

Class 11: Genomics

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Q5 Proportion of MXL with G|G genotype

```
mxl <- read.csv('373531-SampleGenotypes-Homo_sapiens_Variation_Sample_rs8067378.csv')
head(mxl)
```

	Sample..	Male..	Female..	Unknown..	Genotype..	forward..	strand..	Population..	s..	Father
1					NA19648	(F)		A A	ALL, AMR, MXL	-
2					NA19649	(M)		G G	ALL, AMR, MXL	-
3					NA19651	(F)		A A	ALL, AMR, MXL	-
4					NA19652	(M)		G G	ALL, AMR, MXL	-
5					NA19654	(F)		G G	ALL, AMR, MXL	-
6					NA19655	(M)		A G	ALL, AMR, MXL	-
	Mother									
1		-								
2		-								
3		-								
4		-								
5		-								
6		-								

```
View(mxl)
```

How many G|G genotypes I have

```
table(mxl$Genotype..forward.strand.) / nrow(mxl)
```

A A	A G	G A	G G
0.343750	0.328125	0.187500	0.140625