***animal* journal**

**Genome-wide association and pathway analysis of carcass and meat quality traits in Piemontese young bulls.**

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Short title: Genomic study for meat traits in Piemontese bulls

**Supplementary Table S1.** Complete list of the significant single nucleotide polymorphism (SNPs) obtained after standard genome-wide association (GWAS) analysis in Piemontese beef cattle.

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **SNP** | **CHR** | **BP** | ***P*-value** | **LOG** | **effB** | **Trait1** | **MAF** |  |  |  |
| BovineHD2300000877 | 23 | 3907142 | 4.47E-05 | 4.350 | 0.316 | a\* | 0.3568 | 0.0458 | 0.5184 | 8.83 |
| BovineHD2500003345 | 25 | 11960157 | 7.79E-06 | 5.108 | -0.368 | a\* | 0.2699 | 0.0534 | 0.5184 | 10.29 |
| ARS-BFGL-NGS-45457 | 6 | 38715250 | 1.86E-06 | 5.731 | -9.284 | AS | 0.4324 | 42.3079 | 273.8923 | 15.45 |
| MS-rs109570900 | 6 | 38777311 | 3.35E-05 | 4.475 | -8.032 | AS | 0.4620 | 32.0690 | 273.8923 | 11.71 |
| Hapmap49816-BTA-98191 | 6 | 91906227 | 1.78E-05 | 4.751 | -10.840 | AS | 0.1775 | 34.3094 | 273.8923 | 12.53 |
| BovineHD2400005258 | 24 | 19872257 | 4.58E-05 | 4.339 | 0.290 | b\* | 0.3773 | 0.0394 | 0.5880 | 6.70 |
| BovineHD2500003345 | 25 | 11960157 | 3.53E-05 | 4.453 | -0.327 | b\* | 0.2699 | 0.0422 | 0.5880 | 7.17 |
| BovineHD2500003345 | 25 | 11960157 | 1.46E-05 | 4.836 | -0.440 | C\* | 0.2699 | 0.0763 | 0.8440 | 9.04 |
| ARS-BFGL-NGS-76281 | 3 | 31524593 | 3.75E-05 | 4.426 | -0.017 | CDG | 0.3882 | 0.0001 | 0.0040 | 3.56 |
| Hapmap30134-BTC-034283 | 6 | 38464203 | 7.13E-06 | 5.147 | -0.019 | CDG | 0.4810 | 0.0002 | 0.0040 | 4.43 |
| BovineHD0600010655 | 6 | 38538611 | 6.35E-06 | 5.197 | -0.019 | CDG | 0.4869 | 0.0002 | 0.0040 | 4.50 |
| BovineHD0600010657 | 6 | 38541611 | 6.35E-06 | 5.197 | -0.019 | CDG | 0.4869 | 0.0002 | 0.0040 | 4.50 |
| BovineHD0600010666 | 6 | 38574125 | 1.73E-05 | 4.762 | 0.018 | CDG | 0.4814 | 0.0002 | 0.0040 | 4.02 |
| Hapmap26308-BTC-057761 | 6 | 38576012 | 6.37E-09 | 8.196 | 0.025 | CDG | 0.3817 | 0.0003 | 0.0040 | 7.31 |
| BovineHD0600010673 | 6 | 38590515 | 1.30E-05 | 4.886 | 0.018 | CDG | 0.4843 | 0.0002 | 0.0040 | 4.12 |
| MS-rs110839532 | 6 | 38599667 | 1.30E-05 | 4.886 | 0.018 | CDG | 0.4843 | 0.0002 | 0.0040 | 4.12 |
