Supplementary figures

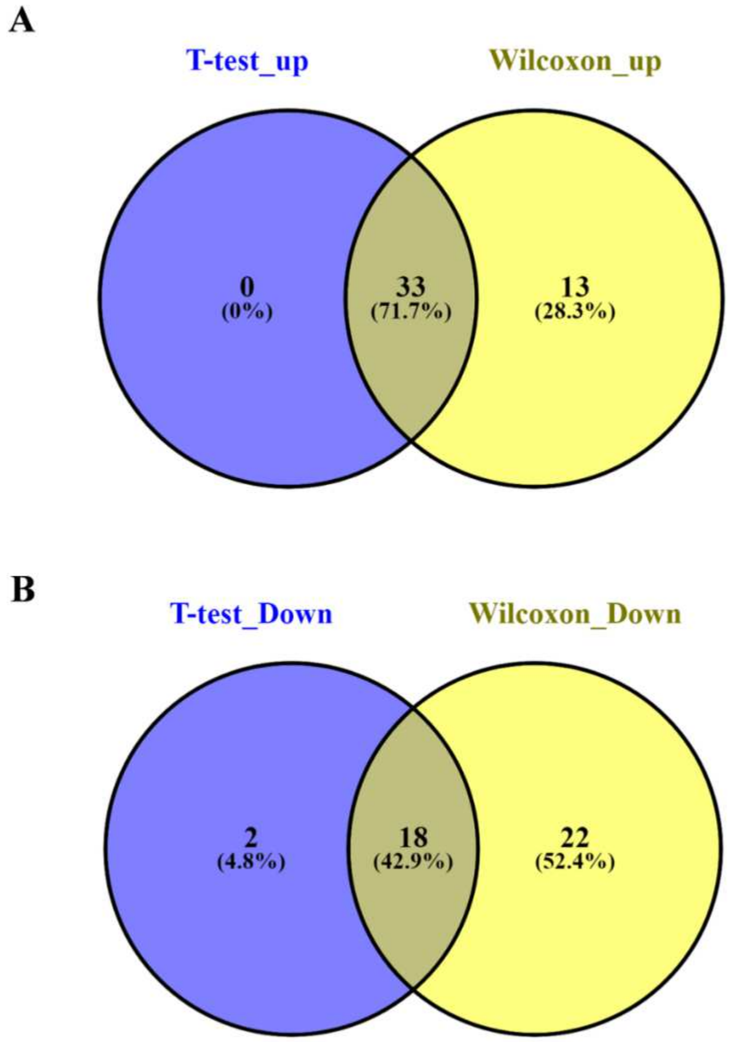

Figure S1. Integrated analysis of up (A) and down regulated (B) genes obtained from the KEAP1 mutation versus WT LUAD tumors.

