Supporting Information

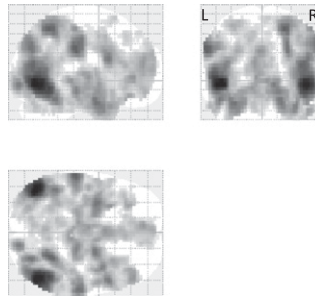## de Quervain et al. 10.1073/pnas.1200857109

Fig. S1. Genotype-independent, subsequent memory analysis for negative information, thresholded at $P < 0.05$, FDR corrected for whole brain. Sagittal, coronal, and axial SPM glass-brain projections are shown. L, left side of the brain; R, right side of the brain.

Table S1. Nominal significance of associated SNPs (negative pictures free recall, $P_{uncorrected} < 0.01$) in the hypothesis-testing sample ($n = 723$)

Affymetrix marker	Chromosome	Position	dbSNP RS ID	Associated gene	Cytoband	Call rate	MAF	HWE P	Association P
SNP_A-8703022	**17**	**62,209,616**	**rs4790904**	***PRKCA***	**q24.2**	**0.997**	**0.20**	**0.697077012**	**0.000002**
SNP_A-1995659	10	12,875,051	rs928337	*CAMK1D*	p13	1.000	0.41	0.353067038	0.00078
SNP_A-1995661	10	12,875,594	rs2493766	*CAMK1D*	p13	0.999	0.37	0.716531688	0.00081
SNP_A-1806035	10	12,887,844	rs4750267	*CAMK1D*	p13	0.997	0.37	0.80609225	0.0012
SNP_A-1936417	10	12,880,848	rs1556408	*CAMK1D*	p13	0.997	0.37	0.797212222	0.0013
SNP_A-8659980	10	12,891,662	rs12358381	*CAMK1D*	p13	1.000	0.27	0.049411446	0.0014
SNP_A-1985684	6	36,127,314	rs17714205	*MAPK14*	p21.31	0.997	0.13	0.524852836	0.0017
SNP_A-8281277	10	12,874,932	rs928336	*CAMK1D*	p13	0.994	0.43	0.170919012	0.0019
SNP_A-2111454	10	12,890,474	rs10906229	*CAMK1D*	p13	0.999	0.35	0.714469219	0.0020
SNP_A-2108498	6	36,184,912	rs3804452	*MAPK14*	p21.31	0.999	0.13	0.550959233	0.0024
SNP_A-2222070	17	62,147,088	rs16960114	*PRKCA*	q24.2	0.993	0.20	0.780677016	0.0028
SNP_A-8281665	10	12,876,558	rs1929389	*CAMK1D*	p13	1.000	0.43	0.18044124	0.0030
SNP_A-1816092	10	49,265,870	rs17697960	*MAPK8*	q11.22	1.000	0.11	0.148347676	0.0033
SNP_A-2000443	10	49,312,216	rs7086275	*MAPK8*	q11.22	0.999	0.42	0.628650983	0.0041
SNP_A-4248684	10	49,290,273	rs9888128	*MAPK8*	q11.22	1.000	0.43	0.729951509	0.0045
SNP_A-2000441	10	49,312,152	rs11101320	*MAPK8*	q11.22	0.994	0.42	0.661763446	0.0047
SNP_A-1781918	10	49,264,246	rs10857560	*MAPK8*	q11.22	0.999	0.43	0.395575993	0.0048
SNP_A-8637914	17	61,737,476	rs7210446	*PRKCA*	q24.2	0.990	0.44	0.87454757	0.0049
SNP_A-4229112	17	64,035,235	rs3785906	*PRKAR1A*	q24.2	1.000	0.23	0.815795241	0.0054
SNP_A-8550960	7	151,186,459	rs6961830	*PRKAG2*	q36.1	0.994	0.18	0.93078015	0.0056
SNP_A-1931100	10	12,872,599	rs4747999	*CAMK1D*	p13	1.000	0.41	0.250623163	0.0056
SNP_A-8470906	17	64,023,836	rs4281788	*PRKAR1A*	q24.2	0.999	0.23	0.770857219	0.0061
SNP_A-2163878	10	49,261,724	rs2698761	*MAPK8*	q11.22	1.000	0.43	0.747074632	0.0062
SNP_A-4222841	10	49,220,700	rs6537561	*MAPK8*	q11.22	1.000	0.43	0.864461361	0.0064
SNP_A-8676867	6	161,418,462	rs9458114	*MAP3K4*	q26	0.997	0.07	0.45633922	0.0077
SNP_A-4292124	10	6,539,234	rs4750491	*PRKCQ*	p15.1	0.994	0.34	0.052291675	0.0081
SNP_A-2146600	17	62,196,905	rs4381631	*PRKCA*	q24.2	0.999	0.47	0.596302414	0.0082
SNP_A-2055994	17	62,148,632	rs4465636	*PRKCA*	q24.2	0.994	0.20	0.584940644	0.0093
SNP_A-2237869	10	12,686,538	rs7906212	*CAMK1D*	p13	0.990	0.07	0.752773631	0.0095
SNP_A-8330608	17	61,738,935	rs4577128	*PRKCA*	q24.2	1.000	0.44	0.583248971	0.0096
SNP_A-8366935	6	161,338,632	rs625977	*MAP3K4*	q26	1.000	0.17	0.586805235	0.0099

Bonferroni-corrected SNPs are in boldface type. HWE, Hardy–Weinberg equilibrium; MAF, minor allele frequency; dbSNP RS, reference SNP sequence number according the National Center for Biotechnology Information SNP data base.

Table S2. Genotype-dependent differences in arousal and valence ratings (*n* = 716)

Genotype, rs4790904	Arousal negative pictures, mean ± SEM	Valence negative pictures, mean ± SEM
AA, *n* = 456	1.67 ± 0.02	2.78 ± 0.01
AG, *n* = 229	1.67 ± 0.02	2.79 ± 0.01
GG, *n* = 31	1.64 ± 0.07	2.76 ± 0.04
	P = 0.9	*P* = 0.8

Table S3. Genotype-dependent performance in the 0- and 2-back task (*n* = 678)

Genotype, rs4790904	Accuracy, 0-back, mean ± SEM	Accuracy, 2-back, mean ± SEM
AA, *n* = 428	0.964 ± 0.002	0.869 ± 0.005
AG, *n* = 219	0.962 ± 0.002	0.873 ± 0.006
GG, *n* = 31	0.971 ± 0.04	0.874 ± 0.016
	P = 0.9	*P* = 0.6

Table S4. Genotype-dependent memory performance (24-h delay) in the hypothesis-testing sample (*n* = 719)

Genotype, rs4790904	Negative pictures, mean ± SEM	Positive pictures, mean ± SEM	Neutral pictures, mean ± SEM	All pictures, mean ± SEM
AA, *n* = 456	7.7 ± 0.2	8.1 ± 0.2	4.8 ± 0.1	20.7 ± 0.4
AG, *n* = 231	7.0 ± 0.2	7.8 ± 0.2	4.2 ± 0.2	19.0 ± 0.5
GG, *n* = 32	5.6 ± 0.4	7.1 ± 0.4	3.7 ± 0.5	16.4 ± 0.8
	P = 0.0001	*P* = 0.07	*P* = 0.0006	*P* = 0.0004