**Evaluation of the potential use of a meta-population for genomic selection in autochthonous beef cattle populations**

E. F. Mouresan, J. J. Cañas-Álvarez, A. González-Rodríguez, S. Munilla, J. Altarriba, C. Díaz, J. A. Baró, A. Molina, J. Piedrafita, L. Varona

***Supplementary Table S1.*** *Accuracy from purebred genomic evaluation in testing populations (h2=0.4)*

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  |  | | Training sets | | | | | | |
|  |  | | AV | ANI | BP | Mo | Pi | Re | RG |
| Validation sets | AV | Gen1 | **0.580**  (0.014) | 0.125  (0.032) | 0.117  (0.022) | 0.135  (0.029) | 0.146  (0.012) | 0.144  (0.015) | 0.137  (0.025) |
| Gen2 | **0.475**  (0.026) | 0.158  (0.021) | 0.112  (0.019) | 0.111  (0.021) | 0.144  (0.018) | 0.112  (0.028) | 0.137  (0.021) |
| Gen3 | **0.437**  (0.029) | 0.171  (0.017) | 0.130  (0.021) | 0.128  (0.019) | 0.138  (0.011) | 0.137  (0.025) | 0.167  (0.012) |
| ANI | Gen1 | 0.170  (0.037) | **0.605**  (0.012) | 0.167  (0.022) | 0.166  (0.022) | 0.106  (0.016) | 0.136  (0.016) | 0.126  (0.019) |
| Gen2 | 0.160  (0.035) | **0.495**  (0.015) | 0.168  (0.009) | 0.188  (0.013) | 0.124  (0.018) | 0.154  (0.019) | 0.155  (0.033) |
| Gen3 | 0.150  (0.029) | **0.454**  (0.020) | 0.151  (0.011) | 0.203  (0.016) | 0.121  (0.014) | 0.192  (0.022) | 0.139  (0.015) |
| BP | Gen1 | 0.121  (0.030) | 0.155  (0.010) | **0.603**  (0.013) | 0.137  (0.017) | 0.131  (0.017) | 0.128  (0.025) | 0.160  (0.022) |
| Gen2 | 0.152  (0.028) | 0.108  (0.012) | **0.475**  (0.008) | 0.153  (0.020) | 0.142  (0.016) | 0.148  (0.026) | 0.159  (0.017) |
| Gen3 | 0.156  (0.026) | 0.106  (0.023) | **0.420**  (0.011) | 0.140  (0.023) | 0.121  (0.012) | 0.107  (0.022) | 0.145  (0.025) |
| Mo | Gen1 | 0.132  (0.018) | 0.164  (0.015) | 0.132  (0.022) | **0.591**  (0.015) | 0.104  (0.019) | 0.149  (0.025) | 0.143  (0.018) |
| Gen2 | 0.130  (0.014) | 0.166  (0.015) | 0.133  (0.024) | **0.486**  (0.023) | 0.141  (0.010) | 0.155  (0.007) | 0.161  (0.006) |
| Gen3 | 0.082  (0.018) | 0.139  (0.011) | 0.143  (0.006) | **0.442**  (0.017) | 0.140  (0.020) | 0.134  (0.016) | 0.142  (0.022) |
| Pi | Gen1 | 0.138  (0.017) | 0.141  (0.014) | 0.177  (0.019) | 0.127  (0.020) | **0.613**  (0.017) | 0.128  (0.026) | 0.101  (0.013) |
| Gen2 | 0.125  (0.026) | 0.149  (0.019) | 0.198  (0.023) | 0.105  (0.012) | **0.525**  (0.017) | 0.124  (0.028) | 0.125  (0.017) |
| Gen3 | 0.112  (0.017) | 0.122  (0.024) | 0.190  (0.011) | 0.148  (0.011) | **0.496**  (0.012) | 0.124  (0.032) | 0.098  (0.022) |
| Re | Gen1 | 0.120  (0.021) | 0.124  (0.027) | 0.131  (0.013) | 0.116  (0.022) | 0.087  (0.015) | **0.608**  (0.015) | 0.132  (0.018) |
| Gen2 | 0.124  (0.021) | 0.128  (0.018) | 0.149  (0.026) | 0.143  (0.023) | 0.101  (0.027) | **0.543**  (0.027) | 0.114  (0.018) |
| Gen3 | 0.131  (0.014) | 0.146  (0.032) | 0.159  (0.021) | 0.137  (0.009) | 0.100  (0.023) | **0.481**  (0.015) | 0.107  (0.011) |
| RG | Gen1 | 0.136  (0.033) | 0.156  (0.024) | 0.168  (0.021) | 0.136  (0.019) | 0.172  (0.032) | 0.126  (0.010) | **0.637**  (0.005) |
| Gen2 | 0.133  (0.025) | 0.158  (0.014) | 0.184  (0.012) | 0.159  (0.022) | 0.163  (0.025) | 0.147  (0.024) | **0.545**  (0.014) |
| Gen3 | 0.123  (0.021) | 0.131  (0.021) | 0.177  (0.018) | 0.161  (0.016) | 0.161  (0.021) | 0.149  (0.028) | **0.474**  (0.024) |

