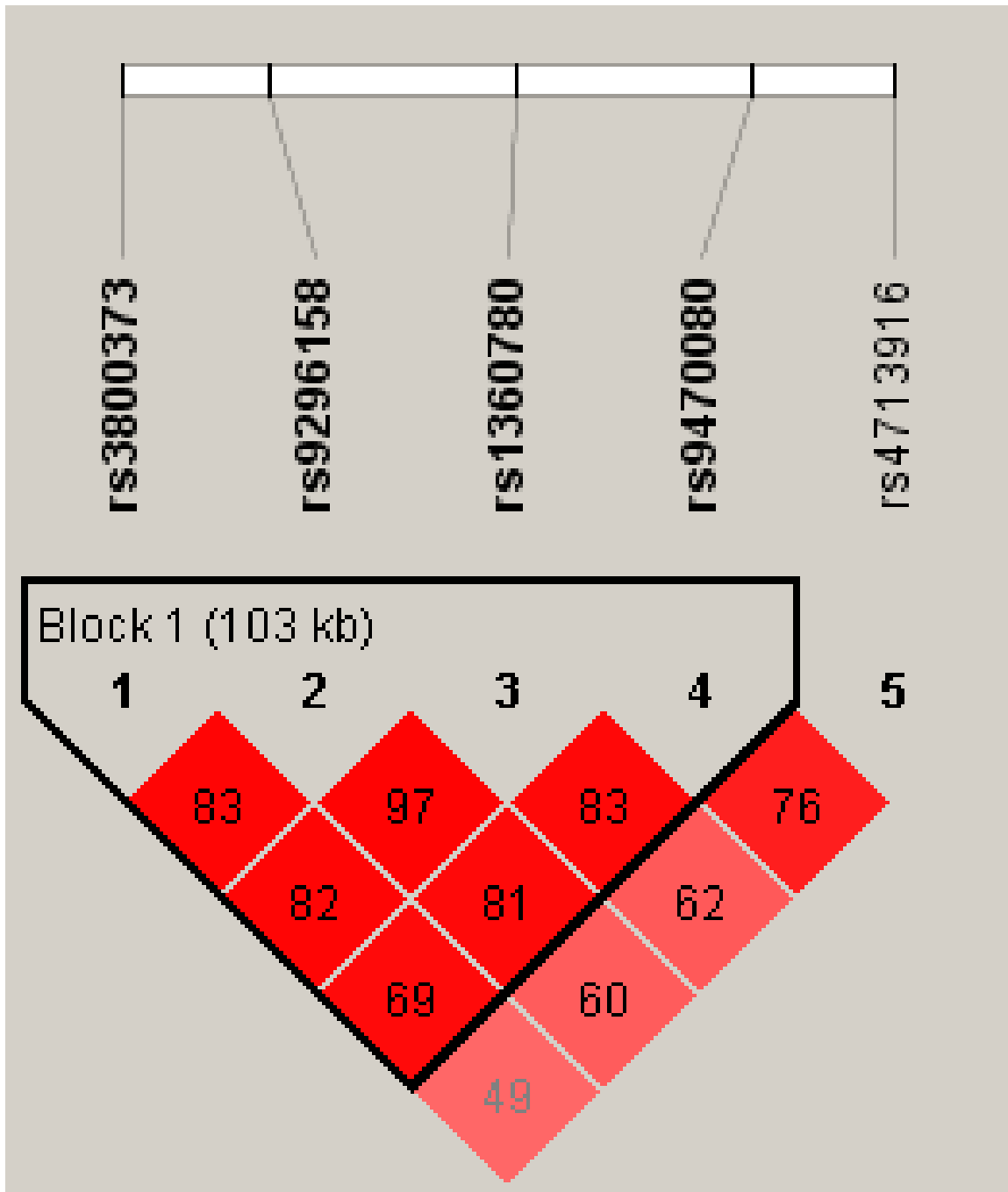


Supplemental Online Figure SF1. Representation of linkage-disequilibrium (LD) structure in the FKBP5 region using r^2



Note. The figure shows the LD plot of all tested SNPs using r^2 as the measure of LD. r^2 values are printed in the respective square for compared SNPs, with darker red values representing higher levels of LD. $r^2 = 1$ would indicate complete LD.

Supplemental Online Table ST1. List of tested *FKBP5* SNPs, their positions on human chromosome 6 (6p21.3-21.2), Hardy-Weinberg Equilibrium test p-value (HWpval), minor allele frequency (MAF) and call rate (N=884). The HWE tests for the SNPs of EDSP respondents without MDE revealed a nominal deviation, which did not withstand Bonferroni-correction for multiple testing (5 SNPs x 2 populations). Although call rates were close to 100%, to exclude genotyping errors we compared the genotypes of rs1360780 and rs9470080 with results of high-throughput genotyping (Illumina 550k Bead Chip, Illumina Inc., San Diego, CA, USA), which is available for these SNPs in a subsample of 169 respondents. 100% concordance in genotyping was observed.

SNP	Position ^a	Function	MDE			No MDE		
			HWpval	MAF	Call Rate	HWpval	MAF	Call Rate
rs3800373	35650454	3' UTR	0.185	0.27	99.37	0.024*	0.25	99.72
rs9296158	35675060	Intron	0.247	0.29	100.00	0.007*	0.28	100.00
rs1360780	35715549	Intron	0.163	0.28	100.00	0.013*	0.29	100.00
rs9470080	35754413	Intron	0.570	0.30	100.00	0.045*	0.32	100.00
rs4713916	35777961-8002	5' flanking (range inserting)	0.800	0.27	100.00	0.031*	0.30	99.86

a Chromosomal positions are given according to the March 2006 (hg18) human reference sequence database (NCBI Build 36.1) of the International Human Genome Sequencing Consortium;

* p < 0.05; for all SNPs: no significant deviation from HWE after Bonferroni-correction for multiple testing (5 SNPs* 2 populations).

