**Supplementary Material for:**

**Comparative selection signature analyses identify genomic footprints in Reggiana cattle, the traditional breed of the Parmigiano Reggiano cheese production system**

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**Supplementary Figure S1.** Average observed heterozygosity (± standard deviation) for each chromosome in the four analysed cattle breeds.

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**Supplementary Figure S2.** Results of the ADMIXTURE analysis in *Bos taurus*.Cross validation error with K from 1 to 29 (top) and plot distribution with K=3, 5, 10 and 15 of the considered breeds.

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**Supplementary Table S1.** Summary of genotyping data: minor allele frequency (MAF) and observed heterozygosity (Het) and their standard deviation (SD) in Reggiana, Brown, Holstein and Simmental cattle breeds.

|  |  |  |
| --- | --- | --- |
| Breed | Average MAF ± SD | Average Het ± SD |
| Reggiana | 0.253 ± 0.145 | 0.340 ± 0.153 |
| Brown | 0.232 ± 0.152 | 0.313 ± 0.168 |
| Holstein | 0.259 ± 0.146 | 0.344 ± 0.152 |
| Simmental | 0.251 ± 0.145 | 0.334 ± 0.151 |

**Supplementary Table S2.** Results of the integrated haplotype score (iHS) analysis in the Reggiana breed including the top 99.5th percentile single nucleotide polymorphisms (SNPs). Reported information includes bovine chromosome (BTA) position of the SNP, the SNP name, the |iHS| value and the gene symbol of the annotated genes ± 200 kbp from the SNP.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| BTA1 | SNP2 | Position | |iHS| value | Annotated genes |
| 1 | DPI-27 | 37381473 | 2.874 | *EPHA3* |
| 1 | ARS-BFGL-NGS-114234 | 45929427 | 2.785 | *TRMT10C, ZBTB11, SENP7, PCNP* |
| 1 | BTB-00052487 | 117704023 | 2.988 | *TSC22D2* |
| 2 | ARS-BFGL-NGS-32858 | 47013329 | 2.804 | *LYPD6B* |
| 2 | Hapmap41178-BTA-120553 | 52511673 | 2.916 | *GTDC1* |
| 2 | BTB-01412441 | 53545307 | 2.925 | *ARHGAP15* |
| 2 | BTB-01391891 | 54536305 | 3.833 | *-* |
| 2 | BTB-00183384 | 54634481 | 3.114 | *-* |
| 2 | Hapmap60963-rs29015781 | 55779254 | 3.020 | *LRP1B* |
| 2 | Hapmap48387-BTA-55128 | 61253063 | 2.988 | *CXCR4* |
| 2 | Hapmap41674-BTA-88236 | 61300454 | 2.803 | *CXCR4, DARS* |
| 2 | ARS-BFGL-NGS-41523 | 64151134 | 3.322 | *NCKAP5* |
| 2 | Hapmap49404-BTA-100549 | 70190436 | 3.636 | *-* |
| 2 | Hapmap35220-BES9\_Contig365\_495 | 70532188 | 2.992 | *EN1* |
| 2 | ARS-BFGL-NGS-1606 | 70931242 | 3.013 | *C1QL2, STEAP3* |
| 2 | ARS-BFGL-NGS-16745 | 71437395 | 2.949 | *TMEM177, CFAP221* |
| 2 | UA-IFASA-2241 | 78787839 | 2.837 | *RF00612, GYPC* |
| 3 | ARS-USMARC-Parent-AY842474-rs29003226 | 51817697 | 2.864 | *CDC7* |
| 3 | ARS-BFGL-NGS-35164 | 51841394 | 2.810 | *CDC7* |
| 3 | INRA-451 | 59220453 | 3.082 | *MCOLN2, LPAR3* |
| 3 | Hapmap53609-rs29011253 | 60566649 | 2.760 | *-* |
| 3 | BTB-00133369 | 67338807 | 2.935 | *PIGK, AK5* |
| 3 | BTA-94549-no-rs | 68497585 | 2.926 | *-* |
| 3 | BTB-00135094 | 70009576 | 3.097 | *TYW3, CRYZ* |
