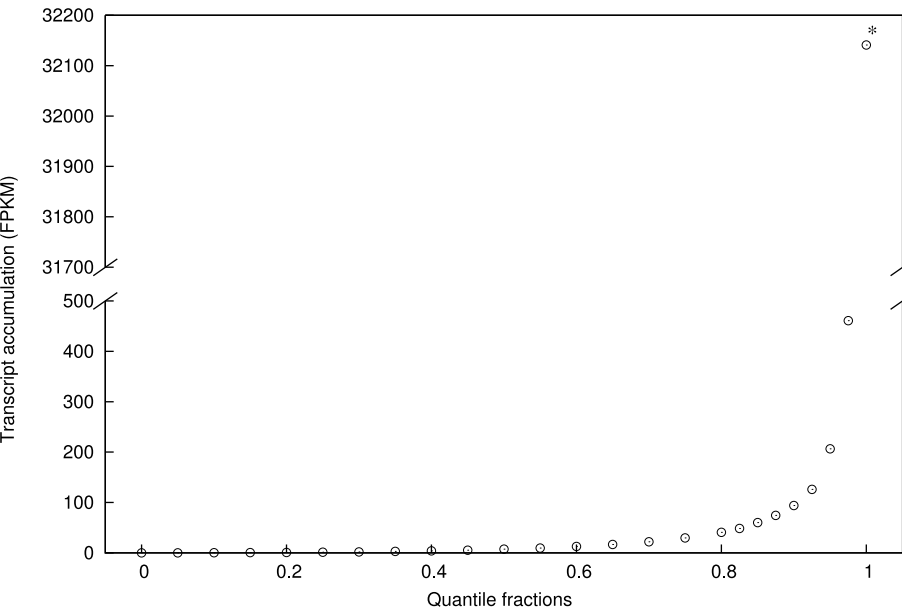


**Figure S1.** Distribution of the transcript accumulation (FPKM) of pooled RNA samples over the quantiles of the number of sequenced gene transcripts. <sup>a, b</sup>



<sup>a</sup> R software, function "quantile" was used

<sup>b</sup> Total amount of sequenced transcripts was 633388 FPKM

\* 5 % (32141 FPKM) of total amount of transcripts