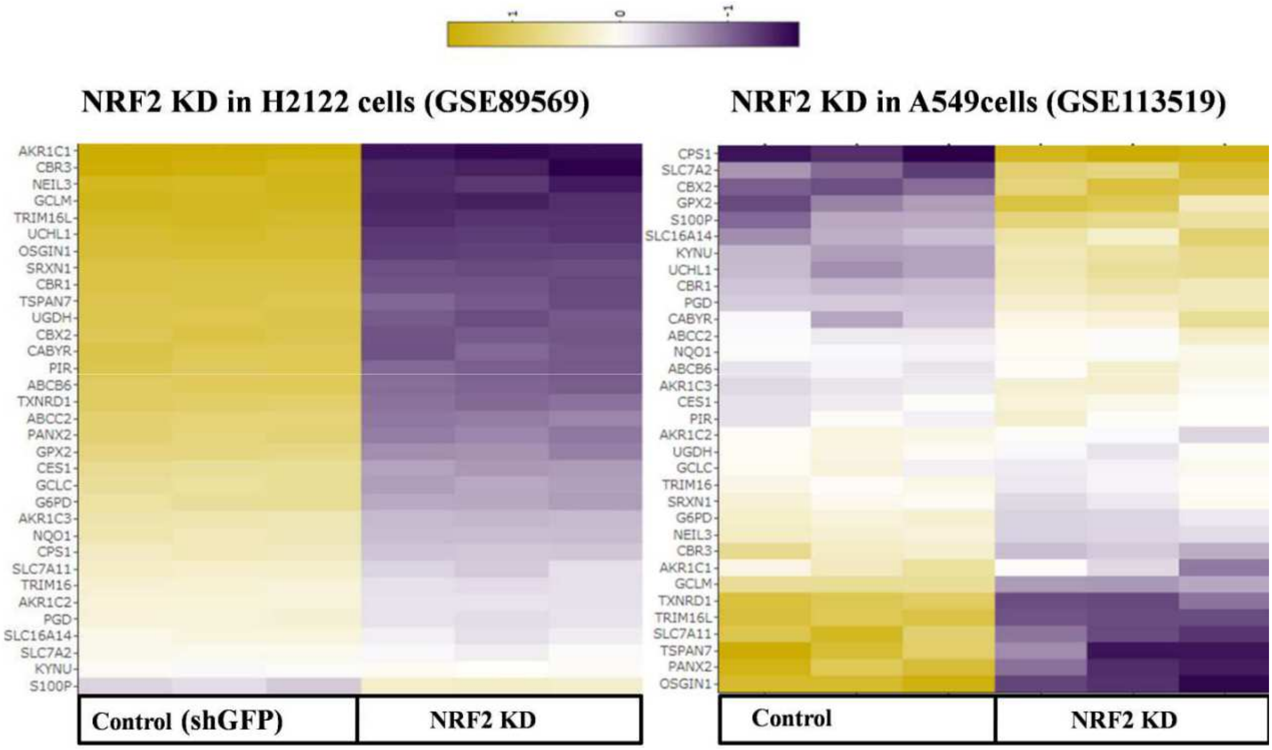

Figure S2. Patterns of KMSGC gene expression in RNA-Seq data of NRF2 knockdown lung adenocarcinoma cell lines such as H2122 from (A) Bar-Peled *et al*, 2017 (GSE89569) [16] and (B) A549 from Olagnier *et al*, 2018 (GSE113519) [15].

