

Supplement to:

Jørgensen, Ruth Eva, Rosa Cheesman, Ole A. Andreassen, Torkild Hovde Lyngstad. 2025. “The Genetics of Partnership Dissolution” *Sociological Science* 12: 76-96.

Supplementary information

Jørgensen et al., *The genetics of partnership dissolution*

Table of contents

Descriptive statistics for analysis sample	2
Supplementary table 1. Basic descriptive statistics for analysis data set	2
Materials regarding the SNP heritability (GWA) analysis	3
Manhattan plots of results from GWAS of partnership dissolution	3
QQ plots and population stratification	5
Materials regarding the polygenic score analyses	7
Supplementary table 2. Numerical results for Figure 1 (event history analysis)	7
Supplementary table 3. Numerical results for Figure 2 (within-family PGI analysis)	8
Analysis of genetic similarities using squared difference PGIs	9

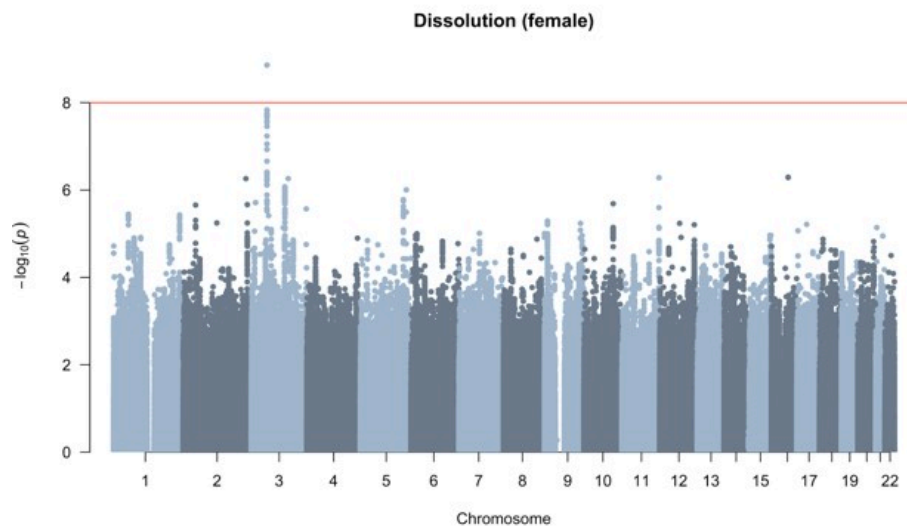
Descriptive statistics for analysis sample

Supplementary table 1. Basic descriptive statistics for analysis data set

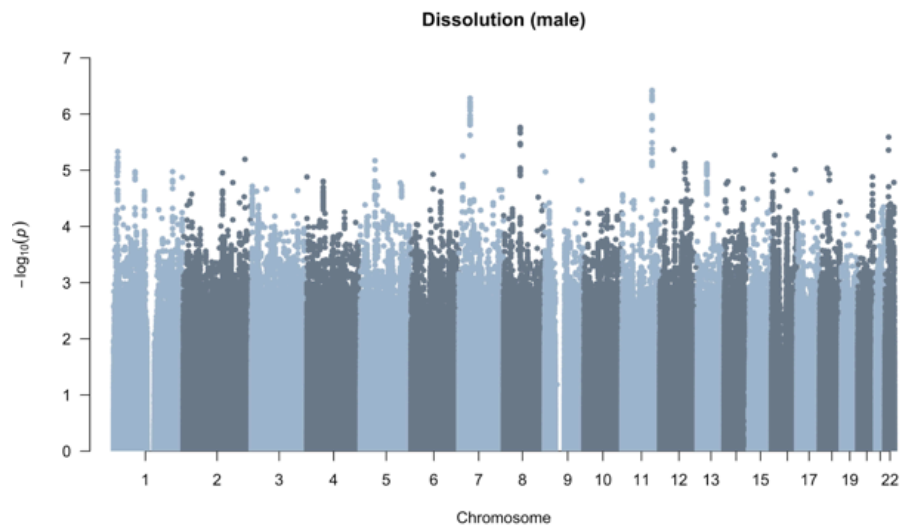
Statistic	Value
Number of individuals	124,476
Number of dissolutions	41,981
Number of person-years	1,542,287
Average # of years of follow-up	12.3
Mean birth cohort	1974
Proportion female	58.2%

