

**Supplementary Table S1, Gene sets that are enriched in Hmga2/GFP-positive and -negative PDAC cells.** This analysis used genes rank ordered according to their log2 fold change (paired comparison) between sorted Hmga2/GFP-positive and Hmga2/GFP-negative cancer cells from primary PDAC of KPC-colors mice. Only top 25 or less gene sets significantly enriched (FDR q-val<0.05) in the GFP-positive and GFP-negative PDAC cancer cells are shown. 3 classes (Hallmark, Curated, and Motif) of annotated genesets from the Molecular Signatures Database (MSigDB) were used, detailed description of the GSEA algorithm is given in Subramanian et al., 2005. Gene sets that are related to the general hypoxic response and cell cycle are highlighted in bold. Size is the number of genes in the indicated geneset. ES = enrichment score. NES = normalized enrichment score. FDR = false discovery rate. FWER = family-wise error rate. NOM p-val = nominal p value. q-val = FDR (0.1)-corrected p value.

NAME	SIZE	ES	NES	NOM p-val	FDR q-val	FWER p-val	RANK AT MAX
<b>Hallmark - GFP-positive</b>							
HALLMARK_HYPOXIA	197	0.6013626	2.7654405	0	0	0	727
HALLMARK_GLYCOLYSIS	198	0.41219902	1.9057528	0	0.00165264	0.001	778
HALLMARK_TGF_BETA_SIGNALING	54	0.4557429	1.8313664	0	0.00477431	0.003	1776
HALLMARK_HEME_METABOLISM	184	0.35285008	1.7988367	0	0.00358073	0.003	1025
HALLMARK_TNFA_SIGNALING_VIA_NFKB	197	0.36692253	1.765372	0	0.00286458	0.003	1178
HALLMARK_MTORC1_SIGNALING	200	0.37022242	1.7238759	0	0.00385617	0.005	699
HALLMARK_P53_PATHWAY	193	0.3238895	1.481823	0	0.0227278	0.023	1187
HALLMARK_PROTEIN_SECRETION	92	0.3447861	1.469612	0	0.02029998	0.024	4515
<b>Curated - GFP-positive</b>							
Q1_HYPOXIA	133	0.7555269	3.3418226	0	0	0	802
GROSS_HYPOXIA_VIA_ELK3_AND_HIF1A_UP	137	0.699667	3.2316911	0	0	0	1439
LEONARD_HYPOXIA	47	0.77416164	3.0425339	0	0	0	697
FARDIN_HYPOXIA_11	32	0.87320334	3.0173016	0	0	0	500
GROSS_HYPOXIA_VIA_HIF1A_DN	104	0.6590951	3.0061028	0	0	0	2137
ELVIDGE_HYPOXIA_UP	163	0.59483755	3.0040722	0	0	0	927
ELVIDGE_HIF1A_AND_HIF2A_TARGETS_DN	100	0.6475315	2.9819386	0	0	0	647
MENSE_HYPOXIA_UP	92	0.69120663	2.9613342	0	0	0	900
PID_HIF1_TFPATHWAY	63	0.7073268	2.839461	0	0	0	551
ELVIDGE_HIF1A_TARGETS_DN	88	0.65053856	2.8192132	0	0	0	647
WINTER_HYPOXIA_UP	85	0.65413207	2.7875495	0	0	0	471
ELVIDGE_HYPOXIA_BY_DMOG_UP	125	0.6231309	2.7474685	0	0	0	688
SEMENZA_HIF1_TARGETS	35	0.78812015	2.7401204	0	0	0	496
GROSS_HIF1A_TARGETS_DN	24	0.823695	2.7126424	0	0	0	800
NAGASHIMA_EGF_SIGNALING_UP	56	0.6661953	2.6607797	0	0	0	1243
KIM_HYPOXIA	25	0.78179026	2.5519912	0	1.12E-04	0.001	697
REACTOME_GLYCOLYSIS	26	0.7821146	2.4842176	0	1.06E-04	0.001	496
WANG_ADIPOGENIC_GENES_REPRESSED_BY_SIRT1	26	0.7484503	2.476059	0	9.99E-05	0.001	496
PEDERSEN_METASTASIS_BY_ERBB2_ISOFORM_1	46	0.6513853	2.47216	0	9.47E-05	0.001	1879
NAGASHIMA_NRG1_SIGNALING_UP	164	0.5298387	2.468677	0	8.99E-05	0.001	1411
HARRIS_HYPOXIA	77	0.5799099	2.4614153	0	8.57E-05	0.001	551
