

Table 1 – Number of differentially methylated probes sorted by genomic region. Q1, probes showing less methylation (<-10%) and higher expression (>0.5 LogFC); Q2, probes showing higher methylation (>10%) and expression; Q3, probes showing higher methylation and less expression (<-0.5 LogFC) ; Q4, probes showing less methylation and expression in HPAEC relative to HPVEC, Genomic regions may overlap between one or more categories (e.g. a probe can be located in 1500bp from upstream and also be associated with Enhancer and/or Promoter)

	All probes		Probes located within 1500bp upstream, 5'UTR and 1st Exon (“non-gene body” probes)			Probes within 1500bp upstream from Transcription Start Site (Excludes 5'UTR/1 st Exon)		
Quadrant number (sup Fig 4)	Probe Count	Proportion to total probes in group	Probe Count	Proportion to total probes in group	Proportion to all analysable probes	Probe Count	Proportion to total probes in group	Proportion to all analysable probes
	351952	100.00%	184099	100.00%	52.31%	130656	100.00%	37.12%
Q1	866	0.25%	462	0.35%	0.13%	292	0.22%	0.08%
Q2	3441	0.98%	955	0.73%	0.27%	619	0.47%	0.18%
Q3	2388	0.68%	1011	0.77%	0.29%	627	0.48%	0.18%
Q4	711	0.20%	301	0.23%	0.09%	179	0.14%	0.05%

	Probes on Enhancer Regions		Promoter Associated Probes			Gene Body Only (not including 5'UTR and 1 st Exon)		
Probe Count	Proportion to total probes in group	Proportion to all analysable probes	Probe Count	Proportion to total probes in group	Proportion to all analysable probes	Probe Count	Proportion to total probes in group	Proportion to all analysable probes
59317	100.00%	16.85%	91601	100.00%	26.03%	146423	100.00%	41.60%
275	0.46%	0.08%	97	0.11%	0.03%	359	0.25%	0.10%
1239	2.09%	0.35%	145	0.16%	0.04%	2220	1.52%	0.63%
960	1.62%	0.27%	214	0.23%	0.06%	1221	0.83%	0.35%
286	0.48%	0.08%	65	0.07%	0.02%	379	0.26%	0.11%