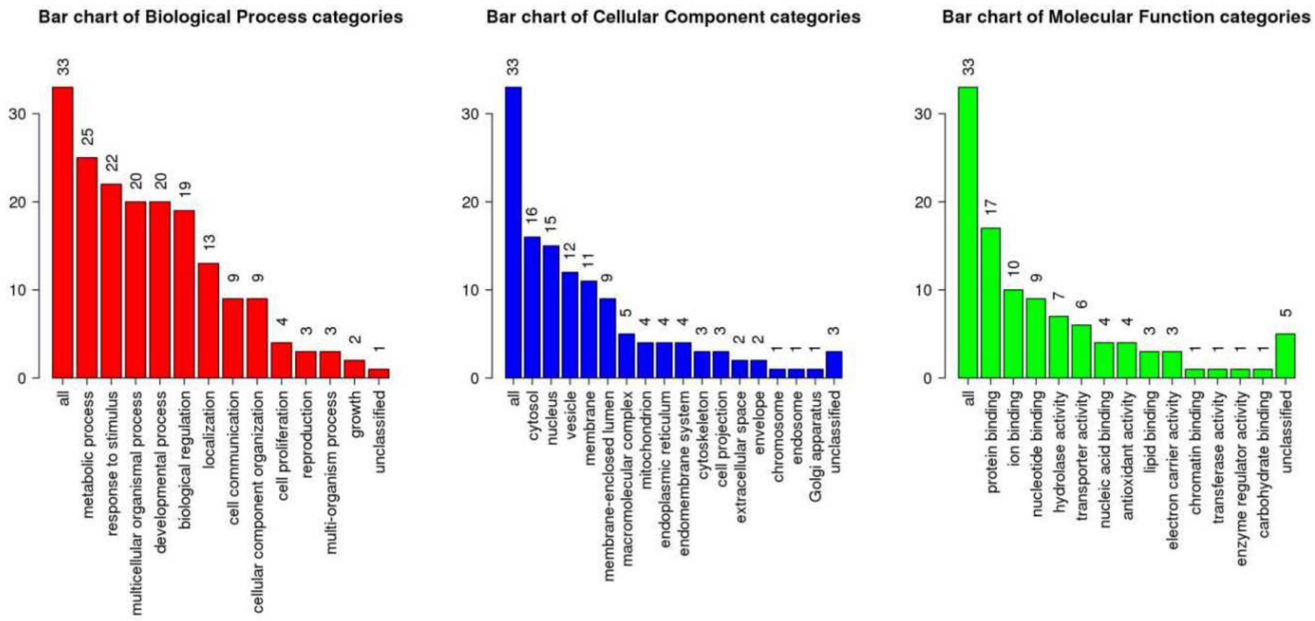

Figure S3. GO slim analysis of KMSGC by using WebGestalt

Table S1: Stratification LUAD tumors based on KEAP1 mutations

Patients barcode	KEAP1 mutation status
TCGA.05.4244	Wildtype
TCGA.05.4249	Wildtype
TCGA.05.4250	Wildtype
TCGA.05.4382	Wildtype
TCGA.05.4384	KEAP1 mutation
TCGA.05.4389	KEAP1 mutation
TCGA.05.4390	Wildtype
TCGA.05.4395	KEAP1 mutation
TCGA.05.4396	Wildtype
TCGA.05.4397	Wildtype
TCGA.05.4398	Wildtype
TCGA.05.4402	Wildtype
TCGA.05.4403	Wildtype
TCGA.05.4405	Wildtype
TCGA.05.4410	Wildtype
TCGA.05.4415	Wildtype
TCGA.05.4417	Wildtype
TCGA.05.4418	KEAP1 mutation
TCGA.05.4420	Wildtype
TCGA.05.4422	Wildtype
TCGA.05.4424	Wildtype
TCGA.05.4425	Wildtype
TCGA.05.4426	Wildtype
TCGA.05.4427	Wildtype
TCGA.05.4430	Wildtype
TCGA.05.4432	Wildtype
TCGA.05.4433	Wildtype
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TCGA.05.5429	Wildtype
TCGA.05.5715	Wildtype
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TCGA.35.4123	Wildtype
TCGA.35.5375	KEAP1 mutation

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TCGA.38.4627	Wildtype
TCGA.38.4628	Wildtype
TCGA.38.4629	Wildtype
TCGA.38.4630	Wildtype
TCGA.38.4631	KEAP1 mutation
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TCGA.44.7662	Wildtype
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TCGA.44.7669	KEAP1 mutation

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TCGA.44.8119	Wildtype
TCGA.44.8120	Wildtype
TCGA.44.A479	Wildtype
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TCGA.44.A47G	Wildtype
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TCGA.91.8497	Wildtype

TCGA.91.8499	Wildtype
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TCGA.91.A4BD	Wildtype
TCGA.93.7347	Wildtype
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TCGA.93.8067	Wildtype
TCGA.93.A4JN	Wildtype
TCGA.93.A4JO	Wildtype
TCGA.93.A4JP	Wildtype
TCGA.93.A4JQ	Wildtype
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TCGA.95.7947	KEAP1 mutation
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TCGA.99.8033	KEAP1 mutation
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TCGA.J2.8194	KEAP1 mutation
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TCGA.J2.A4AG	Wildtype
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TCGA.L4.A4E6	Wildtype
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TCGA.MP.A4TC	Wildtype
TCGA.MP.A4TD	Wildtype
TCGA.MP.A4TE	KEAP1 mutation
TCGA.MP.A4TF	Wildtype
TCGA.MP.A4TH	Wildtype

TCGA.MP.A4TI	Wildtype
TCGA.MP.A4TK	Wildtype
TCGA.MP.A5C7	KEAP1 mutation
TCGA.NJ.A4YF	Wildtype
TCGA.NJ.A4YG	Wildtype
TCGA.NJ.A4YI	Wildtype
TCGA.NJ.A4YP	Wildtype
TCGA.NJ.A4YQ	KEAP1 mutation
TCGA.NJ.A55A	Wildtype
TCGA.NJ.A55O	Wildtype
TCGA.NJ.A55R	KEAP1 mutation
TCGA.O1.A52J	Wildtype

Table S2: List of up and down regulated overlapping genes obtained from the DEG analysis of KEAP1 mutated *versus* WT TCGA LUAD tumors

