**Table S2: Gene annotation - physical versus genetic distance.**

Physical position of the genes was mined from Rat Genome Database. Physical position is indicated in Million bases (Mb) and represent the centre position of gene ((start position + stop position) /2). Genetic distance (cM) was obtained by fitting linear regression for Physical vs Genetic distance of five markers D5Rat98, D5Got131, D5Rat256, D5Wox37, D5Rat235. Equation obtained from trend line, y = 0.3356(x)-49.378. R2=0.9899.

|  |  |  |
| --- | --- | --- |
| mb | cM | *Gene* |
| 171.54 | 8.19 | **D5Rat256** |
| 171.99 | 8.34 | *hypothetical LOC100363381* |
| 172.23 | 8.42 | *caspase activity and apoptosis inhibitor 1* |
| 172.32 | 8.45 | *phospholipase A2, activating protein* |
| 172.42 | 8.48 | *intraflagellar transport 74 homolog (Chlamydomonas)* |
| 172.41 | 8.48 | *leucine rich repeat containing 19* |
| 172.65 | 8.56 | *TEK tyrosine kinase, endothelial* |
| 172.83 | 8.62 | *equatorin, sperm acrosome associated* |
| 172.89 | 8.64 | *myb-like, SWIRM and MPN domains 1* |
| 173.04 | 8.69 | *hypothetical protein LOC100363437* |
| 173.04 | 8.69 | *jun proto-oncogene* |
| 174.02 | 9.02 | *FGGY carbohydrate kinase domain containing* |
| 174.52 | 9.19 | *hook homolog 1 (Drosophila)* |
| 174.65 | 9.24 | *cytochrome P450, family 2, subfamily j, polypeptide 13* |
| 174.73 | 9.26 | *cytochrome P450, family 2, subfamily j, polypeptide 10* |
| 174.81 | 9.29 | *similar to cytochrome P450, family 2, subfamily j, polypeptide 11* |
| 174.94 | 9.33 | *cytochrome P450, family 2, subfamily j, polypeptide 16* |
| 175.07 | 9.37 | *cytochrome P450, family 2, subfamily j, polypeptide 4* |
| 175.13 | 9.39 | *cytochrome P450, family 2, subfamily j, polypeptide 3* |
| 175.15 | 9.40 | *similar to Ab2-162* |
| 175.16 | 9.41 | *cytochrome P450, family 2, subfamily j, polypeptide 5, pseudogene* |
| 175.33 | 9.46 | *similar to hypothetical protein MGC34837* |
| 175.45 | 9.50 | *similar to BWK-1* |
| 175.46 | 9.51 | *similar to TBC1 domain family, member 5* |
| 175.62 | 9.56 | *similar to glyceraldehyde-3-phosphate dehydrogenase* |
| 176.89 | 9.99 | *similar to 60S acidic ribosomal protein P1* |
| 177.41 | 10.16 | *nuclear factor I/A* |
| 177.85 | 10.31 | *similar to ribosomal protein L21* |
| 178.11 | 10.40 | *ribosomal protein S18-like* |
| 178.17 | 10.42 | *TM2 domain containing 1* |
| 178.20 | 10.43 | *hypothetical protein LOC685326* |
| 178.37 | 10.48 | *InaD-like (Drosophila)* |
| 178.72 | 10.60 | *LINE-1 type transposase domain containing 1* |
| 178.74 | 10.61 | *Rho GDP dissociation inhibitor (GDI) alpha-like* |
| 178.79 | 10.62 | *KN motif and ankyrin repeat domains 4* |
| 179.00 | 10.70 | *similar to ubiquitin specific protease 15* |
| 179.05 | 10.71 | *ubiquitin specific peptidase 1* |
| 179.15 | 10.74 | *dedicator of cytokinesis 7* |
| 179.22 | 10.77 | *angiopoietin-like 3* |
| 179.79 | 10.96 | *autophagy related 4C, cysteine peptidase* |
| 179.87 | 10.99 | *hypothetical protein LOC685453* |
| 179.95 | 11.01 | *similar to hypothetical protein DKFZp434P0316* |
| 180.12 | 11.07 | *similar to glyceraldehyde-3-phosphate dehydrogenase* |
| 180.27 | 11.12 | *hypothetical LOC100362448* |
| 180.38 | 11.16 | *similar to ribosomal protein L21* |
| 180.38 | 11.16 | *similar to non-SMC element 1 homolog* |
| 180.50 | 11.20 | *forkhead box D3* |
| 180.63 | 11.24 | *ALG6, alpha-1,3-glucosyltransferase* |
| 180.72 | 11.27 | *integrin beta 3 binding protein (beta3-endonexin)* |
| 180.81 | 11.30 | *EF-hand calcium binding domain 7* |
| 180.92 | 11.34 | *phosphoglucomutase 1* |
| 181.30 | 11.46 | *receptor tyrosine kinase-like orphan receptor 1* |
| 181.73 | 11.61 | *similar to hypothetical protein MGC35130* |
| 182.08 | 11.73 | *40S ribosomal protein SA-like* |
| 182.26 | 11.79 | *cache domain containing 1* |
| 182.51 | 11.87 | *hypothetical protein LOC100359934* |
| 182.63 | 11.91 | *ribonucleoprotein, PTB-binding 2* |
| 182.76 | 11.96 | *Janus kinase 1* |
| 183.12 | 12.08 | *adenylate kinase 4* |
| 183.31 | 12.14 | *DnaJ (Hsp40) homolog, subfamily C, member 6* |
| 183.48 | 12.20 | *leptin receptor overlapping transcript* |
| 183.57 | 12.23 | *leptin receptor* |
| 183.58 | 12.23 | **D5Wox37** |