

**Table S2** Gene annotations and biological process for QTL associated SNPs, including scaffold genome number (Table S3) with its start hit and end (Pavey *et al.* unpubl. data; Table S3), bit score, blast hit scaffold region and blast hit e-value.

| SNP    | Scaffold | hit start | hit end | Bit score | Blast hit region           | Blast hit                            | e-value  | Annotation   | Biol.process                              |
|--------|----------|-----------|---------|-----------|----------------------------|--------------------------------------|----------|--|---|
| 3771*  | 53738    | 723       | 655     | 91.6      | scaffold-53738_10145-13664 | gi 166218146 sp A0MSJ1.1 CRA1B_DANRE | 2.00E-21 | Collagen alpha-1(XXVII) chain B                                  | Skeletal system development               |
| 6501   | 18019    | 18515     | 18582   | 121       | scaffold-18019_12691-13429 | gi 74710067 sp Q6R2W3.1 SCND3_HUMAN  | 7.00E-20 | SCAN domain-containing protein 3                                 | Unknown                                   |
| 13798  | 436174   | 7187      | 7120    | 121       | scaffold-436174_513-2580   | gi 122145283 sp Q0IID7.1 DUS10_BOVIN | 2.00E-47 | Dual specificity protein phosphatase 10                          | Cellular signalisation                    |
| 19208  | 447255   | 1037      | 1104    | 126       | scaffold-447255_500-863    | gi 123885751 sp QQP427.1 PPR35_DANRE | 6.00E-14 | Protein phosphatase 1 regulatory subunit 35                      | Cellular signalisation                    |
| 21462  | 183364   | 2807      | 2758    | 87.9      | scaffold-183364_3863-4414  | gi 464864 sp P35072.1 TCB1_CAEBR     | 9.00E-36 | Transposable element Tcb1 transposase                            | Transposable element                      |
| 28896  | 232830   | 3491      | 3424    | 104       | scaffold-232830_2720-3610  | gi 74821373 sp Q95SX7.1 RTBS_DROME   | 3.00E-17 | Probable RNA-directed DNA polymerase from transposon BS          | RNA-dependant DNA replication             |
| 37687* | 26906    | 1078      | 1040    | 67.6      | scaffold-26906_1850-4864   | gi 141446 sp P03934.1 TC1A_CAEL      | 2.00E-36 | Transposable element Tc1 transposase                             | Transposable element                      |
| 38077  | 208871   | 9749      | 9682    | 126       | scaffold-208871_1928-3130  | gi 172046699 sp Q86TG7.2 PEG10_HUMAN | 6.00E-43 | Retrotransposon-derived protein PEG10                            | Apoptosis and cell differentiation        |
| 38781  | 133600   | 2165      | 2232    | 121       | scaffold-133600_588-6816   | gi 143018392 sp Q9HCG7.2 GBA2_HUMAN  | 1.00E-20 | Non-lysosomal glucosylceramidase                                 | Neuronal development                      |
| 48708  | 453732   | 5661      | 5728    | 121       | scaffold-453732_3049-4594  | gi 51702142 sp Q9D2M8.4 UB2V2_MOUSE  | 8.00E-24 | Ubiquitin-conjugating enzyme E2 variant 2                        | Transcriptional regulation and DNA repair |
|        |          |           |         |           | scaffold-453732_6190-6527  | gi 464864 sp P35072.1 TCB1_CAEBR     | 4.00E-31 | Transposable element Tcb1 transposase                            | Transposable element                      |
| 49883  | 279183   | 2986      | 3053    | 126       | scaffold-279183_1927-2442  | gi 68565602 sp Q92585.3 MAML1_HUMAN  | 2.00E-13 | Mastermind-like protein 1  | Notch signaling pathway                   |
| 51058  | 310208   | 183       | 116     | 126       | scaffold-310208_102-461    | gi 385178693 sp F1Q7Z7.2 DAAF3_DANRE | 3.00E-24 | Dynein assembly factor 3, axonemal                               | Cytoplasm                                 |
| 60023  | 7589     | 4537      | 4604    | 121       | scaffold-7589_379-636      | gi 75041428 sp Q5R7K9.1 EDIL3_PONAB  | 2.00E-35 | EGF-like repeat and discoidin I-like domain-containing protein 3 | Cell adhesion                             |
| 64568  | 15526    | 9006      | 9073    | 121       | scaffold-15526_1724-2397   | gi 464864 sp P35072.1 TCB1_CAEBR     | 2.00E-19 | Transposable element Tcb1 transposase                            | Transposable element                      |
|        |          |           |         |           | scaffold-15526_6444-9312   | gi 122069920 sp Q2KJB1.1 SEP10_BOVIN | 3.00E-69 | Septin-10  | Cell cycle                                |

