25A13,OAS1,UCP2,OPTN,MAPK8,AGL,GALM,FGF21,LDLR,GALE,PEA15,CTH,ABCC3,TCF7L2,PPARGC1A,LGALS3,EPHX2,SLC35D1,PDPK1,RBP1,B3GALT1,PTEN,CXCL3,B4GALNT1,TBC1D4,SMPD4,LECT1,CXCL14,LPL,ABCB11,CHPT1,GPC1,CLCN3,SLCO1B3,CEACAM1,PDK4,RPS6KB1,GLA,ATF3,SPP1,FGFR1,NR2C2,BACE1,FN3K,GPAT4,C5,PANK1,NPC1,IGF2,UGP2,GYG1,SLC37A4,SIRT1,IGFBP3,NCOA1,PLCB3,CD14,Gm15807/Hmgn5,FITM2,PDK2,SDS,CCDC80,SFTPD,PC,PDGFA,PIGL,PPP1CB,ATF6,BCL2,ALDH2,ANXA1,PRKAA2,EGLN3,GNMT,MMP12,PLSCR1,Mup1 (includes others),DPP4,HYAL1,ST3GAL6,SGMS2,FGF1,PPP1R3B,GNAI2,EXOC4,NUCB2,PLPP2,ACSL1
Lipid Metabolism	1KI tumor genes	3.29E-05	IDI1,CAV2,QKI,F2R,CLDN7,HMGCS2,RBP1,Akr1b7,CXCL10,MYC,SCNN1A,SH3YL1,B4GALNT1,TBC1D4,SPTLC2,LPL,RDH16,CXCL14,CAV1,ADA,ABCB11,GPC1,GSTK1,PITPNB,AMACR,ACSL3,SPP1,FFAR4,CIDEC,AFP,VLDLR,LONP2,ACADS,PANK1,IGF2,AKR1D1,CPT2,PTGER2,PDK2,CYP4A11,SQLE,DECR1,PIGP,PDGFA,PIGL,PGAP1,COL4A3,GDF15,HEXA,E2F3,KLB,ACAA2,SIRT4,LIPA,TRIB1,JUN,ANGPTL4,SLC10A2,ANXA5,DECR2,HPGD,MTM1,IGHM,ACSL4,PARK2,MMP12,IFRD1,SMPD3,CYP51A1,DPP4,NSDHL,ENTPD1,PCOLCE2,Scd2,VIM,Cyp2c54 (includes others),BAX,Slco1a4,RETSAT,Cyp4f16/Cyp4f37,ASPA,PCCA,TLR5,S100A9,DLAT,CDKN1A,NUCB2,SLC1A2,G6PC,PLEKHA1,P2RX7,ACSL1,PPARGC1A
Lipid Metabolism	3bKI tumor genes	2.64E-07	ABCG8,SIK3,MYH9,HSD17B13,BMP4,APOB,DDX25,ABAT,Akap9,XDH,CP,KPNA1,ADRB3,HSD17B8,Akr1b7,ABCC6,SCNN1A,ATXN2,RB1,ESRRG,ALDH1L1,BCAT2,APCS,VAMP3,CELA3B,LSS,AMACR,ACAA1,VLDLR,CSF2RB,SCP2,UBR1,Acot1,CYP2B6,ACOT9,DHRS4,PRDX2,HSD17B10,KLF15,SQLE,DECR1,CYP4F8,SLC10A1,KCNE3,PGAP1,PPP1R3C,COL4A3,MVK,GDF15,HEXA,IGFBP7,ANPEP,TGM2,LIPA,AR,JUN,PDE3B,ANXA5,FABP5,SORT1,PDCD6IP,SMPD3,CYP51A1,ALDH5A1,PLAT,STX12,NSDHL,SLC25A13,UCP2,RDH11,ACOX1,SLC6A6,MAPK8,VIM,Cyp2c54 (includes others),RETSAT,ASPA,Ces1e,FGF21,B4GALT6,CLEC7A,LDLR,CDKN1A,NR5A2,PSAP,ABCC3,TCF7L2,PPARGC1A,MVD,HSD3B1,PRPF19,LGALS3,EPHX2,SPHK2,NUS1,TAF10,CLDN7,HMGCS2,TMEM30A,RARG,B3GALT1,RBP1,Cyp2j5,TSC22D3,PTEN,CXCL3,FDFT1,B4GALNT1,TBC1D4,CYP1A2,ADGRF5,SMPD4,RUNX2,RORA,ECI2,LPL,CXCL14,CHPT1,ABCB11,GPC1,CEACAM1,SLCO1B3,PDK4,MFSD2A,RPS6KB1,GLA,SPP1,ATF3,LCN2,NR2C2,AFP,GPAT4,C5,PANK1,NPC1,IGF2,SIRT1,SLC37A4,CPT2,NCOA1,PLCB3,CD14,CCNY,FITM2,PDK2,CCDC80,PPAT,SFTPD,PDGFA,PIGL,SLC13A5,TERT,ATF6,APOC2,GCDH,TGIF1,BCL2,DHCR7,LYST,TIMP1,ANXA1,SAA1,DECR2,PRKAA2,HPGD,OPA1,CYGB,IGHM,LRPPRC,GNMT,PDK1,MMP12,PLSCR1,Mup1 (includes others),DPP4,Slco1a1,ABCD3,ACADSB,SGMS2,ACSM3,FGF1,Cyp4f16/Cyp4f37,FDPS,LOC102724788/PRODH,LPCAT1,ACAT1,NUCB2,Sf1,PLPP2,PTGR2,ACSL1

Supplemental Table 11. E2F1 and/or E2FB HCC upregulated targets

Regulated by	Gene symbol	Entrez Gene Name	Location	Type
E2F1	ACSL3	acyl-CoA synthetase long-chain family member 3	Cytoplasm	enzyme
E2F1	ALCAM	activated leukocyte cell adhesion molecule	Plasma Membrane	other
E2F1	ATXN2L	ataxin 2-like	Nucleus	other
E2F1	AURKA	aurora kinase A	Nucleus	kinase
E2F1	BIRC5	baculoviral IAP repeat containing 5	Cytoplasm	other
E2F1	CAMK2N2	calcium/calmodulin-dependent protein kinase II inhibitor 2	Nucleus	other
E2F1	CCNA2	cyclin A2	Nucleus	other
E2F1	CCNE1	cyclin E1	Nucleus	transcription regulator
E2F1	CDC6	cell division cycle 6	Nucleus	other
E2F1	CDCA5	cell division cycle associated 5	Cytoplasm	other
E2F1	CDK1	cyclin-dependent kinase 1	Nucleus	kinase
E2F1	CEP55	centrosomal protein 55kDa	Cytoplasm	other
E2F1	CHEK1	checkpoint kinase 1	Nucleus	kinase
E2F1	CKAP2	cytoskeleton associated protein 2	Cytoplasm	other
E2F1	CKS1B	CDC28 protein kinase regulatory subunit 1B	Other	kinase
E2F1	DDX50	DEAD (Asp-Glu-Ala-Asp) box polypeptide 50	Nucleus	enzyme
E2F1	DEPDC1B	DEP domain containing 1B	Cytoplasm	other
E2F1	DUSP6	dual specificity phosphatase 6	Cytoplasm	phosphatase
E2F1	E2F3	E2F transcription factor 3	Nucleus	transcription regulator
E2F1	GAS2L3	growth arrest-specific 2 like 3	Other	other
E2F1	GJA1	gap junction protein, alpha 1, 43kDa	Plasma Membrane	transporter
E2F1	HELLS	helicase, lymphoid-specific	Nucleus	enzyme
E2F1	HEXA	hexosaminidase A (alpha polypeptide)	Cytoplasm	enzyme
E2F1	HIST1H4A	histone cluster 1, H4a	Nucleus	other
E2F1	HIVEP2	human immunodeficiency virus type I enhancer binding protein 2	Nucleus	transcription regulator
E2F1	IDI1	isopentenyl-diphosphate delta isomerase 1	Cytoplasm	enzyme
E2F1	IFRD1	interferon-related developmental regulator 1	Nucleus	other
E2F1	MDM2	MDM2 proto-oncogene, E3 ubiquitin protein ligase	Nucleus	transcription regulator
E2F1	MYC	v-myc avian myelocytomatosis viral oncogene homolog	Nucleus	transcription regulator
E2F1	MYEF2	myelin expression factor 2	Nucleus	transcription regulator
E2F1	NFE2L2	nuclear factor, erythroid 2-like 2	Nucleus	transcription regulator
E2F1	NOP58	NOP58 ribonucleoprotein	Nucleus	enzyme
E2F1	PAPSS1	3'-phosphoadenosine 5'-phosphosulfate synthase 1	Cytoplasm	enzyme
E2F1	PBK	PDZ binding kinase	Cytoplasm	kinase
E2F1	PBX3	pre-B-cell leukemia homeobox 3	Nucleus	transcription regulator
E2F1	PIGP	phosphatidylinositol glycan anchor biosynthesis, class P	Cytoplasm	enzyme
E2F1	PLEKHA1	pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 1	Cytoplasm	other
E2F1	PVR	poliovirus receptor	Plasma Membrane	other
E2F1	RAD18	RAD18 E3 ubiquitin protein ligase	Nucleus	other
E2F1	RAD51	RAD51 recombinase	Nucleus	enzyme

Supplemental Table 11. E2F1 and/or E2FB HCC upregulated targets

Regulated by	Gene symbol	Entrez Gene Name	Location	Type
E2F1	RHOB	ras homolog family member B	Cytoplasm	enzyme
E2F1	SHCBP1	SHC SH2-domain binding protein 1	Other	other
E2F1	SLC20A1	solute carrier family 20 (phosphate transporter), member 1	Plasma Membrane	transporter
E2F1	SMC4	structural maintenance of chromosomes 4	Nucleus	transporter
E2F1	SPATS2	spermatogenesis associated, serine-rich 2	Cytoplasm	other
E2F1	STMN1	stathmin 1	Cytoplasm	other
E2F1	TACC3	transforming, acidic coiled-coil containing protein 3	Nucleus	other
E2F1	TOP2A	topoisomerase (DNA) II alpha 170kDa	Nucleus	enzyme
E2F1	TRIB1	tribbles pseudokinase 1	Cytoplasm	kinase
E2F1	UHRF1	ubiquitin-like with PHD and ring finger domains 1	Nucleus	transcription regulator
E2F1	WWTR1	WW domain containing transcription regulator 1	Nucleus	transcription regulator
E2F1;E2F3B	BTG2	BTG family, member 2	Nucleus	transcription regulator
E2F1;E2F3B	CDKN1A	cyclin-dependent kinase inhibitor 1A (p21, Cip1)	Nucleus	kinase
E2F1;E2F3B	EGR2	early growth response 2	Nucleus	transcription regulator
E2F1;E2F3B	EXOC4	exocyst complex component 4	Cytoplasm	transporter
E2F1;E2F3B	JUND	jun D proto-oncogene	Nucleus	transcription regulator
E2F1;E2F3B	LGALS1	lectin, galactoside-binding, soluble, 1	Extracellular Space	other
E2F1;E2F3B	PHLDA3	pleckstrin homology-like domain, family A, member 3	Plasma Membrane	other
E2F1;E2F3B	RRBP1	ribosome binding protein 1	Cytoplasm	other
E2F1;E2F3B	TMEM43	transmembrane protein 43	Nucleus	other
E2F1;E2F3B	TUBB6	tubulin, beta 6 class V	Cytoplasm	other
E2F1;E2F3B	UNC5B	unc-5 netrin receptor B	Plasma Membrane	transmembrane receptor
E2F3B	ABRACL	ABRA C-terminal like	Other	other
E2F3B	ACTB	actin, beta	Cytoplasm	other
E2F3B	ADPRH	ADP-ribosylarginine hydrolase	Other	enzyme
E2F3B	AGO2	argonaute RISC catalytic component 2	Cytoplasm	translation regulator
E2F3B	ARSG	arylsulfatase G	Cytoplasm	enzyme
E2F3B	ATP2B1	ATPase, Ca++ transporting, plasma membrane 1	Plasma Membrane	transporter
E2F3B	CAPG	capping protein (actin filament), gelsolin-like	Nucleus	other
E2F3B	CDKN3	cyclin-dependent kinase inhibitor 3	Cytoplasm	phosphatase
E2F3B	CENPM	centromere protein M	Cytoplasm	other
E2F3B	COL4A1	collagen, type IV, alpha 1	Extracellular Space	other
E2F3B	COL6A3	collagen, type VI, alpha 3	Extracellular Space	other
E2F3B	CSRP1	cysteine and glycine-rich protein 1	Nucleus	other
E2F3B	CTGF	connective tissue growth factor	Extracellular Space	growth factor
E2F3B	CYP51A1	cytochrome P450, family 51, subfamily A, polypeptide 1	Cytoplasm	enzyme
E2F3B	CYR61	cysteine-rich, angiogenic inducer, 61	Extracellular Space	other
E2F3B	DDR1	discoidin domain receptor tyrosine kinase 1	Plasma Membrane	kinase
E2F3B	DLGAP5	discs, large (Drosophila) homolog-associated protein 5	Nucleus	phosphatase

Supplemental Table 11. E2F1 and/or E2FB HCC upregulated targets

Regulated by	Gene symbol	Entrez Gene Name	Location	Type
E2F3B	EIF4EBP2	eukaryotic translation initiation factor 4E binding protein 2	Cytoplasm	translation regulator
E2F3B	FAAP20	Fanconi anemia core complex associated protein 20	Nucleus	other
E2F3B	FDFT1	farnesyl-diphosphate farnesyltransferase 1	Cytoplasm	enzyme
E2F3B	FDPS	farnesyl diphosphate synthase	Cytoplasm	enzyme
E2F3B	FGFR1	fibroblast growth factor receptor 1	Plasma Membrane	kinase
E2F3B	FNDC3B	fibronectin type III domain containing 3B	Cytoplasm	other
E2F3B	GNAI2	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2	Plasma Membrane	other
E2F3B	HAUS8	HAUS augmin-like complex, subunit 8	Cytoplasm	other
E2F3B	HBEGF	heparin-binding EGF-like growth factor	Extracellular Space	growth factor
E2F3B	IQGAP1	IQ motif containing GTPase activating protein 1	Cytoplasm	other
E2F3B	JAG1	jagged 1	Extracellular Space	growth factor
E2F3B	KLF6	Kruppel-like factor 6	Nucleus	transcription regulator
E2F3B	LASP1	LIM and SH3 protein 1	Cytoplasm	transporter
E2F3B	LIPT2	lipoyl(octanoyl) transferase 2 (putative)	Cytoplasm	other
E2F3B	LOXL1	lysyl oxidase-like 1	Extracellular Space	enzyme
E2F3B	LYSMD2	LysM, putative peptidoglycan-binding, domain containing 2	Other	other
E2F3B	MYH9	myosin, heavy chain 9, non-muscle	Cytoplasm	enzyme
E2F3B	NRM	nurim (nuclear envelope membrane protein)	Nucleus	other
E2F3B	PDAP1	PDGFA associated protein 1	Cytoplasm	other
E2F3B	PDGFA	platelet-derived growth factor alpha polypeptide	Extracellular Space	growth factor
E2F3B	PDLIM1	PDZ and LIM domain 1	Cytoplasm	transcription regulator
E2F3B	PLAT	plasminogen activator, tissue	Extracellular Space	peptidase
E2F3B	PRDX2	peroxiredoxin 2	Cytoplasm	enzyme
E2F3B	PSAP	prosaposin	Extracellular Space	other
E2F3B	PVT1	Pvt1 oncogene (non-protein coding)	Other	other
E2F3B	RAB5C	RAB5C, member RAS oncogene family	Cytoplasm	enzyme
E2F3B	SAE1	SUMO1 activating enzyme subunit 1	Cytoplasm	enzyme
E2F3B	SAMD4A	sterile alpha motif domain containing 4A	Cytoplasm	translation regulator
E2F3B	SECISBP2	SECIS binding protein 2	Cytoplasm	translation regulator
E2F3B	SEPT11	septin 11	Nucleus	other
E2F3B	SF1	splicing factor 1	Nucleus	transcription regulator
E2F3B	SLC35A5	solute carrier family 35, member A5	Other	transporter
E2F3B	SLC35C1	solute carrier family 35 (GDP-fucose transporter), member C1	Cytoplasm	transporter
E2F3B	SOX4	SRY (sex determining region Y)-box 4	Nucleus	transcription regulator
E2F3B	SP4	Sp4 transcription factor	Nucleus	transcription regulator
E2F3B	SQLE	squalene epoxidase	Cytoplasm	enzyme
E2F3B	SRXN1	sulfiredoxin 1	Cytoplasm	enzyme
E2F3B	TIMP1	TIMP metallopeptidase inhibitor 1	Extracellular Space	cytokine
E2F3B	TOB1	transducer of ERBB2, 1	Nucleus	transcription regulator
E2F3B	TUBB4B	tubulin, beta 4B class IVb	Cytoplasm	other
E2F3B	UAP1L1	UDP-N-acetylglucosamine pyrophosphorylase 1 like 1	Other	other
E2F3B	UBE2S	ubiquitin-conjugating enzyme E2S	Nucleus	enzyme

Supplemental Table 11. E2F1 and/or E2FB HCC upregulated targets

Regulated by	Gene symbol	Entrez Gene Name	Location	Type
E2F3B	VAMP3	vesicle-associated membrane protein 3	Plasma Membrane	other
E2F3B	WDFY3	WD repeat and FYVE domain containing 3	Cytoplasm	enzyme
E2F3B	YWHAZ	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta	Cytoplasm	enzyme
E2F3B	ZC3HAV1	zinc finger CCCH-type, antiviral 1	Plasma Membrane	other
E2F3B	ZDHHC14	zinc finger, DHHC-type containing 14	Cytoplasm	enzyme
E2F3B	ZFP280D	zinc finger protein 280D	Other	other

Supplemental Table 12. E2F1 and/or E2FB HCC downregulated targets

Regulated by	Gene symbol	Entrez Gene Name	Location	Type
E2F1	BAG4	BCL2-associated athanogene 4	Cytoplasm	other
E2F1	DLST	dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex)	Cytoplasm	enzyme
E2F1	GYPC	glycophorin C (Gerbich blood group)	Plasma Membrane	other
E2F1	PANK1	pantothenate kinase 1	Cytoplasm	kinase
E2F1	PCOLCE2	procollagen C-endopeptidase enhancer 2	Extracellular Space	other
E2F1	POLG2	polymerase (DNA directed), gamma 2, accessory subunit	Cytoplasm	enzyme
E2F1	RFX4	regulatory factor X, 4 (influences HLA class II expression)	Nucleus	transcription regulator
E2F1	RPRD2	regulation of nuclear pre-mRNA domain containing 2	Other	other
E2F1	SCO2	SCO2 cytochrome c oxidase assembly protein	Cytoplasm	other
E2F1	SDC1	syndecan 1	Plasma Membrane	enzyme
E2F1	SHMT1	serine hydroxymethyltransferase 1 (soluble)	Cytoplasm	enzyme
E2F1	SLC29A1	solute carrier family 29 (equilibrative nucleoside transporter), member 1	Plasma Membrane	transporter
E2F1	ZFP213	zinc finger protein 213	Nucleus	transcription regulator
E2F1	ZFP784	zinc finger protein 784	Other	other
E2F1;E2F3B	ALDH4A1	aldehyde dehydrogenase 4 family, member A1	Cytoplasm	enzyme
E2F1;E2F3B	ALS2	amyotrophic lateral sclerosis 2 (juvenile)	Cytoplasm	other
E2F1;E2F3B	DLEU2	deleted in lymphocytic leukemia 2 (non-protein coding)	Other	other
E2F1;E2F3B	MACROD1	MACRO domain containing 1	Cytoplasm	enzyme
E2F1;E2F3B	NRP2	neuropilin 2	Plasma Membrane	kinase
E2F3B	1600002H07RIK	RIKEN cDNA 1600002H07 gene	Other	other
E2F3B	1810014B01RIK	RIKEN cDNA 1810014B01RIK gene	Other	other
E2F3B	4831440E17RIK	RIKEN cDNA 4831440E17RIK gene	Other	other
E2F3B	4930581F22RIK	RIKEN cDNA 4930581F22RIK gene	Other	other
E2F3B	ABCD3	ATP-binding cassette, sub-family D (ALD), member 3	Cytoplasm	transporter
E2F3B	ACAT1	acetyl-CoA acetyltransferase 1	Cytoplasm	enzyme
E2F3B	ACSL1	acyl-CoA synthetase long-chain family member 1	Cytoplasm	enzyme
E2F3B	ACY1	aminoacylase 1	Cytoplasm	peptidase
E2F3B	ADGRF5	adhesion G protein-coupled receptor F5	Plasma Membrane	G-protein coupled receptor
E2F3B	ADK	adenosine kinase	Nucleus	kinase
E2F3B	ADRB3	adrenoceptor beta 3	Plasma Membrane	G-protein coupled receptor
E2F3B	AFMID	arylformamidase	Nucleus	enzyme
E2F3B	AGBL3	ATP/GTP binding protein-like 3	Other	peptidase
E2F3B	AGFG2	ArfGAP with FG repeats 2	Other	other
E2F3B	AGPAT6	1-acylglycerol-3-phosphate O-acyltransferase 6	Cytoplasm	enzyme

