

**Table S1.** Clinical parameters of TCGA COAD cohort

<b>Variables</b>	<b>Patients (n=438)</b>	<b>MST(days)</b>	<b>HR(95%CI)</b>	<b>Log-rank P</b>
<b>Gender</b>				0.545
<b>Female</b>	204	NA	1	
<b>Male</b>	234	2475	1.131(0.759-1.686)	
<b>Age (years) §</b>				0.112
<b>&lt;65</b>	168	NA	1	
<b>≥65</b>	268	2475	1.420(0.919-2.194)	
<b>Tumor stage £</b>				<0.0001
<b>I</b>	73	NA	1	
<b>II</b>	167	2821	2.240(0.781-6.421)	
<b>III</b>	126	NA	4.068(1.434-11.538)	
<b>IV</b>	61	858	11.291(3.980-32.026)	
<b>Tumor stage</b>				<0.0001
<b>I+II</b>	240	3042	1	
<b>III+IV</b>	187	1711	3.097(2.009-4.772)	
<b>AC096751.1</b>				0.016
<b>Low expression</b>	219	2475	1	
<b>High expression</b>	219	NA	0.610(0.407-0.915)	

**Notes:** §Information of age was unavailable in 2 patients; £Information of tumor stage was unavailable in 11 patients.

**Abbreviation:** NA, Not available; TCGA, The Cancer Genome Atlas; MST, median survival time; COAD, colon adenocarcinoma; HR, hazard ratio; CI, confidence interval.

**Table S2.** List of co-expressed genes of AC096751.1

<b>ID</b>	<b>ID</b>	<b>r</b>	<b>pValue</b>
AC096751.1	AC096751.1	1	9.07E-30
AC096751.1	HPGD	0.621	2.32E-12
AC096751.1	FLVCR2	0.376	2.42E-05
AC096751.1	BIRC3	0.361	5.10E-05
AC096751.1	PIM1	0.349	9.07E-05
AC096751.1	DENND5B	0.346	0.000104
AC096751.1	PLAC8	0.344	0.000115
AC096751.1	GCNT3	0.344	0.000115
AC096751.1	CCDC68	0.336	0.000166
AC096751.1	HSD17B2	0.331	0.000208
AC096751.1	RARRES3	0.328	0.000238
AC096751.1	PARP12	0.324	0.000284
AC096751.1	PTPRR	0.319	0.000354
AC096751.1	IRS1	0.318	0.00037
AC096751.1	GRAMD1A	-0.305	0.000403
AC096751.1	DAPK1	0.314	0.000439
AC096751.1	SOCS6	0.312	0.000479
AC096751.1	RND3	0.312	0.000479
AC096751.1	FAM46A	0.311	0.000499
AC096751.1	KCNK1	0.31	0.000521
AC096751.1	KCTD1	0.31	0.000521
AC096751.1	KLF6	0.31	0.000521
AC096751.1	PKIB	0.309	0.000544
AC096751.1	EGFR	0.308	0.000567
AC096751.1	ENDOD1	0.308	0.000567
AC096751.1	IMPA1	0.305	0.000643
AC096751.1	SAMD9	0.304	0.000671
AC096751.1	PAG1	0.3	0.000791
AC096751.1	TMEM133	0.3	0.000791
AC096751.1	GPD2	0.298	0.000859
AC096751.1	RNF213	0.297	0.000895
AC096751.1	PTGS2	0.296	0.000932
AC096751.1	TEAD2	-0.284	0.00097
AC096751.1	MXD1	0.295	0.000971
AC096751.1	APOL2	0.294	0.001011
AC096751.1	RIOK3	0.294	0.001011
AC096751.1	DUSP5	0.293	0.001053
AC096751.1	SEMG2	0.292	0.001096
AC096751.1	EMP1	0.292	0.001096
AC096751.1	EZR	0.291	0.001141
AC096751.1	ARFGAP3	0.291	0.001141
AC096751.1	DPCR1	0.29	0.001188

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<b>AC096751.1</b>	<b>ARHGAP10</b>	0.288	0.001286
<b>AC096751.1</b>	<b>SETMAR</b>	-0.276	0.001337
<b>AC096751.1</b>	<b>PPP4R1</b>	0.287	0.001338
<b>AC096751.1</b>	<b>WDR44</b>	0.287	0.001338
<b>AC096751.1</b>	<b>SMCHD1</b>	0.287	0.001338
<b>AC096751.1</b>	<b>TDGF1</b>	-0.275	0.001391
<b>AC096751.1</b>	<b>SAMD9L</b>	0.286	0.001392
<b>AC096751.1</b>	<b>CALCOCO2</b>	0.286	0.001392
<b>AC096751.1</b>	<b>ARHGAP42</b>	0.285	0.001448
<b>AC096751.1</b>	<b>DPP4</b>	0.285	0.001448
<b>AC096751.1</b>	<b>NYAP2</b>	0.284	0.001506
<b>AC096751.1</b>	<b>CACNG4</b>	0.284	0.001506
<b>AC096751.1</b>	<b>WWC1</b>	0.283	0.001567
<b>AC096751.1</b>	<b>TMCC3</b>	0.283	0.001567
<b>AC096751.1</b>	<b>PNMA1</b>	0.282	0.001629
<b>AC096751.1</b>	<b>HPSE</b>	0.282	0.001629
<b>AC096751.1</b>	<b>SCIN</b>	0.281	0.001694
<b>AC096751.1</b>	<b>TCAF2</b>	0.281	0.001694
<b>AC096751.1</b>	<b>KDSR</b>	0.28	0.001761
<b>AC096751.1</b>	<b>PCSK5</b>	0.279	0.00183
<b>AC096751.1</b>	<b>CDKN2B</b>	0.279	0.00183
<b>AC096751.1</b>	<b>SLC41A2</b>	0.279	0.00183
<b>AC096751.1</b>	<b>EFNA4</b>	-0.267	0.001901
<b>AC096751.1</b>	<b>OXGR1</b>	-0.267	0.001901
<b>AC096751.1</b>	<b>ADAM9</b>	0.277	0.001977
<b>AC096751.1</b>	<b>ARHGAP29</b>	0.277	0.001977
<b>AC096751.1</b>	<b>IGFL2</b>	0.277	0.001977
<b>AC096751.1</b>	<b>C18orf8</b>	0.276	0.002054
<b>AC096751.1</b>	<b>ALDH1B1</b>	-0.264	0.002133
<b>AC096751.1</b>	<b>EXT1</b>	0.275	0.002134
<b>AC096751.1</b>	<b>TCP11L1</b>	0.274	0.002217
<b>AC096751.1</b>	<b>CREG2</b>	0.272	0.002392
<b>AC096751.1</b>	<b>DOCK5</b>	0.272	0.002392
<b>AC096751.1</b>	<b>PHLPP2</b>	0.272	0.002392
<b>AC096751.1</b>	<b>AHNAK</b>	0.272	0.002392
<b>AC096751.1</b>	<b>CPM</b>	0.272	0.002392
<b>AC096751.1</b>	<b>LRRC1</b>	0.272	0.002392
<b>AC096751.1</b>	<b>GBP3</b>	0.271	0.002484
<b>AC096751.1</b>	<b>TEX45</b>	-0.259	0.002577
<b>AC096751.1</b>	<b>PSAPL1</b>	0.27	0.002579
<b>AC096751.1</b>	<b>SHROOM3</b>	0.27	0.002579
<b>AC096751.1</b>	<b>PARP14</b>	0.267	0.002885
<b>AC096751.1</b>	<b>RNF44</b>	-0.255	0.002992
<b>AC096751.1</b>	<b>CASP10</b>	0.266	0.002994

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<b>AC096751.1</b>	<b>STS</b>	0.266	0.002994
<b>AC096751.1</b>	<b>PKN2</b>	0.266	0.002994
<b>AC096751.1</b>	<b>ABCB11</b>	0.266	0.002994
<b>AC096751.1</b>	<b>CYTH3</b>	0.265	0.003107
<b>AC096751.1</b>	<b>NUB1</b>	0.265	0.003107
<b>AC096751.1</b>	<b>IL15</b>	0.265	0.003107
<b>AC096751.1</b>	<b>MBD2</b>	0.265	0.003107
<b>AC096751.1</b>	<b>PSCA</b>	0.264	0.003224
<b>AC096751.1</b>	<b>MYOF</b>	0.264	0.003224
<b>AC096751.1</b>	<b>SYTL4</b>	0.264	0.003224
<b>AC096751.1</b>	<b>WNK2</b>	-0.252	0.003343
<b>AC096751.1</b>	<b>FOXO1</b>	0.263	0.003345
<b>AC096751.1</b>	<b>KIAA1211</b>	0.263	0.003345
<b>AC096751.1</b>	<b>PTPRH</b>	0.262	0.003469
<b>AC096751.1</b>	<b>NPC1</b>	0.262	0.003469
<b>AC096751.1</b>	<b>JOSD1</b>	0.262	0.003469
<b>AC096751.1</b>	<b>RAB27B</b>	0.26	0.003732
<b>AC096751.1</b>	<b>GDA</b>	0.26	0.003732
<b>AC096751.1</b>	<b>GBP2</b>	0.259	0.00387
<b>AC096751.1</b>	<b>DACH1</b>	-0.247	0.00401
<b>AC096751.1</b>	<b>SPON1</b>	0.258	0.004013
<b>AC096751.1</b>	<b>IKZF2</b>	0.258	0.004013
<b>AC096751.1</b>	<b>CP</b>	0.257	0.00416
<b>AC096751.1</b>	<b>RNF152</b>	0.257	0.00416
<b>AC096751.1</b>	<b>VPS4B</b>	0.257	0.00416
<b>AC096751.1</b>	<b>LGR4</b>	0.257	0.00416
<b>AC096751.1</b>	<b>KIF13A</b>	0.257	0.00416
<b>AC096751.1</b>	<b>TMEM9</b>	-0.245	0.00431
<b>AC096751.1</b>	<b>KITLG</b>	0.256	0.004312
<b>AC096751.1</b>	<b>XRN1</b>	0.256	0.004312
<b>AC096751.1</b>	<b>VSTM5</b>	0.256	0.004312
<b>AC096751.1</b>	<b>VAPA</b>	0.256	0.004312
<b>AC096751.1</b>	<b>TTC7A</b>	0.256	0.004312
<b>AC096751.1</b>	<b>SLC1A1</b>	0.255	0.004469
<b>AC096751.1</b>	<b>CD5L</b>	0.254	0.004632
<b>AC096751.1</b>	<b>MT2A</b>	0.254	0.004632
<b>AC096751.1</b>	<b>GJB4</b>	0.254	0.004632
<b>AC096751.1</b>	<b>TRIM69</b>	0.254	0.004632
<b>AC096751.1</b>	<b>RRM2B</b>	0.254	0.004632
<b>AC096751.1</b>	<b>PLA2G2A</b>	0.254	0.004632
<b>AC096751.1</b>	<b>TMEM261</b>	-0.242	0.004797
<b>AC096751.1</b>	<b>NECTIN1</b>	-0.242	0.004797
<b>AC096751.1</b>	<b>CCNYL1</b>	0.253	0.004799
<b>AC096751.1</b>	<b>BTN3A3</b>	0.253	0.004799

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<b>AC096751.1</b>	<b>HOXA7</b>	<b>-0.241</b>	<b>0.00497</b>
<b>AC096751.1</b>	<b>HNRNPA0</b>	<b>-0.241</b>	<b>0.00497</b>
<b>AC096751.1</b>	<b>SERPINB5</b>	<b>0.252</b>	<b>0.004973</b>
<b>AC096751.1</b>	<b>EPHB3</b>	<b>-0.24</b>	<b>0.005149</b>
<b>AC096751.1</b>	<b>LARGE2</b>	<b>-0.24</b>	<b>0.005149</b>
<b>AC096751.1</b>	<b>ANXA1</b>	<b>0.251</b>	<b>0.005151</b>
<b>AC096751.1</b>	<b>BTN3A1</b>	<b>0.251</b>	<b>0.005151</b>
<b>AC096751.1</b>	<b>IL18</b>	<b>0.251</b>	<b>0.005151</b>
<b>AC096751.1</b>	<b>NFKBIA</b>	<b>0.251</b>	<b>0.005151</b>
<b>AC096751.1</b>	<b>DHRS9</b>	<b>0.251</b>	<b>0.005151</b>
<b>AC096751.1</b>	<b>CRB2</b>	<b>-0.239</b>	<b>0.005333</b>
<b>AC096751.1</b>	<b>DDX60L</b>	<b>0.25</b>	<b>0.005336</b>
<b>AC096751.1</b>	<b>TAP1</b>	<b>0.25</b>	<b>0.005336</b>
<b>AC096751.1</b>	<b>SPTBN1</b>	<b>0.25</b>	<b>0.005336</b>
<b>AC096751.1</b>	<b>MBP</b>	<b>0.25</b>	<b>0.005336</b>
<b>AC096751.1</b>	<b>MEST</b>	<b>-0.238</b>	<b>0.005524</b>
<b>AC096751.1</b>	<b>GJB1</b>	<b>-0.238</b>	<b>0.005524</b>
<b>AC096751.1</b>	<b>KRT9</b>	<b>0.249</b>	<b>0.005527</b>
<b>AC096751.1</b>	<b>PDLIM5</b>	<b>0.249</b>	<b>0.005527</b>
<b>AC096751.1</b>	<b>NOCT</b>	<b>0.249</b>	<b>0.005527</b>
<b>AC096751.1</b>	<b>TMEM8B</b>	<b>-0.237</b>	<b>0.00572</b>
<b>AC096751.1</b>	<b>TRAF5</b>	<b>-0.237</b>	<b>0.00572</b>
<b>AC096751.1</b>	<b>HLA-DRB1</b>	<b>0.248</b>	<b>0.005723</b>
<b>AC096751.1</b>	<b>AC005885.1</b>	<b>0.248</b>	<b>0.005723</b>
<b>AC096751.1</b>	<b>COL17A1</b>	<b>0.248</b>	<b>0.005723</b>
<b>AC096751.1</b>	<b>BCL11A</b>	<b>-0.236</b>	<b>0.005923</b>
<b>AC096751.1</b>	<b>MISP3</b>	<b>-0.236</b>	<b>0.005923</b>
<b>AC096751.1</b>	<b>ADGRG6</b>	<b>0.247</b>	<b>0.005926</b>
<b>AC096751.1</b>	<b>DHRSX</b>	<b>-0.235</b>	<b>0.006132</b>
<b>AC096751.1</b>	<b>CACNG1</b>	<b>0.246</b>	<b>0.006136</b>
<b>AC096751.1</b>	<b>GNA13</b>	<b>0.246</b>	<b>0.006136</b>
<b>AC096751.1</b>	<b>LHFPL2</b>	<b>0.246</b>	<b>0.006136</b>
<b>AC096751.1</b>	<b>HLA-DMA</b>	<b>0.245</b>	<b>0.006352</b>
<b>AC096751.1</b>	<b>SYT12</b>	<b>0.245</b>	<b>0.006352</b>
<b>AC096751.1</b>	<b>FRMD3</b>	<b>0.244</b>	<b>0.006575</b>
<b>AC096751.1</b>	<b>NUP50</b>	<b>0.244</b>	<b>0.006575</b>
<b>AC096751.1</b>	<b>PPFIBP2</b>	<b>-0.232</b>	<b>0.006801</b>
<b>AC096751.1</b>	<b>LZTS3</b>	<b>-0.232</b>	<b>0.006801</b>
<b>AC096751.1</b>	<b>VSIG10L</b>	<b>0.243</b>	<b>0.006805</b>
<b>AC096751.1</b>	<b>GBP1</b>	<b>0.243</b>	<b>0.006805</b>
<b>AC096751.1</b>	<b>SP100</b>	<b>0.243</b>	<b>0.006805</b>
<b>AC096751.1</b>	<b>PRDM8</b>	<b>0.243</b>	<b>0.006805</b>
<b>AC096751.1</b>	<b>SH3BP4</b>	<b>-0.231</b>	<b>0.007038</b>
<b>AC096751.1</b>	<b>APOL6</b>	<b>0.242</b>	<b>0.007042</b>

