

**Appendix 1 Enrichment analysis reveals transcription factors associated with the EGR1 promoter region**

Promoter sequences spanning from TSS -1000 to +100 of EGR1 were subjected to ChIP-seq analysis using the UCSC database. Notably, two distinct ChIP-seq segments exhibited significant enrichment of EGR1, highlighted in yellow and blue, respectively, representing prominent peaks. Furthermore, promoter sequences were analyzed using the JAPSAR website to identify binding site sequences, highlighted in green font. Remarkably, an overlap was observed between the identified EGR1 peaks and binding site sequences, suggesting a potential autoregulatory mechanism wherein EGR1 modulates its own transcription.

EGR1 TSS -1000 to 100

CAGCTTCCCCACTTTCGGTCCCCCAAAGGTGGGCTCTTTGCCGGCGGGGACTAGGGAACAGCCTTTTCGG  
 TTCCGGGGGAGCACAGGGGACCCAGGCACCCAGCAGCCCCCATCCCACCGACAGGTGGCAG  
 AGCAAGGCAGCTCACTGCTATACAGTGTCCAAGAACAAGTGCCCGTGACTTCTATCTCAAT  
 TTCCACGACACCCGGAAAGACACCGTGCCATAGATCGAGGCCCGGGGTCAAGG  
 CCCCCTCTCCTGGGCGGCCCTGCCAGGCGGCCAGCCGCTCCTCCCCGCACTCCCGGT  
 TCGTCTCACGGTCCCTGAGGTGGGCGGGCGCCCTGGATGACAGCGATAGAACCCCGGCCGACT  
 CGCCCTCGCCCCGCTCTGGGTCTGGGCTTCCCCAGCCTAGTTCACGCCTAGGAGCCGCC  
 TGAGCAGCCGCGCGGCCAGCGCCACACGCCACGAGCCCTCCCCGCTGGGCGTCCC  
 CGGATCCCGGAGCGCTCGGGCTCCCGGCTTGAACCAGGGAGGAGGGAGGGAGCGAGGGAGC  
 AACCAAGCTGCGACCCGGAAATGCCATATAAGGAGCAGGAAGGATCCCCCGCCGGAA  
 CAACCCTTATTTGGGCAGCACCTTATTTGGAGTGGCCCGATATGGCCCGCCGCTTCCGGCT  
 CTGGGAGGAGGGAAGAAGGCGGAGGGAGGGCAACGCGGGAAGTCCGGAGCTGCGCGGGTCCCGGA  
 GGCCCCGGCGGGCTAGAGCTCTAGGCTTCCCCGAAGCCTGGGCGCCTGGGATGCGGGCGCGG  
 GCGCGGCCCTAGGCTGCAGGATGGAGGTGCCGGGCGCTGTGCGATGGGGGGCTTACGCTACTCC  
 GGGTCTCCCGCGGTCCTGCCATATAGGGCTTCCCTGCCATATGCCATATGGCCATGTACGTCAGC  
 ACGGAGGCGGACCCGTCCTGTTCCAGACCCCTCAATAGAGCGGATCCGGGGAGTTCGCGAGA  
 GATCCAGCGCGCAGAACTTGGGAGCGCCGCGCCATCCGCCGCGCAGCCAG  
 CTTCGCGCCGAGACCGGCCCTGCCAGCCTCCGACG

TSS

>hg19\_dna range=chr5:137800346-137800699 5'pad=0 3'pad=0 strand=+ repeatMasking=none EGR1 first peak  
 >hg19\_dna range=chr5:137801131-137801400 5'pad=0 3'pad=0 strand=+ repeatMasking=none EGR1 second peak  
 EGR1 peak and binding site have overlapping base sequences

Jaspar

Display 102550100All profiles

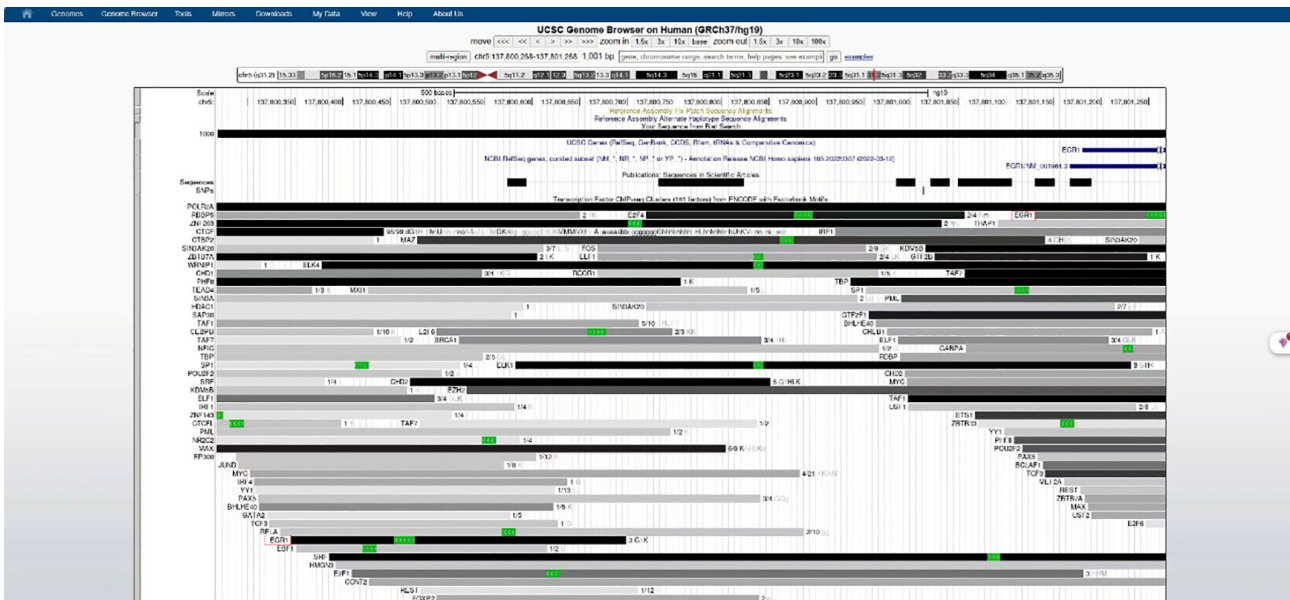
Filter:

