Figure S2: Read length histogram for the HelaS3 cell-line (a). Total number of reads in the HelaS3 cell-line and number (and percentage) of reads that could be mapped using GMAP. Percentages in light blue bars are given with respect to the previous light blue bar (b). Chromosome distribution of read-mappings (c). Number of reads (and percentage) that were considered mapped with high confidence (well-mapped) and number of reads (and percentage) of reads that did not overlap ribosomal RNA genes (d). Chromosome distribution of high confidence read mappings that did not overlap ribosomal RNA genes (e). Number of reads falling entirely into intergenic, intronic and exonic regions (f). Number and percentage (with respect to the previous light blue bar) of reads containing a split (first bar); number and percentage of reads containing at least one split and having intron-consensus di-nucleotides at the ends of all splits (second bar); number and percentage of reads containing at least one split and having intron-consensus di-nucleotides at the ends of all splits and having at least one split-end as an annotated splice site for all splits (third bar, g); Number of introns in these reads (with respect to last blue bar in previous figure, h). Intron length distribution for the previous introns, showing only introns of up to 500bps (i). Percentage of annotated genes identified when using increasing number of reads (j). Percentage of annotated exons identified when using increasing number of reads (k).