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<b>AC096751.1</b>	<b>FABP6</b>	<b>-0.23</b>	<b>0.007283</b>
<b>AC096751.1</b>	<b>CLIC5</b>	<b>0.241</b>	<b>0.007287</b>
<b>AC096751.1</b>	<b>MYO1E</b>	<b>0.241</b>	<b>0.007287</b>
<b>AC096751.1</b>	<b>CD70</b>	<b>0.241</b>	<b>0.007287</b>
<b>AC096751.1</b>	<b>DUSP4</b>	<b>0.241</b>	<b>0.007287</b>
<b>AC096751.1</b>	<b>SLC20A1</b>	<b>0.241</b>	<b>0.007287</b>
<b>AC096751.1</b>	<b>CYFIP2</b>	<b>-0.229</b>	<b>0.007535</b>
<b>AC096751.1</b>	<b>FOXA2</b>	<b>-0.229</b>	<b>0.007535</b>
<b>AC096751.1</b>	<b>ZBED1</b>	<b>-0.229</b>	<b>0.007535</b>
<b>AC096751.1</b>	<b>KANK1</b>	<b>-0.229</b>	<b>0.007535</b>
<b>AC096751.1</b>	<b>CAV2</b>	<b>0.24</b>	<b>0.007539</b>
<b>AC096751.1</b>	<b>FGD6</b>	<b>0.24</b>	<b>0.007539</b>
<b>AC096751.1</b>	<b>ROS1</b>	<b>0.24</b>	<b>0.007539</b>
<b>AC096751.1</b>	<b>GPRC5A</b>	<b>0.24</b>	<b>0.007539</b>
<b>AC096751.1</b>	<b>ITSN1</b>	<b>0.239</b>	<b>0.007799</b>
<b>AC096751.1</b>	<b>BTN3A2</b>	<b>0.239</b>	<b>0.007799</b>
<b>AC096751.1</b>	<b>CMTM8</b>	<b>-0.227</b>	<b>0.008062</b>
<b>AC096751.1</b>	<b>DDX60</b>	<b>0.238</b>	<b>0.008067</b>
<b>AC096751.1</b>	<b>CTXN1</b>	<b>0.238</b>	<b>0.008067</b>
<b>AC096751.1</b>	<b>PPFIA1</b>	<b>0.238</b>	<b>0.008067</b>
<b>AC096751.1</b>	<b>ACTR1B</b>	<b>-0.226</b>	<b>0.008338</b>
<b>AC096751.1</b>	<b>HES6</b>	<b>-0.226</b>	<b>0.008338</b>
<b>AC096751.1</b>	<b>C2CD4D</b>	<b>-0.226</b>	<b>0.008338</b>
<b>AC096751.1</b>	<b>GALNT5</b>	<b>0.237</b>	<b>0.008343</b>
<b>AC096751.1</b>	<b>KRT20</b>	<b>0.237</b>	<b>0.008343</b>
<b>AC096751.1</b>	<b>SRGAP1</b>	<b>0.236</b>	<b>0.008627</b>
<b>AC096751.1</b>	<b>PITPNC1</b>	<b>0.236</b>	<b>0.008627</b>
<b>AC096751.1</b>	<b>DNMT3A</b>	<b>-0.224</b>	<b>0.008916</b>
<b>AC096751.1</b>	<b>ADGRG1</b>	<b>-0.224</b>	<b>0.008916</b>
<b>AC096751.1</b>	<b>DAGLA</b>	<b>-0.224</b>	<b>0.008916</b>
<b>AC096751.1</b>	<b>IKBKE</b>	<b>-0.223</b>	<b>0.009218</b>
<b>AC096751.1</b>	<b>SAMD4A</b>	<b>0.234</b>	<b>0.009223</b>
<b>AC096751.1</b>	<b>UST</b>	<b>0.234</b>	<b>0.009223</b>
<b>AC096751.1</b>	<b>TMEM45B</b>	<b>0.234</b>	<b>0.009223</b>
<b>AC096751.1</b>	<b>TAP2</b>	<b>0.234</b>	<b>0.009223</b>
<b>AC096751.1</b>	<b>RTTN</b>	<b>0.234</b>	<b>0.009223</b>
<b>AC096751.1</b>	<b>CLIP1</b>	<b>0.234</b>	<b>0.009223</b>
<b>AC096751.1</b>	<b>ADAM10</b>	<b>0.234</b>	<b>0.009223</b>
<b>AC096751.1</b>	<b>PLEKHB1</b>	<b>-0.222</b>	<b>0.009529</b>
<b>AC096751.1</b>	<b>ITGA3</b>	<b>0.233</b>	<b>0.009534</b>
<b>AC096751.1</b>	<b>TNFSF9</b>	<b>0.233</b>	<b>0.009534</b>
<b>AC096751.1</b>	<b>CD55</b>	<b>0.233</b>	<b>0.009534</b>
<b>AC096751.1</b>	<b>CYP39A1</b>	<b>-0.221</b>	<b>0.009849</b>
<b>AC096751.1</b>	<b>CAPN2</b>	<b>0.232</b>	<b>0.009854</b>

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<b>AC096751.1</b>	STBD1	0.232	0.009854
<b>AC096751.1</b>	TGFBI	-0.22	0.010179
<b>AC096751.1</b>	TRIB2	0.231	0.010184
<b>AC096751.1</b>	TXNRD1	0.231	0.010184
<b>AC096751.1</b>	TRIM7	0.231	0.010184
<b>AC096751.1</b>	FLNB	0.231	0.010184
<b>AC096751.1</b>	AIM2	0.231	0.010184
<b>AC096751.1</b>	TRPV6	0.231	0.010184
<b>AC096751.1</b>	SPHK2	-0.219	0.010519
<b>AC096751.1</b>	RGS2	0.23	0.010524
<b>AC096751.1</b>	ANKRD12	0.23	0.010524
<b>AC096751.1</b>	IRF1	0.23	0.010524
<b>AC096751.1</b>	HDAC9	0.23	0.010524
<b>AC096751.1</b>	APOL1	0.23	0.010524
<b>AC096751.1</b>	ANKRD16	-0.218	0.010869
<b>AC096751.1</b>	NME4	-0.218	0.010869
<b>AC096751.1</b>	FGF2	0.229	0.010874
<b>AC096751.1</b>	C18orf25	0.229	0.010874
<b>AC096751.1</b>	NMU	0.229	0.010874
<b>AC096751.1</b>	RPIA	-0.217	0.011229
<b>AC096751.1</b>	RNF19B	0.228	0.011234
<b>AC096751.1</b>	MCUB	0.228	0.011234
<b>AC096751.1</b>	RNF19A	0.228	0.011234
<b>AC096751.1</b>	AK4	0.228	0.011234
<b>AC096751.1</b>	RABEP2	-0.216	0.011599
<b>AC096751.1</b>	C19orf73	-0.216	0.011599
<b>AC096751.1</b>	TMEM140	0.227	0.011605
<b>AC096751.1</b>	SMCO2	0.227	0.011605
<b>AC096751.1</b>	TEP1	0.227	0.011605
<b>AC096751.1</b>	LCLAT1	0.227	0.011605
<b>AC096751.1</b>	LEFTY1	-0.215	0.011981
<b>AC096751.1</b>	KCNN4	-0.215	0.011981
<b>AC096751.1</b>	C14orf93	-0.215	0.011981
<b>AC096751.1</b>	INPP5D	-0.215	0.011981
<b>AC096751.1</b>	FAM171A1	-0.215	0.011981
<b>AC096751.1</b>	RABEPK	-0.215	0.011981
<b>AC096751.1</b>	PERM1	0.226	0.011987
<b>AC096751.1</b>	ACHE	0.226	0.011987
<b>AC096751.1</b>	LPIN2	0.226	0.011987
<b>AC096751.1</b>	RARRES1	0.226	0.011987
<b>AC096751.1</b>	ANKH	-0.214	0.012373
<b>AC096751.1</b>	FGFR4	-0.214	0.012373
<b>AC096751.1</b>	ASPHD2	0.225	0.01238
<b>AC096751.1</b>	PLEKHA7	0.225	0.01238

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<b>AC096751.1</b>	<b>MYRFL</b>	<b>0.225</b>	<b>0.01238</b>
<b>AC096751.1</b>	<b>RAPH1</b>	<b>0.225</b>	<b>0.01238</b>
<b>AC096751.1</b>	<b>ANTXR2</b>	<b>0.225</b>	<b>0.01238</b>
<b>AC096751.1</b>	<b>PARP9</b>	<b>0.225</b>	<b>0.01238</b>
<b>AC096751.1</b>	<b>LANCL3</b>	<b>0.225</b>	<b>0.01238</b>
<b>AC096751.1</b>	<b>GNAI3</b>	<b>0.225</b>	<b>0.01238</b>
<b>AC096751.1</b>	<b>CTSE</b>	<b>0.225</b>	<b>0.01238</b>
<b>AC096751.1</b>	<b>AC008687.4</b>	<b>0.225</b>	<b>0.01238</b>
<b>AC096751.1</b>	<b>CNNM4</b>	<b>0.225</b>	<b>0.01238</b>
<b>AC096751.1</b>	<b>EDEM1</b>	<b>0.225</b>	<b>0.01238</b>
<b>AC096751.1</b>	<b>SERPINB8</b>	<b>0.225</b>	<b>0.01238</b>
<b>AC096751.1</b>	<b>GJA3</b>	<b>0.225</b>	<b>0.01238</b>
<b>AC096751.1</b>	<b>ABCA3</b>	<b>0.224</b>	<b>0.012784</b>
<b>AC096751.1</b>	<b>FAM114A1</b>	<b>0.224</b>	<b>0.012784</b>
<b>AC096751.1</b>	<b>PLCL2</b>	<b>0.224</b>	<b>0.012784</b>
<b>AC096751.1</b>	<b>SLMAP</b>	<b>0.223</b>	<b>0.013199</b>
<b>AC096751.1</b>	<b>TRIM36</b>	<b>0.223</b>	<b>0.013199</b>
<b>AC096751.1</b>	<b>LIPH</b>	<b>0.223</b>	<b>0.013199</b>
<b>AC096751.1</b>	<b>ANKRD13C</b>	<b>0.223</b>	<b>0.013199</b>
<b>AC096751.1</b>	<b>PATZ1</b>	<b>-0.211</b>	<b>0.01362</b>
<b>AC096751.1</b>	<b>CREB3L4</b>	<b>-0.211</b>	<b>0.01362</b>
<b>AC096751.1</b>	<b>BCL9</b>	<b>-0.211</b>	<b>0.01362</b>
<b>AC096751.1</b>	<b>C11orf49</b>	<b>-0.211</b>	<b>0.01362</b>
<b>AC096751.1</b>	<b>SNX9</b>	<b>0.222</b>	<b>0.013627</b>
<b>AC096751.1</b>	<b>BARX2</b>	<b>0.222</b>	<b>0.013627</b>
<b>AC096751.1</b>	<b>C6orf106</b>	<b>0.222</b>	<b>0.013627</b>
<b>AC096751.1</b>	<b>CALB1</b>	<b>0.222</b>	<b>0.013627</b>
<b>AC096751.1</b>	<b>TMEM63A</b>	<b>-0.21</b>	<b>0.01406</b>
<b>AC096751.1</b>	<b>FLAD1</b>	<b>-0.21</b>	<b>0.01406</b>
<b>AC096751.1</b>	<b>RPL7A</b>	<b>-0.21</b>	<b>0.01406</b>
<b>AC096751.1</b>	<b>BICDL1</b>	<b>0.221</b>	<b>0.014067</b>
<b>AC096751.1</b>	<b>HLA-C</b>	<b>0.221</b>	<b>0.014067</b>
<b>AC096751.1</b>	<b>ACBD6</b>	<b>-0.209</b>	<b>0.014512</b>
<b>AC096751.1</b>	<b>NCK2</b>	<b>-0.209</b>	<b>0.014512</b>
<b>AC096751.1</b>	<b>C20orf196</b>	<b>-0.209</b>	<b>0.014512</b>
<b>AC096751.1</b>	<b>FAM221B</b>	<b>-0.209</b>	<b>0.014512</b>
<b>AC096751.1</b>	<b>NDRG2</b>	<b>-0.209</b>	<b>0.014512</b>
<b>AC096751.1</b>	<b>KIF12</b>	<b>-0.209</b>	<b>0.014512</b>
<b>AC096751.1</b>	<b>MMP28</b>	<b>0.22</b>	<b>0.014519</b>
<b>AC096751.1</b>	<b>MTF1</b>	<b>0.22</b>	<b>0.014519</b>
<b>AC096751.1</b>	<b>PSEN1</b>	<b>0.22</b>	<b>0.014519</b>
<b>AC096751.1</b>	<b>PLK2</b>	<b>0.22</b>	<b>0.014519</b>
<b>AC096751.1</b>	<b>FAM102B</b>	<b>0.22</b>	<b>0.014519</b>
<b>AC096751.1</b>	<b>ZNF444</b>	<b>-0.208</b>	<b>0.014977</b>

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<b>AC096751.1</b>	<b>FOXA3</b>	<b>-0.208</b>	<b>0.014977</b>
<b>AC096751.1</b>	<b>ACTL10</b>	<b>-0.208</b>	<b>0.014977</b>
<b>AC096751.1</b>	<b>GULP1</b>	<b>0.219</b>	<b>0.014984</b>
<b>AC096751.1</b>	<b>ERRFI1</b>	<b>0.219</b>	<b>0.014984</b>
<b>AC096751.1</b>	<b>ENO2</b>	<b>0.219</b>	<b>0.014984</b>
<b>AC096751.1</b>	<b>CCNG2</b>	<b>0.219</b>	<b>0.014984</b>
<b>AC096751.1</b>	<b>RUBCN</b>	<b>0.219</b>	<b>0.014984</b>
<b>AC096751.1</b>	<b>MT1E</b>	<b>0.219</b>	<b>0.014984</b>
<b>AC096751.1</b>	<b>EEPD1</b>	<b>-0.207</b>	<b>0.015455</b>
<b>AC096751.1</b>	<b>TMEM216</b>	<b>-0.207</b>	<b>0.015455</b>
<b>AC096751.1</b>	<b>PGAP2</b>	<b>-0.207</b>	<b>0.015455</b>
<b>AC096751.1</b>	<b>UGT1A1</b>	<b>0.218</b>	<b>0.015462</b>
<b>AC096751.1</b>	<b>RAP2B</b>	<b>0.218</b>	<b>0.015462</b>
<b>AC096751.1</b>	<b>RALBP1</b>	<b>0.218</b>	<b>0.015462</b>
<b>AC096751.1</b>	<b>ARNTL2</b>	<b>0.218</b>	<b>0.015462</b>
<b>AC096751.1</b>	<b>CYP2C18</b>	<b>0.218</b>	<b>0.015462</b>
<b>AC096751.1</b>	<b>TNFRSF21</b>	<b>0.218</b>	<b>0.015462</b>
<b>AC096751.1</b>	<b>ABCG2</b>	<b>0.218</b>	<b>0.015462</b>
<b>AC096751.1</b>	<b>DUSP18</b>	<b>-0.206</b>	<b>0.015946</b>
<b>AC096751.1</b>	<b>GFOD2</b>	<b>-0.206</b>	<b>0.015946</b>
<b>AC096751.1</b>	<b>ADM</b>	<b>0.217</b>	<b>0.015954</b>
<b>AC096751.1</b>	<b>SLC7A7</b>	<b>0.217</b>	<b>0.015954</b>
<b>AC096751.1</b>	<b>MICB</b>	<b>0.217</b>	<b>0.015954</b>
<b>AC096751.1</b>	<b>ZMYND15</b>	<b>0.217</b>	<b>0.015954</b>
<b>AC096751.1</b>	<b>AHCYL2</b>	<b>0.217</b>	<b>0.015954</b>
<b>AC096751.1</b>	<b>ALCAM</b>	<b>0.217</b>	<b>0.015954</b>
<b>AC096751.1</b>	<b>IRF2BP2</b>	<b>-0.205</b>	<b>0.016451</b>
<b>AC096751.1</b>	<b>LDB1</b>	<b>-0.205</b>	<b>0.016451</b>
<b>AC096751.1</b>	<b>SGMS2</b>	<b>0.216</b>	<b>0.016459</b>
<b>AC096751.1</b>	<b>ZNF165</b>	<b>0.216</b>	<b>0.016459</b>
<b>AC096751.1</b>	<b>RHOF</b>	<b>0.216</b>	<b>0.016459</b>
<b>AC096751.1</b>	<b>TRANK1</b>	<b>0.216</b>	<b>0.016459</b>
<b>AC096751.1</b>	<b>LRRFIP1</b>	<b>0.216</b>	<b>0.016459</b>
<b>AC096751.1</b>	<b>STARD10</b>	<b>-0.204</b>	<b>0.01697</b>
<b>AC096751.1</b>	<b>SLC5A6</b>	<b>-0.204</b>	<b>0.01697</b>
<b>AC096751.1</b>	<b>PIK3CB</b>	<b>0.215</b>	<b>0.016978</b>
<b>AC096751.1</b>	<b>GLI2</b>	<b>0.215</b>	<b>0.016978</b>
<b>AC096751.1</b>	<b>SYNJ1</b>	<b>0.215</b>	<b>0.016978</b>
<b>AC096751.1</b>	<b>EHBP1L1</b>	<b>0.215</b>	<b>0.016978</b>
<b>AC096751.1</b>	<b>CRYZ</b>	<b>0.215</b>	<b>0.016978</b>
<b>AC096751.1</b>	<b>TSPAN1</b>	<b>0.215</b>	<b>0.016978</b>
<b>AC096751.1</b>	<b>SSFA2</b>	<b>0.215</b>	<b>0.016978</b>
<b>AC096751.1</b>	<b>RCAN1</b>	<b>0.215</b>	<b>0.016978</b>
<b>AC096751.1</b>	<b>MNX1</b>	<b>-0.203</b>	<b>0.017503</b>

