

S2 Table. LY6A from C57Bl/6J but not BALB/cJ mice is predicted to be GPI anchored.

Gene (strain)	ω-site prediction	Specificity	Probability	Sequence
<i>Ly6a</i> (C57Bl/6J;DBA/J; AKR/J)	110	100%	Highly Probable	MDTSHTTKSCLLILLVALLCAERAQGLECYQCYGVPFETSCPSITCP YPDGVCVTQEAAVIVDSQTRKVKNNLCLPICPPNIESMEILGTKNV KTSCCQEDLCNVAVP <u>N</u> GGSTWTMAGVLLFSLSSVLLQTLL
<i>Ly6a</i> (CAST/EiJ; PWK/PhJ)	110	0%	Not GPI- anchored	MDTSHTTKSC <u>V</u> LILLVALLCAERAQGLECYQCYGVPFETSCPSITC PYPDGVCVTQEAAVIVDSQTRKVKNNLCLPICPPNIESMEILGTKVN VKTS offense LCNA <u>A</u> AVP <u>N</u> GGSTWTMAGVLLFSLSSVLLQTLL
<i>Ly6a</i> (BALB/C;NOD/S hiLtJ)	110	0%	Not GPI- anchored	MDTSHTTKSCLLILLVALLCAERAQGLECYQCYGVPFETSCPSITCP YPDGVCVTQEAAVIV <u>G</u> SQTRKVKNNLCLPICPPNIESMEILGTKNV KTSCCQEDLCN <u>A</u> AVP <u>N</u> GGSTWTMAGVLLFSLSSVLLQTLL
<i>Ly6c1</i> (C57Bl/6J)	102	100%	Highly Probable	MDTSHTTKSCVLILLVALLCAERAQGLQCYECYGVPIETSCPAVTC RASDGFCIAQNIELIEDSQRRKLKTRQCLSCPAGVPIRDPNIRERT SCCSEDLC <u>N</u> AAVPTAGSTWTMAGVLLFSLSSVVLQTLL
<i>Ly6e</i>	107	100%	Highly Probable	MSATSNMRVFLPVLLAALLGMEQVHSLMCFSCTDQKNNINCLWPV SCQEKDHYCITLSAAAGFGNVNLGYTLNKGCSPICPSENVNLNLGV ASVNSYCCQSSFCNF <u>S</u> AAGLGLRASIPLLGLLSSLALLQLSP

The predGPI prediction model [3] was used to assess the probability that the alleles of *Ly6a* present in permissive and nonpermissive mouse strains encode protein products likely to be modified by a GPI anchor. Within the amino acid sequences, SNPs are highlighted in red and underlined text; predicted GPI-anchor sites (ω-sites) are highlighted in bold green text, and cleaved C-terminal hydrophobic tail sequences are highlighted in magenta text.