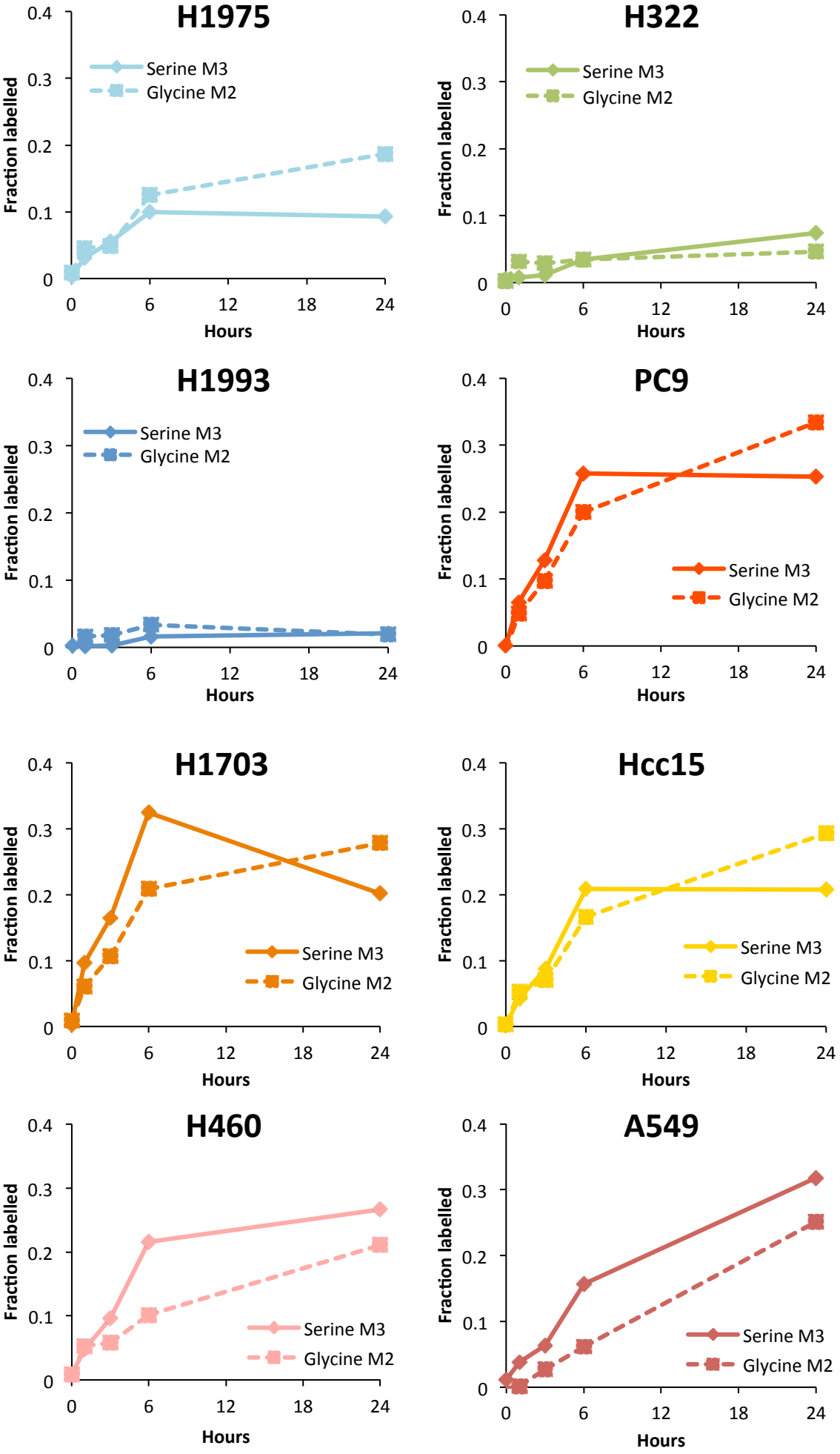
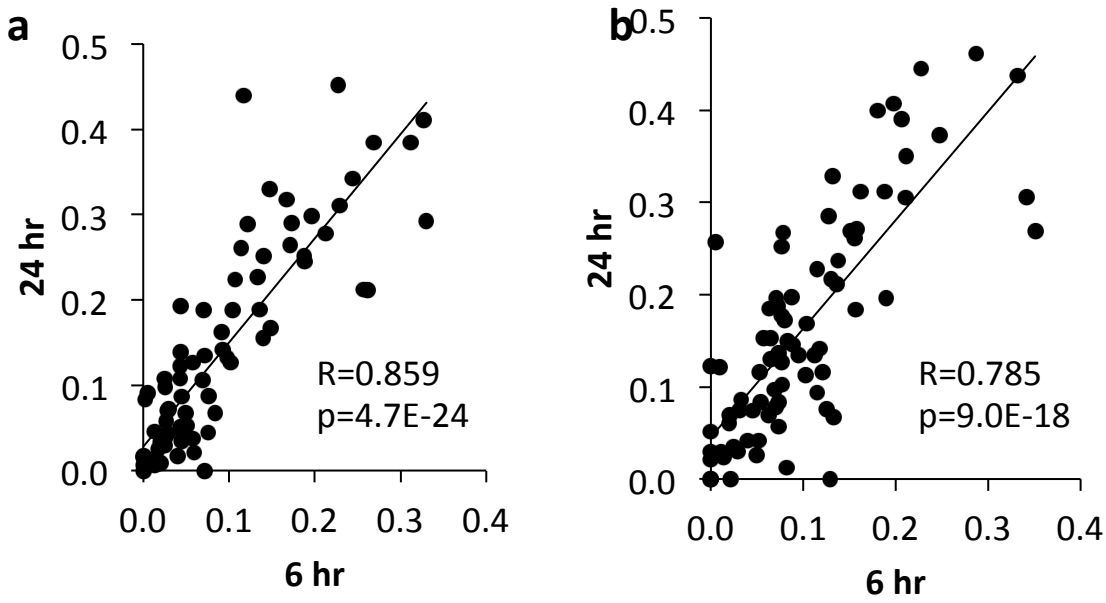
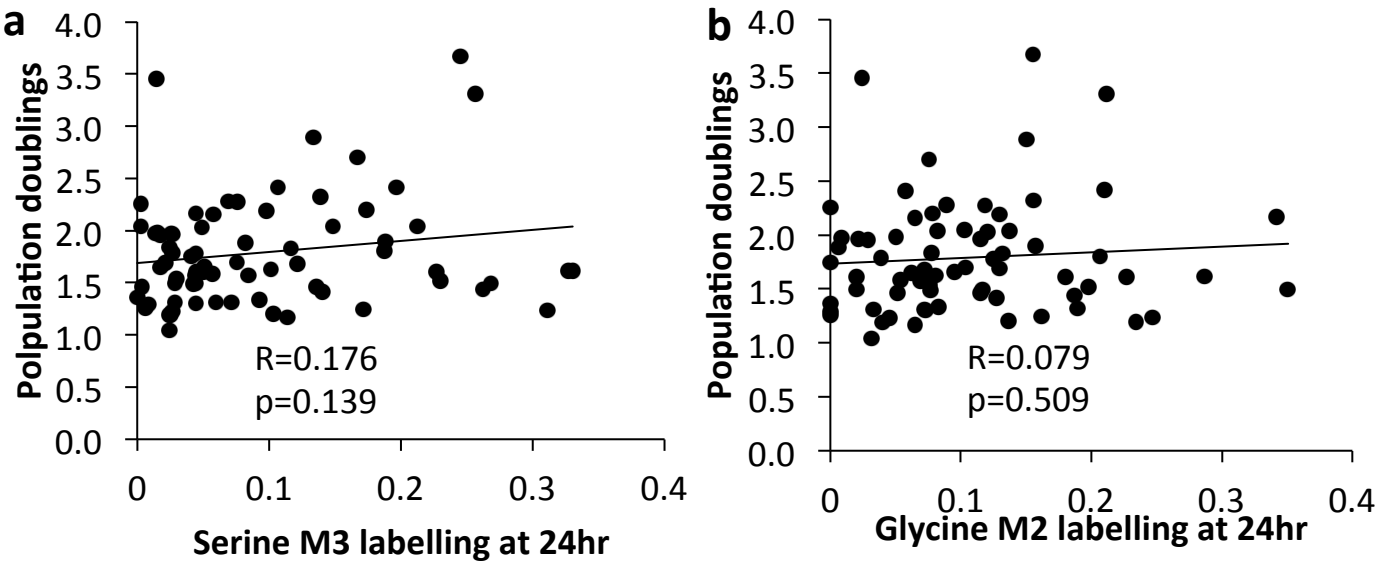


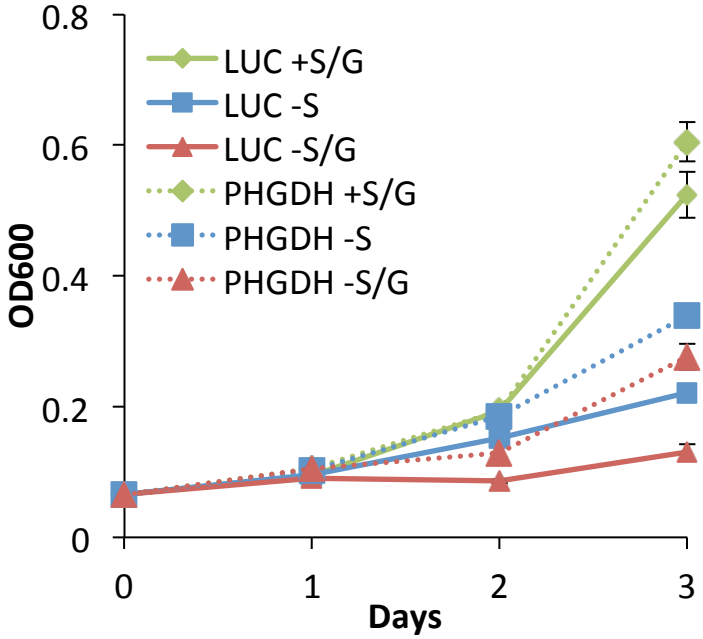
Supplementary Figure 1: Time course of serine and glycine labelling from ^{13}C-glucose in NSCLC cell lines.



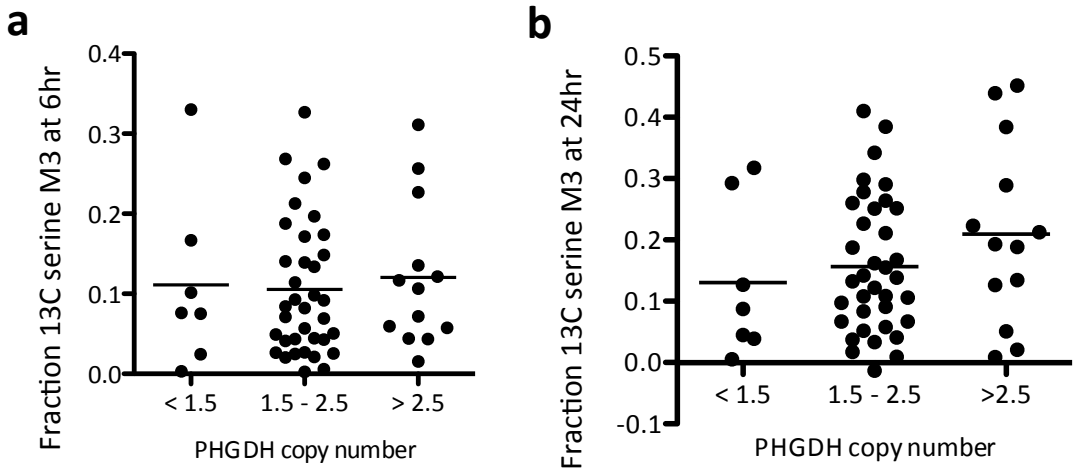
Supplementary Figure 2: Correlation of serine and glycine labelling at 6 and 24 hours. (a) Correlation between serine M3 labelling at 6 hours and 24 hours. (b) Correlation between glycine M2 labelling at 6 hours and 24 hours. Each data point is an individual cell line.



Supplementary Figure 3: Serine (a) or glycine (b) labelling does not correlate with population doubling time. Population doublings were quantified by assaying the relative increase in DNA content over 2 days.



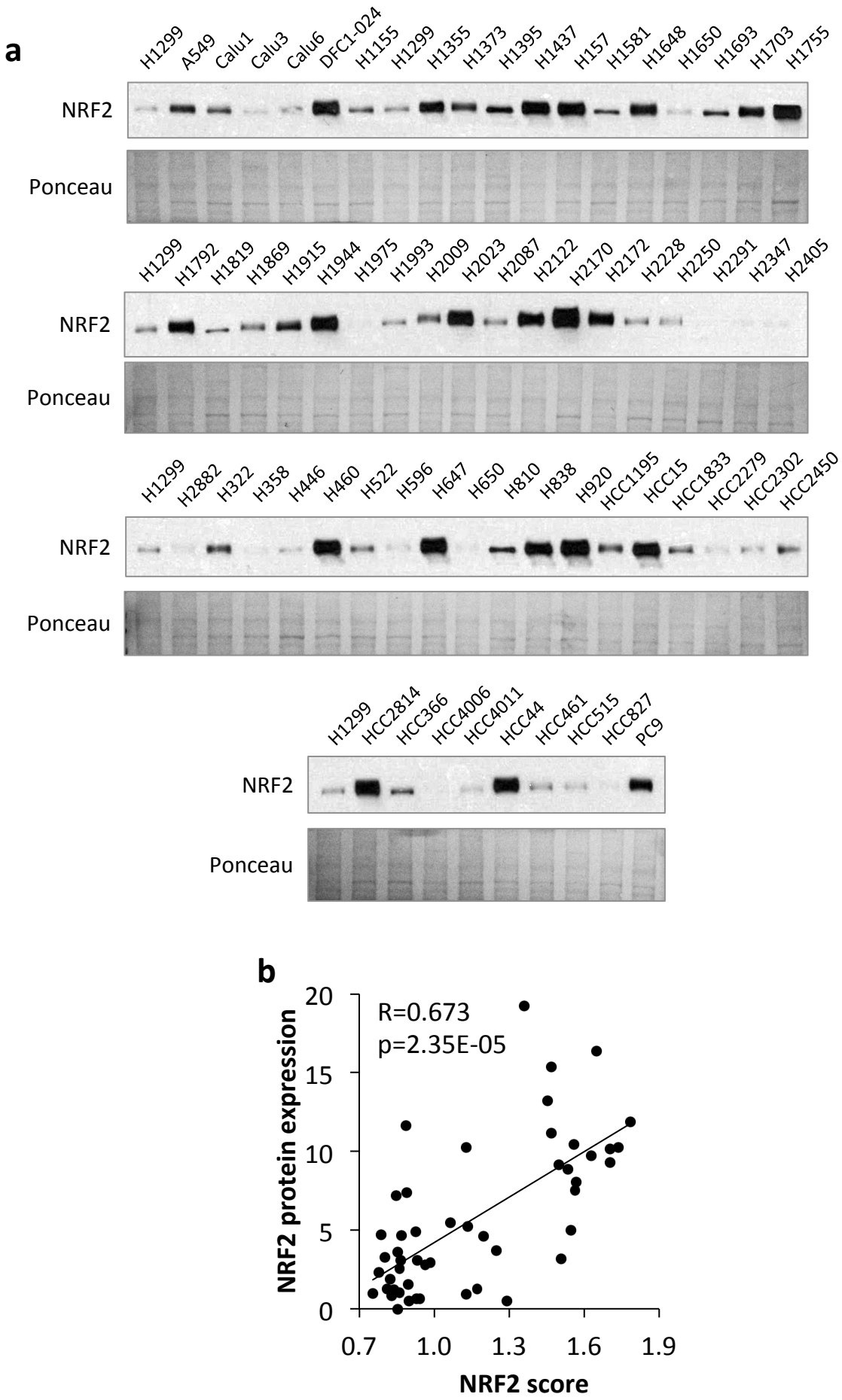
Supplementary Figure 4: PHGDH expression rescues growth of serine low cells in media lacking serine or serine and glycine. H2009 cells were infected with lentivirus expressing luciferase (LUC) or PHGDH and seeded in 96 well plates. Media was changed to full media, media lacking serine, or media lacking serine and glycine. Cell number was quantified by crystal violet staining on the indicated days.



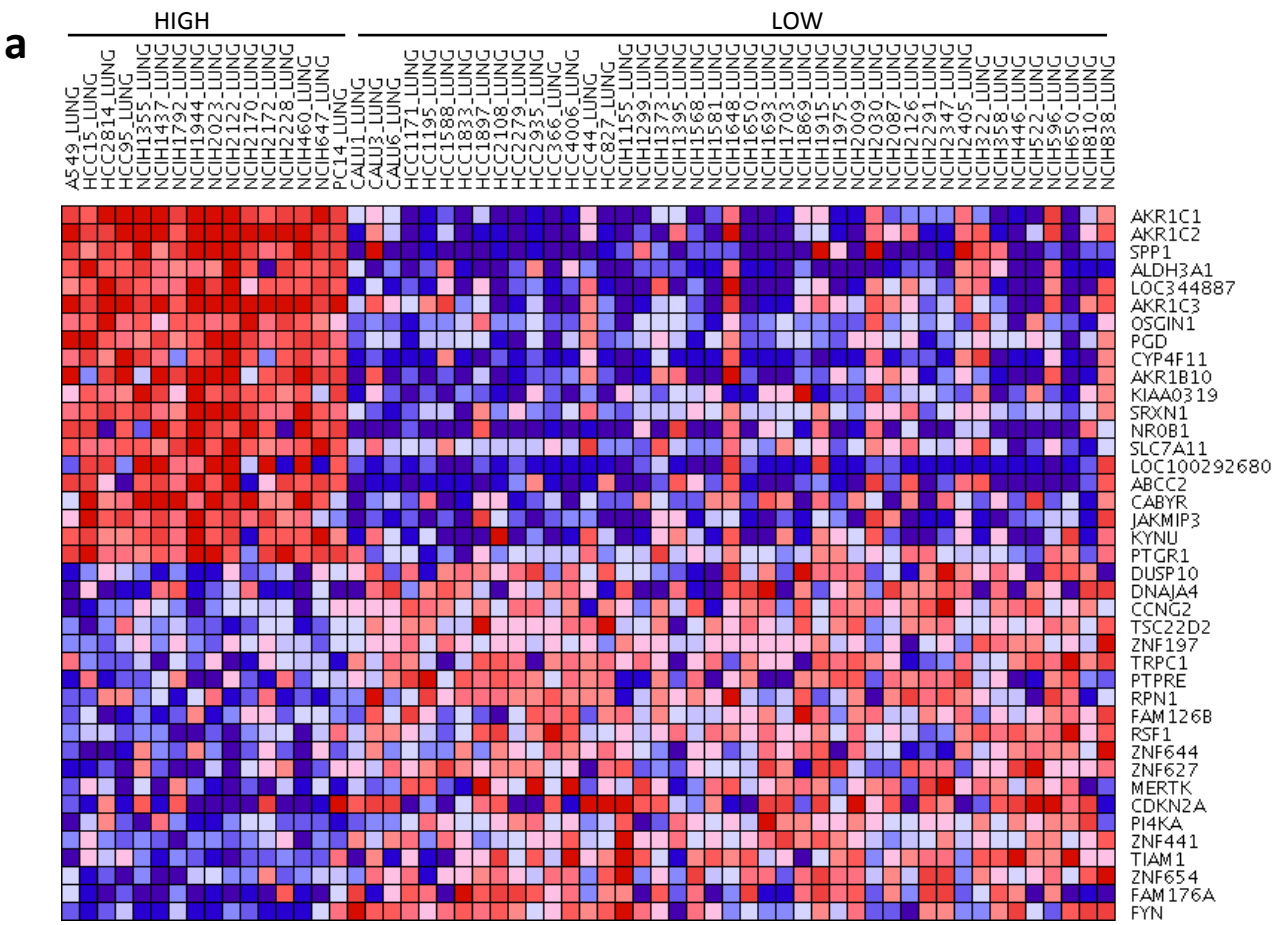
Supplementary Figure 5: Serine biosynthetic activity is not due to an increase in *PHGDH* copy number. *PHGDH* copy number data was obtained from the Broad-Novartis Cancer Cell Line Encyclopedia (CCLE), and the fraction of ^{13}C serine M3 at 6 hours (a) and 24 hours (b) determined relative to copy number. No significant difference was found. *PHGDH* copy number for individual cell lines can be found in Supplementary table 2.

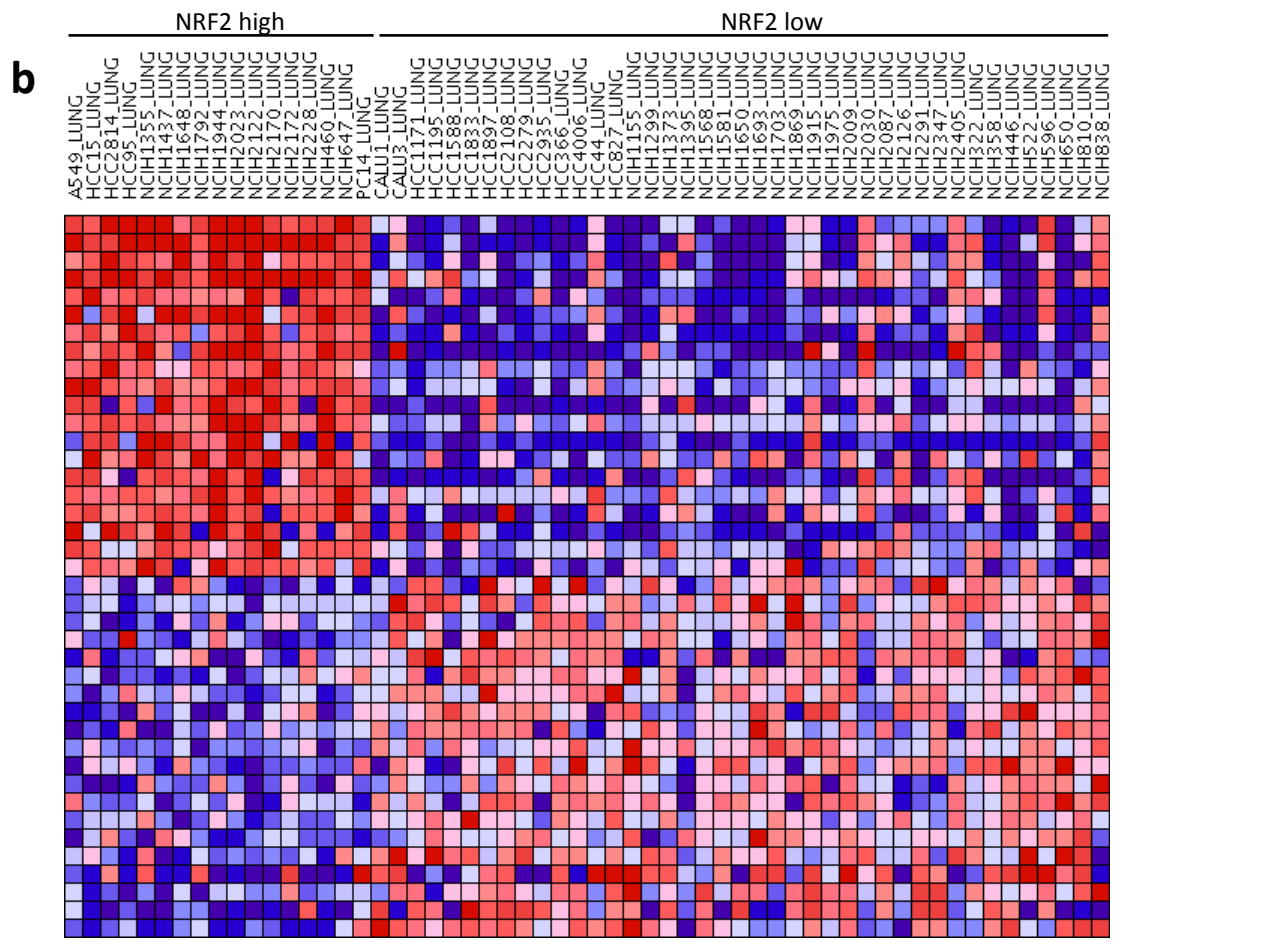
Labelling	Correlation cutoff	Geneset	p-value	q-value
serine 6hr	p<0.05	NFE2L2.V2	1.44E-20	2.71E-18
serine 24hr	p<0.05	NFE2L2.V2	7.89E-17	1.49E-14
glycine 6hr	p<0.05	NFE2L2.V2	1.30E-4	1.56E-3
glycine 24	p<0.05	NFE2L2.V2	3.47E-15	6.55E-13

Supplementary Figure 6: Serine and glycine biosynthesis correlates with a NRF2 target gene signature (gene set NFE2L2.V2). Genes that correlated with the metabolite parameters (pearson correlation, $p<0.05$) were subjected to gene set enrichment analysis (GSEA) using the Broad Institute GSEA software against oncogenic signature gene sets.