| 3 | BTA-10440-no-rs | 70057563 | 2.885 | *TYW3, CRYZ* |
| 3 (ROH) | ARS-BFGL-NGS-32439 | 75251155 | 2.902 | *LRRC7* |
| 3 (ROH) | ARS-BFGL-NGS-8612 | 75279283 | 2.806 | *LRRC7* |
| 3 (ROH) | INRA-142 | 76452556 | 2.842 | *-* |
| 3 (ROH) | BTB-00137261 | 77599781 | 3.102 | *RF00026, GADD45A, GNG12* |
| 3 (ROH) | BTB-00137287 | 77652594 | 3.058 | *RF00026, GADD45A, GNG12* |
| 3 (ROH) | BTB-01168089 | 78669044 | 2.792 | *TCTEX1D1, SGIP1* |
| 5 | ARS-BFGL-NGS-5720 | 96995660 | 2.921 | *GPRC5D, APOLD1, HEBP1, GPRC5A, DDX47* |
| 6 | BTA-108507-no-rs | 12478100 | 3.135 | *-* |
| 6 | ARS-BFGL-NGS-107549 | 16334539 | 3.457 | *-* |
| 6 | BTB-00247622 | 16367079 | 3.532 | *-* |
| 6 | Hapmap44568-BTA-77505 | 16407876 | 2.832 | *-* |
| 6 | ARS-BFGL-NGS-80568 | 17056293 | 3.353 | *LEF1* |
| 6 | ARS-BFGL-NGS-45046 | 17498903 | 2.844 | *PAPSS1* |
| 7 | ARS-BFGL-NGS-35666 | 38039999 | 2.803 | *RNF44, EIF4E1B, FAF2, CDHR2, SNCB, TSPAN17* |
| 10 | ARS-BFGL-NGS-57077 | 68564596 | 2.762 | *PELI2* |
| 11 | Hapmap48122-BTA-91937 | 1818651 | 2.773 | *MALL, MAL, NPHP1* |
| 11 | ARS-BFGL-NGS-105586 | 81697133 | 2.816 | *FAM49A* |
| 12 | BTB-01544419 | 49153380 | 2.900 | *-* |
| 12 | Hapmap24871-BTA-157401 | 75360273 | 3.390 | *RF00026, FARP1* |
| 13 | UA-IFASA-7733 | 37955994 | 2.791 | *DSTN, BANF2, BFSP1, RRBP1* |
| 13 | ARS-BFGL-NGS-18246 | 45034339 | 2.844 | *PITRM1* |
| 13 | ARS-BFGL-NGS-35887 | 46089659 | 3.083 | *ADARB2* |
| 13 | ARS-BFGL-NGS-107916 | 46808920 | 2.817 | *DIP2C* |
| 14 | ARS-BFGL-NGS-40495 | 78423753 | 2.852 | *-* |
| 16 | Hapmap49866-BTA-114054 | 31458337 | 3.032 | *SMYD3* |
| 16 | Hapmap41252-BTA-39046 | 48366828 | 2.796 | *-* |
| 16 | Hapmap60283-rs29014986 | 48816898 | 2.784 | *-* |
| 16 | Hapmap26379-BTA-130999 | 53997980 | 2.860 | *-* |
| 16 | Hapmap49429-BTA-107409 | 68461967 | 3.124 | *PDPN, PRDM2* |
| 17 | BTB-01087937 | 19461407 | 2.865 | *SLC7A11* |
| 17 | Hapmap51443-BTA-40619 | 20682264 | 2.814 | *-* |
| 17 | BTB-01731152 | 28148532 | 2.822 | *RF00100* |
| 17 | BTB-01869986 | 30566646 | 3.319 | *-* |
| 17 | BTB-01426795 | 30798193 | 2.887 | *-* |
| 17 | ARS-BFGL-NGS-74608 | 31986086 | 2.798 | *-* |
| 17 | BTB-01308307 | 33433050 | 2.900 | *-* |
| 17 | BTA-122399-no-rs | 40371968 | 2.859 | *RXFP1* |
| 17 | BTB-00676954 | 43133674 | 2.848 | *-* |
| 17 | Hapmap29721-BTA-131409 | 44455186 | 2.806 | *PGAM5, RF00026, CHFR, ANKLE2, PXMP2, GOLGA3, POLE* |
| 17 | ARS-BFGL-NGS-27620 | 44586221 | 3.048 | *PGAM5, RF00026, P2RX2, LRCOL1, ANKLE2, PXMP2, POLE, FBRSL1* |
| 17 | ARS-BFGL-NGS-105739 | 44725907 | 3.057 | *FBRSL1* |
| 17 | ARS-BFGL-NGS-103650 | 44812935 | 3.342 | *GALNT9* |
| 17 | ARS-BFGL-NGS-86713 | 45036186 | 3.304 | *NOC4L, RF00562, bta-mir-6520, DDX51, GALNT9, EP400* |
| 17 | BTB-00678060 | 45302168 | 2.929 | *bta-mir-2285af-2, MMP17, SFSWAP* |
| 17 | BTA-41003-no-rs | 45331881 | 2.824 | *bta-mir-2285af-2, MMP17, SFSWAP* |
| 17 | Hapmap38384-BTA-117953 | 45517219 | 3.143 | *-* |
| 17 | ARS-BFGL-NGS-79176 | 45561948 | 3.237 | *-* |
