

Supplementary Information

Emotion Recognition Task

Stimuli for the task were created using still images of three men and three women from the FACES database¹. All of the images were converted into grayscale and rescaled to a standard size using Adobe Photoshop CS4 (Adobe Systems Inc., San Jose, CA, USA) and Matlab 7.7 (MathWorks Inc., Natick, MA, USA). Overall brightness and contrast were also normalized for all images. To hide hair and background, an elliptical mask (411 x 570 pixels) was overlaid over each image.

Using WinMorph 3.01 (<http://www.debugmode/winmorph>), facial images of individuals displaying neutral expressions were morphed into images of the same individuals displaying full-intensity emotional expressions (happy, angry, fearful, and angry). In total, images of three men and three women were converted into stimuli for 24 test trials (6 individuals x 4 emotions). Each trial consisted of a sequence of 100 still images that appeared to participants as a dynamic emotional expression transitioning smoothly from 0% to 100% intensity over 8 seconds.

Images were presented on a grey background and a 20" monitor (30.6 x 40.8 cm, resolution 1024 x 768 pixels) at a viewing distance of 55 cm. Before the 24 test trials, participants completed four practice trials, for which images from the FACES database of another individual displaying the four target emotions were used. The test trials appeared in one of two pseudo-randomized testing orders. For each trial, reaction time and accuracy were recorded.

1. Ebner NC, Riediger M, Lindenberger U. FACES--a database of facial expressions in young, middle-aged, and older women and men: development and validation. *Behav Res Methods* 2010; **42**:351-62.

Supplementary Table 1: 23 SNPs across the *OXTR* gene region were analyzed. 10 were excluded from further analyses because of deviation from Hardy-Weinberg Equilibrium (cut-off $p < .05$; SNPs 3, 14, 15, 18, 19, 22, 23), minor allele frequency (MAF) below 5% (SNPs 4 & 20), or genotyping failure (SNP 8). SNPs included in the association test are shown in bold.

	rs number	chr position	Alleles	MAF	HWE p value	% Genotyped
1	rs237917	8812699	C/T	0.296	0.149	96.0
2	rs2268498	8812411	T/C	0.470	0.956	99.0
3	rs3806675	8811646	T/C	0.428	0.029	80.4
4	rs73132859	8811394	G/C	0.036	1.0	98.5
5	rs4564970	8810408	G/C	0.106	0.175	99.5
6	rs237897	8808285	G/A	0.432	0.317	100.0
7	rs2268495	8807535	G/A	0.216	0.783	100.0
8	rs237894	8806531	failed genotyping			
9	rs53576	8804371	G/A	0.36	0.528	99.0
10	rs13316193	8802743	T/C	0.389	0.894	100.0
11	rs237889	8802483	C/T	0.346	0.182	94.5
12	rs2254298	8802228	G/A	0.106	0.175	99.5
13	rs2268494	8802046	T/A	0.056	0.921	99.5
14	rs2268492	8800672	C/T	0.286	0.023	93.0
15	rs4686301	8798586	C/T	0.342	0.045	100.0
16	rs9840864	8798477	G/C	0.218	0.604	99.0
17	rs237887	8797042	A/G	0.379	0.116	99.5
18	rs11706648	8796547	A/C	0.36	0.007	93.5
19	rs237885	8795543	T/G	0.426	<.05	50.8
20	rs2139184	8795494	C/A	0.008	1.0	100.0
21	rs1042778	8794545	G/T	0.437	0.578	99.0
22	rs6770632	8793724	C/A	0.394	<.05	68.8
23	rs9872310	8793381	A/G	0.138	0.035	100.0

Supplementary Table 3: Global p-value, permutation corrected global p-value (shown in brackets), and individual p-values for haplotypes of sizes 5 to 2. p-values for individual SNPs are shown at the bottom of the table.

	Haplotype	Frequency	Chi ²	p
	rs237917 - rs2268498 - rs4564970 - rs237897 - rs2268495			
	Likelihood ratio $\chi^2 = 14.74$, df=5, global p-value = 0.012 (0.046)			
	C-C-G-A-G	0.356	6.984	0.008
	C-T-G-G-G	0.214	0.043	0.835
	T-T-G-G-A	0.156	3.127	0.077
	T-T-C-G-G	0.076	6.519	0.011
	C-C-G-G-A	0.067	0.908	0.341
	T-T-G-A-G	0.054	0.845	0.358
	rs2268498 - rs4564970 - rs237897 - rs2268495 – rs53576			
	Likelihood ratio $\chi^2 = 15.29$, df=6, global p-value = 0.018 (0.032)			
Window 5	C-G-A-G-A	0.279	7.845	0.005
	T-G-G-G-G	0.213	0.072	0.788
	T-G-G-A-G	0.156	2.831	0.092
	T-C-G-G-G	0.089	7.270	0.007
	C-G-A-G-G	0.076	0.115	0.734
	C-G-G-A-G	0.067	0.954	0.329
	T-G-A-G-A	0.061	0.542	0.462
	rs4564970 - rs237897 - rs2268495 – rs53576 – rs13316193			
	Likelihood ratio $\chi^2 = 17.14$, df=7, global p-value = 0.017 (0.043)			
	G-A-G-A-T	0.290	5.565	0.018
	G-G-A-G-C	0.164	1.739	0.183
	G-G-G-G-T	0.155	0.047	0.829
	G-G-G-G-C	0.091	0.344	0.557
	C-G-G-G-T	0.070	7.432	0.006
	G-G-A-G-T	0.057	3.389	0.066
	G-A-G-G-C	0.056	1.003	0.317