***Supplementary Table S2.*** *Accuracy from purebred genomic evaluation in testing populations (h2=0.1)*

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  |  | | Training sets | | | | | | |
|  |  | | AV | ANI | BP | Mo | Pi | Re | RG |
| Validation sets | AV | Gen1 | **0.387**  (0.013) | 0.077  (0.014) | 0.091  (0.031) | 0.054  (0.018) | 0.079  (0.031) | 0.080  (0.025) | 0.063  (0.016) |
| Gen2 | **0.307**  (0.019) | 0.096  (0.024) | 0.105  (0.037) | 0.040  (0.015) | 0.084  (0.043) | 0.087  (0.023) | 0.052  (0.026) |
| Gen3 | **0.270**  (0.021) | 0.091  (0.054) | 0.099  (0.034) | 0.099  (0.013) | 0.073  (0.017) | 0.085  (0.022) | 0.058  (0.022) |
| ANI | Gen1 | 0.076  (0.018) | **0.419**  (0.006) | 0.069  (0.011) | 0.091  (0.013) | 0.079  (0.017) | 0.071  (0.017) | 0.071  (0.017) |
| Gen2 | 0.064  (0.020) | **0.346**  (0.013) | 0.079  (0.014) | 0.094  (0.031) | 0.067  (0.011) | 0.083  (0.023) | 0.091  (0.016) |
| Gen3 | 0.096  (0.006) | **0.284**  (0.011) | 0.090  (0.013) | 0.122  (0.025) | 0.087  (0.014) | 0.085  (0.039) | 0.093  (0.012) |
| BP | Gen1 | 0.106  (0.033) | 0.059  (0.018) | **0.385**  (0.015) | 0.087  (0.039) | 0.077  (0.018) | 0.104  (0.025) | 0.092  (0.019) |
| Gen2 | 0.099  (0.025) | 0.080  (0.018) | **0.292**  (0.013) | 0.086  (0.022) | 0.080  (0.017) | 0.108  (0.014) | 0.082  (0.013) |
| Gen3 | 0.103  (0.021) | 0.084  (0.014) | **0.244**  (0.018) | 0.105  (0.012) | 0.074  (0.017) | 0.059  (0.020) | 0.063  (0.019) |
| Mo | Gen1 | 0.129  (0.017) | 0.077  (0.017) | 0.054  (0.027) | **0.440**  (0.025) | 0.070  (0.031) | 0.067  (0.018) | 0.090  (0.016) |
| Gen2 | 0.119  (0.019) | 0.063  (0.017) | 0.068  (0.011) | **0.377**  (0.017) | 0.070  (0.028) | 0.052  (0.029) | 0.086  (0.033) |
| Gen3 | 0.066  (0.022) | 0.083  (0.021) | 0.059  (0.014) | **0.312**  (0.009) | 0.073  (0.019) | 0.033  (0.017) | 0.081  (0.033) |
| Pi | Gen1 | 0.063  (0.017) | 0.033  (0.020) | 0.076  (0.016) | 0.101  (0.027) | **0.419**  (0.016) | 0.059  (0.028) | 0.080  (0.021) |
| Gen2 | 0.039  (0.032) | 0.055  (0.022) | 0.080  (0.020) | 0.087  (0.016) | **0.362**  (0.015) | 0.057  (0.028) | 0.087  (0.019) |
| Gen3 | 0.050  (0.016) | 0.059  (0.018) | 0.063  (0.033) | 0.095  (0.022) | **0.294**  (0.017) | 0.082  (0.013) | 0.091  (0.009) |
| Re | Gen1 | 0.087  (0.023) | 0.095  (0.009) | 0.030  (0.018) | 0.120  (0.013) | 0.055  (0.017) | **0.380**  (0.036) | 0.078  (0.016) |
| Gen2 | 0.096  (0.027) | 0.113  (0.014) | 0.063  (0.022) | 0.111  (0.009) | 0.090  (0.016) | **0.300**  (0.013) | 0.077  (0.021) |
| Gen3 | 0.091  (0.017) | 0.085  (0.013) | 0.063  (0.033) | 0.123  (0.014) | 0.071  (0.016) | **0.285**  (0.017) | 0.069  (0.011) |
| RG | Gen1 | 0.053  (0.027) | 0.057  (0.025) | 0.103  (0.029) | 0.034  (0.019) | 0.049  (0.021) | 0.045  (0.025) | **0.398**  (0.025) |
| Gen2 | 0.045  (0.018) | 0.070  (0.018) | 0.107  (0.021) | 0.061  (0.020) | 0.068  (0.012) | 0.066  (0.020) | **0.334**  (0.022) |
| Gen3 | 0.051  (0.022) | 0.060  (0.019) | 0.097  (0.039) | 0.073  (0.020) | 0.090  (0.028) | 0.080  (0.022) | **0.291**  (0.019) |