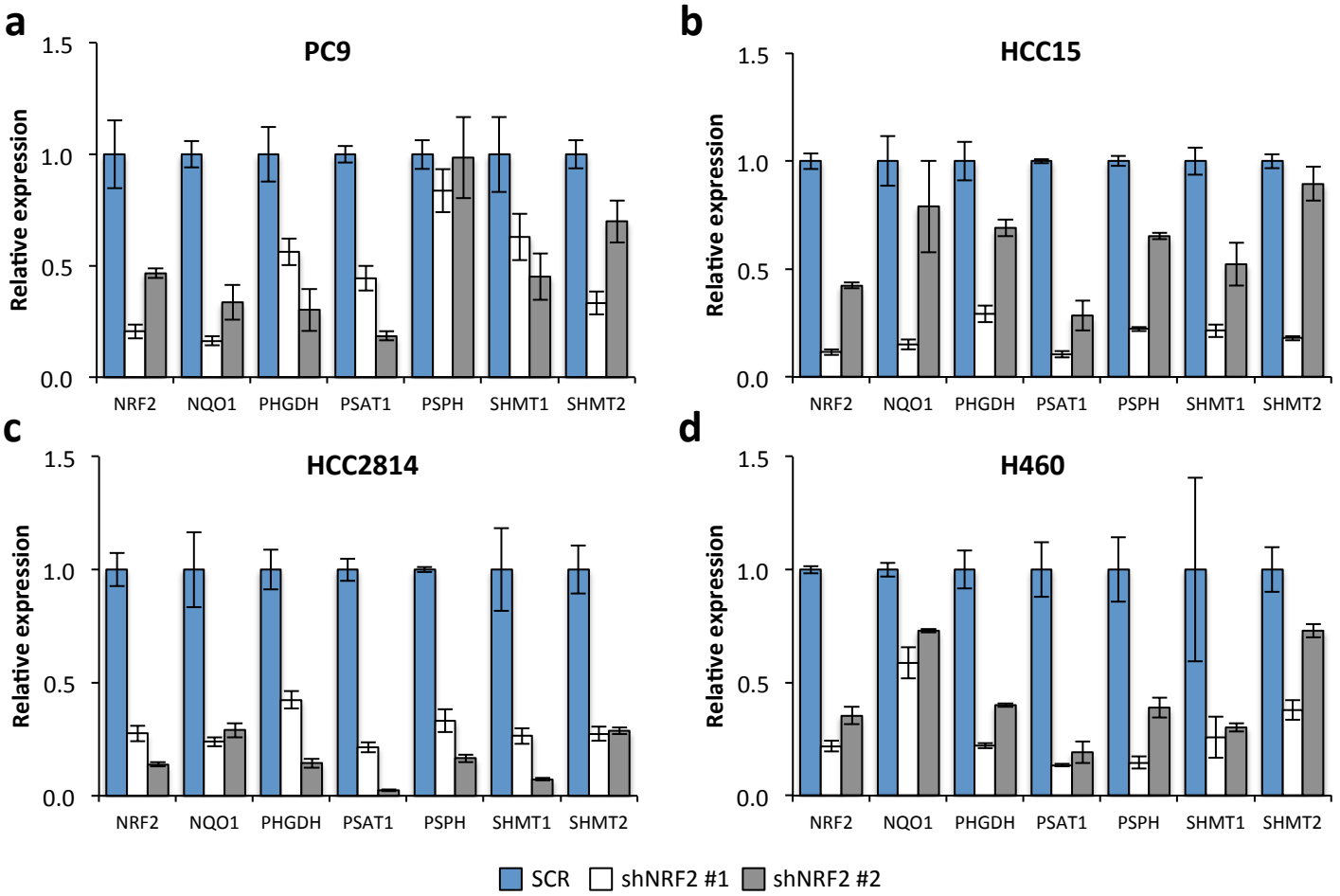


Supplementary Figure 7: Determination of NRF2 nuclear abundance in NSCLC cell lines. (a) Western blot of NRF2 in NSCLC cell line nuclear extracts. Ponceau staining denotes equal protein loading. (b) NRF2 protein expression correlates significantly with a NRF2 activity score (see Supplementary Figure 8).

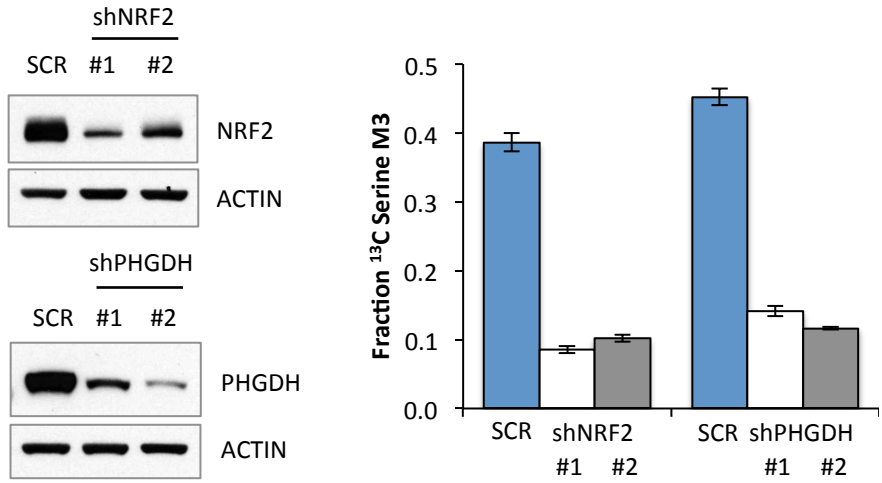




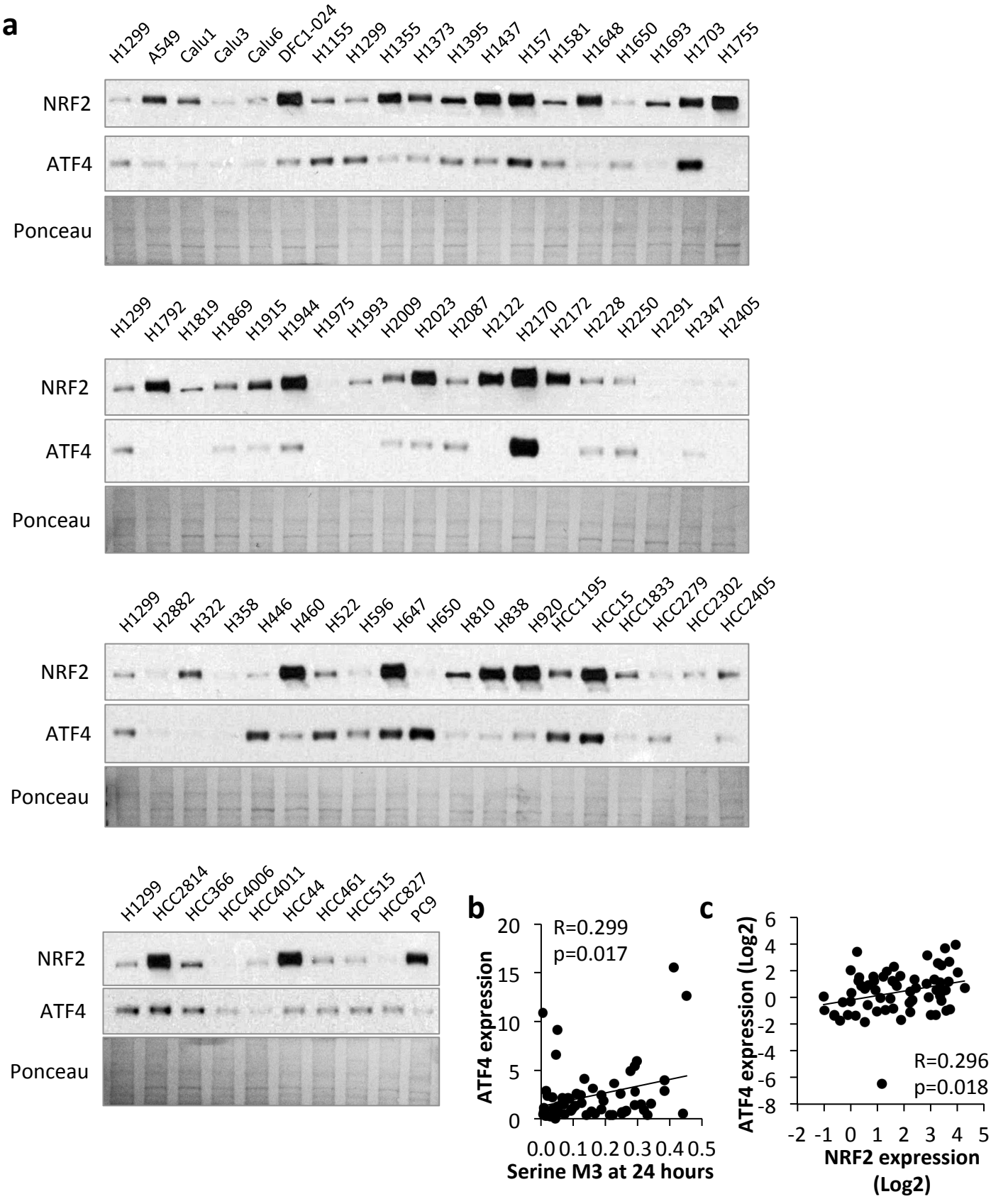
Supplementary Figure 8: Determination of the NRF2 "high" vs. "low" grouping. (a) Cell lines were separated by the expression of five classic NRF2 target genes: *NQO1*, *GCLC*, *GCLM*, *SLC7A11,* and *AKR1C1*. Groups were compared using the Broad-Novartis Cancer Cell Line Encyclopedia (CCLE) differential expression tool. The 20 most upregulated genes from were used to calculate a NRF2 score. (b) The cell lines were separated into "NRF2 high" and "NRF2 low" groups by their NRF2 score.



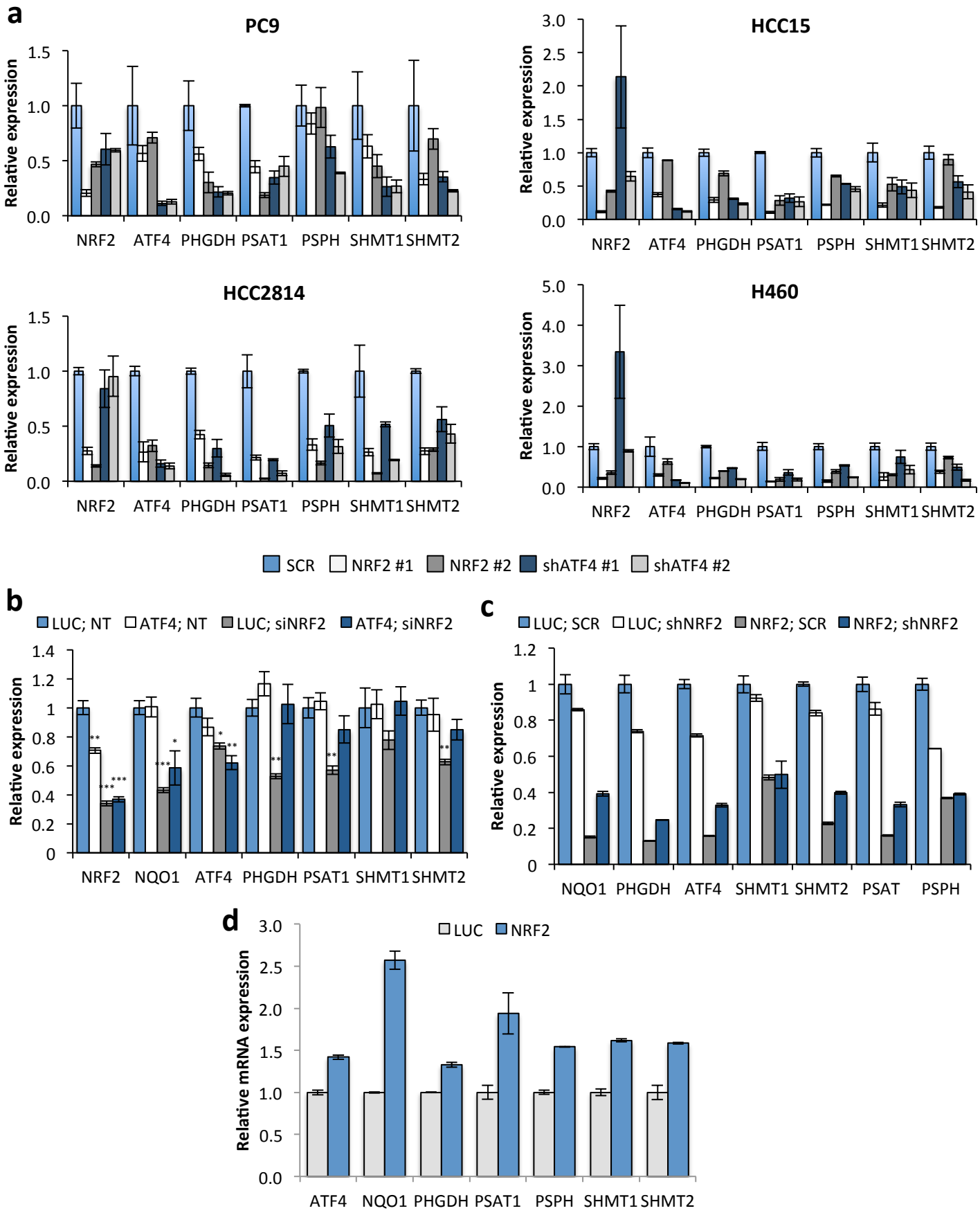
Supplementary Figure 9: NRF2 regulates the expression of serine/glycine biosynthesis enzymes. (a-d) The mRNA expression of cell lines expressing scramble shRNA (SCR) or NRF2 shRNAs was quantified by real-time PCR and normalized to the expression in the scramble controls.



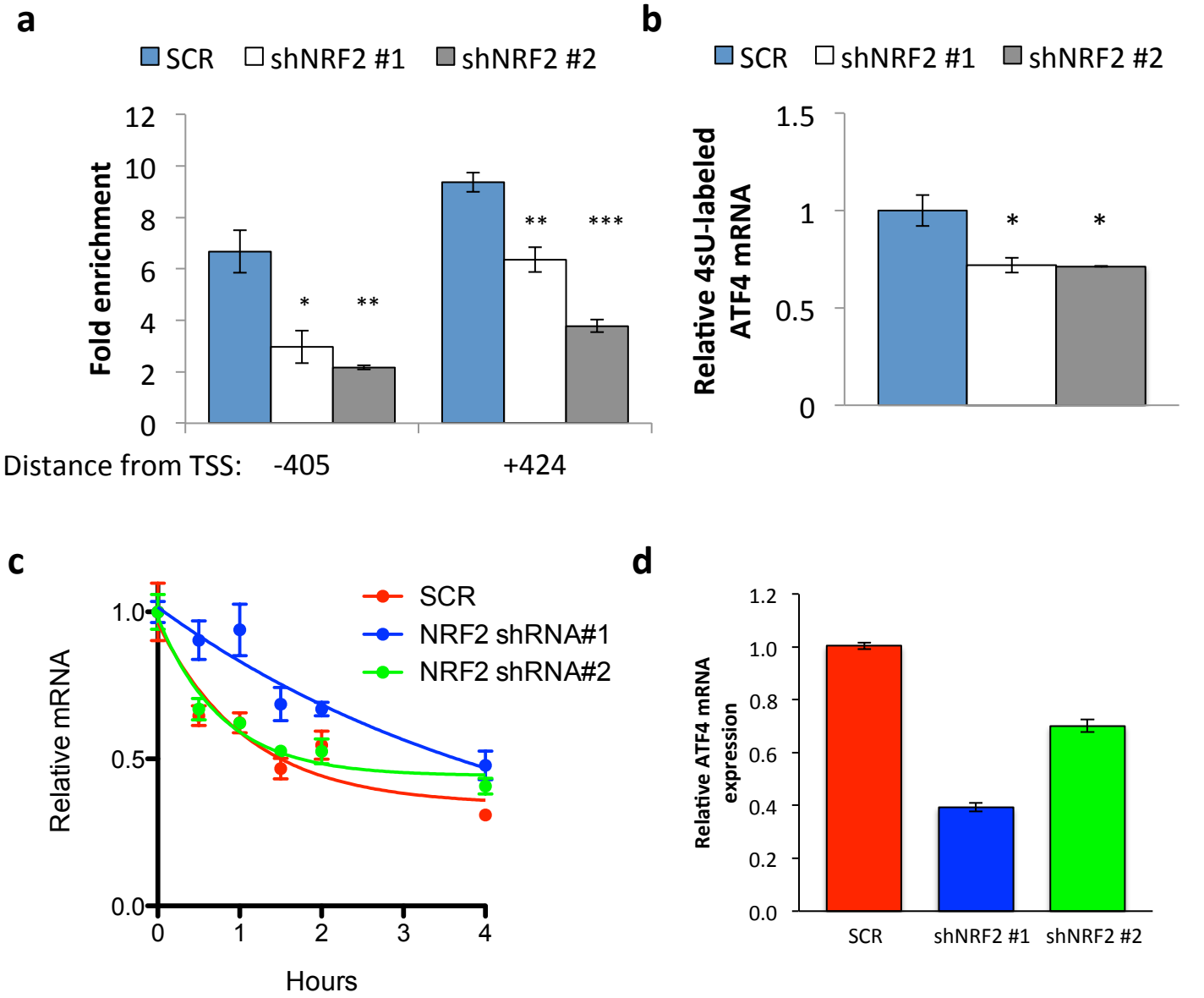
Supplementary Figure 10: NRF2 and PHGDH regulate serine biosynthesis. Cells were grown in the presence of U-^{13}C-glucose for 24 hours and metabolites were extracted and analysed by LC/MS. (Left) Western blot analysis of (Top) NRF2 and ACTIN protein expression in lysates from A549 cells expressing scramble (SCR) or NRF2 shRNAs #1 or #2. Stable cell lines were made by selecting in 1ug/ml puromycin for 5 days. (Bottom) Western blot analysis of PHGDH and ACTIN protein expression in lysates from A549 cells expressing scramble (SCR) or PHGDH shRNAs #1 or #2. Protein expression was analysed 3 days after infection with lentivirus. (Right) Analysis of the fractional ^{13}C-labelling of serine derived from glucose.



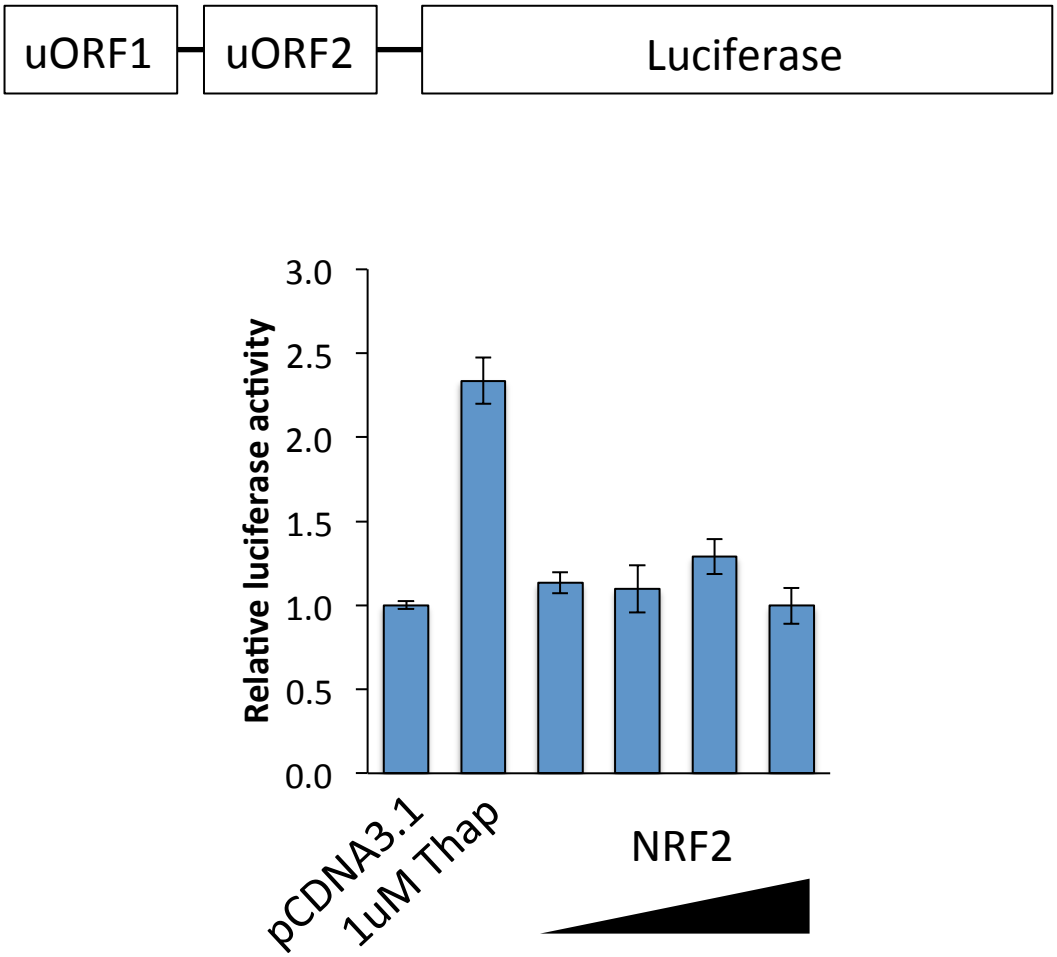
Supplementary Figure 11: Determination of NRF2 and ATF4 nuclear abundance in NSCLC cell lines. (a) Western blot of NRF2 and ATF4 in NSCLC cell line nuclear extracts. Ponceau staining denotes equal protein loading. NRF2 and Ponceau blots are from Supplementary Figure 6. (b) ATF4 protein expression correlates with serine biosynthesis. (c) ATF4 expression correlates with NRF2 expression.



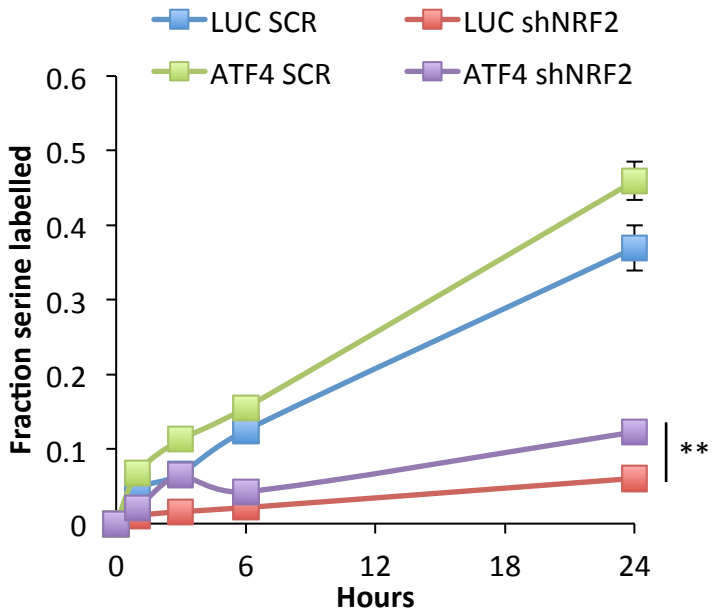
Supplementary Figure 12: NRF2 regulates the expression of serine/glycine biosynthesis genes through ATF4. (a) The mRNA expression of cell lines expressing scramble shRNA (SCR), NRF2 or ATF4 shRNAs was quantified by real-time PCR and normalized to the expression in the scramble controls. (b) ATF4 rescues the expression of serine biosynthesis enzymes in A549 cells transfected with NRF2 siRNA. (c) The specificity of shNRF2 #1 is demonstrated by partial rescue of NQO1, ATF4, and ATF4 target gene expression by reintroduction of a NRF2 cDNA. shNRF2 #1 targets the NRF2 5'UTR and not the NRF2 cDNA. (d) Ectopic NRF2 expression in H1975 cells induces the expression of NQO1, ATF4, and serine biosynthesis genes.



