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# CORRIGENDUM

# QUANTIFYING ALTERNATIVE SPLICING FROM PAIRED-END RNA-SEQ DATA

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In Figure 4(d) of Rossell et al. (2014) (Section 4.3), we followed the standard pipeline for BitSeq and used the bowtie aligner (versus Tophat for the other methods, casper, Cufflinks and BitSeq). The BitSeq authors noted that we used the bowtie1 version, which gave very low mapping rates (<2% aligned reads in both samples). Figure 1 below uses bowtie2, which gives mapping rates >70% (the MAD between replicates also drops, from 0.098 to 0.062). We thank the Bitseq authors for alerting us to bowtie2.

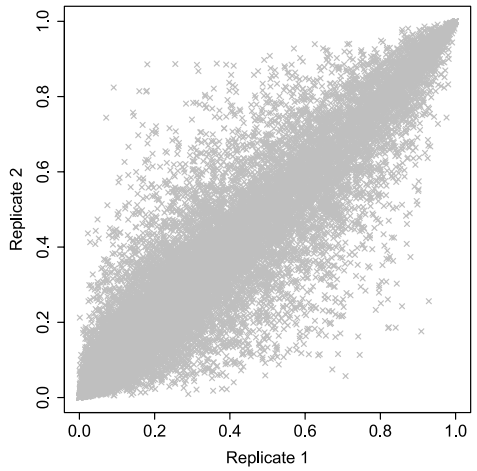


FIG. 1. *Corrected Figure* 4d, *right panel*.

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## REFERENCE

ROSSELL, D., STEPHAN-OTTO ATTOLINI, C., KROISS, M. and STÖCKER, A. (2014). Quantifying alternative splicing from paired-end RNA-sequencing data. *Ann. Appl. Stat.* **8** 309–330. MR3191992

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