

Table S11. Partitioning contribution of androgen (AR) and estrogen (ER) responsive-genes in GIANT anthropometric traits with "baseline" model.

| Trait | AR | | ER | |
|--------|-----------------------------|-----------------------------|-----------------------------|-----------------------------|
| | M h^2_g (SE) [^] | F h^2_g (SE) [^] | M h^2_g (SE) [^] | F h^2_g (SE) [^] |
| BMI | 8% (1%) | 6% (1%)* | 3% (1%) | 5% (1%) |
| HIP | 8% (1%) | 8% (1%) | 3% (1%) | 5% (1%) |
| HIP-a | 10% (1%) | 10% (1%) | 4% (1%) | 4% (1%) |
| WC | 8% (1%) | 7% (1%) | 3% (1%) | 5% (1%) |
| WC-a | 12% (2%) | 10% (1%) | 5% (1%) | 6% (1%) |
| WHR | 7% (2%) | 8% (1%) | 5% (1%) | 4% (1%) |
| WHR-a | 9% (2%) | 9% (2%) | 7% (1%)* | 4% (1%) |
| HEIGHT | 13% (1%)* | 13% (1%)* | 4% (1%) | 5% (1%) |
| WEIGHT | 12% (1%) | 7% (1%) | 3% (1%)* | 5% (1%) |

Abbreviations: h^2_g heritability; *** P<0.001; * P<0.05; conditional on baseline model

% h^2_g computed as (h^2_g in category) / (h^2_g total) with corresponding standard error estimated using delta method

[^] P-value on the coefficient of enrichment measured jointly with 51 known functional categories (including genic and regulatory)