Materials regarding the SNP heritability (GWA) analysis

Manhattan plots of results from GWAS of partnership dissolution



Supplementary figure 1. Manhattan plot of the $-\log_{10}(P)$ value of $\beta_{PartnershipDissolution}$ for all SNPs, ordered by chromosome and base position in women. The red horizontal line indicates the thresholds for genome-wide significant hits ($P = 5 \times 10^{-8}$).



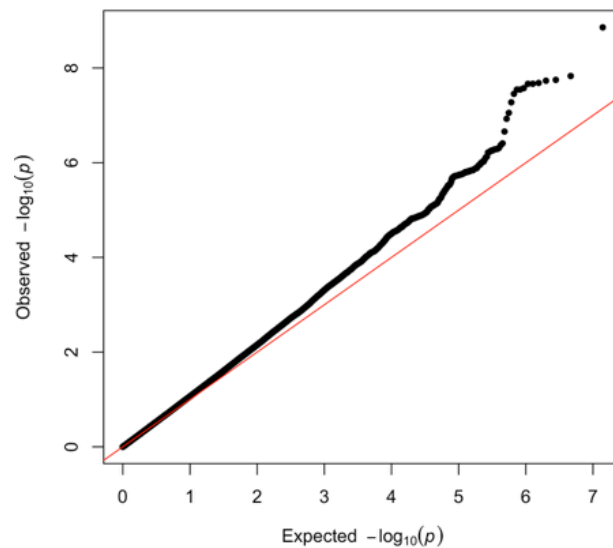
Supplementary figure 2. Manhattan plot of the $-\log_{10}(P)$ value of $\beta_{PartnershipDissolution}$ for all SNPs, ordered by chromosome and base position in men.

QQ plots and population stratification

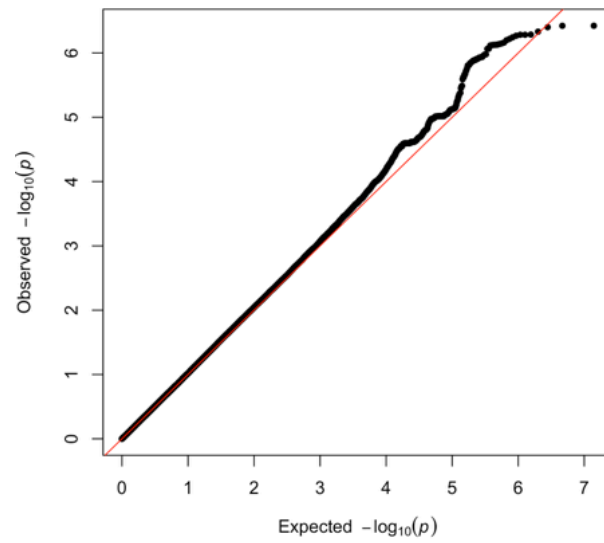
When some observed p -values are lower (more statistically significant) than expected under the null hypothesis, the points shown in the QQ plots will shift towards the y-axis (see fig. III). We observe a relatively early divergence between the expected values (as indicated by the red line) and observed ones (black points), particularly evident for females. This suggests that many moderately significant p -values are more significant than expected under the null hypothesis. Rather than being caused by thousands of true positives; this is often caused by population stratification, which involves systematic differences in allele frequencies among subpopulations within the studied group of individuals. As a result, many p -values are smaller than expected from chance alone.

To address issues related to population stratification, one potential approach is to conduct a within-family Genome-Wide Association Study (GWAS). However, the modest sample size in such studies may lead to a lack of sufficient statistical power, making it challenging to detect meaningful associations.

