|  | Length |  |  |
| ---: | :---: | :---: | :---: |
| Percent ID | $\geq \mathbf{5 0} \mathbf{b p}$ | $\geq \mathbf{1 0 0} \mathbf{b p}$ | $\geq \mathbf{2 0 0} \mathbf{b p}$ |
| $\geq 90 \%$ | $383,576(79,248)$ | $137,396(41,378)$ | $40,644(18,374)$ |
| $\geq 92 \%$ | $299,143(56,749)$ | $94,605(26,727)$ | $26,407(11,215)$ |
| $\geq 94 \%$ | $217,428(37,879)$ | $60,234(16,051)$ | $16,051(6,324)$ |
| $\geq 96 \%$ | $143,912(22,683)$ | $34,945(8,370)$ | $8,707(3,052)$ |
| $\geq 98 \%$ | $84,182(11,510)$ | $17,484(3,518)$ | $3,678(1,050)$ |
| $100 \%$ | $38,897(5,068)$ | $5,131(700)$ | $466(79)$ |

Table S1. Percent identity in chimp-rodent alignments. Counts of the number of blocks in multiple alignments of the chimpanzee, mouse, and rat genomes that are a given length and whose nucleotide sequences are a given percent identical (across all three species). Only nucleotides (A,C,T,G), and not indels nor missing data, count as identical. The number in parentheses gives the count of these blocks that contain at least one alignment column where chimpanzee, mouse, and rat have an identical nucleotide and human has a different one (human diff). The 466 blocks $\geq 200 \mathrm{bp}$ and $100 \%$ identical are analogous to (but not identical to) the ultraconserved elements described in ref. 32, which used the human, mouse and rat genomes.