| MS-rs43702361 | 6 | 38599672 | 1.32E-05 | 4.879 | 0.018 | CDG | 0.4835 | 0.0002 | 0.0040 | 4.12 |
| MS-rs109241256 | 6 | 38599864 | 1.12E-05 | 4.952 | 0.018 | CDG | 0.4846 | 0.0002 | 0.0040 | 4.20 |
| MS-rs41255599 | 6 | 38599993 | 1.30E-05 | 4.886 | 0.018 | CDG | 0.4843 | 0.0002 | 0.0040 | 4.12 |
| BovineHD0600010685 | 6 | 38616248 | 1.30E-05 | 4.886 | 0.018 | CDG | 0.4846 | 0.0002 | 0.0040 | 4.12 |
| ARS-BFGL-NGS-45457 | 6 | 38715250 | 2.44E-11 | 10.613 | 0.028 | CDG | 0.4324 | 0.0004 | 0.0040 | 9.61 |
| MS-rs109570900 | 6 | 38777311 | 1.07E-08 | 7.971 | 0.024 | CDG | 0.4620 | 0.0003 | 0.0040 | 7.08 |
| MS-rs110251642 | 6 | 38808241 | 3.34E-08 | 7.476 | 0.023 | CDG | 0.4752 | 0.0003 | 0.0040 | 6.51 |
| BovineHD4100004576 | 6 | 38834676 | 3.19E-08 | 7.496 | 0.023 | CDG | 0.4766 | 0.0003 | 0.0040 | 6.52 |
| BovineHD0600010755 | 6 | 38866381 | 5.33E-08 | 7.273 | 0.022 | CDG | 0.4781 | 0.0003 | 0.0040 | 6.26 |
| Hapmap31285-BTC-041097 | 6 | 38869785 | 3.34E-08 | 7.476 | 0.023 | CDG | 0.4752 | 0.0003 | 0.0040 | 6.51 |
| Hapmap33628-BTC-041023 | 6 | 38939012 | 1.23E-08 | 7.909 | 0.024 | CDG | 0.4583 | 0.0003 | 0.0040 | 7.07 |
| BovineHD0600010795 | 6 | 39185743 | 1.22E-06 | 5.915 | 0.020 | CDG | 0.4931 | 0.0002 | 0.0040 | 5.07 |
| BovineHD4100004612 | 6 | 39340446 | 2.11E-06 | 5.676 | -0.020 | CDG | 0.4145 | 0.0002 | 0.0040 | 5.04 |
| Hapmap31044-BTC-071337 | 6 | 39346170 | 1.10E-06 | 5.960 | -0.021 | CDG | 0.4142 | 0.0002 | 0.0040 | 5.31 |
| BovineHD0600010842 | 6 | 39441548 | 3.66E-06 | 5.437 | -0.020 | CDG | 0.3630 | 0.0002 | 0.0040 | 4.66 |
| BovineHD0600008146 | 6 | 29225507 | 4.04E-05 | 4.394 | 0.629 | CL | 0.2617 | 0.1531 | 0.7387 | 20.72 |
| ARS-BFGL-NGS-70946 | 10 | 14574453 | 4.15E-05 | 4.382 | -0.552 | CL | 0.4237 | 0.1489 | 0.7387 | 20.16 |
| Hapmap30134-BTC-034283 | 6 | 38464203 | 2.82E-06 | 5.550 | -8.421 | CW | 0.4810 | 35.4019 | 639.2217 | 5.54 |
| BovineHD0600010655 | 6 | 38538611 | 2.18E-06 | 5.662 | -8.516 | CW | 0.4869 | 36.2401 | 639.2217 | 5.67 |
| BovineHD0600010657 | 6 | 38541611 | 2.18E-06 | 5.662 | -8.516 | CW | 0.4869 | 36.2401 | 639.2217 | 5.67 |
| BovineHD0600010666 | 6 | 38574125 | 2.14E-05 | 4.670 | 7.593 | CW | 0.4814 | 28.7844 | 639.2217 | 4.50 |
| Hapmap26308-BTC-057761 | 6 | 38576012 | 4.81E-07 | 6.318 | 9.212 | CW | 0.3817 | 40.0582 | 639.2217 | 6.27 |
