Figure S1

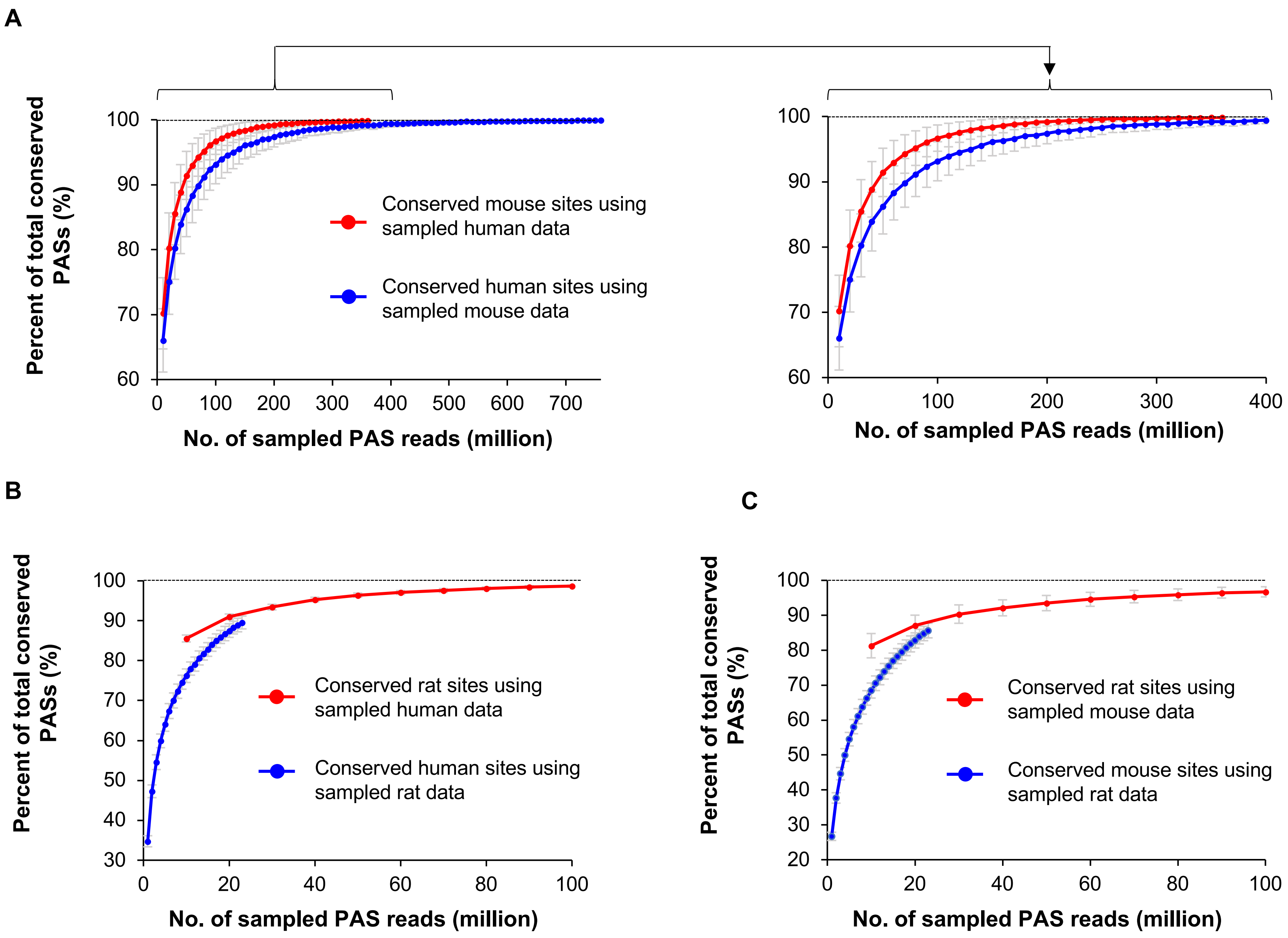

Figure S1. Assessment of completeness of identified conserved PASs by random sampling of PAS data. (A) Conserved PASs between human and mouse. **(B)** Conserved PASs between human and rat. **(C)** Conserved PASs between mouse and rat. PAS reads were randomly sampled, starting with 1 or 10 million PAS reads and increasing by 1 or 10 million PAS reads each step. Each sampling step was repeated 5 times, and the average and standard deviation of percent of total conserved PASs identified were calculated and plotted. All mouse conserved PASs were identified when ~200 million human PAS reads were used, whereas all human conserved sites were identified when ~400 million mouse PAS reads were used (A). This result indicates that identification of conserved PASs in human and mouse genomes is quite complete. By contrast, neither human nor mouse conserved PASs could be completely identified when all rat PAS reads were used (B and C).