SNPStats results

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Descriptive statistics

Response variable: status **Type:** categorical

	n	missing	unique
All subjects	179	0	2
status=0-control	77 (43.02%)	---	---
status=1-cese	102 (56.98%)	---	---

Covariate: age **Type:** quantitative

	n	missing	unique	mean	.05	.10	.25	.50	.75	.90	.95
All subjects	179	0	59	50.29	22.9	29	40	51	61	69	76.1
status = 0-control	77	0	41	44.81	21.8	28.6	36	48	52	57.4	61
status = 1-cese	102	0	49	54.43	25.05	30	42.25	58	66	74	77

lowest: 18, 19, 20, 21, 22 highest: 77, 78, 80, 82, 86

Covariate: gender **Type:** categorical

	n	missing	unique
All subjects	179	0	2
status=0-control	77	0	2
status=1-cese	102	0	2

	FeMale	Male
All subjects	116 (65%)	63 (35%)
status=0-control	46 (60%)	31 (40%)
status=1-cese	70 (69%)	32 (31%)

Single-SNP analysis

SNP: rs4256

Percentage of typed samples: 179/179 (100%)

rs4256 allele frequencies (n=179)						
	All subjects		status=0-control		status=1-cese	
Allele	**Count**	**Proportion**	**Count**	**Proportion**	**Count**	**Proportion**
A	219	0.61	91	0.59	128	0.63
C	139	0.39	63	0.41	76	0.37

rs4256 genotype frequencies (n=179)						
	All subjects		status=0-control		status=1-cese	
Genotype	**Count**	**Proportion**	**Count**	**Proportion**	**Count**	**Proportion**
A/A	66	0.37	28	0.36	38	0.37
A/C	87	0.49	35	0.45	52	0.51
C/C	26	0.15	14	0.18	12	0.12

rs4256 exact test for Hardy-Weinberg equilibrium (n=179)						
	N11	**N12**	**N22**	**N1**	**N2**	**P-value**
All subjects	66	87	26	219	139	0.87
status=0-control	28	35	14	91	63	0.64
status=1-cese	38	52	12	128	76	0.41

rs4256 association with response status (n=179, adjusted by age+gender)							
Model	**Genotype**	**status=0-control**	**status=1-cese**	**OR (95% CI)**	**P-value**	**AIC**	**BIC**
Codominant	A/A	28 (36.4%)	38 (37.2%)	1.00			
	C/A	35 (45.5%)	52 (51%)	0.88 (0.44-1.76)	0.45	234.2	250.1
	C/C	14 (18.2%)	12 (11.8%)	0.54 (0.20-1.43)			
Dominant	A/A	28 (36.4%)	38 (37.2%)	1.00	0.47	233.3	246
	C/A-C/C	49 (63.6%)	64 (62.8%)	0.79 (0.41-1.52)			
Recessive	A/A-C/A	63 (81.8%)	90 (88.2%)	1.00	0.23	232.3	245.1
	C/C	14 (18.2%)	12 (11.8%)	0.58 (0.24-1.41)			
Overdominant	A/A-C/C	42 (54.5%)	50 (49%)	1.00	0.87	233.8	246.5
	C/A	35 (45.5%)	52 (51%)	1.06 (0.56-1.98)			
Log-additive	---	---	---	0.76 (0.48-1.22)	0.26	232.5	245.3

Interaction analysis with covariate gender

rs4256 and gender cross-classification interaction table (n=179, adjusted by age)						
	FeMale			**Male**		
	status=0-control	**status=1-cese**	**OR (95% CI)**	**status=0-control**	**status=1-cese**	**OR (95% CI)**
A/A	16	22	1.00	12	16	0.97 (0.34-2.74)
C/A	19	39	1.14 (0.46-2.79)	16	13	0.57 (0.21-1.59)
C/C	11	9	0.49 (0.15-1.56)	3	3	0.88 (0.15-5.24)
Interaction p-value: 0.43						