| BovineHD0600010673 | 6 | 38590515 | 3.25E-05 | 4.488 | 7.408 | CW | 0.4843 | 27.4132 | 639.2217 | 4.29 |
| MS-rs110839532 | 6 | 38599667 | 3.25E-05 | 4.488 | 7.408 | CW | 0.4843 | 27.4132 | 639.2217 | 4.29 |
| MS-rs43702361 | 6 | 38599672 | 3.29E-05 | 4.483 | 7.408 | CW | 0.4835 | 27.4122 | 639.2217 | 4.29 |
| MS-rs109241256 | 6 | 38599864 | 2.79E-05 | 4.554 | 7.478 | CW | 0.4846 | 27.9328 | 639.2217 | 4.37 |
| MS-rs41255599 | 6 | 38599993 | 3.25E-05 | 4.488 | 7.408 | CW | 0.4843 | 27.4132 | 639.2217 | 4.29 |
| BovineHD0600010685 | 6 | 38616248 | 3.25E-05 | 4.488 | 7.408 | CW | 0.4846 | 27.4144 | 639.2217 | 4.29 |
| ARS-BFGL-NGS-45457 | 6 | 38715250 | 8.32E-08 | 7.080 | 9.611 | CW | 0.4324 | 45.3451 | 639.2217 | 7.09 |
| MS-rs109570900 | 6 | 38777311 | 5.55E-06 | 5.256 | 8.113 | CW | 0.4620 | 32.7199 | 639.2217 | 5.12 |
| MS-rs110251642 | 6 | 38808241 | 5.98E-06 | 5.223 | 8.018 | CW | 0.4752 | 32.0629 | 639.2217 | 5.02 |
| BovineHD4100004576 | 6 | 38834676 | 7.97E-06 | 5.098 | 7.901 | CW | 0.4766 | 31.1429 | 639.2217 | 4.87 |
| BovineHD0600010755 | 6 | 38866381 | 7.71E-06 | 5.113 | 7.885 | CW | 0.4781 | 31.0245 | 639.2217 | 4.85 |
| Hapmap31285-BTC-041097 | 6 | 38869785 | 5.98E-06 | 5.223 | 8.018 | CW | 0.4752 | 32.0629 | 639.2217 | 5.02 |
| Hapmap33628-BTC-041023 | 6 | 38939012 | 3.92E-06 | 5.407 | 8.279 | CW | 0.4583 | 34.0334 | 639.2217 | 5.32 |
| BovineHD0600011056 | 6 | 40563707 | 4.55E-05 | 4.342 | -10.471 | CW | 0.1410 | 26.5563 | 639.2217 | 4.15 |
| ARS-BFGL-NGS-4893 | 19 | 6895198 | 3.07E-05 | 4.513 | 7.536 | CW | 0.4284 | 27.8162 | 639.2217 | 4.35 |
| BovineHD0900013319 | 9 | 48330996 | 1.54E-05 | 4.811 | 0.209 | PL | 0.4288 | 0.0215 | 0.1644 | 13.06 |
| BovineHD0400032408 | 4 | 1.13E+08 | 3.34E-05 | 4.476 | -0.378 | H\* | 0.4573 | 0.0709 | 1.0140 | 6.99 |
| BovineHD2500003345 | 25 | 11960157 | 3.13E-05 | 4.504 | -0.417 | H\* | 0.2699 | 0.0686 | 1.0140 | 6.77 |
| BovineHD2300001826 | 23 | 7245409 | 3.56E-05 | 4.448 | 0.608 | L\* | 0.3692 | 0.1720 | 3.6370 | 4.73 |
| ARS-BFGL-NGS-114722 | 8 | 28464160 | 2.02E-05 | 4.695 | 0.011 | pH | 0.1939 | 0.0000 | 0.0002 | 22.78 |
| BTA-76623-no-rs | 6 | 71154473 | 9.69E-06 | 5.014 | -0.433 | EUS | 0.1194 | 0.0395 | 0.4135 | 9.55 |
| ARS-BFGL-NGS-116123 | 11 | 94686959 | 4.83E-05 | 4.316 | 0.263 | EUS | 0.3240 | 0.0303 | 0.4135 | 7.33 |