PRAMOONJAGO_SOX4_TARGETS_UP	51	0.6568234	2.4390717	0	8.18E-05	0.001	530
REACTOME_GLYCOSE_METABOLISM	58	0.59936976	2.4262369	0	7.82E-05	0.001	1038
AMIT_DELAYED_EARLY_GENES	18	0.80801666	2.3946455	0	7.50E-05	0.001	2734
PID_HIF2PATHWAY	34	0.66005015	2.3848462	0	7.20E-05	0.001	206
<b>Motif - GFP-positive</b>							
V\$HIF1_Q5	231	0.39235276	2.0176015	0	0.0084398	0.002	1613
<b>Hallmark - GFP-negative</b>							
HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION	189	-0.7360357	-2.1867032	0	0	0	1390
HALLMARK_E2F_TARGETS	195	-0.5808843	-1.7286623	0	0.00238013	0.006	3540
HALLMARK_COAGULATION	131	-0.5922391	-1.7270943	0	0.00158675	0.006	2282
HALLMARK_ANGIOGENESIS	35	-0.6632232	-1.7166897	0	0.00158404	0.008	1127
HALLMARK_MYOGENESIS	190	-0.5460951	-1.629204	0	0.00563015	0.035	2318
HALLMARK_G2M_CHECKPOINT	193	-0.5417711	-1.6161727	0	0.00563176	0.041	2549
HALLMARK_APICAL_JUNCTION	195	-0.5382791	-1.5981194	0	0.00654015	0.056	2111
HALLMARK_INTERFERON_GAMMA_RESPONSE	187	-0.5247333	-1.551441	0	0.01208107	0.114	2621
HALLMARK_INTERFERON_ALPHA_RESPONSE	89	-0.5359042	-1.5451324	0.00209424	0.01180763	0.125	2485
HALLMARK_APICAL_SURFACE	44	-0.5746088	-1.5121665	0.02455357	0.01666682	0.185	2339
<b>Curated - GFP-negative</b>							
ANASTASSIOU_CANCER_MESENCHYMAL_TRANSITION_SIGNATURE	63	-0.8568471	-2.3630607	0	0	0	1158
BOQUEST_STEM_CELL_UP	246	-0.7733492	-2.3204596	0	0	0	1475
TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR_NORMAL_DN	66	-0.8289813	-2.290811	0	0	0	1187
TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_NORMAL_UP	63	-0.8185398	-2.2722008	0	0	0	1070
SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP	318	-0.7487881	-2.2693477	0	0	0	2188
NABA_CORE_MATRISOME	251	-0.7488236	-2.2507753	0	0	0	2199
PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP	192	-0.7468457	-2.22359	0	0	0	2027
NABA_ECM_GLYCOPROTEINS	177	-0.7448465	-2.2097406	0	0	0	2177
KIM_GLI2_TARGETS_UP	80	-0.7759727	-2.1768982	0	0	0	2252
VECCHI_GASTRIC_CANCER_ADVANCED_VS_EARLY_UP	162	-0.7353241	-2.171968	0	0	0	1224
<b>Motif - GFP-negative</b>							
V\$GATA_C	242	-0.5707218	-1.7075081	0	0.01995597	0.086	2361
V\$POU6F1_01	220	-0.5520641	-1.6704702	0	0.03299948	0.167	1767

**Supplementary Table S2, A stringent list of *Blimp1*-dependent genes that are either induced or repressed under hypoxia.** To derive this gene list, the following criteria were used: genes that are hypoxia-induced (red font) or repressed (blue font) as defined by a log2 fold change > 1 or < -0.7; fold change induced by hypoxia was impacted by *Blimp1* knockdown more than 2-fold (hypoxia-sh*Blimp1*/normoxia-sh*Blimp1* fold change over hypoxia-shControl/normoxia-shControl fold change > 1 or < -1 by log2 value); log2 fold change of sh*Blimp1*/shControl > 0.6 or < -0.6. Column 3-10 show TPM of indicated sample; column 11 shows log2 fold change of hypoxia-shControl/normoxia-shControl by DESeq2; column 12 shows log2 fold change of hypoxia-sh*Blimp1*/hypoxia-shControl by DESeq2.