Matrix ID	Name	Score	Relative score	Sequence ID	Start	End	Strand	Predicted sequence
MA0162.2	MA0162.2.EGR1	16.213522	0.9538132715370483	EGR1	292	305	+	GCTCTCCCCCGCA
MA0162.2	MA0162.2.EGR1	14.5056715	0.9355236234429649	EGR1	383	396	+	CCCTCGCCCCGCT
MA0162.2	MA0162.2.EGR1	13.1271105	0.9207603894384563	EGR1	1059	1072	+	CTTCGCGCCGCA
MA0162.2	MA0162.2.EGR1	12.381396	0.9127744150104505	EGR1	1040	1053	+	CATCCGCGCCGCA
MA0162.2	MA0162.2.EGR1	12.063826	0.9093734989191459	EGR1	1027	1040	+	GAGCCGCGCCGCC
MA0162.4	MA0162.4.EGR1	14.189755	0.9078886793876008	EGR1	800	813	-	CCGCGCCCGCC
MA0162.5	MA0162.5.EGR1	11.720642	0.9041905874570929	EGR1	386	395	+	TCGCCCCGCG
MA0162.2	MA0162.2.EGR1	11.42462	0.9025281387036078	EGR1	1086	1099	+	CCCCAGCCTCCGCA
MA0162.5	MA0162.5.EGR1	11.365128	0.8972558207813758	EGR1	802	811	-	GCGCCCGCGC
MA0162.5	MA0162.5.EGR1	11.318152	0.8963395105262527	EGR1	484	493	-	ACGCCAGGC
MA0162.4	MA0162.4.EGR1	13.463276	0.8951842928836917	EGR1	384	397	+	CCTCGCCCCGCTC
MA0162.2	MA0162.2.EGR1	10.408893	0.8916505527235009	EGR1	543	556	-	CCCTCGCTCCCTCC
MA0162.2	MA0162.2.EGR1	10.365023	0.8911807420611944	EGR1	1030	1043	+	CCGCGCCGCCATC
MA0162.2	MA0162.2.EGR1	10.195637	0.8893667608222012	EGR1	940	953	-	GGTCCGCTCCGTC
MA0162.5	MA0162.5.EGR1	10.744426	0.885148236509544	EGR1	295	304	+	CCTCCCCGCG
MA0162.2	MA0162.2.EGR1	9.392305	0.8807637545693674	EGR1	692	705	-	CTCCTCGCCTTC
MA0162.2	MA0162.2.EGR1	8.590367	0.8721756695873241	EGR1	797	810	-	CGCCCGCGCCGCA
MA0162.5	MA0162.5.EGR1	9.92071	0.8690805965731452	EGR1	336	345	-	CCGCCCCGCC
MA0162.5	MA0162.5.EGR1	9.918124	0.8690301648151892	EGR1	798	807	-	CCGCGCCGCG
MA0162.5	MA0162.5.EGR1	9.918124	0.8690301648151892	EGR1	804	813	-	CCGCGCCGCG
MA0162.2	MA0162.2.EGR1	8.183985	0.8678236526995592	EGR1	377	390	+	GACTCGCCCTCGCC
MA0162.5	MA0162.5.EGR1	9.843793	0.867580237821974	EGR1	332	341	-	CCGCCACCT
MA0162.4	MA0162.4.EGR1	11.710306	0.8645290518206684	EGR1	334	347	-	GCCCCCGCCGCCAC
MA0162.4	MA0162.4.EGR1	11.681345	0.8640225901382546	EGR1	293	306	+	CTCTCCCCCGCAC
MA0162.3	MA0162.3.EGR1	11.106431	0.8624768768102979	EGR1	294	307	+	TCCTCCCCCGCACT
MA0162.2	MA0162.2.EGR1	7.4407067	0.8598637675160669	EGR1	689	702	-	CCTCGCCTTCTTC
MA0162.5	MA0162.5.EGR1	9.417667	0.8592681130529998	EGR1	781	790	-	GCGCCAGGC
MA0162.2	MA0162.2.EGR1	7.369345	0.8590995451678771	EGR1	747	760	-	TAGCCGCGCCGGG
MA0162.2	MA0162.2.EGR1	7.3068523	0.8584302991083358	EGR1	1037	1050	+	CGCCATCCGCGCC
MA0162.2	MA0162.2.EGR1	7.163466	0.8568947512334246	EGR1	1080	1093	+	CCCCTGCCCCAGCC
MA0162.4	MA0162.4.EGR1	11.22189	0.8559878310457374	EGR1	802	815	-	GCCCGCGCCGCGC
MA0162.2	MA0162.2.EGR1	7.048623	0.8556648800421255	EGR1	803	816	-	GGCCCGCGCCCGCG
MA0162.2	MA0162.2.EGR1	6.907245	0.8541508408573475	EGR1	1056	1069	+	CAGCTTCGCGCC
MA0162.4	MA0162.4.EGR1	11.069701	0.853326405591214	EGR1	378	391	+	ACTCGCCCTCGCC
MA0162.5	MA0162.5.EGR1	8.953744	0.8502186912368739	EGR1	380	389	+	TCGCCCTCGC
MA0162.2	MA0162.2.EGR1	6.5031905	0.8498237540325527	EGR1	663	676	+	CGGCCGCTCCGGC
MA0162.4	MA0162.4.EGR1	10.795865	0.8485376676247709	EGR1	482	495	-	GGACGCCAGCGGG
MA0162.2	MA0162.2.EGR1	6.3581796	0.8482708082214393	EGR1	1043	1056	+	CCGCGCCCGCAGCC
MA0162.5	MA0162.5.EGR1	8.81953	0.8476006672515622	EGR1	1030	1039	+	CCGCCCGCCG
MA0162.5	MA0162.5.EGR1	8.81953	0.8476006672515622	EGR1	1043	1052	+	CCGCCCGCCG
MA0162.5	MA0162.5.EGR1	8.81953	0.8476006672515622	EGR1	1062	1071	+	CCGCCCGCCG
