Supplementary Materials

Dual Targeting of the FOXM1-ELF3 Reciprocal Transcriptional Circuit as a Promising Therapeutic Strategy for Refractory NSCLC

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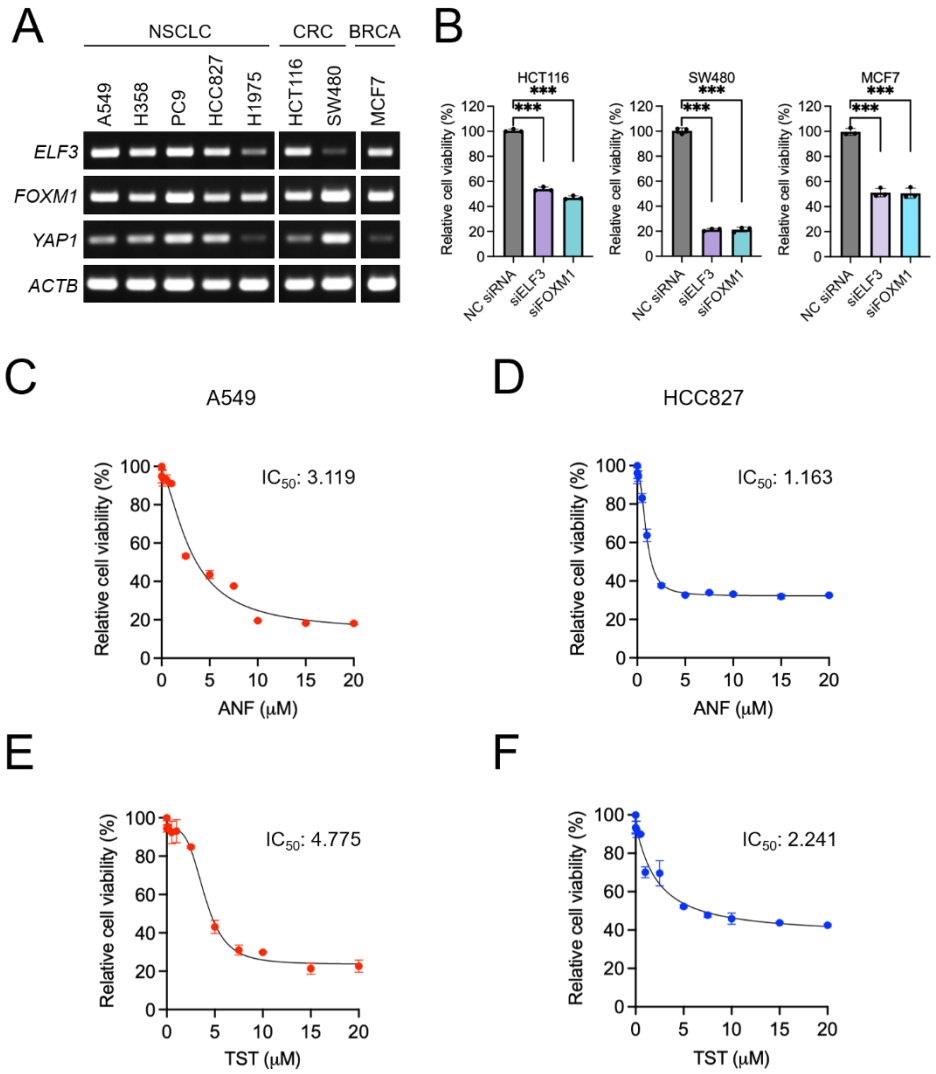


Figure S1. Expression levels of FOXM1, ELF3, and YAP1 in various cancer cell lines and reduced cell viability by genetic knockdown or drug treatment. Dose-dependent effects of auranofin (ANF) and thiostrepton (TST) on NSCLC cell viability. (A) mRNA levels of ELF3, FOXM1, and YAP1 in various NSCLC, CRC, and BRCA cell lines. (B) Cell viabilities demonstrating effects of inhibition by siELF3 and siFOXM1 transfection in HCT116, SW480, and MCF7 cells. (C, D) Relative cell viability of A549 (C) and HCC827 (D) cells treated with increasing concentrations of ANF (0.01 to 20 μM) for 48 h. (E, F) Relative cell viability of A549 (E) and HCC827 (F) cells treated with increasing concentrations of TST (0.01 to 20 μM) for 48 h. Cell viability was assessed using a luminescence-based CellTiter-Glo assay. Both drugs showed a dose-dependent decrease in cell viability in both cell lines. Data are presented as mean ± SD (n = 3). The IC_{50} values of ANF and TST were 3.119 μM and 4.775 μM for A549 cells, and 1.163 μM and 2.241 μM for HCC827 cells, respectively.

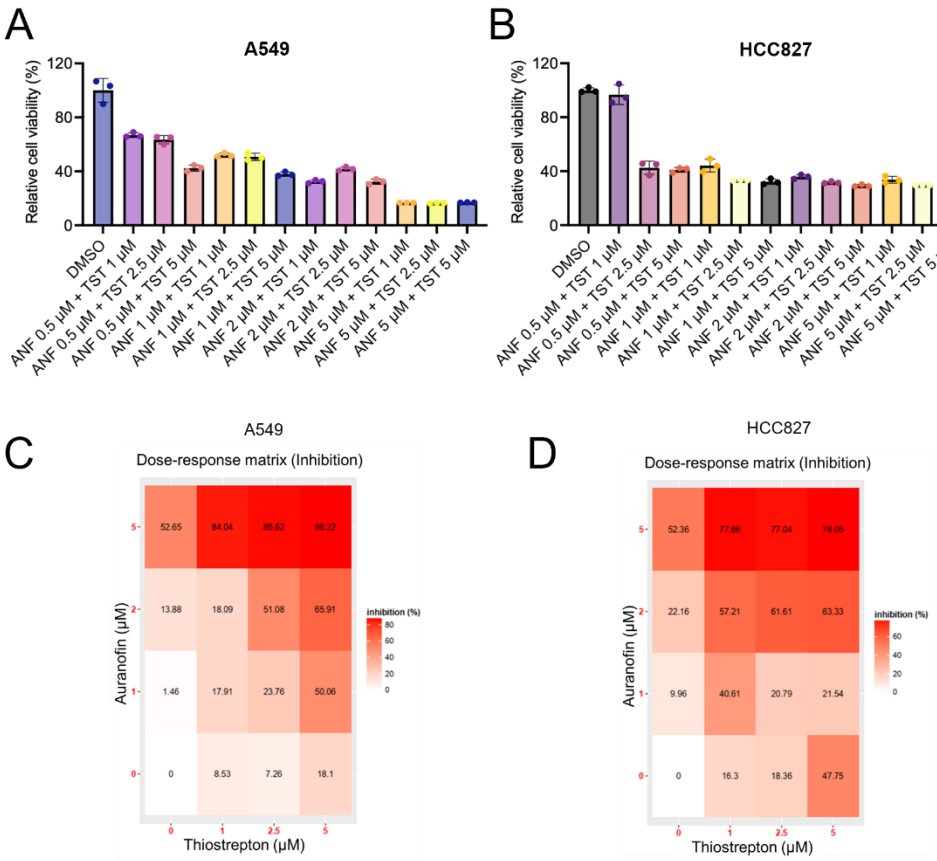


Figure S2. Synergistic effects of combined ANF and TST treatment on NSCLC cell viability. (A, B) Relative cell viability of A549 (A) and HCC827 (B) cells treated with increasing concentrations of ANF and TST, either individually or in dual inhibition, for 48 h. (C, D) Dose-response matrices showing percentage inhibition in A549 (C) and HCC827 (D) cells across various dose combinations of ANF and TST. Inhibition is represented as a heatmap, with darker red indicating greater inhibition. ZIP synergy scoring was used to quantify drug interaction effects. A ZIP synergy score >10 indicates synergism, ~0 indicates additivity, and <−10 indicates antagonism. Data are presented as mean ± SD (n = 3).

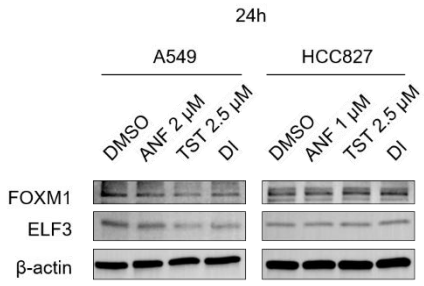


Figure S3. Western blot analysis of FOXM1 and ELF3 protein expression after 24 h of single-agent or dual treatment in both A549 and HCC827 cells. β-actin served as a loading control.

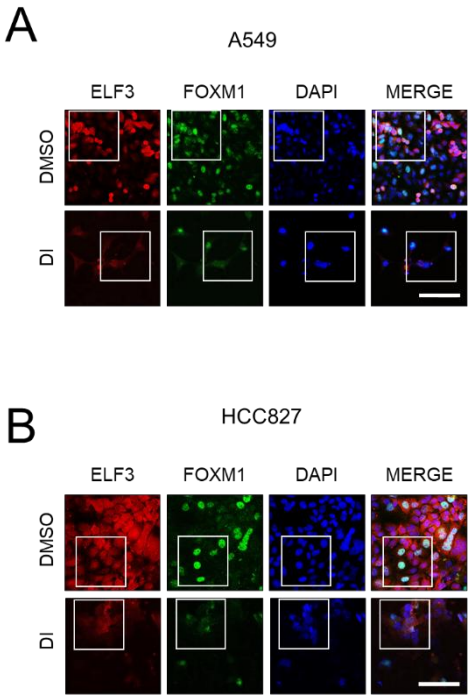


Figure S4. ICC staining of nuclear ELF3 and FOXM1 protein levels following pharmacological inhibition by ANF and TST combination. (A, B) Fluorescence of ELF3 (red) and FOXM1 (green) in A549 (A) and HCC827 (B) cells co-treated with ANF and TST (DI) for 48 h. Co-treatment of ANF and TST significantly reduced the nuclear intensity of their respective targets and partially affected each other's expression. White squares on each image indicate magnified spots in Figure 4E and 4F. Scale bars 50 μm.

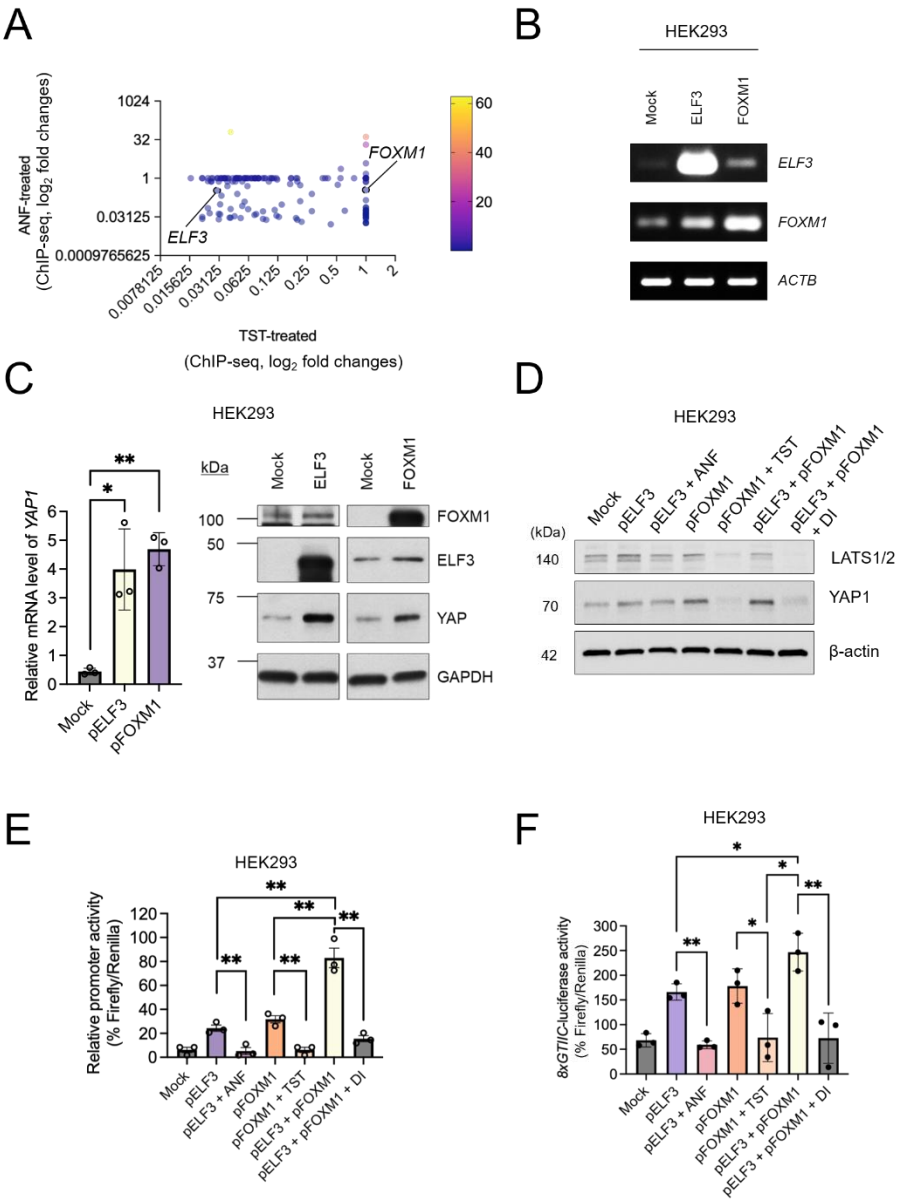


Figure S5. Reciprocal regulation of FOXM1 and ELF3 induced by TST and ANF treatment. (A) Comparison of TF occupancy of target gene promoters (log2, fold changes) through ChIP-seq in TST or ANF-treated A549 cells. In TST-treated A549 cells, relative ChIP-seq peak intensity of ELF3 is reduced to approximately 0.003 and that of FOXM1 is also reduced to approximately 0.6 in ANF-treated A549 cells. (B, C) A reciprocal increment of FOXM1 and ELF3 expression detected by RT-PCR (B) and real-time PCR analysis showing significantly increased YAP1 mRNA expression (left) and western blotting analysis (right) confirming elevated YAP1 protein expression upon ELF3 and FOXM1 overexpression in HEK293 cells (C). GAPDH served as loading control. (D) Western blot analysis indicating increased YAP1 protein expression upon ELF3 and FOXM1 overexpression in HEK293 cells. Treatment with ANF and TST reduced YAP1 protein levels. β-actin served as loading control. (E) Dual luciferase assay for activation of YAP1 promoter by ELF3 and FOXM1 overexpression in HEK293 cells. Data are presented as mean ± SD (n = 3). **P < 0.01. (F) Dual luciferase assay for transactivation of YAP1-responsive 8×GTIIC-luciferase plasmids by ELF3 and FOXM1 in HEK293 cells. Data are presented as mean ± SD (n = 3). *P < 0.05, **P < 0.01.

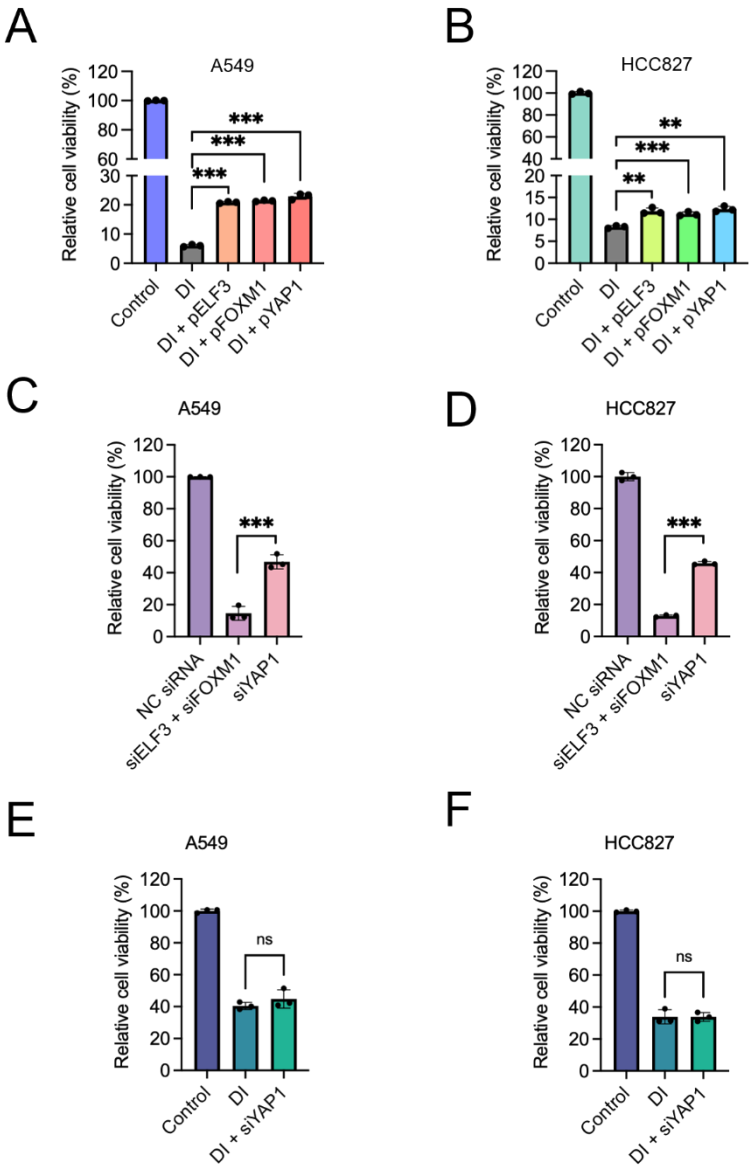


Figure S6. Functional contribution of YAP1 to FOXM1–ELF3 circuit-dependent cell viability (A-B) Rescue of cell viability by dual inhibition (ANF and TST) with ELF3, FOXM1, and YAP1 overexpression in A549 (A) and HCC827 (B) cells. Data are presented as mean ± SD (n = 3). **P < 0.01, ***P < 0.001. (C-D) Relative cell viability following treatment with NC siRNA, combined siELF3+siFOXM1, or siYAP1 in A549 (C) and HCC827 (D) cells. Data are presented as mean ± SD (n = 3). (E-F) Changes in cell viability by dual inhibition and siYAP1 transfection in A549 (E) and HCC827 (F) cells. Data are presented as mean ± SD (n = 3).

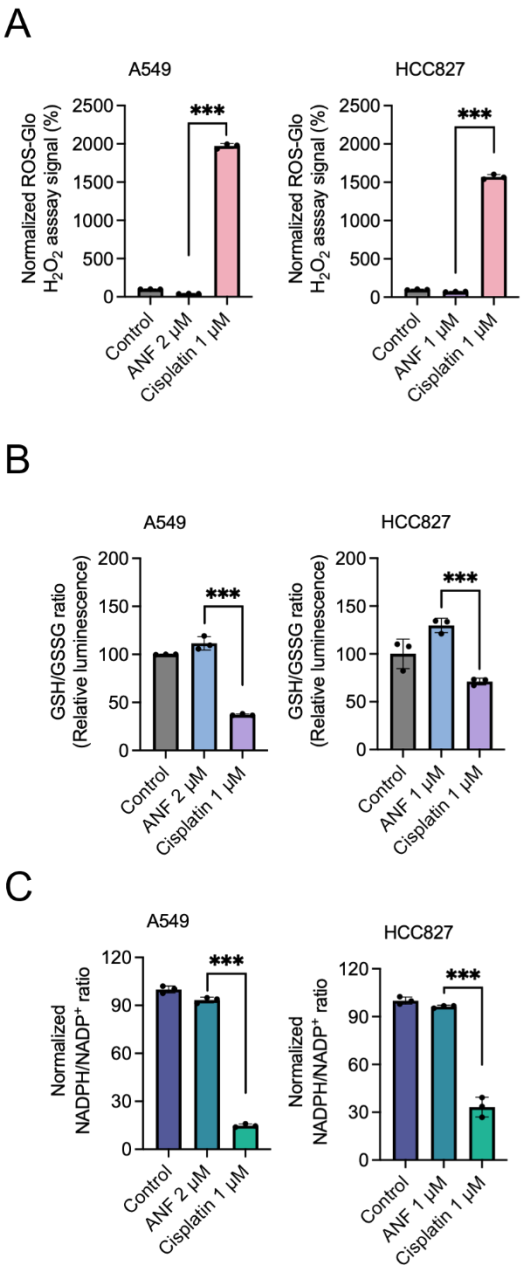


Figure S7. Assessment of oxidative-stress markers following auranofin (ANF) treatment in NSCLC cell lines. (A) Normalized reactive oxygen species (ROS) levels in ANF-treated A549 and HCC827 cell lines for 48 h. Cells treated with cisplatin (1 μM) served as a positive control for oxidative stress. (B) Normalized GSH/GSSG ratio in ANF-treated A549 and HCC827 cell lines. (C) Normalized NADPH/$NADP^+$ ratio in ANF-treated A549 and HCC827 cell lines. Data are presented as mean ± SD (n = 3). DMSO was used as a negative control.

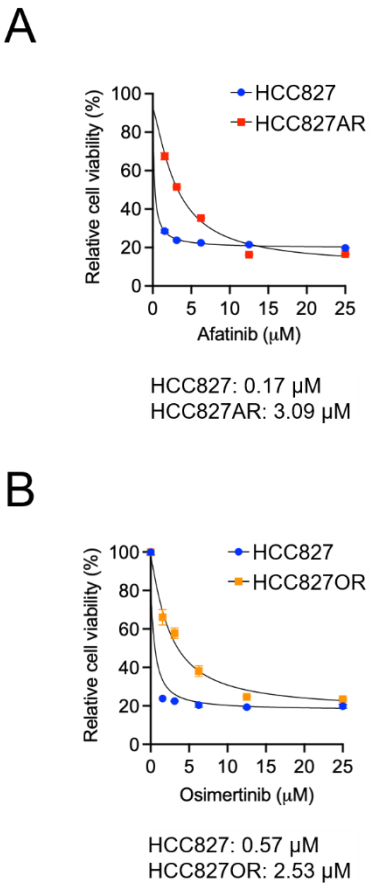


Figure S8. The IC_{50} for afatinib- and osimertinib- resistant HCC827 cells (A) Dose-response curves showing a rightward shift in afatinib sensitivity in HCC827AR cells relative to parental HCC827 cells. The IC_{50} of afatinib for HCC827AR is 18.2-fold higher than HCC827. Data are presented as mean ± SD (n = 3). (B) Dose-response curves showing a rightward shift in osimertinib sensitivity in HCC827AR cells relative to parental HCC827 cells. The IC_{50} of osimertinib for HCC827OR is 4.4-fold higher than HCC827. Data are presented as mean ± SD (n = 3).

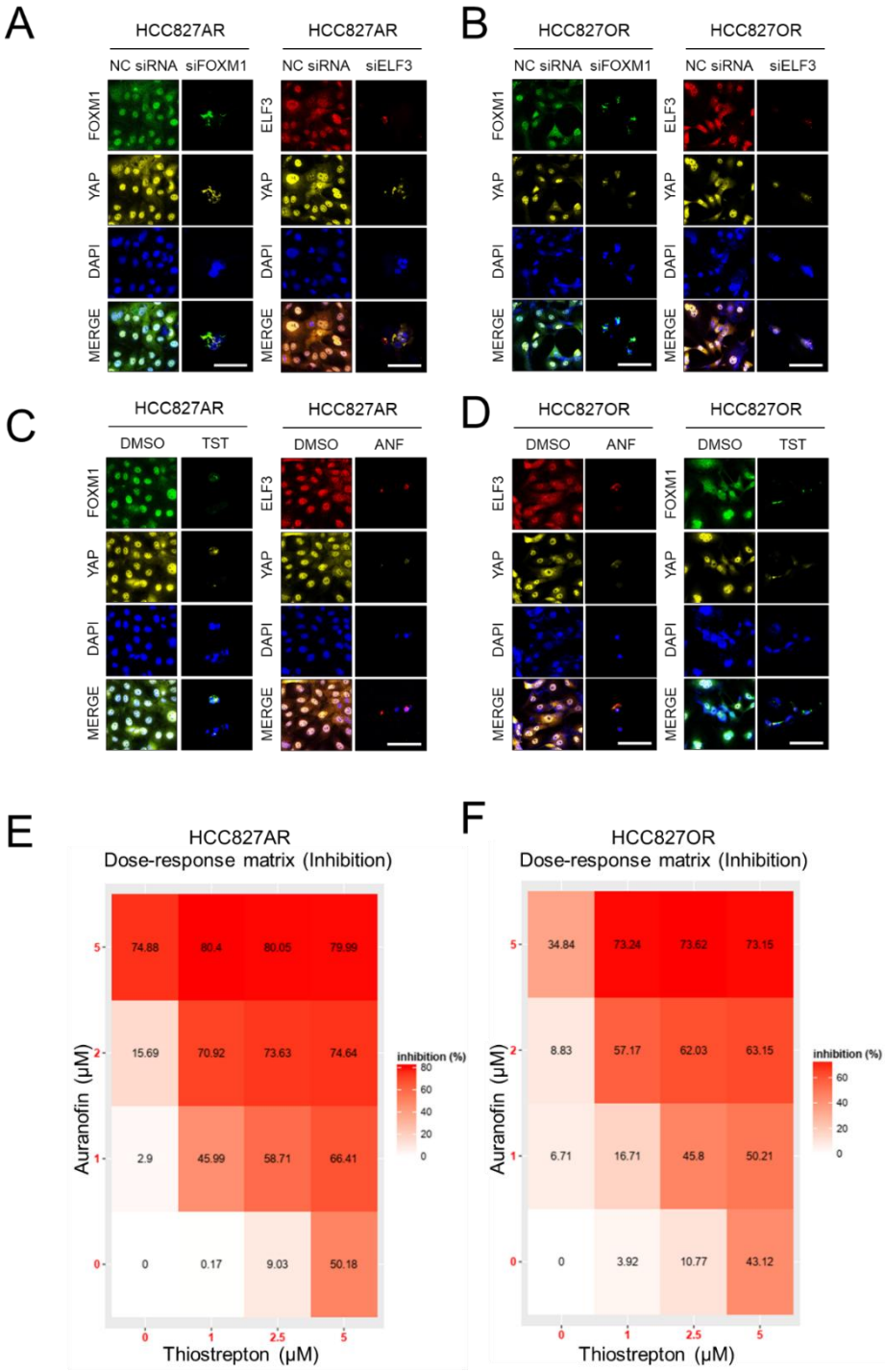


Figure S9. ELF3 and FOXM1 inhibition affects YAP1 expression by siRNA transfection and dual inhibition of ANF and TST in TKI-resistant HCC827 cells. (A, B) ICC images showing reduction of YAP1 expression by ELF3 and FOXM1 knockdowns in HCC827AR (A) and HCC827OR (B). Scale bars 50 μm. (C, D) ICC images showing reduction of YAP1 expression by ANF and TST treatment for 48 hours in HCC827AR (C) and HCC827OR (D). Scale bars 50 μm. (E, F) Dose-response matrices showing percentage inhibition in HCC827AR (E) and HCC827OR (F) cells across various dose combinations of ANF and TST. Both cell lines exhibit strong synergy in the high-dose combination zones.

