

Ensembl
genomes:

Homo sapiens
Pan troglodytes
Macaca mulatta
Bos taurus
Canis familiaris

↓ Intron extraction (< 50000 bp)

<i>Homo sapiens</i> :	163347 introns
<i>Pan troglodytes</i> :	160601 introns
<i>Macaca mulatta</i> :	158457 introns
<i>Bos taurus</i> :	153659 introns
<i>Canis familiaris</i> :	173320 introns

↓ Orthology (1:1)

11835 introns

↓ Size selection (200-1600 bp)

4849 introns

↓ Cross-species size conservation

2750 introns

↓ Flanking exons size filter (> 40 bp)

2608 introns

↓ Single copy gene filter ($e < 10^{-4}$)

1344 introns

↓ Molecular clock filter (K score < 0.1)

890 introns

↓ Divergence filter (scaling factor < 1.15)
(total primates branch
length > 0.075 subs./pos.)

225 introns

↓ Visual inspection

224 introns