**Genotype imputation from various low-density SNP panels and its impact on accuracy of genomic breeding values in pigs**

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***Table S1*** *Number of SNPs selected for low-density SNP panels in pigs*

|  |  |  |  |
| --- | --- | --- | --- |
| **Chr.** | **Chr****size (Mb)** | **Evenly-spaced SNPs selected for LD panel** | **LD7K** |
| **LD300** | **LD500** | **LD800** | **LD1K** | **LD2K** | **LD3K** | **LD4K** | **LD5K** |
| 1 | 315.32 | 36 | 61 | 99 | 124 | 254 | 383 | 511 | 637 | 808 |
| 2 | 162.57 | 19 | 32 | 50 | 64 | 128 | 190 | 252 | 314 | 459 |
| 3 | 144.79 | 17 | 28 | 46 | 57 | 113 | 169 | 226 | 281 | 415 |
| 4 | 143.47 | 17 | 28 | 45 | 57 | 115 | 176 | 236 | 295 | 447 |
| 5 | 111.51 | 13 | 22 | 35 | 44 | 90 | 134 | 181 | 222 | 324 |
| 6 | 157.77 | 18 | 31 | 50 | 63 | 127 | 191 | 255 | 326 | 458 |
| 7 | 134.76 | 15 | 26 | 42 | 53 | 106 | 162 | 216 | 272 | 410 |
| 8 | 148.49 | 17 | 29 | 46 | 58 | 116 | 173 | 233 | 292 | 428 |
| 9 | 153.67 | 18 | 30 | 49 | 61 | 123 | 182 | 243 | 305 | 443 |
| 10 | 79.10 | 9 | 15 | 25 | 32 | 64 | 95 | 128 | 160 | 233 |
| 11 | 87.69 | 10 | 17 | 28 | 35 | 71 | 107 | 144 | 182 | 272 |
| 12 | 63.59 | 8 | 13 | 20 | 25 | 50 | 76 | 104 | 131 | 232 |
| 13 | 218.64 | 25 | 43 | 69 | 86 | 177 | 267 | 357 | 442 | 601 |
| 14 | 153.85 | 18 | 30 | 49 | 61 | 125 | 188 | 255 | 321 | 485 |
| 15 | 157.68 | 18 | 31 | 49 | 63 | 123 | 185 | 248 | 304 | 433 |
| 16 | 86.90 | 10 | 17 | 28 | 34 | 70 | 106 | 142 | 180 | 281 |
| 17 | 69.70 | 8 | 14 | 22 | 28 | 56 | 85 | 114 | 146 | 237 |
| 18 | 61.22 | 7 | 12 | 20 | 24 | 50 | 75 | 102 | 128 | 209 |
| X | 144.29 | 17 | 23 | 30 | 34 | 46 | 51 | 58 | 60 | 81 |
| Y | 1.64 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| **Total** | **2 596.65** | **300** | **502** | **802** | **1 003** | **2 004** | **2 995** | **4 005** | **4 998** | **7 256** |
| Chr.: Chromosome; The low-density panels contained 300 (LD300), 502 (LD500), 802 (LD800), 1 003 (LD1K), 2 004 (LD2K), 2 995 (LD3K), 4 005 (LD4K), 4 998 (LD5K) and 7 256 (LD7K) markers. |

