

Supplementary Table S1. Patient characteristics

Characteristic	Cohort 1 ^a	Cohort 2 ^b	CKS2 immunohistochemistry cohort ^c
No. of patients	150	135	47
Age (years)			
Median	54.9	52.9	54.7
Range	23.8-84.2	21.8-83.9	29.7 – 84.2
Histology			
Squamous	150	135	45
Adenosquamous			2
FIGO stage			
1B-2B	103	104	28
3B-4A	47	31	19
Tumor volume (cm ³) ^d			
Median	43.8	30.8	47.8
Range	1.9-321.0	2.8-266.8	2.8 – 321.0
Pelvic lymph node status			
Positive	64		22
Negative	86		25
Abbreviations: FIGO, Federation International de Gynecologie et d'Obstetrique.			
^a Assayed with WG-6 v3 Illumina bead arrays.			
^b Assayed with HT-12 v4 Illumina bead arrays.			
^c Includes 41 cohort 1 patients.			
^d Calculated from pre-treatment magnetic resonance images based on 3 orthogonal diameters (a,b,c) as $(\pi/6)^x abc$.			

Supplementary Table S2A. Cellular compartments enriched in the transcriptional program associated with CKS2 expression in patients

Top 20 cellular components from GSEA analysis are listed.

Cohort 1					
Gene Set Name	Cellular compartment	# Genes in Gene Set (K)	# Genes in Overlap (k)	p-value	FDR q-value
GO_CATALYTIC_COMPLEX		1038	194	2.26E-68	1.31E-65
GO_MITOCHONDRION	Mitochondrion	1633	240	1.30E-63	3.54E-61
GO_NUCLEOPLASM_PART	Nucleus	708	154	1.83E-63	3.54E-61
GO_RIBONUCLEOPROTEIN_COMPLEX		721	153	1.61E-61	2.33E-59
GO_CHROMOSOME	Chromosome	880	159	6.51E-54	7.55E-52
GO_ENVELOPE	Envelope	1090	173	2.32E-50	2.25E-48
GO_TRANSFERASE_COMPLEX		703	135	5.58E-49	4.63E-47
GO_MITOCHONDRIAL_PART	Mitochondrion	953	155	1.68E-46	1.22E-44
GO_NUCLEOLUS	Nucleus	848	145	3.46E-46	2.23E-44
GO_CYTOSKELETON	Cytoskeleton	1967	233	5.47E-45	3.17E-43
GO_MICROTUBULE_CYTOSKELETON	Cytoskeleton	1068	154	1.21E-39	6.41E-38
GO_MITOCHONDRIAL_ENVELOPE	Mitochondrion	691	119	2.46E-38	1.19E-36
GO_CYTOSKELETAL_PART	Cytoskeleton	1436	172	9.51E-34	4.24E-32
GO_ORGANELLE_INNER_MEMBRANE	Envelope	525	94	7.33E-32	3.04E-30
GO_MICROTUBULE_ORGANIZING_CENTER	Cytoskeleton	623	101	1.87E-30	7.25E-29
GO_CHROMOSOMAL_REGION	Chromosome	330	69	7.20E-28	2.61E-26
GO_CENTROSOME	Cytoskeleton	487	84	1.98E-27	6.75E-26
GO_CHROMOSOME_CENTROMERIC_REGION	Chromosome	174	50	2.72E-27	8.78E-26
GO_NUCLEAR_BODY	Nucleus	349	69	2.40E-26	7.33E-25
GO_RIBOSOME	Others	226	55	6.45E-26	1.87E-24

Cohort 2					
Gene Set Name	Cellular compartment	# Genes in Gene Set (K)	# Genes in Overlap (k)	p-value	FDR q-value
GO_MITOCHONDRION	Mitochondrion	1633	282	4.98E-92	2.89E-89
GO_RIBONUCLEOPROTEIN_COMPLEX		721	164	9.83E-71	2.85E-68
GO_MITOCHONDRIAL_PART	Mitochondrion	953	187	1.45E-69	2.80E-67
GO_ENVELOPE	Envelope	1090	190	4.87E-62	7.07E-60
GO_CHROMOSOME	Chromosome	880	168	1.20E-60	1.39E-58
GO_MITOCHONDRIAL_ENVELOPE	Mitochondrion	691	143	3.54E-56	3.42E-54
GO_NUCLEOLUS	Nucleus	848	158	1.51E-55	1.25E-53
GO_CATALYTIC_COMPLEX		1038	172	6.91E-53	5.01E-51
GO_ORGANELLE_INNER_MEMBRANE	Envelope	525	113	2.67E-46	1.72E-44
GO_NUCLEOPLASM_PART	Nucleus	708	130	4.86E-45	2.82E-43
GO_TRANSFERASE_COMPLEX		703	118	5.49E-37	2.89E-35
GO_RIBOSOME	Others	226	65	3.87E-35	1.87E-33
GO_CHROMOSOMAL_REGION	Chromosome	330	77	1.91E-34	8.54E-33
GO_MICROTUBULE_CYTOSKELETON	Cytoskeleton	1068	144	6.33E-34	2.62E-32
GO_CYTOSKELETON	Cytoskeleton	1967	207	1.21E-32	4.67E-31
GO_MITOCHONDRIAL_MATRIX	Mitochondrion	412	81	1.39E-30	5.06E-29
GO_CHROMOSOME_CENTROMERIC_REGION	Chromosome	174	51	2.66E-28	9.08E-27
GO_RIBOSOMAL_SUBUNIT	Others	163	49	8.31E-28	2.68E-26
GO_MICROTUBULE_ORGANIZING_CENTER	Cytoskeleton	623	96	2.50E-27	7.63E-26
GO_CYTOSKELETAL_PART	Cytoskeleton	1436	154	3.16E-25	9.18E-24

