Table HIV dementia hazard ratios for CPE score, HIV-CAUSAL collaboration, 1998–2013

	Person-years		No. of events		Unadjusted hazard ratio (95% CI)		IPW-adjusted hazard ratio (95% CI)	
CPE score	Overall	Excluding efavirenz	Overall	Excluding efavirenz	Overall	Excluding efavirenz	Overall	Excluding efavirenz
Low	140,962	82,323	127	95	1.00 (Reference)	1.00 (Reference)	1.00 (Reference)	1.00 (Reference)
Medium	86,799	46,219	72	46	0.97 (0.72, 1.30)	0.98 (0.68, 1.40)	1.01 (0.73, 1.39)	1.04 (0.72, 1.50)
High	32,097	28,930	36	34	1.55 (1.06, 2.26)	1.33 (0.89, 1.98)	1.74 (1.15, 2.65)	1.80 (1.10, 2.95)

Abbreviations: CI = confidence interval; CPE = CNS penetration effectiveness; IPW = inverse probability weighting.

symptoms or neuropsychiatric issues. Efavirenz is commonly used as part of the regimens with low and medium CPE scores. However, an analysis that excludes individuals initiating a regimen with efavirenz does not materially affect our results (table). We agree with Beardsley and Le that future studies are needed to examine the effect of CNS penetration on the incidence of HIV dementia.

1. Caniglia EC, Cain LE, Justice A, et al. Antiretroviral penetration into the CNS and incidence of AIDS-defining neurologic conditions. Neurology 2014;83:134–141.
2. Berger JR, Clifford DB. The relationship of CPE to HIV dementia: slain by an ugly fact? Neurology 2014;83:109–110.
3. World Health Organization. March 2014 supplement to the 2013 consolidated guidelines on the use of antiretroviral drugs for treating and preventing HIV infection. Available at: www.who.int/hiv/pub/guidelines/arv2013/arvs2013upplement_march2014/en/. Accessed July 22, 2014.

CORRECTION

Novel *CLN3* mutation causing autophagic vacuolar myopathy

In the article "Novel *CLN3* mutation causing autophagic vacuolar myopathy" by A. Cortese et al. (*Neurology*® 2014;82:2072–2076), there is an error in the Results regarding the *ASPHD1* variant. The *ASPHD1* variant should have been described as a duplication: c.513_515dup resulting in p.(Gly172dup), which might retain some functionality (this is a known issue with the software used to annotate the variants in the whole exome sequencing data). The authors regret the error.

Author disclosures are available upon request (journal@neurology.org).