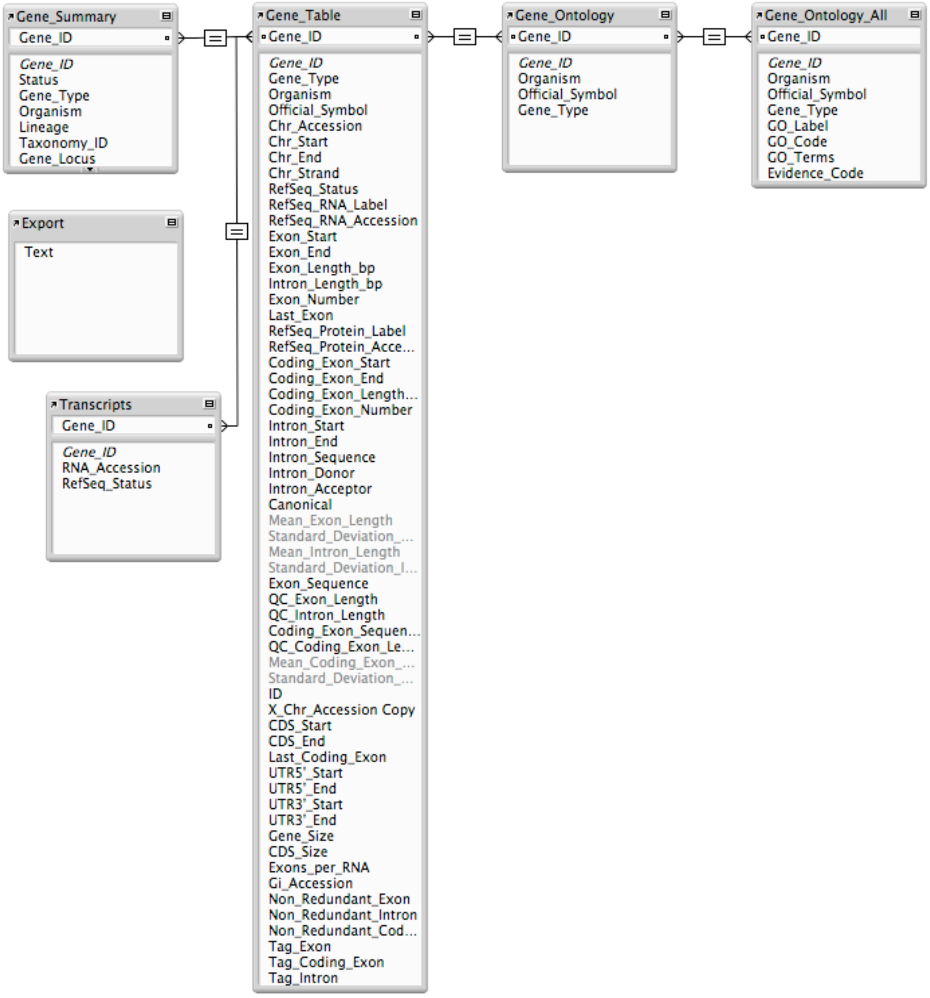
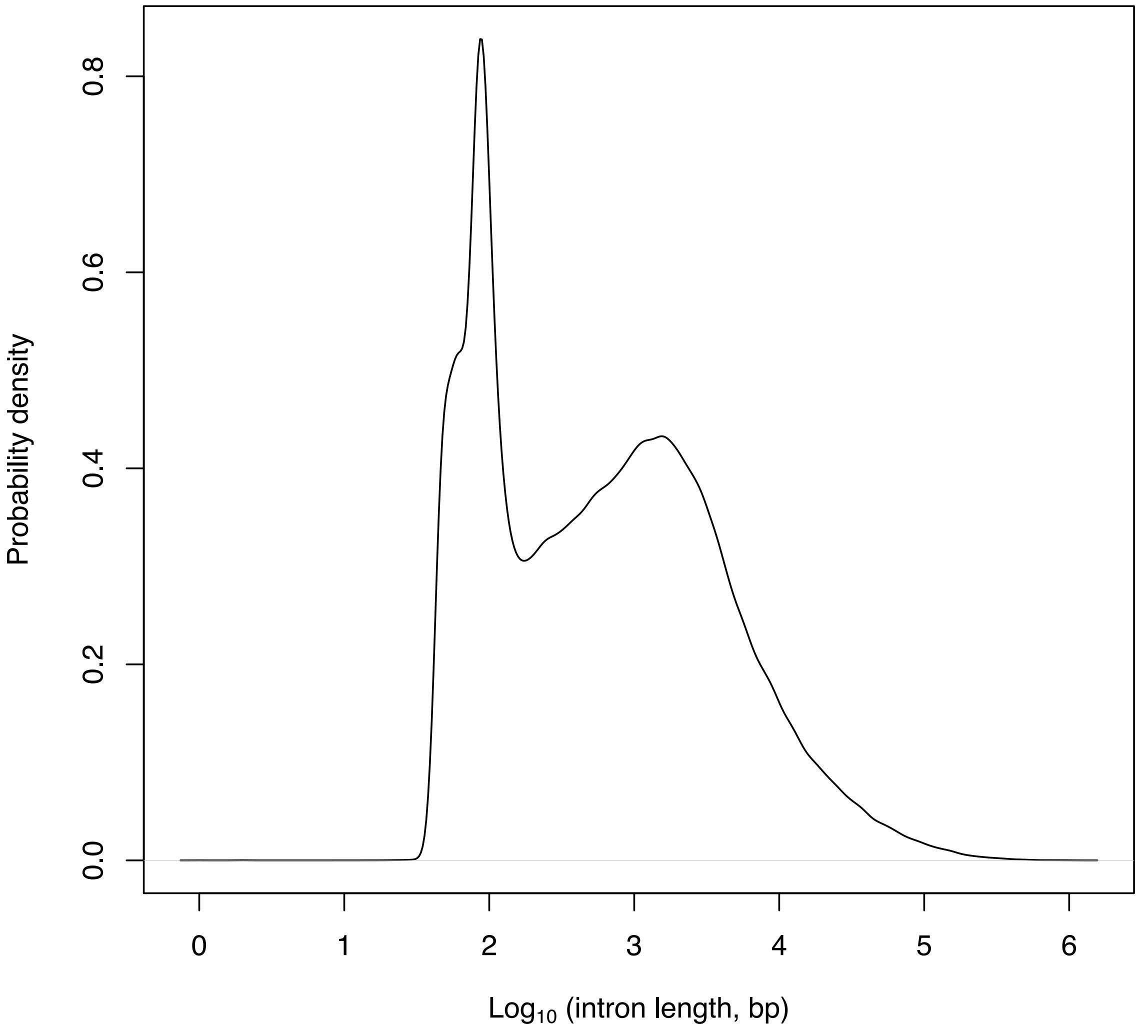