Immunohistochemistry cohort					
Gene Set Name	Cellular compartment	# Genes in Gene Set (K)	# Genes in Overlap (k)	p-value	FDR q-value
GO_CATALYTIC_COMPLEX		1038	116	2.04E-23	1.18E-20
GO_CYTOSKELETON	Cytoskeleton	1967	174	6.04E-23	1.75E-20
GO_MITOCHONDRION	Mitochondrion	1633	150	2.12E-21	4.09E-19
GO_TRANSFERASE_COMPLEX		703	83	1.58E-18	2.29E-16
GO_MICROTUBULE_CYTOSKELETON	Cytoskeleton	1068	107	3.58E-18	4.15E-16
GO_NUCLEOPLASM_PART	Nucleus	708	82	8.07E-18	7.80E-16
GO_RIBONUCLEOPROTEIN_COMPLEX		721	82	2.38E-17	1.97E-15
GO_CYTOSKELETAL_PART	Cytoskeleton	1436	127	5.81E-17	4.21E-15
GO_VACUOLE	Others	1180	110	2.09E-16	1.34E-14
GO_CHROMOSOME	Chromosome	880	88	4.06E-15	2.36E-13
GO_ENVELOPE	Envelope	1090	98	8.69E-14	4.58E-12
GO_NUCLEAR_BODY	Nucleus	349	48	9.83E-14	4.75E-12
GO_VACUOLAR_MEMBRANE	Others	587	65	1.69E-13	7.55E-12
GO_VACUOLAR_PART	Others	694	72	2.19E-13	9.06E-12
GO_NUCLEAR_SPECK	Nucleus	194	33	2.01E-12	7.76E-11
GO_MICROTUBULE_ORGANIZING_CENTER	Cytoskeleton	623	65	2.50E-12	9.05E-11
GO_CELL_PROJECTION	Cytoskeleton	1786	133	4.37E-12	1.49E-10
GO_GOLGI_APPARATUS	Others	1445	114	4.67E-12	1.50E-10
GO_INTRACELLULAR_VESICLE	Others	1259	101	3.13E-11	9.54E-10
GO_LYTIC_VACUOLE	Others	526	56	3.72E-11	1.08E-09

Supplementary Table S2B. Hallmarks enriched in the transcriptional program associated with CKS2 expression in patients

Top 20 hallmarks from GSEA analysis are listed.

Cohort 1				
Gene Set Name	# Genes in Gene Set (K)	# Genes in Overlap (k)	p-value	FDR q-value
HALLMARK_E2F_TARGETS	200	53	5.91E-27	2.96E-25
HALLMARK_G2M_CHECKPOINT	200	48	1.61E-22	2.68E-21
HALLMARK_MYC_TARGETS_V1	200	48	1.61E-22	2.68E-21
HALLMARK_OXIDATIVE_PHOSPHORYLATION	200	47	1.14E-21	1.43E-20
HALLMARK_DNA_REPAIR	150	35	2.09E-16	2.09E-15
HALLMARK_MITOTIC_SPINDLE	200	40	4.67E-16	3.89E-15
HALLMARK_MTORC1_SIGNALING	200	27	1.80E-07	1.28E-06
HALLMARK_P53_PATHWAY	200	26	6.32E-07	3.95E-06
HALLMARK_ADIPOGENESIS	200	25	2.13E-06	1.18E-05
HALLMARK_PROTEIN_SECRETION	96	16	3.58E-06	1.79E-05
HALLMARK_UNFOLDED_PROTEIN_RESPONSE	113	17	7.55E-06	3.43E-05
HALLMARK_FATTY_ACID_METABOLISM	158	20	1.78E-05	7.40E-05
HALLMARK_APOPTOSIS	161	20	2.34E-05	9.02E-05
HALLMARK_UV_RESPONSE_UP	158	19	5.82E-05	2.08E-04
HALLMARK_APICAL_JUNCTION	200	21	1.75E-04	5.23E-04
HALLMARK_GLYCOLYSIS	200	21	1.75E-04	5.23E-04
HALLMARK_PI3K_AKT_MTOR_SIGNALING	105	14	1.78E-04	5.23E-04
HALLMARK_HEME_METABOLISM	200	19	1.18E-03	3.28E-03
HALLMARK_PEROXISOME	104	11	5.45E-03	1.43E-02
HALLMARK_INTERFERON_GAMMA_RESPONSE	200	17	6.46E-03	1.54E-02

Cohort 2				
Gene Set Name	# Genes in Gene Set (K)	# Genes in Overlap (k)	p-value	FDR q-value
HALLMARK_E2F_TARGETS	200	73	1.97E-47	4.92E-46
HALLMARK_MYC_TARGETS_V1	200	73	1.97E-47	4.92E-46
HALLMARK_G2M_CHECKPOINT	200	55	7.51E-29	1.25E-27
HALLMARK_OXIDATIVE_PHOSPHORYLATION	200	50	2.68E-24	3.36E-23
HALLMARK_DNA_REPAIR	150	39	6.32E-20	6.32E-19
HALLMARK_MITOTIC_SPINDLE	200	44	3.21E-19	2.67E-18
HALLMARK_MTORC1_SIGNALING	200	34	8.53E-12	6.09E-11
HALLMARK_MYC_TARGETS_V2	58	14	1.28E-07	8.01E-07
HALLMARK_UNFOLDED_PROTEIN_RESPONSE	113	19	3.81E-07	2.12E-06
HALLMARK_HEME_METABOLISM	200	26	6.09E-07	3.05E-06
HALLMARK_PI3K_AKT_MTOR_SIGNALING	105	16	1.14E-05	5.20E-05
HALLMARK_PROTEIN_SECRETION	96	15	1.57E-05	6.53E-05
HALLMARK_ADIPOGENESIS	200	23	2.05E-05	7.90E-05
HALLMARK_UV_RESPONSE_UP	158	19	5.66E-05	2.02E-04
HALLMARK_INTERFERON_GAMMA_RESPONSE	200	22	6.05E-05	2.02E-04
HALLMARK_SPERMATOGENESIS	135	17	7.67E-05	2.40E-04
HALLMARK_GLYCOLYSIS	200	21	1.70E-04	5.00E-04
HALLMARK_FATTY_ACID_METABOLISM	158	16	1.41E-03	3.93E-03
HALLMARK_WNT_BETA_CATENIN_SIGNALING	42	7	1.99E-03	5.24E-03
HALLMARK_INTERFERON_ALPHA_RESPONSE	97	11	3.14E-03	7.86E-03

