SNPStats results

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Descriptive statistics

Response variable: status **Type:** categorical

	n	missing	unique
All subjects	380	0	2
status=0-control	244 (64.21%)	---	---
status=1-cese	136 (35.79%)	---	---

Covariate: ethnicity **Type:** categorical

	n	missing	unique
All subjects	380	0	2
status=0-control	244	0	2
status=1-cese	136	0	2

	1	2
All subjects	251 (66%)	129 (34%)
status=0-control	172 (70%)	72 (30%)
status=1-cese	79 (58%)	57 (42%)

Covariate: gender **Type:** categorical

	n	missing	unique
All subjects	380	0	2
status=0-control	244	0	2
status=1-cese	136	0	2

	FeMale	Male
All subjects	229 (60%)	151 (40%)
status=0-control	144 (59%)	100 (41%)
status=1-cese	85 (62%)	51 (38%)

Single-SNP analysis

SNP: rs4256

Percentage of typed samples: 380/380 (100%)

rs4256 allele frequencies (n=380)						
	All subjects		status=0-control		status=1-cese	
Allele	**Count**	**Proportion**	**Count**	**Proportion**	**Count**	**Proportion**
A	458	0.6	286	0.59	172	0.63
C	302	0.4	202	0.41	100	0.37

rs4256 genotype frequencies (n=380)						
	All subjects		status=0-control		status=1-cese	
Genotype	**Count**	**Proportion**	**Count**	**Proportion**	**Count**	**Proportion**

A/A	135	0.36	82	0.34	53	0.39
A/C	188	0.49	122	0.5	66	0.49
C/C	57	0.15	40	0.16	17	0.12

rs4256 exact test for Hardy-Weinberg equilibrium (n=380)

	N11	**N12**	**N22**	**N1**	**N2**	**P-value**
All subjects	135	188	57	458	302	0.59
status=0-control	82	122	40	286	202	0.69
status=1-cese	53	66	17	172	100	0.71

rs4256 association with response status (n=380, adjusted by ethnicity+gender)

Model	**Genotype**	**status=0-control**	**status=1-cese**	**OR (95% CI)**	**P-value**	**AIC**	**BIC**
Codominant	A/A	82 (33.6%)	53 (39%)	1.00	0.51	497.9	517.6
	C/A	122 (50%)	66 (48.5%)	0.87 (0.55-1.38)			
	C/C	40 (16.4%)	17 (12.5%)	0.68 (0.35-1.32)			
Dominant	A/A	82 (33.6%)	53 (39%)	1.00	0.38	496.5	512.2
	C/A-C/C	162 (66.4%)	83 (61%)	0.82 (0.53-1.28)			
Recessive	A/A-C/A	204 (83.6%)	119 (87.5%)	1.00	0.32	496.2	512
	C/C	40 (16.4%)	17 (12.5%)	0.73 (0.40-1.36)			
Overdominant	A/A-C/C	122 (50%)	70 (51.5%)	1.00	0.89	497.2	513
	C/A	122 (50%)	66 (48.5%)	0.97 (0.64-1.48)			
Log-additive	---	---	---	0.83 (0.61-1.14)	0.26	495.9	511.7

Interaction analysis with covariate ethnicity

rs4256 and ethnicity cross-classification interaction table (n=380, adjusted by gender)

	1			**2**		
	status=0-control	**status=1-cese**	**OR (95% CI)**	**status=0-control**	**status=1-cese**	**OR (95% CI)**
A/A	55	29	1.00	27	24	1.74 (0.85-3.55)
C/A	90	39	0.84 (0.46-1.51)	32	27	1.63 (0.82-3.23)
C/C	27	11	0.81 (0.35-1.87)	13	6	0.87 (0.30-2.53)

Interaction p-value: 0.69

ethnicity within rs4256 (n=380, adjusted by gender)

		status=0-control	**status=1-cese**	**OR (95% CI)**
A/A	**1**	55	29	1.00
	2	27	24	1.74 (0.85-3.55)
C/A	**1**	90	39	1.00
	2	32	27	**1.95 (1.03-3.68)**
C/C	**1**	27	11	1.00
	2	13	6	1.08 (0.32-3.59)