Supplemental Table 12. E2F1 and/or E2FB HCC downregulated targets

Regulated by	Gene symbol	Entrez Gene Name	Location	Type
E2F3B	AHCTF1	AT hook containing transcription factor 1	Nucleus	transcription regulator
E2F3B	AHCY	adenosylhomocysteinase	Cytoplasm	enzyme
E2F3B	AI314180	KIAA0368	Cytoplasm	other
E2F3B	AKAP1	A kinase (PRKA) anchor protein 1	Cytoplasm	other
E2F3B	AKAP8	A kinase (PRKA) anchor protein 8	Nucleus	other
E2F3B	ALDH7A1	aldehyde dehydrogenase 7 family, member A1	Cytoplasm	enzyme
E2F3B	AMIGO1	adhesion molecule with Ig-like domain 1	Plasma Membrane	other
E2F3B	AP2B1	adaptor-related protein complex 2, beta 1 subunit	Plasma Membrane	transporter
E2F3B	AP3M1	adaptor-related protein complex 3, mu 1 subunit	Cytoplasm	transporter
E2F3B	AP5M1	adaptor-related protein complex 5, mu 1 subunit	Cytoplasm	other
E2F3B	ARHGAP5	Rho GTPase activating protein 5	Cytoplasm	enzyme
E2F3B	ARIH1	ariadne RBR E3 ubiquitin protein ligase 1	Cytoplasm	enzyme
E2F3B	ARRDC3	arrestin domain containing 3	Plasma Membrane	other
E2F3B	ATF6	activating transcription factor 6	Cytoplasm	transcription regulator
E2F3B	B3GALNT2	beta-1,3-N-acetylgalactosaminyltransferase 2	Cytoplasm	enzyme
E2F3B	BAZ1B	bromodomain adjacent to zinc finger domain, 1B	Nucleus	transcription regulator
E2F3B	BIRC6	baculoviral IAP repeat containing 6	Cytoplasm	enzyme
E2F3B	CAND1	cullin-associated and neddylation-dissociated 1	Cytoplasm	transcription regulator
E2F3B	CCP110	centriolar coiled coil protein 110kDa	Cytoplasm	other
E2F3B	CDKN2AIP	CDKN2A interacting protein	Nucleus	transcription regulator
E2F3B	CHD9	chromodomain helicase DNA binding protein 9	Cytoplasm	other
E2F3B	CNOT6L	CCR4-NOT transcription complex, subunit 6-like	Cytoplasm	enzyme
E2F3B	COPG2	coatomer protein complex, subunit gamma 2	Cytoplasm	transporter
E2F3B	CUTC	cutC copper transporter	Cytoplasm	other
E2F3B	D15ERTD621E	DNA segment, Chr 15, ERATO Doi 621, expressed	Other	other
E2F3B	DANCR	differentiation antagonizing non-protein coding RNA	Other	other
E2F3B	DDI2	DNA-damage inducible 1 homolog 2	Plasma Membrane	transporter
E2F3B	DPY19L1	dpy-19-like 1 (C. elegans)	Other	other
E2F3B	EIF3A	eukaryotic translation initiation factor 3, subunit A	Cytoplasm	other
E2F3B	EIF4G1	eukaryotic translation initiation factor 4 gamma, 1	Cytoplasm	translation regulator
E2F3B	ELF1	E74-like factor 1 (ets domain transcription factor)	Nucleus	transcription regulator
E2F3B	EPHB6	EPH receptor B6	Plasma Membrane	kinase

Supplemental Table 12. E2F1 and/or E2FB HCC downregulated targets

Regulated by	Gene symbol	Entrez Gene Name	Location	Type
E2F3B	ERCC6L2	excision repair cross-complementation group 6-like 2	Other	enzyme
E2F3B	FBXO21	F-box protein 21	Extracellular Space	enzyme
E2F3B	FBXO30	F-box protein 30	Extracellular Space	other
E2F3B	GCN1	GCN1 eIF2 alpha kinase activator homolog	Cytoplasm	translation regulator
E2F3B	GDE1	glycerophosphodiester phosphodiesterase 1	Plasma Membrane	enzyme
E2F3B	GGNBP2	gametogenetin binding protein 2	Other	other
E2F3B	GM5617	predicted gene 5617	Other	other
E2F3B	GM608	predicted gene 608	Other	other
E2F3B	GPHN	gephyrin	Plasma Membrane	enzyme
E2F3B	GSPT1	G1 to S phase transition 1	Cytoplasm	translation regulator
E2F3B	GTF2I	general transcription factor IIi	Nucleus	transcription regulator
E2F3B	GTF3C2	general transcription factor IIIC, polypeptide 2, beta 110kDa	Nucleus	transcription regulator
E2F3B	GTPBP10	GTP-binding protein 10 (putative)	Cytoplasm	other
E2F3B	HERPUD1	homocysteine-inducible, endoplasmic reticulum stress-inducible, ubiquitin-like domain member 1	Cytoplasm	other
E2F3B	HIPK1	homeodomain interacting protein kinase 1	Nucleus	kinase
E2F3B	HNRNPD	heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA binding protein 1, 37kDa)	Nucleus	transcription regulator
E2F3B	HNRNPR	heterogeneous nuclear ribonucleoprotein R	Nucleus	other
E2F3B	HSPA4	heat shock 70kDa protein 4	Cytoplasm	other
E2F3B	IPMK	inositol polyphosphate multikinase	Nucleus	kinase
E2F3B	IREB2	iron-responsive element binding protein 2	Cytoplasm	translation regulator
E2F3B	KIF13A	kinesin family member 13A	Cytoplasm	transporter
E2F3B	KIF1B	kinesin family member 1B	Cytoplasm	transporter
E2F3B	KPNA1	karyopherin alpha 1 (importin alpha 5)	Nucleus	transporter
E2F3B	LACTB	lactamase, beta	Cytoplasm	other
E2F3B	LATS2	large tumor suppressor kinase 2	Nucleus	kinase
E2F3B	LPP	LIM domain containing preferred translocation partner in lipoma	Nucleus	other
E2F3B	LYST	lysosomal trafficking regulator	Cytoplasm	transporter
E2F3B	MAPK1IP1L	mitogen-activated protein kinase 1 interacting protein 1-like	Nucleus	other
E2F3B	MARCH5	membrane-associated ring finger (C3HC4) 5	Cytoplasm	enzyme
E2F3B	MARVELD1	MARVEL domain containing 1	Other	other
E2F3B	MCCC1	methylcrotonoyl-CoA carboxylase 1 (alpha)	Cytoplasm	enzyme
E2F3B	MCCC2	methylcrotonoyl-CoA carboxylase 2 (beta)	Cytoplasm	enzyme
E2F3B	MCM10	minichromosome maintenance complex component 10	Nucleus	other
E2F3B	MEMO1	mediator of cell motility 1	Cytoplasm	other

Supplemental Table 12. E2F1 and/or E2FB HCC downregulated targets

Regulated by	Gene symbol	Entrez Gene Name	Location	Type
E2F3B	MON2	MON2 homolog, regulator of endosome-to-Golgi trafficking	Cytoplasm	other
E2F3B	MSH3	mutS homolog 3	Nucleus	enzyme
E2F3B	MTHFD1	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1, methenyltetrahydrofolate cyclohydrolase, formyltetrahydrofolate synthetase	Cytoplasm	enzyme
E2F3B	MTMR4	myotubularin related protein 4	Cytoplasm	phosphatase
E2F3B	MTO1	mitochondrial tRNA translation optimization 1	Cytoplasm	enzyme
E2F3B	MTRR	5-methyltetrahydrofolate-homocysteine methyltransferase reductase	Cytoplasm	enzyme
E2F3B	NAA16	N(alpha)-acetyltransferase 16, NatA auxiliary subunit	Nucleus	enzyme
E2F3B	NASP	nuclear autoantigenic sperm protein (histone-binding)	Nucleus	other
E2F3B	NAV2	neuron navigator 2	Nucleus	other
E2F3B	NEO1	neogenin 1	Plasma Membrane	transcription regulator
E2F3B	NFIB	nuclear factor I/B	Nucleus	transcription regulator
E2F3B	NFIX	nuclear factor I/X (CCAAT-binding transcription factor)	Nucleus	transcription regulator
E2F3B	NOL7	nucleolar protein 7, 27kDa	Nucleus	other
E2F3B	NUP153	nucleoporin 153kDa	Nucleus	transporter
E2F3B	NXT2	nuclear transport factor 2-like export factor 2	Nucleus	transporter
E2F3B	PA2G4	proliferation-associated 2G4, 38kDa	Nucleus	transcription regulator
E2F3B	PABPC1	poly(A) binding protein, cytoplasmic 1	Cytoplasm	translation regulator
E2F3B	PAICS	phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoimidazole succinocarboxamide synthetase	Cytoplasm	enzyme
E2F3B	PAN3	PAN3 poly(A) specific ribonuclease subunit	Cytoplasm	other
E2F3B	PDK1	pyruvate dehydrogenase kinase, isozyme 1	Cytoplasm	kinase
E2F3B	PDP2	pyruvate dehyrogenase phosphatase catalytic subunit 2	Cytoplasm	phosphatase
E2F3B	PEBP1	phosphatidylethanolamine binding protein 1	Cytoplasm	other
E2F3B	PHLPP1	PH domain and leucine rich repeat protein phosphatase 1	Cytoplasm	enzyme
E2F3B	PIH1D1	PIH1 domain containing 1	Other	other
E2F3B	PPP1CB	protein phosphatase 1, catalytic subunit, beta isozyme	Cytoplasm	phosphatase
E2F3B	PPP2R3A	protein phosphatase 2, regulatory subunit B'', alpha	Nucleus	phosphatase
E2F3B	PRPF19	pre-mRNA processing factor 19	Nucleus	other
E2F3B	PRPF4B	pre-mRNA processing factor 4B	Nucleus	kinase

Supplemental Table 12. E2F1 and/or E2FB HCC downregulated targets

Regulated by	Gene symbol	Entrez Gene Name	Location	Type
E2F3B	RAB2A	RAB2A, member RAS oncogene family	Cytoplasm	enzyme
E2F3B	RAD23B	RAD23 homolog B, nucleotide excision repair protein	Nucleus	other
E2F3B	RB1	retinoblastoma 1	Nucleus	transcription regulator
E2F3B	RBM33	RNA binding motif protein 33	Other	other
E2F3B	RBM39	RNA binding motif protein 39	Nucleus	transcription regulator
E2F3B	RCL1	RNA terminal phosphate cyclase-like 1	Nucleus	enzyme
E2F3B	RETSAT	retinol saturase (all-trans-retinol 13,14-reductase)	Cytoplasm	enzyme
E2F3B	RICTOR	RPTOR independent companion of MTOR, complex 2	Cytoplasm	other
E2F3B	RIF1	replication timing regulatory factor 1	Nucleus	other
E2F3B	RMND5A	required for meiotic nuclear division 5 homolog A	Nucleus	other
E2F3B	RORA	RAR-related orphan receptor A	Nucleus	ligand-dependent nuclear receptor
E2F3B	SERBP1	SERPINE1 mRNA binding protein 1	Cytoplasm	other
E2F3B	SF3B2	splicing factor 3b, subunit 2, 145kDa	Nucleus	other
E2F3B	SFPQ	splicing factor proline/glutamine-rich	Nucleus	other
E2F3B	SIN3A	SIN3 transcription regulator family member A	Nucleus	transcription regulator
E2F3B	SLC15A4	solute carrier family 15 (oligopeptide transporter), member 4	Cytoplasm	transporter
E2F3B	SLC25A32	solute carrier family 25 (mitochondrial folate carrier), member 32	Cytoplasm	transporter
E2F3B	SLC35A3	solute carrier family 35 (UDP-N-acetylglucosamine (UDP-GlcNAc) transporter), member A3	Cytoplasm	transporter
E2F3B	SLC35E3	solute carrier family 35, member E3	Other	other
E2F3B	SMARCC1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 1	Nucleus	transcription regulator
E2F3B	SMARCD2	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 2	Nucleus	transcription regulator
E2F3B	SMPD4	sphingomyelin phosphodiesterase 4, neutral membrane (neutral sphingomyelinase-3)	Cytoplasm	enzyme
E2F3B	SOS1	son of sevenless homolog 1 (Drosophila)	Cytoplasm	other
E2F3B	STARD7	StAR-related lipid transfer (START) domain containing 7	Other	other
E2F3B	STEAP2	STEAP family member 2, metalloreductase	Plasma Membrane	transporter
E2F3B	STK11IP	serine/threonine kinase 11 interacting protein	Cytoplasm	other
E2F3B	STX12	syntaxin 12	Cytoplasm	other
E2F3B	SYNCRIP	synaptotagmin binding, cytoplasmic RNA interacting protein	Nucleus	other

Supplemental Table 12. E2F1 and/or E2FB HCC downregulated targets

Regulated by	Gene symbol	Entrez Gene Name	Location	Type
E2F3B	SYNE2	spectrin repeat containing, nuclear envelope 2	Nucleus	other
E2F3B	TAF10	TAF10 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 30kDa	Nucleus	transcription regulator
E2F3B	TAF15	TAF15 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 68kDa	Nucleus	other
E2F3B	TANGO2	transport and golgi organization 2 homolog	Cytoplasm	other
E2F3B	TAOK1	TAO kinase 1	Cytoplasm	kinase
E2F3B	TARDBP	TAR DNA binding protein	Nucleus	transcription regulator
E2F3B	TBC1D4	TBC1 domain family, member 4	Cytoplasm	other
E2F3B	TCF7L2	transcription factor 7-like 2 (T-cell specific, HMG-box)	Nucleus	transcription regulator
E2F3B	TFDP2	transcription factor Dp-2 (E2F dimerization partner 2)	Nucleus	transcription regulator
E2F3B	TGS1	trimethylguanosine synthase 1	Nucleus	enzyme
E2F3B	TLE2	transducin-like enhancer of split 2	Nucleus	transcription regulator
E2F3B	TMEM245	transmembrane protein 245	Other	other
E2F3B	TMTC3	transmembrane and tetratricopeptide repeat containing 3	Other	other
E2F3B	TNPO1	transportin 1	Nucleus	transporter
E2F3B	TOMM70A	translocase of outer mitochondrial membrane 70 homolog A (S. cerevisiae)	Cytoplasm	transporter
E2F3B	TRIM33	tripartite motif containing 33	Nucleus	transcription regulator
E2F3B	TRIP4	thyroid hormone receptor interactor 4	Nucleus	transcription regulator
E2F3B	TTC14	tetratricopeptide repeat domain 14	Other	other
E2F3B	TTC7A	tetratricopeptide repeat domain 7A	Plasma Membrane	other
E2F3B	TYW1	tRNA-yW synthesizing protein 1 homolog (S. cerevisiae)	Other	other
E2F3B	U2SURP	U2 snRNP-associated SURP domain containing	Nucleus	other
E2F3B	UBE3C	ubiquitin protein ligase E3C	Nucleus	enzyme
E2F3B	UBE4B	ubiquitination factor E4B	Cytoplasm	other
E2F3B	UBR5	ubiquitin protein ligase E3 component n-recognin 5	Nucleus	enzyme
E2F3B	UGP2	UDP-glucose pyrophosphorylase 2	Cytoplasm	enzyme
E2F3B	USP34	ubiquitin specific peptidase 34	Extracellular Space	peptidase
E2F3B	USP38	ubiquitin specific peptidase 38	Other	peptidase
E2F3B	VPS13A	vacuolar protein sorting 13 homolog A (S. cerevisiae)	Cytoplasm	transporter
E2F3B	WAPAL	wings apart-like homolog (Drosophila)	Nucleus	other
E2F3B	WHSC1L1	Wolf-Hirschhorn syndrome candidate 1-like 1	Nucleus	enzyme
E2F3B	XIAP	X-linked inhibitor of apoptosis, E3 ubiquitin protein ligase	Cytoplasm	enzyme
E2F3B	XPNPEP3	X-prolyl aminopeptidase 3, mitochondrial	Cytoplasm	peptidase
E2F3B	XPO4	exportin 4	Nucleus	transporter

Supplemental Table 12. E2F1 and/or E2FB HCC downregulated targets

Regulated by	Gene symbol	Entrez Gene Name	Location	Type
E2F3B	XYLB	xylulokinase homolog (H. influenzae)	Cytoplasm	kinase
E2F3B	YTHDF3	YTH N(6)-methyladenosine RNA binding protein 3	Cytoplasm	other
E2F3B	ZBTB44	zinc finger and BTB domain containing 44	Other	other
E2F3B	ZC3H8	zinc finger CCCH-type containing 8	Nucleus	transcription regulator
E2F3B	ZCCHC2	zinc finger, CCHC domain containing 2	Cytoplasm	other
E2F3B	ZFP191	zinc finger protein 191	Nucleus	transcription regulator
E2F3B	ZFP318	zinc finger protein 381	Nucleus	other
E2F3B	ZFP644	zinc finger protein 644	Nucleus	other
E2F3B	ZFP68	zinc finger protein 68	Nucleus	other
E2F3B	ZHX3	zinc fingers and homeoboxes 3	Nucleus	transcription regulator

Supplemental Table 13. Expression of E2F1 and E2F3B putative direct targets in human liver disease

Group	Affymetrix ID	Gene Symbol	Regulated by	Normal medain	Cirrhotic medain	Dysplastic medain	Early HCC medain	Advanced HCC medain	Fold change Cirrhotic vs. Normal	Cirrhotic adj.pvalue	Fold change Adv HCC vs. Normal	Advanced HCC adj.pvalue
Advanced HCC	201292_at	TOP2A	E2F1	3.78	3.98	3.95	5.60	8.28	**1.05**	0.116	**2.19**	0.000 *
Advanced HCC	219148_at	PBK	E2F1	3.48	3.53	3.51	4.43	6.61	**1.02**	0.237	**1.90**	0.000 *
Advanced HCC	203764_at	DLGAP5	E2F3B	3.43	3.64	3.56	4.47	6.36	**1.06**	0.081	**1.85**	0.000 *
Advanced HCC	209714_s_at	CDKN3	E2F3B	4.49	4.53	4.45	5.77	7.76	**1.01**	0.624	**1.73**	0.000 *
Advanced HCC	227350_at	HELLS	E2F1	3.44	3.91	3.73	4.39	5.75	**1.14**	0.017 *	**1.67**	0.000 *
Advanced HCC	210559_s_at	CDK1	E2F1	4.55	4.95	4.86	5.71	7.54	**1.09**	0.137	**1.66**	0.000 *
Advanced HCC	218252_at	CKAP2	E2F1	4.31	5.00	4.74	5.46	6.61	**1.16**	0.006 *	**1.54**	0.000 *
Advanced HCC	225655_at	UHRF1	E2F1	4.07	4.46	4.27	4.99	6.13	**1.10**	0.074	**1.51**	0.000 *
Advanced HCC	203418_at	CCNA2	E2F1	4.08	4.12	3.96	4.49	6.14	**1.01**	0.702	**1.51**	0.000 *
Advanced HCC	203968_s_at	CDC6	E2F1	3.31	3.41	3.47	3.59	4.97	**1.03**	0.121	**1.50**	0.000 *
Advanced HCC	204092_s_at	AURKA	E2F1	5.20	5.44	5.61	6.20	7.76	**1.05**	0.060	**1.49**	0.000 *
Advanced HCC	226980_at	DEPDC1B	E2F1	2.91	3.05	2.93	3.25	4.32	**1.05**	0.002 *	**1.48**	0.000 *
Advanced HCC	218542_at	CEP55	E2F1	3.09	3.05	3.05	3.32	4.52	**0.99**	0.837	**1.47**	0.000 *
Advanced HCC	219493_at	SHCBP1	E2F1	3.06	3.20	3.15	3.47	4.28	**1.05**	0.036 *	**1.40**	0.000 *
Advanced HCC	209218_at	SQLE	E2F3B	7.05	7.27	6.64	8.69	9.63	**1.03**	0.650	**1.37**	0.000 *
Advanced HCC	203693_s_at	E2F3	E2F1	5.00	6.24	5.85	6.36	6.59	**1.25**	0.002 *	**1.32**	0.000 *
Advanced HCC	222593_s_at	SPATS2	E2F3B	5.35	5.88	5.70	6.44	6.86	**1.10**	0.001 *	**1.28**	0.000 *
Advanced HCC	202779_s_at	UBE2S	E2F3B	6.21	6.36	6.16	7.12	7.91	**1.02**	0.161	**1.27**	0.000 *
Advanced HCC	200783_s_at	STMN1	E2F1	5.90	6.16	5.84	6.61	7.46	**1.04**	0.045 *	**1.26**	0.000 *
Advanced HCC	201417_at	SOX4	E2F3B	6.99	8.52	8.35	8.09	8.82	**1.22**	0.000 *	**1.26**	0.000 *
Advanced HCC	224753_at	CDCA5	E2F1	5.31	5.24	5.28	5.59	6.71	**0.99**	0.935	**1.26**	0.000 *
Advanced HCC	210334_x_at	BIRC5	E2F1	5.19	5.23	5.08	5.43	6.52	**1.01**	0.295	**1.26**	0.000 *
Advanced HCC	225827_at	AGO2	E2F3B	6.06	6.27	6.34	6.96	7.54	**1.04**	0.255	**1.24**	0.000 *
Advanced HCC	238756_at	GAS2L3	E2F1	5.85	6.61	6.76	6.21	7.24	**1.13**	0.006 *	**1.24**	0.000 *
Advanced HCC	232676_x_at	MYEF2	E2F1	4.69	5.14	4.77	4.96	5.80	**1.10**	0.001 *	**1.24**	0.007 *
Advanced HCC	211980_at	COL4A1	E2F3B	8.17	9.71	9.14	9.83	9.93	**1.19**	0.001 *	**1.22**	0.000 *
Advanced HCC	201667_at	GJA1	E2F1	7.06	7.85	7.73	7.66	8.47	**1.11**	0.074	**1.20**	0.002 *
Advanced HCC	218741_at	CENPM	E2F3B	4.84	4.90	4.87	5.14	5.71	**1.01**	0.515	**1.18**	0.000 *
Advanced HCC	201897_s_at	CKS1B	E2F1	8.49	8.50	8.60	8.83	9.96	**1.00**	0.886	**1.17**	0.000 *
Advanced HCC	218308_at	TACC3	E2F1	5.44	5.54	5.37	5.77	6.37	**1.02**	0.221	**1.17**	0.000 *
Advanced HCC	201664_at	SMC4	E2F1	7.42	7.41	7.53	8.06	8.66	**1.00**	0.933	**1.17**	0.000 *
Advanced HCC	200639_s_at	YWHAZ	E2F3B	9.37	10.03	9.90	10.33	10.82	**1.07**	0.003 *	**1.16**	0.000 *
Advanced HCC	213523_at	CCNE1	E2F1	4.83	4.93	4.90	5.12	5.56	**1.02**	0.363	**1.15**	0.000 *

