

Table S5. Characteristic pathways of methylated genes in subtypes

cluster	MyList	Biological Process (GO)
1	<i>LOC728392</i>	None
1	<i>EVC</i>	GO:0003416 endochondral bone growth;GO:0098868 bone growth;GO:0045880 positive regulation of smoothened signaling pathway
1	<i>HOXB4</i>	GO:0048103 somatic stem cell division;GO:0048539 bone marrow development;GO:0060218 hematopoietic stem cell differentiation
2	<i>CAPN8</i>	GO:0007586 digestion;GO:0006508 proteolysis;GO:0019538 protein metabolic process
2	<i>CSTA</i>	GO:0018149 peptide cross-linking;GO:0030216 keratinocyte differentiation;GO:0009913 epidermal cell differentiation
2	<i>GSDMC</i>	GO:0070269 pyroptosis;GO:0042742 defense response to bacterium;GO:0009617 response to bacterium
2	<i>HEBP1</i>	GO:0007623 circadian rhythm;GO:0048511 rhythmic process;GO:0008150 biological_process
2	<i>HRH1</i>	GO:0032962 positive regulation of inositol trisphosphate biosynthetic process;GO:0032960 regulation of inositol trisphosphate biosynthetic process;GO:0071420 cellular response to histamine
2	<i>KRTAP2.4</i>	None
2	<i>MAP4K5</i>	GO:0000165 MAPK cascade;GO:0006468 protein phosphorylation;GO:0016310 phosphorylation
2	<i>MIR135B</i>	GO:1904754 positive regulation of vascular associated smooth muscle cell migration;GO:1905564 positive regulation of vascular endothelial cell proliferation;GO:0014911 positive regulation of smooth muscle cell migration
2	<i>SLAMF7</i>	GO:0042267 natural killer cell mediated cytotoxicity;GO:0002228 natural killer cell mediated immunity;GO:0001909 leukocyte mediated cytotoxicity
2	<i>UCA1</i>	GO:0010468 regulation of gene expression;GO:0060255 regulation of macromolecule metabolic process;GO:0019222 regulation of metabolic process
2	<i>SNORD114.29</i>	None