MA0162.2	MA0162.2.EGR1	5.841346	0.8427359512525668	EGR1	331	344	-	CGCCCGCCACCTC
MA0162.3	MA0162.3.EGR1	9.273761	0.840630528440203	EGR1	795	808	-	CCCGGCCCGCATC
MA0162.4	MA0162.4.EGR1	10.333047	0.8404440870638041	EGR1	796	809	-	GCCCGCGCCCGCAT
MA0162.3	MA0162.3.EGR1	9.1927805	0.8396652026258443	EGR1	385	398	+	CTCGCCCCGCTCT
MA0162.2	MA0162.2.EGR1	5.3005843	0.8369448487777864	EGR1	750	763	-	CTTAGCCGCGCC
MA0162.2	MA0162.2.EGR1	5.2210727	0.8360933456765679	EGR1	695	708	-	CCCCTCCCTCCGCC
MA0162.2	MA0162.2.EGR1	5.167436	0.835518943135983	EGR1	1079	1092	+	GCCCCTGCCCCAGC
MA0162.4	MA0162.4.EGR1	10.028896	0.8351252220722396	EGR1	330	343	-	GCCCGCCACCTCA
MA0162.2	MA0162.2.EGR1	4.7306314	0.8308411298497141	EGR1	121	134	-	TTGCCTTGCCACC
MA0162.2	MA0162.2.EGR1	4.5724688	0.8291473409278306	EGR1	109	122	+	ATCCACCGACAGG
MA0162.2	MA0162.2.EGR1	4.4399047	0.8277276907811395	EGR1	269	282	+	CCCCTGCCAGGCG
MA0162.2	MA0162.2.EGR1	4.1895103	0.8250461770538605	EGR1	844	857	-	CCCCATCCGACAGC
MA0162.2	MA0162.2.EGR1	3.905218	0.8220016429022641	EGR1	937	950	-	CCGCCCTCCGTCGTG
MA0162.2	MA0162.2.EGR1	3.7972858	0.8208457806013022	EGR1	675	688	-	CCTCTCCAGAGC
MA0162.3	MA0162.3.EGR1	7.583398	0.8204805542606844	EGR1	1042	1055	+	TCCGCCGCGCAGC
MA0162.2	MA0162.2.EGR1	3.7209058	0.8200278146136758	EGR1	801	814	-	CCCGCGCCCGCGCC
MA0162.2	MA0162.2.EGR1	3.5881782	0.8186064129283533	EGR1	1074	1087	+	GACCGGCCCTGCC
MA0162.3	MA0162.3.EGR1	7.3732505	0.8179754920508496	EGR1	1061	1074	+	TCCGCCGCGCAGG
MA0162.2	MA0162.2.EGR1	3.4524295	0.8171526588436151	EGR1	375	388	+	CCGACTCGCCCTCG
MA0162.2	MA0162.2.EGR1	3.4094152	0.8166920118433323	EGR1	252	265	+	CCGCCCTCCTGGG
MA0162.2	MA0162.2.EGR1	2.945271	0.8117214158531728	EGR1	536	549	-	TCCTCCCTCCTCC
MA0162.2	MA0162.2.EGR1	2.8590753	0.810798332015026	EGR1	1053	1066	+	AGCCAGCTTCCGCC
MA0162.4	MA0162.4.EGR1	8.62718	0.8106125633663006	EGR1	794	807	-	CCGCGCCCGCATCC
MA0162.2	MA0162.2.EGR1	2.777149	0.8099209694629922	EGR1	124	137	-	GCCTTGCTCTGCC
MA0162.2	MA0162.2.EGR1	2.7071834	0.8091716964714892	EGR1	1062	1075	+	CCGCCGCGCAGGA
MA0162.2	MA0162.2.EGR1	2.6788352	0.808868110910529	EGR1	698	711	-	TTGCCCTCCCTCC
MA0162.2	MA0162.2.EGR1	2.571873	0.8077226352847169	EGR1	696	709	-	GCCCTCCCTCCGC
MA0162.2	MA0162.2.EGR1	2.4110997	0.8060008881295762	EGR1	1073	1086	+	GGACCGGCCCTGCG
MA0162.3	MA0162.3.EGR1	6.21576	0.8041776275201115	EGR1	481	494	-	GACGCCAGGCGGG
MA0162.4	MA0162.4.EGR1	8.24962	0.8040099494283515	EGR1	1041	1054	+	ATCCGCCGCGCAG
MA0162.2	MA0162.2.EGR1	2.202343	0.8037652788602213	EGR1	533	546	-	CTCCTCCTCCCTG
MA0162.5	MA0162.5.EGR1	6.5690584	0.8037023426086309	EGR1	550	559	-	GCTCCCTCGC
MA0162.2	MA0162.2.EGR1	2.1822662	0.8035502736633152	EGR1	70	83	-	TGTGCTCCCCGGA
MA0162.2	MA0162.2.EGR1	2.1321342	0.803013401540141	EGR1	1046	1059	+	CCGCCGCGCCAGC
MA0162.2	MA0162.2.EGR1	2.131194	0.803003334022905	EGR1	249	262	+	GCCCGCCTCCTCT
MA0162.2	MA0162.2.EGR1	2.0270956	0.8018885256427233	EGR1	263	276	+	GGCGGCCCTGCGC
MA0162.2	MA0162.2.EGR1	2.0143116	0.8017516196639789	EGR1	975	988	-	GATCCGCTCTATT
MA0162.3	MA0162.3.EGR1	5.9487824	0.8009951183568478	EGR1	801	814	-	CCCGCGCCCGCGCC
MA0162.4	MA0162.4.EGR1	8.074243	0.8009430110718295	EGR1	1028	1041	+	AGCCGCCGCGGCCA
MA0162.2	MA0162.2.EGR1	1.920058	0.8007422431857049	EGR1	42	55	-	CCCTAGTCCCGGCC
MA0162.4	MA0162.4.EGR1	8.049063	0.8005026755936692	EGR1	779	792	-	AGGCCCGCAGGCTT
MA0162.2	MA0162.2.EGR1	1.8548676	0.8000441082284295	EGR1	453	466	+	CGCCAGCGCCACA