Test for interaction in the trend: 0.66

rs4256 within ethnicity (n=380, adjusted by gender)

		status=0-control	**status=1-cese**	**OR (95% CI)**
1	**A/A**	55	29	1.00
	C/A	90	39	0.84 (0.46-1.51)
	C/C	27	11	0.81 (0.35-1.87)
2	**A/A**	27	24	1.00
	C/A	32	27	0.94 (0.44-1.99)
	C/C	13	6	0.50 (0.16-1.53)

Test for interaction in the trend: 0.69

SNP: rs0519

Percentage of typed samples: 380/380 (100%)

rs0519 allele frequencies (n=380)						
	All subjects		**status=0-control**		**status=1-cese**	
Allele	**Count**	**Proportion**	**Count**	**Proportion**	**Count**	**Proportion**
G	511	0.67	322	0.66	189	0.69
A	249	0.33	166	0.34	83	0.31

rs0519 genotype frequencies (n=380)						
	All subjects		**status=0-control**		**status=1-cese**	
Genotype	**Count**	**Proportion**	**Count**	**Proportion**	**Count**	**Proportion**
A/A	37	0.1	24	0.1	13	0.1
G/A	175	0.46	118	0.48	57	0.42
G/G	168	0.44	102	0.42	66	0.49

rs0519 exact test for Hardy-Weinberg equilibrium (n=380)						
	N11	**N12**	**N22**	**N1**	**N2**	**P-value**
All subjects	168	175	37	511	249	0.42
status=0-control	102	118	24	322	166	0.26
status=1-cese	66	57	13	189	83	0.84

rs0519 association with response status (n=380, adjusted by ethnicity+gender)

Model	Genotype	status=0-control	status=1-cese	OR (95% CI)	P-value	AIC	BIC
Codominant	G/G	102 (41.8%)	66 (48.5%)	1.00	0.47	497.7	517.4
	A/G	118 (48.4%)	57 (41.9%)	0.76 (0.48-1.18)			
	A/A	24 (9.8%)	13 (9.6%)	0.90 (0.42-1.91)			
Dominant	G/G	102 (41.8%)	66 (48.5%)	1.00	0.25	495.9	511.7
	A/G-A/A	142 (58.2%)	70 (51.5%)	0.78 (0.51-1.19)			
Recessive	G/G-A/G	220 (90.2%)	123 (90.4%)	1.00	0.93	497.2	513
	A/A	24 (9.8%)	13 (9.6%)	1.03 (0.50-2.12)			
Overdominant	G/G-A/A	126 (51.6%)	79 (58.1%)	1.00	0.23	495.8	511.6
	A/G	118 (48.4%)	57 (41.9%)	0.77 (0.50-1.18)			
Log-additive	---	---	---	0.87 (0.62-1.21)	0.4	496.5	512.3

Interaction analysis with covariate ethnicity

rs0519 and ethnicity cross-classification interaction table (n=380, adjusted by gender)						
	1			**2**		
	status=0-control	**status=1-cese**	**OR (95% CI)**	**status=0-control**	**status=1-cese**	**OR (95% CI)**
G/G	70	38	1.00	32	28	1.65 (0.86-3.15)
A/G	84	31	0.70 (0.39-1.24)	34	26	1.43 (0.75-2.73)
A/A	18	10	1.05 (0.44-2.53)	6	3	0.91 (0.22-3.85)
Interaction p-value: 0.59						

ethnicity within rs0519 (n=380, adjusted by gender)				
G/G		**status=0-control**	**status=1-cese**	**OR (95% CI)**
	1	70	38	1.00
	2	32	28	1.65 (0.86-3.15)
A/G		**status=0-control**	**status=1-cese**	**OR (95% CI)**
	1	84	31	1.00
	2	34	26	**2.06 (1.07-3.97)**
A/A		**status=0-control**	**status=1-cese**	**OR (95% CI)**
	1	18	10	1.00
	2	6	3	0.86 (0.18-4.25)
Test for interaction in the trend: 0.74				

rs0519 within ethnicity (n=380, adjusted by gender)				
		status=0-control	**status=1-cese**	**OR (95% CI)**
1	**G/G**	70	38	1.00
	A/G	84	31	0.70 (0.39-1.24)
	A/A	18	10	1.05 (0.44-2.53)
		status=0-control	**status=1-cese**	**OR (95% CI)**
2	**G/G**	32	28	1.00
	A/G	34	26	0.87 (0.42-1.78)
	A/A	6	3	0.55 (0.13-2.43)

