*Table S4:*

General consensus loop sizes and thus position relative to the start of the first loop at the first loop base determined for human HB2, as well as HEK293T TEV (intact cohesin) and HRV (cleaved cohesin) cells of the IGF/H19 region at HS 11p 15.5-15.4. The subchromosomal domain size is calculated for domains with defined borders only from the sum of the loop sizes present.

|  |  |  |
| --- | --- | --- |
| **Loop**  **[#]** | **Loop Size**  **[kbp]** | **Domain/Linker**  **[#]** |
| 1 | 15.0 | Domain 1 |
| 2 | 45.9 |
| 3 | 56.0 |
| 4 | 43.0 |
| 5 | 56.7 |
| 6 | 48.1 |
| 7 | 63.2 | Linker 2 |
| 8 | 45.9 | Domain 2  728.5 |
| 9 | 59.6 |
| 10 | 51.7 |
| 11 | 37.3 |
| 12 | 76.1 |
| 13 | 28.7 |
| 14 | 46.7 |
| 15 | 25.1 |
| 16 | 76.8 |
| 17 | 25.8 |
| 18 | 59.6 |
| 19 | 13.6 |
| 20 | 42.3 |
| 21 | 47.4 |
| 22 | 51.7 |
| 23 | 40.2 |
| 24 | 33.7 | Linker 2 |
| 25 | 48.1 | Domain 3  403.4 |
| 26 | 39.5 |
| 27 | 44.5 |
| 28 | 63.2 |
| 29 | 46.7 |
| 30 | 53.8 |
| 31 | 48.8 |
| 32 | 25.1 |
| 33 | 33.7 |
| 34 | 43.1 | Linker 3 |
| 35 | 46.7 | Domain 4 |
| 36 | 73.2 |
| 37 | 43.8 |
| 38 | 63.2 |
| 39 | 62.4 |
| Average  StdDev  StdErr | 48.6±14.5±2.4  46.7±15.1±8.7 | Loops  Linker |