Supplementary figures 3 and 4 show QQ plots for women and men accordingly.



Supplementary figure 3. Quantile-quantile (QQ) plot of the data shown in Manhattan plot supplementary figure 1 (women).



Supplementary figure 4. Quantile-quantile (QQ) plot of the data shown in Manhattan plot supplementary figure 2 (men).

Materials regarding the polygenic score analyses

Supplementary table 2. Numerical results for Figure 1 (event history analysis)

Polygenic index	Men					Women				
	Beta	SE	P	Lower	Upper	Beta	SE	P	Lower	Upper
Number of sex partners	0.084	0.010	0.000	0.065	0.103	0.115	0.008	0.000	0.100	0.130
Depression	0.035	0.010	0.001	0.015	0.054	0.045	0.008	0.000	0.029	0.061
Cigarettes per day	0.028	0.008	0.001	0.012	0.044	0.031	0.007	0.000	0.018	0.044
Autism spectrum disorder	0.016	0.008	0.045	0.000	0.032	0.042	0.007	0.000	0.029	0.055
Loneliness	0.029	0.009	0.002	0.010	0.047	0.018	0.008	0.017	0.003	0.033
ADHD	0.011	0.008	0.170	-0.005	0.028	0.010	0.007	0.152	-0.004	0.023
Drinks per week	0.016	0.008	0.056	0.000	0.031	-0.006	0.007	0.323	-0.019	0.006
BMI	-0.004	0.008	0.627	-0.021	0.012	-0.003	0.007	0.688	-0.016	0.011
Being a 'morning person'	-0.009	0.009	0.301	-0.027	0.008	-0.001	0.007	0.899	-0.015	0.013
Neuroticism	0.000	0.011	0.985	-0.021	0.022	-0.019	0.009	0.035	-0.036	-0.001
Height	-0.014	0.008	0.086	-0.030	0.002	-0.006	0.007	0.394	-0.019	0.008
Number of children ever born	-0.029	0.009	0.001	-0.046	-0.012	-0.039	0.007	0.000	-0.052	-0.025
Subjective well-being	-0.038	0.013	0.004	-0.064	-0.012	-0.045	0.011	0.000	-0.066	-0.024
Age at 1st birth	-0.059	0.012	0.000	-0.082	-0.036	-0.067	0.009	0.000	-0.086	-0.049
Age at 1st sex	-0.051	0.010	0.000	-0.071	-0.032	-0.085	0.008	0.000	-0.101	-0.069
Educational attainment	-0.106	0.011	0.000	-0.127	-0.086	-0.114	0.008	0.000	-0.131	-0.098

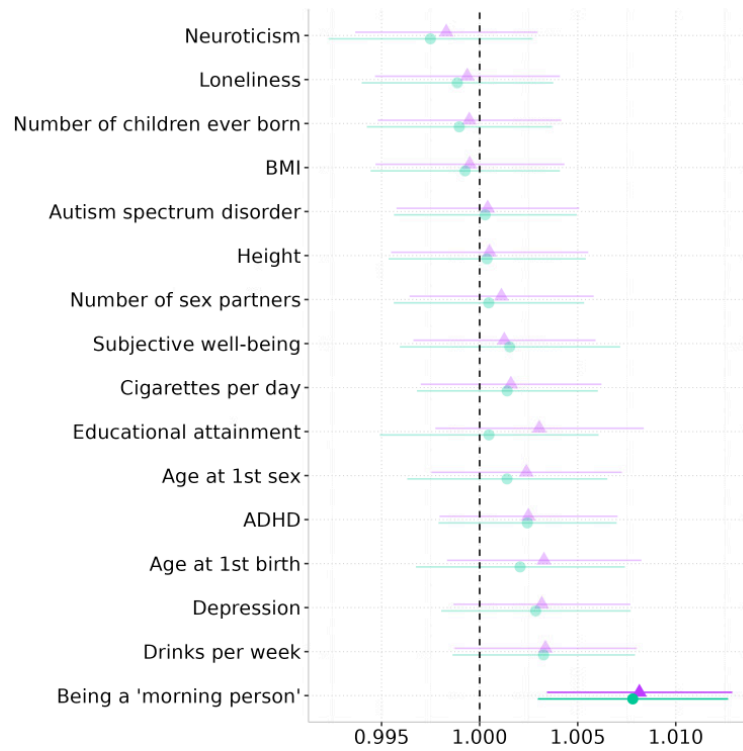
Supplementary table 3. Numerical results for Figure 2 (within-family PGI analysis)