gender within rs4256 (n=179, adjusted by age)				
A/A		**status=0-control**	**status=1-cese**	**OR (95% CI)**
	FeMale	16	22	1.00
	Male	12	16	0.97 (0.34-2.74)
C/A		**status=0-control**	**status=1-cese**	**OR (95% CI)**
	FeMale	19	39	1.00
	Male	16	13	0.50 (0.19-1.31)
C/C		**status=0-control**	**status=1-cese**	**OR (95% CI)**
	FeMale	11	9	1.00
	Male	3	3	1.78 (0.26-12.01)
Test for interaction in the trend: 0.91				

rs4256 within gender (n=179, adjusted by age)				
FeMale		**status=0-control**	**status=1-cese**	**OR (95% CI)**
	A/A	16	22	1.00
	C/A	19	39	1.14 (0.46-2.79)
	C/C	11	9	0.49 (0.15-1.56)
Male		**status=0-control**	**status=1-cese**	**OR (95% CI)**
	A/A	12	16	1.00
	C/A	16	13	0.59 (0.20-1.76)
	C/C	3	3	0.90 (0.14-5.64)
Test for interaction in the trend: 0.43				

SNP: rs0519

Percentage of typed samples: 179/179 (100%)

rs0519 allele frequencies (n=179)

	All subjects		status=0-control		status=1-cese	
Allele	**Count**	**Proportion**	**Count**	**Proportion**	**Count**	**Proportion**
G	244	0.68	105	0.68	139	0.68
A	114	0.32	49	0.32	65	0.32

rs0519 genotype frequencies (n=179)						
	All subjects		status=0-control		status=1-cese	
Genotype	**Count**	**Proportion**	**Count**	**Proportion**	**Count**	**Proportion**
A/A	14	0.08	6	0.08	8	0.08
G/A	86	0.48	37	0.48	49	0.48
G/G	79	0.44	34	0.44	45	0.44

rs0519 exact test for Hardy-Weinberg equilibrium (n=179)						
	N11	**N12**	**N22**	**N1**	**N2**	**P-value**
All subjects	79	86	14	244	114	0.17
status=0-control	34	37	6	105	49	0.44
status=1-cese	45	49	8	139	65	0.36

rs0519 association with response status (n=179, adjusted by age+gender)							
Model	**Genotype**	**status=0-control**	**status=1-cese**	**OR (95% CI)**	**P-value**	**AIC**	**BIC**
Codominant	G/G	34 (44.2%)	45 (44.1%)	1.00			
	A/G	37 (48%)	49 (48%)	0.82 (0.42-1.59)	0.82	235.4	251.4
	A/A	6 (7.8%)	8 (7.8%)	0.80 (0.23-2.71)			
Dominant	G/G	34 (44.2%)	45 (44.1%)	1.00	0.54	233.4	246.2
	A/G-A/A	43 (55.8%)	57 (55.9%)	0.82 (0.43-1.55)			
Recessive	G/G-A/G	71 (92.2%)	94 (92.2%)	1.00	0.84	233.8	246.5
	A/A	6 (7.8%)	8 (7.8%)	0.89 (0.27-2.85)			
Overdominant	G/G-A/A	40 (52%)	53 (52%)	1.00	0.61	233.5	246.3
	A/G	37 (48%)	49 (48%)	0.85 (0.45-1.60)			
Log-additive	---	---	---	0.86 (0.52-1.43)	0.56	233.5	246.2

Interaction analysis with covariate gender

rs0519 and gender cross-classification interaction table (n=179, adjusted by age)						
	FeMale			Male		
	status=0-control	**status=1-cese**	**OR (95% CI)**	**status=0-control**	**status=1-cese**	**OR (95% CI)**
G/G	20	27	1.00	14	18	0.97 (0.37-2.51)
A/G	21	37	1.01 (0.44-2.33)	16	12	0.56 (0.21-1.51)
A/A	5	6	0.67 (0.16-2.70)	1	2	1.77 (0.14-23.01)
Interaction p-value: 0.48						

gender within rs0519 (n=179, adjusted by age)				
		status=0-control	**status=1-cese**	**OR (95% CI)**
G/G	**FeMale**	20	27	1.00
	Male	14	18	0.97 (0.37-2.51)
		status=0-control	**status=1-cese**	**OR (95% CI)**
A/G	**FeMale**	21	37	1.00
	Male	16	12	0.55 (0.21-1.45)
		status=0-control	**status=1-cese**	**OR (95% CI)**
A/A	**FeMale**	5	6	1.00
	Male	1	2	2.65 (0.16-43.48)
Test for interaction in the trend: 0.88				

rs0519 within gender (n=179, adjusted by age)				
FeMale		**status=0-control**	**status=1-cese**	**OR (95% CI)**
	G/G	20	27	1.00