| 17 | Hapmap28761-BTA-159815 | 45637897 | 2.825 | *-* |
| 17 | ARS-BFGL-BAC-27022 | 45697242 | 3.420 | *-* |
| 17 | ARS-BFGL-NGS-9657 | 46895925 | 3.561 | *FZD10* |
| 17 | ARS-BFGL-NGS-115236 | 47192942 | 3.068 | *RF00026, RF00100, RFLNA, NCOR2* |
| 17 | Hapmap39519-BTA-85553 | 51369492 | 2.824 | *-* |
| 17 | Hapmap49158-BTA-41145 | 53987189 | 2.924 | *CAMKK2, P2RX4, P2RX7, IFT81* |
| 17 | BTB-00679561 | 54482037 | 2.922 | *PPTC7, TCTN1, PPP1CC, RAD9B, HVCN1* |
| 17 | ARS-BFGL-NGS-5696\* | 54765150 | 3.000 | *MYL2, CCDC63, CUX2* |
| 17 | Hapmap43572-BTA-41227\* | 54798284 | 2.797 |
| 17 | ARS-BFGL-NGS-21400\* | 54862080 | 2.908 |
| 17 (ROH) | ARS-BFGL-BAC-34676\* | 54925511 | 2.806 |
| 17 (ROH) | Hapmap48751-BTA-41232 | 55767778 | 2.829 | *TMEM233, CIT* |
| 17 (ROH) | BTA-25636-no-rs | 55916308 | 2.976 | *CCDC60* |
| 17 (ROH) | ARS-BFGL-NGS-54784 | 56479267 | 3.087 | *-* |
| 17 (ROH) | BTB-00680019 | 56987958 | 2.853 | *TAOK3* |
| 17 (ROH) | BTB-00680348\* | 57375842 | 2.878 | *RF00026, KSR2, NOS1* |
| 17 (ROH) | ARS-BFGL-NGS-112404\* | 57495561 | 3.128 |
| 17 (ROH) | ARS-BFGL-NGS-116162\* | 57562662 | 2.913 |
| 17 (ROH) | ARS-BFGL-NGS-10055\* | 57716043 | 2.930 |
| 17 (ROH) | ARS-BFGL-NGS-27713 | 57937352 | 3.291 | *TESC, NOS1, FBXO21FBXW8* |
| 17 (ROH) | BTB-00681880\* | 58741798 | 3.214 | *MED13L* |
| 17 (ROH) | BTB-00681839\* | 58796978 | 3.044 |
| 17 (ROH) | ARS-BFGL-NGS-54448\* | 58989148 | 2.991 |
| 17 (ROH) | ARS-BFGL-NGS-75591 | 59530888 | 2.800 | *-* |
| 17 (ROH) | ARS-BFGL-NGS-1369 | 59560283 | 2.924 | *-* |
| 17 | BTB-01095540 | 59953298 | 3.201 | *-* |
| 24 | Hapmap38797-BTA-99366 | 21431369 | 2.800 | *GALNT1* |
| 24 | ARS-BFGL-NGS-53865 | 29888368 | 2.767 | *CHST9* |
| 24 | BTA-57840-no-rs | 32183082 | 2.941 | *HRH4, IMPACT* |
| 24 | BTB-00886759 | 34511917 | 2.875 | *ABHD3, MIB1* |
| 24 | Hapmap57118-rs29009938 | 38934184 | 2.769 | *EPB41L3* |
| 24 | ARS-BFGL-NGS-98552 | 40627809 | 2.798 | *PTPRM* |
| 25 | ARS-BFGL-NGS-42870 | 29938832 | 3.235 | *-* |
| 25 | Hapmap23619-BTC-057878 | 31203678 | 2.957 | *RF00026* |
| 26 | BTB-00930720 | 21034491 | 2.830 | *RF00026, ERLIN1, DNMBP, CHUK, CPN1* |
| 26 | ARS-BFGL-NGS-119202 | 23161478 | 2.849 | *MFSD13A, ACTR1A, SUFU* |
| 28 | ARS-BFGL-NGS-41944 | 15601752 | 2.830 | *CCDC6, ANK3* |
| 29 (ROH) | ARS-BFGL-NGS-118102 | 16069820 | 3.182 | *-* |
| 29 (ROH) | ARS-BFGL-NGS-2529 | 16569370 | 3.077 | *bta-mir-708* |
| 29 (ROH) | ARS-BFGL-NGS-39422 | 16996267 | 3.867 | *TENM4* |
| 29 (ROH) | ARS-BFGL-NGS-1508 | 17291020 | 3.178 | *TENM4* |
| 29 (ROH) | BTB-01012731 | 22198059 | 2.919 | *GAS2* |
| 29 (ROH) | BTA-106551-no-rs | 22648358 | 3.197 | *ANO5* |
| 29  | BTB-00934783 | 23661968 | 3.050 | *-* |
| 29 | Hapmap43319-BTA-65094 | 24529656 | 3.116 | *PRMT3* |
| 29 | BTB-01013468 | 24721139 | 3.005 | *NAV2* |
| 29 | Hapmap41325-BTA-65112 | 24898216 | 2.885 | *NAV2* |
| 29 | ARS-BFGL-NGS-9185 | 24940506 | 3.077 | *bta-mir-449d* |
| 29 | ARS-BFGL-NGS-39535 | 25169363 | 3.180 | *NAV2* |
| 29 | ARS-BFGL-NGS-91937 | 25338021 | 2.944 | *RF00408* |
