



**Supplementary Figure 1. Quality control analysis of the STRT-N RNA sequencing library.**

A) Graph showing total number of mapped reads. B) Total number of ERCC Spike- in reads per sample. C) Quality check of the 5'-end spike-in rate. D) Mapped rate calculated by dividing the total number of reads with total number of mapped reads. E) Mapped/Spike-in reads, a quality check of the overall amount of mRNA present in each sample. F) Coding 5'-end of the mRNA molecules. On the x-axis of all the samples we have developmental stages. Hypoxia is shown in red, normoxia in blue and ultrahypoxia in green.