

Supplemental Materials for

Genetic and Environmental Influences on Executive Functions and Intelligence in Middle  
Childhood

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**Supplemental Table 1***Descriptive Statistics for Cognitive Tasks Before Screening*

Measure	<i>n</i>	<i>M</i>	<i>SD</i>	Min	Max	Range	Skew	Kurtosis
Flanker	11712	94	9.14	51	116	65	-1	1.49
List	11669	96.64	12.09	36	136	100	-0.54	0.87
Card	11713	92.52	9.51	50	120	70	-0.82	2.04
Picture	11706	102.81	12.07	76	136	60	0.25	-0.4
NBack2	9468	0.71	0.17	0	1	1	-1.04	1.49
StroopRT	4848	75.55	64.1	-260.9	413.36	674.26	0.2	0.82
StroopACC	4849	-0.04	0.06	-1	0.25	1.25	-3.3	33.01
SST	9598	299.69	85.07	-692	702.69	1394.69	-1.23	9.5
PI	11597	-0.2	1.99	-9	7	16	-0.02	0.27
RI	11644	-1.55	2.14	-15	14	29	-0.54	4.6
MatrixR	11620	17.9	3.84	0	32	32	-0.4	0.8
PicVocab	11718	84.45	8.12	29	119	90	0.11	0.64

*Note.* Descriptive statistics for cognitive tasks before data screening. List = list sort; Card = card sort; Picture = picture sequence; NBack = accuracy on 2-back trials; StroopACC = Accuracy Diff Score = difference in accuracy between incongruent and congruent trials (incongruent trials - congruent trials); StroopRT = RT Diff Score = difference in reaction time (RT) between incongruent and congruent trials (incongruent trials - congruent trials); SST = stop signal RT, calculated by the mean “go” trial RT - the mean stop signal delay; RAVLT = Rey auditory verbal learning task; PI = proactive interference; RI = retroactive interference.; Matrix = matrix reasoning; PicVoc = picture vocabulary.

