

Supplementary Table 1. Comparison of mRNA expression between two clusters

Gene	Cluster 1	Cluster 2	Fisher's p-value	Adjusted p-value
<i>MET</i>	15325.21	10501.05	0.004006	7.121778e-03
<i>SERPINA1</i>	61629.54	38354.61	0.005308	7.720727e-03
<i>TIMP1</i>	19703.83	15160.10	0.04248	5.248000e-02
<i>PROS1</i>	9213.393	6428.974	0.01116	1.373538e-02
<i>FN1</i>	654094.0	309384.4	0.005028	7.720727e-03
<i>CDKN2A</i>	355.11553	81.67595	0.001668	3.336000e-03
<i>CDKN2B</i>	390.6521	240.3759	0.03195	3.651429e-02
<i>TG</i>	300425.5	721943.5	3.53e-10	1.882667e-09
<i>DNAH9</i>	14.25255	30.98896	8.792e-05	2.009600e-04
<i>TFF3</i>	75.44333	2263.83774	8.379e-07	2.234400e-06
<i>CRABP1</i>	224.5220	954.2775	5.348e-08	1.711360e-07
<i>TPO</i>	4595.554	25621.680	2.743e-10	1.882667e-09
<i>JAK2</i>	180.2953	215.2441	0.04822	5.143680e-02
<i>KIT</i>	165.1687	722.5089	2.678e-15	4.284800e-14
<i>KDR</i>	1040.618	2131.501	2.315e-09	9.260000e-09
<i>NFE2L2</i>	3122.581	3633.828	0.00687	9.160000e-03

Adjusted p-values were obtained using method of Benjamini Hochberg