# 6660187

We used the ssizeRNA R package to calculate power (p) across samples (n) at an FDR of 0.05.60 Important parameters for ssize RNA include the variability (dispersions for the samples and genes), which were calculated directly from our EiaD length scaled TPM values by the edgeR packages estimateCommonDisp and estimateTagwiseDisp. The code to calculate the power is given as â€˜power\_calc.R.'

# 6639890

In accordance with the study by Cooper et al.,[4] who reported adequate sedation during TEE in 90.9% using Dex and 64.4% with midazolam and considering an Î± type error of 0.05 and study power of 80%, we calculated our sample size to be 35 patients in each group (http://www.stat.ubc.ca/~rollin/stats/ssize/b2.html). Initially, 70 patients were enrolled in the study; however, because 2 patients declined to participate in the study, a total of 68 patients were finally randomized in Dex (n = 34) and propofol (n = 34) groups using online randomization software (http://www.graphpad.com/quickcalcs/randomize2/). The patientsâ€™ allocation list was referred to a 3rd person and was concealed from the researchers. In the propofol group, one patient did not receive sedation due to an unplanned change in the patient's examination by the echocardiographer, and in two patients propofol was discontinued because of difficult TEE probe insertion. In the Dex group, all 34 patients finished the study, and they were entered into the statistical analyses [Figure 1]. This study was single-blinded, with only the patients being unaware of drug allocation for their sedation.

# 6555531

Male Syrian golden hamsters 6â€“8 weeks-old were used for vaccination studies. Sample size was calculated using two sample inference for comparing two means (https://www.stat.ubc.ca/~rollin/stats/ssize/n2.html) [25]. A sample size of n = 9 was selected on the assumption of a vaccine trial resulting in a mean of 40 worms per hamster for Î¼1 (adjuvant control) and 25 worms per hamster for Î¼2 (test group), Ïƒ = 11, two-sided test, with Î± = 0.05 and power of 0.80. A total of 45 hamsters were divided into 5 groups (9 hamsters/group) including 1) vaccinated with 10 Î¼g of Ov-EVs, 2) vaccinated with 50 Î¼g of rOv-LEL-TSP-2, 3) vaccinated with 50 Î¼g of rOv-LEL-TSP-3, 4) vaccinated with 50 Î¼g of rOv-LEL-TSP-2 plus 50 Î¼g of rOv-LEL-TSP-3. Both EVs and recombinant proteins were formulated with an equal volume of a colloidal suspension of aluminium hydroxide gel (alum) (Invivogen, USA) and CpG ODN 1826 (10 Î¼g) (Invivogen, USA). A fifth group of hamsters were injected with 10 Î¼g of alum/CpG only (adjuvant control group) as a control group. Vaccines were injected intraperitoneally on days 0, 14 and 28; and hamsters were challenged with 50 metacercariae via the oral route on day 42 (2 weeks after last vaccination). Hamsters were finally sacrificed at 8 weeks post-challenge. Blood was collected for serum by heart puncture after euthanasia and bile was collected from the gall bladder. Whole livers were collected to investigate the number of flukes.

# 6511655

Direct, indirect and total effects of various exposures on pre- and postoperative eGFRAnalysis performed assuming a direct causal path between tumor size and postoperative eGFRDirect effectsIndirect effectsTotal effectsÎ² (95% CI)Î² (95% CI)Î² (95% CI)Preoperative eGFRâ€ƒCharlson comorbidity indexâˆ’0.5 (âˆ’2.1, 1.0)-âˆ’0.5 (âˆ’2.1, 1.0)â€ƒAge (years)âˆ’0.9 (âˆ’1.0, âˆ’0.8)0.0 (âˆ’0.1, 0.1) aâˆ’0.9 (âˆ’1.0, âˆ’0.8)â€ƒTumor Ssize (cm)âˆ’1.0 (âˆ’1.4, âˆ’0.6)-âˆ’1.0 (âˆ’1.4, âˆ’0.6)Postoperative eGFRâ€ƒCharlson comorbidity indexâˆ’1.7 (âˆ’2.9, âˆ’0.5)âˆ’0.2 (âˆ’1.0, 0.5) bâˆ’1.9 (âˆ’3.4, âˆ’0.5)â€ƒAge (years)âˆ’0.2 (âˆ’0.3, âˆ’0.1)âˆ’0.4 (âˆ’0.5, âˆ’0.4) câˆ’0.7 (âˆ’0.8, âˆ’0.6)â€ƒTumor size (cm)1.0 (0.6, 1.3)âˆ’0.5 (âˆ’0.7, âˆ’0.3) d0.5 (0.1, 0.9)â€ƒPreoperative eGFR0.5 (0.4, 0.5)-0.5 (0.4, 0.5)Analysis performed assuming no direct causal path between tumor size and postoperative eGFRDirect effectsIndirect effectsTotal effectsÎ² (95% CI)Î² (95% CI)Î² (95% CI)Preoperative eGFRâ€ƒCharlson comorbidity indexâˆ’0.4 (âˆ’1.8, 1.0)-âˆ’0.4 (âˆ’1.8, 1.0)â€ƒAge (years)âˆ’0.9 (âˆ’1.0, âˆ’0.6)0.0 (âˆ’0.1, 0.1) aâˆ’0.9 (âˆ’1.3, âˆ’0.6)â€ƒTumor size (cm)âˆ’0.9 (âˆ’1.3, âˆ’0.6)-âˆ’0.9 (âˆ’1.3, âˆ’0.6)Postoperative eGFRâ€ƒCharlson comorbidity indexâˆ’1.7 (âˆ’2.8, âˆ’0.6)âˆ’0.2 (âˆ’0.8, 0.5) bâˆ’1.9 (âˆ’3.2, âˆ’0.6)â€ƒAge (years)âˆ’0.2 (âˆ’0.4, âˆ’0.2)âˆ’0.4 (âˆ’0.5, âˆ’0.3) câˆ’0.7 (âˆ’0.8, âˆ’0.6)â€ƒTumor size (cm)-âˆ’0.4 (âˆ’0.6, âˆ’0.2) dâˆ’0.4 (âˆ’0.6, âˆ’0.2)â€ƒPreoperative eGFR0.4 (0.4, 0.5)-0.4 (0.4, 0.5)