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<b>AC096751.1</b>	<b>MEX3A</b>	<b>-0.203</b>	<b>0.017503</b>
<b>AC096751.1</b>	<b>SLC25A26</b>	<b>-0.203</b>	<b>0.017503</b>
<b>AC096751.1</b>	<b>ANKLE2</b>	<b>0.214</b>	<b>0.017511</b>
<b>AC096751.1</b>	<b>ITPRIPL2</b>	<b>0.214</b>	<b>0.017511</b>
<b>AC096751.1</b>	<b>CRYBA4</b>	<b>0.214</b>	<b>0.017511</b>
<b>AC096751.1</b>	<b>ETV7</b>	<b>0.214</b>	<b>0.017511</b>
<b>AC096751.1</b>	<b>GAREM1</b>	<b>0.214</b>	<b>0.017511</b>
<b>AC096751.1</b>	<b>SGMS1</b>	<b>0.214</b>	<b>0.017511</b>
<b>AC096751.1</b>	<b>AHR</b>	<b>0.214</b>	<b>0.017511</b>
<b>AC096751.1</b>	<b>BTNL8</b>	<b>0.214</b>	<b>0.017511</b>
<b>AC096751.1</b>	<b>PLEKHN1</b>	<b>0.214</b>	<b>0.017511</b>
<b>AC096751.1</b>	<b>SLC2A8</b>	<b>-0.202</b>	<b>0.018051</b>
<b>AC096751.1</b>	<b>MAP1LC3A</b>	<b>-0.202</b>	<b>0.018051</b>
<b>AC096751.1</b>	<b>TRIM68</b>	<b>-0.202</b>	<b>0.018051</b>
<b>AC096751.1</b>	<b>ZSCAN2</b>	<b>-0.202</b>	<b>0.018051</b>
<b>AC096751.1</b>	<b>SEPHS1</b>	<b>-0.202</b>	<b>0.018051</b>
<b>AC096751.1</b>	<b>RAET1E</b>	<b>0.213</b>	<b>0.01806</b>
<b>AC096751.1</b>	<b>RALB</b>	<b>0.213</b>	<b>0.01806</b>
<b>AC096751.1</b>	<b>AKR1B10</b>	<b>0.213</b>	<b>0.01806</b>
<b>AC096751.1</b>	<b>COL4A3BP</b>	<b>0.213</b>	<b>0.01806</b>
<b>AC096751.1</b>	<b>PRDX5</b>	<b>-0.201</b>	<b>0.018614</b>
<b>AC096751.1</b>	<b>MSRB2</b>	<b>-0.201</b>	<b>0.018614</b>
<b>AC096751.1</b>	<b>CHRM3</b>	<b>-0.201</b>	<b>0.018614</b>
<b>AC096751.1</b>	<b>SPAG9</b>	<b>0.212</b>	<b>0.018623</b>
<b>AC096751.1</b>	<b>NAPG</b>	<b>0.212</b>	<b>0.018623</b>
<b>AC096751.1</b>	<b>FSTL3</b>	<b>0.212</b>	<b>0.018623</b>
<b>AC096751.1</b>	<b>ROCK1</b>	<b>0.212</b>	<b>0.018623</b>
<b>AC096751.1</b>	<b>RPL15</b>	<b>-0.2</b>	<b>0.019192</b>
<b>AC096751.1</b>	<b>CAT</b>	<b>-0.2</b>	<b>0.019192</b>
<b>AC096751.1</b>	<b>SMTN</b>	<b>-0.2</b>	<b>0.019192</b>
<b>AC096751.1</b>	<b>ARHGEF19</b>	<b>-0.2</b>	<b>0.019192</b>
<b>AC096751.1</b>	<b>POLR3C</b>	<b>-0.2</b>	<b>0.019192</b>
<b>AC096751.1</b>	<b>NCOA2</b>	<b>0.211</b>	<b>0.019201</b>
<b>AC096751.1</b>	<b>CDCP1</b>	<b>0.211</b>	<b>0.019201</b>
<b>AC096751.1</b>	<b>IL6R</b>	<b>0.211</b>	<b>0.019201</b>
<b>AC096751.1</b>	<b>MAP3K6</b>	<b>0.211</b>	<b>0.019201</b>
<b>AC096751.1</b>	<b>BDKRB1</b>	<b>0.211</b>	<b>0.019201</b>
<b>AC096751.1</b>	<b>CDC42BPA</b>	<b>0.211</b>	<b>0.019201</b>
<b>AC096751.1</b>	<b>MAX</b>	<b>0.211</b>	<b>0.019201</b>
<b>AC096751.1</b>	<b>CAB39</b>	<b>0.211</b>	<b>0.019201</b>
<b>AC096751.1</b>	<b>ACTBL2</b>	<b>0.211</b>	<b>0.019201</b>
<b>AC096751.1</b>	<b>HLA-E</b>	<b>0.211</b>	<b>0.019201</b>
<b>AC096751.1</b>	<b>MUC17</b>	<b>0.211</b>	<b>0.019201</b>
<b>AC096751.1</b>	<b>HIPK1</b>	<b>0.21</b>	<b>0.019795</b>

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<b>AC096751.1</b>	DENND1C	0.21	0.019795
<b>AC096751.1</b>	SMPDL3A	0.21	0.019795
<b>AC096751.1</b>	C11orf86	0.21	0.019795
<b>AC096751.1</b>	BMP8B	0.21	0.019795
<b>AC096751.1</b>	CHMP2B	0.21	0.019795
<b>AC096751.1</b>	SEC24A	0.21	0.019795
<b>AC096751.1</b>	RNF144A	0.21	0.019795
<b>AC096751.1</b>	CAV1	0.209	0.020405
<b>AC096751.1</b>	SECTM1	0.209	0.020405
<b>AC096751.1</b>	UBR2	0.209	0.020405
<b>AC096751.1</b>	DSC2	0.209	0.020405
<b>AC096751.1</b>	SPATA5	0.209	0.020405
<b>AC096751.1</b>	PLEC	0.209	0.020405
<b>AC096751.1</b>	MAFF	0.209	0.020405
<b>AC096751.1</b>	AHNAK2	0.209	0.020405
<b>AC096751.1</b>	BCL10	0.208	0.021031
<b>AC096751.1</b>	TMBIM1	0.208	0.021031
<b>AC096751.1</b>	RAB12	0.208	0.021031
<b>AC096751.1</b>	RPS6KA5	0.208	0.021031
<b>AC096751.1</b>	ITIH4	0.208	0.021031
<b>AC096751.1</b>	SPATS2L	0.208	0.021031
<b>AC096751.1</b>	FEZ2	0.208	0.021031
<b>AC096751.1</b>	EDN3	0.208	0.021031
<b>AC096751.1</b>	ZCCHC2	0.208	0.021031
<b>AC096751.1</b>	HRASLS2	0.208	0.021031
<b>AC096751.1</b>	SI	0.208	0.021031
<b>AC096751.1</b>	IRF8	0.208	0.021031
<b>AC096751.1</b>	TFAP2A	0.207	0.021674
<b>AC096751.1</b>	PDE4D	0.207	0.021674
<b>AC096751.1</b>	PTPRU	0.207	0.021674
<b>AC096751.1</b>	PLLP	0.207	0.021674
<b>AC096751.1</b>	SLC2A5	0.207	0.021674
<b>AC096751.1</b>	S100A16	0.207	0.021674
<b>AC096751.1</b>	SGPP2	0.207	0.021674
<b>AC096751.1</b>	SP110	0.206	0.022335
<b>AC096751.1</b>	EPS8	0.206	0.022335
<b>AC096751.1</b>	IGSF5	0.206	0.022335
<b>AC096751.1</b>	CYTH1	0.206	0.022335
<b>AC096751.1</b>	S100A10	0.206	0.022335
<b>AC096751.1</b>	RBBP8	0.206	0.022335
<b>AC096751.1</b>	JAK2	0.205	0.023012
<b>AC096751.1</b>	ZNFX1	0.205	0.023012
<b>AC096751.1</b>	EVI5	0.205	0.023012
<b>AC096751.1</b>	IFIT5	0.205	0.023012

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<b>AC096751.1</b>	LMO7	0.205	0.023012
<b>AC096751.1</b>	ATP2B1	0.205	0.023012
<b>AC096751.1</b>	BBS7	0.205	0.023012
<b>AC096751.1</b>	MTUS1	0.204	0.023707
<b>AC096751.1</b>	TBC1D1	0.204	0.023707
<b>AC096751.1</b>	RBMXL1	0.204	0.023707
<b>AC096751.1</b>	ME1	0.204	0.023707
<b>AC096751.1</b>	NR3C2	0.204	0.023707
<b>AC096751.1</b>	BMP2	0.204	0.023707
<b>AC096751.1</b>	MXI1	0.203	0.024421
<b>AC096751.1</b>	SLC9A7	0.203	0.024421
<b>AC096751.1</b>	AARD	0.203	0.024421
<b>AC096751.1</b>	ASS1	0.203	0.024421
<b>AC096751.1</b>	CDA	0.203	0.024421
<b>AC096751.1</b>	RPE65	0.203	0.024421
<b>AC096751.1</b>	STAT1	0.203	0.024421
<b>AC096751.1</b>	SPATA46	0.203	0.024421
<b>AC096751.1</b>	FP565260.3	0.203	0.024421
<b>AC096751.1</b>	LCOR	0.202	0.025153
<b>AC096751.1</b>	ZDHHC18	0.202	0.025153
<b>AC096751.1</b>	ARHGEF18	0.202	0.025153
<b>AC096751.1</b>	LAMA3	0.202	0.025153
<b>AC096751.1</b>	RAMP1	0.202	0.025153
<b>AC096751.1</b>	TPCN2	0.202	0.025153
<b>AC096751.1</b>	DTX3L	0.202	0.025153
<b>AC096751.1</b>	AC020914.1	0.2	0.026674
<b>AC096751.1</b>	NKX3-1	0.2	0.026674
<b>AC096751.1</b>	KCNIP1	0.2	0.026674
<b>AC096751.1</b>	HHLA2	0.2	0.026674
<b>AC096751.1</b>	SLC45A4	0.2	0.026674
<b>AC096751.1</b>	CLCF1	0.2	0.026674
<b>AC096751.1</b>	PDP1	0.2	0.026674
<b>AC096751.1</b>	HLA-B	0.2	0.026674
<b>AC096751.1</b>	NCR1	0.2	0.026674
<b>AC096751.1</b>	FECH	0.2	0.026674

**Table S3.**Survival analysis results of AC096751.1 co-expressed genes (Only gene list with P<0.05 is shown ).

<b>ID</b>	<b>P</b>	<b>HR</b>	<b>Low 95%CI</b>	<b>High 95%CI</b>
<b>DAPK1</b>	0.002093399	1.946256078	1.273405483	2.974632018
<b>EVI5</b>	0.00210591	0.502695535	0.324274713	0.779286176
<b>CRYBA4</b>	0.004681786	1.848958507	1.20765074	2.830824713
<b>KCTD1</b>	0.00826329	1.766290773	1.158025855	2.694053055
<b>DPCR1</b>	0.010646043	1.74395656	1.138116395	2.67229652
<b>ENO2</b>	0.011888209	1.729654848	1.128621112	2.650761943
<b>PHLPP2</b>	0.018535165	0.605717061	0.39906461	0.919382848
<b>SLMAP</b>	0.019496164	0.610854644	0.403949433	0.923737888
<b>BCL10</b>	0.020595917	0.607591107	0.398504742	0.926380327
<b>CYP39A1</b>	0.021761359	0.61571128	0.406877283	0.931731499
<b>RAPH1</b>	0.02180111	0.611877998	0.402141925	0.931001374
<b>RPS6KA5</b>	0.022551623	0.610973258	0.400088503	0.93301437
<b>HIPK1</b>	0.024819195	0.622342649	0.411288391	0.94170023
<b>FGFR4</b>	0.026558587	0.619632194	0.405925141	0.945849413
<b>GNA13</b>	0.027605398	0.626467405	0.413229031	0.949743073
<b>NMU</b>	0.031748336	1.585489847	1.041082907	2.414580088
<b>TGFBI</b>	0.035851527	0.639686146	0.42145633	0.970915221
<b>SLC2A5</b>	0.040183693	1.542052002	1.019586205	2.332244556
<b>ADAM9</b>	0.04050391	0.647144756	0.426754196	0.98135259
<b>SEC24A</b>	0.041295492	0.648328635	0.427585651	0.98303116
<b>EFNA4</b>	0.042195168	0.650934846	0.430178796	0.984976894
<b>CHMP2B</b>	0.043383665	0.653217658	0.432127815	0.987423846
<b>SLC25A26</b>	0.045173679	0.656052247	0.434323254	0.990977449

**Table S4.** Functional enrichment analysis results of AC096751.1 co-expressed genes

Category	Term	Count	P Value
KEGG_PATHWAY	hsa05200:Pathways in cancer	24	4.10E-04
KEGG_PATHWAY	hsa05168:Herpes simplex infection	15	4.55E-04
KEGG_PATHWAY	hsa05222:Small cell lung cancer	9	0.002137336
KEGG_PATHWAY	hsa05416:Viral myocarditis	7	0.004386428
KEGG_PATHWAY	hsa04668:TNF signaling pathway	9	0.008713227
KEGG_PATHWAY	hsa05332:Graft-versus-host disease	5	0.011899509
KEGG_PATHWAY	hsa04612:Antigen processing and presentation	7	0.017281288
KEGG_PATHWAY	hsa05330:Allograft rejection	5	0.017653712
KEGG_PATHWAY	hsa04940:Type I diabetes mellitus	5	0.026940128
KEGG_PATHWAY	hsa04810:Regulation of actin cytoskeleton	12	0.029018217
KEGG_PATHWAY	hsa05145:Toxoplasmosis	8	0.030561909
KEGG_PATHWAY	hsa02010:ABC transporters	5	0.031336006
KEGG_PATHWAY	hsa00600:Sphingolipid metabolism	5	0.038676926
KEGG_PATHWAY	hsa05140:Leishmaniasis	6	0.044129353
KEGG_PATHWAY	hsa04071:Sphingolipid signaling pathway	8	0.045659678
GOTERM_CC_DIRECT	GO:0045121~membrane raft	24	1.37E-09
GOTERM_BP_DIRECT	GO:0060333~interferon-gamma-mediated signaling pathway	13	1.60E-07
GOTERM_BP_DIRECT	GO:0007165~signal transduction	58	5.81E-07
GOTERM_CC_DIRECT	GO:0005886~plasma membrane	144	1.90E-06
GOTERM_CC_DIRECT	GO:0070062~extracellular exosome	102	2.79E-05
GOTERM_CC_DIRECT	GO:0005765~lysosomal membrane	20	4.70E-05
GOTERM_CC_DIRECT	GO:0048471~perinuclear region of cytoplasm	33	6.16E-05
GOTERM_MF_DIRECT	GO:0005102~receptor binding	23	7.63E-05
GOTERM_CC_DIRECT	GO:0005737~cytoplasm	165	9.32E-05
GOTERM_MF_DIRECT	GO:0005515~protein binding	257	9.73E-05
GOTERM_CC_DIRECT	GO:0016324~apical plasma membrane	20	1.05E-04
GOTERM_CC_DIRECT	GO:0000139~Golgi membrane	30	3.14E-04
GOTERM_CC_DIRECT	GO:0005856~cytoskeleton	22	3.33E-04
GOTERM_CC_DIRECT	GO:0005794~Golgi apparatus	39	3.35E-04
GOTERM_MF_DIRECT	GO:0042803~protein homodimerization activity	35	3.38E-04
GOTERM_CC_DIRECT	GO:0005913~cell-cell adherens junction	20	3.94E-04
GOTERM_BP_DIRECT	GO:0043547~positive regulation of GTPase activity	29	4.32E-04
GOTERM_BP_DIRECT	GO:0002474~antigen processing and presentation of peptide antigen via MHC class I	6	7.87E-04
GOTERM_BP_DIRECT	GO:0006939~smooth muscle contraction	5	8.70E-04
GOTERM_BP_DIRECT	GO:0060337~type I interferon signaling pathway	8	0.001016401
GOTERM_BP_DIRECT	GO:0032436~positive regulation of proteasomal ubiquitin-dependent protein catabolic process	8	0.001016401
GOTERM_CC_DIRECT	GO:0005829~cytosol	108	0.001034324
GOTERM_CC_DIRECT	GO:0016020~membrane	77	0.001075629
GOTERM_BP_DIRECT	GO:0030148~sphingolipid biosynthetic process	7	0.001148912
GOTERM_BP_DIRECT	GO:0002250~adaptive immune response	12	0.00118282

