Quality filtering auf comparative AUGUSTUS

filter criterion

1. tx must have ≥ 4 CDS exons
   - difficult cases such as single exon genes are skipped
2. tx does not match a gene annotated as non-coding or pseudogene
3.

   either **90%** of tx has at least **low RNA-Seq support**, i.e.
   - introns: ≥ 1 spliced reads (any strain)
   - exons: ≥ 10 reads per kilobase of mRNA (any strain)

   or **80%** of tx has **high RNA-Seq support**, i.e.
   - introns: ≥ 10 spliced reads (any strain)
   - exons: ≥ 1000 reads per kilobase of mRNA (any strain)