| 29 | ARS-BFGL-NGS-56290 | 25466622 | 3.145 | *.* |
| 29 | ARS-BFGL-NGS-12494 | 25632177 | 2.883 | *E2F8* |
| 29 | Hapmap45305-BTA-65247 | 27881130 | 2.859 | *OR8B4* |
| 29 | ARS-BFGL-NGS-94355 | 28154066 | 3.373 | *PANX3, TBRG1, NRGN, ESAM, SIAE, SPA17, VSIG2, MSANTD2* |
| 29 | BTB-01017247\* | 28440651 | 2.928 | *CCDC15, HEPACAM, RF00100, ROBO3, ROBO4, SLC37A2, TMEM218* |
| 29 | ARS-BFGL-NGS-37244\* | 28518134 | 3.356 |
| 29 | ARS-BFGL-NGS-102700\* | 28539785 | 3.083 |
| 29 | ARS-BFGL-NGS-18412 | 28560818 | 3.516 | *SLC37A2, TMEM218* |
| 29 | UA-IFASA-5034 | 28684366 | 2.872 | *-* |
| 29 | ARS-BFGL-NGS-23652 | 28731093 | 3.411 | *PKNOX2* |
| 29 | ARS-BFGL-NGS-25532 | 29117496 | 3.082 | *SSLP1, PATE1, bta-mir-2285ce, PATE2, PATE3, RF00099, STT3A, CHEK1, ACRV1* |
| 29 | ARS-BFGL-NGS-105093 | 29536191 | 2.895 | *SRPRA, RPUSD4, FAM118B, FOXRED1* |
| 29 | ARS-BFGL-NGS-17769 | 29928524 | 2.930 | *KIRREL3* |
| 29 | ARS-BFGL-NGS-29938 | 29953458 | 3.429 | *KIRREL3* |
| 29 | ARS-BFGL-NGS-52511\* | 30103989 | 3.638 | *-* |
| 29 | Hapmap40782-BTA-65467\* | 30157180 | 3.149 |
| 29 | BTA-65463-no-rs\* | 30188256 | 3.184 |
| 29 | ARS-BFGL-NGS-109714 | 31764186 | 2.933 | *ETS1* |
| 29 | BTB-01020010 | 31875920 | 3.165 | *ETS1* |
| 29 | Hapmap40017-BTA-65421 | 31971753 | 3.697 | *ETS1* |
| 29 | ARS-BFGL-NGS-87575\* | 32078660 | 3.455 | *FLI1, KCNJ1, KCNJ5, FLI1, KCNJ1, ARHGAP32* |
| 29 | ARS-BFGL-NGS-12309\* | 32128256 | 3.210 |
| 29 | UA-IFASA-7219\* | 32253717 | 3.111 |
| 29 | Hapmap58618-rs29012371 | 32801728 | 3.502 | *-* |
| 29 | BTB-01023253 | 32940189 | 2.905 | *JAM3* |
| 29 | Hapmap49699-BTA-65589 | 33406139 | 3.084 | *-* |
| 29 | Hapmap60712-rs29014894 | 33436030 | 2.989 | *-* |
| 29 | ARS-BFGL-NGS-24911 | 33487878 | 2.909 | *-* |
| 29 | ARS-BFGL-NGS-34282 | 33704537 | 3.060 | *-* |
| 29 | ARS-BFGL-NGS-36490 | 34592350 | 3.303 | *OPCML* |
| 29 | UA-IFASA-9704 | 34687068 | 3.022 | *NTM* |
| 29 | ARS-BFGL-NGS-12285 | 34751748 | 2.976 | *NTM* |
| 29 | Hapmap53268-rs29022154 | 34808241 | 3.001 | *NTM* |
| 29 | UA-IFASA-6129 | 34835983 | 3.236 | *NTM* |
| 29 | ARS-BFGL-NGS-28392\* | 35237784 | 3.426 | *RF00619* |
| 29 | ARS-BFGL-NGS-115969\* | 35373548 | 3.039 |
| 29 | ARS-BFGL-NGS-89027\* | 35393862 | 2.754 |
| 29 | BTB-01027202\* | 35564539 | 3.085 |
| 29 | ARS-BFGL-NGS-39172 | 36048959 | 3.679 | *NFRKB, PRDM10, TMEM45B* |
| 29 | ARS-BFGL-NGS-2990 | 36088900 | 3.211 | *NFRKB, PRDM10, TMEM45B* |
| 29 | ARS-BFGL-NGS-29244 | 36130086 | 3.291 | *NFRKB, PRDM10, TMEM45B* |
| 29 | ARS-BFGL-NGS-4431 | 36619214 | 3.258 | *ADAMTS8, ADAMTS15* |
| 29 | ARS-BFGL-NGS-17583 | 36932109 | 3.173 | *SNX19* |
| 29 | ARS-BFGL-NGS-111280 | 36986707 | 2.845 | *MS4A8, SNX19, MS4A18* |
| 29 | ARS-BFGL-NGS-56408 | 37168472 | 2.916 | *MS4A15, PTGDR2, MS4A8, MS4A10, CCDC86, TMEM109, TMEM132A, MS4A18, PRPF19* |
| 29 | ARS-BFGL-NGS-104963 | 40438138 | 3.100 | *FTH1, FADS1, FADS3, RAB3IL1, BEST1, FADS2* |
| 29 | ARS-BFGL-NGS-110249 | 40565850 | 2.845 | *FTH1, BEST1, INCENP* |