<b>GOTERM_CC_DIRECT</b>	GO:0005768~endosome	15	0.001319108
<b>GOTERM_CC_DIRECT</b>	GO:0005764~lysosome	15	0.001375498
<b>GOTERM_MF_DIRECT</b>	GO:0008289~lipid binding	12	0.001386535
<b>GOTERM_MF_DIRECT</b>	GO:0005125~cytokine activity	13	0.001512396
<b>GOTERM_CC_DIRECT</b>	GO:0005925~focal adhesion	21	0.001584375
<b>GOTERM_BP_DIRECT</b>	GO:0050714~positive regulation of protein secretion	6	0.001842935
<b>GOTERM_BP_DIRECT</b>	GO:0006915~apoptotic process	27	0.002059684
<b>GOTERM_BP_DIRECT</b>	GO:0008283~cell proliferation	20	0.002097451
<b>GOTERM_BP_DIRECT</b>	GO:0035970~peptidyl-threonine dephosphorylation	4	0.00216249
<b>GOTERM_MF_DIRECT</b>	GO:0098641~cadherin binding involved in cell-cell adhesion	17	0.002509195
<b>GOTERM_BP_DIRECT</b>	GO:0007173~epidermal growth factor receptor signaling pathway	7	0.002574223
<b>GOTERM_BP_DIRECT</b>	GO:0070373~negative regulation of ERK1 and ERK2 cascade	7	0.003078721
<b>GOTERM_BP_DIRECT</b>	GO:0034612~response to tumor necrosis factor	5	0.003135578
<b>GOTERM_CC_DIRECT</b>	GO:0005903~brush border	7	0.003369631
<b>GOTERM_BP_DIRECT</b>	GO:0031018~endocrine pancreas development	5	0.003634017
<b>GOTERM_BP_DIRECT</b>	GO:0016477~cell migration	12	0.003853907
<b>GOTERM_MF_DIRECT</b>	GO:0042605~peptide antigen binding	5	0.004778395
<b>GOTERM_CC_DIRECT</b>	GO:0016323~basolateral plasma membrane	12	0.004803495
<b>GOTERM_MF_DIRECT</b>	GO:0004871~signal transducer activity	13	0.005062333
<b>GOTERM_BP_DIRECT</b>	GO:0071549~cellular response to dexamethasone stimulus	5	0.005445393
<b>GOTERM_BP_DIRECT</b>	GO:0000186~activation of MAPKK activity	6	0.005473974
<b>GOTERM_BP_DIRECT</b>	GO:0009267~cellular response to starvation	6	0.006003441
<b>GOTERM_CC_DIRECT</b>	GO:0031234~extrinsic component of cytoplasmic side of plasma membrane	7	0.006261178
<b>GOTERM_BP_DIRECT</b>	GO:0006810~transport	18	0.006351654
<b>GOTERM_CC_DIRECT</b>	GO:0009986~cell surface	24	0.007516947
<b>GOTERM_BP_DIRECT</b>	GO:0008285~negative regulation of cell proliferation	19	0.010241769
<b>GOTERM_CC_DIRECT</b>	GO:0046581~intercellular canaliculus	3	0.011517577
<b>GOTERM_BP_DIRECT</b>	GO:0019882~antigen processing and presentation	6	0.011593807
<b>GOTERM_BP_DIRECT</b>	GO:0050852~T cell receptor signaling pathway	10	0.011691908
<b>GOTERM_MF_DIRECT</b>	GO:0008134~transcription factor binding	15	0.011747008
<b>GOTERM_CC_DIRECT</b>	GO:0016021~integral component of membrane	149	0.012082895
<b>GOTERM_MF_DIRECT</b>	GO:0046983~protein dimerization activity	10	0.012647885
<b>GOTERM_CC_DIRECT</b>	GO:0030176~integral component of endoplasmic reticulum membrane	8	0.01380885
<b>GOTERM_BP_DIRECT</b>	GO:0042517~positive regulation of tyrosine phosphorylation of Stat3 protein	5	0.014213954
<b>GOTERM_BP_DIRECT</b>	GO:0071407~cellular response to organic cyclic compound	6	0.015402059
<b>GOTERM_BP_DIRECT</b>	GO:0006953~acute-phase response	5	0.015535716
<b>GOTERM_MF_DIRECT</b>	GO:0005518~collagen binding	6	0.016438932
<b>GOTERM_BP_DIRECT</b>	GO:0048661~positive regulation of smooth muscle cell proliferation	6	0.016470103
<b>GOTERM_BP_DIRECT</b>	GO:0010508~positive regulation of autophagy	5	0.016932325

<b>GOTERM_BP_DIRECT</b>	GO:0098609~cell-cell adhesion	14	0.018244476
<b>GOTERM_MF_DIRECT</b>	GO:0046934~phosphatidylinositol-4,5-bisphosphate 3-kinase activity	6	0.01871617
<b>GOTERM_MF_DIRECT</b>	GO:0046703~natural killer cell lectin-like receptor binding	3	0.019712865
<b>GOTERM_BP_DIRECT</b>	GO:0002480~antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-independent	3	0.019731328
<b>GOTERM_CC_DIRECT</b>	GO:0005615~extracellular space	46	0.01976956
<b>GOTERM_BP_DIRECT</b>	GO:0006979~response to oxidative stress	8	0.019828792
<b>GOTERM_CC_DIRECT</b>	GO:0005901~caveola	6	0.021162436
<b>GOTERM_BP_DIRECT</b>	GO:0030155~regulation of cell adhesion	5	0.021582427
<b>GOTERM_BP_DIRECT</b>	GO:0031623~receptor internalization	5	0.021582427
<b>GOTERM_MF_DIRECT</b>	GO:0042626~ATPase activity, coupled to transmembrane movement of substances	5	0.023252335
<b>GOTERM_MF_DIRECT</b>	GO:0043236~laminin binding	4	0.023292493
<b>GOTERM_BP_DIRECT</b>	GO:0015949~nucleobase-containing small molecule interconversion	4	0.023322355
<b>GOTERM_BP_DIRECT</b>	GO:0000188~inactivation of MAPK activity	4	0.023322355
<b>GOTERM_MF_DIRECT</b>	GO:0019911~structural constituent of myelin sheath	3	0.024241121
<b>GOTERM_BP_DIRECT</b>	GO:0008015~blood circulation	5	0.025075547
<b>GOTERM_BP_DIRECT</b>	GO:0007267~cell-cell signaling	13	0.025265057
<b>GOTERM_BP_DIRECT</b>	GO:0032355~response to estradiol	7	0.025748741
<b>GOTERM_BP_DIRECT</b>	GO:0042552~myelination	5	0.026942364
<b>GOTERM_CC_DIRECT</b>	GO:0042612~MHC class I protein complex	3	0.028281188
<b>GOTERM_CC_DIRECT</b>	GO:0043296~apical junction complex	3	0.028281188
<b>GOTERM_BP_DIRECT</b>	GO:0071230~cellular response to amino acid stimulus	5	0.02889017
<b>GOTERM_BP_DIRECT</b>	GO:0070166~enamel mineralization	3	0.029175003
<b>GOTERM_BP_DIRECT</b>	GO:0007175~negative regulation of epidermal growth factor-activated receptor activity	3	0.029175003
<b>GOTERM_BP_DIRECT</b>	GO:0046854~phosphatidylinositol phosphorylation	7	0.029592511
<b>GOTERM_CC_DIRECT</b>	GO:0005813~centrosome	18	0.032967339
<b>GOTERM_BP_DIRECT</b>	GO:0036092~phosphatidylinositol-3-phosphate biosynthetic process	5	0.033030657
<b>GOTERM_CC_DIRECT</b>	GO:0071556~integral component of luminal side of endoplasmic reticulum membrane	4	0.033033828
<b>GOTERM_CC_DIRECT</b>	GO:0005789~endoplasmic reticulum membrane	31	0.033407473
<b>GOTERM_CC_DIRECT</b>	GO:0043231~intracellular membrane-bounded organelle	22	0.033656529
<b>GOTERM_BP_DIRECT</b>	GO:0006955~immune response	18	0.034076904
<b>GOTERM_MF_DIRECT</b>	GO:0000983~transcription factor activity, RNA polymerase II core promoter sequence-specific	3	0.034412471
<b>GOTERM_BP_DIRECT</b>	GO:0030212~hyaluronan metabolic process	3	0.0344439
<b>GOTERM_BP_DIRECT</b>	GO:0071985~multivesicular body sorting pathway	3	0.0344439
<b>GOTERM_BP_DIRECT</b>	GO:0031581~hemidesmosome assembly	3	0.0344439
<b>GOTERM_MF_DIRECT</b>	GO:0019904~protein domain specific binding	11	0.034887836
<b>GOTERM_CC_DIRECT</b>	GO:0030659~cytoplasmic vesicle membrane	8	0.035039436



<b>GOTERM_BP_DIRECT</b>	GO:0006468~protein phosphorylation	19	0.036113396
<b>GOTERM_CC_DIRECT</b>	GO:0031982~vesicle	8	0.037669909
<b>GOTERM_CC_DIRECT</b>	GO:0012507~ER to Golgi transport vesicle membrane	5	0.03785539
<b>GOTERM_BP_DIRECT</b>	GO:0034097~response to cytokine	5	0.039858342
<b>GOTERM_BP_DIRECT</b>	GO:0016337~single organismal cell-cell adhesion	7	0.039972213
<b>GOTERM_MF_DIRECT</b>	GO:0017017~MAP kinase tyrosine/serine/threonine phosphatase activity	3	0.040013397
<b>GOTERM_BP_DIRECT</b>	GO:0048546~digestive tract morphogenesis	3	0.040049631
<b>GOTERM_BP_DIRECT</b>	GO:0010288~response to lead ion	3	0.040049631
<b>GOTERM_BP_DIRECT</b>	GO:0042981~regulation of apoptotic process	11	0.04040461
<b>GOTERM_BP_DIRECT</b>	GO:0030324~lung development	6	0.040561252
<b>GOTERM_BP_DIRECT</b>	GO:0006869~lipid transport	6	0.040561252
<b>GOTERM_BP_DIRECT</b>	GO:0000209~protein polyubiquitination	10	0.04056262
<b>GOTERM_CC_DIRECT</b>	GO:0005887~integral component of plasma membrane	46	0.04136926
<b>GOTERM_BP_DIRECT</b>	GO:0007259~JAK-STAT cascade	4	0.044320235
<b>GOTERM_BP_DIRECT</b>	GO:0007498~mesoderm development	4	0.044320235
<b>GOTERM_BP_DIRECT</b>	GO:0014066~regulation of phosphatidylinositol 3-kinase signaling	6	0.044558434
<b>GOTERM_MF_DIRECT</b>	GO:0019003~GDP binding	5	0.04475615
<b>GOTERM_BP_DIRECT</b>	GO:0007411~axon guidance	9	0.045125926
<b>GOTERM_BP_DIRECT</b>	GO:0003407~neural retina development	3	0.045972305
<b>GOTERM_BP_DIRECT</b>	GO:0071364~cellular response to epidermal growth factor stimulus	4	0.047884246
<b>GOTERM_BP_DIRECT</b>	GO:0043123~positive regulation of I-kappaB kinase/NF-kappaB signaling	9	0.047945551
<b>GOTERM_BP_DIRECT</b>	GO:0048015~phosphatidylinositol-mediated signaling	7	0.048641276
<b>GOTERM_BP_DIRECT</b>	GO:0046967~cytosol to ER transport	2	0.04905126
<b>GOTERM_CC_DIRECT</b>	GO:0001772~immunological synapse	4	0.049514809

**Table S5.**GSEA analysis results between high - and low -AC096751.1 phenotypes in COAD

<b>NAME</b>	<b>SIZ</b>	<b>ES</b>	<b>NES</b>	<b>NOM</b>	<b>FDR</b>
	<b>E</b>			<b>p-val</b>	<b>q-val</b>
<b>GOBP_MITOCHONDRIAL_ELECTRON_TRANSPORT_CYTOCHROME_C_TO_OXYGEN</b>	19	0.8097	1.8951	<0.01	0.2409
		5765	869		0937
<b>GOBP_PYRIMIDINE_RIBONUCLEOSIDE_TRIPHOSPHATE_METABOLIC_PROCESS</b>	18	0.6589	1.8834	0.00199	0.2094
		0646	474	6008	7339
<b>GOBP_RIBOSOMAL_SMALL_SUBUNIT_ASSEMBLY</b>	19	0.7950	1.8794	0.00200	0.2010
		74	417	8032	365
<b>HP_MACROCYTIC_ANEMIA</b>	56	0.6040	1.9071	0.00200	0.2495
		6446	213	8032	2225
<b>HP_ABNORMALITY_OF_THE_MUSCULATURE_OF_THE_HAND</b>	86	0.4852	1.8840	0.00204	0.2210
		0508	91	499	944
<b>GOBP_PYRIMIDINE_NUCLEOTIDE_METABOLIC_PROCESS</b>	49	0.5522	1.8774	0.00385	0.1949
		471	265	3565	6028
<b>GOCC_SMALL_RIBOSOMAL_SUBUNIT</b>	71	0.7418	1.8859	0.00398	0.2393
		0776	416	4064	4138
<b>HP_ERYTHROID_HYPOPLASIA</b>	24	0.8169	1.8959	0.00575	0.2486
		176	482	8158	0276
<b>HP_PERSISTENCE_OF_HEMOGLOBIN_F</b>	28	0.7473	1.8698	0.00582	0.1903
		389	34	5243	4462
<b>HP_DEVELOPMENTAL_GLAUCOMA</b>	60	0.5488	1.8760	0.00591	0.1880
		402	072	716	4759
<b>HP_PARTIAL_DUPLICATION_OF_THE_PHALANX_OF_HAND</b>	38	0.6239	1.9027	0.00773	0.2406
		7784	42	6944	28
<b>HP_ELEVATED_RED_CELL_ADENOSINE_DEAMINASE_LEVEL</b>	21	0.8364	1.8197	0.00775	0.2208
		585	936	1938	3934
<b>HP_NONIMMUNE_HYDROPS_FETALIS</b>	40	0.6683	1.8779	0.00784	0.1989
		55	552	3138	1496

<b>HP_SPRENGEL_ANOMALY</b>	49	0.5791	1.8853	0.00796	0.2326
		8614	256	8128	9795
<b>GOCC_RESPIRASOME</b>	97	0.7015	1.9069	0.00796	0.2390
		9495	755	8128	6949
<b>GOCC_LARGE_RIBOSOMAL_SUBUNIT</b>	114	0.7398	1.8796	0.00798	0.2062
		391	082	4032	7543
<b>GOBP_GLYCOSYL_COMPOUND_BIOSYNTHETIC_PROCESS</b>	40	0.6155	1.8843	0.008	0.2273
		5165	865		2924
<b>GOBP_POSITIVE_REGULATION_OF_VIRAL_TRANSCRIPTION</b>	26	0.6461	1.8925	0.01008	0.2384
		892	848	0645	8051
<b>HP_MALIGNANT_GENITOURINARY_TRACT_TUMOR</b>	25	0.7796	1.8254	0.01158	0.2129
		479	523	3012	4136
<b>HP_PURE_RED_CELL_APLASIA</b>	24	0.7858	1.8163	0.01158	0.2208
		8164	51	3012	4205
<b>GOBP_PYRIMIDINE_NUCLEOTIDE_BIOSYNTHETIC_PROCESS</b>	29	0.6148	1.8372	0.01169	0.2107
		1655	493	5907	2827
<b>GOCC_CYTOCHROME_COMPLEX</b>	35	0.7108	1.8537	0.012	0.2052
		879	82		9208
<b>HP_APLASIA_OF_THE_FINGERS</b>	65	0.5068	1.8170	0.012	0.2230
		1686	01		8485
<b>HP_THROMBOCYTOSIS</b>	48	0.5769	1.8474	0.01207	0.2103
		792	312	2435	4196
<b>HP_INCREASED_MEAN_CORPUSCULAR_VOLUME</b>	36	0.6408	1.8373	0.01377	0.2145
		331	37	9528	4826
<b>GOCC_RESPIRATORY_CHAIN_COMPLEX</b>	83	0.7057	1.8836	0.01380	0.2153
		394	89	6706	4465
<b>GOBP_PYRIMIDINE_RIBONUCLEOTIDE_BIOSYNTHETIC_PROCESS</b>	22	0.6492	1.8457	0.01386	0.2097
		74	6	1386	2957
<b>GOBP_ATP_SYNTHESIS_COUPLED_ELECTRON_TRANSPORT</b>	97	0.7013	1.8657	0.01397	0.1899

