**Table S12. The true value, posterior mean and 95% credible interval for the 12 dimensional multinomial distribution used in the simulation study with multiple distinct 3D chromosomal structures.**

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  |  |  |  |  |  |  |  |  |
| Structure |  |  |  |  | 1 | Mean2 | 2.50% quantile | 97.50% quantile |
| 1 | 0 |  | 0 | 0 | 0.5 | 0.48 | 0.43 | 0.52 |
| 2 | 0 |  |  | 0 | 0 | 0.00 | 0.00 | 0.01 |
| 3 | 0 | 0 | 0 | 0 | 0 | 0.02 | 0.00 | 0.07 |
| 4 | 0 | 0 |  | 0 | 0 | 0.00 | 0.00 | 0.00 |
| 5 |  | 0 | 0 | 0 | 0 | 0.01 | 0.00 | 0.03 |
| 6 |  | 0 |  | 0 | 0 | 0.00 | 0.00 | 0.00 |
| 7 | 0 |  | 0 | 1 | 0 | 0.00 | 0.00 | 0.00 |
| 8 | 0 |  |  | 1 | 0.5 | 0.49 | 0.43 | 0.53 |
| 9 | 0 | 0 | 0 | 1 | 0 | 0.00 | 0.00 | 0.01 |
| 10 | 0 | 0 |  | 1 | 0 | 0.00 | 0.00 | 0.02 |
| 11 |  | 0 | 0 | 1 | 0 | 0.00 | 0.00 | 0.01 |
| 12 |  | 0 |  | 1 | 0 | 0.00 | 0.00 | 0.01 |
|  |  |  |  |  |  |  |  |  |

1The true value for the 12 dimensional multinomial distribution .

2The posterior mean provided by the BACH-MIX algorithm.