Table 7. Summary statistics of gene methylation among clusters by Kruskal-Wallis Tests and ANOVA

Marker	Cluster 1 Mean (SD)	Cluster 2 Mean (SD)	Cluster 3 Mean (SD)	*P* value
Original markers (MINT clones)				
MINT1	0.43 (0.18)	0.01 (0.08)	0.24 (0.25)	<0.0001
MINT2	0.39 (0.21)	0.03 (0.11)	0.31 (0.25)	<0.0001
MINT27	0.43 (0.18)	0.04 (0.14)	0.39 (0.21)	<0.0001
MINT12	0.39 (0.21)	0.03 (0.11)	0.22 (0.25)	<0.0001
MINT31	0.39 (0.21)	0.03 (0.11)	0.27 (0.25)	<0.0001
MINT17	0.36 (0.23)	0.01 (0.08)	0.15 (0.23)	<0.0001
Type-C genes (Genes methylated in cancer)				
P14/ARF	0.18 (0.18)	0.02 (0.05)	0.07 (0.12)	0.006
MLH1	0.39 (0.21)	0.00 (0.00)	0.00 (0.00)	<0.0001
THBS1	0.05 (0.12)	0.00 (0.00)	0.02 (0.07)	0.003
THBS2	0.21 (0.13)	0.07 (0.07)	0.12 (0.11)	<0.0001
MGMT	0.29 (0.26)	0.12 (0.18)	0.25 (0.27)	0.005
COX2	0.03 (0.09)	0.02 (0.07)	0.05 (0.10)	0.69
Megalin	0.16 (0.16)	0.05 (0.10)	0.14 (0.17)	0.004
RIZ1	0.27 (0.30)	0.02 (0.06)	0.02 (0.07)	<0.0001
P16 (CDKN2A)	0.20 (0.15)	0.03 (0.02)	0.14 (0.18)	<0.0001
RASSF1A	0.11 (0.16)	0.06 (0.09)	0.09 (0.14)	0.21
DAPK	0.05 (0.08)	0.03 (0.04)	0.07 (0.08)	0.12
TIMP3	0.41 (0.23)	0.06 (0.11)	0.14 (0.20)	<0.0001

Marker	Cluster 1 Mean (SD)	Cluster 2 Mean (SD)	Cluster 3 Mean (SD)	*P* value
hTERT	0.15 (0.13)	0.07 (0.13)	0.18 (0.19)	0.003
Neurog1	0.45 (0.27)	0.10 (0.15)	0.29 (0.22)	<0.0001
SOCS1	0.22 (0.17)	0.07 (0.10)	0.05 (0.09)	0.0007
RUNX3	0.21 (0.20)	0.03 (0.04)	0.08 (0.12)	0.0002
Type-A genes (Genes methylated in both normal and cancer)				
ER alpha	0.33 (0.18)	0.31 (0.14)	0.38 (0.14)	0.22
MyoD1	0.37 (0.20)	0.35 (0.19)	0.46 (0.13)	0.03
N33	0.39 (0.14)	0.41 (0.14)	0.46 (0.11)	0.26
SFRP1	0.48 (0.16)	0.54 (0.14)	0.54 (0.14)	0.37
HPP1	0.34 (0.20)	0.33 (0.17)	0.38 (0.13)	0.40