		052	482	2056	5367
<b>GOBP_TRANSLATIONAL_INITIATION</b>	187	0.6253	1.8907	0.01541	0.2346
		4344	079	4258	656
<b>HP_DUPLICATION_OF_THUMB_PHALANX</b>	52	0.5609	1.8402	0.01596	0.2127
		048	189	8064	6551
<b>HP_RETICULOCYTOPENIA</b>	33	0.6592	1.8338	0.01714	0.2100
		152	314	2856	4379
<b>HP_ABSENT_THUMB</b>	43	0.5928	1.8061	0.01778	0.2245
		2184	135	656	7473
<b>GOBP_NUCLEAR_TRANSCRIBED_MRNA_CATABOLIC_PROCESS_NONSENSE_MEDIATED_DECAY</b>	120	0.6876	1.8699	0.01785	0.1946
		306	847	7144	0963
<b>GOCC_NADH_DEHYDROGENASE_COMPLEX</b>	47	0.7240	1.8095	0.01785	0.2242
		4844	207	7144	4042
<b>GOMF_HEME_COPPER_TERMINAL_OXIDASE_ACTIVITY</b>	27	0.7138	1.8410	0.01792	0.2149
		9174	796	8287	5976
<b>GOCC_POLYSOME</b>	68	0.5861	1.8118	0.01953	0.2229
		052	67	125	9328
<b>GOBP_RIBOSOME_ASSEMBLY</b>	59	0.6545	1.8148	0.01980	0.2205
		0543	459	198	792
<b>HP_OSTEOSARCOMA</b>	32	0.6886	1.8510	0.02067	0.2067
		585	729	6691	493
<b>GOBP_PROTEIN_LOCALIZATION_TO_ENDOPLASMIC_RETICULUM</b>	142	0.6407	1.8588	0.02148	0.1994
		394	123	4375	3988
<b>HP_ABNORMAL_NUMBER_OF_ERYTHROID_PRECURSORS</b>	35	0.6831	1.8329	0.02169	0.2012
		0463	296	6253	5581
<b>GOBP_NUCLEAR_TRANSCRIBED_MRNA_CATABOLIC_PROCESS</b>	199	0.5579	1.8339	0.02325	0.2136
		004	305	5814	806
<b>GOCC_INNER_MITOCHONDRIAL_MEMBRANE_PROTEIN_COMPLEX</b>	115	0.6654	1.8804	0.02366	0.2101
		8157	523	864	2625

<b>GOMF_RRNA_BINDING</b>	59	0.6754	1.8336	0.024	0.2066
		749	972		01
<b>KIM_ALL_DISORDERS_DURATION_CORR_DN</b>	140	0.6540	1.9901	0.00200	0.1498
		722	317	4008	4359
<b>REACTOME_CELLULAR_RESPONSE_TO_STARVATION</b>	152	0.7049	2.0064	0.00610	0.1528
		533	285	998	479
<b>POMEROY_MEDULLOBLASTOMA_PROGNOSIS_DN</b>	41	0.7308	2.0160	0.00396	0.1538
		307	6	0396	171
<b>ABE_INNER_EAR</b>	40	0.6629	1.9954	<0.01	0.1565
		771	26		3266
<b>BILANGES_SERUM_RESPONSE_TRANSLATION</b>	31	0.7599	2.0213	<0.01	0.1670
		049	73		9052
<b>PECE_MAMMARY_STEM_CELL_UP</b>	129	0.6893	2.0873	<0.01	0.1765
		1526	373		1685
<b>REACTOME_SELENOAMINO_ACID_METABOLISM</b>	108	0.7819	1.9385	0.00606	0.1793
		981	908	0606	4799
<b>REACTOME_SIGNALING_BY_ROBO_RECEPTORS</b>	211	0.5846	1.9180	0.01375	0.1814
		635	821	2456	2438
<b>REACTOME_METABOLISM_OF_AMINO_ACIDS_AND_DERIVATIVES</b>	351	0.5553	1.9417	0.01192	0.1843
		761	307	843	0115
<b>REACTOME_ABORTIVE_ELONGATION_OF_HIV_1_TRANSCRIPT_IN_THE_ABSENCE_OF_TAT</b>	23	0.7153	1.9203	0.00787	0.1862
		411	76	4016	203
<b>REACTOME_SULFUR_AMINO_ACID_METABOLISM</b>	27	0.6797	2.0255	<0.01	0.1888
		315	697		2619
<b>IRITANI_MAD1_TARGETS_DN</b>	44	0.6950	1.9038	0.00766	0.1929
		7444	482	2835	095
<b>HOLLEMAN_ASParAGINASE_RESISTANCE_B_ALL_UP</b>	24	0.7625	1.9218	0.00580	0.1935
		29	668	2708	6276
<b>BILANGES_SERUM_AND_RAPAMYCIN_SENSITIVE_GENES</b>	65	0.7924	1.9427	0.00397	0.1951

		459	29	6143	6295
<b>LU_EZH2_TARGETS_UP</b>	266	0.5557	1.9068	0.00986	0.1961
		083	847	1933	1442
<b>LI_DCP2_BOUND_MRNA</b>	86	0.6638	1.9477	<0.01	0.1984
		779	97		0229
<b>REACTOME_RESPONSE_OF_EIF2AK4_GCN2_TO_AMINO_ACID_DEFICIENCY</b>	101	0.7863	1.8972	0.00801	0.1994
		9054	919	6032	1425
<b>REACTOME_GLYCOGEN_STORAGE_DISEASES</b>	16	0.6988	1.9237	<0.01	0.1996
		649	996		9879
<b>HOLLEMAN_VINCRIStINE_RESISTANCE_ALL_DN</b>	20	0.8265	2.1197	<0.01	0.2036
		086	588		4022
<b>REACTOME_EUKARYOTIC_TRANSLATION_INITIATION</b>	119	0.7648	1.8875	0.01	0.2037
		525	512		6892
<b>SCHLOSSER_MYC_AND_SERUM_RESPONSE_SYNERGY</b>	31	0.7730	1.9587	<0.01	0.2053
		823	839		3678
<b>MODY_HIPPOCAMPUS_PRENATAL</b>	40	0.7057	1.9519	0.00584	0.2055
		355	062	7953	3882
<b>REACTOME_NONSENSE_MEDIATED_DECAY_NMD</b>	115	0.7192	1.8898	0.01964	0.2068
		848	947	6365	6089
<b>KEGG_RNA_POLYMERASE</b>	27	0.7189	2.0328	0.00194	0.2110
		6124	858	1748	4845
<b>REACTOME_REGULATION_OF_EXPRESSION_OF_SLITS_AND_ROBOS</b>	167	0.6611	1.8800	0.01789	0.2116
		499	644	2644	7171
<b>SANSOM_APC_TARGETS_REQUIRE_MYC</b>	211	0.5263	1.8758	0.00588	0.2124
		152	723	2353	5995
<b>YAMASHITA_LIVER_CANCER_WITH_EPCAM_UP</b>	53	0.6332	1.8616	0.01553	0.2135
		689	396	3981	7
<b>CHNG_MULTIPLE_MYELOMA_HYPERPLOID_UP</b>	53	0.8681	2.0510	<0.01	0.2163
		068	442		1287

<b>REACTOME_INFLUENZA_INFECTION</b>	155	0.6626	1.8695	0.01832	0.2183
		491	244	9939	0134
<b>LEE_LIVER_CANCER_MYC_UP</b>	50	0.5221	1.8616	<0.01	0.2206
		27	784		3102
<b>KEGG_HUNTINGTONS_DISEASE</b>	161	0.5381	1.8552	0.00988	0.2206
		4065	914	1423	4999
<b>WP_CYTOPLASMIC_RIBOSOMAL_PROTEINS</b>	88	0.8081	1.8486	0.00608	0.2211
		169	186	5193	3793
<b>ANDERSEN_LIVER_CANCER_KRT19_UP</b>	34	0.7039	1.8510	0.00595	0.2226
		739	748	2381	4992
<b>HEDENFALK_BREAST_CANCER_BRACX_UP</b>	18	0.6628	1.8617	0.00617	0.2280
		1587	351	284	4987
<b>REACTOME_EUKARYOTIC_TRANSLATION_ELONGATION</b>	93	0.8152	1.8366	0.00617	0.2408
		0456	524	284	7116
<b>REACTOME_ACTIVATION_OF_THE_MRNA_UPON_BINDING_OF_THE_CAP_BINDING_COMPLEX _AND_EIFS_AND_SUBSEQUENT_BINDING_TO_43S</b>	59	0.7443	1.8269	0.01603	0.2419
		236	695	2064	3038
<b>KEGG_RIBOSOME</b>	87	0.8197	1.8240	0.00609	0.2420
		25	659	7561	3016
<b>REACTOME_SRP_DEPENDENT_COTRANSLATIONAL_PROTEIN_TARGETING_TO_MEMBRANE</b>	112	0.7434	1.8287	0.026	0.2444
		9856	617		8845
<b>REACTOME_RNA_POLYMERASE_III_CHAIN_ELONGATION</b>	18	0.6752	1.8306	0.00596	0.2471
		262	139	4215	056

**Table S6.** DEG between high - and low -AC096751.1 phenotypes in COAD

<b>ID</b>	<b>Log FC</b>	<b>Log CPM</b>	<b>P value</b>	<b>FDR</b>
<b>PAEP</b>	5.455820773	3.325170379	2.14E-51	3.76E-47
<b>NNAT</b>	-2.462139553	2.406100716	4.35E-35	3.81E-31
<b>CHRNA4</b>	3.87875452	-2.832738107	5.15E-29	3.01E-25
<b>HPGD</b>	-1.380231843	5.085415306	9.06E-29	3.97E-25
<b>SFTPC</b>	-5.868055242	0.157546519	1.19E-28	4.19E-25
<b>UTS2B</b>	-2.238340142	-1.921312495	1.75E-26	5.11E-23
<b>CALCA</b>	3.163409564	2.10559192	8.99E-26	2.25E-22
<b>COL2A1</b>	2.822532384	2.055521233	3.13E-25	6.85E-22
<b>TFAP2B</b>	4.814463555	-2.05169447	5.07E-25	9.87E-22
<b>COLEC10</b>	-1.901340754	-1.217024581	1.72E-24	3.02E-21
<b>CLEC2A</b>	4.189372656	-2.663736615	7.42E-24	1.18E-20
<b>GCG</b>	-3.277575242	1.721928869	1.84E-22	2.68E-19
<b>NEUROD4</b>	3.766214905	-3.476906121	6.68E-21	9.01E-18
<b>ZNF479</b>	3.899499629	-3.281261692	1.19E-20	1.49E-17
<b>UGT3A1</b>	3.572165938	-2.997036039	1.38E-20	1.62E-17
<b>IGDCC3</b>	2.563253926	-0.993600729	7.39E-20	8.09E-17
<b>SULT1C4</b>	1.946011809	1.66166825	2.22E-19	2.29E-16
<b>DPCR1</b>	-2.474726603	-0.641051447	5.47E-19	5.33E-16
<b>NMRK2</b>	3.282380553	-2.694089472	1.01E-18	9.30E-16
<b>LHX3</b>	2.858201606	-2.490324291	1.61E-18	1.41E-15
<b>GALP</b>	3.51559122	-3.499260293	1.72E-18	1.43E-15
<b>IRGM</b>	2.272557372	-2.634843472	2.04E-18	1.63E-15
<b>SPRR2E</b>	3.827456634	0.205928492	5.86E-18	4.46E-15
<b>IGF2</b>	2.563406708	10.49892132	7.75E-18	5.66E-15
<b>SFTPA1</b>	-3.439079681	-0.478289005	8.42E-18	5.91E-15
<b>MYBPC3</b>	-1.48711947	-0.72412177	1.04E-17	7.03E-15
<b>CHRND</b>	2.779526746	-2.042282053	1.68E-17	1.08E-14
<b>CPA1</b>	-3.415027205	-1.881128102	1.73E-17	1.08E-14
<b>LRP1B</b>	2.14079152	-1.579753304	3.92E-17	2.37E-14
<b>FGF6</b>	2.91374155	-3.712582017	6.94E-17	3.92E-14
<b>NCAN</b>	2.069471865	-2.591667918	7.81E-17	4.28E-14
<b>CRNN</b>	3.121376294	-3.60935195	8.49E-17	4.51E-14
<b>TEX19</b>	1.666377162	-1.836186616	9.36E-17	4.83E-14
<b>KRT78</b>	2.822613577	-2.021934903	1.13E-16	5.57E-14
<b>SPRR2B</b>	3.129010161	-3.678003165	1.14E-16	5.57E-14
<b>CER1</b>	2.520803791	-2.203849013	1.47E-16	6.85E-14
<b>HSF5</b>	-1.99545602	-2.612251274	1.48E-16	6.85E-14
<b>PSCA</b>	-2.380693502	2.753820518	1.73E-16	7.79E-14
<b>SOHLH1</b>	3.217355233	-0.87598646	1.96E-16	8.59E-14
<b>TCAP</b>	-1.342674905	0.49314832	2.07E-16	8.85E-14
<b>CACNG6</b>	2.571855257	-2.348208956	2.26E-16	9.44E-14
<b>PPP1R17</b>	2.936777338	-3.121890288	2.53E-16	1.03E-13



<b>LCE3D</b>	3.16397936	-3.504363046	5.08E-16	2.02E-13
<b>ALK</b>	-2.076681305	-1.875248666	5.62E-16	2.19E-13
<b>BTBD18</b>	-1.748492802	-2.427795621	6.52E-16	2.45E-13
<b>NLRP4</b>	2.427579094	-2.462632298	6.58E-16	2.45E-13
<b>COX8C</b>	2.486207698	-3.403147774	7.59E-16	2.77E-13
<b>UNCX</b>	3.181024653	-2.975161822	1.86E-15	6.51E-13
<b>PAX2</b>	1.931472173	-2.011428735	1.96E-15	6.75E-13
<b>PRSS56</b>	3.0779817	2.524854341	2.50E-15	8.44E-13
<b>ADAD2</b>	-2.074390989	-2.246377052	3.51E-15	1.16E-12
<b>KRTAP4-6</b>	3.125411344	-3.474655447	9.14E-15	2.91E-12
<b>AIRE</b>	1.96966077	0.107194373	1.53E-14	4.72E-12
<b>GPR50</b>	2.78225342	-3.512308452	1.95E-14	5.90E-12
<b>DHRS9</b>	-1.388689122	4.241384982	2.94E-14	8.73E-12
<b>CTRB1</b>	-2.843935669	-3.285432994	3.48E-14	1.02E-11
<b>PNLIP</b>	-4.197716375	-2.264222644	3.56E-14	1.02E-11
<b>CHST8</b>	1.797092714	-2.300392537	5.16E-14	1.46E-11
<b>INHBB</b>	1.147711395	3.368747483	5.47E-14	1.50E-11
<b>OR1N2</b>	3.024651126	-3.356161211	6.49E-14	1.75E-11
<b>SP8</b>	1.769885776	0.470026551	7.22E-14	1.92E-11
<b>TCHH</b>	1.555387264	0.242670279	1.07E-13	2.80E-11
<b>WIPF3</b>	-1.266558754	1.550177233	1.28E-13	3.25E-11
<b>SBK2</b>	2.646050718	-3.338877219	1.71E-13	4.23E-11
<b>CNBD2</b>	-1.2221705	-1.135123687	1.72E-13	4.23E-11
<b>KCNJ9</b>	1.438795994	-2.338008577	1.74E-13	4.23E-11
<b>HCN4</b>	1.531837305	-2.65326836	2.47E-13	5.94E-11
<b>CELA2A</b>	-2.365614471	-3.108354642	2.86E-13	6.78E-11
<b>HRH3</b>	2.446853002	-2.597516531	3.55E-13	8.30E-11
<b>CLCA4</b>	-1.904798845	4.992553007	3.86E-13	8.89E-11
<b>PNMT</b>	-1.612884443	-0.339086253	3.97E-13	9.03E-11
<b>NEUROD2</b>	1.759126895	-2.333313622	4.08E-13	9.17E-11
<b>MMP8</b>	-1.961985253	0.571850369	4.37E-13	9.70E-11
<b>PAK5</b>	2.841729235	-1.772739671	4.60E-13	9.98E-11
<b>CRCT1</b>	2.981378717	-2.212261362	4.61E-13	9.98E-11
<b>OPRD1</b>	1.476703756	0.695543527	7.70E-13	1.58E-10
<b>DHRS2</b>	1.332597941	2.501048869	7.94E-13	1.59E-10
<b>CTRB2</b>	-2.339125468	-3.115584479	8.19E-13	1.59E-10
<b>SHISA7</b>	1.626093487	-2.647678966	9.57E-13	1.84E-10
<b>CYP3A4</b>	-1.520113957	0.482015723	1.27E-12	2.42E-10
<b>SLC8A3</b>	-1.379487399	-1.628510541	1.30E-12	2.45E-10
<b>KCNQ2</b>	1.974924013	-0.044041484	1.36E-12	2.54E-10
<b>CELA3A</b>	-1.94394047	-2.217306856	2.54E-12	4.55E-10
<b>TMCO2</b>	-1.945719141	-3.354927364	3.05E-12	5.41E-10
<b>NFE4</b>	-1.739892722	-2.877466698	3.36E-12	5.89E-10
<b>PDYN</b>	2.560031059	-3.636925717	3.44E-12	5.96E-10

