Table S3: Enrichment analysis of 501 differential methylated prakriti specific regions (mPSR) for genomic context and histone occupancy.

Overall Distribution

#501	No of Feature	Features in the array	Chi-square Test	
			P-value	Odds Ratio
Upstream Promoter	21	5360	0.04	1.55
Promoter	75	49331	<0.0001	0.73
5'UTR	36	19790	0.06	0.69
Gene Body	301	99219	0.009	1.2
3'UTR	19	3967	0.005	1.01
Downstream	17	9083	0.23	0.62
Non-Intergenic	32	12649	0.97	0.97
CpG Island Context				
Upstream Promoter	17	4397	0.09	1.5
Promoter	67	40871	0.0005	0.63
5'UTR	34	18469	0.058	0.71
Gene Body	256	81611	0.012	1.21
3'UTR	16	3097	0.0054	2
Downstream	12	7402	0.111	0.62
Non-Intergenic	25	9979	0.89	0.97
CpG shore context				
Upstream Promoter	4	963	0.21	1.5
Promoter	8	8460	0.01	0.63
5'UTR	2	1321	0.59	0.71
Gene Body	45	17608	0.43	1.21
3'UTR	3	870	0.44	2
Downstream	5	1681	0.03	0.62
Non-Intergenic	7	2670	0.66	0.97