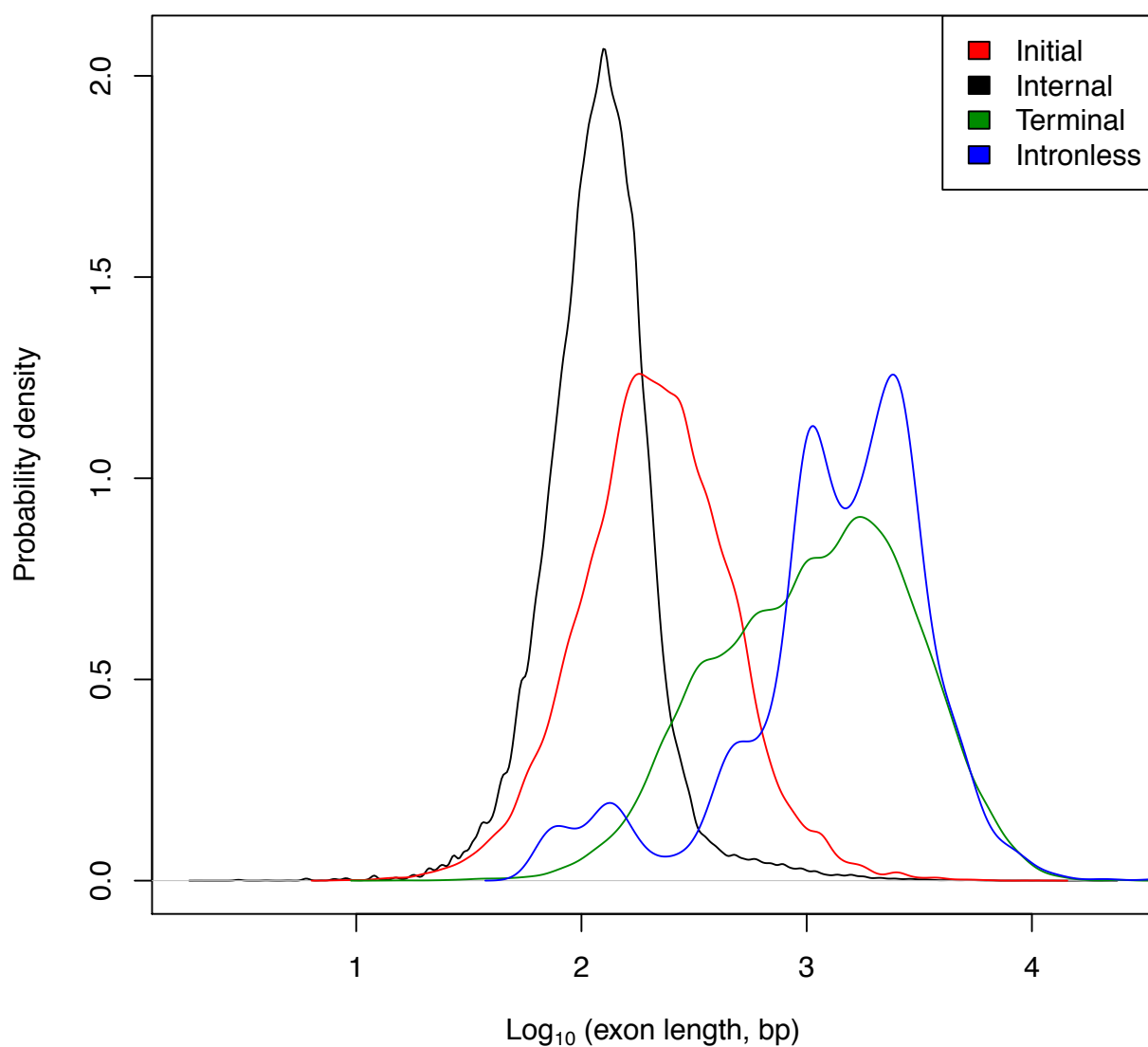
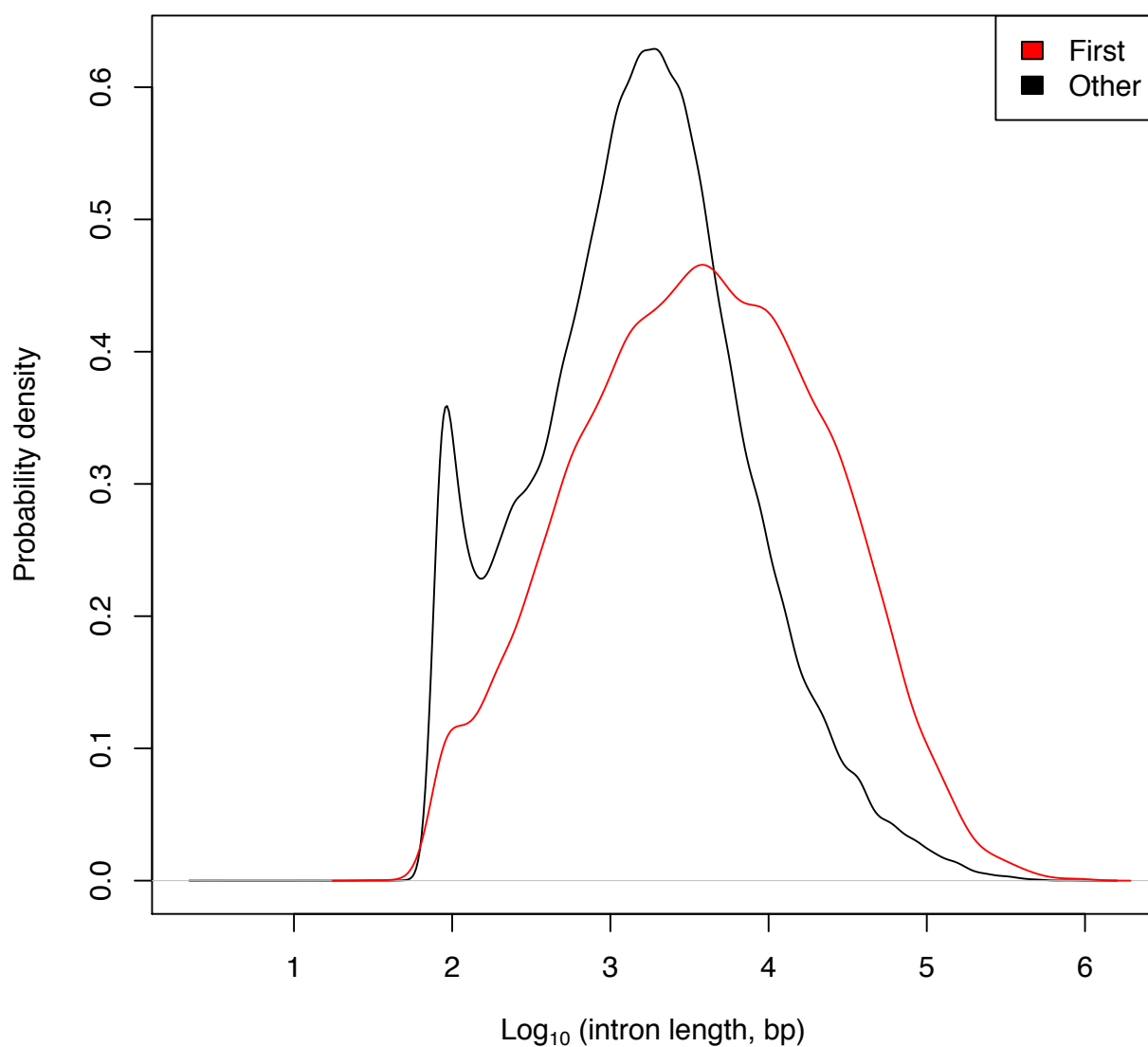