|         |        |       |       |      |                            |                                      |           |  |                               |
|---------|--------|-------|-------|------|----------------------------|--------------------------------------|-----------|--|-------------------------------|
| 69063*  | 54791  | 5526  | 5459  | 121  | scaffold-54791_3224-3664   | gi 81880352 sp Q9CPY0.1 MRM2_MOUSE   | 2.00E-47  | rRNA methyltransferase 2, mitochondrial                    | rRNA methylation              |
| 74955*  | 76647  | 1518  | 1452  | 124  | scaffold-76647_2170-5490   | gi 83288218 sp Q53GS7.2 GLE1_HUMAN   | 3.00E-36  | Nucleoporin GLE1   | mRNA export                   |
|         |        |       |       |      | scaffold-76647_6723-7102   | gi 464865 sp Q04202.1 TCB2_CAEBR     | 6.00E-20  | Transposable element Tcb2 transposase                      | Transposable element          |
| 78628*  | 78598  | 5211  | 5144  | 126  | scaffold-78598_2145-2291   | gi 9910620 sp O43715.1 TRIA1_HUMAN   | 5.00E-26  | TP53-regulated inhibitor of apoptosis 1                    | Apoptosis                     |
| 78917   | 183364 | 2847  | 2914  | 102  | scaffold-183364_3863-4414  | gi 464864 sp P35072.1 TCB1_CAEBR     | 9.00E-36  | Transposable element Tcb1 transposase                      | Transposable element          |
| 80526   | 232830 | 3500  | 3567  | 126  | scaffold-232830_2720-3610  | gi 74821373 sp Q95SX7.1 RTBS_DROME   | 3.00E-17  | Probable RNA-directed DNA polymerase from transposon BS    | RNA-dependant DNA replication |
| 88186   | 336919 | 2690  | 2757  | 126  | scaffold-336919_2507-2698  | gi 81898999 sp Q8C627.1 F221B_MOUSE  | 5.00E-16  | Protein FAM221B  | <i>Unknown</i>                |
| 93783   | 334686 | 526   | 459   | 126  | scaffold-334686_207-1019   | gi 134035372 sp Q6A085.2 ZN629_MOUSE | 1.00E-30  | Zinc finger protein 629                                    | Transcriptional regulation    |
| 97205   | 34582  | 2640  | 2706  | 124  | scaffold-34582_9401-10219  | gi 464864 sp P35072.1 TCB1_CAEBR     | 3.00E-37  | Transposable element Tcb1 transposase                      | Transposable element          |
|         |        |       |       |      | scaffold-34582_17105-17316 | gi 50403735 sp P33005.2 KALM_CHICK   | 2.00E-29  | Anosmin-1  | Cell adhesion                 |
| 101670* | 183364 | 2838  | 2766  | 97.1 | scaffold-183364_3863-4414  | gi 464864 sp P35072.1 TCB1_CAEBR     | 9.00E-36  | Transposable element Tcb1 transposase                      | Transposable element          |
| 110970* | 12855  | 20623 | 20586 | 71.3 | scaffold-12855_2228-14681  | gi 338817941 sp Q9QXZ0.2 MACF1_MOUSE | 1.00E-62  | Microtubule-actin cross-linking factor 1                   | <i>Multiple</i>               |
|         | 32096  | 8942  | 9009  | 121  | scaffold-32096_1541-5542   | gi 338817989 sp Q9UPN3.4 MACF1_HUMAN | 2.00E-103 | Microtubule-actin cross-linking factor 1, isoforms 1/2/3/5 | <i>Multiple</i>               |
| 114899  | 84221  | 5438  | 5371  | 126  | scaffold-78598_3908-8097   | gi 145566945 sp Q2NKQ1.2 SGSM1_HUMAN | 3.00E-63  | Small G protein signaling modulator 1                      | Golgi apparatus               |
|         |        |       |       |      | scaffold-84221_5333-6762   | gi 82100806 sp Q8AXC7.1 PGFRA_TAKRU  | 1.00E-92  | Platelet-derived growth factor receptor alpha              | Chemotaxis and development    |
| 114971  | 340942 | 1     | 61    | 113  | scaffold-340942_931-1155   | gi 123792664 sp Q0V8T9.1 CTP5A_MOUSE | 3.00E-21  | Contactin-associated protein like 5-1                      | Cell adhesion                 |
| 123874* | 228433 | 1365  | 1432  | 121  | scaffold-228433_10-3697    | gi 425906075 sp Q8NF91.4 SYNE1_HUMAN | 2.00E-22  | Nesprin-1  | Cytoskeleton and organelle    |
| 131325  | 300418 | 2369  | 2302  | 126  | scaffold-300418_521-4385   | gi 17367145 sp Q9ULA0.1 DNPEP_HUMAN  | 6.00E-19  | Aspartyl aminopeptidase                                    | Protein metabolism            |
| 136924  | 64513  | 1788  | 1721  | 126  | scaffold-64513_1202-1897   | gi 75056157 sp Q9GLY5.1 ITIH3_RABIT  | 6.00E-37  | Inter-alpha-trypsin inhibitor heavy chain H3               | Hyaluronan metabolism         |

|         |        |      |      |     |                           |                                     |          |   |                               |
|---------|--------|------|------|-----|---------------------------|-------------------------------------|----------|---|-------------------------------|
|         | 272191 | 699  | 766  | 121 | scaffold-272191_683-862   | gi 3024056 sp Q63416.1 ITIH3_RAT    | 9.00E-17 | Inter-alpha-trypsin inhibitor heavy chain H3            | Hyaluronan metabolism         |
| 138429  | 232830 | 3491 | 3424 | 99  | scaffold-232830_2720-3610 | gi 74821373 sp Q95SX7.1 RTBS_DROME  | 3.00E-17 | Probable RNA-directed DNA polymerase from transposon BS | RNA-dependant DNA replication |
| 147541* | 392290 | 308  | 375  | 126 | scaffold-392290_2121-2231 | gi 75077434 sp Q4U0T9.1 CSRP3_BOVIN | 4.00E-18 | Cysteine and glycine-rich protein 3                     | Cardiac muscle development    |
| 155423  | 31593  | 2825 | 2892 | 121 | scaffold-31593_6120-6725  | gi 464864 sp P35072.1 TCB1_CAEBR    | 6.00E-36 | Transposable element Tcb1 transposase                   | Transposable element          |

\* Annotated SNP with potential divergent selection.