**Table S5:** Alternative strategies for bioinformatic processing of ant transcriptomes do not significantly affect read mapping.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Species | Caste | Strategy used in manuscript | Alternative strategy | Spearman’s correlation of FPKM values | |
| Transcriptome wide | Chemosensory genes only |
| *C. floridanus* | Major worker | read1+2  50bp | read1 50bp | 0.995 | 0.996 |
| read1 34bp | 0.990 | 0.991 |
| read2 50bp | 0.995 | 0.997 |
| read2 34bp | 0.990 | 0.991 |
| Minor worker | read1+2  50bp | read1 50bp | 0.995 | 0.998 |
| read1 34bp | 0.990 | 0.990 |
| read2 50bp | 0.994 | 0.997 |
| read2 34bp | 0.989 | 0.991 |
| Male | 34bp | 50bp | 0.995 | 0.974 |
| *H. saltator* | Worker | read1+2  50bp | read1 50bp | 0.990 | 0.997 |
| read1 34bp | 0.971 | 0.992 |
| read2 50bp | 0.990 | 0.996 |
| read2 34bp | 0.973 | 0.990 |
| Male | 50bp | 34bp | 0.980 | 0.982 |