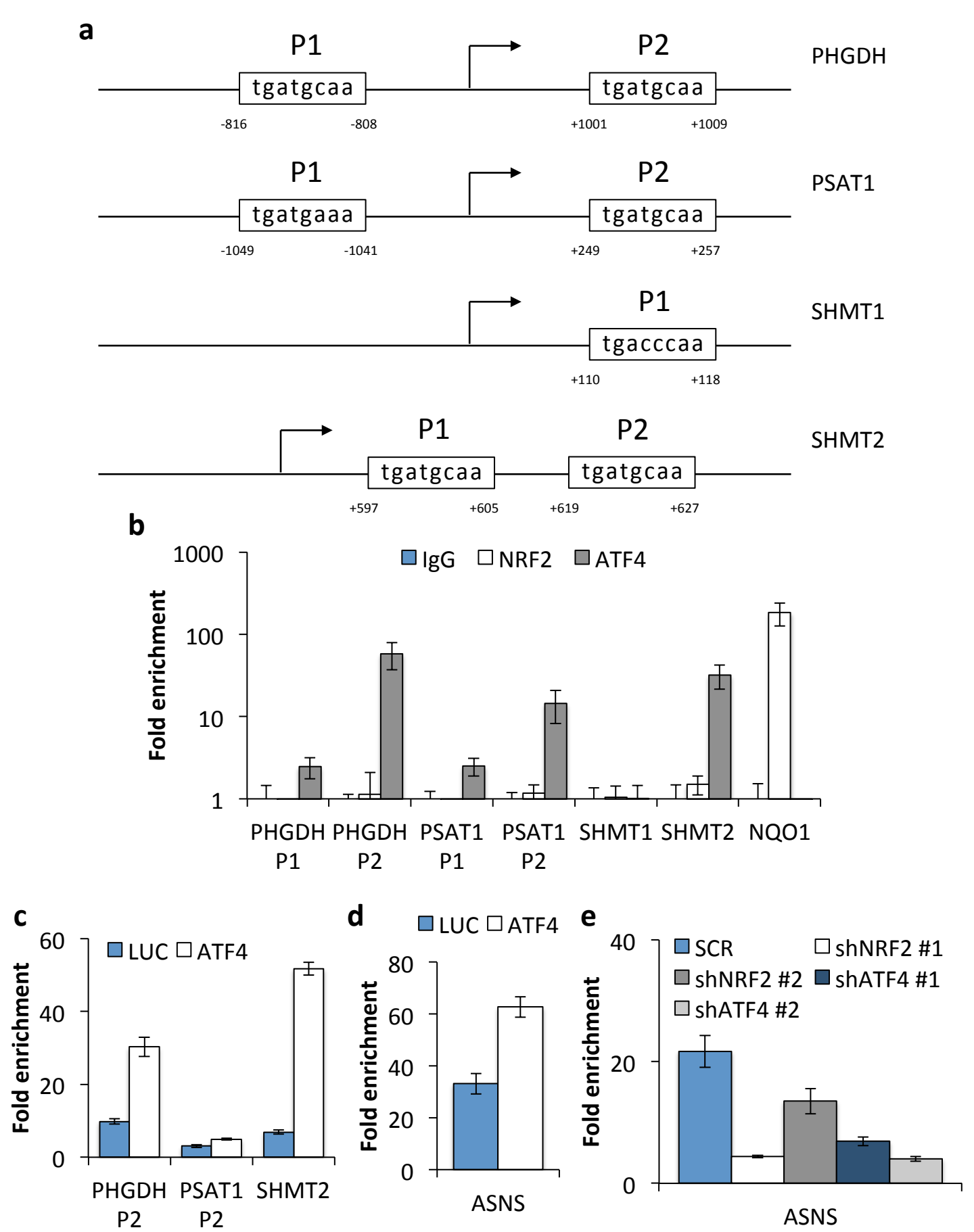
Supplementary Figure 13: NRF2 regulates ATF4 transcription. (a) Chromatin immunopriciptiation of RNA pol II (pSer5) binding to the ATF4 promoter. (b) Analysis of the levels of newly synthesized ATF4 transcript using4-thioruidine (4sU) pulse-labeling. Cells were labelled with 4sU for 60 minutes, after which time the RNA was purified and the 4sU residue linked to a biotin molecule. The biotinylated RNA was purified with streptavidin beads, cDNA was transcribed and levels are assayed by real-time PCR. ATF4 levels were normalized to β-actin. (c-d) Determination of ATF4 mRNA half-life. (c) ATF4 half-life was examined following 5ug/mL Actinomycin D treatment for the indicated times in A549 cells stably expressing scramble or NRF2 shRNA. ATF4 mRNA levels were normalized to time 0. (d) Total ATF4 mRNA expression levels in the cells from (c).



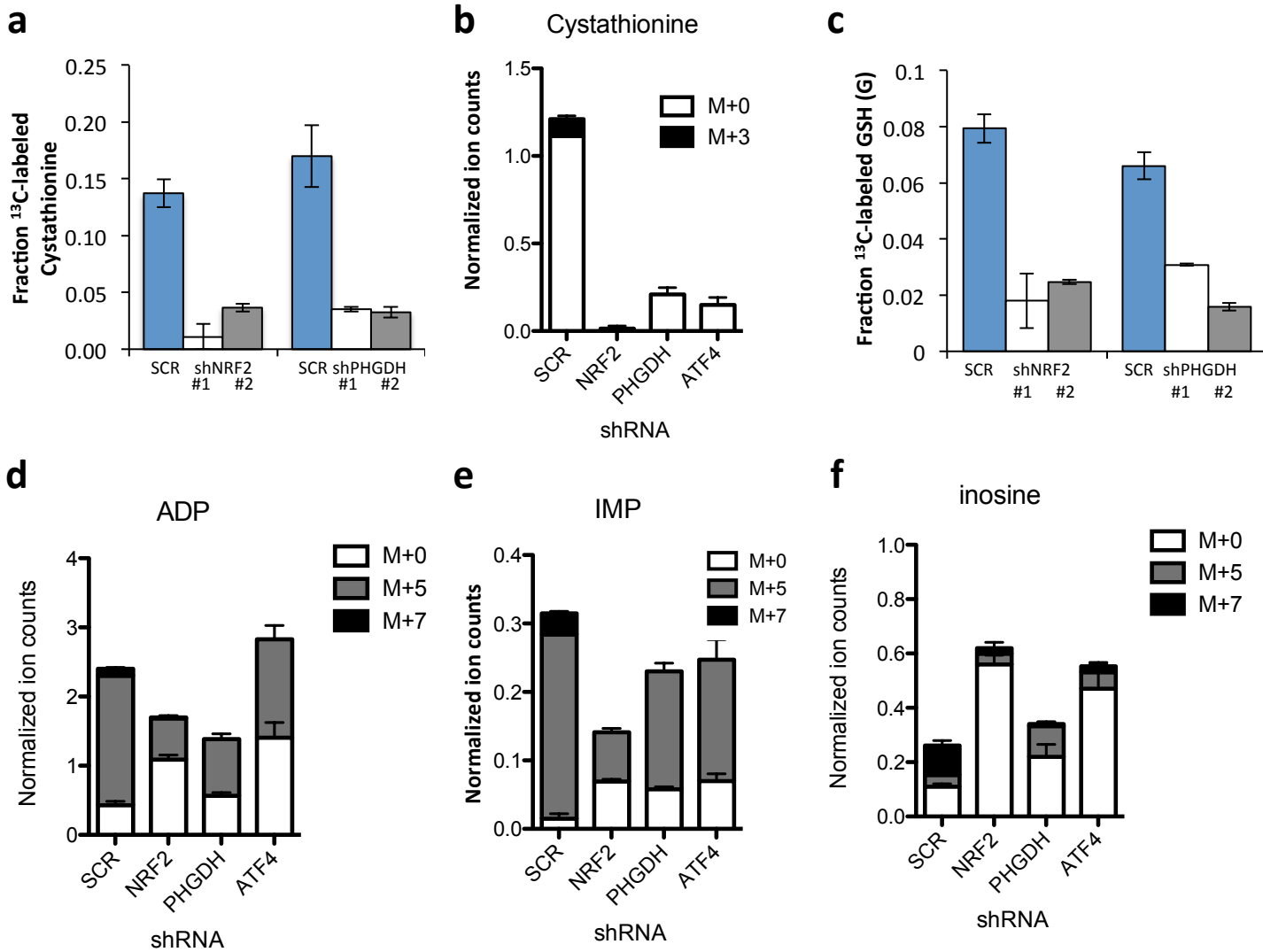
Supplementary Figure 14: Determination of ATF4 translation in a reporter assay. 293Ts were co-transfected with the ATF4 translation reporter, a renilla control plasmid, and pcDNA 3.1 or pcDNA3.1-NRF2 (range 1-200ng). Alternatively cells were treated with 1uM thapsigargin for 4 hours.



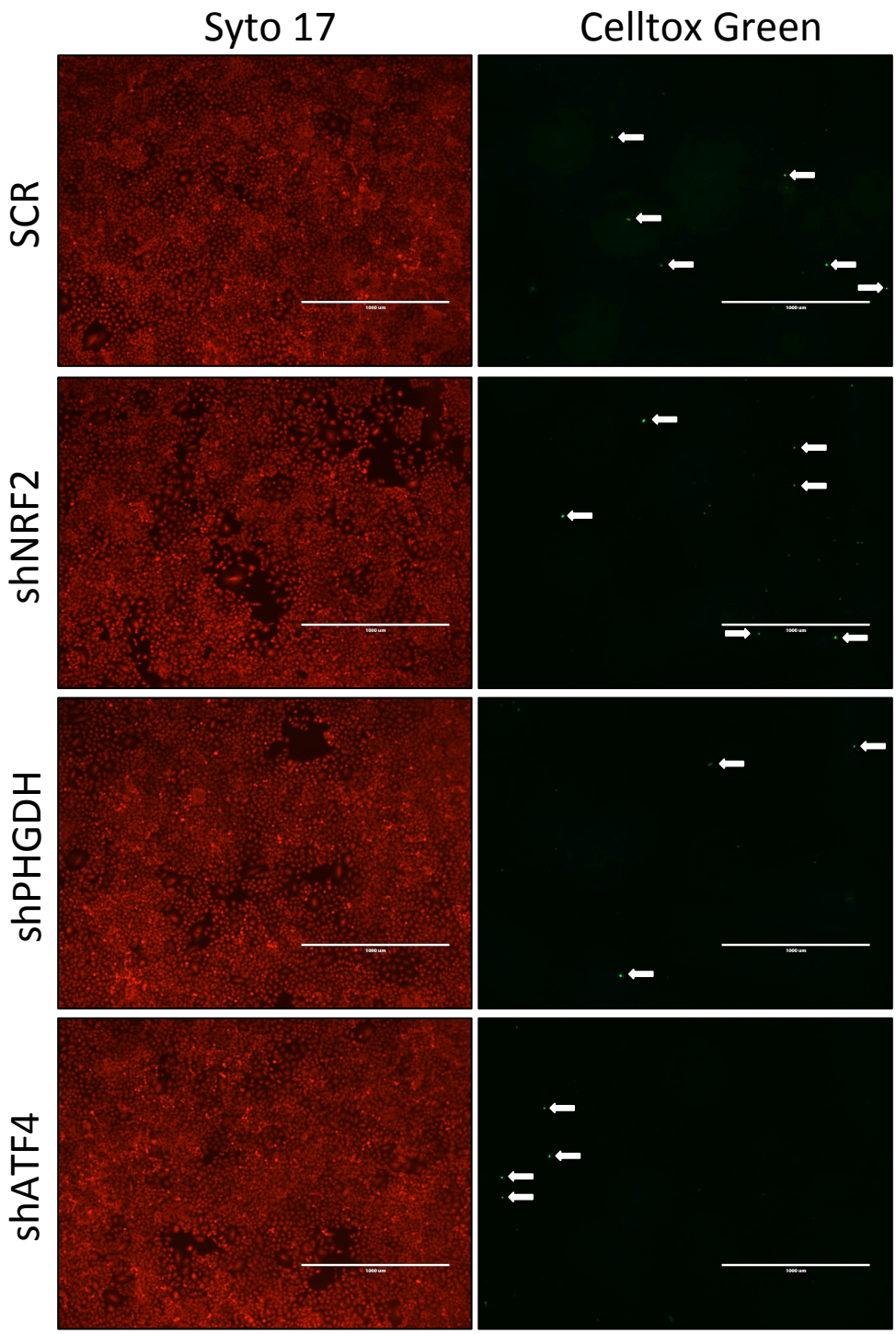
Supplementary Figure 15: ATF4 partially rescues serine biosynthesis following NRF2 knockdown. A549 cells were infected with lentivirus encoding mATF4 prior to infection with scramble or NRF2-targeting lentivirus. Cells were fed ^{13}C-glucose for the indicated time points, metabolites extracted, and fraction serine labelling determined by LC/MS.



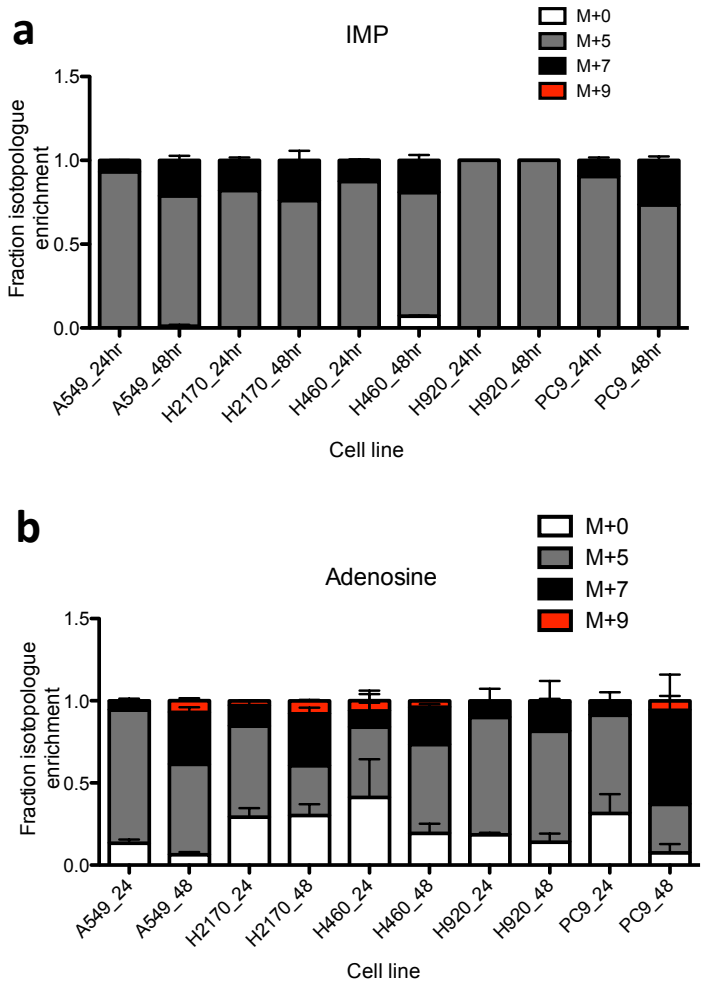
Supplementary Figure 16: Identification of ATF4 binding sites on the PHGDH, PSAT1 and SHMT2 promoters. (a) Putative ATF4 binding sites in the PHGDH, PSAT1, SHMT1 and SHMT2 promoters. (b) ATF4 binds to PHGDH P2, PSAT1 P2 and SHMT2 in A549 cells. NRF2 does not bind at these sites, despite binding to the NQO1 promoter. (c-d) ATF4 overexpression increases ATF4 binding to PHGDH, PSAT1, SHMT2 (c) and the classic ATF4 target ASNS (d) in H1975 cells. (e) NRF2 and ATF4 knockdown decreases ATF4 binding to ASNS in A549 cells.



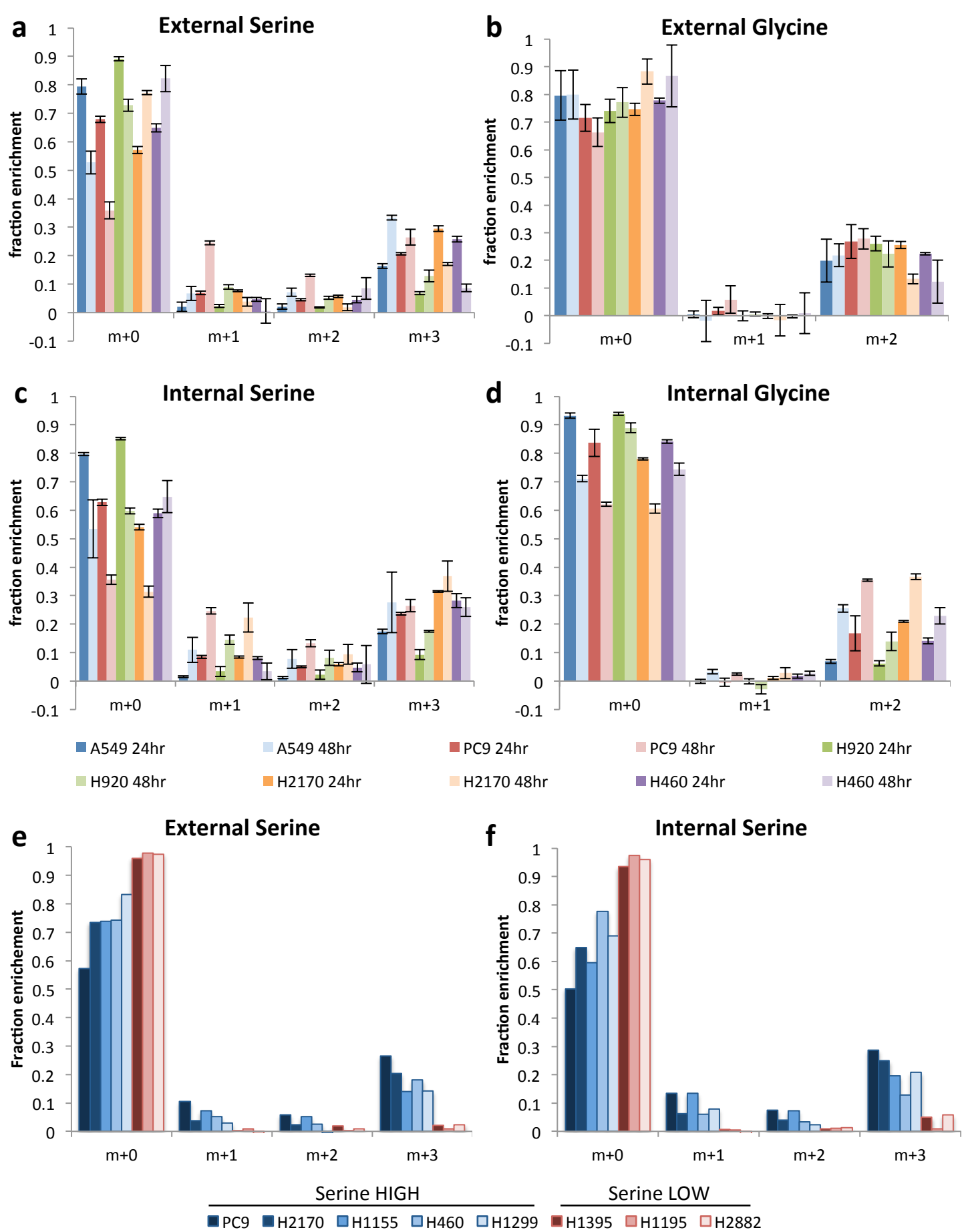
Supplementary Figure 17: Knockdown of NRF2, PHGDH, or ATF4 in A549 cells decreases incorporation of PHGDH-derived serine into downstream metabolites. Decreased labelling is observed in cystathionine (M +3) (a,b), the glycine moiety on glutathione (M+2) (c), and M+7 labelling of ADP (d) IMP (e) and inosine (f). (d-f) M+0 denotes no carbons labelled, M+5 denotes labelling on the ribose moiety, M+7 labelling denotes 5 carbons from ribose and 2 carbons from glycine or one-carbon units, and M+9 labelling denotes 5 carbons from ribose, 2 carbons from glycine, and 2 carbons from one-carbon units. No M+9 labelling was detected.



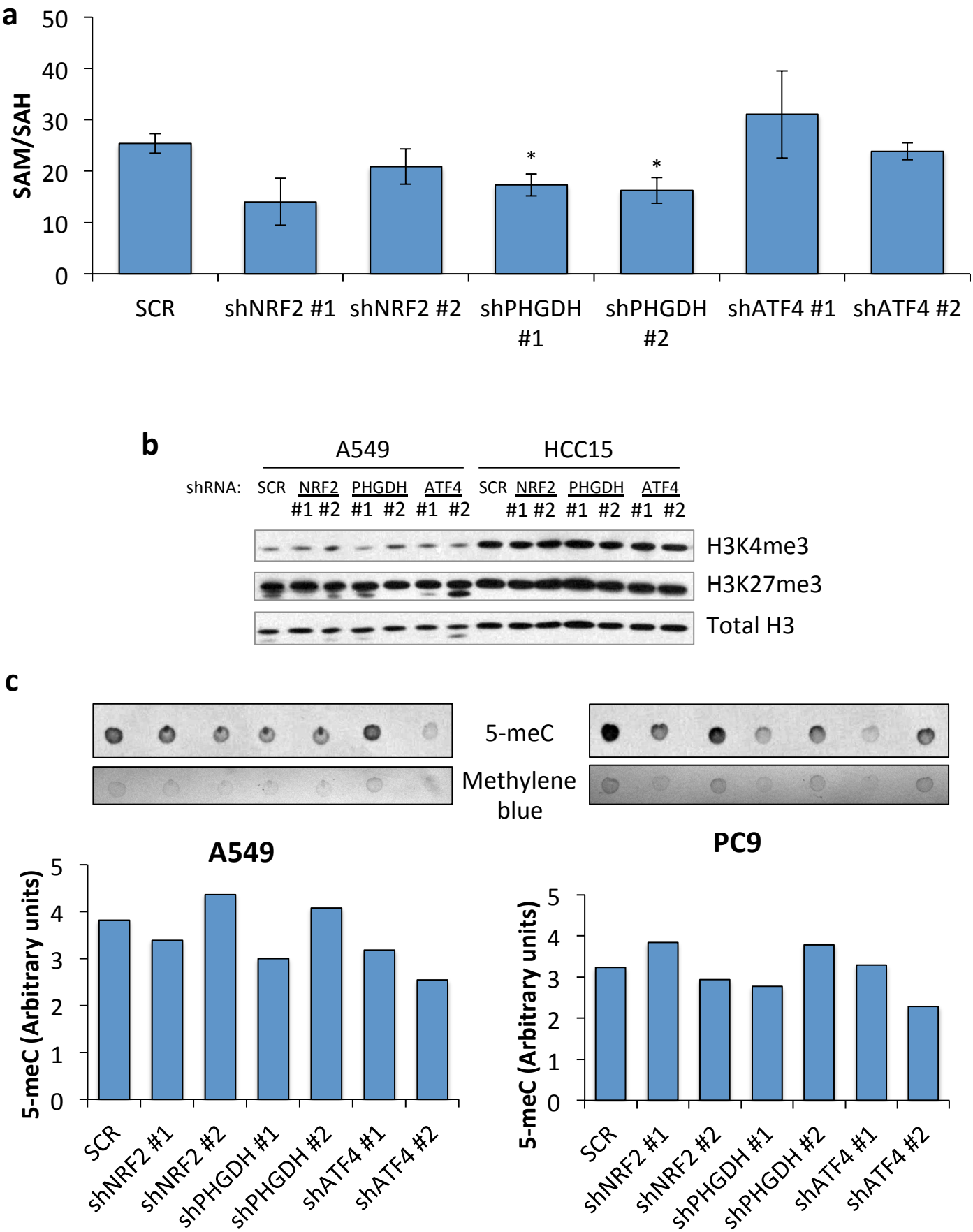
Supplementary Figure 18: No loss of viability of cells expressing SCR, NRF2, PHGDH, and ATF4 shRNAs at the time of metabolite extraction. Cells were stained with Syto17 to label all cells, and Celltox Green to label apoptotic cells. Apoptotic cells were rare in all populations.



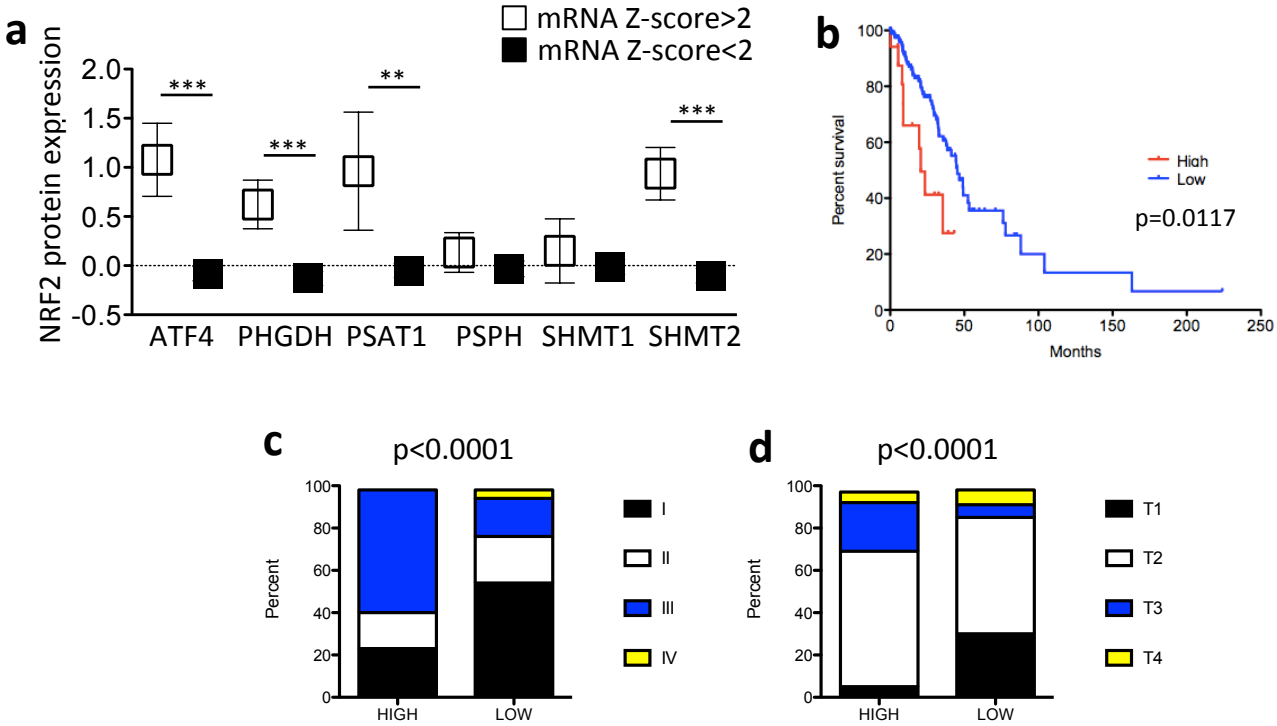
Supplementary Figure 19: Metabolite labeling in serine high cell lines. PHGDH-derived serine is incorporated into nucleotide precursors inosine monophosphate (IMP) (a) and adenosine (b) through the generation of glycine and one-carbon units. Cells were labelled with ^{13}C-glucose for 24 or 48 hours as indicated. M+0 denotes no carbons labelled, M+5 denotes labelling on the ribose moiety, M+7 labelling denotes 5 carbons from ribose and 2 carbons from glycine or one-carbon units, and M+9 labelling denotes 5 carbons from ribose, 2 carbons from glycine, and 2 carbons from one-carbon units.