Gene_id (mouse)	Gene_id (human)	shGFP_nor_1	shGFP_nor_2	shGFP_hyp_1	shGFP_hyp_2	shBlimp1_nor_1	shBlimp1_nor_2	shBlimp1_hyp_1	shBlimp1_hyp_2	hypoxia- induced log2 fold change (DESeq2)	Blimp1KD- induced log2 fold change under hypoxia
Adm	ADM	0.50	0.99	77.22	74.40	0.14	0.28	18.92	17.32	5.83	-2.09
Pgf	PGF	4.59	4.08	210.67	211.02	5.76	5.96	44.56	42.71	5.30	-2.35
Ndrgr1	NDRG1	23.57	21.70	799.46	793.79	21.10	19.10	382.26	383.18	4.96	-1.16
Ddit3	DDIT3	15.75	14.45	509.79	539.43	20.74	19.72	336.18	344.42	4.88	-0.73
Cdkn1a	CDKN1A	11.92	10.95	334.52	344.47	20.54	21.53	176.32	176.59	4.69	-1.05
Dusp1	DUSP1	12.89	13.79	365.56	361.60	23.93	19.65	203.74	200.55	4.58	-0.95
Trim15	TRIM15	0.28	0.25	12.77	15.06	0.81	0.92	6.56	6.85	4.44	-1.05
Serpine1	SERPINE1	115.68	114.42	2796.51	2794.48	201.47	192.61	767.86	735.82	4.43	-2.00
Prdm1	PRDM1	0.00	0.00	2.78	2.23	0.14	0.07	1.30	1.86	4.40	-0.63
Mgarpl	MGARP	0.48	0.16	19.32	16.10	0.26	0.67	4.94	7.21	4.40	-1.43
Hmox1	HMOX1	33.41	33.54	705.55	718.51	56.10	58.49	293.18	295.53	4.23	-1.38
Vwa1	VWA1	0.22	0.36	8.72	8.33	0.18	0.43	1.42	2.36	4.04	-1.95
Fos	FOS	3.28	3.50	62.31	62.57	3.23	3.37	17.09	16.74	3.93	-1.94
Kctd11	KCTD11	12.98	14.80	235.85	241.20	10.51	10.24	74.80	72.03	3.93	-1.80
Nos2	NOS2	0.04	0.00	2.54	2.82	2.92	2.44	10.97	10.59	3.89	1.74
Vldlr	VLDLR	2.31	2.26	37.97	36.24	2.58	2.73	20.31	19.36	3.81	-1.00
Ero1l	ERO1A	31.40	30.25	486.12	481.81	30.15	28.64	163.40	163.01	3.80	-1.67
Pmaip1	PMAIP1	12.15	14.05	185.79	181.20	16.80	16.54	100.40	96.87	3.63	-1.00
Fgf18	FGF18	1.58	1.05	26.09	25.09	2.60	2.46	13.88	13.11	3.62	-0.94
Efr3b	EFR3B	0.03	0.00	1.23	1.42	0.06	0.03	12.62	12.72	3.62	2.94
Vegfa	VEGFA	25.59	24.62	328.87	320.89	23.25	22.54	140.40	136.90	3.52	-1.33
P2rx7	P2RX7	0.19	0.21	4.02	3.06	0.35	0.25	17.11	16.32	3.38	2.04
S1pr1	S1PR1	0.40	0.30	5.45	6.26	0.25	0.50	0.70	0.95	3.30	-2.29
Efn3	EFNA3	0.70	0.75	11.56	12.33	1.38	0.93	5.19	6.40	3.21	-0.96
Ypel3	YPEL3	8.47	9.34	101.50	93.24	11.26	14.32	34.87	29.57	3.21	-1.65
Adssl1	ADSSL1	4.06	2.71	35.77	38.72	3.24	2.46	13.54	14.52	3.15	-1.45
Grin1	GRIN1	0.06	0.00	0.90	0.83	0.00	0.00	0.05	0.05	3.12	-2.27
Hyal1	HYAL1	0.92	0.92	9.96	9.86	0.70	0.51	3.52	3.47	3.06	-1.48
Rhob	RHOB	61.84	57.34	562.55	555.40	75.78	71.90	266.66	262.28	3.05	-1.18
Cox7a1	COX7A1	3.28	3.13	43.19	38.39	7.71	9.91	16.72	29.86	2.97	-0.75
Trim40	TRIM40	0.39	0.73	6.77	6.88	0.60	0.69	3.54	3.47	2.97	-0.90