	A/G	21	37	1.01 (0.44-2.33)
	A/A	5	6	0.67 (0.16-2.70)
Male		**status=0-control**	**status=1-cese**	**OR (95% CI)**
	G/G	14	18	1.00
	A/G	16	12	0.58 (0.20-1.68)
	A/A	1	2	1.83 (0.14-24.56)
Test for interaction in the trend: 0.48				

SNP: rs0270

Percentage of typed samples: 179/179 (100%)

rs0270 allele frequencies (n=179)						
	All subjects		**status=0-control**		**status=1-cese**	
Allele	**Count**	**Proportion**	**Count**	**Proportion**	**Count**	**Proportion**
A	202	0.56	85	0.55	117	0.57
G	156	0.44	69	0.45	87	0.43

rs0270 genotype frequencies (n=179)						
	All subjects		**status=0-control**		**status=1-cese**	
Genotype	**Count**	**Proportion**	**Count**	**Proportion**	**Count**	**Proportion**
A/A	56	0.31	23	0.3	33	0.32
A/G	90	0.5	39	0.51	51	0.5
G/G	33	0.18	15	0.19	18	0.18

rs0270 exact test for Hardy-Weinberg equilibrium (n=179)						
	N11	**N12**	**N22**	**N1**	**N2**	**P-value**
All subjects	56	90	33	202	156	0.88
status=0-control	23	39	15	85	69	1
status=1-cese	33	51	18	117	87	1

rs0270 association with response status (n=179, adjusted by age+gender)							
Model	**Genotype**	**status=0-control**	**status=1-cese**	**OR (95% CI)**	**P-value**	**AIC**	**BIC**
Codominant	A/A	23 (29.9%)	33 (32.4%)	1.00			
	G/A	39 (50.6%)	51 (50%)	0.66 (0.32-1.38)	0.48	234.3	250.3
	G/G	15 (19.5%)	18 (17.6%)	0.64 (0.25-1.62)			
Dominant	A/A	23 (29.9%)	33 (32.4%)	1.00	0.23	232.4	245.1
	G/A-G/G	54 (70.1%)	69 (67.7%)	0.65 (0.33-1.31)			
Recessive	A/A-G/A	62 (80.5%)	84 (82.3%)	1.00	0.64	233.6	246.3
	G/G	15 (19.5%)	18 (17.6%)	0.82 (0.36-1.85)			
Overdominant	A/A-G/G	38 (49.4%)	51 (50%)	1.00	0.45	233.2	246
	G/A	39 (50.6%)	51 (50%)	0.78 (0.41-1.48)			
Log-additive	---	---	---	0.78 (0.49-1.23)	0.29	232.7	245.4

Interaction analysis with covariate gender

rs0270 and gender cross-classification interaction table (n=179, adjusted by age)						
	FeMale			**Male**		
	status=0-control	**status=1-cese**	**OR (95% CI)**	**status=0-control**	**status=1-cese**	**OR (95% CI)**
A/A	13	20	1.00	10	13	0.83 (0.26-2.60)
G/A	21	36	0.74 (0.29-1.93)	18	15	0.45 (0.16-1.27)
G/G	12	14	0.54 (0.17-1.65)	3	4	0.98 (0.18-5.42)
Interaction p-value: 0.54						

gender within rs0270 (n=179, adjusted by age)				
A/A		**status=0-control**	**status=1-cese**	**OR (95% CI)**
	FeMale	13	20	1.00

