<COMP: Please publish these supplemental tables online only, with links to this material provided in the main text.>

Supplemental Table 1. Differences in self-reported symptom scores among the cognitive problems subgroups at enrollment (n = 199)

Symptom score	More Frequent n = 18	Persistent n = 28	Almost Never n = 153	Statistic	p-value and post hoc comparisons
			Mean (SD)		
POMS tension/anxiety[a]	7.8 (5.64)	11.5 (6.26)	6.5 (4.94)	$F(2,196) = 10.2$	$p < .001$; 2 > 1,3
POMS fatigue/inertia[b]	6.0 (14.00)	7.0 (11.75)	4.0 (5.00)	KW = 10.4	$p = .005$; 1 > 3
BDI-II[b]	7.0 (9.50)	6.0 (7.75)	3.0 (5.00)	KW = 19.7	$p < .001$; 1,2 > 3
PAOFI total[a]	26.6 (13.25)	33.4 (15.47)	13.8 (8.64)	$F(2,195) = 38.4$	$p < .001$; 1,2 > 3
Memory subscale[a]	10.2 (6.79)	11.6 (4.73)	6.2 (3.84)	$F(2,32.4) = 20.1$[c]	$p < .001$; 2 > 3
HLCIF subscale[b]	8.0 (8.50)	8.0 (8.00)	1.0 (3.00)	KW = 47.6	$p < .001$; 1,2 > 3
Language & communication subscale[b]	5.6 (5.00)	9.5 (7.13)	3.4 (4.69)	KW = 33.7	$p < .001$; 1,2 > 3
Use of hands & sensory-perceptual subscale[b]	3.0 (6.00)	2.5 (5.00)	1.0 (3.00)	KW = 15.9	$p < .001$; 1,2 > 3
			n (%)		
Pain (yes)	13 (72.2%)	16 (57.1%)	65 (42.5%)	$\chi^2 = 7.0$	$p = .030$; 1 > 3
Neuropathic symptoms (yes)	11 (61.1%)	12 (42.9%)	26 (17.0%)	FE	$p < .001$; 1,2 > 3

Abbreviations: SD, standard deviation; POMS, Profile of Mood States; KW, Kruskal-Wallis test; BDI-II, Beck Depression Inventory II; PAOFI, Patient Assessment of Own Functioning Inventory; HLCIF, Higher-Level Cognitive and Intellectual Functions; FE, Fisher's exact test.

[a]Although actual means and SDs are reported for each subgroup, analysis of variance was performed on the transformed variable due to its non-normal distribution.

[b]Medians and interquartile ranges are shown, and the non-parametric KW test was performed, for the untransformed variable due to its non-normal distribution after transformation.

[c]The Welch test was used due to a significant Levene statistic (p=.012).

Supplemental Table 2. Differences in cognitive domain z-scores among the three cognitive problems subgroups at enrollment (*n* = 199)

Cognitive domain z-score	More Frequent *n* = 18	Persistent *n* = 28	Almost Never *n* = 153	Statistic	p-value
			Mean (SD)		
Attention[a]	-0.59 (1.626)	-0.13 (1.200)	0.10 (1.209)	KW = 4.7	.098
Concentration[a]	0.18 (1.194)	0.08 (0.724)	0.09 (0.831)	KW = 0.7	.712
Mental flexibility[a]	0.00 (0.684)	-0.03 (1.109)	0.26 (0.994)	KW = 1.6	.448
Executive function	-0.13 (0.655)	-0.45 (0.590)	-0.20 (0.664)	F(2,196)=1.9	.151
Psychomotor speed[a]	-0.05 (1.078)	0.04 (1.019)	0.19 (1.097)	KW = 0.2	.920
Verbal memory	-0.26 (0.883)	-0.21 (0.634)	-0.05 (0.718)	F(2,196)=1.1	.323
Visual memory[a]	0.06 (0.780)	0.19 (0.671)	0.28 (0.512)	KW = 1.6	.455
Visual working memory[a]	0.03 (1.013)	0.24 (0.996)	-0.10 (1.139)	KW = 5.4	.066

SD = standard deviation; KW = Kruskal-Wallis test.

[a]Medians and interquartile ranges are shown, and the nonparametric KW test was performed, for the untransformed variable due to its non-normal distribution after transformation.

