**Table S3. Mean susceptibility and infectivity following selection using the conventional animal model or the Indirect Genetic Effects model with a logistic link function**.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Selection** | | | Mean susceptibility | Mean infectivity | R0 |
| **None** | | | 0.22 | 0.22 | 4.46 |
| **Conventional animal effect** | | EBV | 0.10 | 0.22 | 2.14±0.04 |
| **Direct effect** | | EBVD | 0.11 | 0.21 | 2.06±0.03 |
| **Indirect effect** | | EBVs | 0.13 | 0.18 | 2.13±0.06 |
| **Index** | Ix=EBVD+ (n-1) EBVs | | 0.11 | 0.20 | 2.03±0.03 |

Population with variation in both infectivity and susceptibility following a skewed multiple allele genetic architecture. 10000 groups of size 10. Proportion selected was 0.10. Values ± standard error when greater than 0.005.