# 6498921

To calculate the sample size and to compare the mean difference in SEI scores between the 2 groups, a pilot study was first done on 10 subjects. The mean decrease in SEI score in the tacrolimus group was 1.8 and, in the dexamethasone, group was 1.5, respectively. The common SD was 0.4. Assuming 1:1 randomization, 90% power (alpha = 0.05), and a precision error of 5% to detect difference of 20% or more in SEI score between 2 groups, the estimated sample size in each group was calculated to be 38 (https://www.stat.ubc.ca/~rollin/stats/ssize/n1.html).

# 6450625

Male B6.Cg-Spp1tm1Blh/J (Spp1-/-) mice (OPN deficient mice) and C57BL/6J (wt) were both from Jackson Laboratory (Sacramento, CA) and the mice were fed irradiated HFD (60 kcal% fat, D12492i, Research Diets, New Brunswick, NJ) or irradiated LFD (10 kcal% fat, D12450Bi, Research Diets) from the age of 7 weeks for 16 weeks. The number of animals per group was determined by power calculation (wt mice on LFD: n = 24, wt mice on HFD: n = 26, Spp1-/- mice on HFD: n = 19). For the power calculation to determine group size, the online tool available at http://www.stat.ubc.ca/~rollin/stats/ssize/n2.html, employing a 2 sided test was used with data from previous experiments.

# 6445081

Pooled CSF samples were made up from de-identified remaining aliquots from clinical routine analyses. After one freezing cycle, samples were thawed for 1â€‰hour to obtain room temperature, pooled, and then aliquoted and stored at âˆ’80â€‰Â°C. This procedure is approved by the Ethics Committee at University of Gothenburg (EPN 140811). These aliquots were used as quality control (QC) samples in the study, but also for the method development and structural studies. For the clinical study, CSF samples were obtained from 20 AD patients [9 men; mean (SD) age: 64 (5) years] and 20 healthy non-AD control individuals [9 men; 61 (7) years]. The AD patients were obtained from the memory clinic at the Sahlgrenska University Hospital, MÃ¶lndal. Informed consent was obtained from all patients and controls of the study. AD was diagnosed according to the NINCDS-ADRDA criteria39. The clinical procedures have been described previously40. The AD diagnoses were evaluated by two independent specialized physicians that were blinded to the results of CSF biomarkers, but had full access to other clinical data. More specifically, an AD diagnosis was established if the patient fulfilled general dementia criteria and in addition had no or mild white matter changes on magnetic resonance imaging and predominant parietotemporal lobe symptoms, i.e. episodic memory loss and difficulties in interpreting sensory information. If the two evaluators had different opinions, the patient was discussed until a consensus decision could be made in terms of the diagnosis. Healthy controls were recruited through senior citizen organizations, e.g., at information meetings on dementia, and a small proportion are relatives of patients. To be regarded as healthy, the controls should not experience or exhibit any cognitive decline at the time of inclusion in the study. The study was approved by the ethical committee at the University of Gothenburg. The study was conducted according to the Declaration of Helsinki. To estimate the required number of CSF samples to be used, a power analysis was performed via the web-tool at the University of British Columbia homepage (https://www.stat.ubc.ca/~rollin/stats/ssize/n2.html).

# 6459539

The sample size required for comparing two populations was calculated using a web-based sample size calculator designed by the University of British Columbia, Canada (https://www.stat.ubc.ca/~rollin/stats/ssize/b2.html). Since no studies were conducted previously in these selected areas, based on local knowledge, we assumed that 30% and 40% of the cattle owners would have knowledge and awareness about rabies in the eastern and southern areas, respectively. With a confidence level of 95% and the statistical power of 80%, 562 cattle owners (281 from each study area) were required to be selected and interviewed. Twenty-five villages from Phuentsholing and Samphelling, and all the 12 villages from Kanglung sub-district were selected for this study.

