

Table S3: Type of rVarBase elements in DMPs

Type*	group B	group A	Expected B (B vs A)	Expected A (B vs A)	p-value (B vs A)	Expected B (B vs Bck)	p-value (B vs bck)	Expected A (A vs Bck)
TssA	604	532	622	514	2.80E-01	552	2.10E-02	457
TssAFlnk	805	664	804	665	9.70E-01	735	6.40E-03	608
TxFlnk	455	189	352	292	9.40E-17	365	1.10E-06	299
Tx	533	338	477	394	7.70E-05	603	2.80E-03	498
TxWk	1281	936	1213	1004	1.40E-03	1321	2.20E-01	1092
EnhG	525	348	478	395	9.50E-04	553	2.20E-01	457
Enh	1085	918	1096	907	6.00E-01	1097	7.10E-01	908
ZNF/Rpts	194	140	183	151	2.30E-01	199	7.50E-01	164
Inactive region	18	8	14	12	2.00E-01	19	9.20E-01	16
TssBiv	326	368	380	314	2.80E-05	325	9.70E-01	270
BivFlnk	244	363	332	275	2.10E-13	247	8.50E-01	207
EnhBiv	379	532	499	412	1.60E-16	433	7.00E-03	361

*Classification performed by RoadMap Epigenomics

bck: background based on 450K Illumina, cl: Cluster

TssA: Active TSS; TssAFlnk: Flanking Active TSS; TxFlnk: Transcr. at gene 5' and 3'; Tx: Strong transcription; TxWk: W

p-value (A vs bck)
2.40E-04
1.70E-02
4.70E-11
4.80E-14
1.20E-07
1.00E-07
7.20E-01
5.80E-02
7.10E-02
8.50E-10
1.00E-28
1.10E-20

Weak