Up regulated genes						
T-test			**Wilcoxon test**			**Overlapping genes-33**
Gene name	Fold Change	P-value	Gene name	Fold Change	P-value	AKR1C2
AKR1C2	6.22577199	6.22E-36	AKR1C2	7.973287	4.38E-31	AKR1C1
AKR1C1	5.27539217	1.12E-31	GPX2	6.594421	4.59E-25	GPX2
GPX2	5.18901554	9.72E-29	AKR1C1	6.14441	2.27E-30	ABCC2
ABCC2	3.46148392	6.19E-13	ABCC2	4.711354	1.84E-14	AKR1C3
AKR1C3	3.43028499	4.10E-31	UCHL1	4.013097	1.60E-20	CABYR
CABYR	3.02191006	1.47E-26	AKR1C3	3.829775	1.54E-29	UCHL1
UCHL1	2.98582679	6.73E-20	CABYR	3.128283	6.94E-27	TRIM16L
TRIM16L	2.88041915	4.17E-35	TRIM16L	3.120047	2.63E-34	S100P
S100P	2.84567569	2.83E-12	CPS1	3.08974	6.43E-05	CPS1
CPS1	2.60283699	7.50E-06	S100P	3.03509	4.07E-14	SLC7A11
SLC7A11	2.5799527	2.30E-29	SLC7A11	2.938262	5.92E-25	NQO1
NQO1	2.51708219	4.13E-33	NQO1	2.87386	7.96E-30	SRXN1
SRXN1	2.3574174	1.37E-32	SRXN1	2.691927	3.90E-32	OSGIN1
OSGIN1	2.34650288	4.32E-24	OSGIN1	2.648101	4.76E-28	TXNRD1
TXNRD1	2.15744664	1.91E-30	TXNRD1	2.568179	1.14E-28	GCLC
GCLC	2.02594655	3.91E-19	SLC7A2	2.497097	4.09E-08	CES1
CES1	2.01479231	2.03E-08	KYNU	2.479675	3.01E-10	PANX2
PANX2	2.00428378	8.95E-30	G6PD	2.396941	7.64E-26	G6PD
G6PD	1.93433109	1.46E-22	TSPAN7	2.375416	3.73E-15	TSPAN7
TSPAN7	1.92053673	6.55E-13	SLC16A14	2.210635	6.62E-11	CBR1
CBR1	1.91808199	3.49E-13	GCLC	2.198029	1.20E-22	CBX2
CBX2	1.86309965	3.43E-22	PANX2	2.162661	4.84E-26	KYNU
KYNU	1.81552807	6.07E-09	CES1	2.071875	1.67E-09	PIR
PIR	1.80576355	3.19E-31	SMOC1	2.052403	0.029573514	NEIL3
NEIL3	1.75752271	8.75E-16	PIR	2.04217	6.36E-28	UGDH
UGDH	1.73315733	8.45E-23	CBX2	2.011997	5.33E-23	PGD
PGD	1.72352446	1.83E-31	UGDH	2.005381	1.60E-24	CBR3
CBR3	1.7144523	1.30E-12	MAP2	2.00048	4.24E-13	SLC7A2
SLC7A2	1.66490371	3.08E-07	TRIM16	1.928616	3.17E-28	TRIM16
TRIM16	1.66402986	3.76E-28	ABP1	1.892875	0.012664322	ABCB6
ABCB6	1.56239919	5.58E-24	CARD14	1.831906	5.69E-11	GCLM
GCLM	1.55687797	2.33E-24	CBR1	1.825556	3.36E-18	SLC16A14
SLC16A14	1.51836805	2.25E-09	PGD	1.810587	4.61E-33	
			NEIL3	1.775105	1.57E-16	
			GSR	1.768656	1.88E-27	
			ABCB6	1.765827	1.88E-27	

RASD1	1.746061	3.72E-08
BTBD11	1.654456	1.02E-10
GCLM	1.653446	1.21E-26
CA12	1.636828	0.00062899
CBR3	1.571071	6.73E-16
PTGR1	1.542664	8.21E-22
SDCBP2	1.539571	4.67E-08
SLC16A4	1.528676	1.58E-05
CMBL	1.526846	2.05E-13
PDE4D	1.503486	1.44E-06

Down regulated genes

T-test			**Wilcoxon test**			**Overlapping genes-18**
Gene name	Fold Change	P-value	Gene name	Fold Change	P-value	SLC1A7
SLC1A7	-2.83848361	1.12E-26	MFSD4	-2.81405	3.62268E-15	MFSD4
MFSD4	-2.07753994	7.49E-16	SPTB	-2.45716	3.21694E-07	TFPI2
TFPI2	-2.05201566	6.05E-08	ITGB8	-2.43343	2.9137E-12	SYT12
SYT12	-2.04680282	7.47E-11	VSIG1	-2.41088	1.96069E-09	VSIG1
VSIG1	-2.02727732	1.96E-10	SLC1A7	-2.30125	1.85683E-16	DNAH11
DNAH11	-1.9951635	1.17E-11	DNAH11	-2.25243	4.04801E-12	LRRN4
LRRN4	-1.96372587	7.54E-11	TFPI2	-2.14113	1.76192E-08	ITGB8
ITGB8	-1.91106113	3.66E-11	CDH3	-2.12914	1.32474E-11	SLC34A2
SLC34A2	-1.89286364	2.69E-09	RASGRF1	-2.11221	2.26878E-10	CDH3
CDH3	-1.86592525	2.25E-09	CX3CL1	-2.09048	4.07063E-18	TNC
TNC	-1.81785732	1.51E-12	PNMAL1	-2.00915	6.30043E-07	HLA-DQB2
HLA-DQB2	-1.75300661	1.10E-12	SLC34A2	-1.96616	4.6371E-12	PIGR
PIGR	-1.69879051	8.91E-07	DPP4	-1.94342	1.20195E-08	ADORA1
ADORA1	-1.68597835	1.30E-12	LRRN4	-1.8957	2.71948E-11	RASGRF1
RASGRF1	-1.67357752	4.18E-11	TNC	-1.85354	9.18543E-14	CX3CL1
CX3CL1	-1.66778141	5.83E-19	PIGR	-1.8277	1.73535E-07	FCGBP
FCGBP	-1.60231062	4.52E-11	SYT12	-1.80663	3.74867E-10	HOXD1
HOXD1	-1.58549362	1.79E-09	RYR1	-1.80004	1.46321E-07	
PLAT	-1.50994419	2.08E-21	WDR66	-1.79436	1.82765E-10	
ISM1	-1.50443224	1.35E-14	HOXD1	-1.78407	3.04136E-09	
			NMNAT2	-1.76644	2.64268E-06	
			PHYHD1	-1.76614	6.67837E-08	
			EFS	-1.71796	3.88067E-11	
			MT1E	-1.69422	1.2784E-09	
			STAC	-1.68343	8.12307E-09	
			TDRD10	-1.68115	1.43524E-05	
			ARHGAP20	-1.66822	7.6091E-13	

