

Supplementary figure legends

Supplementary figure 1: DNA methylation of *Ly49r* 5'-region in the 129/S6 (SvEvTac) mouse Ly49R-expressing NK cells.

Sodium bisulfite sequencing of 12A8-positive NK cells (Ly49R positive). This region is ~700bp long and is amplified using the same primer sets used to amplify *Ly49d* and *r* in the 129/B6 F1 hybrid. All clones presented here are unique. The curved arrow represents the transcriptional start site.

Supplementary figure 2: Gel-shift assay with T-cell extract

Double-stranded probes harbouring the region of interest in exon 1 (refer to Figure 6) for the activating *Ly49d* and *h* of the B6 strain and the corresponding region for the inhibitory *Ly49a* and *Ly49c* were used in gel-shift experiments with nuclear extract from FACS-sorted T-cells. The amount and source of T-cell extract used in this assay is different from that used in Figure 6 (independent FACS sort). The bracket indicates the protein complexes bound most significantly by the activating *Ly49d* and *h* probes but not the inhibitory *Ly49a* and *c* in T-cells. The arrow indicates another protein complex specific to the activating *Ly49* probes in T-cells.