Dhrs9	DHRS9	4.81	4.55	41.54	41.84	3.41	4.67	17.21	17.13	2.93	-1.35
Cidea	CIDEA	0.00	0.00	3.45	3.92	0.00	0.00	2.63	1.06	2.91	-0.66
Nudt18	NUDT18	4.85	4.62	38.03	41.31	5.21	4.11	20.46	19.81	2.86	-1.07
Rnf208	RNF208	1.41	0.86	12.03	13.17	0.85	1.29	4.23	1.70	2.86	-1.75
Car9	CA9	0.44	0.35	4.94	5.38	0.48	0.58	0.36	0.74	2.81	-2.16
Selenbp1	SELENBP1	5.29	5.16	41.03	45.45	2.57	3.28	12.57	10.89	2.80	-1.89
Col11a1	COL11A1	0.23	0.12	2.29	1.68	0.08	0.13	0.41	0.31	2.79	-1.97
Hif3a	HIF3A	0.00	0.00	0.37	0.74	0.03	0.00	0.00	0.00	2.77	-1.76
Mfsd9	MFSD9	1.41	2.23	13.51	16.00	2.06	2.62	6.38	6.16	2.76	-1.26
Kif26b	KIF26B	0.06	0.06	0.89	0.91	0.02	0.22	0.56	0.44	2.69	-0.69
Tsc22d3	TSC22D3	6.82	6.67	47.12	49.69	6.22	5.93	22.22	20.50	2.65	-1.27
Slc2a1	SLC2A1	163.16	168.34	1135.26	1145.50	119.37	129.40	469.11	468.07	2.62	-1.39
Ovol1	OVOL1	0.18	0.24	2.36	2.48	0.06	0.33	1.38	1.14	2.53	-0.76
Lif	LIF	20.76	21.35	132.10	138.73	21.00	22.06	19.63	20.11	2.51	-2.85
L1cam	L1CAM	0.15	0.04	1.44	0.95	0.13	0.23	0.66	0.61	2.48	-0.71
Hilpda	HILPDA	83.58	83.38	525.19	512.16	96.28	103.19	198.35	205.99	2.46	-1.46
Ier3	IER3	302.39	292.24	1756.94	1790.91	317.06	337.39	497.53	519.42	2.41	-1.90
Tnc	TNC	0.80	0.98	5.69	5.22	1.71	1.78	1.35	1.21	2.36	-2.00
Ptges	PTGES	0.33	0.25	2.78	2.17	0.10	0.16	0.26	0.11	2.36	-2.26
Rusc2	RUSC2	17.19	18.10	103.77	98.80	20.44	20.18	45.22	44.54	2.35	-1.27
Csn3	CSN3	0.00	0.10	1.09	1.77	0.00	0.00	0.20	0.09	2.35	-1.33
231007B0C2orf54		7.04	7.36	42.25	42.16	9.00	9.70	26.21	24.88	2.35	-0.81
Hoga1	HOGA1	1.68	1.96	12.27	11.60	2.07	1.52	4.89	6.31	2.34	-1.03
Tmem95	TMEM95	0.32	1.72	11.55	8.93	1.06	0.36	3.55	3.49	2.27	-1.02
Kcnc3	KCNC3	0.03	0.09	0.89	0.73	0.00	0.00	0.14	0.16	2.21	-1.24
Rab11fip5	RAB11FIP5	11.09	10.35	54.63	55.87	8.85	8.01	21.41	19.96	2.19	-1.51
Ctgf	CTGF	316.07	315.25	1608.21	1583.71	132.44	132.05	237.53	231.93	2.17	-2.87
31100430C9orf72		19.50	19.04	99.04	97.36	19.89	20.12	38.84	36.43	2.17	-1.48
Lhfp12	LHFP12	2.43	2.46	12.98	12.39	3.61	3.70	7.04	7.58	2.15	-0.86
Olfml3	OLFML3	0.00	0.00	0.71	1.29	0.08	0.16	0.10	0.44	2.10	-0.74
Hspb8	HSPB8	0.19	0.00	2.08	1.45	0.31	0.00	0.00	0.46	2.08	-1.15
Clmn	CLMN	0.18	0.15	1.05	0.90	0.14	0.05	0.14	0.19	2.06	-1.94
Rsb1	RSBN1	14.23	13.61	62.96	62.38	11.97	10.41	24.53	24.92	2.00	-1.44
Mxi1	MXI1	17.67	18.60	77.33	79.31	25.79	25.33	51.18	49.58	1.94	-0.74
