

Appendix B. Differences among clusters in the frequency (%) of hypermethylation for each individual gene identified. The table shows the values for 28 genes that are differentially methylated ($p < 0.05$).

Gene	Cluster								P-Value	
	1 (N=9)		2 (N=21)		3 (N=15)		4 (N=13)			
	N	%	N	%	N	%	N	%	Fisher test raw value	Holm correction
<i>ALOX12</i>	1	11.1	4	19	5	33.3	13	100	<.0001	<.0001
<i>APC</i>	0	0	2	9.5	3	20	12	92.3	<.0001	<.0001
<i>CCNA1</i>	0	0	0	0	10	66.7	12	92.3	<.0001	<.0001
<i>CFTR</i>	0	0	0	0	8	53.3	13	100	<.0001	<.0001
<i>COL18A1</i>	0	0	1	4.8	13	86.7	12	92.3	<.0001	<.0001
<i>ERG</i>	0	0	0	0	11	73.3	11	84.6	<.0001	<.0001
<i>EYA4</i>	0	0	0	0	10	66.7	10	76.9	<.0001	<.0001
<i>GADD45A</i>	0	0	0	0	11	73.3	10	76.9	<.0001	<.0001
<i>GF11</i>	0	0	0	0	12	80	11	84.6	<.0001	<.0001
<i>GSTM2</i>	1	11.1	18	85.7	1	6.7	13	100	<.0001	<.0001
<i>GSTP1</i>	0	0	7	33.3	2	13.3	13	100	<.0001	<.0001
<i>KLK10</i>	0	0	1	4.8	11	73.3	11	84.6	<.0001	<.0001
<i>MET</i>	0	0	0	0	12	80	13	100	<.0001	<.0001
<i>MFAP4</i>	0	0	1	4.8	11	73.3	11	84.6	<.0001	<.0001
<i>MMP14</i>	0	0	0	0	12	80	12	92.3	<.0001	<.0001
<i>MT1A</i>	0	0	0	0	7	46.7	11	84.6	<.0001	<.0001
<i>MYCL2</i>	0	0	0	0	10	66.7	7	53.8	<.0001	.0001
<i>NEU1</i>	0	0	0	0	11	73.3	13	100	<.0001	<.0001
<i>PDGFRB</i>	0	0	1	4.8	5	33.3	13	100	<.0001	<.0001
<i>PENK</i>	0	0	1	4.8	9	60	11	84.6	<.0001	<.0001
<i>POMC</i>	0	0	1	4.8	11	73.3	9	69.2	<.0001	.0001
<i>RARA</i>	0	0	0	0	9	60	10	76.9	<.0001	<.0001
<i>RARB</i>	0	0	2	9.5	1	6.7	13	100	<.0001	<.0001
<i>SCGB3A1</i>	0	0	1	4.8	7	46.7	13	100	<.0001	<.0001
<i>SEPT9</i>	0	0	0	0	12	80	10	76.9	<.0001	<.0001
<i>TAL1</i>	0	0	0	0	12	80	12	92,308	<.0001	<.0001
<i>TBX1</i>	0	0	0	0	11	73,333	11	84,615	<.0001	<.0001
<i>TERT</i>	0	0	0	0	11	73,333	12	92,308	<.0001	<.0001