





CORRECTION **OPEN**

Correction to: For whom the bell tolls: psychopathological and neurobiological correlates of a DNA methylation index of time-to-death

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Correction to: *Translational Psychiatry* <https://doi.org/10.1038/s41398-022-02164-w>, published online 24 September 2022

The original version of this article unfortunately contained some mistakes. The authors noticed formatting issues and errors in the tables. These are as follows:

- Table 1: Standard deviation for IL10 (NCPTSD column) should read “.26”, not “26”
- Table 2: NC-PTSD header misaligned

- Table 3: Formatting is misaligned (e.g., there are no results in the right columns)
- Covariates is spelled wrong
- Table 3 note refers to entering neuropsychological variables into second step, but it was GrimAge Residuals that were entered into second step
- Table 4: GFAP and NFL results are not in the correct row

The correct tables can be found below. The original article has been corrected.

Table 1. Participant characteristics and descriptive statistics.

Variable	NCPTSD (N = 647)		TRACTS (N = 434)	
	M (SD)	n (%)	M (SD)	n (%)
Demographics				
Sex (male)		407 (62.9)		392 (90.3)
Age	51.85 (10.60)		32.44 (8.63)	
Race				
White		525 (81.1)		322 (74.2)
Black/African American		80 (12.4)		37 (8.5)
Asian		8 (1.2)		6 (1.4)
American Indian/Alaska Native		57 (8.8)		3 (0.7)
Hawaiian/Other Pacific Islander		2 (0.3)		2 (0.5)
Unknown		38 (5.9)		2 (0.5)
Psychiatric				
Lifetime PTSD severity/Dx	60.12 (32.93)	389 (60.1)	69.00 (32.98)	351 (76.8)
# of Trauma types	9.90 (4.26)		1.95 (1.80)	
Lifetime AUD severity/Dx	8.03 (7.81)	376 (58.8)		286 (65.9)
Lifetime Non-AUD SUD severity/Dx	5.24 (9.53)	191 (29.7)		137 (31.6)
Lifetime ASPD severity/Dx	5.19 (5.80)	22 (4.8)		
Neuropsychological				
AGNG				11.56 (9.19)
Stroop ^b				26.59 (12.14)
CVLT-II ^c				48.33 (9.88)
Biological				
CRP (log)			-0.77 (0.29)	
GGT (log)			1.39 (0.24)	
WBC			6.28 (1.71)	
AB40 (log)			2.32 (0.07)	
AB42 (log)			0.91 (0.08)	
BDNF (log)	3.41 (0.38)		3.10 (0.47)	
GFAP (log)			1.79 (0.16)	
NFL (log)			0.72 (0.19)	
NSE (log)	4.32 (0.26)		4.07 (0.21)	
TAU4 (log)			0.16 (0.23)	
PNF (log)			1.41 (0.35)	
Eotaxin (log)			1.61 (0.14)	
IL10 (log)	-0.10 (26)		-0.16 (0.21)	
IL6 (log)	0.19 (0.31)		0.14 (0.27)	
TNF- α (log)	0.53 (0.20)		0.43 (0.13)	

NCPTSD National Center for PTSD cohort, TRACTS Translational Research Center for TBI and stress disorders cohort, M mean, SD standard deviation, PTSD posttraumatic stress disorder, dx diagnosis, CRP C-reactive protein, GGT gamma-glutamyl transferase, WBC total measured white blood cell counts, AGNG affective go/no-go task, CVLT-II California verbal learning test second edition, AB40/AB42 amyloid β 40/42, BDNF brain-derived neurotrophic factor, GFAP glial fibrillary acidic protein, NFL neurofilament light, NSE neuron-specific enolase, PNF phosphorylated neurofilament heavy, IL10/6 interleukin 6/10, TNF- α tumor necrosis factor.

^aRaw scores for total commission error = Total positive commissions + total negative commissions.

^bScaled scores adjusted for performance = Inhibition - (Color naming + Word reading)/2.

^cTotal words recalled across five learning trials.

Table 2. Psychopathology as a predictor of GrimAge residuals in both cohorts.

