

**Table S1: The suggestive significant single nucleotide polymorphisms (SNPs) for milk composition traits in dairy cattle**

| Trait | Locus       | Chr | Position   | $-\log_{10}(P)$ | Effect (SE)  | Ref. | MA | Ref. freq. | Annotation | Gene name | Gene description   |
|-------|-------------|-----|------------|-----------------|--------------|------|----|------------|------------|-----------|--|
| FP    | rs134637616 | 5   | 93,945,655 | 5.74            | 0.11 (0.02)  | G    | T  | 0.66       | intron     | MGST1     | microsomal glutathione S-transferase 1   |
|       | rs211210569 | 5   | 93,945,738 | 6.76            | 0.11 (0.02)  | C    | T  | 0.62       | intron     | MGST1     | microsomal glutathione S-transferase 1   |
|       | rs210744919 | 5   | 93,949,810 | 6.43            | -0.11 (0.02) | G    | A  | 0.41       | intron     | MGST1     | microsomal glutathione S-transferase 1   |
|       | rs41630614  | 14  | 1,514,056  | 5.09            | 0.09 (0.02)  | T    | G  | 0.68       | upstream   | ZNF7      | zinc finger protein 7  |
|       | rs110984572 | 14  | 1,653,693  | 7.85            | -0.17 (0.03) | C    | T  | 0.89       | upstream   | FOXH1     | forkhead box H1  |
|       | rs134432442 | 14  | 1,736,599  | 74.54           | -0.33 (0.02) | C    | T  | 0.52       | missense   | CPSF1     | cleavage and polyadenylation specific factor 1                                   |
|       | rs211309638 | 14  | 1,757,935  | 10.01           | -0.20 (0.03) | C    | T  | 0.89       | upstream   | ADCK5     | aarF domain containing kinase 5  |
|       | rs137071126 | 14  | 1,765,835  | 84.41           | -0.36 (0.02) | C    | G  | 0.48       | synonymous | SLC52A2   | solute carrier family 52 member 2  |
|       | rs109421300 | 14  | 1,801,116  | 89.79           | -0.38 (0.02) | T    | C  | 0.46       | intron     | DGAT1     | diacylglycerol O-acyltransferase 1   |
|       | rs137787931 | 14  | 1,880,378  | 67.95           | 0.32 (0.02)  | T    | C  | 0.55       | intron     | MROH1     | maestro heat like repeat family member 1   |
|       | rs109742607 | 14  | 2,217,163  | 16.15           | 0.16 (0.02)  | A    | G  | 0.69       | intron     | IQANK1    | IQ motif and ankyrin repeat containing 1   |
|       | rs110323635 | 14  |            | 16.15           | -0.16 (0.02) | A    | G  | 0.31       | missense   | MAPK15    | mitogen-activated protein kinase 15  |
|       |             |     | 2,239,085  |                 |              |      |    |            |            |           |  |
|       | rs109617015 | 14  | 2,386,688  | 17.86           | -0.22 (0.03) | A    | G  | 0.16       | intron     | ZC3H3     | zinc finger CCCH-type containing 3   |
|       | rs109529219 | 14  | 2,468,020  | 21.47           | -0.22 (0.02) | G    | A  | 0.22       | intron     | RHPN1     | rhophilin Rho GTPase binding protein 1   |
|       | rs110060785 | 14  | 2,553,525  | 4.91            | 0.10 (0.02)  | C    | T  | 0.67       | upstream   | GPIHBP1   | glycosylphosphatidylinositol anchored high density lipoprotein binding protein 1 |
|       | rs109958270 | 14  | 2,605,493  | 7.81            | 0.12 (0.02)  | C    | T  | 0.78       | intergenic | -         | -  |
|       | rs110626984 | 14  | 2,674,264  | 5.40            | -0.11 (0.02) | T    | C  | 0.30       | intron     | SLC45A4   | solute carrier family 45 member 4  |
|       | rs110043428 | 14  | 2,790,501  | 12.49           | 0.14 (0.02)  | A    | G  | 0.53       | intergenic | -         | -  |
|       | rs109476486 | 14  | 2,826,632  | 12.41           | -0.17 (0.02) | T    | G  | 0.20       | upstream   | LYPD2     | LY6/PLAUR domain containing 2  |
|       | rs134312854 | 14  | 2,898,515  | 4.95            | -0.09 (0.02) | C    | A  | 0.44       | downstream | ARC       | activity regulated cytoskeleton associated protein                               |

