Table S1: Standardized variance components for Wave 2 processing speed measures

	Full Cholesky			Reduced Cholesky		
	a^2	c^2	e^2	a^2	c^2	e^2
Trails Number	.25 (.06, .37)	.04 (.00, .20)	.71 (.62, .80)	.26 (.09, .38)	.03 (.00, .18)	.71 (.62, .81)
Trails Letter	.34 (.11, .47)	.05 (.00, .24)	.61 (.53, .71)	.39 (.18, .48)	.00 (.00, .17)	.61 (.52, .70)
Stroop Word	.55 (.39, .63)	.02 (.00, .15)	.43 (.36, .50)	.57 (.50, .64)	.00	.43 (.36, .50)
Stroop Color	.46 (.26, .58)	.05 (.00, .23)	.48 (.41, .57)	.52 (.44, .59)	.00	.48 (.41, .56)
Reaction Time Left	.35 (.15, .45)	.02 (.00, .18)	.63 (.55, .72)	.37 (.27, .45)	.00	.63 (.55, .73)
Reaction Time Right	.28 (.08, .43)	.07 (.00, .25)	.65 (.56, .74)	.36 (.26, .44)	.00	.64 (.56, .74)

Reported values represent the proportion of measure variance accounted for by the genetic (a^2), common environmental (c^2), and unique environmental (e^2) influences with 95% Confidence Intervals. The a^2 term is the heritability of that measure.

Table S2: Wave 2 model comparisons

Model	-2LL	df	AIC	$\Delta\chi^2$	Δ df	p
Full Cholesky	16589	6702	3185	---	---	---
Reduced Cholesky	16592	6720	3151	2.24	18	1.0
Single Factor	17338.	6744	3850	746.3	24	<.0001
Correlated Factor	16614.	6737	3140	22.2	17	0.18
Higher Order	**16616**	**6739**	**3138**	**23.8**	**19**	**0.20**

The reduced Cholesky is compared to the full Cholesky. All other models are compared to the reduced Cholesky. –2LL = Negative Log-Likelihood; df = degrees of freedom; AIC = Akaike information criterion; $\Delta\chi^2$= likelihood ratio test (difference in -2LL between the model and its comparison model); Δdf = difference in df between the model and its comparison model. Best fitting model is shown in bold font.

Table S3: Correlations among processing speed measures at wave 2

Phenotypic	Trails Number	Trails Letter	Word Reading	Color Naming	Reaction Left
Trails Letter	.57 (.53, .61)				
Word Reading	.26 (.20, .32)	.32 (.26, .37)			
Color Naming	.31 (.26, .37)	.33 (.28, .39)	.64 (.61, .68)		
Reaction Left	.19 (.14, .25)	.16 (.10, .22)	.25 (.19, .31)	.26 (.20, .32)	
Reaction Right	.18 (.12, .23)	.19 (.13, .25)	.24 (.18, .29)	.23 (.17, .29)	.64 (.60, .67)
Genetic	**Trails Number**	**Trails Letter**	**Word Reading**	**Color Naming**	**Reaction Left**
Trails Letter	.98 (.77, 1.0)				
Word Reading	.27 (.08, .52)	.43 (.29, .65)			
Color Naming	.50 (.31, .85)	.53 (.39, .79)	.69 (.61, .76)		
Reaction Left	.29 (.05, .59)	.27 (.08, .50)	.41 (.26, .55)	.42 (.26, .57)	
Reaction Right	.97 (.77, 1.0)	.27 (.07, .49)	.37 (.22, .52)	.33 (.16. .49)	.93 (.83, 1.0)
Unique Environmental	**Trails Number**	**Trails Letter**	**Word Reading**	**Color Naming**	**Reaction Left**
Trails Letter	.41 (.32, .48)				
Word Reading	.28 (.18, .38)	.22 (.12, .32)			
Color Naming	.22 (.12, .32)	.17, (.07, .28)	.60 (.51, .66)		
Reaction Left	.16 (.06, .26)	.10 NS	.13 (.02, .23)	.14 (.03, .24)	
Reaction Right	.13 (.03, .23)	.15 (.05, .25)	.13 (.03, .24)	.15 (.05, .26)	.47 (.38, .54)

Phenotypic, genetic, and unique environmental correlations were derived from the reduced Cholesky. 95% confidence intervals are presented in the parentheses. NS=nonsignificant.

