**Supplementary Table S1**. Top five GO terms of biological processes using cut-off of 1% for each method of selection signatures in rabbits.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Method** | XP-CLR |  |  |  |  |
| **Genes** | 579 |  |  |  |  |
| **Name** | **GO term** | **P-value** | **Odds ratio** | **Combined Score** | **Genes** |
| ribosomal small subunit export from nucleus | GO:0000056 | 6.74E-03 | 15.26 | 76.27 | *LTV1; RPS15* |
| ventricular compact myocardium morphogenesis | GO:0003223 | 6.74E-03 | 15.26 | 76.27 | *DSP; BMPR1A* |
| regulation of anion channel activity | GO:0010359 | 6.74E-03 | 15.26 | 76.27 | *TCAF2; TCAF1* |
| maintenance of protein location in extracellular region | GO:0071694 | 6.74E-03 | 15.26 | 76.27 | *FBN2; NBL1* |
| glutamate catabolic process | GO:0006538 | 6.74E-03 | 15.26 | 76.27 | *GLUD1; GLUD2* |
| **Method** | XP-EHH |  |  |  |  |
| **Genes** | 443 |  |  |  |  |
| **Name** | **GO term** | **P-value** | **Odds ratio** | **Combined Score** | **Genes** |
| regulation of osteoclast development | GO:2001204 | 4.16E-03 | 19.55 | 107.20 | *NOTCH2; FBN1* |
| detection of chemical stimulus involved in sensory perception | GO:0050907 | 1.90E-07 | 6.83 | 105.77 | *OR4A8; OR4C12; OR4C45; OR4C11; OR4A47; OR4P4; OR4C15; OR2A4; OR4A15; OR4C13; OR4S2; OR4C46* |
| aminoglycoside antibiotic metabolic process | GO:0030647 | 7.58E-03 | 14.66 | 71.58 | *AKR1B10; AKR1B1* |
| daunorubicin metabolic process | GO:0044597 | 7.58E-03 | 14.66 | 71.58 | *AKR1B10; AKR1B1* |
| positive regulation of TORC1 signaling | GO:1904263 | 7.58E-03 | 14.66 | 71.58 | *RRAGA; LARS* |
| **Method** | normalised-Fst |  |  |  |  |
| **Genes** | 368 |  |  |  |  |
| **Term** | **GO term** | **P-value** | **Odds ratio** | **Combined Score** | **Genes** |
| citrate metabolic process | GO:0006101 | 3.43E-03 | 21.57 | 122.47 | *STAT5A; STAT5B* |
| interleukin-15-mediated signaling pathway | GO:0035723 | 9.31E-04 | 14.94 | 104.24 | *STAT5A; STAT5B; STAT3* |
| cellular response to interleukin-15 | GO:0071350 | 9.31E-04 | 14.94 | 104.24 | *STAT5A; STAT5B; STAT3* |
| oxaloacetate metabolic process | GO:0006107 | 4.75E-03 | 18.49 | 98.94 | *STAT5A; STAT5B* |
| valine metabolic process | GO:0006573 | 4.75E-03 | 18.49 | 98.94 | *STAT5A; STAT5B* |

Gene Ontology (GO) knowledgebase is the world's largest source of information on the functions of genes. Odds ratios are used to compare the relative odds of the occurrence of the outcome of interest given exposure to the variable of interest. The odds ratio is calculated using the analysed genes and GO terms of the datable. XP-CLR = cross population – composite likelihood ratio. XP-EHH = cross population – extended haplotype homozygosity. Fst = Wright’s fixation index. TORC1 = mammalian target of rapamycin complex 1.

**Supplementary Table S2**. Annotated Genes in the selection signatures of intramuscular fat in rabbits.

See the ‘Supplementary Table S2.xlsx’ file

**Supplementary Table S3**. First ten go ontology (GO) terms of biological processes using genes located in genomic regions that exceeded a cut-off of 1% in at least two methods of selection signatures in rabbits.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO term’s CODE** | **Term** | **P-value** | **Odds Ratio** | **Combined Score** | **Annotated Mouse Genes** |
| GO:0072528 | pyrimidine-containing compound biosynthetic process | 1.67E-02 | 59.52 | 243.65 | *TPK1* |
| GO:0070417 | cellular response to cold | 1.67E-02 | 59.52 | 243.65 | *SAXO1* |
| GO:0010665 | regulation of cardiac muscle cell apoptotic process | 1.67E-02 | 59.52 | 243.65 | *LTK* |
| GO:0044003 | modification by symbiont of host morphology or physiology | 1.94E-02 | 51.02 | 201.04 | *RRAGA* |
| GO:1904526 | regulation of microtubule binding | 1.94E-02 | 51.02 | 201.04 | *TTBK2* |
| GO:2000483 | negative regulation of interleukin-8 secretion | 1.94E-02 | 51.02 | 201.04 | *MAPKBP1* |
| GO:0042723 | thiamine-containing compound metabolic process | 1.94E-02 | 51.02 | 201.04 | *TPK1* |
| GO:0033629 | negative regulation of cell adhesion mediated by integrin | 1.94E-02 | 51.02 | 201.04 | *ACER2* |
| GO:0060292 | long term synaptic depression | 1.94E-02 | 51.02 | 201.04 | *SLC24A2* |
| GO:0060850 | regulation of transcription involved in cell fate commitment | 1.94E-02 | 51.02 | 201.04 | *RORA* |

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