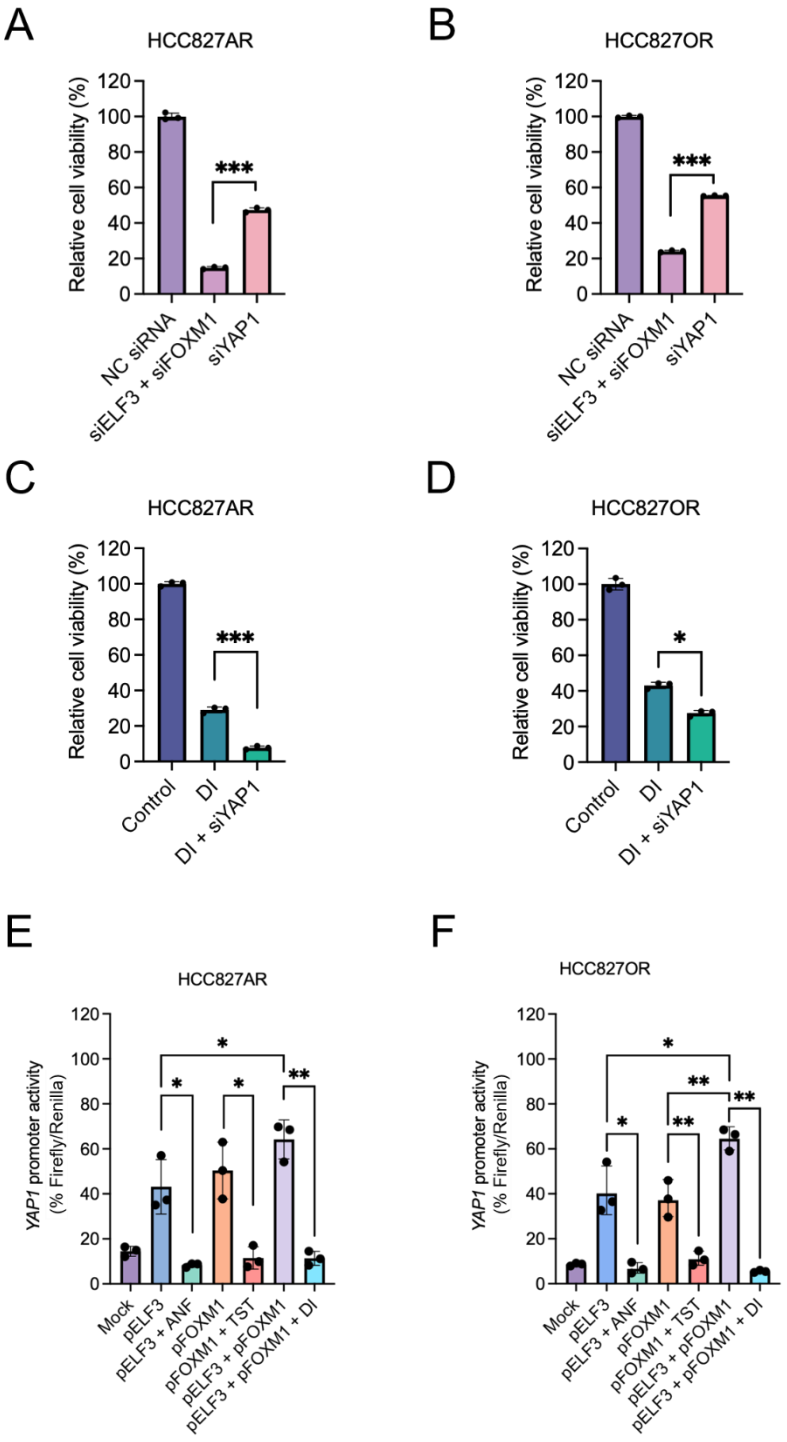


Figure S10. (A-B) Changes in cell viability following NC siRNA, siELF3+siFOXM1, and siYAP1 transfection in HCC827AR (A) and HCC827OR (B) cells. Data are presented as mean ± SD (n = 3). (C-D) Changes of cell viabilities by dual inhibition and siYAP1 transfection in HCC827AR (C) and HCC827OR (D) cells. DMSO was used as negative control. Data are presented as mean ± SD (n = 3). (E) Promoter activity assays in HCC827AR cells demonstrating similar synergistic activation of YAP1 promoter upon ELF3 and FOXM1 co-expression, and subsequent suppression by inhibitor treatments. (F) Promoter activity assays in HCC827OR cells demonstrate similar synergistic activation of YAP1 promoter upon ELF3 and FOXM1 co-expression, and subsequent suppression by inhibitor treatments. Data are presented as mean ± SD (n = 3). *P < 0.05, **P < 0.01, ***P < 0.001.

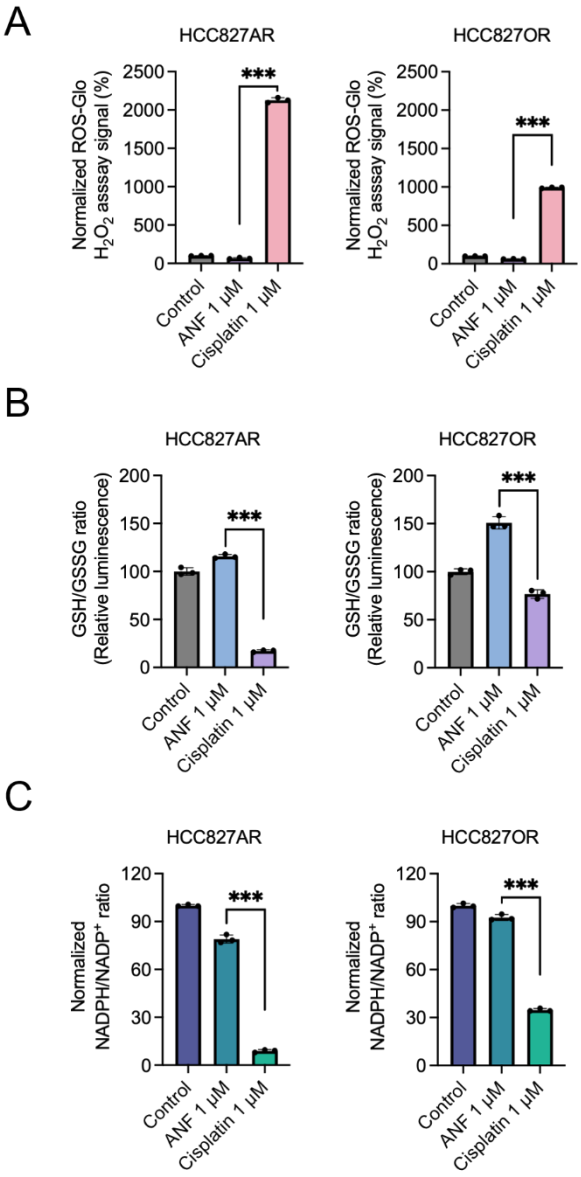


Figure S11. Assessment of oxidative-stress markers following auranofin (ANF) treatment in TKI-resistant cell lines. (A) Normalized reactive oxygen species (ROS) levels in ANF-treated HCC827AR and HCC827OR cell lines for 48 h. Cisplatin (1 μM) was treated as a positive control to produce ROS in cells. (B) Normalized GSH/GSSG ratio in ANF-treated HCC827AR and HCC827OR cell lines. (C) Normalized NADPH/$NADP^+$ ratio in ANF-treated HCC827AR and HCC827OR cell lines. Data are presented as mean ± SD (n = 3). DMSO was used as negative control.

Table S1. siRNAs used in this study. All siRNAs were purchased from Qiagen.

siRNA	Cat. No.	Sequences
Negative control	SI03650318	N/A
siELF3	SI04265660	5'-uugguagcugauccaguccag-3'
siFOXM1	SI04166309	5'-ugguuaauaaucuugauccca-3'

Table S2. Primer sets for RT-PCR.

Gene	FWD / REV	Sequence
ELF3	FWD	5'-ttagcaactacttcagtgcgatgt-3'
	REV	5'-gttcttctccacttggtagctgat-3'
FOXM1	FWD	5'-atctcagcaccactcccttg-3'
	REV	5'-cttgctgaggctgtcattca-3'
YAP1	FWD	5'-gtggcacctatcactctcga-3'
	REV	5'-tggcttcaaggtagtctggg-3'
ACTB	FWD	5'-catcgagcacggcatcgtca-3'
	REV	5'-tagcacagcctggatagcaa-3'

Table S3. Primer sets for ChIP-PCR amplifying promoter sequences.

Gene	FWD / REV	Sequence
ELF3	FWD	5'-gttgcagatgctggctacaa-3'
	REV	5'-catccaggtatgcaggtgtg-3'
FOXM1	FWD	5'-gtacgatttcccccagtgag-3'
	REV	5'-gcggagcgttaaggtcac-3'
YAP1	FWD	5'-ccctgaggctgtgcttagaa-3'
	REV	5'-acctcatagttgttggggca-3'

Table S4. Sequencing depth and quality metrics for ChIP-seq libraries analyzed in this study.

Sample	Sequencing depth (reads)	Trimmed reads	Mapped reads	Unmapped reads	Mapping rate (%)	Number of peaks
549ANFE3	26,279,275	22,409,881	18,908,231	3,501,650	84.37	126,214
549CONE3	31,438,986	24,410,103	21,102,066	3,308,037	86.45	171,597
549CONF1	23,819,735	22,095,734	17,366,622	4,729,112	78.60	156,335
549TSTF1	28,095,513	26,638,787	16,264,007	10,374,780	61.05	56,695
827ANFE3	46,752,921	43,830,026	34,897,784	8,932,242	79.62	184,282
827CONE3	35,105,680	33,384,839	27,001,512	6,383,327	80.88	165,786
827CONF1	32,539,577	30,805,144	22,965,499	7,839,645	74.55	189,103
827TSTF1	41,085,376	39,028,329	29,533,662	9,494,667	75.67	153,305
ARANFE3	26,690,139	25,196,118	17,770,305	7,425,813	70.53	97,547
ARCONE3	32,908,295	30,878,015	24,235,766	6,642,249	78.49	175,051
ARCONF1	48,008,533	45,102,261	31,359,444	13,742,817	69.53	192,920
ARTSTF1	42,702,301	40,494,475	28,196,763	12,297,712	69.63	195,587

Reads were aligned to the human genome (UCSC hg19) with Bowtie2; peaks were called with MACS2 ($q < 0.01$). Each condition represents a single library without biological replicates. CON, control; ANF, auranofin; TST, thiostrepton; AR, afatinib-resistant HCC827.

Table S5. Overall survival rate according to FOXM1 alterations (TCGA, Firehose legacy; luad_tcga). P = 0.0001.

Patient ID	Study ID	Number at Risk	Status	Survival Rate	Time (months)
Altered Group					
TCGA-05-4395	luad_tcga	128	deceased	0.9921875	0
TCGA-55-A493	luad_tcga	127	censored	0.9921875	0.92
TCGA-91-6849	luad_tcga	126	censored	0.9921875	1.15
TCGA-91-8499	luad_tcga	125	censored	0.9921875	1.18
TCGA-64-5775	luad_tcga	124	deceased	0.984185988	2.04
TCGA-95-7562	luad_tcga	123	deceased	0.976184476	2.86
TCGA-05-4415	luad_tcga	122	deceased	0.968182964	2.99
TCGA-86-A4D0	luad_tcga	121	deceased	0.960181452	3.81
TCGA-55-6975	luad_tcga	120	deceased	0.95217994	3.88
TCGA-50-6591	luad_tcga	119	deceased	0.944178427	3.91
TCGA-69-8255	luad_tcga	118	censored	0.944178427	4.24
TCGA-73-4670	luad_tcga	117	censored	0.944178427	4.3
TCGA-62-8394	luad_tcga	116	deceased	0.936038958	4.57
TCGA-78-7146	luad_tcga	115	deceased	0.927899489	5.68
TCGA-55-6978	luad_tcga	114	deceased	0.91976002	5.78
TCGA-86-6851	luad_tcga	113	censored	0.91976002	5.88
TCGA-50-6595	luad_tcga	112	deceased	0.911547877	6.21
TCGA-91-6848	luad_tcga	111	censored	0.911547877	7.36
TCGA-69-7973	luad_tcga	110	censored	0.911547877	7.56
TCGA-78-7536	luad_tcga	109	deceased	0.903185052	8.02
TCGA-50-5072	luad_tcga	108	deceased	0.894822228	8.21
TCGA-49-AAR9	luad_tcga	107	deceased	0.886459403	8.54
TCGA-49-4507	luad_tcga	106	deceased	0.878096579	8.8
TCGA-44-8119	luad_tcga	105	censored	0.878096579	9.36
TCGA-91-6831	luad_tcga	104	censored	0.878096579	10.18
TCGA-78-8660	luad_tcga	103	deceased	0.869571369	10.55
TCGA-78-7542	luad_tcga	102	deceased	0.86104616	10.55
TCGA-73-A9RS	luad_tcga	101	deceased	0.85252095	11.17
TCGA-86-8585	luad_tcga	100	censored	0.85252095	11.6
TCGA-38-4631	luad_tcga	99	deceased	0.843909627	11.63
TCGA-55-8620	luad_tcga	98	deceased	0.835298305	12.32
TCGA-95-7944	luad_tcga	97	censored	0.835298305	12.39
TCGA-91-6836	luad_tcga	96	censored	0.835298305	13.7
TCGA-67-6217	luad_tcga	95	censored	0.835298305	13.86
TCGA-MP-A4TI	luad_tcga	94	deceased	0.826412152	14.09
TCGA-50-5931	luad_tcga	93	deceased	0.817526	14.26
TCGA-62-8398	luad_tcga	92	deceased	0.808639848	14.59
TCGA-05-4434	luad_tcga	91	deceased	0.799753696	15.01
TCGA-55-8087	luad_tcga	90	censored	0.799753696	15.18
TCGA-97-8176	luad_tcga	89	deceased	0.790767699	15.37
TCGA-95-7947	luad_tcga	88	censored	0.790767699	15.67
TCGA-55-A494	luad_tcga	87	censored	0.790767699	15.8
TCGA-49-6742	luad_tcga	86	deceased	0.781572726	16.03
TCGA-44-6779	luad_tcga	85	deceased	0.772377753	16.43
TCGA-95-7043	luad_tcga	84	deceased	0.76318278	16.52

Patient ID	Study ID	Number at Risk	Status	Survival Rate	Time (months)
TCGA-91-8496	luad_tcga	83	censored	0.76318278	16.59
TCGA-55-8514	luad_tcga	82	censored	0.76318278	17.08
TCGA-55-8301	luad_tcga	81	censored	0.76318278	17.54
TCGA-44-7661	luad_tcga	80	deceased	0.753642995	18.3
TCGA-55-7913	luad_tcga	79	deceased	0.74410321	18.43
TCGA-95-7567	luad_tcga	78	censored	0.74410321	18.66
TCGA-44-7669	luad_tcga	77	deceased	0.734439532	18.86
TCGA-L4-A4E5	luad_tcga	76	censored	0.734439532	18.99
TCGA-44-7660	luad_tcga	75	censored	0.734439532	19.45
TCGA-78-7154	luad_tcga	74	deceased	0.724514673	19.48
TCGA-55-8205	luad_tcga	73	censored	0.724514673	19.68
TCGA-55-7994	luad_tcga	72	censored	0.724514673	19.81
TCGA-55-8512	luad_tcga	71	deceased	0.714310241	19.94
TCGA-55-A4DF	luad_tcga	70	deceased	0.704105809	20.17
TCGA-50-5044	luad_tcga	69	deceased	0.693901377	20.5
TCGA-97-8552	luad_tcga	68	censored	0.693901377	20.57
TCGA-55-7726	luad_tcga	67	censored	0.693901377	21.42
TCGA-50-5935	luad_tcga	66	deceased	0.68338772	21.45
TCGA-86-8358	luad_tcga	65	censored	0.68338772	21.45
TCGA-99-8033	luad_tcga	64	deceased	0.672709787	21.55
TCGA-78-7150	luad_tcga	63	deceased	0.662031854	21.88
TCGA-49-6767	luad_tcga	62	censored	0.662031854	22.24
TCGA-55-8089	luad_tcga	61	deceased	0.651178873	23.06
TCGA-44-6148	luad_tcga	60	censored	0.651178873	23.13
TCGA-73-4659	luad_tcga	59	deceased	0.640141943	23.36
TCGA-05-4397	luad_tcga	58	deceased	0.629105013	24.01
TCGA-86-A4JF	luad_tcga	57	deceased	0.618068083	24.21
TCGA-44-2668	luad_tcga	56	deceased	0.607031153	25
TCGA-50-6592	luad_tcga	55	deceased	0.595994222	25.53
TCGA-73-4666	luad_tcga	54	censored	0.595994222	26.28
TCGA-78-7220	luad_tcga	53	deceased	0.584749048	26.51
TCGA-83-5908	luad_tcga	52	censored	0.584749048	27.07
TCGA-55-7570	luad_tcga	51	censored	0.584749048	27.07
TCGA-MN-A4N1	luad_tcga	50	censored	0.584749048	27.17
TCGA-49-4487	luad_tcga	49	deceased	0.572815394	28.09
TCGA-44-5644	luad_tcga	48	censored	0.572815394	28.35
TCGA-44-7670	luad_tcga	47	censored	0.572815394	28.98
TCGA-55-7995	luad_tcga	46	censored	0.572815394	29.2
TCGA-49-4510	luad_tcga	45	deceased	0.560086163	29.43
TCGA-MP-A4TE	luad_tcga	44	deceased	0.547356932	29.43
TCGA-05-4420	luad_tcga	43	censored	0.547356932	29.96
TCGA-55-5899	luad_tcga	42	censored	0.547356932	30.55
TCGA-86-7701	luad_tcga	41	censored	0.547356932	31.11
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TCGA-86-7953	luad_tcga	38	censored	0.533673009	32.75
TCGA-44-5643	luad_tcga	37	censored	0.533673009	33.28
TCGA-55-7910	luad_tcga	36	censored	0.533673009	34.17
TCGA-53-7624	luad_tcga	35	deceased	0.518425209	34.26

Patient ID	Study ID	Number at Risk	Status	Survival Rate	Time (months)
TCGA-86-7711	luad_tcga	34	deceased	0.503177409	34.36
TCGA-53-A4EZ	luad_tcga	33	censored	0.503177409	35.18
TCGA-86-7955	luad_tcga	32	censored	0.503177409	35.22
TCGA-38-4630	luad_tcga	31	deceased	0.486945879	35.25
TCGA-44-7667	luad_tcga	30	censored	0.486945879	36.04
TCGA-50-8457	luad_tcga	29	censored	0.486945879	36.96
TCGA-86-8054	luad_tcga	28	censored	0.486945879	37.71
TCGA-78-7155	luad_tcga	27	deceased	0.468910847	38.47
TCGA-55-1594	luad_tcga	26	censored	0.468910847	38.7
TCGA-62-A471	luad_tcga	25	censored	0.468910847	40.93
TCGA-50-6590	luad_tcga	24	deceased	0.449372895	42.31
TCGA-55-6968	luad_tcga	23	deceased	0.429834943	42.48
TCGA-44-2655	luad_tcga	22	censored	0.429834943	43.5
TCGA-38-4632	luad_tcga	21	deceased	0.409366612	44.58
TCGA-05-4398	luad_tcga	20	censored	0.409366612	47.01
TCGA-62-8402	luad_tcga	19	deceased	0.387821001	49.21
TCGA-50-5068	luad_tcga	18	deceased	0.36627539	49.24
TCGA-50-5946	luad_tcga	17	censored	0.36627539	53.12
TCGA-49-4514	luad_tcga	16	censored	0.36627539	55.85
TCGA-50-5942	luad_tcga	15	censored	0.36627539	60.68
TCGA-49-AAR3	luad_tcga	14	censored	0.36627539	62.19
TCGA-97-7547	luad_tcga	13	censored	0.36627539	64.55
TCGA-75-5125	luad_tcga	12	deceased	0.335752441	66.59
TCGA-55-1596	luad_tcga	11	censored	0.335752441	67.84
TCGA-49-AAR2	luad_tcga	10	censored	0.335752441	73.06
TCGA-75-6206	luad_tcga	9	censored	0.335752441	85.09
TCGA-MP-A4SV	luad_tcga	8	deceased	0.293783386	86.07
TCGA-64-5774	luad_tcga	7	censored	0.293783386	87.91
TCGA-78-7167	luad_tcga	6	deceased	0.244819488	88.07
TCGA-80-5608	luad_tcga	5	censored	0.244819488	93.04
TCGA-38-4625	luad_tcga	4	censored	0.244819488	97.67
TCGA-75-7027	luad_tcga	3	censored	0.244819488	100.49
TCGA-49-AARQ	luad_tcga	2	censored	0.244819488	221.16
TCGA-78-7163	luad_tcga	1	censored	0.244819488	238.11
Unaltered Group					
TCGA-05-4244	luad_tcga	378	censored	1	0
TCGA-86-8281	luad_tcga	377	censored	1	0
TCGA-05-4410	luad_tcga	376	censored	1	0
TCGA-NJ-A4YI	luad_tcga	375	deceased	0.997333333	0.13
TCGA-55-8506	luad_tcga	374	censored	0.997333333	0.36
TCGA-NJ-A55O	luad_tcga	373	censored	0.997333333	0.43
TCGA-35-3615	luad_tcga	372	censored	0.997333333	0.46
TCGA-NJ-A55A	luad_tcga	371	censored	0.997333333	0.49
TCGA-97-7938	luad_tcga	370	deceased	0.994637838	0.59
TCGA-86-8672	luad_tcga	369	deceased	0.991942342	0.62
TCGA-50-6673	luad_tcga	368	deceased	0.989246847	0.72
TCGA-86-8074	luad_tcga	367	censored	0.989246847	0.79
TCGA-93-A4JO	luad_tcga	366	deceased	0.986543987	1.08
TCGA-73-4677	luad_tcga	365	deceased	0.983841126	1.25

Patient ID	Study ID	Number at Risk	Status	Survival Rate	Time (months)
TCGA-91-A4BC	luad_tcga	364	censored	0.983841126	1.45
TCGA-99-8032	luad_tcga	363	censored	0.983841126	1.45
TCGA-55-8616	luad_tcga	362	censored	0.983841126	1.58
TCGA-NJ-A4YP	luad_tcga	361	censored	0.983841126	1.64
TCGA-L9-A5IP	luad_tcga	360	deceased	0.981108234	1.91
TCGA-91-6830	luad_tcga	359	censored	0.981108234	1.97
TCGA-05-5715	luad_tcga	358	censored	0.981108234	2.04
TCGA-MP-A4TC	luad_tcga	357	deceased	0.978360032	2.43
TCGA-91-6835	luad_tcga	356	censored	0.978360032	2.6
TCGA-MN-A4N5	luad_tcga	355	censored	0.978360032	2.76
TCGA-95-8494	luad_tcga	354	censored	0.978360032	2.76
TCGA-44-2666	luad_tcga	353	deceased	0.975588474	3.19
TCGA-55-A490	luad_tcga	352	deceased	0.972816916	3.25
TCGA-55-7727	luad_tcga	351	censored	0.972816916	3.91
TCGA-05-4250	luad_tcga	350	deceased	0.970037439	3.98
TCGA-86-8055	luad_tcga	349	deceased	0.967257962	4.07
TCGA-38-A44F	luad_tcga	348	censored	0.967257962	4.37
TCGA-69-7978	luad_tcga	347	censored	0.967257962	4.4
TCGA-86-8056	luad_tcga	346	censored	0.967257962	4.57
TCGA-67-6216	luad_tcga	345	censored	0.967257962	4.63
TCGA-05-5423	luad_tcga	344	censored	0.967257962	4.96
TCGA-55-8092	luad_tcga	343	deceased	0.964437968	5.06
TCGA-MP-A4T8	luad_tcga	342	deceased	0.961617974	5.29
TCGA-97-8174	luad_tcga	341	deceased	0.95879798	5.39
TCGA-69-7765	luad_tcga	340	censored	0.95879798	5.42
TCGA-MP-A4T7	luad_tcga	339	deceased	0.955969667	5.49
TCGA-55-6712	luad_tcga	338	deceased	0.953141354	5.62
TCGA-67-6215	luad_tcga	337	censored	0.953141354	5.72
TCGA-78-7158	luad_tcga	336	deceased	0.950304624	5.88
TCGA-35-4123	luad_tcga	335	censored	0.950304624	5.98
TCGA-69-7974	luad_tcga	334	censored	0.950304624	6.04
TCGA-93-8067	luad_tcga	333	censored	0.950304624	6.11
TCGA-69-7761	luad_tcga	332	censored	0.950304624	6.11
TCGA-55-7914	luad_tcga	331	deceased	0.947433613	6.14
TCGA-L9-A443	luad_tcga	330	deceased	0.944562602	6.34
TCGA-69-7760	luad_tcga	329	censored	0.944562602	6.64
TCGA-71-8520	luad_tcga	328	deceased	0.941682838	6.9
TCGA-44-7662	luad_tcga	327	censored	0.941682838	7.16
TCGA-35-4122	luad_tcga	326	censored	0.941682838	7.39
TCGA-55-6979	luad_tcga	325	deceased	0.938785353	7.79
TCGA-55-7284	luad_tcga	324	deceased	0.935887867	7.98
TCGA-05-4402	luad_tcga	323	deceased	0.932990381	8.02
TCGA-71-6725	luad_tcga	322	censored	0.932990381	8.41
TCGA-50-5936	luad_tcga	321	deceased	0.930083869	8.44
TCGA-78-7166	luad_tcga	320	deceased	0.927177357	8.48
TCGA-44-8120	luad_tcga	319	censored	0.927177357	8.54
TCGA-35-5375	luad_tcga	318	censored	0.927177357	8.67
TCGA-05-4418	luad_tcga	317	deceased	0.924252507	9
TCGA-05-5429	luad_tcga	316	deceased	0.921327658	9.03

Patient ID	Study ID	Number at Risk	Status	Survival Rate	Time (months)
TCGA-73-4676	luad_tcga	315	deceased	0.918402808	9.23
TCGA-50-5930	luad_tcga	314	deceased	0.915477958	9.26
TCGA-44-A47B	luad_tcga	313	censored	0.915477958	9.43
TCGA-78-7161	luad_tcga	312	deceased	0.912543734	9.56
TCGA-4B-A93V	luad_tcga	311	deceased	0.90960951	9.86
TCGA-05-4396	luad_tcga	310	deceased	0.906675286	9.95
TCGA-MP-A4TD	luad_tcga	309	deceased	0.903741061	10.09
TCGA-L9-A444	luad_tcga	308	censored	0.903741061	10.09
TCGA-50-7109	luad_tcga	307	deceased	0.900797279	10.12
TCGA-91-6828	luad_tcga	306	censored	0.900797279	10.61
TCGA-MP-A4TF	luad_tcga	305	deceased	0.897843846	11.04
TCGA-50-6593	luad_tcga	304	deceased	0.894890412	11.04
TCGA-MP-A4TJ	luad_tcga	303	deceased	0.891936978	11.14
TCGA-55-7907	luad_tcga	302	deceased	0.888983545	11.27
TCGA-44-A47G	luad_tcga	301	censored	0.888983545	11.53
TCGA-49-6761	luad_tcga	300	censored	0.888983545	11.63
TCGA-05-4422	luad_tcga	299	censored	0.888983545	11.99
TCGA-50-6594	luad_tcga	298	deceased	0.886000378	12.16
TCGA-91-6840	luad_tcga	297	censored	0.886000378	12.22
TCGA-86-6562	luad_tcga	296	deceased	0.883007134	12.35
TCGA-49-4490	luad_tcga	295	deceased	0.880013889	12.65
TCGA-67-3774	luad_tcga	294	censored	0.880013889	12.65
TCGA-44-8117	luad_tcga	293	censored	0.880013889	12.65
TCGA-69-7979	luad_tcga	292	censored	0.880013889	13.4
TCGA-44-A4SU	luad_tcga	291	deceased	0.876989787	13.44
TCGA-69-8254	luad_tcga	290	censored	0.876989787	13.44
TCGA-69-7980	luad_tcga	289	censored	0.876989787	13.5
TCGA-62-A46Y	luad_tcga	288	deceased	0.873944683	13.6
TCGA-69-7764	luad_tcga	287	censored	0.873944683	13.6
TCGA-86-A4P7	luad_tcga	286	censored	0.873944683	13.63
TCGA-44-A4SS	luad_tcga	285	censored	0.873944683	13.63
TCGA-55-8619	luad_tcga	284	censored	0.873944683	13.67
TCGA-55-8507	luad_tcga	283	censored	0.873944683	13.73
TCGA-86-8668	luad_tcga	282	censored	0.873944683	13.9
TCGA-53-7813	luad_tcga	281	censored	0.873944683	13.93
TCGA-69-8253	luad_tcga	280	censored	0.873944683	13.99
TCGA-05-4384	luad_tcga	279	censored	0.873944683	13.99
TCGA-67-3773	luad_tcga	278	censored	0.873944683	14.03
TCGA-49-4505	luad_tcga	277	deceased	0.870789648	14.06
TCGA-91-8497	luad_tcga	276	deceased	0.867634613	14.26
TCGA-L4-A4E6	luad_tcga	275	censored	0.867634613	14.29
TCGA-97-8179	luad_tcga	274	censored	0.867634613	14.29
TCGA-55-6543	luad_tcga	273	censored	0.867634613	14.29
TCGA-55-8505	luad_tcga	272	censored	0.867634613	14.45
TCGA-L9-A50W	luad_tcga	271	deceased	0.86443301	14.52
TCGA-55-7725	luad_tcga	270	censored	0.86443301	14.52
TCGA-86-8359	luad_tcga	269	deceased	0.861219504	14.59
TCGA-55-8615	luad_tcga	268	censored	0.861219504	14.65
TCGA-67-4679	luad_tcga	267	censored	0.861219504	14.72