***Supplementary Table S3.*** *Accuracy from genomic evaluation in admixed ×2 populations in the generation 1 (h2=0.4).*

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  |  | Validation sets | | | | | | |
|  |  | AV | ANI | BP | Mo | Pi | Re | RG |
| Training sets | AV-ANI | **0.475**  (0.013) | **0.498**  (0.012) | 0.150  (0.015) | 0.180  (0.012) | 0.153  (0.018) | 0.126  (0.015) | 0.167  (0.018) |
| AV-BP | **0.481**  (0.020) | 0.179  (0.032) | **0.500**  (0.016) | 0.144  (0.024) | 0.169  (0.007) | 0.141  (0.010) | 0.186  (0.027) |
| AV-Mo | **0.480**  (0.017) | 0.178  (0.026) | 0.160  (0.015) | **0.504**  (0.018) | 0.136  (0.013) | 0.126  (0.023) | 0.163  (0.027) |
| AV-Pi | **0.477**  (0.016) | 0.164  (0.028) | 0.140  (0.025) | 0.126  (0.021) | **0.525**  (0.012) | 0.111  (0.009) | 0.180  (0.028) |
| AV-Re | **0.482**  (0.016) | 0.174  (0.028) | 0.146  (0.019) | 0.150  (0.024) | 0.120  (0.024) | **0.518**  (0.017) | 0.175  (0.021) |
| AV-RG | **0.478**  (0.013) | 0.150  (0.020) | 0.150  (0.024) | 0.154  (0.014) | 0.111  (0.020) | 0.140  (0.017) | **0.545**  (0.011) |
| ANI-BP | 0.121  (0.018) | **0.495**  (0.013) | **0.498**  (0.016) | 0.176  (0.018) | 0.185  (0.009) | 0.140  (0.015) | 0.167  (0.022) |
| ANI-Mo | 0.126  (0.023) | **0.497**  (0.011) | 0.170  (0.018) | **0.506**  (0.015) | 0.158  (0.007) | 0.126  (0.028) | 0.139  (0.016) |
| ANI-Pi | 0.120  (0.024) | **0.491**  (0.014) | 0.149  (0.016) | 0.162  (0.020) | **0.529**  (0.010) | 0.117  (0.017) | 0.164  (0.016) |
| ANI-Re | 0.124  (0.015) | **0.494**  (0.013) | 0.149  (0.013) | 0.181  (0.023) | 0.151  (0.024) | **0.518**  (0.015) | 0.153  (0.022) |
| ANI-RG | 0.114  (0.024) | **0.490**  (0.016) | 0.162  (0.015) | 0.185  (0.011) | 0.134  (0.015) | 0.137  (0.024) | **0.543**  (0.011) |
| BP-Mo | 0.138  (0.038) | 0.173  (0.012) | **0.499**  (0.019) | **0.501**  (0.017) | 0.172  (0.015) | 0.137  (0.014) | 0.158  (0.028) |
| BP-Pi | 0.134  (0.016) | 0.159  (0.033) | **0.498**  (0.014) | 0.122  (0.022) | **0.531**  (0.011) | 0.124  (0.013) | 0.181  (0.015) |
| BP-Re | 0.135  (0.020) | 0.165  (0.025) | **0.499**  (0.016) | 0.144  (0.021) | 0.163  (0.017) | **0.521**  (0.016) | 0.172  (0.021) |
| BP-RG | 0.133  (0.028) | 0.144  (0.023) | **0.497**  (0.017) | 0.151  (0.010) | 0.152  (0.015) | 0.153  (0.019) | **0.544**  (0.012) |
| Mo-Pi | 0.138  (0.023) | 0.154  (0.012) | 0.151  (0.010) | **0.499**  (0.016) | **0.526**  (0.012) | 0.110  (0.014) | 0.152  (0.024) |
| Mo-Re | 0.140  (0.025) | 0.165  (0.014) | 0.165  (0.019) | **0.506**  (0.016) | 0.132  (0.016) | **0.517**  (0.015) | 0.142  (0.016) |
| Mo-RG | 0.134  (0.031) | 0.143  (0.015) | 0.165  (0.023) | **0.505**  (0.017) | 0.118  (0.017) | 0.136  (0.026) | **0.542**  (0.011) |
| Pi-Re | 0.141  (0.015) | 0.150  (0.017) | 0.141  (0.019) | 0.128  (0.025) | **0.527**  (0.013) | **0.514**  (0.015) | 0.168  (0.020) |
| Pi-RG | 0.130  (0.020) | 0.125  (0.012) | 0.145  (0.011) | 0.131  (0.008) | **0.523**  (0.011) | 0.124  (0.017) | **0.542**  (0.009) |
| Re-RG | 0.134  (0.022) | 0.133  (0.016) | 0.153  (0.012) | 0.151  (0.009) | 0.103  (0.016) | **0.521**  (0.015) | **0.543**  (0.011) |

