

Agilent Community Design Epigenetic Research Panels

Mouse and Rat Methyl-Seq Panels

Epigenetic modifications regulate gene expression without changes in the DNA sequence, accounting for a wide range of phenotypic variation in populations. DNA methylation is the most common type of epigenetic modification that plays a critical role in regulating gene expression. Methylation sequencing (methyl-seq) coupled with SureSelect target enrichment allows you to assess genome-wide DNA methylation without having to sequence the entire genome.

The Agilent Community Design program now offers two methyl-seq panels that enable global DNA methylation profiling in the two key animal models, the rat and the mouse (Table 1). These two panels were designed in collaboration with a group led by Dr. Richard Lee, Assistant Professor of Psychiatry and Behavior Sciences at the Johns Hopkins University. Each panel targets a comprehensive set of CpG islands, shores, shelves, and regulatory elements, where differential DNA methylation occurs, based on the rat Genome Build rn4 and the mouse Genome Build mm9, respectively. The scientists from Dr. Lee's group have published several studies using these two panels.¹⁻⁴ They provide important insights on tissue-specific differential methylation as well as methylation changes in response to environmental influences.

The Agilent Community Design program offers NGS panels designed by or in collaboration with experts in various research fields. These Agilent Community Design panels are priced significantly lower than a custom-made panel of equivalent size. They are produced upon order placement and are ready to ship in as little as two weeks.

Agilent has not validated the performance of the panels in the Agilent Community Design program.

Table 1. The Genome Build and the size of the community designs for epigenetic research.

Panel Name	Genome Build	Panel Size (Mb, Mega bases)
SureSelect Community Design Rat Methyl-Seq	<i>rn4</i>	97
SureSelect Community Design Mouse Methyl-Seq	<i>mm9</i>	109

Table 2. Ordering information for the SureSelect Community Design Rat and Mouse Methyl-Seq panels. These part numbers cover the capture probe libraries only. Library prep and target enrichment reagent kits must be purchased separately.

Part Number	Product Description
5191-6702	SureSelect XT Community Design Rat Methyl-Seq, 16 rxn
5191-6703	SureSelect XT Community Design Rat Methyl-Seq, 96 rxn
5191-6704	SureSelect XT Community Design Mouse Methyl-Seq, 16 rxn
5191-6705	SureSelect XT Community Design Mouse Methyl-Seq, 96 rxn

References

1. Hing, B. *et al.* Chronic social stress induces DNA methylation changes at an evolutionary conserved intergenic region in chromosome X. *Epigenetics* **2018** *13*, 627-641. DOI: 10.1080/15592294.2018.1486654
2. Hing, B. *et al.* Adaptation of the targeted capture Methyl-Seq platform for the mouse genome identifies novel tissue-specific DNA methylation patterns of genes involved in neurodevelopment. *Epigenetics* **2015** *10*, 581-596.
3. Uli, N. *et al.* Age-specific changes in genome-wide methylation enrich for Foxa2 and estrogen receptor alpha binding sites. *PLoS ONE* **2018** *13*, e0203147. <https://doi.org/10.1371/journal.pone.0203147>
4. Seifuddin, F. *et al.* Genome-wide Methyl-Seq analysis of blood-brain targets of glucocorticoid exposure. *Epigenetics* **2017** *12:8*, 637-652. DOI: 10.1080/15592294.2017.1334025

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