Test for interaction in the trend: 0.59

SNP: rs0270

Percentage of typed samples: 380/380 (100%)

rs0270 allele frequencies (n=380)						
	All subjects		**status=0-control**		**status=1-cese**	
Allele	**Count**	**Proportion**	**Count**	**Proportion**	**Count**	**Proportion**
A	433	0.57	271	0.56	162	0.6
G	327	0.43	217	0.44	110	0.4

rs0270 genotype frequencies (n=380)						
	All subjects		**status=0-control**		**status=1-cese**	
Genotype	**Count**	**Proportion**	**Count**	**Proportion**	**Count**	**Proportion**
A/A	121	0.32	73	0.3	48	0.35
A/G	191	0.5	125	0.51	66	0.49
G/G	68	0.18	46	0.19	22	0.16

rs0270 exact test for Hardy-Weinberg equilibrium (n=380)						
	N11	**N12**	**N22**	**N1**	**N2**	**P-value**
All subjects	121	191	68	433	327	0.68
status=0-control	73	125	46	271	217	0.61
status=1-cese	48	66	22	162	110	1

rs0270 association with response status (n=380, adjusted by ethnicity+gender)							
Model	**Genotype**	**status=0-control**	**status=1-cese**	**OR (95% CI)**	**P-value**	**AIC**	**BIC**
Codominant	A/A	73 (29.9%)	48 (35.3%)	1.00	0.62	498.3	518
	G/A	125 (51.2%)	66 (48.5%)	0.83 (0.51-1.33)			
	G/G	46 (18.9%)	22 (16.2%)	0.75 (0.40-1.42)			
Dominant	A/A	73 (29.9%)	48 (35.3%)	1.00	0.35	496.4	512.1
	G/A-G/G	171 (70.1%)	88 (64.7%)	0.81 (0.51-1.27)			
Recessive	A/A-G/A	198 (81.2%)	114 (83.8%)	1.00	0.55	496.9	512.6
	G/G	46 (18.9%)	22 (16.2%)	0.84 (0.48-1.48)			
Overdominant	A/A-G/G	119 (48.8%)	70 (51.5%)	1.00	0.67	497.1	512.8
	G/A	125 (51.2%)	66 (48.5%)	0.91 (0.60-1.39)			
Log-additive	---	---	---	0.86 (0.63-1.17)	0.34	496.3	512.1

Interaction analysis with covariate ethnicity

rs0270 and ethnicity cross-classification interaction table (n=380, adjusted by gender)						
	1			**2**		
	status=0-control	**status=1-cese**	**OR (95% CI)**	**status=0-control**	**status=1-cese**	**OR (95% CI)**
A/A	50	26	1.00	23	22	1.88 (0.89-4.01)
G/A	90	39	0.84 (0.46-1.55)	35	27	1.52 (0.76-3.04)
G/G	32	14	0.88 (0.40-1.94)	14	8	1.09 (0.41-2.94)

Interaction p-value: 0.81

ethnicity within rs0270 (n=380, adjusted by gender)

		status=0-control	status=1-cese	OR (95% CI)
A/A	**1**	50	26	1.00
	2	23	22	1.88 (0.89-4.01)
		status=0-control	**status=1-cese**	**OR (95% CI)**
G/A	**1**	90	39	1.00
	2	35	27	1.80 (0.96-3.37)
		status=0-control	**status=1-cese**	**OR (95% CI)**
G/G	**1**	32	14	1.00
	2	14	8	1.25 (0.42-3.67)