Supplemental Table 13. Expression of E2F1 and E2F3B putative direct targets in human liver disease

Group	Affymetrix ID	Gene Symbol	Regulated by	Normal medain	Cirrhotic medain	Dysplastic medain	Early HCC medain	Advanced HCC medain	Fold change Cirrhotic vs. Normal	Cirrhotic adj.pvalue	Fold change Adv HCC vs. Normal	Advanced HCC adj.pvalue
Advanced HCC	217946_s_at	SAE1	E2F3B	7.01	7.22	7.14	7.55	8.00	**1.03**	0.310	**1.14**	0.000 *
Advanced HCC	201662_s_at	ACSL3	E2F1	8.50	9.16	9.09	8.94	9.47	**1.08**	0.237	**1.11**	0.054
Advanced HCC	238670_at	RAD18	E2F1	4.83	4.62	4.90	5.02	5.32	**0.96**	0.925	**1.10**	0.033 *
Advanced HCC	200618_at	LASP1	E2F3B	9.22	9.58	9.16	9.69	10.12	**1.04**	0.036 *	**1.10**	0.000 *
Advanced HCC	223096_at	NOP58	E2F1	9.70	9.66	9.84	10.23	10.56	**1.00**	0.515	**1.09**	0.000 *
Advanced HCC	236265_at	SP4	E2F3B	6.63	6.93	6.23	6.91	7.21	**1.05**	0.273	**1.09**	0.008 *
Advanced HCC	224926_at	EXOC4	E2F1, E2F3B	7.41	7.45	7.45	7.83	8.01	**1.00**	0.473	**1.08**	0.000 *
Advanced HCC	201275_at	FDPS	E2F3B	9.84	9.13	9.16	9.77	10.52	**0.93**	1.000	**1.07**	0.008 *
Advanced HCC	205024_s_at	RAD51	E2F1	4.50	4.36	4.27	4.41	4.78	**0.97**	1.000	**1.06**	0.015 *
Advanced HCC	221699_s_at	DDX50	E2F1	8.10	8.15	7.95	8.23	8.59	**1.01**	0.515	**1.06**	0.006 *
Advanced HCC	208313_s_at	SF1	E2F3B	7.92	8.09	8.09	8.21	8.40	**1.02**	0.123	**1.06**	0.002 *
Advanced HCC	208881_x_at	IDI1	E2F1	9.62	9.39	9.38	9.98	10.18	**0.98**	0.837	**1.06**	0.022 *
Advanced HCC	208647_at	FDFT1	E2F3B	9.13	9.54	9.05	9.44	9.65	**1.05**	0.116	**1.06**	0.091
Advanced HCC	225032_at	FNDC3B	E2F3B	9.95	9.88	9.88	9.94	10.43	**0.99**	0.760	**1.05**	0.134
Advanced HCC	208668_x_at	HMGN2	E2F3B	11.08	11.23	11.01	11.36	11.58	**1.01**	0.065	**1.05**	0.002 *
Advanced HCC	208770_s_at	EIF4EBP2	E2F3B	8.67	8.50	8.55	8.70	9.02	**0.98**	1.000	**1.04**	0.013 *
Advanced HCC	202290_at	PDAP1	E2F3B	7.56	7.48	7.25	7.43	7.85	**0.99**	0.933	**1.04**	0.100
Advanced HCC	205967_at	HIST1H4A	E2F1	8.19	7.81	7.90	8.00	8.43	**0.95**	0.936	**1.03**	0.347
Advanced HCC	202314_at	CYP51A1	E2F3B	9.13	8.87	8.82	9.23	9.36	**0.97**	0.990	**1.03**	0.337
Advanced HCC	215716_s_at	ATP2B1	E2F3B	7.92	7.76	7.66	7.61	8.11	**0.98**	0.886	**1.02**	0.043 *
Advanced HCC	201156_s_at	RAB5C	E2F3B	7.80	7.77	7.69	7.66	7.93	**1.00**	0.904	**1.02**	0.557
Advanced HCC	225592_at	NRM	E2F3B	6.48	6.55	6.40	6.30	6.56	**1.01**	0.310	**1.01**	0.202
Advanced HCC	39729_at	PRDX2	E2F3B	10.73	10.56	10.59	10.55	10.74	**0.98**	0.935	**1.00**	0.718
Early HCC	225252_at	SRXN1	E2F3B	7.12	7.68	7.72	9.06	8.99	**1.08**	0.081	**1.26**	0.000 *
Early HCC	205463_s_at	PDGFA	E2F3B	5.43	6.53	5.93	6.67	6.60	**1.20**	0.002 *	**1.22**	0.017 *
Early HCC	209043_at	PAPSS1	E2F1	7.43	7.86	7.31	8.33	8.12	**1.06**	0.040 *	**1.09**	0.001 *
Early HCC	213051_at	ZC3HAV1	E2F3B	8.17	8.69	8.54	9.05	8.95	**1.06**	0.003 *	**1.10**	0.000 *
Early HCC	212642_s_at	HIVEP2	E2F1	6.48	6.84	6.98	7.11	6.68	**1.06**	0.002 *	**1.03**	0.067
Early HCC	213726_x_at	TUBB4B	E2F3B	9.43	9.45	9.56	10.12	10.08	**1.00**	0.446	**1.07**	0.003 *
Early HCC	201765_s_at	HEXA	E2F1	8.68	9.06	9.04	9.22	9.11	**1.04**	0.006 *	**1.05**	0.002 *
Early HCC	218634_at	PHLDA3	E2F1, E2F3B	6.23	6.34	6.39	6.53	6.12	**1.02**	0.019 *	**0.98**	0.771
Early HCC	201307_at	SEPT11	E2F3B	7.97	8.13	7.96	8.32	8.24	**1.02**	0.273	**1.03**	0.083

Supplemental Table 13. Expression of E2F1 and E2F3B putative direct targets in human liver disease

Group	Affymetrix ID	Gene Symbol	Regulated by	Normal medain	Cirrhotic medain	Dysplastic medain	Early HCC medain	Advanced HCC medain	Fold change Cirrhotic vs. Normal	Cirrhotic adj.pvalue	Fold change Adv HCC vs. Normal	Advanced HCC adj.pvalue
Early HCC	201952_at	ALCAM	E2F1	9.90	9.86	10.10	10.30	10.05	**1.00**	0.933	**1.02**	0.203
Early HCC	202133_at	WWTR1	E2F1	8.92	9.12	8.50	9.23	8.52	**1.02**	0.153	**0.95**	1.000
Early HCC	200801_x_at	ACTB	E2F3B	12.94	13.10	13.07	13.29	13.16	**1.01**	0.040 *	**1.02**	0.002 *
Dysplastic	229711_s_at	MDM2	E2F1	7.55	8.19	8.49	8.35	8.15	**1.08**	0.002 *	**1.08**	0.002 *
Dysplastic	212662_at	PVR	E2F1	6.66	7.28	7.47	7.33	6.93	**1.09**	0.040 *	**1.04**	0.249
Dysplastic	201204_s_at	RRBP1	E2F1, E2F3B	9.91	10.48	10.98	10.52	10.28	**1.06**	0.092	**1.04**	0.455
Dysplastic	222647_at	SLC35C1	E2F3B	7.63	8.32	8.35	8.22	7.40	**1.09**	0.255	**0.97**	0.940
Dysplastic	226748_at	LYSMD2	E2F3B	8.59	8.99	8.99	8.62	8.46	**1.05**	0.003 *	**0.99**	0.640
Dysplastic	224250_s_at	SECISBP2	E2F3B	8.07	7.77	8.42	8.01	8.27	**0.96**	0.936	**1.03**	0.258
Dysplastic	202704_at	TOB1	E2F3B	10.13	10.28	10.57	10.39	10.07	**1.01**	0.702	**0.99**	0.592
Dysplastic	202146_at	IFRD1	E2F1	8.13	7.94	8.28	8.26	8.10	**0.98**	0.933	**1.00**	0.672
Dysplastic	226247_at	PLEKHA1	E2F1	8.33	8.35	8.42	8.31	8.38	**1.00**	0.624	**1.01**	0.415
Dysplastic	204082_at	PBX3	E2F1	7.83	7.46	7.91	7.82	7.69	**0.95**	1.000	**0.98**	1.000
Dysplastic	201336_at	VAMP3	E2F3B	9.74	9.82	9.83	9.82	9.76	**1.01**	0.123	**1.00**	0.347
Dysplastic	218519_at	SLC35A5	E2F3B	7.94	7.93	7.96	7.64	7.63	**1.00**	0.886	**0.96**	1.000
Dysplastic	201806_s_at	ATXN2L	E2F1	6.25	5.98	6.27	6.21	6.26	**0.96**	1.000	**1.00**	0.672
Cirrhotic	201860_s_at	PLAT	E2F1	5.01	6.71	5.40	6.00	5.57	**1.34**	0.001 *	**1.11**	0.237
Cirrhotic	203570_at	LOXL1	E2F3B	4.95	6.35	5.17	5.60	5.08	**1.28**	0.000 *	**1.03**	0.578
Cirrhotic	201438_at	COL6A3	E2F3B	7.51	8.94	8.15	8.37	8.26	**1.19**	0.003 *	**1.10**	0.249
Cirrhotic	209099_x_at	JAG1	E2F3B	8.13	9.64	8.89	8.92	8.78	**1.19**	0.000 *	**1.08**	0.002 *
Cirrhotic	201666_at	TIMP1	E2F3B	10.36	12.02	11.72	11.26	10.21	**1.16**	0.052	**0.99**	0.950
Cirrhotic	201236_s_at	BTG2	E2F1, E2F3B	7.77	8.83	7.93	7.50	7.37	**1.14**	0.023 *	**0.95**	0.950
Cirrhotic	209101_at	CTGF	E2F3B	8.28	9.32	8.57	8.08	8.45	**1.13**	0.014 *	**1.02**	0.660
Cirrhotic	202284_s_at	CDKN1A	E2F1, E2F3B	8.51	9.55	9.31	8.82	7.94	**1.12**	0.005 *	**0.93**	1.000
Cirrhotic	200791_s_at	IQGAP1	E2F3B	8.40	9.19	8.64	8.46	8.58	**1.09**	0.001 *	**1.02**	0.592
Cirrhotic	201105_at	LGALS1	E2F1, E2F3B	9.88	10.56	9.76	10.11	10.11	**1.07**	0.005 *	**1.02**	0.455
Cirrhotic	201289_at	CYR61	E2F3B	9.86	10.41	9.99	8.66	7.79	**1.06**	0.065	**0.79**	1.000
Cirrhotic	1007_s_at	DDR1	E2F3B	7.08	7.47	7.00	6.82	7.05	**1.06**	0.001 *	**1.00**	0.337
Cirrhotic	217795_s_at	TMEM43	E2F1, E2F3B	7.05	7.42	7.14	7.20	7.09	**1.05**	0.026 *	**1.01**	0.258
Cirrhotic	208891_at	DUSP6	E2F1	10.21	10.74	10.21	9.86	9.64	**1.05**	0.005 *	**0.94**	1.000
Cirrhotic	238505_at	ADPRH	E2F3B	4.91	5.17	5.07	4.86	4.82	**1.05**	0.042 *	**0.98**	1.000

Supplemental Table 13. Expression of E2F1 and E2F3B putative direct targets in human liver disease

Group	Affymetrix ID	Gene Symbol	Regulated by	Normal medain	Cirrhotic medain	Dysplastic medain	Early HCC medain	Advanced HCC medain	Fold change Cirrhotic vs. Normal	Cirrhotic adj.pvalue	Fold change Adv HCC vs. Normal	Advanced HCC adj.pvalue
Cirrhotic	214755_at	UAP1L1	E2F3B	4.07	4.26	4.10	4.26	4.14	**1.05**	0.006 *	**1.02**	0.160
Cirrhotic	201920_at	SLC20A1	E2F1	8.68	9.04	8.99	8.78	8.79	**1.04**	0.161	**1.01**	0.347
Cirrhotic	211926_s_at	MYH9	E2F3B	8.35	8.68	8.57	8.58	8.66	**1.04**	0.007 *	**1.04**	0.015 *
Cirrhotic	1555832_s_at	KLF6	E2F3B	10.75	11.16	10.52	10.62	10.12	**1.04**	0.515	**0.94**	1.000
Cirrhotic	208690_s_at	PDLIM1	E2F3B	9.98	10.35	10.02	10.30	10.21	**1.04**	0.002 *	**1.02**	0.258
Cirrhotic	209191_at	TUBB6	E2F1, E2F3B	7.06	7.31	7.00	6.45	6.45	**1.04**	0.161	**0.91**	1.000
Cirrhotic	200621_at	CSRP1	E2F3B	9.26	9.59	9.24	9.09	8.53	**1.04**	0.026 *	**0.92**	1.000
Cirrhotic	202431_s_at	MYC	E2F1	9.43	9.67	9.62	8.55	9.35	**1.03**	0.310	**0.99**	0.771
Cirrhotic	201146_at	NFE2L2	E2F1	10.46	10.72	10.61	10.05	9.97	**1.02**	0.065	**0.95**	1.000
Cirrhotic	200871_s_at	PSAP	E2F3B	11.58	11.87	11.71	11.74	11.79	**1.02**	0.001 *	**1.02**	0.002 *
Cirrhotic	211535_s_at	FGFR1	E2F3B	7.20	7.30	7.19	6.76	6.84	**1.01**	0.123	**0.95**	1.000
Cirrhotic	201040_at	GNAI2	E2F3B	8.47	8.58	8.39	8.38	8.43	**1.01**	0.161	**1.00**	0.939
Cirrhotic	223361_at	ABRACL	E2F3B	7.36	7.44	7.41	7.17	7.03	**1.01**	0.446	**0.95**	0.991
Cirrhotic	41856_at	UNC5B	E2F1, E2F3B	7.18	7.19	7.11	6.97	6.98	**1.00**	0.624	**0.97**	1.000
Normal	212099_at	RHOB	E2F1	12.03	11.79	11.62	11.54	10.49	**0.98**	0.994	**0.87**	1.000
Normal	202241_at	TRIB1	E2F1	11.43	10.87	10.66	10.24	10.24	**0.95**	1.000	**0.90**	1.000
Normal	203752_s_at	JUND	E2F1, E2F3B	10.70	10.44	10.67	10.42	10.10	**0.98**	0.925	**0.94**	1.000
Normal	212845_at	SAMD4A	E2F3B	9.33	8.75	8.83	8.49	8.29	**0.94**	1.000	**0.89**	1.000
Normal	221689_s_at	PIGP	E2F1	9.15	8.90	8.85	9.06	8.99	**0.97**	1.000	**0.98**	1.000
Normal	219247_s_at	ZDHHC14	E2F3B	7.44	7.20	7.09	7.44	7.33	**0.97**	1.000	**0.99**	1.000
Normal	205249_at	EGR2	E2F1, E2F3B	7.37	6.62	6.11	5.49	5.23	**0.90**	1.000	**0.71**	1.000
Normal	212602_at	WDFY3	E2F3B	6.61	6.56	6.57	6.42	6.50	**0.99**	0.886	**0.98**	0.928
Normal	38037_at	HBEGF	E2F3B	6.44	6.42	6.25	5.84	5.80	**1.00**	0.577	**0.90**	1.000
Normal	230706_s_at	CAMK2N2	E2F1	5.67	5.67	5.65	5.58	5.59	**1.00**	0.925	**0.99**	0.940
Normal	226308_at	HAUS8	E2F3B	5.51	5.28	5.34	5.36	5.49	**0.96**	1.000	**1.00**	0.950
Normal	229423_at	CHEK1	E2F1	4.98	4.61	4.76	4.78	4.91	**0.92**	1.000	**0.99**	0.736

**P*-value vs. control Wilcoxon method with Benjamini–Hochberg (BH) correction.

Supplemental Table 14. General IPA functions for E2F1 and E2F3B putative direct targets