ADORA1	-1.65107	5.5017E-14
EYA2	-1.62576	6.62599E-06
SLC16A9	-1.62531	9.41522E-06
FCGBP	-1.6187	3.58409E-10
ROS1	-1.59788	9.29278E-09
ACHE	-1.59169	1.77681E-07
APLP1	-1.58662	2.23898E-05
VSTM2L	-1.58221	3.30746E-07
HLA-DQB2	-1.55569	1.11452E-12
KCNJ15	-1.53328	4.84457E-09
SEMA3A	-1.52598	1.70285E-07
CRABP2	-1.51135	9.76477E-06
ESPN	-1.50643	1.41822E-05

Table S4: Prediction of NRF2 binding sites of KMSGC by using the *in silico* analysis and NRF2-A549 cells ENCODE and Olagnier *et al*, 2018 (GSE113519) ChIP-Seq datas.

in silico analysis results					
Chr	**Start**	**End**	**Annotation**	**Distance to TSS**	**Gene Name**
chr2	220082669	220082680	intron (NM_005689, intron 1 of 18)	1064	ABCB6
chr10	101539728	101539739	Intergenic	-2621	ABCC2
chr10	101535777	101535788	Intergenic	-6572	ABCC2
chr10	101524554	101524565	Intergenic	-17795	ABCC2
chr10	101543924	101543935	intron (NM_000392, intron 1 of 31)	1575	ABCC2
chr10	4995798	4995809	Intergenic	-9650	AKR1C1
chr10	4999262	4999273	Intergenic	-6186	AKR1C1
chr10	5054973	5054984	intron (NM_001354, intron 1 of 10)	5246	AKR1C2
chr10	5114098	5114109	intron (NM_001253908, intron 1 of 8)	-22464	AKR1C3
chr10	5138029	5138040	intron (NM_003739, intron 1 of 8)	1467	AKR1C3
chr18	21772352	21772363	intron (NM_018030, intron 4 of 13)	52910	CABYR
chr18	21753406	21753417	intron (NM_018030, intron 7 of 13)	33964	CABYR
chr18	21727932	21727943	intron (NM_138644, intron 3 of 5)	8490	CABYR
chr18	21712935	21712946	3' UTR (NM_001135993, exon 14 of 14)	-5979	CABYR
chr18	21766008	21766019	intron (NM_018030, intron 4 of 13)	46566	CABYR
chr18	21773824	21773835	intron (NM_018030, intron 4 of 13)	54382	CABYR
chr17	77743996	77744007	Intergenic	-7975	CBX2
chr16	55852121	55852132	intron (NM_001025195, intron 7 of 13)	14948	CES1
chr16	55870438	55870449	Intergenic	-3369	CES1
chr16	55839857	55839868	intron (NM_001025195, intron 12 of 13)	27212	CES1
chr16	55868163	55868174	Intergenic	-1094	CES1
chr6	53413045	53413056	Intergenic	-3124	GCLC
chr6	53316051	53316062	Intergenic	93870	GCLC