# 6333381

The sample size was calculated on the basis that the rate of HIV status disclosure to children in Malawi may be either high or low. In a recent study conducted in Kenya, Vreeman and colleagues [18] reported disclosure rates among children of 12 and 14 years of age of 44 per cent and 62 per cent, respectively. We used a sample size calculator developed by Rollin Bryant, https://www.stat.ubc.ca/~rollin/stats/ssize/b2.html. This sample size calculating formula was based on the estimation of sample size and power for comparing two binomial proportions in Bernard Rosner's Fundamentals of Biostatistics [19]. A sample size of 320 was required to provide 90 per cent power to detect a difference in the prevalence of HIV disclosure between different age groups, with a 5 per cent chance that a significant difference was due to chance [19]. Assuming a response rate of 75 per cent, approximately 427 potential participants were approached to participate in the survey.

# 6304442

Firstly, 100 high-quality grains (plump grains with undamaged awns and hulls) were randomly chosen from each population for trait measurements. The grain length (GL), seed (hulled grain) length (SL) and seed width (SW) were measured with a digital caliper. Because the awn is an important accessory structure of seed and can affect the activity of seed dispersal, the awn length (AL) was also measured. From these measurements, the seed size (Ssize = SL Ã— SW), seed shape (Sshape = SL/SW) and awn-length/grain-length ratio (AGL) were calculated. Then, another 100 grains were randomly selected from the mixed seed pool of each population. They were oven-dried and weighed (M100grain). Then, they were hulled and weighed to obtain the weight of 100 seeds (M100seed). This procedure was repeated three times to avoid biases, and the mean value was recorded.

All seed characteristics varied greatly and showed significant differences among the 15 populations except for AGL (Table 2, and also seeSupporting Informationâ€”Table S2). The seed width (SW) ranged from 0.98 mm (HLJYC) to 1.51 mm (JXJX), which was negatively correlated with latitude (R = âˆ’0.827, P < 0.01), and the seed length (SL) ranged from 8.03 mm (HLJYC) to 11.30 mm (LNSY). As expected, the estimated Ssize and Sshape were significantly correlated with latitude (Rsize = âˆ’0.630, Rshape = 0.767, P < 0.05) as well. M100grain ranged from 0.83 g (HLJYC) to 1.73 g (JXJX), with a mean value of 1.44 g. The average value of M100seed was 1.13 g, and it ranged from 0.57 g (HJLYC) to 1.50 g (JXJX) among the populations. As a function of M100grain and M100seed, SPR was significantly correlated with latitude (R = 0.739, P < 0.01), with a mean value of 0.22. The populations located at high latitudes showed relatively high SPRs. WC was also associated with latitude (R = 0.610, P < 0.05), with a mean value of 0.23 and a range from 0.09 (JSBY) to 0.46 (JLDH). The grain length (GL) ranged from 28.98 mm (HLJYC) to 45.84 mm (HBHH). The corresponding awn length (AL) ranged from 16.78 mm (HLJYC) to 28.87 mm (HBHH). AGL showed no significant difference among populations, with a mean value of 0.60, indicating a constant ratio between AL and GL.Table 2.