Supplementary Figure S1. Analysis of exon number of transcripts considering GeneBase 1.1 Human "Gene_Table" records with a "VALIDATED" or "REVIEWED" RefSeq status, with an "NM_" (protein-coding RNAs, black line) or "NR_" (non-coding RNAs, red line) type of corresponding RefSeq RNA accession number, belonging to "REVIEWED" or "VALIDATED" genes, excluding genes not in current annotation release.



Supplementary Figure S2. Exon length distribution considering GeneBase 1.1 Human "Gene_Table" records with a "VALIDATED" or "REVIEWED" RefSeq status, with an "NM_" or "NR_" type of corresponding RefSeq RNA accession number, belonging to genes with a "VALIDATED" or "REVIEWED" RefSeq status, excluding "not in current annotation release" records. Initial indicates the first exons, terminal the last exon, intronless indicates unique exon transcripts and internal indicates the remaining exons.



Supplementary Figure S3. Intron length distribution considering GeneBase 1.1 Human "Gene_Table" records with a "VALIDATED" or "REVIEWED" RefSeq status, with an "NM_" or "NR_" type of corresponding RefSeq RNA accession number, belonging to genes with a "VALIDATED" or "REVIEWED" RefSeq status, excluding "not in current annotation release" records. First intron lengths are indicated in red, other intron lengths in black.