chr6	53383078	53383089	intron (NM_001498, intron 3 of 15)	26843	GCLC
chr1	94470740	94470751	intron (NM_000350, intron 44 of 49)	-95592	GCLM
chr1	94430206	94430217	Intergenic	-55058	GCLM
chr1	94390951	94390962	Intergenic	-15803	GCLM
chr14	65421101	65421112	intron (NM_198686, intron 1 of 6)	-11484	GPX2
chr2	143348755	143348766	Intergenic	-286434	KYNU
chr2	143732013	143732024	intron (NM_001032998, intron 8 of 11)	96824	KYNU
chr2	143545067	143545078	Intergenic	-90122	KYNU
chr2	143591012	143591023	Intergenic	-44177	KYNU
chr2	143518234	143518245	Intergenic	-116955	KYNU
chr2	143442928	143442939	Intergenic	-192261	KYNU
chr2	143276473	143276484	Intergenic	-358716	KYNU
chr2	143560938	143560949	Intergenic	-74251	KYNU
chr2	143680029	143680040	intron (NM_001032998, intron 3 of 11)	44840	KYNU
chr2	143734293	143734304	intron (NM_001032998, intron 8 of 11)	99104	KYNU
chr4	178219158	178219169	Intergenic	-11827	NEIL3
chr4	178128918	178128929	Intergenic	-102067	NEIL3
chr4	178296772	178296783	Intergenic	65787	NEIL3
chr4	178293902	178293913	Intergenic	62917	NEIL3
chr4	178071979	178071990	Intergenic	-159006	NEIL3
chr4	178128313	178128324	Intergenic	-102672	NEIL3
chr16	69760908	69760919	promoter-TSS (NM_001286137)	-343	NQO1
chr16	69768969	69768980	Intergenic	-8404	NQO1
chr16	83976952	83976963	Intergenic	-9869	OSGIN1
chr1	10440740	10440751	3' UTR (NM_015074, exon 47 of 47)	-18303	PGD
chrX	15514662	15514673	Intergenic	-2957	PIR
chr2	230964071	230964082	Intergenic	-30362	SLC16A14
chr2	230934484	230934495	promoter-TSS (NM_152527)	-775	SLC16A14
chr2	230984820	230984831	Intergenic	-51111	SLC16A14
chr2	230861341	230861352	intron (NM_174899, intron 2 of 3)	72368	SLC16A14

chr2	230974017	230974028	Intergenic	-40308	SLC16A14
chr2	230973814	230973825	Intergenic	-40105	SLC16A14
chr2	230983545	230983556	Intergenic	-49836	SLC16A14
chr4	139173880	139173891	Intergenic	-10383	SLC7A11
chr4	139115227	139115238	intron (NM_014331, intron 6 of 11)	48270	SLC7A11
chr4	139156848	139156859	intron (NM_014331, intron 2 of 11)	6649	SLC7A11
chr8	17318002	17318013	Intergenic	-36589	SLC7A2
chr8	17357190	17357201	intron (NM_001008539, intron 1 of 11)	2599	SLC7A2
chr20	641249	641260	TTS (NM_033129)	-7241	SRXN1
chr17	18633473	18633484	intron (NM_001353225, intron 2 of 3)	8143	TRIM16L
chrX	38529382	38529393	intron (NM_004615, intron 2 of 7)	108657	TSPAN7
chrX	38525780	38525791	intron (NM_004615, intron 2 of 7)	105055	TSPAN7
chrX	38376403	38376414	Intergenic	-44322	TSPAN7
chrX	38423767	38423778	intron (NM_004615, intron 1 of 7)	3042	TSPAN7
chrX	38353468	38353479	Intergenic	-67257	TSPAN7
chrX	38492848	38492859	intron (NM_004615, intron 1 of 7)	72123	TSPAN7
chrX	38319262	38319273	Intergenic	-101463	TSPAN7
chrX	38512599	38512610	intron (NM_004615, intron 1 of 7)	91874	TSPAN7
chrX	38379982	38379993	Intergenic	-40743	TSPAN7
chr12	104613290	104613301	intron (NM_001093771, intron 1 of 16)	3739	TXNRD1
chr12	104667784	104667795	intron (NM_001093771, intron 3 of 16)	-12670	TXNRD1
chr12	104674045	104674056	intron (NM_001093771, intron 3 of 16)	-6409	TXNRD1
chr4	41259458	41259469	promoter-TSS (NR_102709)	566	UCHL1
chr4	39516837	39516848	intron (NM_001184701, intron 1 of 10)	12375	UGDH

ENCODE-NRF2-A549 ChIP-Seq results

Chr	Start	End	Annotation	Distance to TSS	Gene Name
chr2	220082581	220082774	intron (NM_005689, intron 1 of 18)	1061	ABCB6
chr10	101544969	101545111	intron (NM_000392, intron 2 of 31)	2685	ABCC2