The measured seed traits and estimated parameters of 15 Zizania latifolia populations, SEs were shown in brackets. GL, grain length; AL, awn length; AGL, AL/GL; SW, seed width; SL, seed length; Sshape, SL/SW; Ssize, SL Ã— SW; M100grain, the weight of 100 grains; M100seed, the weight of 100 seeds; SPR, seed-pericarp ratio; WC, relative water content. The superior labelled letters indicate significant differences according to multiple comparisons followed by LSD tests.PopulationGL (mm)AL (mm)AGLSW (mm)SL (mm)SshapeSsizeM100grain (g)M100seed (g)SPRWCHLJYC28.98a (4.59)16.78a (3.62)0.58 (0.05)0.98a (0.10)8.03a (1.21)8.20a (1.07)7.86a (1.80)0.83a (0.02)0.57a (0.02)0.32a (0.02)0.25a (0.03)HLJMDJ45.32b (5.02)26.77b (3.31)0.59 (0.02)1.14b (0.13)10.73b (1.69)9.45b (1.33)12.19b (2.75)1.64b (0.09)1.13b (0.10)0.31a (0.04)0.31b (0.04)JLDH41.41c (7.50)25.70b (6.20)0.62 (0.04)1.14b (0.12)10.13c (1.01)8.92ab (1.48)11.51bd (1.48)1.42c (0.09)1.03c (0.07)0.27b (0.01)0.46c (0.05)LNSY44.80b (6.61)27.25b (5.32)0.61 (0.04)1.25c (0.09)11.30d (0.82)9.06ab (0.77)14.10c (1.68)1.62b (0.02)1.25d (0.05)0.23c (0.02)0.34b (0.04)BJHD39.76cd (5.27)21.61c (3.57)0.54 (0.03)1.07c (0.14)9.66c (1.00)9.04a (1.02)10.33b (2.11)1.17d (0.02)0.85bc (0.03)0.28b (0.01)0.26a (0.03)SDTZ44.60b (5.77)26.69b (3.97)0.60 (0.04)1.35d (0.12)10.16c (0.76)7.50ac (0.80)13.77c (1.71)1.45cd (0.04)1.08bc (0.04)0.25bc (0.01)0.20a (0.03)JSSQ40.08cd (8.85)25.26b (7.23)0.63 (0.05)1.31cd (0.16)9.03e (0.99)6.91c (0.52)11.78b (2.57)1.29e (0.03)0.90e (0.05)0.30ab (0.02)0.16d (0.01)JSBY40.04cd (5.44)23.54c (3.90)0.59 (0.05)1.31cd (0.14)10.45bc (1.07)7.97a (0.60)13.70c (2.54)1.52d (0.08)1.23d (0.08)0.19d (0.01)0.09e (0.01)HBWH38.00d (6.26)23.44c (4.99)0.62 (0.04)1.21c (0.25)8.74e (0.97)7.22abc (1.34)10.57d (2.74)1.13f (0.03)0.90e (0.02)0.20d (0.01)0.35b (0.04)AHAQ34.10e (6.87)20.39c (5.61)0.60 (0.06)1.41d (0.15)9.70c (1.09)6.90c (0.98)13.63c (2.35)1.31e (0.03)1.21bd (0.02)0.07e (0.01)0.14d (0.02)HBJZ41.83c (5.91)25.92b (4.37)0.62 (0.03)1.37d (0.11)10.67b (0.83)7.81a (0.82)14.57c (1.65)1.58bd (0.05)1.35f (0.07)0.15f (0.02)0.17d (0.01)HBJY33.64e (3.96)19.90c (3.34)0.59 (0.04)1.39d (0.10)10.07c (0.69)7.22c (0.56)14.04c (1.69)1.50cd (0.05)1.27df (0.03)0.16f (0.00)0.18d (0.02)HBHH45.84b (7.85)28.87b (6.17)0.63 (0.03)1.42d (0.10)10.24bc (0.98)7.23c (0.75)14.49c (1.92)1.63b (0.03)1.36f (0.04)0.16f (0.01)0.19d (0.02)JXDA45.78b (5.54)28.35b (5.04)0.62 (0.05)1.26c (0.11)9.77c (0.68)7.76a (0.71)12.30b (1.58)1.37ce (0.05)1.02c (0.03)0.26bc (0.01)0.12f (0.01)JXJX38.33cd (5.75)23.56c (4.47)0.61 (0.04)1.51e (0.14)9.74c (0.98)6.46c (0.78)14.68c (2.33)1.73g (0.05)1.50g (0.06)0.14f (0.02)0.16d (0.02)Mean40.08 (5.01)24.26 (3.42)0.60 (0.04)1.29 (0.13)9.93 (0.83)7.78(0.86)12.80(1.85)1.44(0.23)1.13(0.23)0.22(0.07)0.23(0.03)

A PCA on the seed traits showed that the first two principal components accounted for 79.59 % of the total variance [seeSupporting Informationâ€”Table S3]. PC1, which explained 50.52 % of the total variance, had its high loadings for SW, Ssize, M100grain and M100seed; Sshape greatly determined PC2, which contributed to 29.07 % of the total variance. A scatterplot of PC1 scores against PC2 scores showed that the morphological variation of the northernmost population HLJYC is distinct [seeSupporting Informationâ€”Fig. S2].

The correlations between the seed characteristics and the first two principal climate components showed that SW, Sshape, Ssize, SPR and WC were significantly correlated with PC1clim [seeSupporting Informationâ€”Table S5]. Multiple regression analyses further indicated that SW was negatively affected by Temperature Seasonality (bio4) (R = âˆ’0.800, P < 0.01); Sshape was positively impacted by the Mean Diurnal Range (bio2) (R = 0.733, P < 0.01); Ssize was significantly correlated with the Mean Temperature of Warmest Quarter (bio10) (R = 0.646, P < 0.01); SPR decreased with increased Annual Precipitation (bio12) (R = âˆ’0.711, P < 0.01); and WC was negatively correlated with the Mean Temperature of Driest Quarter (bio9) (R = âˆ’0.648, P < 0.01) (Fig. 3).

The variations of seed characteristics were significantly correlated with the climatic variables: (A) seed width (SW) vs. Temperature Seasonality (bio4); (B) seed shape (Sshape) vs. Mean Diurnal Range (bio2); (C) seed size (Ssize) vs. Mean Temperature of Warmest Quarter (bio10); (D) seed-pericarp ratio (SPR) vs. Annual Precipitation (bio12); (E) relative water content (WC) vs. Mean Temperature of Driest Quarter (bio9).

Latitude is a proxy for many climatic variables. For instance, the latitudinal gradient was proved to cause local environment changes that could lead to corresponding phenotypic variations in seeds (Boulli et al. 2001; Murray et al. 2003; Daws et al. 2006; Cochrane et al. 2015). It is now well established that local climatic variables can be associated with a number of seed traits, including seed size (Daws and Jensen 2011), desiccation tolerance (Daws et al. 2004) and longevity (Kochanek et al. 2010). Though the relative contribution of genetic differentiation and phenotypic plasticity on the variations of seed traits was yet to be clarified, our results indicated that Z. latifolia tended to produce relatively larger seeds with lower moisture content and lower investments in seed pericarp at lower latitudes. These variation trends in seed characteristics offered opportunities to screen out a batch of individuals with ideal seed traits during the neo-domestication. Multiple regression analyses further indicated that seed width (SW), seed size (Ssize), seed shape (Sshape), seed-pericarp ratio (SPR) and relative water content (WC) were significantly correlated with climatic variables (Fig. 3), which could not only imply the ecological significances for variations in seed characteristics, but also could be taken as references when artificially modifying a particular seed trait.

