**Ultra-low density genotype panels for breed assignment of Angus and Hereford cattle**

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**Supplementary Material**

**Supplementary Table S1** *Number of SNPs chosen per autosome (BTA) for each of the ultra-low density i.e. 100, 200, 300, 400, 500, 600, 700, 800, 900 and 1 000 SNP genotype panels*

|  |  |
| --- | --- |
|  | Single nucleotide polymorphism density |
| BTA | 100 | 200 | 300 | 400 | 500 | 600 | 700 | 800 | 900 | 1 000 |
| 1 | 6 | 12 | 18 | 24 | 30 | 36 | 42 | 48 | 54 | 61 |
| 2 | 5 | 10 | 15 | 20 | 25 | 30 | 35 | 40 | 45 | 50 |
| 3 | 5 | 10 | 15 | 20 | 26 | 31 | 36 | 41 | 46 | 51 |
| 4 | 5 | 10 | 14 | 19 | 24 | 29 | 34 | 38 | 43 | 48 |
| 5 | 4 | 8 | 12 | 16 | 21 | 25 | 29 | 33 | 37 | 41 |
| 6 | 4 | 9 | 13 | 17 | 22 | 26 | 30 | 34 | 39 | 43 |
| 7 | 5 | 9 | 14 | 18 | 23 | 27 | 32 | 36 | 41 | 45 |
| 8 | 5 | 10 | 15 | 19 | 24 | 29 | 34 | 39 | 44 | 49 |
| 9 | 4 | 8 | 12 | 16 | 20 | 24 | 28 | 32 | 36 | 40 |
| 10 | 4 | 9 | 13 | 17 | 22 | 26 | 30 | 34 | 39 | 43 |
| 11 | 4 | 9 | 13 | 17 | 22 | 26 | 30 | 35 | 39 | 44 |
| 12 | 3 | 6 | 9 | 13 | 16 | 19 | 22 | 25 | 28 | 32 |
| 13 | 4 | 7 | 11 | 14 | 18 | 22 | 25 | 29 | 32 | 36 |
| 14 | 3 | 7 | 10 | 13 | 17 | 20 | 23 | 27 | 30 | 34 |
| 15 | 3 | 7 | 10 | 14 | 17 | 21 | 24 | 28 | 31 | 35 |
| 16 | 3 | 6 | 10 | 13 | 16 | 19 | 22 | 26 | 29 | 32 |
| 17 | 3 | 7 | 10 | 13 | 17 | 20 | 23 | 26 | 30 | 33 |
| 18 | 3 | 6 | 8 | 11 | 14 | 17 | 19 | 22 | 25 | 28 |
| 19 | 3 | 6 | 9 | 11 | 14 | 17 | 20 | 23 | 26 | 29 |
| 20 | 3 | 6 | 9 | 12 | 15 | 19 | 22 | 25 | 28 | 31 |
| 21 | 3 | 5 | 8 | 11 | 14 | 16 | 19 | 22 | 24 | 26 |
| 22 | 3 | 5 | 8 | 10 | 13 | 15 | 18 | 20 | 23 | 25 |
| 23 | 2 | 4 | 6 | 9 | 11 | 13 | 15 | 17 | 19 | 22 |
| 24 | 3 | 4 | 8 | 10 | 11 | 15 | 18 | 20 | 23 | 25 |
| 25 | 2 | 4 | 6 | 9 | 10 | 12 | 14 | 16 | 18 | 20 |
| 26 | 2 | 4 | 7 | 9 | 11 | 13 | 15 | 18 | 20 | 21 |
| 27 | 2 | 4 | 5 | 8 | 9 | 11 | 13 | 14 | 16 | 18 |
| 28 | 2 | 4 | 6 | 8 | 9 | 11 | 13 | 15 | 17 | 19 |
| 29 | 2 | 4 | 6 | 9 | 9 | 11 | 15 | 17 | 18 | 19 |

Supplementary Table S2 *Correlations of the predicted breed proportion in the Angus (n=5 470; below diagonal) and Hereford (n=5 187; above diagonal) populations among the different density genotype panels including the gold-standard (gold) panel. Single nucleotide polymorphisms were selected using the Global Index statistic*