chr10	101520086	101520356	Intergenic	-22134	ABCC2
chr10	101535727	101535906	Intergenic	-6538	ABCC2
chr10	101594148	101594418	exon (NM_000392, exon 24 of 32)	51928	ABCC2
chr10	4995662	4995932	Intergenic	-9657	AKR1C1
chr10	4983820	4984003	Intergenic	-21542	AKR1C1
chr10	4989958	4990228	Intergenic	-15361	AKR1C1
chr10	5062507	5062690	Intergenic	-2374	AKR1C2
chr10	5051568	5051669	intron (NM_001354, intron 1 of 10)	-5413	AKR1C2
chr10	5075630	5075819	Intergenic	-15233	AKR1C3
chr10	5137902	5138172	intron (NM_003739, intron 1 of 8)	1469	AKR1C3
chr10	5113969	5114237	intron (NM_001253908, intron 1 of 8)	-22465	AKR1C3
chr10	5121057	5121327	intron (NM_001253908, intron 1 of 8)	-15376	AKR1C3
chr18	21754086	21754356	intron (NM_018030, intron 7 of 13)	34773	CABYR
chr18	21717118	21717388	Intergenic	-1667	CABYR
chr21	37442018	37442288	promoter-TSS (NM_001757)	-69	CBR1
chr17	77743865	77744135	Intergenic	-7977	CBX2
chr17	77738642	77738912	Intergenic	-13200	CBX2
chr16	55870288	55870558	Intergenic	-3348	CES1
chr6	53412985	53413121	Intergenic	-3126	GCLC
chr1	94374911	94375147	5' UTR (NM_002061, exon 1 of 7)	125	GCLM
chr1	94429335	94429424	Intergenic	-54226	GCLM
chr14	65409431	65409701	promoter-TSS (NM_002083)	57	GPX2
chr2	143630978	143631187	Intergenic	-4112	KYNU
chr2	143632017	143632287	Intergenic	-3043	KYNU
chr4	178229533	178229613	Intergenic	-1418	NEIL3
chr16	69760750	69761049	promoter-TSS (NM_001286137)	-329	NQO1
chr16	83986669	83986804	promoter-TSS (NM_182981)	-90	OSGIN1
chr22	50608460	50608730	promoter-TSS (NR_027691)	-565	PANX2
chr1	10448166	10448350	Intergenic	-10791	PGD
chr1	10447672	10447942	Intergenic	-11242	PGD

chrX	15511347	15511489	5' UTR (NM_003662, exon 1 of 10)	293	PIR
chr4	139163559	139163670	promoter-TSS (NM_014331)	-112	SLC7A11
chr4	139173736	139174006	Intergenic	-10368	SLC7A11
chr4	139156747	139156944	intron (NM_014331, intron 2 of 11)	6657	SLC7A11
chr20	633997	634297	promoter-TSS (NM_080725)	-133	SRXN1
chrX	38429702	38429972	intron (NM_004615, intron 1 of 7)	9106	TSPAN7
chr12	104613165	104613452	intron (NM_001093771, intron 1 of 16)	3752	TXNRD1
chr12	104682531	104682641	intron (NM_001261445, intron 1 of 14)	2126	TXNRD1
chr12	104680586	104680849	5' UTR (NM_001261445, exon 1 of 15)	258	TXNRD1
chr12	104671170	104671440	intron (NM_001093771, intron 3 of 16)	-9155	TXNRD1
chr12	104680129	104680399	promoter-TSS (NM_001261445)	-196	TXNRD1
chr4	41259304	41259574	promoter-TSS (NR_102709)	541	UCHL1
chr4	39516751	39517052	intron (NM_001184701, intron 1 of 10)	12316	UGDH

Olagnier et al, 2018 ChIP-Seq results

Chr	Start	End	Dist to Start	Position	Gene List
10	101,535,606	101,536,203	-6,655	upstream	ABCC2
10	101,539,576	101,540,297	-2,367	upstream	ABCC2
10	101,543,344	101,545,578	2,561	in gene	ABCC2
10	101,594,080	101,594,553	51,777	in gene	ABCC2
10	4,998,865	4,999,628	-6,158	upstream	AKR1C1
10	5,051,234	5,052,009	8,719	in gene	AKR1C2
10	5,052,669	5,052,882	7,439	in gene	AKR1C2
10	5,061,156	5,061,353	-1,105	upstream	AKR1C2
10	5,061,822	5,063,377	-2,337	upstream	AKR1C2
10	5,135,177	5,135,517	-1,272	upstream	AKR1C3
10	5,137,996	5,138,593	1,560	in gene	AKR1C3
17	77,743,096	77,744,490	-7,945	upstream	CBX2
2	211,413,724	211,414,001	71,479	in gene	CPS1
6	53,409,665	53,409,992	-25	upstream	GCLC

