**Table S4. The structural variations of chromatin correlate with genetic and epigenetic features.**

**(A)** In the HindIII sample, the structural variations correlate with genetic and epigenetic features.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  |  |  |  |  |
| Genomic and epigenetic features | Low1 | High2 | Diff3 | P-value4 |
| Gene density | 5.0724 | 7.4052 | 2.3327 | **0.0003** |
| Gene expression | 1.2926 | 1.5806 | 0.2880 | 0.1625 |
| H3K36me3 | -0.6512 | -0.4699 | 0.1813 | **0.0017** |
| H3K27me3 | 0.1328 | 0.1927 | 0.0599 | **0.0500** |
| H3K4me3 | 0.0097 | 0.0140 | 0.0043 | **3.0E-5** |
| RNA polymerase II | 0.0067 | 0.0082 | 0.0016 | **0.0002** |
| Chromatin accessibility | 0.0346 | 0.0462 | 0.0116 | **1.9E-05** |
| DNA replication time | -0.2214 | 0.0392 | 0.2606 | **0.0006** |
| H3K9me3 | -0.0836 | -0.1682 | -0.0846 | **0.0001** |
| H4K20me3 | -0.1531 | -0.2222 | -0.0691 | **0.0199** |
| Genome-nuclear lamina interaction | 0.1098 | -0.0482 | -0.1580 | **0.0011** |
|  |  |  |  |  |

1Mean of genetic and epigenetic features in regions with low structural variations.

2Mean of genetic and epigenetic features in regions with high structural variations.

3Difference of genetic and epigenetic features between regions with high structural variations and regions with low structural variations.

4Two sample t-test p-value. Significant p-values (< 0.05) are highlighted in bold font.

**(B)** In the NcoI sample, the structural variations correlate with genetic and epigenetic features.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  |  |  |  |  |
| Genomic and epigenetic features | Low1 | High2 | Diff3 | P-value4 |
| Gene density | 5.4071 | 7.4885 | 2.0814 | **0.0011** |
| Gene expression | 1.3047 | 1.6100 | 0.3053 | 0.1418 |
| H3K36me3 | -0.6686 | -0.4350 | 0.2335 | **2.6E-05** |
| H3K27me3 | 0.1196 | 0.2090 | 0.0894 | **0.0010** |
| H3K4me3 | 0.0100 | 0.0144 | 0.0044 | **1.7E-05** |
| RNA polymerase II | 0.0068 | 0.0083 | 0.0015 | **0.0003** |
| Chromatin accessibility | 0.0347 | 0.0476 | 0.0129 | **1.0E-06** |
| DNA replication time | -0.2379 | 0.0837 | 0.3215 | **8.0E-06** |
| H3K9me3 | -0.0926 | -0.1733 | -0.0807 | **4.7E-05** |
| H4K20me3 | -0.1346 | -0.2433 | -0.1086 | **0.0001** |
| Genome-nuclear lamina interaction | 0.1387 | -0.0875 | -0.2262 | **1.0E-06** |
|  |  |  |  |  |

1Mean of genetic and epigenetic features in regions with low structural variations.

2Mean of genetic and epigenetic features in regions with high structural variations.

3Difference of genetic and epigenetic features between regions with high structural variations and regions with low structural variations.

4Two sample t-test p-value. Significant p-values (< 0.05) are highlighted in bold font.