

Zuin et al., Table S 8

NIPBL ChIP signals in HB2 cells on different repeat classes.

RPKM measure (reads per kilobase per 10 million reads) was calculated similar to the RNA-seq analyses [56] and an enrichment compared to the input material (control) was calculated.

| class | length (bp) | % of total genomic sequence | ChIP signal (RPKM) | | Enrichment |
|--------------------------|-------------|-----------------------------|--------------------|--------------|--------------|
| | | | NIPBL | ChIP control | |
| SINE-Alu | 306745172 | 9.91 | 1.68 | 1.56 | 1.08 |
| SINE-MIR | 84349685 | 2.72 | 4.75 | 4.97 | 0.96 |
| SINE-Other | 571757 | 0.02 | 5.94 | 5.76 | 1.03 |
| LINE-L1 | 512445461 | 16.55 | 2.08 | 1.96 | 1.07 |
| LINE-L2 | 103990071 | 3.36 | 5.08 | 5.18 | 0.98 |
| LINE-CR1 | 10860002 | 0.35 | 4.55 | 4.48 | 1.02 |
| LINE-RTE | 3643770 | 0.12 | 4.08 | 3.79 | 1.08 |
| LINE-Other | 201745 | 0.01 | 4.89 | 4.75 | 1.03 |
| LTR-ERV1-MaLR | 110849894 | 3.58 | 4 | 3.88 | 1.03 |
| LTR-ERV1 | 56136298 | 1.81 | 4.86 | 4.81 | 1.01 |
| LTR-ERV1 | 83494001 | 2.7 | 3.2 | 3.06 | 1.04 |
| LTR-ERV1 | 8842596 | 0.29 | 1.94 | 1.72 | 1.13 |
| LTR-Gypsy | 2301837 | 0.07 | 5.28 | 5.15 | 1.03 |
| LTR-ERV | 191609 | 0.01 | 5.36 | 4.77 | 1.12 |
| DNA-TcMar-Tigger | 33986503 | 1.1 | 3.15 | 3.03 | 1.04 |
| DNA-TcMar-Mariner | 2830187 | 0.09 | 3.29 | 3.11 | 1.06 |
| DNA-TcMar-Tc2 | 1669939 | 0.05 | 3.24 | 3.08 | 1.05 |
| DNA-TcMar | 318232 | 0.01 | 3.82 | 3.53 | 1.08 |
| DNA-hAT-Charlie | 45014464 | 1.45 | 4.17 | 4.03 | 1.04 |
| DNA-hAT-Blackjack | 3419498 | 0.11 | 4.31 | 4.22 | 1.02 |
| DNA-hAT-Tip100 | 6614899 | 0.21 | 4.35 | 4.32 | 1.01 |
| DNA-hAT | 1687099 | 0.05 | 4.11 | 4.09 | 1.01 |
| DNA-Other | 2734962 | 0.09 | 4.06 | 3.79 | 1.07 |
| Satellite-acro | 31038 | 0 | 14.04 | 11.47 | 1.22 |
| Satellite-centr | 8243430 | 0.27 | 10.45 | 9.17 | 1.14 |
| Satellite-telo | 254147 | 0.01 | 3.2 | 4.27 | 0.75 |
| Satellite | 4025177 | 0.13 | 18.3 | 17.69 | 1.03 |
| rRNA | 175474 | 0.01 | 265.35 | 19.96 | 13.3 |
| LSU-rRNA_Hsa | 68641 | 0.002 | 442.08 | 28.92 | 15.28 |
| SSU-rRNA_Hsa | 16619 | 0.001 | 947.81 | 66.34 | 14.29 |
| 5S | 90214 | 0.003 | 5.15 | 4.59 | 1.12 |
| tRNA | 102988 | 0 | 8.09 | 13.2 | 0.61 |
| scRNA | 122042 | 0 | 3.5 | 3.5 | 1 |
| snRNA | 337551 | 0.01 | 5.57 | 4.13 | 1.35 |
| srpRNA | 263136 | 0.01 | 4.09 | 4.24 | 0.96 |
| RNA | 118748 | 0 | 4.73 | 5.74 | 0.82 |
| Low_complexity | 16922589 | 0.55 | 2.79 | 2.35 | 1.19 |
| Simple_repeat | 26087578 | 0.84 | 2.78 | 3.15 | 0.88 |
| Other_repeat | 6109487 | 0.2 | 1.85 | 1.83 | 1.01 |