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| **Table S2a.** Descriptive statistics on imputation rates per chromosome in pigs. |
|   | **Duroc** |   | **Landrace** |
| **Chr** | **LD300** | **LD500** | **LD800** | **LD1K** | **LD2K** | **LD3K** | **LD4K** | **LD5K** |   | **LD300** | **LD500** | **LD800** | **LD1K** | **LD2K** | **LD3K** | **LD4K** | **LD5K** |
| **1** | 0.82 | 0.85 | 0.89 | 0.91 | 0.94 | 0.95 | 0.97 | 0.97 |  | 0.91 | 0.93 | 0.95 | 0.95 | 0.97 | 0.98 | 0.99 | 0.99 |
| **2** | 0.78 | 0.83 | 0.87 | 0.89 | 0.93 | 0.95 | 0.96 | 0.97 |  | 0.91 | 0.93 | 0.94 | 0.96 | 0.97 | 0.98 | 0.98 | 0.98 |
| **3** | 0.72 | 0.8 | 0.83 | 0.86 | 0.91 | 0.93 | 0.95 | 0.96 |  | 0.89 | 0.91 | 0.92 | 0.94 | 0.96 | 0.97 | 0.98 | 0.98 |
| **4** | 0.76 | 0.81 | 0.85 | 0.87 | 0.91 | 0.95 | 0.96 | 0.96 |  | 0.9 | 0.91 | 0.93 | 0.94 | 0.97 | 0.98 | 0.98 | 0.98 |
| **5** | 0.76 | 0.79 | 0.82 | 0.85 | 0.9 | 0.92 | 0.94 | 0.95 |  | 0.87 | 0.91 | 0.92 | 0.93 | 0.96 | 0.97 | 0.98 | 0.98 |
| **6** | 0.75 | 0.81 | 0.85 | 0.85 | 0.91 | 0.94 | 0.96 | 0.96 |  | 0.86 | 0.89 | 0.92 | 0.91 | 0.95 | 0.97 | 0.97 | 0.98 |
| **7** | 0.82 | 0.84 | 0.86 | 0.87 | 0.92 | 0.94 | 0.95 | 0.96 |  | 0.92 | 0.93 | 0.93 | 0.95 | 0.96 | 0.97 | 0.98 | 0.98 |
| **8** | 0.78 | 0.82 | 0.84 | 0.87 | 0.92 | 0.95 | 0.96 | 0.96 |  | 0.86 | 0.89 | 0.92 | 0.93 | 0.96 | 0.97 | 0.98 | 0.98 |
| **9** | 0.81 | 0.83 | 0.85 | 0.88 | 0.92 | 0.94 | 0.95 | 0.96 |  | 0.91 | 0.93 | 0.94 | 0.95 | 0.97 | 0.98 | 0.98 | 0.98 |
| **10** | 0.73 | 0.77 | 0.8 | 0.83 | 0.87 | 0.91 | 0.93 | 0.94 |  | 0.87 | 0.91 | 0.9 | 0.92 | 0.94 | 0.96 | 0.97 | 0.97 |
| **11** | 0.75 | 0.79 | 0.8 | 0.84 | 0.89 | 0.92 | 0.94 | 0.95 |  | 0.89 | 0.91 | 0.93 | 0.94 | 0.96 | 0.97 | 0.98 | 0.98 |
| **12** | 0.76 | 0.75 | 0.78 | 0.8 | 0.86 | 0.92 | 0.93 | 0.94 |  | 0.87 | 0.88 | 0.9 | 0.91 | 0.95 | 0.96 | 0.97 | 0.97 |
| **13** | 0.82 | 0.84 | 0.89 | 0.9 | 0.93 | 0.95 | 0.96 | 0.97 |  | 0.92 | 0.93 | 0.95 | 0.96 | 0.97 | 0.98 | 0.98 | 0.99 |
| **14** | 0.78 | 0.82 | 0.88 | 0.89 | 0.93 | 0.94 | 0.96 | 0.97 |  | 0.9 | 0.92 | 0.95 | 0.96 | 0.97 | 0.98 | 0.98 | 0.99 |
| **15** | 0.77 | 0.81 | 0.86 | 0.87 | 0.92 | 0.94 | 0.96 | 0.97 |  | 0.89 | 0.91 | 0.93 | 0.94 | 0.97 | 0.97 | 0.98 | 0.98 |
| **16** | 0.77 | 0.8 | 0.84 | 0.86 | 0.91 | 0.94 | 0.95 | 0.96 |  | 0.9 | 0.91 | 0.93 | 0.95 | 0.96 | 0.97 | 0.98 | 0.98 |
| **17** | 0.8 | 0.83 | 0.87 | 0.86 | 0.91 | 0.95 | 0.95 | 0.96 |  | 0.91 | 0.91 | 0.94 | 0.94 | 0.96 | 0.97 | 0.98 | 0.98 |
| **18** | 0.7 | 0.73 | 0.8 | 0.8 | 0.9 | 0.93 | 0.95 | 0.96 |   | 0.85 | 0.86 | 0.91 | 0.92 | 0.95 | 0.97 | 0.97 | 0.97 |

Chr.: Chromosome; The low-density panels contained 300 (LD300), 502 (LD500), 802 (LD800), 1 003 (LD1K), 2 004 (LD2K), 2 995 (LD3K), 4 005 (LD4K), 4 998 (LD5K) and 7 256 (LD7K) markers.