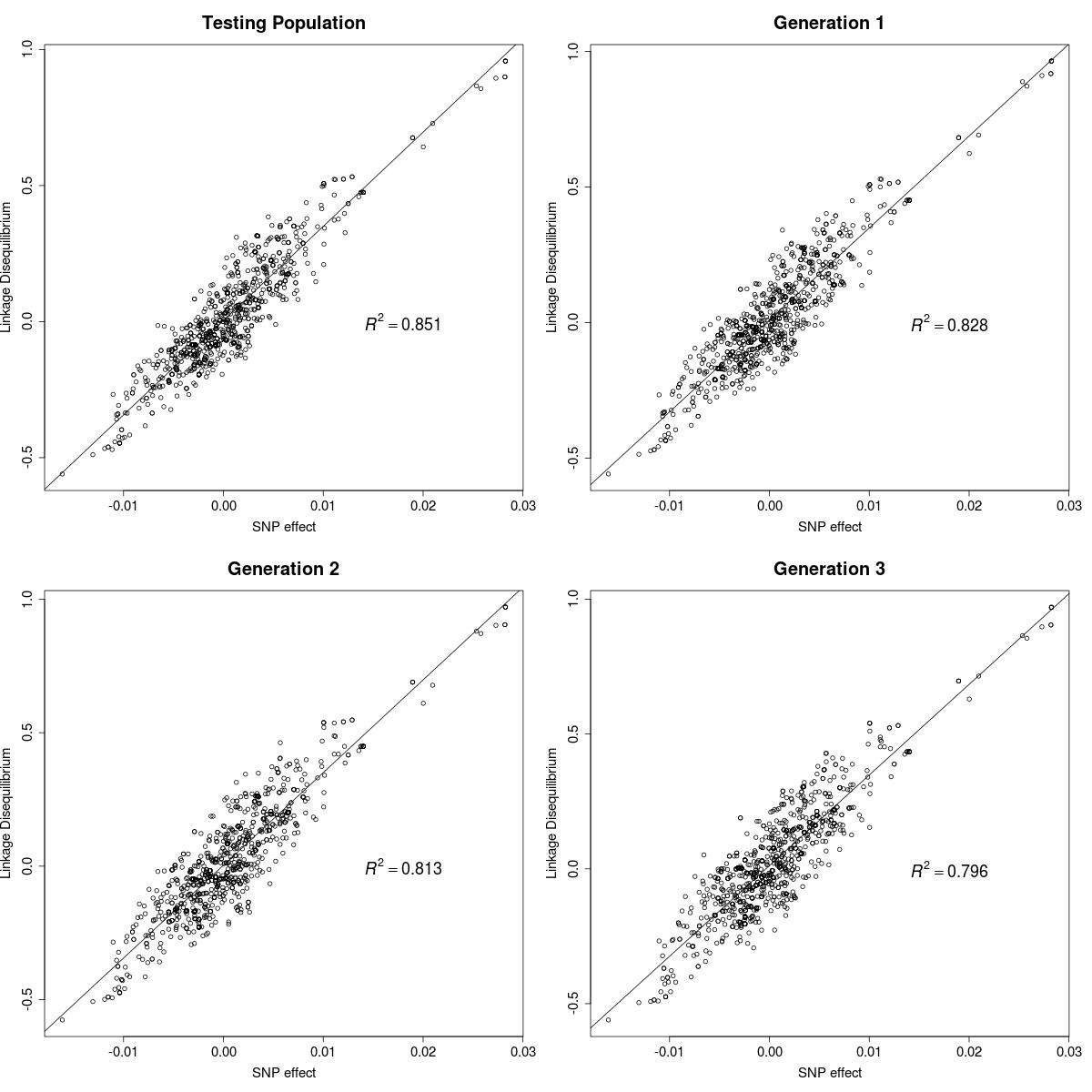
***Supplementary Table S4.*** *Accuracy from genomic evaluation in admixed ×2 populations in the generation 1 (h2=0.1).*