Eda2r	EDA2R	0.03	0.00	0.64	0.21	0.03	0.03	0.04	0.17	1.90	-0.76
Adamts4	ADAMTS4	0.25	0.17	1.38	1.29	0.46	0.70	0.52	0.55	1.87	-0.91
Cybrd1	CYBRD1	1.84	1.98	7.61	7.82	2.78	2.75	26.89	25.53	1.79	1.61
Dkk2	DKK2	0.32	0.68	2.42	2.23	0.41	0.57	0.89	1.50	1.77	-0.79
App12	APPL2	19.97	18.65	78.83	70.20	21.66	21.19	30.93	26.81	1.76	-1.45
Cttnbp2nl	CTTNBP2NL	31.32	30.49	114.99	119.24	22.80	21.72	43.36	42.47	1.75	-1.55
4930452B0C3orf67		4.15	4.74	16.39	17.54	7.54	6.40	10.90	10.97	1.73	-0.71

Abcb1a	ABCB1	18.82	21.47	74.87	72.32	14.03	13.19	25.23	26.39	1.71	-1.60
Pim1	PIM1	29.48	30.03	108.57	109.86	32.75	32.91	51.19	50.72	1.70	-1.19
Arrb1	ARRB1	11.84	11.26	43.39	41.44	10.79	11.03	17.74	16.99	1.70	-1.38
Ltbp2	LTBP2	0.57	0.56	2.29	2.14	3.37	3.35	5.00	4.89	1.67	0.98
Pkp1	PKP1	3.52	3.62	14.46	11.82	3.86	3.70	4.51	4.60	1.67	-1.54
Pdgfa	PDGFA	21.46	17.68	74.23	69.32	31.50	27.56	40.71	41.92	1.67	-0.87
Col6a5	COL6A5	0.00	0.00	0.10	0.25	0.00	0.02	1.27	0.93	1.64	1.70
Pitpnm3	PITPNM3	0.07	0.19	0.57	0.63	0.08	0.04	0.02	0.13	1.63	-1.60
Nipal1	NIPAL1	4.73	5.14	17.99	16.44	5.49	5.75	9.33	10.75	1.61	-0.85
Fam71f2	FAM71F2	0.58	1.17	4.81	3.58	1.60	2.11	2.60	1.75	1.61	-0.67
Tnfrsf19	TNFRSF19	0.00	0.00	0.28	0.28	0.00	0.04	1.39	1.67	1.51	1.51
Unc5c	UNC5C	0.24	0.19	0.81	0.81	0.14	0.05	0.26	0.16	1.50	-1.50
Arhgap31	ARHGAP31	0.06	0.08	0.45	0.31	1.06	0.80	0.82	1.16	1.48	0.91
Atp6v0a4	ATP6V0A4	0.19	0.45	1.39	1.28	0.32	0.05	3.70	2.89	1.48	0.94
Dusp5	DUSP5	79.88	89.16	258.61	244.99	97.89	92.86	142.04	132.28	1.41	-0.97
Procr	PROCR	226.23	235.40	678.19	685.86	201.28	193.25	221.35	213.62	1.40	-1.75
Hbegf	HBEGF	85.29	89.13	253.75	249.96	135.08	133.96	125.38	126.80	1.37	-1.10
Smtnl2	SMTNL2	12.74	11.77	34.26	37.22	1.36	2.04	13.55	14.61	1.36	-1.40
Slc4a11	SLC4A11	9.86	9.44	28.97	26.89	2.00	1.79	15.22	14.11	1.34	-1.00
Cry2	CRY2	4.18	4.90	13.39	12.70	5.85	5.56	8.20	8.40	1.34	-0.73
Rassf2	RASSF2	0.06	0.11	0.38	0.37	0.14	0.14	0.17	0.15	1.30	-0.66
Itpk1	ITPK1	47.92	49.04	135.23	131.06	48.15	43.50	48.79	47.21	1.29	-1.56
Cd59a	CD59	0.47	0.89	2.87	1.94	1.56	1.06	1.56	0.91	1.27	-0.64
Fgfr3	FGFR3	0.16	0.47	1.07	1.00	1.15	0.95	7.92	8.39	1.24	2.51
Cth	CTH	31.61	28.59	75.19	83.58	23.40	24.37	18.95	17.74	1.22	-2.16
Cyp26b1	CYP26B1	0.75	0.82	2.09	2.32	5.65	4.61	7.43	6.97	1.22	1.46
Chst4	CHST4	0.00	0.00	0.35	0.70	0.09	0.10	3.30	2.37	1.19	1.28
Emp2	EMP2	34.10	33.79	87.51	85.98	25.54	23.47	24.02	24.81	1.18	-1.91