Test for interaction in the trend: 0.58

rs0270 within ethnicity (n=380, adjusted by gender)

		status=0-control	status=1-cese	OR (95% CI)
1	**A/A**	50	26	1.00
	G/A	90	39	0.84 (0.46-1.55)
	G/G	32	14	0.88 (0.40-1.94)
		status=0-control	**status=1-cese**	**OR (95% CI)**
2	**A/A**	23	22	1.00
	G/A	35	27	0.80 (0.37-1.74)
	G/G	14	8	0.58 (0.20-1.66)

Test for interaction in the trend: 0.81

Multiple-SNP analysis

Linkage disequilibrium analysis

D statistic

```
       rs4256 rs0519 rs0270
rs4256      .  0.196 0.2263
rs0519      .      . 0.1852
rs0270      .      .      .
```

D' statistic

```
       rs4256 rs0519 rs0270
rs4256      . 0.9928 0.9997
rs0519      .      . 0.9921
rs0270      .      .      .
```

r statistic

```
       rs4256 rs0519 rs0270
rs4256      . 0.8534 0.9341
rs0519      .      . 0.7969
rs0270      .      .      .
```

P-values

```
       rs4256 rs0519 rs0270
rs4256      .      0      0
rs0519      .      .      0
rs0270      .      .      .
```

Haplotype analysis

Haplotype frequencies estimation (n=380)

	rs4256	rs0519	rs0270	Total	group.0.control	group.1.cese	Cumulative frequency
1	A	G	A	0.5683	0.5553	0.5916	0.5683
2	C	A	G	0.3262	0.3402	0.3012	0.8945

3	C	G	G	0.0712	0.0738	0.0665	0.9657
4	A	G	G	0.0329	0.0307	0.0368	0.9986
5	A	A	A	0.0014	NA	0.004	1

Haplotype association with response (n=380, adjusted by ethnicity+gender)						
	rs4256	**rs0519**	**rs0270**	**Freq**	**OR (95% CI)**	**P-value**
1	A	G	A	0.5683	1.00	---
2	C	A	G	0.3262	0.84 (0.59 - 1.18)	0.31
3	C	G	G	0.0712	0.83 (0.45 - 1.55)	0.56
4	A	G	G	0.0329	1.11 (0.50 - 2.43)	0.8
rare	*	*	*	0.0014	**833050856.68 (833050856.63 - 833050856.73)**	<0.0001
Global haplotype association p-value: 0.46						

Haplotype interaction analysis with covariate ethnicity

Haplotype and ethnicity cross-classification interaction table (n=380, adjusted by gender)			
		1	**2**
Haplotype	**Frequency**	**OR (95% CI)**	**OR (95% CI)**
AGA	0.5683	1.00	1.97 (0.99 - 3.95)
CAG	0.3262	0.87 (0.57 - 1.34)	1.56 (0.84 - 2.89)
CGG	0.0712	0.96 (0.44 - 2.12)	1.33 (0.45 - 3.97)
AGG	0.0329	1.21 (0.47 - 3.10)	1.86 (0.45 - 7.65)
rare	0.0014	Inf	Inf
Interaction p-value: 0.98			

Haplotypes within ethnicity (n=380, adjusted by gender)			
		1	**2**
Haplotype	**Frequency**	**OR (95% CI)**	**OR (95% CI)**
AGA	0.5683	1.00	1.00
CAG	0.3262	0.87 (0.57 - 1.34)	0.79 (0.44 - 1.42)
CGG	0.0712	0.96 (0.44 - 2.12)	0.68 (0.25 - 1.86)
AGG	0.0329	1.21 (0.47 - 3.10)	0.94 (0.23 - 3.84)
rare	0.0014	Inf	Inf

ethnicity whithin haplotypes (n=380, adjusted by gender)			
		1	**2**
Haplotype	**Frequency**	**OR (95% CI)**	**OR (95% CI)**
AGA	0.5683	1.00	1.97 (0.99 - 3.95)
CAG	0.3262	1.00	**1.79 (1.04 - 3.07)**
CGG	0.0712	1.00	1.39 (0.40 - 4.80)
AGG	0.0329	1.00	1.55 (0.30 - 7.90)
rare	0.0014	1.00	0.00 (-Inf - Inf)

<<< Step 3: Customize analysis