Patient ID	Study ID	Number at Risk	Status	Survival Rate	Time (months)
TCGA-38-6178	luad_tcga	266	censored	0.861219504	14.72
TCGA-05-4417	luad_tcga	265	censored	0.861219504	14.95
TCGA-05-5420	luad_tcga	264	censored	0.861219504	15.01
TCGA-50-5939	luad_tcga	263	deceased	0.857944905	15.11
TCGA-55-6970	luad_tcga	262	deceased	0.854670306	15.24
TCGA-44-A47A	luad_tcga	261	censored	0.854670306	15.31
TCGA-73-4668	luad_tcga	260	censored	0.854670306	15.34
TCGA-55-7816	luad_tcga	259	deceased	0.851370421	15.37
TCGA-55-8299	luad_tcga	258	deceased	0.848070535	15.41
TCGA-L9-A8F4	luad_tcga	257	censored	0.848070535	15.64
TCGA-55-8097	luad_tcga	256	censored	0.848070535	15.64
TCGA-95-7948	luad_tcga	255	censored	0.848070535	15.64
TCGA-50-5051	luad_tcga	254	deceased	0.844731675	15.7
TCGA-55-8302	luad_tcga	253	censored	0.844731675	15.7
TCGA-97-7941	luad_tcga	252	censored	0.844731675	15.9
TCGA-44-A479	luad_tcga	251	censored	0.844731675	15.97
TCGA-55-7573	luad_tcga	250	censored	0.844731675	16
TCGA-91-7771	luad_tcga	249	censored	0.844731675	16.16
TCGA-97-8177	luad_tcga	248	censored	0.844731675	16.39
TCGA-S2-AA1A	luad_tcga	247	censored	0.844731675	16.85
TCGA-55-8621	luad_tcga	246	censored	0.844731675	16.92
TCGA-55-8204	luad_tcga	245	censored	0.844731675	16.92
TCGA-49-6745	luad_tcga	244	censored	0.844731675	17.15
TCGA-93-A4JQ	luad_tcga	243	censored	0.844731675	17.28
TCGA-93-7348	luad_tcga	242	censored	0.844731675	17.44
TCGA-55-8614	luad_tcga	241	censored	0.844731675	17.61
TCGA-55-7911	luad_tcga	240	censored	0.844731675	17.64
TCGA-55-8510	luad_tcga	239	censored	0.844731675	17.71
TCGA-97-A4M3	luad_tcga	238	censored	0.844731675	17.74
TCGA-55-8094	luad_tcga	237	censored	0.844731675	17.77
TCGA-97-8172	luad_tcga	236	censored	0.844731675	17.9
TCGA-55-A57B	luad_tcga	235	censored	0.844731675	17.94
TCGA-55-8203	luad_tcga	234	censored	0.844731675	17.97
TCGA-J2-A4AD	luad_tcga	233	deceased	0.841106217	18.07
TCGA-97-8175	luad_tcga	232	censored	0.841106217	18.1
TCGA-55-8511	luad_tcga	231	censored	0.841106217	18.13
TCGA-95-A4VN	luad_tcga	230	censored	0.841106217	18.17
TCGA-97-7937	luad_tcga	229	censored	0.841106217	18.53
TCGA-L9-A7SV	luad_tcga	228	censored	0.841106217	18.56
TCGA-55-7903	luad_tcga	227	censored	0.841106217	18.63
TCGA-97-A4M6	luad_tcga	226	censored	0.841106217	18.66
TCGA-97-8171	luad_tcga	225	censored	0.841106217	18.66
TCGA-67-3772	luad_tcga	224	censored	0.841106217	18.82
TCGA-05-4403	luad_tcga	223	censored	0.841106217	18.99
TCGA-93-A4JP	luad_tcga	222	censored	0.841106217	18.99
TCGA-MP-A4TK	luad_tcga	221	deceased	0.837300307	19.12
TCGA-78-7147	luad_tcga	220	deceased	0.833494396	19.25
TCGA-69-A59K	luad_tcga	219	censored	0.833494396	19.42
TCGA-62-A46P	luad_tcga	218	deceased	0.829671028	19.51

Patient ID	Study ID	Number at Risk	Status	Survival Rate	Time (months)
TCGA-44-6145	luad_tcga	217	censored	0.829671028	19.55
TCGA-55-A492	luad_tcga	216	censored	0.829671028	19.58
TCGA-55-8090	luad_tcga	215	deceased	0.825812093	19.65
TCGA-55-8091	luad_tcga	214	censored	0.825812093	19.71
TCGA-97-A4M1	luad_tcga	213	censored	0.825812093	19.74
TCGA-NJ-A55R	luad_tcga	212	censored	0.825812093	19.81
TCGA-91-A4BD	luad_tcga	211	censored	0.825812093	19.81
TCGA-95-A4VP	luad_tcga	210	censored	0.825812093	19.88
TCGA-86-7954	luad_tcga	209	censored	0.825812093	19.88
TCGA-05-4382	luad_tcga	208	censored	0.825812093	19.94
TCGA-55-A4DG	luad_tcga	207	censored	0.825812093	19.97
TCGA-55-7283	luad_tcga	206	censored	0.825812093	20.01
TCGA-67-3771	luad_tcga	205	censored	0.825812093	20.04
TCGA-67-3770	luad_tcga	204	censored	0.825812093	20.04
TCGA-05-4405	luad_tcga	203	censored	0.825812093	20.04
TCGA-97-A4LX	luad_tcga	202	censored	0.825812093	20.17
TCGA-NJ-A7XG	luad_tcga	201	censored	0.825812093	20.27
TCGA-55-8508	luad_tcga	200	censored	0.825812093	20.27
TCGA-97-A4M2	luad_tcga	199	censored	0.825812093	20.5
TCGA-86-7714	luad_tcga	198	deceased	0.821641324	20.53
TCGA-78-7148	luad_tcga	197	deceased	0.817470556	20.57
TCGA-55-A491	luad_tcga	196	censored	0.817470556	20.57
TCGA-64-1677	luad_tcga	195	deceased	0.8132784	20.63
TCGA-97-A4M7	luad_tcga	194	censored	0.8132784	20.66
TCGA-55-A48Y	luad_tcga	193	censored	0.8132784	20.7
TCGA-97-A4M5	luad_tcga	192	censored	0.8132784	20.83
TCGA-95-A4VK	luad_tcga	191	censored	0.8132784	21.39
TCGA-55-A48Z	luad_tcga	190	censored	0.8132784	21.39
TCGA-97-A4M0	luad_tcga	189	censored	0.8132784	21.42
TCGA-97-8547	luad_tcga	188	censored	0.8132784	21.58
TCGA-99-AA5R	luad_tcga	187	censored	0.8132784	21.62
TCGA-44-6774	luad_tcga	186	censored	0.8132784	21.62
TCGA-L9-A743	luad_tcga	185	censored	0.8132784	21.81
TCGA-05-4425	luad_tcga	184	censored	0.8132784	21.98
TCGA-05-5428	luad_tcga	183	censored	0.8132784	22.01
TCGA-55-7576	luad_tcga	182	censored	0.8132784	22.01
TCGA-55-8208	luad_tcga	181	censored	0.8132784	22.14
TCGA-49-AAQV	luad_tcga	180	deceased	0.808760186	22.24
TCGA-93-7347	luad_tcga	179	censored	0.808760186	22.44
TCGA-55-A48X	luad_tcga	178	censored	0.808760186	22.63
TCGA-69-7763	luad_tcga	177	censored	0.808760186	22.67
TCGA-44-7659	luad_tcga	176	censored	0.808760186	22.7
TCGA-86-8075	luad_tcga	175	deceased	0.804138699	22.8
TCGA-78-7160	luad_tcga	174	deceased	0.799517213	22.9
TCGA-55-1592	luad_tcga	173	deceased	0.794895726	23.03
TCGA-86-8280	luad_tcga	172	censored	0.794895726	23.03
TCGA-55-7728	luad_tcga	171	censored	0.794895726	23.13
TCGA-55-7724	luad_tcga	170	censored	0.794895726	23.16
TCGA-44-6775	luad_tcga	169	censored	0.794895726	23.16

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TCGA-93-A4JN	luad_tcga	168	censored	0.794895726	23.59
TCGA-55-8096	luad_tcga	167	deceased	0.790135871	23.62
TCGA-44-7672	luad_tcga	166	censored	0.790135871	23.62
TCGA-J2-8194	luad_tcga	165	censored	0.790135871	23.78
TCGA-44-6146	luad_tcga	164	censored	0.790135871	23.92
TCGA-05-4433	luad_tcga	163	censored	0.790135871	23.98
TCGA-J2-8192	luad_tcga	162	censored	0.790135871	24.28
TCGA-86-8073	luad_tcga	161	censored	0.790135871	24.31
TCGA-MP-A4TH	luad_tcga	160	censored	0.790135871	24.34
TCGA-99-7458	luad_tcga	159	censored	0.790135871	24.54
TCGA-55-6984	luad_tcga	158	deceased	0.785135011	24.97
TCGA-05-4432	luad_tcga	157	censored	0.785135011	25
TCGA-05-4430	luad_tcga	156	censored	0.785135011	25
TCGA-55-7815	luad_tcga	155	censored	0.785135011	25.39
TCGA-97-7554	luad_tcga	154	censored	0.785135011	25.46
TCGA-05-4426	luad_tcga	153	censored	0.785135011	25.99
TCGA-55-8513	luad_tcga	152	censored	0.785135011	25.99
TCGA-78-7539	luad_tcga	151	censored	0.785135011	25.99
TCGA-05-4427	luad_tcga	150	censored	0.785135011	25.99
TCGA-38-7271	luad_tcga	149	deceased	0.779865649	26.28
TCGA-86-A4P8	luad_tcga	148	censored	0.779865649	26.45
TCGA-86-8674	luad_tcga	147	censored	0.779865649	26.48
TCGA-44-4112	luad_tcga	146	deceased	0.774524103	26.54
TCGA-69-8453	luad_tcga	145	censored	0.774524103	26.71
TCGA-78-7145	luad_tcga	144	deceased	0.769145464	27.14
TCGA-50-8460	luad_tcga	143	censored	0.769145464	27.23
TCGA-95-8039	luad_tcga	142	censored	0.769145464	27.27
TCGA-86-8671	luad_tcga	141	censored	0.769145464	27.56
TCGA-91-6847	luad_tcga	140	censored	0.769145464	27.66
TCGA-44-6147	luad_tcga	139	censored	0.769145464	27.76
TCGA-44-5645	luad_tcga	138	censored	0.769145464	27.99
TCGA-86-8673	luad_tcga	137	censored	0.769145464	28.32
TCGA-38-4629	luad_tcga	136	deceased	0.763489982	28.38
TCGA-64-5779	luad_tcga	135	censored	0.763489982	28.38
TCGA-64-5815	luad_tcga	134	censored	0.763489982	28.45
TCGA-49-4488	luad_tcga	133	deceased	0.757749456	28.55
TCGA-55-7281	luad_tcga	132	censored	0.757749456	28.65
TCGA-49-AAR4	luad_tcga	131	deceased	0.751965109	28.88
TCGA-05-5425	luad_tcga	130	censored	0.751965109	28.98
TCGA-55-8206	luad_tcga	129	censored	0.751965109	29.17
TCGA-44-7671	luad_tcga	128	censored	0.751965109	29.2
TCGA-86-A456	luad_tcga	127	censored	0.751965109	29.43
TCGA-55-8085	luad_tcga	126	censored	0.751965109	29.7
TCGA-49-4512	luad_tcga	125	deceased	0.745949388	29.73
TCGA-62-A472	luad_tcga	124	censored	0.745949388	29.89
TCGA-05-4424	luad_tcga	123	censored	0.745949388	29.99
TCGA-73-4675	luad_tcga	122	deceased	0.739835049	30.29
TCGA-53-7626	luad_tcga	121	deceased	0.73372071	30.52
TCGA-86-8669	luad_tcga	120	censored	0.73372071	30.81

Patient ID	Study ID	Number at Risk	Status	Survival Rate	Time (months)
TCGA-86-8278	luad_tcga	119	censored	0.73372071	31.01
TCGA-78-7535	luad_tcga	118	deceased	0.727502738	31.18
TCGA-86-8279	luad_tcga	117	censored	0.727502738	31.18
TCGA-55-7227	luad_tcga	116	deceased	0.721231162	31.27
TCGA-78-7156	luad_tcga	115	deceased	0.714959587	32.06
TCGA-44-6777	luad_tcga	114	deceased	0.708688012	32.42
TCGA-J2-A4AG	luad_tcga	113	censored	0.708688012	32.46
TCGA-86-8076	luad_tcga	112	censored	0.708688012	32.62
TCGA-55-7574	luad_tcga	111	deceased	0.702303435	32.69
TCGA-55-6982	luad_tcga	110	deceased	0.695918858	32.69
TCGA-49-4506	luad_tcga	109	deceased	0.689534282	32.82
TCGA-44-3919	luad_tcga	108	deceased	0.683149705	33.71
TCGA-44-3918	luad_tcga	107	censored	0.683149705	34.03
TCGA-99-8025	luad_tcga	106	censored	0.683149705	34.82
TCGA-J2-A4AE	luad_tcga	105	censored	0.683149705	35.45
TCGA-49-4494	luad_tcga	104	deceased	0.676580958	35.51
TCGA-75-6214	luad_tcga	103	deceased	0.670012211	36.63
TCGA-99-8028	luad_tcga	102	censored	0.670012211	36.73
TCGA-50-8459	luad_tcga	101	censored	0.670012211	36.76
TCGA-64-1680	luad_tcga	100	censored	0.670012211	36.99
TCGA-05-4390	luad_tcga	99	censored	0.670012211	36.99
TCGA-44-3396	luad_tcga	98	censored	0.670012211	37.12
TCGA-49-AARN	luad_tcga	97	deceased	0.663104868	37.29
TCGA-38-4627	luad_tcga	96	deceased	0.656197526	37.68
TCGA-86-7713	luad_tcga	95	censored	0.656197526	38.01
TCGA-44-2661	luad_tcga	94	censored	0.656197526	38.07
TCGA-44-3398	luad_tcga	93	censored	0.656197526	38.21
TCGA-64-1681	luad_tcga	92	deceased	0.649064944	38.34
TCGA-MN-A4N4	luad_tcga	91	censored	0.649064944	38.6
TCGA-64-1678	luad_tcga	90	censored	0.649064944	39.06
TCGA-73-7498	luad_tcga	89	censored	0.649064944	39.06
TCGA-62-A470	luad_tcga	88	deceased	0.641689206	39.22
TCGA-78-7540	luad_tcga	87	deceased	0.634313468	39.32
TCGA-78-8648	luad_tcga	86	deceased	0.62693773	39.72
TCGA-78-7152	luad_tcga	85	deceased	0.619561992	39.91
TCGA-62-8395	luad_tcga	84	censored	0.619561992	39.95
TCGA-49-AARE	luad_tcga	83	deceased	0.61209739	40.37
TCGA-55-6985	luad_tcga	82	censored	0.61209739	40.51
TCGA-50-5932	luad_tcga	81	deceased	0.604540632	40.57
TCGA-55-6969	luad_tcga	80	censored	0.604540632	40.7
TCGA-91-6829	luad_tcga	79	deceased	0.596888219	41.33
TCGA-MP-A4T9	luad_tcga	78	deceased	0.589235806	41.56
TCGA-50-6597	luad_tcga	77	deceased	0.581583393	41.66
TCGA-95-7039	luad_tcga	76	censored	0.581583393	41.79
TCGA-44-2662	luad_tcga	75	censored	0.581583393	42.05
TCGA-97-7546	luad_tcga	74	censored	0.581583393	42.21
TCGA-62-8397	luad_tcga	73	censored	0.581583393	42.35
TCGA-44-2665	luad_tcga	72	censored	0.581583393	42.74
TCGA-64-5778	luad_tcga	71	censored	0.581583393	42.87

Patient ID	Study ID	Number at Risk	Status	Survival Rate	Time (months)
TCGA-75-5147	luad_tcga	70	censored	0.581583393	43.79
TCGA-44-2657	luad_tcga	69	censored	0.581583393	44.38
TCGA-44-2659	luad_tcga	68	censored	0.581583393	44.91
TCGA-05-4389	luad_tcga	67	censored	0.581583393	44.97
TCGA-55-6981	luad_tcga	66	deceased	0.572771523	45.3
TCGA-55-6971	luad_tcga	65	censored	0.572771523	45.99
TCGA-49-4501	luad_tcga	64	deceased	0.563821968	46.68
TCGA-44-2656	luad_tcga	63	censored	0.563821968	46.94
TCGA-NJ-A4YQ	luad_tcga	62	censored	0.563821968	47.04
TCGA-50-5066	luad_tcga	61	censored	0.563821968	47.37
TCGA-62-A46O	luad_tcga	60	deceased	0.554424935	47.77
TCGA-50-5941	luad_tcga	59	censored	0.554424935	48.42
TCGA-55-1595	luad_tcga	58	censored	0.554424935	48.59
TCGA-38-4628	luad_tcga	57	deceased	0.544698182	49.01
TCGA-MP-A4SY	luad_tcga	56	deceased	0.534971429	49.31
TCGA-75-6212	luad_tcga	55	deceased	0.525244675	49.8
TCGA-05-4249	luad_tcga	54	censored	0.525244675	50.03
TCGA-78-7633	luad_tcga	53	deceased	0.515334399	50.2
TCGA-73-7499	luad_tcga	52	deceased	0.505424122	50.3
TCGA-64-5781	luad_tcga	51	censored	0.505424122	51.22
TCGA-73-4658	luad_tcga	50	deceased	0.495315639	52.56
TCGA-49-6743	luad_tcga	49	censored	0.495315639	53.25
TCGA-78-7537	luad_tcga	48	deceased	0.484996563	53.29
TCGA-55-6972	luad_tcga	47	deceased	0.474677488	53.61
TCGA-62-A46S	luad_tcga	46	deceased	0.464358412	54.3
TCGA-49-6744	luad_tcga	45	censored	0.464358412	55.29
TCGA-62-A46R	luad_tcga	44	deceased	0.453804812	56.67
TCGA-64-1676	luad_tcga	43	censored	0.453804812	56.77
TCGA-50-5944	luad_tcga	42	censored	0.453804812	57.49
TCGA-MP-A4SW	luad_tcga	41	deceased	0.442736401	58.41
TCGA-MP-A4T6	luad_tcga	40	deceased	0.431667991	58.8
TCGA-O1-A52J	luad_tcga	39	deceased	0.420599581	59.07
TCGA-50-5055	luad_tcga	38	deceased	0.409531171	60.12
TCGA-44-6778	luad_tcga	37	censored	0.409531171	61.24
TCGA-97-7553	luad_tcga	36	censored	0.409531171	61.43
TCGA-97-7552	luad_tcga	35	censored	0.409531171	63.47
TCGA-78-7159	luad_tcga	34	censored	0.409531171	64.85
TCGA-62-A46U	luad_tcga	33	censored	0.409531171	67.9
TCGA-55-6980	luad_tcga	32	censored	0.409531171	69.28
TCGA-55-6987	luad_tcga	31	censored	0.409531171	70.2
TCGA-NJ-A4YF	luad_tcga	30	censored	0.409531171	70.99
TCGA-50-5045	luad_tcga	29	deceased	0.395409407	71.42
TCGA-62-A46V	luad_tcga	28	censored	0.395409407	72.24
TCGA-MP-A5C7	luad_tcga	27	censored	0.395409407	73.85
TCGA-NJ-A4YG	luad_tcga	26	censored	0.395409407	74.28
TCGA-49-4486	luad_tcga	25	deceased	0.379593031	76.15
TCGA-78-8655	luad_tcga	24	censored	0.379593031	77.53
TCGA-75-5146	luad_tcga	23	censored	0.379593031	77.79
TCGA-50-5933	luad_tcga	22	deceased	0.362338802	78.61

Patient ID	Study ID	Number at Risk	Status	Survival Rate	Time (months)
TCGA-55-6642	luad_tcga	21	censored	0.362338802	80.45
TCGA-64-1679	luad_tcga	20	censored	0.362338802	81.73
TCGA-73-4662	luad_tcga	19	censored	0.362338802	82.62
TCGA-80-5611	luad_tcga	18	censored	0.362338802	85.25
TCGA-44-6776	luad_tcga	17	censored	0.362338802	85.94
TCGA-MP-A4T4	luad_tcga	16	deceased	0.339692627	85.97
TCGA-62-8399	luad_tcga	15	censored	0.339692627	88.57
TCGA-55-6983	luad_tcga	14	censored	0.339692627	92.74
TCGA-50-5049	luad_tcga	13	censored	0.339692627	101.64
TCGA-78-7162	luad_tcga	12	deceased	0.311384908	104.11
TCGA-55-6986	luad_tcga	11	censored	0.311384908	107.13
TCGA-75-7025	luad_tcga	10	censored	0.311384908	108.57
TCGA-78-8662	luad_tcga	9	deceased	0.276786585	110.41
TCGA-78-7153	luad_tcga	8	censored	0.276786585	119.42
TCGA-38-4626	luad_tcga	7	censored	0.276786585	120.7
TCGA-49-AARO	luad_tcga	6	censored	0.276786585	123.49
TCGA-78-7149	luad_tcga	5	censored	0.276786585	129.43
TCGA-49-AAR0	luad_tcga	4	censored	0.276786585	156.54
TCGA-78-7143	luad_tcga	3	deceased	0.18452439	162.98
TCGA-49-AARR	luad_tcga	2	censored	0.18452439	163.99
TCGA-78-8640	luad_tcga	1	censored	0.18452439	232

Table S6. Overall survival rate according to ELF3 alterations (TCGA, Firehose legacy; luad_tcga). P = 0.0085.

Patient ID	Study ID	Number at Risk	Status	Survival Rate	Time (months)
Altered Group					
TCGA-05-4244	luad_tcga	137	censored	1	0
TCGA-55-8506	luad_tcga	136	censored	1	0.36
TCGA-NJ-A55A	luad_tcga	135	censored	1	0.49
TCGA-97-7938	luad_tcga	134	deceased	0.992537313	0.59
TCGA-93-A4JO	luad_tcga	133	deceased	0.985074627	1.08
TCGA-55-8616	luad_tcga	132	censored	0.985074627	1.58
TCGA-NJ-A4YP	luad_tcga	131	censored	0.985074627	1.64
TCGA-L9-A5IP	luad_tcga	130	deceased	0.97749713	1.91
TCGA-64-5775	luad_tcga	129	deceased	0.969919633	2.04
TCGA-05-5715	luad_tcga	128	censored	0.969919633	2.04
TCGA-95-7562	luad_tcga	127	deceased	0.96228247	2.86
TCGA-05-4415	luad_tcga	126	deceased	0.954645308	2.99
TCGA-50-6591	luad_tcga	125	deceased	0.947008145	3.91
TCGA-69-7978	luad_tcga	124	censored	0.947008145	4.4
TCGA-97-8174	luad_tcga	123	deceased	0.939308892	5.39
TCGA-MP-A4T7	luad_tcga	122	deceased	0.931609639	5.49
TCGA-93-8067	luad_tcga	121	censored	0.931609639	6.11
TCGA-50-6595	luad_tcga	120	deceased	0.923846225	6.21
TCGA-L9-A443	luad_tcga	119	deceased	0.916082811	6.34
TCGA-69-7760	luad_tcga	118	censored	0.916082811	6.64

Patient ID	Study ID	Number at Risk	Status	Survival Rate	Time (months)
TCGA-91-6848	luad_tcga	117	censored	0.916082811	7.36
TCGA-55-7284	luad_tcga	116	deceased	0.908185546	7.98
TCGA-78-7536	luad_tcga	115	deceased	0.90028828	8.02
TCGA-71-6725	luad_tcga	114	censored	0.90028828	8.41
TCGA-78-7166	luad_tcga	113	deceased	0.892321127	8.48
TCGA-49-AAR9	luad_tcga	112	deceased	0.884353974	8.54
TCGA-05-5429	luad_tcga	111	deceased	0.876386821	9.03
TCGA-4B-A93V	luad_tcga	110	deceased	0.868419669	9.86
TCGA-05-4396	luad_tcga	109	deceased	0.860452516	9.95
TCGA-MP-A4TF	luad_tcga	108	deceased	0.852485363	11.04
TCGA-86-8585	luad_tcga	107	censored	0.852485363	11.6
TCGA-38-4631	luad_tcga	106	deceased	0.844443048	11.63
TCGA-86-6562	luad_tcga	105	deceased	0.836400733	12.35
TCGA-49-4490	luad_tcga	104	deceased	0.828358418	12.65
TCGA-44-8117	luad_tcga	103	censored	0.828358418	12.65
TCGA-69-8254	luad_tcga	102	censored	0.828358418	13.44
TCGA-69-7980	luad_tcga	101	censored	0.828358418	13.5
TCGA-49-4505	luad_tcga	100	deceased	0.820074834	14.06
TCGA-MP-A4TI	luad_tcga	99	deceased	0.81179125	14.09
TCGA-97-8176	luad_tcga	98	deceased	0.803507666	15.37
TCGA-55-7816	luad_tcga	97	deceased	0.795224082	15.37
TCGA-95-7947	luad_tcga	96	censored	0.795224082	15.67
TCGA-55-8302	luad_tcga	95	censored	0.795224082	15.7
TCGA-55-A494	luad_tcga	94	censored	0.795224082	15.8
TCGA-49-6742	luad_tcga	93	deceased	0.786673285	16.03
TCGA-91-8496	luad_tcga	92	censored	0.786673285	16.59
TCGA-55-8514	luad_tcga	91	censored	0.786673285	17.08
TCGA-93-7348	luad_tcga	90	censored	0.786673285	17.44
TCGA-97-A4M3	luad_tcga	89	censored	0.786673285	17.74
TCGA-J2-A4AD	luad_tcga	88	deceased	0.777733816	18.07
TCGA-55-8511	luad_tcga	87	censored	0.777733816	18.13
TCGA-44-7661	luad_tcga	86	deceased	0.7686904	18.3
TCGA-55-7903	luad_tcga	85	censored	0.7686904	18.63
TCGA-97-A4M6	luad_tcga	84	censored	0.7686904	18.66
TCGA-97-8171	luad_tcga	83	censored	0.7686904	18.66
TCGA-67-3772	luad_tcga	82	censored	0.7686904	18.82
TCGA-05-4403	luad_tcga	81	censored	0.7686904	18.99
TCGA-69-A59K	luad_tcga	80	censored	0.7686904	19.42
TCGA-44-7660	luad_tcga	79	censored	0.7686904	19.45
TCGA-62-A46P	luad_tcga	78	deceased	0.758835394	19.51
TCGA-55-8205	luad_tcga	77	censored	0.758835394	19.68
TCGA-NJ-A55R	luad_tcga	76	censored	0.758835394	19.81
TCGA-55-8512	luad_tcga	75	deceased	0.748717589	19.94
TCGA-05-4405	luad_tcga	74	censored	0.748717589	20.04
TCGA-55-A4DF	luad_tcga	73	deceased	0.738461184	20.17
TCGA-55-8508	luad_tcga	72	censored	0.738461184	20.27
TCGA-50-5044	luad_tcga	71	deceased	0.728060322	20.5
TCGA-78-7148	luad_tcga	70	deceased	0.71765946	20.57
TCGA-55-A491	luad_tcga	69	censored	0.71765946	20.57