1 Chromosome regions overlapping runs of homozygosity (ROH) islands reported by Mastrangelo *et al.* (2018b) in the Reggiana cattle breed are indicated with “(ROH)”.

2 Consecutive SNPs are indicated with an asterisk “\*”) in the SNP column.

**Supplementary Table S3.** Results of the pairwise fixation index FST analysis of Reggiana *vs* the three cosmopolitan breeds (Brown, Holstein and Simmental). Reported information includes the bovine chromosome (BTA) position (start and end nucleotide position on the chromosome) of the top 99.5th percentile of the mean FST values (mFST) in 1 Mbp sliding windows and the annotated genes in the corresponding chromosome regions. Overlapping or adjacent windows were merged. However, the total number of all sliding windows (overlapping or partially overlapping) is reported in the text.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| BTA1 | Starting window position  | End window position | mFST | Annotated genes in the genomic windows |
| Brown |
| 5 | 16500000 | 17500000 | 0.286 | *-* |
| 5 | 19500000 | 20500000 | 0.387 | *RF00001, ATP2B1* |
| 5 | 33000000 | 34000000 | 0.279 | *AMIGO2, SLC38A2, PCED1B, SLC38A4, SLC38A1* |
| 5 | 41500000 | 42500000 | 0.300 | *bta-mir-2428, RF00026, ABCD2, KIF21A, CPNE8* |
| 5 | 75500000 | 77000000 | 0.307 | *SSTR3, bta-mir-1835, ELFN2, RF00026, RF00026, ALG10, IL2RB, RAC2, CYTH4, CARD10, USP18, C1QTNF6, MFNG, SYT10, TMPRSS6, USP18, SYT10* |
| 6 | 31000000 | 32500000 | 0.335 | *RF00026, GRID2* |
| 6 | 39000000 | 40000000 | 0.326 | *SLIT2* |
| 6 | 67500000 | 70500000 | 0.307 | *bta-mir-4449, CHIC2, CWH43, DCUN1D4, FIP1L1, GSX2, KIT, LNX1,* *LRRC66, OCIAD1, OCIAD2, PDGFRA, RASL11B, RF00026, RF00568, SCFD2, SGCB, SPATA18, USP46,*  |
| 6 | 79000000 | 80500000 | 0.279 | *RF00001, TECRL, RF00001, TECRL, BMP10, GKN1, RF00100, PROKR1,* *GKN3P, GKN2, NFU1, ANTXR1, GFPT1, AAK1, ARHGAP25* |
| 11 | 67000000 | 69500000 | 0.350 | *ANTXR1, ANXA4, ASPRV1, C11H2orf42, CAPN13, CAPN14, EHD3, GALNT14, GFPT1, GMCL1, LCLAT, MXD1, NFU1, PCBP1, PCYOX1, SNRNP27, SNRPG, TIA1, AAK1* |
| 12 | 72500000 | 73500000 | 0.315 | *DZIP1, CLDN10, DNAJC3, UGGT2, HS6ST3* |
| 16 | 24500000 | 26000000 | 0.290 | *RF00096, DUSP10* |
| 29 | 26500000 | 27500000 | 0.308 | *M-SAA3.2, OR8D4, RF00026, OR4D5, RF00056,* *OR10S1, OR10G6, OR10D3, TMEM225, VWA5A* |
| Holstein |
| 1 | 76500000 | 77500000 | 0.287 | *CLDN16, CLDN1, IL1RAP, TMEM207, P3H2, TP63* |
| 2 | 0 | 1000000 | 0.291 | *RF00026, LGSN, NIPA1, OCA2, HERC2* |
| 4 | 76000000 | 77000000 | 0.424 | *bta-mir-2420, RF00392, RF00392, RF00411, RF00026, PURB, bta-mir-4657, TMED4, IGFBP3, IGFBP1, ADCY1, RAMP3, TBRG4, CCM2, MYO1G,* *H2AFV, PPIA, ZMIZ2, DDX56, NPC1L1, OGDH, NUDCD3* |
| 4 | 83500000 | 84500000 | 0.296 | *RF00001* |
| 5 | 25000000 | 26000000 | 0.288 | *MUCL1, GLYCAM1, GPR84, bta-mir-148b, HNRNPA1, SMUG1, HOXC4, HOXC5, METAP2, USP44, PPP1R1A, PDE1B, GTSF1, ITGA5, COPZ1, NFE2, CBX5, NCKAP1L, ZNF385A* |
| 6 (ROH) | 37000000 | 38000000 | 0.314 | *MED28, DCAF16, LAP3, FAM184B, NCAPG, LCORL* |
| 7 | 41000000 | 42000000 | 0.315 | *OR6F1, OR11L1, RF00001, OR2M4, TRIM58, OR2W3, OR2L13* |
| 8 | 103000000 | 104000000 | 0.297 | *MIR455, ORM1, RF00416, RF00560, KIF12, AKNA, ATP6V1G1, TNFSF15, ZNF618, COL27A1, WHRN, TMEM268* |
| 8 | 106000000 | 107000000 | 0.307 | *RF00413, ASTN2* |
| 9 | 55000000 | 56000000 | 0.299 | *RF00100, RF00026* |
| 14 | 22000000 | 23500000 | 0.457 | *SOX17, RP1, LYPLA1, XKR4, MRPL15RPS20, RF01277, RF00003, MOS, TGS1, CHCHD7, SDR16C5, SDR16C6, XKR4, LYN, PLAG1, TMEM68* |
