**Table S1.** The correlation ( 95 % Confidence Interval) between the diagonal and off-diagonal values of **A22**1 and **G**1 averaged across generations for both genotyping scenarios2

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Truncation  Point3 | Correlation Between A22 and G | | | | | |
| Scenario1 | | Scenario2 | | |
| Diagonal  Elements | Off-Diagonal Elements | Diagonal  Elements | Off-Diagonal Elements |
| Full | 0.184 (0.16-0.20) | 0.560 (0.55-0.57) | 0.180 (0.16-0.20) | 0.507 (0.50-0.52) |
| 10 | 0.165 (0.14-0.18) | 0.566 (0.56-0.58) | 0.188 (0.17-0.21) | 0.513 (0.50-0.52) |
| 5 | 0.167 (0.15-0.19) | 0.562 (0.55-0.57) | 0.193 (0.17-0.21) | 0.510 (0.50-0.52) |
| 4 | 0.164 (0.14-0.18) | 0.559 (0.55-0.57) | 0.192 (0.17-0.21) | 0.506 (0.50-0.52) |
| 3 | 0.141 (0.12-0.16) | 0.552 (0.54-0.66) | 0.206 (0.19-0.23) | 0.514 (0.50-0.52) |
| 2 | 0.200 (0.18-0.22) | 0.577 (0.57-0.59) | 0.223 (0.20-0.24) | 0.517 (0.51-0.53) |
| 1 | 0.149 (0.13-0.17) | 0.520 (0.51-0.53) | 0.207 (0.19-0.23) | 0.498 (0.49-0.51) |

1 **A22** matrix refers to the pedigree-based relationship for genotyped animals and **G** refers to the adjusted and weighted genomic relationship matrix used when generating the combined pedigree and genomic relationship matrix (**H**).

2 Scenario1: selection candidates did not have phenotype and genotype information when estimated breeding values were predicted. Scenario2: selection candidates had phenotype and genotype information when estimated breeding values were predicted.

3 Truncation point refers to utilizing information on relatives and their associated progeny that are 1, 2, 3, 4, 5, 10 ancestral generation generations back from the selection candidates when breeding values were estimated. Under the Full truncation scenario all available information was utilized when EBV were estimated within each generation.