	Category	B-H p-valu	Genes
E2F1 upregulated	Cell Cycle	3.41E-10	WWTR1,SMC4,CAMK2N2,E2F3,CHEK1,STMN1,MYC,RAD51,CCNA2,RHOB,TOP2A,JUND,CDCA5,NFE2L2,TACC3,GJA1,UHRF1,CDC6,CKAP2,MDM2,HELLS,AURKA,BIRC5,CDK1,CCNE1,CDKN1A,BTG2,RAD18,CKS1B,CEP55,LGALS1
E2F1 upregulated	Cell Death and Survival	3.41E-10	DUSP6,UNC5B,CAMK2N2,E2F3,PBK,CHEK1,RAD51,STMN1,MYC,TRIB1,CCNA2,EGR2,RHOB,NOP58,TOP2A,JUND,IFRD1,NFE2L2,SLC20A1,TACC3,GJA1,UHRF1,RRBP1,PHLDA3,CDC6,MDM2,CKAP2,HELLS,AURKA,PVR,BIRC5,CDK1,CCNE1,TUBB6,PBX3,BTG2,CDKN1A,RAD18,ALCAM,LGALS1
E2F1 upregulated	Cellular Development	7.32E-09	DUSP6,WWTR1,UNC5B,CAMK2N2,E2F3,PBK,CHEK1,STMN1,MYC,RAD51,TRIB1,CCNA2,HIST1H4A,EGR2,RHOB,NOP58,TOP2A,CDCA5,JUND,IFRD1,NFE2L2,SLC20A1,TACC3,GJA1,UHRF1,RRBP1,CDC6,HELLS,MDM2,AURKA,BIRC5,CDK1,HIVEP2,CCNE1,EXOC4,PBX3,BTG2,CDKN1A,CKS1B,ALCAM,LGALS1
E2F1 upregulated	Cellular Growth and Proliferation	7.32E-09	DUSP6,WWTR1,UNC5B,HEXA,CAMK2N2,E2F3,PBK,CHEK1,STMN1,MYC,RAD51,TRIB1,CCNA2,EGR2,RHOB,NOP58,TOP2A,CDCA5,JUND,NFE2L2,SLC20A1,TACC3,GJA1,UHRF1,CDC6,HELLS,MDM2,AURKA,BIRC5,CDK1,HIVEP2,CCNE1,EXOC4,PBX3,BTG2,CDKN1A,RAD18,CKS1B,ALCAM,PLEKHA1,LGALS1
E2F1 upregulated	DNA Replication, Recombination, and Repair	1.63E-07	SMC4,E2F3,PBK,CHEK1,RAD51,MYC,STMN1,CCNA2,TOP2A,CDCA5,TACC3,GJA1,UHRF1,PHLDA3,CDC6,HELLS,MDM2,AURKA,BIRC5,CDK1,CCNE1,CDKN1A,BTG2,RAD18,CKS1B,LGALS1
E2F1 upregulated	Cancer	1.71E-07	DEPDC1B,IDI1,UNC5B,SMC4,PBK,STMN1,MYC,EGR2,RHOB,JUND,GJA1,ACSL3,MYEF2,RRBP1,CKAP2,HELLS,AURKA,BTG2,RAD18,ALCAM,CEP55,DUSP6,WWTR1,GAS2L3,E2F3,CAMK2N2,CHEK1,RAD51,CCNA2,TRIB1,NOP58,TOP2A,CDCA5,IFRD1,NFE2L2,SLC20A1,UHRF1,DDX50,PHLDA3,CDC6,MDM2,PVR,ATXN2L,BIRC5,CDK1,HIVEP2,CCNE1,EXOC4,PBX3,TUBB6,CDKN1A,CKS1B,PAPSS1,SPATS2,LGALS1
E2F1 upregulated	Connective Tissue Development and Function	4.74E-07	E2F3,CHEK1,STMN1,MYC,CCNA2,EGR2,RHOB,NOP58,JUND,CDCA5,NFE2L2,SLC20A1,GJA1,UHRF1,CDC6,MDM2,CKAP2,HELLS,AURKA,BIRC5,HIVEP2,CCNE1,BTG2,CDKN1A,RAD18,CKS1B
E2F1 upregulated	Organismal Injury and Abnormalities	4.88E-07	DEPDC1B,IDI1,UNC5B,SMC4,PBK,MYC,STMN1,EGR2,RHOB,JUND,ACSL3,GJA1,MYEF2,RRBP1,CKAP2,HELLS,AURKA,BTG2,RAD18,ALCAM,CEP55,WWTR1,DUSP6,GAS2L3,CAMK2N2,E2F3,CHEK1,RAD51,CCNA2,TRIB1,NOP58,TOP2A,CDCA5,IFRD1,NFE2L2,SLC20A1,UHRF1,DDX50,PHLDA3,CDC6,MDM2,PVR,ATXN2L,BIRC5,CDK1,HIVEP2,CCNE1,EXOC4,PBX3,TUBB6,CDKN1A,CKS1B,PAPSS1,SPATS2,LGALS1
E2F1 upregulated	Tumor Morphology	4.88E-07	GJA1,UHRF1,CDC6,MDM2,BIRC5,CDK1,CHEK1,MYC,RAD51,STMN1,TRIB1,CCNE1,RHOB,CDKN1A,BTG2,CKS1B,ALCAM,NFE2L2,LGALS1
E2F1 upregulated	Cellular Assembly and Organization	4.88E-07	WWTR1,UNC5B,SMC4,HEXA,GAS2L3,CHEK1,RAD51,MYC,STMN1,CCNA2,RHOB,TOP2A,IFRD1,TACC3,GJA1,UHRF1,RRBP1,CDC6,HELLS,MDM2,CKAP2,AURKA,PVR,BIRC5,CDK1,CCNE1,BTG2,CDKN1A,RAD18
E2F1 upregulated	Connective Tissue Disorders	5.01E-07	UNC5B,MDM2,BIRC5,CDK1,CHEK1,STMN1,MYC,CCNE1,EGR2,RHOB,CDKN1A,TOP2A,JUND,NFE2L2
E2F1 upregulated	Reproductive System Disease	1.18E-06	DEPDC1B,WWTR1,SMC4,CAMK2N2,E2F3,CHEK1,RAD51,STMN1,MYC,TRIB1,CCNA2,EGR2,RHOB,TOP2A,JUND,IFRD1,NFE2L2,SLC20A1,GJA1,ACSL3,UHRF1,RRBP1,DDX50,PHLDA3,CDC6,MDM2,AURKA,BIRC5,CDK1,HIVEP2,CCNE1,TUBB6,EXOC4,BTG2,CDKN1A,CKS1B,ALCAM,SPATS2,CEP55,LGALS1
E2F1 upregulated	Respiratory Disease	2.15E-06	MYEF2,DUSP6,CDC6,HELLS,MDM2,AURKA,BIRC5,CDK1,STMN1,MYC,CCNA2,CDKN1A,TOP2A,CKS1B,ALCAM,CDCA5,NFE2L2,LGALS1
E2F1 upregulated	Cellular Movement	2.77E-06	DUSP6,WWTR1,UNC5B,E2F3,PBK,MYC,STMN1,CCNA2,TRIB1,EGR2,RHOB,TOP2A,JUND,NFE2L2,GJA1,CDC6,MDM2,CKAP2,AURKA,PVR,BIRC5,CDK1,BTG2,CDKN1A,ALCAM,CEP55,LGALS1
E2F1 upregulated	Renal and Urological Disease	1.50E-05	ACSL3,DUSP6,WWTR1,UNC5B,HELLS,MDM2,AURKA,ATXN2L,E2F3,BIRC5,CDK1,MYC,STMN1,RAD51,TRIB1,CCNA2,EXOC4,RHOB,BTG2,CDKN1A,TOP2A,NFE2L2

Supplemental Table 14. General IPA functions for E2F1 and E2F3B putative direct targets

	Category	B-H p-valu	Genes
E2F1 upregulated	Hematological Disease	2.19E-05	E2F3,CHEK1,MYC,STMN1,RAD51,TRIB1,CCNA2,EGR2,RHOB,TOP2A,NFE2L2,SLC20A1,RRBP1,HELLS,MDM2,AURKA,BIRC5,CDK1,EXOC4,PBX3,CDKN1A,BTG2,PAPSS1,CEP55,LGALS1
E2F1 upregulated	Immunological Disease	2.19E-05	MDM2,AURKA,BIRC5,CDK1,CHEK1,RAD51,MYC,STMN1,CCNA2,EGR2,RHOB,CDKN1A,BTG2,TOP2A,NFE2L2,LGALS1
E2F1 upregulated	Gene Expression	2.39E-05	WWTR1,E2F3,MYC,CCNA2,EGR2,RHOB,TOP2A,JUND,IFRD1,NFE2L2,SLC20A1,GJA1,UHRF1,RRBP1,CKAP2,MDM2,HELLS,BIRC5,CDK1,HIVEP2,CCNE1,PBX3,CDKN1A,BTG2,LGALS1
E2F1 upregulated	Cell Morphology	2.40E-05	TACC3,GJA1,WWTR1,HEXA,HELLS,MDM2,AURKA,E2F3,BIRC5,CDK1,HIVEP2,CHEK1,RAD51,STMN1,MYC,TRIB1,CCNA2,RHOB,CDKN1A,RAD18,NFE2L2,LGALS1
E2F1 upregulated	Cellular Function and Maintenance	2.40E-05	WWTR1,UNC5B,HEXA,GAS2L3,CHEK1,MYC,STMN1,RAD51,EGR2,RHOB,IFRD1,NFE2L2,TACC3,GJA1,RRBP1,CKAP2,MDM2,PVR,AURKA,BIRC5,CDK1,HIVEP2,CDKN1A,BTG2,RAD18,LGALS1
E2F1 upregulated	Tissue Morphology	4.29E-05	SLC20A1,GJA1,TACC3,UHRF1,DUSP6,HELLS,MDM2,E2F3,BIRC5,HIVEP2,STMN1,MYC,TRIB1,CCNA2,CCNE1,SHCBP1,EGR2,RHOB,CDKN1A,BTG2,RAD18,ALCAM,NFE2L2,LGALS1
E2F1 upregulated	Embryonic Development	5.08E-05	SLC20A1,TACC3,GJA1,WWTR1,DUSP6,MDM2,AURKA,E2F3,BIRC5,CHEK1,RAD51,MYC,CCNA2,CCNE1,EGR2,PBX3,BTG2,CDKN1A,PLEKHA1,NFE2L2
E2F1 upregulated	Renal and Urological System Development and Function	5.90E-05	MYC,DUSP6,NOP58,CDKN1A,UNC5B,CDCA5,AURKA,E2F3,BIRC5
E2F1 upregulated	Tissue Development	7.74E-05	WWTR1,HEXA,E2F3,CHEK1,STMN1,MYC,RAD51,TRIB1,CCNA2,EGR2,RHOB,JUND,NFE2L2,SLC20A1,GJA1,TACC3,RRBP1,CDC6,MDM2,AURKA,BIRC5,CDK1,HIVEP2,CCNE1,PBX3,BTG2,CDKN1A,RAD18,PLEKHA1,LGALS1
E2F1 upregulated	Developmental Disorder	7.78E-05	SLC20A1,GJA1,TACC3,UHRF1,WWTR1,CDC6,HEXA,HELLS,MDM2,AURKA,E2F3,BIRC5,MYC,CCNA2,TRIB1,CCNE1,EGR2,PBX3,EXOC4,CDKN1A,NFE2L2
E2F1 upregulated	Digestive System Development and Function	8.50E-05	MYC,SLC20A1,CCNE1,GJA1,CDKN1A,JUND,NFE2L2,LGALS1
E2F1 upregulated	Hepatic System Development and Function	8.50E-05	MYC,SLC20A1,CCNE1,CDKN1A,JUND,E2F3,NFE2L2,LGALS1
E2F1 upregulated	Organ Development	8.50E-05	SLC20A1,GJA1,E2F3,BIRC5,MYC,TRIB1,CCNE1,EGR2,NOP58,CDKN1A,JUND,NFE2L2,LGALS1
E2F1 upregulated	Skeletal and Muscular System Development and Function	1.40E-04	GJA1,RRBP1,DUSP6,WWTR1,MDM2,E2F3,BIRC5,HIVEP2,MYC,STMN1,CCNA2,TRIB1,CCNE1,CDKN1A,JUND,NFE2L2
E2F1 upregulated	Cell-To-Cell Signaling and Interaction	1.73E-04	MYC,GJA1,RHOB,CDKN1A,TOP2A,MDM2,PVR,BIRC5,CHEK1
E2F1 upregulated	Inflammatory Response	1.73E-04	GJA1,IDI1,MDM2,E2F3,PBK,BIRC5,MYC,CCNA2,SHCBP1,EGR2,CDKN1A,TOP2A,ALCAM,PLEKHA1,NFE2L2,LGALS1
E2F1 upregulated	Cellular Response to Therapeutics	1.73E-04	AURKA,NFE2L2
E2F1 upregulated	Hematological System Development and Function	1.73E-04	SLC20A1,GJA1,TACC3,MDM2,HELLS,BIRC5,CDK1,HIVEP2,CHEK1,MYC,TRIB1,HIST1H4A,SHCBP1,EGR2,CDKN1A,BTG2,TOP2A,NFE2L2,LGALS1
E2F1 upregulated	Hematopoiesis	1.73E-04	MYC,SLC20A1,TACC3,GJA1,EGR2,CDKN1A,HELLS,NFE2L2,BIRC5,CDK1,HIVEP2,CHEK1

Supplemental Table 14. General IPA functions for E2F1 and E2F3B putative direct targets

	Category	B-H p-valu	Genes
E2F1 upregulated	Dermatological Diseases and Conditions	1.96E-04	MYC,GJA1,CDKN1A,HELLS,MDM2,BIRC5,NFE2L2
E2F1 upregulated	Cardiovascular System Development and Function	2.15E-04	MYC,TRIB1,CCNA2,GJA1,CDKN1A,E2F3,NFE2L2,BIRC5
E2F1 upregulated	Hereditary Disorder	4.33E-04	MYC,CCNA2,EXOC4,WWTR1,CDKN1A,BIRC5
E2F1 upregulated	Skeletal and Muscular Disorders	5.00E-04	MYC,DUSP6,CDKN1A,JUND,MDM2,E2F3,CAMK2N2,BIRC5
E2F1 upregulated	Organ Morphology	5.29E-04	MYC,TRIB1,GJA1,TACC3,DUSP6,CDKN1A,HELLS,MDM2,BIRC5,NFE2L2,HIVEP2
E2F1 upregulated	Cardiovascular Disease	5.75E-04	SLC20A1,GJA1,DUSP6,MDM2,AURKA,CAMK2N2,E2F3,BIRC5,CDK1,MYC,CCNA2,CCNE1,PBX3,CDKN1A,TOP2A,ALCAM,JUND
E2F1 upregulated	Hair and Skin Development and Function	7.15E-04	MYC,CCNE1,CDKN1A,E2F3,NFE2L2
E2F1 upregulated	Endocrine System Disorders	8.63E-04	UNC5B,SMC4,CAMK2N2,E2F3,BIRC5,CDK1,CHEK1,MYC,CDKN1A,TOP2A,ALCAM,CDCA5,LGALS1
E2F1 upregulated	Reproductive System Development and Function	8.63E-04	MYC,SLC20A1,TRIB1,GJA1,CCNE1,NOP58,CDKN1A,RAD18,HEXA,E2F3
E2F1 upregulated	Neurological Disease	9.32E-04	GJA1,DUSP6,UNC5B,HEXA,E2F3,BIRC5,CDK1,CHEK1,MYC,TRIB1,EGR2,CDKN1A,BTG2,TOP2A,IFRD1,NFE2L2,LGALS1
E2F1 upregulated	Lymphoid Tissue Structure and Development	1.02E-03	SLC20A1,TACC3,GJA1,MDM2,HELLS,BIRC5,HIVEP2,CHEK1,MYC,TRIB1,EGR2,CDKN1A,ALCAM,NFE2L2
E2F1 upregulated	Organismal Survival	1.18E-03	SLC20A1,TACC3,GJA1,UHRF1,HEXA,HELLS,MDM2,AURKA,CAMK2N2,E2F3,BIRC5,CDK1,CHEK1,MYC,RAD51,CCNA2,CCNE1,EGR2,PBX3,CDKN1A,TOP2A,CKS1B,NFE2L2,LGALS1
E2F1 upregulated	Post-Translational Modification	1.21E-03	WWTR1,DUSP6,CDC6,AURKA,PBK,BIRC5,CDK1,CHEK1,RAD51,CCNE1,CDKN1A,CKS1B,LGALS1
E2F1 upregulated	Gastrointestinal Disease	1.65E-03	IDI1,DUSP6,WWTR1,UNC5B,SMC4,GAS2L3,PBK,CHEK1,MYC,RAD51,CCNA2,EGR2,NOP58,TOP2A,JUND,CDCA5,NFE2L2,SLC20A1,GJA1,ACSL3,MYEF2,DDX50,CDC6,MDM2,HELLS,CKAP2,PVR,AURKA,ATXN2L,BIRC5,CDK1,HIVEP2,EXOC4,CDKN1A,PAPSS1,RAD18,ALCAM,CEP55,LGALS1
E2F1 upregulated	Nervous System Development and Function	2.04E-03	GJA1,UNC5B,E2F3,NFE2L2,CDK1,CHEK1
E2F1 upregulated	Free Radical Scavenging	3.03E-03	MYC,CDKN1A,BIRC5,NFE2L2,PBK
E2F1 upregulated	Molecular Transport	3.03E-03	MYC,TRIB1,CDKN1A,JUND,BIRC5,PBK,NFE2L2
E2F1 upregulated	Organismal Development	3.21E-03	SLC20A1,GJA1,UHRF1,WWTR1,DUSP6,MDM2,AURKA,E2F3,BIRC5,CDK1,CHEK1,RAD51,MYC,CCNA2,CCNE1,EGR2,PBX3,CDKN1A,CKS1B,JUND,PLEKHA1,IFRD1,NFE2L2,LGALS1

Supplemental Table 14. General IPA functions for E2F1 and E2F3B putative direct targets

	Category	B-H p-valu	Genes
E2F1 upregulated	Respiratory System Development and Function	3.41E-03	MYC,GJA1,PBX3,BTG2,CDKN1A,HEXA,MDM2,NFE2L2,LGALS1
E2F1 upregulated	Energy Production	3.47E-03	CDC6,TOP2A,CDK1
E2F1 upregulated	Nucleic Acid Metabolism	3.47E-03	STMN1,CDC6,TOP2A,CDK1
E2F1 upregulated	Small Molecule Biochemistry	3.47E-03	STMN1,CDC6,TOP2A,PBK,CDK1,CHEK1
E2F1 upregulated	Amino Acid Metabolism	3.65E-03	PBK,CDK1,CHEK1
E2F1 upregulated	Cellular Compromise	4.03E-03	MYC,CDKN1A,MDM2
E2F1 upregulated	Protein Trafficking	4.03E-03	MDM2,PLEKHA1,CEP55
E2F1 upregulated	Cell-mediated Immune Response	4.26E-03	EGR2,CDKN1A,BIRC5,CHEK1
E2F1 upregulated	Hepatic System Disease	4.26E-03	MYC,SLC20A1,CDKN1A,JUND,NFE2L2
E2F3B upregulated	Cancer	4.95E-09	DLGAP5,MYH9,CTGF,ATP2B1,UNC5B,KLF6,FNDC3B,SLC35C1,ZDHHC14,SECISBP2,FDFT1,EGR2,JUND,SOX4,LIPT2,COL4A1,HMGN2,RRBP1,FGFR1,ZC3HAV1,YWHAZ,HBEGF,UBE2S,DDR1,SP4,COL6A3,BTG2,LOXL1,PDLIM1,CYR61,JAG1,SAMD4A,PRDX2,SQLE,EIF4EBP2,PDGFA,IQGAP1,CDKN3,WDFY3,TIMP1,CYP51A1,LASP1,PLAT,SLC35A5,HAUS8,TUBB4B,ACTB,PHLDA3,TOB1,AGO2,FDPS,PDAP1,GNAI2,TUBB6,EXOC4,PVT1,UAP1L1,CDKN1A,PSAP,SF1,LGALS1
E2F3B upregulated	Organismal Injury and Abnormalities	4.95E-09	DLGAP5,MYH9,CTGF,ATP2B1,UNC5B,KLF6,FNDC3B,SLC35C1,ZDHHC14,SECISBP2,FDFT1,EGR2,JUND,SOX4,LIPT2,COL4A1,HMGN2,RRBP1,FGFR1,ZC3HAV1,YWHAZ,HBEGF,UBE2S,DDR1,SP4,COL6A3,BTG2,LOXL1,PDLIM1,TMEM43,CYR61,JAG1,SAMD4A,PRDX2,SQLE,PDGFA,IQGAP1,CDKN3,WDFY3,TIMP1,CYP51A1,LASP1,PLAT,SLC35A5,HAUS8,TUBB4B,ACTB,PHLDA3,TOB1,AGO2,PDAP1,FDPS,GNAI2,EXOC4,TUBB6,PVT1,UAP1L1,CDKN1A,PSAP,SF1,LGALS1
E2F3B upregulated	Cellular Movement	4.78E-07	CTGF,MYH9,PDGFA,KLF6,UNC5B,FNDC3B,IQGAP1,CDKN3,EGR2,TIMP1,JUND,LASP1,PLAT,SOX4,COL4A1,FGFR1,ACTB,YWHAZ,AGO2,HBEGF,DDR1,GNAI2,CDKN1A,BTG2,PDLIM1,SF1,JAG1,CYR61,LGALS1,PRDX2
E2F3B upregulated	Cardiovascular System Development and Function	1.10E-05	SOX4,MYH9,COL4A1,CTGF,PDGFA,FGFR1,KLF6,UNC5B,YWHAZ,AGO2,HBEGF,DDR1,TIMP1,CDKN1A,PSAP,JUND,JAG1,CYR61,CYP51A1,LASP1,PRDX2,LGALS1,PLAT
E2F3B upregulated	Organismal Development	1.10E-05	MYH9,CTGF,EIF4EBP2,PDGFA,UNC5B,KLF6,SLC35C1,FNDC3B,IQGAP1,SECISBP2,FDFT1,EGR2,TIMP1,JUND,LASP1,CYP51A1,PLAT,SOX4,COL4A1,FGFR1,ZC3HAV1,YWHAZ,HBEGF,AGO2,DDR1,SP4,GNAI2,COL6A3,CDKN1A,LOXL1,BTG2,PSAP,JAG1,CYR61,LGALS1,PRDX2
E2F3B upregulated	Cellular Growth and Proliferation	1.64E-05	DLGAP5,MYH9,CTGF,EIF4EBP2,PDGFA,UNC5B,KLF6,CSRP1,FNDC3B,IQGAP1,SECISBP2,CDKN3,FDFT1,SAE1,EGR2,TIMP1,JUND,LASP1,PLAT,SOX4,COL4A1,TUBB4B,ACTB,FGFR1,YWHAZ,TOB1,HBEGF,AGO2,DDR1,SP4,GNAI2,PDAP1,EXOC4,COL6A3,BTG2,CDKN1A,PSAP,SF1,JAG1,CYR61,LGALS1,PRDX2
E2F3B upregulated	Visual System Development and Function	2.27E-05	CTGF,TIMP1,PDGFA,FGFR1,CYR61,PLAT,LGALS1
E2F3B upregulated	Cell Death and Survival	3.81E-05	MYH9,CTGF,PDGFA,ATP2B1,KLF6,UNC5B,IQGAP1,CDKN3,FDFT1,EGR2,TIMP1,VAMP3,JUND,PLAT,SOX4,COL4A1,HAUS8,RRBP1,PHLDA3,ACTB,FGFR1,YWHAZ,AGO2,HBEGF,UBE2S,SRXN1,DDR1,GNAI2,FDPS,TUBB6,CDKN1A,BTG2,PSAP,JAG1,CYR61,LGALS1,PRDX2

Supplemental Table 14. General IPA functions for E2F1 and E2F3B putative direct targets

