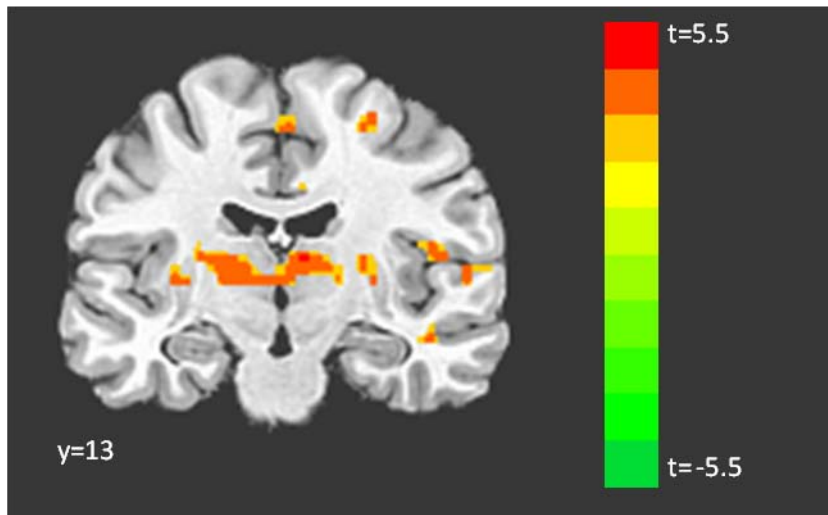


Supplementary Figure 1. Regions showing an effect of genotype in a whole brain t-test (SS > L carriers)^a



^aContrast displayed in neurological convention (left=left) at corrected $p < .05$, $t > 2.95$, color bar indicates t statistic. Coordinates for all regions showing an effect of genotype are displayed in Table 1.

Supplementary Table 1. Regions showing an effect of 5-HTTLPR genotype in a whole brain regression (SS > LS > LL)^a

Region	Side	BA	x	y	z	voxels	r
Thalamus (anterior nucleus)	L	-	-6.9	-3.0	4.8	81	0.50
Fusiform gyrus	L	-	-27.5	-61.4	-12.3	42	0.59
Putamen	L	-	20.6	-3.0	4.8	32	0.51
Middle temporal gyrus	R	21	44.7	-6.4	-12.3	28	0.50
Superior temporal gyrus	R	22	58.4	-44.2	8.3	25	0.47
Middle frontal gyrus	R	6	27.5	7.3	53.0	23	0.53
Medial frontal gyrus	R	10/32	6.9	52.0	1.4	19	0.47
Middle temporal gyrus	R	21	-55.0	-30.5	-2.0	17	0.53
Superior temporal gyrus	R	-	41.3	-33.9	1.4	17	0.52
Supramarginal gyrus	L	40	-55.0	-51.1	32.3	17	0.49
Middle frontal gyrus	L	6	-27.5	-6.4	53.0	15	0.47
Putamen	L	-	-20.6	14.2	1.4	14	0.53
Superior temporal gyrus	R	39	41.3	-54.5	25.5	13	0.53
Culmen	R	-	27.5	-47.7	-22.7	12	0.51
Caudate	R	-	13.8	14.2	4.8	12	0.45
Middle temporal gyrus	R	37	48.1	-47.7	-5.5	11	0.54
Superior temporal gyrus	L	38	-48.1	-7.3	-12.3	7	0.41
Amygdala	R	-	17.2	-3.0	-8.9	7	0.43
Precuneus	R	7	6.9	-47.7	53.0	7	0.52

^aAll clusters survived corrected $p < .05$, $t > 2.95$. Coordinates indicate the peak of the cluster. Asterisk indicates a region which was identified as a supra-cluster, and the sub-cluster peaks are listed directly below it.

Supplementary Table 2. Pairwise comparison of individual genotype groups^a

Region	LS vs LL		SS vs LL		SS vs LS	
	p	mean difference	p	mean difference	p	mean difference
Thalamus (anterior nucleus)	.503	0.02	<.001	0.16	<.001	0.14
Fusiform gyrus	.040	0.14	<.001	0.39	<.001	0.25
Putamen	.624	0.02	<.001	0.16	<.001	0.14
Middle temporal gyrus	.074	0.05	<.001	0.19	<.001	0.14
Superior temporal gyrus	.997	0.00	<.001	0.19	<.001	0.19
Middle frontal gyrus	.030	0.10	<.001	0.21	.005	0.11
Medial frontal gyrus	.154	0.09	<.001	0.29	.001	0.20
Middle temporal gyrus	.128	0.07	<.001	0.19	.002	0.12
Superior temporal gyrus	.116	0.04	<.001	0.12	.001	0.08
Supramarginal gyrus	.311	0.06	<.001	0.30	<.001	0.24
Middle frontal gyrus	.026	0.11	<.001	0.21	.026	0.10
Putamen	.527	0.03	.001	0.21	.001	0.18
Superior temporal gyrus	.399	0.03	<.001	0.16	.001	0.12
Culmen	.009	0.14	<.001	0.28	.006	0.14
Caudate	.244	0.06	.001	0.21	.003	0.15
Middle temporal gyrus	.025	0.09	<.001	0.23	<.001	0.14
Superior temporal gyrus	.337	0.04	<.001	0.22	<.001	0.18
Amygdala	.245	0.08	<.001	0.31	.001	0.22
Precuneus	.836	-0.01	<.001	0.12	<.001	0.13

^a p-value obtained from pairwise post-hoc comparisons after ANOVA. Table shows that the majority of clusters did not show significant differences between LL and LS individuals, whereas SS individuals were significantly different from both LL and LS individuals.

Supplementary Table 3. Beta values obtained from interaction analysis of 5-HTTLPR, brain activation and responses to the task

Brain Region	Neural ROI (β)	5HTTLPR genotype (β)	Interaction term (β)
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Outcome: Anxiety in response to task

Amygdala	-.146, p = .62	-.058, p = .75	.132, p = .64
BA9	-.207, p = .39	-.228, p = .20	.496, p = .04*
Left Insula	-.225, p = .20	.546, p = .03*	-.269, p = .28

Outcome: Success at regulating anxiety

Amygdala	-.327, p = .26	-.06, p = .72	.389, p = .17
BA9	-.082, p = .75	-.072, p = .70	.127, p = .62
Left Insula	.053, p = .75	-.754, p = .003**	.580, p = .017*

^a Functional clusters were obtained from SS > L carriers analysis. Interaction analyses examined amygdala (peak at x= 17, y=-3, z=-12), insula (peak at x=-31, y=-20, z=-15), dorsomedial prefrontal cortex (peak at x=-14, y=35, z=36).