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Panel Density | 100 | 200 | 300 | 400 | 500 | 600 | 700 | 800 | 900 | 1,000 | Gold |
| 100 |  | 0.995 | 0.993 | 0.992 | 0.992 | 0.991 | 0.991 | 0.991 | 0.991 | 0.991 | 0.989 |
| 200 | 0.993 |  | 0.997 | 0.997 | 0.996 | 0.996 | 0.996 | 0.996 | 0.996 | 0.995 | 0.994 |
| 300 | 0.991 | 0.996 |  | 0.998 | 0.998 | 0.998 | 0.998 | 0.998 | 0.997 | 0.997 | 0.995 |
| 400 | 0.990 | 0.996 | 0.997 |  | 0.999 | 0.998 | 0.998 | 0.998 | 0.999 | 0.998 | 0.996 |
| 500 | 0.989 | 0.995 | 0.997 | 0.998 |  | 0.999 | 0.999 | 0.999 | 0.999 | 0.999 | 0.997 |
| 600 | 0.989 | 0.995 | 0.997 | 0.998 | 0.998 |  | 0.999 | 0.999 | 0.999 | 0.999 | 0.997 |
| 700 | 0.988 | 0.994 | 0.997 | 0.998 | 0.998 | 0.999 |  | 0.999 | 0.999 | 0.999 | 0.998 |
| 800 | 0.988 | 0.994 | 0.997 | 0.998 | 0.998 | 0.999 | 0.999 |  | 0.999 | 0.999 | 0.998 |
| 900 | 0.988 | 0.994 | 0.997 | 0.997 | 0.998 | 0.998 | 0.999 | 0.999 |  | 0.999 | 0.998 |
| 1 000 | 0.988 | 0.994 | 0.996 | 0.997 | 0.998 | 0.998 | 0.999 | 0.999 | 0.999 |  | 0.998 |
| Gold | 0.983 | 0.990 | 0.993 | 0.994 | 0.995 | 0.995 | 0.996 | 0.996 | 0.996 | 0.997 |  |

**Supplementary Table S3** *The number of common single nucleotide polymorphsims (selected using the Global Index selection method) between each genotype panel density in the Angus population (n=5 470;**below diagonal), the Hereford population (n=5 187;**above diagonal) as well as between the Angus and Hereford populations for the same density (on the diagonal)*

|  |  |
| --- | --- |
|  | Panel Density |
| Panel Density | 100 | 200 | 300 | 400 | 500 | 600 | 700 | 800 | 900 | 1 000 |
| 100 | 2 | 100 | 99 | 96 | 98 | 98 | 99 | 99 | 99 | 99 |
| 200 | 99 | 2 | 183 | 190 | 191 | 192 | 196 | 196 | 197 | 196 |
| 300 | 99 | 177 | 4 | 257 | 274 | 289 | 282 | 289 | 294 | 289 |
| 400 | 98 | 188 | 255 | 12 | 347 | 354 | 362 | 385 | 381 | 380 |
| 500 | 98 | 188 | 261 | 337 | 18 | 418 | 429 | 450 | 455 | 480 |
| 600 | 98 | 193 | 293 | 360 | 410 | 24 | 491 | 517 | 543 | 550 |
| 700 | 98 | 192 | 274 | 369 | 436 | 484 | 33 | 563 | 592 | 609 |
| 800 | 99 | 197 | 284 | 388 | 456 | 514 | 588 | 39 | 644 | 677 |
| 900 | 100 | 197 | 398 | 374 | 455 | 529 | 590 | 636 | 50 | 730 |
| 1 000 | 100 | 197 | 290 | 382 | 478 | 530 | 603 | 679 | 723 | 63 |



**Supplementary Figure S1** *Allele frequencies for each of the 300 SNPs selected using in Pairwise Fst method in Angus population versus the Hereford (♦), Holstein (▪), Belgian Blue (▲), Limousin (×), Simmental (–) and Charolais (•) populations*



**Supplementary Figure S2** *The Angus breed proportion of all Angus animals (n=5 740) using the gold-standard genotype panel (x-axis) and the 300 single nucleotide polymorphism genotype panel (y-axis) (SNPs selected using the Global Index method)*