**Table S11. Posterior mean and 95% credible interval for parameters in the simulation study with single consensus 3D chromosomal structure.** We use the posterior samples in chain 3 (after burn-in and thin) for statistical inference. The true values for , , , and are , , , and , respectively.

|  |  |  |  |
| --- | --- | --- | --- |
|  |  |  |  |
| Variable | Posterior mean | 2.5% quantile | 97.5% quantile |
|  | 4.0045 | 3.8814 | 4.1186 |
|  | -0.9999 | -1.0206 | -0.9824 |
|  | 0.1020 | 0.0738 | 0.1278 |
|  | -0.0854 | -0.1063 | -0.0644 |
|  | 0.0950 | 0.0721 | 0.1097 |
|  |  |  |  |