

Interweaving between genetic and epigenetic studies on asthma

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Supplemental Table1. *Summary on the number of CpGs on each gene and their 0.5 MB neighboring SNPs, and the number of ANOVA models fitted for each gene, along with the*

number of significant results after controlling FDR. To thoroughly examine whether IL4 and TLE4 have methQTLs, all available SNPs were assessed for their associations with DNAm.

Gene	Number of CpGs	Number of unique SNPs	Number of models	Number of significant results
<i>DUSP22</i>	24	2,432	53,964	47
<i>IKZF3</i>	7	3,119	18,512	26
<i>IL4</i>	4	1,531	6,116	0
<i>RUNX1</i>	7	3,992	96,723	17
<i>TLE4</i>	37	1,947	13,575	0

Supplemental Table2. *Summary on the number of CpGs on each gene and their 2 MB neighboring SNPs, and the number of ANOVA models fitted for each gene, along with the number of significant results after controlling FDR. To thoroughly examine whether IL4 and TLE4 have methQTLs, all available SNPs were assessed for their associations with DNAm.*

Gene	Number of CpGs	Number of unique SNPs	Number of models	Number of significant results
<i>DUSP22</i>	24	7,879	184,555	177
<i>IKZF3</i>	7	10,658	70,659	23
<i>IL4</i>	4	5,859	23,398	0
<i>RUNX1</i>	7	11,127	366,444	23
<i>TLE4</i>	37	7,368	51,512	0