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  |  | Validation sets | | | | | | |
|  |  | AV | ANI | BP | Mo | Pi | Re | RG |
| Training sets | AV-ANI | **0.303**  (0.020) | **0.318**  (0.011) | 0.094  (0.027) | 0.101  (0.014) | 0.045  (0.019) | 0.078  (0.016) | 0.071  (0.022) |
| AV-BP | **0.299**  (0.023) | 0.056  (0.014) | **0.317**  (0.023) | 0.122  (0.023) | 0.086  (0.018) | 0.064  (0.012) | 0.113  (0.028) |
| AV-Mo | **0.298**  (0.020) | 0.066  (0.021) | 0.090  (0.019) | **0.334**  (0.036) | 0.071  (0.015) | 0.092  (0.013) | 0.051  (0.017) |
| AV-Pi | **0.299**  (0.021) | 0.079  (0.019) | 0.097  (0.021) | 0.105  (0.019) | **0.335**  (0.021) | 0.051  (0.015) | 0.069  (0.033) |
| AV-Re | **0.301**  (0.021) | 0.069  (0.022) | 0.108  (0.016) | 0.097  (0.026) | 0.045  (0.029) | **0.299**  (0.025) | 0.058  (0.018) |
| AV-RG | **0.295**  (0.020) | 0.075  (0.019) | 0.105  (0.020) | 0.116  (0.017) | 0.060  (0.025) | 0.097  (0.026) | **0.317**  (0.039) |
| ANI-BP | 0.085  (0.015) | **0.315**  (0.013) | **0.313**  (0.025) | 0.074  (0.021) | 0.076  (0.010) | 0.058  (0.019) | 0.103  (0.026) |
| ANI-Mo | 0.065  (0.020) | **0.315**  (0.010) | 0.072  (0.019) | **0.327**  (0.037) | 0.061  (0.011) | 0.086  (0.018) | 0.040  (0.030) |
| ANI-Pi | 0.071  (0.020) | **0.317**  (0.017) | 0.081  (0.013) | 0.060  (0.013) | **0.331**  (0.020) | 0.047  (0.007) | 0.056  (0.031) |
| ANI-Re | 0.085  (0.014) | **0.318**  (0.014) | 0.095  (0.014) | 0.058  (0.012) | 0.034  (0.023) | **0.298**  (0.026) | 0.047  (0.015) |
| ANI-RG | 0.066  (0.016) | **0.318**  (0.014) | 0.089  (0.012) | 0.070  (0.017) | 0.048  (0.032) | 0.086  (0.028) | **0.311**  (0.039) |
| BP-Mo | 0.060  (0.024) | 0.054  (0.019) | **0.312**  (0.028) | **0.333**  (0.035) | 0.099  (0.020) | 0.073  (0.017) | 0.085  (0.018) |
| BP-Pi | 0.064  (0.029) | 0.065  (0.023) | **0.313**  (0.026) | 0.077  (0.015) | **0.338**  (0.018) | 0.030  (0.011) | 0.098  (0.041) |
| BP-Re | 0.076  (0.027) | 0.055  (0.020) | **0.315**  (0.028) | 0.073  (0.019) | 0.073  (0.018) | **0.293**  (0.025) | 0.091  (0.031) |
| BP-RG | 0.056  (0.020) | 0.064  (0.021) | **0.315**  (0.026) | 0.092  (0.014) | 0.086  (0.025) | 0.075  (0.029) | **0.320**  (0.043) |
| Mo-Pi | 0.047  (0.026) | 0.072  (0.025) | 0.073  (0.023) | **0.326**  (0.039) | **0.336**  (0.019) | 0.062  (0.016) | 0.037  (0.022) |
| Mo-Re | 0.057  (0.023) | 0.067  (0.028) | 0.086  (0.023) | **0.327**  (0.039) | 0.060  (0.015) | **0.301**  (0.026) | 0.029  (0.012) |
| Mo-RG | 0.040  (0.008) | 0.073  (0.023) | 0.084  (0.023) | **0.328**  (0.037) | 0.072  (0.027) | 0.106  (0.021) | **0.308**  (0.038) |
| Pi-Re | 0.065  (0.028) | 0.079  (0.021) | 0.091  (0.011) | 0.058  (0.022) | **0.331**  (0.019) | **0.290**  (0.026) | 0.044  (0.031) |
| Pi-RG | 0.047  (0.021) | 0.085  (0.038) | 0.090  (0.013) | 0.071  (0.019) | **0.333**  (0.019) | 0.063  (0.021) | **0.311**  (0.042) |
| Re-RG | 0.056  (0.017) | 0.077  (0.011) | 0.103  (0.012) | 0.072  (0.020) | 0.044  (0.025) | **0.301**  (0.024) | **0.312**  (0.042) |