Immunohistochemistry cohort				
Gene Set Name	# Genes in Gene Set (K)	# Genes in Overlap (k)	p-value	FDR q-value
HALLMARK_MYC_TARGETS_V1	200	28	8.69E-09	4.34E-07
HALLMARK_E2F_TARGETS	200	26	1.33E-07	3.32E-06
HALLMARK_MTORC1_SIGNALING	200	21	5.60E-05	9.33E-04
HALLMARK_APOPTOSIS	161	18	8.27E-05	1.03E-03
HALLMARK_G2M_CHECKPOINT	200	20	1.62E-04	1.62E-03
HALLMARK_UV_RESPONSE_DN	144	16	2.16E-04	1.80E-03
HALLMARK_PI3K_AKT_MTOR_SIGNALING	105	13	2.85E-04	2.03E-03
HALLMARK_MITOTIC_SPINDLE	200	19	4.47E-04	2.79E-03
HALLMARK_UNFOLDED_PROTEIN_RESPONSE	113	13	5.84E-04	3.06E-03
HALLMARK_UV_RESPONSE_UP	158	16	6.12E-04	3.06E-03
HALLMARK_ESTROGEN_RESPONSE_EARLY	200	18	1.17E-03	4.49E-03
HALLMARK_HYPOXIA	200	18	1.17E-03	4.49E-03
HALLMARK_OXIDATIVE_PHOSPHORYLATION	200	18	1.17E-03	4.49E-03
HALLMARK_FATTY_ACID_METABOLISM	158	15	1.71E-03	6.12E-03
HALLMARK_DNA_REPAIR	150	14	2.81E-03	9.37E-03
HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY	49	7	3.14E-03	9.83E-03
HALLMARK_BILE_ACID_METABOLISM	112	11	5.21E-03	1.53E-02
HALLMARK_GLYCOLYSIS	200	16	6.70E-03	1.68E-02
HALLMARK_HEME_METABOLISM	200	16	6.70E-03	1.68E-02
HALLMARK_INFLAMMATORY_RESPONSE	200	16	6.70E-03	1.68E-02

Table S3. CKS2 correlating genes encoding mitochondrial proteins

Spearman's rank test (ρ , p -value) with Benjamini-Hochberg correction for multiple testing (FDR q -value) based on average expression value of two CKS2 probes on the arrays.

Cellular component ontology terms: Mitochondrion, Mitochondrion_part, Mitochondrion_envelope, Mitochondrial_matrix

