**Genome-wide identification of runs of homozygosity islands and associated genes in local dairy cattle breeds**

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**Supplementary materials**

***Supplementary Table S1*** *Mean Linkage Disequilibrium (r2) for all pairwise combinations of SNPs with a distance lower than 500 kb. The r2 value was estimated within each ROH islands and for each autosome (BTA)*

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Breed | BTA | Start bp | End bp | Length (bp) | *r2* ROH island | *r2* BTA |
| Cinisara | 8 | 18 112 643 | 18 420 652 | 308 010 | 0.024 | 0.078 |
| 10 | 56 464 919 | 56 792 715 | 327 797 | 0.077 | 0.073 |
| 13 | 30 530 185 | 30 878 341 | 348 157 | 0.081 | 0.072 |
| 16 | 43 922 935 | 45 552 538 | 1 629 604 | 0.290 | 0.075 |
| 23 | 60 163 | 6 423 288 | 6 363 126 | 0.080 | 0.061 |
| 23 | 10 870 036 | 11 251 946 | 381 911 | 0.053 |  |
| 23 | 13 517 193 | 13 793 884 | 276 692 | 0.040 |  |
| 28 | 27 655 543 | 32 996 400 | 5 340 858 | 0.051 | 0.056 |
| 28 | 34 157 181 | 39 007 759 | 4 850 579 | 0.062 |  |
| 28 | 39 700 262 | 40 191 764 | 491 503 | 0.069 |  |
| 28 | 40 782 405 | 46 224 056 | 5 441 652 | 0.051 |  |
| Italian Holstein | 3 | 91 930 742 | 93 497 168 | 1 566 427 | 0.121 | 0.129 |
| 5 | 99 527 745 | 99 569 438 | 41 694 | 0.280 | 0.122 |
| 7 | 49 145 480 | 49 715 020 | 569 541 | 0.060 | 0.135 |
| 10 | 34 907 534 | 40 294 545 | 5 387 012 | 0.168 | 0.133 |
| 10 | 49 889 790 | 62 309 052 | 12 419 263 | 0.150 |  |
| 10 | 63 095 461 | 67 118 053 | 4 022 593 | 0.168 |  |
| 13 | 51 880 463 | 56 190 025 | 4 309 563 | 0.191 | 0.123 |
| 20 | 24 266 877 | 26 460 587 | 2 193 711 | 0.137 | 0.135 |
| 20 | 29 545 545 | 31 848 979 | 2 303 435 | 0.135 |  |
| 20 | 34 817 221 | 36 570 529 | 1 753 309 | 0.142 |  |
| 26 | 19 727 292 | 21 226 405 | 1 499 114 | 0.203 | 0.120 |
| Modicana | 1 | 130 168 696 | 132 182 348 | 2 013 653 | 0.189 | 0.119 |
| 4 | 35 763 942 | 37 877 098 | 2 113 157 | 0.141 | 0.139 |
| 4 | 51 406 099 | 57 744 446 | 6 338 348 | 0.152 |  |
| 5 | 27 542 987 | 33 508 142 | 5 965 156 | 0.160 | 0.136 |
| 5 | 78 776 781 | 82 786 530 | 4 009 750 | 0.178 |  |
| 6 | 34 324 052 | 41 343 408 | 7 019 357 | 0.192 | 0.125 |
| 8 | 29 767 566 | 32 749 041 | 2 981 476 | 0.081 | 0.119 |
| 8 | 40 422 559 | 40 921 256 | 498 698 | 0.184 |  |
| Reggiana | 1 | 150 141 293 | 151 550 746 | 1 409 454 | 0.137 | 0.088 |
| 1 | 151 736 540 | 152 412 536 | 675 997 | 0.098 |  |
| 3 | 71 141 852 | 71 167 977 | 26 126 | 0.006 | 0.082 |
| 3 | 73 035 441 | 79 378 528 | 6 343 088 | 0.077 |  |
| 6 | 38 689 886 | 39 346 170 | 656 285 | 0.387 | 0.083 |
| 17 | 56 941 968 | 61 788 328 | 4 846 361 | 0.124 | 0.085 |
| 26 | 9 078 964 | 10 441 474 | 1 362 511 | 0.097 | 0.086 |
| 29 | 15 819 913 | 23 142 122 | 7 322 210 | 0.075 | 0.072 |

ROH = Runs of homozygosity; SNPs = Single nucleotide polymorphisms.

***Supplementary Table S2*** *Position, number of SNPs and number of genes within genomic region, gene symbol and full names for all annotated genes in each cattle breed (see excel file).*