

Duplicate Genes in Cotton et al. 2014 DNA Methylation Study

In the 2014 DNA methylation study, Cotton et al. mapped DNA methylation marks to their nearest Transcriptional Start Site (TSS) [1]. For example, the research group measured DNA methylation at three positions which each mapped to NLGN4X.

Table 1: An example of a duplicate gene (NLGN4X) in Cotton et al. 2014 which was associated with multiple DNA methylation positions.

Gene	Position (DNAm)	Start (bp) [hg38]	End (bp) [hg38]	Escape Status
NLGN4X	6227074	5840637	6228867	escape
NLGN4X	6227846	5840637	6228867	escape
NLGN4X	6228664	5840637	6228867	escape

1. Cotton, A.M., et al., *Landscape of DNA methylation on the X chromosome reflects CpG density, functional chromatin state and X-chromosome inactivation*. Human Molecular Genetics, 2014. **24**(6): p. 1528-1539.