| 16 | 41500000 | 42500000 | 0.358 | *KIAA2013, RF00020, NPPB, NPPA, RF02158, RF02157, RF02156, bta-mir-12050, FBXO2, TNFRSF1B, TNFRSF8, MIIP, MFN2, PLOD1, CLCN6, MTHFR, DRAXIN, MAD2L2, FBXO6, FBXO44, DISP3, UBIAD1, ANGPTL7, MTOR, AGTRAP* |
| 17 | 18000000 | 19000000 | 0.294 | *NDUFC1, MGARP, RF00026, MGST2, SETD7, RAB33B, NOCT, MAML3, NAA15, ELF2,*  |
| 18 | 13500000 | 15000000 | 0.347 | *ACSF3, ANKRD11, APRT, bta-mir-2327, CBFA2T3, CDH15, CDK10, CDT1, CHMP1A, CPNE7, CTU2, CYBA, DBNDD1, DEF8, DPEP1, FANCA, GALNS, GAS8, MC1R, MVD, PIEZO1, RF00003, RF00324,* *RNF166, RPL13, SHCBP1, SLC22A31, SNAI3, SPATA2L, SPG7, SPIRE2, TCF25, TRAPPC2L,* *TUBB3, VPS35, VPS9D1, ZC3H18, ZFPM1, ZNF276, ZNF469* |
| 20 | 30500000 | 32000000 | 0.296 | *RF00026, RF00017, PAIP1, TMEM267, CCL28, HMGCS1, NIM1K, FGF10, NNT,* *C20H5orf34, RF00302, bta-mir-12004, ZNF131, SELENOP, CCDC152, GHR* |
| 20 | 43500000 | 45000000 | 0.482 | *-* |
| 22 | 22000000 | 23000000 | 0.341 | *RF02196, LRRN1, SETMAR* |
| 24 | 17500000 | 18500000 | 0.313 | *RF00026* |
| 26 | 21500000 | 23500000 | 0.408 | *RF00156, SEMA4G, MRPL43, TWNK, KAZALD1, TLX1, LBX1, FGF8, NPM3, RF00001, HPS6, RF00099, PITX3, NFKB2, FBXL15, bta-mir-146b, TRIM8, CYP17A1, CYP17A1, SLF2, LZTS2, SFXN3, POLL, DPCD, KCNIP2, LDB1, NOLC1, ELOVL3, PSD, CUEDC2, MFSD13A, ACTR1A, ARL3, WBP1L, CYP17A1, PAX2, BTRC, FBXW4, OGA, ARMH3, PPRC1, GBF1, SUFU, SFXN2* |
| Simmental |
| 4 | 54500000 | 56000000 | 0.201 | *GPR85, PPP1R3A, BMT2, LSMEM1, IFRD1, ZNF277, TMEM168* |
| 5 | 13500000 | 14500000 | 0.158 | *RF00026, SLC6A15* |
| 5 | 22500000 | 24000000 | 0.157 | *RF00026, PLEKHG7, UBE2N, MRPL42, SOCS2, EEA1, NUDT4, CRADD, PLXNC1* |
| 6 | 61000000 | 62500000 | 0.182 | *SHISA3, bta-mir-2285cs, RF00100, BEND4, ATP8A1, GRXCR1, RF00100, GRXCR1* |
| 6 | 64500000 | 66000000 | 0.165 | *COX7B2, GABRG1, GABRA2, GABRA4, GABRB1* |
| 6 | 69000000 | 71500000 | 0.310 | *GSX2, RF00026, RF00026, CHIC2, FIP1L1, LNX1, PDGFRA, KIT, KDR, SRD5A3, TMEM165, PDCL2, CLOCK, EXOC1L, CEP135, NMU, EXOC1* |
| 6 | 91500000 | 92500000 | 0.164 | *SOWAHB, SEPT11, CCNI, CCNG2, CXCL13, CNOT6L, SHROOM3* |
| 7 | 42000000 | 43500000 | 0.171 | *ARID3A, AZU1, BSG, C2CD4C, CDC34, CFD, ELANE, FGF22, FSTL3, GZMM, HCN2, KISS1R, LYPD8, MADCAM1, MED16, MGC137030,* *MIER2, MISP, ODF3L2, OR2G6, OR2T1, OR2T11, OR2T27, OR2T6, PALM, PGBD2, PLPP2, PLPPR3, POLRMT, PRSS57, PRTN3, PTBP1, R3HDM4, RF00026, RNF126, SH3BP5L, SHC, THEG, TPGS1, ZNF672, ZNF692* |
| 7 | 67500000 | 68500000 | 0.164 | *SGCD, TIMD4* |
| 11 | 59000000 | 60000000 | 0.180 | *C11H2orf74, AHSA2, USP34* |
| 11 | 93500000 | 94500000 | 0.154 | *OR1J2, OR1N2, OR1N1, OR1Q1, OR1B1, OR1L1, OR1L3, OR5C1, OR1K1, PDCL, RF00594, RF00579, ZBTB6, ZBTB26, GPR21, RF00026, RC3H2, RABGAP1, STRBP* |
| 11 | 95500000 | 96500000 | 0.159 | *bta-mir-181b-2, RF00026, RPL35, RF00264, HSPA5, RF00026, RF00020, ADGRD2, NR5A1, OLFML2A, WDR38, ARPC5L, GOLGA1, RABEPK, NR6A1, SCAI, PPP6C, GAPVD1, MAPKAP1* |
| 16 | 13000000 | 14000000 | 0.157 | RF00001, RGS18 |
| 18 | 13500000 | 15000000 | 0.185 | *ZNF469, CYBA, MVD, SNAI3, bta-mir-2327, CDT1, APRT, TRAPPC2L, SLC22A31, RPL13, RF00324, CPNE7, CHMP1A, CDK10, SPATA2L, VPS9D1, MC1R, DBNDD1, RF00003, ZC3H18, CTU2, RNF166, PIEZO1, CBFA2T3, ACSF3, CDH15, SPG7, DPEP1, ZNF276, FANCA, SPIRE2, TCF25, TUBB3, DEF8, GAS8, SHCBP1, VPS35, ZFPM1, GALNS, ANKRD11ZNF469, CYBA, MVD, SNAI3, bta-mir-2327, CDT1, APRT, TRAPPC2L, SLC22A31, RPL13, RF00324, CPNE7, CHMP1A, CDK10, SPATA2L, VPS9D1, MC1R, DBNDD1, RF00003, ZC3H18, CTU2, RNF166, PIEZO1, CBFA2T3, ACSF3, CDH15, SPG7, DPEP1, ZNF276, FANCA, SPIRE2, TCF25, TUBB3, DEF8, GAS8, SHCBP1, VPS35, ZFPM1, GALNS, ANKRD11* |
| 29 | 7500000 | 9000000 | 0.182 | *DENR, RAB38, TMEM135, FZD4, PRSS23, ME3, TMEM135* |