Bmp2	BMP2	7.91	6.64	16.89	20.81	9.43	7.89	12.07	11.97	1.17	-0.72
Srgap3	SRGAP3	1.12	1.12	3.33	2.55	1.04	0.87	0.77	1.12	1.17	-1.52
Slc36a1	SLC36A1	7.51	7.95	20.37	18.93	7.69	7.55	51.78	49.36	1.17	1.24
Ereg	EREG	41.71	44.43	107.58	106.34	43.58	43.83	47.97	45.11	1.15	-1.30
Klhdc1	KLHDC1	2.64	3.29	7.38	7.21	2.61	2.94	2.42	2.96	1.06	-1.26
Abca6	ABCA6	0.06	0.04	0.33	0.21	0.10	0.07	2.14	2.05	1.06	2.01
Comp	COMP	0.00	0.09	0.39	0.51	0.00	0.00	1.16	2.04	1.01	0.88
Lpcat4	LPCAT4	157.70	147.49	105.78	103.18	129.65	126.57	198.73	188.74	-0.71	0.78
Fah	FAH	41.33	43.89	31.26	26.48	40.71	40.94	13.66	15.22	-0.72	-1.03
Itga6	ITGA6	125.16	126.03	79.29	76.63	108.37	96.16	28.04	27.87	-0.85	-1.57
Kif4	KIF4A	20.25	21.39	12.14	13.00	25.62	23.31	34.11	31.85	-0.88	1.27
Prr11	PRR11	64.08	66.25	38.04	38.28	67.64	63.78	87.21	83.02	-0.93	1.04
Aldh3a1	ALDH3A1	10.72	12.46	6.15	6.61	36.28	34.15	50.56	47.16	-0.97	2.66
Mki67	MKI67	97.50	105.10	58.64	56.83	118.44	101.95	157.74	153.75	-0.97	1.32
Mms22l	MMS22L	33.00	33.00	18.30	18.71	34.37	31.65	41.93	43.31	-0.99	1.08
Cenpf	CENPF	21.36	21.71	11.86	11.91	22.84	20.23	33.59	33.20	-1.02	1.37
Dhfr	DHFR	16.39	26.26	14.76	14.42	30.12	27.81	46.99	45.33	-1.02	1.54
Myd88	MYD88	39.88	39.64	20.56	22.68	31.21	32.36	42.01	40.91	-1.02	0.80
Nek2	NEK2	50.14	54.33	27.69	29.03	48.44	50.16	64.71	69.06	-1.03	1.12
Kif20b	KIF20B	61.69	62.12	32.87	32.49	83.77	75.44	99.64	96.07	-1.08	1.47
Ncapg	NCAPG	57.39	55.91	26.34	31.30	65.41	64.74	81.78	82.52	-1.13	1.38
Cd1d1	CD1D	1.58	1.49	0.64	0.48	1.63	1.66	2.43	1.34	-1.16	0.80
Kif14	KIF14	10.22	10.11	5.09	4.96	9.23	7.88	11.81	11.85	-1.17	1.10
Iqgap3	IQGAP3	44.25	45.47	21.99	22.40	39.50	38.51	47.01	46.00	-1.17	0.95
Csrp2	CSRP2	170.72	182.25	79.09	93.65	151.10	150.27	160.71	168.61	-1.18	0.80
Kif20a	KIF20A	109.26	108.18	51.96	55.10	159.18	150.03	216.69	220.75	-1.18	1.91
Spag5	SPAG5	63.67	61.67	32.28	29.18	84.86	78.99	91.33	89.50	-1.19	1.44
Aspm	ASPM	15.94	15.07	7.82	7.30	16.20	12.91	18.97	18.03	-1.20	1.17
Hmmr	HMMR	65.88	71.71	32.19	32.97	74.55	67.44	94.84	92.39	-1.23	1.40
Gtse1	GTSE1	40.10	37.21	16.80	18.70	42.09	42.22	49.28	46.20	-1.27	1.28
Pcca	PCCA	18.93	18.21	7.27	9.52	14.97	14.51	3.93	2.84	-1.27	-1.26
Mcm3	MCM3	283.09	276.42	122.71	121.60	263.29	264.97	260.42	260.76	-1.36	0.98
Ccnb1	CCNB1	171.49	167.97	73.75	72.12	187.72	181.20	181.21	187.40	-1.38	1.22
