S2 Table. Summary of 16 genes selected for analysis of transitional-CpG methylation

Gene	Expression pattern	CpG islands	Nearest retroelements		MSP position (kb)	Intermediate methylation density (%)
			Type	Distance (kb)		
CDH1	Housekeeping gene	Presence	*Alu*	0.3	–0.1	11-30
ARRDC4	Housekeeping gene	Presence	*Alu*	1.3	–0.3	11-30
PPARG	Housekeeping gene	Presence	*Alu*	2.3	–1.5	21-40
TRAPPC2L	Housekeeping gene	Presence	*Alu*	3.8	–0.8	41-60
MMP2	Housekeeping gene	Presence	*LTR*	0.6	–0.3	31-50
CDKN2A	Housekeeping gene	Presence	*LTR*	2.4	–1.6	11-30
RUNX2	Housekeeping gene	Presence	*LTR*	6.3	–3.1	21-40
RUNX3	Housekeeping gene	Presence	*LTR*	8.3	–1.4	41-60
TFF3	Stomach antrum, mucous epithelial cells	Absence	*Alu*	0.5	–0.2	31-50
TFF2	Stomach, mucous epithelial cells	Absence	*L1*	2.7	–0.2	31-50
TFF1	Intestine, mucous epithelial cells	Absence	*Alu*	0.5	0.0	31-50
PGC	Stomach, epithelial cells	Absence	*Alu*	1.6	–0.2	31-50
ATP4B	Stomach, parietal cells	Absence	*Alu*	1.5	–0.1	41-60
GHRL	Stomach, epithelial cells	Absence	*Alu*	0.8	–0.2	41-60
PGA	Stomach, chief cells	Absence	*Alu*	1.2	0.0	31-50
APC	Inactive gene	Absence	*Alu*	0.9	–0.1	31-50