Supplementary Figure 20: Analysis of the intracellular and extracellular labelling of serine and glycine in serine high cell lines. (a-b) Extracellular labelling of (a) serine and (b) glycine at 24 and 48 hours after ^{13}C-glucose labelling. (c-d) Intracellular labelling of (c) serine and (d) glycine at 24 and 48 hours after ^{13}C-glucose labelling. (e-f) Extracellular (e) and intracellular (f) labeling of serine labeling in serine high (blue) and serine low (red) cell lines 6 hours after ^{13}C-glucose labelling.



Supplementary Figure 21: Analysis of the s-adenosyl methionine/s-adenosyl homocysteine ratio and methylation of cellular targets in cells following knockdown of NRF2, PHGDH and ATF4. (a) SAM/SAH ratio following NRF2, PHGDH and ATF4 knockdown in A549 cells. SAM and SAH levels were determined by LC/MS. (b) Western analysis of histone methylation from histone extracts. (c) Dot blot analysis of methyl-cytosine levels in DNA. Bar graphs indicate normalization of methyl-cytosine levels to DNA loading (methylene blue staining).



Supplementary Figure 22: High expression of PHGDH, PSAT1 and SHMT2 confers poor prognosis in NSCLC. (a) Patient samples with high ATF4, PHGDH, PSAT1 or SHMT2 mRNA expression (Z-score >2) have elevated NRF2 protein expression. (b) Kaplan-Meier survival analysis of patients from TCGA with a high (red) or low (blue) expression of PHGDH, PSAT1 and SHMT2. The p-value was calculated using the Mantel-Cox test. (c-d) Association of tumour stage (c) and primary tumour pathological spread (d) associated with PHGHD, PSAT1 and SHMT2 expression. The p-value was calculated using the Chi-square test.

Supplementary Table 1: Gene expression correlations with 13C- serine and glycine labelling at 6 and 24 hours

Serine 6hr			Serine 24hr			Glycine 6hr			Glycine 24hr		
Rank	Gene	Pearson	Rank	Gene	Pearson	Rank	Gene	Pearson	Rank	Gene	Pearson
1	LOC100128361	0.605	1	APOO	0.545	1	LOC100128361	0.501	1	PHGDH	0.531
2	PHGDH	0.562	2	CENPJ	0.527	2	NUDT10	0.501	2	TCEB2	0.486
3	TCEB2	0.554	3	PHGDH	0.525	3	KLHL14	0.496	3	MAPK10	0.465
4	LEO1	0.519	4	NIPSNAP3A	0.508	4	ROR2	0.491	4	LEO1	0.460
5	EGFL6	0.508	5	LEO1	0.506	5	DLK1	0.488	5	KBTBD6	0.457
6	CENPJ	0.500	6	LSM14A	0.504	6	CD1D	0.484	6	CENPJ	0.450
7	EIF2S2	0.487	7	POLA1	0.504	7	LOC100507043	0.484	7	LOC100128361	0.438
8	NFE2L2	0.482	8	KBTBD6	0.503	8	MAPK10	0.482	8	KBTBD7	0.427
9	FANCC	0.474	9	KIF11	0.501	9	ZBTB8B	0.475	9	PAQR4	0.427
10	RHBDL3	0.463	10	FANCC	0.500	10	RUNDC3B	0.469	10	C20orf112	0.423
11	MAPK10	0.459	11	NUP133	0.499	11	TBC1D24	0.468	11	ZNF768	0.421
12	KBTBD6	0.443	12	KIAA1841	0.494	12	ZCCHC12	0.465	12	MAS1L	0.417
13	PPIA	0.443	13	TCEB2	0.493	13	D4S234E	0.465	13	EPHX1	0.416
14	XPA	0.439	14	COL5A2	0.492	14	40058	0.458	14	EGFL6	0.415
15	CAMSAP2	0.439	15	PHF16	0.479	15	BTN1A1	0.454	15	LOC100506995	0.415
16	C3orf25	0.434	16	HSD17B10	0.474	16	PPM1E	0.453	16	MED4	0.415
17	EPHX1	0.433	17	C1orf124	0.468	17	PRL	0.453	17	PPIA	0.413
18	NUP133	0.431	18	GSTA4	0.466	18	HOTAIR	0.451	18	SRGAP3	0.412
19	C16orf59	0.426	19	TIMM23	0.466	19	ATCAY	0.450	19	AIMP2	0.407
20	GGCT	0.426	20	ZNF566	0.464	20	PPIA	0.444	20	FANCC	0.407
21	FAM8A1	0.425	21	DDX46	0.463	21	CPA1	0.444	21	COL3A1	0.406
22	RNF20	0.425	22	KCMF1	0.463	22	CDK13	0.443	22	EIF2S2	0.406
23	HIST1H3F	0.424	23	NDUFA1	0.462	23	TCEB2	0.442	23	USP7	0.402
24	POLA1	0.423	24	EIF2S2	0.460	24	PHGDH	0.441	24	LRRC57	0.402
25	NIPSNAP3A	0.421	25	RHBDL3	0.458	25	PAQR4	0.441	25	LPAR6	0.401
26	SNRPE	0.421	26	SLC47A1	0.458	26	SNRPE	0.436	26	SUCLA2	0.399
27	LOC100507043	0.419	27	HIBCH	0.457	27	C15orf59	0.434	27	SLC43A2	0.396
28	C1orf131	0.419	28	COX7B	0.456	28	NSD1	0.432	28	C1QB	0.396
29	C19orf76	0.416	29	MAS1L	0.453	29	FAM8A1	0.429	29	D2HGDH	0.394
30	ENAH	0.416	30	RIOK1	0.453	30	LOC150622	0.428	30	PIK3C2B	0.393
31	PAQR4	0.416	31	SIX3	0.452	31	RGS12	0.428	31	C1orf131	0.390
32	PASK	0.413	32	LIN9	0.451	32	GPR61	0.423	32	NHSL1	0.389
33	PHTF2	0.411	33	SUCLA2	0.450	33	CBLN2	0.422	33	COL5A2	0.388
34	CBLN2	0.410	34	GSTM4	0.446	34	CUL3	0.420	34	LOC100132735	0.386
35	PHF8	0.409	35	DNAJB7	0.446	35	DSCR6	0.417	35	XPA	0.385
36	TBC1D7	0.408	36	MLLT11	0.445	36	POLA1	0.417	36	BTG2	0.384
37	ECI1	0.408	37	CBLN2	0.445	37	EFCAB1	0.416	37	PNMT	0.383
38	USP7	0.408	38	CUL3	0.444	38	LOC643201	0.416	38	RNF20	0.383
39	NHSL1	0.406	39	C16orf59	0.442	39	KBTBD2	0.415	39	IGFBP2	0.381
40	CROT	0.406	40	HDDC2	0.441	40	MIR600HG	0.415	40	PASK	0.379
41	RFXAP	0.405	41	ENAH	0.441	41	LOC283547	0.415	41	GGCT	0.379
42	PGD	0.405	42	PIR	0.441	42	ITGB1BP2	0.414	42	PHF16	0.377
43	MAS1L	0.405	43	LOC100128361	0.440	43	DYNLT1	0.413	43	MMP19	0.377
44	IRAK1BP1	0.404	44	TIMM21	0.438	44	C3orf25	0.413	44	SKP2	0.376
45	SUCLA2	0.403	45	ALDH1A1	0.435	45	HOXA10	0.411	45	ECI1	0.375
46	TDP2	0.400	46	MED4	0.435	46	ECI1	0.408	46	NAA60	0.375
47	LOC283547	0.398	47	TDP2	0.434	47	KIAA2022	0.408	47	LOC100506597	0.374
48	STRBP	0.397	48	TBCE	0.434	48	SLC7A3	0.408	48	ARID1B	0.372
49	CUL3	0.397	49	TAF9B	0.433	49	EGFL6	0.406	49	PHF8	0.372
50	IPO9	0.397	50	RHEB	0.431	50	C9orf16	0.404	50	LSM14A	0.371
51	DDX46	0.396	51	COL3A1	0.430	51	LOC100506530	0.403	51	PSMA2	0.371

52	PNMT	0.396	52	HAUS1	0.429	52	ATRNL1	0.403	52	FLJ34503	0.371
53	RBMX	0.395	53	CCDC90A	0.428	53	EIF2AK1	0.402	53	C16orf59	0.369
54	LSM14A	0.394	54	C14orf142	0.427	54	LEO1	0.402	54	LOC283688	0.368
55	UBE2L3	0.394	55	PEG3-AS1	0.427	55	SOWAHA	0.401	55	SARM1	0.368
56	MED4	0.394	56	UBE2L3	0.425	56	KIAA0146	0.401	56	ALDH1A1	0.368
57	RPS27A	0.393	57	LOC100132735	0.425	57	HADH	0.401	57	ARHGAP35	0.368
58	NFIA	0.393	58	FECH	0.424	58	FRMPD3	0.401	58	LOC283547	0.368
59	YWHAG	0.393	59	CCDC34	0.423	59	LOC100134361	0.399	59	PURB	0.367
60	DLGAP1	0.392	60	USP7	0.422	60	DKFZP586I1420	0.399	60	CUL3	0.367
61	GTF2A2	0.391	61	TCP1	0.422	61	GGCT	0.397	61	C9orf125	0.366
62	MRS2	0.391	62	LOC100507486	0.421	62	HPCA	0.395	62	SAP18	0.366
63	EEF1A1	0.391	63	ING5	0.420	63	NASP	0.395	63	PPARGC1B	0.365
64	C9orf125	0.391	64	FAM8A1	0.419	64	SNX13	0.395	64	RFX7	0.362
65	FLJ34503	0.391	65	EIF1AX	0.419	65	PASK	0.394	65	UBE2L3	0.362
66	KBTBD7	0.387	66	HAUS7	0.418	66	TCEAL2	0.393	66	PGD	0.361
67	KLRD1	0.387	67	RNGTT	0.417	67	STRBP	0.391	67	OSR2	0.361
68	SKP2	0.387	68	PDHA1	0.416	68	CENPJ	0.391	68	TRAF7	0.360
69	PA2G4	0.387	69	RNF20	0.416	69	ZNF513	0.390	69	FAM53B	0.360
70	KRT5	0.385	70	IKBKAP	0.416	70	HOXA11	0.390	70	RFXAP	0.360
71	ALDH3A1	0.385	71	KLHL15	0.416	71	LOC100506597	0.389	71	HOXA11	0.360
72	COX5A	0.384	72	IREB2	0.415	72	SLC18A3	0.388	72	PIR	0.359
73	UBQLN2	0.383	73	LIG1	0.414	73	MPHOSPH8	0.388	73	RCBTB1	0.359
74	GMNN	0.383	74	DLX1	0.413	74	RAB26	0.386	74	NIPSNAP3A	0.359
75	FECH	0.383	75	GTF2A2	0.413	75	BGN	0.386	75	CIC	0.358
76	YAE1D1	0.382	76	OIP5	0.411	76	PHF8	0.385	76	SULF2	0.358
77	BTG2	0.381	77	C15orf59	0.411	77	LOC100506995	0.381	77	MYBL2	0.357
78	LRRC57	0.380	78	RP2	0.411	78	CHRNA3	0.380	78	SEPHS1	0.357
79	SMC1A	0.380	79	JAM3	0.411	79	CHST1	0.380	79	KLRD1	0.357
80	PSMA2	0.379	80	EIF3K	0.410	80	RMST	0.379	80	SKP1	0.355
81	GALNTL1	0.378	81	NDUFS1	0.409	81	SH2B1	0.379	81	TMEM97	0.355
82	HSD17B10	0.377	82	PHTF2	0.409	82	SLC27A3	0.378	82	CYBASC3	0.354
83	CAMKK1	0.377	83	ASF1A	0.407	83	TAS1R1	0.378	83	GMNN	0.354
84	DNAJB7	0.376	84	MAGOHB	0.407	84	GRIPAP1	0.377	84	HIST1H3D	0.353
85	FBN2	0.376	85	PA2G4	0.406	85	TCF20	0.377	85	UTP14C	0.352
86	MRAP2	0.375	86	PSMG1	0.406	86	SCN4B	0.377	86	NDUFA10	0.352
87	HOXB13	0.375	87	SIRT1	0.405	87	FAM123A	0.376	87	YAE1D1	0.351
88	ITGB1BP2	0.375	88	CDK8	0.405	88	PRAC	0.375	88	PTCH1	0.351
89	KIF11	0.375	89	PEG3	0.405	89	RBM8A	0.374	89	C16orf54	0.350
90	AIMP2	0.374	90	TBC1D7	0.405	90	ATP8A2	0.374	90	POLA1	0.350
91	PIR	0.374	91	TMEM237	0.405	91	LAG3	0.373	91	NUP133	0.350
92	TBC1D24	0.374	92	HTATSF1	0.404	92	LOC100507194	0.372	92	TAS2R41	0.349
93	SOSTDC1	0.374	93	NR0B1	0.404	93	HNRNPA3	0.372	93	SOX12	0.349
94	IGFBP2	0.373	94	TPMT	0.403	94	PPP1R16B	0.372	94	MGC16025	0.349
95	ATRNL1	0.372	95	DZIP1	0.403	95	SHF	0.371	95	DLX1	0.348
96	JAM3	0.372	96	POMP	0.402	96	KHK	0.371	96	C3orf25	0.348
97	CCDC90A	0.372	97	TCF12	0.401	97	EIF2S2	0.370	97	ABCC5	0.347
98	IQCA1	0.371	98	SHPRH	0.401	98	DNASE1L2	0.370	98	HIST1H3F	0.347
99	ASF1A	0.370	99	MTERFD3	0.400	99	BRD3	0.369	99	AKR1C2	0.347
100	PRL	0.368	100	C19orf40	0.400	100	SEC31B	0.369	100	SOX2	0.346
101	ING5	0.368	101	SPHAR	0.400	101	ING5	0.369	101	TBC1D7	0.346
102	OLA1	0.368	102	ID2	0.399	102	C1orf173	0.369	102	HFE2	0.346
103	IREB2	0.368	103	SLC25A14	0.398	103	RFXAP	0.368	103	RNF114	0.345
104	SLC25A14	0.367	104	C5orf44	0.398	104	CHRNB4	0.368	104	PKD1	0.344
105	RNGTT	0.367	105	APOOL	0.398	105	C1QA	0.366	105	ALG1	0.342

106	AKR1C1	0.367	106	C21orf128	0.398	106	NRXN2	0.366	106	KRT5	0.341
107	C20orf112	0.367	107	UBR3	0.397	107	LYSMD4	0.365	107	TAF11	0.341
108	C1QB	0.366	108	EXO1	0.397	108	PDZD4	0.365	108	HOXA10	0.341
109	PSMC2	0.366	109	CCAR1	0.397	109	ZSCAN29	0.364	109	ZSCAN29	0.341
110	LOC83954	0.366	110	C1orf131	0.396	110	NDUFA4	0.364	110	PRPF38A	0.340
111	MIR600HG	0.366	111	SOX12	0.396	111	NT5M	0.364	111	OPA1	0.340
112	ANKRD16	0.366	112	GLI1	0.396	112	ZIC3	0.364	112	BRD3	0.339
113	LOC283688	0.364	113	ANKRD16	0.395	113	RHBDL3	0.364	113	FAM215A	0.339
114	SOHLH1	0.364	114	FH	0.395	114	SLC25A14	0.362	114	PEG3-AS1	0.339
115	LIG1	0.364	115	ABCB10	0.395	115	FGF7	0.362	115	IREB2	0.338
116	CCBL1	0.364	116	EMID2	0.395	116	CRMP1	0.362	116	DNAJB7	0.338
117	TCP1	0.364	117	RBM17	0.395	117	ROGDI	0.361	117	UNC5B	0.338
118	NTRK2	0.363	118	UCHL1	0.394	118	C16orf59	0.361	118	GATA2	0.338
119	C11orf53	0.363	119	LOC100506935	0.393	119	TMEM107	0.360	119	ING5	0.338
120	CHRNA5	0.363	120	IFT88	0.393	120	GATA4	0.360	120	ENAH	0.337
121	MAGOHB	0.362	121	EXOSC3	0.393	121	NFIA	0.360	121	TBC1D24	0.336
122	RBM34	0.361	122	IER3IP1	0.392	122	LOC100506388	0.358	122	AKR1C1	0.336
123	ROR2	0.360	123	NUP160	0.392	123	TNRC6B	0.358	123	RBM17	0.335
124	RFX7	0.360	124	PSMA2	0.391	124	WNK3	0.358	124	GNG4	0.335
125	CD1D	0.359	125	IPO9	0.391	125	BTNL9	0.357	125	CDCA7	0.334
126	LPAR6	0.359	126	NFYB	0.391	126	ANKS6	0.357	126	KIF11	0.334
127	LOC100506935	0.359	127	SEPHS1	0.391	127	NFE2L2	0.357	127	RELL2	0.334
128	SKP1	0.359	128	PASK	0.391	128	ZZEF1	0.357	128	VPS39	0.334
129	CMTM5	0.358	129	ITGB1BP2	0.390	129	PHF16	0.356	129	DLGAP1	0.333
130	ZSCAN29	0.357	130	ATP5G3	0.390	130	IRAK1BP1	0.356	130	HTATSF1	0.333
131	LIN9	0.356	131	PRL	0.390	131	ZBTB34	0.355	131	STRBP	0.333
132	DENND2C	0.356	132	BRP44	0.390	132	SIX6	0.355	132	LIG1	0.333
133	HOXA10	0.356	133	XPA	0.389	133	MAK	0.354	133	BCL9	0.332
134	RNF187	0.356	134	NFIA	0.389	134	BTG2	0.354	134	PIK3R1	0.332
135	OIP5	0.355	135	TOR3A	0.389	135	HOXB13	0.354	135	FOLH1	0.332
136	TAF11	0.355	136	LOC149086	0.389	136	SENP7	0.353	136	RAI1	0.331
137	MYCBP2	0.354	137	SARM1	0.388	137	LOC83954	0.352	137	LOC100506935	0.331
138	IKBKAP	0.354	138	SMC1A	0.388	138	ODZ3	0.352	138	NUP210P1	0.331
139	MRPL30	0.354	139	FGD1	0.387	139	TRO	0.352	139	TUFM	0.331
140	CDCA7	0.353	140	RFXAP	0.387	140	FANCC	0.351	140	HDLBP	0.331
141	KIAA0319	0.353	141	EPB41L5	0.387	141	COL2A1	0.350	141	LINC00479	0.329
142	MRPL44	0.352	142	UBA2	0.387	142	TLX1	0.350	142	SOHLH1	0.329
143	UHRF1BP1	0.352	143	SRSF1	0.386	143	PABPC5	0.350	143	ALDH3A2	0.329
144	NASP	0.352	144	SNRPE	0.386	144	CITED1	0.350	144	39872	0.329
145	NR0B1	0.351	145	CCBL1	0.385	145	SOHLH1	0.349	145	IGFBP5	0.329
146	PSAT1	0.351	146	SNX12	0.385	146	ING3	0.349	146	TDP2	0.328
147	RNPS1	0.351	147	MAP1A	0.385	147	ZNF768	0.349	147	IRAK1BP1	0.328
148	CRMP1	0.351	148	AFG3L2	0.385	148	PSMA2	0.348	148	IQCA1	0.328
149	PCNA	0.351	149	GAS7	0.385	149	ZNF460	0.347	149	MPLKIP	0.328
150	COX7B	0.350	150	GSG2	0.384	150	CCP110	0.347	150	CBLN2	0.328
151	C1orf111	0.350	151	SEMA6D	0.384	151	CHRM4	0.347	151	SKA3	0.326
152	HDLBP	0.350	152	EEF1A1	0.384	152	LOC100507739	0.347	152	GSTM4	0.326
153	KCNS2	0.349	153	NDUFA6	0.383	153	PHTF2	0.346	153	SLC35A4	0.325
154	OPN1SW	0.349	154	SKP2	0.383	154	PKNOX1	0.346	154	DSCC1	0.325
155	AKR1C2	0.349	155	CMTM5	0.381	155	FBXW2	0.346	155	INTS6-AS1	0.324
156	HR	0.349	156	SCARA5	0.381	156	GTF2IRD1	0.345	156	CMTM5	0.324
157	MGC16025	0.348	157	HIST1H3F	0.380	157	FGF12	0.345	157	COX5A	0.324
158	HDDC2	0.348	158	RPS27A	0.380	158	AP3B2	0.344	158	GTF2IRD1	0.323
159	RNASEH1	0.348	159	C9orf125	0.379	159	NFATC2IP	0.344	159	C1orf129	0.323

160	ILKAP	0.348	160	PGD	0.379	160	SYBU	0.343	160	ANKRD13B	0.322
161	SHPRH	0.348	161	RAB11FIP2	0.379	161	IGFBP2	0.343	161	POLR1D	0.322
162	EHMT1	0.347	162	HNRNPA0	0.379	162	PABPC1L	0.342	162	HNRNPA0	0.322
163	DYNLL1	0.346	163	ZNF271	0.379	163	CNOT6	0.342	163	MRS2	0.322
164	ATRX	0.345	164	HOXB13	0.378	164	TAGAP	0.342	164	DYNLL1	0.321
165	GAL3ST2	0.345	165	CHUK	0.378	165	SRRM2	0.342	165	DDX46	0.321
166	WDR76	0.344	166	RCBTB1	0.378	166	ZNF821	0.341	166	FRAT2	0.321
167	MLST8	0.344	167	KIAA1586	0.378	167	C19orf76	0.341	167	PDS5B	0.321
168	LMNB1	0.344	168	ZNF507	0.377	168	OLA1	0.341	168	ZCCHC3	0.321
169	HIST1H3G	0.343	169	OLA1	0.377	169	GAS8	0.341	169	HR	0.320
170	KLHL14	0.343	170	MFF	0.377	170	LUC7L2	0.341	170	SYBU	0.320
171	SIX3	0.343	171	DNA2	0.376	171	PRR14L	0.341	171	SLC29A3	0.320
172	PHF16	0.343	172	ZNF192	0.376	172	GNL1	0.340	172	C9orf16	0.320
173	IAPP	0.343	173	IPO7	0.376	173	H2AFV	0.340	173	TUBB2B	0.319
174	ZCCHC10	0.342	174	TIMM17A	0.376	174	CXCR4	0.339	174	TRIL	0.319
175	BEX1	0.342	175	DTL	0.375	175	FAM172A	0.339	175	TRIM26	0.319
176	GSTA4	0.342	176	DSTYK	0.375	176	HDAC10	0.339	176	SOSTDC1	0.319
177	KIAA0101	0.342	177	WDR76	0.375	177	MEGF11	0.339	177	HSD17B10	0.319
178	TMEM237	0.342	178	NXT2	0.375	178	NIPSNAP3A	0.339	178	PTPLAD1	0.318
179	ANP32B	0.342	179	TSNAX	0.375	179	PRPH	0.338	179	REV1	0.318
180	ZNF192	0.341	180	GIP	0.375	180	DPY19L2P3	0.338	180	TTF2	0.317
181	SAP18	0.341	181	TRAPPC2	0.375	181	LDB3	0.337	181	CYP4F12	0.317
182	COL5A2	0.341	182	LOC647946	0.374	182	TXN2	0.337	182	MAGEF1	0.317
183	PAFAH1B3	0.341	183	ATP5A1	0.374	183	HDAC4	0.336	183	POLD2	0.317
184	SEMA3F	0.341	184	BTNL9	0.373	184	ZNF346	0.336	184	PIGX	0.317
185	RNASEH2B	0.341	185	DLGAP1	0.373	185	PRKDC	0.336	185	NT5C3	0.317
186	MARK1	0.341	186	RPS16	0.373	186	GABRG3	0.335	186	NFE2L2	0.316
187	MRPS31	0.341	187	EPHX1	0.373	187	ZNF662	0.335	187	NUDT15	0.316
188	PTCH1	0.341	188	MRPL30	0.373	188	KBTBD6	0.335	188	SLC6A8	0.316
189	FGF12	0.341	189	GMNN	0.372	189	RNF187	0.335	189	TRAF3IP1	0.316
190	MAPKBP1	0.340	190	ATP5J	0.372	190	LOC157627	0.335	190	TCP1	0.316
191	REV1	0.340	191	NRG2	0.372	191	HADHA	0.335	191	KIF22	0.315
192	TAF9B	0.339	192	LYRM7	0.370	192	ERP44	0.334	192	HIBCH	0.315
193	TPMT	0.339	193	TDRD3	0.370	193	GPRIN1	0.334	193	CLDN8	0.314
194	NAA60	0.338	194	MRS2	0.370	194	CDK5	0.334	194	CYCS	0.314
195	RCBTB1	0.338	195	C1orf31	0.369	195	KBTBD7	0.334	195	HADH	0.313
196	ANKRD13B	0.338	196	NARS	0.369	196	EPHA5	0.334	196	CDK8	0.313
197	CELA3A	0.338	197	MSL3	0.368	197	TMEM132C	0.333	197	SEMA3F	0.313
198	ERP44	0.338	198	SMC2	0.368	198	SPIRE2	0.333	198	MADD	0.312
199	SOX12	0.338	199	ALMS1	0.367	199	CUX1	0.333	199	SEMA6D	0.312
200	C1orf31	0.338	200	KIF14	0.367	200	CDKN2B-AS1	0.333	200	CCDC34	0.312
201	COL3A1	0.337	201	ZNF324B	0.367	201	HUWE1	0.333	201	ZCCHC10	0.312
202	SESTD1	0.337	202	IDE	0.367	202	CCDC136	0.333	202	MSX2	0.312
203	HNRNPA3	0.337	203	SAP18	0.367	203	ZNF48	0.332	203	RNF187	0.312
204	PPM1E	0.337	204	TSHZ1	0.366	204	ATPIF1	0.332	204	DDX49	0.312
205	WASF1	0.336	205	GBX2	0.366	205	CHN2	0.332	205	ENDOG	0.312
206	HIST1H3D	0.336	206	DMXL1	0.366	206	RAPGEF4	0.331	206	SLC4A11	0.311
207	LOC100132735	0.336	207	ISLR2	0.366	207	PPIP5K1	0.331	207	RPS27A	0.310
208	GSTM3	0.336	208	RNF138	0.365	208	DLX4	0.331	208	PRR15	0.310
209	LINC00487	0.336	209	C14orf162	0.365	209	MGC45800	0.331	209	PNKD	0.310
210	TP53AIP1	0.336	210	PGBD1	0.364	210	AIF1L	0.330	210	C19orf76	0.310
211	ZCCHC12	0.335	211	CABYR	0.363	211	PEX6	0.330	211	PIGS	0.310
212	HIBCH	0.335	212	FAM104B	0.363	212	D2HGDH	0.330	212	GAL3ST2	0.309
213	C9orf16	0.335	213	CCP110	0.362	213	RALA	0.330	213	TOP1MT	0.309

