

Table S1. Overview of identification and replication of number of SNPs associated with hormone levels in UK biobank.

Trait	Sex	Discovery analysis				Replication analysis			Variance explained [°]
		N	N SNPs $p < 5 \times 10^{-8}$	N lead SNPs*	N loci	N	N_SNPs $p < 0.05$	N SNPs replicated†	
<i>Testosterone</i>	Male	140,216	15,436	154	59	69,933	137	92	8.1%
	Female	139,591	6,028	83	47	69,916	81	63	3.6%
<i>SHBG</i>	Male	129,700	24,586	303	81	64,804	291	213	20.5%
	Female	150,365	16,024	234	76	75,325	221	153	13.0%

*FUMA: $R^2 = 0.05$, distance=10,000bp, UKB European ref panel

† Replication based on same direction of effect and one-sided p-value < Bonferroni corrected p-value ($0.05/N$ discovery lead SNPs)

° Variance explained calculated as: $[2 \times EAF \times (1 - EAF) \times GX^2] / \text{varX}$ (where varX is the variance of X)