

Table 1 The sequence of forward and reverse primers used in RT-PCR analysis.

Gene	NCBI Gene ID	Forward and reverse primers	Product length
ACOT17	572757	F: AAGATGATCGAGGAGGCAGG R: GAGTGCTTGGAGGTGTAGGT	173
AK3L1	205	F: TGCTGCCAGGCTAAGACAGTACAA R: TCTTCCTGGTTCTTCCATTGGGCA	199
ALDOA	226	F: GAGAACACCGAGGAGAACCG R: TGGGTGGTAGTCTCGCCATT	230
AM	133	F: CTCTGAGTCGTGGGAAGAGG R: CGTGTGCTTGTGGCTTAGAA	402
ANGPTL4	51129	F: AGATGAATGTCCTGGCGCAC R: GGATCCTGCTGTTCTGAGCC	231
ANKRD37	353322	F: AAATTCTCCCGTGCTAGGGC R: TGCTGCCTTGTGTAGTGGAG	325
BNIP3L	665	F: CACCTCGCTCGCAGACACCAC R: GAGAGCAGCAGAGATGGAAGGAAAAC	316
CAIX	768	F: TACAGCTGAACTTCCGAGCG R: CTAGGCTCCAGTCTCGGCTA	269
CDKN3	1033	F: GACTCCTGACATAGCCAGCT R: ATTGCCCCGGATCCTCTTAG	204
DDIT4	54541	F: CTAGCCTTTGGGACCGCTT R: CGACACCCCATCCAGGTAAG	227
ENO1	2023	F: ATGGTGTCTCATCGTTCCGGG R: TGAGGAGCTGGTTGTACTTGG	133
HIF1A	3091	F: CATAAAGTCTGCAACATGGAAGGT R: ATTTGATGGGTGAGGAATGGGTT	148
HK2	3099	F: TCACGGAGCTCAACCATGAC R: CTGCAGTAGGGTGAGTGGTG	147
HPRT1	3251	F: TGGCGTCGTGATTAGTGATG R: TATCCAACACTTCGTGGGGT	504
LDHA	3939	F: CTGTTCCACTTAAGGCCCCCTC R: CCAGCCTTTCCCCCATTAGG	670
MIF	4282	F: TATTACGACATGAACGCGGC R: ACCGTTTATTCTCCCCACCA	161
MRPS17	51373	F: ATAGTCTTGGCGGAGGTGAC R: GGCATCGTGAGCAAAGTAGG	194
NDRG1	10397	F: TTTCTGCCTCTCCTCCACAG R: AAGGACACTCATCACAGCCA	153
PDHA1	5160	F: TTCTCAGAAGCCGGCAAGC R: CCATTGCCCCCGTAGAAGTT	450
PDK1	5163	F: CGGATCAGAAACCGACACAA R: AGATGGACTTCCTTTGCCTTTTC	204
PFKFB3	5209	F: ATCTACCTGAACGTGGAGTCCGTCTG R: TCAGTGTTTCCTGGAGGAGTCAGC	270
PFKFB4	5210	F: GGGATGGCGTCCCCACGGG R: CGTCTCCGTTCTCGGGTG	420
PGAM1	5223	F: CTGCACCCACTCCCTTCATA R: TCACTGGTCATGGCTTAGCA	181
PKM	5315	F: GCCGCCTGGACATTGATTC R: CCATGAGAGAAGTTCAGACGAG	145
P4HA1	5033	F: ATGAAGATCAGGTTGGGGCA	196

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		R: TGTTCATCCACAGTTCCGT	
SLC2A1	6513	F: TTGGCTCCGGTATCGTCAAC R: GGTCCGGCCTTTAGTCTCAG	446
SLC2A3	6515	F: GTGCACTGTCACCTTGCTCTG R: AACCTACTGTTTGAGGAGCCAG	596
TPI1	7167	F: GGGGCTTTTACTGGGGAGAT R: CCAATGCAGGCGATTACTCC	170
VEGFA	7422	F: CTCTACCTCCACCATGCCAAGT R: ATCTGGTTCCCGAAACCCTGAG	577 445

Table 2. Spearman’s rank coefficients for 12 hypoxia target genes in melanoma patients’ transcriptomic datasets. For significant positive correlations the R value is marked in green.

	<i>CA9</i>	<i>PFKFB4</i>	<i>AK3L1</i>	<i>HK2</i>	<i>PDK1</i>	<i>VEGFA</i>	<i>ADM</i>	<i>ANKRD37</i>	<i>DDIT4</i>	<i>ANGPTL4</i>	<i>BNIP3L</i>	<i>SLC2A1</i>
<i>CA9</i>		0.319	0.314	0.315	0.185	0.380	0.234	0.275	0.275	0.274	0.205	0.350
<i>PFKFB4</i>	0.319		0.319	0.453	0.158	0.372	0.244	0.465	0.250	0.218	0.032	0.355
<i>AK3L1</i>	0.314	0.319		0.509	0.167	0.341	0.392	0.452	0.307	0.257	0.597	0.345
<i>HK2</i>	0.315	0.453	0.509		0.072	0.346	0.337	0.370	0.274	0.306	0.209	0.323
<i>PDK1</i>	0.185	0.158	0.167	0.072		0.203	0.203	0.185	0.186	0.048	0.136	0.314
<i>VEGFA</i>	0.380	0.372	0.341	0.346	0.203		0.366	0.336	0.481	0.553	0.272	0.396
<i>ADM</i>	0.234	0.244	0.392	0.337	0.203	0.366		0.364	0.403	0.445	0.239	0.363
<i>ANKRD37</i>	0.275	0.465	0.452	0.370	0.185	0.336	0.364		0.365	0.117	0.267	0.548
<i>DDIT4</i>	0.275	0.250	0.307	0.274	0.186	0.481	0.403	0.365		0.401	0.012	0.257
<i>ANGPTL4</i>	0.274	0.218	0.257	0.306	0.048	0.553	0.445	0.117	0.401		0.247	0.153
<i>BNIP3L</i>	0.205	0.032	0.597	0.209	0.136	0.272	0.239	0.267	0.012	0.247		0.153
<i>SLC2A1</i>	0.350	0.355	0.345	0.323	0.314	0.396	0.363	0.548	0.257	0.153	0.153	