	Male	10	13	0.83 (0.26-2.60)
G/A		**status=0-control**	**status=1-cese**	**OR (95% CI)**
	FeMale	21	36	1.00
	Male	18	15	0.60 (0.24-1.51)
G/G		**status=0-control**	**status=1-cese**	**OR (95% CI)**
	FeMale	12	14	1.00
	Male	3	4	1.82 (0.31-10.65)
Test for interaction in the trend: 0.73				

rs0270 within gender (n=179, adjusted by age)				
FeMale		**status=0-control**	**status=1-cese**	**OR (95% CI)**
	A/A	13	20	1.00
	G/A	21	36	0.74 (0.29-1.93)
	G/G	12	14	0.54 (0.17-1.65)
Male		**status=0-control**	**status=1-cese**	**OR (95% CI)**
	A/A	10	13	1.00
	G/A	18	15	0.54 (0.17-1.69)
	G/G	3	4	1.18 (0.20-6.98)
Test for interaction in the trend: 0.54				

Multiple-SNP analysis

Linkage disequilibrium analysis

D statistic

	rs4256	rs0519	rs0270
rs4256	.	0.1947	0.219
rs0519	.	.	0.1796
rs0270	.	.	.

D' statistic

	rs4256	rs0519	rs0270
rs4256	.	0.9998	0.9997
rs0519	.	.	0.9997
rs0270	.	.	.

r statistic

	rs4256	rs0519	rs0270
rs4256	.	0.8578	0.9063
rs0519	.	.	0.7776
rs0270	.	.	.

P-values

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

Haplotype analysis

Haplotype frequencies estimation (n=179)							
	rs4256	**rs0519**	**rs0270**	**Total**	**group.0.control**	**group.1.cese**	**Cumulative frequency**
1	A	G	A	0.5642	0.5519	0.5735	0.5642
2	C	A	G	0.3184	0.3182	0.3186	0.8827
3	C	G	G	0.0698	0.0909	0.0539	0.9525
4	A	G	G	0.0475	0.039	0.0539	1

Haplotype association with response (n=179, adjusted by age+gender)

	rs4256	rs0519	rs0270	Freq	OR (95% CI)	P-value
1	A	G	A	0.5642	1.00	---
2	C	A	G	0.3184	0.83 (0.49 - 1.41)	0.49
3	C	G	G	0.0698	0.56 (0.23 - 1.40)	0.22
4	A	G	G	0.0475	1.00 (0.32 - 3.10)	1
Global haplotype association p-value: 0.59						

Haplotype interaction analysis with covariate gender

Haplotype and gender cross-classification interaction table (n=179, adjusted by age)			
		FeMale	**Male**
Haplotype	**Frequency**	**OR (95% CI)**	**OR (95% CI)**
AGA	0.5642	1.00	0.68 (0.24 - 1.90)
CAG	0.3184	0.83 (0.44 - 1.58)	0.57 (0.22 - 1.46)
AGG	0.0475	0.80 (0.19 - 3.35)	1.01 (0.16 - 6.41)
CGG	0.0698	0.50 (0.17 - 1.48)	0.54 (0.10 - 3.00)
Interaction p-value: 0.93			

Haplotypes within gender (n=179, adjusted by age)			
		FeMale	**Male**
Haplotype	**Frequency**	**OR (95% CI)**	**OR (95% CI)**
AGA	0.5642	1.00	1.00
CAG	0.3184	0.83 (0.44 - 1.58)	0.84 (0.34 - 2.08)
AGG	0.0475	0.80 (0.19 - 3.35)	1.49 (0.23 - 9.53)
CGG	0.0698	0.50 (0.17 - 1.48)	0.79 (0.15 - 4.18)

gender whithin haplotypes (n=179, adjusted by age)			
		FeMale	**Male**
Haplotype	**Frequency**	**OR (95% CI)**	**OR (95% CI)**
AGA	0.5642	1.00	0.68 (0.24 - 1.90)
CAG	0.3184	1.00	0.68 (0.30 - 1.57)
AGG	0.0475	1.00	1.25 (0.14 - 11.36)
CGG	0.0698	1.00	1.08 (0.16 - 7.31)

<<< Step 3: Customize analysis