Supplementary Table 1. Goodness-of-fit statistics for alternative biometric models for psychoneurometric and DSM-IV diagnostic symptom composite variables.

Variable	model	df	-2LL	AIC	BIC (n adj)
THT $_{PsyNeuro}$	ACE	447	824.314	-69.686	-109.799
	AE [a,b]	**448**	**824.314**	**-71.686**	**-110.967**
	CE	448	829.264	-66.736	-108.492
	E	449	853.632	-44.386	-97.475
DIS $_{PsyNeuro}$	ACE	447	898.921	4.921	-72.496
	AE [a,b]	**448**	**899.055**	**3.055**	**-73.596**
	CE	448	911.081	15.081	-67.583
	E	449	986.241	88.241	-31.171
THT $_{PsyNeuro}$ x DIS $_{PsyNeuro}$	ACE	447	543.724	-350.276	-250.094
	AE [a,b]	**448**	**543.724**	**-352.276**	**-251.262**
	CE	448	546.092	-349.908	-250.078
	E	449	549.830	-348.170	-249.377
Distress Symptoms	ACE	464	-585.784	-1513.784	-836.562
	AE [a,b]	**465**	**-585.784**	**-1515.784**	**-837.734**
	CE	465	-582.750	-1512.750	-836.217
	E	466	-565.091	-1497.091	-828.559
Fear Symptoms	ACE	464	-694.277	-1622.277	-890.809
	AE [a,b]	**465**	**-694.277**	**-1624.277**	**-891.981**
	CE	465	-686.664	-1616.664	-888.174
	E	466	-667.353	-1599.353	-879.690
Substance Use Symptoms	ACE	464	-1208.750	-2136.750	-1148.045
	AE [a,b]	**465**	**-1208.612**	**-2138.612**	**-1149.148**
	CE	465	-1197.339	-2127.339	-1143.511
	E	466	-1142.951	-2074.951	-1117.489

Note. Biometric parameters were estimated for bolded models; *df* = degrees of freedom; *-2LL* = -2 times log-likelihood; *AIC* = Akaike's Information Criterion (χ^2 - 2*df*); *BIC (n adj)* = sample size adjusted Bayesian Information Criterion. THT $_{PsyNeuro}$ and DIS $_{PsyNeuro}$ = threat sensitivity and weak response inhibition assessed using neurophysiological and self-report indicators; THT $_{PsyNeuro}$ x DIS $_{PsyNeuro}$ = interaction term computed as the product of mean-centered scores for the two traits. Symptom variables reflect aggregates of symptom counts for Fear, Distress, and Substance Use disorders.

[a] The difference in goodness-of-fit between the full model (ACE) and reduced model (AE) did not reach significance, indicating the more parsimonious AE model was selected.

[b] The difference in goodness-of-fit between the E model and the full (ACE) or reduced (AE) model was significant, indicating that inclusion of the A path (reflecting a contribution of additive genetic influences) resulted in improved model fit ($p < .05$).