Showing 1 to 83 of 83 entries  
 PreviousNext

>hg19\_dna range=chr5:137800346-137800699 5'pad=0 3'pad=0 strand=+ repeatMasking=none  
GACTTCCTATCCTCAATTTCCCAGCGACACCCGAAAGACACCGTGCCAT  
AGATCGAGGCCCGGGGTCAAGGCCCGCCTCTCCTGGGCGGCCCTGCCC  
AGGCGGGCCCAGCCGCTCCTCCCCCGCACTCCCGGTTTCGCTCTCACGGTC  
CCTGAGGTGGGCGGGCGGGCCCTGGATGACAGCGATAGAACCCCGGCCCG  
ACTCGCCCTCGCCCCGCTCTGGGTCTGGGCTTCCCCAGCCTAGTTCACG  
CCTAGGAGCCGCCTGAGCAGCCGCGCGCCCAGCGCCACACGCCACGAGCC  
CTCCCCGCCTGGGCGTCCCCGGATCCCGCGAGCGCTCGGGCTCCCGGCTT  
GGAA

>hg19\_dna range=chr5:137801131-137801400 5'pad=0 3'pad=0 strand=+ repeatMasking=none  
CCAGACCCTTCAAATAGAGGCGGATCCGGGGAGTCGCGAGAGATCCCAGC  
GCGCAGAACTTGGGGAGCCGCCGCCCATCCGCCGCCGAGCCAGCTTC  
CGCCGCCGAGGACCGGCCCTGCCCCAGCCTCCGCAGCCGCGGCGCGTC  
CACGCCCCCGCGCCCAGGGCGAGTCGGGGTCGCCGCCTGCACGCTTCT  
CAGTGTTCCCCGCGCCCCGCATGTAACCCGGCCAGGCCCCCGCAACTGTG  
TCCCCTGCAGCTCCAGCCCC



**Figure S1** EGR1 regulated its own transcription. The promoter sequences from TSS -1000 to 100 of the EGR1 were selected and put into the UCSC database to obtain ChIP-seq results. The ChIP-seq results indicate enrichment of EGR1 on its own promoter region, suggesting its involvement in self-transcriptional regulation (highlighted by the red box in the figure below).

**Table S1** Senescence related genes list

GO: senescence related genes

*ABI3*  
*ABL1*  
*AKT3*  
*ARG2*  
*ATM*  
*ATR*  
*B2M*  
*BCL6*  
*BMAL1*  
*BMPR1A*  
*BRC A2*  
*CALR*  
*CDK2*  
*CDK6*  
*CDKN1A*  
*CDKN1B*  
*CDKN2A*  
*CDKN2B*  
*CGAS*  
*CHEK1*  
*CHEK2*  
*CITED2*  
*COMP*  
*CTC1*  
*DNAJA3*  
*ECRG4*  
*EEF1E1*  
*ERCC1*  
*FBXO4*  
*FBXO5*  
*FZR1*  
*H2AX*  
*HLA-G*  
*HMGA1*  
*HMGA2*  
*HRAS*

**Table S1** (*continued*)**Table S1** (*continued*)

GO: senescence related genes

*ID2*  
*IGF1R*  
*ING2*  
*KAT5*  
*KAT6A*  
*KIR2DL4*  
*LMNA*  
*MAGEA2*  
*MAP2K1*  
*MAP2K3*  
*MAP2K4*  
*MAP2K6*  
*MAP2K7*  
*MAP3K3*  
*MAP3K5*  
*MAPK10*  
*MAPK11*  
*MAPK14*  
*MAPK8*  
*MAPK9*  
*MAPKAPK5*  
*MIF*  
*MME*  
*MNT*  
*MORC3*  
*NEK4*  
*NEK6*  
*NPM1*  
*NSMCE2*  
*NUAK1*  
*NUP62*  
*OPA1*  
*PAWR*  
*PLA2R1*  
*PLK2*  
*PML*

**Table S1** (*continued*)**Table S1** (*continued*)

GO: senescence related genes

*PNPT1*  
*PRELP*  
*PRKCD*  
*PRMT6*  
*PTEN*  
*RBL1*  
*ROMO1*  
*RSL1D1*  
*SERPINE1*  
*SIRT1*  
*SIRT6*  
*SMC5*  
*SMC6*  
*SPI1*  
*SRF*  
*TBX2*  
*TBX3*  
*TERF2*  
*TERT*  
*TOP2B*  
*TP53*  
*TP63*  
*TWIST1*  
*ULK3*  
*VASH1*  
*WNT1*  
*WNT16*  
*WRN*  
*YBX1*  
*YPEL3*  
*ZKSCAN3*  
*ZMIZ1*  
*ZMPSTE24*  
*ZNF277*

Search the word “senescence” in the GO database (Gene Ontology Resource) yields a list of genes.