**Supplemental Table 2***Model Comparison Fit Statistics for Behavioral Genetic Models of Latent Variables*

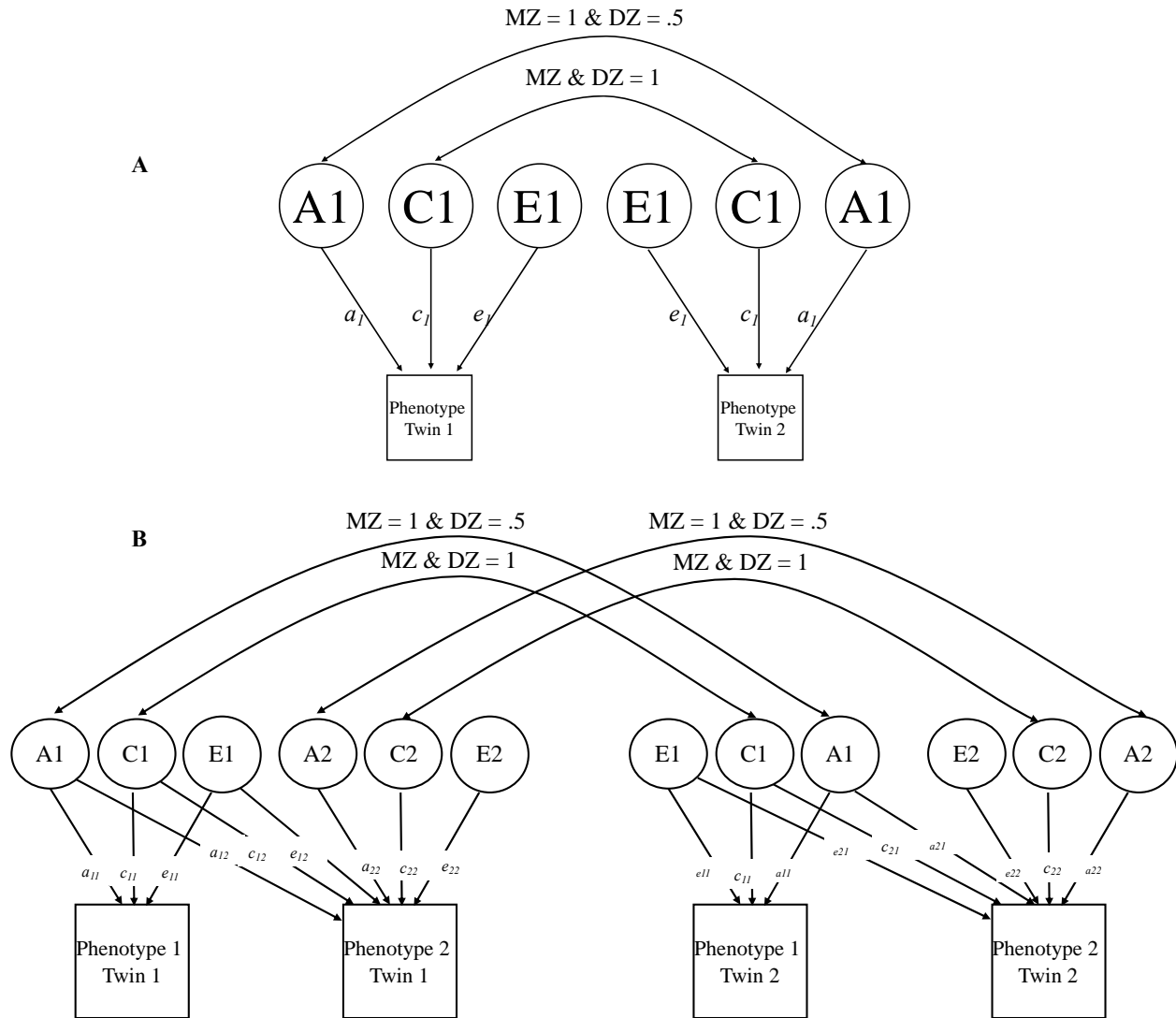
<b>Model</b>	$\chi^2$	<u>Model Fit</u>			<u>Model fit vs. full Model</u>			
		<i>df</i>	<i>p</i>	RMSEA	CFI	$\Delta\chi^2$	<i>df</i>	<i>p</i>
Full ACE: EF & UPD	185.75	100	< .001	.048	.872			
Without cEF	185.80	101	< .001	.047	.874	0.05	1	.823
Without eEF	197.45	101	< .001	.050	.860	11.70	1	.001
Without aEF	196.62	101	< .001	.050	.858	10.87	1	.001
Without aEF & cEF	250.77	102	< .001	.062	.779	65.02	2	< .001
Without cUPD	185.99	101	< .001	.047	.874	0.24	1	.625
Without eUPD	185.75	101	< .001	.047	.874	0.00	1	1.00
Without aUPD	185.99	101	< .001	.047	.874	0.24	1	.626
Without aUPD & cUPD	214.63	102	< .001	.054	.832	28.88	1	< .001
Full ACE: IQ	15.06	17	.591	.000	1.00			
Without cIQ	20.68	18	.296	.020	.994	5.62	1	.018
Without eIQ	15.07	18	.657	.000	1.00	0.01	1	.906
Without aIQ	21.74	18	.244	.024	.991	6.68	1	.010
Without aIQ & cIQ	133.25	19	< .001	.127	.738	118.19	2	< .001
Genetic Cholesky	283.44	190	< .001	.036	.930			
Without aEF to IQ	298.61	191	< .001	.040	.920	15.18	1	< .001
Without aUPD to IQ	284.82	191	< .001	.036	.933	1.38	1	.240
Without cEF to IQ	284.85	191	< .001	.036	.933	1.42	1	.234
Without cUPD to IQ	285.67	191	< .001	.036	.932	2.23	1	.135
Without eEF to IQ	283.45	191	< .001	.036	.930	0.01	1	.916
Without a&cEF to IQ	383.23	192	< .001	.052	.861	99.79	2	< .001

*Note.* A=additive genetic influences, C=shared environmental influences, E=nonshared

environmental influences. EF=Common EF, UPD=Updating-Specific, and IQ=latent IQ.

Indented models are nested within preceding non-indented models,  $\Delta\chi^2 p < .05$  indicates that a significant reduction in model fit and that a significant parameter was dropped from the model.