SNP: single nucleotide polymorphism; CHR: chromosome; BP: SNP location in bp; LOG: -log10(*P*-value); effB: SNP effect; MAF: minor allele frequency; : variance explained by the SNP, calculated as *2pqa2,* where *p* is the frequency of one allele, *q = 1-p* is the frequency of the second allele, and *a* is the estimated additive genomic effect; : additive genomic variance; proportion of genomic variance explained by each SNP, calculated as .

1Trait: AS: age at slaughtering; CW: carcass weight; CDG: carcass daily gain, carcass; EUS: carcass conformation according to the EU linear grading system (Commission of the European Communities 1982). The six main grades (S, E, U, R, O, P from best to worst) were furtherly subdivided in + or – subclasses and then converted into numerical scores (EUS) ranging from 18 (S+ class) to 1 (P- class); PL: purge loss; CL: cooking loss; L\*: lightness; a\*: redness; b\*: yellowness; C\*: chroma; H\*: hue

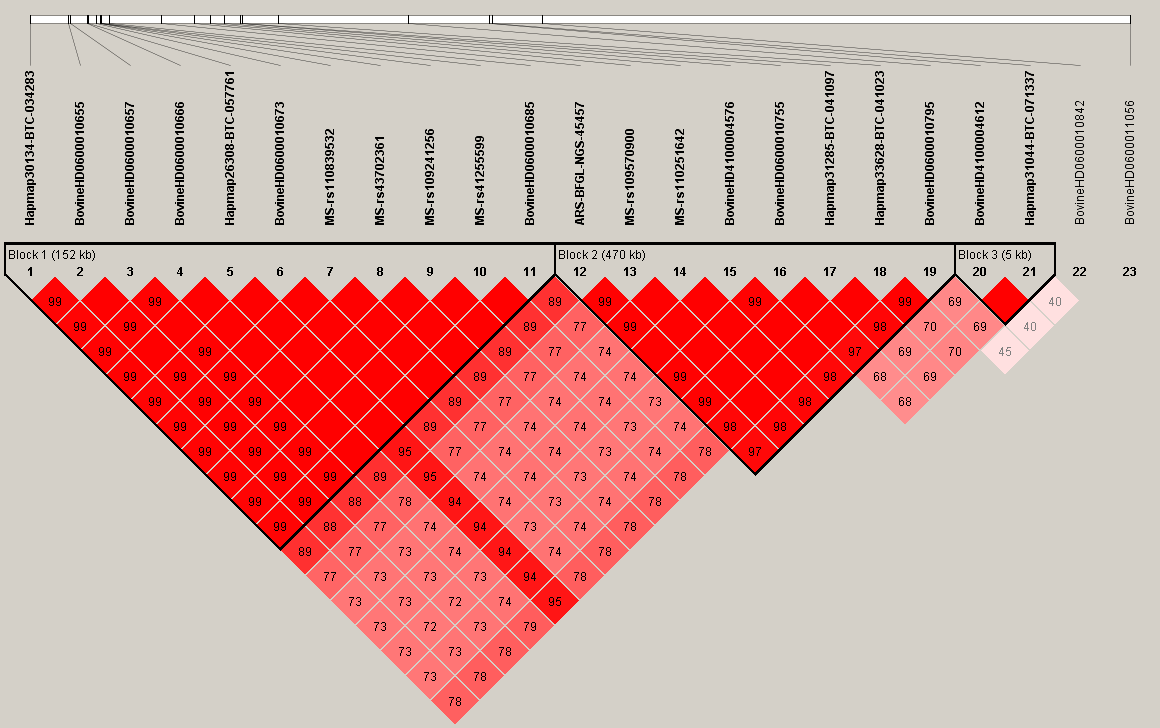
**Supplementary Table S2.** Significantly enriched gene ontology (GO) terms and Kyoto Encyclopaedia of Genes and Genomes (KEGG) pathways for carcass and meat quality traits in Piemontese beef cattle.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **ID** | **Term** | **Nr. Genes** | **% AG** | **FDR** | **Associated Genes Found** |
| ***1a\**** |  |  |  |  |  |
| KEGG:04728 | dopaminergic synapse | 12 | 21.1 | 0.042 | [AKT3, CACNA1B, CACNA1D, CAMK2D, GNG3, GRIA2, ITPR1, ITPR2, ITPR3, MAPK10, PLCB1, PRKCG] |
| GO\_MF:0005262 | calcium channel activity | 14 | 25.0 | 0.014 | [CACNA1B, CACNA1D, CACNG5, CACNG7, FAM155A, ITPR1, ITPR2, ITPR3, ORAI3, SLC24A4, TPCN2, TRPC3, TRPM8, TRPV5] |
| GO\_MF:0022890 | inorganic cation transmembrane transporter activity | 32 | 13.9 | 0.029 | [ATP5G3, CACNA1B, CACNA1D, CACNG5, CACNG7, CNGA3, COX7A2L, FAM155A, GRIA2, ITPR1, ITPR2, ITPR3, KCND2, KCNIP4, KCNK3, LOC534223, NDUFA4L2, ORAI3, SLC12A6, SLC20A2, SLC24A4, SLC30A3, SLC36A1, SLC5A1, SLC6A11, SLC9A1, SLC9A8, SLC9B2, TPCN2, TRPC3, TRPM8, TRPV5] |
| GO\_BP:0098662 | inorganic cation transmembrane transport | 33 | 12.5 | 0.047 | [ATP5G3, CACNA1B, CACNA1D, CACNG5, CACNG7, CNGA3, COX7A2L, FAM155A, ITPR1, ITPR2, ITPR3, KCND2, KCNIP4, KCNK3, KEL, LOC534223, NDUFA4L2, NEDD4L, ORAI3, SLC12A6, SLC20A2, SLC24A4, SLC30A3, SLC36A1, SLC9A1, SLC9A8, SLC9B2, STIM1, TESC, TPCN2, TRPC3, TRPM8, TRPV5] |