Seed size often varies among plant species, populations and individuals (Westoby et al. 1992; Moles et al. 2005). From a macroevolutionary perspective, interspecific seed size tends to increase towards the equator, showing a latitudinal trend (Baskin and Baskin 2014). We found a similar pattern in Z. latifolia populations. The seed size (Ssize) of Z. latifolia was negatively correlated with latitude and positively correlated with the Mean Temperature of Warmest Quarter (bio10). Moles and Westoby (2003) suggested that the length of the growing period might positively affect seed size because longer growing seasons provide more time for carbon accumulation, which could be an explanation for this phenomenon. However, our findings were contrary to the knowledge about among-population variations in seed size that usually increased with latitude (Cochrane et al. 2015). The genus Zizania was reported to originate in North America and then dispersed into eastern Asia via the land bridge, which meant that the distribution range of Z. latifolia had expanded from north to south (Xu et al. 2008, 2010). Actually, the populations of Z. latifolia in the Yangtze River Basin were adjacent to the speciesâ€™ southern edge. Our results may support the view that natural selection favours larger seeds towards the geographic limit (Metz et al. 2010). The ecological and evolutionary significance underlying the latitudinal seed size variance of Z. latifolia should be soundly investigated in future. Nevertheless, the populations at lower latitudes produced larger seeds, which could be predominant in grain crop domestication.

There are abundant variations in the seed characteristics among Z. latifolia populations along a latitudinal gradient. Among the measured seed traits, SW, Sshape, Ssize, SPR and WC were significantly associated with climatic variables. In general, Z. latifolia produces larger seeds with lower moisture content and lower investments in seed pericarp at lower latitudes. The low germination percentage and strong dormancy of seed may be potential obstacles for neo-domestication as a grain crop. A prominent genetic structure was found in Z. latifolia populations, which could be mainly attributed to IBD. This study provided fundamental information on morphological and genetic variations in Z. latifolia populations. Nevertheless, more researches on deciphering the genetic basis of important domestication traits are still needed to promote the neo-domestication of Z. latifolia.

# 6416033

Station houses (firefighters) and police headquarters (police officers) were identified in 10 cities in the suburban areas of Boston, Massachusetts and Phoenix, Arizona and these cities were randomized to 12 months in the intervention and control group via a computerized randomization program. The study was designed to detect a 5â€Šmg/dL increase in Î±1 HDL in the treatment group versus the control group with 80% statistical power and a significance level (alpha) of 0.05. The 12-month improvement in alpha1 should be at least 5â€Šmg/dL greater in the treatment group than the control group (eg, 5â€Šmg/dL vs 0â€Šmg/dL). The standard deviation of that change is estimated to be 6.0â€Šmg/dL for the combined group (about 8â€Šmg/dL for the treatment group and 4â€Šmg/dL for the control group). Sample size calculations indicate we need 46 participants to complete the trial (eg. 23 intervention, 23 control) to achieve 80% power to find a significant difference (Pâ€Š<â€Š0.05) between intervention and control. Sample size calculator used for these calculations: http://stat.ubc.ca/âˆ¼rollin/stats/ssize/n2.html

# 6223832

bThe detection power (1â€‰âˆ’â€‰Î²) was calculated using the online tool at https://www.stat.ubc.ca/~rollin/stats/ssize/n2.html with Î± (type I error rate) at 0.05

# 6220373

1https://www.stat.ubc.ca/rollin/stats/ssize/n2.html

# 6271315

Thyroid gland size was expressed as a ratio comparing thyroid size to the zygomatic salivary gland using the following formula:T:Ssize ratio:Number of pixels in thyroidROINumber of pixels in salivaryROI

# 6191930

Differential gene expression (DGE) analysis was applied to detect relationships between distinct maternal diagnoses and UCB gene expression levels using the limma package (Ritchie et al., 2015). The covariates maternal tobacco use, maternal alcohol use, RIN, batch, biological sex, gestational age, mode of delivery and ethnicity were included in all models to adjust for their potential confounding influence on UCB gene expression between main group effects, and the significance threshold was a nominal P-valueâ€¯<â€¯0.05. This P-value threshold was used to yield a sufficient number of genes to include within functional annotation and gene network analyses, described below. Power and sample size was estimated using the R package ssize.fdr (Orr and Liu, 2015).

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# 6536278

The study sample size was determined using a free online sample size calculator from Department of Statistics, Faculty of Science, The University of British Columbia, Vancouver, Canada (available at: http://www.stat.ubc.ca/~rollin/stats/ssize/n2.html). According to data from a pilot study (10), it is estimated that at least 26 subjects would be needed in each of the groups, with ?Î± level p=0.05 and the test power adjusted to 90%, to detect a statistically significant difference between the two groups (if it exists). Statistical analysis was performed using IBM SPSS Statistics 20 by the person blinded to group allocation. Discrete data were compared using ?Ï‡2-test and Fisher exact test. The normality of distribution of continuous data was assessed using Kolmogorov-Smirnov test. Ordinal data and continuous data that were not normally distributed were expressed as median and range. Mann-Whitney test was used to compare data differences between the two groups. Normally distributed continuous data were expressed as arithmetic mean and standard deviation (SD) or standard error of the mean (SEM). These data were compared using 2-factor analysis of variance with repeated measures on 1 factor, with least significant difference (LSD) method of post hoc analysis. The level of statistical significance of the observed differences was set at p<0.05.

