Supplementary Table 1. Genetic variants associated at (*p* < 5 × 10-8) with inverse normally transformed AMH levels in premenopausal women.

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Locus | SNP | Chromosome | Base pair position | EA | OA | EAF | Imputation quality | Effect (SE) | *p*-value | Percentage of variance in AMH explained |
| *AMH* | rs10417628 | 19 | 2251817 | T | C | 0.02 | 0.83 | –0.34 (0.05) | 1.2 × 10-11 | 0.50% |
| *TEX41* | rs13009019 | 2 | 145670572 | A | G | 0.69 | 0.95 | –0.09 (0.01) | 7.2 × 10-10 | 0.35% |
| *MCM8* | rs16991615 | 20 | 5948227 | A | G | 0.07 | 0.99 | 0.16 (0.03) | 1.2 × 10-8 | 0.30% |
| *CDCA7* | rs11683493 | 2 | 174259325 | T | C | 0.57 | 0.97 | –0.08 (0.01) | 1.7 × 10-8 | 0.32% |

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AMH, anti-Müllerian hormone; SNP, single nucleotide polymorphism; EA, effect allele; OA, other allele; EAF, effect allele frequency; SE, standard error.