**Table S2** Senescence related genes were analyzed by ChIP-X

TF	Target/ Input	Targets/ Database	Fraction/Input	Fraction/ Database	Difference	P value	Z-score	Combined Score	Genes
EGR1-20690147	45	6207	0.445544554	0.206872417	0.238672137	6.37E-08	-1.038470727	17.20722818	NEK6; SRF; IGF1R; PRKCD; CDKN1A; MAP2K3; MAP2K7; BCL6; SIRT6; SIRT1; ABL1; NUA1; PRMT6; YPEL3; TERF2; TWIST1; TOP2B; CITED2; MAPKAPK5; ZMPSTE24; ID2; MAPK10; MAPK11; SERPINE1; ING2; PAWR; SMC5; ZMIZ1; COMP; MNT; HMGA1; HMGA2; FZR1; CHEK1; SPI1; AKT3; TBX3; TBX2; HRAS; LMNA; YBX1; WNT16; WNT1; TERT; CDK6
MITF-21258399	42	5578	0.415841584	0.185908546	0.229933039	8.16E-08	-0.737519192	12.03696641	NEK6; IGF1R; ERCC1; ZMIZ1; PRKCD; CDKN1A; CDKN1B; MAP2K3; BCL6; HLA-G; RBL1; SIRT1; NSMCE2; MIF; ULK3; MME; MNT; NPM1; HMGA1; HMGA2; ABL1; CHEK2; PRELP; AKT3; TBX2; CALR; MORC3; TERF2; KAT5; TWIST1; TOP2B; CITED2; LMNA; YBX1; MAPKAPK5; ID2; SERPINE1; TERT; CDK6; OPA1; ATM; RSL1D1
HNF4A-19822575	40	6083	0.396039604	0.202739635	0.193299969	7.10E-06	-0.543068375	6.43839126	NEK4; NEK6; TP53; IGF1R; ZMIZ1; PRKCD; PLK2; CDKN1A; CDKN1B; MAP2K3; MAP2K6; BCL6; COMP; PNPT1; RBL1; SIRT1; NSMCE2; HMGA2; ABL1; CHEK2; NUA1; AKT3; EEF1E1; TERF2; LMNA; BMPR1A; YBX1; MAPK9; MAPK8; ZNF277; ZMPSTE24; ID2; MAPK14; MAPK10; SERPINE1; ING2; CDK6; OPA1; ATM; ROMO1
FLI1-21571218	36	5834	0.356435644	0.194440741	0.161994902	1.06E-04	0.402214697	-3.681693044	MAP3K5; ZKSCAN3; NEK4; NEK6; FBXO4; TP53; MAP3K3; IGF1R; ERCC1; SMC5; ZMIZ1; CDKN1A; MAP2K3; MAP2K1; MAP2K7; DNAJA3; PNPT1; SIRT6; SIRT1; NSMCE2; PRMT6; SPI1; YPEL3; MORC3; TERF2; KAT5; CITED2; LMNA; BRCA2; MAPK14; SERPINE1; ING2; OPA1; ATM; ATR; RSL1D1
RUNX1-21571218	34	5071	0.336633663	0.169010799	0.167622865	3.37E-05	-0.438440999	4.515010425	NEK6; PTEN; FBXO4; IGF1R; ERCC1; ZMIZ1; CDKN1B; MAP2K3; MAP2K1; MAP2K7; BCL6; DNAJA3; PNPT1; RBL1; SIRT6; SIRT1; MIF; MNT; NPM1; HMGA1; SPI1; YPEL3; MORC3; VASH1; KAT5; TOP2B; CITED2; HRAS; LMNA; ZNF277; ID2; SERPINE1; OPA1; ATM
SOX2-21211035	26	3420	0.257425743	0.113984802	0.143440941	5.16E-05	-1.044225553	10.30809376	NEK6; PTEN; FBXO4; FBXO5; MAP3K3; SMC5; ZMIZ1; CDKN2B; MAP2K3; MAP2K1; MAP2K7; HLA-G; NSMCE2; NPM1; ABL1; CHEK2; PRMT6; AKT3; TBX3; MORC3; CITED2; MAPK9; ID2; MAPK10; CDK2; OPA1
PPARD-21283829	26	3447	0.257425743	0.114884682	0.142541061	5.89E-05	-0.416346227	4.054941244	NEK6; PTEN; ZMIZ1; CDKN1A; CDKN2B; MAP2K6; BCL6; DNAJA3; HLA-G; ABL1; CHEK2; CHEK1; PRMT6; YPEL3; TBX3; TBX2; TWIST1; CITED2; LMNA; ZNF277; MAPKAPK5; ID2; MAPK10; SERPINE1; OPA1; B2M
FOXA2-19822575	25	2968	0.247524752	0.098920144	0.148604608	1.37E-05	-0.985666558	11.03940836	AKT3; ZKSCAN3; NEK6; SRF; TBX3; TBX2; IGF1R; ZMIZ1; CDKN1A; BCL6; CITED2; LMNA; COMP; YBX1; MAPK9; BRCA2; MAPK14; MAPK10; SERPINE1; ING2; PAWR; CDK6; CHEK2; NUA1; RSL1D1
E2F4-21247883	24	2998	0.237623762	0.099920011	0.137703752	4.84E-05	-0.856432159	8.510324563	YPEL3; PTEN; TP53; IGF1R; CDKN1B; TERF2; MAP2K1; VASH1; DNAJA3; HRAS; BMPR1A; ARG2; SIRT1; MAPKAPK5; ULK3; BRCA2; MNT; WNT1; PAWR; CDK2; CHEK1; ATM; PRMT6; RSL1D1