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| **Table S2b.** Descriptive statistics on imputation rates per chromosome in pigs. |
|   |   | **Yorkshire** |
| **Chr** | **LD300** | **LD500** | **LD800** | **LD1K** | **LD2K** | **LD3K** | **LD4K** | **5K** |
| **1** | 0.91 | 0.93 | 0.94 | 0.95 | 0.97 | 0.98 | 0.98 | 0.99 |
| **2** | 0.91 | 0.93 | 0.94 | 0.95 | 0.97 | 0.98 | 0.98 | 0.99 |
| **3** | 0.88 | 0.9 | 0.91 | 0.94 | 0.95 | 0.96 | 0.97 | 0.98 |
| **4** | 0.9 | 0.91 | 0.92 | 0.93 | 0.96 | 0.97 | 0.98 | 0.98 |
| **5** | 0.88 | 0.91 | 0.92 | 0.93 | 0.95 | 0.97 | 0.97 | 0.98 |
| **6** | 0.84 | 0.88 | 0.91 | 0.92 | 0.95 | 0.97 | 0.97 | 0.98 |
| **7** | 0.92 | 0.93 | 0.94 | 0.95 | 0.96 | 0.97 | 0.98 | 0.98 |
| **8** | 0.88 | 0.91 | 0.92 | 0.94 | 0.96 | 0.97 | 0.97 | 0.98 |
| **9** | 0.91 | 0.92 | 0.94 | 0.94 | 0.96 | 0.97 | 0.98 | 0.98 |
| **10** | 0.85 | 0.87 | 0.9 | 0.91 | 0.95 | 0.95 | 0.97 | 0.97 |
| **11** | 0.87 | 0.9 | 0.92 | 0.93 | 0.96 | 0.97 | 0.98 | 0.98 |
| **12** | 0.87 | 0.88 | 0.91 | 0.92 | 0.94 | 0.96 | 0.97 | 0.97 |
| **13** | 0.9 | 0.94 | 0.95 | 0.95 | 0.97 | 0.98 | 0.98 | 0.99 |
| **14** | 0.9 | 0.92 | 0.94 | 0.95 | 0.97 | 0.97 | 0.98 | 0.98 |
| **15** | 0.9 | 0.91 | 0.93 | 0.95 | 0.96 | 0.97 | 0.97 | 0.98 |
| **16** | 0.9 | 0.89 | 0.93 | 0.94 | 0.96 | 0.97 | 0.97 | 0.98 |
| **17** | 0.9 | 0.91 | 0.93 | 0.94 | 0.96 | 0.97 | 0.98 | 0.98 |
| **18** | 0.84 | 0.87 | 0.91 | 0.91 | 0.95 | 0.96 | 0.97 | 0.98 |

Chr.: Chromosome; The low-density panels contained 300 (LD300), 502 (LD500), 802 (LD800),

1 003 (LD1K), 2 004 (LD2K), 2 995 (LD3K), 4 005 (LD4K), 4 998 (LD5K) and 7 256 (LD7K) markers.

***Table S3.*** *Number of animals in training and validation populations used for genomic predictions in the three major Canadian pig breeds*

|  |  |  |  |
| --- | --- | --- | --- |
| **Breed** | **Trait** | **Training** | **Validation** |
| Duroc (DU) | Growth rate | 875 | 426 |
| Backfat thickness | 874 | 430 |
| Loin muscle depth at 100 kg | 875 | 429 |
| Loin intramuscular fat | 688 | 215 |
| Landrace (LA) | Growth rate | 1 570 | 692 |
| Backfat thickness | 1 570 | 365 |
| Loin muscle depth at 100 kg | 1 570 | 86 |
| Total number of piglets born per litter | 1 023 | 733 |
| Yorkshire (YO) | Growth rate | 1 935 | 985 |
| Backfat thickness | 1 937 | 499 |
| Loin muscle depth at 100 kg | 1 930 | 125 |
| Total number of piglets born per litter | 1 280 | 1 081 |

***Table S4.*** *Number of animals in the validation population with no, one, or two parents in the reference population in pigs*

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Breed** | **No parents** | **One parent** | **Two parents** | **Total** |
| **Duroc (DU)** | 270 (61%) | 158 (35%) | 19 (4%) | 447 |
| **Landrace (LA)** | 319 (43%) | 233 (31%) | 196 (26%) | 748 |
| **Yorkshire (YO)** | 523 (48%) | 304 (28%) | 262 (24%) | 1 089 |