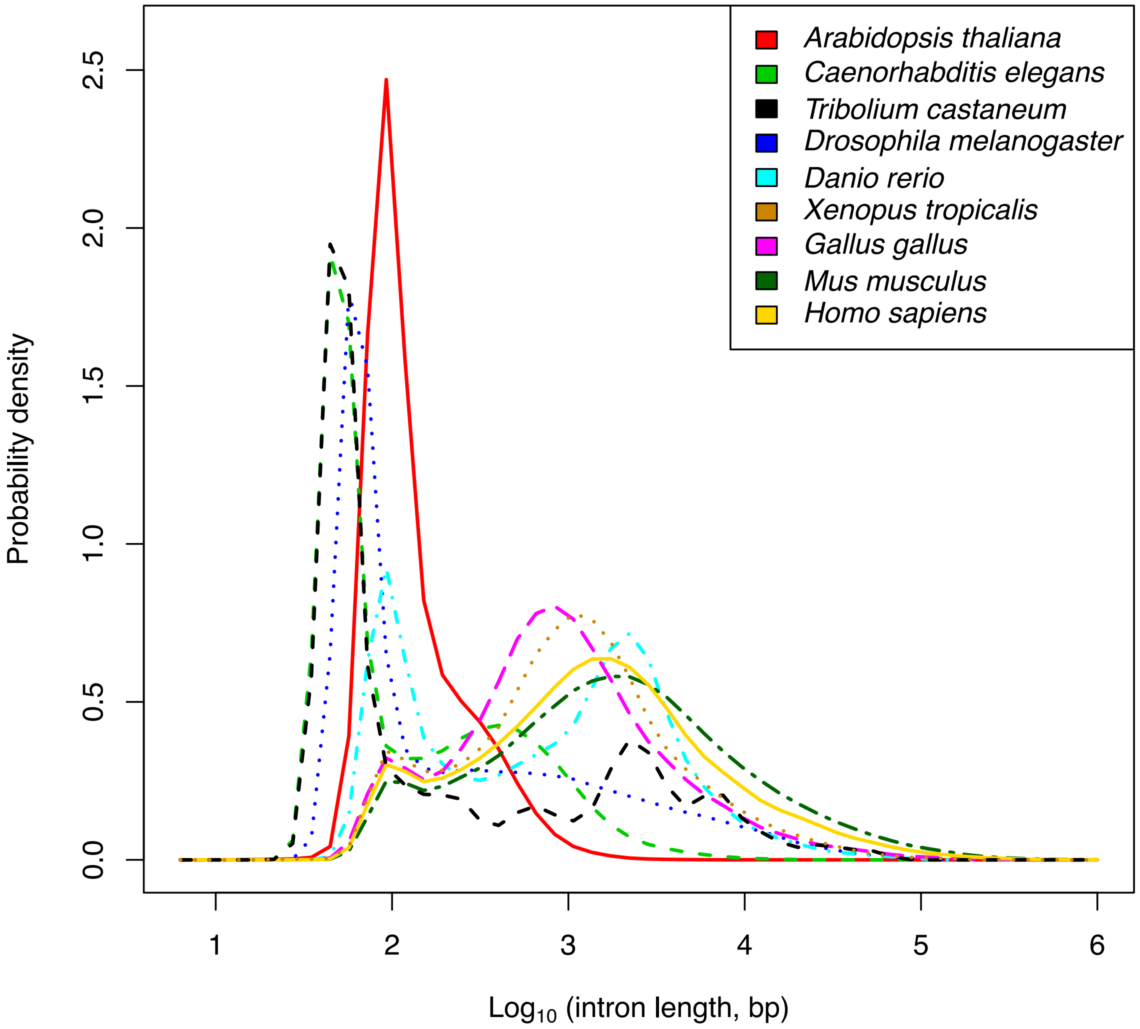


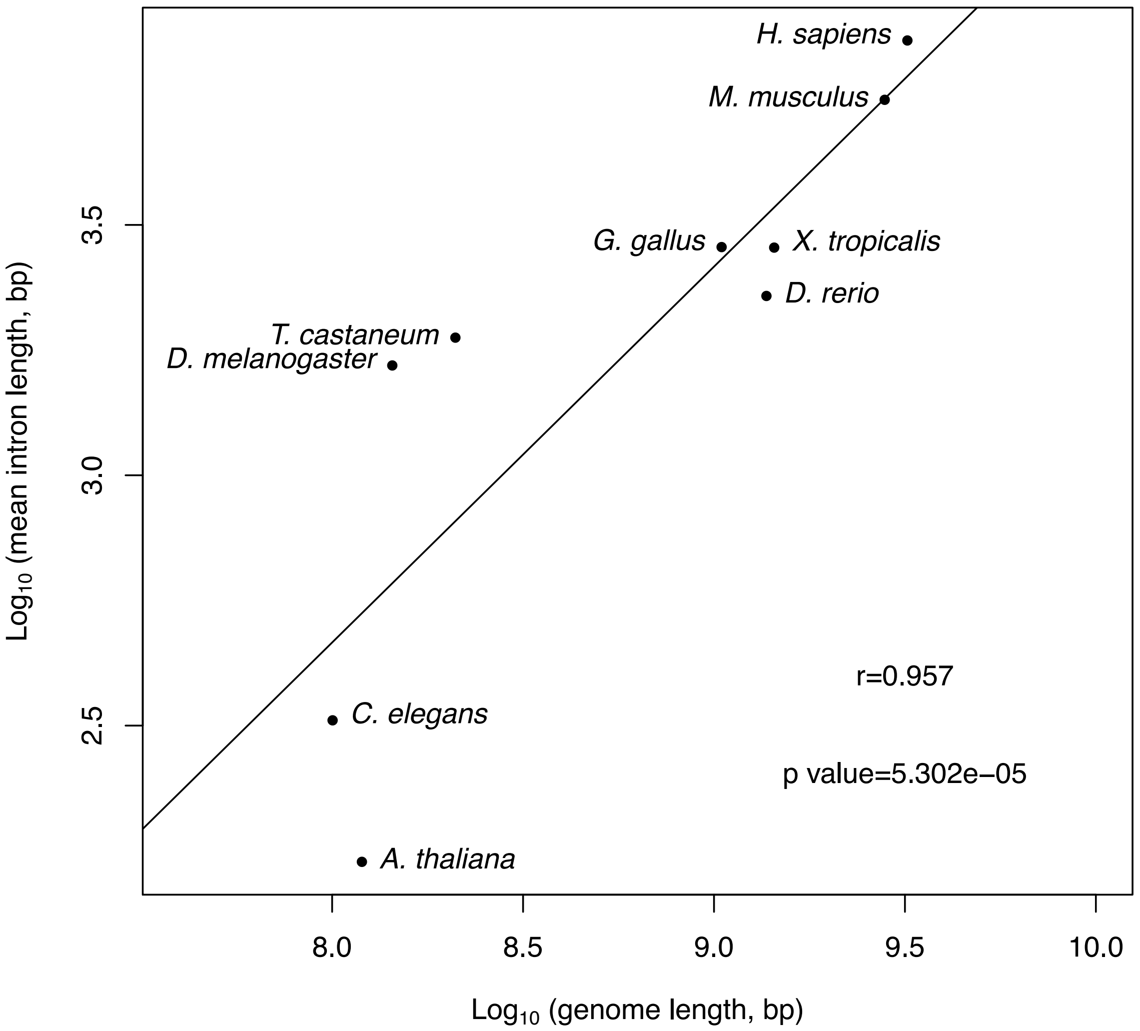
Supplementary Figure S1. Graph of GeneBase table relationships. The HTML file generated by FileMaker Pro containing a full description of the database ("Database Design Report") is shown in Supplementary File S1.



