Figure S6

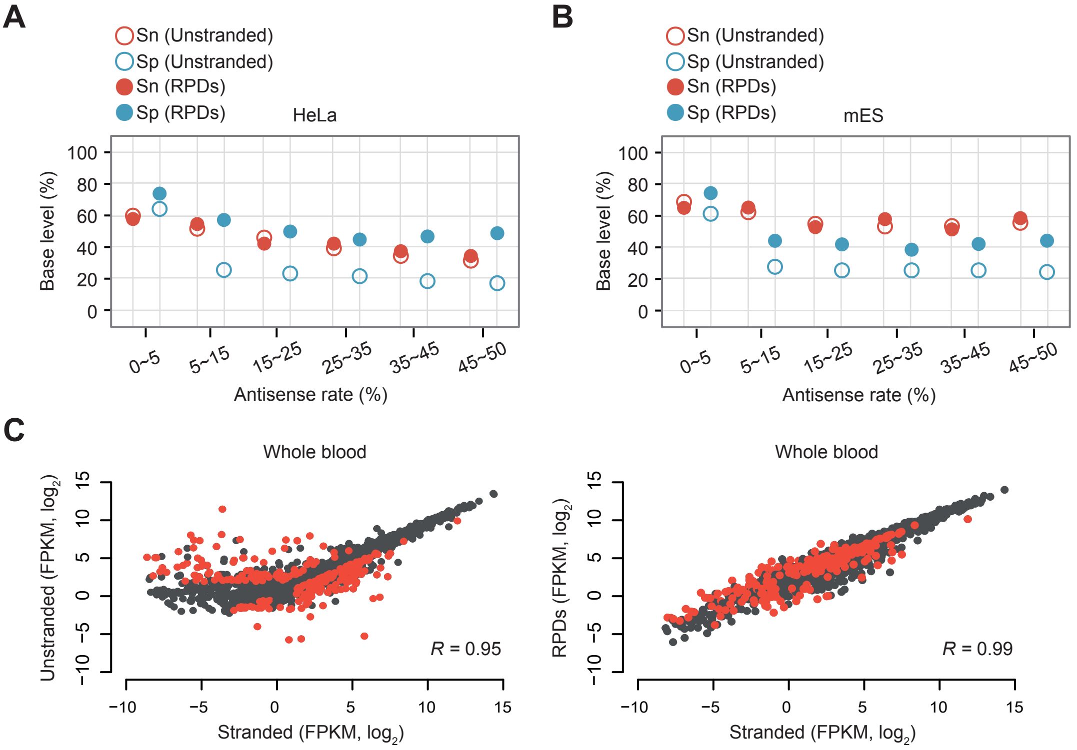

Figure S6. Effectiveness of the *k*MC model

(A-B) Sensitivity (SN, red) and specificity (SP, blue) were measured for the resulting assembly across the antisense-overlapping loci with different fractions of antisense reads using unstranded reads (open circles) and RPDs (solid circles) from HeLa (A) and mES cells (B). (C) Comparisons of gene expression values (FPKM, $\log_2$) estimated with stranded (X-axis) and unstranded reads (Y-axis, left) or RPDs (Y-axis, right) from whole blood cells (Zhao et al. 2015). The gene expression values were averaged from four biological replicates of whole blood cells. Otherwise, as in Figs. 2E,F.

References

Zhao S, Zhang Y, Gordon W, Quan J, Xi H, Du S, von Schack D, Zhang B. 2015. Comparison of stranded and non-stranded RNA-seq transcriptome profiling and investigation of gene overlap. *BMC genomics* **16**: 675.