# Table S3
# Summary of the 32 RNA-Sequencing samples

| Horse | Total sequences Raw reads[a] | Sequences after trimming[b] | Per sequence GC content (%) | Aligned pairs[c] | Alignment rate[d] | Total count[e] |
|---|---|---|---|---|---|---|
| H1-0h | 19717258 | 8502094 | 49 | 7358186 | 86.2% | 5197583 |
| H1-24h | 67308470 | 32342562 | 50 | 2884440 | 88.9% | 2180946 |
| H1-48h | 19839515 | 9954298 | 50 | 8838404 | 88.5% | 6823863 |
| H1-72h | 14432128 | 7358130 | 50 | 6582181 | 89.1% | 4900818 |
| H2-0h | 18178744 | 9085634 | 51 | 7880970 | 86.5% | 5655934 |
| H2-24h | 12681202 | 6069612 | 50.5 | 5437735 | 89.3% | 4184830 |
| H2-48h | 30143876 | 15499068 | 50 | 1411214 | 90.7% | 1082339 |
| H2-72h | 12826353 | 6530807 | 49.5 | 5933521 | 90.4% | 4429069 |
| H3-0h | 20960250 | 10117417 | 50 | 9154720 | 90.2% | 6380111 |
| H3-24h | 15509308 | 7851773 | 50 | 7119652 | 90.4% | 5369106 |
| H3-48h | 16948027 | 8578848 | 51 | 7836263 | 91.1% | 5985166 |
| H3-72h | 25647761 | 13313650 | 50.5 | 1225096 | 91.6% | 9310609 |
| H4-0h | 28670134 | 13715002 | 51 | 1194665 | 86.8% | 8575720 |
| H4-24h | 20422712 | 10795659 | 51 | 9902068 | 91.4% | 7521370 |
| H4-48h | 15788862 | 8014918 | 51 | 7388535 | 91.9% | 5582761 |
| H4-72h | 18383955 | 9131700 | 51 | 8317166 | 90.8% | 6402180 |
| H5-0h | 22947695 | 9857331 | 50.5 | 8960958 | 90.6% | 6415387 |
| H5-24h | 21849937 | 10419618 | 51 | 9440102 | 90.3% | 7128889 |
| H5-48h | 24772671 | 12453536 | 51 | 1146623 | 91.7% | 8804639 |
| H5-72h | 23018161 | 11156075 | 51 | 1032539 | 92.2% | 7980186 |
| H6-0h | 18112353 | 9450237 | 50 | 8529686 | 90.0% | 6110302 |
| H6-24h | 18419612 | 10260890 | 51 | 9328179 | 90.6% | 7078320 |
| H6-48h | 19130571 | 10543071 | 50 | 9721228 | 91.8% | 7310548 |
| H6-72h | 18810862 | 10857330 | 50 | 1017581 | 93.3% | 7657996 |
| H7-0h | 18438679 | 8526023 | 50 | 7893428 | 92.1% | 5666816 |
| H7-24h | 20176785 | 10709870 | 50 | 1004868 | 93.5% | 7528436 |
| H7-48h | 25947827 | 14121856 | 50.5 | 1313489 | 92.6% | 1025650 |
| H7-72h | 21821418 | 11656927 | 51 | 1096165 | 93.6% | 8616341 |
| H8-0h | 24180545 | 13500189 | 50 | 1252684 | 92.4% | 9231933 |
| H8-24h | 18784516 | 9993324 | 51 | 9351613 | 93.2% | 7172256 |
| H8-48h | 22175150 | 11562073 | 50.5 | 1080717 | 93.1% | 7870190 |
| H8-72h | 19340153 | 9988254 | 50 | 9287351 | 92.6% | 6542845 |

[a] Count of the total number of sequences processed.
[b] Number of sequences actually used for the rest of the analysis after quality filtering.
[c] Number of aligned pairs mapped to the annotated equine genome.
[d] Concordant pair alignment rate to the annotated equine genome.
[e] Counts of reads assigned to a gene feature in the annotation file.