Supporting Information

Rietveld et al. 10.1073/pnas.1222171110

SI Text

Swedish Twin Registry TwinGene Study (TG). Between December 2010 and May 2011, 9,836 Swedish twins were genotyped by the SNP&SEQ Technology Platform, Uppsala, using the Illumina HumanOmniExpress BeadChip genotyping platform. A detailed description of the analysis to detect pedigree errors is available in ref. 1. All genetic analyses reported in the present article are based on the dataset with cryptically related respondents removed from the sample.

Rotterdam Study. Genotyping of the Rotterdam Study (RS) samples was performed in the Genetic Laboratory, Department of Internal Medicine, Erasmus Medical Center, Rotterdam (HuGeF) using the Illumina, HumanHap 550K (RS-I and RS-II) and Illumina 610K Quad (RS-III) chip. Ethnic outliers and individuals with a mismatch between sex and typed X-linked markers, excess autosomal heterozygosity, or within-sample cryptic relatedness were removed.

RS and TG. In addition to the study-specific quality-control filters, additional control filters were imposed to prevent estimating spurious heritability due to different genotyping platforms across the two samples or due to the presence of twins in TG. SNPs with minor allele frequency <0.01, missing rate >0.05, or Hardy-Weinberg equilibrium test P value < 0.001 were excluded. Individuals with less than 95% of genotyped SNPs available were dropped, as were individuals with missing phenotypic information. In all analyses, one twin per family in the TG sample was always excluded. If only one twin from a pair had answered both survey questions, the individual with complete phenotypic data was included in the analysis. If both twins had complete phenotypic data, one of them was chosen at random for inclusion. The quality-control procedures resulted in a dataset of 627,011 SNPs for 6,767 individuals in the Swedish Twin Registry (STR); 517,635 SNPs for 3,878 individuals in RS-I; 498,999 SNPs for 2,085 individuals in RS-II; and 510,681 SNPs for 2,993 individuals in RS-III.

1. Benjamin DJ, et al. (2012) The genetic architecture of economic and political preferences. *Proc Natl Acad Sci USA* 109(21):8026–8031.

Table S1. Additional GREML (common narrow heritability) estimates of subjective well-being (SWB): Only SNPs in both datasets and no-relatedness threshold

Dataset	No. SNPs	Happy ("...I was happy")				Enjoy ("...I enjoyed life")				Combined			
		n	h^2_{SNP}	SE	P value	n	h^2_{SNP}	SE	P value	n	h^2_{SNP}	SE	P value
Only SNPs in both datasets	283,289	11,439	0.11	0.05	0.01	11,512	0.03	0.05	0.31	11,415	0.08	0.05	0.05
No-relatedness threshold	852,597	15,584	0.08	0.03	0.01	15,687	0.03	0.04	0.18	15,548	0.06	0.03	0.04

This table reports genomic-relatedness-matrix restricted maximum-likelihood (GREML) estimates for *Happy*, *Enjoy*, and *Combined* for the pooled sample (combining TG and RS). We estimated the matrix of genetic relatedness after omitting one twin per pair in the Swedish data. In the first analysis, we restricted the analyses to individuals whose relatedness did not exceed 0.025 and only SNPs that were available in all datasets. In the second analysis, we included all individuals and all SNPs. n is the number of individuals used in the analyses after the relatedness threshold has been applied. In all analyses we control for sex, age, age-squared, and the first 20 principal components of the variance-covariance matrix of the genotypic data. The P value is from a likelihood ratio test of the null hypothesis that the fraction of variance explained is equal to zero.

Table S2. Variance decomposition: Twin analyses in SALT

ACE decomposition	a^2	c^2	e^2	$-2 \ln L$
Same-sex and opposite-sex DZ				
Happy	0.04 (0.00–0.16)	0.06 (0.00–0.08)	0.91 (0.84–0.95)	24593.30
Enjoy	0.07 (0.00–0.16)	0.03 (0.00–0.11)	0.90 (0.84–0.95)	25289.21
Combined	0.03 (0.00–0.17)	0.08 (0.00–0.13)	0.89 (0.88–0.92)	23681.61
Only same-sex pairs included				
Happy	0.05 (0.00–0.15)	0.04 (0.00–0.10)	0.91 (0.85–0.96)	17652.16
Enjoy	0.08 (0.00–0.14)	0.00 (0.00–0.06)	0.92 (0.86–0.97)	18060.22
Combined	0.06 (0.00–0.17)	0.05 (0.00–0.13)	0.89 (0.83–0.95)	17047.92

The upper section reports estimates of an additive genetic/common environmental/unique environmental (ACE) model with same-sex and opposite-sex dizygotic (DZ) pairs included. The genetic and environmental factors are assumed to be the same in men and women. The lower section reports estimates from an ACE model with only same-sex pairs included. All models allow the liability threshold to vary by age and sex. The variance components are constrained to be the same in men and women. The Swedish Twin Registry's Screening Across the Lifespan Twin Study (SALT) sample is restricted to twin pairs in which both members responded to the survey and such that the age range is the same as in the TG sample. The SALT individuals used in these twin analyses are a superset of the TG sample used in the GREML analyses.