AR-19668381	23	3519	0.227722772	0.117284362	0.11043841	0.001314404	-0.181045024	1.201120035	MAP3K5; NEK6; IGF1R; ZMIZ1; CDKN2B; MAP2K4; MAP2K1; MAP2K7; MAP2K6; HLA-G; HMGA2; ABL1; AKT3; TBX2; EEF1E1; MORC3; PML; BMPR1A; ID2; BRCA2; MAPK11; TERT; ATM
CUX1-19635798	22	3052	0.217821782	0.101719771	0.116102011	4.70E-04	-2.475332783	18.96652163	MAP3K5; PLA2R1; NEK6; SRF; TBX2; FBXO4; TP53; EEF1E1; DNAJA3; MAGEA2; MAPKAPK5; ZMPSTE24; KIR2DL4; WNT1; NUP62; CDK6; CDK2; OPA1; FZR1; CHEK1; B2M; ATR
SOX2-20726797	20	2564	0.198019802	0.085455273	0.112564529	3.30E-04	-0.865487134	6.939112646	WRN; NEK6; TBX3; IGF1R; ERCC1; PLK2; TERF2; CDKN2B; MAP2K6; BCL6; LMNA; ARG2; ID2; MME; HMGA2; NUP62; SERPINE1; OPA1; ATM; RSL1D1
DACH1-20351289	19	1698	0.188118812	0.056592454	0.131526358	3.86E-06	-1.537506576	19.1665382	NEK4; PTEN; FBXO5; MAP3K3; ZMIZ1; PLK2; MAP2K7; CITED2; PNPT1; BMPR1A; SIRT1; MAPKAPK5; NPM1; HMGA1; HMGA2; NUP62; PAWR; OPA1; PRMT6
POU3F2-20337985	16	1702	0.158415842	0.05672577	0.101690072	1.88E-04	-1.120346427	9.608671602	AKT3; EEF1E1; SMC6; CDKN2B; CDKN2A; TWIST1; WNT16; MAPK8; MME; HMGA2; MAPK10; CDK6; OPA1; CHEK1; ATM; PRMT6
JUN-21703547	16	1585	0.158415842	0.05282629	0.105589552	8.37E-05	0	0	TP53; PLK2; CDKN1A; CDKN1B; MAP2K3; BCL6; COMP; PNPT1; NSMCE2; ID2; MNT; NPM1; MAPK10; SERPINE1; PAWR; PRMT6
GATA1-21571218	16	2601	0.158415842	0.086688442	0.0717274	0.013520886	0.646786987	-2.783460502	SPI1; MAP3K5; NEK6; MAP3K3; IGF1R; ERCC1; ZMIZ1; CDKN1A; CITED2; NSMCE2; ULK3; ID2; ABL1; CDK6; OPA1; ATR
PHF8-20622854	14	1490	0.138613861	0.049660045	0.088953816	4.96E-04	-0.533975974	4.063091069	SIRT1; FBXO4; ULK3; ID2; CALR; NPM1; NUP62; MAPK14; PLK2; ABL1; DNAJA3; B2M; TOP2B; RBL1
SMAD3-18955504	14	1936	0.138613861	0.06452473	0.074089131	0.005552163	-0.201226442	1.045083137	NEK6; TBX3; IGF1R; CDKN1A; MAP2K3; PML; TOP2B; MAPK8; MNT; NUP62; SERPINE1; PAWR; ABL1; FZR1
SMAD2-18955504	14	1936	0.138613861	0.06452473	0.074089131	0.005552163	-0.201226442	1.045083137	NEK6; TBX3; IGF1R; CDKN1A; MAP2K3; PML; TOP2B; MAPK8; MNT; NUP62; SERPINE1; PAWR; ABL1; FZR1
GABP-19822575	14	2639	0.138613861	0.087954939	0.050658922	0.059651343	1.108705824	-3.125706276	FBXO5; MORC3; VASH1; MAP2K7; KAT5; SIRT6; MIF; ZMPSTE24; ID2; MAPK14; ING2; OPA1; RSL1D1; ROMO1
E2F1-21310950	13	1145	0.128712871	0.038161578	0.090551293	1.34E-04	-1.369194142	12.21402011	FBXO5; MIF; BRCA2; EEF1E1; MNT; HMGA1; ERCC1; SMC6; CDKN1A; CDKN1B; PAWR; CHEK1; RBL1
ETS1-20019798	13	1607	0.128712871	0.053559525	0.075153346	0.00298483	-0.348930314	2.028754977	TERF2; MAP2K3; DNAJA3; KAT5; PNPT1; RBL1; ZNF277; SIRT6; MAPKAPK5; ZMPSTE24; OPA1; CHEK2; PRMT6
GATA2-19941826	13	2410	0.128712871	0.080322624	0.048390248	0.061648609	0.149476076	-0.41648588	SPI1; MAP3K5; NEK6; MORC3; ERCC1; ZMIZ1; MAP2K3; NSMCE2; MME; OPA1; FZR1; NUA1; ATM
GATA2-21571218	12	1111	0.118811881	0.037028396	0.081783485	3.85E-04	-0.783039623	6.157424657	MAP3K5; ULK3; MNT; MAP3K3; IGF1R; SERPINE1; SMC5; ZMIZ1; CDKN1A; ING2; MAP2K3; LMNA
SMAD4-21741376	12	2738	0.118811881	0.091254499	0.027557382	0.210250663	0	0	TBX3; TP63; MAP3K3; IGF1R; ZMIZ1; VASH1; MAP2K6; TOP2B; LMNA; ID2; HMGA2; NUA1