<b>BARX1</b>	1.691389229	-0.259556361	5.21E-12	8.62E-10
<b>CHRNA2</b>	2.042761335	-3.190945488	6.43E-12	1.03E-09
<b>SLC1A6</b>	1.834970028	-3.434209537	8.12E-12	1.29E-09
<b>TDRD12</b>	-1.237054104	-1.516326361	8.24E-12	1.29E-09
<b>CD70</b>	-1.193851493	1.432471366	9.15E-12	1.41E-09
<b>ABCB11</b>	-1.270773532	-2.107297794	9.22E-12	1.41E-09
<b>PRSS41</b>	1.456611503	-0.983107083	1.01E-11	1.51E-09
<b>KRT14</b>	2.720442947	2.355297442	1.11E-11	1.63E-09
<b>CDH22</b>	1.984282904	-1.498088471	1.12E-11	1.63E-09
<b>CELF3</b>	1.334198828	1.34714077	1.21E-11	1.74E-09
<b>SEZ6</b>	1.605158147	-1.428244034	1.23E-11	1.76E-09
<b>DLX2</b>	1.456959662	-1.531068336	1.45E-11	1.99E-09
<b>TMPRSS5</b>	1.188163331	1.215840547	1.57E-11	2.13E-09
<b>PRH2</b>	1.44047523	-2.489834284	2.09E-11	2.71E-09
<b>TCP11</b>	1.958915549	0.628046368	2.30E-11	2.96E-09
<b>SERPINB7</b>	-1.879016888	0.650112055	2.89E-11	3.67E-09
<b>PNLDC1</b>	1.342523085	-1.597788641	3.07E-11	3.87E-09
<b>DDX53</b>	-3.147571219	-2.41742091	3.14E-11	3.94E-09
<b>RGR</b>	1.773931954	-1.055324704	3.99E-11	4.85E-09
<b>RNF17</b>	1.665438007	-3.143353885	4.60E-11	5.45E-09
<b>ARHGAP36</b>	1.889941336	-2.657382982	4.69E-11	5.51E-09
<b>ATP2B3</b>	1.70121118	-2.618004557	7.48E-11	8.46E-09
<b>SEC14L4</b>	1.556686352	-0.377906383	7.91E-11	8.89E-09
<b>ERVW-1</b>	-1.376610531	-1.581971543	8.04E-11	8.98E-09
<b>KRT7</b>	-1.209797366	4.110393537	8.90E-11	9.87E-09
<b>KRT6C</b>	1.948661231	-1.072132021	9.09E-11	1.00E-08
<b>CACNA2D2</b>	1.025266962	2.907545249	9.84E-11	1.07E-08
<b>SRRM4</b>	1.765300976	-2.728533085	1.17E-10	1.24E-08
<b>MAGEB1</b>	-3.028804539	-3.717088833	1.28E-10	1.36E-08
<b>UMODL1</b>	1.112933414	0.717474722	1.35E-10	1.41E-08
<b>SLITRK6</b>	1.489366187	3.640262314	1.42E-10	1.49E-08
<b>FBN3</b>	1.505139225	-2.368332795	1.50E-10	1.53E-08
<b>SPRR3</b>	2.385699135	1.429251748	1.72E-10	1.71E-08
<b>CCDC141</b>	-1.115074419	-1.294554774	2.72E-10	2.62E-08
<b>CACNG7</b>	1.67991275	-2.720958717	3.11E-10	2.93E-08
<b>GRIN2C</b>	1.015413002	0.66198504	3.67E-10	3.39E-08
<b>EEF1A2</b>	1.291485377	1.582386617	3.84E-10	3.53E-08
<b>CPNE6</b>	1.250244443	-0.167454221	3.93E-10	3.58E-08
<b>P2RY4</b>	-1.216599884	-2.623647067	4.51E-10	4.06E-08
<b>CAPN6</b>	1.340517885	4.041772872	4.99E-10	4.43E-08
<b>ALPP</b>	-1.64562261	-0.096982685	5.00E-10	4.43E-08
<b>TMEM249</b>	1.075664405	-0.134121212	5.22E-10	4.57E-08
<b>CLCA2</b>	1.706035925	0.32499038	6.13E-10	5.32E-08
<b>PPBP</b>	-2.170318006	6.34585552	7.29E-10	6.26E-08

<b>PCSK2</b>	1.592723522	-1.608734244	9.60E-10	8.01E-08
<b>RIMS2</b>	-1.666060074	-1.222038836	9.79E-10	8.14E-08
<b>SPRR2D</b>	1.959262185	0.956288191	1.06E-09	8.76E-08
<b>SERPINB13</b>	2.736705482	-2.058738202	1.18E-09	9.64E-08
<b>AC011473.4</b>	2.091699385	-3.587649334	1.46E-09	1.15E-07
<b>ACTL6B</b>	1.466350588	-3.249490202	1.47E-09	1.15E-07
<b>HMX2</b>	1.6543069	-2.435922227	1.47E-09	1.15E-07
<b>CLDN6</b>	-1.562265872	-0.891066946	1.50E-09	1.17E-07
<b>RHBDL3</b>	1.14009119	0.434193314	1.64E-09	1.26E-07
<b>UGT2B4</b>	2.173370275	-0.20174877	2.02E-09	1.49E-07
<b>CYP4F8</b>	1.298865172	-0.629100978	2.27E-09	1.64E-07
<b>NDST4</b>	1.845492741	-3.175543407	2.55E-09	1.80E-07
<b>NKX2-2</b>	1.583254033	-1.601034935	2.55E-09	1.80E-07
<b>INSL4</b>	2.413989629	-1.175278026	2.68E-09	1.86E-07
<b>CALML5</b>	-2.273861934	-1.992306365	2.81E-09	1.94E-07
<b>C5orf58</b>	-1.037876506	-1.735089575	2.92E-09	2.01E-07
<b>IL36G</b>	1.222289947	-1.891129026	2.99E-09	2.05E-07
<b>ANPEP</b>	-1.155797369	7.161288308	3.36E-09	2.24E-07
<b>GCGR</b>	1.177633758	-2.25130132	3.57E-09	2.37E-07
<b>CIDEC</b>	-1.006543467	1.671178547	3.66E-09	2.42E-07
<b>RS1</b>	1.25955313	-3.054273066	3.68E-09	2.42E-07
<b>FOXI1</b>	1.682684633	-0.479592005	4.83E-09	3.08E-07
<b>LEFTY2</b>	1.148378372	0.353095606	4.89E-09	3.10E-07
<b>SCRT1</b>	1.280838422	-2.617093698	5.85E-09	3.66E-07
<b>GLYATL2</b>	-1.228849147	-1.349026152	6.34E-09	3.90E-07
<b>GPR87</b>	-1.948147881	-1.890206479	6.45E-09	3.95E-07
<b>INSRR</b>	1.063315874	-2.445268642	7.38E-09	4.43E-07
<b>NTNG1</b>	-1.300477194	-1.722775507	7.44E-09	4.43E-07
<b>ADAM2</b>	1.777040571	-3.335065132	7.71E-09	4.55E-07
<b>ALDOB</b>	-1.025146468	5.547756919	7.93E-09	4.62E-07
<b>MEGF11</b>	1.041476981	0.386090685	8.00E-09	4.64E-07
<b>CELA3B</b>	-1.434188142	-2.383918049	8.03E-09	4.64E-07
<b>C20orf85</b>	1.739171978	-2.502521014	8.15E-09	4.70E-07
<b>VWA5B2</b>	1.095715836	0.466411695	8.25E-09	4.74E-07
<b>LEFTY1</b>	1.155277139	6.321533592	9.19E-09	5.16E-07
<b>NAT8L</b>	1.084865481	0.505084139	9.97E-09	5.57E-07
<b>CCDC155</b>	1.427208279	-2.874974706	1.05E-08	5.83E-07
<b>ITLN2</b>	1.679096063	0.6358475	1.13E-08	6.13E-07
<b>LRRTM1</b>	1.480192499	0.252495947	1.20E-08	6.47E-07
<b>BMP3</b>	-1.1499052	0.914480767	1.32E-08	7.04E-07
<b>KIF19</b>	1.149967323	1.847846877	1.50E-08	7.85E-07
<b>FGF21</b>	1.331636376	-3.470099748	1.71E-08	8.85E-07
<b>QRFPR</b>	-1.736711044	-1.734904854	2.06E-08	1.04E-06
<b>PHF21B</b>	1.339902143	-3.122491513	2.43E-08	1.20E-06

<b>TAS2R30</b>	-1.613823866	-2.866099183	2.44E-08	1.20E-06
<b>USP41</b>	1.027094403	-2.051916019	2.48E-08	1.21E-06
<b>KRT76</b>	-2.257514856	-3.563908016	3.02E-08	1.43E-06
<b>CPS1</b>	1.436976038	4.42241397	3.29E-08	1.54E-06
<b>PCDHA1</b>	1.523009509	-2.146860766	3.52E-08	1.62E-06
<b>ANXA8L1</b>	-1.072530351	-1.787954743	3.70E-08	1.69E-06
<b>PTH2R</b>	1.575880566	-1.298939013	3.88E-08	1.76E-06
<b>SPRR2A</b>	1.829327248	0.946647399	4.06E-08	1.82E-06
<b>SLC26A3</b>	-1.179878857	7.406954368	4.08E-08	1.83E-06
<b>SEMG2</b>	-1.940789397	-1.821519076	4.13E-08	1.84E-06
<b>PSG9</b>	-2.456744059	-3.248984906	4.52E-08	2.00E-06
<b>A2ML1</b>	-1.612475068	0.316025451	4.53E-08	2.00E-06
<b>SYNGR4</b>	-1.192763413	0.071144104	5.01E-08	2.17E-06
<b>HRG</b>	1.441570096	-3.119608232	5.42E-08	2.34E-06
<b>AC010422.3</b>	1.032795565	1.905839048	5.46E-08	2.34E-06
<b>CNMD</b>	-1.291103929	-3.310846572	5.49E-08	2.35E-06
<b>ADGRA1</b>	1.454558391	-3.421129509	5.55E-08	2.36E-06
<b>SH3GL2</b>	1.235520063	-1.193773724	7.08E-08	2.89E-06
<b>EPHA7</b>	1.071642448	1.248143004	7.09E-08	2.89E-06
<b>MLN</b>	-2.010778002	-2.279278042	7.44E-08	3.00E-06
<b>HTR2C</b>	2.087913234	-2.335425318	7.53E-08	3.02E-06
<b>KRT24</b>	2.002689731	-2.678487359	7.77E-08	3.07E-06
<b>DPYSL5</b>	1.356810903	-1.59769035	7.77E-08	3.07E-06
<b>SFTPD</b>	-1.06092138	-2.287668046	7.96E-08	3.14E-06
<b>FAM83A</b>	-1.066072008	1.642678363	8.86E-08	3.41E-06
<b>ADGRD2</b>	1.097729983	-2.357265801	8.90E-08	3.42E-06
<b>HPN</b>	1.230507478	2.315805719	9.17E-08	3.49E-06
<b>ZFR2</b>	1.125197101	-2.634539878	9.36E-08	3.54E-06
<b>ORM1</b>	-1.825574524	1.776117953	1.08E-07	4.01E-06
<b>PLSCR5</b>	-2.229568086	-3.616716022	1.09E-07	4.01E-06
<b>SCRT2</b>	1.662829435	-3.571194228	1.32E-07	4.73E-06
<b>LCN6</b>	-1.104442253	-2.719957558	1.57E-07	5.49E-06
<b>FAM9C</b>	-1.145494933	-3.422728219	1.70E-07	5.80E-06
<b>LIPC</b>	1.218534769	0.66502447	1.98E-07	6.60E-06
<b>KRT6A</b>	1.51171034	3.669255108	1.98E-07	6.60E-06
<b>AMY2A</b>	-1.639029008	-3.462558581	2.15E-07	7.07E-06
<b>CDH16</b>	-1.336133231	1.499704389	2.74E-07	8.59E-06
<b>REG3A</b>	1.601378841	7.995142696	3.28E-07	1.01E-05
<b>DLX1</b>	1.183074417	-1.113477782	3.52E-07	1.07E-05
<b>CA6</b>	1.590979932	-1.559318578	3.52E-07	1.07E-05
<b>LMX1A</b>	1.377630741	-2.182366956	3.61E-07	1.09E-05
<b>PCOLCE2</b>	-1.027148657	0.554127664	3.80E-07	1.13E-05
<b>GNG13</b>	1.075195125	-1.246392158	3.89E-07	1.15E-05
<b>IVL</b>	1.935794139	-1.278514244	3.90E-07	1.16E-05

<b>IL1RAPL2</b>	-1.71926242	-2.880461471	3.98E-07	1.17E-05
<b>FOXN4</b>	1.222937243	-3.310641981	4.24E-07	1.24E-05
<b>COX7B2</b>	-1.966537569	-3.111071188	4.61E-07	1.34E-05
<b>GPR22</b>	-1.153278497	-2.279866749	4.69E-07	1.35E-05
<b>LRTM2</b>	1.052173957	-3.411412176	5.09E-07	1.46E-05
<b>PON1</b>	-1.278757495	-0.945240411	5.16E-07	1.47E-05
<b>IRX4</b>	-1.718776348	-3.116241545	5.60E-07	1.57E-05
<b>SCGB3A2</b>	-1.441865854	-3.026701648	5.69E-07	1.59E-05
<b>SERPINA11</b>	1.378179449	-1.811214954	6.01E-07	1.66E-05
<b>LKAAEAR1</b>	1.331958674	-3.37368198	6.30E-07	1.72E-05
<b>GPR83</b>	1.1770591	-0.269450184	6.69E-07	1.81E-05
<b>SCEL</b>	-1.088131856	1.697057034	6.93E-07	1.86E-05
<b>AKAIN1</b>	1.403897457	-2.437698672	7.03E-07	1.87E-05
<b>HTR3E</b>	1.135562809	-2.10531703	7.56E-07	2.00E-05
<b>CNGA3</b>	-1.193455476	-0.477960055	7.61E-07	2.01E-05
<b>HTR3C</b>	1.488664513	-2.229110873	8.66E-07	2.23E-05
<b>RGS7</b>	1.194365512	-1.757266771	9.09E-07	2.32E-05
<b>BRDT</b>	-1.156148158	-3.457943499	9.96E-07	2.51E-05
<b>APOA2</b>	1.490466446	0.106074343	1.13E-06	2.78E-05
<b>TMIGD1</b>	-1.316058297	0.851301429	1.17E-06	2.85E-05
<b>TAS2R46</b>	-1.228466891	-3.488484295	1.23E-06	2.96E-05
<b>F7</b>	1.102001808	1.457242184	1.30E-06	3.10E-05
<b>RETNLB</b>	1.080975389	4.277457507	1.31E-06	3.11E-05
<b>TCF23</b>	1.20021154	-1.655390852	1.66E-06	3.83E-05
<b>SI</b>	-1.084575822	4.016751472	1.69E-06	3.87E-05
<b>MROH2A</b>	1.235634632	-2.814313256	1.71E-06	3.90E-05
<b>DBH</b>	-1.018779801	-0.434679727	1.73E-06	3.93E-05
<b>IL36B</b>	-1.485255972	-2.164042876	1.77E-06	4.01E-05
<b>TMPRSS11E</b>	1.585345467	-0.232020961	1.92E-06	4.29E-05
<b>SLC18A1</b>	1.059510597	1.895254921	2.08E-06	4.57E-05
<b>CBLN4</b>	1.265128306	-1.765051863	2.28E-06	4.97E-05
<b>SYNPR</b>	1.198667481	-0.251976384	2.32E-06	5.04E-05
<b>SIX2</b>	1.024686629	0.952835916	2.36E-06	5.11E-05
<b>SLC7A10</b>	1.193148778	-1.212881712	2.66E-06	5.59E-05
<b>KRT31</b>	-1.596779565	-1.612257678	2.73E-06	5.71E-05
<b>CALB1</b>	-1.469845281	3.888137885	2.77E-06	5.76E-05
<b>GABRA4</b>	1.173149584	0.558600712	2.86E-06	5.90E-05
<b>LIPF</b>	1.732069425	-2.941925123	3.02E-06	6.15E-05
<b>RFX6</b>	1.25369584	-0.634922452	3.46E-06	6.91E-05
<b>GHRH</b>	1.179160298	-3.433510976	3.82E-06	7.46E-05
<b>NOL4</b>	1.058766961	-1.1998089	4.31E-06	8.25E-05
<b>KLK4</b>	1.028265065	0.35637354	4.48E-06	8.51E-05
<b>AQP8</b>	-1.144743706	3.247293326	5.06E-06	9.37E-05
<b>CHGB</b>	1.200485926	2.836162831	5.69E-06	0.000103233