PROBE_ID	Entrz ID	Gene Symbol	HALLMARK	Cohort 1			Cohort 2		
				ρ	p -value	FDR q -value	ρ	p -value	FDR q -value
ILMN_1676846	6059	ABCE1	MYC TARGETS V1	0.30	2.1E-04	4.5E-03	0.49	1.5E-09	1.6E-07
ILMN_1806408	37	ACADVL	OXPHOS; FATTY ACID METABOLISM	-0.43	4.3E-08	9.8E-06	-0.49	1.2E-09	1.3E-07
ILMN_2388507	207	AKT1		-0.34	2.4E-05	9.0E-04	-0.47	8.7E-09	6.7E-07
ILMN_1665331	275	AMT		-0.36	7.2E-06	3.8E-04	-0.43	2.3E-07	9.0E-06
ILMN_1677487	55139	ANKZF1		-0.44	1.4E-08	4.4E-06	-0.45	3.2E-08	1.9E-06
ILMN_2052598	83787	ARMC10		0.33	3.9E-05	1.3E-03	0.42	5.4E-07	1.8E-05
ILMN_1654497	84896	ATAD1		0.41	1.8E-07	2.7E-05	0.48	4.7E-09	4.1E-07
ILMN_1701269	509	ATP5C1	OXPHOS, Complex V	0.45	9.8E-09	3.5E-06	0.52	6.7E-11	1.3E-08
ILMN_1794912	10476	ATP5H	OXPHOS, Complex V	0.42	7.6E-08	1.4E-05	0.53	3.5E-11	8.0E-09
ILMN_1652806	522	ATP5J	OXPHOS, Complex V	0.28	4.5E-04	7.8E-03	0.37	8.0E-06	1.6E-04
ILMN_1791332	539	ATP5O	OXPHOS, Complex V	0.34	2.4E-05	9.0E-04	0.41	6.2E-07	2.0E-05
ILMN_1700625	27109	ATP5S		0.32	5.1E-05	1.6E-03	0.42	3.5E-07	1.3E-05
ILMN_1679782	282991	BLOC1S2		0.35	8.3E-06	4.2E-04	0.42	3.5E-07	1.3E-05
ILMN_1783333	56942	C16orf61		0.42	8.7E-08	1.6E-05	0.45	3.0E-08	1.8E-06
ILMN_1658110	125228	C18orf19		0.31	1.0E-04	2.6E-03	0.45	4.3E-08	2.4E-06
ILMN_2406892	8725	C19orf2		0.28	6.2E-04	9.9E-03	0.39	3.9E-06	8.8E-05
ILMN_2350607	79133	C20orf7		0.29	4.0E-04	7.2E-03	0.41	8.4E-07	2.5E-05
ILMN_1758806	755	C21orf2		-0.31	9.7E-05	2.5E-03	-0.38	5.1E-06	1.1E-04
ILMN_1671387	285343	C3orf23		0.30	1.6E-04	3.7E-03	0.41	6.6E-07	2.1E-05
ILMN_1728057	135154	C6orf57		0.38	1.2E-06	1.1E-04	0.42	5.0E-07	1.7E-05
ILMN_2081335	55744	C7orf44		0.37	4.4E-06	2.7E-04	0.43	2.6E-07	9.9E-06
ILMN_1727618	137682	C8orf38		0.30	1.7E-04	3.8E-03	0.48	4.9E-09	4.3E-07
ILMN_1709043	55848	C9orf46		0.32	7.7E-05	2.1E-03	0.54	1.3E-11	3.3E-09
ILMN_1659189	84270	C9orf89		0.40	4.3E-07	5.0E-05	0.49	2.0E-09	2.0E-07
ILMN_2410540	835	CASP2		-0.32	5.6E-05	1.7E-03	-0.43	1.8E-07	7.6E-06
ILMN_1716368	201973	CCDC111		0.32	5.0E-05	1.5E-03	0.43	2.7E-07	1.0E-05
ILMN_1703718	10574	CCT7	MYC TARGETS V1	0.29	3.3E-04	6.2E-03	0.44	7.7E-08	3.8E-06
ILMN_1747911	983	CDK1	E2F TARGETS; G2M CHECKPOINT; MITOTIC SPINDLE; GLYCOLYSIS	0.54	1.1E-12	3.5E-09	0.61	0.0E+00	0.0E+00
ILMN_1744295	1029	CDKN2A	E2F TARGETS	0.31	1.1E-04	2.8E-03	0.56	1.7E-12	6.0E-10
ILMN_1672149	118487	CHCHD1		0.45	7.2E-09	2.8E-06	0.51	1.8E-10	3.0E-08
ILMN_1673026	54927	CHCHD3		0.33	3.2E-05	1.1E-03	0.46	2.7E-08	1.6E-06
ILMN_1669281	1201	CLN3		-0.35	1.0E-05	5.0E-04	-0.43	2.5E-07	9.6E-06
ILMN_1756572	27235	COQ2		0.40	4.6E-07	5.2E-05	0.55	7.0E-12	2.1E-09
ILMN_1663512	1329	COX5B	OXPHOS, Complex IV	0.31	1.0E-04	2.6E-03	0.41	6.0E-07	2.0E-05
ILMN_1783636	1337	COX6A1	OXPHOS, Complex IV	0.35	9.5E-06	4.7E-04	0.52	8.1E-11	1.5E-08
ILMN_1701293	1347	COX7A2	OXPHOS, Complex IV	0.34	2.4E-05	9.1E-04	0.38	5.1E-06	1.1E-04
ILMN_2184049	1349	COX7B	OXPHOS, Complex IV	0.31	9.8E-05	2.5E-03	0.51	2.3E-10	3.6E-08
ILMN_2206272	728294	D2HGDH	FATTY ACID METABOLISM	-0.44	1.8E-08	5.3E-06	-0.39	2.4E-06	5.9E-05
ILMN_1735402	8816	DCAF5		-0.33	4.2E-05	1.4E-03	-0.40	2.1E-06	5.2E-05
ILMN_1747506	9704	DHX34		-0.34	2.3E-05	8.8E-04	-0.43	1.7E-07	7.3E-06
ILMN_1724826	10059	DNM1L	PROTEIN SECRETION	0.30	2.2E-04	4.5E-03	0.50	6.5E-10	8.4E-08
ILMN_1671568	55268	ECHDC2		-0.42	8.1E-08	1.5E-05	-0.52	9.6E-11	1.8E-08
ILMN_1722309	2021	ENDOG		0.37	2.3E-06	1.7E-04	0.61	0.0E+00	0.0E+00
ILMN_1701457	81889	FAHD1		0.30	2.1E-04	4.5E-03	0.42	4.0E-07	1.4E-05
ILMN_2378696	84340	GFM2		0.36	6.7E-06	3.6E-04	0.42	5.3E-07	1.8E-05
ILMN_1728467	27069	GHITM		0.37	3.1E-06	2.1E-04	0.44	6.7E-08	3.4E-06
ILMN_1708414	54552	GNL3L		-0.39	7.8E-07	7.7E-05	-0.40	1.8E-06	4.7E-05
ILMN_1723139	2820	GPD2	FATTY ACID METABOLISM	0.31	8.8E-05	2.3E-03	0.43	3.5E-07	1.3E-05
ILMN_1670817	80273	GRPEL1	OXPHOS	0.33	3.2E-05	1.1E-03	0.47	8.5E-09	6.5E-07
ILMN_2393243	29083	GTPBP8		0.30	1.7E-04	3.8E-03	0.38	5.2E-06	1.1E-04
ILMN_2398903	10456	HAX1	GLYCOLYSIS	0.38	1.7E-06	1.3E-04	0.39	2.9E-06	6.9E-05
ILMN_2057220	10247	HRSP12		0.28	6.6E-04	1.0E-02	0.41	9.5E-07	2.8E-05
ILMN_1803775	3336	HSPE1	MYC TARGETS V1; MYC TARGETS V2; MTORC	0.30	2.3E-04	4.7E-03	0.53	4.7E-11	1.0E-08
ILMN_2182198	3396	ICT1		0.33	4.8E-05	1.5E-03	0.50	4.4E-10	6.0E-08
ILMN_2239754	3437	IFIT3		0.28	6.0E-04	9.6E-03	0.41	1.2E-06	3.4E-05
ILMN_2219556	81689	ISCA1	OXPHOS; HEME METABOLISM	0.41	1.8E-07	2.7E-05	0.70	4.1E-21	5.3E-18
ILMN_1701512	9692	KIAA0391		0.35	1.2E-05	5.5E-04	0.44	7.3E-08	3.6E-06
ILMN_1765132	114294	LACTB		0.35	1.2E-05	5.4E-04	0.41	6.3E-07	2.0E-05
ILMN_2400297	5601	MAPK9		0.28	5.6E-04	9.0E-03	0.38	4.4E-06	9.8E-05
ILMN_2198499	92014	MCART1		0.33	3.5E-05	1.2E-03	0.44	1.3E-07	5.9E-06
ILMN_1656913	4190	MDH1	OXPHOS; FATTY ACID METABOLISM; GLYCOLYSIS	0.36	8.0E-06	4.1E-04	0.40	1.6E-06	4.3E-05
ILMN_2048636	4200	ME2	GLYCOLYSIS	0.30	1.8E-04	3.9E-03	0.48	4.9E-09	4.3E-07
ILMN_2090558	27249	MMADHC		0.35	9.6E-06	4.7E-04	0.48	4.1E-09	3.6E-07
ILMN_2076658	65008	MRPL1		0.36	8.3E-06	4.3E-04	0.51	3.3E-10	4.8E-08
ILMN_2316540	65003	MRPL11	OXPHOS	0.38	1.3E-06	1.1E-04	0.40	2.0E-06	5.2E-05
ILMN_1671158	28998	MRPL13		0.35	9.8E-06	4.7E-04	0.59	7.3E-14	4.2E-11
ILMN_2103720	29088	MRPL15	OXPHOS	0.32	5.9E-05	1.7E-03	0.43	2.5E-07	9.7E-06
ILMN_2230672	29074	MRPL18		0.32	5.7E-05	1.7E-03	0.53	2.9E-11	6.8E-09
ILMN_2189424	55052	MRPL20		0.31	1.0E-04	2.6E-03	0.38	4.5E-06	9.9E-05
ILMN_2348050	219927	MRPL21		0.41	1.8E-07	2.7E-05	0.51	1.8E-10	2.9E-08

