

Table 1. Basic description of the resilience meta-analysis sample composition.

Dataset	N	Cases (n)	Cases (%)	Age range	Age (mean $\pm$ SD)	Females	Males	RS-11 (mean $\pm$ SD)
BiDirect Study	1,453	Depression (526), ACE (243)	52.92	37-73	56 $\pm$ 8	688	765	56 $\pm$ 12
FOR2107 consortium	1,789	MDD (795), BP (133)	51.87	18-65	36 $\pm$ 13	1,131	658	56 $\pm$ 13
PROCAM-2 Study	3,879	Depression (421)	10.85	32-88	60 $\pm$ 9	1,822	2,057	61 $\pm$ 10
SHIP-LEGEND	2,230	MDD (374)	16.77	29-89	56 $\pm$ 14	1,177	1,053	64 $\pm$ 9
SHIP-TREND (B1)	752	MDD (126)	16.76	29-89	57 $\pm$ 13	427	325	62 $\pm$ 12
SHIP-TREND (B2)	1,578	MDD (317)	20.09	28-89	57 $\pm$ 14	767	811	61 $\pm$ 12
LIFE-Adult-Study	4,141	Depression (360)	8.69	18-79	64 $\pm$ 13	2,166	1,975	60 $\pm$ 11
Total	15,822	Depression (2,919), BP (133), ACE (243)	20.83	18-89	55	8,178	7,644	60

B1: batch 1, B2: batch 2, N: sample size, BP: bipolar disorder, MDD: major depressive disorder, ACE: acute coronary event, SD: standard deviation, RS-11: 11-item resilience scale

Table 2. Correlation between polygenic scores for personality characteristics and RS-11 scores in PROCAM-2.

PGS Catalog ID	Phenotype	Method	Publication ID	# PGS SNPs	# Valid SNPs	% Valid SNPs	r	p-value	FDR
PGS001829	Depression	Penalized regression (bigstatsr)	PGP000263	7,534	7,530	99.9	0.0097	0.5453	0.5907
PGS002213	Neuroticism	LDpred2 (bigsnpr)	PGP000263	950,183	944,901	99.4	-0.0670	3.02E-05	0.0004
PGS002209	Chronotype	LDpred2 (bigsnpr)	PGP000263	955,439	950,000	99.4	-0.0312	0.0522	0.1131
PGS002222	Self-injurious behavior	LDpred2 (bigsnpr)	PGP000263	761,279	756,897	99.4	-0.0170	0.2912	0.4731
PGS002231	Educational attainment	LDpred2 (bigsnpr)	PGP000263	950,845	945,206	99.4	-0.0333	0.0384	0.1131
PGS002154	General happiness	LDpred2 (bigsnpr)	PGP000263	806,011	801,523	99.4	-0.0505	0.0017	0.0108
PGS001016	Sensitivity / hurt feelings	snpnet	PGP000244	7,922	7,370	93.0	-0.0329	0.0405	0.1131
PGS001017	Suffer from 'nerves'	snpnet	PGP000244	3,348	3,074	91.8	-0.0224	0.1634	0.3034
PGS001021	Feelings of worry or anxiety	snpnet	PGP000244	9,747	9,110	93.5	-0.0320	0.0464	0.1131
PGS001091	Loneliness	snpnet	PGP000244	660	574	87.0	-0.0136	0.3965	0.5154
PGS001398	Friendship satisfaction	snpnet	PGP000244	659	590	89.5	0.0042	0.7926	0.7926
PGS001401	Health satisfaction	snpnet	PGP000244	1,814	1,662	91.6	0.0110	0.4920	0.5814

PGS: polygenic score, SNPs: single-nucleotide polymorphisms, FDR: false discovery rate

Table 3. Genomic loci suggested for trait resilience through variant-based meta-analysis.

