

Mouse Genotyping

Universal Genotyping Array Service



Content and Design Characteristics

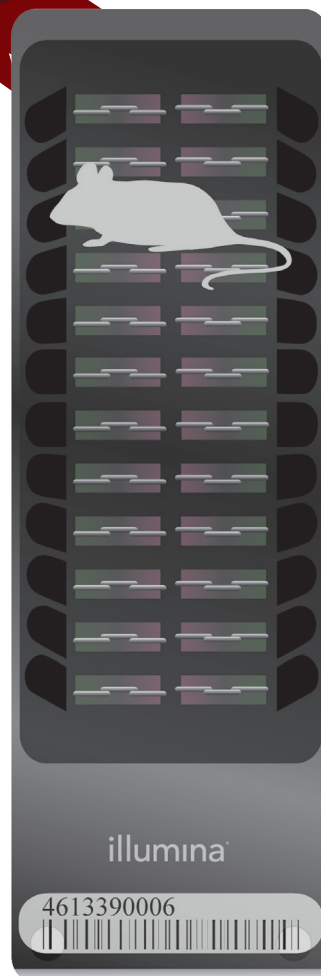
The Mouse Universal Genotyping Array (MUGA) provides 7,851 SNP markers built on the Illumina® Infinium platform. The SNP markers are distributed throughout the mouse genome (average spacing of 325 Kb, standard deviation of 191 Kb). The SNPs were selected to be maximally informative and independent — making the array a highly cost-effective tool for many genotyping applications by maximizing information per marker.

The MUGA design criteria makes it optimal for detecting heterozygous regions and discriminating between haplotypes in homozygous regions. The array's allele frequencies and haplotypes were derived from the 8 laboratory mouse strains that are founders of the Collaborative Cross (A/J, C57BL/6J, 129S1/SvImJ, NOD/LtJ, NZO/HILtJ, CAST/EiJ, PWK/PhJ, WSB/EiJ).

Performance

Based on analysis of 200 DNA samples, the MUGA array provided excellent concordance among biological replicates, and between parents and F1 offspring.

- >95% of the SNPs provide robust and replicable genotypes in varied classical and wild-derived *Mus musculus* laboratory strains.
- As expected, the call rate for other mouse species decreases, but it still provides genotype calls for ~7,000 SNP in the divergent SPRET/EiJ inbred strain.
- Initial analysis in 18 inbred strains (129S1/SvImJ, A/J, AKR/J, C3H/HeJ, C57BL/6J, CAST/EiJ, CBA/J, DBA/2J, FVB/NJ, KK/H1J, LP/J, NOD/LtJ, NZO/HILtJ, PWK/PhJ, SJL/J, SKIVE/EiJ, TIRANO/EiJ and WSB/EiJ) shows the percent of informative autosomal SNPs in pairwise strain combinations typically varies between 25% to 50%. A spreadsheet of genotypes for these strains can be found at <http://csbio.unc.edu/CCstatus/index.py>.
- Notably, >10% (i.e., 750) SNPs are informative even between closely related strains (e.g., 129S1/SvImJ and LP/J5).



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GeneSeek can also assist with custom SNP genotyping panels.



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* MUGA content and design were done at the University of North Carolina at Chapel Hill by Catherine Welsh, Leonard McMillan and Fernando Pardo-Manuel de Villena.

**This work was supported by NIH grants (MH090338/CA134240) and Ellison Medical Foundation. A complete array description will appear in an upcoming publication.

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