ILMN_1663220	29093	MRPL22		0.35	1.3E-05	5.9E-04	0.43	2.1E-07	8.4E-06
ILMN_1766154	51263	MRPL30		0.50	5.9E-11	7.4E-08	0.56	0.0E+00	0.0E+00
ILMN_1749432	64983	MRPL32		0.39	8.0E-07	7.8E-05	0.49	1.5E-09	1.6E-07
ILMN_1800197	64979	MRPL36		0.28	6.5E-04	1.0E-02	0.39	2.4E-06	5.9E-05
ILMN_1726391	54148	MRPL39		0.39	1.1E-06	9.7E-05	0.50	5.4E-10	7.1E-08
ILMN_2356895	28977	MRPL42		0.42	6.1E-08	1.2E-05	0.50	7.5E-10	9.2E-08
ILMN_1808301	84311	MRPL45		0.35	1.0E-05	4.9E-04	0.45	4.8E-08	2.6E-06
ILMN_1722838	26589	MRPL46		0.32	6.9E-05	1.9E-03	0.42	5.4E-07	1.8E-05
ILMN_2391522	57129	MRPL47		0.42	1.0E-07	1.8E-05	0.56	1.9E-12	6.7E-10
ILMN_1664833	54534	MRPL50		0.58	1.3E-14	6.0E-11	0.72	3.6E-23	5.0E-20
ILMN_2097421	51258	MRPL51		0.29	3.4E-04	6.4E-03	0.47	6.6E-09	5.3E-07
ILMN_1658486	116541	MRPL54		0.28	4.8E-04	8.2E-03	0.48	5.0E-09	4.3E-07
ILMN_2405915	64963	MRPS11	OXPHOS	0.34	1.9E-05	7.7E-04	0.37	8.6E-06	1.7E-04
ILMN_1804851	51373	MRPS17		0.32	5.3E-05	1.6E-03	0.41	1.1E-06	3.2E-05
ILMN_1658416	51023	MRPS18C		0.55	4.6E-13	1.6E-09	0.58	0.0E+00	0.0E+00
ILMN_1655377	56945	MRPS22	OXPHOS	0.28	6.0E-04	9.6E-03	0.53	5.5E-11	1.2E-08
ILMN_1687359	51649	MRPS23		0.49	1.2E-10	1.4E-07	0.54	1.1E-11	2.9E-09
ILMN_1718424	28957	MRPS28		0.36	5.3E-06	3.2E-04	0.46	3.2E-08	1.9E-06
ILMN_1674706	10797	MTHFD2	E2F TARGETS; G2M CHECKPOINT; MITOTIC SPINDLE; MTORC; UPR	0.34	1.8E-05	7.3E-04	0.47	8.4E-09	6.5E-07
ILMN_1772302	10588	MTHFS		0.35	1.4E-05	6.2E-04	0.42	5.4E-07	1.8E-05
ILMN_1737738	55967	NDUFA12		0.38	1.4E-06	1.2E-04	0.51	3.3E-10	4.8E-08
ILMN_1751258	4697	NDUFA4	OXPHOS, Complex I	0.30	1.6E-04	3.6E-03	0.48	5.3E-09	4.5E-07
ILMN_1759729	4702	NDUFA8	OXPHOS, Complex I	0.29	2.9E-04	5.6E-03	0.52	1.0E-10	1.9E-08
ILMN_1682857	91942	NDUFAF2		0.35	1.1E-05	5.1E-04	0.54	1.6E-11	3.9E-09
ILMN_1770589	4710	NDUFB4	OXPHOS, Complex I	0.33	5.3E-05	1.6E-03	0.41	7.8E-07	2.4E-05
ILMN_2369924	4712	NDUFB6	OXPHOS, Complex I	0.42	1.2E-07	2.0E-05	0.63	2.8E-16	2.5E-13
ILMN_1733603	4717	NDUFC1	OXPHOS, Complex I	0.28	5.3E-04	8.7E-03	0.44	1.1E-07	5.2E-05
ILMN_1812312	4724	NDUFS4	OXPHOS, Complex I	0.36	5.5E-06	3.2E-04	0.45	4.9E-08	2.7E-06
ILMN_2406468	27247	NFU1		0.29	3.1E-04	5.9E-03	0.39	3.7E-06	8.5E-05
ILMN_2414399	4830	NME1	MYC TARGETS V1; DNA REPAIR; E2F TARGETS	0.30	1.6E-04	3.7E-03	0.52	1.7E-10	2.8E-08
ILMN_2389347	2908	NR3C1	HEME METABOLISM	0.28	5.3E-04	8.7E-03	0.45	4.0E-08	2.2E-06
ILMN_1703324	23590	PDSS1		0.33	3.1E-05	1.1E-03	0.54	9.0E-12	2.6E-09
ILMN_1689525	5366	PMAIP1		0.29	3.1E-04	6.0E-03	0.39	4.3E-06	9.5E-05
ILMN_1662587	375775	PNPLA7		-0.37	2.8E-06	1.9E-04	-0.39	2.9E-06	6.9E-05
ILMN_1687785	27068	PPA2		0.33	3.9E-05	1.3E-03	0.49	1.7E-09	1.8E-07
ILMN_1748831	23368	PPP1R13B		-0.40	2.9E-07	3.7E-05	-0.48	4.5E-09	4.0E-07
ILMN_1810467	5518	PPP2R1A		-0.42	9.2E-08	1.6E-05	-0.49	2.3E-09	2.2E-07
