

Description of Additional Supplementary Files

File Name: Supplementary Data 1

Description: Results of longitudinal differential gene expression analysis across time in females.

File Name: Supplementary Data 2

Description: Results of longitudinal differential gene expression analysis across time in males.

File Name: Supplementary Data 3

Description: Results of cross-sectional differential gene expression analysis across age in females.

File Name: Supplementary Data 4

Description: Results of cross-sectional differential gene expression analysis across age in males.

File Name: Supplementary Data 5

Description: Significance of longitudinal multivariate adaptive shrinkage analysis across time in both sexes (LFSR).

File Name: Supplementary Data 6

Description: Effect size estimates from longitudinal multivariate adaptive shrinkage analysis across time in both sexes.

File Name: Supplementary Data 7

Description: Results of longitudinal differential gene expression analysis across puberty stages in females.

File Name: Supplementary Data 8

Description: Results of longitudinal differential gene expression analysis across puberty stages in males.

File Name: Supplementary Data 9

Description: Results of cross-sectional differential gene expression analysis across puberty stages in females.

File Name: Supplementary Data 10

Description: Results of cross-sectional differential gene expression analysis across puberty stages in males.

File Name: Supplementary Data 11

Description: Results of cross-sectional differential gene expression of pre and post-menarche in females.

File Name: Supplementary Data 12

Description: Results of cis interaction eQTL mapping.

File Name: Supplementary Data 13

Description: Results of Transcriptome-Wide Association Study of age at menarche.

File Name: Supplementary Data 14

Description: Overlap of genes associated with age at menarche via TWAS and differentially expressed genes.

File Name: Supplementary Data 15

Description: Overlap of genes associated with asthma via TWAS (Zhang et al, 2019) and differentially expressed genes.