# **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 (DNAme)** | **Start (bp) [hg38]** | **End (bp) [hg38]** | **Escape Status** |
| --- | --- | --- | --- | --- |
| [NLGN4X](http://www.ensembl.org/Homo_sapiens/Location/View?r=X:5840637-6228867) | 6227074 | 5840637 | 6228867 | escape |
| [NLGN4X](http://www.ensembl.org/Homo_sapiens/Location/View?r=X:5840637-6228867) | 6227846 | 5840637 | 6228867 | escape |
| [NLGN4X](http://www.ensembl.org/Homo_sapiens/Location/View?r=X:5840637-6228867) | 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.