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|-------|-------------|-----|------------|-----------------|--------------|------|----|------------|-------------|-----------|--|
| FP    | rs110545978 | 14  | 3,186,141  | 15.28           | 0.18 (0.02)  | T    | C  | 0.83       | intergenic  | -         | -  |
|       | rs109289626 | 14  | 3,433,372  | 5.78            | -0.11 (0.02) | A    | G  | 0.43       | intron      | TRAPPC9   | trafficking protein particle complex subunit 9 |
|       | rs110461662 | 14  | 3,765,019  | 5.22            | -0.09 (0.02) | G    | A  | 0.58       | intron      | DENND3    | DENN domain containing 3                       |
|       | rs136880486 | 14  | 4,078,923  | 11.13           | -0.13 (0.02) | T    | C  | 0.28       | upstream    | AGO2      | argonaute RISC catalytic component 2           |
|       | rs110017379 | 14  | 4,364,952  | 5.33            | -0.09 (0.02) | T    | C  | 0.56       | intron      | TRAPPC9   | trafficking protein particle complex subunit 9 |
|       | rs109917734 | 14  | 4,398,699  | 5.60            | -0.10 (0.02) | G    | A  | 0.50       | intron      | TRAPPC9   | trafficking protein particle complex subunit 9 |
|       | rs109086264 | 14  | 4,414,829  | 4.65            | 0.08 (0.02)  | A    | C  | 0.40       | intron      | TRAPPC9   | trafficking protein particle complex subunit 9 |
|       | rs110755656 | 14  | 5,274,635  | 7.65            | 0.11 (0.02)  | G    | T  | 0.76       | intergenic  | -         | -  |
|       | rs110359329 | 14  | 7,428,315  | 6.09            | -0.09 (0.02) | A    | G  | 0.58       | intergenic  | -         | -  |
|       | rs109396809 | 19  | 42,493,794 | 4.64            | 0.41 (0.08)  | C    | T  | 0.41       | downstream  | U6        | U6 spliceosomal RNA                            |
| PP    | rs43703015  | 6   | 87,390,576 | 6.52            | 0.05 (0.01)  | T    | C  | 0.61       | missense    | CSN3      | casein kappa                                   |
|       | rs43703016  | 6   | 8,7390,612 | 6.52            | 0.05 (0.01)  | C    | A  | 0.61       | missense    | CSN3      | casein kappa                                   |
|       | rs110014544 | 6   | 87,390,673 | 6.52            | 0.05 (0.01)  | G    | A  | 0.61       | synonymous  | CSN3      | casein kappa                                   |
|       | rs109787476 | 6   | 87,390,681 | 6.43            | 0.05 (0.01)  | T    | A  | 0.61       | 3 prime UTR | CSN3      | casein kappa                                   |
|       | rs110398459 | 6   | 87,733,586 | 4.78            | 0.05 (0.01)  | G    | T  | 0.26       | intron      | ENAM      | enamelin                                       |
|       | rs110398459 | 6   | 87,743,848 | 5.03            | -0.04 (0.01) | A    | G  | 0.38       | intron      | ENAM      | enamelin                                       |
|       | rs134432442 | 14  | 1,736,599  | 28.13           | -0.09 (0.01) | C    | T  | 0.52       | missense    | CPSF1     | cleavage and polyadenylation specific factor 1 |
|       | rs137071126 | 14  | 1,765,835  | 30.83           | -0.10 (0.01) | C    | G  | 0.48       | synonymous  | SLC52A2   | solute carrier family 52 member 2              |
|       | rs109421300 | 14  | 1,801,116  | 30.96           | -0.10 (0.01) | T    | C  | 0.46       | intron      | DGAT1     | diacylglycerol O-acyltransferase 1             |
|       | rs137787931 | 14  | 1,880,378  | 23.91           | 0.09 (0.01)  | T    | C  | 0.55       | intron      | MROH1     | maestro heat like repeat family member 1       |
|       | rs109742607 | 14  | 2,217,163  | 6.59            | 0.04 (0.01)  | A    | G  | 0.69       | intron      | IQANK1    | IQ motif and ankyrin repeat containing 1       |
|       | rs110323635 | 14  | 2,239,085  | 4.96            | -0.04 (0.01) | A    | G  | 0.31       | missense    | MAPK15    | mitogen-activated protein kinase 15            |
|       | rs109617015 | 14  | 2,386,688  | 8.31            | -0.07 (0.01) | A    | G  | 0.16       | intron      | ZC3H3     | zinc finger CCCH-type containing 3             |
|       | rs109529219 | 14  | 2,468,020  | 9.81            | -0.07 (0.01) | G    | A  | 0.22       | intron      | RHPN1     | rhophilin Rho GTPase binding protein 1         |
|       | rs110545978 | 14  | 3,186,141  | 8.33            | 0.06 (0.01)  | T    | C  | 0.83       | intergenic  | -         | -  |

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|-------|-------------|-----|------------|-----------------|---------------|------|----|------------|------------|-----------|--|
| PP    | rs136880486 | 14  | 4,078,923  | 5.58            | -0.05 (0.01)  | T    | C  | 0.28       | upstream   | AGO2      | argonaute RISC catalytic component 2                   |
|       | rs110755656 | 14  | 5,274,635  | 5.94            | 0.05 (0.01)   | G    | T  | 0.76       | intergenic | -         | -  |
|       | rs109841945 | 14  | 6,276,199  | 4.74            | -0.04 (0.01)  | C    | T  | 0.54       | intergenic | -         | -  |
| LP    | rs137513051 | 19  | 42,932,520 | 5.16            | -0.03 (0.01)  | T    | C  | 0.89       | intron     | KCNH4     | potassium voltage-gated channel subfamily H member 4   |
|       | rs136271679 | 19  | 42,988,287 | 4.95            | -0.03 (0.01)  | C    | T  | 0.89       | intron     | STAT5B    | signal transducer and activator of transcription 5B    |
|       | rs378183369 | 29  | 9,563,396  | 8.89            | -0.03 (0.004) | A    | G  | 0.74       | intron     | PICALM    | phosphatidylinositol binding clathrin assembly protein |

Chr = chromosome; SE = standard error; Ref. = reference allele; MA= minor allele; Ref. freq. = reference allele frequency; FP = fat percentage; PP = protein percentage.