**Supplementary Table 1** Equine primer pair details: gene symbol, primer sequence, annealing temperature, product size and accession number for all genes used for qRT-PCR analysis.

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| --- | --- | --- | --- | --- | --- |
| Gene symbol | Ta (oC) | Product size (bp) | Forward sequence | Reverse sequence | Accession no. |
| LIFR | 58 | 280 | GTTTCCTTAATTCCAGACACTC | CAACGTAGCATCTAATTCCC | XM\_023625722.1 |
| LIF | 65 | 264 | GGAGTTGTGCCCCTGCTGCTA | CGTGGGAAAGGGCGGGAAGTC | XM\_023646870.1;  XM\_023646869.1;  XM\_023646868.1;  XM\_023646867.1;  XM\_023646866.1 |
| PTGFR | 58 | 185 | CTTAGCCCTTGTCGTTTCA | TGTTGGCCATTGTCACC | NM\_001081806.3;  XM\_005610256.3; XM\_023640208.1;  XM\_014739993.2;  XM\_023640207.1 |
| INSR | 62 | 101 | CGAGTTGGATTATTGCCTCAAAG | CGTACTCACTCTGATTGTGCTTCTG | XM\_023644612.1;  XM\_023644611.1;  XM\_023644610.1;  XM\_023644609.1;  XM\_023644608.1;  XM\_023644607.1 |
| IL6ST | 62 | 259 | GCACTGTTGATTATTCTCCTG | GTTGAAGCATCTTTGGTCCT | NM\_001301172.2;  XM\_023625263.1;  XM\_005604257.3;  XM\_005604255.3;  XM\_023625262.1 |
| IGF1 | 60 | 137 | ACGCTCTTCAGTTCGTGTGT | CAGCCTCCTCAGATCACAGC | XM\_005606472.3;  XM\_005606471.3;  XM\_005606470.3;  XM\_005606469.3;  NM\_001082498.2 |
| OXTR | 62 | 218 | CATCGTGCTGGCCTTCATCGTGTG | GGTAGCCGGAGGAGCAGCAGAGGA | XM\_014731360.2;  XM\_023620041.1;  XM\_023620040.1 |
| NDN | 58 | 222 | CGGTAGTTACAAGAAATGGTG | CGACCCTTCACATAGATGAG | XM\_001492612.4 |
| H19 | 58 | 224 | GTCTCTGTTCCTTTACTTTCC | GTTCCTTTAGCTTAACCTTCC | NR\_027326.1 |
| SNRPN | 60 | 109 | GATCTCAGCAACAGCAAATACC | CTACCTGGATGTTCCAATACTG | XM\_005602853.1; XM\_005602852.1 ; XM\_005602849.1; XM\_005602848.1; XM\_005602847.1; XM\_005602850.1; XM\_005602851.1 |
| PEG10 | 62 | 216 | AGAGTTTACCCACCCATGAG | GAGTAATCAGGCCATCTTTCAC | NM\_001172559.2 |
| SLC2A1 | 63 | 308 | CACGGGCTTCGTGCCCATGT | GGGTCACGTCTGCCGTTCCG | NM\_001163971.2;  XM\_005607003.3 |
| SLC1A4 | 63 | 365 | TGTGTGGCCGCGGTGTTCAT | GGCGACGTCTCCTCCTCCGA | XM\_001493515.3 |
| SLC1A5 | 60 | 104 | TCAGCCTGCCGGTTCACGAC | TCCTGCCCCAAAGGCGTCAC | XM\_001917363.1 |
| SLC2A3 | 58 | 233 | CCAGGAGATGAAAGATGAGAG | ATAGTATTAACCACACCCGCA | XM\_001498757.1 |
| SLC2A5 | 63 | 281 | CCGATTAAGAAGGAAGGGAG | TTTCTGCCAAGTCTATTCACC | NM\_001081877.1 |
| SLC5A1 | 60 | 104 | TCAGCCTGCCGGTTCACGAC | TCCTGCCCCAAAGGCGTCAC | XM\_001917363.1 |
| SLC7A5 | 60 | 297 | GAAAGGTGACATCTCCAATCTG | GTGATAGTTCCCGAAGTCCA | XM\_001916639.4 |
| SLC38A2 | 62 | 377 | CAGCCTGACACAACCAGCGGC | GGGTGACAGCCACTAACACAGCC | XM\_001489523.3 |
| SLC43A2 | 60 | 181 | CATCCACTCTGCCGTCGGGG | REV 5' GCCCAGCAGCCCCACATTCA | XM\_001502290.1 |
| GAPDH | 53 | 112 | AGGCCATCACCATCTTCCAG | CCAGCCTTCTCCAAGGTAGT | NM\_001163856.1 |
| HPRT1 | 58 | 232 | GAGATGTGATGAAGGAGATGG | CTTTCCAGTTAAAGTTGAGAGG | XM\_001490189.2 |
| SRP14 | 55 | 101 | CTGAAGAAGTATGACGGTCG | CCATCAGTAGCTCTCAACAG | XM\_001503583.2 |