214	AQP10	0.335	214	LOC255352	0.362	214	UHRF1BP1	0.330	214	WFDC9	0.309
215	TIMM23	0.334	215	TSN	0.362	215	LOC100288152	0.330	215	ILKAP	0.309
216	EIF3J	0.334	216	R3HDM1	0.362	216	MPLKIP	0.329	216	GSTA4	0.309
217	PNKD	0.334	217	CTPS	0.361	217	YWHAG	0.329	217	DYNLT1	0.309
218	HOXA11	0.334	218	DHX9	0.361	218	PTPN18	0.329	218	EMID2	0.309
219	TMEM97	0.334	219	PDE3B	0.361	219	SDK1	0.329	219	ELFN1	0.308
220	DHRS11	0.333	220	EID2	0.360	220	WDR76	0.329	220	SULF1	0.308
221	CDK8	0.333	221	POP4	0.360	221	TULP4	0.328	221	LCMT2	0.308
222	RNFT2	0.333	222	NEFH	0.360	222	RNPS1	0.328	222	SESTD1	0.308
223	NUDT10	0.333	223	MEGF11	0.359	223	GNG4	0.328	223	SPNS1	0.308
224	ANP32A	0.333	224	LSM2	0.359	224	E2F2	0.327	224	CHGB	0.308
225	DYNLT1	0.333	225	CCDC138	0.359	225	TCF24	0.327	225	UBQLN2	0.308
226	MPLKIP	0.332	226	CUTA	0.359	226	HSD17B10	0.327	226	PA2G4	0.307
227	OPA1	0.332	227	LOC100129195	0.359	227	CDK5R1	0.326	227	TPD52L1	0.307
228	TAS2R41	0.332	228	PSAT1	0.358	228	RC3H2	0.326	228	DENND2C	0.307
229	RBM10	0.331	229	CAND2	0.358	229	TP53I11	0.325	229	THAP4	0.307
230	RBM20	0.331	230	CD247	0.358	230	FLJ34503	0.325	230	CIZ1	0.307
231	HAUS7	0.331	231	ZC3H12B	0.358	231	CROT	0.324	231	NFIA	0.306
232	FOLH1	0.331	232	COX6B1	0.358	232	UBE2QL1	0.324	232	CELA3A	0.306
233	THAP4	0.331	233	BMPR1A	0.358	233	KCNS2	0.324	233	LOC100506497	0.306
234	SRGAP3	0.330	234	RBM34	0.357	234	RBP1	0.324	234	EIF2AK1	0.306
235	SLC2A9	0.330	235	METTL9	0.357	235	HIST1H1E	0.323	235	NUFIP1	0.306
236	SLTM	0.330	236	PSMC2	0.357	236	KIF22	0.323	236	PDE8B	0.306
237	PIN4	0.330	237	AP3M1	0.357	237	L1CAM	0.323	237	KANK4	0.306
238	DHX9	0.330	238	EPS15L1	0.357	238	ENAH	0.323	238	HCFC1	0.305
239	PCYT1B	0.330	239	MAPK10	0.356	239	ARID1B	0.323	239	TPRXL	0.305
240	CBX2	0.330	240	SKA3	0.356	240	GRIA2	0.323	240	LBR	0.305
241	C1orf124	0.329	241	DYNLL1	0.356	241	DSCC1	0.323	241	MYCBP2	0.305
242	CLDN8	0.328	242	VTA1	0.356	242	HES6	0.323	242	FASTKD5	0.305
243	FUZ	0.328	243	HIST1H1E	0.356	243	EBF3	0.323	243	ADAL	0.304
244	HN1	0.328	244	KPTN	0.355	244	C11orf53	0.322	244	ERP44	0.304
245	VSIG4	0.328	245	CCDC167	0.355	245	UBQLN2	0.322	245	HIST1H4F	0.304
246	KPTN	0.328	246	TAC1	0.354	246	C11orf31	0.322	246	LRP4	0.304
247	CCDC34	0.328	247	NDUFS3	0.354	247	MAB21L3	0.322	247	CDK13	0.304
248	AUTS2	0.327	248	C20orf112	0.354	248	TAB1	0.322	248	TET2	0.303
249	HIST1H1E	0.327	249	MTMR9	0.354	249	SERF2	0.322	249	OXGR1	0.303
250	POLD2	0.327	250	KBTBD7	0.354	250	C19orf57	0.321	250	FBXL18	0.303
251	NUP160	0.327	251	SLC25A15	0.354	251	REEP1	0.321	251	COL14A1	0.303
252	XXYLT1	0.327	252	TOMM5	0.353	252	NUDT11	0.321	252	XXYLT1	0.303
253	APOO	0.327	253	SKP1	0.353	253	PCYT1B	0.321	253	SMAD9	0.302
254	SKA3	0.326	254	CITED1	0.353	254	MOGAT2	0.320	254	CDK5RAP2	0.302
255	PPIL1	0.326	255	TBP	0.353	255	TAF12	0.319	255	ALDH3A1	0.302
256	ZXDB	0.326	256	LOC100507043	0.353	256	NT5C3	0.319	256	RNASEH2B	0.302
257	LBR	0.326	257	TCF4	0.352	257	EFNB3	0.319	257	TIGD1	0.302
258	PRPF38A	0.326	258	C5orf42	0.352	258	C1QB	0.319	258	RBP1	0.302
259	ARV1	0.325	259	TAF11	0.352	259	XKR6	0.319	259	DHRS11	0.301
260	PARD6G	0.325	260	C2orf56	0.352	260	OPA1	0.319	260	LSM5	0.301
261	GSTM4	0.325	261	BOLA3-AS1	0.351	261	LPAR6	0.318	261	NUCKS1	0.301
262	GPLD1	0.325	262	NKAP	0.351	262	TOX	0.318	262	FZD1	0.300
263	POLR1D	0.325	263	TUBB2B	0.351	263	USP7	0.318	263	MGC45800	0.300
264	PLCD4	0.324	264	KIRREL2	0.351	264	MAML1	0.318	264	CDR1	0.300
265	DMRT3	0.324	265	KCNMB1	0.351	265	CD2BP2	0.318	265	TCF12	0.300
266	NUFIP1	0.324	266	LYRM4	0.351	266	KDM4A	0.318	266	CHRNA5	0.300
267	GBX2	0.324	267	C6orf162	0.351	267	REV3L	0.318	267	FUZ	0.300

268	DSCC1	0.324	268	POLR3K	0.350	268	RBM23	0.318	268	FGF7	0.299
269	LOC100131354	0.324	269	MDM1	0.350	269	REV1	0.318	269	ZC3H12B	0.299
270	C15orf59	0.323	270	LMNB1	0.350	270	TUBB2B	0.318	270	TMEM189	0.299
271	NDUFA10	0.323	271	PAFAH1B3	0.350	271	SMC1A	0.318	271	ZACN	0.299
272	PDXP	0.323	272	NLN	0.350	272	HOXA6	0.318	272	SH2B1	0.299
273	D2HGDH	0.323	273	WFDC9	0.349	273	YAE1D1	0.317	273	IGLV5-45	0.299
274	TCEAL7	0.323	274	HINT3	0.349	274	S100A1	0.317	274	CDAN1	0.299
275	LRP4	0.322	275	HDLBP	0.349	275	SYNDIG1	0.317	275	MCM3	0.298
276	HADH	0.322	276	PIN4	0.349	276	PRPF38A	0.317	276	H19	0.298
277	FAM53B	0.322	277	EGFL6	0.349	277	KIDINS220	0.316	277	C7orf26	0.298
278	SOX2	0.322	278	CXorf36	0.349	278	FBXL16	0.316	278	ID2	0.298
279	PTPLAD1	0.322	279	KIAA0101	0.349	279	RNGTT	0.316	279	KIAA0664L3	0.298
280	HAUS1	0.322	280	ZCCHC10	0.349	280	C22orf46	0.316	280	ANP32A	0.298
281	RIOK1	0.322	281	NOL7	0.349	281	KIF26B	0.315	281	PEG3	0.297
282	TOR3A	0.322	282	CAMSAP2	0.349	282	MEPCE	0.315	282	MMP28	0.297
283	CD247	0.322	283	EID3	0.349	283	RFX4	0.315	283	PSAT1	0.297
284	ING3	0.322	284	GALNT13	0.348	284	PIN4	0.315	284	PPIP5K1	0.297
285	HIST1H4F	0.321	285	C16orf87	0.348	285	TMEM151B	0.314	285	HOXB13	0.297
286	LSM5	0.321	286	SAE1	0.348	286	PENK	0.314	286	CCKBR	0.297
287	TTLL10	0.321	287	PPM1F	0.348	287	LOC339400	0.314	287	MLST8	0.297
288	TAF15	0.321	288	DLD	0.348	288	XRCC5	0.314	288	ASF1A	0.297
289	LYSMD4	0.321	289	GNPAT	0.348	289	USP42	0.313	289	UQCRC2	0.297
290	TROVE2	0.321	290	MYEOV2	0.347	290	FZD3	0.313	290	FOXO1	0.296
291	PPARGC1B	0.321	291	NHEJ1	0.347	291	GTF3C5	0.312	291	BLCAP	0.296
292	BCLAF1	0.321	292	NUP153	0.346	292	MTOR	0.312	292	SLC47A2	0.296
293	UCHL1	0.321	293	LRP3	0.346	293	SKP2	0.312	293	FAM65B	0.296
294	NXT2	0.320	294	TREML1	0.346	294	C20orf112	0.312	294	CYP26A1	0.296
295	EMID2	0.320	295	ROR2	0.346	295	PDXP	0.312	295	RNPS1	0.296
296	ZC3H12B	0.320	296	GYG2	0.346	296	FBLL1	0.312	296	NDUFAB1	0.296
297	ODZ3	0.320	297	ESD	0.346	297	SESN1	0.312	297	NCOA1	0.296
298	GATA4	0.320	298	DLX2	0.345	298	ATAT1	0.311	298	FAM8A1	0.296
299	TRIM11	0.320	299	URB2	0.345	299	ADCK2	0.311	299	FBXL19	0.296
300	NRCAM	0.319	300	ACN9	0.345	300	C7orf59	0.310	300	LINC00487	0.295
301	KIF14	0.319	301	C10orf140	0.345	301	IPO9	0.310	301	OIP5	0.295
302	SLC47A2	0.319	302	NUCKS1	0.345	302	BEX2	0.310	302	NFATC2IP	0.295
303	KRT13	0.318	303	PTCH1	0.345	303	VPS39	0.309	303	ROR2	0.295
304	DTL	0.318	304	ANGPT4	0.345	304	ZNF436	0.309	304	FZD5	0.295
305	RBM17	0.318	305	SKA1	0.345	305	PIDD	0.309	305	SEPT7P2	0.295
306	CCKBR	0.318	306	RPS19	0.345	306	MRAP2	0.309	306	RHBDL3	0.295
307	ALDH3A2	0.318	307	AMMECR1L	0.345	307	TNFRSF4	0.309	307	MPHOSPH8	0.294
308	GNG4	0.318	308	ISOC1	0.345	308	USP22	0.309	308	NDUFB5	0.294
309	UNC5B	0.318	309	HDAC4	0.345	309	LINC00487	0.308	309	ANKRD16	0.294
310	SEPHS1	0.317	310	ATRNL1	0.345	310	HIST1H3F	0.308	310	CEL	0.294
311	KLHL10	0.317	311	TGFBR3	0.344	311	MEOX2	0.308	311	TBCCD1	0.294
312	RAB26	0.317	312	HNRNPC	0.344	312	GATA2	0.308	312	LOC100506104	0.294
313	ZNF507	0.317	313	PSMD1	0.344	313	ATP5J2	0.308	313	GPX2	0.294
314	TRAPPC2	0.316	314	PDE8B	0.344	314	ULBP1	0.307	314	ZNF629	0.293
315	PIK3R1	0.316	315	DDX49	0.344	315	UBE2L3	0.307	315	HNRNPUL2	0.293
316	PRPS2	0.316	316	ATRX	0.344	316	TEKT2	0.307	316	AFG3L2	0.293
317	PDZD4	0.316	317	IRAK1BP1	0.344	317	CACNB3	0.307	317	OPN1SW	0.293
318	CENPH	0.315	318	TEX30	0.343	318	TRIM58	0.307	318	CASKIN2	0.293
319	C4orf45	0.315	319	CENPF	0.343	319	MADD	0.307	319	RGS7BP	0.293
320	SOX7	0.315	320	C4orf45	0.343	320	NAALAD2	0.307	320	WASF1	0.293
321	GTF2IRD1	0.315	321	GNAZ	0.343	321	ZC3H12B	0.306	321	KRT13	0.292

322	D4S234E	0.314	322	PPP2R5D	0.342	322	UBE2I	0.306	322	TAC1	0.292
323	RAC3	0.314	323	CLTCL1	0.342	323	LOC100505920	0.306	323	MRPS31	0.292
324	LOC339166	0.314	324	ANP32B	0.342	324	MGC16025	0.306	324	RBM10	0.292
325	PABPC5	0.314	325	RAB4A	0.342	325	DMRT3	0.306	325	FTSJD2	0.292
326	IP6K3	0.314	326	PDHA2	0.341	326	DCST1	0.306	326	FGFR3	0.292
327	NOL7	0.314	327	STK32B	0.341	327	C22orf32	0.306	327	NR0B1	0.292
328	CCNB2	0.314	328	COL14A1	0.341	328	CYCS	0.306	328	ODZ3	0.292
329	TNFRSF4	0.314	329	ENDOG	0.341	329	FAM168B	0.305	329	SNRPE	0.291
330	ATAT1	0.314	330	CCKBR	0.341	330	PNKD	0.305	330	ITPA	0.291
331	TUBB2B	0.314	331	MARK4	0.341	331	LMNB1	0.305	331	C1orf187	0.291
332	TUFM	0.313	332	URI1	0.340	332	SLC36A1	0.305	332	HTN1	0.291
333	LAG3	0.313	333	CDH10	0.340	333	DCAF12L2	0.305	333	RABGAP1	0.290
334	GTF3C5	0.313	334	KCNS2	0.340	334	DMRT2	0.305	334	CBX2	0.290
335	HOTAIR	0.313	335	ANKRD54	0.340	335	ASMT	0.305	335	HOXA4	0.289
336	BUB1B	0.313	336	TAS1R1	0.339	336	GARS	0.304	336	SIX3	0.289
337	CHD5	0.313	337	FXN	0.339	337	SLC25A4	0.304	337	MAGOHB	0.289
338	GIP	0.313	338	PPIA	0.339	338	ZNF764	0.304	338	LPCAT3	0.289
339	GLI1	0.313	339	PCMT1	0.339	339	UCK1	0.304	339	FABP4	0.289
340	PKD1	0.313	340	LOC730101	0.339	340	LOC729852	0.304	340	TCF20	0.289
341	INA	0.312	341	FAM20B	0.339	341	GRM2	0.304	341	GAS7	0.289
342	GSG2	0.312	342	ANKRD26P3	0.339	342	SHPRH	0.304	342	CLEC2L	0.289
343	APOOL	0.312	343	PARG	0.339	343	MYCBP2	0.304	343	RNF40	0.289
344	FAM172A	0.312	344	ZBTB5	0.338	344	ZNF184	0.304	344	LOC100505946	0.289
345	RBM12	0.312	345	POLR2I	0.338	345	PHF2	0.303	345	RP9	0.288
346	MAPK12	0.312	346	HNRNPA3	0.338	346	SYNGR4	0.303	346	SDK1	0.288
347	EFCAB1	0.312	347	AHI1	0.338	347	DLGAP1	0.303	347	HOXA13	0.288
348	DLK1	0.312	348	MRPL44	0.338	348	UQCR10	0.303	348	SHMT1	0.288
349	TBCCD1	0.311	349	FAM168B	0.338	349	FLJ13197	0.303	349	OR7D2	0.288
350	RBBP4	0.311	350	KIAA0319	0.337	350	ID4	0.303	350	NASP	0.288
351	MRI1	0.311	351	PNKD	0.337	351	KIAA0664L3	0.303	351	PCNA	0.287
352	KPNA3	0.311	352	CDCA7	0.337	352	RCC2	0.303	352	HOXC6	0.287
353	LINC00052	0.311	353	NDUFA5	0.337	353	LOC389023	0.302	353	MRPS18A	0.287
354	KBTBD2	0.311	354	FUZ	0.337	354	CCKBR	0.302	354	C6orf47	0.287
355	DEK	0.310	355	HADH	0.337	355	PELI2	0.302	355	ZNF770	0.287
356	CYP26A1	0.310	356	PAK1IP1	0.336	356	COL3A1	0.302	356	NHEJ1	0.286
357	DPYSL4	0.310	357	LOC285819	0.336	357	HTATSF1	0.302	357	SLCO1A2	0.286
358	MLLT11	0.310	358	GPLD1	0.336	358	PANK1	0.302	358	RFC4	0.286
359	NUCKS1	0.310	359	C20orf7	0.336	359	USP37	0.302	359	SLC12A3	0.286
360	PURB	0.310	360	PIBF1	0.336	360	HNRNPA0	0.302	360	DSG3	0.286
361	MIR205	0.310	361	EXOC2	0.336	361	FBXL21	0.302	361	IDH1	0.286
362	ANO7	0.310	362	ZXDB	0.336	362	ILKAP	0.302	362	MRPS9	0.286
363	BRD3	0.310	363	OSTM1	0.335	363	SRGAP3	0.302	363	SLC25A14	0.286
364	DLX1	0.310	364	CHAMP1	0.335	364	ZXDC	0.302	364	SMAD6	0.286
365	CLUL1	0.310	365	PNMT	0.335	365	CAMTA1	0.301	365	RCC2	0.285
366	NAA16	0.309	366	DPY19L3	0.335	366	CRIP3	0.301	366	DVL3	0.285
367	SULF1	0.309	367	HSF2	0.334	367	LOC728537	0.301	367	ZNF48	0.285
368	EIF1AX	0.309	368	FBXO9	0.334	368	FAM53B	0.301	368	FAR2	0.285
369	ESD	0.309	369	FAM210A	0.333	369	LRRC57	0.300	369	DCTPP1	0.285
370	EXOSC8	0.309	370	BCLAF1	0.333	370	GPRASP1	0.300	370	HCN4	0.285
371	E2F2	0.309	371	ARV1	0.333	371	CERK	0.300	371	POMP	0.285
372	DSCR6	0.309	372	MRAP2	0.333	372	IP6K3	0.300	372	NUP160	0.284
373	EMD	0.308	373	TBXA2R	0.332	373	ANP32B	0.300	373	MTOR	0.284
374	RABIF	0.308	374	DMXL2	0.332	374	CABP7	0.300	374	CRYAB	0.284
375	SLC6A8	0.308	375	39876	0.332	375	JAKMIP2	0.300	375	RBBP6	0.284

376	PSMG1	0.308	376	HSDL2	0.332	376	SLC25A35	0.299	376	KIAA1704	0.284
377	MGC45800	0.308	377	MMP12	0.332	377	RNF40	0.299	377	DROSHA	0.283
378	SLCO1A2	0.308	378	RBM45	0.332	378	CHRNA5	0.299	378	TBRG4	0.283
379	RTF1	0.308	379	E2F2	0.332	379	PPP1R7	0.299	379	IAPP	0.283
380	DDX42	0.307	380	BUB1B	0.331	380	ZRSR2	0.299	380	GUCY2F	0.283
381	GRIA2	0.307	381	SGTB	0.331	381	PHKA2	0.299	381	TAF2	0.283
382	TRO	0.307	382	PLAA	0.331	382	CDCA7	0.299	382	IBA57	0.283
383	ENDOG	0.307	383	TMEM97	0.331	383	NDUFA10	0.299	383	HSPB2	0.282
384	PELI2	0.307	384	ZNF260	0.331	384	GUCA2B	0.299	384	KPTN	0.282
385	EPHA5	0.307	385	PFDN6	0.330	385	THAP9	0.298	385	FAM168B	0.282
386	CEP78	0.307	386	UBQLN2	0.330	386	PON1	0.298	386	UHRF1BP1	0.282
387	ZNF770	0.306	387	HIST1H1D	0.330	387	LOC100507353	0.298	387	SEPHS2	0.282
388	ANKRD54	0.306	388	C9orf91	0.330	388	GGA1	0.297	388	PLEKHA2	0.282
389	PDE3B	0.306	389	SRSF3	0.329	389	SCN3B	0.297	389	KIAA0564	0.282
390	CADM3	0.306	390	TBC1D24	0.329	390	KCNH3	0.297	390	LOC100129195	0.281
391	LGALSL	0.306	391	ROCK1	0.329	391	POU4F2	0.297	391	C11orf49	0.281
392	TREML1	0.306	392	SMCP	0.329	392	RFC2	0.297	392	FBLN1	0.281
393	SPAST	0.306	393	AK5	0.329	393	INA	0.297	393	CCNB2	0.281
394	RBP1	0.306	394	NOL12	0.329	394	MED4	0.297	394	TNNI1	0.281
395	ADAL	0.305	395	RBMX	0.328	395	DECR2	0.296	395	CHD6	0.281
396	LOC100505515	0.305	396	SUMO1	0.328	396	RBBP4	0.296	396	PROSER1	0.281
397	TET1	0.305	397	FANCB	0.328	397	LOC339166	0.296	397	GSG2	0.281
398	DUT	0.305	398	OSBPL11	0.328	398	NHSL1	0.296	398	ZC3H4	0.281
399	ALMS1	0.305	399	ILKAP	0.328	399	EEF1A1	0.296	399	PER2	0.280
400	TAB1	0.305	400	MIR600HG	0.328	400	SLC26A10	0.296	400	KBTBD2	0.280
401	LINC00479	0.305	401	LOC100506343	0.328	401	ERCC3	0.296	401	NAA16	0.280
402	URB2	0.305	402	NDUFA4	0.328	402	CALB1	0.296	402	FAT2	0.280
403	CNTLN	0.305	403	ERF	0.328	403	C7orf29	0.296	403	ATP5G3	0.279
404	REV3L	0.304	404	HAT1	0.327	404	CENPH	0.295	404	CCDC101	0.279
405	ISOC1	0.304	405	RBM10	0.327	405	ATRX	0.295	405	GPR124	0.279
406	ZACN	0.304	406	TET1	0.327	406	DTNBP1	0.295	406	CCDC50	0.279
407	RFC4	0.304	407	TTF2	0.327	407	SOX18	0.295	407	PELI2	0.279
408	PSIP1	0.304	408	WT1	0.327	408	DDX25	0.295	408	IPO9	0.279
409	CYP4F11	0.304	409	LAS1L	0.327	409	TCEAL7	0.294	409	PPP3R2	0.278
410	HTATSF1	0.303	410	DISC1	0.327	410	BCL9	0.294	410	GTF3C5	0.278
411	SLITRK5	0.303	411	ZNF420	0.327	411	RPS27A	0.294	411	ABCC1	0.278
412	PDCD2	0.303	412	SBF2	0.327	412	CBX3	0.294	412	LOC100507534	0.278
413	ANKS6	0.303	413	LIN54	0.327	413	KRTAP2-4	0.294	413	SLC7A5	0.278
414	C7orf26	0.303	414	GKAP1	0.326	414	NEFH	0.294	414	HADHA	0.278
415	TSHB	0.303	415	KLRD1	0.326	415	PBRM1	0.294	415	CDC23	0.277
416	SNX12	0.302	416	ARL3	0.326	416	HNRNPAB	0.294	416	EHMT1	0.277
417	KIAA0564	0.302	417	BBIP1	0.325	417	C10orf95	0.294	417	SHPRH	0.277
418	CITED1	0.302	418	ZNF711	0.325	418	ITM2C	0.294	418	TMEM237	0.277
419	CCP110	0.302	419	ACER3	0.325	419	BEX1	0.294	419	39881	0.277
420	AGFG1	0.302	420	CACYBP	0.325	420	GAL3ST2	0.294	420	KPNA3	0.277
421	HBG2	0.302	421	DSCC1	0.325	421	HOXD8	0.294	421	TRIM13	0.277
422	RNF8	0.301	422	PDCD2	0.325	422	SYK	0.293	422	MYCBPAP	0.277
423	CABYR	0.301	423	KIF4A	0.325	423	NONO	0.293	423	HNRNPM	0.277
424	NUSAP1	0.301	424	LOC100506108	0.324	424	ZNF620	0.293	424	FECH	0.276
425	MTMR8	0.301	425	FASTKD5	0.324	425	GALNTL1	0.293	425	NDUFA8	0.276
426	ABCB10	0.301	426	SMAD2	0.324	426	ZBTB5	0.293	426	FERD3L	0.276
427	MCM3	0.301	427	SEH1L	0.324	427	SESTD1	0.293	427	ZNF436	0.276
428	MDM1	0.301	428	HOXC9	0.323	428	TMEM198	0.292	428	PLCD4	0.276
429	ZCCHC3	0.300	429	FBXO43	0.323	429	NNT	0.292	429	MLLT11	0.276