NCPTSD				
Variable	β	B	SE	p
Covariates:				
PC1	0.075	9.148	4.616	0.048
PC2	-0.023	-2.722	4.443	0.540
PC3	-0.003	-0.397	4.594	0.931
CD8-T	0.064	7.720	4.646	0.097
CD4-T	-0.038	-3.163	3.245	0.330
NK	-0.241	-23.402	3.566	<0.001
B-cell	-0.145	-16.815	4.304	<0.001
Monocytes	-0.044	-7.601	6.932	0.273
Sex	0.344	3.178	0.359	<0.001
Primary Predictors				
Externalizing Factor Score	0.345	0.351	0.044	<0.001
Distress Factor Score	-0.120	-0.178	0.095	0.062
Fear Factor Score	0.018	0.008	0.025	0.738
Lifetime PTSD Severity	0.056	0.008	0.006	0.215
TRACTS				
Variable	β	B	SE	p
Covariates:				
PC1	-0.186	-15.297	3.984	<0.001
PC2	0.022	2.064	4.485	<0.001
PC3	0.053	4.814	4.288	0.262
CD8-T	-0.233	-20.689	4.174	<0.001
CD4-T	-0.144	-9.883	3.346	0.003
NK	-0.238	-23.583	4.639	<0.001
B-cell	-0.051	-7.153	7.010	0.308
Monocytes	-0.108	-14.293	6.473	0.028
Sex	-0.150	-1.691	0.527	0.001
Primary Predictors:				
Lifetime AUD dx	0.077	0.541	0.339	0.112
Lifetime non-AUD SUD dx	0.104	0.747	0.339	0.028
Lifetime PTSD dx	0.149	1.165	1.220	0.001

Results based on hierarchical regression models with covariates entered into the first step and psychopathology variables entered in the second. The ΔR^2 coefficients were significant for the second step across models. *PC* Principal component, *CD* Cluster of differentiation, *NK* Natural killer, *PTSD* Posttraumatic stress disorder, *AUD* Alcohol use disorder, *SUD* Substance use disorder, *dx* Diagnosis, β Standardized beta, *B* Unstandardized beta *SE* Standard error for unstandardized beta.

Table 3. GrimAge residuals as a predictor of neuropsychological constructs.


Variable	AGNG			Stroop			CVLT-II		
	β	<i>p</i>	<i>p</i> _{adj}	β	<i>p</i>	<i>p</i> _{adj}	β	<i>p</i>	<i>p</i> _{adj}
Covariates									
Sex	0.011	0.835	–	–0.003	0.955	–	0.033	0.518	–
Age	0.006	0.901	–	–0.041	0.429	–	–0.171	0.001	–
Primary Predictor:									
GrimAge Residuals	0.136	0.007	0.021	0.052	0.318	.318	–0.122	0.015	0.023

Results based on hierarchical regression models with covariates entered into the first step and GrimAge Residuals entered in the second. ΔR^2 coefficients were significant for the second step across models with significant second step effects. *AGNG* Affective Go/No-Go Task, *CVLT-II* California Verbal Learning Test: Second edition, *PTSD* Posttraumatic stress disorder, *AUD* Alcohol use disorder, *MDD* Major depressive disorder, *p*_{adj} *p*-value adjusted for multiple testing by controlling the false discovery rate (FDR) of 5%.

Table 4. Associations between GrimAge residuals and metabolic, immune, and neurology markers.

Variable	TRACTS			NCPTSD		
	β	<i>p</i>	<i>p</i> _{adj}	β	<i>p</i>	<i>p</i> _{adj}
Metabolic, Immune, and Oxidative Stress						
MetS	0.139	<0.001	<0.001	–	–	–
WBC	0.324	<0.001	<0.001	–	–	–
GGT	0.161	0.001	0.003	–	–	–
Inflammatory Markers						
CRP	0.220	<0.001	<0.001	–	–	–
Eotaxin	0.108	0.026	0.059	–	–	–
IL10	0.072	0.165	0.264	0.049	0.281	0.281
IL6	0.286	<0.001	<0.001	0.341	<0.001	<0.001
TNF-alpha	0.077	0.135	0.240	0.156	<0.001	<0.001
Neurologic Markers						
GFAP	–0.132	0.008	0.021	–	–	–
NFL	–0.055	0.266	0.387	–	–	–
pNF	0.001	0.985	0.985	–	–	–
AB42	0.052	0.316	0.421	–	–	–
AB40	0.080	0.122	0.240	–	–	–
NSE	0.043	0.391	0.447	0.072	0.107	0.143
BDNF	0.043	0.386	0.447	0.071	0.114	0.143
Tau4	0.025	0.661	0.705	–	–	–

Results based on hierarchical regression models controlling for age and sex (covariate effects not shown for simplicity). The ΔR^2 coefficients were significant for the second step across models with significant second step effects. *MetS* Metabolic Syndrome, *WBC* Total measured white blood cell count, *GGT* Gamma-Glutamyl Transferase, *CRP* C-reactive protein, *IL10/IL6* Interleukin 10/6, *TNF-alpha* Tumor necrosis factor, *GFAP* Glial fibrillary acidic protein, *NFL* Neurofilament light, *pNF* Phosphorylated neurofilament heavy chain, *AB42/AB40* Amaloyd beta 40/42, *NSE* Neuron specific enolase, *BDNF* Brain derived neurotrophic factor, *p*_{adj} *p*-value adjusted for multiple testing by controlling the false discovery rate (FDR) of.

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