Table S3. Descriptive statistics: Single-question SWB measures

SWB measure	Sample	n	% Rarely or none of the time (less than 1 d)	% Some or a little of the time (1–2 d)	% Occasionally or a moderate amount of time (3–4 d)	% Most or all of the time (5–7 d)
Happy	RS-I	3,842	7.0	7.7	15.9	69.5
	RS-II	2,075	4.5	11.0	22.3	62.2
	RS-III	2,992	2.9	9.8	20.3	67.1
	STR	6,675	5.1	11.0	44.9	39.0
	STR+RS	15,584	5.1	10.0	30.0	55.0
Enjoy	RS-I	3,866	6.1	7.0	13.3	73.6
	RS-II	2,080	4.2	10.3	17.9	67.6
	RS-III	2,990	2.6	8.7	15.7	72.9
	STR	6,751	2.4	3.7	27.0	66.9
	STR+RS	15,687	3.6	6.3	20.3	69.8

This table provides summary statistics for the SWB measures used in the GREML analysis.

Table S4. Descriptive statistics: Combined SWB measure

SWB measure	Sample	n	0 (%)	1 (%)	2 (%)	3 (%)	4 (%)	5 (%)	6 (%)
Combined	RS-I	3,830	3.2	2.1	5.0	6.4	8.2	11.5	63.5
	RS-II	2,070	2.7	1.7	6.4	6.3	12.0	15.9	55.1
	RS-III	2,989	1.4	1.4	5.2	5.8	11.0	14.3	61.0
	STR	6,659	1.1	1.3	3.8	8.0	21.4	28.7	35.8
	STR+RS	15,548	1.9	1.6	4.7	6.9	14.9	20.0	50.0

This table provides summary statistics for the combined SWB measure used in the GREML analysis.

Table S5. Descriptive statistics: GREML and Twin Analysis samples

Sample	n	% Female	Mean age (SD)	No. *Happy* (%high)	No. *Enjoy* (%high)	No. *Combined* (%high)
GREML						
RS-I	3,878	58.6	72.42 (7.35)	3,842 (69.5%)	3,866 (73.6%)	3,830 (63.5%)
RS-II	2,085	54.3	64.72 (7.93)	2,075 (62.2%)	2,080 (67.5%)	2,070 (55.1%)
RS-III	2,993	56.3	57.03 (6.78)	2,992 (67.0%)	2,990 (72.9%)	2,989 (60.1%)
RS	8,956	56.8	65.48 (9.91)	8,909 (67.0%)	8,936 (72.0%)	8,889 (60.7%)
TG	6,767	52.6	67.59 (8.92)	6,675 (38.9%)	6,751 (66.9%)	6,659 (35.8%)
TG+RS	15,723	55.0	66.39 (9.35)	15,584 (55.0%)	15,687 (69.8%)	15,548 (50.0%)
SALT						
SALT MZ	5,398	53.8	73.85 (5.21)	1,952 (37.8%)	3,308 (62.9%)	1,781 (34.6%)
SALT DZ	8,950	52.8	74.16 (5.21)	3,156 (37.0%)	5,460 (62.6%)	2,856 (33.6%)
SALT OS	5,682	50.0	76.19 (7.50)	1,917 (35.6%)	3,385 (61.2%)	1,703 (31.8%)

This table provides summary statistics for the variables used in the GREML and SALT analysis. DZ, dizygotic same-sex pairs; MZ, monozygotic; OS, opposite-sex DZ pairs. The TG sample is the subset of the SALT sample that has been genotyped, and in the TG (but not SALT) sample, one twin per family has been removed. The SALT sample is restricted to twin pairs in which both members responded to the survey and such that the age range is the same as in the TG sample. No. *Happy* refers to the number of observation individuals with nonmissing data for *Happy*; analogously for No. *Enjoy* and No. *Combined*. For *Happy* and *Enjoy*, "%high" refers to the fraction of individuals who chose the highest response category for the SWB question; for *Combined*, it is the fraction coded as high for both questions.