### Estimated polygenic score AUC using LDSC/AVENGEME approach.

| Phenotype     | N      | AVENGEME $h^2$ | LDSC $h^2$ | LDSC intercept | Prevalence | Sampling | Est. AUC (LDSC $h^2$) | Est. AUC (AVENGEME $h^2$) | Obs. AUC (pT1) | Obs. AUC (DBSLMM) |
|---------------|--------|----------------|------------|----------------|------------|----------|----------------------|--------------------------|----------------|------------------|
| Depression    | 143265 | 0.097          | 0.1        | 0.997          | 0.15       | 0.318    | 0.567                | 0.565                    | 0.549          | 0.559            |
| T2D           | 152599 | 0.14           | 0.118      | 0.999          | 0.05       | 0.168    | 0.58                 | 0.599                    | 0.592          | 0.642            |
| CAD           | 184305 | 0.078          | 0.055      | 0.887          | 0.03       | 0.33     | 0.599                | 0.59                     | 0.576          | 0.597            |
| IBD           | 34652  | 0.165          | 0.183      | 1.069          | 0.013      | 0.592    | 0.631                | 0.615                    | 0.604          | 0.677            |
| MultiScier    | 27148  | 0.133          | 0.02       | 1.062          | 0.002      | 0.36     | 0.515                | 0.623                    | 0.615          | 0.657            |
| RheuArth      | 58284  | 0.101          | 0.143      | 1.065          | 0.005      | 0.246    | 0.631                | 0.584                    | 0.582          | 0.632            |
| Breast_Cancer | 228951 | 0.142          | 0.15       | 1.103          | 0.125      | 0.537    | 0.635                | 0.629                    | 0.602          | 0.658            |
| Prostate_Cancer | 140254 | 0.218          | 0.188      | 1.081          | 0.125      | 0.564    | 0.652                | 0.673                    | 0.632          | 0.691            |

Note. N, GWAS sample size; Est. AUC (LDSC $h^2$), AUC estimated by AVENGEME given SNP-based heritability estimated by LDSC; Prevalence, population prevalence of the outcome; Sampling, sampling fraction of cases and controls in GWAS sample calculated as $N_{\text{case}}/(N_{\text{case}}+N_{\text{control}})$; Est. AUC (AVENGEME $h^2$), AUC estimated by AVENGEME given SNP-based heritability estimated by AVENGEME; Obs. AUC (pT1), Observed AUC of polygenic scores based on pT+clump polygenic score using a p-value threshold of 1; Obs. AUC (DBSLMM), Observed AUC of polygenic scores based on DBLMM polygenic score.