

# Lab assignment

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Download SSalzbergDNA23andMe.txt file from personal genome project(PGP): [personalgenomes.org](http://personalgenomes.org)

Position: chr1:87222711

The variant's dbSNP identifier is: rs10873824

The alleles is : A > G / A > T

The allele frequency of the variation is:

A=0.20686 (25975/125568, TOPMED)

A=0.1950 (15347/78696, PAGE\_STUDY)

A=0.2195 (6876/31326, GnomAD) (- 6 less)

A=0.212 (1063/5008, 1000G)

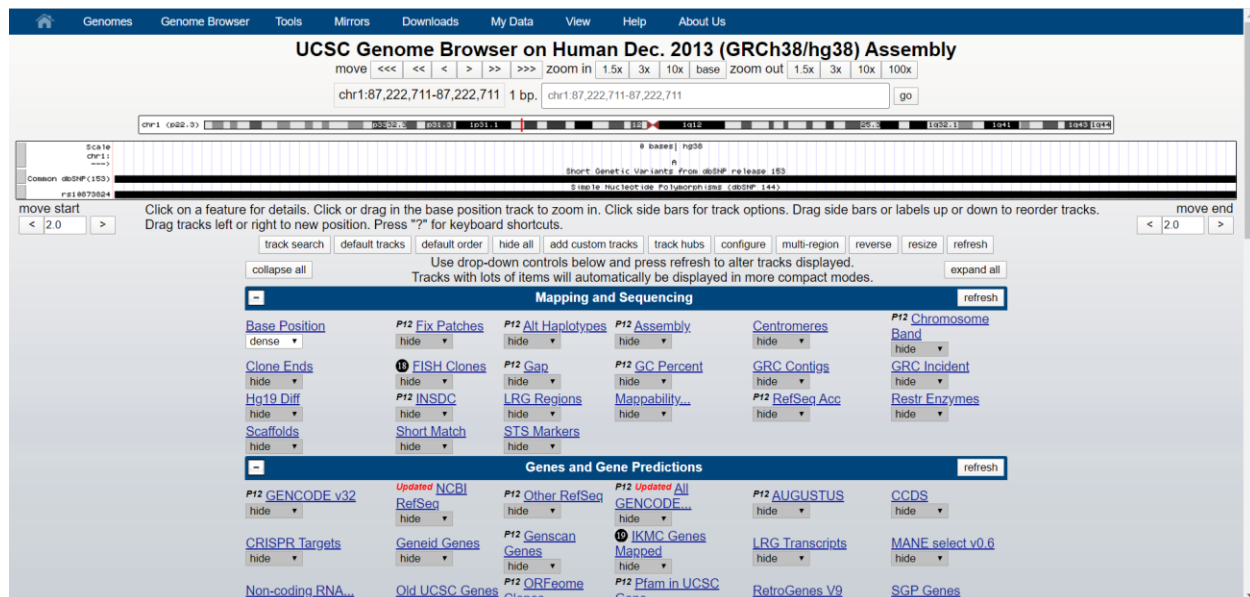
A=0.272 (1220/4480, Estonian)

A=0.275 (1059/3854, ALSPAC)

A=0.270 (1003/3708, TWINSUK)

A=0.26 (155/600, NorthernSweden)

A=0.34 (74/216, Vietnamese)



Reference SNP (rs) Report

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Released July 9, 2019

**rs10873824**

<b>Organism</b>	<i>Homo sapiens</i>	<b>Clinical Significance</b>	Not Reported in ClinVar
<b>Position</b>	chr1:87222711 (GRCh38.p12)	<b>Gene : Consequence</b>	LINC02801 : Intron Variant
<b>Alleles</b>	A>G / A>T	<b>Publications</b>	1 citation
<b>Variation Type</b>	SNV Single Nucleotide Variation	<b>Genomic View</b>	<a href="#">See rs on genome</a>
<b>Frequency</b>	A=0.20686 (25975/125568, TOPMED) A=0.1950 (15347/78696, PAGE_STUDY) A=0.2195 (6876/31326, GnomAD) (-6 less) A=0.212 (1063/5008, 1000G) A=0.272 (1220/4480, Estonian) A=0.275 (1059/3854, ALSPAC) A=0.270 (1003/3708, TWINSUK) A=0.26 (155/600, NorthernSweden) A=0.34 (74/216, Vietnamese)		

**Variant Details**

**Clinical Significance**

**Genomic Placements**

Sequence name	Change
GRCh37.p13 chr 1	NC_000001.10:g.87688394A>G

The known clinical relevance paper is:

<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4011843/pdf/pone.0096374.pdf>

ncbi.nlm.nih.gov/snp/?term=rs10873824

dbSNP

SNP rs10873824

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Search results

Items: 2

rs10873824 [*Homo sapiens*]

1.

Variant type: SNV  
Alleles: A>G, T [Show Flanks]  
Chromosome: 1:87222711  
Gene: LINC02801 (Varview)  
Functional Consequence: intron\_variant  
Validated: by frequency by cluster  
MAF: A=0.195016/15347 (PAGE\_STUDY)  
A=0.20686/25975 (TOPMED)  
A=0.21226/1063 (1000Genomes)  
A=0.219496/6876 (GnomAD)  
A=0.258333/155 (NorthernSweden)  
A=0.270496/1003 (TWINSUK)  
A=0.272321/1220 (Estonian)  
A=0.274779/1059 (ALSPAC)  
A=0.342593/74 (Vietnamese)  
HGVS: NC\_000001.11:g.87222711A>G, NC\_000001.11:g.87222711A>T, NC\_000001.10:g.87688394A>G, NC\_000001.10:g.87688394A>T  
PubMed LitVar

rs61259767 has merged into rs10873824 [*Homo sapiens*]

2.

Variant type: SNV  
Alleles: A>G, T [Show Flanks]

Find related data  
Database: Select  
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rs10873824[All Fields]  
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rs10873824 (2) SNP  
rs4233323 (3) SNP  
rs10737721 (2) SNP  
rs12403601 (2) SNP

The paper directly investigated the molecular genetic basis of heredity of mathematical ability. The SNPs (rs789859) which I randomly choose shows significant association with the heredity of mathematical ability after Bonferroni correction. And the SNP (rs789859) is located in a region on chromosome 3q29 that has been previously linked to learning difficulties and autism. rs789859 lies 1.3 kbp downstream of LSG1, and 700 bp upstream of FAM43A, mapping within the potential promoter/regulatory region of the latter.