Table S2 (continued)

Table S2 (continued)

TF	Target/ Input	Targets/ Database	Fraction/ Input	Fraction/ Database	Difference	P value	Z-score	Combined Score	Genes
MYC-19915707	12	2979	0.118811881	0.099286762	0.019525119	0.300927819	0.956358722	-1.148476699	<i>EEF1E1; IGF1R; CDKN2A; MAP2K3; MAPK9; HMGA1; MAPK10; TERT; PAWR; ABL1; CDK6; PRMT6</i>
AR-20517297	12	2047	0.118811881	0.068224237	0.050587644	0.042924524	1.035178448	-3.259064701	<i>TBX2; SMC6; MAP2K1; DNAJA3; RBL1; ZNF277; ARG2; ULK3; HMGA2; NUP62; ABI3; ROMO1</i>
E2F4-17652178	11	1002	0.108910891	0.033395547	0.075515344	5.96E-04	-1.541405127	11.44423833	<i>FBXO5; TP53; BRCA2; MNT; NPM1; CDKN1A; CDK6; CHEK1; B2M; YBX1; RBL1</i>
SCL-21571218	11	1784	0.108910891	0.059458739	0.049452152	0.038245506	0.762913501	-2.489943074	<i>SPI1; MAP3K5; IGF1R; ZMIZ1; CDKN1B; MAP2K3; VASH1; NSMCE2; TERT; ABL1; OPA1</i>
TP53-18474530	10	827	0.099009901	0.027562992	0.071446909	5.14E-04	-0.826628917	6.259551978	<i>TBX2; ID2; CALR; MAPK10; PLK2; CDKN1A; MAP2K6; NUA1; CITED2; MAPK9</i>
NANOG-16153702	10	1686	0.099009901	0.056192508	0.042817393	0.058366534	-0.176656593	0.501883606	<i>CALR; EEF1E1; ERCC1; TWIST1; CITED2; MAPK8; ID2; MAPK14; CDK6; B2M</i>
FOXP3-21729870	10	1404	0.099009901	0.046793761	0.05221614	0.020363055	0	0	<i>PTEN; MNT; MAPK14; ZMIZ1; CDKN1B; BCL6; OPA1; ATR; CITED2; PNPT1</i>
E2F1-17053090	10	1726	0.099009901	0.057525663	0.041484238	0.066124393	0.700539747	-1.90281837	<i>TBX3; TP53; IGF1R; CDKN1B; MAP2K6; RBL1; MNT; PAWR; CHEK2; CHEK1</i>
DNAJC2-21179169	9	899	0.089108911	0.029962672	0.059146239	0.003497064	-0.619406201	3.503257047	<i>MAP3K5; TBX3; MAP3K3; NUP62; TERF2; MAP2K7; BCL6; FZR1; TOP2B</i>
ELF1-20517297	9	1020	0.089108911	0.033995467	0.055113444	0.007776577	-0.204050488	0.990999569	<i>YPEL3; SRF; ERCC1; TERF2; CHEK2; HRAS; COMP; PRELP; ROMO1</i>
TFAP2C-20629094	9	1203	0.089108911	0.040094654	0.049014257	0.020693953	0.358398274	-1.389837603	<i>TP63; NSMCE2; IGF1R; ERCC1; FZR1; CHEK2; NUA1; LMNA; MAPK9</i>
CLOCK-20551151	8	407	0.079207921	0.013564858	0.065643063	8.06E-05	-1.568180304	14.78177623	<i>SERPINE1; CDKN1A; CDKN1B; YPEL3; BCL6; CALR; LMNA; MAPK14</i>
RUNX1-17652178	8	1003	0.079207921	0.033428876	0.045779045	0.020508639	-0.383458945	1.490470049	<i>PTEN; ZMPSTE24; NPM1; NUP62; SERPINE1; CDKN1B; DNAJA3; YBX1</i>
CTNNB1-20460455	8	988	0.079207921	0.032928943	0.046278978	0.01894291	-8.49E-04	0.00336817	<i>AKT3; SIRT6; NSMCE2; ZMPSTE24; MAP2K4; MAP2K6; CDK6; WNT16</i>
GATA2-21666600	8	837	0.079207921	0.02789628	0.05131164	0.007619133	0	0	<i>NSMCE2; MAPK14; SERPINE1; SMC6; CDKN2B; FZR1; CHEK2; LMNA</i>
PAX3-FKHR-20663909	8	1063	0.079207921	0.03542861	0.043779311	0.027701267	0.228430335	-0.819214484	<i>MME; IGF1R; HMGA2; ZMIZ1; PLK2; MAP2K6; CDK6; CITED2</i>
MYC-20876797	8	1406	0.079207921	0.046860419	0.032347502	0.102567558	0.706297883	-1.608405264	<i>AKT3; FBXO5; ID2; WNT1; ERCC1; ECRG4; OPA1; PML</i>
TFEB-21752829	7	808	0.069306931	0.026929743	0.042377188	0.019973393	0	0	<i>SIRT1; CALR; NPM1; CDKN2B; BCL6; KAT5; ATM</i>
SMAD3-21741376	7	1460	0.069306931	0.048660179	0.020646752	0.222227658	0	0	<i>TBX3; HMGA2; MAPK10; ZMIZ1; VASH1; MAP2K6; NUA1</i>
EOMES-21245162	7	932	0.069306931	0.031062525	0.038244406	0.038783999	0.341916031	-1.111140771	<i>ARG2; TBX3; ZMPSTE24; ERCC1; CDKN2A; MAP2K4; MAP2K1</i>
EWS-ERG-20517297	7	1038	0.069306931	0.034595387	0.034711543	0.062015949	0.651623555	-1.811750465	<i>SMC6; ABI3; BCL6; PRMT6; COMP; YBX1; PRELP</i>
TFAP2A-17053090	7	1904	0.069306931	0.063458206	0.005848725	0.461669791	2.433902499	-1.881176338	<i>CDKN1B; MAP2K1; MAP2K6; DNAJA3; CHEK2; NUA1; RSL1D1</i>
SPI1-20517297	7	1249	0.069306931	0.041627783	0.027679148	0.129345863	1.228592615	-2.512797911	<i>SPI1; ZNF277; YPEL3; TP63; SMC6; TERF2; LMNA</i>
TP63-19390658	6	179	0.059405941	0.005965871	0.053440069	3.88E-05	-2.138652635	21.72313433	<i>TP53; TWIST1; ID2; CITED2; PML; TBX2</i>
CREB1-15753290	6	957	0.059405941	0.031895747	0.027510193	0.105244426	-0.543216623	1.223035802	<i>ZNF277; ARG2; MAPKAPK5; BRCA2; BCL6; ATM</i>
EST1-17652178	6	1001	0.059405941	0.033362218	0.026043722	0.122918099	0.173360719	-0.363405154	<i>TP53; ZMPSTE24; MAP2K6; OPA1; DNAJA3; RBL1</i>
TP53-16413492	5	449	0.04950495	0.014964671	0.034540279	0.018575014	-1.26500443	5.042229129	<i>CDKN1A; MAP2K6; ATM; RBL1; MAPK9</i>
SMAD4-19686287	5	405	0.04950495	0.0134982	0.03600675	0.012476789	-0.621606208	2.725050265	<i>SERPINE1; CDKN1A; PTEN; TP53; MAPK8</i>
TRIM28-17542650	5	3568	0.04950495	0.118917478	-0.069412527	0.994723827	5.959613286	-0.031527197	<i>IGF1R; TBX3; TERF2; ID2; CDK6</i>
MYC-18940864	5	746	0.04950495	0.024863352	0.024641599	0.108564876	0.676821235	-1.502818845	<i>PTEN; TBX2; FBXO5; TOP2B; ERCC1</i>
HNF4A-19761587	5	1126	0.04950495	0.03752833	0.011976621	0.33019363	1.484753945	-1.645220269	<i>PTEN; SRF; CDKN1A; CDKN1B; CITED2</i>
ERG-20517297	5	1062	0.04950495	0.035395281	0.01410967	0.288053508	1.823855364	-2.269986842	<i>ARG2; TBX3; IGF1R; ABI3; VASH1</i>
EGR1-19374776	4	68	0.03960396	0.002266364	0.037337596	1.03E-04	-1.754213846	16.10432109	<i>ABL1; NPM1; CDK6; CALR</i>
ESR1-15608294	4	98	0.03960396	0.003266231	0.036337729	3.94E-04	-1.475324906	11.56483002	<i>SERPINE1; TP53; TERT; HRAS</i>

Table S2 (continued)

Table S2 (continued)