Patient ID	Study ID	Number at Risk	Status	Survival Rate	Time (months)
TCGA-55-7726	luad_tcga	68	censored	0.71765946	21.42
TCGA-50-5935	luad_tcga	67	deceased	0.706948125	21.45
TCGA-05-5428	luad_tcga	66	censored	0.706948125	22.01
TCGA-49-AAQV	luad_tcga	65	deceased	0.696072	22.24
TCGA-44-7659	luad_tcga	64	censored	0.696072	22.7
TCGA-86-8075	luad_tcga	63	deceased	0.685023238	22.8
TCGA-55-7728	luad_tcga	62	censored	0.685023238	23.13
TCGA-55-7724	luad_tcga	61	censored	0.685023238	23.16
TCGA-44-6146	luad_tcga	60	censored	0.685023238	23.92
TCGA-05-4433	luad_tcga	59	censored	0.685023238	23.98
TCGA-86-A4JF	luad_tcga	58	deceased	0.673212493	24.21
TCGA-55-6984	luad_tcga	57	deceased	0.661401747	24.97
TCGA-44-2668	luad_tcga	56	deceased	0.649591002	25
TCGA-55-7815	luad_tcga	55	censored	0.649591002	25.39
TCGA-38-7271	luad_tcga	54	deceased	0.637561539	26.28
TCGA-73-4666	luad_tcga	53	censored	0.637561539	26.28
TCGA-86-8674	luad_tcga	52	censored	0.637561539	26.48
TCGA-44-4112	luad_tcga	51	deceased	0.625060332	26.54
TCGA-69-8453	luad_tcga	50	censored	0.625060332	26.71
TCGA-78-7145	luad_tcga	49	deceased	0.612303999	27.14
TCGA-MN-A4N1	luad_tcga	48	censored	0.612303999	27.17
TCGA-44-6147	luad_tcga	47	censored	0.612303999	27.76
TCGA-49-4487	luad_tcga	46	deceased	0.598993042	28.09
TCGA-86-8673	luad_tcga	45	censored	0.598993042	28.32
TCGA-64-5815	luad_tcga	44	censored	0.598993042	28.45
TCGA-49-4488	luad_tcga	43	deceased	0.585062972	28.55
TCGA-55-7281	luad_tcga	42	censored	0.585062972	28.65
TCGA-49-AAR4	luad_tcga	41	deceased	0.570793143	28.88
TCGA-55-7995	luad_tcga	40	censored	0.570793143	29.2
TCGA-MP-A4TE	luad_tcga	39	deceased	0.556157421	29.43
TCGA-53-7626	luad_tcga	38	deceased	0.5415217	30.52
TCGA-78-7535	luad_tcga	37	deceased	0.526885978	31.18
TCGA-MP-A4TA	luad_tcga	36	deceased	0.512250257	31.21
TCGA-55-8207	luad_tcga	35	censored	0.512250257	32.1
TCGA-J2-A4AG	luad_tcga	34	censored	0.512250257	32.46
TCGA-53-A4EZ	luad_tcga	33	censored	0.512250257	35.18
TCGA-86-7955	luad_tcga	32	censored	0.512250257	35.22
TCGA-J2-A4AE	luad_tcga	31	censored	0.512250257	35.45
TCGA-44-7667	luad_tcga	30	censored	0.512250257	36.04
TCGA-49-AARN	luad_tcga	29	deceased	0.494586455	37.29
TCGA-64-1681	luad_tcga	28	deceased	0.476922653	38.34
TCGA-78-7155	luad_tcga	27	deceased	0.459258851	38.47
TCGA-MN-A4N4	luad_tcga	26	censored	0.459258851	38.6
TCGA-73-7498	luad_tcga	25	censored	0.459258851	39.06
TCGA-78-7540	luad_tcga	24	deceased	0.440123065	39.32
TCGA-78-8648	luad_tcga	23	deceased	0.42098728	39.72
TCGA-49-AARE	luad_tcga	22	deceased	0.401851494	40.37
TCGA-55-6985	luad_tcga	21	censored	0.401851494	40.51
TCGA-62-A471	luad_tcga	20	censored	0.401851494	40.93

Patient ID	Study ID	Number at Risk	Status	Survival Rate	Time (months)
TCGA-95-7039	luad_tcga	19	censored	0.401851494	41.79
TCGA-50-6590	luad_tcga	18	deceased	0.379526411	42.31
TCGA-49-4501	luad_tcga	17	deceased	0.357201328	46.68
TCGA-05-4398	luad_tcga	16	censored	0.357201328	47.01
TCGA-05-4249	luad_tcga	15	censored	0.357201328	50.03
TCGA-78-7537	luad_tcga	14	deceased	0.331686948	53.29
TCGA-62-A46S	luad_tcga	13	deceased	0.306172567	54.3
TCGA-MP-A4T6	luad_tcga	12	deceased	0.280658187	58.8
TCGA-44-6778	luad_tcga	11	censored	0.280658187	61.24
TCGA-97-7547	luad_tcga	10	censored	0.280658187	64.55
TCGA-55-1596	luad_tcga	9	censored	0.280658187	67.84
TCGA-NJ-A4YG	luad_tcga	8	censored	0.280658187	74.28
TCGA-50-5933	luad_tcga	7	deceased	0.24056416	78.61
TCGA-62-8399	luad_tcga	6	censored	0.24056416	88.57
TCGA-80-5608	luad_tcga	5	censored	0.24056416	93.04
TCGA-78-8662	luad_tcga	4	deceased	0.18042312	110.41
TCGA-78-7143	luad_tcga	3	deceased	0.12028208	162.98
TCGA-49-AARR	luad_tcga	2	censored	0.12028208	163.99
TCGA-78-8640	luad_tcga	1	censored	0.12028208	232
Unaltered Group					
TCGA-05-4395	luad_tcga	367	deceased	0.997275204	0
TCGA-86-8281	luad_tcga	366	censored	0.997275204	0
TCGA-05-4410	luad_tcga	365	censored	0.997275204	0
TCGA-NJ-A4YI	luad_tcga	364	deceased	0.994535437	0.13
TCGA-NJ-A55O	luad_tcga	363	censored	0.994535437	0.43
TCGA-35-3615	luad_tcga	362	censored	0.994535437	0.46
TCGA-86-8672	luad_tcga	361	deceased	0.991780492	0.62
TCGA-50-6673	luad_tcga	360	deceased	0.989025546	0.72
TCGA-86-8074	luad_tcga	359	censored	0.989025546	0.79
TCGA-55-A493	luad_tcga	358	censored	0.989025546	0.92
TCGA-91-6849	luad_tcga	357	censored	0.989025546	1.15
TCGA-91-8499	luad_tcga	356	censored	0.989025546	1.18
TCGA-73-4677	luad_tcga	355	deceased	0.986239558	1.25
TCGA-91-A4BC	luad_tcga	354	censored	0.986239558	1.45
TCGA-99-8032	luad_tcga	353	censored	0.986239558	1.45
TCGA-91-6830	luad_tcga	352	censored	0.986239558	1.97
TCGA-MP-A4TC	luad_tcga	351	deceased	0.983429759	2.43
TCGA-91-6835	luad_tcga	350	censored	0.983429759	2.6
TCGA-MN-A4N5	luad_tcga	349	censored	0.983429759	2.76
TCGA-95-8494	luad_tcga	348	censored	0.983429759	2.76
TCGA-44-2666	luad_tcga	347	deceased	0.980595667	3.19
TCGA-55-A490	luad_tcga	346	deceased	0.977761576	3.25
TCGA-86-A4D0	luad_tcga	345	deceased	0.974927484	3.81
TCGA-55-6975	luad_tcga	344	deceased	0.972093393	3.88
TCGA-55-7727	luad_tcga	343	censored	0.972093393	3.91
TCGA-05-4250	luad_tcga	342	deceased	0.969251014	3.98
TCGA-86-8055	luad_tcga	341	deceased	0.966408636	4.07
TCGA-69-8255	luad_tcga	340	censored	0.966408636	4.24
TCGA-73-4670	luad_tcga	339	censored	0.966408636	4.3

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TCGA-38-A44F	luad_tcga	338	censored	0.966408636	4.37
TCGA-62-8394	luad_tcga	337	deceased	0.963540955	4.57
TCGA-86-8056	luad_tcga	336	censored	0.963540955	4.57
TCGA-67-6216	luad_tcga	335	censored	0.963540955	4.63
TCGA-05-5423	luad_tcga	334	censored	0.963540955	4.96
TCGA-55-8092	luad_tcga	333	deceased	0.960647438	5.06
TCGA-MP-A4T8	luad_tcga	332	deceased	0.957753922	5.29
TCGA-69-7765	luad_tcga	331	censored	0.957753922	5.42
TCGA-55-6712	luad_tcga	330	deceased	0.954851637	5.62
TCGA-78-7146	luad_tcga	329	deceased	0.951949353	5.68
TCGA-67-6215	luad_tcga	328	censored	0.951949353	5.72
TCGA-55-6978	luad_tcga	327	deceased	0.949038193	5.78
TCGA-78-7158	luad_tcga	326	deceased	0.946127033	5.88
TCGA-86-6851	luad_tcga	325	censored	0.946127033	5.88
TCGA-35-4123	luad_tcga	324	censored	0.946127033	5.98
TCGA-69-7974	luad_tcga	323	censored	0.946127033	6.04
TCGA-69-7761	luad_tcga	322	censored	0.946127033	6.11
TCGA-55-7914	luad_tcga	321	deceased	0.943179596	6.14
TCGA-71-8520	luad_tcga	320	deceased	0.94023216	6.9
TCGA-44-7662	luad_tcga	319	censored	0.94023216	7.16
TCGA-35-4122	luad_tcga	318	censored	0.94023216	7.39
TCGA-69-7973	luad_tcga	317	censored	0.94023216	7.56
TCGA-55-6979	luad_tcga	316	deceased	0.937256742	7.79
TCGA-05-4402	luad_tcga	315	deceased	0.934281324	8.02
TCGA-50-5072	luad_tcga	314	deceased	0.931305905	8.21
TCGA-50-5936	luad_tcga	313	deceased	0.928330487	8.44
TCGA-44-8120	luad_tcga	312	censored	0.928330487	8.54
TCGA-35-5375	luad_tcga	311	censored	0.928330487	8.67
TCGA-49-4507	luad_tcga	310	deceased	0.925335873	8.8
TCGA-05-4418	luad_tcga	309	deceased	0.922341258	9
TCGA-73-4676	luad_tcga	308	deceased	0.919346644	9.23
TCGA-50-5930	luad_tcga	307	deceased	0.916352029	9.26
TCGA-44-8119	luad_tcga	306	censored	0.916352029	9.36
TCGA-44-A47B	luad_tcga	305	censored	0.916352029	9.43
TCGA-78-7161	luad_tcga	304	deceased	0.913337713	9.56
TCGA-MP-A4TD	luad_tcga	303	deceased	0.910323397	10.09
TCGA-L9-A444	luad_tcga	302	censored	0.910323397	10.09
TCGA-50-7109	luad_tcga	301	deceased	0.907299067	10.12
TCGA-91-6831	luad_tcga	300	censored	0.907299067	10.18
TCGA-78-8660	luad_tcga	299	deceased	0.904264622	10.55
TCGA-78-7542	luad_tcga	298	deceased	0.901230177	10.55
TCGA-91-6828	luad_tcga	297	censored	0.901230177	10.61
TCGA-50-6593	luad_tcga	296	deceased	0.898185481	11.04
TCGA-MP-A4TJ	luad_tcga	295	deceased	0.895140784	11.14
TCGA-73-A9RS	luad_tcga	294	deceased	0.892096088	11.17
TCGA-55-7907	luad_tcga	293	deceased	0.889051391	11.27
TCGA-44-A47G	luad_tcga	292	censored	0.889051391	11.53
TCGA-49-6761	luad_tcga	291	censored	0.889051391	11.63
TCGA-05-4422	luad_tcga	290	censored	0.889051391	11.99

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TCGA-50-6594	luad_tcga	289	deceased	0.885975089	12.16
TCGA-91-6840	luad_tcga	288	censored	0.885975089	12.22
TCGA-55-8620	luad_tcga	287	deceased	0.882888067	12.32
TCGA-95-7944	luad_tcga	286	censored	0.882888067	12.39
TCGA-67-3774	luad_tcga	285	censored	0.882888067	12.65
TCGA-69-7979	luad_tcga	284	censored	0.882888067	13.4
TCGA-44-A4SU	luad_tcga	283	deceased	0.879768322	13.44
TCGA-62-A46Y	luad_tcga	282	deceased	0.876648576	13.6
TCGA-69-7764	luad_tcga	281	censored	0.876648576	13.6
TCGA-86-A4P7	luad_tcga	280	censored	0.876648576	13.63
TCGA-44-A4SS	luad_tcga	279	censored	0.876648576	13.63
TCGA-55-8619	luad_tcga	278	censored	0.876648576	13.67
TCGA-91-6836	luad_tcga	277	censored	0.876648576	13.7
TCGA-55-8507	luad_tcga	276	censored	0.876648576	13.73
TCGA-67-6217	luad_tcga	275	censored	0.876648576	13.86
TCGA-86-8668	luad_tcga	274	censored	0.876648576	13.9
TCGA-53-7813	luad_tcga	273	censored	0.876648576	13.93
TCGA-69-8253	luad_tcga	272	censored	0.876648576	13.99
TCGA-05-4384	luad_tcga	271	censored	0.876648576	13.99
TCGA-67-3773	luad_tcga	270	censored	0.876648576	14.03
TCGA-91-8497	luad_tcga	269	deceased	0.873389659	14.26
TCGA-50-5931	luad_tcga	268	deceased	0.870130742	14.26
TCGA-L4-A4E6	luad_tcga	267	censored	0.870130742	14.29
TCGA-97-8179	luad_tcga	266	censored	0.870130742	14.29
TCGA-55-6543	luad_tcga	265	censored	0.870130742	14.29
TCGA-55-8505	luad_tcga	264	censored	0.870130742	14.45
TCGA-L9-A50W	luad_tcga	263	deceased	0.866822261	14.52
TCGA-55-7725	luad_tcga	262	censored	0.866822261	14.52
TCGA-86-8359	luad_tcga	261	deceased	0.863501102	14.59
TCGA-62-8398	luad_tcga	260	deceased	0.860179944	14.59
TCGA-55-8615	luad_tcga	259	censored	0.860179944	14.65
TCGA-67-4679	luad_tcga	258	censored	0.860179944	14.72
TCGA-38-6178	luad_tcga	257	censored	0.860179944	14.72
TCGA-05-4417	luad_tcga	256	censored	0.860179944	14.95
TCGA-05-4434	luad_tcga	255	deceased	0.85680669	15.01
TCGA-05-5420	luad_tcga	254	censored	0.85680669	15.01
TCGA-50-5939	luad_tcga	253	deceased	0.853420102	15.11
TCGA-55-8087	luad_tcga	252	censored	0.853420102	15.18
TCGA-55-6970	luad_tcga	251	deceased	0.850020022	15.24
TCGA-44-A47A	luad_tcga	250	censored	0.850020022	15.31
TCGA-73-4668	luad_tcga	249	censored	0.850020022	15.34
TCGA-55-8299	luad_tcga	248	deceased	0.846592522	15.41
TCGA-L9-A8F4	luad_tcga	247	censored	0.846592522	15.64
TCGA-55-8097	luad_tcga	246	censored	0.846592522	15.64
TCGA-95-7948	luad_tcga	245	censored	0.846592522	15.64
TCGA-50-5051	luad_tcga	244	deceased	0.84312288	15.7
TCGA-97-7941	luad_tcga	243	censored	0.84312288	15.9
TCGA-44-A479	luad_tcga	242	censored	0.84312288	15.97
TCGA-55-7573	luad_tcga	241	censored	0.84312288	16

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TCGA-91-7771	luad_tcga	240	censored	0.84312288	16.16
TCGA-97-8177	luad_tcga	239	censored	0.84312288	16.39
TCGA-44-6779	luad_tcga	238	deceased	0.839580347	16.43
TCGA-95-7043	luad_tcga	237	deceased	0.836037814	16.52
TCGA-S2-AA1A	luad_tcga	236	censored	0.836037814	16.85
TCGA-55-8621	luad_tcga	235	censored	0.836037814	16.92
TCGA-55-8204	luad_tcga	234	censored	0.836037814	16.92
TCGA-49-6745	luad_tcga	233	censored	0.836037814	17.15
TCGA-93-A4JQ	luad_tcga	232	censored	0.836037814	17.28
TCGA-55-8301	luad_tcga	231	censored	0.836037814	17.54
TCGA-55-8614	luad_tcga	230	censored	0.836037814	17.61
TCGA-55-7911	luad_tcga	229	censored	0.836037814	17.64
TCGA-55-8510	luad_tcga	228	censored	0.836037814	17.71
TCGA-55-8094	luad_tcga	227	censored	0.836037814	17.77
TCGA-97-8172	luad_tcga	226	censored	0.836037814	17.9
TCGA-55-A57B	luad_tcga	225	censored	0.836037814	17.94
TCGA-55-8203	luad_tcga	224	censored	0.836037814	17.97
TCGA-97-8175	luad_tcga	223	censored	0.836037814	18.1
TCGA-95-A4VN	luad_tcga	222	censored	0.836037814	18.17
TCGA-55-7913	luad_tcga	221	deceased	0.832254838	18.43
TCGA-97-7937	luad_tcga	220	censored	0.832254838	18.53
TCGA-L9-A7SV	luad_tcga	219	censored	0.832254838	18.56
TCGA-95-7567	luad_tcga	218	censored	0.832254838	18.66
TCGA-44-7669	luad_tcga	217	deceased	0.828419562	18.86
TCGA-L4-A4E5	luad_tcga	216	censored	0.828419562	18.99
TCGA-93-A4JP	luad_tcga	215	censored	0.828419562	18.99
TCGA-MP-A4TK	luad_tcga	214	deceased	0.824548442	19.12
TCGA-78-7147	luad_tcga	213	deceased	0.820677323	19.25
TCGA-78-7154	luad_tcga	212	deceased	0.816806204	19.48
TCGA-44-6145	luad_tcga	211	censored	0.816806204	19.55
TCGA-55-A492	luad_tcga	210	censored	0.816806204	19.58
TCGA-55-8090	luad_tcga	209	deceased	0.81289804	19.65
TCGA-55-8091	luad_tcga	208	censored	0.81289804	19.71
TCGA-97-A4M1	luad_tcga	207	censored	0.81289804	19.74
TCGA-91-A4BD	luad_tcga	206	censored	0.81289804	19.81
TCGA-55-7994	luad_tcga	205	censored	0.81289804	19.81
TCGA-95-A4VP	luad_tcga	204	censored	0.81289804	19.88
TCGA-86-7954	luad_tcga	203	censored	0.81289804	19.88
TCGA-05-4382	luad_tcga	202	censored	0.81289804	19.94
TCGA-55-A4DG	luad_tcga	201	censored	0.81289804	19.97
TCGA-55-7283	luad_tcga	200	censored	0.81289804	20.01
TCGA-67-3771	luad_tcga	199	censored	0.81289804	20.04
TCGA-67-3770	luad_tcga	198	censored	0.81289804	20.04
TCGA-97-A4LX	luad_tcga	197	censored	0.81289804	20.17
TCGA-NJ-A7XG	luad_tcga	196	censored	0.81289804	20.27
TCGA-97-A4M2	luad_tcga	195	censored	0.81289804	20.5
TCGA-86-7714	luad_tcga	194	deceased	0.808707844	20.53
TCGA-97-8552	luad_tcga	193	censored	0.808707844	20.57
TCGA-64-1677	luad_tcga	192	deceased	0.804495824	20.63

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TCGA-97-A4M7	luad_tcga	191	censored	0.804495824	20.66
TCGA-55-A48Y	luad_tcga	190	censored	0.804495824	20.7
TCGA-97-A4M5	luad_tcga	189	censored	0.804495824	20.83
TCGA-95-A4VK	luad_tcga	188	censored	0.804495824	21.39
TCGA-55-A48Z	luad_tcga	187	censored	0.804495824	21.39
TCGA-97-A4M0	luad_tcga	186	censored	0.804495824	21.42
TCGA-86-8358	luad_tcga	185	censored	0.804495824	21.45
TCGA-99-8033	luad_tcga	184	deceased	0.800123564	21.55
TCGA-97-8547	luad_tcga	183	censored	0.800123564	21.58
TCGA-99-AA5R	luad_tcga	182	censored	0.800123564	21.62
TCGA-44-6774	luad_tcga	181	censored	0.800123564	21.62
TCGA-L9-A743	luad_tcga	180	censored	0.800123564	21.81
TCGA-78-7150	luad_tcga	179	deceased	0.7956536	21.88
TCGA-05-4425	luad_tcga	178	censored	0.7956536	21.98
TCGA-55-7576	luad_tcga	177	censored	0.7956536	22.01
TCGA-55-8208	luad_tcga	176	censored	0.7956536	22.14
TCGA-49-6767	luad_tcga	175	censored	0.7956536	22.24
TCGA-93-7347	luad_tcga	174	censored	0.7956536	22.44
TCGA-55-A48X	luad_tcga	173	censored	0.7956536	22.63
TCGA-69-7763	luad_tcga	172	censored	0.7956536	22.67
TCGA-78-7160	luad_tcga	171	deceased	0.791000655	22.9
TCGA-55-1592	luad_tcga	170	deceased	0.78634771	23.03
TCGA-86-8280	luad_tcga	169	censored	0.78634771	23.03
TCGA-55-8089	luad_tcga	168	deceased	0.781667069	23.06
TCGA-44-6148	luad_tcga	167	censored	0.781667069	23.13
TCGA-44-6775	luad_tcga	166	censored	0.781667069	23.16
TCGA-73-4659	luad_tcga	165	deceased	0.776929692	23.36
TCGA-93-A4JN	luad_tcga	164	censored	0.776929692	23.59
TCGA-55-8096	luad_tcga	163	deceased	0.772163253	23.62
TCGA-44-7672	luad_tcga	162	censored	0.772163253	23.62
TCGA-J2-8194	luad_tcga	161	censored	0.772163253	23.78
TCGA-05-4397	luad_tcga	160	deceased	0.767337232	24.01
TCGA-J2-8192	luad_tcga	159	censored	0.767337232	24.28
TCGA-86-8073	luad_tcga	158	censored	0.767337232	24.31
TCGA-MP-A4TH	luad_tcga	157	censored	0.767337232	24.34
TCGA-99-7458	luad_tcga	156	censored	0.767337232	24.54
TCGA-05-4432	luad_tcga	155	censored	0.767337232	25
TCGA-05-4430	luad_tcga	154	censored	0.767337232	25
TCGA-97-7554	luad_tcga	153	censored	0.767337232	25.46
TCGA-50-6592	luad_tcga	152	deceased	0.762288961	25.53
TCGA-05-4426	luad_tcga	151	censored	0.762288961	25.99
TCGA-55-8513	luad_tcga	150	censored	0.762288961	25.99
TCGA-78-7539	luad_tcga	149	censored	0.762288961	25.99
TCGA-05-4427	luad_tcga	148	censored	0.762288961	25.99
TCGA-86-A4P8	luad_tcga	147	censored	0.762288961	26.45
TCGA-78-7220	luad_tcga	146	deceased	0.757067804	26.51
TCGA-83-5908	luad_tcga	145	censored	0.757067804	27.07
TCGA-55-7570	luad_tcga	144	censored	0.757067804	27.07
TCGA-50-8460	luad_tcga	143	censored	0.757067804	27.23

Patient ID	Study ID	Number at Risk	Status	Survival Rate	Time (months)
TCGA-95-8039	luad_tcga	142	censored	0.757067804	27.27
TCGA-86-8671	luad_tcga	141	censored	0.757067804	27.56
TCGA-91-6847	luad_tcga	140	censored	0.757067804	27.66
TCGA-44-5645	luad_tcga	139	censored	0.757067804	27.99
TCGA-44-5644	luad_tcga	138	censored	0.757067804	28.35
TCGA-38-4629	luad_tcga	137	deceased	0.751541761	28.38
TCGA-64-5779	luad_tcga	136	censored	0.751541761	28.38
TCGA-05-5425	luad_tcga	135	censored	0.751541761	28.98
TCGA-44-7670	luad_tcga	134	censored	0.751541761	28.98
TCGA-55-8206	luad_tcga	133	censored	0.751541761	29.17
TCGA-44-7671	luad_tcga	132	censored	0.751541761	29.2
TCGA-49-4510	luad_tcga	131	deceased	0.745804801	29.43
TCGA-86-A456	luad_tcga	130	censored	0.745804801	29.43
TCGA-55-8085	luad_tcga	129	censored	0.745804801	29.7
TCGA-49-4512	luad_tcga	128	deceased	0.739978201	29.73
TCGA-62-A472	luad_tcga	127	censored	0.739978201	29.89
TCGA-05-4420	luad_tcga	126	censored	0.739978201	29.96
TCGA-05-4424	luad_tcga	125	censored	0.739978201	29.99
TCGA-73-4675	luad_tcga	124	deceased	0.734010635	30.29
TCGA-55-5899	luad_tcga	123	censored	0.734010635	30.55
TCGA-86-8669	luad_tcga	122	censored	0.734010635	30.81
TCGA-86-8278	luad_tcga	121	censored	0.734010635	31.01
TCGA-86-7701	luad_tcga	120	censored	0.734010635	31.11
TCGA-86-8279	luad_tcga	119	censored	0.734010635	31.18
TCGA-55-7227	luad_tcga	118	deceased	0.727790206	31.27
TCGA-78-7156	luad_tcga	117	deceased	0.721569777	32.06
TCGA-44-6777	luad_tcga	116	deceased	0.715349348	32.42
TCGA-86-8076	luad_tcga	115	censored	0.715349348	32.62
TCGA-55-7574	luad_tcga	114	deceased	0.709074354	32.69
TCGA-55-6982	luad_tcga	113	deceased	0.702799359	32.69
TCGA-86-7953	luad_tcga	112	censored	0.702799359	32.75
TCGA-49-4506	luad_tcga	111	deceased	0.696467834	32.82
TCGA-44-5643	luad_tcga	110	censored	0.696467834	33.28
TCGA-44-3919	luad_tcga	109	deceased	0.69007822	33.71
TCGA-44-3918	luad_tcga	108	censored	0.69007822	34.03
TCGA-55-7910	luad_tcga	107	censored	0.69007822	34.17
TCGA-53-7624	luad_tcga	106	deceased	0.683568049	34.26
TCGA-86-7711	luad_tcga	105	deceased	0.677057877	34.36
TCGA-99-8025	luad_tcga	104	censored	0.677057877	34.82
TCGA-38-4630	luad_tcga	103	deceased	0.670484499	35.25
TCGA-49-4494	luad_tcga	102	deceased	0.663911122	35.51
TCGA-75-6214	luad_tcga	101	deceased	0.657337744	36.63
TCGA-99-8028	luad_tcga	100	censored	0.657337744	36.73
TCGA-50-8459	luad_tcga	99	censored	0.657337744	36.76
TCGA-50-8457	luad_tcga	98	censored	0.657337744	36.96
TCGA-64-1680	luad_tcga	97	censored	0.657337744	36.99
TCGA-05-4390	luad_tcga	96	censored	0.657337744	36.99
TCGA-44-3396	luad_tcga	95	censored	0.657337744	37.12
TCGA-38-4627	luad_tcga	94	deceased	0.65034479	37.68