<b>KIF1A</b>	1.040059092	0.941348924	5.83E-06	0.000104919
<b>AKAP4</b>	-1.159291566	-1.976167345	6.01E-06	0.000107804
<b>ANKRD34C</b>	1.247375821	-3.589733934	6.72E-06	0.000118862
<b>CACNG4</b>	-1.063727225	2.336925204	6.82E-06	0.000120246
<b>SOHLH2</b>	-1.419136705	-2.070169281	7.06E-06	0.00012386
<b>MAGEB2</b>	-1.992414241	-0.579434297	7.28E-06	0.000126893
<b>KLK13</b>	1.067034787	-0.51282841	7.64E-06	0.000132212
<b>SLITRK1</b>	1.410744984	-3.581544674	7.82E-06	0.000134392
<b>ALPPL2</b>	-1.190984371	2.47789863	8.45E-06	0.00014381
<b>ATP6V0A4</b>	1.055196816	-1.414245216	9.02E-06	0.000151421
<b>KRT9</b>	-1.012319367	-3.238618065	9.22E-06	0.000153974
<b>MUC15</b>	1.456966054	-2.219333137	9.68E-06	0.000159845
<b>XAGE2</b>	-1.808962879	-1.808414008	1.01E-05	0.000164496
<b>POU3F3</b>	1.048796203	-1.86806727	1.07E-05	0.000172582
<b>CNTN5</b>	1.187266099	-2.589475135	1.12E-05	0.00017861
<b>GFY</b>	1.155077302	-3.13489963	1.34E-05	0.000206705
<b>HIST1H4C</b>	-1.487047722	2.253037179	1.37E-05	0.000209621
<b>TRPV6</b>	-1.13485009	0.899081358	1.41E-05	0.000215684
<b>UPK2</b>	-1.077626176	-0.743070621	1.42E-05	0.000216651
<b>HS3ST4</b>	1.418823059	-0.235006914	1.44E-05	0.000218624
<b>ACTBL2</b>	-1.144936111	-2.52228056	1.47E-05	0.000221517
<b>SLCO1A2</b>	1.06392193	-1.217702555	1.47E-05	0.000221833
<b>SLC6A2</b>	1.41483817	-2.222592277	1.47E-05	0.000222007
<b>TMPRSS11D</b>	1.289941605	-3.083001116	1.56E-05	0.000231348
<b>REG3G</b>	-1.658377924	-0.065033224	1.58E-05	0.000234379
<b>NEUROD1</b>	1.521181383	-0.159254131	1.84E-05	0.000263949
<b>TBX4</b>	1.103203816	0.275787257	1.84E-05	0.000264279
<b>ZPBP2</b>	-1.12558078	-3.118840938	1.85E-05	0.000264824
<b>KCNC2</b>	1.3914501	-2.467029689	1.97E-05	0.000278433
<b>BPIFB4</b>	1.36307	-3.484054024	2.34E-05	0.000319043
<b>SLC10A2</b>	-1.652554517	-2.685726753	2.39E-05	0.000323862
<b>SLURP1</b>	1.241910514	-3.351437732	2.46E-05	0.000332226
<b>CA1</b>	-1.125328837	3.284431918	2.54E-05	0.000340671
<b>PCSK1</b>	1.065772313	5.086658269	2.65E-05	0.000351976
<b>TUBA3C</b>	-1.678644007	-3.283817168	2.75E-05	0.00036331
<b>SLC38A8</b>	1.160550364	-2.669416324	2.75E-05	0.00036331
<b>ANKRD34B</b>	1.149465206	-3.024732677	2.77E-05	0.000364455
<b>MYBPHL</b>	1.118876875	-0.558534906	2.84E-05	0.000370229
<b>MAGEC1</b>	-1.766799968	-2.235964611	3.02E-05	0.000391743
<b>SP9</b>	1.476159349	-1.499783862	3.09E-05	0.000397231
<b>SLC30A10</b>	-1.002782647	-1.089751727	3.14E-05	0.000401186
<b>CLPS</b>	-1.561650033	-2.981534836	3.32E-05	0.000421658
<b>SPRR1A</b>	1.408086339	0.84222544	3.50E-05	0.000437299
<b>RPTN</b>	-1.604655949	-2.843601984	3.59E-05	0.000445504

<b>NKX2-5</b>	1.197036039	-2.708422535	3.72E-05	0.000457521
<b>SFTPB</b>	-1.197280462	0.722946789	3.72E-05	0.000457521
<b>SLC36A2</b>	1.053655149	-3.57386111	3.79E-05	0.000465843
<b>KCNE1B</b>	-1.529444356	-1.380753954	4.14E-05	0.000496502
<b>ANXA8</b>	-1.217741801	-1.512656003	4.15E-05	0.00049755
<b>MS4A12</b>	-1.06152352	3.317541034	4.38E-05	0.000519716
<b>NHLH2</b>	1.356809635	-1.602425103	4.38E-05	0.000519716
<b>GSX1</b>	1.156607961	-3.439566749	4.41E-05	0.000522765
<b>TKTL1</b>	1.391449925	0.893977857	4.43E-05	0.000523732
<b>HSD3B2</b>	-1.143277422	-0.775882722	4.50E-05	0.000529268
<b>INSL5</b>	-1.312826278	-1.136401805	4.65E-05	0.000545304
<b>GDF10</b>	1.159520598	1.127218941	4.67E-05	0.000546804
<b>DAZ1</b>	1.816757088	-3.46557901	5.16E-05	0.000594926
<b>KRT13</b>	1.024830918	-0.050267276	5.20E-05	0.000597986
<b>KRT5</b>	1.307461575	3.752473133	5.47E-05	0.000625891
<b>CNPY1</b>	1.130801145	-3.252149028	5.52E-05	0.000629496
<b>CRISP3</b>	-1.474739329	-3.326274713	5.59E-05	0.000636181
<b>CCDC190</b>	1.30570221	-1.716021437	5.65E-05	0.000640593
<b>PAX7</b>	1.583026048	-0.537417348	6.00E-05	0.000674102
<b>FOXR2</b>	1.544757242	-3.669269745	6.17E-05	0.00069018
<b>LCN15</b>	1.244454742	5.656950865	6.97E-05	0.000759527
<b>MUC16</b>	-1.069871046	1.225839054	7.54E-05	0.000806974
<b>DMRT1</b>	1.270752307	-1.710486211	7.94E-05	0.000840587
<b>IFNK</b>	-1.286961629	-3.654647063	7.97E-05	0.000842582
<b>HIST1H1B</b>	-1.29125851	3.281342721	8.78E-05	0.000906862
<b>POU5F2</b>	-1.015630983	-2.679188817	8.78E-05	0.000906862
<b>CLDN8</b>	-1.28242253	0.198302867	9.32E-05	0.000954424
<b>HIST1H4D</b>	-1.260000086	1.80701295	9.67E-05	0.000984683
<b>NTS</b>	-1.254919642	2.513937584	9.72E-05	0.000988852
<b>BRINP3</b>	1.147682142	0.576712819	0.000108159	0.001077285
<b>KRTAP13-2</b>	-1.272705137	-3.339338189	0.000115078	0.001137161
<b>GC</b>	1.301862444	-3.173059503	0.000116538	0.001148989
<b>PSAPL1</b>	-1.294235336	-1.564879962	0.000120085	0.001174711
<b>HIST1H4F</b>	1.569104577	-1.831521911	0.000123732	0.001203011
<b>LCN8</b>	1.098985645	-2.543127272	0.000164142	0.001517625
<b>TBX5</b>	1.206332606	-2.004452939	0.00016708	0.001535874
<b>CPB1</b>	-1.157551951	-1.571661647	0.00018106	0.001631867
<b>HIST1H2BO</b>	-1.090138805	0.914031325	0.000218915	0.001892294
<b>CT45A1</b>	-1.649937937	-2.976959656	0.000220593	0.001903051
<b>TRIM71</b>	1.051241338	-0.186310634	0.000232016	0.00198209
<b>LRRC53</b>	1.160724897	-2.964498748	0.000233996	0.001991598
<b>11-Mar</b>	1.087333495	-3.592032111	0.000252393	0.002109897
<b>PAGE2</b>	1.080463915	-3.577203944	0.000291123	0.002370487
<b>SSX1</b>	-1.647567942	-3.460640374	0.000293042	0.00238156

<b>REG1B</b>	1.19452104	6.927395912	0.000293741	0.002386132
<b>TEX15</b>	-1.159977928	-3.091763936	0.000308843	0.002486918
<b>ZIC4</b>	-1.396251346	-2.764807107	0.00038686	0.00296401
<b>PIP</b>	1.010729367	-3.424654191	0.000393514	0.003006771
<b>CLPSL1</b>	-1.377399839	-3.301128892	0.00042546	0.003196878
<b>PNMA5</b>	1.441611028	2.630083872	0.000444708	0.003311695
<b>DCAF4L2</b>	-1.583191875	-2.711888476	0.000456197	0.00338575
<b>OTOP3</b>	-1.199681696	-3.241997401	0.000526444	0.003771378
<b>HIST1H1D</b>	-1.063336504	1.884717849	0.000576363	0.004074048
<b>SOX21</b>	-1.016395538	-2.701560782	0.000582663	0.004110297
<b>HIST1H1A</b>	-1.339973526	-3.524797392	0.000614555	0.004302378
<b>SSX5</b>	1.304791988	-3.509225395	0.000714199	0.004840448
<b>HAND1</b>	-1.007689624	0.150128226	0.000740713	0.004973074
<b>PTF1A</b>	-1.160166067	-1.125245819	0.000743644	0.004985115
<b>SAGE1</b>	1.146086463	-2.513457428	0.001821466	0.009910085
<b>FGL1</b>	1.021462337	-0.750700965	0.002317434	0.011969541
<b>TAAR1</b>	-1.114927363	-3.437069014	0.003324611	0.015923615
<b>MAGEA12</b>	1.294130666	1.187904434	0.00343474	0.016312923
<b>CSAG3</b>	1.022079497	-2.546316893	0.005409409	0.023117243
<b>CSAG1</b>	1.081832341	0.35954189	0.006358055	0.026188137
<b>SFTA3</b>	-1.161041651	-1.800515598	0.006766066	0.027462178
<b>MT4</b>	-1.066899531	-0.882531009	0.008054238	0.031292284
<b>CXorf67</b>	-1.049342469	-3.004583696	0.010746722	0.039020307
<b>SPRR2F</b>	1.058365605	-1.095205669	0.013989163	0.047654494
<b>MAGEA9</b>	1.01509734	-3.594548206	0.014354068	0.048638898



**Table S7.** Survival analysis results of DEG between high - and low -AC096751.1 phenotypes in COAD OS (Only gene list with P<0.05 is shown ).

<b>ID</b>	<b>P</b>	<b>HR</b>	<b>Low 95%CI</b>	<b>High 95%CI</b>
<b>COX8C</b>	0.003675859	1.860622743	1.223786796	2.828856301
<b>PNMA5</b>	0.007848828	1.777282954	1.163122031	2.715738001
<b>PCOLCE2</b>	0.013690667	1.711254184	1.116408425	2.623046206
<b>TAS2R30</b>	0.01442023	1.691660366	1.110232037	2.577582613
<b>AQP8</b>	0.017066227	0.60147528	0.396098115	0.913340656
<b>COLEC10</b>	0.018999405	0.604562301	0.397018326	0.920601272
<b>EPHA7</b>	0.019309313	0.605979641	0.39829806	0.921951077
<b>SLC38A8</b>	0.019959953	1.635028911	1.080654648	2.473796363
<b>ALPP</b>	0.020135118	1.648264896	1.081387651	2.512306447
<b>ITLN2</b>	0.02052065	0.61121153	0.403000384	0.92699548
<b>GCG</b>	0.021026946	0.613833632	0.405530371	0.929133191
<b>DPCR1</b>	0.023376864	1.631880162	1.068620831	2.492027842
<b>GLYATL2</b>	0.023987821	0.621798967	0.411606996	0.93932795
<b>GFY</b>	0.026389779	1.601463781	1.056794432	2.426854424
<b>PNLDC1</b>	0.026596309	1.610906349	1.056914423	2.455278506
<b>GPR83</b>	0.03274764	1.579881157	1.038240632	2.404090527
<b>PCSK1</b>	0.03710554	0.642766157	0.424211455	0.973920737
<b>ZFR2</b>	0.046216879	1.52394574	1.007093193	2.306053337

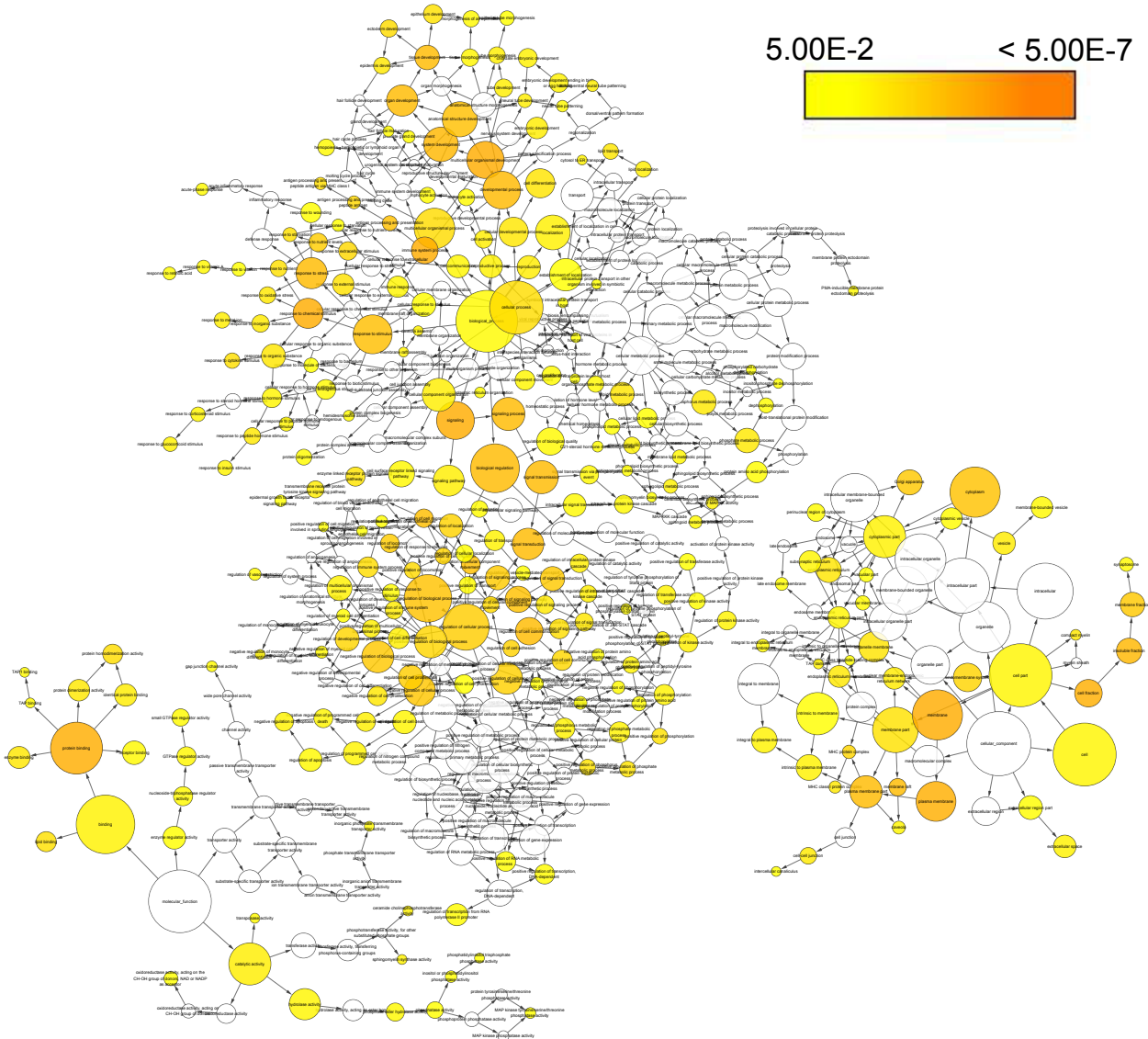
**Table S8.** Functional enrichment analysis results of DEG between high - and low -AC096751.1 phenotypes in COAD

<b>Category</b>	<b>Term</b>	<b>Count</b>	<b>PValue</b>
<b>GOTERM_CC_DIRECT</b>	GO:0005576~extracellular region	73	4.22E-12
<b>GOTERM_CC_DIRECT</b>	GO:0005615~extracellular space	64	1.90E-11
<b>GOTERM_CC_DIRECT</b>	GO:0001533~cornified envelope	12	7.27E-10
<b>GOTERM_BP_DIRECT</b>	GO:0008544~epidermis development	15	8.63E-10
<b>GOTERM_MF_DIRECT</b>	GO:0005198~structural molecule activity	22	8.99E-09
<b>GOTERM_BP_DIRECT</b>	GO:0031424~keratinization	10	2.95E-07
<b>GOTERM_BP_DIRECT</b>	GO:0018149~peptide cross-linking	10	4.25E-07
<b>GOTERM_MF_DIRECT</b>	GO:0004252~serine-type endopeptidase activity	19	1.64E-06
<b>GOTERM_BP_DIRECT</b>	GO:0030216~keratinocyte differentiation	11	1.98E-06
<b>GOTERM_CC_DIRECT</b>	GO:0045334~clathrin-coated endocytic vesicle	6	6.15E-06
<b>GOTERM_CC_DIRECT</b>	GO:0042599~lamellar body	5	8.42E-06
<b>GOTERM_MF_DIRECT</b>	GO:0005179~hormone activity	11	1.06E-05
<b>GOTERM_BP_DIRECT</b>	GO:0006508~proteolysis	26	1.53E-05
<b>GOTERM_BP_DIRECT</b>	GO:0010842~retina layer formation	6	5.29E-05
<b>GOTERM_CC_DIRECT</b>	GO:0005882~intermediate filament	11	5.87E-05
<b>GOTERM_BP_DIRECT</b>	GO:0035881~amacrine cell differentiation	4	6.98E-05
<b>GOTERM_MF_DIRECT</b>	GO:0001228~transcriptional activator activity, RNA polymerase II transcription regulatory region sequence-specific binding	10	7.39E-05
<b>GOTERM_BP_DIRECT</b>	GO:0007585~respiratory gaseous exchange	6	4.62E-04
<b>GOTERM_BP_DIRECT</b>	GO:0006810~transport	18	4.64E-04
<b>GOTERM_BP_DIRECT</b>	GO:0044267~cellular protein metabolic process	10	4.81E-04
<b>GOTERM_CC_DIRECT</b>	GO:0045095~keratin filament	9	6.36E-04
<b>GOTERM_BP_DIRECT</b>	GO:0007271~synaptic transmission, cholinergic	6	6.90E-04
<b>GOTERM_MF_DIRECT</b>	GO:0015464~acetylcholine receptor activity	5	8.15E-04
<b>GOTERM_MF_DIRECT</b>	GO:0004889~acetylcholine-activated cation-selective channel activity	5	8.15E-04
<b>GOTERM_CC_DIRECT</b>	GO:0005887~integral component of plasma membrane	45	8.22E-04
<b>GOTERM_CC_DIRECT</b>	GO:0005892~acetylcholine-gated channel complex	5	0.001005