1Chromosome regions overlapping runs of homozygosity (ROH) islands reported by Mastrangelo *et al.* (2018b) in the Reggiana cattle breed are indicated with “(ROH)”.

**Supplementary Table S4.** Results of the pairwise Cross-Population Extended Haplotype Homozygosity (XP-EHH) analysis of Reggiana *vs* the three cosmopolitan breeds (Brown, Holstein and Simmental). Reported information includes the bovine chromosome (BTA) position [start and end nucleotide position on the chromosome determined by the corresponding single nucleotide polymorphism (SNP) positions], the number of SNPs in the window, the averaged XP-EPP value, the averaged log value and the annotated genes in the reported chromosome regions.

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| BTA | Start position | End position | Start SNP | End SNP | N. of SNPs | Averaged XP-EHH | Averaged log value | Annotated genes |
| Brown |
| 5 | 71914501 | 72264476 | ARS-BFGL-NGS-111053 | ARS-BFGL-NGS-79121 | 9 | -3.833 | 3.919 | *RF00407, RF00598, LARGE1* |
| 5 | 73581692 | 74079648 | ARS-BFGL-NGS-100454 | BTA-73985-no-rs | 12 | -3.783 | 3.835 | *RASD2, TOM1, HMOX1, MCM5, MB, RBFOX2* |
| 5 | 74740570 | 75224515 | ARS-BFGL-NGS-118891 | ARS-BFGL-NGS-117321 | 12 | -3.590 | 3.487 | *RF00026, EIF3D, MYH9, TXN2, FOXRED2, IFT27, PVALB, CACNG2* |
| 6 | 59716766 | 60085027 | Hapmap50098-BTA-76549 | ARS-BFGL-NGS-112982 | 11 | -3.927 | 4.100 | *APBB2* |
| 6 | 70431058 | 70716954 | Hapmap23983-BTC-070420 | BTB-00263209 | 10 | -3.617 | 3.532 | *RF00026, RF00026, KDR* |
| 6 | 80685724 | 80858441 | Hapmap26275-BTC-043486 | Hapmap24320-BTC-043265 | 5 | -3.713 | 3.690 | *EPHA5* |
| 6 | 88075494 | 89359390 | Hapmap39947-BTA-77207 | BTB-01458572 | 18 | -3.696 | 3.669 | *RF00100, CXCL8, CXCL5, CXCL2, CXCL3, GRO1,* *EPGN, COX18, ALB, AFP, AFM, RASSF6, EREG, ANKRD17, MTHFD2L* |
| 6 | 89732280 | 89935361 | ARS-BFGL-NGS-2935 | ARS-BFGL-NGS-83505 | 8 | -4.114 | 4.423 | *PARM1* |
| 6 | 90260850 | 91800062 | BTB-01496160 | BTA-77154-no-rs | 30 | -4.070 | 4.346 | *RCHY1, RF00003, CXCL9, CXCL10, CXCL11, STBD1,* *RF00026, SOWAHB, THAP6, G3BP2, PPEF2, NAAA, NUP54, CCDC158, 11-Sep, SCARB2, CDKL2, USO1, SDAD1, ART3, SHROOM3* |
| 6 | 92383295 | 92430962 | Hapmap52160-rs29020798 | BTB-00270310 | 3 | -3.526 | 3.378 | *CNOT6L* |
| 6 | 93019845 | 93233475 | ARS-BFGL-NGS-66691 | Hapmap53128-rs29022916 | 5 | -3.426 | 3.213 | *FRAS1* |
| 6 | 96162959 | 96424013 | Hapmap36567-SCAFFOLD30438\_8760 | Hapmap48078-BTA-77495 | 9 | -3.985 | 4.195 | *RF00156, RASGEF1B* |
| 13 | 44978611 | 45082428 | ARS-BFGL-NGS-23830 | BTA-99048-no-rs | 4 | -3.541 | 3.399 | *PITRM1* |
| 13 | 45936412 | 46049129 | ARS-BFGL-NGS-101531 | Hapmap42872-BTA-22214 | 4 | -3.455 | 3.259 | *ADARB2* |
| Holstein |
| 10 | 44727501 | 44820482 | ARS-BFGL-NGS-97032 | Hapmap51024-BTA-67203 | 5 | -3.481 | 3.312 | *GNG2* |
| 20 | 24479790 | 24565655 | Hapmap53329-rs29023196 | ARS-BFGL-NGS-108866 | 3 | -3.370 | 3.128 | *SNX18* |
| 20 | 28062228 | 28317303 | BTA-50190-no-rs | ARS-BFGL-NGS-31598 | 6 | -3.284 | 2.993 | *PARP8* |
