

## SUPPLEMENTAL MATERIAL - FIGURE LEGENDS

Ebeling et al. (2011) Genome-based analysis of the non-human primate *Macaca fascicularis* as a model for drug safety assessment.

**Figure S1.** Allele combination counts of SNPs in the *M. fascicularis* genome draft

**Figure S2.** Tissue specific gene expression in *M. fascicularis*

Genes with tissue specific expression and robust expressions level (EST-counts) were selected from NCBI's Unigene EST database (<http://www.ncbi.nlm.nih.gov/UniGene/>). The expression levels ( $\log_2$ ) of *M. fascicularis* orthologs of 6 liver (*F7*, *TTR*, *AGT*, *APOB*, *CRP*, *CYP3A5*) and 7 testes (*KIF2B*, *TNP2*, *SPATA20*, *SPATA21*, *SPZ1*, *TSGA13*, *TSKS*) specific genes is shown in liver, testes, bladder, spleen and kidney samples from three animals. The expression levels of three housekeeping genes (*GAPDH*, *POLR2B* and *POLR2C*) are shown as reference and the detection limit of the microarray platform is depicted by a hatched line.