Supplementary material 2. Expected ratios of Fop_X/Fop_A, π_{4x}/π_{4A} and π_{0x}/π_{0A} for the overlap region

Sex-specific selection coefficients	h	Fop_X/Fop_A	π_{4x}/π_{4A}	π_{0x}/π_{0A}	Comments
$s_{fX} = s_{mX} = s_{fA} = s_{mX} > 0$	0	1.002	< 0.75	<< 0.75	Equal selection in both sexes and for A and X. Recessivity of deleterious mutations.
$s_{fX} = s_{mX} = s_{fA} = s_{mX} > 0$	0.5	~ 1	0.75	0.75	Equal selection in both sexes and for A and X. Semidominance of fitness effects.
$s_{fX} = s_{mX} = s_{fA} = s_{mX} > 0$	1	~ 1	> 0.75	1	Equal selection in both sexes and for A and X. Dominance of deleterious mutations.
$s_{mX} = 0$; $s_{fX} = s_{fA} = s_{mX} > 0$	0 -1	< 1	< 1	1.5	Selection purely on females on the X, but on both sexes for A.
$s_{mX} = 0$; $s_{mA} = 0$, $s_{fA} = s_{fX} > 0$ or $s_{fA} = 0$, $s_{mA} = s_{fX} > 0$	0 -1	~1	0.75	0.75	Selection purely on females on the X, and either mode of sex-specific selection for A.

s_{fX}: selection coefficient in females against deleterious mutations on the X chromosome. s_{mX}: selection coefficient in males for the X chromosome. s_{fA}: selection coefficient in females for the autosomes. s_{mA}: selection coefficient in males on the autosomes. h: dominance coefficient.

The equilibrium Fop_x/Fop_A and π_{4x}/π_{4A} ratios in the first three rows are as in McVean and Charlesworth (1999, Figure 4). The values in the last two rows are based on numerical results from an extension of the approach of McVean and Charlesworth (1999) to the case of different selection regimes in the two sexes, using a scaled selection intensity of similar magnitude to that estimated in Table 4.

The predicted equilibrium π_{0x}/π_{0A} ratios under strong purifying selection for $h > 0$ are given approximately by the expression $3h(s_{fA} + s_{mA})/2(2h\, s_{fX} + s_{mx})$, which corresponds to the ratios of the frequencies of deleterious X-linked and autosomal mutations under mutation-selection balance equilibrium (Charlesworth and Charlesworth 2010, p.161); this is because diversities for sites with low frequency mutations are approximately twice the frequency of the mutations.