| ***1b\**** |  |  |  |  |  |
| GO\_MF:0005262 | calcium channel activity | 13 | 23.2 | 0.021 | [CACNA1D, CACNB3, CACNG7, FAM155A, ITGAV, ITPR3, ORAI3, PKD2, SLC24A4, TPCN2, TRPC3, TRPM8, TRPV5] |
| GO\_BP:0034030 | ribonucleoside bisphosphate biosynthetic process | 5 | 71.4 | 0.019 | [ACAT1, ACOT7, PANK2, PAPSS1, PPCDC] |
| GO\_BP:0034033 | purine nucleoside bisphosphate biosynthetic process | 5 | 71.4 | 0.019 | [ACAT1, ACOT7, PANK2, PAPSS1, PPCDC] |
| ***1C\**** |  |  |  |  |  |
| KEGG:04713 | circadian entrainment | 10 | 21.7 | 0.043 | [CACNA1D, CAMK2D, GNAI1, GRIA1, GRIA2, ITPR1, ITPR3, PLCB1, PRKCG, PRKG1] |
| KEGG:04730 | long-term depression | 8 | 27.6 | 0.048 | [GNAI1, GRIA1, GRIA2, ITPR1, ITPR3, PLCB1, PRKCG, PRKG1] |
| GO\_MF:0005262 | calcium channel activity | 12 | 21.4 | 0.035 | [CACNA1D, CACNG5, CACNG7, FAM155A, ITGAV, ITPR1, ITPR3, ORAI3, SLC24A4, TPCN2, TRPC3, TRPV6] |
| GO\_MF:0008324 | cation transmembrane transporter activity | 36 | 12.9 | 0.013 | [ATP5G3, CACNA1D, CACNG5, CACNG7, CNGA3, COX7A2L, FAM155A, GRIA1, GRIA2, ITGAV, ITPR1, ITPR3, KCND2, KCNIP4, KCNK3, LOC534223, NDUFA4L2, ORAI3, SCN2A, SLC12A6, SLC1A4, SLC20A2, SLC24A4, SLC28A1, SLC30A3, SLC30A4, SLC36A1, SLC39A11, SLC5A1, SLC6A11, SLC6A16, SLC9A8, SLC9B2, TPCN2, TRPC3, TRPV6] |
| GO\_BP:0015671 | oxygen transport | 4 | 57.1 | 0.047 | [HBA, HBM, HBQ1, HBZ] |
| GO\_BP:0015672 | monovalent inorganic cation transport | 23 | 12.6 | 0.049 | [ATP5G3, CACNA1D, CNGA3, COMMD9, COX7A2L, KCND2, KCNIP4, KCNK3, LOC534223, NDUFA4L2, NEDD4L, NKAIN2, NNT, SCN2A, SLC12A6, SLC20A2, SLC24A4, SLC36A1, SLC5A1, SLC9A8, SLC9B2, TESC, TSC1] |
| GO\_MF:0022890 | inorganic cation transmembrane transporter activity | 34 | 14.8 | 0.002 | [ATP5G3, CACNA1D, CACNG5, CACNG7, CNGA3, COX7A2L, FAM155A, GRIA1, GRIA2, ITGAV, ITPR1, ITPR3, KCND2, KCNIP4, KCNK3, LOC534223, NDUFA4L2, ORAI3, SCN2A, SLC12A6, SLC20A2, SLC24A4, SLC28A1, SLC30A3, SLC36A1, SLC39A11, SLC5A1, SLC6A11, SLC6A16, SLC9A8, SLC9B2, TPCN2, TRPC3, TRPV6] |
| GO\_MF:0046873 | metal ion transmembrane transporter activity | 28 | 13.5 | 0.030 | [CACNA1D, CACNG5, CACNG7, CNGA3, FAM155A, ITGAV, ITPR1, ITPR3, KCND2, KCNIP4, KCNK3, LOC534223, ORAI3, SCN2A, SLC12A6, SLC20A2, SLC24A4, SLC28A1, SLC30A3, SLC39A11, SLC5A1, SLC6A11, SLC6A16, SLC9A8, SLC9B2, TPCN2, TRPC3, TRPV6] |