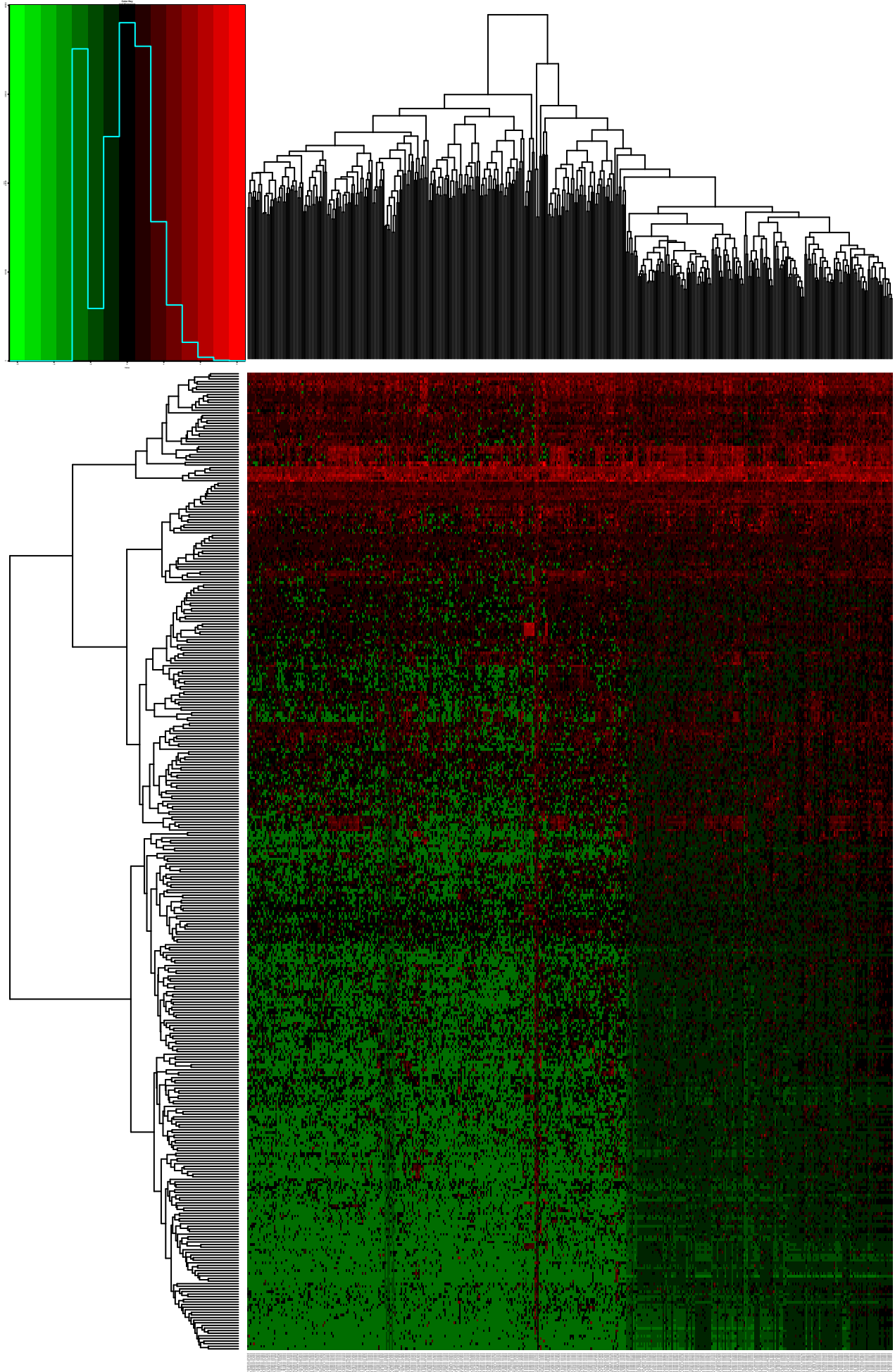
<b>GOTERM_MF_DIRECT</b>	GO:0008236~serine-type peptidase activity	7	0.001156
<b>GOTERM_BP_DIRECT</b>	GO:0007626~locomotory behavior	8	0.001207
<b>GOTERM_CC_DIRECT</b>	GO:0034774~secretory granule lumen	4	0.001314
<b>GOTERM_MF_DIRECT</b>	GO:0042166~acetylcholine binding	5	0.001316
<b>GOTERM_MF_DIRECT</b>	GO:0005125~cytokine activity	11	0.00184
<b>GOTERM_MF_DIRECT</b>	GO:0000977~RNA polymerase II regulatory region sequence-specific DNA binding	12	0.001961
<b>GOTERM_BP_DIRECT</b>	GO:0098655~cation transmembrane transport	6	0.00228
<b>GOTERM_BP_DIRECT</b>	GO:0007417~central nervous system development	9	0.002326
<b>GOTERM_MF_DIRECT</b>	GO:0005230~extracellular ligand-gated ion channel activity	5	0.003249
<b>GOTERM_BP_DIRECT</b>	GO:0042391~regulation of membrane potential	7	0.003297
<b>GOTERM_BP_DIRECT</b>	GO:0007267~cell-cell signaling	13	0.00405
<b>GOTERM_MF_DIRECT</b>	GO:0015276~ligand-gated ion channel activity	5	0.004476
<b>GOTERM_BP_DIRECT</b>	GO:0071377~cellular response to glucagon stimulus	5	0.007274
<b>GOTERM_BP_DIRECT</b>	GO:0048468~cell development	5	0.007274
<b>GOTERM_BP_DIRECT</b>	GO:0032094~response to food	4	0.007377
<b>GOTERM_MF_DIRECT</b>	GO:0005160~transforming growth factor beta receptor binding	5	0.007791
<b>GOTERM_BP_DIRECT</b>	GO:0043408~regulation of MAPK cascade	5	0.00794
<b>GOTERM_BP_DIRECT</b>	GO:0030154~cell differentiation	18	0.00885
<b>GOTERM_CC_DIRECT</b>	GO:0000786~nucleosome	7	0.00902
<b>GOTERM_BP_DIRECT</b>	GO:0050796~regulation of insulin secretion	6	0.009557
<b>GOTERM_MF_DIRECT</b>	GO:0008083~growth factor activity	9	0.011585
<b>GOTERM_BP_DIRECT</b>	GO:0006811~ion transport	8	0.011826
<b>GOTERM_BP_DIRECT</b>	GO:0010862~positive regulation of pathway-restricted SMAD protein phosphorylation	5	0.013734
<b>GOTERM_CC_DIRECT</b>	GO:0005891~voltage-gated calcium channel complex	4	0.017207
<b>GOTERM_MF_DIRECT</b>	GO:0005200~structural constituent of cytoskeleton	7	0.017592
<b>GOTERM_BP_DIRECT</b>	GO:0071320~cellular response to cAMP	5	0.017999
<b>GOTERM_BP_DIRECT</b>	GO:0007283~spermatogenesis	15	0.018178

<b>GOTERM_BP_DIRECT</b>	GO:0007268~chemical synaptic transmission	11	0.018789
<b>GOTERM_CC_DIRECT</b>	GO:0031093~platelet alpha granule lumen	5	0.020385
<b>GOTERM_BP_DIRECT</b>	GO:0043085~positive regulation of catalytic activity	6	0.02041
<b>GOTERM_MF_DIRECT</b>	GO:0046983~protein dimerization activity	8	0.02329
<b>GOTERM_MF_DIRECT</b>	GO:0005249~voltage-gated potassium channel activity	5	0.02341
<b>GOTERM_BP_DIRECT</b>	GO:0003007~heart morphogenesis	4	0.023543
<b>GOTERM_BP_DIRECT</b>	GO:0007210~serotonin receptor signaling pathway	3	0.025303
<b>GOTERM_BP_DIRECT</b>	GO:0021527~spinal cord association neuron differentiation	3	0.025303
<b>GOTERM_BP_DIRECT</b>	GO:0044241~lipid digestion	3	0.025303
<b>GOTERM_BP_DIRECT</b>	GO:0070588~calcium ion transmembrane transport	7	0.02823
<b>GOTERM_BP_DIRECT</b>	GO:0006334~nucleosome assembly	7	0.02823
<b>GOTERM_BP_DIRECT</b>	GO:0002009~morphogenesis of an epithelium	3	0.029148
<b>GOTERM_CC_DIRECT</b>	GO:0043195~terminal bouton	5	0.030104
<b>GOTERM_BP_DIRECT</b>	GO:0060395~SMAD protein signal transduction	5	0.031961
<b>GOTERM_MF_DIRECT</b>	GO:0030246~carbohydrate binding	9	0.032009
<b>GOTERM_BP_DIRECT</b>	GO:0009888~tissue development	3	0.03321
<b>GOTERM_BP_DIRECT</b>	GO:0007586~digestion	5	0.033626
<b>GOTERM_MF_DIRECT</b>	GO:0043565~sequence-specific DNA binding	17	0.036029
<b>GOTERM_BP_DIRECT</b>	GO:0021893~cerebral cortex GABAergic interneuron fate commitment	2	0.038335
<b>GOTERM_BP_DIRECT</b>	GO:0003218~cardiac left ventricle formation	2	0.038335
<b>GOTERM_BP_DIRECT</b>	GO:0003326~pancreatic A cell fate commitment	2	0.038335
<b>GOTERM_BP_DIRECT</b>	GO:0003329~pancreatic PP cell fate commitment	2	0.038335
<b>GOTERM_MF_DIRECT</b>	GO:0005245~voltage-gated calcium channel activity	4	0.03888
<b>GOTERM_MF_DIRECT</b>	GO:0004806~triglyceride lipase activity	3	0.039705
<b>GOTERM_BP_DIRECT</b>	GO:0006366~transcription from RNA polymerase II promoter	17	0.041449
<b>GOTERM_BP_DIRECT</b>	GO:0001580~detection of chemical stimulus involved in sensory perception of bitter taste	4	0.041919
<b>GOTERM_BP_DIRECT</b>	GO:0030326~embryonic limb morphogenesis	4	0.041919
<b>GOTERM_BP_DIRECT</b>	GO:0048663~neuron fate commitment	3	0.041942

<b>GOTERM_BP_DIRECT</b>	GO:0048265~response to pain	3	0.041942
<b>GOTERM_BP_DIRECT</b>	GO:0008203~cholesterol metabolic process	5	0.042698
<b>GOTERM_BP_DIRECT</b>	GO:0007218~neuropeptide signaling pathway	6	0.046422
<b>GOTERM_BP_DIRECT</b>	GO:0045653~negative regulation of megakaryocyte differentiation	3	0.046594
<b>GOTERM_CC_DIRECT</b>	GO:0045211~postsynaptic membrane	9	0.048761
<b>GOTERM_CC_DIRECT</b>	GO:0070062~extracellular exosome	66	0.049893
<b>KEGG_PATHWAY</b>	hsa04972:Pancreatic secretion	10	3.33E-05
<b>KEGG_PATHWAY</b>	hsa04080:Neuroactive ligand-receptor interaction	14	0.001097
<b>KEGG_PATHWAY</b>	hsa04974:Protein digestion and absorption	7	0.004382
<b>KEGG_PATHWAY</b>	hsa04260:Cardiac muscle contraction	6	0.010041
<b>KEGG_PATHWAY</b>	hsa05034:Alcoholism	9	0.012504
<b>KEGG_PATHWAY</b>	hsa00910:Nitrogen metabolism	3	0.035128
<b>KEGG_PATHWAY</b>	hsa04726:Serotonergic synapse	6	0.045492
<b>KEGG_PATHWAY</b>	hsa05410:Hypertrophic cardiomyopathy (HCM)	5	0.048034

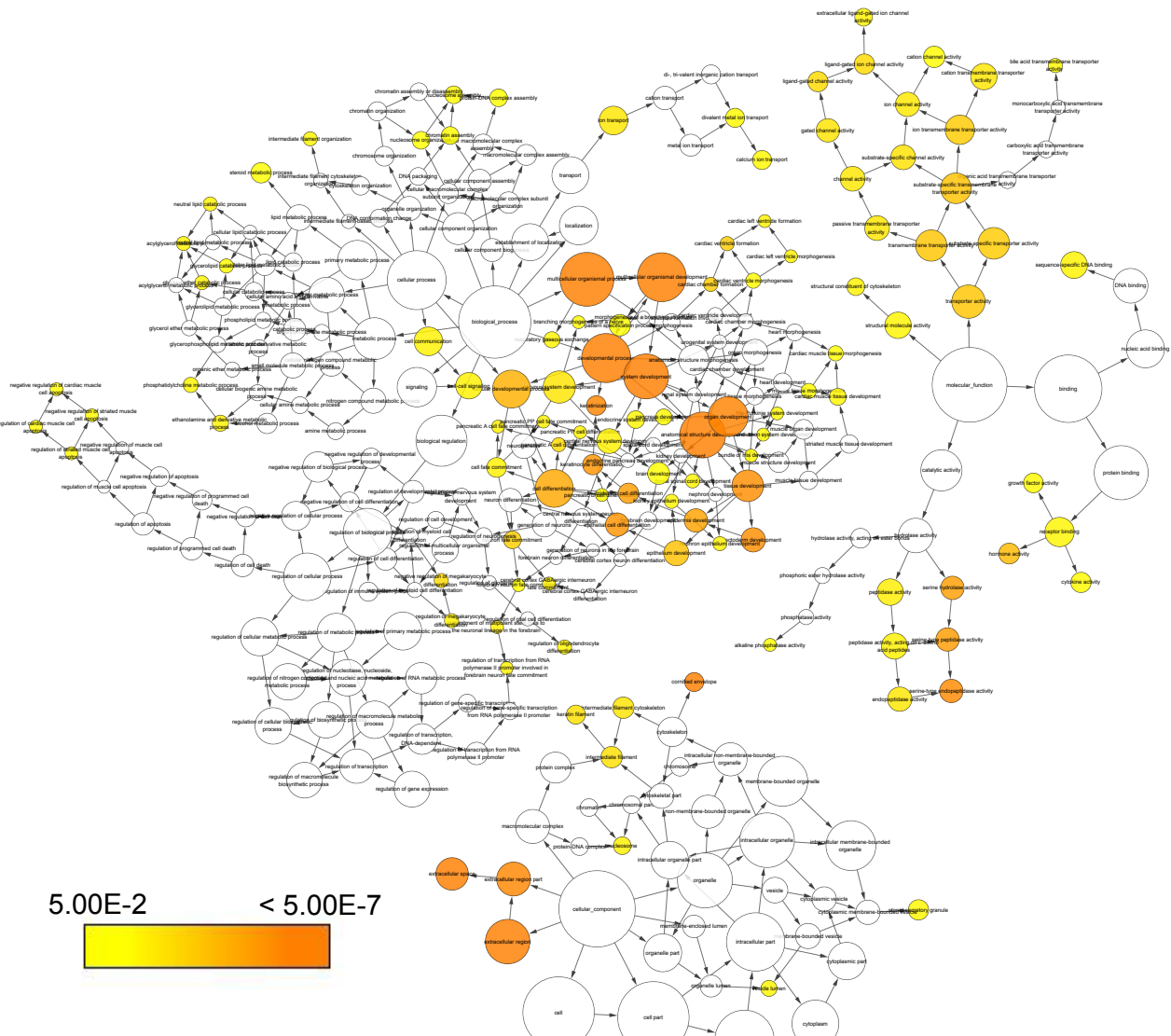


**Figure S1.** BiNGO enrichment results of AC096751.1 co-expressed genes.



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**Figure S2.** Heat map of the differentially expressed genes between high- and low-AC096751.1 expression phenotypes in COAD.



**Figure S3.** BiNGO enrichment results of DEGs between high- and low-AC096751.1 expression phenotypes in COAD.