**Table S5.** Pearson *correlation (\*100) between genomic estimated breeding values (GEBVs) from imputed (from evenly-spaced low-density panels) and from actual 60K genotypes when no, one, or two parents were included in the reduced reference population and Pearson correlation for the full reference population in pigs*

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Scenario** | **Trait** | **Breed** | **NVal** | **LD300** | **LD500** | **LD800** | **LD1K** | **LD2K** | **LD3K** | **LD4K** | **LD5K** |
| NP | BFAT | LA | 124 | 87 | 89 | 93 | 95 | 98 | 98 | 99 | 99 |
| NP | BFAT | DU | 255 | 72 | 80 | 87 | 89 | 94 | 97 | 98 | 98 |
| NP | BFAT | YO | 192 | 87 | 92 | 94 | 96 | 98 | 99 | 99 | 99 |
| NP | GRATE | YO | 436 | 89 | 92 | 94 | 95 | 97 | 99 | 99 | 99 |
| NP | GRATE | LA | 274 | 84 | 88 | 94 | 94 | 97 | 98 | 99 | 99 |
| NP | GRATE | DU | 252 | 81 | 87 | 91 | 93 | 97 | 98 | 99 | 99 |
| NP | LOIND | YO | 18 | 82 | 80 | 89 | 90 | 96 | 99 | 99 | 99 |
| NP | LOIND | LA | 10 | 75 | 91 | 93 | 98 | 95 | 99 | 99 | 99 |
| NP | LOIND | DU | 254 | 78 | 88 | 93 | 94 | 97 | 99 | 99 | 99 |
| NP | LIMF | DU | 112 | 88 | 89 | 94 | 97 | 97 | 99 | 99 | 99 |
| NP | TBORN | YO | 523 | 95 | 96 | 98 | 98 | 99 | 99 | 100 | 100 |
| NP | TBORN | LA | 310 | 89 | 93 | 96 | 96 | 99 | 99 | 99 | 100 |
| 1P | BFAT | YO | 130 | 94 | 96 | 96 | 98 | 99 | 99 | 99 | 100 |
| 1P | BFAT | LA | 109 | 91 | 93 | 97 | 97 | 98 | 99 | 99 | 100 |
| 1P | BFAT | DU | 156 | 81 | 86 | 91 | 94 | 98 | 98 | 99 | 99 |
| 1P | GRATE | YO | 296 | 93 | 95 | 96 | 97 | 99 | 99 | 99 | 100 |
| 1P | GRATE | LA | 227 | 91 | 94 | 96 | 97 | 99 | 99 | 99 | 99 |
| 1P | GRATE | DU | 155 | 86 | 92 | 93 | 95 | 97 | 99 | 99 | 99 |
| 1P | LOIND | YO | 37 | 91 | 93 | 94 | 97 | 99 | 99 | 100 | 100 |
| 1P | LOIND | LA | 30 | 95 | 94 | 99 | 98 | 99 | 99 | 100 | 100 |
| 1P | LOIND | DU | 156 | 88 | 92 | 95 | 96 | 98 | 99 | 99 | 100 |
| 1P | LIMF | DU | 94 | 87 | 93 | 95 | 95 | 98 | 99 | 99 | 100 |
| 1P | TBORN | YO | 300 | 97 | 98 | 99 | 99 | 100 | 100 | 100 | 100 |
| 1P | TBORN | LA | 231 | 93 | 96 | 97 | 98 | 99 | 99 | 100 | 100 |
| **DU**: Duroc breed; **LA**: Landrace breed; **YO**: Yorkshire breed; **GRATE**: growth rate; **BFAT**: backfat thickness, **LOIND**: loin muscle depth adjusted to 100 Kg of live weight (loin depth); **LIMF**: loin intramuscular fat; **TBORN**: total number of piglets born per litter (total born); **NP**: no parents of validation animals in the reference population; **1P**: One parent of validation animals in the reference population; **2P**: both parents of validation animals in the reference population; **FR**: full reference population; **NVAL**: number of animals in the validation population. The low-density panels contained 300 (LD300), 502 (LD500), 802 (LD800), 1 003 (LD1K), 2 004 (LD2K), 2 995 (LD3K), 4 005 (LD4K), 4 998 (LD5K) and 7 256 (LD7K) markers. |

