

Supplementary Methods

DNA was extracted from 23 blood samples from the following seven species: white-handed gibbon (*Hylobates lar*, 6 samples), siamang (*Symphalangus syndactylus*, 3 samples), red-cheeked gibbon (*Nomascus gabriellae*, 2 samples), southern white-cheeked gibbon (*Nomascus siki*, 2 samples), northern white-cheeked gibbon (*Nomascus leucogenys*, 6 samples), Bornean gibbon (*Hylobates muelleri*, 1 sample), agile gibbon (*Hylobates agilis*, 3 samples). All samples were sourced from the Deutsches Primatenzentrum, Goettingen, Germany. These samples are of diverse origins throughout the EU.

All samples were screened via PCR using four primer pairs designed against the *pol* genes of GALV and KoRV. These analyses were performed using the primer pairs KoRV-pol-F to KoRV-pol-R and KoRVmgbf to KoRVmgbr designed against the KoRV *pol* gene, sequences and conditions described in Tarlinton et al. (2006), the primer pair ERV1 (5' TGG GCC GAG AAG GCA CCT AT 3') to ERVR1 (5' CCA TTC AAA CGC GAA CAA TG 3') designed against MLV, under the same conditions and the primer pair GALV-pol-F (5' AGA TCG ACC CGG CGT GTA CT 3') to GALV-pol-R (5' CCA TTC AAA CGC GAA CAA TG 3') designed against the GALV *pol* gene, again under the same conditions. One sample from each species was also screened using the degenerate gammaretrovirus primer pair PRO (5' GTK TTI KTI GAY ACI GGI KC 3') to CT (5' AGI AGG TCR TCI ACR TAS TG 3') [from Martin et al. (1999)], which were designed to amplify MLV-related ERVs. These analyses were performed in 50 μ l reactions with 2x MgCl₂-free buffer, 20 pmol each primer, 3 μ M MgCl₂, 100 μ M each dNTP, 2.5 Units Taq polymerase with 2 minutes at 95°C, 40 cycles of 94°C for 20 seconds, 44.8°C for 30 seconds, 72°C for 60 seconds, followed by 2 minutes at 72°C.

DNA quality was confirmed for all samples using primers based on the β -actin gene as described in Tarlinton et al. (2006).

For the *in silico* screening, reference genomes screened were as follows: marmoset (*Callithrix jacchus*) Callithrix_jacchus-3.2, aye-aye (*Daubentonia madagascariensis*) DauMad_1.0, gorilla (*Gorilla gorilla*) gorGor3.1, human (*Homo sapiens*) GRCh37.p10, crab-

eating macaque (*Macaca fascicularis*) MacFas_Jun2011, rhesus macaque (*Macaca mulatta*) Mmul_051212, lemur (*Microcebus murinus*) micMur1, gibbon (*Nomascus leucogenys*) Nleu_3.0, bushbaby (*Otolemur garnettii*) OtoGar3, bonobo (*Pan paniscus*) panpan1, chimpanzee (*Pan troglodytes*) Pan_troglodytes-2.1.4, orangutan (*Pongo abelii*) P_pygmaeus_2.0.2, baboon (*Papio anubis*) Panu_2.0, squirrel monkey (*Saimiri boliviensis*) SaiBol1.0, tarsier (*Tarsius syrichta*) tarSyr1, guinea pig (*Cavia porcellus*) Cavpor3.0, chinchilla (*Chinchilla lanigera*) ChiLan1.0, hamster (*Cricetulus griseus*) CriGri_1.0, kangaroo rat (*Dipodomys ordii*) dipOrd1, naked mole rat (*Heterocephalus glaber*) HetGla_female_1.0, jerboa (*Jaculus jaculus*) JacJac1.0, vole (*Microtus ochrogaster*) MicOch1.0, mouse (*Mus musculus*) GRCm38.p1, degu (*Octodon degus*) OctDeg1.0 and rat (*Rattus norvegicus*) Rnor_5.0.

Martin, J., Herniou, E., Cook, J., O'Neill, R.W., Tristem, M., 1999. Interclass Transmission and Phyletic Host Tracking in Murine Leukemia Virus-Related Retroviruses. *J. Virol.* 73, 2442-2449.

Tarlinton, R.E., Meers, J., Young, P.R., 2006. Retroviral invasion of the koala genome. *Nature* 442, 79-81.