Patient ID	Study ID	Number at Risk	Status	Survival Rate	Time (months)
TCGA-86-8054	luad_tcga	93	censored	0.65034479	37.71
TCGA-86-7713	luad_tcga	92	censored	0.65034479	38.01
TCGA-44-2661	luad_tcga	91	censored	0.65034479	38.07
TCGA-44-3398	luad_tcga	90	censored	0.65034479	38.21
TCGA-55-1594	luad_tcga	89	censored	0.65034479	38.7
TCGA-64-1678	luad_tcga	88	censored	0.65034479	39.06
TCGA-62-A470	luad_tcga	87	deceased	0.642869562	39.22
TCGA-78-7152	luad_tcga	86	deceased	0.635394335	39.91
TCGA-62-8395	luad_tcga	85	censored	0.635394335	39.95
TCGA-50-5932	luad_tcga	84	deceased	0.627830116	40.57
TCGA-55-6969	luad_tcga	83	censored	0.627830116	40.7
TCGA-91-6829	luad_tcga	82	deceased	0.620173652	41.33
TCGA-MP-A4T9	luad_tcga	81	deceased	0.612517187	41.56
TCGA-50-6597	luad_tcga	80	deceased	0.604860722	41.66
TCGA-44-2662	luad_tcga	79	censored	0.604860722	42.05
TCGA-97-7546	luad_tcga	78	censored	0.604860722	42.21
TCGA-62-8397	luad_tcga	77	censored	0.604860722	42.35
TCGA-55-6968	luad_tcga	76	deceased	0.596902028	42.48
TCGA-44-2665	luad_tcga	75	censored	0.596902028	42.74
TCGA-64-5778	luad_tcga	74	censored	0.596902028	42.87
TCGA-44-2655	luad_tcga	73	censored	0.596902028	43.5
TCGA-75-5147	luad_tcga	72	censored	0.596902028	43.79
TCGA-44-2657	luad_tcga	71	censored	0.596902028	44.38
TCGA-38-4632	luad_tcga	70	deceased	0.588374856	44.58
TCGA-44-2659	luad_tcga	69	censored	0.588374856	44.91
TCGA-05-4389	luad_tcga	68	censored	0.588374856	44.97
TCGA-55-6981	luad_tcga	67	deceased	0.579593142	45.3
TCGA-55-6971	luad_tcga	66	censored	0.579593142	45.99
TCGA-44-2656	luad_tcga	65	censored	0.579593142	46.94
TCGA-NJ-A4YQ	luad_tcga	64	censored	0.579593142	47.04
TCGA-62-A46O	luad_tcga	63	deceased	0.570393251	47.77
TCGA-50-5941	luad_tcga	62	censored	0.570393251	48.42
TCGA-55-1595	luad_tcga	61	censored	0.570393251	48.59
TCGA-38-4628	luad_tcga	60	deceased	0.560886697	49.01
TCGA-62-8402	luad_tcga	59	deceased	0.551380143	49.21
TCGA-50-5068	luad_tcga	58	deceased	0.541873588	49.24
TCGA-MP-A4SY	luad_tcga	57	deceased	0.532367034	49.31
TCGA-75-6212	luad_tcga	56	deceased	0.52286048	49.8
TCGA-78-7633	luad_tcga	55	deceased	0.513353926	50.2
TCGA-73-7499	luad_tcga	54	deceased	0.503847372	50.3
TCGA-64-5781	luad_tcga	53	censored	0.503847372	51.22
TCGA-73-4658	luad_tcga	52	deceased	0.494157999	52.56
TCGA-49-6743	luad_tcga	51	censored	0.494157999	53.25
TCGA-55-6972	luad_tcga	50	deceased	0.484274839	53.61
TCGA-49-6744	luad_tcga	49	censored	0.484274839	55.29
TCGA-49-4514	luad_tcga	48	censored	0.484274839	55.85
TCGA-62-A46R	luad_tcga	47	deceased	0.473971119	56.67
TCGA-64-1676	luad_tcga	46	censored	0.473971119	56.77
TCGA-50-5944	luad_tcga	45	censored	0.473971119	57.49

Patient ID	Study ID	Number at Risk	Status	Survival Rate	Time (months)
TCGA-MP-A4SW	luad_tcga	44	deceased	0.463199048	58.41
TCGA-O1-A52J	luad_tcga	43	deceased	0.452426977	59.07
TCGA-50-5055	luad_tcga	42	deceased	0.441654906	60.12
TCGA-50-5942	luad_tcga	41	censored	0.441654906	60.68
TCGA-97-7553	luad_tcga	40	censored	0.441654906	61.43
TCGA-49-AAR3	luad_tcga	39	censored	0.441654906	62.19
TCGA-97-7552	luad_tcga	38	censored	0.441654906	63.47
TCGA-78-7159	luad_tcga	37	censored	0.441654906	64.85
TCGA-75-5125	luad_tcga	36	deceased	0.429386715	66.59
TCGA-62-A46U	luad_tcga	35	censored	0.429386715	67.9
TCGA-55-6980	luad_tcga	34	censored	0.429386715	69.28
TCGA-55-6987	luad_tcga	33	censored	0.429386715	70.2
TCGA-NJ-A4YF	luad_tcga	32	censored	0.429386715	70.99
TCGA-50-5045	luad_tcga	31	deceased	0.41553553	71.42
TCGA-62-A46V	luad_tcga	30	censored	0.41553553	72.24
TCGA-49-AAR2	luad_tcga	29	censored	0.41553553	73.06
TCGA-MP-A5C7	luad_tcga	28	censored	0.41553553	73.85
TCGA-49-4486	luad_tcga	27	deceased	0.400145325	76.15
TCGA-78-8655	luad_tcga	26	censored	0.400145325	77.53
TCGA-75-5146	luad_tcga	25	censored	0.400145325	77.79
TCGA-55-6642	luad_tcga	24	censored	0.400145325	80.45
TCGA-64-1679	luad_tcga	23	censored	0.400145325	81.73
TCGA-73-4662	luad_tcga	22	censored	0.400145325	82.62
TCGA-75-6206	luad_tcga	21	censored	0.400145325	85.09
TCGA-80-5611	luad_tcga	20	censored	0.400145325	85.25
TCGA-44-6776	luad_tcga	19	censored	0.400145325	85.94
TCGA-MP-A4T4	luad_tcga	18	deceased	0.37791503	85.97
TCGA-MP-A4SV	luad_tcga	17	deceased	0.355684734	86.07
TCGA-64-5774	luad_tcga	16	censored	0.355684734	87.91
TCGA-78-7167	luad_tcga	15	deceased	0.331972418	88.07
TCGA-55-6983	luad_tcga	14	censored	0.331972418	92.74
TCGA-38-4625	luad_tcga	13	censored	0.331972418	97.67
TCGA-75-7027	luad_tcga	12	censored	0.331972418	100.49
TCGA-50-5049	luad_tcga	11	censored	0.331972418	101.64
TCGA-78-7162	luad_tcga	10	deceased	0.298775176	104.11
TCGA-55-6986	luad_tcga	9	censored	0.298775176	107.13
TCGA-75-7025	luad_tcga	8	censored	0.298775176	108.57
TCGA-78-7153	luad_tcga	7	censored	0.298775176	119.42
TCGA-38-4626	luad_tcga	6	censored	0.298775176	120.7
TCGA-49-AARO	luad_tcga	5	censored	0.298775176	123.49
TCGA-78-7149	luad_tcga	4	censored	0.298775176	129.43
TCGA-49-AAR0	luad_tcga	3	censored	0.298775176	156.54
TCGA-49-AARQ	luad_tcga	2	censored	0.298775176	221.16
TCGA-78-7163	luad_tcga	1	censored	0.298775176	238.11

Table S7. Over-represented genes (n = 46) identified by ChIP-seq peak analysis in A549 cells (TST/DMSO and ANF/DMSO peak intensity ratios).

No.	Gene	Chromosome Peak Area	A549 TST/DMSO	A549 ANF/DMSO
1	ZNF648	chr1:181998612-181999012	93.19	38.49
2	PAX2	chr10:102575322-102575722	70.73	5.81
3	FGF8	chr10:103499843-103500243	24.63	29.12
4	BAG3	chr10:121401851-121402251	47.64	21.31
5	LRRC27	chr10:134184924-134185324	18.32	1.84
6	MICAL2	chr11:12284755-12285155	6.95	25.43
7	FOXJ2	chr12:8183714-8184428	20.76	1.70
8	SP7	chr12:53718958-53719358	2.66	11.80
9	RFX4	chr12:107113891-107114291	23.28	29.00
10	NOS1	chr12:117786424-117786824	37.44	44.85
11	ARID4A	chr14:58766155-58766555	28.51	15.50
12	ASB7	chr15:101244124-101244785	39.88	5.88
13	SETD1A	chr16:30968480-30968880	33.38	4.75
14	SALL1	chr16:51539928-51540328	5.60	26.44
15	IRF8	chr16:86082485-86082885	44.12	24.21
16	HOXB2	chr17:46620704-46621104	53.50	1.48
17	BPTF	chr17:65875091-65875491	10.83	9.03
18	SOX9	chr17:69953404-69953804	57.38	3.45
19	FOXJ1	chr17:74131470-74131870	31.31	39.38
20	SMAD2	chr18:45424775-45425175	44.12	43.84
21	SSBP4	chr19:18527472-18527872	33.66	13.83
22	MYT1L	chr2:2643119-2643519	71.63	10.48
23	TAF1B	chr2:9996293-9996693	18.05	11.26
24	DTNB	chr2:25896762-25897162	30.23	3.09
25	EPAS1	chr2:46583354-46583754	33.38	1.63
26	HAT1	chr2:172823993-172824393	90.22	2.24
27	JAG1	chr20:10783881-10784281	1.68	24.10
28	MMP9	chr20:44642568-44642968	5.51	23.98
29	TFAP2C	chr20:55344665-55345065	61.17	35.25
30	TMPRSS6	chr22:37465755-37466155	4.36	43.96
31	MAFF	chr22:38607331-38607731	4.28	33.02
32	CBX7	chr22:39548658-39549058	53.50	21.64
33	FOXP1	chr3:70588435-70588835	11.19	19.19
34	ZFP42	chr4:188931671-188932071	86.70	25.99
35	BDP1	chr5:70744176-70744576	33.02	20.30
36	F2RL1	chr5:76091562-76091962	17.33	10.71
37	EGR1	chr5:137800543-137800943	19.85	105.32
38	ZNF354B	chr5:178287379-178287779	21.75	8.59
39	AUTS2	chr7:70084118-70084518	52.69	46.52
40	MAGI2	chr7:78265844-78266244	15.79	20.86
41	HGF	chr7:81347004-81347404	4.79	26.77
42	KDM4C	chr9:6866925-6867325	42.04	7.80
43	RORB	chr9:76834974-76835374	48.00	7.92
44	ZNF462	chr9:109168399-109168799	46.92	9.26
45	MED27	chr9:134717982-134718382	19.04	1.53
46	FOXO4	chrX:70315377-70315777	45.11	18.26

Table S8. Counter-represented genes (n = 491) identified by ChIP-seq peak analysis in A549 cells (TST/DMSO and ANF/DMSO peak intensity ratios).

No.	Gene	Chromosome Peak Area	A549 TST/DMSO	A549 ANF/DMSO
1	PRDM16	chr1:3360029-3360429	0.04	4.35
2	ZBTB48	chr1:6646606-6647006	0.07	37.82
3	CAMTA1	chr1:7288302-7288702	63.06	0.04
4	CAMTA1	chr1:7532279-7532679	0.03	2.37
5	CAMTA1	chr1:7622687-7623087	0.13	13.21
6	CAMTA1	chr1:7700296-7701009	0.04	1.94
7	PAX7	chr1:18901997-18902397	13.27	0.06
8	GRHL3	chr1:24669962-24670362	0.04	10.60
9	RUNX3	chr1:25256052-25256452	0.03	34.47
10	RPS6KA1	chr1:26855315-26855715	0.02	2.47
11	AKIRIN1	chr1:39457013-39457413	11.28	0.10
12	HEYL	chr1:40104806-40105206	0.06	5.57
13	RLF	chr1:40708600-40709000	0.04	18.51
14	ZNF691	chr1:43352091-43352491	0.05	15.62
15	SSBP3	chr1:54740001-54740401	0.03	29.79
16	SSBP3	chr1:54777499-54777899	38.80	0.05
17	SSBP3	chr1:54872195-54872595	0.03	6.36
18	ACOT11	chr1:55089790-55090190	0.17	30.12
19	MYSM1	chr1:59200833-59201233	31.04	0.06
20	BARHL2	chr1:91112839-91113239	0.03	21.53
21	FNBP1L	chr1:93914600-93915000	0.08	37.26
22	ASH1L	chr1:155499620-155500020	0.10	25.77
23	USF1	chr1:161015336-161015736	0.03	4.13
24	LMX1A	chr1:165302364-165302764	0.23	16.17
25	POU2F1	chr1:167257715-167258115	65.23	0.09
26	TBX19	chr1:168281918-168282318	0.26	11.82
27	LHX4	chr1:180230432-180230832	0.03	21.42
28	CDC73	chr1:193103491-193103891	0.05	18.41
29	CDC73	chr1:194489604-194490004	0.09	27.44
30	PKP1	chr1:201278615-201279015	57.11	0.03
31	ELF3	chr1:202000256-202000656	0.05	2.90
32	SOX13	chr1:204090912-204091312	0.03	40.39
33	NSL1	chr1:212962600-212963000	2.43	0.05
34	PARP1	chr1:226596239-226596639	0.06	46.63
35	ZNF678	chr1:227792603-227793003	0.18	25.66
36	ZNF678	chr1:227820340-227820740	0.03	5.02
37	WNT3A	chr1:228192094-228192494	0.05	2.51
38	WNT3A	chr1:228223525-228223925	0.02	9.79
39	NUP133	chr1:229615186-229615586	57.29	0.03
40	NUP133	chr1:229623607-229624007	0.09	20.86
41	ARID4B	chr1:235412317-235412717	0.14	36.59
42	ARID4B	chr1:235412738-235413138	0.04	16.29
43	HNRNPU	chr1:245021070-245021470	0.06	3.23
44	SMYD3	chr1:246002268-246002668	0.03	4.33
45	SH3BP5L	chr1:249116962-249117362	23.10	0.05
46	KLF6	chr10:3735495-3735895	0.12	1.89
47	KLF6	chr10:4082145-4082545	0.08	24.76

No.	Gene	Chromosome Peak Area	A549 TST/DMSO	A549 ANF/DMSO
48	KLF6	chr10:4152077-4152477	41.68	0.06
49	TAF3	chr10:7868977-7869377	0.04	17.07
50	TAF3	chr10:7957250-7957951	0.03	1.48
51	TAF3	chr10:7974518-7974918	0.07	17.18
52	TAF3	chr10:8020750-8021150	49.89	0.04
53	GATA3	chr10:8097732-8098132	0.04	23.54
54	GATA3	chr10:8724053-8724453	66.31	0.04
55	GATA3	chr10:8753161-8753561	0.03	10.95
56	ITGA8	chr10:15608484-15608884	0.06	17.96
57	MLLT10	chr10:21823603-21824003	28.15	0.02
58	CREM	chr10:35409953-35410353	26.80	0.03
59	CREM	chr10:35433860-35434260	0.02	12.05
60	ZNF33B	chr10:43072225-43072625	0.08	12.60
61	ERCC6	chr10:50650301-50650701	0.05	7.02
62	PRF1	chr10:72390211-72390611	10.47	0.08
63	ZMIZ1	chr10:80886516-80886916	0.03	12.60
64	ZMIZ1	chr10:81032645-81033045	0.10	19.86
65	HHEX	chr10:94450050-94450450	0.04	34.03
66	ZNF518A	chr10:97889475-97889875	0.05	2.54
67	ERLIN1	chr10:101890196-101890596	0.06	41.50
68	CHUK	chr10:101987500-101987900	43.67	0.37
69	PAX2	chr10:102489432-102489832	0.04	2.04
70	FGF8	chr10:103539662-103540062	23.73	0.11
71	PITX3	chr10:103989666-103990066	0.04	1.56
72	CTBP2	chr10:126747896-126748664	51.34	0.03
73	EBF3	chr10:131764587-131764987	63.06	0.05
74	PWWP2B	chr10:134232098-134232498	0.03	22.20
75	IRF7	chr11:614846-615246	0.02	2.44
76	DEAF1	chr11:642478-642878	0.22	12.70
77	ASCL2	chr11:2257928-2258328	29.42	0.04
78	ASCL2	chr11:2280852-2281252	0.03	7.58
79	CD81	chr11:2372845-2373245	0.02	31.35
80	CD81	chr11:2404926-2405326	0.07	27.22
81	LMO1	chr11:8332332-8332732	0.05	19.86
82	NRIP3	chr11:9025797-9026197	0.03	18.85
83	MICAL2	chr11:12296011-12296411	0.13	17.85
84	TEAD1	chr11:12769746-12770146	0.03	9.14
85	TEAD1	chr11:12840911-12841311	9.39	0.05
86	LMO2	chr11:33891862-33892262	0.07	23.31
87	ALX4	chr11:44285678-44286078	0.04	34.47
88	ALX4	chr11:44337636-44338036	0.03	3.30
89	ALX4	chr11:44355556-44355956	18.23	0.59
90	ALX4	chr11:44383617-44384017	14.98	0.09
91	ALX4	chr11:44418927-44419327	18.77	0.05
92	CREB3L1	chr11:46289030-46289430	0.36	9.59
93	LRP5	chr11:68093968-68094368	0.02	2.04
94	LRP5	chr11:68121827-68122227	57.74	0.10
95	GAL	chr11:68443454-68443854	0.06	38.60
96	KMT2A	chr11:118305859-118306259	0.09	29.34

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97	CDON	chr11:125911874-125912274	0.03	23.09
98	BARX2	chr11:129217881-129218281	48.18	0.05
99	FOXM1	chr12:2978226-2978626	1.00	0.71
100	TEAD4	chr12:3073366-3073766	0.02	23.65
101	LRP6	chr12:12420114-12420514	0.03	2.89
102	VDR	chr12:48327454-48327854	0.05	44.29
103	ATF1	chr12:51157281-51157681	0.03	2.75
104	NR4A1	chr12:52444474-52444874	0.05	1.68
105	RARG	chr12:53619365-53619765	0.36	37.82
106	STAT6	chr12:57502474-57502874	0.04	25.10
107	ANKS1B	chr12:99210271-99210671	42.04	0.04
108	ANKS1B	chr12:100277825-100278225	63.06	0.04
109	RFX4	chr12:106989147-106989547	0.03	37.71
110	TBX3	chr12:115032986-115033386	82.10	0.04
111	TBX3	chr12:115325430-115325830	79.03	0.04
112	TBX3	chr12:115390590-115390990	0.03	34.81
113	MED13L	chr12:116144574-116144974	0.07	7.69
114	MED13L	chr12:116439560-116439960	0.20	20.08
115	NOS1	chr12:117804065-117804465	72.81	0.04
116	RNF10	chr12:120972416-120972816	0.03	46.07
117	PSMD9	chr12:122348271-122348671	0.04	2.59
118	ZNF84	chr12:133614131-133614531	21.21	0.04
119	HMGB1	chr13:31003145-31003545	51.25	0.09
120	FOXO1	chr13:41107447-41107847	0.07	26.33
121	TNFSF11	chr13:43148866-43149266	0.19	1.39
122	KLF5	chr13:73685784-73686184	22.11	0.11
123	KLF12	chr13:74235549-74235949	0.11	9.03
124	KLF12	chr13:74710130-74710530	0.14	1.58
125	SOX1	chr13:112575733-112576133	1.94	0.08
126	TFDP1	chr13:114238382-114238782	0.07	2.90
127	ZNF219	chr14:21572218-21572618	0.07	2.89
128	HIF1A	chr14:62162089-62162489	0.04	62.81
129	ESR2	chr14:64804808-64805208	0.04	9.45
130	FOS	chr14:75695222-75695622	0.05	7.02
131	JDP2	chr14:75895391-75895791	0.11	1.40
132	ESRRB	chr14:76957459-76957859	0.06	13.05
133	ESRRB	chr14:77040532-77040932	0.04	29.67
134	IRF2BPL	chr14:77422920-77423320	0.09	34.47
135	IRF2BPL	chr14:77499637-77500037	0.17	42.62
136	ASB2	chr14:94413596-94413996	0.03	29.12
137	TUNAR	chr14:96361952-96362352	0.03	4.24
138	BCL11B	chr14:99509465-99509865	23.73	0.04
139	BCL11B	chr14:99531030-99531430	79.30	0.04
140	SETD3	chr14:99817074-99817474	0.05	1.57
141	YY1	chr14:100707967-100708367	0.04	13.01
142	KLF13	chr15:31571154-31571554	9.05	0.03
143	KLF13	chr15:31673982-31674382	0.05	2.90
144	GREM1	chr15:33010405-33010805	0.04	21.53
145	ZNF770	chr15:35280426-35280826	33.02	0.04

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146	ZNF770	chr15:35297798-35298198	0.03	21.08
147	MGA	chr15:41913155-41913555	3.35	0.05
148	ONECUT1	chr15:53099197-53099597	32.12	0.06
149	CCPG1	chr15:55653749-55654149	0.05	25.32
150	NEDD4	chr15:56250928-56251328	0.06	14.86
151	NEDD4	chr15:56318522-56318922	0.15	27.89
152	RORA	chr15:60884937-60885337	0.02	26.10
153	MAP2K5	chr15:67829186-67829586	1.50	0.33
154	MAP2K5	chr15:67868239-67868639	45.56	0.05
155	ARNT2	chr15:80724112-80724512	49.16	0.03
156	ZSCAN2	chr15:85167288-85167688	0.04	16.73
157	RGMA	chr15:93586404-93586804	0.12	36.93
158	RGMA	chr15:93880896-93881296	13.72	0.02
159	NR2F2	chr15:96895614-96896014	5.06	0.08
160	NR2F2	chr15:96900243-96900643	0.05	59.58
161	ASB7	chr15:101193274-101193674	0.05	13.27
162	E4F1	chr16:2275789-2276189	0.08	34.58
163	NLRC3	chr16:3599226-3599626	0.14	19.19
164	ZNF768	chr16:30545572-30545972	0.03	1.96
165	ZNF785	chr16:30596264-30596664	0.03	22.53
166	ZNF689	chr16:30610507-30611187	0.07	21.19
167	RNF40	chr16:30773074-30773474	0.03	1.54
168	RNF40	chr16:30786787-30787187	0.03	29.23
169	ZNF629	chr16:30798595-30798995	0.13	25.18
170	SETD1A	chr16:30968980-30969380	9.03	0.05
171	BCKDK	chr16:31121361-31121761	0.32	7.58
172	ZNF423	chr16:49829372-49829772	0.07	36.77
173	ZNF423	chr16:49872519-49872919	15.52	0.07
174	TOX3	chr16:52580931-52581331	0.17	4.36
175	NLRC5	chr16:57094618-57095018	0.03	47.08
176	NLRC5	chr16:57100248-57100648	25.72	0.04
177	TAT	chr16:71598828-71599228	0.05	19.34
178	ZFHX3	chr16:72563200-72563600	0.06	17.18
179	ZFHX3	chr16:72639926-72640326	0.16	23.43
180	ZFHX3	chr16:73028361-73028761	2.96	0.04
181	MAF	chr16:79468011-79468411	1.96	0.02
182	CYB5D2	chr17:4047091-4047491	0.05	25.66
183	PELP1	chr17:4566955-4567355	25.27	0.05
184	MED11	chr17:4632369-4632961	15.97	0.12
185	PER1	chr17:8053324-8053724	0.36	2.94
186	ZNF624	chr17:16569983-16570383	0.06	5.02
187	FOXN1	chr17:26854894-26855294	0.04	8.81
188	LHX1	chr17:35196661-35197061	0.08	21.64
189	CDK12	chr17:37638924-37639324	0.10	20.64
190	RARA	chr17:38470786-38471186	0.04	1.80
191	RARA	chr17:38474414-38474814	0.05	15.95
192	RARA	chr17:38498231-38498631	4.79	0.06
193	RARA	chr17:38512556-38512956	0.04	27.78
194	JUP	chr17:39832985-39833720	0.09	7.47

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195	STAT3	chr17:40469840-40470240	0.05	5.09
196	EZH1	chr17:40872745-40873145	0.06	25.77
197	MEOX1	chr17:41711981-41712381	0.05	6.17
198	HDAC5	chr17:42159497-42159897	41.32	0.08
199	HDAC5	chr17:42160829-42161229	0.03	12.60
200	CDK5RAP3	chr17:46048377-46048777	11.38	0.02
201	HOXB3	chr17:46640183-46640583	0.05	21.53
202	NOG	chr17:54670730-54671130	18.23	0.05
203	BCAS3	chr17:59313684-59314084	0.03	3.01
204	HELZ	chr17:65063310-65063710	0.03	1.45
205	BPTF	chr17:65820922-65821322	0.08	26.14
206	BPTF	chr17:65895487-65895887	0.32	10.93
207	FOXJ1	chr17:74124261-74124661	68.21	0.21
208	JMJD6	chr17:74721729-74722129	27.97	0.05
209	EIF4A3	chr17:78120422-78120822	0.03	1.37
210	EIF4A3	chr17:78123203-78123603	0.13	25.43
211	MRPL12	chr17:79673941-79674341	0.06	8.04
212	FOXK2	chr17:80559525-80559925	0.05	22.20
213	PIK3C3	chr18:39324664-39325064	0.12	16.51
214	SMAD2	chr18:45486504-45486904	0.05	1.83
215	ZBTB7C	chr18:45698839-45699239	60.81	0.03
216	TCF4	chr18:53233133-53233533	0.07	16.84
217	ZNF407	chr18:72509032-72509432	0.05	8.81
218	ZNF516	chr18:74070123-74070523	0.15	26.10
219	ZNF236	chr18:74559369-74559769	0.05	17.68
220	ZNF236	chr18:74639047-74639447	0.11	13.50
221	NFATC1	chr18:77151994-77152394	0.03	25.43
222	SBNO2	chr19:1122803-1123203	0.05	6.89
223	TCF3	chr19:1636634-1637034	0.04	5.80
224	AP3D1	chr19:2123699-2124099	4.34	0.03
225	ZNF57	chr19:2906840-2907240	40.96	0.04
226	NFIC	chr19:3358478-3358878	0.05	2.03
227	NFIC	chr19:3384382-3384782	0.12	23.31
228	NFIC	chr19:3397149-3397549	0.10	15.62
229	UHRF1	chr19:4910777-4911177	0.06	41.17
230	SAFB	chr19:5623969-5624369	0.03	25.55
231	GTF2F1	chr19:6381335-6381735	0.07	17.51
232	ZNF557	chr19:7088879-7089279	0.03	22.76
233	ZNF44	chr19:12326804-12327204	0.08	50.20
234	KLF2	chr19:16435546-16435946	12.10	0.43
235	ZNF208	chr19:22193193-22193593	0.03	32.80
236	ZNF676	chr19:22395062-22395462	0.04	30.34
237	ZNF726	chr19:24106005-24106405	25.36	0.08
238	ZNF507	chr19:32784492-32784892	17.42	0.06
239	ZNF30	chr19:35416120-35416520	0.03	17.29
240	ZBTB32	chr19:36207280-36207680	0.06	3.17
241	ZNF529	chr19:37064281-37064681	0.06	47.86
242	ACTN4	chr19:39189805-39190205	0.05	36.15
243	ACTN4	chr19:39193550-39193950	0.05	2.45