430	PRKX	0.300	430	PFAS	0.323	430	DYDC2	0.292	430	PPM1E	0.276
431	CDC23	0.300	431	ELFN1	0.323	431	FAM215A	0.292	431	TSHZ1	0.275
432	ZNF768	0.300	432	RABIF	0.323	432	RND2	0.292	432	MFNG	0.275
433	TET2	0.300	433	CDH2	0.322	433	PIPOX	0.292	433	RBM45	0.275
434	LOC100134361	0.299	434	KCTD15	0.322	434	NXT2	0.292	434	SRRM2	0.275
435	LINC00523	0.299	435	CDK5RAP2	0.322	435	JAM3	0.292	435	RAB26	0.275
436	COL2A1	0.299	436	UCK2	0.322	436	FARP1	0.292	436	LOC100130950	0.275
437	TBX1	0.299	437	SPAST	0.322	437	MECP2	0.292	437	NTRK2	0.275
438	KIRREL2	0.299	438	KIAA1549	0.322	438	KIAA0895	0.291	438	CAMKMT	0.275
439	FARSB	0.299	439	KDELC1	0.322	439	SHISA8	0.291	439	CRMP1	0.275
440	FANCE	0.299	440	SLC25A30	0.322	440	SYP	0.291	440	TOR3A	0.274
441	POLR3K	0.299	441	KIAA2022	0.322	441	SAP18	0.291	441	HAUS7	0.274
442	C16orf93	0.299	442	ZNF281	0.322	442	AK1	0.291	442	MMEL1	0.274
443	PARG	0.299	443	KIAA0895	0.321	443	SEPHS1	0.291	443	GPR137B	0.274
444	PIGX	0.298	444	RBPMS2	0.321	444	ZNF678	0.291	444	FLJ11235	0.274
445	C14orf142	0.298	445	INTS7	0.321	445	IQCA1	0.291	445	SLC9A3R1	0.274
446	CASKIN2	0.298	446	GLA	0.321	446	CD8A	0.291	446	RIOK1	0.273
447	RP2	0.298	447	AGFG1	0.321	447	TET2	0.291	447	SRSF6	0.273
448	LOC100130950	0.298	448	COX20	0.321	448	ZNF500	0.291	448	RFC3	0.273
449	RP9	0.298	449	RPP30	0.321	449	CNTLN	0.290	449	BTNL9	0.273
450	TRAV8-6	0.298	450	HOXC6	0.321	450	UBE2V2	0.290	450	TCAP	0.273
451	NUDT15	0.298	451	CIZ1	0.321	451	PURB	0.290	451	PI15	0.273
452	TCF12	0.297	452	RBBP9	0.320	452	C22orf39	0.290	452	C7	0.273
453	GUCY2F	0.297	453	FOPNL	0.320	453	TBC1D2B	0.290	453	FLT3	0.272
454	ALDH1A1	0.297	454	CRYAB	0.320	454	TAF1	0.290	454	JAM3	0.272
455	GRIPAP1	0.297	455	ZCCHC2	0.319	455	HOXD9	0.289	455	NKX2-5	0.272
456	PLA2G10	0.297	456	RBM12	0.319	456	DHX9	0.289	456	MIR600HG	0.272
457	HUWE1	0.297	457	DPYSL4	0.319	457	XPA	0.288	457	ZNF488	0.272
458	SLC48A1	0.297	458	KLHL14	0.319	458	LOC283588	0.288	458	PTH2R	0.272
459	TCAP	0.296	459	CTIF	0.319	459	CIC	0.288	459	ZZEF1	0.272
460	PRDX1	0.296	460	AKR1C1	0.319	460	MLL3	0.288	460	GLI1	0.272
461	SLC25A15	0.296	461	PEPD	0.319	461	RAB39A	0.288	461	EIF4E2	0.272
462	ELFN1	0.296	462	CHRNA5	0.319	462	VANGL2	0.287	462	ZIC3	0.272
463	EIF3K	0.296	463	ZNF529	0.319	463	FNDC5	0.287	463	CARD9	0.271
464	FBLL1	0.296	464	MYCBP2	0.319	464	LOC100130950	0.287	464	HDDC2	0.271
465	MGC27345	0.296	465	KPNA3	0.318	465	ZKSCAN1	0.287	465	PSMC2	0.271
466	RMI1	0.295	466	GABPA	0.318	466	UBN2	0.287	466	RP9P	0.271
467	HNRNPM	0.295	467	NUDT11	0.318	467	TAF11	0.287	467	ATRX	0.271
468	KIAA1549	0.295	468	ZIM2	0.318	468	SUCLA2	0.286	468	BUB1B	0.271
469	CDK5RAP2	0.295	469	COX5A	0.318	469	GPR182	0.286	469	C16orf79	0.271
470	NUP153	0.295	470	ID4	0.318	470	RUNDC3A	0.286	470	KIAA0319	0.271
471	NUP210P1	0.295	471	CA4	0.318	471	SCG3	0.286	471	EIF3K	0.271
472	NELL2	0.295	472	WFDC1	0.318	472	LINC00282	0.286	472	TBX3	0.271
473	LSM2	0.295	473	MRPS9	0.318	473	GNRH2	0.285	473	PPP1R15B	0.270
474	LOC149086	0.294	474	GNAI1	0.318	474	ARHGEF6	0.285	474	PPIL1	0.270
475	PARP16	0.294	475	RBM26	0.318	475	CXorf57	0.285	475	LOC730101	0.270
476	NDUFA1	0.294	476	TUB	0.317	476	LOC100506343	0.285	476	GYG2	0.270
477	POMP	0.294	477	PSMA4	0.317	477	GYG2	0.285	477	RMI1	0.270
478	40059	0.294	478	FAM55C	0.316	478	TPO	0.285	478	NDUFA1	0.270
479	C2orf56	0.294	479	FAM172A	0.316	479	MLL5	0.284	479	EARS2	0.270
480	TAS1R1	0.294	480	SLC25A17	0.316	480	RPAIN	0.284	480	ABCB6	0.270
481	TRMT6	0.294	481	ZCCHC7	0.316	481	IGLV5-45	0.284	481	PHF2	0.270
482	KIAA2022	0.294	482	MCM3	0.316	482	NUDCD3	0.284	482	USP42	0.270
483	MTMR9	0.294	483	SENP6	0.316	483	HOXA4	0.284	483	CCAR1	0.270

484	TUSC5	0.293	484	PLCXD1	0.316	484	RGS7	0.284	484	ATP5J	0.270
485	TXN	0.293	485	FAM155B	0.315	485	KIAA1549	0.284	485	ZNF192	0.270
486	IFT88	0.293	486	PALM	0.315	486	LDOC1L	0.284	486	PIAS1	0.269
487	HDAC2	0.293	487	PCNA	0.315	487	MAPK12	0.284	487	E4F1	0.269
488	PER2	0.293	488	TMEM14A	0.315	488	MAGEF1	0.283	488	AMBRA1	0.269
489	SERPINB13	0.293	489	PRPF38A	0.315	489	C7orf41	0.283	489	SLC2A9	0.269
490	CSDC2	0.292	490	ESCO2	0.315	490	KIAA0182	0.283	490	FAM122B	0.269
491	CLN6	0.292	491	GNAL	0.315	491	CA5B	0.283	491	UPF3A	0.269
492	NKAP	0.292	492	PHF8	0.315	492	BUD31	0.283	492	COL2A1	0.269
493	ZZEF1	0.292	493	PHF10	0.315	493	CHD5	0.283	493	SERPINF1	0.269
494	NT5M	0.292	494	PARD6G	0.315	494	CCDC90A	0.283	494	TIMP3	0.269
495	ZNF343	0.292	495	IQCA1	0.314	495	ATP6V1G1	0.283	495	INHBC	0.269
496	SNRNP25	0.292	496	SPRYD7	0.314	496	SMARCD3	0.282	496	HDAC4	0.269
497	RNF114	0.291	497	TOB1	0.314	497	TRIM11	0.282	497	SMCHD1	0.269
498	CDAN1	0.291	498	MTO1	0.314	498	NIPBL	0.282	498	SPICE1	0.269
499	LOC730101	0.291	499	UPF3A	0.314	499	MAPK11	0.281	499	PPFIBP2	0.269
500	ARHGAP35	0.291	500	NSMCE4A	0.314	500	ARF5	0.281	500	MAML1	0.269
501	FAM215A	0.291	501	CHRDL2	0.314	501	SLC25A25	0.281	501	PARN	0.269
502	MRPS26	0.291	502	HDHD2	0.314	502	ZFP106	0.281	502	LOC83954	0.269
503	NUDT11	0.291	503	MELK	0.313	503	HIST1H3G	0.281	503	SLC6A5	0.268
504	PPPDE1	0.291	504	ORC5	0.313	504	SHC2	0.281	504	AKR1C3	0.268
505	SRSF1	0.291	505	ZNF225	0.313	505	GIP	0.281	505	KANK1	0.268
506	RAB4A	0.290	506	ECI1	0.313	506	IWS1	0.281	506	GATS	0.268
507	ZNF213	0.290	507	NDUFA8	0.313	507	BEND4	0.281	507	MFAP3	0.268
508	FERD3L	0.290	508	39872	0.313	508	CBX7	0.281	508	ATG4B	0.268
509	SH3GL3	0.290	509	SLC35B4	0.313	509	SULT4A1	0.280	509	PRR24	0.268
510	UBE2I	0.290	510	LSM5	0.313	510	BARX1	0.280	510	IFT88	0.268
511	TIMM21	0.290	511	MTMR10	0.312	511	C5orf24	0.280	511	C5orf42	0.268
512	PLA2G2D	0.290	512	CXorf67	0.312	512	HSD17B1	0.280	512	GPLD1	0.268
513	MADD	0.289	513	BEX1	0.312	513	PGAP1	0.280	513	BRP44	0.268
514	HRG	0.289	514	LOC283688	0.312	514	SARM1	0.280	514	RBM20	0.268
515	SRSF6	0.289	515	WASF1	0.312	515	RABGAP1	0.280	515	LIFR-AS1	0.267
516	SMAD9	0.289	516	CENPH	0.312	516	PTCH1	0.280	516	PLCL1	0.267
517	TRAV12-1	0.289	517	ZMAT4	0.312	517	CDK5RAP2	0.280	517	TAF3	0.267
518	TSNAX	0.289	518	NCOA1	0.312	518	PHIP	0.280	518	HUWE1	0.267
519	KIAA0895	0.289	519	CBX2	0.312	519	CDK8	0.279	519	LOC284804	0.267
520	TTF1	0.288	520	ZCCHC3	0.312	520	FOXD2	0.279	520	ZNF219	0.267
521	THAP5	0.288	521	NENF	0.312	521	ZNF396	0.279	521	MORF4L1	0.267
522	FANCI	0.288	522	CNTLN	0.312	522	SKP1	0.279	522	C1orf111	0.267
523	LOC100506597	0.288	523	KCNJ12	0.311	523	KLHL9	0.279	523	B4GALT5	0.267
524	C1orf35	0.288	524	DENND2C	0.311	524	HIST1H3D	0.279	524	PRR12	0.267
525	FAM48A	0.288	525	ABHD13	0.311	525	DCUN1D2	0.278	525	USP8	0.267
526	TAF3	0.288	526	MOGAT2	0.311	526	GTF2I	0.278	526	CADM3	0.266
527	FOPNL	0.288	527	LOC154092	0.311	527	KLRD1	0.278	527	C9orf29	0.266
528	MAPK6	0.288	528	B9D2	0.311	528	PAFAH1B3	0.278	528	TRIM11	0.266
529	HDAC10	0.288	529	NDUFA10	0.311	529	RGS7BP	0.278	529	CRIP2	0.266
530	ATP5J2	0.287	530	BLMH	0.311	530	RIMS3	0.278	530	SCAF8	0.266
531	UNK	0.287	531	KIFC1	0.311	531	TMOD2	0.278	531	GSTA1	0.265
532	SPP1	0.287	532	IGLV5-45	0.311	532	UNC5B	0.278	532	ALG5	0.265
533	NT5C3	0.287	533	BYSL	0.311	533	RBMX	0.278	533	MUT	0.265
534	MAFG	0.287	534	TAF3	0.311	534	HMGB1	0.278	534	TAB1	0.265
535	FAM122B	0.287	535	LOC100131354	0.311	535	PGF	0.278	535	HERC2	0.265
536	NENF	0.287	536	TIPRL	0.311	536	DAB2IP	0.277	536	RALA	0.265
537	LAS1L	0.287	537	NUFIP1	0.311	537	PKD1	0.277	537	HIST1H3G	0.265

538	RASL10B	0.287	538	OGG1	0.310	538	MGC27345	0.277	538	CDH2	0.265
539	SLC35A4	0.287	539	HNRNPM	0.310	539	CEL	0.277	539	EFNB1	0.265
540	CAPRIN1	0.287	540	IQSEC2	0.310	540	MCM6	0.277	540	HNRNPA3	0.265
541	CYBASC3	0.287	541	TXNL1	0.310	541	MICAL1	0.277	541	EMD	0.265
542	ACN9	0.286	542	TRIM58	0.310	542	MLST8	0.277	542	RAP1GAP	0.264
543	RAPGEF4	0.286	543	RSL24D1	0.310	543	LOC90246	0.277	543	NFATC3	0.264
544	KCMF1	0.286	544	PKD1	0.310	544	SBK1	0.277	544	KCNS2	0.264
545	AMZ2P1	0.286	545	S1PR1	0.310	545	C15orf17	0.277	545	MAZ	0.264
546	TSTD2	0.286	546	RAVER2	0.310	546	CHGB	0.276	546	SEC31B	0.264
547	GNRH2	0.286	547	MYOM2	0.309	547	PCDHGB7	0.276	547	MRPL44	0.264
548	ANGPT4	0.286	548	EIF4E2	0.309	548	SOSTDC1	0.276	548	TMEM199	0.264
549	RC3H2	0.286	549	CCNE1	0.309	549	STX17	0.276	549	SEMA3D	0.264
550	GNL1	0.286	550	EDNRB	0.309	550	C7orf44	0.276	550	SLC27A3	0.264
551	PHB2	0.285	551	MZT1	0.309	551	TNFRSF19	0.276	551	EXOSC8	0.264
552	TWIST1	0.285	552	FARSB	0.309	552	GLCCI1	0.276	552	NRAS	0.264
553	ID2	0.285	553	ICA1L	0.309	553	CCDC78	0.276	553	SCGB3A2	0.263
554	PHF10	0.285	554	SNRPC	0.309	554	ZCCHC18	0.276	554	WHSC1L1	0.263
555	RNF138	0.285	555	EPHA5	0.309	555	PLEKHM3	0.276	555	XRCC5	0.263
556	SLC6A5	0.285	556	C1QB	0.308	556	TRIM24	0.276	556	NR2F6	0.263
557	SFRP4	0.285	557	COL11A1	0.308	557	C14orf142	0.276	557	NKRF	0.263
558	HMGB1	0.285	558	LRRC58	0.308	558	PFDN6	0.275	558	TOB1	0.263
559	CUX1	0.285	559	TIMM50	0.308	559	C1orf35	0.275	559	NDRG2	0.263
560	CIZ1	0.284	560	CEP192	0.308	560	C5orf45	0.275	560	RAC1	0.263
561	EID3	0.284	561	GALNTL1	0.308	561	GSTA4	0.275	561	PALM	0.263
562	NOL12	0.284	562	SLC39A6	0.308	562	VAMP2	0.275	562	DDX56	0.263
563	DISC1	0.284	563	RFC3	0.308	563	DCAKD	0.275	563	HOXA7	0.263
564	GRIK1-AS1	0.284	564	FGF7	0.308	564	PLXNB1	0.275	564	KAT8	0.262
565	DNA2	0.284	565	ATP7B	0.308	565	SLC47A2	0.275	565	CUX1	0.262
566	SLC6A15	0.284	566	S1PR5	0.307	566	SERTM1	0.275	566	SMPD2	0.262
567	C9orf4	0.284	567	PPP1R15B	0.307	567	DLG3	0.275	567	MIPEP	0.262
568	SLC25A30	0.284	568	YAE1D1	0.307	568	DNA2	0.275	568	CCP110	0.262
569	C20orf7	0.284	569	GRIK1-AS1	0.307	569	IAPP	0.275	569	HIST1H1D	0.262
570	HHEX	0.283	570	USP9X	0.307	570	DMXL2	0.275	570	EEF1A1	0.262
571	PART1	0.283	571	UQCR10	0.307	571	GABRD	0.275	571	HOXC13	0.262
572	SAE1	0.283	572	ARID1B	0.307	572	ULK2	0.274	572	GNRH2	0.262
573	COX20	0.283	573	LOC100507739	0.306	573	CLUL1	0.274	573	RBM38	0.262
574	METTL9	0.283	574	CHST10	0.306	574	HNRNPF	0.274	574	OR10H2	0.262
575	AFG3L2	0.283	575	ZIC3	0.306	575	DENND1A	0.274	575	EID3	0.262
576	LYRM7	0.283	576	PGAP1	0.306	576	EHMT1	0.274	576	LOC100131733	0.262
577	40058	0.283	577	TUBB2A	0.306	577	HHATL	0.274	577	PRTG	0.262
578	SRSF3	0.282	578	FERD3L	0.306	578	GALR2	0.274	578	PHIP	0.262
579	TRMT11	0.282	579	CELA3A	0.306	579	FAM49A	0.273	579	EN1	0.262
580	NRG2	0.282	580	GTF2A1	0.306	580	ZNF510	0.273	580	FBN2	0.261
581	DTNBP1	0.282	581	RP9	0.306	581	TSN	0.273	581	LPHN3	0.261
582	SDCCAG8	0.282	582	UBE2A	0.305	582	C14orf93	0.273	582	SCARA5	0.261
583	CLCA4	0.282	583	ZNF343	0.305	583	FAXC	0.273	583	FOXH1	0.261
584	GLRA2	0.282	584	NEDD4	0.305	584	LRRTM2	0.273	584	PABPC1L	0.261
585	C9orf29	0.282	585	CDAN1	0.305	585	TRIL	0.273	585	CCDC90A	0.261
586	LY6G6D	0.282	586	SLC18A3	0.305	586	RPRM	0.273	586	PLXNB1	0.261
587	POLE3	0.282	587	KLHL10	0.304	587	TBC1D7	0.272	587	MCCC1	0.261
588	BEND4	0.282	588	ARMCX5-GPRASP2	0.304	588	CEP192	0.272	588	GRIK1-AS1	0.261
589	INHBC	0.282	589	PDS5B	0.304	589	HLCS	0.272	589	TMEM198	0.261
590	SMCHD1	0.282	590	LIMS1	0.304	590	SYNE2	0.272	590	VAMP2	0.261
591	GALNT13	0.282	591	SEC22C	0.304	591	SLTM	0.272	591	KIAA0895	0.260

592	HNRNPA0	0.281	592	GNL3L	0.304	592	RNF157	0.272	592	DMXL2	0.260
593	LOC151658	0.281	593	NLRP8	0.304	593	CIB2	0.272	593	ABHD16A	0.260
594	TPRXL	0.281	594	PARPBP	0.304	594	CAMSAP2	0.271	594	TREML1	0.260
595	RPL27A	0.281	595	FBXO10	0.304	595	GNMT	0.271	595	CAMSAP2	0.260
596	ACBD6	0.281	596	CRMP1	0.304	596	PSIP1	0.271	596	CSDC2	0.260
597	DCTPP1	0.281	597	ENY2	0.304	597	PHF10	0.271	597	RBMX	0.260
598	TCF20	0.281	598	ACTC1	0.304	598	ZNF192	0.271	598	ACAD9	0.260
599	ATCAY	0.281	599	HOXA11	0.304	599	MTMR8	0.270			
600	NKRF	0.281	600	MORF4L1	0.304	600	WFDC1	0.270			
601	BYSL	0.281	601	PDXP	0.304	601	C9orf4	0.270			
602	MTOR	0.281	602	HOTAIR	0.303	602	CARHSP1	0.270			
603	CEP192	0.281	603	KCTD20	0.303	603	TCF25	0.270			
604	TSHZ1	0.280	604	KCTD7	0.303	604	LIG1	0.270			
605	KDM1B	0.280	605	NUSAP1	0.303	605	TMEM169	0.270			
606	DGCR9	0.280	606	LATS1	0.303	606	GALR3	0.270			
607	TMEM107	0.280	607	RABL5	0.303	607	SMAD9	0.270			
608	SRI	0.280	608	ALPK2	0.303	608	TRMU	0.269			
609	ABCB6	0.280	609	BCL7C	0.303	609	FBXW7	0.269			
610	SEC31B	0.280	610	HDAC8	0.302	610	KRT5	0.269			
611	ORC5	0.280	611	ZNF565	0.302	611	RCBTB1	0.269			
612	TSPAN7	0.280	612	PLCG1	0.302	612	KLHDC9	0.269			
613	SHMT1	0.280	613	LOC100507654	0.302	613	AATK	0.269			
614	WDR61	0.280	614	NCAPG2	0.302	614	C6orf47	0.269			
615	FBXO9	0.279	615	ADSL	0.302	615	ZNF775	0.269			
616	SYBU	0.279	616	SYBU	0.302	616	KCTD20	0.269			
617	ZMYND19	0.279	617	SESN1	0.302	617	SVOP	0.269			
618	TMEM151B	0.279	618	RABEPK	0.302	618	ARMCX5-GPRASP2	0.269			
619	IGLV5-45	0.279	619	DLK1	0.302	619	MRPL44	0.269			
620	SLC35B4	0.279	620	HOXC8	0.302	620	H2AFY	0.269			
621	BRP44	0.279	621	ZNF24	0.302	621	POU2F1	0.269			
622	IWS1	0.279	622	LRP4	0.301	622	NCBP1	0.268			
623	PTCHD2	0.279	623	CEP78	0.301	623	DCTPP1	0.268			
624	SYNCRIP	0.279	624	MTCP1NB	0.301	624	CCDC88C	0.268			
625	WDR17	0.279	625	NRCAM	0.301	625	TBX1	0.268			
626	MFF	0.279	626	RMI1	0.301	626	TRAF3IP2-AS1	0.268			
627	TCF4	0.279	627	WTIP	0.301	627	CREBBP	0.268			
628	MAK	0.279	628	GATA4	0.301	628	SECISBP2	0.268			
629	TUB	0.279	629	ERAL1	0.301	629	RPL27A	0.268			
630	PSMA4	0.279	630	TMEM151B	0.301	630	TSHZ1	0.267			
631	SULF2	0.279	631	PPIL1	0.301	631	HIP1	0.267			
632	RAVER2	0.279	632	TAF5	0.301	632	REEP2	0.267			
633	LINC00277	0.279	633	CENPV	0.300	633	AP4E1	0.267			
634	HDC	0.279	634	RARS2	0.300	634	SULF1	0.267			
635	39872	0.279	635	NDUFAF4	0.300	635	DLX3	0.267			
636	TOMM5	0.279	636	PTGR2	0.300	636	LOC100506629	0.267			
637	DLD	0.279	637	CDC7	0.300	637	NPTX2	0.267			
638	MTR	0.278	638	CAPN7	0.300	638	KCNC1	0.267			
639	MARK4	0.278	639	SLMO1	0.300	639	TARDBP	0.267			
640	LUC7L2	0.278	640	APITD1	0.300	640	NELL2	0.267			
641	PYCR2	0.278	641	SAMD14	0.300	641	LINC00324	0.266			
642	PPP1R16B	0.278	642	PES1	0.300	642	CDH24	0.266			
643	RBM45	0.278	643	ZFR	0.300	643	PRRC2B	0.266			
644	FANCL	0.278	644	C19orf12	0.299	644	ARHGAP35	0.266			
645	CTRB2	0.278	645	CHAT	0.299	645	MFHAS1	0.266			