# 6162092

We analyzed the sequences and occurrence patterns of the TCRs belonging to these 78 clusters in order to assess their potential biological significance and prioritize them for further study (Table 3). Each cluster was assigned two scores (Figure 6): a size score (Ssize, x-axis), reflecting the significance of seeing a cluster of that size given the total number of TCRs clustered for its associated allele, and a co-occurrence score (ZCO, y-axis), reflecting the degree to which the TCRs in that cluster co-occur within its allele-positive cohort subset (see Materials and methods). In computing the co-occurrence score, we defined a subset of individuals with an apparent enrichment for the member TCRs in each cluster; the size of this enriched subset of subjects is given in the â€˜Subjectsâ€™ column in Table 3. We rank ordered the 78 clusters based on the sum of their size and co-occurrence scores (weighted to equalize dynamic range); the top five clusters are presented in greater detail in Figure 7 and Figure 8. HLA associations, member TCR and enriched subject counts, cluster center TCR sequences, scores, and annotations for all 78 clusters are given in Table 3.

Each point represents one of the 78 significant HLA-restricted TCR clusters, plotted based on a normalized cluster size score (Ssize, x-axis) and an aggregate TCR co-occurrence score for the member TCRs (ZCO, y-axis). Markers are colored by the locus of the restricting HLA allele and sized based on the strength of the association between cluster member TCRs and the HLA allele. The database annotations associated to TCRs in each cluster are summarized with text labels using the following abbreviations: B19Â =Â parvovirus B19, INFÂ =Â influenza, EBVÂ =Â Epstein Barr Virus, RAÂ =Â rheumatoid arthritis, MSÂ =Â multiple sclerosis, MELAÂ =Â melanoma, T1DÂ =Â type one diabetes, CMVÂ =Â cytomegalovirus. Clusters labeled â€˜coCMVâ€™ are significantly associated (P<1Ã—10âˆ’5) with CMV seropositivity (see main text discussion of cluster #3). Clusters labeled 1â€“5 are discussed in the text and examined in greater detail in Figure 7 and Figure 8.Figure 6â€”source data 1.Paired TCRÎ± chain sequences from the pairSEQ dataset of (Howie et al., 2015) for all clusters with at least 2 matched TCRÎ² chains, along with a score for each cluster that assesses the degree of sequence similarity among the partner chains.Click here to view.(8.2K, tds)

Clusters 3â€“5; see preceding legend for details.Table 3.HLA-restricted TCR clusters with size (Ssize) and co-occurrence (ZCO) scores, annotations (abbreviated as in Figure 6), and validation scores.RankHLA alleleAllele frequencyTCRsSubjectsCluster center

We used this co-occurrence score ZCO together with a log-transformed version of the cluster size p-value,Ssize=âˆ’log10â¡(Psize)

for visualizing clustering results in Figure 6 (Ssize on the x-axis and ZCO on the y-axis) and prioritizing individual clusters for detailed follow-up.

# 6223127

There are dozens of power and sample size calculations available in R (Supplementary File 9), but they are scattered among dozens of different package libraries: samplesize, ssize.fdr, pwr, powerpkg, powerAnalysis, powerbydesign, Sample.Size, samplesize4surveys, etc. There are also basic power and sample size functions in the default stats library. Often specific power and sample size libraries will address specific types of statistical tests and experimental designs, while other libraries may be more general. Several examples are shown using the functions power.t.test() and power.anova.test() in Supplementary file 9.

In the first examples, the power.t.test() is used to calculate 3 single estimates for sample size, power and delta. Then power.t.test() is used to compute 9 estimates of sample size (Fig. 6d), power (Fig. 6e) and delta (Fig. 6f) to plot some basic power and sample size curves. Likewise, in the second series of examples, the power.anova.test() function is used to calculate 3 single estimates of sample size (Fig. 6g), power (Fig. 6h) and delta (Fig. 6i), before multiple sequences of estimates are calculated and plotted. Finally, ssize.twoSampVary() from the ssize.fdr package library is used to calculate power estimates for a typical gene expression microarray analysis (Fig. 6j).

# 6139626

Power analyses should be done during the experimental design process to estimate the sample size needed to detect a difference that is scientifically important (27). Sample sizes that are too large wastes resources, whereas sample sizes that are too low are subject to false negative results (type II error). There is also a balance between theoretically ideal and practically feasible that needs to be considered when designing experiments. There are a number of online calculators for power analysis that are easy to use, including http://powerandsamplesize.com/, http://clincalc.com/stats/samplesize.aspx, and https://www.stat.ubc.ca/~rollin/stats/ssize/n2.html. The main assumption of the power analysis is that the data involve random sampling. Two other considerations are 1) the power analysis is performed a priori to set a preplanned sample size and 2) the effect size is the smallest of interest rather than a preobserved value. A more indepth discussion of power, including bias that occurs when small sample pilot studies are used to estimate the expected effect size in prospective power analysis, is beyond the scope of this article (2).