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244	MED29	chr19:39888343-39888743	6.68	0.02
245	SERTAD1	chr19:40931506-40931906	43.94	0.04
246	POU2F2	chr19:42617603-42618003	84.98	0.07
247	ZNF234	chr19:44653118-44653518	0.04	41.39
248	ZNF227	chr19:44711638-44712312	0.05	11.15
249	ZNF180	chr19:45004292-45004692	0.01	1.67
250	LIG1	chr19:48622281-48622681	0.04	41.72
251	LIG1	chr19:48673195-48673595	0.28	1.71
252	TEAD2	chr19:49865284-49865684	0.09	7.28
253	MED25	chr19:50321452-50321852	0.21	16.91
254	PTOV1	chr19:50359224-50359624	0.02	20.97
255	IL4I1	chr19:50426977-50427377	0.11	53.44
256	ZNF83	chr19:53192991-53193391	0.03	1.67
257	ZNF415	chr19:53608868-53609268	0.06	15.73
258	ZNF628	chr19:55981760-55982160	0.36	23.20
259	ZNF71	chr19:57138362-57138762	0.26	26.88
260	ZNF835	chr19:57178721-57179121	0.02	10.60
261	ZNF17	chr19:57912015-57912415	0.17	2.74
262	ZNF17	chr19:57933606-57934006	62.43	0.05
263	ZNF8	chr19:58790580-58790980	0.12	1.34
264	ZNF324	chr19:58977853-58978253	0.03	14.69
265	MYT1L	chr2:2506399-2506799	0.06	36.48
266	MYT1L	chr2:2669469-2669869	0.19	1.70
267	TAF1B	chr2:9948284-9948684	0.11	10.93
268	KIF3C	chr2:26194906-26195306	8.49	0.02
269	ZNF512	chr2:27814234-27814634	0.04	7.01
270	SIX3	chr2:45125456-45125856	0.07	1.35
271	SIX2	chr2:45240996-45241396	0.04	5.43
272	EPAS1	chr2:46556114-46556825	6.65	0.03
273	ASB3	chr2:53580455-53580855	13.54	0.37
274	ASB3	chr2:53669820-53670220	0.03	3.16
275	ASB3	chr2:53943626-53944026	54.49	0.04
276	MEIS1	chr2:66673106-66673506	0.08	28.67
277	MEIS1	chr2:66805224-66805624	8.22	0.06
278	PPP3R1	chr2:68416006-68416406	68.75	0.08
279	DYSF	chr2:71831527-71831927	0.03	11.60
280	TET3	chr2:74211327-74211727	0.04	1.59
281	TLX2	chr2:74740339-74740739	32.66	0.06
282	TCF7L1	chr2:85347268-85347668	18.05	0.07
283	TCF7L1	chr2:85540093-85540854	0.04	13.94
284	AFF3	chr2:100312999-100313399	0.03	3.68
285	PDCL3	chr2:101172066-101172466	0.10	48.42
286	PDCL3	chr2:101245818-101246218	0.04	3.07
287	EN1	chr2:119603851-119604251	0.07	21.08
288	EPC2	chr2:149388488-149388888	0.04	17.29
289	NR4A2	chr2:156543016-156543416	19.13	0.08
290	ACVR1	chr2:158773410-158773810	0.05	42.06
291	DLX2	chr2:173116937-173117337	0.08	30.79
292	DLX2	chr2:173118162-173118562	33.57	0.07

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293	SP3	chr2:174740604-174741004	0.06	51.21
294	NEUROD1	chr2:182549846-182550246	0.05	29.79
295	HECW2	chr2:197431278-197431678	0.06	7.56
296	BMPR2	chr2:203285562-203285962	0.06	12.27
297	BMPR2	chr2:203352501-203352901	0.03	11.82
298	IHH	chr2:219920270-219920781	15.34	0.04
299	PTPRN	chr2:220178875-220179574	13.54	0.05
300	PID1	chr2:230095613-230096013	47.28	0.05
301	PID1	chr2:230172418-230172818	0.05	19.19
302	PTMA	chr2:232520699-232521099	0.03	21.53
303	ASB18	chr2:237110762-237111162	0.04	60.69
304	HDAC4	chr2:239958467-239958867	0.05	5.46
305	HDAC4	chr2:240018839-240019239	0.05	38.04
306	HDAC4	chr2:240281762-240282162	0.06	21.86
307	HDAC4	chr2:240383408-240383808	0.05	4.26
308	HDAC4	chr2:240408102-240408502	0.07	22.87
309	ZNF343	chr20:2489094-2489494	0.34	10.87
310	MAVS	chr20:3847946-3848346	0.03	36.15
311	SMOX	chr20:4065873-4066273	0.03	42.28
312	SMOX	chr20:4130371-4130771	0.05	2.54
313	BMP2	chr20:6688482-6688882	31.31	0.07
314	BMP2	chr20:7021351-7021751	37.08	0.04
315	RRBP1	chr20:17614966-17615366	0.03	3.34
316	RRBP1	chr20:17656408-17656808	0.03	62.81
317	NKX2-2	chr20:21486535-21486935	0.07	1.55
318	NKX2-2	chr20:21537950-21538350	1.77	0.05
319	E2F1	chr20:32272959-32273359	0.05	4.84
320	PXMP4	chr20:32303824-32304224	0.06	30.01
321	PXMP4	chr20:32307835-32308235	0.04	29.45
322	SRC	chr20:36008815-36009215	0.02	29.00
323	LPIN3	chr20:39969378-39969778	0.36	10.37
324	NCOA3	chr20:46252350-46252750	0.26	2.67
325	SNAI1	chr20:48611048-48611448	3.23	0.05
326	CEBPB	chr20:48805594-48805994	0.04	40.61
327	CEBPB	chr20:48807501-48807901	2.01	0.03
328	NFATC2	chr20:49926205-49926605	0.03	18.85
329	SALL4	chr20:50532317-50532717	16.06	0.07
330	ZFP64	chr20:50601835-50602235	47.37	0.19
331	BMP7	chr20:55759953-55760353	2.08	0.04
332	BMP7	chr20:55841620-55842020	0.06	24.60
333	CTCFL	chr20:56040122-56040522	37.99	0.06
334	TAF4	chr20:60540999-60541399	0.03	31.91
335	TAF4	chr20:60665339-60665739	30.95	0.03
336	CABLES2	chr20:60964173-60964573	0.13	25.32
337	BHLHE23	chr20:61630408-61630808	27.43	0.54
338	ZBTB46	chr20:62400008-62400408	0.13	4.46
339	ZBTB46	chr20:62434179-62434579	0.07	18.07
340	MYT1	chr20:62790936-62791336	0.07	42.50
341	MYT1	chr20:62861194-62861594	0.05	29.23

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342	ERG	chr21:39829266-39829666	24.36	0.04
343	ERG	chr21:39873548-39873948	0.12	47.75
344	ERG	chr21:39975708-39976108	6.05	0.07
345	ERG	chr21:40033215-40033615	0.05	2.76
346	PKNOX1	chr21:44395257-44395657	0.04	12.38
347	ZNF74	chr22:20709115-20709515	0.06	17.18
348	SGSM1	chr22:25212264-25212664	24.82	0.03
349	MRTFA	chr22:40845810-40846210	0.02	18.18
350	RAF1	chr3:12726824-12727224	6.86	0.05
351	WNT7A	chr3:13832383-13832783	0.09	33.13
352	WNT7A	chr3:13920758-13921158	0.04	19.52
353	ANKRD28	chr3:15900481-15900881	0.06	11.26
354	EOMES	chr3:27770299-27770699	0.06	12.49
355	CSRNP1	chr3:39188643-39189043	0.36	25.66
356	RAD54L2	chr3:51571450-51571850	0.09	2.79
357	MITF	chr3:69986982-69987382	0.03	11.60
358	FOXP1	chr3:71213345-71213745	0.04	5.70
359	FOXP1	chr3:71492551-71492951	39.52	0.03
360	FOXP1	chr3:71538113-71538513	70.82	0.04
361	POU1F1	chr3:87481542-87481942	66.49	0.06
362	POU1F1	chr3:87670507-87670907	28.87	0.21
363	NFKBIZ	chr3:101568183-101568583	0.24	1.45
364	NAA50	chr3:113454604-113455004	69.83	0.06
365	DRD3	chr3:113861020-113861420	0.20	23.76
366	GSK3B	chr3:119812618-119813018	0.04	17.85
367	ZNF148	chr3:125094066-125094466	0.03	5.00
368	CNBP	chr3:128901610-128902010	0.04	3.79
369	ZBTB38	chr3:141128034-141128434	0.05	6.13
370	ZIC4	chr3:147003857-147004257	0.03	43.62
371	WWTR1	chr3:149345871-149346271	0.03	3.73
372	P2RY1	chr3:152602449-152602849	3.44	0.02
373	MECOM	chr3:168959161-168959561	0.06	27.55
374	MECOM	chr3:169210362-169210762	13.27	0.27
375	PPARGC1A	chr4:23456567-23456967	0.03	22.31
376	STIM2	chr4:27345132-27345532	54.49	0.05
377	CLOCK	chr4:56411832-56412232	0.04	1.55
378	ANKRD17	chr4:73992185-73992585	9.30	0.06
379	HNRNPD	chr4:83294719-83295119	0.05	3.29
380	NKX6-1	chr4:85007609-85008009	0.02	33.45
381	H2AZ1	chr4:100870759-100871159	0.08	22.98
382	TET2	chr4:106101655-106102055	52.33	0.03
383	ANK2	chr4:114274089-114274489	62.88	0.06
384	ANKRD50	chr4:125446687-125447087	0.03	4.90
385	MAML3	chr4:140780310-140780710	3.35	0.05
386	NR3C2	chr4:149635373-149635773	3.44	0.02
387	ZFP42	chr4:188872910-188873310	116.02	0.04
388	FBXL7	chr5:15553482-15553882	25.90	0.05
389	PRDM9	chr5:23728254-23728654	24.91	0.64
390	SUB1	chr5:32585788-32586188	0.04	1.86

No.	Gene	Chromosome Peak Area	A549 TST/DMSO	A549 ANF/DMSO
391	ZNF131	chr5:43121587-43121987	0.06	9.39
392	GPBP1	chr5:56459951-56460351	27.16	0.08
393	PIK3R1	chr5:67517776-67518176	14.08	0.04
394	OCLN	chr5:68781922-68782322	0.09	43.96
395	AP3B1	chr5:77588825-77589225	32.03	0.04
396	SSBP2	chr5:81046680-81047080	0.07	34.03
397	MEF2C	chr5:88613660-88614060	0.02	13.05
398	GIN1	chr5:102419732-102420358	0.05	13.16
399	WNT8A	chr5:137434485-137434885	0.07	8.48
400	PPARGC1B	chr5:149110844-149111244	0.09	42.95
401	FGF18	chr5:170895132-170895532	0.06	27.78
402	SQSTM1	chr5:179260032-179260432	0.02	4.61
403	FOXF2	chr6:1389447-1389847	0.19	19.74
404	FOXF2	chr6:1408591-1408991	0.04	18.63
405	FOXC1	chr6:1614870-1615270	0.02	10.93
406	TFAP2A	chr6:10376547-10376947	0.12	43.62
407	ATXN1	chr6:16844491-16844891	0.03	21.53
408	NUP153	chr6:17635407-17635807	0.05	11.82
409	NUP153	chr6:17673147-17673547	0.05	19.07
410	ID4	chr6:19688935-19689335	0.06	24.88
411	SOX4	chr6:21595965-21596365	25.99	0.05
412	ZKSCAN8P1	chr6:28139292-28139692	16.88	0.06
413	TFEB	chr6:41691854-41692254	2.56	0.03
414	PHIP	chr6:79786580-79786980	43.76	0.04
415	ZNF292	chr6:87849518-87849918	0.02	7.02
416	ANKRD6	chr6:90227494-90228187	19.49	0.02
417	SIM1	chr6:100899389-100899789	6.59	0.04
418	FOXO3	chr6:109010458-109010858	0.04	24.54
419	ESR1	chr6:152077274-152077674	0.06	3.34
420	EIF3B	chr7:2390968-2391368	62.25	0.12
421	ETV1	chr7:13543014-13543414	0.27	15.28
422	SP4	chr7:21201558-21201958	0.10	21.53
423	SP4	chr7:21492849-21493249	66.79	0.37
424	IL6	chr7:22706842-22707242	23.55	0.03
425	CREB5	chr7:28438448-28438848	3.50	0.24
426	CREB5	chr7:28449925-28450325	20.49	0.03
427	CDK13	chr7:40148722-40149122	29.51	0.04
428	IKZF1	chr7:50481281-50481681	0.04	3.78
429	EGFR	chr7:55201018-55201418	0.18	22.87
430	ZNF92	chr7:64898607-64899007	38.08	0.03
431	AUTS2	chr7:68098928-68099328	0.03	17.96
432	GTF2IRD1	chr7:73918493-73918893	0.03	2.72
433	MAGI2	chr7:77649323-77649723	37.99	0.07
434	BHLHA15	chr7:97841958-97842358	0.06	17.62
435	SMURF1	chr7:98646270-98646670	0.03	3.45
436	TFEC	chr7:115536751-115537151	57.83	0.02
437	TFEC	chr7:115735040-115735828	0.31	15.35
438	WNT2	chr7:116979355-116979945	0.03	12.27
439	SMO	chr7:128828054-128828454	19.76	0.04

No.	Gene	Chromosome Peak Area	A549 TST/DMSO	A549 ANF/DMSO
440	REPIN1	chr7:150065358-150065758	2.98	0.65
441	KMT2C	chr7:151999939-152000339	0.05	34.14
442	EN2	chr7:155184126-155184526	0.04	20.41
443	SHH	chr7:155745606-155746006	0.38	15.73
444	SHH	chr7:155803664-155804064	0.08	24.32
445	ZNF596	chr8:182333-182733	0.08	2.29
446	ZNF596	chr8:189429-189829	0.04	9.26
447	TNKS	chr8:9331643-9332043	0.05	21.42
448	PIWIL2	chr8:22217412-22217812	0.04	2.67
449	NRG1	chr8:32837318-32837718	0.08	7.92
450	ANK1	chr8:41593788-41594188	0.03	20.00
451	IKBKB	chr8:42127504-42127904	0.02	26.22
452	HGSNAT	chr8:43095756-43096156	2.81	0.09
453	HGSNAT	chr8:43102041-43102441	0.04	32.02
454	PRKDC	chr8:48764142-48764542	30.77	0.12
455	MYBL1	chr8:67524994-67525394	2.49	0.05
456	EYA1	chr8:71953213-71953613	33.75	0.03
457	ZFAT	chr8:135296882-135297282	0.02	16.18
458	ZNF707	chr8:144777709-144778109	0.03	35.92
459	FOXH1	chr8:145702274-145702674	0.04	7.19
460	FOXH1	chr8:145703899-145704299	0.04	10.48
461	ZNF250	chr8:146126186-146126948	0.08	17.84
462	DMRT1	chr9:948002-948402	44.30	0.03
463	CAAP1	chr9:26892169-26892569	0.01	10.04
464	PAX5	chr9:36839030-36839430	0.03	17.85
465	RORB	chr9:76965652-76966052	0.03	20.75
466	ZNF367	chr9:99193896-99194296	22.65	0.10
467	ZNF510	chr9:99539905-99540305	0.04	5.69
468	ZNF782	chr9:99637733-99638133	0.05	35.92
469	ANKS6	chr9:101505198-101505870	5.69	0.06
470	NR4A3	chr9:102581803-102582203	0.06	1.42
471	NR4A3	chr9:102610536-102610936	0.07	4.68
472	RNF20	chr9:104297287-104297687	53.35	0.09
473	ZNF462	chr9:109622829-109623229	0.03	25.43
474	AKNA	chr9:117101468-117101868	0.04	5.46
475	AKNA	chr9:117108004-117108404	0.06	20.64
476	AKNA	chr9:117138907-117139307	0.04	27.33
477	TLR4	chr9:120614480-120614880	0.06	23.31
478	CRB2	chr9:126080948-126081348	0.17	1.38
479	LMX1B	chr9:129378131-129378531	0.06	6.69
480	LMX1B	chr9:129464765-129465165	17.96	0.05
481	ZBTB43	chr9:129579587-129580345	0.07	21.75
482	PRRX2	chr9:132437974-132438374	0.05	22.42
483	FUBP3	chr9:133517038-133517438	0.04	27.97
484	ABL1	chr9:133636066-133636466	0.11	18.96
485	GFI1B	chr9:135849586-135849986	0.06	11.93
486	RXRA	chr9:137297483-137297883	0.25	43.73
487	RPS6KA3	chrX:20789627-20790027	0.06	3.34
488	MBTPS2	chrX:21857446-21857846	0.05	5.80

No.	Gene	Chromosome Peak Area	A549 TST/DMSO	A549 ANF/DMSO
489	MED14	chrX:40594779-40595179	0.12	1.79
490	TFE3	chrX:48880618-48881018	0.05	1.36
491	TAF1	chrX:70711693-70712093	0.26	8.70

Table S9. Under-represented genes (n = 830) identified by ChIP-seq peak analysis in A549 cells (TST/DMSO and ANF/DMSO peak intensity ratios).

No.	Gene	Chromosome Peak Area	A549 TST/DMSO	A549 ANF/DMSO
1	AGRN	chr1:955393-955793	0.07	0.03
2	AGRN	chr1:961080-961480	0.05	0.08
3	AGRN	chr1:997903-998303	0.14	0.07
4	HES5	chr1:2459315-2459715	0.03	0.04
5	PRDM16	chr1:3014342-3014742	0.20	0.03
6	PRDM16	chr1:3251514-3251914	0.04	0.07
7	CAMTA1	chr1:6999380-6999780	0.07	0.04
8	CAMTA1	chr1:7023286-7023686	0.05	0.08
9	CAMTA1	chr1:7263710-7264110	0.04	0.07
10	CAMTA1	chr1:7280758-7281158	0.06	0.03
11	CAMTA1	chr1:7641987-7642387	0.03	0.06
12	ZBTB17	chr1:16269188-16269588	0.05	0.06
13	ZBTB40	chr1:22655423-22655823	0.06	0.04
14	GRHL3	chr1:24611434-24611834	0.07	0.03
15	RUNX3	chr1:25257224-25257624	0.03	0.06
16	RUNX3	chr1:25354399-25354799	0.06	0.18
17	GMEB1	chr1:28987729-28988129	0.02	0.03
18	HDAC1	chr1:32779838-32780238	0.08	0.11
19	ZNF362	chr1:33686632-33687032	0.04	0.03
20	ZNF362	chr1:33722457-33722857	0.04	0.10
21	ZC3H12A	chr1:37945372-37945772	0.18	0.11
22	FOXD2	chr1:47903052-47903452	0.38	0.58
23	GLIS1	chr1:54204336-54204736	0.11	0.04
24	ACOT11	chr1:54965501-54965901	0.04	0.05
25	TNNI3K	chr1:74975758-74976158	0.36	0.29
26	GFI1	chr1:92949725-92950125	0.18	0.03
27	FNBP1L	chr1:93886890-93887290	0.38	0.14
28	NHLH2	chr1:116371242-116371642	0.06	0.04
29	GABPB2	chr1:151043861-151044261	0.05	0.04
30	POGZ	chr1:151422122-151422522	0.07	0.05
31	S100A10	chr1:151920652-151921052	0.10	0.06
32	JTB	chr1:153948587-153948987	0.12	0.03
33	HAX1	chr1:154249476-154249876	0.04	0.05
34	ASH1L	chr1:155311006-155311406	0.06	0.10
35	ASH1L	chr1:155506621-155507021	0.04	0.03
36	MIR9-1HG	chr1:156390570-156390970	0.03	0.04
37	MIR9-1HG	chr1:156391305-156391705	0.02	0.04
38	PBX1	chr1:164298572-164298972	0.15	0.03
39	PBX1	chr1:164756680-164757080	0.12	0.03

No.	Gene	Chromosome Peak Area	A549 TST/DMSO	A549 ANF/DMSO
40	PBX1	chr1:164822805-164823205	0.03	0.03
41	DCAF6	chr1:167920720-167921120	0.04	0.06
42	IER5	chr1:181057443-181057843	0.07	0.04
43	IER5	chr1:181058530-181058930	0.14	0.75
44	IER5	chr1:181108780-181109180	0.12	0.03
45	DHX9	chr1:182809643-182810043	0.05	0.03
46	CDC73	chr1:193342283-193342683	0.09	0.27
47	CDC73	chr1:193390993-193391393	0.04	0.07
48	CDC73	chr1:193941585-193941985	0.03	0.04
49	CDC73	chr1:194682583-194682983	0.14	0.13
50	NR5A2	chr1:199925542-199925942	0.34	0.05
51	NR5A2	chr1:200010409-200010809	0.04	0.09
52	ZNF281	chr1:200409595-200409995	0.07	0.37
53	PKP1	chr1:201237527-201237927	0.06	0.05
54	PKP1	chr1:201268025-201268425	0.18	0.05
55	KDM5B	chr1:202738743-202739143	0.02	0.27
56	SOX13	chr1:204071397-204072116	0.04	0.06
57	NUCKS1	chr1:205701409-205701809	0.10	0.07
58	PACC1	chr1:212587916-212588316	0.07	0.53
59	ATF3	chr1:212733316-212733716	0.03	0.04
60	PROX1	chr1:214156029-214156429	0.08	0.03
61	ESRRG	chr1:216909375-216909775	0.08	0.03
62	MTARC2	chr1:220901546-220901946	0.10	0.19
63	WNT3A	chr1:228195761-228196161	0.04	0.18
64	NUP133	chr1:229580297-229580697	0.06	0.08
65	ARID4B	chr1:235315172-235315572	0.05	0.04
66	ZBTB18	chr1:244304981-244305381	0.09	0.15
67	ZBTB18	chr1:244330827-244331227	0.15	0.14
68	SMYD3	chr1:246670497-246670897	0.08	0.05
69	ZNF692	chr1:249152764-249153164	0.04	0.06
70	KLF6	chr10:3733898-3734298	0.12	0.07
71	KLF6	chr10:3786879-3787279	0.04	0.08
72	KLF6	chr10:3828133-3828533	0.13	0.03
73	KLF6	chr10:3838308-3838708	0.06	0.07
74	KLF6	chr10:3930765-3931165	0.19	0.03
75	ASB13	chr10:5648354-5648754	0.11	0.04
76	ASB13	chr10:5661326-5661726	0.03	0.03
77	TAF3	chr10:7859494-7859894	0.04	0.03
78	GATA3	chr10:8165685-8166085	0.03	0.21
79	ITGA8	chr10:15612079-15612479	0.03	0.07
80	MLLT10	chr10:21843374-21843774	0.03	0.10
81	MLLT10	chr10:22014543-22014943	0.06	0.06
82	MKX	chr10:28019548-28019948	0.08	0.07
83	ZNF438	chr10:31101180-31101580	0.04	0.05
84	ZEB1	chr10:31609593-31609993	0.07	0.04
85	ZEB1	chr10:31937757-31938157	0.04	0.06
86	EPC1	chr10:32548152-32548552	0.04	0.12
87	EPC1	chr10:32698268-32698668	0.08	0.03
88	CREM	chr10:35416351-35416751	0.03	0.02

No.	Gene	Chromosome Peak Area	A549 TST/DMSO	A549 ANF/DMSO
89	CREM	chr10:35466082-35466482	0.03	0.08
90	ZNF248	chr10:38170590-38170990	0.06	0.08
91	TET1	chr10:70466723-70467123	0.05	0.08
92	ECD	chr10:74927473-74927873	0.03	0.02
93	ZMIZ1	chr10:80840471-80840871	0.03	0.12
94	ZMIZ1	chr10:80845016-80845416	0.06	0.67
95	ZMIZ1	chr10:80949782-80950182	0.04	0.05
96	ZMIZ1	chr10:80999086-80999486	0.04	0.37
97	BMPR1A	chr10:88516347-88516747	0.07	0.37
98	PTEN	chr10:89628990-89629737	0.06	0.05
99	PCGF5	chr10:92988018-92988418	0.02	0.19
100	PAX2	chr10:102467377-102467777	0.08	0.06
101	PAX2	chr10:102469169-102469569	0.05	0.03
102	NFKB2	chr10:104154937-104155657	0.68	0.02
103	TCF7L2	chr10:114760638-114761038	0.03	0.05
104	TCF7L2	chr10:115018291-115018691	0.07	0.05
105	ABLIM1	chr10:116354301-116354701	0.06	0.15
106	ABLIM1	chr10:116380125-116380525	0.13	0.05
107	ABLIM1	chr10:116496880-116497280	0.06	0.03
108	ATE1	chr10:123671166-123671566	0.03	0.12
109	ATE1	chr10:123687256-123687656	0.21	0.06
110	CTBP2	chr10:126703037-126703437	0.04	0.33
111	EBF3	chr10:131757156-131757556	0.04	0.04
112	STK32C	chr10:134085185-134085585	0.04	0.04
113	STK32C	chr10:134120396-134120796	0.05	0.08
114	STK32C	chr10:134145228-134145628	0.03	0.04
115	PWWP2B	chr10:134209221-134209621	0.03	0.05
116	PWWP2B	chr10:134237514-134237914	0.03	0.03
117	TSPAN32	chr11:2331545-2331945	0.03	0.03
118	TSPAN32	chr11:2337923-2338323	0.18	0.09
119	LMO1	chr11:8263925-8264325	0.03	0.03
120	LMO1	chr11:8285171-8285571	0.36	0.46
121	MICAL2	chr11:12188713-12189113	0.17	0.03
122	MICAL2	chr11:12284131-12284531	0.03	0.04
123	TEAD1	chr11:12774571-12774971	0.09	0.03
124	BMAL1	chr11:13299931-13300331	0.06	0.03
125	PTH	chr11:13508716-13509116	0.05	0.09
126	SOX6	chr11:15984893-15985293	0.03	0.03
127	MYOD1	chr11:17732643-17733043	0.17	0.09
128	PAX6	chr11:31832636-31833036	0.03	0.07
129	WT1	chr11:32355223-32355623	0.13	0.03
130	CREB3L1	chr11:46272396-46272796	0.02	0.03
131	PSMC3	chr11:47447349-47447749	0.03	0.03
132	CPSF7	chr11:61197104-61197504	0.03	0.10
133	RPS6KA4	chr11:64148055-64148455	0.03	0.03
134	KAT5	chr11:65480580-65480980	0.14	0.03
135	CST6	chr11:65780579-65780979	0.03	0.04
136	GAL	chr11:68421637-68422037	0.06	0.08
137	GAL	chr11:68456164-68456865	0.03	0.08

No.	Gene	Chromosome Peak Area	A549 TST/DMSO	A549 ANF/DMSO
138	ARRB1	chr11:74975030-74975430	0.11	0.03
139	DRD2	chr11:113345883-113346283	0.05	0.04
140	ZBTB16	chr11:114054041-114054441	0.03	0.04
141	BCL9L	chr11:118783301-118783701	0.15	0.07
142	FLI1	chr11:128508308-128508708	0.28	0.24
143	TEAD4	chr12:3149075-3149475	0.11	0.05
144	TNFRSF1A	chr12:6450129-6450529	0.04	0.06
145	MED21	chr12:27187686-27188086	0.04	0.04
146	ARID2	chr12:46147278-46147678	0.03	0.04
147	ARID2	chr12:46160386-46160786	0.31	0.05
148	ZNF641	chr12:48736686-48737086	0.03	0.04
149	ACVR1B	chr12:52381939-52382339	0.05	0.06
150	NR4A1	chr12:52419761-52420161	0.06	0.05
151	SP1	chr12:53764849-53765249	0.04	0.02
152	ATF7	chr12:53955940-53956340	0.06	0.08
153	ATF7	chr12:53994199-53994599	0.02	0.09
154	HOXC10	chr12:54376285-54376685	0.04	0.12
155	AGAP2	chr12:58129718-58130321	0.04	0.06
156	HMGA2	chr12:66331552-66331952	0.03	0.06
157	CAND1	chr12:67649668-67650068	0.13	0.06
158	CAND1	chr12:67662849-67663249	0.05	0.12
159	CAND1	chr12:67697736-67698136	0.06	0.06
160	E2F7	chr12:77718495-77718895	0.04	0.04
161	PPP1R12A	chr12:80388088-80388488	0.21	0.04
162	NR2C1	chr12:95431210-95431610	0.02	0.05
163	NR2C1	chr12:95465462-95465862	0.08	0.10
164	ELK3	chr12:96593799-96594199	0.02	0.06
165	SPIC	chr12:101910443-101910843	0.09	0.04
166	ASCL1	chr12:103352182-103352582	0.04	0.08
167	ASCL1	chr12:103355815-103356215	0.07	0.03
168	ASCL1	chr12:103440229-103440629	0.03	0.06
169	NFYB	chr12:104532228-104532628	0.09	0.14
170	POLR3B	chr12:106753219-106753619	0.05	0.02
171	RFX4	chr12:106994865-106995265	0.03	0.06
172	PRDM4	chr12:108122265-108122665	0.12	0.08
173	FOXN4	chr12:109722317-109722717	0.05	0.05
174	FOXN4	chr12:109760663-109761063	0.07	0.73
175	TBX3	chr12:115122008-115122408	0.06	0.68
176	TBX3	chr12:115249517-115249917	0.02	0.07
177	TBX3	chr12:115475725-115476125	0.06	0.04
178	MED13L	chr12:115889503-115889903	0.11	0.06
179	MED13L	chr12:116043908-116044308	0.10	0.03
180	MED13L	chr12:116517215-116517615	0.03	0.06
181	PSMD9	chr12:122339407-122339807	0.02	0.04
182	MLXIP	chr12:122514445-122514845	0.13	0.58
183	MLXIP	chr12:122517125-122517525	0.04	0.04
184	MLXIP	chr12:122583351-122583751	0.05	0.02
185	MLXIP	chr12:122606927-122607327	0.02	0.07
186	PUS1	chr12:132420176-132420576	0.05	0.21