Table 3. Spearman’s rank coefficients for 12 hypoxia target genes in multiple myeloma patients’ transcriptomic datasets. For significant positive and negative correlations, the R value is marked in green and pink, respectively.

	<i>CA9</i>	<i>PFKFB4</i>	<i>AK3L1</i>	<i>HK2</i>	<i>PDK1</i>	<i>NDRG1</i>	<i>P4HA1</i>	<i>SLC2A1</i>	<i>DDIT4</i>	<i>ANGPTL4</i>	<i>BNIP3L</i>	<i>PFKFB3</i>
<i>CA9</i>		0.087	-0.065	0.041	-0.037	-0.101	-0.013	0.143	-0.004	0.166	-0.037	0.023
<i>PFKFB4</i>	0.087		-0.123	-0.152	-0.027	0.077	0.078	0.178	-0.096	-0.022	0.183	0.070
<i>AK3L1</i>	-0.065	-0.123		0.241	-0.018	0.008	-0.380	0.014	0.018	-0.136	-0.149	-0.003
<i>HK2</i>	0.041	-0.152	0.241		0.058	-0.164	-0.292	0.034	0.161	-0.009	-0.354	-0.029
<i>PDK1</i>	-0.037	-0.027	-0.018	0.058		0.028	0.062	0.005	0.034	0.022	0.166	0.054
<i>NDRG1</i>	-0.101	0.077	0.008	-0.164	0.028		0.020	0.073	0.100	-0.025	0.003	0.060
<i>P4HA1</i>	-0.013	0.078	-0.380	-0.292	0.062	0.020		-0,018	0.111	0.045	0.237	-0.034
<i>SLC2A1</i>	0.143	0.178	0.014	0.034	0.005	0.073	-0,018		-0.010	-0.058	-0.084	-0.049
<i>DDIT4</i>	-0.004	-0.096	0.018	0.161	0.034	0.100	0.111	-0.010		0.032	-0.087	-0.078
<i>ANGPTL4</i>	0.166	-0.022	-0.136	-0.009	0.022	-0.025	0.045	-0.058	0.032		-0.077	0.052
<i>BNIP3L</i>	-0.037	0.183	-0.149	-0.354	0.166	0.003	0.237	-0.084	-0.087	-0.077		0.212
<i>PFKFB3</i>	0.023	0.070	-0.003	-0.029	0.054	0.060	-0.034	-0.049	-0.078	0.052	0.212	

Table 4. Spearman’s rank coefficients for 11 genes, forming NF-kappa B signature, in multiple myeloma patients’ transcriptomic datasets. For significant positive correlations the R value is marked in green.

	<i>BIRC3</i>	<i>TNFAIP3</i>	<i>NFKB2</i>	<i>IL2 RG</i>	<i>NFKBIE</i>	<i>RELB</i>	<i>NFKBIA</i>	<i>CD74</i>	<i>PLEK</i>	<i>MALT1</i>	<i>Wnt10A</i>
<i>BIRC3</i>		0.620	0.439	0.378	0.515	0.553	0.496	0.564	0.484	0.404	0.477
<i>TNFAIP3</i>	0.620		0.556	0.568	0.590	0.599	0.602	0.560	0.606	0.584	0.550
<i>NFKB2</i>	0.439	0.556		0.595	0.375	0.628	0.392	0.495	0.509	0.532	0.549
<i>IL2RG</i>	0.378	0.568	0.595		0.396	0.462	0.333	0.472	0.485	0.476	0.543
<i>NFKBIE</i>	0.515	0.590	0.375	0.396		0.461	0.471	0.489	0.399	0.353	0.494
<i>RELB</i>	0.553	0.599	0.628	0.462	0.495		0.531	0.451	0.451	0.469	0.478
<i>NFKBIA</i>	0.496	0.602	0.392	0.333	0.471	0.531		0.418	0.328	0.355	0.346
<i>CD74</i>	0.564	0.560	0.495	0.472	0.489	0.451	0.418		0.524	0.335	0.467
<i>PLEK</i>	0.484	0.606	0.509	0.485	0.399	0.451	0.328	0.524		0.486	0.428
<i>MALT1</i>	0.404	0.584	0.532	0.476	0.353	0.469	0.355	0.335	0.486		0.405
<i>Wnt10A</i>	0.477	0.550	0.549	0.543	0.494	0.478	0.346	0.467	0.428	0.405	