



In this example, exon 2 has twice as many reads mapping to it than exon 1. Does this also mean that it is twice as abundant? Exon 2 is also twice as long as exon 1 and the longer a feature, the higher the chance that a read originated from it. In this case abundance was most likely equal. In general, we have to account for the length of the transcript (i.e. its exons). There are two main ways to normalise: RPKM/FPKM and TPM.