

Additional file 1. Normal methylation ranges and thresholds calculated on different sets of healthy individuals by Southern blot, MS-MLPA and pyrosequencing.

A) Southern blot.

<i>H19/IGF2:IG-DMR</i> MI (n=50)	
Mean	52
Standard Dev.	4
+2 SD	60
- 2 SD	44

<i>KCNQ1OT1:TSS-DMR</i> MI (n=40)	
Mean	51
Standard Dev.	4
- 2 SD	43

B) MS-MLPA.

<i>H19/IGF2:IG-DMR HhaI probes</i>						<i>KCNQ1OT1:TSS-DMR HhaI probes</i>				
Controls (50)	(1) L05772	(2) L16503	(3) L08764	(4) L20532	ALL PROBES	(1) L19204	(2) L05782	(3) L06781	(4) L19191	ALL PROBES
Mean	0.48	0.51	0.52	0.55	0.52	0.53	0.49	0.51	0.56	0.52
Standard Dev.	0.02	0.04	0.03	0.04	0.03	0.03	0.02	0.03	0.04	0.03
Max value	0.52	0.58	0.58	0.61		0.59	0.54	0.57	0.63	
Min value	0.44	0.43	0.46	0.48		0.48	0.45	0.44	0.49	
+3 SD	0.54	0.63	0.61	0.67	0.61	0.61	0.56	0.60	0.69	0.61
+2 SD	0.52	0.59	0.58	0.63	0.58	0.59	0.54	0.57	0.65	0.58
+1 SD	0.50	0.55	0.55	0.59	0.55	0.56	0.52	0.54	0.60	0.55
Mean	0.48	0.51	0.52	0.55	0.52	0.53	0.49	0.51	0.56	0.52
-1 SD	0.46	0.47	0.49	0.51	0.49	0.50	0.47	0.48	0.52	0.49
-2 SD	0.44	0.43	0.46	0.47	0.46	0.47	0.45	0.45	0.48	0.46
-3 SD	0.42	0.39	0.43	0.43	0.43	0.44	0.43	0.42	0.44	0.43

C) Pyrosequencing.

ICR1: 40–52%

***H19* promoter:** 44–54%;

DMR2: 41–52%

ICR2: 39–50%.