**Supplemental Tables**

**Table S1A. Breeding: CD19-*Cre/Cre; Pcgf6+/fl* xEμ-*myc; Pcgf6+/fl***

|  |  |  |
| --- | --- | --- |
| **Genotype** | **Expected frequency** | **Observed frequency** |
| CD19-*Cre; Pcgf6+/+* | 12.50% | 21/173 | 12.14% |
| CD19-*Cre; Pcgf6+/fl* | 25% | 52/173 | 30.06% |
| CD19-*Cre; Pcgf6fl/fl* | 12.50% | 30/173 | 17.34% |
| CD19-*Cre*; Eμ-*myc*; *Pcgf6+/+* | 12.50% | 36/173 | 20.81% |
| CD19-*Cre*; Eμ-*myc*; *Pcgf6+/fl* | 25% | 29/173 | 16.76% |
| CD19-*Cre*; Eμ-*myc*; *Pcgf6fl/fl* | 12.50% | 5/173 | 2.89% |

**Table S1B. Breeding: CD19*-Cre; Mga+/fl* x Eμ-*myc; Mga+/fl***

|  |  |  |
| --- | --- | --- |
| **Genotype** | **Expected frequency** | **Observed frequency** |
| *Mga+/+* | 6.25% | 6/96 | 6.25% |
| *Mga+/fl* | 12.50% | 23/96 | 23.96% |
| *Mgafl/fl* | 6.25% | 2/96 | 2.08% |
| Eμ-*myc*; *Mga+/+* | 6.25% | 7/96 | 7.29% |
| Eμ-*myc*; *Mga+/fl* | 12.50% | 3/96 | 3.13% |
| Eμ-*myc*; *Mgafl/fl* | 6.25% | 9/96 | 9.38% |
| CD19-*Cre*; *Mga+/+* | 6.25% | 11/96 | 11.46% |
| CD19-*Cre*; *Mga+/fl* | 12.50% | 19/96 | 19.79% |
| CD19-*Cre*; *Mgafl/fl* | 6.25% | 3/96 | 3.13% |
| CD19-Cre; Eμ-*myc*; *Mga+/+* | 6.25% | 4/96 | 4.17% |
| CD19-Cre; Eμ-*myc*; *Mga+/fl* | 12.50% | 5/96 | 5.21% |
| CD19-Cre; Eμ-*myc*; *Mgafl/fl* | 6.25% | 4/96 | 4.17% |

**Table S1. Breeding Strategy.** Each table shows the expected (assuming mendelian distribution) and observed frequencies of the indicated compound genotypes, based on the crosses shown at the top. **(A**) *Pcgf6* mutant cohort. Here all siblings are positive for CD19-*Cre*, as this transgene was first bred to homozygosity in one of the parents (CD19-*Cre/Cre*). Note that Eμ-*myc* and *Pcgf6* segregated in a sub-Mendelian manner  (p <0.0001 ), consistent with their close genomic location on chromosome 19 (Lefebure et al. 2017) ([http://www.informatics.jax.org/marker/MGI:1918291](http://www.informatics.jax.org/marker/MGI%3A1918291)). **(B**) *Mga* mutant cohort. In line with published data (Washkowitz et al. 2015), *Mgafl/fl*mice were recovered at sub-Mendelian frequencies (p < 0.005), confirming that *Mgafl* is a hypomorphic allele.