	Haplotype	Frequency	Chi ²	p
Window 4	rs2268498 - rs4564970 - rs237897 - rs2268495			
	Likelihood ratio $\chi^2 = 16.13$, df=5, global p-value = 0.006 (0.026)			
	C-G-A-G	0.355	7.842	0.005
	T-G-G-G	0.218	0.001	0.973
	T-G-G-A	0.155	2.626	0.105
	T-C-G-G	0.091	7.551	0.006
	C-G-G-A	0.067	0.952	0.329
	T-G-A-G	0.066	1.467	0.226
	rs4564970 - rs237897 - rs2268495 - rs53576			
	Likelihood ratio $\chi^2 = 14.83$, df=4, global p-value = 0.005 (0.031)			
	G-A-G-A	0.347	7.630	0.006
	G-G-G-G	0.241	0.061	0.804
G-G-A-G	0.217	4.136	0.041	
C-G-G-G	0.010	6.440	0.011	
G-A-G-G	0.082	0.488	0.485	
Window 3	rs237917 - rs2268498 - rs4564970			
	Likelihood ratio $\chi^2 = 9.90$, df=3, global p-value = 0.019 (0.021)			
	C-C-G	0.458	4.888	0.027
	C-T-G	0.227	0.295	0.587
	T-T-G	0.210	3.178	0.075
	T-T-C	0.082	5.299	0.021
	rs2268498 - rs4564970 - 237897			
	Likelihood ratio $\chi^2 = 14.40$, df=4, global p-value = 0.006 (0.030)			
	T-G-G	0.374	1.665	0.197
	C-G-A	0.356	7.450	0.006
	C-G-G	0.10	0.270	0.603

T-C-G	0.092	7.669	0.006
T-G-A	0.066	1.368	0.242

rs4564970 – rs237897 – rs2268495

Likelihood ratio $\chi^2 = 14.66$, df=3, global p-value = **0.002 (0.005)**

G-A-G	0.421	9.805	0.002
G-G-G	0.252	0.010	0.917
G-G-A	0.223	3.867	0.049
C-G-G	0.104	6.387	0.012

rs237897 – rs2268495 – rs53576

Likelihood ratio $\chi^2 = 10.01$ df=3, global p-value = **0.018 (0.023)**

G-G-G	0.344	1.866	0.170
A-G-A	0.341	7.610	0.006
G-A-G	0.223	4.104	0.043
A-G-G	0.080	0.500	0.481

rs2254298 – rs2268494 – rs9840864

Likelihood ratio $\chi^2 = 8.23$ df=3, global p-value = **0.042 (0.046)**

G-T-G	0.771	0.336	0.562
A-T-C	0.093	6.269	0.012
G-T-C	0.070	2.386	0.122
G-A-C	0.060	0.151	0.697

Window 2

Haplotype	Frequency	Chi ²	p
rs237917 - rs2268498			
Likelihood ratio $\chi^2 = 8.43$, df=2, global p-value = 0.015 (0.012)			
C-C	0.469	5.493	0.019
T-T	0.291	7.691	0.006
C-T	0.241	0.039	0.844

rs2268498 - rs4564970

Likelihood ratio $\chi^2 = 10.02$, df=2, global p-value = **0.007 (0.021)**

C-G	0.456	6.059	0.014
T-G	0.439	0.913	0.339
T-C	0.091	7.098	0.008

rs4564970 - rs237897

Likelihood ratio $\chi^2 = 12.87$, df=2, global p-value = **0.002 (0.007)**

G-G	0.474	2.400	0.121
G-A	0.421	9.805	0.002
C-G	0.104	6.387	0.012

rs237897 - rs2268495

Likelihood ratio $\chi^2 = 10.33$, df=2, global p-value = **0.006 (0.003)**

A-G	0.422	9.832	0.002
G-G	0.355	2.340	0.126
G-A	0.223	3.848	0.050

Single SNPs	rs number	MAF	Chi ²	p
	rs237917	0.296	7.026	0.008
	rs2268498	0.470	5.763	0.017
	rs4564970	0.106	9.832	0.002
	rs237897	0.432	3.863	0.049
	rs53576	0.216	5.980	0.014
	rs2254298	0.106	5.680	0.017