# 6082457

This was calculated with the sample size calculator of the Department of Statistics, University of British Columbia, Canada, available online (http://www.stat.ubc.ca/~rollin/stats/ssize/b2.html).

# 6041520

The Statistical Package for Social Science version15.0 software (SPSS, Chicago, IL., USA) was used to conduct the statistical analyses. Anthropometric and scar features were categorized as categorical variables or continuous variables. Comparisons between the groups were made using the Studentâ€™st-test or Mann- Whitney U test as appropriate. Categorical variables were compared using the Ï‡2 test or Fisherâ€™s exact test as appropriate. One Way Anovaand Kruskal- Wallis variance analysis were used for multi- group comparison of continuous variables. If the differences were significant, pair â€“wise comparisons would be based on the Mann-Whitney U-test or Bonferroni correction to establish which subgroups were different. All of the reported p-values were two-tailed, and those less than 0.05 were considered to be statistically significant. The statistical program on the website of the statistical department of the University of British Colombia was used to calculate the sample size and the power of our study (https://www.stat.ubc.ca/~rollin/stats/ssize/b1.html). According to SG status, the inclusion of 45 patients in each study group with 80% confidence interval and p <0.05 significance level was calculated as sufficient for the sample size of our study.

# 5980571

Sample size calculations were performed using online resources (OpenEpi, Atlanta, Georgia; http://www.stat.ubc.ca/~rollin/stats/ssize/b2.html) to determine the number of students needed per group (students with access to the training course and students who were not given access to the training course) to detect a significant difference in DOGiBAT quiz score with training. Pilot data was utilized from 10 untrained veterinary students who scored 3 cases (cluster size 30) with a baseline correct response rate of 75%. Using independent samples, an alphaâ€‰=â€‰0.05 and 80% power, the required sample size to detect a significant difference (defined as a 20% increase in number of correct scores) between the 2 groups was calculated. When sample sizes were adjusted for clustering by students (ie, each student answered multiple questions), and assuming an intraclass correlation of 0.75, the required sample size was determined to be 35 students in the trained group and 35 students in the untrained group.

# 5885166

Most studies estimate that the mean time from onset of PD to dementia is 10 years,22 and that up to 80% of patients with PD develop dementia during the disease course.20 Therefore, predicting imminent risk may be more informative. Accordingly, the MoPaRDS was assessed for a mean (SD) of 4.4 (1.4) years and can also be used to predict annual dementia conversion rates during this time. In clinical practice, it may be most useful to divide the scale into 3 groups; low risk indicates that the development of short-term dementia is extremely unlikely (0.6% per year), high risk indicates a need for intensive surveillance (14.9% risk per year), and intermediate scores (5.8% risk per year) indicate a need for moderate surveillance and caution in using medications that are prone to cause sedation or hallucinations. Moreover, the MoPaRDS can be measured serially through time. Although some items do not change (sex) or are seen commonly in early disease (RBD, orthostatic hypotension) others, such as MCI or hallucination, more often occur late.23 Therefore, scores should generally rise as dementia becomes imminent (note that we cannot assess this hypothesis directly using the methods of this study). The MoPaRDS may also be useful for randomized clinical trials, both for trials with dementia as an outcome and as a means to stratify patients in nondementia trials. For example, if one were to use a MoPaRDS of 4 or greater in a 3-year parallel-design clinical trial against PDD, an agent that reduces dementia risk by 50% would require a sample size of 69 patients (assuming 80% power with Pâ€‰=â€‰.05) to demonstrate a significant benefit (binominal probability, 2 proportions; https://www.stat.ubc.ca/~rollin/stats/ssize/b2.html). By contrast, without using stratification, the same clinical trial would require 568 patients, an 8-fold increase.

# 5859111

Psmc1fl/fl;CaMKIIÎ±-Cre and control (Psmc1fl/fl;CaMKIIÎ±-Wt or Psmc1fl/wt;CaMKIIÎ±-Wt) littermate mice were housed under identical conditions and genotyped as described previously11. Mice had ad libitum access to food and water. Female mice were used in all analyses. Cortex (50â€‰mg), hippocampus (10â€‰mg) and cerebellum (30â€‰mg) were rapidly micro-dissected from mouse brain, snap-frozen in liquid nitrogen and transferred directly to âˆ’80â€‰Â°C for storage until extraction. Samples were collected at the same time on each day over a period of 4 months before tissue extraction for 1H NMR Spectroscopy. The number of mice used at each age in NMR spectroscopy was determined by power calculations using online software (https://www.stat.ubc.ca/~rollin/stats/ssize/n2.html) based on unpublished pilot data of nâ€‰=â€‰3 mice at each age (power 0.80; alpha 0.05). Actual number of mice used at each age met or exceeded power calculations and is provided in Supplementary TableÂ 1. All procedures were authorised and approved by the University of Nottingham ethics committee and carried out in accordance with the UK Animals (Scientific Procedures) Act 1986.

