

Additional File 1. The top 250 genes correlated with HIF-1 α in the TCGA dataset were clustered using the KEGG pathway enrichment analysis. The HIF-1 α correlated genes belonging to the “Cytokine-cytokine receptor interaction” pathway were reported according to their correlation coefficients (p-value < 0.001).

Gene	r-value	p-value
OSMR	0.52	7.04E-10
IL1RAP	0.48	1.54E-08
IL-1 β	0.44	3.03E-07
IL7R	0.44	3.44E-07
TGFBR2	0.43	5.40E-07
IL1R1	0.43	5.56E-07
IL1A	0.42	1.36E-06
IL6ST	0.41	2.30E-06
INHBA	0.41	2.40E-06
IL6	0.41	2.63E-06