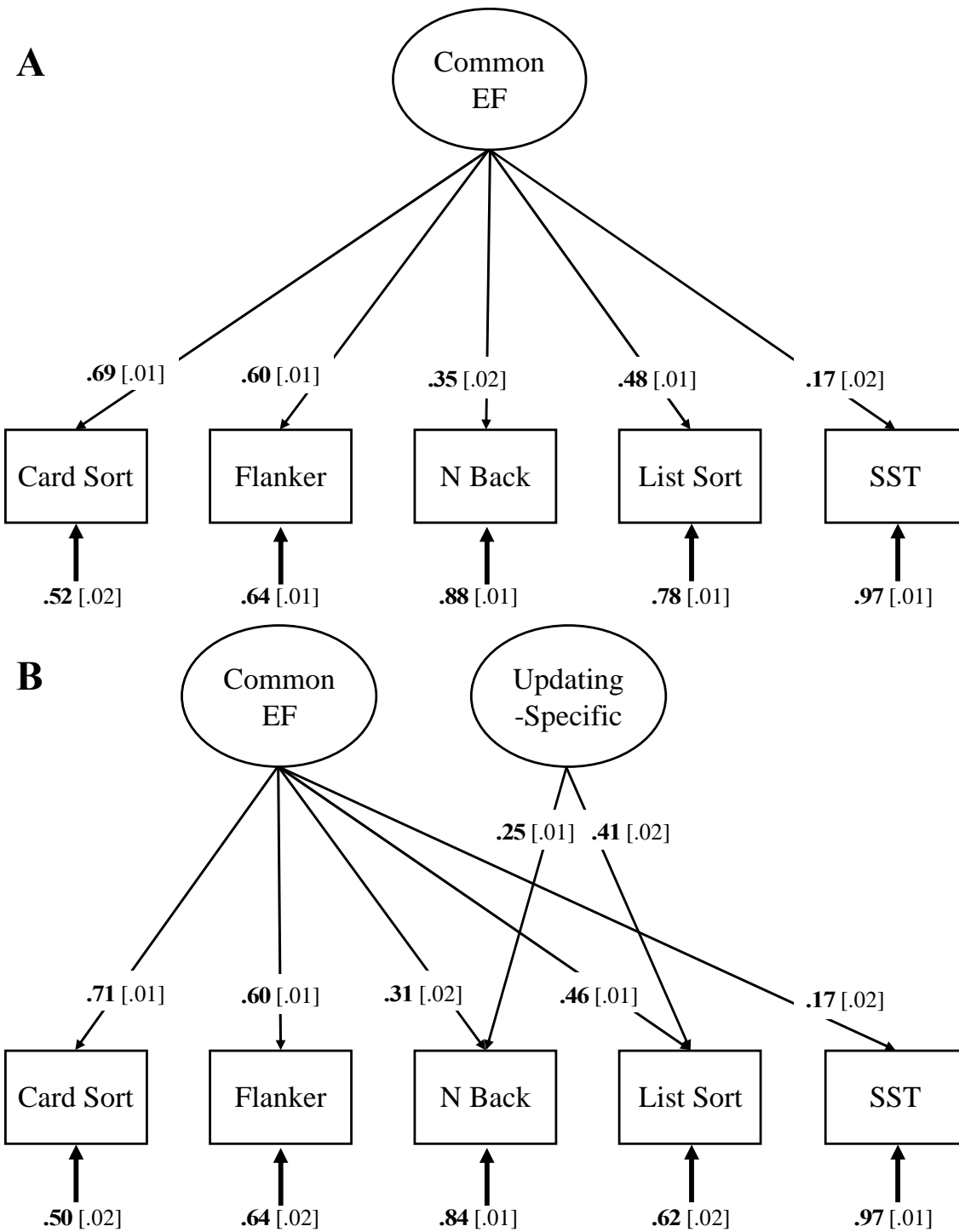
The genetic Cholesky decomposition was used to derive the genetic and environmental correlations of the EF and IQ latent variables. It did not contain a cross path from eUPD to eIQ because the E variance component for Updating-Specific EF was estimated at 0 in the EF model without IQ.



**Supplemental Figure 1.** Path diagrams for the univariate twin model (panel A) and the bivariate Cholesky decomposition (panel B). Each phenotype's variance is decomposed into three components: additive genetic (A), shared environmental (C, those that lead siblings to be more similar), and nonshared environmental (E, those that lead siblings to be uncorrelated). The correlations between the A variance components for twin 1 and twin 2 are fixed at 1 for MZ twins and .5 for DZ twins, reflecting the average proportion of shared segregating DNA for MZ and DZ twins. Because both MZ and DZ twins are reared together, the C variance components for twin 1 and twin 2 are correlated at 1 for both MZ and DZ twin pairs. Finally, the E variance

