

**Table S5. Diversity across regions of the human X chromosome, with ampliconic and low diversity regions included.** Diversity, measured as the average number of pairwise differences per site ( $\pi$ ) between the X chromosomes of 26 unrelated genetic females, in each region of the human X chromosome is presented first unnormalized for mutation rate variation, then normalized using human-chimpanzee (hg19-panTro4) divergence and separately normalized for human-macaque (hg19-rheMac3) divergence. The regions analyzed include the pseudoautosomal region 1 (PAR1), pseudoautosomal region 2 (PAR2), X-transposed region (XTR) and the non-pseudoautosomal region either including the XTR (nonPAR) or excluding the XTR (nonPAR<sub>minus\_XTR</sub>). The ampliconic and lowdiversity regions have not been filtered out. *P* values from permutation tests with 10,000 replicates are shown between each recombining and nonPAR region.

Region	Human-Chimpanzee		Human-Macaque		Human-Dog		Human-Mouse		
	Uncorrected $\pi$	Divergence	$\pi$	Divergence	$\pi$	Divergence	$\pi$	Divergence	
nonPAR	0.000512	0.009814	0.053489	0.049702	0.010444	0.234423	0.002183	0.305070	0.001678
nonPAR <sub>minus_XTR</sub>	0.000506	0.009782	0.053056	0.049512	0.011036	0.234372	0.002157	0.304460	0.001661
PAR1	0.001505	0.022643	0.066482	0.099892	0.015070	0.337717	0.004457	NA	0.000000
<i>p vs. nonPAR</i>	<b>0.0000</b>		<b>0.0388</b>		<b>0.0000</b>		<b>0.0000</b>		NA
<i>p vs. nonPAR<sub>minus_XTR</sub></i>	<b>0.0000</b>		<b>0.0500</b>		<b>0.0000</b>		<b>0.0000</b>		NA
PAR2	0.000643	0.008720	0.078348	0.040967	0.016677	0.218771	0.002940	0.257609	0.002497
<i>p vs. nonPAR</i>	<i>0.1429</i>		<i>0.1342</i>		<i>0.1092</i>		<i>0.1298</i>		<i>0.0947</i>
<i>p vs. nonPAR<sub>minus_XTR</sub></i>	<i>0.1553</i>		<i>0.1421</i>		<i>0.1132</i>		<i>0.1372</i>		<i>0.0993</i>
XTR	0.000747	0.010937	0.068256	0.056953	0.013108	0.245717	0.003038	0.336725	0.002217
<i>p vs. nonPAR</i>	<b>0.0000</b>		<b>0.0000</b>		<b>0.0000</b>		<b>0.0000</b>		<b>0.0000</b>