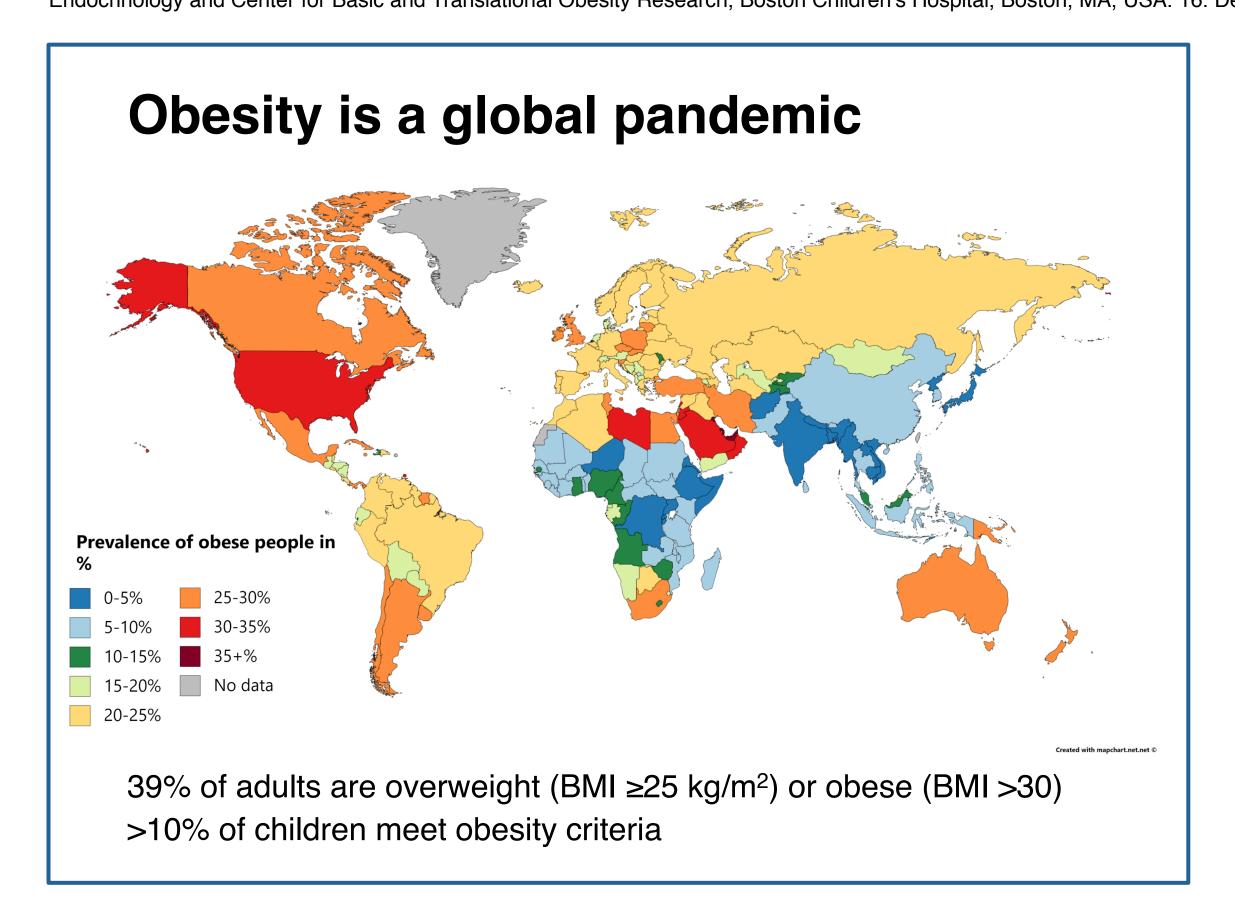
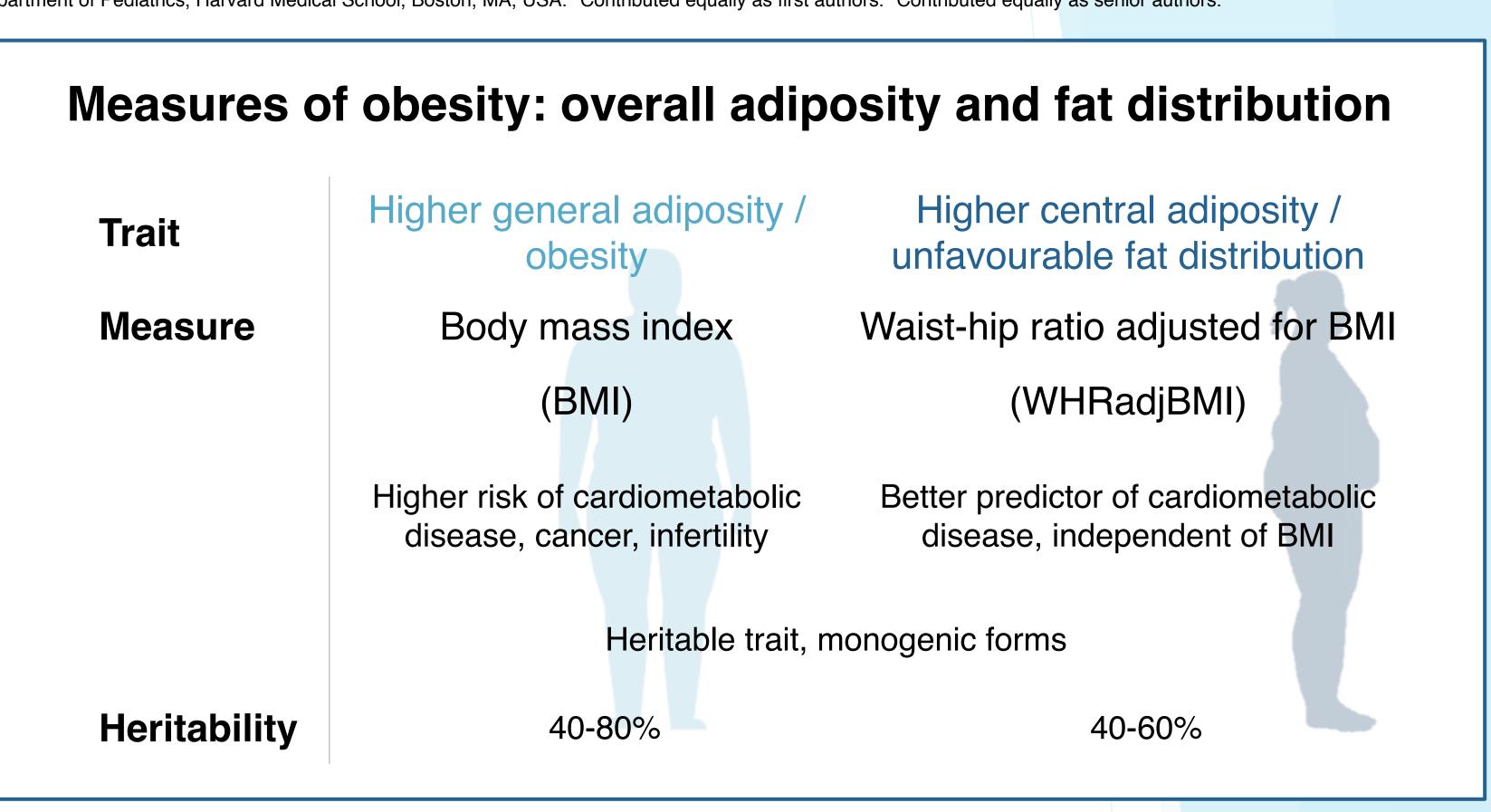


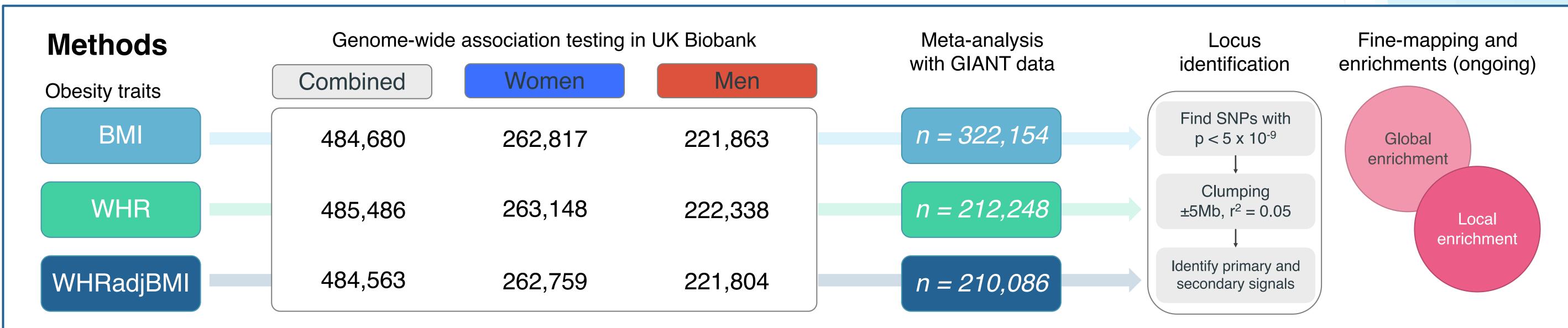
## Meta-analysis of genome-wide association studies for body fat distribution in 694,649 individuals of European ancestry

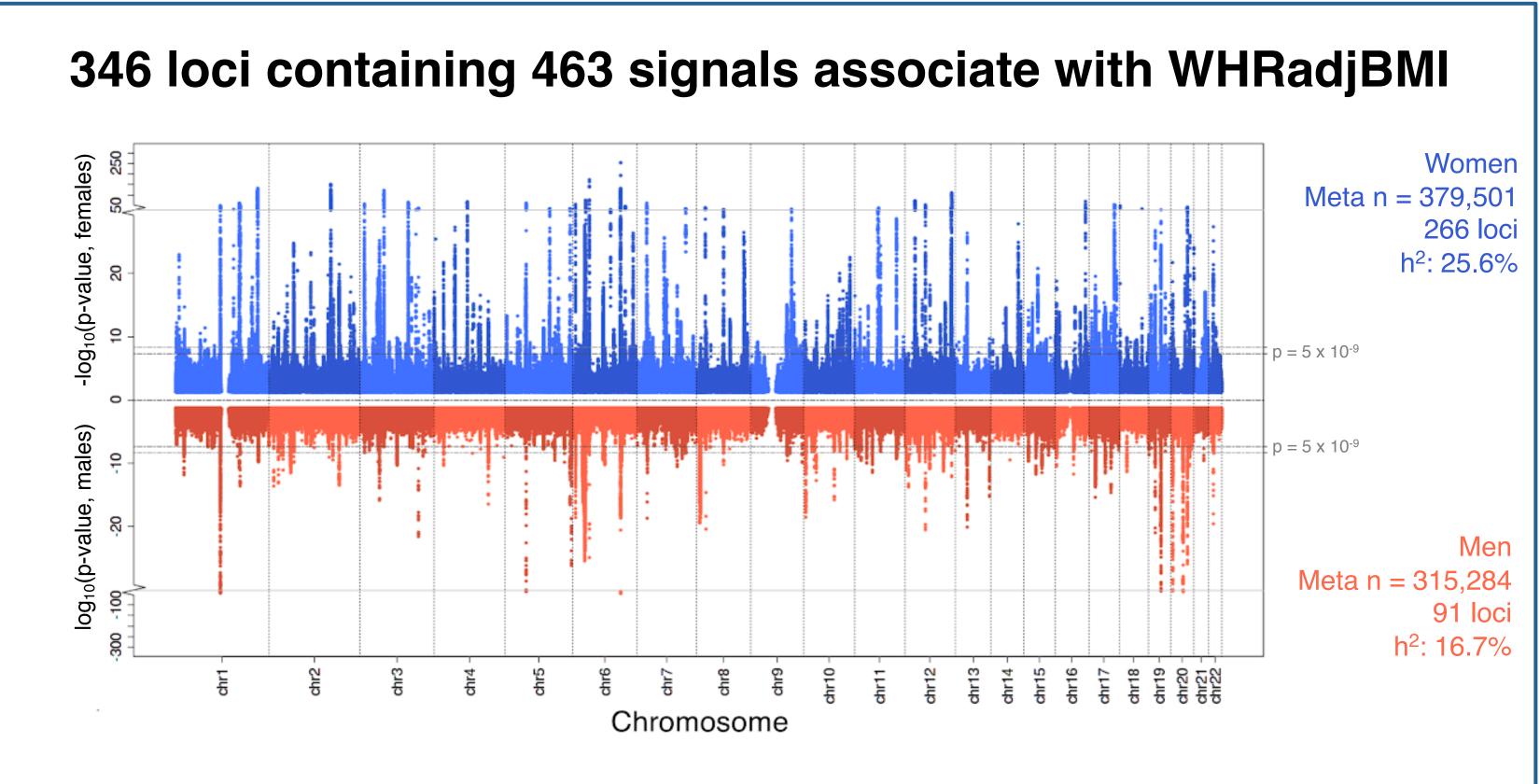