| GO\_BP:0098655 | cation transmembrane transport | 34 | 11.0 | 0.048 | [ATP5G3, CACNA1D, CACNG5, CACNG7, CNGA3, COX7A2L, FAM155A, ITGAV, ITPR1, ITPR3, KCND2, KCNIP4, KCNK3, LOC534223, NDUFA4L2, NEDD4L, NPSR1, ORAI3, SCN2A, SLC12A6, SLC1A4, SLC20A2, SLC24A4, SLC30A3, SLC30A4, SLC36A1, SLC39A11, SLC9A8, SLC9B2, STIM1, TESC, TPCN2, TRPC3, TRPV6] |
| GO\_BP:0098660 | inorganic ion transmembrane transport | 34 | 11.4 | 0.046 | [ATP5G3, CACNA1D, CACNG5, CACNG7, CLCA4, CNGA3, COX7A2L, FAM155A, ITGAV, ITPR1, ITPR3, KCND2, KCNIP4, KCNK3, LOC534223, NDUFA4L2, NEDD4L, NPSR1, ORAI3, SCN2A, SLC12A6, SLC1A4, SLC20A2, SLC24A4, SLC30A3, SLC36A1, SLC39A11, SLC9A8, SLC9B2, STIM1, TESC, TPCN2, TRPC3, TRPV6] |
| GO\_BP:0098662 | inorganic cation transmembrane transport | 32 | 12.2 | 0.044 | [ATP5G3, CACNA1D, CACNG5, CACNG7, CNGA3, COX7A2L, FAM155A, ITGAV, ITPR1, ITPR3, KCND2, KCNIP4, KCNK3, LOC534223, NDUFA4L2, NEDD4L, NPSR1, ORAI3, SCN2A, SLC12A6, SLC20A2, SLC24A4, SLC30A3, SLC36A1, SLC39A11, SLC9A8, SLC9B2, STIM1, TESC, TPCN2, TRPC3, TRPV6] |
| ***1CL*** |  |  |  |  |  |
| GO\_BP:0051963 | regulation of synapse assembly | 9 | 34.6 | 0.027 | [ADGRL1, EFNA5, EPHB1, NTRK1, NTRK2, PTK2, PVRL1, WNT5A, WNT7A] |
| ***1CW*** |  |  |  |  |  |
| GO\_BP:0035418 | protein localization to synapse | 5 | 55.6 | 0.038 | [ASIC2, CDK5, DLG4, NSG1, SNAP47] |
| ***1EUS*** |  |  |  |  |  |
| GO\_BP:0014070 | response to organic cyclic compound | 31 | 14.2 | 0.029 | [BCL2, BMP4, BMP7, CSN3, CTNNB1, DDIT4, DROSHA, EFNA5, EGFR, GABRB1, GABRB3, GABRG2, GNG2, HCN1, HID1, HNF4G, IL10, IL1RN, KCNJ8, LRP6, LRRK2, NCOR1, NR1H2, PPP3CA, PRKCE, PRKCG, PRMT2, RECQL5, SLC9A1, SLIT3, UFSP2] |

%AG: percentage of genes associated with the significant pathways with respect to the total number of genes in the pathway; FDR: false discovery rate

1See Supplementary Table S1 for trait definition

**Supplementary Figure S1.** Haploview plot of pairwise D′ in the region at ~38.46-40.56 Mb on *Bos taurus autosome* (BTA6) in Piemontese beef cattle: red, Dʹ = 1.0 and logarithm of the odds (LOD) ≥ 2.0; blue, D′ = 1.0 and LOD < 2.0; white, D′ < 1.0 and LOD < 2.0; shades of pink/red, D′ < 1.0 and LOD ≥ 2.0. LD blocks are defined by a black line.

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