	Category	B-H p-valu	Genes
E2F3B upregulated	Reproductive System Disease	3.81E-05	SQLE,MYH9,CTGF,PDGFA,ATP2B1,KLF6,FNDC3B,SLC35C1,IQGAP1,ZDHHC14,CDKN3,FDFT1,EGR2,WDFY3,TIMP1,JUND,CYP51A1,LASP1,PLAT,SOX4,COL4A1,HAUS8,RRBP1,TUBB4B,FGFR1,PHLDA3,YWHAZ,ZC3HAV1,AGO2,HBEGF,UBE2S,DDR1,PDAP1,GNAI2,FDPS,EXOC4,TUBB6,COL6A3,BTG2,LOXL1,CDKN1A,PDLIM1,SF1,CYR61,JAG1,SAMD4A,LGALS1
E2F3B upregulated	Cellular Assembly and Organization	4.53E-05	DLGAP5,MYH9,RAB5C,CTGF,EIF4EBP2,ATP2B1,PDGFA,UNC5B,CSRP1,IQGAP1,TIMP1,VAMP3,JUND,LASP1,PLAT,HAUS8,RRBP1,ACTB,FGFR1,YWHAZ,DDR1,SP4,GNAI2,COL6A3,EXOC4,BTG2,CDKN1A,PSAP,JAG1,CYR61,LGALS1
E2F3B upregulated	Cellular Function and Maintenance	4.53E-05	DLGAP5,RAB5C,MYH9,CTGF,EIF4EBP2,ATP2B1,PDGFA,UNC5B,CSRP1,FNDC3B,IQGAP1,EGR2,VAMP3,LASP1,PLAT,HAUS8,RRBP1,FGFR1,ACTB,DDR1,SP4,GNAI2,BTG2,CDKN1A,PSAP,JAG1,CYR61,LGALS1
E2F3B upregulated	Renal and Urological Disease	6.15E-05	DLGAP5,CTGF,MYH9,ATP2B1,KLF6,SECISBP2,FDFT1,WDFY3,TIMP1,JUND,CYP51A1,PLAT,SLC35A5,COL4A1,TUBB4B,FGFR1,ACTB,PHLDA3,HBEGF,DDR1,SP4,FDPS,COL6A3,PVT1,BTG2,CDKN1A,LOXL1,PDLIM1,PSAP,CYR61,PRDX2
E2F3B upregulated	Inflammatory Response	6.23E-05	CTGF,MYH9,UNC5B,CSRP1,SLC35C1,EGR2,TIMP1,CYP51A1,PLAT,COL4A1,TUBB4B,ACTB,FGFR1,AGO2,TOB1,HBEGF,DDR1,GNAI2,CDKN1A,PSAP,PDLIM1,CYR61,JAG1,PRDX2,LGALS1
E2F3B upregulated	Hereditary Disorder	6.23E-05	MYH9,COL4A1,CTGF,ATP2B1,FGFR1,ACTB,YWHAZ,FDPS,FDFT1,EGR2,COL6A3,LOXL1,PDLIM1,PSAP,TMEM43,JAG1,CYP51A1,PRDX2
E2F3B upregulated	Skeletal and Muscular Disorders	6.23E-05	SQLE,CTGF,PDGFA,ATP2B1,NRM,IQGAP1,FDFT1,EGR2,TIMP1,JUND,CYP51A1,PLAT,SOX4,COL4A1,TUBB4B,FGFR1,ACTB,YWHAZ,HBEGF,DDR1,GNAI2,FDPS,COL6A3,CDKN1A,LOXL1,PDLIM1,TMEM43,CYR61,JAG1,LGALS1,PRDX2
E2F3B upregulated	Hematological Disease	7.54E-05	MYH9,CTGF,PDGFA,IQGAP1,FDFT1,EGR2,TIMP1,CYP51A1,PLAT,SOX4,COL4A1,TUBB4B,RRBP1,FGFR1,ACTB,YWHAZ,ZC3HAV1,HBEGF,DDR1,FDPS,COL6A3,EXOC4,CDKN1A,BTG2,JAG1,CYR61,LGALS1
E2F3B upregulated	Cardiovascular Disease	7.54E-05	SOX4,COL4A1,CTGF,MYH9,TUBB4B,PDGFA,FGFR1,KLF6,HBEGF,DDR1,SP4,GNAI2,TIMP1,CDKN1A,TMEM43,JUND,JAG1,CYR61,SAMD4A,CYP51A1,PRDX2,PLAT
E2F3B upregulated	Gastrointestinal Disease	7.54E-05	SOX4,DLGAP5,COL4A1,CTGF,TUBB4B,PDGFA,FGFR1,HBEGF,GNAI2,CDKN3,COL6A3,TIMP1,LOXL1,CDKN1A,BTG2,JUND,CYR61,JAG1,CYP51A1,LGALS1,PLAT
E2F3B upregulated	Hepatic System Disease	7.54E-05	CDKN3,CTGF,COL4A1,PDGFA,TIMP1,FGFR1,CDKN1A,HBEGF,JUND,PLAT
E2F3B upregulated	Cell-To-Cell Signaling and Interaction	7.81E-05	MYH9,CTGF,PDGFA,ACTB,FGFR1,KLF6,HBEGF,CSRP1,IQGAP1,GNAI2,EGR2,TIMP1,CDKN1A,CYR61,JAG1,LGALS1,PLAT,PRDX2
E2F3B upregulated	Hematological System Development and Function	7.81E-05	SOX4,CTGF,COL4A1,MYH9,ACTB,UNC5B,HBEGF,TOB1,CSRP1,SLC35C1,DDR1,GNAI2,EGR2,TIMP1,CDKN1A,VAMP3,PSAP,JUND,CYR61,JAG1,LGALS1,PLAT,PRDX2
E2F3B upregulated	Tissue Development	7.87E-05	DLGAP5,CTGF,MYH9,EIF4EBP2,PDGFA,UNC5B,CSRP1,SLC35C1,FNDC3B,IQGAP1,SECISBP2,EGR2,TIMP1,JUND,CYP51A1,PLAT,SOX4,COL4A1,RRBP1,ACTB,FGFR1,YWHAZ,AGO2,TOB1,HBEGF,DDR1,SP4,GNAI2,COL6A3,EXOC4,LOXL1,BTG2,CDKN1A,PSAP,CYR61,JAG1,PRDX2,LGALS1
E2F3B upregulated	Endocrine System Disorders	7.97E-05	CTGF,MYH9,UNC5B,KLF6,FNDC3B,ZDHHC14,CDKN3,EGR2,TIMP1,LASP1,PLAT,COL4A1,TUBB4B,RRBP1,FGFR1,HBEGF,DDR1,GNAI2,PDAP1,FDPS,COL6A3,CDKN1A,BTG2,LOXL1,CYR61,PRDX2
E2F3B upregulated	Cellular Development	8.19E-05	DLGAP5,MYH9,CTGF,EIF4EBP2,PDGFA,UNC5B,KLF6,CSRP1,FNDC3B,IQGAP1,SECISBP2,CDKN3,FDFT1,EGR2,TIMP1,JUND,PLAT,SOX4,COL4A1,RRBP1,FGFR1,ACTB,YWHAZ,AGO2,TOB1,HBEGF,DDR1,SP4,GNAI2,EXOC4,COL6A3,CDKN1A,BTG2,PSAP,JAG1,CYR61,LGALS1,PRDX2
E2F3B upregulated	Cell Morphology	9.12E-05	CTGF,MYH9,EIF4EBP2,PDGFA,RRBP1,ATP2B1,ACTB,FGFR1,UNC5B,YWHAZ,HBEGF,CSRP1,IQGAP1,DDR1,SP4,EXOC4,TIMP1,CDKN1A,BTG2,PSAP,CYR61,LASP1,LGALS1,PLAT
E2F3B upregulated	Organismal Survival	1.13E-04	MYH9,CTGF,PDGFA,ATP2B1,KLF6,FNDC3B,SLC35C1,SECISBP2,CDKN3,FDFT1,EGR2,TIMP1,CYP51A1,PLAT,SOX4,COL4A1,FGFR1,ACTB,HBEGF,AGO2,SRXN1,DDR1,SP4,GNAI2,CDKN1A,PSAP,CYR61,JAG1

Supplemental Table 14. General IPA functions for E2F1 and E2F3B putative direct targets

	Category	B-H p-valu	Genes
E2F3B upregulated	Developmental Disorder	1.41E-04	MYH9,CTGF,PDGFA,SLC35C1,FDFT1,EGR2,TIMP1,CYP51A1,PLAT,SOX4,COL4A1,FGFR1,ACTB,HBEGF,AGO2,DDR1,GNAI2,FDPS,COL6A3,EXOC4,CDKN1A,LOXL1,PSAP,TMEM43,JAG1
E2F3B upregulated	Connective Tissue Development and Function	1.51E-04	SOX4,CTGF,PDGFA,FGFR1,ACTB,KLF6,HBEGF,TOB1,FNDC3B,IQGAP1,DDR1,GNAI2,EGR2,TIMP1,BTG2,CDKN1A,JUND,CYR61,JAG1,PLAT,LGALS1
E2F3B upregulated	Embryonic Development	2.59E-04	MYH9,CTGF,EIF4EBP2,PDGFA,KLF6,CSRP1,SLC35C1,FNDC3B,SECISBP2,EGR2,TIMP1,JUND,CYP51A1,PLAT,SOX4,COL4A1,FGFR1,AGO2,HBEGF,DDR1,SP4,COL6A3,CDKN1A,LOXL1,BTG2,PSAP,JAG1,CYR61,LGALS1,PRDX2
E2F3B upregulated	Organ Development	2.59E-04	SOX4,CTGF,MYH9,PDGFA,FGFR1,HBEGF,TOB1,SLC35C1,DDR1,EGR2,COL6A3,TIMP1,LOXL1,CDKN1A,PSAP,JUND,CYR61,JAG1,CYP51A1,LGALS1
E2F3B upregulated	Organ Morphology	2.59E-04	SOX4,CTGF,PDGFA,FGFR1,AGO2,HBEGF,SLC35C1,IQGAP1,DDR1,SP4,EGR2,TIMP1,CDKN1A,LOXL1,PSAP,JUND,JAG1,CYP51A1,LASP1,PLAT
E2F3B upregulated	Nervous System Development and Function	2.59E-04	SOX4,COL4A1,MYH9,EIF4EBP2,FGFR1,ACTB,YWHAZ,CSRP1,HBEGF,IQGAP1,SECISBP2,DDR1,SP4,GNAI2,EGR2,EXOC4,CDKN1A,BTG2,PSAP,JAG1,CYR61,LGALS1,PLAT
E2F3B upregulated	Respiratory System Development and Function	2.59E-04	SOX4,CTGF,PDGFA,FGFR1,CDKN1A,LOXL1,HBEGF,SLC35C1,LGALS1
E2F3B upregulated	Digestive System Development and Function	3.98E-04	CTGF,PDGFA,FGFR1,TOB1,HBEGF,IQGAP1,GNAI2,TIMP1,LOXL1,CDKN1A,PSAP,JUND,JAG1,CYP51A1,LGALS1
E2F3B upregulated	Hepatic System Development and Function	3.98E-04	CTGF,TIMP1,CDKN1A,HBEGF,TOB1,JUND,LGALS1
E2F3B upregulated	Dermatological Diseases and Conditions	5.21E-04	SQLE,COL4A1,COL6A3,LOXL1,PSAP,JAG1,CYP51A1
E2F3B upregulated	Infectious Diseases	5.21E-04	SOX4,SQLE,RAB5C,EIF4EBP2,HMGN2,TUBB4B,FGFR1,ACTB,ZC3HAV1,AGO2,FDPS,SAE1,TIMP1,PVT1,BTG2,VAMP3,CYP51A1,LGALS1,PLAT,PRDX2
E2F3B upregulated	Connective Tissue Disorders	5.89E-04	SQLE,MYH9,CTGF,PDGFA,UNC5B,NRM,FDFT1,EGR2,TIMP1,JUND,CYP51A1,PLAT,SOX4,COL4A1,TUBB4B,FGFR1,ACTB,YWHAZ,HBEGF,DDR1,FDPS,GNAI2,COL6A3,CDKN1A,JAG1,CYR61,PRDX2,LGALS1
E2F3B upregulated	Neurological Disease	6.27E-04	CTGF,MYH9,ATP2B1,KLF6,UNC5B,CDKN3,FDFT1,EGR2,WDFY3,TIMP1,CYP51A1,PLAT,SOX4,COL4A1,TUBB4B,FGFR1,ACTB,YWHAZ,AGO2,TOB1,HBEGF,FDPS,COL6A3,PVT1,BTG2,CDKN1A,PDLIM1,PSAP,CYR61,JAG1,PRDX2,LGALS1
E2F3B upregulated	Skeletal and Muscular System Development and Function	7.20E-04	SOX4,MYH9,CTGF,PDGFA,RRBP1,FGFR1,TOB1,HBEGF,FNDC3B,DDR1,COL6A3,TIMP1,CDKN1A,JUND,SF1,JAG1,CYR61,PLAT
E2F3B upregulated	Inflammatory Disease	8.97E-04	SQLE,MYH9,CTGF,NRM,FDFT1,EGR2,WDFY3,TIMP1,VAMP3,CYP51A1,PLAT,COL4A1,TUBB4B,FGFR1,AGO2,TOB1,HBEGF,DDR1,GNAI2,FDPS,COL6A3,CDKN1A,LOXL1,PDLIM1,JAG1,LGALS1,PRDX2
E2F3B upregulated	Respiratory Disease	1.13E-03	SOX4,MYH9,TUBB4B,FGFR1,ACTB,YWHAZ,AGO2,DDR1,FDPS,FDFT1,TIMP1,CDKN1A,VAMP3,CYR61,CYP51A1,PRDX2,LGALS1,PLAT

Supplemental Table 14. General IPA functions for E2F1 and E2F3B putative direct targets

	Category	B-H p-valu	Genes
E2F3B upregulated	Gene Expression	1.13E-03	CTGF,EIF4EBP2,PDGFA,KLF6,IQGAP1,EGR2,TIMP1,JUND,SOX4,HMGN2,RRBP1,FGFR1,YWHAZ,ZC3HAV1,TOB1,AGO2,HBEGF,SP4,PVT1,CDKN1A,BTG2,PDLIM1,JAG1,CYR61,SAMD4A,LGALS1
E2F3B upregulated	Tissue Morphology	1.13E-03	CTGF,MYH9,EIF4EBP2,PDGFA,KLF6,SLC35C1,IQGAP1,FDFT1,EGR2,TIMP1,PLAT,SOX4,COL4A1,FGFR1,HBEGF,AGO2,TOB1,DDR1,SP4,FDPS,GNAI2,LOXL1,CDKN1A,PSAP,JAG1,PRDX2,LGALS1
E2F3B upregulated	Immune Cell Trafficking	1.13E-03	MYH9,COL4A1,CTGF,FGFR1,ACTB,UNC5B,DDR1,GNAI2,EGR2,TIMP1,CDKN1A,CYR61,LGALS1,PLAT
E2F3B upregulated	Metabolic Disease	1.13E-03	MYH9,CTGF,COL4A1,FGFR1,ACTB,YWHAZ,HBEGF,FDPS,FDFT1,WDFY3,TIMP1,BTG2,PSAP,LGALS1,PLAT
E2F3B upregulated	Psychological Disorders	1.13E-03	MYH9,CTGF,TUBB4B,ATP2B1,ACTB,FGFR1,YWHAZ,TOB1,FNDC3B,UBE2S,FDPS,FDFT1,EGR2,WDFY3,TIMP1,BTG2,PSAP,PDLIM1,CYP51A1,PLAT,LGALS1,PRDX2
E2F3B upregulated	Immunological Disease	1.47E-03	MYH9,COL4A1,TUBB4B,FGFR1,YWHAZ,HBEGF,AGO2,TOB1,IQGAP1,EGR2,TIMP1,CDKN1A,BTG2,PDLIM1,JAG1,CYR61,CYP51A1,PLAT,LGALS1
E2F3B upregulated	Protein Synthesis	1.81E-03	SOX4,EIF4EBP2,RRBP1,BTG2,AGO2,TOB1,SAMD4A
E2F3B upregulated	Small Molecule Biochemistry	2.77E-03	SQLE,PDGFA,FGFR1,IQGAP1,FDPS,GNAI2,FDFT1,TIMP1,CDKN1A,PSAP,CYP51A1,PRDX2,LGALS1
E2F3B upregulated	Lipid Metabolism	2.77E-03	FDPS,FDFT1,SQLE,PDGFA,TIMP1,FGFR1,CDKN1A,PSAP,CYP51A1,PRDX2
E2F3B upregulated	Renal and Urological System Development and Function	3.10E-03	SOX4,TIMP1,FGFR1,CDKN1A,HBEGF,PSAP,JAG1
E2F3B upregulated	Tumor Morphology	3.68E-03	TIMP1,FGFR1,KLF6,BTG2,CDKN1A,HBEGF,IQGAP1,CYR61,JAG1,PLAT,LGALS1
E2F3B upregulated	Hair and Skin Development and Function	5.68E-03	GNAI2,DLGAP5,CTGF,TIMP1,FGFR1,CDKN1A,UNC5B,HBEGF,CYR61
E2F3B upregulated	DNA Replication, Recombination, and Repair	6.00E-03	GNAI2,DLGAP5,PDGFA,FGFR1,CDKN1A,HBEGF,CYR61,IQGAP1,LGALS1
E2F3B upregulated	Cell Cycle	6.98E-03	DLGAP5,HAUS8,FGFR1,KLF6,HBEGF,UBE2S,CDKN3,TIMP1,CDKN1A,BTG2,PSAP,CYR61,LGALS1
E2F3B upregulated	Ophthalmic Disease	7.58E-03	COL4A1,TIMP1,ACTB,LOXL1,CDKN1A,JAG1,CYP51A1,LGALS1
E2F3B upregulated	Cell-mediated Immune Response	7.80E-03	GNAI2,MYH9,COL4A1,EGR2,ACTB,CDKN1A,LGALS1
E2F3B upregulated	Vitamin and Mineral Metabolism	8.11E-03	FDPS,FDFT1,SQLE,CYP51A1
E2F3B upregulated	Organismal Functions	8.45E-03	PDGFA,FGFR1,KLF6,HBEGF,PLAT
E2F3B upregulated	Hematopoiesis	9.60E-03	EGR2,CDKN1A
E2F3B upregulated	Lymphoid Tissue Structure and Development	9.60E-03	EGR2,CDKN1A
E2F3B upregulated	Cell Signaling	1.21E-02	GNAI2,SAE1,CTGF,PDGFA,FGFR1,CDKN1A,ZC3HAV1,PSAP,CYR61,IQGAP1,PRDX2,LGALS1
E2F3B upregulated	Nucleic Acid Metabolism	1.58E-02	GNAI2,IQGAP1,LGALS1

Supplemental Table 14. General IPA functions for E2F1 and E2F3B putative direct targets

	Category	B-H p-valu	Genes
E2F3B upregulated	Auditory and Vestibular System Development and Function	1.58E-02	EGR2,PSAP,DDR1,PLAT
E2F3B upregulated	Cellular Compromise	1.80E-02	FGFR1,HBEGF,PSAP,PLAT
E2F3B upregulated	Reproductive System Development and Function	1.82E-02	PDGFA,HBEGF,PSAP,JUND,LASP1
E2F3B upregulated	Post-Translational Modification	1.82E-02	GNAI2,CDKN1A,CYR61,IQGAP1,PRDX2
E2F3B upregulated	Molecular Transport	1.82E-02	TIMP1,CDKN1A,PSAP
E2F3B upregulated	Carbohydrate Metabolism	1.82E-02	PSAP
E2F3B upregulated	Drug Metabolism	1.82E-02	TIMP1,CDKN1A,PSAP
E2F3B upregulated	Endocrine System Development and Function	1.82E-02	TIMP1,CDKN1A,PSAP
E2F3B upregulated	Auditory Disease	1.82E-02	MYH9,ACTB,PSAP,JAG1
E2F3B upregulated	Nutritional Disease	1.82E-02	GNAI2,EGR2,TIMP1,CDKN1A,PSAP
E2F1 downregulated	Organismal Injury and Abnormalities	1.59E-02	SCO2,RFX4,SDC1,POLG2,DLST,ALS2,BAG4
E2F1 downregulated	Cellular Function and Maintenance	1.59E-02	SCO2,SDC1,DLST,ALS2,BAG4
E2F1 downregulated	Hereditary Disorder	1.59E-02	SCO2,SDC1,POLG2,ALS2
E2F1 downregulated	Skeletal and Muscular Disorders	1.59E-02	SCO2,SDC1,POLG2,ALS2
E2F1 downregulated	Neurological Disease	1.59E-02	SCO2,RFX4,SDC1,POLG2,PCOLCE2,ALS2
E2F1 downregulated	Molecular Transport	1.59E-02	PANK1,SDC1,PCOLCE2,SHMT1,SLC29A1,PITPNB
E2F1 downregulated	Nucleic Acid Metabolism	1.59E-02	PANK1,DLST,SHMT1,SLC29A1
E2F1 downregulated	Small Molecule Biochemistry	1.59E-02	PANK1,SDC1,DLST,PCOLCE2,SHMT1,SLC29A1,BAG4,PITPNB
E2F1 downregulated	Amino Acid Metabolism	1.59E-02	PANK1,SHMT1,SLC29A1
E2F1 downregulated	Vitamin and Mineral Metabolism	1.59E-02	PANK1,SHMT1
E2F1 downregulated	Behavior	1.59E-02	ALS2,SLC29A1
E2F1 downregulated	Ophthalmic Disease	1.59E-02	SCO2,POLG2