646	ZNF513	0.278	646	NAA60	0.299	646	C3orf70	0.266
647	XRCC5	0.278	647	HOXC13	0.299	647	C2orf70	0.266
648	ZBTB5	0.277	648	TRO	0.299	648	HYAL4	0.266
649	THAP9	0.277	649	THAP4	0.299	649	PCDH8	0.266
650	TAF5L	0.277	650	IL17F	0.299	650	POLD2	0.266
651	GYG2	0.277	651	EXOSC8	0.298	651	EMD	0.265
652	ATP5J	0.277	652	THAP9	0.298	652	MOAP1	0.265
653	AP3M1	0.277	653	TEKT2	0.298	653	SLC6A8	0.265
654	TP63	0.277	654	METTL8	0.298	654	SHROOM1	0.265
655	KIAA1704	0.277	655	ZRANB3	0.297	655	DNALI1	0.265
656	NONO	0.277	656	RPRD1A	0.297	656	FAM122B	0.265
657	EIF4E2	0.277	657	NQO2	0.297	657	MTMR9	0.265
658	CIC	0.276	658	QRSL1	0.297	658	LIMK2	0.265
659	OSR2	0.276	659	MTCH2	0.297	659	OSR2	0.265
660	C9orf116	0.276	660	ENOX1	0.297	660	PCK2	0.265
661	SEMA3D	0.276	661	U2AF1	0.296	661	UBE2N	0.265
662	RAI1	0.276	662	PIGX	0.296	662	KIF1A	0.265
663	KIFC1	0.276	663	GLRX2	0.296	663	SKA3	0.265
664	SRP14	0.276	664	C6orf165	0.296	664	SLC22A9	0.264
665	SLC7A5	0.276	665	TNNT3	0.296	665	NHP2L1	0.264
666	SIGLECP3	0.276	666	RAC3	0.296	666	HBBP1	0.264
667	DLX4	0.276	667	GLRA2	0.296	667	C16orf53	0.264
668	LOC100506388	0.275	668	COL4A6	0.296	668	TRAPPC2	0.264
669	SLC47A1	0.275	669	TRAF3IP1	0.296	669	LOC146336	0.264
670	FASTKD5	0.275	670	FKBP5	0.296	670	CCDC101	0.264
671	CCAR1	0.275	671	MED29	0.296	671	DLL1	0.264
672	UBA2	0.275	672	FAM215A	0.296	672	LOC100505760	0.264
673	PRPF19	0.275	673	TAF15	0.296	673	SRP14	0.264
674	R3HDM1	0.275	674	RNF187	0.296	674	PNMT	0.264
675	DMXL2	0.275	675	DTNBP1	0.296	675	C9orf29	0.264
676	LOC100507194	0.275	676	SPP1	0.296	676	SOX4	0.263
677	LPHN3	0.275	677	AMZ2P1	0.296	677	DPYSL4	0.263
678	ALDH5A1	0.275	678	LRRC57	0.295	678	SLC22A17	0.263
679	HAUS2	0.275	679	RNASEH2B	0.295	679	CDK5R2	0.263
680	DTYMK	0.275	680	CUTC	0.295	680	ZDHHC4	0.263
681	MMP19	0.274	681	BEND4	0.295	681	PA2G4	0.263
682	CUTA	0.274	682	NHSL1	0.295	682	LOC100506802	0.263
683	GPR182	0.274	683	RIC8B	0.295	683	TIA1	0.263
684	TRA2B	0.274	684	PHLPP2	0.295	684	WRB	0.263
685	SOX18	0.274	685	TROVE2	0.295	685	HOXC6	0.263
686	DAPK2	0.274	686	LOC401588	0.295	686	VAPB	0.263
687	FOXD1	0.274	687	EIF5A2	0.294	687	KIRREL2	0.263
688	GPR61	0.273	688	CCDC77	0.294	688	TMEM18	0.263
689	LHFPL4	0.273	689	C9orf50	0.294	689	ELL3	0.263
690	OR51B6	0.273	690	ASPM	0.294	690	HNRNPA2B1	0.262
691	ZNF271	0.273	691	C5orf24	0.294	691	DPY19L3	0.262
692	RHEB	0.273	692	RNF114	0.294	692	RBM34	0.262
693	ALG1	0.273	693	SCML2	0.294	693	CPT2	0.262
694	SRY	0.273	694	LOC100506874	0.294	694	RAC1	0.262
695	ELK1	0.273	695	BTRC	0.294	695	HDLBP	0.262
696	REEP1	0.273	696	CHPT1	0.294	696	PRSS16	0.262
697	C16orf87	0.272	697	API5	0.294	697	ARHGAP19	0.262
698	ABCC5	0.272	698	CHD5	0.294	698	PSMC2	0.262
699	RSL24D1	0.272	699	CAP2	0.294	699	RNF20	0.262

700	CBS	0.272	700	COPS8	0.294	700	GABRR1	0.262
701	NT5DC2	0.272	701	THAP5	0.294	701	RELL2	0.261
702	FH	0.272	702	ANK2	0.293	702	RPL13	0.261
703	PDHA1	0.272	703	MRPS31	0.293	703	HMX2	0.261
704	FOXH1	0.272	704	ZCCHC12	0.293	704	KIF11	0.261
705	TBCE	0.272	705	HBBP1	0.293	705	C21orf33	0.261
706	STON1	0.272	706	BMP6	0.293	706	TIMM17B	0.261
707	RND2	0.272	707	SNRNP48	0.292	707	ALDH5A1	0.261
708	OLFM2	0.272	708	UNG	0.292	708	CDK19	0.261
709	MRPS9	0.272	709	CXorf56	0.292	709	PIRT	0.260
710	TRAF7	0.272	710	MAPK11	0.292	710	NUP62CL	0.260
711	VANGL2	0.272	711	MLST8	0.292	711	GATS	0.260
712	FAM161A	0.272	712	U2AF1L4	0.292	712	KDM1A	0.260
713	NARG2	0.272	713	RBM18	0.292	713	CNTNAP2	0.260
714	POU2F1	0.271	714	SH2D6	0.292	714	AIMP2	0.260
715	CAND2	0.271	715	SFRP4	0.291	715	C14orf132	0.260
716	LOC100144597	0.271	716	NKX2-5	0.291	716	PHF21B	0.260
717	DDX49	0.271	717	LOC100128139	0.291			
718	SNRPC	0.271	718	WDR61	0.291			
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720	CAMKMT	0.271	720	AKR1C2	0.290			
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725	ESCO2	0.271	725	SLITRK5	0.290			
726	TRMT61B	0.270	726	GSTM3	0.290			
727	NUP188	0.270	727	FAM161A	0.290			
728	DNASE1L2	0.270	728	C15orf2	0.289			
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730	S1PR5	0.270	730	C19orf76	0.289			
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732	SP4	0.270	732	LOC100144597	0.289			
733	CXorf36	0.270	733	PTPRN	0.289			
734	NDUFB10	0.270	734	SNRPD2	0.289			
735	USP42	0.270	735	SYP	0.289			
736	MCM8	0.270	736	WDR41	0.289			
737	KANK1	0.270	737	CRIP2	0.289			
738	FAM162B	0.270	738	ZNF184	0.289			
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740	COL4A6	0.269	740	PLCB4	0.289			
741	SMARCE1	0.269	741	C2orf76	0.289			
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743	E2F3	0.269	743	MEX3B	0.289			
744	PHIP	0.269	744	GLE1	0.289			
745	LOC100507534	0.269	745	WDR62	0.288			
746	MDGA1	0.269	746	C2orf44	0.288			
747	ZNF346	0.269	747	TWIST1	0.288			
748	SARM1	0.269	748	PRPF4B	0.288			
749	SEPT7P2	0.269	749	TUFM	0.288			
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751	HRH3	0.269	751	LINC00478	0.288			
752	NEFH	0.269	752	KCNK3	0.287			
753	AP4E1	0.268	753	PI15	0.287			

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755	PHF2	0.268	755	SLTM	0.287
756	MRPS18A	0.268	756	TATDN3	0.287
757	DNAH8	0.268	757	LBR	0.287
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759	TARBP1	0.268	759	MCM8	0.287
760	NDUFS3	0.268	760	LOC401324	0.287
761	RUNDC3B	0.268	761	ZNF546	0.287
762	LOC100506995	0.268	762	LOC339166	0.287
763	C18orf56	0.268	763	ZNF770	0.287
764	DUS1L	0.268	764	CRY1	0.287
765	DZIP1	0.268	765	INA	0.286
766	NCOA1	0.268	766	ZNF615	0.286
767	ATP2B3	0.268	767	TIMM17B	0.286
768	SLC22A8	0.268	768	HSBP1	0.286
769	NCS1	0.268	769	SH3BP5L	0.286
770	PSMG3	0.267	770	SH3GL3	0.285
771	ANKRD26P3	0.267	771	GNRH2	0.285
772	XPO5	0.267	772	SALL3	0.285
773	LOC100506679	0.267	773	RNFT2	0.285
774	EID2	0.267	774	MSRB3	0.285
775	GNMT	0.267	775	ZNF227	0.285
776	CELSR2	0.267	776	CKAP2	0.285
777	MADCAM1	0.267	777	RBM3	0.285
778	NRM	0.266	778	MBLAC2	0.285
779	HIST1H1D	0.266	779	NECAB2	0.285
780	SESN1	0.266	780	RPP40	0.285
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782	ZNF460	0.266	782	PCDH10	0.284
783	CACYBP	0.266	783	NOSIP	0.284
784	C6orf162	0.265	784	NDUFAB1	0.284
785	RELL2	0.265	785	SOHLH1	0.284
786	ASNS	0.265	786	DIXDC1	0.284
787	HFE2	0.265	787	LANCL1	0.284
788	MYBL2	0.265	788	SMAD6	0.284
789	GTF2F2	0.265	789	SLC22A8	0.284
790	CHRNB4	0.265	790	HIST1H2AM	0.284
791	RABEPK	0.265	791	LOC100506679	0.284
792	DECR2	0.265	792	IAPP	0.284
793	LOC730098	0.265	793	TNFRSF4	0.284
794	GLA	0.265	794	ECEL1	0.283
795	APITD1	0.265	795	TYRP1	0.283
796	TEK	0.264	796	FMN2	0.283
797	DSG3	0.264	797	E2F3	0.283
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1044	ATP5J2	0.263			
1045	PTDSS2	0.263			
1046	MAP2	0.263			
1047	POLR2F	0.263			
1048	HCCS	0.263			
1049	OPA1	0.263			
1050	C14orf2	0.263			
1051	SRI	0.263			
1052	TARDBP	0.263			
1053	LINC00282	0.262			
1054	ACER1	0.262			
1055	C17orf81	0.262			
1056	SNRPD1	0.262			
1057	ANKRD13B	0.262			
1058	DYNLT1	0.262			
1059	ANO7	0.262			
1060	ID1	0.262			
1061	CHORDC1	0.262			
1062	FAM98B	0.262			
1063	TRIML2	0.262			
1064	JOSD2	0.262			
1065	POLR2D	0.262			
1066	UCK1	0.262			
1067	UQCRC2	0.262			
1068	HR	0.262			
1069	HOXD9	0.261			
1070	C9orf4	0.261			
1071	CCNB1	0.261			
1072	LOC100506597	0.261			
1073	METTL15	0.261			
1074	RRP12	0.261			
1075	GPR52	0.261			
1076	DYX1C1	0.261			
1077	PABPC5	0.261			

1078	LOC100506828	0.261
1079	ZNF768	0.261
1080	C16orf93	0.261
1081	PQBP1	0.261
1082	DPY19L2	0.261
1083	LHX2	0.261
1084	FAR2	0.261
1085	PSMD10	0.261
1086	ARHGAP11A	0.261
1087	UCP3	0.261
1088	ZC3H14	0.260
1089	DEGS1	0.260
1090	EIF2S3	0.260
1091	TUBE1	0.260

Supplementary Table 2 - PHGDH copy number in NSCLC cell lines

Cell line	PHGDH copy #	Cell line	PHGDH copy #
H1693	0.80218117	H1568	2.46912521
H650	1.33783482	H1581	2.48165059
H596	1.41539036	H1437	2.49251122
H1975	1.47120675	PC9	2.55177301
A549	1.47733806	H446	2.57183841
Hcc2935	1.48617087	Hcc44	2.58613932
Calu-3	1.49692299	H1703	2.65866131
H1755	1.52298317	HCC1195	2.66881629
H1395	1.59074215	H1792	2.6896156
H460	1.59526931	H522	2.69670928
Hcc1171	1.61250094	H2087	2.83883697
H2122	1.66612888	H1869	3.03584893
Hcc2279	1.68225919	H647	3.22209716
Calu-6	1.68692987	Hcc366	3.3689523
H2347	1.68845063	H2172	3.51591453
H2228	1.70751707	H838	4.2251425
H1373	1.74303314		
H1648	1.74508825		
H1355	1.74629828		
H2009	1.76810016		
H322	1.77817831		
H1299	1.78052168		
HCC95	1.83999265		
Hcc4006	1.84101324		
H1944	1.87826419		
H1915	1.9121557		
H2126	1.92398827		
H1155	1.98384595		
H2030	2.00722174		
H1650	2.08117748		
H2405	2.1178494		
H2291	2.14860458		
Calu-1	2.19755611		
H2170	2.20763245		
Hcc15	2.26466868		
Hcc827	2.27379155		
H2023	2.32430598		
Hcc1897	2.42183403		
H810	2.44020102		
H358	2.45513099		

Supplementary Table 3 - NRF2 score and CCLE gene expression data for NSCLC cell lines

NRF2 score	Description	NQO1	GCLC	GCLM	SLC7A11	AKR1C1	PHGDH	PSAT1	PSPH	SHMT1	SHMT2
1.55	A549_LUNG	13.24	11.17	11.07	11.12	13.07	7.98	11.45	9.18	7.94	9.67
0.87	CALU1_LUNG	11.31	6.08	9.80	8.77	8.21	7.54	10.27	8.38	7.34	9.32
1.13	CALU3_LUNG	11.82	10.30	8.98	10.73	9.09	8.71	9.61	8.87	7.55	10.07
0.90	CALU6_LUNG	11.62	8.64	7.77	8.75	7.62	9.52	10.82	6.27	8.63	10.30
0.83	HCC1171_LUNG	12.15	9.35	8.90	8.97	3.92	6.44	10.18	8.84	7.02	9.39
0.89	HCC1195_LUNG	11.24	10.81	8.76	8.65	5.09	5.91	10.55	8.75	7.12	9.95
1.63	HCC15_LUNG	13.79	12.56	10.67	10.63	12.00	9.03	10.26	8.46	8.25	9.64
0.98	HCC1588_LUNG	12.32	10.90	9.13	10.11	5.92	9.43	12.24	9.96	6.30	10.52
0.79	HCC1833_LUNG	12.26	9.88	12.17	9.38	4.56	4.58	9.63	8.60	6.97	9.98
1.02	HCC1897_LUNG	12.90	10.18	9.72	8.41	7.51	5.84	8.60	7.75	7.05	9.45
0.86	HCC2108_LUNG	11.62	8.92	9.60	8.25	3.99	5.84	9.83	8.68	6.96	9.25
0.82	HCC2279_LUNG	10.68	10.99	10.16	8.41	4.26	7.39	9.86	9.70	7.21	8.99
1.53	HCC2814_LUNG	13.49	11.12	10.10	10.69	14.19	8.51	10.48	8.86	8.63	9.27
0.95	HCC2935_LUNG	12.03	11.38	8.80	8.44	5.34	7.71	11.23	9.27	7.64	8.20
0.80	HCC366_LUNG	11.71	11.04	10.87	9.60	3.92	8.35	10.59	8.97	5.69	8.65
0.83	HCC4006_LUNG	11.55	10.72	8.93	8.32	4.67	8.49	10.79	11.00	7.74	9.26
1.13	HCC44_LUNG	12.42	10.45	10.38	11.33	9.18	7.87	11.23	8.91	6.33	10.41
0.86	HCC827_LUNG	11.10	9.33	10.14	7.72	4.48	6.87	10.87	10.52	8.09	10.26
1.54	HCC95_LUNG	12.82	13.15	12.10	11.24	14.11	9.50	11.32	10.19	7.90	9.72
0.78	NCIH1155_LUNG	10.87	8.59	9.20	8.08	4.61	10.05	11.13	8.67	7.44	10.01
0.93	NCIH1299_LUNG	11.02	8.70	9.63	7.19	4.64	8.50	11.35	8.40	7.50	9.66
1.56	NCIH1355_LUNG	13.18	10.42	10.79	10.98	13.84	7.22	10.62	8.28	7.54	9.98
1.06	NCIH1373_LUNG	12.89	13.54	9.67	11.20	8.35	8.35	10.45	7.44	7.16	9.24
1.13	NCIH1395_LUNG	11.95	8.87	9.69	8.76	7.89	6.78	10.92	7.80	7.52	10.65
1.65	NCIH1437_LUNG	13.88	9.51	11.71	10.20	14.78	10.30	10.56	7.92	7.93	10.33
0.88	NCIH1568_LUNG	11.43	9.42	9.37	7.89	4.30	9.60	9.80	8.36	7.38	9.40
0.85	NCIH1581_LUNG	10.82	9.04	8.68	8.07	5.45	8.25	9.75	9.02	7.01	9.28
1.47	NCIH1648_LUNG	12.09	9.83	10.06	10.61	10.83	7.68	9.17	8.32	7.39	9.74
0.81	NCIH1650_LUNG	12.43	8.82	9.48	8.58	4.59	9.19	10.99	8.65	7.76	8.72
0.85	NCIH1693_LUNG	9.82	9.33	9.68	7.93	4.09	7.02	10.55	8.65	6.87	9.88
0.89	NCIH1703_LUNG	12.93	9.29	10.11	10.12	4.79	10.21	12.50	9.72	7.55	9.52
1.50	NCIH1792_LUNG	12.91	11.04	10.02	11.60	13.46	8.44	10.58	7.31	6.74	9.02
0.97	NCIH1869_LUNG	12.85	12.48	11.15	9.37	8.37	9.61	11.27	9.65	7.43	9.88
1.20	NCIH1915_LUNG	12.22	10.36	11.64	9.67	9.25	8.89	10.83	9.62	7.38	9.74
1.74	NCIH1944_LUNG	13.05	10.80	12.07	11.71	14.21	7.37	10.56	8.51	7.54	9.49
0.93	NCIH1975_LUNG	11.59	8.95	8.82	7.08	5.00	8.06	10.20	9.02	8.60	10.29
0.87	NCIH2009_LUNG	12.63	10.78	10.87	8.85	4.75	7.91	10.79	8.82	7.75	8.95
1.70	NCIH2023_LUNG	13.05	11.89	11.52	10.86	13.89	7.75	10.91	8.52	7.18	9.12
1.40	NCIH2030_LUNG	13.38	9.57	10.08	10.04	10.57	5.62	4.31	7.33	6.80	9.13
0.99	NCIH2087_LUNG	12.66	12.20	10.49	9.82	5.61	10.68	11.00	8.36	9.08	10.61
1.79	NCIH2122_LUNG	13.15	11.82	11.48	12.14	14.42	9.31	11.91	9.31	8.50	10.83
1.09	NCIH2126_LUNG	12.18	10.72	8.64	10.59	6.18	8.39	10.28	7.76	7.15	8.96
1.47	NCIH2170_LUNG	13.60	11.49	10.54	11.08	13.60	9.71	11.58	9.36	8.10	9.26
1.45	NCIH2172_LUNG	13.26	11.82	10.63	10.34	12.25	7.97	10.40	9.24	6.43	8.65
1.51	NCIH2228_LUNG	13.74	11.81	10.82	10.39	13.41	8.38	10.72	8.40	7.70	9.56
0.85	NCIH2291_LUNG	11.97	9.08	9.27	9.37	6.30	6.54	11.63	8.80	6.30	9.48
0.90	NCIH2347_LUNG	11.72	9.57	9.45	8.44	6.26	5.84	9.82	6.79	6.18	9.20
1.29	NCIH2405_LUNG	12.50	10.95	8.86	9.82	11.15	6.97	8.64	8.65	6.11	8.67
1.25	NCIH322_LUNG	13.17	11.60	9.96	11.12	6.16	7.79	6.06	7.62	7.50	9.09

NRF2 score	Description	AKR1C2	AKR1C3	AKR1B10	LOC344887	CYP4F11	ALDH3A1	SPP1	OSGIN1	PGD
1.55	A549_LUNG	14.70	14.03	14.27	7.55	7.69	10.48	12.47	7.71	12.32
0.87	CALU1_LUNG	4.86	8.49	3.89	4.66	3.75	6.13	3.80	5.29	8.74
1.13	CALU3_LUNG	10.25	12.52	11.81	6.53	3.88	4.12	13.61	5.67	9.89
0.90	CALU6_LUNG	7.23	9.79	3.89	4.58	3.50	5.32	4.28	5.15	9.62
0.83	HCC1171_LUNG	4.44	8.82	5.36	4.86	3.54	3.76	4.07	4.98	8.44
0.89	HCC1195_LUNG	5.30	10.51	3.73	4.58	3.68	4.97	4.85	5.61	9.63
1.63	HCC15_LUNG	13.29	12.72	6.19	8.79	9.24	12.91	9.64	8.37	12.40
0.98	HCC1588_LUNG	7.64	12.89	4.81	6.70	6.26	9.46	3.82	5.56	9.72
0.79	HCC1833_LUNG	4.45	7.09	3.82	3.97	3.65	4.32	3.99	5.99	10.03
1.02	HCC1897_LUNG	4.81	9.46	6.59	7.18	3.47	3.98	4.07	7.66	10.02
0.86	HCC2108_LUNG	4.83	3.54	3.81	4.13	3.92	4.05	4.91	5.60	8.62
0.82	HCC2279_LUNG	4.32	4.99	4.12	5.24	3.56	4.92	4.01	5.51	8.09
1.53	HCC2814_LUNG	13.85	14.02	13.20	10.74	6.96	9.70	12.34	9.65	11.50
0.95	HCC2935_LUNG	5.33	7.61	5.49	5.49	3.95	7.61	4.52	6.20	10.03
0.80	HCC366_LUNG	4.39	3.88	5.00	4.45	3.72	3.89	3.89	5.21	7.87
0.83	HCC4006_LUNG	4.09	4.00	5.94	4.99	3.49	6.86	4.02	5.37	9.40
1.13	HCC44_LUNG	9.35	11.07	9.49	8.57	5.42	5.37	4.23	7.31	10.71
0.86	HCC827_LUNG	5.00	6.80	5.09	4.56	3.77	3.99	4.81	5.56	8.99
1.54	HCC95_LUNG	15.12	13.84	13.32	10.02	10.50	9.77	11.64	7.63	11.27
0.78	NCIH1155_LUNG	3.95	3.66	3.53	4.36	3.40	4.21	5.12	4.66	9.36
0.93	NCIH1299_LUNG	5.76	4.66	4.21	4.29	3.84	4.87	10.48	6.34	9.58
1.56	NCIH1355_LUNG	14.28	12.73	6.82	9.19	8.86	10.88	13.46	8.21	10.91
1.06	NCIH1373_LUNG	4.56	7.95	8.89	8.85	5.12	5.12	5.90	6.32	10.24
1.13	NCIH1395_LUNG	11.22	9.28	10.30	4.12	3.72	4.96	4.18	6.15	9.69
1.65	NCIH1437_LUNG	14.99	13.97	13.79	8.58	7.64	9.11	9.18	6.77	11.92
0.88	NCIH1568_LUNG	5.59	5.63	3.90	5.35	3.73	4.35	5.49	5.67	8.45
0.85	NCIH1581_LUNG	4.50	4.45	3.63	4.14	3.60	4.23	5.45	4.82	10.01
1.47	NCIH1648_LUNG	14.58	13.37	13.49	10.53	8.22	8.97	5.51	6.54	10.75
0.81	NCIH1650_LUNG	4.34	4.27	5.05	4.33	3.54	4.35	4.29	5.38	8.65
0.85	NCIH1693_LUNG	3.98	4.99	3.81	4.03	3.69	4.26	4.14	5.56	8.67
0.89	NCIH1703_LUNG	3.77	4.72	3.72	4.33	3.73	4.04	3.78	6.35	9.74
1.50	NCIH1792_LUNG	12.47	12.63	12.86	8.66	4.28	8.52	12.97	8.25	10.59
0.97	NCIH1869_LUNG	7.48	10.29	5.58	6.51	3.97	5.16	4.01	5.73	9.84
1.20	NCIH1915_LUNG	8.22	11.56	5.10	7.20	3.13	3.92	13.22	5.72	9.05
1.74	NCIH1944_LUNG	14.66	14.06	14.39	10.64	8.20	9.26	14.31	8.45	11.70
0.93	NCIH1975_LUNG	5.42	9.64	8.21	4.19	3.50	4.18	8.54	5.29	8.71
0.87	NCIH2009_LUNG	4.46	8.40	5.90	4.52	3.55	4.14	3.93	5.25	10.25
1.70	NCIH2023_LUNG	15.05	13.93	14.04	9.68	9.14	7.58	13.51	8.00	12.69
1.40	NCIH2030_LUNG	11.51	12.32	8.43	7.79	7.85	4.14	13.55	8.37	10.19
0.99	NCIH2087_LUNG	9.70	10.72	9.76	6.35	3.69	4.62	4.03	5.74	9.77
1.79	NCIH2122_LUNG	14.54	13.64	14.25	10.31	10.18	12.64	13.82	8.10	12.69
1.09	NCIH2126_LUNG	11.29	10.29	8.04	7.50	3.92	5.03	3.92	6.18	10.35
1.47	NCIH2170_LUNG	14.24	13.97	7.03	7.01	8.38	10.73	13.00	9.14	12.04
1.45	NCIH2172_LUNG	14.77	14.19	11.35	9.07	4.22	4.13	10.47	7.59	11.13
1.51	NCIH2228_LUNG	14.13	13.53	12.81	9.24	8.58	11.43	11.98	8.63	11.61
0.85	NCIH2291_LUNG	4.98	6.47	4.75	5.81	3.99	4.80	4.08	5.46	8.59
0.90	NCIH2347_LUNG	5.20	8.05	5.78	5.18	3.85	4.16	4.50	6.27	9.33
1.29	NCIH2405_LUNG	11.76	12.39	8.65	7.49	6.37	8.47	13.97	5.23	9.88
1.25	NCIH322_LUNG	12.14	9.10	6.08	8.00	8.96	9.41	11.48	8.43	10.24