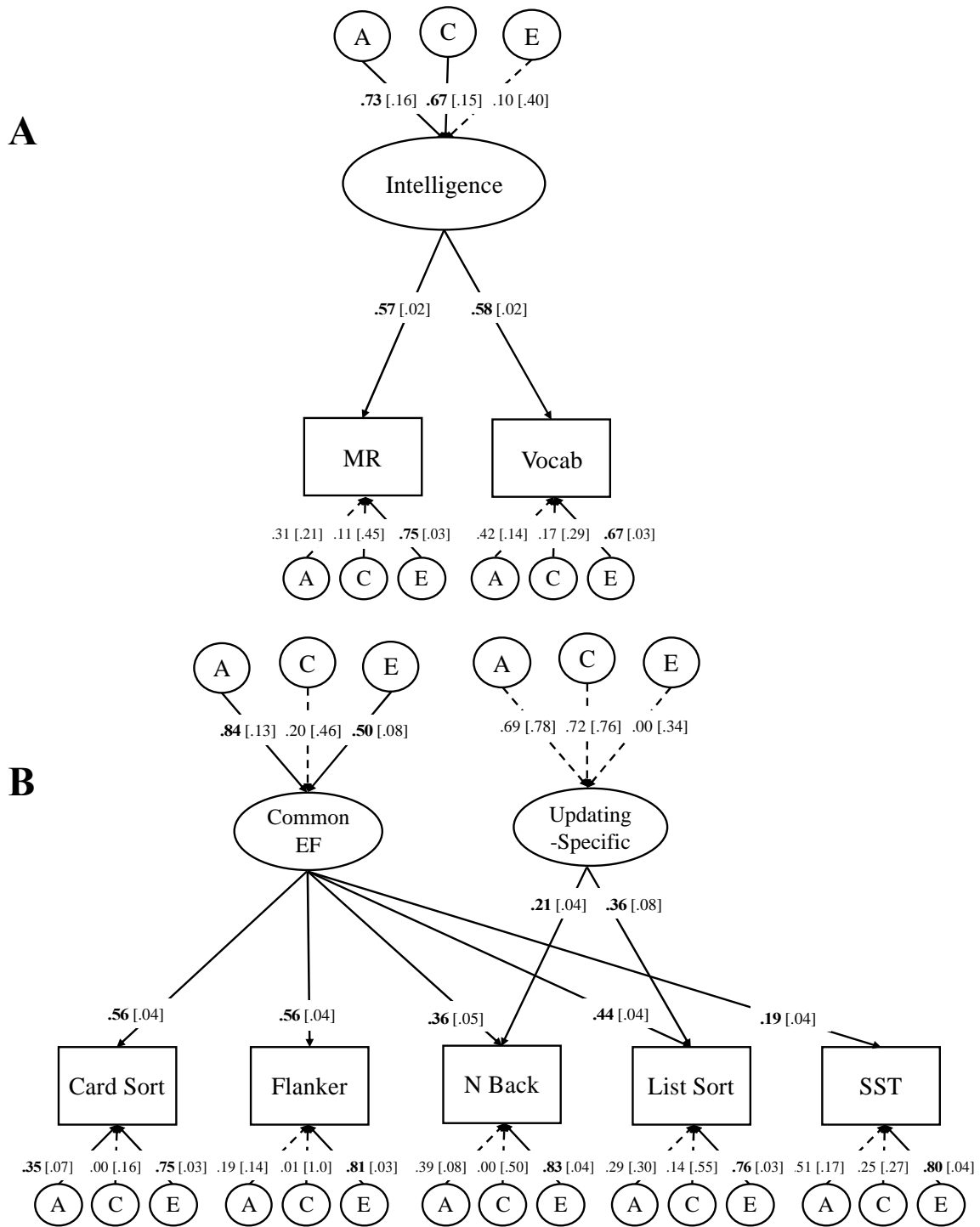
components are not correlated, as they represent environmental influences unique to each twin.

The lower-case italicized letters (*a*, *c*, *e*) are path coefficients. Squaring these estimates indicates the variance explained in the phenotype by A, C, or E, respectively. The use of the same subscripts indicates that the parameters are constrained to be equal across twin 1 and twin 2.



**Supplemental Figure 2.** Phenotypic factor models of executive functions (EFs). Ellipses indicate latent variables; rectangles indicate observed variables. Numbers on single-headed arrows indicate standardized factor loadings [standard errors]. Numbers at the ends of arrows are

residual variances. Double headed arrows between latent factors indicate correlations. Solid lines and boldface type indicate  $p < .05$ . Panel A depicts the path diagram of a unitary factor model of Common EF,  $\chi^2(5) = 123.52, p < .001, RMSEA = .045, CFI = .971$ . Panel B depicts the path diagram of the phenotypic factor model of Common EF and Updating-Specific ability,  $\chi^2(4) = 43.48, p < .001, RMSEA = .029, CFI = .990$ .



**Supplemental Figure 3.** Twin models of latent Common Executive Functioning (EF) and Updating-Specific variables,  $\chi^2(100) = 185.75, p < .001, RMSEA = .048, CFI = .872$  (panel A) and intelligence (IQ),  $\chi^2(17) = 15.06, p = .591, RMSEA = .000, CFI = 1.00$  (panel B). A



indicates additive genetic influences, C indicates shared environmental influences, and E indicates nonshared environmental influences. Solid lines and boldface type indicate  $p < .05$ ; dashed lines indicate  $p > .05$ , determined with chi-square difference tests for variance components.