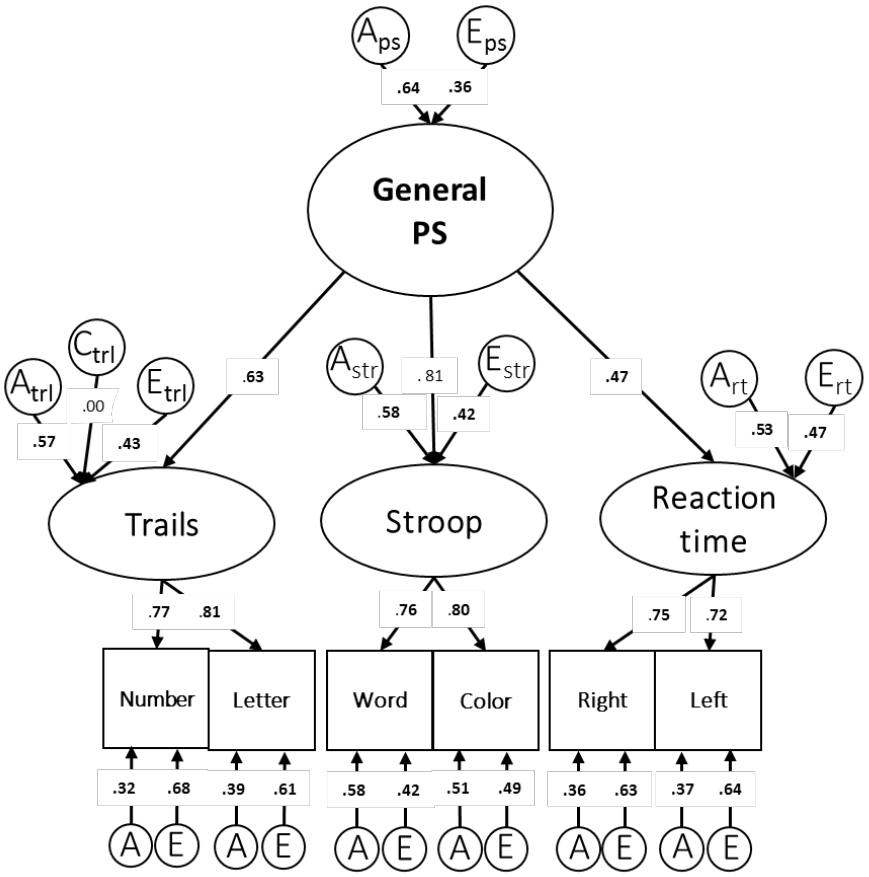

Figure S1: Wave 2 Higher Order Factor model. Standardized variance components are presented; "A" indicates the heritability of the related factor, "C" indicates the common environmental influences, and "E' indicates the unique environmental influences. As explained in the footnote above, the standardized

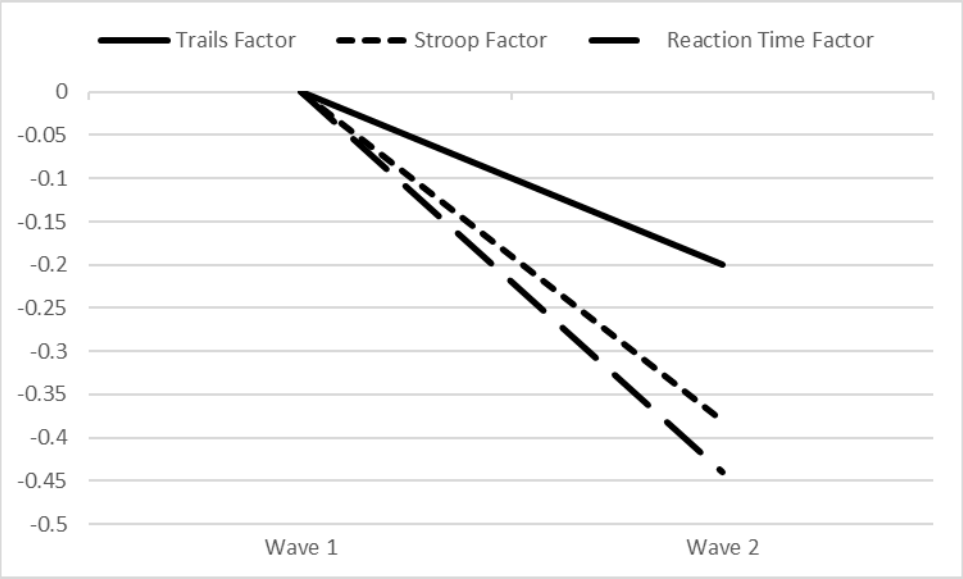

Figure S2: Change over time in test-specific factors. The Y-axis shows slowing in processing speed in standard deviation units. At wave 1, all test-specific factors were centered at 0 with a standard deviation of 1. The general PS factor is not shown as it followed the same trajectory as the Trails factor. The 95 percent confidence intervals of the general PS factor (-.20 SD; 95%CI [-.13, -.27]) and Trails factor (-.20 SD; 95%CI [-.14, -.27]). did not overlap with the confidence intervals of the Reaction time factor (-.38 SD; 95%CI [-.33, -.44]) or Stroop factor (-.44 SD; 95%CI [-.38, -.51]), indicating a significant difference in change. Participants had a mean age of 56 years at wave 1 and 62 years at wave 2.