NRF2 score	Description	KIAA0319	SRXN1	NR0B1	SLC7A11	CABYR	ABCC2	LOC100292680	JAKMIP3
1.55	A549_LUNG	5.58	11.50	9.53	11.12	6.66	10.11	4.58	5.12
0.87	CALU1_LUNG	4.23	10.08	3.83	8.77	4.16	4.03	4.49	3.72
1.13	CALU3_LUNG	5.47	8.58	3.76	10.73	5.39	4.56	4.15	4.11
0.90	CALU6_LUNG	4.62	7.98	3.83	8.75	5.78	4.20	4.60	3.91
0.83	HCC1171_LUNG	3.99	8.19	4.78	8.97	5.09	4.00	4.41	4.19
0.89	HCC1195_LUNG	4.54	9.56	4.00	8.65	7.75	4.25	4.65	3.81
1.63	HCC15_LUNG	6.72	11.60	9.93	10.63	9.41	10.48	10.10	7.59
0.98	HCC1588_LUNG	4.01	9.38	3.80	10.11	4.30	4.25	4.11	4.16
0.79	HCC1833_LUNG	4.79	7.09	3.78	9.38	4.67	4.52	4.04	3.70
1.02	HCC1897_LUNG	4.46	10.81	8.74	8.41	7.01	4.07	4.60	6.83
0.86	HCC2108_LUNG	4.23	8.93	3.88	8.25	6.85	4.33	4.22	4.79
0.82	HCC2279_LUNG	4.11	10.56	3.91	8.41	4.53	5.21	4.71	4.26
1.53	HCC2814_LUNG	6.24	12.09	3.92	10.69	7.52	7.11	9.99	6.24
0.95	HCC2935_LUNG	5.49	8.85	3.64	8.44	4.92	8.05	4.28	3.81
0.80	HCC366_LUNG	4.58	8.39	4.17	9.60	6.07	4.32	4.28	4.26
0.83	HCC4006_LUNG	3.94	9.75	3.76	8.32	4.40	3.93	4.25	4.40
1.13	HCC44_LUNG	4.77	11.39	4.25	11.33	6.48	4.28	4.39	4.45
0.86	HCC827_LUNG	4.01	8.95	3.85	7.72	5.00	7.28	4.38	3.84
1.54	HCC95_LUNG	5.83	11.57	9.34	11.24	8.01	3.95	4.96	7.00
0.78	NCIH1155_LUNG	5.40	8.64	3.75	8.08	5.22	3.86	3.83	3.81
0.93	NCIH1299_LUNG	4.87	9.52	6.48	7.19	7.52	4.03	4.66	3.84
1.56	NCIH1355_LUNG	7.31	12.18	4.58	10.98	9.32	9.79	10.30	5.92
1.06	NCIH1373_LUNG	4.49	9.49	3.85	11.20	6.35	4.89	5.13	4.99
1.13	NCIH1395_LUNG	5.17	9.39	9.61	8.76	5.08	9.76	4.28	5.18
1.65	NCIH1437_LUNG	6.96	11.43	10.73	10.20	9.17	10.74	10.88	6.73
0.88	NCIH1568_LUNG	4.90	10.40	3.77	7.89	5.23	6.96	4.02	3.97
0.85	NCIH1581_LUNG	5.62	9.99	3.80	8.07	7.27	4.92	4.12	4.52
1.47	NCIH1648_LUNG	4.28	10.98	8.47	10.61	7.42	9.47	9.43	4.86
0.81	NCIH1650_LUNG	4.31	9.57	3.84	8.58	5.21	4.49	4.53	4.06
0.85	NCIH1693_LUNG	5.51	9.40	6.10	7.93	8.26	4.05	4.40	3.76
0.89	NCIH1703_LUNG	5.36	10.04	5.74	10.12	7.59	4.13	4.44	4.15
1.50	NCIH1792_LUNG	5.60	10.93	9.19	11.60	9.60	8.43	7.69	6.02
0.97	NCIH1869_LUNG	7.36	9.70	4.35	9.37	4.42	4.76	4.30	4.07
1.20	NCIH1915_LUNG	4.19	10.78	8.37	9.67	8.12	5.39	9.72	4.88
1.74	NCIH1944_LUNG	7.60	12.47	10.23	11.71	8.07	11.64	8.25	7.16
0.93	NCIH1975_LUNG	4.45	10.04	3.87	7.08	5.03	4.59	4.26	4.29
0.87	NCIH2009_LUNG	4.47	9.02	4.04	8.85	7.40	3.96	4.30	3.85
1.70	NCIH2023_LUNG	6.51	12.57	9.84	10.86	9.67	9.69	11.17	6.64
1.40	NCIH2030_LUNG	7.06	10.57	8.31	10.04	6.45	9.98	4.49	6.78
0.99	NCIH2087_LUNG	4.69	10.50	3.80	9.82	4.26	4.60	4.55	5.59
1.79	NCIH2122_LUNG	7.02	12.84	8.86	12.14	8.83	11.22	10.97	6.75
1.09	NCIH2126_LUNG	5.06	11.43	5.68	10.59	7.32	9.21	4.27	3.82
1.47	NCIH2170_LUNG	6.78	11.99	11.09	11.08	9.67	4.28	5.16	5.98
1.45	NCIH2172_LUNG	6.62	11.08	8.77	10.34	7.37	7.10	10.44	6.87
1.51	NCIH2228_LUNG	5.94	11.29	3.85	10.39	7.44	10.28	4.38	5.62
0.85	NCIH2291_LUNG	5.20	8.29	3.87	9.37	3.98	4.10	4.18	3.95
0.90	NCIH2347_LUNG	4.65	10.01	3.68	8.44	7.77	4.68	4.17	3.89
1.29	NCIH2405_LUNG	4.45	10.45	5.34	9.82	6.51	8.92	4.45	5.12
1.25	NCIH322_LUNG	5.87	10.24	5.37	11.12	4.92	9.15	4.39	3.99

NRF2 score	Description	KYNU	PTGR1
1.55	A549_LUNG	10.16	12.84
0.87	CALU1_LUNG	4.82	12.07
1.13	CALU3_LUNG	8.85	8.65
0.90	CALU6_LUNG	6.79	10.34
0.83	HCC1171_LUNG	5.13	10.55
0.89	HCC1195_LUNG	7.13	7.87
1.63	HCC15_LUNG	10.97	13.36
0.98	HCC1588_LUNG	4.58	9.32
0.79	HCC1833_LUNG	4.18	6.73
1.02	HCC1897_LUNG	4.46	10.94
0.86	HCC2108_LUNG	11.74	9.23
0.82	HCC2279_LUNG	4.27	10.46
1.53	HCC2814_LUNG	8.55	12.19
0.95	HCC2935_LUNG	5.88	9.71
0.80	HCC366_LUNG	4.44	10.04
0.83	HCC4006_LUNG	4.66	9.84
1.13	HCC44_LUNG	9.95	11.80
0.86	HCC827_LUNG	6.66	8.98
1.54	HCC95_LUNG	8.72	12.23
0.78	NCIH1155_LUNG	4.13	10.24
0.93	NCIH1299_LUNG	4.71	9.52
1.56	NCIH1355_LUNG	9.74	11.60
1.06	NCIH1373_LUNG	7.82	12.79
1.13	NCIH1395_LUNG	8.67	10.13
1.65	NCIH1437_LUNG	10.65	12.30
0.88	NCIH1568_LUNG	6.28	11.07
0.85	NCIH1581_LUNG	4.88	9.94
1.47	NCIH1648_LUNG	9.87	11.56
0.81	NCIH1650_LUNG	4.48	10.30
0.85	NCIH1693_LUNG	4.45	10.39
0.89	NCIH1703_LUNG	8.19	9.42
1.50	NCIH1792_LUNG	9.12	12.08
0.97	NCIH1869_LUNG	5.15	9.53
1.20	NCIH1915_LUNG	8.28	11.36
1.74	NCIH1944_LUNG	11.83	13.27
0.93	NCIH1975_LUNG	7.32	11.46
0.87	NCIH2009_LUNG	7.04	10.11
1.70	NCIH2023_LUNG	9.98	13.58
1.40	NCIH2030_LUNG	10.21	11.06
0.99	NCIH2087_LUNG	5.46	10.75
1.79	NCIH2122_LUNG	10.71	12.54
1.09	NCIH2126_LUNG	4.33	12.17
1.47	NCIH2170_LUNG	5.04	9.48
1.45	NCIH2172_LUNG	10.15	12.85
1.51	NCIH2228_LUNG	9.56	13.54
0.85	NCIH2291_LUNG	4.57	12.06
0.90	NCIH2347_LUNG	5.30	10.25
1.29	NCIH2405_LUNG	7.81	10.14
1.25	NCIH322_LUNG	4.86	9.64

NRF2 score	Description	NQO1	GCLC	GCLM	SLC7A11	AKR1C1	PHGDH	PSAT1	PSPH
0.94	NCIH358_LUNG	12.48	10.74	9.97	9.11	4.44	9.38	10.45	8.35
0.75	NCIH446_LUNG	5.07	8.96	8.37	5.35	4.73	9.86	10.01	8.09
1.70	NCIH460_LUNG	13.23	10.90	11.58	11.12	13.68	8.87	11.38	6.76
0.86	NCIH522_LUNG	12.47	9.36	8.83	7.35	4.57	9.19	10.56	9.39
1.17	NCIH596_LUNG	11.88	11.75	8.83	9.67	12.98	7.87	9.86	9.73
1.56	NCIH647_LUNG	13.10	10.99	10.95	12.12	13.87	10.29	11.75	8.18
0.84	NCIH650_LUNG	10.15	9.45	8.96	7.11	4.11	4.08	7.59	8.60
0.93	NCIH810_LUNG	9.11	10.61	10.10	6.11	7.00	8.74	10.68	8.92
1.36	NCIH838_LUNG	12.99	10.04	11.61	9.13	9.98	8.20	9.76	8.05
1.57	PC14_LUNG (PC9)	12.45	11.11	11.77	11.00	13.36	9.80	11.20	9.72

NRF2 score	Description	AKR1C2	AKR1C3	AKR1B10	LOC344887	CYP4F11	ALDH3A1	SPP1	OSGIN1
0.94	NCIH358_LUNG	5.01	6.71	4.57	4.38	3.45	7.02	10.55	5.97
0.75	NCIH446_LUNG	4.11	3.69	3.35	4.35	3.51	3.90	4.07	4.42
1.70	NCIH460_LUNG	14.21	13.62	13.72	8.84	8.97	10.43	13.69	8.09
0.86	NCIH522_LUNG	7.78	3.83	3.91	4.36	3.71	4.02	3.88	7.25
1.17	NCIH596_LUNG	13.76	12.55	11.90	7.33	5.60	9.28	5.68	5.54
1.56	NCIH647_LUNG	13.64	13.40	12.61	9.77	7.71	10.51	12.96	7.26
0.84	NCIH650_LUNG	4.39	4.30	4.03	3.93	3.70	4.25	4.13	5.23
0.93	NCIH810_LUNG	9.07	10.65	4.14	4.35	3.46	4.46	5.47	4.84
1.36	NCIH838_LUNG	12.02	12.46	9.00	6.35	6.54	9.93	5.17	6.54
1.57	PC14_LUNG (PC9)	13.80	13.97	12.90	9.24	8.12	10.84	12.44	6.68

NRF2 score	Description	KIAA0319	SRXN1	NR0B1	SLC7A11	CABYR	ABCC2
0.94	NCIH358_LUNG	4.15	9.63	3.82	9.11	7.04	4.06
0.75	NCIH446_LUNG	4.52	8.88	3.85	5.35	5.32	3.80
1.70	NCIH460_LUNG	6.83	12.42	10.99	11.12	9.45	9.63
0.86	NCIH522_LUNG	5.78	9.21	3.90	7.35	8.70	3.98
1.17	NCIH596_LUNG	4.60	9.63	3.94	9.67	5.15	4.08
1.56	NCIH647_LUNG	4.95	11.66	9.26	12.12	8.57	9.98
0.84	NCIH650_LUNG	4.32	8.14	3.91	7.11	6.55	3.72
0.93	NCIH810_LUNG	5.52	9.68	7.66	6.11	4.52	4.67
1.36	NCIH838_LUNG	5.85	11.03	5.84	9.13	7.60	9.12
1.57	PC14_LUNG (PC9)	7.09	11.14	10.00	11.00	5.91	9.21

NRF2 score	Description	KYNU	PTGR1	LOC100292680	JAKMIP3	SHMT1	SHMT2	PGD
0.94	NCIH358_LUNG	7.57	10.26	4.28	3.66	8.64	9.99	10.13
0.75	NCIH446_LUNG	4.36	8.94	4.31	4.12	7.03	9.59	10.06
1.70	NCIH460_LUNG	9.82	12.67	10.42	6.02	8.17	10.09	11.86
0.86	NCIH522_LUNG	4.28	8.38	4.30	4.47	5.84	8.51	10.49
1.17	NCIH596_LUNG	6.24	11.81	4.08	4.69	7.22	8.96	9.78
1.56	NCIH647_LUNG	11.23	13.03	4.27	4.68	7.20	9.84	12.27
0.84	NCIH650_LUNG	10.73	11.67	4.39	4.54	5.48	7.73	8.23
0.93	NCIH810_LUNG	4.86	8.17	4.61	4.03	7.53	10.04	9.42
1.36	NCIH838_LUNG	9.51	11.97	9.93	7.01	7.11	8.71	10.70
1.57	PC14_LUNG (PC9)	8.17	12.84	8.92	4.44	8.68	10.03	11.01

Supplementary Table 4 - Real-time PCR primers

ChIP primers

Gene Name	Forward	Reverse
Non-specific	TAAAAAGTAGAGTGGTTGGAGTGATGACG	TCTCAGTTTTTGCCCTTATTTAATCCC
NQO1	CCCTTTTAGCCTTGGCACGAAA	TGCACCCAGGGAAGTGTGTTGTAT
ASNS	TGGTTGGTCCTCGCAGGCAT	CGCTTATACCGACCTGGCTCCT
PHGDH P1	CAGGTCCCCGCTCTTTTAT	TCTTTCCTCTGGTGGCCTAA
PHGDH P2	CGTAAGGCAGCAAACACGTA	CCAGCGATAAACCAAAGGTG
PSAT1 P1	TTCTCTAAACGGGGCAGTTG	CAGAATACCCTCCCCCTACC
PSAT1 P2	GTTTGCATCCCTGCGTGT	CCGAGCTTCCTCACCAACT
SHMT1	GCAGAGTGCACCTTCCTGA	GCCCACCTACCGGAACAC
SHMT2	GGCAAATGAGCGGAGTTTT	TGCCCGAGAGTAAGCCAATA
ATF4 –405	Qiagen catalog # GPH1008975 (–)01A	
ATF4 +424	Qiagen catalog # GPH1008975(+)01A	

Real-time PCR primers

Gene Name	Forward	Reverse
PHGDH	ATCTCTCACGGGGGTTGTG	AGGCTCGCATCAGTGTCC
PSAT1	ACTTCCTGTCCAAGCCAGTGGA	CTGCACCTTGTATTCCAGGACC
PSPH	ACTTCCTGTCCAAGCCAGTGGA	CTGCACCTTGTATTCCAGGACC
SHMT1	TGAACACTGCCATGTGGTGACC	TCTTTGCCAGTCTTGGGATCC
SHMT2	GCCTCATTGACTACAACCAGCTG	ATGTCTGCCAGCAGGTGTGCTT
bACTIN	CAACCGCGAGAAGATGACC	ATCACGATGCCAGTGGTACG
NRF2	GAGAGCCCAGTCTTCATTGC	TTGGCTTCTGGACTTGGAAC
NQO1	TGAAGAAGAAAGGATGGGAGGT	GGCCTTCTTTATAAGCCAGAACA
ATF4	GTTCTCCAGCGACAAGGCTA	GCATCCAAGTCGAAACTCCTT

Supplementary Table 5 - Vectors

Vectors

Vector Name	Mature antisense sequence
pLKO.1 scramble - SHC002 (SIGMA)	TTGGTGCTCTTCATCTTGTTG
pLKO.1 shNRF2 - TRCN0000007555 (#1)	ATTTCACATCACAGTAGGAGC
pLKO.1 shNRF2 - TRCN0000007558 (#2)	TTGTGTTTAGTGAAATGCCGG
pLKO.1 shNRF2 – TRCN0000281950 (#3)	AAATGATCTAAATCTTGCTCT
pLKO.1 shPHGDH - TRCN0000233029 (#1)	AATAAGGCCTTCACAGTCCTG
pLKO.1 shPHGDH - TRCN0000233031 (#2)	CTTTCACCAGCAGCTTAGCGT
pLKO.1 shATF4 - TRCN0000329751 (#1)	GAATGATCTGGAGTGGAGGAC
pLKO.1 shATF4 - TRCN0000329696 (#2)	CTATACCCAACAGGGCATCCA
pLenti CMV puro - luciferase	N/A
pLenti CMV puro - PHGDH	N/A
pLenti CMV puro – NRF2	N/A
pLenti CMV puro – mATF4 (addgene # 24874)	N/A

Supplementary Note

The human genome sequence reveals more than 20 genes for amino acid transporters. These transporters fall into two classes. Sodium coupled transporters that use the sodium gradient to drive amino acid uptake against a concentration gradient. Amino acid exchange systems (e.g. antiporters) that cannot mediate net amino acid uptake against a gradient, but can exchange an abundant intracellular amino acid (e.g. Ser) for another amino acid from outside the cell (e.g. Gly or cystine) and thus facilitate the elevation of intracellular Gly or cystine above the extracellular concentration at the expense of dissipating the Ser gradient. These antiporters allow cells to import amino acids without altering the osmolarity or (assuming only neutral amino acid exchange) charge. Even at steady state, these antiporters are highly active in exchanging intracellular for extracellular amino acids (e.g. Ser_{in} for Ser_{out} or Gly_{in} for Gly_{out}) with no net movement of amino acids across the cytoplasmic membrane. For further discussions of how these antiporters work, see references[1-5].

The mechanism of action of these transporters is relevant to the discussion: They could potentially be exchanging the intracellular ^{13}C-Ser and ^{13}C-Gly for extracellular ^{12}C-Ser and ^{12}C-Gly with no net import of Ser and Gly (e.g. Ser_{in}-Ser_{out} and Gly_{in}-Gly_{out} antiport as discussed above), in which case they provide no net Ser and Gly movement but could quickly dilute the intracellular ^{13}C-Ser and ^{13}C-Gly isotope by exchanging it for extracellular ^{12}C-Ser and ^{12}C-Gly. To test this possibility we examined the media at 24 and 48 hours after ^{13}C-glucose was added to the cells and found that the majority of ^{13}C-Ser and ^{13}C-Gly had escaped the cells (Supplementary Figure 20). In fact the ^{13}C-Ser/total-Ser and ^{13}C-Gly/total-Gly ratio outside the cell was greater than or equal to the ^{13}C-Ser/total-Ser and ^{13}C-Gly/total-Gly ratio inside the cell at both time points (up to 30% labeled), despite the massive excess of media Ser and Gly compared to intracellular Ser and Gly. We also compared the intracellular and extracellular serine labeling in both serine-high and serine-low cells at an earlier time point of 6 hours and found that the intracellular and extracellular serine pools had equilibrated in all cell lines (Supplementary Fig. 20e,f), demonstrating that the rate of exchange is fast and does not differ between serine high and low cell lines. Thus, it is likely that the true contribution of glucose-derived serine and glycine to downstream metabolites is significantly higher due to the isotope dilution effect.

We also observe slow kinetics in intracellular glycine labeling, which is likely influenced by the rate at which intracellular ^{13}C-Ser/^{12}C-Ser and intracellular ^{13}C-Gly/^{12}C-Gly reach steady state. We examined the labeling in serine in a panel of cell lines and found that a plateau is reached by 6 hours (Supplemental Figure 1). However, this was not true for glycine. We observe a doubling in the intracellular labeling of the M+2 isotopologue of glycine from 24 to 48 hours in cell lines

(Supplementary Figure 20). The longer time required for intracellular ^{13}C-Gly/^{12}C-Gly to reach steady state could be explained by the fact that this isotope ratio is influenced not only by exchange of intracellular ^{13}C-Ser for extracellular ^{12}C-Ser but also by exchange of intracellular ^{13}C-Gly for extracellular ^{12}C-Gly. The total quantity of Ser and Gly in the media vastly exceeds the total Ser and Gly in the cytosol at any one time, but this experiment shows that over 48 hours the cell has produced at least one third as much Ser and Gly from glucose as was present in the media (not including the amount of glucose-derived intracellular Ser and Gly that was used for anabolic processes).

Importantly, we observe that serine high cell lines have a low rate of serine consumption and little to no glycine consumption. In fact, most serine high cell lines demonstrate net glycine export, which in the case of H920 and H2170 vastly exceeds serine consumption. We have estimated the rate of serine and glycine consumption in these lines and found them to be the following:

Cell line	serine consumption	glycine consumption
A549	5.4 nmol/hr/10^6 cells	0.625 nmol/hr/10^6 cells
PC9	3.05 nmol/hr/10^6 cells	1.28 nmol/hr/10^6 cells
H920	14.35 nmol/hr/10^6 cells	-81.9 nmol/hr/10^6 cells
H2170	4.4 nmol/hr/10^6 cells	-30.75 nmol/hr/10^6 cells
H460	7.5 nmol/hr/10^6 cells	-6.625 nmol/hr/10^6 cells

Comparisons with published data[6] show the serine consumption rates of these lines to be lower than high serine consuming lines in their study and similar to the rate they observed for A549 cells, which demonstrated minimal serine consumption. Furthermore, we estimate that at 6 hours, when the intracellular and extracellular serine has equilibrated (Supplementary Figure 1, Supplementary Figure 20), the extracellular labeling exceeds the amount of serine consumed:

Cell line	serine consumption (% of total)	serine labeling (% of total)
A549	10.1	16.4
PC9	5.7	20.6
H920	26.9	6.8
H2170	8.2	29.5
H460	14.1	25.8

These results suggest that the majority of the serine in these cell lines is derived from glucose, rather than consumption from the media.

Consistent with the slow equilibration of ^{13}C-Gly/^{12}C-Gly, we observe a significant increase in glutathione and nucleotide labeling at 48 hours compared to 24 hours

(Figures 4d, 4e, Supplementary Figure 19a,b). These results demonstrate that PHGDH-derived serine and glycine contribute significantly to the glutathione and nucleotide pools and that ^{13}C-glucose tracing underestimates the contribution due to ^{13}C/^{12}C label exchange. Consistent with this finding, depletion of NRF2, ATF4 or PHGDH significantly reduces the total levels of these metabolites (Figs. 4f,g).

It should also be pointed out that sodium-independent amino acid transporters can exchange intracellular Ser for extracellular cystine, so the production of intracellular Ser can be used to import cystine for glutathione synthesis. So, although we do not observe a major conversion of intracellular Ser to Cys, it is possible that Ser synthesis is critical for high rates of cystine import needed to provide the Cys needed for glutathione synthesis.

We also observe that ATF4 is capable of rescuing serine biosynthesis in cells expressing shNRF2 during the initial time points in the time course, which reflect the true rate of serine biosynthesis. This is consistent with the ability of ATF4 to rescue the expression of serine biosynthesis enzyme expression. However, there is a defect observed at later time points, which reflect the later equilibration phase. Thus, ATF4 may rescue serine biosynthesis, but ^{13}C-serine may not be retained well in cells lacking NRF2.

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