**Table S1 Accuracy of conventional and genomic selection with varying number of phenotypes and phenotyped animals.**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| NoPheno | NoDaughters | rsires | rcows | rnon-pheno | NoPhenoCows | NoPhenoTotal |
| **Conventional selection, 100 sires** | | | | | | |
| Variable resources for phenotyping | | | | | | |
| 1 | 100 | 0.93 | 0.62 | 0.56 | 10,000 | 10,000 |
| 2 | 100 | 0.96 | 0.70 | 0.59 | 10,000 | 20,000 |
| 5 | 100 | 0.97 | 0.81 | 0.64 | 10,000 | 50,000 |
| 10 | 100 | 0.98 | 0.89 | 0.66 | 10,000 | 100,000 |
| Fixed resources for phenotyping | | | | | | |
| 1 | 1000 | 0.99 | 0.63 | 0.59 | 100,000 | 100,000 |
| 2 | 500 | 0.99 | 0.71 | 0.61 | 50,000 | 100,000 |
| 5 | 200 | 0.99 | 0.82 | 0.64 | 20,000 | 100,000 |
| 10 | 100 | 0.98 | 0.89 | 0.66 | 10,000 | 100,000 |
| **Genomic selection** | | | | | | |
| Variable resources for phenotyping | | | | | | |
| 1 | - | - | 0.62 | 0.56 | 10,000 | 10,000 |
| 2 | - | - | 0.70 | 0.63 | 10,000 | 20,000 |
| 5 | - | - | 0.81 | 0.71 | 10,000 | 50,000 |
| 10 | - | - | 0.89 | 0.76 | 10,000 | 100,000 |
| Fixed resources for phenotyping | | | | | | |
| 1 | - | - | 0.63 | 0.93 | 100,000 | 100,000 |
| 2 | - | - | 0.71 | 0.90 | 50,000 | 100,000 |
| 5 | - | - | 0.82 | 0.84 | 20,000 | 100,000 |
| 10 | - | - | 0.89 | 0.76 | 10,000 | 100,000 |

NoRec = Number of phenotypic records per lactation, NoDaughters = number or daughters per sire, rsire = accuracy for sires, rcows = accuracy for cows, rnon-pheno = accuracy for non-phenotyped animals, NoPhenoCows = number of phenotyped cows, NoPhenoTotal = total number of phenotypes (number of phenotypes per lactation times the number of phenotyped cows).