TF	Target/ Input	Targets/ Database	Fraction/ Input	Fraction/ Database	Difference	P value	Z-score	Combined Score	Genes
IRF1-19129219	4	196	0.03960396	0.006532462	0.033071498	0.004673182	-1.03287758	5.542333477	<i>FBXO4; NSMCE2; ZKSCAN3; TBX3</i>
ZNF274-21170338	4	327	0.03960396	0.010898547	0.028705414	0.025504289	-0.190276145	0.698105798	<i>ZMPSTE24; HMGA1; CDK6; MAPK9</i>
NOTCH1-21737748	4	245	0.03960396	0.008165578	0.031438382	0.009977441	0	0	<i>SERPINE1; SIRT1; IGF1R; BCL6</i>
PADI4-21655091	4	1037	0.03960396	0.034562058	0.005041902	0.463779665	0	0	<i>MAPKAPK5; OPA1; MAGEA2; CITED2</i>
CDX2-20551321	4	504	0.03960396	0.01679776	0.0228062	0.091841949	0.182899076	-0.436705585	<i>TERT; CITED2; PNPT1; RBL1</i>
KDM6A-18722178	4	479	0.03960396	0.015964538	0.023639422	0.079756439	0.277605542	-0.70200273	<i>MAPKAPK5; DNAJA3; CHEK2; CHEK1</i>
POU5F1-16153702	4	622	0.03960396	0.020730569	0.018873391	0.159294221	0.640785751	-1.177124923	<i>TBX3; ZMPSTE24; ID2; MAP3K3</i>
GABP-17652178	4	1001	0.03960396	0.033362218	0.006241742	0.436948805	1.444338643	-1.19582464	<i>TP53; ZMPSTE24; ING2; YBX1</i>
NANOG-21062744	4	840	0.03960396	0.027996267	0.011607693	0.314462223	1.41817053	-1.640669185	<i>SIRT6; NSMCE2; HMGA2; CDKN1B</i>
EWS-FLI1-20517297	4	574	0.03960396	0.019130783	0.020473178	0.129937865	0.86856684	-1.7724834	<i>WRN; BCL6; BRCA2; PRMT6</i>
STAT1-20625510	4	656	0.03960396	0.021863751	0.017740209	0.181446903	1.088072773	-1.857114137	<i>MAP2K3; PLA2R1; CHEK1; ERCC1</i>
GATA1-19941826	3	967	0.02970297	0.032229036	-0.002526066	0.635935591	2.008427197	-0.909130625	<i>SPI1; NSMCE2; OPA1</i>
ELK1-19687146	3	917	0.02970297	0.030562592	-8.60E-04	0.599976158	2.070385408	-1.057688188	<i>SMC6; ING2; YBX1</i>
ERG-21242973	3	321	0.02970297	0.010698574	0.019004397	0.095681078	0.515522579	-1.209794735	<i>SMC5; TWIST1; TBX2</i>
STAT6-20620947	3	508	0.02970297	0.016931076	0.012771894	0.245780707	1.171557731	-1.644065209	<i>BCL6; IGF1R; HMGA1</i>
TCF4-18268006	3	470	0.02970297	0.015664578	0.014038392	0.212216814	1.080842359	-1.675464342	<i>PRKCD; ID2; PNPT1</i>
ESR2-21235772	3	424	0.02970297	0.014131449	0.015571521	0.173180577	1.003431128	-1.759436641	<i>PRKCD; CDK6; NUA1</i>
SOX2-16153702	2	1278	0.01980198	0.042594321	-0.022792341	0.93217848	2.115214466	-0.148553585	<i>CALR; CDK6</i>
ELF1-17652178	2	133	0.01980198	0.004432742	0.015369238	0.075654547	0.564499755	-1.457300003	<i>TP53; DNAJA3</i>
SCL-19346495	2	252	0.01980198	0.00839888	0.0114031	0.20973698	0.986524066	-1.540852936	<i>MAP3K5; HMGA2</i>
EGR1-19032775	2	276	0.01980198	0.009198773	0.010603207	0.23932524	1.220594414	-1.745366788	<i>CDKN1B; MAP2K1</i>
HIF1A-21447827	2	321	0.01980198	0.010698574	0.009103407	0.295183823	1.451433858	-1.770977162	<i>MIF; CITED2</i>
IKZF1-21737484	1	155	0.00990099	0.005165978	0.004735012	0.408802209	0	0	<i>PRKCD</i>
CTNNB1-20615089	1	637	0.00990099	0.021230503	-0.011329513	0.885489433	2.043934098	-0.248572544	<i>SIRT6</i>
HTT-18923047	1	566	0.00990099	0.018864151	-0.008963161	0.853921486	1.88642235	-0.297896321	<i>MAPK8</i>
MYCN-21190229	1	373	0.00990099	0.012431676	-0.002530686	0.717680462	2.083827107	-0.691269735	<i>CHEK1</i>
MYCN-19997598	1	234	0.00990099	0.00779896	0.00210203	0.54743469	2.136683744	-1.287377837	<i>NUP62</i>
VDR-20736230	1	230	0.00990099	0.007665645	0.002235346	0.541262045	2.187721164	-1.342936457	<i>CDK6</i>
ESR1-21235772	1	228	0.00990099	0.007598987	0.002302003	0.538144537	2.191677672	-1.358025069	<i>PRKCD</i>
NOTCH1-17114293	1	134	0.00990099	0.004466071	0.005434919	0.365355736	2.43698755	-2.453763237	<i>RBL1</i>
SMAD-19615063	1	124	0.00990099	0.004132782	0.005768208	0.343570235	2.569512895	-2.745174354	<i>TBX3</i>
SALL1-21062744	1	105	0.00990099	0.003499533	0.006401457	0.300118039	2.55362224	-3.073487171	<i>MME</i>
ZNF263-19887448	1	71	0.00990099	0.002366351	0.007534639	0.215137646	2.990669243	-4.595095231	<i>CDK6</i>
TP63-17297297	1	40	0.00990099	0.001333156	0.008567835	0.128792352	3.701858212	-7.587157738	<i>CDKN1A</i>

Senescence related genes were put into ChIP-X software for analysis.