Supplemental Table 14. General IPA functions for E2F1 and E2F3B putative direct targets

	Category	B-H p-valu	Genes
E2F1 downregulated	Cellular Growth and Proliferation	2.32E-02	SDC1,ALS2,SLC29A1
E2F1 downregulated	Cancer	2.32E-02	SDC1
E2F1 downregulated	Tumor Morphology	2.32E-02	SDC1
E2F1 downregulated	Cellular Movement	2.32E-02	SDC1,PCOLCE2,ALS2,BAG4
E2F1 downregulated	Inflammatory Response	2.32E-02	SDC1,PCOLCE2,SLC29A1,ALS2,BAG4
E2F1 downregulated	Hematological System Development and Function	2.32E-02	SDC1,PCOLCE2,SLC29A1,BAG4
E2F1 downregulated	Immune Cell Trafficking	2.32E-02	SDC1,PCOLCE2,BAG4
E2F1 downregulated	Carbohydrate Metabolism	2.32E-02	BAG4,PITPNB
E2F1 downregulated	Organismal Functions	2.32E-02	SDC1
E2F1 downregulated	Cellular Assembly and Organization	2.76E-02	SDC1,POLG2,ALS2,BAG4
E2F1 downregulated	Connective Tissue Disorders	2.76E-02	SDC1
E2F1 downregulated	Immunological Disease	2.76E-02	SDC1
E2F1 downregulated	Developmental Disorder	2.76E-02	SCO2,RFX4,SDC1,ALS2
E2F1 downregulated	Digestive System Development and Function	2.76E-02	PANK1,SHMT1
E2F1 downregulated	Hepatic System Development and Function	2.76E-02	PANK1,SHMT1
E2F1 downregulated	Organ Development	2.76E-02	PANK1,RFX4,SDC1,SHMT1
E2F1 downregulated	Skeletal and Muscular System Development and Function	2.76E-02	SDC1,ALS2
E2F1 downregulated	Cell-To-Cell Signaling and Interaction	2.76E-02	SDC1,SLC29A1,ALS2
E2F1 downregulated	Cardiovascular Disease	2.76E-02	SCO2,SDC1,BAG4
E2F1 downregulated	Drug Metabolism	2.76E-02	SHMT1,SLC29A1
E2F1 downregulated	Metabolic Disease	2.76E-02	SCO2,SDC1
E2F1 downregulated	Inflammatory Disease	2.76E-02	SDC1
E2F1 downregulated	Cell Morphology	2.87E-02	SDC1,POLG2,ALS2
E2F1 downregulated	Lipid Metabolism	2.87E-02	PANK1,SDC1,PCOLCE2,BAG4,PITPNB

Supplemental Table 14. General IPA functions for E2F1 and E2F3B putative direct targets

	Category	B-H p-valu	Genes
E2F1 downregulated	Nutritional Disease	2.87E-02	PANK1,SDC1
E2F1 downregulated	Infectious Diseases	2.87E-02	PANK1,SDC1,DLST
E2F1 downregulated	Psychological Disorders	2.87E-02	PANK1,SDC1,SLC29A1
E2F1 downregulated	Embryonic Development	3.27E-02	RFX4,SDC1,DLST,BAG4
E2F1 downregulated	Tissue Development	3.27E-02	RFX4,SDC1,ALS2
E2F1 downregulated	Organ Morphology	3.27E-02	RFX4,SDC1,ALS2
E2F1 downregulated	Post-Translational Modification	3.27E-02	SCO2,SHMT1
E2F1 downregulated	Nervous System Development and Function	3.27E-02	RFX4,SLC29A1,ALS2
E2F1 downregulated	Organismal Development	3.27E-02	RFX4,SDC1,ALS2
E2F1 downregulated	Protein Synthesis	3.27E-02	SCO2,SHMT1,BAG4
E2F1 downregulated	Cell Signaling	3.27E-02	SCO2,ALS2
E2F1 downregulated	Cellular Development	4.06E-02	SDC1,ALS2,SLC29A1
E2F1 downregulated	DNA Replication, Recombination, and Repair	4.06E-02	POLG2,SLC29A1
E2F1 downregulated	Free Radical Scavenging	4.26E-02	SCO2,DLST,ALS2
E2F1 downregulated	Auditory Disease	4.44E-02	SDC1
E2F1 downregulated	Cell Death and Survival	4.55E-02	SDC1,DLST,SLC29A1,ALS2,BAG4
E2F1 downregulated	Tissue Morphology	4.55E-02	SDC1,ALS2
E2F1 downregulated	Cellular Compromise	4.55E-02	SDC1,ALS2
E2F1 downregulated	Cardiovascular System Development and Function	5.44E-02	SDC1,BAG4
E2F1 downregulated	Renal and Urological System Development and Function	6.14E-02	SDC1
E2F1 downregulated	Renal and Urological Disease	8.14E-02	DLST,BAG4
E2F1 downregulated	Reproductive System Disease	8.45E-02	SDC1
E2F1 downregulated	Reproductive System Development and Function	8.96E-02	SDC1

Supplemental Table 14. General IPA functions for E2F1 and E2F3B putative direct targets

	Category	B-H p-valu	Genes
E2F1 downregulated	Connective Tissue Development and Function	9.47E-02	SDC1
E2F1 downregulated	Humoral Immune Response	9.91E-02	SDC1
E2F3B downregulate	Cancer	4.46E-04	CCP110,GTF3C2,SLC35E3,SMARCD2,SFPQ,GTPBP10,SLC15A4,KPNA1,RICTOR,TOMM70A,ADRB3,RCL1,IPMK,FAM91A1,KIF13A,PRPF4B,TARDBP,HIPK1,AHCY,ALDH7A1,AFMID,SERBP1,PABPC1,WAPL,DPY19L1,SYNCRIP,AGFG2,MON2,ERCC6L2,ARHGAP5,MTMR4,PPP2R3A,YTHDF3,ACY1,FBXO30,AHCTF1,KIAA0368,ZNF644,RBM39,PHLPP1,TRIM33,NOL7,AKAP8,TRIP4,EIF4G1,TYW1,XYLB,RIF1,ADK,SOS1,EIF3A,MCM10,XPO4,LPP,FBXO21,UBE3C,PAICS,RETSAT,TGS1,SIN3A,SF3B2,NUP153,IREB2,TCF7L2,TAF15,AKAP1,NAV2,PRPF19,MSH3,KIF1B,VPS13A,TAF10,STARD7,RBM33,LATS2,USF3,HSPA4,GSPT1,ADGRF5,TBC1D4,ZNF318,SMPD4,RORA,GDE1,AP5M1,NEO1,DDI2,NAA16,TFDP2,LACTB,SYNE2,UBE4B,DLEU2,USP38,TNPO1,MACROD1,BIRC6,GPAT4,ELF1,ZBTB44,ARIH1,CAND1,TTC14,WHSC1L1,NASP,UGP2,AGBL3,CUTC,BAZ1B,MCCC2,PEBP1,TMTC3,NFIX,PA2G4,XPNPEP3,GTF2I,TLE2,PPP1CB,ATF6,TAOK1,GPHN,MARVELD1,PDP2,EPHB6,LYST,STEAP2,ZNF24,MCCC1,PDK1,RAD23B,UBR5,ABCD3,AP3M1,MTRR,TMEM245,HERPUD1,MTHFD1,ALS2,MTO1,ZHX3,XIAP,CDKN2AIP,U2SURP,CHD9,PAN3,TTC7A,AMIGO1,TANGO2,ACAT1,SLC25A32,NFIB,SMARCC1,USP34,ACSL1
E2F3B downregulate	Organismal Injury and Abnormalities	4.46E-04	CCP110,GTF3C2,SFPQ,SMARCD2,SLC35E3,GTPBP10,RICTOR,KPNA1,SLC15A4,TOMM70A,ADRB3,RCL1,IPMK,FAM91A1,KIF13A,PRPF4B,TARDBP,HIPK1,ALDH7A1,AHCY,AFMID,PABPC1,SERBP1,WAPL,SLC35A3,DPY19L1,SYNCRIP,MON2,AGFG2,ERCC6L2,ARHGAP5,MTMR4,PPP2R3A,YTHDF3,ACY1,AHCTF1,FBXO30,KIAA0368,ZNF644,RBM39,PHLPP1,TRIM33,NOL7,AKAP8,TRIP4,EIF4G1,TYW1,XYLB,RIF1,ADK,SOS1,EIF3A,MCM10,B3GALNT2,XPO4,LPP,FBXO21,UBE3C,MEMO1,PAICS,TGS1,RETSAT,SIN3A,NUP153,SF3B2,IREB2,TCF7L2,TAF15,AKAP1,NAV2,PRPF19,KIF1B,MSH3,VPS13A,TAF10,STARD7,RBM33,LATS2,USF3,HSPA4,GSPT1,ADGRF5,TBC1D4,ZNF318,SMPD4,RORA,GDE1,AP5M1,NEO1,DDI2,NAA16,TFDP2,LACTB,SYNE2,UBE4B,DLEU2,MACROD1,TNPO1,USP38,BIRC6,GPAT4,ZBTB44,ELF1,CAND1,ARIH1,TTC14,WHSC1L1,NASP,UGP2,AGBL3,CUTC,BAZ1B,MCCC2,PEBP1,TMTC3,NFIX,PA2G4,XPNPEP3,GTF2I,TLE2,PPP1CB,ATF6,GPHN,TAOK1,MARVELD1,PDP2,EPHB6,LYST,STEAP2,ZNF24,MCCC1,PDK1,RAD23B,UBR5,ABCD3,AP3M1,MTRR,TMEM245,HERPUD1,MTHFD1,ALS2,MTO1,XIAP,ZHX3,CDKN2AIP,CHD9,U2SURP,PAN3,TTC7A,AMIGO1,TANGO2,ACAT1,SLC25A32,NFIB,SMARCC1,USP34,ACSL1
E2F3B downregulate	Renal and Urological Disease	4.46E-04	NAV2,TRIM33,AKAP8,XPNPEP3,GTF3C2,KIF1B,VPS13A,SLC35E3,SMARCD2,GPHN,LATS2,TYW1,ADRB3,XYLB,EPHB6,GSPT1,LYST,AP5M1,MCCC1,ALDH7A1,UBE3C,UBR5,PABPC1,MTRR,SYNE2,DPY19L1,ZHX3,SIN3A,ARHGAP5,ARIH1,NASP,NUP153,UGP2,CHD9,ACAT1,SMARCC1,USP34,MCCC2,PHLPP1
E2F3B downregulate	Tissue Morphology	1.07E-02	NFIX,VPS13A,GPHN,TAF10,RICTOR,ADRB3,IPMK,TBC1D4,RORA,TARDBP,ZNF24,MCM10,HIPK1,RAD23B,MEMO1,SYNE2,UBE4B,BIRC6,SYNCRIP,GPAT4,ALS2,TGS1,XIAP,ARHGAP5,AHCTF1,SMARCC1,IREB2,TCF7L2,ACSL1
E2F3B downregulate	Organismal Development	1.07E-02	NOL7,PRPF19,NFIX,AKAP8,KIF1B,GTF2I,VPS13A,PPP1CB,GPHN,TAF10,RICTOR,LATS2,KPNA1,RCL1,RORA,SOS1,MCM10,HIPK1,RAD23B,UBE4B,BIRC6,SYNCRIP,GPAT4,TGS1,ALS2,XIAP,ARHGAP5,NUP153,AHCTF1,NFIB,SMARCC1,IREB2,TCF7L2
E2F3B downregulate	Hematological Disease	1.22E-02	NAV2,NFIX,AKAP8,KIF1B,MSH3,VPS13A,GPHN,EIF4G1,RBM33,ADRB3,ZC3H8,IPMK,RIF1,RORA,STEAP2,ADK,PDK1,LPP,AHCY,UBE3C,MTRR,SYNE2,DLEU2,BIRC6,MTHFD1,ALS2,XIAP,ELF1,ARIH1,WHSC1L1,MTMR4,CHD9,AHCTF1,FBXO30,SLC25A32,SMARCC1,IREB2,USP34
E2F3B downregulate	Developmental Disorder	1.22E-02	TRIM33,PRPF19,NFIX,AKAP8,GPHN,LATS2,ADRB3,ADK,SOS1,ZNF24,TARDBP,MCM10,MCCC1,B3GALNT2,TFDP2,HIPK1,RAD23B,AHCY,MEMO1,SYNE2,MTRR,SLC35A3,MTHFD1,ALS2,NASP,TTC7A,ACAT1,NFIB,SMARCC1,IREB2,TCF7L2,MCCC2
E2F3B downregulate	Hereditary Disorder	1.22E-02	XPNPEP3,KIF1B,VPS13A,ATF6,GPHN,EIF4G1,ADRB3,LYST,SOS1,TARDBP,ADK,MCCC1,B3GALNT2,TFDP2,AHCY,ALDH7A1,MTRR,SYNE2,SLC35A3,ALS2,MTO1,XIAP,ACY1,TTC7A,ACAT1,ZNF644,MCCC2
E2F3B downregulate	Metabolic Disease	1.22E-02	MTRR,GPHN,MTO1,ADRB3,RORA,STEAP2,ADK,ACY1,TARDBP,ACAT1,MCCC1,B3GALNT2,PDK1,TCF7L2,MCCC2,AHCY

Supplemental Table 14. General IPA functions for E2F1 and E2F3B putative direct targets

	Category	B-H p-valu	Genes
E2F3B downregulate	Nucleic Acid Metabolism	1.39E-02	ABCD3,SLC35A3,RICTOR,MTHFD1,GPAT4,EPHB6,UGP2,RORA,ADK,B3GALNT2,MCCC2,AHCY,PHLPP1
E2F3B downregulate	Small Molecule Biochemistry	1.39E-02	PEBP1,ATF6,TAF10,SLC15A4,ADRB3,XYLB,EPHB6,SMPD4,ADK,B3GALNT2,PDK1,AHCY,AFMID,ABCD3,MTRR,SLC35A3,MTHFD1,GPAT4,UGP2,TTC7A,ACAT1,SLC25A32,IREB2,ACSL1,PHLPP1,MCCC2
E2F3B downregulate	Carbohydrate Metabolism	1.39E-02	XYLB,MTRR,SMPD4,UGP2,SLC35A3,PPP1CB,ATF6,TAF10,B3GALNT2,GPAT4
E2F3B downregulate	Reproductive System Disease	2.80E-02	NAV2,CCP110,MSH3,VPS13A,SMARCD2,STARD7,KPNA1,RBM33,RICTOR,TOMM70A,ADRB3,USF3,TBC1D4,ZNF318,FAM91A1,RORA,KIF13A,PRPF4B,TARDBP,NEO1,HIPK1,ALDH7A1,LACTB,PABPC1,WAPL,SYNE2,USP38,TNPO1,BIRC6,MON2,ERCC6L2,ELF1,ZBTB44,CAND1,NASP,UGP2,ACY1,AHCTF1,ZNF644,BAZ1B,RBM39,TMTC3,NOL7,NFIX,PPP1CB,ATF6,TRIP4,GPHN,EIF4G1,MARVELD1,TYW1,XYLB,EPHB6,LYST,RIF1,ZNF24,SOS1,EIF3A,MCCC1,XPO4,LPP,UBE3C,UBR5,MEMO1,TMEM245,ALS2,MTO1,TGS1,XIAP,SIN3A,NUP153,CHD9,PAN3,IREB2,USP34,ACSL1
E2F3B downregulate	DNA Replication, Recombination, and Repair	3.41E-02	TRIM33,PRPF19,MSH3,SFPQ,SMARCD2,TAOK1,KPNA1,EIF4G1,IPMK,RIF1,ADK,EIF3A,MCM10,HIPK1,RAD23B,AHCY,UBR5,PABPC1,WAPL,ABCD3,MACROD1,CDKN2AIP,SF3B2,BAZ1B,SMARCC1
E2F3B downregulate	Organ Morphology	3.41E-02	NFIX,UBE4B,KIF1B,GTF2I,VPS13A,SYNCRIP,KPNA1,RICTOR,LATS2,ALS2,ARHGAP5,RORA,NFIB,SMARCC1,IREB2,RAD23B,TCF7L2
E2F3B downregulate	Nervous System Development and Function	3.41E-02	NFIX,KIF1B,VPS13A,PPP1CB,SFPQ,GPHN,RICTOR,LATS2,RORA,TARDBP,ZNF24,AHCY,SYNE2,AP3M1,UBE4B,SYNCRIP,HNRNPD,ALS2,XIAP,ARHGAP5,AMIGO1,NFIB,SMARCC1,IREB2,TCF7L2,PHLPP1
E2F3B downregulate	Lipid Metabolism	3.46E-02	PEBP1,ABCD3,SMPD4,ACAT1,ATF6,TAF10,PDK1,GPAT4,ACSL1,ADRB3
E2F3B downregulate	Cell Cycle	3.80E-02	UBR5,PABPC1,TRIM33,WAPL,CCP110,NFIX,PRPF19,MSH3,GTF2I,BIRC6,SMARCD2,SFPQ,TAF10,LATS2,KPNA1,GSPT1,NASP,SF3B2,KIF13A,AHCTF1,MCM10,BAZ1B,SMARCC1,PDK1
E2F3B downregulate	Cell Death and Survival	3.80E-02	PEBP1,TRIM33,CCP110,PRPF19,NFIX,PA2G4,KIF1B,MSH3,AP2B1,VPS13A,PPP1CB,SFPQ,ATF6,GPHN,TAF10,EIF4G1,RICTOR,LATS2,EPHB6,HSPA4,ZC3H8,IPMK,SMPD4,ADK,TARDBP,EIF3A,MCM10,PDK1,RAD23B,MEMO1,WAPL,UBE4B,BIRC6,HERPUD1,ALS2,SIN3A,XIAP,PPP2R3A,AHCTF1,NFIB,SMARCC1,IREB2,TCF7L2,AKAP1,PHLPP1
E2F3B downregulate	Embryonic Development	3.80E-02	UBR5,TRIM33,NOL7,PRPF19,NFIX,TAF10,RICTOR,XIAP,NASP,NUP153,IPMK,RORA,SOS1,ZNF24,TARDBP,AHCTF1,MCM10,NFIB,SMARCC1,HIPK1,RAD23B,TCF7L2
E2F3B downregulate	Gastrointestinal Disease	3.80E-02	CCP110,GTF3C2,SFPQ,GTPBP10,SLC15A4,KPNA1,RICTOR,TOMM70A,ADRB3,RCL1,FAM91A1,KIF13A,PRPF4B,TARDBP,HIPK1,AHCY,ALDH7A1,SERBP1,PABPC1,SYNCRIP,MON2,AGFG2,ERCC6L2,ARHGAP5,MTMR4,PPP2R3A,YTHDF3,ACY1,AHCTF1,FBXO30,KIAA0368,ZNF644,RBM39,PHLPP1,NOL7,TRIM33,EIF4G1,TYW1,XYLB,RIF1,SOS1,ADK,EIF3A,MCM10,XPO4,LPP,FBXO21,UBE3C,PAICS,TGS1,RETSAT,SIN3A,NUP153,SF3B2,IREB2,TCF7L2,AKAP1,NAV2,KIF1B,MSH3,VPS13A,TAF10,STARD7,LATS2,RBM33,USF3,GSPT1,TBC1D4,SMPD4,ZNF318,RORA,GDE1,NEO1,DDI2,NAA16,TFDP2,LACTB,SYNE2,UBE4B,USP38,MACROD1,TNPO1,BIRC6,ELF1,ARIH1,TTC14,WHSC1L1,NASP,UGP2,AGBL3,CUTC,BAZ1B,MCCC2,TMTC3,NFIX,PA2G4,XPNPEP3,TLE2,PPP1CB,ATF6,TAOK1,PDP2,LYST,STEAP2,ZNF24,MCCC1,PDK1,UBR5,ABCD3,AP3M1,MTRR,TMEM245,HERPUD1,MTHFD1,MTO1,ALS2,ZHX3,CDKN2AIP,U2SURP,CHD9,PAN3,TTC7A,TANGO2,ACAT1,NFIB,SMARCC1,USP34,ACSL1
E2F3B downregulate	Hepatic System Disease	3.80E-02	NAV2,CCP110,MSH3,GTF3C2,KIF1B,SFPQ,RBM33,RICTOR,LATS2,KPNA1,TOMM70A,USF3,RCL1,TBC1D4,SMPD4,ZNF318,RORA,PRPF4B,GDE1,TFDP2,ALDH7A1,PABPC1,SYNE2,USP38,BIRC6,AGFG2,MON2,ARHGAP5,ARIH1,WHSC1L1,NASP,UGP2,YTHDF3,ACY1,AHCTF1,KIAA0368,ZNF644,BAZ1B,MCCC2,TRIM33,NFIX,PA2G4,XPNPEP3,ATF6,TYW1,XYLB,LYST,STEAP2,ADK,EIF3A,LPP,FBXO21,UBE3C,UBR5,MTRR,HERPUD1,PAICS,MTHFD1,ALS2,RETSAT,MTO1,ZHX3,SIN3A,SF3B2,U2SURP,CHD9,PAN3,NFIB,IREB2,USP34,TCF7L2,ACSL1
E2F3B downregulate	Behavior	3.99E-02	RORA,PPP1CB,SFPQ,HNRNPD,AHCY,PHLPP1