***Table S5.*** *Cont.*

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Scenario** | **Trait** | **Breed** | **NVal** | **LD300** | **LD500** | **LD800** | **LD1K** | **LD2K** | **LD3K** | **LD4K** | **LD5K** |
| 2P | BFAT | YO | 177 | 97 | 97 | 98 | 99 | 99 | 99 | 100 | 100 |
| 2P | BFAT | LA | 132 | 95 | 97 | 98 | 98 | 99 | 99 | 100 | 100 |
| 2P | BFAT | DU | 19 | 94 | 88 | 94 | 92 | 97 | 97 | 99 | 99 |
| 2P | GRATE | YO | 253 | 97 | 98 | 98 | 99 | 99 | 100 | 100 | 100 |
| 2P | GRATE | LA | 191 | 97 | 97 | 98 | 99 | 99 | 99 | 99 | 100 |
| 2P | GRATE | DU | 19 | 90 | 97 | 97 | 97 | 98 | 99 | 100 | 100 |
| 2P | LOIND | YO | 70 | 98 | 99 | 99 | 99 | 100 | 100 | 100 | 100 |
| 2P | LOIND | LA | 46 | 96 | 98 | 99 | 99 | 100 | 100 | 100 | 100 |
| 2P | LOIND | DU | 19 | 94 | 97 | 99 | 98 | 98 | 99 | 99 | 100 |
| 2P | LIMF | DU | 9 | 99 | 99 | 99 | 99 | 100 | 99 | 100 | 100 |
| 2P | TBORN | YO | 258 | 99 | 99 | 100 | 99 | 100 | 100 | 100 | 100 |
| 2P | TBORN | LA | 192 | 97 | 98 | 98 | 99 | 99 | 99 | 100 | 100 |
| FR | BFAT | YO | 499 | 93 | 95 | 96 | 97 | 99 | 99 | 99 | 100 |
| FR | BFAT | LA | 365 | 91 | 93 | 96 | 97 | 98 | 99 | 99 | 99 |
| FR | BFAT | DU | 430 | 77 | 83 | 89 | 91 | 96 | 97 | 98 | 99 |
| FR | GRATE | YO | 985 | 93 | 95 | 95 | 97 | 98 | 99 | 99 | 99 |
| FR | GRATE | LA | 692 | 90 | 93 | 96 | 96 | 98 | 99 | 99 | 99 |
| FR | GRATE | DU | 426 | 83 | 89 | 92 | 94 | 97 | 98 | 99 | 99 |
| FR | LOIND | YO | 125 | 95 | 96 | 97 | 98 | 99 | 99 | 100 | 100 |
| FR | LOIND | LA | 125 | 94 | 96 | 98 | 99 | 99 | 99 | 100 | 100 |
| FR | LOIND | DU | 429 | 83 | 90 | 94 | 95 | 97 | 99 | 99 | 99 |
| FR | LIMF | DU | 215 | 88 | 92 | 94 | 96 | 98 | 99 | 99 | 99 |
| FR | TBORN | YO | 1 081 | 96 | 97 | 98 | 99 | 99 | 100 | 100 | 100 |
| FR | TBORN | LA | 733 | 92 | 95 | 97 | 97 | 99 | 99 | 100 | 100 |
| **DU**: Duroc breed; **LA**: Landrace breed; **YO**: Yorkshire breed; **GRATE**: growth rate; **BFAT**: backfat thickness, **LOIND**: loin muscle depth adjusted to 100 Kg of live weight (loin depth); **LIMF**: loin intramuscular fat; **TBORN**: total number of piglets born per litter (total born); **NP**: no parents of validation animals in the reference population; **1P**: One parent of validation animals in the reference population; **2P**: both parents of validation animals in the reference population; **FR**: full reference population; **NVAL**: number of animals in the validation population. The low-density panels contained 300 (LD300), 502 (LD500), 802 (LD800), 1 003 (LD1K), 2 004 (LD2K), 2 995 (LD3K), 4 005 (LD4K), 4 998 (LD5K) and 7 256 (LD7K) markers. |

**Figure S1** Imputation accuracy of 60K SNP panel from different evenly-spaced low-density panels, and from panels with double or quadruple SNP density at the beginning and end (tails) of chromosomes (5% of chromosome size) in three pig breeds

**Concordance rate (%)**