**S4 Table. Performance of heterogeneous kinship estimators in ~0.75X sequencing data of 762 Chinese and Malays.**

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Call set** | **Method** | **Unrelated**  **(289,205 pairs)** | | **3rd degree**  **(148 pairs)** | | **2nd degree**  **(147 pairs)** | | **PO/FS**  **(437 pairs)** | | **Self-kinship**  **(762 individuals)** | |
| **RMSE** | **BIAS** | **RMSE** | **BIAS** | **RMSE** | **BIAS** | **RMSE** | **BIAS** | **RMSE** | **BIAS** |
| BEAGLE | SEEKIN | 0.005 | -0.002 | 0.008\* | 0.004\* | 0.010\* | 0.006\* | 0.021\* | 0.015\* | 0.045 | 0.022 |
| PC-Relate | 0.003\* | 0.000\* | 0.013 | -0.012 | 0.025 | -0.024 | 0.048 | -0.047 | 0.035 | 0.026 |
| REAP | 0.003\* | -0.001 | 0.015 | -0.014 | 0.028 | -0.028 | 0.052 | -0.051 | 0.030\* | 0.017\* |
| RelateAdmix | 0.003\* | 0.002 | 0.016 | -0.015 | 0.030 | -0.029 | 0.057 | -0.056 | -- | -- |
| BEAGLE+1KG3 | SEEKIN | 0.003 | -0.001 | 0.003\* | 0.001\* | 0.004\* | 0.001\* | 0.007\* | 0.003\* | 0.018 | 0.002\* |
| PC-Relate | 0.002\* | 0.000\* | 0.005 | -0.004 | 0.010 | -0.009 | 0.020 | -0.020 | 0.017\* | -0.014 |
| REAP | 0.002\* | -0.001 | 0.008 | -0.008 | 0.014 | -0.014 | 0.024 | -0.023 | 0.018 | -0.017 |
| RelateAdmix | 0.002\* | 0.001 | 0.005 | -0.005 | 0.009 | -0.009 | 0.016 | -0.016 | -- | -- |

RMSE is the root mean squared error and BIAS is defined as the mean difference to the array-based estimates from PC-Relate for each type of relatedness. Negative values of BIAS suggest underestimation for results based on sparse sequencing data and vice versa.

\* Smallest magnitude of RMSE or BIAS in each call set and each type of relatedness.