ILMN_2395969	10935	PRDX3	MYC TARGETS V1; OXPHOS; ADIPOGENESIS	0.31	1.2E-04	2.9E-03	0.38	7.2E-06	1.4E-04
ILMN_1717707	118672	PSTK		0.33	3.1E-05	1.1E-03	0.42	5.4E-07	1.8E-05
ILMN_2225709	26024	PTCD1		-0.29	2.6E-04	5.1E-03	-0.44	1.2E-07	5.5E-06
ILMN_2311548	51651	PTRH2		0.30	1.7E-04	3.8E-03	0.51	3.0E-10	4.5E-08
ILMN_1763080	5859	QARS		-0.31	1.1E-04	2.8E-03	-0.42	3.3E-07	1.2E-05
ILMN_1760635	5889	RAD51C	E2F TARGETS	0.45	9.6E-09	3.4E-06	0.56	1.9E-12	6.7E-10
ILMN_1739810	10743	RAI1		-0.45	1.2E-08	3.9E-06	-0.43	1.6E-07	6.8E-06
ILMN_1806266	5910	RAP1GDS1	FATTY ACID METABOLISM	0.33	3.9E-05	1.3E-03	0.52	6.8E-11	1.3E-08
ILMN_1660723	112724	RDH13		-0.30	1.8E-04	4.0E-03	-0.40	1.7E-06	4.4E-05
ILMN_1669310	89941	RHOT2	OXPHOS; MITOTIC SPINDLE	-0.34	2.5E-05	9.4E-04	-0.44	7.8E-08	3.8E-06
ILMN_2119535	8737	RIPK1		-0.29	3.7E-04	6.8E-03	-0.39	2.8E-06	6.8E-05
ILMN_1774823	6164	RPL34	MYC TARGETS V1	0.35	9.1E-06	4.5E-04	0.54	1.8E-11	4.4E-09
ILMN_1728975	6341	SCO1		0.39	7.5E-07	7.5E-05	0.37	1.0E-05	1.9E-04
ILMN_1701655	80024	SLC24A6		-0.30	1.6E-04	3.7E-03	-0.47	7.2E-09	5.8E-07
ILMN_1810727	283130	SLC25A45		-0.28	4.4E-04	7.7E-03	-0.39	3.6E-06	8.2E-05
ILMN_1720311	91137	SLC25A46		0.38	1.5E-06	1.2E-04	0.48	6.9E-09	5.6E-07
ILMN_1800425	6548	SLC9A1		-0.33	4.8E-05	1.5E-03	-0.40	2.0E-06	5.1E-05
ILMN_1661945	81892	SLRP		0.30	1.8E-04	4.1E-03	0.51	1.8E-10	2.9E-08
ILMN_1728168	51012	SLMO2		0.31	1.4E-04	3.4E-03	0.43	1.4E-07	6.3E-06
ILMN_1754529	6687	SPG7		-0.40	3.9E-07	4.6E-05	-0.53	4.1E-11	9.2E-09
ILMN_2192032	6728	SRP19		0.29	4.1E-04	7.2E-03	0.46	2.1E-08	1.3E-06
ILMN_1809478	6742	SSBP1	MYC TARGETS V1	0.37	2.4E-06	1.7E-04	0.48	3.9E-09	3.5E-07
ILMN_1660787	8803	SUCLA2	OXPHOS; FATTY ACID METABOLISM	0.43	4.0E-08	9.4E-06	0.45	3.4E-08	2.0E-06
ILMN_1711994	10312	TCIRG1	OXPHOS	-0.32	6.5E-05	1.9E-03	-0.41	8.5E-07	2.6E-05
ILMN_1722239	1678	TIMM8A		0.29	2.9E-04	5.6E-03	0.48	2.9E-09	2.7E-07
ILMN_1653709	26520	TIMM9	OXPHOS	0.33	2.9E-05	1.0E-03	0.49	1.6E-09	1.7E-07
ILMN_2175265	8834	TMEM11		0.28	4.1E-04	7.3E-03	0.54	1.4E-11	3.5E-09
ILMN_2217809	84233	TMEM126A		0.35	1.5E-05	6.4E-04	0.46	1.7E-08	1.1E-06
ILMN_1766851	55863	TMEM126B		0.41	2.2E-07	3.0E-05	0.45	5.4E-08	2.9E-06
ILMN_1808661	401505	TOMM5		0.50	5.0E-11	7.0E-08	0.66	1.7E-18	1.9E-15
ILMN_1706558	55006	TRMT61B		0.33	3.7E-05	1.3E-03	0.42	4.8E-07	1.7E-05
ILMN_1680314	7295	TXN	GLYCOLYSIS	0.44	1.6E-08	4.9E-06	0.59	4.3E-14	2.6E-11
ILMN_1737585	57176	VARS2		-0.32	8.5E-05	2.3E-03	-0.43	3.1E-07	1.2E-05
ILMN_1750088	7444	VRK2		0.40	4.4E-07	5.0E-05	0.47	1.8E-08	1.2E-06
ILMN_1734316	10730	YME1L1		0.33	3.7E-05	1.3E-03	0.45	5.3E-08	2.8E-06
ILMN_1789492	29801	ZDHHC8		-0.39	7.7E-07	7.7E-05	-0.40	1.4E-06	3.9E-05
ILMN_1760718	83637	ZMIZ2		-0.36	4.4E-06	2.8E-04	-0.49	1.7E-09	1.7E-07