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***Supplementary Figure S1.*** *Accuracy from single-breed genomic evaluation under different genetic architecture scenarios.*

PG=Polygenic effects, 10G(20%)=Polygenic effects + 10 genes explaining 20% of the genetic variance, 4G(50%)=Polygenic effects + 4 genes explaining 50% of the genetic variance, Ex=Polygenic effects drawn from an exponential distribution, LMAF=polygenic effects with low allelic frequencies (≤0.05), 4MG=4 major genes.



***Supplementary Figure S2.*** *Relationship between the linkage disequilibrium with a causal gene with an additive effect of 20.16 units and the estimated SNP effects for the 1000 closest markers in one case of the 4MG scenario.*

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***Supplementary Figure S3.*** *Accuracy from admixed ×2 genomic evaluation under different genetic architecture scenarios.*

PG=Polygenic effects, 10G(20%)=Polygenic effects + 10 genes explaining 20% of the genetic variance, 4G(50%)=Polygenic effects + 4 genes explaining 50% of the genetic variance, Ex=Polygenic effects drawn from an exponential distribution, LMAF=polygenic effects with low allelic frequencies (≤0.05), 4MG=4 major genes.

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***Supplementary Figure S4.*** *Accuracy from admixed ×7 genomic evaluation under different genetic architecture scenarios.*

PG=Polygenic effects, 10G(20%)=Polygenic effects + 10 genes explaining 20% of the genetic variance, 4G(50%)=Polygenic effects + 4 genes explaining 50% of the genetic variance, Ex=Polygenic effects drawn from an exponential distribution, LMAF=polygenic effects with low allelic frequencies (≤0.05), 4MG=4 major genes.