Birc5	BIRC5	101.06	97.54	40.47	41.70	100.67	104.42	102.81	107.68	-1.43	1.24
Ckap2	CKAP2	83.54	87.45	33.74	34.51	99.82	94.65	95.29	90.92	-1.48	1.32
Fkbp11	FKBP11	43.73	40.64	16.76	16.32	28.96	32.85	4.29	5.82	-1.48	-1.51
Fgfr4	FGFR4	6.10	7.65	2.10	2.86	4.73	4.92	4.55	6.13	-1.53	0.84
Ddit4l	DDIT4L	3.53	2.78	0.95	1.10	3.80	1.96	3.81	4.70	-1.56	1.45
Dhrs3	DHRS3	7.64	7.97	2.42	2.97	9.64	10.17	9.28	9.19	-1.56	1.38
Ect2	ECT2	240.77	250.66	93.71	91.64	209.05	191.24	221.74	225.35	-1.57	1.16
Vcam1	VCAM1	35.34	32.90	13.25	12.25	73.63	72.00	89.61	87.17	-1.58	2.65
Bop1	BOP1	310.92	306.48	118.82	112.93	237.82	238.71	208.29	204.26	-1.58	0.72
Hsph1	HSPH1	186.38	191.77	66.05	68.60	209.14	198.81	231.64	227.11	-1.65	1.66
Cdc20	CDC20	169.89	171.79	61.02	53.97	167.28	176.37	160.76	159.91	-1.74	1.37
Pik3c2g	PIK3C2G	0.51	0.57	0.08	0.12	1.16	1.35	0.86	1.06	-1.92	1.89
Ccna2	CCNA2	309.92	308.54	87.96	90.35	322.39	318.48	220.81	227.38	-1.95	1.22
Shcbp1	SHCBP1	224.66	232.81	65.40	62.36	230.49	232.65	155.23	159.28	-2.00	1.18
Shmt1	SHMT1	107.28	110.18	27.57	28.76	85.68	88.14	61.23	59.00	-2.10	0.96

**Supplementary Table S3, GO terms enriched in hypoxia-induced, *Blimp1*-dependent genes by FuncAssociate 3.0.** Hypoxia-induced, *Blimp1*-dependent genes (n=1022) were defined through the comparison of transcriptomes (RNA-Seq) from 688M cells cultured under normoxia and hypoxia (0.5% O<sub>2</sub>) for 24 hours *in vitro*. Usage of FuncAssociate tool was reported by Berriz et al. Bioinformatics 2009.

Gene number in query & attribute	Gene number in attribute	Odds ratio (log10)	Nominal p value	Adjusted p value	Attribute ID	Attribute name
12	41	0.86045969	1.47E-06	0.002	GO:0007044	cell-substrate junction assembly
39	248	0.51600292	4.04E-09	<0.001	GO:0001525	angiogenesis
36	267	0.436450368	8.09E-07	<0.001	GO:0036293	response to decreased oxygen levels
35	262	0.431617058	1.43E-06	0.002	GO:0001666	response to hypoxia
38	288	0.425759838	6.98E-07	<0.001	GO:0070482	response to oxygen levels
51	471	0.328575062	4.29E-06	0.009	GO:0009986	cell surface
62	586	0.318933512	8.84E-07	<0.001	GO:0030334	regulation of cell migration
64	623	0.304558112	1.62E-06	0.002	GO:2000145	regulation of cell motility
69	684	0.296373513	1.22E-06	0.001	GO:0040012	regulation of locomotion
66	666	0.286950834	3.82E-06	0.007	GO:0051270	regulation of cellular component movement