Sara L. Pulit<sup>1,2,3\*</sup>, Charli Stoneman<sup>4\*</sup>, Andrew P. Morris<sup>5,6</sup>, Andrew R. Wood<sup>4</sup>, Craig A. Glastonbury<sup>1</sup>, Jessica Tyrrell<sup>4</sup>, Loïc Yengo<sup>7</sup>, Teresa Ferreira<sup>1</sup>, Eirini Marouli<sup>8</sup>, Yingjie Ji<sup>4</sup>, Jian Yang<sup>7,9</sup>, Samuel Jones<sup>4</sup>, Robin Beaumont<sup>4</sup>, Damien C. Croteau-Chonka<sup>10</sup>, Thomas W. Winkler<sup>11</sup>, GIANT Consortium, Andrew. T. Hattersley<sup>4</sup>, Ruth J. F. Loos<sup>12</sup>, Joel N. Hirschhorn<sup>13,14,15,16</sup>, Peter M. Visscher<sup>7,9</sup>, Timothy M. Frayling<sup>4#</sup>, Hanieh Yaghootkar<sup>4#</sup>, Cecilia M. Lindgren<sup>1,3,6#</sup>

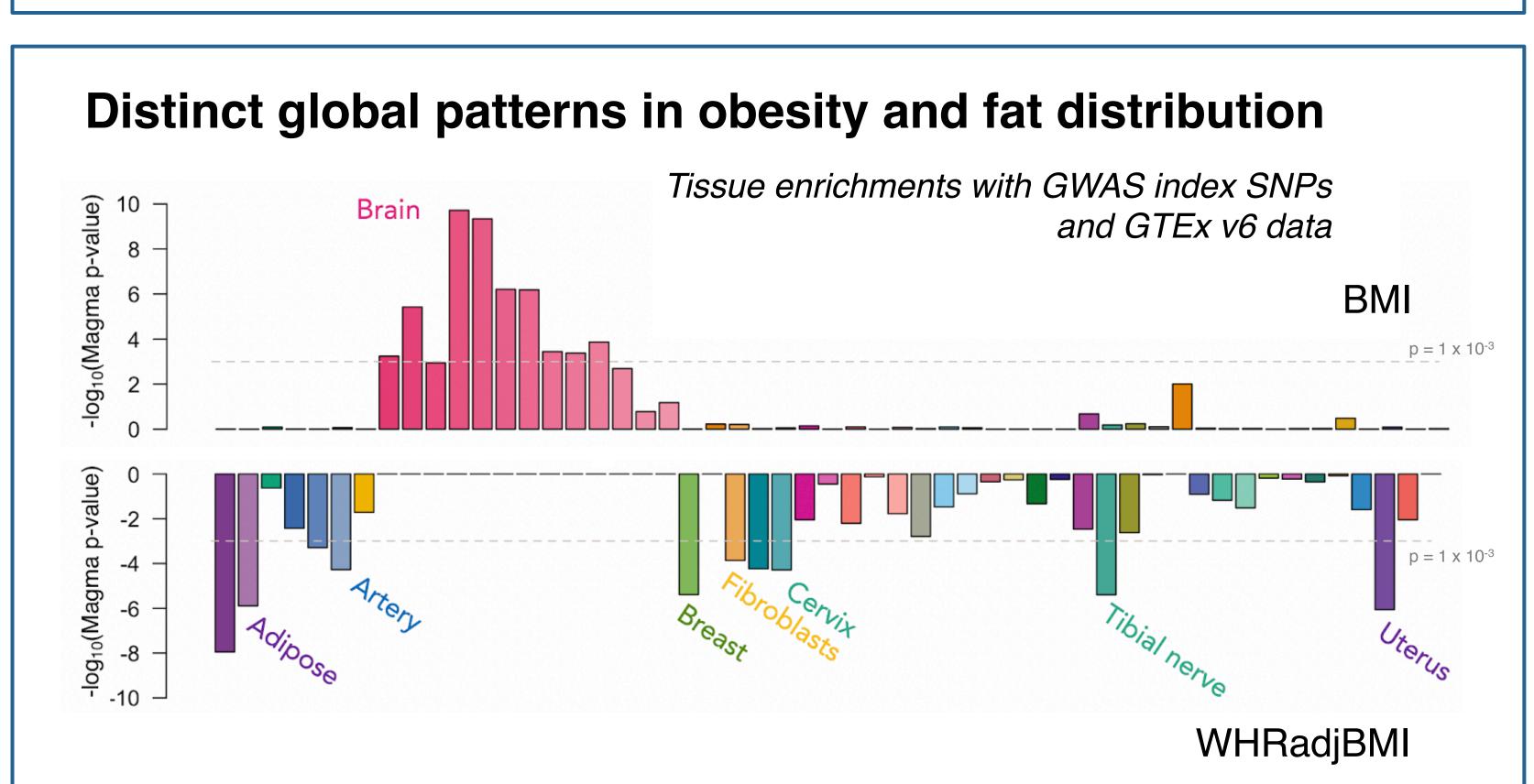
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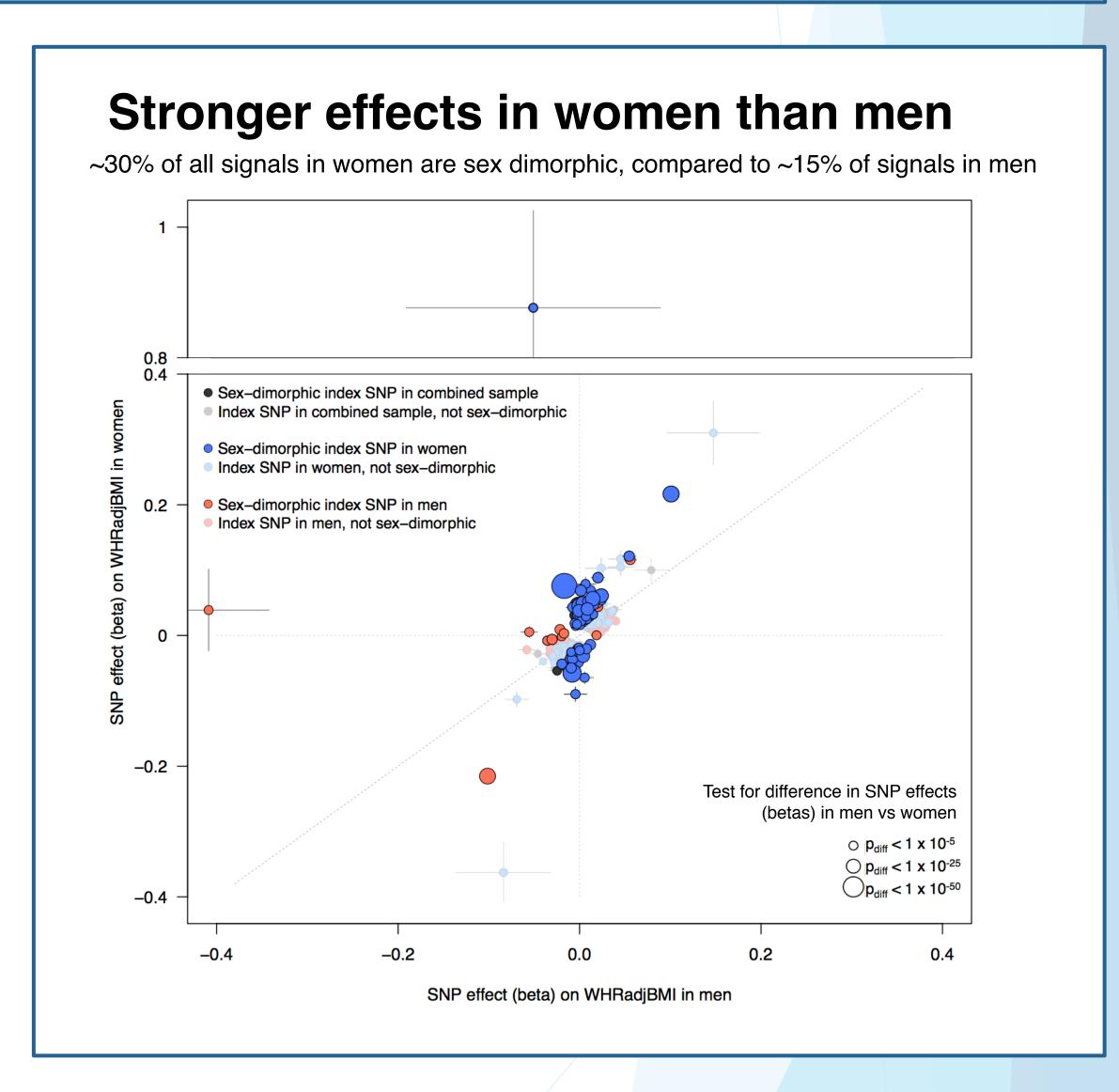












## Conclusions

Expanding sample size from ~300k to ~700k increases the number of associated loci ~10-fold

Signature of sex dimorphism in WHRadjBMI persists; many more associated loci in women than men

Additional work (e.g., fine-mapping) can help elucidate causal mechanisms, biological interplay underlying fat distribution and its comorbidities.