Supplemental Table 14. General IPA functions for E2F1 and E2F3B putative direct targets

	Category	B-H p-valu	Genes
E2F3B downregulate	RNA Post-Transcriptional Modification	4.01E-02	PABPC1,RCL1,SF3B2,PRPF19,PRPF4B,TARDBP,CNOT6L,SYNCRIP,SFPQ,HNRNPD,RBM39
E2F3B downregulate	Molecular Transport	4.70E-02	PEBP1,ABCD3,KIF1B,RAB2A,TNPO1,SLC35A3,PPP1CB,ATF6,TAF10,GPAT4,KPNA1,SLC15A4,TOMM70A,XIAP,UGP2,KIF13A,STEAP2,ADK,TTC7A,ACAT1,SLC25A32,PDK1,IREB2,ACSL1
E2F3B downregulate	Amino Acid Metabolism	4.72E-02	AFMID,MTRR,SLC25A32,MTHFD1,SLC15A4,MCCC2,AHCY
E2F3B downregulate	Post-Translational Modification	5.67E-02	UBR5,TRIM33,PRPF19,UBE4B,BIRC6,HERPUD1,PPP1CB,XIAP,PDP2,ARIH1,CAND1,LYST,NUP153,MTMR4,PPP2R3A,AHCTF1,PHLPP1,UBE3C
E2F3B downregulate	Protein Synthesis	5.67E-02	UBR5,STX12,PABPC1,UBE4B,SYNCRIP,HERPUD1,HNRNPD,ATF6,KPNA1,EIF4G1,XIAP,ARIH1,CDKN2AIP,NUP153,PPP2R3A,ACY1,AGBL3,EIF3A,AHCTF1,KIAA0368,NAA16,IREB2,PHLPP1
E2F3B downregulate	Cell Signaling	5.67E-02	UBR5,NUP153,AHCTF1
E2F3B downregulate	Connective Tissue Development and Function	6.60E-02	ARHGAP5,NFIX,TBC1D4,GTF2I,ADK,GPAT4,LATS2,ADRB3
E2F3B downregulate	Gene Expression	6.60E-02	PEBP1,NFIX,PA2G4,GTF3C2,GTF2I,TLE2,SFPQ,ATF6,TAF10,TRIP4,EIF4G1,HSPA4,ZC3H8,RORA,TARDBP,ZNF24,SOS1,EIF3A,NEO1,TFDP2,HIPK1,UBR5,SYNCRIP,HNRNPD,XIAP,ZHX3,SIN3A,ELF1,CAND1,WHSC1L1,AHCTF1,NFIB,SMARCC1,IREB2,RBM39,TCF7L2,TAF15
E2F3B downregulate	Cell Morphology	7.19E-02	PEBP1,TRIM33,PRPF19,SYNE2,NFIX,UBE4B,SYNCRIP,GPHN,TAOK1,TAF10,LATS2,RICTOR,GPAT4,ALS2,RIF1,TBC1D4,ADGRF5,RORA,TARDBP,NEO1,NFIB,PDK1,TCF7L2,PHLPP1
E2F3B downregulate	Cellular Assembly and Organization	8.64E-02	NFIX,SMARCD2,ATF6,GPHN,RICTOR,HSPA4,TBC1D4,NUP153,TARDBP,EIF3A,AMIGO1,ACAT1,NEO1,BAZ1B,SMARCC1
E2F3B downregulate	Cellular Development	9.09E-02	UBR5,PRPF19,MSH3,BIRC6,SFPQ,GPHN,GPAT4,RICTOR,XIAP,NUP153,RORA,KIF13A,PRPF4B,TARDBP,ZNF24,EIF3A,NFIB,SMARCC1,PDK1,PHLPP1
E2F3B downregulate	Cellular Growth and Proliferation	9.09E-02	PRPF19,MSH3,SFPQ,LATS2,RICTOR,HSPA4,RCL1,IPMK,KIF13A,RORA,PRPF4B,TARDBP,NEO1,HIPK1,AHCY,WAPL,UBE4B,CNOT6L,BIRC6,ELF1,ARHGAP5,ARIH1,NASP,PHLPP1,PEBP1,TRIM33,NFIX,PA2G4,GTF2I,PPP1CB,ATF6,GPHN,EIF4G1,EPHB6,HNRNPR,STEAP2,ZNF24,SOS1,ADK,EIF3A,MCM10,PDK1,UBR5,MEMO1,HNRNPD,MTHFD1,ALS2,XIAP,SIN3A,CDKN2AIP,NUP153,SF3B2,ACAT1,NFIB,SMARCC1,TCF7L2
E2F3B downregulate	Tumor Morphology	9.09E-02	HSPA4,XIAP
E2F3B downregulate	Connective Tissue Disorders	9.09E-02	MEMO1,MTRR,NFIX,SLC35A3,STEAP2,SOS1,TFDP2,BAZ1B,MTHFD1,IREB2
E2F3B downregulate	Immunological Disease	9.09E-02	NAV2,NFIX,AKAP8,MSH3,KIF1B,VPS13A,STARD7,GPHN,EIF4G1,RBM33,ADRB3,EPHB6,ZC3H8,IPMK,RIF1,HNRNPR,STEAP2,PDK1,LPP,AHCY,UBE3C,SYNE2,DLEU2,BIRC6,MTHFD1,ALS2,XIAP,ELF1,ARIH1,WHSC1L1,MTMR4,CHD9,AHCTF1,FBXO30,SLC25A32,SMARCC1,USP34
E2F3B downregulate	Cellular Function and Maintenance	9.09E-02	TRIM33,PRPF19,NFIX,AP3M1,UBE4B,KIF1B,GPHN,RICTOR,MTHFD1,ALS2,RIF1,SOS1,TTC7A,PDK1,IREB2,PHLPP1
E2F3B downregulate	Tissue Development	9.09E-02	NOL7,NFIX,GPHN,GPAT4,RICTOR,TGS1,ADRB3,ARHGAP5,NUP153,RORA,STEAP2,SOS1,ZNF24,NFIB,SMARCC1,PDK1,HIPK1,TCF7L2,RAD23B,PHLPP1
E2F3B downregulate	Digestive System Development and Function	9.09E-02	ADK,NFIB,TCF7L2

Supplemental Table 14. General IPA functions for E2F1 and E2F3B putative direct targets

	Category	B-H p-valu	Genes
E2F3B downregulate	Organ Development	9.09E-02	NOL7,NUP153,NFIX,RORA,ADK,NFIB,SMARCC1,RICTOR,RAD23B
E2F3B downregulate	Skeletal and Muscular System Development and Function	9.09E-02	NOL7,NFIX,NEO1
E2F3B downregulate	Cell-To-Cell Signaling and Interaction	9.09E-02	SYNE2,NEO1,GPHN,RICTOR,ALS2,TCF7L2
E2F3B downregulate	Inflammatory Response	9.09E-02	ARIH1,SYNE2,HNRNPR,STEAP2,ADK,SLC25A32,STARD7,RICTOR,PDK1,AHCY
E2F3B downregulate	Hematological System Development and Function	9.09E-02	RORA,SOS1,SMARCC1,RICTOR,PDK1,XIAP,PHLPP1
E2F3B downregulate	Hematopoiesis	9.09E-02	RORA,SMARCC1,RICTOR,PHLPP1
E2F3B downregulate	Cardiovascular System Development and Function	9.09E-02	RORA,PRPF4B,ZNF24,EIF3A,PPP1CB
E2F3B downregulate	Skeletal and Muscular Disorders	9.09E-02	MEMO1,MTRR,NFIX,SYNE2,AKAP8,KIF1B,SLC35A3,EIF4G1,LATS2,MTHFD1,MTO1,ALS2,ADRB3,SOS1,TFDP2,BAZ1B,SMARCC1,B3GALNT2,IREB2,HIPK1,RAD23B,TCF7L2,ACSL1
E2F3B downregulate	Cardiovascular Disease	9.09E-02	CAND1,HSPA4,MTRR,PPP1CB,SLC25A32,IREB2,TOMM70A,MTO1,ACSL1,ADRB3
E2F3B downregulate	Endocrine System Disorders	9.09E-02	MEMO1,NFIX,TCF7L2,ADRB3
E2F3B downregulate	Neurological Disease	9.09E-02	PEBP1,PRPF19,NFIX,MSH3,KIF1B,VPS13A,SFPQ,PPP1CB,GPHN,EIF4G1,TYW1,ADRB3,RORA,PRPF4B,ADK,TARDBP,ZNF24,B3GALNT2,HIPK1,PDK1,AHCY,ALDH7A1,MTRR,UBE4B,SLC35A3,BIRC6,HERPUD1,MTHFD1,ALS2,XIAP,SIN3A,ZBTB44,ACAT1,NFIB,SMARCC1,IREB2,TCF7L2
E2F3B downregulate	Lymphoid Tissue Structure and Development	9.09E-02	RORA,SMARCC1,RICTOR,PHLPP1
E2F3B downregulate	Cellular Compromise	9.09E-02	UBE4B,SMARCD2,ATF6,GPHN,LATS2,ALS2,ADRB3,XIAP,ARHGAP5,HSPA4,NUP153,TARDBP,SMARCC1,IREB2,ACSL1
E2F3B downregulate	Cell-mediated Immune Response	9.09E-02	RICTOR,PHLPP1
E2F3B downregulate	Humoral Immune Response	9.09E-02	SOS1,SMARCC1,RICTOR,PDK1
E2F3B downregulate	Antimicrobial Response	9.09E-02	AHCY
E2F3B downregulate	Vitamin and Mineral Metabolism	9.09E-02	MTRR,SLC25A32,GPHN,MTHFD1,RETSAT
E2F3B downregulate	Drug Metabolism	9.09E-02	MTRR,SLC25A32
E2F3B downregulate	Endocrine System Development and Function	9.09E-02	ACAT1,TCF7L2

Supplemental Table 14. General IPA functions for E2F1 and E2F3B putative direct targets

	Category	B-H p-valu	Genes
E2F3B downregulate	Ophthalmic Disease	9.09E-02	ZNF644,ATF6,B3GALNT2,ADRB3,RAD23B
E2F3B downregulate	Psychological Disorders	9.09E-02	PRPF19,UBE4B,MSH3,VPS13A,PRPF4B,TARDBP,BIRC6,SFPQ,EIF4G1,ADRB3,AHCY
E2F3B downregulate	Organismal Survival	1.10E-01	TRIM33,PRPF19,NFIX,MSH3,KIF1B,GTF2I,ATF6,GPHN,TAF10,KPNA1,RICTOR,LATS2,TBC1D4,ADGRF5,RIF1,IPMK,RORA,ADK,SOS1,ZNF24,TARDBP,MCM10,HIPK1,RAD23B,AFMID,SYNE2,UBE4B,BIRC6,HNRNPD,TGS1,SIN3A,XIAP,ARHGAP5,NASP,AHCTF1,NFIB,SMARCC1,IREB2,TCF7L2
E2F3B downregulate	Cellular Movement	1.21E-01	PEBP1,CCP110,KIF13A,AHCTF1,BIRC6,LATS2,PDK1,XIAP
E2F3B downregulate	Hair and Skin Development and Function	1.21E-01	PEBP1,RORA,NFIB
E2F3B downregulate	Reproductive System Development and Function	1.21E-01	NUP153,NFIX,KIF1B,KPNA1
E2F3B downregulate	Respiratory System Development and Function	1.21E-01	UBR5,NOL7,GTF2I
E2F3B downregulate	RNA Damage and Repair	1.21E-01	GSPT1,CNOT6L,HNRNPD
E2F3B downregulate	Visual System Development and Function	1.21E-01	WAPL,RAD23B
E2F3B downregulate	Nutritional Disease	1.21E-01	ADRB3
E2F3B downregulate	Protein Degradation	1.22E-01	UBR5,ARIH1,STX12,CDKN2AIP,UBE4B,PPP2R3A,ACY1,AGBL3,KIAA0368,HERPUD1,ATF6,NAA16
E2F3B downregulate	Respiratory Disease	1.40E-01	ADRB3
E2F3B downregulate	Inflammatory Disease	1.40E-01	ARIH1,SYNE2,HNRNPR,ADK,SLC25A32,STARD7,ADRB3,AHCY
E2F3B downregulate	Protein Trafficking	1.54E-01	AP3M1,KIF1B,RAB2A,KIF13A,TNPO1,STEAP2,PAN3,GPHN,KPNA1,TOMM70A
E2F3B downregulate	Dermatological Diseases and Conditions	1.62E-01	ARIH1,EPHB6,SYNE2,HNRNPR,TTC7A,SLC25A32,STARD7,AHCY
E2F3B downregulate	RNA Trafficking	1.62E-01	EIF3A
E2F3B downregulate	Infectious Diseases	1.62E-01	AP3M1,ADK
E2F3B downregulate	Hepatic System Development and Function	1.79E-01	ADK
E2F3B downregulate	Energy Production	1.79E-01	ABCD3

Supplemental Table 15. Liver IPA functions for E2F1 and E2F3B putative direct targets

	Category	B-H p-value	Genes
E2F1 upregulated	Liver Proliferation	9.48E-05	MYC,SLC20A1,CCNE1,CDKN1A,JUND,NFE2L2,LGALS1
E2F1 upregulated	Liver Necrosis/Cell Death	6.34E-03	MYC,SLC20A1,CDKN1A,JUND,NFE2L2
E2F1 upregulated	Liver Regeneration	1.36E-02	CCNE1,BIRC5,NFE2L2
E2F1 upregulated	Liver Hyperplasia/Hyperproliferation	1.44E-02	GJA1,MYEF2,RRBP1,UNC5B,MDM2,AURKA,ATXN2L,GAS2L3,BIRC5,HIVEP2,MYC,TRIB1,CCNA2,CCNE1,NOP58,CDKN1A,TOP2A,CKS1B,ALCAM,IFRD1,NFE2L2
E2F1 upregulated	Biliary Hyperplasia	2.20E-02	MYC
E2F1 upregulated	Hepatocellular Carcinoma	2.20E-02	GJA1,MYEF2,RRBP1,UNC5B,MDM2,AURKA,ATXN2L,GAS2L3,HIVEP2,MYC,TRIB1,CCNA2,NOP58,CDKN1A,TOP2A,CKS1B,ALCAM,IFRD1,NFE2L2
E2F1 upregulated	Liver Hypoplasia	2.55E-02	SLC20A1,TACC3
E2F1 upregulated	Liver Cholestasis	2.75E-02	GJA1,CDKN1A,NFE2L2
E2F1 upregulated	Liver Damage	6.84E-02	CDKN1A,JUND,NFE2L2
E2F1 upregulated	Liver Failure	6.84E-02	TOP2A
E2F1 upregulated	Glutathione Depletion In Liver	6.84E-02	NFE2L2
E2F1 upregulated	Liver Fibrosis	9.16E-02	NFE2L2,LGALS1
E2F1 upregulated	Liver Cirrhosis	1.77E-01	TOP2A,NFE2L2
E2F1 upregulated	Liver Steatosis	6.41E-01	CDKN1A
E2F3B upregulated	Liver Proliferation	9.25E-04	CTGF,TIMP1,CDKN1A,HBEGF,TOB1,JUND,LGALS1
E2F3B upregulated	Liver Fibrosis	1.53E-03	CTGF,TIMP1,FGFR1,HBEGF,LGALS1
E2F3B upregulated	Liver Necrosis/Cell Death	1.36E-02	TIMP1,CDKN1A,HBEGF,JUND
E2F3B upregulated	Liver Hyperplasia/Hyperproliferation	1.36E-02	SQLE,UNC5B,FNDC3B,SLC35C1,IQGAP1,CDKN3,WDFY3,TIMP1,CYP51A1,SLC35A5,SOX4,COL4A1,HAUS8,RRBP1,TUBB4B,FGFR1,ACTB,AGO2,TOB1,UBE2S,SP4,COL6A3,CDKN1A,LOXL1,PSAP,CYR61,JAG1,SAMD4A
E2F3B upregulated	Hepatocellular Carcinoma	1.36E-02	SQLE,UNC5B,FNDC3B,IQGAP1,CDKN3,WDFY3,CYP51A1,SLC35A5,SOX4,COL4A1,HAUS8,RRBP1,TUBB4B,FGFR1,ACTB,AGO2,TOB1,UBE2S,SP4,COL6A3,CDKN1A,LOXL1,PSAP,CYR61,JAG1,SAMD4A
E2F3B upregulated	Liver Cirrhosis	1.52E-02	CTGF,TIMP1,FGFR1,JAG1
E2F3B upregulated	Liver Adhesion	1.89E-02	CTGF
E2F3B upregulated	Liver Dysfunction	2.88E-02	FDFT1
E2F3B upregulated	Liver Damage	7.98E-02	TIMP1,CDKN1A,JUND
E2F3B upregulated	Liver Inflammation/Hepatitis	1.71E-01	TIMP1,CYR61
E2F3B upregulated	Liver Failure	1.92E-01	TIMP1
E2F3B upregulated	Liver Regeneration	2.59E-01	TOB1

Supplemental Table 15. Liver IPA functions for E2F1 and E2F3B putative direct targets

	Category	B-H p-value	Genes
E2F3B upregulated	Liver Hepatomegaly	2.65E-01	FDFT1
E2F3B upregulated	Liver Enlargement	2.65E-01	FDFT1
E2F3B upregulated	Liver Cholestasis	2.97E-01	CDKN1A
E2F3B upregulated	Liver Steatosis	3.06E-01	CDKN1A,HBEGF
E2F1 downregulated	Liver Steatosis	2.67E-01	PANK1
E2F1 downregulated	Liver Hyperplasia/Hyperproliferation	1.00E+00	RPRD2,ALS2,SLC29A1,PITPNB
E2F1 downregulated	Hepatocellular Carcinoma	1.00E+00	RPRD2,ALS2,SLC29A1,PITPNB
E2F3B downregulated	Liver Hyperplasia/Hyperproliferation	2.51E-02	NAV2,CCP110,MSH3,GTF3C2,KIF1B,SFPQ,RBM33,RICTOR,LATS2,KPNA1,TOMM70A,USF3,RCL1,TBC1D4,SMPD4,ZNF318,RORA,PRPF4B,GDE1,TFDP2,ALDH7A1,SYNE2,USP38,BIRC6,AGFG2,MON2,ARHGAP5,ARIH1,WHSC1L1,NASP,UGP2,YTHDF3,ACY1,AHCTF1,KIAA0368,ZNF644,BAZ1B,MCCC2,TRIM33,NFIX,PA2G4,XPNPEP3,ATF6,TYW1,XYLB,LYST,STEAP2,EIF3A,LPP,FBXO21,UBE3C,UBR5,MTRR,PAICS,HERPUD1,MTHFD1,ALS2,RETSAT,MTO1,ZHX3,SIN3A,SF3B2,U2SURP,CHD9,PAN3,NFIB,IREB2,USP34,TCF7L2,ACSL1
E2F3B downregulated	Hepatocellular Carcinoma	2.51E-02	NAV2,CCP110,MSH3,GTF3C2,KIF1B,SFPQ,RBM33,RICTOR,LATS2,KPNA1,TOMM70A,USF3,RCL1,TBC1D4,SMPD4,ZNF318,RORA,PRPF4B,GDE1,TFDP2,ALDH7A1,SYNE2,USP38,BIRC6,AGFG2,MON2,ARHGAP5,ARIH1,WHSC1L1,NASP,UGP2,YTHDF3,ACY1,AHCTF1,KIAA0368,ZNF644,BAZ1B,MCCC2,TRIM33,NFIX,PA2G4,XPNPEP3,ATF6,TYW1,XYLB,LYST,STEAP2,EIF3A,LPP,FBXO21,UBE3C,UBR5,MTRR,PAICS,HERPUD1,MTHFD1,ALS2,RETSAT,MTO1,ZHX3,SIN3A,SF3B2,U2SURP,CHD9,PAN3,NFIB,IREB2,USP34,TCF7L2,ACSL1
E2F3B downregulated	Liver Steatosis	1.91E-01	RORA,STEAP2,ADK,ATF6
E2F3B downregulated	Liver Dysfunction	1.91E-01	ATF6
E2F3B downregulated	Liver Damage	2.08E-01	ADK
E2F3B downregulated	Liver Inflammation/Hepatitis	2.08E-01	ADK
E2F3B downregulated	Liver Cholestasis	3.12E-01	UGP2,ACSL1
E2F3B downregulated	Hepatocellular Peroxisome Proliferation	3.12E-01	ABCD3
E2F3B downregulated	Liver Failure	3.43E-01	ADRB3
E2F3B downregulated	Liver Proliferation	3.79E-01	BIRC6
E2F3B downregulated	Liver Fibrosis	5.30E-01	RORA,ADK
E2F3B downregulated	Liver Necrosis/Cell Death	6.31E-01	TAF10,XIAP
E2F3B downregulated	Liver Cirrhosis	6.49E-01	ADK,ADRB3