No.	Gene	Chromosome Peak Area	A549 TST/DMSO	A549 ANF/DMSO
187	SUPT20H	chr13:37633550-37633950	0.07	0.06
188	NUFIP1	chr13:45488164-45488564	0.10	0.05
189	NUFIP1	chr13:45534532-45534932	0.06	0.08
190	GTF2F2	chr13:45737558-45737958	0.08	0.03
191	KLF12	chr13:74477683-74478083	0.04	0.02
192	SOX1	chr13:112534493-112534893	0.23	0.06
193	ZNF219	chr14:21566567-21566967	0.11	0.03
194	ZNF219	chr14:21589565-21589965	0.02	0.06
195	CEBPE	chr14:23584336-23584736	0.13	0.05
196	IL25	chr14:23844705-23845105	0.06	0.05
197	NPAS3	chr14:33698488-33698888	0.07	0.11
198	FOXA1	chr14:38057159-38057559	0.08	0.11
199	PSMC6	chr14:53169383-53169783	0.04	0.06
200	BMP4	chr14:54434554-54434954	0.02	0.03
201	OTX2	chr14:57215825-57216225	0.13	0.05
202	SIX1	chr14:61115053-61115453	0.12	0.54
203	MAX	chr14:65569400-65569800	0.04	0.03
204	MAX	chr14:65624073-65624473	0.04	0.13
205	VSX2	chr14:74724428-74724828	0.03	0.04
206	FOS	chr14:75754335-75754735	0.04	0.04
207	JDP2	chr14:75894160-75894560	0.09	0.03
208	JDP2	chr14:75919866-75920266	0.14	0.03
209	JDP2	chr14:75930995-75931395	0.31	0.33
210	BATF	chr14:76015307-76015707	0.10	0.03
211	IRF2BPL	chr14:77472914-77473314	0.03	0.11
212	IRF2BPL	chr14:77493164-77493564	0.34	0.05
213	IRF2BPL	chr14:77500115-77500515	0.05	0.03
214	GTF2A1	chr14:81685761-81686161	0.05	0.06
215	ASB2	chr14:94405480-94405880	0.06	0.09
216	DICER1	chr14:95512077-95512477	0.03	0.06
217	BCL11B	chr14:99434649-99435049	0.05	0.07
218	BCL11B	chr14:99625591-99625991	0.38	0.06
219	YY1	chr14:100744862-100745262	0.03	0.05
220	AKT1	chr14:105247045-105247445	0.09	0.10
221	UBE3A	chr15:25641170-25641570	0.06	0.03
222	KLF13	chr15:31678189-31678589	0.04	0.04
223	MGA	chr15:41990287-41990687	0.20	0.06
224	TP53BP1	chr15:43803665-43804065	0.34	0.04
225	GABPB1	chr15:50588927-50589327	0.04	0.23
226	LEO1	chr15:52263677-52264077	0.09	0.01
227	ONECUT1	chr15:53217408-53217808	0.02	0.08
228	PYGO1	chr15:55879950-55880350	0.04	0.03
229	NEDD4	chr15:56092868-56093268	0.07	0.03
230	RFX7	chr15:56383559-56383959	0.02	0.04
231	RORA	chr15:60996388-60996788	0.03	0.03
232	RORA	chr15:61173921-61174321	0.02	0.05
233	RORA	chr15:61693982-61694382	0.06	0.05
234	ZNF609	chr15:64838659-64839059	0.03	0.02
235	ZNF609	chr15:64908910-64909310	0.13	0.09

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236	MAP2K1	chr15:66716889-66717289	0.06	0.13
237	MAP2K1	chr15:66746879-66747279	0.06	0.12
238	SMAD3	chr15:67309717-67310117	0.14	0.09
239	ARID3B	chr15:74881027-74881427	0.14	0.12
240	ISL2	chr15:76627628-76628028	0.05	0.04
241	ZSCAN2	chr15:85144145-85144545	0.03	0.04
242	ZNF710	chr15:90607190-90607590	0.04	0.02
243	ZNF774	chr15:90895526-90895926	0.62	0.03
244	CRTC3	chr15:91073156-91073556	0.03	0.06
245	CRTC3	chr15:91194992-91195392	0.08	0.05
246	RGMA	chr15:93594438-93594838	0.03	0.18
247	ASB7	chr15:101228719-101229119	0.02	0.63
248	ELOB	chr16:2827899-2828299	0.06	0.06
249	ZNF205	chr16:3174635-3175035	0.03	0.03
250	ZNF263	chr16:3321269-3321669	0.05	0.05
251	TFAP4	chr16:4323393-4323793	0.04	0.03
252	NUBP1	chr16:10844609-10845009	0.07	0.57
253	CIITA	chr16:10972464-10972864	0.04	0.10
254	LITAF	chr16:11661949-11662349	0.04	0.08
255	SGF29	chr16:28590542-28590942	0.05	0.09
256	SGF29	chr16:28591509-28591909	0.02	0.03
257	ZNF764	chr16:30565149-30565549	0.04	0.03
258	ZNF764	chr16:30568787-30569187	0.05	0.03
259	ZNF689	chr16:30621816-30622216	0.05	0.28
260	SETD1A	chr16:30989450-30989850	0.08	0.07
261	ZNF668	chr16:31072787-31073187	0.03	0.12
262	ZNF423	chr16:49712920-49713320	0.14	0.03
263	SALL1	chr16:51024954-51025354	0.13	0.07
264	SALL1	chr16:51121060-51121460	0.03	0.04
265	NLRC5	chr16:57097438-57097838	0.08	0.03
266	E2F4	chr16:67226823-67227223	0.02	0.21
267	FHOD1	chr16:67280549-67281250	0.03	0.54
268	NFATC3	chr16:68119667-68120067	0.38	0.03
269	WWP2	chr16:69804424-69804824	0.05	0.11
270	WWP2	chr16:69922715-69923115	0.06	0.06
271	WWP2	chr16:69971397-69971797	0.03	0.05
272	HYDIN	chr16:71073844-71074244	0.06	0.04
273	HYDIN	chr16:71085328-71085728	0.09	0.03
274	HYDIN	chr16:71095402-71095802	0.09	0.08
275	HYDIN	chr16:71131871-71132271	0.06	0.07
276	ZFHX3	chr16:72908057-72908457	0.06	0.04
277	ZFHX3	chr16:72940545-72940945	0.05	0.07
278	ZFP1	chr16:75199293-75199693	0.13	0.11
279	WWOX	chr16:78896913-78897313	0.03	0.09
280	CDH13	chr16:83093681-83094081	0.06	0.10
281	ZFPM1	chr16:88570346-88570746	0.07	0.03
282	BHLHA9	chr17:1162512-1162912	0.06	0.08
283	BHLHA9	chr17:1169761-1170161	0.04	0.05
284	BHLHA9	chr17:1171340-1172001	0.16	0.44

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285	MYBBP1A	chr17:4452126-4452526	0.03	0.17
286	MYBBP1A	chr17:4455461-4455861	0.02	0.07
287	MYBBP1A	chr17:4458390-4459188	0.02	0.01
288	CAMTA2	chr17:4889143-4889543	0.07	0.04
289	MED31	chr17:6554796-6555196	0.05	0.05
290	TP53	chr17:7571422-7571822	0.10	0.08
291	KDM6B	chr17:7746889-7747289	0.05	0.06
292	MYOCD	chr17:12588433-12588833	0.12	0.07
293	NCOR1	chr17:16039680-16040080	0.06	0.03
294	NCOR1	chr17:16083702-16084102	0.08	0.03
295	SREBF1	chr17:17727828-17728518	0.07	0.02
296	CRLF3	chr17:29151175-29151575	0.13	0.03
297	LHX1	chr17:35191410-35191810	0.07	0.10
298	HNF1B	chr17:36105110-36105510	0.03	0.08
299	MLLT6	chr17:36860763-36861163	0.66	0.03
300	MLLT6	chr17:36879133-36879533	0.05	0.11
301	IKZF3	chr17:37910512-37911237	0.04	0.02
302	RARA	chr17:38519539-38519939	0.03	0.09
303	RARA	chr17:38526996-38527396	0.03	0.02
304	TOP2A	chr17:38551994-38552394	0.04	0.06
305	HAP1	chr17:39890477-39890877	0.03	0.03
306	JUP	chr17:39891313-39891713	0.03	0.05
307	JUP	chr17:39933830-39934230	0.03	0.03
308	JUP	chr17:39942021-39942421	0.13	0.10
309	JUP	chr17:39947813-39948213	0.03	0.11
310	STAT5B	chr17:40408147-40408547	0.25	0.05
311	STAT3	chr17:40521938-40522338	0.12	0.05
312	BRCA1	chr17:41209995-41210395	0.07	0.16
313	ETV4	chr17:41656109-41656509	0.22	0.02
314	MPP3	chr17:41903092-41903492	0.03	0.16
315	MPP3	chr17:41910895-41911295	0.04	0.48
316	TBX21	chr17:45810110-45810510	0.11	0.04
317	NFE2L1	chr17:46125108-46125508	0.03	0.03
318	SKAP1	chr17:46546535-46546935	0.06	0.33
319	ZNF652	chr17:47432773-47433173	0.06	0.06
320	DLX3	chr17:48075409-48075809	0.05	0.05
321	BCAS3	chr17:58830772-58831172	0.04	0.05
322	BCAS3	chr17:59121431-59121831	0.03	0.09
323	TBX2	chr17:59483247-59483647	0.06	0.06
324	INTS2	chr17:59993225-59993625	0.19	0.04
325	MED13	chr17:60232506-60232906	0.02	0.15
326	SMURF2	chr17:62662388-62662788	0.04	0.05
327	SOX9	chr17:69536104-69536504	0.13	0.12
328	SOX9	chr17:70144744-70145144	0.13	0.05
329	WBP2	chr17:73859432-73859832	0.04	0.05
330	MRPL12	chr17:79670152-79670552	0.24	0.01
331	FOXK2	chr17:80479575-80479975	0.05	0.10
332	FOXK2	chr17:80512908-80513308	0.18	0.15
333	FOXK2	chr17:80513517-80513917	0.34	0.05

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334	GATA6	chr18:19750457-19750857	0.03	0.03
335	GATA6	chr18:19758078-19758478	0.03	0.09
336	ZNF521	chr18:22950029-22950429	0.03	0.07
337	ASXL3	chr18:31322759-31323159	0.03	0.29
338	ZNF397	chr18:32820435-32820835	0.06	0.13
339	ZNF24	chr18:32923984-32924384	0.13	0.03
340	SMAD2	chr18:45299937-45300337	0.05	0.12
341	SMAD2	chr18:45453633-45454340	0.12	0.03
342	ZBTB7C	chr18:45742952-45743352	0.02	0.07
343	TCF4	chr18:53483417-53483817	0.03	0.03
344	NEDD4L	chr18:55821991-55822391	0.12	0.06
345	NEDD4L	chr18:55912916-55913316	0.03	0.06
346	NEDD4L	chr18:55922562-55922962	0.12	0.03
347	GALR1	chr18:75461887-75462287	0.06	0.12
348	GALR1	chr18:75617573-75617973	0.06	0.21
349	NFATC1	chr18:77153995-77154395	0.09	0.06
350	FSTL3	chr19:675177-675577	0.03	0.03
351	NFIC	chr19:3339318-3339718	0.03	0.11
352	NFIC	chr19:3420993-3421393	0.03	0.02
353	MATK	chr19:3775427-3775827	0.04	0.04
354	UHRF1	chr19:4925200-4925600	0.03	0.03
355	RFX2	chr19:6056239-6056639	0.04	0.06
356	ZNF557	chr19:7073746-7074146	0.09	0.06
357	ZNF627	chr19:11708252-11708652	0.10	0.04
358	ZNF627	chr19:11726115-11726763	0.56	0.03
359	NFIX	chr19:13197689-13198089	0.02	0.03
360	RFX1	chr19:14118013-14118413	0.04	0.06
361	KLF2	chr19:16421466-16421866	0.18	0.04
362	MED26	chr19:16696198-16696598	0.08	0.09
363	SSBP4	chr19:18523535-18523935	0.03	0.10
364	SSBP4	chr19:18544918-18545318	0.22	0.09
365	ELL	chr19:18562206-18562606	0.05	0.04
366	ELL	chr19:18630256-18630656	0.23	0.23
367	CRTC1	chr19:18886857-18887257	0.02	0.04
368	PBX4	chr19:19729008-19729408	0.06	0.33
369	ZNF90	chr19:20187422-20187822	0.06	0.18
370	ZNF90	chr19:20236346-20236746	0.11	0.04
371	ZNF85	chr19:21147442-21147842	0.09	0.33
372	ZNF676	chr19:22347700-22348100	0.10	0.06
373	ZNF726	chr19:24097900-24098300	0.04	0.06
374	ZNF254	chr19:24260517-24260917	0.24	0.04
375	ZNF254	chr19:24325208-24325608	0.02	0.12
376	UQCRFS1	chr19:29613084-29613484	0.19	0.03
377	UQCRFS1	chr19:29677069-29677469	0.20	0.01
378	ZNF507	chr19:32756598-32756998	0.03	0.04
379	CEBPA	chr19:33770662-33771062	0.03	0.03
380	CEBPA	chr19:33771648-33772048	0.07	0.09
381	ZNF181	chr19:35225187-35225587	0.02	0.06
382	ZNF30	chr19:35417875-35418275	0.34	0.04

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383	ZNF30	chr19:35433004-35433404	0.05	0.11
384	LSR	chr19:35739778-35740178	0.05	0.04
385	ZBTB32	chr19:36193519-36193919	0.03	0.03
386	ZNF146	chr19:36714348-36714748	0.03	0.10
387	ZNF527	chr19:37861527-37861927	0.09	0.11
388	ACTN4	chr19:39212391-39212791	0.25	0.02
389	ZNF780B	chr19:40561762-40562162	0.27	0.03
390	AKT2	chr19:40766167-40766567	0.04	0.07
391	AKT2	chr19:40779784-40780184	0.03	0.72
392	AKT2	chr19:40790503-40790903	0.04	0.06
393	AKT2	chr19:40803505-40803905	0.07	0.03
394	ZNF574	chr19:42578329-42578729	0.04	0.05
395	ZNF575	chr19:44036327-44036727	0.03	0.08
396	ZNF226	chr19:44694429-44694829	0.10	0.05
397	BCL3	chr19:45245189-45245589	0.04	0.01
398	BCL3	chr19:45256544-45256944	0.04	0.05
399	RELB	chr19:45540936-45541336	0.03	0.04
400	ERCC1	chr19:45918395-45918795	0.15	0.02
401	ERCC1	chr19:45926450-45926850	0.08	0.13
402	ERCC1	chr19:45970847-45971247	0.09	0.04
403	PRKD2	chr19:47194697-47195097	0.08	0.07
404	MEIS3	chr19:47917800-47918200	0.09	0.04
405	NAPA	chr19:47991278-47991678	0.06	0.02
406	NAPA	chr19:48014096-48014496	0.03	0.13
407	MED25	chr19:50324561-50324961	0.06	0.04
408	IZUMO2	chr19:50651244-50651644	0.03	0.02
409	ZNF845	chr19:53840283-53840683	0.02	0.18
410	ZNF813	chr19:53971304-53971704	0.07	0.11
411	ZNF331	chr19:54065712-54066112	0.03	0.04
412	NAT14	chr19:55996319-55996719	0.20	0.04
413	ZNF784	chr19:56135727-56136127	0.08	0.05
414	ZNF784	chr19:56137128-56137528	0.06	0.06
415	ZNF787	chr19:56631691-56632091	0.32	0.04
416	ZSCAN5B	chr19:56708223-56708623	0.05	0.03
417	ZNF71	chr19:57126383-57126783	0.09	0.03
418	ZNF17	chr19:57922399-57922799	0.06	0.02
419	ZNF773	chr19:58011081-58011481	0.02	0.02
420	ZNF606	chr19:58513747-58514147	0.04	0.29
421	ZNF837	chr19:58891983-58892383	0.04	0.02
422	MYT1L	chr2:1974233-1974633	0.03	0.04
423	MYT1L	chr2:2713729-2714129	0.03	0.04
424	SOX11	chr2:5649049-5649449	0.04	0.07
425	ITGB1BP1	chr2:9563318-9563718	0.09	0.10
426	GRHL1	chr2:10091445-10091845	0.08	0.19
427	GRHL1	chr2:10123662-10124062	0.07	0.06
428	MYCN	chr2:16368465-16368865	0.03	0.03
429	MYCN	chr2:16401694-16402094	0.03	0.16
430	OSR1	chr2:19557845-19558245	0.03	0.03
431	NCOA1	chr2:24713695-24714095	0.10	0.15

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432	NCOA1	chr2:24822325-24822725	0.04	0.12
433	DTNB	chr2:25896093-25896493	0.05	0.05
434	KIF3C	chr2:26141755-26142155	0.20	0.05
435	KIF3C	chr2:26181521-26181921	0.02	0.33
436	SOS1	chr2:39344151-39344551	0.05	0.14
437	SIX3	chr2:45171153-45171553	0.02	0.05
438	EPAS1	chr2:46524904-46525304	0.04	0.03
439	EPAS1	chr2:46526718-46527118	0.12	0.06
440	EPCAM	chr2:47537982-47538382	0.03	0.06
441	ASB3	chr2:53228146-53228546	0.05	0.02
442	BCL11A	chr2:60721108-60721508	0.09	0.10
443	BCL11A	chr2:60779017-60779417	0.09	0.06
444	OTX1	chr2:63277180-63277580	0.06	0.09
445	MEIS1	chr2:66661984-66662384	0.06	0.04
446	PCBP1	chr2:70325614-70326014	0.16	0.05
447	FIGLA	chr2:71017620-71018020	0.05	0.05
448	DYSF	chr2:71862060-71862460	0.09	0.05
449	TET3	chr2:74214752-74215152	0.03	0.03
450	TET3	chr2:74266719-74267119	0.06	0.03
451	TCF7L1	chr2:85500803-85501203	0.04	0.18
452	ATOH8	chr2:85983424-85983824	0.05	0.03
453	ARID5A	chr2:97213005-97213780	0.04	0.05
454	AFF3	chr2:100527721-100528121	0.03	0.10
455	NPAS2	chr2:101491161-101491561	0.07	0.03
456	POU3F3	chr2:105478902-105479302	0.13	0.04
457	FHL2	chr2:106015401-106015801	0.09	0.71
458	IL1B	chr2:113573753-113574153	0.09	0.12
459	PAX8	chr2:113976111-113976511	0.03	0.12
460	PAX8	chr2:114004211-114004611	0.09	0.05
461	EN1	chr2:119426049-119426449	0.04	0.04
462	GLI2	chr2:121453199-121453977	0.08	0.02
463	GLI2	chr2:121565018-121565418	0.06	0.02
464	GLI2	chr2:121625563-121625963	0.13	0.03
465	GLI2	chr2:121708260-121708660	0.10	0.02
466	GLI2	chr2:121815878-121816278	0.06	0.03
467	TFCP2L1	chr2:121992535-121992935	0.11	0.03
468	EPC2	chr2:149356139-149356539	0.07	0.16
469	NR4A2	chr2:157136669-157137069	0.02	0.04
470	CSRNP3	chr2:166342335-166342735	0.05	0.06
471	DLX2	chr2:173080383-173080783	0.05	0.03
472	ITGA6	chr2:173165617-173166017	0.06	0.03
473	ITGA6	chr2:173291906-173292684	0.02	0.06
474	SP3	chr2:174797356-174797756	0.07	0.02
475	SP3	chr2:174830313-174830713	0.03	0.03
476	ATF2	chr2:176027826-176028226	0.02	0.06
477	HOXD4	chr2:177016311-177016711	0.46	0.08
478	NFE2L2	chr2:178129382-178129782	0.09	0.02
479	NEUROD1	chr2:182544175-182544575	0.02	0.03
480	STAT1	chr2:191878679-191879079	0.05	0.58

No.	Gene	Chromosome Peak Area	A549 TST/DMSO	A549 ANF/DMSO
481	HECW2	chr2:197111046-197111446	0.03	0.05
482	ANKRD44	chr2:197859147-197859547	0.06	0.21
483	ANKRD44	chr2:198063265-198063665	0.03	0.05
484	KLF7	chr2:207984464-207984864	0.02	0.05
485	KLF7	chr2:208157039-208157439	0.02	0.08
486	CREB1	chr2:208394166-208394566	0.03	0.02
487	ZNF142	chr2:219516290-219516690	0.09	0.38
488	SP100	chr2:231276615-231277015	0.04	0.03
489	GBX2	chr2:237087774-237088174	0.05	0.04
490	HDAC4	chr2:240005694-240006094	0.03	0.03
491	HDAC4	chr2:240080327-240080727	0.08	0.24
492	HDAC4	chr2:240171352-240171752	0.03	0.03
493	HDAC4	chr2:240207353-240207753	0.05	0.09
494	HDAC4	chr2:240429322-240429722	0.04	0.02
495	SNED1	chr2:241937884-241938284	0.04	0.15
496	SNED1	chr2:241967165-241967565	0.09	0.03
497	RBCK1	chr20:412960-413360	0.05	0.02
498	ZNF343	chr20:2505027-2505427	0.10	0.06
499	EBF4	chr20:2723727-2724127	0.07	0.03
500	DDRGK1	chr20:3185291-3185691	0.17	0.05
501	AP5S1	chr20:3798324-3798724	0.06	0.05
502	MAVS	chr20:3845148-3845548	0.03	0.04
503	SMOX	chr20:4117128-4117528	0.02	0.02
504	SMOX	chr20:4140608-4141008	0.27	0.51
505	SMOX	chr20:4141305-4141705	0.04	0.07
506	SMOX	chr20:4150497-4150897	0.32	0.30
507	BMP2	chr20:6768185-6768585	0.12	0.13
508	JAG1	chr20:10761584-10761984	0.03	0.05
509	RRBP1	chr20:17598228-17598628	0.04	0.03
510	RRBP1	chr20:17606937-17607337	0.07	0.03
511	RRBP1	chr20:17662163-17662563	0.07	0.09
512	ZNF133	chr20:18239202-18239602	0.03	0.06
513	ZNF133	chr20:18268799-18269199	0.08	0.02
514	PAX1	chr20:21705254-21705654	0.03	0.07
515	ASXL1	chr20:31012063-31012463	0.04	0.04
516	PXMP4	chr20:32295299-32295699	0.04	0.12
517	ZNF341	chr20:32368009-32368409	0.02	0.03
518	ITCH	chr20:32927364-32927764	0.02	0.07
519	ITCH	chr20:32950271-32950671	0.03	0.03
520	SRC	chr20:35981733-35982133	0.05	0.06
521	SRC	chr20:36000329-36000729	0.03	0.04
522	LPIN3	chr20:39968536-39968936	0.03	0.02
523	TOX2	chr20:42564085-42564485	0.07	0.07
524	TOX2	chr20:42616580-42616980	0.04	0.27
525	HNF4A	chr20:43017296-43017696	0.21	0.53
526	YWHAB	chr20:43514582-43514982	0.02	0.07
527	ZNF335	chr20:44590951-44591351	0.13	0.03
528	ZNF335	chr20:44600094-44600494	0.06	0.03
529	CD40	chr20:44762507-44762907	0.07	0.24

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530	ZMYND8	chr20:45851863-45852263	0.05	0.03
531	ZMYND8	chr20:45889069-45889469	0.25	0.04
532	ZMYND8	chr20:45928211-45928611	0.07	0.04
533	ZMYND8	chr20:46030999-46031399	0.04	0.03
534	NCOA3	chr20:46199936-46200336	0.05	0.03
535	NCOA3	chr20:46242444-46242844	0.05	0.04
536	SNAI1	chr20:48602097-48602497	0.09	0.04
537	CEBPB	chr20:48850072-48850472	0.03	0.09
538	NFATC2	chr20:49988846-49989246	0.05	0.03
539	NFATC2	chr20:50057891-50058291	0.05	0.04
540	SALL4	chr20:50418136-50418536	0.06	0.04
541	SALL4	chr20:50441661-50442061	0.05	0.27
542	ZFP64	chr20:50774914-50775314	0.04	0.05
543	ZFP64	chr20:50780267-50780667	0.02	0.09
544	ZNF217	chr20:52210261-52210661	0.05	0.08
545	TFAP2C	chr20:55181544-55181944	0.02	0.03
546	TFAP2C	chr20:55449999-55450399	0.07	0.05
547	TAF4	chr20:60562050-60562778	0.02	0.09
548	SS18L1	chr20:60723393-60723793	0.04	0.09
549	ADRM1	chr20:60879784-60880184	0.03	0.03
550	GATA5	chr20:61078640-61079040	0.11	0.05
551	GMEB2	chr20:62223345-62223745	0.03	0.04
552	ZBTB46	chr20:62375902-62376302	0.06	0.13
553	ZBTB46	chr20:62382406-62382806	0.04	0.06
554	ZBTB46	chr20:62406364-62406764	0.13	0.04
555	ZBTB46	chr20:62417727-62418127	0.13	0.04
556	SIM2	chr21:38074375-38074775	0.08	0.03
557	ETS2	chr21:40213164-40213564	0.05	0.03
558	PCP4	chr21:41256513-41257299	0.03	0.06
559	PKNOX1	chr21:44411551-44411951	0.08	0.06
560	RRP1B	chr21:45079344-45079744	0.03	0.19
561	TBX1	chr22:19728923-19729323	0.02	0.07
562	MED15	chr22:20958307-20958707	0.03	0.09
563	HIC2	chr22:21807533-21807933	0.11	0.05
564	SMARCB1	chr22:24175623-24176023	0.09	0.06
565	OSM	chr22:30653776-30654176	0.08	0.04
566	MB	chr22:35987192-35987592	0.04	0.06
567	SOX10	chr22:38373898-38374298	0.04	0.11
568	EP300	chr22:41534288-41534688	0.18	0.04
569	TEF	chr22:41778517-41778917	0.07	0.37
570	MKRN2	chr3:12596286-12596686	0.02	0.05
571	RAF1	chr3:12682875-12683275	0.03	0.03
572	ANKRD28	chr3:15803380-15803780	0.16	0.05
573	ZNF621	chr3:40566265-40566665	0.03	0.19
574	CTNNB1	chr3:41158962-41159362	0.36	0.04
575	ASB14	chr3:57313394-57313794	0.03	0.03
576	FEZF2	chr3:62357839-62358239	0.03	0.06
577	ATXN7	chr3:63954452-63954852	0.05	0.13
578	TMF1	chr3:69101143-69101543	0.03	0.21

