

Additional file 6: Tab. S1: Genes in the region 10 - 25 Mb on BTA5 found to be expressed in the pigmented skin transcriptome of RTS-affected and wild type animals

| Gene | Name | Position [Mb] ¹ | Number of exons ² | | | Comment |
|------------|--|----------------------------|------------------------------|-----------|-----------------|---|
| | | | RTS A | wild type | RTS B, RTS C | |
| MYF6 | myogenic factor 6 (herculin) | 10,330,470 | 3 | 3 | 3 | |
| LIN7A | lin-7 homolog A (C. elegans) | 10,566,010 | 6 | 6 | 6 | |
| ACSS3 | acyl-CoA synthetase short-chain family member 3 | 10,731,243 | 16 | 16 | 16 | |
| CCDC59 | coiled-coil domain containing 59 | 11,378,864 | 4 | 4 | 4 | |
| METTL25 | methyltransferase like 25 | 12,007,564 | 9 | 9 | 9 | |
| TMTC2 | transmembrane and tetratricopeptide repeat containing 2 | 12,290,944 | 13 | 13 | 13 | |
| LOC781108 | PRKR-interacting protein 1 pseudogene | 13,756,337 | 1 | 1 | 1 | |
| SLC6A15 | solute carrier family 6 (neutral amino acid transporter), member 15 | 14,572,179 | 12 | 12 | 12 | |
| ALX1 | ALX homeobox 1 | 14,991,697 | 4 | 4 | 4 | |
| RASSF9 | Ras association (RalGDS/AF-6) domain family (N-terminal) member 9 | 15,546,053 | 2 | 2 | 2 | |
| C5H12orf29 | chromosome 5 open reading frame, human C12orf29 | 17,892,374 | 7 | 7 | 7 | |
| CEP290 | centrosomal protein 290kDa | 17,998,514 | 55;56 | 55;56 | 55;56 | |
| TMTC3 | transmembrane and tetratricopeptide repeat containing 3 | 17,998,756 | 14;13 | 14;13 | 14;13 | |
| KITLG | KIT ligand | 18,420,198 | 9;8 | 9;8 | 9;8 | Additional exon 1 |
| DUSP6 | dual specificity phosphatase 6 | 19,280,061 | 3 | 3 | 3 | |
| POC1B | POC1 centriolar protein B | 19,462,615 | 12* | 12;10 | 12 | No RTS-associated splicing |
| GALNT4 | UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 4 (GalNAc-T4) | 19,461,415 | 1 | 1 | 1 | |
| ATP2B1 | ATPase, Ca ⁺⁺ transporting, plasma membrane 1 | 19,670,561 | 21 | 21 | 21 | 2 transcription start sites, no RTS-associated splicing |

| | | | | | | |
|--------------|--|------------|----------------|----------------|------------|--|
| KERA | keratocan | 21,003,034 | 3 | 3 | 3 | |
| LUM | lumican | 21,047,145 | 4;3 | 4;3 | 4;3 | 2 transcription start sites, additional exon 1 |
| DCN | decorin | 21,119,087 | 8 | 8 | 8 | 2 transcription start sites |
| BTG1 | B-cell translocation gene 1, anti-proliferative | 22,088,782 | 2 | 2 | 2 | |
| LOC784883 | putative gamma-taxilin-like protein CYorf15B | 22,526,151 | 3 | 3 | 3 | |
| LOC519417 | pleckstrin homology domain-containing family G member 7 | 22,719,202 | 16 | 16 | 16 | |
| EEA1 | early endosome antigen 1 | 22,932,444 | 30*;29*; 28 | 30*;29*; 28 | 30*;29*;28 | 2 previously unknown additional exons |
| NUDT4 | nudix (nucleoside diphosphate linked moiety X)-type motif 4 | 23,348,044 | 5 | 5 | 5 | |
| UBE2N | ubiquitin carrier protein N ubiquitin-conjugating enzyme E2 N ubiquitin-protein ligase N | 23,411,877 | 4 | 4 | 4 | |
| MRPL42 | mitochondrial ribosomal protein L42 | 23,426,113 | 7,7*,6 | 7,7*,6 | 7,7*,6 | |
| SOCS2 | suppressor of cytokine signaling 2 | 23,524,065 | 3 | 3 | 3 | |
| CRADD | CASP2 and RIPK1 domain containing adaptor with death domain | 23,629,05 | 3 | 3 | 3 | additional exon 3 compared to annotation 104 |
| PLXNC1 | plexin C1 | 24,072,234 | 31;30 | 31;30 | 31;30 | |
| CEP83 | centrosomal protein 83kDa | 24,374,925 | 17;16 | 17;16 | 17;16 | |
| LOC100848598 | uncharacterized LOC100848598 | 24,380,708 | 3;2 | 3;2 | 3;2 | |
| TMCC3 | transmembrane and coiled-coil domain family 3 | 24,537,335 | 4 | 4 | 4 | |
| NDUFA12 | NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 12 | 24,873,028 | 4;3 | 4;3 | 4;3 | |
| NR2C1 | nuclear receptor subfamily 2, group C, member 1 | 24,922,158 | 14 | 14 | 14 | |
| FGD6 | FYVE, RhoGEF and PH domain containing 6 | 25,031,325 | 21, 20* | 21 | 21 | |

¹First base of exon 1 according to *Bos taurus* genome assembly UMD3.1.1.

²Number of exons in pigmented skin of three individuals (RTS A, RTS B, RTS C) with “rat-tail” phenotype and an individual with wild type phenotype.

*Splice variants compared annotation release 104 of the *Bos taurus* genome assembly