Supplemental Table 16. E2F1 and E2F3B direct upregulated targets in canonical IPA pathways

Category		B-H p-value	Genes
Cell Cycle: G2/M DNA Damage Checkpoint Regulation	E2F1 upregulated	7.84E-09	CDKN1A,CKS1B,TOP2A,MDM2,AURKA,CDK1,CHEK1
	E2F3B upregulated	9.73E-02	CDKN1A,YWHAZ
ATM Signaling	E2F1 upregulated	2.37E-05	RAD51,CDKN1A,MDM2,CDK1,CHEK1
	E2F3B upregulated	3.37E-01	CDKN1A
Cell Cycle: G1/S Checkpoint Regulation	E2F1 upregulated	2.98E-05	MYC,CCNE1,CDKN1A,MDM2,E2F3
	E2F3B upregulated	3.39E-01	CDKN1A
Cyclins and Cell Cycle Regulation	E2F1 upregulated	6.84E-05	CCNA2,CCNE1,CDKN1A,E2F3,CDK1
	E2F3B upregulated	4.62E-01	CDKN1A
Superpathway of Cholesterol Biosynthesis	E2F1 upregulated	2.27E-01	IDI1
	E2F3B upregulated	1.77E-04	FDPS,SQLE,FDFT1,CYP51A1
Hepatic Fibrosis / Hepatic Stellate Cell Activation	E2F3B upregulated	2.88E-05	COL4A1,CTGF,MYH9,COL6A3,PDGFA,TIMP1,FGFR1,KLF6

Supplemental Table 17. Expression of E2F1 and E2F3B targets in HCC samples with normal or elevated E2F1 copy numbers

Gene	Regulated by	Mean expression in E2F1 diploid samples	Mean expression in E2F1 copy number increased samples	Wilcox adj. *P* -value	
E2F1	NA	-0.004	0.390	0.000	*
E2F3	E2F1	0.258	0.289	1.000	
ACSL3	E2F1	-0.055	0.080	1.000	
ALCAM	E2F1	0.047	0.057	1.000	
ATXN2L	E2F1	-0.049	0.038	1.000	
AURKA	E2F1	0.066	0.716	0.000	*
BIRC5	E2F1	0.082	0.606	0.000	*
CAMK2N2	E2F1	-0.031	0.019	1.000	
CCNA2	E2F1	-0.070	0.281	0.000	*
CCNE1	E2F1	0.288	0.221	0.052	
CDC6	E2F1	0.067	0.396	0.005	*
CDCA5	E2F1	-0.082	0.522	0.000	*
CDK1	E2F1	-0.040	0.370	0.000	*
CEP55	E2F1	0.084	0.402	0.000	*
CHEK1	E2F1	-0.074	0.331	0.009	*
CKAP2	E2F1	-0.162	0.055	0.601	
DDX50	E2F1	-0.131	0.239	1.000	
DEPDC1B	E2F1	-0.039	0.258	0.000	*
DUSP6	E2F1	0.066	-0.228	1.000	
GAS2L3	E2F1	-0.031	0.327	1.000	
GJA1	E2F1	-0.066	-0.066	1.000	
HELLS	E2F1	-0.006	0.429	0.002	*
HEXA	E2F1	-0.009	-0.195	1.000	
HIST1H4A	E2F1	-0.028	0.160	1.000	
HIVEP2	E2F1	-0.146	-0.346	1.000	
IDI1	E2F1	-0.049	0.192	0.984	
IFRD1	E2F1	0.255	0.139	1.000	
MDM2	E2F1	0.105	0.071	1.000	
MYC	E2F1	0.436	0.281	1.000	
MYEF2	E2F1	0.113	0.189	1.000	
NFE2L2	E2F1	0.050	-0.370	1.000	
NOP58	E2F1	0.087	0.279	1.000	
PAPSS1	E2F1	-0.035	0.210	1.000	
PBK	E2F1	-0.212	0.059	0.021	*
PBX3	E2F1	-0.035	-0.055	1.000	
PIGP	E2F1	-0.179	-0.383	1.000	
PLEKHA1	E2F1	-0.105	-0.044	1.000	
PVR	E2F1	0.001	0.286	0.045	*
RAD18	E2F1	0.082	0.179	1.000	
RAD51	E2F1	-0.023	0.586	0.000	*
RHOB	E2F1	0.026	-0.234	1.000	
SHCBP1	E2F1	0.001	0.237	0.008	*
SLC20A1	E2F1	-0.033	0.170	0.601	
SMC4	E2F1	0.006	0.169	1.000	
SPATS2	E2F1	0.053	0.264	0.401	
STMN1	E2F1	-0.145	0.317	0.000	*
TACC3	E2F1	-0.016	0.387	0.000	*
TOP2A	E2F1	-0.022	0.437	0.000	*

Supplemental Table 17. Expression of E2F1 and E2F3B targets in HCC samples with normal or elevated E2F1 copy numbers

Gene	Regulated by	Mean expression in E2F1 diploid samples	Mean expression in E2F1 copy number increased samples	Wilcox adj. *P* -value	
TRIB1	E2F1	0.103	0.068	1.000	
UHRF1	E2F1	-0.050	0.242	0.004	*
WWTR1	E2F1	0.036	-0.073	1.000	
BTG2	E2F1;E2F3B	-0.034	0.070	0.385	
CDKN1A	E2F1;E2F3B	0.021	-0.028	1.000	
EGR2	E2F1;E2F3B	-0.022	-0.099	1.000	
EXOC4	E2F1;E2F3B	0.228	0.247	1.000	
JUND	E2F1;E2F3B	-0.118	0.135	1.000	
LGALS1	E2F1;E2F3B	0.069	0.180	1.000	
PHLDA3	E2F1;E2F3B	-0.005	0.202	1.000	
RRBP1	E2F1;E2F3B	-0.045	0.342	0.027	*
TMEM43	E2F1;E2F3B	0.088	0.231	1.000	
TUBB6	E2F1;E2F3B	-0.011	0.070	1.000	
UNC5B	E2F1;E2F3B	-0.006	0.138	1.000	
ABRACL	E2F3B	-0.149	-0.230	1.000	
ACTB	E2F3B	0.096	0.434	1.000	
ADPRH	E2F3B	0.031	-0.061	1.000	
AGO2	E2F3B	0.861	1.216	1.000	
ARSG	E2F3B	0.085	0.125	1.000	
ATP2B1	E2F3B	0.003	0.363	0.514	
CAPG	E2F3B	-0.046	0.172	0.128	
CDKN3	E2F3B	-0.032	0.408	0.000	*
CENPM	E2F3B	-0.081	0.654	0.000	*
COL4A1	E2F3B	0.046	-0.039	1.000	
COL6A3	E2F3B	0.008	0.052	1.000	
CSRP1	E2F3B	0.051	0.026	1.000	
CTGF	E2F3B	-0.137	-0.012	1.000	
CYP51A1	E2F3B	0.152	0.474	0.799	
CYR61	E2F3B	-0.037	-0.198	1.000	
DDR1	E2F3B	0.039	0.083	1.000	
DLGAP5	E2F3B	0.014	0.504	0.000	*
EIF4EBP2	E2F3B	-0.141	0.017	1.000	
FAAP20	E2F3B	-0.083	-0.048	1.000	
FDFT1	E2F3B	-0.380	-0.268	1.000	
FDPS	E2F3B	0.557	0.983	0.146	
FGFR1	E2F3B	-0.082	-0.155	1.000	
FNDC3B	E2F3B	0.059	0.163	1.000	
GNAI2	E2F3B	-0.059	0.025	1.000	
HAUS8	E2F3B	-0.080	0.371	0.002	*
HBEGF	E2F3B	-0.030	-0.087	1.000	
IQGAP1	E2F3B	0.091	0.113	1.000	
JAG1	E2F3B	0.028	0.273	1.000	
KLF6	E2F3B	0.007	0.007	1.000	
LASP1	E2F3B	0.080	0.307	1.000	
LIPT2	E2F3B	0.034	0.137	1.000	
LOXL1	E2F3B	0.165	0.216	1.000	
LYSMD2	E2F3B	-0.037	-0.311	1.000	

Supplemental Table 17. Expression of E2F1 and E2F3B targets in HCC samples with normal or elevated E2F1 copy numbers

Gene	Regulated by	Mean expression in E2F1 diploid samples	Mean expression in E2F1 copy number increased samples	Wilcox adj. *P* -value	
MYH9	E2F3B	0.002	0.031	1.000	
NRM	E2F3B	0.164	0.706	0.001	*
PDAP1	E2F3B	0.337	0.667	0.961	
PDGFA	E2F3B	0.115	0.303	1.000	
PDLIM1	E2F3B	-0.157	-0.024	1.000	
PLAT	E2F3B	-0.029	-0.178	1.000	
PRDX2	E2F3B	-0.023	0.174	1.000	
PSAP	E2F3B	-0.083	-0.016	1.000	
PVT1	E2F3B	0.986	0.758	1.000	
RAB5C	E2F3B	0.284	0.085	1.000	
SAE1	E2F3B	0.099	0.645	0.110	
SAMD4A	E2F3B	-0.171	-0.405	1.000	
SECISBP2	E2F3B	-0.181	-0.303	1.000	
SEPT12	E2F3B	-0.152	-0.153	1.000	
SF1	E2F3B	0.007	0.037	1.000	
SLC35A5	E2F3B	0.101	-0.265	1.000	
SLC35C1	E2F3B	0.021	-0.147	1.000	
SOX4	E2F3B	0.053	0.238	1.000	
SP4	E2F3B	0.006	0.073	1.000	
SQLE	E2F3B	0.496	1.029	0.049	*
SRXN1	E2F3B	0.016	0.064	1.000	
TIMP1	E2F3B	-0.023	-0.136	1.000	
TOB1	E2F3B	0.264	-0.040	1.000	
TUBB4B	E2F3B	-0.120	0.335	0.176	
UAP1L1	E2F3B	0.096	0.150	1.000	
UBE2S	E2F3B	-0.037	0.395	0.000	*
VAMP3	E2F3B	-0.360	-0.504	1.000	
WDFY3	E2F3B	-0.205	-0.405	1.000	
YWHAZ	E2F3B	0.912	1.254	1.000	
ZC3HAV1	E2F3B	0.133	-0.233	1.000	
ZDHHC14	E2F3B	-0.275	-0.071	0.924	

Supplemental Table 18. Expression of E2F1 and E2F3B targets in HCC samples with normal or elevated E2F3 copy numbers

Gene	Regulated by	Mean expression in E2F3 diploid samples	Mean expression in E2F3 copy number increased samples	Wilcox adj. *P*-value	
E2F1	NA	0.042	0.228	1.000	
E2F3	E2F1	-0.004	0.643	0.001	*
ATXN2L	E2F1	-0.056	0.027	1.000	
AURKA	E2F1	0.285	0.252	1.000	
BIRC5	E2F1	0.240	0.260	1.000	
CAMK2N2	E2F1	-0.018	-0.011	1.000	
CCNA2	E2F1	0.038	0.045	1.000	
CCNE1	E2F1	0.266	0.268	1.000	
CDC6	E2F1	0.083	0.292	1.000	
CDCA5	E2F1	0.042	0.200	1.000	
CDK1	E2F1	0.038	0.161	1.000	
CEP55	E2F1	0.218	0.139	1.000	
CHEK1	E2F1	-0.072	0.228	0.180	
CKAP2	E2F1	-0.082	-0.109	1.000	
DDX50	E2F1	-0.094	0.097	1.000	
DEPDC1B	E2F1	0.049	0.063	1.000	
DUSP6	E2F1	0.069	-0.159	1.000	
GAS2L3	E2F1	0.091	0.069	1.000	
GJA1	E2F1	-0.004	-0.152	1.000	
HELLS	E2F1	0.051	0.242	1.000	
HEXA	E2F1	-0.053	-0.088	1.000	
HIST1H4A	E2F1	0.042	0.016	1.000	
HIVEP2	E2F1	-0.096	-0.366	1.000	
IDI1	E2F1	-0.077	0.172	0.937	
IFRD1	E2F1	0.248	0.177	1.000	
MDM2	E2F1	0.185	-0.030	1.000	
MYC	E2F1	0.463	0.282	1.000	
MYEF2	E2F1	0.178	0.080	1.000	
NFE2L2	E2F1	-0.066	-0.106	1.000	
NOP58	E2F1	0.032	0.306	1.000	
PAPSS1	E2F1	0.088	-0.020	1.000	
PBK	E2F1	-0.138	-0.111	1.000	
PBX3	E2F1	-0.006	-0.090	1.000	
PIGP	E2F1	-0.277	-0.198	1.000	
PLEKHA1	E2F1	-0.119	-0.039	1.000	
PVR	E2F1	0.179	-0.030	1.000	
RAD18	E2F1	0.101	0.128	1.000	
RAD51	E2F1	0.121	0.235	1.000	
RHOB	E2F1	0.009	-0.146	1.000	
SHCBP1	E2F1	0.118	0.018	1.000	
SLC20A1	E2F1	0.090	-0.050	1.000	
SMC4	E2F1	0.056	0.059	1.000	
SPATS2	E2F1	0.109	0.135	1.000	
STMN1	E2F1	-0.128	0.180	0.016	*
TACC3	E2F1	0.124	0.095	1.000	
TOP2A	E2F1	0.062	0.207	1.000	
TRIB1	E2F1	0.176	-0.025	1.000	

Supplemental Table 18. Expression of E2F1 and E2F3B targets in HCC samples with normal or elevated E2F3 copy numbers

Gene	Regulated by	Mean expression in E2F3 diploid samples	Mean expression in E2F3 copy number increased samples	Wilcox adj. *P*-value
UHRF1	E2F1	-0.019	0.126	1.000
WWTR1	E2F1	0.039	-0.049	1.000
BTG2	E2F1;E2F3B	0.013	-0.022	1.000
CDKN1A	E2F1;E2F3B	0.032	-0.031	1.000
EGR2	E2F1;E2F3B	0.068	-0.204	1.000
EXOC4	E2F1;E2F3B	0.150	0.350	1.000
JUND	E2F1;E2F3B	-0.040	-0.034	1.000
LGALS1	E2F1;E2F3B	0.209	-0.040	1.000
PHLDA3	E2F1;E2F3B	0.128	-0.032	1.000
RRBP1	E2F1;E2F3B	0.050	0.115	1.000
TMEM43	E2F1;E2F3B	0.233	-0.004	1.000
TUBB6	E2F1;E2F3B	0.144	-0.164	1.000
UNC5B	E2F1;E2F3B	0.035	0.047	1.000
ABRACL	E2F3B	-0.008	-0.404	1.000
ACTB	E2F3B	0.357	-0.010	1.000
ADPRH	E2F3B	0.122	-0.164	1.000
AGO2	E2F3B	0.764	1.263	1.000
ARSG	E2F3B	0.106	0.086	1.000
ATP2B1	E2F3B	0.067	0.186	1.000
CAPG	E2F3B	0.022	0.025	1.000
CDKN3	E2F3B	0.041	0.199	1.000
CENPM	E2F3B	0.063	0.274	1.000
COL4A1	E2F3B	0.089	-0.077	1.000
COL6A3	E2F3B	0.119	-0.112	1.000
CSRP1	E2F3B	0.173	-0.137	1.000
CTGF	E2F3B	-0.081	-0.121	1.000
CYP51A1	E2F3B	0.197	0.332	1.000
CYR61	E2F3B	0.016	-0.231	1.000
DDR1	E2F3B	0.001	0.125	0.961
DLGAP5	E2F3B	0.107	0.255	1.000
EIF4EBP2	E2F3B	-0.229	0.100	0.474
FAAP20	E2F3B	-0.016	-0.149	1.000
FDFT1	E2F3B	-0.319	-0.380	1.000
FDPS	E2F3B	0.662	0.733	1.000
FGFR1	E2F3B	-0.028	-0.212	1.000
FNDC3B	E2F3B	0.113	0.064	1.000
GNAI2	E2F3B	0.090	-0.202	1.000
HAUS8	E2F3B	0.054	0.075	1.000
HBEGF	E2F3B	0.027	-0.152	1.000
IQGAP1	E2F3B	0.223	-0.074	1.000
JAG1	E2F3B	0.119	0.087	1.000
KLF6	E2F3B	0.049	-0.051	1.000
LASP1	E2F3B	0.080	0.250	1.000
LIPT2	E2F3B	0.055	0.082	1.000
LOXL1	E2F3B	0.397	-0.118	1.000
LYSMD2	E2F3B	-0.024	-0.260	1.000
MYH9	E2F3B	0.041	-0.030	1.000

Supplemental Table 18. Expression of E2F1 and E2F3B targets in HCC samples with normal or elevated E2F3 copy numbers

Gene	Regulated by	Mean expression in E2F3 diploid samples	Mean expression in E2F3 copy number increased samples	Wilcox adj. *P*-value	
NRM	E2F3B	0.051	0.728	0.002	*
PDAP1	E2F3B	0.422	0.469	1.000	
PDGFA	E2F3B	0.138	0.225	1.000	
PDLIM1	E2F3B	-0.206	0.011	1.000	
PLAT	E2F3B	-0.034	-0.135	1.000	
PRDX2	E2F3B	0.033	0.048	1.000	
PSAP	E2F3B	-0.005	-0.140	1.000	
PVT1	E2F3B	0.939	0.880	1.000	
RAB5C	E2F3B	0.208	0.240	1.000	
SAE1	E2F3B	0.143	0.450	1.000	
SAMD4A	E2F3B	-0.199	-0.308	1.000	
SECISBP2	E2F3B	-0.312	-0.092	1.000	
SEPT12	E2F3B	-0.055	-0.287	1.000	
SF1	E2F3B	-0.028	0.078	1.000	
SLC35A5	E2F3B	0.055	-0.110	1.000	
SLC35C1	E2F3B	0.019	-0.103	1.000	
SOX4	E2F3B	0.003	0.262	1.000	
SP4	E2F3B	0.017	0.041	1.000	
SQLE	E2F3B	0.548	0.824	1.000	
SRXN1	E2F3B	0.014	0.054	1.000	
TIMP1	E2F3B	0.025	-0.173	1.000	
TOB1	E2F3B	0.151	0.192	1.000	
TUBB4B	E2F3B	0.089	-0.066	1.000	
UAP1L1	E2F3B	0.078	0.162	1.000	
UBE2S	E2F3B	0.088	0.115	1.000	
VAMP3	E2F3B	-0.335	-0.504	1.000	
WDFY3	E2F3B	-0.137	-0.449	1.000	
YWHAZ	E2F3B	0.995	1.053	1.000	
ZC3HAV1	E2F3B	0.079	-0.067	1.000	
ZDHHC14	E2F3B	-0.165	-0.275	1.000	

Supplemental Table 19: Oligonucleotide sequences used for genotyping

Allele(s)	Primer 1	Primer 2	Primer 3
$E2f3a^{+}$, $E2f3a^{1KI}$ $E2f3a^{+}$, $E2f3a^{3bKI}$	CATCTCTCGCTCCTGCTCTT	GACCCTCCTCTCTCCAGACC	
Cre	CCTGTTTTGCACGTTCACCG	ATGCTTCTGTCCGTTTGCCG	
$E2f1^{+}$, $E2f1^{-}$	AGCCACTGGATATGATTCTTGGAC	AGAAGTCACGCTATGAAACCTCAC	AGTGCCAGCGGGGCTGCTAAAG
$E2f3a^{+}$, $E2f3a^{-}$	CTCCAGACCCCCGATTATTT	TCCAGTGCACTACTCCCTCC	GCTAGCAGTGCCCTTTTGTC
$E2f3b^{+}$, $E2f3b^{-}$	CCCCATTTCCCAAAGTCCTA	TGTTAGACTCGGGGTGCTTT	AAAGCGCCTTTGAGAGAT

Supplemental Table 20: Oligonucleotide sequences used for ChIP-qPCR

Gene	Primer 1	Primer 2
CDC6	AAAGGCTCTGTGACTACAGCCA	GATCCTTCTCACGTCTCTCACA
CDKN1A	CGGAGTGGAAGCAGTTTTG	GGTAATGGCATAGGGGTTGA
CHEK1	GCTCAGACGATACTCTCGCCTC	CGCTAACCCAAGACGGGAG
RAD51	AGCTGGGAACTGCAACTCAT	CGCCTCACACACTCACCTC
RBM4	CGGACGCCAATTACCTAAGA	GCGCCATGAAGCTAAAGACT
TIMELESS	GAGTGAGTGTGTGGCGAGAG	CGGGAGACTAAGGAGCAGAG
TOP2A	CGCACGAGAAAACAAGTGAG	TCCGTCCAGAAGAACCAATC
TUB4A4	ATGGAGGGATGAATGGTTATGC	CTTTTTGGGTCTGGCTTCTTTCAC
UHFR1	AGAGTTCAGGGGGTCTGTACC	ACTCGGCATTTGGGAGTTG
UPF3B	AGATGGCGGAATTGCTAATG	ATGCCCCTTGTGATAAGTCG