# 6054794

Bones were scanned in 70% ethanol on a 1076 machine (Skyscan, Kontich, Belgium) with voxel size 18â€‰Î¼m, filter aluminum (Al) 0.5â€‰mm, exposure 1180â€‰ms, voltage 63â€‰kV, and 166â€‰Î¼A of current. Threeâ€dimensional (3D) reconstructions were visualized by CTVol Version 2.1 (Bruker). BMD was measured in reference to 0.25 and 0.75â€‰g/cm3 calcium phosphate standards with 2â€‰mm diameter (Skyscan). Images were reconstructed using NRecon Version 1.6.9.3 (SkyScan) and analyzed by CTAn Version 1.13.2.1 (SkyScan 2003â€11; Bruker 2012â€13). Sections 0.5 to 1.5â€‰mm or 2.15 to 2.58â€‰mm from distal growth plate and 0.45â€‰mm of midâ€shaft bone between distal growth plate and minor trochanter underwent automated segmentation into cancellous and cortical bone with grayscale thresholds 80/255 and 85/255. L5 vertebral body trabecular regions were interpolated between three manually selected elliptic planes. Morphometry was obtained using twoâ€dimensional (2D)/3D techniques. Sample sizes required for a power of 0.8 for distal femoral BMD measurement were estimated as nâ€‰=â€‰7 to 9 per genotype using http://www.stat.ubc.ca/~rollin/stats/ssize/n2.html on April 10, 2014.

# 5831411

Twenty young subjects participated in a pilot study on complex multiplication learning (72 repetitions, 10 problems). Based on accuracy scores at baseline, we classified 11 participants as â€œaverageâ€ and 9 participants as â€œbelow averageâ€. At post-training, the â€œbelow averageâ€ participants obtained a mean difference score in accuracy between trained and untrained problems of 41.11%. The â€œaverageâ€ participants achieved a mean difference score of 23.18%. Based on these findings, we performed a sample-size estimation analysis. Results showed that at least 16 participants have to be included in each group to find a between-group difference of 17.93 (Î¼1 = 41.11, Î¼2 = 23.18, Ïƒ = 17.54; Î± = 0.05, two-sided; power 0.80, http://www.stat.ubc.ca/~rollin/stats/ssize/n2.html). Our previous fMRI studies on arithmetic learning tested about 18 participants. For this study, we planned to recruit at least 25 subjects in each age group in order to detect even smaller group differences as the one found in the pilot study.

# 5827979

In a pilot study by Yinon [38] the RHI in normotensive pregnancies was 1.8, and in PE 1.5; in most populations standard deviation is 0.5 [37]. For 80% power and a two sided Î±â€‰=â€‰0.05 and considering a 0.3 difference clinically relevant, the sample size for each group would be 44 (http://www.stat.ubc.ca/~rollin/stats/ssize/n2.html); which we consider the sample size for our cross-sectional study comparing pre-eclamptic patients with normotensive controls. The sample size of this study will be 90 patients, 45 in each group.

# 5845509

Study size was calculated using the University of British Columbia (UBC) power calculator inference for proportions (http://www.stat.ubc.ca/~rollin/stats/ssize/b2.html). An estimated adherence rate of 80% for frequently seen patients was utilized based on previous publications (Kitney et al.) whilst those seen infrequently were estimated to have an adherence rate of 55%. Using a 2-sided test, alpha cut-off of 0.05, we calculated a required sample size of 110 patients to achieve 80% power.

# 6112156

For all experiments, sample size was chosen using a power analysis based on pilot experiments that provided an estimate of effect size (http://ww.stat.ubc.ca/~rollin/stats/ssize/n2.html). Mice used for immunohistochemical analysis were selected randomly from a set of genotyped animals (genotypes were known to investigators). Mouse and human tissue sections used for immunohistochemical analysis were selected randomly. For mouse tissues, sections were prepared using an approximately equal representation of all levels of the spinal cord, and of those, all were imaged and quantified. The sections were only not used if NeuN or Chat immunostaining failed. For iMN survival assays, assays were repeated at least twice, with each round containing 3 biologically independent iMN conversions. iMNs from the 3 biologically independent iMN conversions in one representative round was used to generate the Kaplan-Meier plot shown. iMN survival times were confirmed by manual longitudinal tracking by an individual who was blinded to the identity of the genotype and condition of each sample. To select 50 iMNs per condition for analysis, >50 neurons were selected for tracking randomly at day 1 of the assay. Subsequently, the survival values for 50 cells were selected at random using the RAND function in Microsoft Excel. For quantification of immunofluorescence, samples were quantified by an individual who was blinded to the identity of the genotype of each sample.

# 5936669

Since the surgeons involved in the study used different post-operative rehabilitation protocols and rehabilitation could potentially affect outcomes, sample size was determined to detect a difference in proportions of patients meeting the MCID pain reduction at 2-weeks post-operative. Prior to study initiation, each surgeon reviewed a consecutive sample of their patients to determine the rate of patients achieving the MCID pain reduction threshold. In this analysis, 9/10 (90%) of one surgeonâ€™s patients met this threshold compared to 6/11 (55%) of the other surgeonâ€™s patients. Using a standard, publicly-available sample size calculator for differences in proportions comparing 2 independent samples (www.stat.ubc.ca/~rollin/stats/ssize/b2.html), greater than or equal to 30 patients per group would be needed to detect a significant difference in the 2-week pain outcome at a power of 0.80 and an alpha of 0.05.