**Figure S1**. Linkage disequilibrium (r2) decay for SNP in the marker panel in the founder population for the swine and cattle population.



**Table S1.** Mean (95 % Confidence Interval)1 true breeding value response per generation for trait 1, trait 2 and the index across different genotyping2 and phenotyping3 scenarios for the swine population.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Phenotyping  Scenario | Genotyping Scenario | Trait 1 | Trait 2 | Index |
| dense\_dense | Pblup | 0.272 (0.269-0.274)\* | 0.276 (0.274-0.277)\* | 0.290 (0.289-0.29)\* |
| random20 | 0.265 (0.262-0.267) | 0.293 (0.292-0.294)\* | 0.302 (0.301-0.302)\* |
| index20 | 0.265 (0.263-0.268) | 0.301 (0.3-0.302)\* | 0.307 (0.307-0.308)\* |
| random40 | 0.263 (0.26-0.266) | 0.299 (0.298-0.3)\* | 0.306 (0.305-0.307)\* |
| index40 | 0.263 (0.261-0.266) | 0.304 (0.303-0.305)\* | 0.310 (0.309-0.311)\* |
| random60 | 0.262 (0.26-0.265) | 0.303 (0.302-0.305)\* | 0.309 (0.308-0.310)\* |
| index60 | 0.264 (0.262-0.267) | 0.306 (0.305-0.307) | 0.312 (0.311-0.312) |
| random80 | 0.263 (0.26-0.266) | 0.306 (0.304-0.307) | 0.311 (0.31-0.312) |
| index80 | 0.264 (0.262-0.267) | 0.307 (0.306-0.308) | 0.312 (0.311-0.313) |
| All | 0.264 (0.261-0.266) | 0.308 (0.307-0.309) | 0.313 (0.312-0.314) |
| dense\_sparse | Pblup | 0.279 (0.277-0.282)\* | 0.245 (0.243-0.248)\* | 0.270 (0.268-0.272)\* |
| random20 | 0.272 (0.269-0.274) | 0.267 (0.264-0.269)\* | 0.284 (0.282-0.286)\* |
| index20 | 0.273 (0.271-0.276) | 0.278 (0.276-0.281)\* | 0.292 (0.291-0.294)\* |
| random40 | 0.267 (0.265-0.270)\* | 0.275 (0.273-0.278)\* | 0.289 (0.288-0.291)\* |
| index40 | 0.271 (0.268-0.273) | 0.282 (0.28-0.285)\* | 0.295 (0.293-0.296)\* |
| random60 | 0.270 (0.268-0.273) | 0.280 (0.278-0.283)\* | 0.293 (0.292-0.295)\* |
| index60 | 0.274 (0.272-0.277) | 0.285 (0.282-0.287) | 0.297 (0.295-0.299) |
| random80 | 0.272 (0.269-0.275) | 0.284 (0.281-0.286) | 0.296 (0.295-0.298) |
| index80 | 0.271 (0.269-0.274) | 0.287 (0.285-0.29) | 0.298 (0.297-0.300) |
| All | 0.273 (0.271-0.276) | 0.288 (0.286-0.29) | 0.299 (0.298-0.301) |

1 Within a phenotype scenario, a genotyping scenario with a \* is statistically different ( P-value < 0.05) from the scenario where all animals are genotyped (i.e. all).

2 See Table 1 for a description of the genotyping scenarios.

3 The dense\_dense phenotype strategy refers to all individuals obtaining a phenotype for both of the traits that are in the index. The dense\_sparse phenotype strategy refers to all individuals obtaining a phenotype for the first trait while only a fraction (20 % in swine and 40 % in cattle) of the individuals obtained a phenotype for the second trait.

**Table S2.** Mean (95 % Confidence Interval) true breeding value response per generation for trait 1, trait 2 and the index across different genotyping1 and phenotyping2 scenarios for the cattle population.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Phenotyping  Scenario | Genotyping Scenario | Trait 1 | Trait 2 | Index |
| dense\_dense | pblup | 0.189 (0.186-0.192) | 0.229 (0.228-0.231)\* | 0.241 (0.24-0.242)\* |
| random20 | 0.184 (0.181-0.187) | 0.245 (0.243-0.246)\* | 0.253 (0.252-0.254)\* |
| index20 | 0.187 (0.184-0.19) | 0.252 (0.25-0.253)\* | 0.259 (0.258-0.261)\* |
| random40 | 0.180 (0.177-0.183) | 0.249 (0.248-0.25)\* | 0.257 (0.255-0.258)\* |
| index40 | 0.184 (0.181-0.187) | 0.255 (0.254-0.257)\* | 0.262 (0.261-0.263)\* |
| random60 | 0.184 (0.181-0.187) | 0.253 (0.252-0.255)\* | 0.26 (0.259-0.262)\* |
| index60 | 0.185 (0.182-0.188) | 0.257 (0.256-0.259) | 0.264 (0.263-0.265) |
| random80 | 0.185 (0.182-0.188) | 0.256 (0.254-0.257)\* | 0.263 (0.261-0.264)\* |
| index80 | 0.185 (0.182-0.188) | 0.258 (0.257-0.26) | 0.265 (0.264-0.266) |
| all | 0.186 (0.183-0.189) | 0.260 (0.258-0.261) | 0.266 (0.265-0.267) |
| dense\_sparse | pblup | 0.189 (0.185-0.192)\* | 0.203 (0.201-0.205)\* | 0.220 (0.218-0.222)\* |
| random20 | 0.176 (0.172-0.180) | 0.222 (0.22-0.224)\* | 0.234 (0.232-0.235)\* |
| index20 | 0.179 (0.175-0.182) | 0.232 (0.23-0.234)\* | 0.243 (0.241-0.244)\* |
| random40 | 0.178 (0.174-0.181) | 0.228 (0.226-0.23)\* | 0.239 (0.238-0.241)\* |
| index40 | 0.178 (0.175-0.182) | 0.235 (0.233-0.237)\* | 0.245 (0.243-0.247)\* |
| random60 | 0.179 (0.175-0.182) | 0.231 (0.229-0.233)\* | 0.242 (0.240-0.244)\* |
| index60 | 0.179 (0.175-0.182) | 0.237 (0.235-0.239) | 0.246 (0.245-0.248) |
| random80 | 0.179 (0.176-0.183) | 0.237 (0.235-0.239) | 0.247 (0.245-0.248) |
| index80 | 0.177 (0.173-0.180) | 0.240 (0.238-0.242) | 0.249 (0.247-0.250) |
| all | 0.180 (0.176-0.183) | 0.240 (0.238-0.242) | 0.249 (0.247-0.251) |

1 Within a phenotype scenario, a genotyping scenario with a \* is statistically different ( P-value < 0.05) from the scenario where all animals are genotyped (i.e. all).

2 See Table 1 for a description of the heritability, genotyping and phenotyping scenarios.