Table S4A. Cellular compartments enriched in a list of genes downregulated by a factor of at least 1.5 under acute hypoxia in either HeLa or SiHa cells

Top 20 cellular components from GSEA analysis are listed.

Gene Set Name	# Genes in Gene Set (K)	# Genes in Overlap (k)	p-value	FDR q-value
GO_NUCLEOLUS	848	145	1.62E-78	9.38E-76
GO_MITOCHONDRION	1633	192	8.70E-76	2.52E-73
GO_RIBONUCLEOPROTEIN_COMPLEX	721	125	2.89E-68	5.59E-66
GO_CHROMOSOME	880	135	6.23E-67	9.03E-65
GO_ENVELOPE	1090	147	2.36E-65	2.74E-63
GO_MITOCHONDRIAL_PART	953	129	2.03E-57	1.96E-55
GO_MICROTUBULE_CYTOSKELETON	1068	128	6.60E-51	5.47E-49
GO_CHROMOSOMAL_REGION	330	74	8.65E-49	6.27E-47
GO_MITOCHONDRIAL_ENVELOPE	691	101	5.01E-48	3.23E-46
GO_CHROMOSOME_CENTROMERIC_REGION	174	54	4.74E-44	2.75E-42
GO_CYTOSKELETAL_PART	1436	133	2.61E-40	1.37E-38
GO_ORGANELLE_INNER_MEMBRANE	525	79	1.28E-38	6.17E-37
GO_CONDENSED_CHROMOSOME	195	51	1.58E-37	7.03E-36
GO_CENTROSOME	487	71	6.74E-34	2.79E-32
GO_CYTOSKELETON	1967	146	2.20E-33	8.49E-32
GO_MICROTUBULE_ORGANIZING_CENTER	623	78	1.75E-32	6.35E-31
GO_MITOCHONDRIAL_MATRIX	412	63	2.07E-31	7.08E-30
GO_SPINDLE	289	53	1.31E-30	4.23E-29
GO_KINETOCHORE	120	37	1.81E-30	5.52E-29
GO_CONDENSED_CHROMOSOME_CENTROMERIC	102	34	2.09E-29	6.06E-28

Table S4B. Hallmarks enriched in a list of genes downregulated by a factor of at least 1.5 under acute hypoxia in either HeLa or SiHa cells

Top 20 hallmarks from GSEA analysis are listed.

Gene Set Name	# Genes in Gene Set (K)	# Genes in Overlap (k)	p-value	FDR q-value
HALLMARK_E2F_TARGETS	200	81	1.48E-76	7.41E-75
HALLMARK_G2M_CHECKPOINT	200	71	2.45E-62	6.13E-61
HALLMARK_MYC_TARGETS_V1	200	58	2.45E-45	4.09E-44
HALLMARK_MYC_TARGETS_V2	58	32	1.68E-36	2.09E-35
HALLMARK_MTORC1_SIGNALING	200	46	2.81E-31	2.81E-30
HALLMARK_UNFOLDED_PROTEIN_RESPONSE	113	21	4.35E-13	3.63E-12
HALLMARK_CHOLESTEROL_HOMEOSTASIS	74	17	1.97E-12	1.41E-11
HALLMARK_ESTROGEN_RESPONSE_LATE	200	24	1.54E-10	8.57E-10
HALLMARK_OXIDATIVE_PHOSPHORYLATION	200	24	1.54E-10	8.57E-10
HALLMARK_MITOTIC_SPINDLE	200	22	4.60E-09	2.27E-08
HALLMARK_DNA_REPAIR	150	19	4.99E-09	2.27E-08
HALLMARK_UV_RESPONSE_UP	158	19	1.19E-08	4.95E-08
HALLMARK_FATTY_ACID_METABOLISM	158	18	6.64E-08	2.55E-07
HALLMARK_ADIPOGENESIS	200	18	2.22E-06	7.92E-06
HALLMARK_GLYCOLYSIS	200	17	9.02E-06	3.01E-05
HALLMARK_APOPTOSIS	161	15	1.00E-05	3.13E-05
HALLMARK_ESTROGEN_RESPONSE_EARLY	200	16	3.46E-05	9.93E-05
HALLMARK_ANDROGEN_RESPONSE	101	11	3.58E-05	9.93E-05
HALLMARK_PI3K_AKT_MTOR_SIGNALING	105	11	5.13E-05	1.35E-04
HALLMARK_SPERMATOGENESIS	135	12	1.19E-04	2.97E-04

Table S4C. Genes encoding mitochondria proteins* downregulated by a factor of at least 1.5 under acute hypoxia in either HeLa or SiHa cells