Supplemental Online Table ST2. Associations between baseline adverse events and SNPs of the *FKBP5* gene. Presence of potential gene-environment correlations (rGE) were tested by evaluating the association between *FKBP5* polymorphisms and the exposure to adverse events. Associations at the nominal level of significance were almost exclusively found for rs4713916 with carriers of the major allele (AG/GG) being less frequently exposed to adverse events compared to non-carriers (AA). No effect withstood correction for multiple testing.

	Proportion of Respondents with Respective Adverse Event ^c among ...			<i>ab vs aa</i> OR (95%CI) ^a	<i>bb vs aa</i> OR (95%CI) ^a	<i>ab vs bb</i> OR (95%CI) ^a
	Subjects Homozygous for the Minor Allele 'aa'	Heterozygous Subjects 'ab'	Subjects Homozygous for the Major Allele 'bb'			
Lifetime adverse event until baseline	n (%) ^a	n (%) ^a	n (%) ^a			
rs3800373 (CC/CA/AA)^b						
<i>Any adverse event</i>	29 (40.3)	102 (33.4)	166 (32.9)	0.8 (0.46-1.36)	0.8 (0.45-1.28)	1.0 (0.76-1.41)
<i>Any separation event</i>	19 (26.4)	73 (23.9)	130 (25.8)	0.9 (0.51-1.68)	1.0 (0.57-1.78)	0.9 (0.65-1.29)
<i>Any trauma</i>	14 (19.4)	43 (14.1)	61 (12.1)	0.7 (0.37-1.46)	0.6 (0.31-1.17)	1.2 (0.79-1.87)
<i>Any severe trauma</i>	11 (15.3)	32 (10.5)	47 (9.3)	0.7 (0.33-1.49)	0.6 (0.29-1.23)	1.2 (0.72-1.90)
rs9296158 (AA/AG/GG)^b						
<i>Any adverse event</i>	38 (42.7)	102 (31.5)	158 (33.6)	0.7 (0.40-1.07)	0.7 (0.44-1.13)	0.9 (0.68-1.26)
<i>Any separation event</i>	26 (29.2)	74 (22.8)	123 (26.1)	0.8 (0.44-1.29)	0.9 (0.53-1.47)	0.9 (0.61-1.20)
<i>Any trauma</i>	18 (20.2)	41 (12.7)	59 (12.5)	0.6 (0.33-1.16)	0.6 (0.33-1.09)	1.0 (0.67-1.60)
<i>Any severe trauma</i>	15 (16.9)	29 (9.0)	46 (9.8)	0.5 (0.26-1.04)	0.6 (0.29-1.07)	0.9 (0.57-1.53)
rs1360780 (TT/CT/CC)^b						
<i>Any adverse event</i>	39 (43.3)	105 (32.1)	154 (33.0)	0.7 (0.40-1.06)	0.7 (0.41-1.07)	1.0 (0.72-1.33)
<i>Any separation event</i>	27 (30.0)	75 (22.9)	121 (25.9)	0.7 (0.43-1.24)	0.8 (0.51-1.39)	0.9 (0.62-1.22)
<i>Any trauma</i>	18 (20.0)	43 (13.2)	57 (12.2)	0.7 (0.35-1.22)	0.6 (0.32-1.06)	1.1 (0.72-1.72)
<i>Any severe trauma</i>	15 (16.7)	30 (9.2)	45 (9.6)	0.5 (0.27-1.07)	0.6 (0.29-1.06)	1.0 (0.59-1.60)
rs9470080 (TT/CT/CC)^b						
<i>Any adverse event</i>	41 (39.8)	112 (31.4)	145 (34.2)	0.7 (0.45-1.14)	0.8 (0.51-1.27)	0.9 (0.65-1.21)
<i>Any separation event</i>	29 (28.2)	81 (22.7)	113 (26.7)	0.8 (0.47-1.28)	0.9 (0.58-1.54)	0.8 (0.58-1.14)
<i>Any trauma</i>	20 (19.4)	45 (12.6)	53 (12.5)	0.6 (0.35-1.14)	0.6 (0.34-1.10)	1.0 (0.66-1.58)
<i>Any severe trauma</i>	17 (16.5)	32 (9.0)	41 (9.7)	0.5 (0.27-0.99)*	0.6 (0.30-1.04)	0.9 (0.57-1.53)
rs4713916 (AA/AG/GG)^b						
<i>Any adverse event</i>	39 (44.8)	109 (31.9)	150 (33.0)	0.6 (0.36-0.96)*	0.6 (0.38-0.99)*	1.0 (0.70-1.29)
<i>Any separation event</i>	29 (33.3)	79 (23.1)	115 (25.3)	0.6 (0.36-1.02)*	0.7 (0.41-1.13)	0.9 (0.64-1.24)
<i>Any trauma</i>	19 (21.8)	43 (12.6)	56 (12.3)	0.5 (0.28-0.97)*	0.5 (0.28-0.93)*	1.0 (0.67-1.58)
<i>Any severe trauma</i>	16 (18.4)	31 (9.1)	43 (9.5)	0.5 (0.23-0.88)*	0.5 (0.24-0.89)*	1.0 (0.59-1.57)

a "n (%)" = number and percentage of respondents; "OR" = odds ratio of a multiple logistic regression; "CI" = confidence interval;

b minor alleles: rs3800373: C; rs9296158: A; rs1360780: T; rs9470080: T; rs4713916: A;

c reference group: without the respective adverse event until baseline;

* p < 0.05 for an OR controlled for age and gender; no effect withstood correction for multiple testing.