Locus	Lead variant	Lead rsID	Lead p	Size (bp)	Start (bp)	End (bp)	# SNPs	protein-coding Mapped/eQTL Genes
1	3:112515187:A:G	rs6797028	9.44E-06	5812	112512647	112518459	12	<i>CD200R1L, CD200R1, GTPBP8, NEPRO</i>
2	3:193598924:C:T	rs78180970	4.88E-06	19899	193598924	193618823	3	-
3	7:11555542:C:G	rs17633522	8.10E-06	7089	11554555	11561644	4	<i>THSD7A</i>
4	14:40818021:C:T	rs61989120	2.97E-06	96875	40763557	40860432	12	-
5	17:19771057:C:G	rs112155453	3.93E-06	164542	19612489	19777031	5	<i>CCDC144A, SLC47A1, ALDH3A2, SLC47A2, ULK2, AKAP10, SPECC1, LGALS9B</i>

bp: base pairs, eQTL: expression quantitative trait loci.

Table 4. Protein-coding candidate genes suggested for trait resilience through gene-based meta-analysis.

Symbol	Chr	Start	End	Weight	Z-score	p-value	I ²	Het.p
<i>RIT1</i>	1	155867599	155881195	15799	4.402	1.07E-05	0	0.748
<i>KHDC4</i>	1	155882834	155904191	15798	4.354	1.34E-05	0	0.737
<i>RXFP4</i>	1	155911480	155912625	15791	4.370	1.24E-05	0	0.770
<i>ARHGEF2</i>	1	155916630	155976861	15793	4.328	1.50E-05	0	0.774
<i>ESRRG</i>	1	216676588	217311097	15793	3.906	9.37E-05	0	0.996
<i>ROBO1*</i>	3	78646390	79816965	15794	5.029	4.93E-07	0	0.991
<i>PCDHB1</i>	5	140430979	140433512	15795	3.948	7.87E-05	12.5	0.335
<i>ZBTB24</i>	6	109783797	109804440	15799	3.935	8.31E-05	0	0.883
<i>GJE1</i>	6	142454227	142456288	15801	4.391	1.13E-05	6.5	0.378
<i>PRR18</i>	6	166719168	166721936	15789	3.952	7.74E-05	0	0.706
<i>MICALL2</i>	7	1468101	1499138	11643	3.971	7.17E-05	0	0.717
<i>TBX20</i>	7	35242042	35293758	15795	3.913	9.13E-05	0	0.821
<i>SEMA3D</i>	7	84624869	84816171	15793	4.078	4.54E-05	11.6	0.341
<i>ABCB8</i>	7	150725510	150744869	11654	4.457	8.31E-06	0	0.998
<i>PAXIP1</i>	7	154735397	154794794	15799	4.398	1.10E-05	0	0.734
<i>ROR2</i>	9	94325373	94712444	15797	4.313	1.61E-05	0	0.570
<i>PALM2</i>	9	112403068	112713755	15795	3.988	6.67E-05	0	0.639
<i>RRM1</i>	11	4115937	4160106	15795	4.209	2.56E-05	33.4	0.173
<i>BATF2</i>	11	64755415	64764517	15795	4.248	2.15E-05	0	0.664
<i>SUDS3</i>	12	118814185	118855840	15800	4.083	4.45E-05	0	0.988
<i>SDR39U1</i>	14	24908972	24912111	15802	3.893	9.92E-05	0	0.514
<i>NIPA2</i>	15	23004684	23034427	15787	3.958	7.56E-05	39.7	0.127
<i>DNASE1</i>	16	3661729	3730144	15789	3.972	7.13E-05	0	0.658
<i>SCNN1B</i>	16	23289552	23392620	15794	4.005	6.19E-05	0	0.434
<i>NSMCE1</i>	16	27236312	27280115	15793	4.014	5.97E-05	0	0.529
<i>ASPHD1</i>	16	29911696	29931185	15786	3.981	6.87E-05	0	0.813
<i>KCTD13</i>	16	29916333	29938356	15783	4.033	5.50E-05	0	0.799
<i>CIB3*</i>	19	16272179	16284336	15790	4.752	2.02E-06	0	0.691
<i>CEACAM6</i>	19	42254885	42276113	15791	4.246	2.18E-05	0	0.832
<i>LYPD4*</i>	19	42341148	42348760	15786	4.778	1.77E-06	0.3	0.421
<i>DMRTC2</i>	19	42348806	42356401	15793	4.031	5.55E-05	29.8	0.201
<i>MB</i>	22	36002811	36033998	15788	4.563	5.04E-06	22.2	0.260
<i>PANX2</i>	22	50609160	50618723	15782	4.176	2.97E-05	0	0.676

*genome-wide significant