Polygenic index	Single PGI models					Multiple PGI model				
	Beta	SE	P	Lower	Upper	Beta	SE	P	Lower	Upper
ADHD	-0.003	0.049	0.944	-0.099	0.092	-0.023	0.049	0.639	-0.120	0.073
Age at 1st birth	-0.289	0.094	0.004	-0.390	-0.188	-0.059	0.071	0.403	-0.198	0.079
Age at 1st sex	-0.332	0.050	0.003	-0.434	-0.234	-0.147	0.063	0.008	-0.287	-0.042
Autism spectrum disorder	0.034	0.075	0.042	-0.059	0.127	0.028	0.049	0.563	-0.068	0.125
BMI	-0.108	0.048	0.024	-0.201	-0.014	-0.006	0.007	0.913	-0.105	0.094
Being a 'morning person'	-0.133	0.048	0.006	-0.228	-0.039	0.004	0.056	0.937	-0.104	0.113
Cigarettes per day	0.166	0.048	0.001	0.072	0.259	0.067	0.049	0.166	-0.029	0.166
Depression	0.295	0.049	0.000	0.199	0.391	0.101	0.016	0.000	0.020	0.183
Drinks per week	0.051	0.048	0.240	-0.037	0.150	0.022	0.049	0.648	-0.074	0.119
Educational attainment	-0.298	0.051	0.000	-0.398	-0.198	-0.152	0.056	0.020	-0.280	-0.024
Height	-0.047	0.052	0.369	-0.168	0.076	0.003	0.053	0.952	-0.101	0.107
Loneliness	0.207	0.049	0.028	-0.480	0.366	0.101	0.058	0.081	-0.013	0.214
Neuroticism	0.074	0.047	0.121	-0.015	0.167	-0.194	0.065	0.003	-0.322	-0.067
Number of children ever born	-0.145	0.047	0.002	-0.237	-0.053	-0.035	0.052	0.499	-0.137	0.067
Number of sex partners	0.163	0.048	0.001	0.069	0.256	0.054	0.059	0.394	-0.062	0.171
Subjective well-being	-0.299	0.048	0.000	-0.393	-0.205	-0.282	0.078	0.000	-0.436	-0.128

Analysis of genetic similarities using squared difference PGIs

We also estimated models using the squared difference between partners' PGIs in order to assess whether genetic similarity between partners is associated with partnership dissolution. The squared difference approach implies that results are uninformative about the direction of the difference (man highest vs. woman highest), but we can learn whether being different from one's partner in genetic dispositions is associated with dissolution risk. An association could emerge from mechanisms related to partners' mutual understanding of the underlying phenotype, or increased tolerance and support from a spouse who has similar life experiences.

Supplementary figure 5 shows that all but one squared difference parameter estimates were non-significant. The exception is 'being a morning person', which was associated with a slightly higher odds of partnership dissolution (OR 1.008, 95 % CI 1.003–1.012). This is a miniscule association, and we refrain from interpreting this parameter estimate further given the risk of making a type 1 error.



Supplementary figure 5. Coefficient plot from a discrete time event-history model showing OR for partnership dissolution by PGI for single PGI models (green circles) and all PGIs, assessed simultaneously (purple triangles). Horizontal error-bars represent 95% confidence intervals (CIs). All PGIs were z-standardized. Non-significant estimates (where the CI includes 1.0) are shown in weaker colors. All models were adjusted for genotyping batch, chip and 10 principal components of ancestry.