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579	MITF	chr3:69789719-69790119	0.04	0.04
580	FOXP1	chr3:71325898-71326298	0.26	0.04
581	ZXDC	chr3:126193653-126194053	0.08	0.06
582	CNBP	chr3:128890744-128891144	0.17	0.03
583	NCK1	chr3:136581126-136581526	0.60	0.05
584	SOX14	chr3:137489951-137490351	0.06	0.06
585	FOXL2	chr3:138654598-138654998	0.03	0.02
586	ZBTB38	chr3:141169232-141169632	0.04	0.29
587	TFDP2	chr3:141830020-141830420	0.02	0.07
588	XRN1	chr3:142102829-142103229	0.10	0.04
589	ZIC1	chr3:147301924-147302324	0.20	0.03
590	ZIC1	chr3:147381704-147382104	0.02	0.03
591	ZIC1	chr3:147512824-147513224	0.07	0.19
592	ZIC1	chr3:147635977-147636377	0.05	0.12
593	WWTR1	chr3:149335967-149336367	0.38	0.02
594	WWTR1	chr3:149375322-149375722	0.04	0.37
595	MED12L	chr3:150803564-150803964	0.04	0.12
596	MED12L	chr3:151104141-151104541	0.09	0.07
597	MECOM	chr3:169379832-169380629	0.06	0.68
598	ZNF721	chr4:475902-476302	0.06	0.10
599	TNIP2	chr4:2743962-2744362	0.08	0.06
600	TNIP2	chr4:2757074-2758099	0.09	0.04
601	LDB2	chr4:16801288-16801688	0.20	0.04
602	LDB2	chr4:16864939-16865339	0.04	0.07
603	PPARGC1A	chr4:23377217-23377617	0.02	0.04
604	APBB2	chr4:40969581-40969981	0.03	0.09
605	APBB2	chr4:40995966-40996366	0.04	0.06
606	APBB2	chr4:41169851-41170251	0.18	0.10
607	ANKRD17	chr4:74073315-74073715	0.06	0.04
608	HNRNPD	chr4:82871020-82871420	0.05	0.11
609	SMARCAD1	chr4:95115413-95115813	0.07	0.05
610	BMPR1B	chr4:95636106-95636506	0.15	0.03
611	PPP3CA	chr4:102205757-102206157	0.12	0.37
612	PPP3CA	chr4:102222585-102222985	0.07	0.09
613	NFKB1	chr4:103422861-103423261	0.15	0.08
614	NPNT	chr4:106879203-106879603	0.26	0.04
615	NEUROG2	chr4:113441891-113442291	0.05	0.03
616	MAML3	chr4:140714076-140714476	0.04	0.08
617	MAML3	chr4:141007413-141007813	0.11	0.15
618	MAML3	chr4:141014154-141014554	0.05	0.07
619	SMAD1	chr4:146448774-146449174	0.20	0.21
620	NR3C2	chr4:149200092-149200492	0.05	0.17
621	NR3C2	chr4:149200695-149201095	0.23	0.07
622	TLR2	chr4:154625767-154626167	0.23	0.09
623	HELT	chr4:185986536-185986936	0.04	0.04
624	HELT	chr4:185994737-185995137	0.08	0.03
625	IRX4	chr5:2301029-2301429	0.02	0.04
626	IRX2	chr5:2334775-2335175	0.02	0.04
627	IRX2	chr5:2537546-2537946	0.09	0.05

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628	FBXL7	chr5:15739215-15739615	0.20	0.06
629	PRDM9	chr5:23413685-23414085	0.09	0.09
630	PRDM9	chr5:23609334-23609734	0.22	0.08
631	PRDM9	chr5:23691222-23691622	0.05	0.06
632	PRDM9	chr5:23707413-23707813	0.08	0.03
633	PRDM9	chr5:23847421-23847821	0.10	0.23
634	NIPBL	chr5:36992713-36993113	0.06	0.27
635	DAB2	chr5:39600563-39600963	0.05	0.03
636	ZNF131	chr5:43112183-43112583	0.02	0.03
637	MAP3K1	chr5:56112690-56113090	0.04	0.03
638	MAP3K1	chr5:56143122-56143522	0.06	0.06
639	GPBP1	chr5:56469200-56469600	0.03	0.04
640	PIK3R1	chr5:67242904-67243304	0.07	0.12
641	RAD17	chr5:68699017-68699417	0.02	0.03
642	BDP1	chr5:70809279-70809982	0.04	0.05
643	ZNF366	chr5:71921751-71922151	0.11	0.09
644	HEXB	chr5:73980559-73980959	0.03	0.03
645	F2RL1	chr5:76108624-76109024	0.23	0.08
646	F2RL1	chr5:76114643-76115043	0.14	0.04
647	AP3B1	chr5:77282743-77283143	0.03	0.03
648	AP3B1	chr5:77489425-77489825	0.05	0.05
649	ELL2	chr5:95257679-95258079	0.04	0.17
650	LOX	chr5:121412957-121413357	0.04	0.14
651	FAM13B	chr5:137391849-137392249	0.08	0.06
652	NRG2	chr5:139252691-139253091	0.03	0.03
653	NRG2	chr5:139348388-139348788	0.05	0.06
654	FGF1	chr5:142092734-142093134	0.02	0.01
655	NR3C1	chr5:142858492-142858892	0.04	0.05
656	NR3C1	chr5:142911495-142911895	0.04	0.09
657	ABLIM3	chr5:148521291-148521691	0.03	0.15
658	TNIP1	chr5:150436405-150436805	0.31	0.04
659	TNIP1	chr5:150460010-150460410	0.25	0.11
660	PWWP2A	chr5:159556623-159557023	0.02	0.28
661	FGF18	chr5:170864973-170865732	0.06	0.10
662	FGF18	chr5:170883448-170883848	0.26	0.05
663	FGF18	chr5:170972792-170973192	0.34	0.03
664	CREBRF	chr5:172483254-172483654	0.04	0.39
665	NKX2-5	chr5:172643255-172643655	0.03	0.05
666	SQSTM1	chr5:179233789-179234189	0.05	0.02
667	SQSTM1	chr5:179244538-179244938	0.10	0.02
668	SQSTM1	chr5:179254727-179255127	0.09	0.02
669	FOXF2	chr6:1390580-1390980	0.09	0.03
670	TFAP2A	chr6:10018984-10019384	0.04	0.05
671	HIVEP1	chr6:12009307-12009707	0.05	0.11
672	EDN1	chr6:12299974-12300374	0.05	0.02
673	EDN1	chr6:12459122-12459522	0.05	0.06
674	ID4	chr6:19804848-19805248	0.03	0.05
675	ID4	chr6:19823841-19824241	0.23	0.05
676	E2F3	chr6:20401987-20402387	0.03	0.12

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677	ZNF184	chr6:27550946-27551346	0.05	0.03
678	ZSCAN12	chr6:28367265-28367665	0.03	0.26
679	ZNF311	chr6:28979345-28979745	0.04	0.06
680	PFDN6	chr6:33257511-33257911	0.14	0.09
681	HMGA1	chr6:34211915-34212315	0.08	0.04
682	TEAD3	chr6:35461398-35461798	0.12	0.03
683	MAPK14	chr6:36038946-36039346	0.02	0.07
684	TFEB	chr6:41650979-41651379	0.03	0.04
685	TRERF1	chr6:42420300-42420700	0.05	0.24
686	VEGFA	chr6:43738642-43739042	0.13	0.05
687	PHIP	chr6:79766222-79766622	0.03	0.04
688	AKIRIN2	chr6:88487468-88487868	0.05	0.04
689	ANKRD6	chr6:90240622-90241022	0.02	0.06
690	POU3F2	chr6:98919866-98920266	0.02	0.03
691	POU3F2	chr6:99048149-99048549	0.02	0.05
692	POU3F2	chr6:99273330-99273730	0.04	0.05
693	POU3F2	chr6:99292701-99293101	0.05	0.03
694	VGLL2	chr6:117489000-117489400	0.07	0.07
695	PRKN	chr6:162003255-162003655	0.06	0.05
696	EIF3B	chr7:2380123-2380523	0.03	0.33
697	EIF3B	chr7:2382962-2383362	0.07	0.14
698	EIF3B	chr7:2398273-2398673	0.05	0.08
699	EIF3B	chr7:2410995-2411642	0.05	0.04
700	ZNF853	chr7:6687437-6687837	0.03	0.05
701	ZNF12	chr7:6746033-6746433	0.06	0.21
702	ETV1	chr7:14080667-14081067	0.08	0.03
703	AGMO	chr7:15111899-15112299	0.16	0.13
704	AHR	chr7:17248006-17248406	0.09	0.04
705	SP4	chr7:21466532-21466932	0.04	0.04
706	CDCA7L	chr7:21985507-21985907	0.03	0.03
707	HOXA10	chr7:27219793-27220588	0.03	0.02
708	ZMIZ2	chr7:44819412-44819812	0.11	0.07
709	PURB	chr7:44934574-44934974	0.02	0.03
710	EGFR	chr7:55122303-55122703	0.04	0.03
711	EGFR	chr7:55160123-55160523	0.04	0.21
712	EGFR	chr7:55220057-55220457	0.05	0.15
713	EGFR	chr7:55323163-55323563	0.11	0.02
714	ZNF716	chr7:57640521-57640921	0.06	0.37
715	AUTS2	chr7:68820711-68821111	0.03	0.06
716	AUTS2	chr7:68937763-68938163	0.06	0.07
717	AUTS2	chr7:68995494-68995894	0.29	0.04
718	BAZ1B	chr7:72905997-72906700	0.05	0.35
719	MLXIPL	chr7:73037381-73037781	0.28	0.05
720	GTF2IRD1	chr7:73890558-73890958	0.04	0.11
721	GTF2I	chr7:74049311-74049711	0.04	0.13
722	MAGI2	chr7:78959440-78959840	0.10	0.33
723	HGF	chr7:81298766-81299166	0.03	0.05
724	HGF	chr7:81388645-81389045	0.14	0.09
725	ZSCAN25	chr7:99241641-99242041	0.07	0.05

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726	ZKSCAN1	chr7:99606363-99606763	0.08	0.03
727	TFR2	chr7:100226904-100227304	0.06	0.04
728	NAMPT	chr7:105925470-105925870	0.05	0.04
729	FOXP2	chr7:113723433-113723833	0.04	0.23
730	FOXP2	chr7:113968402-113968802	0.02	0.18
731	TFEC	chr7:115556380-115556780	0.04	0.03
732	MET	chr7:116382243-116382643	0.02	0.03
733	WNT2	chr7:116964054-116964793	0.03	0.04
734	ASB15	chr7:123234942-123235342	0.03	0.02
735	NRF1	chr7:129229210-129229610	0.07	0.06
736	STRA8	chr7:134932337-134932737	0.07	0.05
737	CREB3L2	chr7:137567147-137567547	0.21	0.13
738	CREB3L2	chr7:137592901-137593301	0.04	0.04
739	ZNF425	chr7:148822862-148823262	0.05	0.33
740	ZNF398	chr7:148844074-148844474	0.03	0.29
741	ZNF746	chr7:149191028-149191428	0.05	0.05
742	KMT2C	chr7:152066991-152067391	0.05	0.05
743	KMT2C	chr7:152132012-152132412	0.34	0.06
744	SHH	chr7:155636434-155636834	0.04	0.74
745	SHH	chr7:155868080-155868480	0.07	0.10
746	SHH	chr7:155889561-155889961	0.04	0.04
747	SHH	chr7:155898256-155898656	0.08	0.03
748	DEFB1	chr8:6735017-6735417	0.02	0.04
749	TNKS	chr8:9399312-9400002	0.34	0.05
750	TNKS	chr8:9413865-9414265	0.03	0.10
751	NKX2-6	chr8:23605552-23605952	0.17	0.06
752	NRG1	chr8:31502549-31502949	0.05	0.18
753	NRG1	chr8:32427564-32427964	0.05	0.05
754	ANK1	chr8:41729670-41730070	0.04	0.06
755	HGSNAT	chr8:43092714-43093114	0.10	0.36
756	HGSNAT	chr8:43094953-43095353	0.04	0.21
757	HGSNAT	chr8:43096594-43096994	0.37	0.15
758	PRKDC	chr8:48687867-48688267	0.05	0.06
759	TCEA1	chr8:54929135-54929535	0.14	0.03
760	TOX	chr8:59716914-59717314	0.03	0.12
761	MYBL1	chr8:67454940-67455340	0.07	0.09
762	NCOA2	chr8:71254307-71254707	0.12	0.03
763	NCOA2	chr8:71315178-71315578	0.20	0.30
764	RBM12B	chr8:94746530-94746930	0.05	0.05
765	GEM	chr8:95246618-95247018	0.03	0.13
766	KLF10	chr8:103641355-103641755	0.04	0.15
767	KLF10	chr8:103665939-103666339	0.11	0.02
768	KLF10	chr8:103679536-103679936	0.12	0.04
769	ABRA	chr8:107871591-107871991	0.03	0.12
770	MYC	chr8:128749742-128750142	0.31	0.01
771	AGO2	chr8:141566166-141566566	0.03	0.03
772	AGO2	chr8:141644246-141644646	0.03	0.04
773	MAFA	chr8:144507666-144508066	0.03	0.16
774	ZNF707	chr8:144781089-144781489	0.03	0.06

No.	Gene	Chromosome Peak Area	A549 TST/DMSO	A549 ANF/DMSO
775	ZNF7	chr8:146052838-146053238	0.06	0.04
776	ZNF250	chr8:146127530-146128287	0.20	0.02
777	DMRT1	chr9:864257-864657	0.06	0.15
778	RFX3	chr9:3460125-3460525	0.03	0.02
779	RFX3	chr9:3526066-3526466	0.01	0.02
780	RFX3	chr9:3591791-3592191	0.08	0.03
781	GLIS3	chr9:4011192-4011592	0.18	0.04
782	JAK2	chr9:4985806-4986206	0.16	0.05
783	IL33	chr9:6213582-6213982	0.24	0.07
784	NFIB	chr9:14312855-14313255	0.03	0.03
785	SNAPC3	chr9:15374980-15375380	0.03	0.06
786	IFT74	chr9:27019708-27020108	0.06	0.04
787	PAX5	chr9:36838253-36838653	0.06	0.05
788	PAX5	chr9:36922640-36923040	0.06	0.03
789	PAX5	chr9:37024744-37025144	0.04	0.04
790	KLF9	chr9:73033580-73033980	0.20	0.02
791	RORB	chr9:77015864-77016264	0.13	0.03
792	NXNL2	chr9:91204535-91204935	0.07	0.03
793	ZNF782	chr9:99639808-99640208	0.03	0.06
794	TDRD7	chr9:100186404-100186804	0.06	0.04
795	ANKS6	chr9:101490769-101491169	0.05	0.03
796	NR4A3	chr9:102534104-102534504	0.03	0.03
797	INVS	chr9:103041164-103041564	0.04	0.05
798	ZNF462	chr9:109309712-109310112	0.04	0.04
799	ZFP37	chr9:115823542-115823942	0.07	0.07
800	DAB2IP	chr9:124307744-124308144	0.03	0.13
801	LHX2	chr9:126758844-126759244	0.10	0.05
802	NR6A1	chr9:127531727-127532127	0.03	0.15
803	PBX3	chr9:128510300-128510700	0.06	0.12
804	ZBTB43	chr9:129599224-129599624	0.05	0.05
805	ABL1	chr9:133605274-133605674	0.06	0.09
806	MED27	chr9:134727311-134727711	0.10	0.03
807	MED27	chr9:134907384-134907784	0.04	0.33
808	MED27	chr9:134955317-134955717	0.04	0.29
809	RXRA	chr9:137122268-137122668	0.05	0.05
810	RXRA	chr9:137161648-137162048	0.05	0.23
811	RXRA	chr9:137186392-137186792	0.06	0.04
812	RXRA	chr9:137268293-137268693	0.08	0.03
813	RXRA	chr9:137273273-137273673	0.03	0.03
814	RXRA	chr9:137296412-137296812	0.04	0.06
815	RXRA	chr9:137388350-137388750	0.17	0.04
816	NOTCH1	chr9:139420365-139420765	0.04	0.04
817	GRIN1	chr9:140040259-140040659	0.03	0.05
818	TBL1X	chrX:9267148-9267548	0.10	0.03
819	TBL1X	chrX:9682894-9683294	0.03	0.05
820	RPS6KA3	chrX:20285299-20285699	0.04	0.03
821	SAT1	chrX:23826286-23826686	0.05	0.23
822	ARX	chrX:25038877-25039277	0.02	0.07
823	MED14	chrX:40582288-40582688	0.24	0.10

No.	Gene	Chromosome Peak Area	A549 TST/DMSO	A549 ANF/DMSO
824	CASK	chrX:42025189-42025589	0.04	0.04
825	KDM6A	chrX:44836717-44837117	0.06	0.09
826	ZNF41	chrX:47329133-47329533	0.29	0.02
827	CHM	chrX:85192301-85192701	0.04	0.05
828	BEX1	chrX:102291208-102291608	0.07	0.05
829	NKRF	chrX:118739990-118740390	0.03	0.12
830	ZIC3	chrX:136511517-136511917	0.06	0.04

Table S10. 151 pan-cancer specific oncogenic transcription factors identified through ChIP-seq. Cell line: A549, fold changes (inhibitor-treated/DMSO).

No.	Gene	Chromosome Peak Area	A549 TST/DMSO	A549 ANF/DMSO
1	HNF1B	chr17:36091207-36091607	0.031	0.744
2	MYC	chr8:128665024-128665424	0.073	1.000
3	SOX10	chr22:38380286-38380686	0.198	0.744
4	SATB2	chr2:199903610-199904010	0.056	1.000
5	GTF3A	chr13:28007219-28007619	1.000	1.000
6	POU2AF1	chr11:111226612-111227012	1.000	1.000
7	RUNX1	chr21:36732303-36732703	0.407	1.000
8	MYB	chr6:135476862-135477262	1.000	0.036
9	ZNF217	chr20:52210261-52210661	0.054	0.083
10	PAX8	chr2:114004211-114004611	0.088	0.051
11	PHOX2A	chr11:71971642-71972042	0.036	1.000
12	FOXA1	chr14:38053550-38053950	0.043	0.744
13	GATA3	chr10:8165685-8166085	0.033	0.209
14	TFAP2A	chr6:9934667-9935067	0.108	1.000
15	ZEB2	chr2:145271016-145271416	1.000	0.030
16	SOX9	chr17:69667993-69668393	0.114	1.000
17	ETV6	chr12:11789244-11789644	0.192	1.000
18	ESR1	chr6:152079661-152080061	0.047	1.000
19	TP63	chr3:189582953-189583353	0.051	1.000
20	KLF5	chr13:73766698-73767098	1.000	1.000
21	IRF4	chr6:436507-436907	0.030	1.000
22	NFE2L2	chr2:178129382-178129782	0.095	0.024
23	SOX2	chr3:181431150-181431550	1.000	1.000
24	TRPS1	chr8:116046799-116047199	0.032	1.000
25	PREB	chr2:27354939-27355339	0.035	1.000
26	MITF	chr3:69950566-69950966	0.030	1.000
27	KLF4	chr9:110249141-110249541	0.093	1.000
28	FLI1	chr11:128508308-128508708	0.279	0.244
29	JUNB	chr19:12902156-12902556	1.000	0.018
30	FOXM1	chr12:2978226-2978626	1.000	0.707
31	SPDEF	chr6:34514429-34514829	1.000	0.139
32	HNF4A	chr20:43017296-43017696	0.212	0.531
33	TFAP2B	chr6:50892863-50893263	1.000	1.000
34	HES1	chr3:193866377-193866777	0.039	1.000
35	DLX5	chr7:96666093-96666493	0.057	1.000
36	MECOM	chr3:168853650-168854050	0.382	1.000
37	CDX2	chr13:28537099-28537499	1.000	0.037
38	SPI1	chr11:47376659-47377059	0.021	1.000
39	JUN	chr1:59219401-59219801	1.000	0.055

No.	Gene	Chromosome Peak Area	A549 TST/DMSO	A549 ANF/DMSO
40	PPARG	chr3:12337120-12337520	0.072	1.000
41	CEBPB	chr20:48850072-48850472	0.088	0.026
42	ELF3	chr1:201977222-201977622	0.030	0.331
43	PHOX2B	chr4:41829911-41830311	1.000	0.058
44	HMGA1	chr6:34211915-34212315	0.075	0.040
45	HAND2	chr4:174427959-174428359	0.049	1.000
46	ETV5	chr3:185842542-185842942	0.079	1.000
47	CEBPA	chr19:33762135-33762535	0.026	0.744
48	POU2F2	chr19:42589092-42589492	0.038	1.000
49	WT1	chr11:32355223-32355623	0.128	0.031
50	TEAD1	chr11:12635049-12635449	0.021	1.000
51	EPAS1	chr2:46526718-46527118	0.116	0.058
52	TBX3	chr12:115249517-115249917	0.024	0.068
53	TCF3	chr19:1635648-1636048	0.067	1.000
54	IRF8	chr16:85925398-85925798	0.024	1.000
55	STAT3	chr17:40518772-40519172	0.101	0.744
56	AHR	chr7:17367624-17368024	0.171	1.000
57	RARA	chr17:38474414-38474814	0.048	0.244
58	HES6	chr2:239148392-239149372	0.167	0.592
59	RARG	chr12:53619365-53619765	0.360	1.000
60	GATA2	chr3:128216600-128217000	0.026	0.744
61	MAFG	chr17:79882600-79883000	1.000	1.479
62	SOX8	chr16:1075187-1075587	0.514	0.553
63	GLIS2	chr16:4371661-4372061	0.123	0.883
64	ZNF652	chr17:47387360-47387760	0.091	1.000
65	EHF	chr11:34595897-34596297	1.000	1.000
66	ETS2	chr21:40213164-40213564	0.052	0.028
67	ZEB1	chr10:31609593-31609993	0.072	0.037
68	MYBL2	chr20:42292082-42292482	0.033	1.000
69	PAX3	chr2:222896113-222896513	0.087	1.000
70	RFX5	chr1:151320520-151320920	0.038	0.492
71	IRF6	chr1:209979288-209979688	1.000	0.049
72	TBX2	chr17:59483247-59483647	0.062	0.062
73	GRHL3	chr1:24606098-24606498	0.079	1.000
74	IKZF1	chr7:50436516-50436916	0.036	1.000
75	SALL1	chr16:51207755-51208155	0.054	0.744
76	HLF	chr17:53419079-53419767	0.121	1.000
77	NCOA3	chr20:46199936-46200336	0.045	0.033
78	RXRA	chr9:137150076-137150476	0.073	1.000
79	AFF3	chr2:100507807-100508207	0.061	1.000
80	ARID5A	chr2:97206478-97206878	0.607	0.054

No.	Gene	Chromosome Peak Area	A549 TST/DMSO	A549 ANF/DMSO
81	SOX17	chr8:55386217-55386617	0.069	1.000
82	XBP1	chr22:29193623-29194023	0.027	1.000
83	PITX1	chr5:134368635-134369035	0.074	1.000
84	MLXIPL	chr7:73037381-73037781	0.279	0.052
85	HHEX	chr10:94519565-94519965	0.061	0.492
86	FOS	chr14:75695222-75695622	0.046	1.000
87	KLF6	chr10:3930765-3931165	0.192	0.028
88	ARNT2	chr15:80719704-80720104	0.103	1.000
89	RUNX3	chr1:25273979-25274379	0.033	1.000
90	CREB3L4	chr1:153942113-153942513	1.000	1.000
91	GATA6	chr18:19750457-19750857	0.031	0.025
92	OLIG1	chr21:34447905-34448305	1.000	0.029
93	ETS1	chr11:127669468-127669868	0.171	1.000
94	ELF1	chr13:41592330-41592730	1.000	0.024
95	MGA	chr15:41911591-41911991	0.058	1.000
96	PPARD	chr6:35323334-35323734	0.066	1.000
97	KLF15	chr3:126025922-126026322	0.035	1.000
98	VDR	chr12:48312336-48312736	0.051	1.000
99	ETV4	chr17:41656109-41656509	0.219	0.020
100	KLF10	chr8:103679536-103679936	0.121	0.035
101	ONECUT2	chr18:55107277-55107677	1.000	0.744
102	SOX6	chr11:16625241-16625992	0.016	1.000
103	THRA	chr17:38218681-38219081	0.436	0.016
104	MAF	chr16:79487282-79487682	0.059	1.000
105	SOX4	chr6:21469969-21470369	0.049	1.000
106	HEY1	chr8:80658324-80658724	1.000	0.030
107	BATF	chr14:76015307-76015707	0.032	0.096
108	KLF9	chr9:73033580-73033980	0.198	0.024
109	MEIS1	chr2:66682185-66682585	0.198	1.000
110	PBX1	chr1:164423688-164424088	0.047	1.000
111	PGR	chr11:100918337-100918737	1.000	1.000
112	NR3C1	chr5:142755164-142755564	0.046	0.744
113	PRRX1	chr1:170645046-170645446	1.000	1.000
114	NFIX	chr19:13197689-13198089	0.021	0.031
115	FOXJ3	chr1:42638989-42639389	1.000	0.056
116	NFATC4	chr14:24854178-24854578	1.000	1.000
117	CEBPG	chr19:33864154-33864554	1.000	0.045
118	TFEB	chr6:41650979-41651379	0.032	0.039
119	RELB	chr19:45540936-45541336	0.031	0.041
120	SMAD3	chr15:67309717-67310117	0.137	0.094
121	PPARA	chr22:46585317-46585717	1.000	0.073

No.	Gene	Chromosome Peak Area	A549 TST/DMSO	A549 ANF/DMSO
122	NR1I3	chr1:161207255-161207655	1.000	0.071
123	RFX4	chr12:106980545-106980945	1.000	0.341
124	MEF2A	chr15:100162680-100163080	0.108	1.000
125	OLIG2	chr21:34414631-34415031	0.043	1.000
126	AKNA	chr9:117112382-117112782	1.000	1.000
127	IRF1	chr5:131827307-131827707	1.000	1.000
128	TCF20	chr22:42550314-42550714	1.000	1.000
129	TCF7L1	chr2:85335457-85335857	1.000	1.000
130	CREB3L2	chr7:137567147-137567547	0.212	0.127
131	PBX3	chr9:128510300-128510700	0.057	0.122
132	NR2F2	chr15:96923856-96924256	0.079	1.000
133	HMGA2	chr12:66282656-66283056	0.026	1.000
134	ATF3	chr1:212733316-212733716	0.025	0.043
135	SOX13	chr1:204071397-204072116	0.041	0.063
136	TCF12	chr15:57497383-57497783	0.079	1.000
137	ZNF362	chr1:33686632-33687032	0.041	0.029
138	PLSCR1	chr3:146249968-146250368	0.756	1.000
139	CREB3L1	chr11:46272396-46272796	0.021	0.026
140	ZNF395	chr8:28209031-28209431	1.000	0.042
141	TET2	chr4:106001169-106001569	1.000	1.000
142	FOXJ1	chr17:74120962-74121362	1.000	0.042
143	TEAD2	chr19:49862555-49862955	1.000	0.018
144	DEAF1	chr11:655373-655773	0.062	1.000
145	EGR1	chr5:137800133-137800533	0.549	1.000
146	ZNF331	chr19:54057856-54058256	0.038	0.744
147	TFEC	chr7:115556380-115556780	0.040	0.029
148	NFATC1	chr18:77163662-77164062	0.047	1.000
149	TSC22D1	chr13:44989931-44990331	1.000	0.018
150	HIF3A	chr19:46805400-46805800	1.000	0.036
151	YAP1	chr11:102082229-102082629	0.024	0.767

Table S11. Eleven LUAD-specific oncogenic transcription factors identified through ChIP-seq. Cell line: A549, fold changes (inhibitor-treated/DMSO).

No.	Gene	Chromosome Peak Area	A549 TST/DMSO	A549 ANF/DMSO
1	EPAS1	chr2:46526718-46527118	0.116	0.058
2	ELF3	chr1:201977222-201977622	0.030	0.331
3	AHR	chr7:17367624-17368024	0.171	1.000
4	CREB3L2	chr7:137567147-137567547	0.212	0.127
5	RUNX1	chr21:36732303-36732703	0.407	1.000
6	CREB3L1	chr11:46272396-46272796	0.021	0.026
7	NR3C1	chr5:142755164-142755564	0.046	0.744
8	STAT3	chr17:40518772-40519172	0.101	0.744
9	XBP1	chr22:29193623-29194023	0.027	1.000
10	FOXM1	chr12:2978226-2978626	1.000	0.707
11	YAP1	chr11:102082229-102082629	0.024	0.767

Table S12. Synergistic ZIP scores across NSCLC cell lines. Synergy scores were calculated using the ZIP scoring method by SynergyFinder 2.0. Synergistic effect is shown in all cell lines as a result of ANF and TST combination.

Cell Line	Mutation	Synergy Score (ZIP)	Most Synergistic Score	Method
A549	K-Ras (G12S)	25.27	27.08	ZIP
H1975	EGFR (T790M, L858R)	23.21	23.92	ZIP
HCC827	EGFR (E19Δ)	18.42	20.52	ZIP
HCC827AR	EGFR (E19Δ)	30.43	32.86	ZIP
HCC827OR	EGFR (E19Δ)	31.14	33.19	ZIP