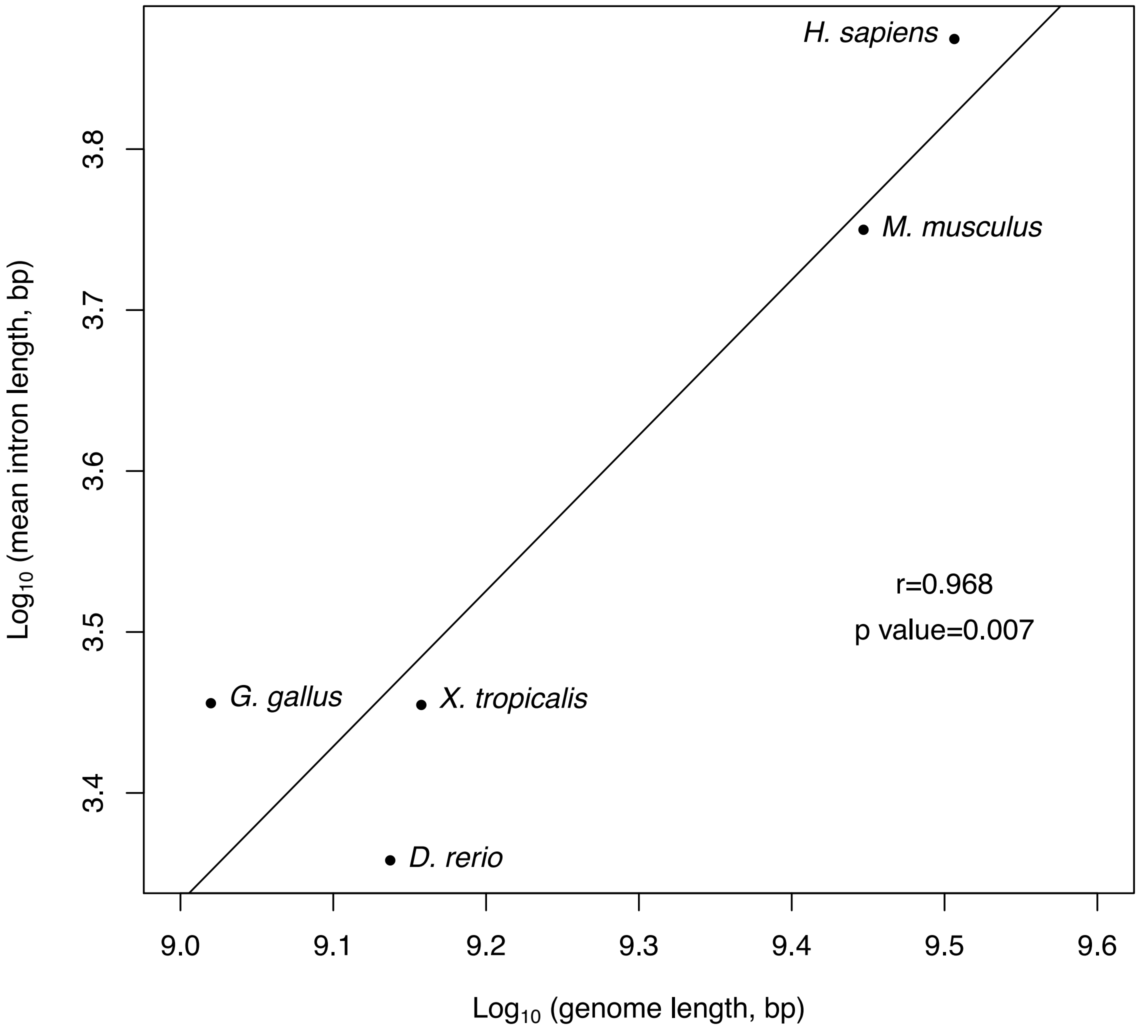
Supplementary Figure S2. Intron length distribution considering GeneBase "Gene_Table" records with a "VALIDATED" or "REVIEWED" RefSeq status, with an "NM_" or "NR_" type of corresponding RefSeq RNA accession number.



Supplementary Figure S3. Intron length distribution in some representative organisms, considering a set of non redundant GeneBase "Gene_Table" records belonging to gene entries currently annotated on the most recent genome annotation, with a "VALIDATED" or "REVIEWED" RefSeq status and an "NM_" or "NR_" type of corresponding RefSeq RNA accession number.



Supplementary Figure S4. Correlation between intron and genome lengths in some representative organisms. Mean intron lengths derive from Table 2. Genome lengths derive from NCBI Genome database.



Supplementary Figure S5. Correlation between intron and genome lengths in *Vertebrata*. Mean intron lengths derive from Table 2. Genome lengths derive from NCBI Genome database.