* Cellular component ontology terms: Mitochondrion, Mitochondrion_part, Mitochondrion_envelope, Mitochondrial_matrix

PROBE_ID	Entrez ID	Gene Symbol	Hallmark
ILMN_1676846	6059	ABCE1	MYC TARGETS V1
ILMN_2284941	10061	ABCF2	
ILMN_2338268	83451	ABHD11	
ILMN_1667641	31	ACACA	
ILMN_2098743	55856	ACOT13	
ILMN_2252621	11332	ACOT7	
ILMN_2066124	10939	AFG3L2	OXPHOS
ILMN_1707169	79814	AGMAT	
ILMN_1757807	64850	AGXT2L1	
ILMN_1667183	9131	AIFM1	OXPHOS
ILMN_1794825	224	ALDH3A2	
ILMN_1652505	27301	APEX2	
ILMN_1721623	79135	APOO	
ILMN_1662895	84334	APOPT1	
ILMN_1738530	55210	ATAD3A	
ILMN_2131936	83858	ATAD3B	
ILMN_1673991	471	ATIC	
ILMN_2341363	498	ATP5A1	OXPHOS
ILMN_1721989	515	ATP5F1	OXPHOS
ILMN_1712430	516	ATP5G1	OXPHOS
ILMN_1809027	55101	ATP5SL	
ILMN_1768396	54998	AURKAIP1	
ILMN_1738529	617	BCS1L	
ILMN_2311089	672	BRCA1	
ILMN_1693410	140707	BRI3BP	
ILMN_1666967	51660	BRP44L	OXPHOS
ILMN_1783333	56942	C16orf61	
ILMN_1798728	8725	C19orf2	
ILMN_1668996	708	C1QBP	MYC TARGETS V1
ILMN_2262543	79133	C20orf7	
ILMN_2394132	55471	C2orf56	
ILMN_1813236	221545	C6orf136	
ILMN_1793012	55744	C7orf44	
ILMN_1779751	154791	C7orf55	
ILMN_1709043	55848	C9orf46	
ILMN_1736568	835	CASP2	
ILMN_1786046	842	CASP9	
ILMN_1775919	63933	CCDC90A	
ILMN_1747911	983	CDK1	
ILMN_1679971	84902	CEP89	
ILMN_1740170	400916	CHCHD10	
ILMN_1813938	131474	CHCHD4	
ILMN_2352326	80347	COASY	

ILMN_1801378	51805	COQ3	
ILMN_2382758	1385	CREB1	
ILMN_1709775	1431	CS	OXPHOS
ILMN_1685796	7812	CSDE1	
ILMN_2382488	348180	CTU2	
ILMN_1684321	80777	CY5B	
ILMN_1815115	1537	CYC1	MYC TARGETS V1
ILMN_1676191	55157	DARS2	
ILMN_2090123	54505	DHX29	
ILMN_2403555	22907	DHX30	
ILMN_2310589	56616	DIABLO	
ILMN_1803312	27292	DIMT1	
ILMN_1664682	1763	DNA2	
ILMN_1672496	3301	DNAJA1	
ILMN_1662334	9093	DNAJA3	
ILMN_2112049	728489	DNLZ	
ILMN_2152768	1841	DTYMK	
ILMN_1718044	60528	ELAC2	
ILMN_2139827	113115	FAM54A	
ILMN_1758728	2189	FANCG	
ILMN_1784871	2194	FASN	
ILMN_2129859	79072	FASTKD3	
ILMN_1656189	112812	FDX1L	
ILMN_2160929	2237	FEN1	
ILMN_1719392	2271	FH	OXPHOS, OXPHOS
ILMN_1730325	80308	FLAD1	
ILMN_1661596	28982	FLVCR1	
ILMN_1762312	55572	FOXRED1	
ILMN_1725471	2710	GK	
ILMN_1737912	51022	GLRX2	
ILMN_3251251	54552	GNL3L	
ILMN_1656145	2805	GOT1	
ILMN_1686587	84705	GTPBP3	
ILMN_1719906	3033	HADH	
ILMN_1787762	55127	HEATR1	
ILMN_1656977	26275	HIBCH	
ILMN_1673711	3326	HSP90AB1	MYC TARGETS V1
ILMN_1774410	3329	HSPD1	MYC TARGETS V1, V2
ILMN_1803775	3336	HSPE1	MYC TARGETS V1, V2
ILMN_1769883	3416	IDE	
ILMN_2091347	3417	IDH1	OXPHOS
ILMN_1789018	3609	ILF3	
ILMN_1735432	23479	ISCU	OXPHOS
ILMN_1723211	79944	L2HGDH	
ILMN_1710668	3954	LETM1	
ILMN_2136423	92935	MARS2	
ILMN_1811367	27430	MAT2B	
ILMN_1767679	27349	MCAT	
ILMN_1803988	4170	MCL1	
ILMN_2048636	4200	ME2	

ILMN_1803005	25974	MMACHC	
ILMN_1799106	64757	MOSC1	
ILMN_1757134	84769	MPV17L2	
ILMN_1690371	65003	MRPL11	OXPHOS
ILMN_1699603	6182	MRPL12	
ILMN_2103720	29088	MRPL15	OXPHOS
ILMN_2230672	29074	MRPL18	
ILMN_1693352	55052	MRPL20	
ILMN_1654250	219927	MRPL21	
ILMN_1663220	29093	MRPL22	
ILMN_2398995	79590	MRPL24	
ILMN_2230592	11222	MRPL3	
ILMN_1749432	64983	MRPL32	
ILMN_1783681	64981	MRPL34	OXPHOS
ILMN_1753016	51318	MRPL35	OXPHOS
ILMN_2041327	51253	MRPL37	
ILMN_1719656	64978	MRPL38	
ILMN_1681230	51073	MRPL4	
ILMN_2356895	28977	MRPL42	
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