**Table S3 Intensity of sire pre-selection and selection by scenario and relative cost of phenotyping to genotyping**

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| --- | --- | --- | --- | --- | --- | --- |
|  | Relative cost of phenotyping (P) to genotyping (G) | | | | | |
|  | Pre-selection for testing based on PA | | | Selection of sires based on gEBVs | | |
| Scenario | $P:$G = 1:2 | $P:$G = 1:1 | $P:$G = 2:1 | $P:$G = 1:2 | $P:$G = 1:1 | $P:$G = 2:1 |
| C11 | 3.19 | 3.19 | 3.19 | 0.80 | 0.80 | 0.80 |
| G10 | 2.89 | 2.65 | 2.41 | 1.33 | 1.70 | 2.02 |
| G9 | 2.62 | 2.37 | 2.09 | 1.75 | 2.06 | 2.34 |
| G8 | 2.43 | 2.17 | 1.87 | 1.99 | 2.26 | 2.53 |
| G5 | 2.03 | 1.72 | 1.36 | 2.40 | 2.64 | 2.87 |
| G2 | 1.72 | 1.36 | 0.92 | 2.64 | 2.87 | 3.08 |
| G1 | 1.62 | 1.25 | 0.77 | 2.71 | 2.93 | 3.14 |

$P:$G = relative cost of phenotyping ($P) to genotyping ($G), PA = parent average, gEBV = genomic breeding value. The pre-selection step selects the animals with the highest parent average out of all available new born males to send into testing (progeny of genomical). The selection step selects the sires with the highest breeding values out of all tested males to use in artificial insemination. The scenarios are named C/G for conventional/genomic with numbers indicating the number of phenotype records per lactation.