6	53,412,707	53,413,638	-3,193	upstream	GCLC
1	94,373,936	94,375,444	36	in gene	GCLM
2	143,625,855	143,626,160	-9,211	upstream	KYNU
2	143,628,268	143,628,521	-6,811	upstream	KYNU
2	143,630,925	143,632,304	-4,091	upstream	KYNU
4	178,229,311	178,229,741	-1,487	upstream	NEIL3
16	69,760,128	69,762,066	-363	upstream	NQO1
16	83,985,898	83,987,573	4,016	in gene	OSGIN1
1	10,471,540	10,471,741	12,579	in gene	PGD
1	10,474,785	10,475,941	16,547	in gene	PGD
1	10,476,216	10,476,438	17,187	in gene	PGD
1	10,476,527	10,476,830	17,603	in gene	PGD
4	139,143,256	139,143,579	20,095	in gene	SLC7A11
4	139,156,581	139,157,505	6,639	in gene	SLC7A11
4	139,163,119	139,163,744	-17	upstream	SLC7A11
17	18,625,091	18,625,407	-186	upstream	TRIM16L
17	18,626,900	18,627,142	1,606	in gene	TRIM16L
12	104,609,420	104,610,033	9	in gene	TXNRD1
12	104,612,631	104,614,373	3,785	in gene	TXNRD1
12	104,670,612	104,671,587	61,801	in gene	TXNRD1
12	104,679,576	104,683,538	71,145	in gene	TXNRD1
4	41,258,754	41,260,230	462	in gene	UCHL1
4	39,516,284	39,517,062	12,386	in gene	UGDH
4	39,517,292	39,517,928	11,762	in gene	UGDH
4	39,528,889	39,529,166	258	in gene	UGDH
4	39,529,245	39,529,710	-254	upstream	UGDH

Table S5: Fold change values of KMSGC obtained from the RNA-Seq data of NRF2 knockdown lung cancer cell lines

KMSGC expression in H2122 cells after NRF2 knockdown- Bar-Peled *et al*, 2017 (GSE89569)	
Gene	**Fold change (NRF2 KD vs. Control)**
AKR1C1	-3.31
CBR3	-3.17
NEIL3	-3.14
GCLM	-3.01
TRIM16L	-2.88
UCHL1	-2.75
OSGIN1	-2.69
SRXN1	-2.50
CBR1	-2.46
CABYR	-2.43
CBX2	-2.43
UGDH	-2.38
TSPAN7	-2.36
PIR	-2.35
ABCB6	-2.20
TXNRD1	-2.05
PANX2	-1.89
ABCC2	-1.86
GPX2	-1.69
CES1	-1.45

KMSGC expression in A549 cells after NRF2 knockdown- Olagnier *et al*, 2018 (GSE113519)	
Gene	**Fold change (NRF2 KD vs. Control)**
TXNRD1	-3.6
TRIM16L	-3.5
SLC7A11	-3.45
OSGIN1	-3.21
GCLM	-2.82
G6PD	-2.56
AKR1C1	-2.51
PANX2	-2.48
SRXN1	-2.38
TRIM16	-2.37
UGDH	-2.29
AKR1C2	-2.22
GCLC	-2.16
NQO1	-2.07
TSPAN7	-2.07
ABCC2	-2.01
AKR1C3	-1.84
PGD	-1.69
NEIL3	-1.68
ABCB6	-1.63

GCLC	-1.40
G6PD	-1.35
AKR1C3	-1.10
NQO1	-1.03
CPS1	-0.94
SLC7A11	-0.75
TRIM16	-0.62
PGD	-0.59
AKR1C2	-0.57
SLC16A14	-0.49
SLC7A2	-0.34
KYNU	-0.10
S100P	0.45

CES1	-1.61
CBR3	-1.46
KYNU	-1.45
CBR1	-1.43
UCHL1	-1.38
PIR	-1.31
GPX2	-0.98
CABYR	-0.82
CBX2	-0.27
S100P	-0.12
CPS1	0.12
SLC7A2	0.37
SLC16A14	0.5

Table S6: List of primers used in this study for the qRT-PCR analysis

mRNA	Function	Sequence
CBX2	Forward	5′-AGTGCATCCTGAGCAAGCG-3′
	Reverse	5′-TCCCAGCTGTTATGTTTGGAGG-3′
G6PD	Forward	5′-TGACCTGGCCAAGAAGAAGA-3′
	Reverse	5′-CAAAGAAGTCCTCCAGCTTG-3′
AKR1C1	Forward	5′-CGAGAAGAACCATGGGTGGA-3′
	Reverse	5′-GGCACAAAGGACTGGGTCC-3′
NQO1	Forward	5′-GGAGAGTTTGCTTACACTTACGC-3′
	Reverse	5′-AGTGGTGATGGAAAGCACTGCCTTC-3′
TRM16L	Forward	5′-GTCCTTCTGTGTGCATTGGG-3′
	Reverse	5′-TCTGACACCGACACCAGAAC-3′
NEIL3	Forward	5′-CAAGCGTCCTAATTGTGGTCA-3′
	Reverse	5′-CCCTGCTAGATGTCCAACTGATT-3′
UCHL1	Forward	5′-CCTGTGGCACAATCGGACTTA-3′
	Reverse	5′-CATCTACCCGACATTGGCCTT-3′
TSPAN7	Forward	5′-ACCAAACCTGTGATAACCTGTCT-3′
	Reverse	5′-AGGGAGATATAGGTGCCCAGA-3′