Supplemental Table 3. Differences in candidate gene single nucleotide polymorphism distributions among the three cognitive problems subgroups (n=199)

Gene	Variation	Chr	Chr Position[a]	Function	MAF[b]	Alleles	n	Statistic	*p*-value	Model[d]
DNA REPAIR										
PARP1	rs2271347	1	226361797	intronic	.142	G>A	197	FE	.541	A
PARP1	rs1136410	1	226367601	missense	.197	T>C	197	FE	.485	A
PARP1	rs3219090	1	226376990	intronic	.363[c]	G>A	175	FE	.588	A
PARP1	rs3219058	1	226385093	intronic	.255	G>A	199	FE	.590	A
ERCC3	rs2134794	2	127273303	intronic	.231	A>C	199	FE	.437	A
ERCC3	rs4150477	2	127274970	intronic	.379	C>T	199	FE	.570	A
ERCC3	rs4150407	2	127292055	intronic	.483	A>G	199	FE	.993	A
ERCC3	rs4150402	2	127292558	intronic	.175	G>A	198	FE	.759	A
ERCC5	rs751402	13	102845848	UTR-5	.311	C>T	197	FE	.990	A
ERCC5	rs2296147	13	102846025	UTR-5	.298	T>C	197	FE	.035	A
ERCC5	rs2296148	13	102846195	UTR-5	.071	C>T	189	FE	.285	A
ERCC5	rs4771436	13	102849670	intronic	.275	T>G	196	FE	.887	A
ERCC5	rs11069498	13	102850972	intronic	.420[c]	A>G	196	FE	.790	A
ERCC5	rs4150355	13	102870962	intronic	.245	C>T	199	FE	.453	A
ERCC5	rs4150360	13	102872412	intronic	.478[c]	T>C	199	FE	.537	A
ERCC5	rs873601	13	102875987	UTR-3	.451	A>G	196	$\chi^2 = 6.4$	.041	D
ERCC2	rs13181	19	45351661	missense	.237	T>G	199	FE	.433	A
ERCC2	rs1799787	19	45352886	nearGene-3	.182	C>T	199	FE	.723	A
ERCC2	rs3916874	19	45353668	intronic	.142	C>G	192	FE	.640	A
ERCC2	rs238416	19	45353791	intronic	.333	G>A	197	FE	.528	A
ERCC2	rs50872	19	45359191	intronic	.183	C>T	196	FE	.992	A
ERCC2	rs50871	19	45359257	intronic	.465[c]	G>T	198	FE	.246	A
ERCC2	rs1799786	19	45364780	intronic	.194	C>T	170	FE	.411	A
ERCC2	rs238406	19	45365051	cds-synon	.364	G>T	194	FE	.788	A
OXIDATIVE STRESS										
GPX1	rs1050450	3	49357401	missense; UTR-3	.218	G>A	187	FE	.369	A

Gene	Variation	Chr	Chr Position[a]	Function	MAF[b]	Alleles	n	Statistic	*p*-value	Model[d]
SEPP1	rs3877899	5	42801166	missense	.173	G>A	190	FE	.151	A
SEPP1	rs230819	5	42805863	intronic	.494	A>C	191	FE	.131	A
SEPP1	rs28919892	5	42809206	intronic	.243	T>C	197	FE	.220	A
SOD2	rs8031	6	159679608	intronic	.367	A>T	199	FE	.128	A
SOD2	rs5746136	6	159682052	UTR-3	.306	G>A	198	FE	.170	A
SOD2	rs4880	6	159692840	missense	.411	T>C	194	FE	.197	A
CAT	rs769214	11	34438170	nearGene-5	.473	A>G	195	FE	.033	R
CAT	rs1001179	11	34438684	nearGene-5	.126	G>A	169	FE	.554	A
CAT	rs525938	11	34442046	intronic	.438	A>G	197	FE	.207	A
CAT	rs2179625	11	34445599	intronic	.224	T>G	198	FE	.813	A
CAT	rs511895	11	34466182	intronic	.193	G>A	195	FE	.181	A
CAT	rs10488736	11	34467705	intronic	.359	C>T	198	FE	.516	A
CAT	rs566979	11	34469100	intronic	.489	T>G	199	FE	.528	A
SOD1	rs1041740	21	31667849	intronic	.243	C>T	194	FE	.989	A

Abbreviations: Chr, chromosome; MAF, minor allele frequency; PARP1, poly(ADP-ribose) polymerase 1; FE, Fisher's exact test; A, additive model; ERCC2, ERCC excision repair 2, TFIIH core complex helicase subunit; cds-synon, synonymous change; nearGene-3, within 3 prime 500 base pairs to gene; R, recessive model; ERCC3, ERCC excision repair 3, TFIIH core complex helicase subunit; ERCC5, ERCC excision repair 5, endonuclease; UTR-5, 5 prime untranslated region; D, dominant model; UTR-3, 3 prime untranslated region; CAT, catalase; nearGene-5, within 5 prime 2000 base pairs of gene; SEPP1, selenoprotein P, plasma, 1; SOD1, superoxide dismutase 1, soluble; SOD2, superoxide dismutase 2, mitochondrial; GPX1, glutathione peroxidase 1.

[a]Chromosome position is reported using the GRCh38.p2 assembly in dbSNP.
[b]Unless otherwise noted, MAFs are reported from the 1000 Genomes Project.
[c]CEU MAF reported.
[d]We selected the genetic model that best fit the data by maximizing the significance of the p value when a significant difference in minor allele frequency was found.