| 20 | 34228714 | 34460986 | Hapmap54938-rs29013720 | BTA-50400-no-rs | 6 | -3.215 | 2.881 | *-* |
| 20 | 34710584 | 34965270 | BTA-15204-no-rs | ARS-BFGL-BAC-31754 | 5 | -3.257 | 3.076 | *RF00004, RF00001* |
| 20 | 35666579 | 36739131 | ARS-BFGL-NGS-34478 | BTB-00780480 | 21 | -3.456 | 3.274 | *RF00416, RF00560, RF00026, RF00026, GDNF, LIFR,* *EGFLAM, WDR70* |
| 20 | 37388845 | 37911470 | Hapmap53888-rs29021190 | Hapmap49835-BTA-104494 | 11 | -3.286 | 2.995 | *SLC1A3* |
| 20 | 39181409 | 39722083 | ARS-BFGL-NGS-115190 | ARS-BFGL-NGS-73590 | 14 | -3.453 | 3.264 | *RAD1, RF00003, BRIX1, TTC23L, C1QTNF3, NAJC21, RAI14* |
| 20 | 41025188 | 41104184 | ARS-BFGL-NGS-63070 | Hapmap43599-BTA-50578 | 4 | -3.410 | 3.195 | *SUB1* |
| 20 | 45677327 | 45971800 | ARS-BFGL-NGS-37203 | Hapmap58446-rs29021863 | 7 | -3.333 | 3.069 | *-* |
| Simmental |
| 5 | 60241477 | 60299953 | ARS-BFGL-NGS-7741 | ARS-BFGL-NGS-110018 | 3 | -3.876 | 3.975 | *CCDC38, AMDHD1, HAL* |
| 5 | 60983725 | 61058294 | ARS-BFGL-NGS-44773 | Hapmap39777-BTA-73723 | 3 | -3.998 | 4.196 | *CFAP54* |
| 5 | 61907183 | 62128735 | ARS-BFGL-NGS-115187 | ARS-BFGL-NGS-100699 | 5 | -3.847 | 3.928 | *-* |
| 5 | 67994388 | 68293598 | ARS-BFGL-NGS-119231 | ARS-BFGL-NGS-33119 | 10 | -4.107 | 4.419 | *CHST11* |
| 6 | 68331252 | 71428675 | Hapmap49432-BTA-107930 | ARS-BFGL-NGS-37727 | 44 | -5.433 | 7.608 | *bta-mir-4449, RF00568, GSX2, RF00026, RF00026,* *RF00026, RF00026, RF00026, USP46, RASL11B, CHIC2,* *KIT, KDR, SRD5A3, TMEM165, PDCL2, EXOC1L, CEP135, SCFD2, FIP1L1, LNX1, PDGFRA, CLOCK, NMU, EXOC1* |
| 7 | 43047351 | 43105247 | ARS-BFGL-NGS-112360 | ARS-BFGL-NGS-74330 | 3 | -3.886 | 4.001 | *C2CD4C, MIER2, THEG* |
| 7 | 43715046 | 43792866 | ARS-BFGL-NGS-22438 | ARS-BFGL-NGS-109750 | 4 | -3.812 | 3.867 | *C7H19orf24, EFNA2, PWWP3A* |
| 7 | 44326829 | 44403367 | Hapmap49311-BTA-78907 | ARS-BFGL-NGS-69626 | 3 | -3.724 | 3.709 | *SOWAHA* |

**Supplementary Table S5.** Gene enrichment analysis over the Gene Ontology (GO; Biological Process) resource of the genome regions under selection in *Bos taurus*.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Term1 | Description2 | Overlap3 | *p*-value4 | Genes5 |
| GO:0006892 | post-Golgi vesicle-mediated transport  | 4/59 | 8.10E-03 | *CHIC2, ARL3, GBF1, EXOC1* |
| GO:0030318 | melanocyte differentiation  | 2/8 | 2.28E-02 | *KIT, HPS6* |
| GO:0006702 | androgen biosynthetic process  | 2/11 | 2.28E-02 | *SRD5A3, CYP17A1* |
| GO:0043549 | regulation of kinase activity  | 4/102 | 2.28E-02 | *PDGFRA, LDB1, KIT, KDR* |
| GO:0051091 | positive regulation of sequence-specific DNA binding transcription factor activity  | 5/216 | 2.28E-02 | *TRIM8, KIT, PPRC1, CLOCK, NFKB2* |
| GO:0008209 | androgen metabolic process  | 2/21 | 4.42E-02 | *SRD5A3, CYP17A1* |

1Identifier retrieved from the GO resource.

2Brief explanation of the functional term.

3Number of input genes associated to the functional term over the number of genes directly associated to the functional term.

4Adjusted *p*-value.

5Genes of the input set associated to the functional term.