

	SNP	slope	intercept	rvalue	pvalue	stderr
STX3 threshold = 0.001	rs78578195	0.151545603	0.026644268	0.078284099	1.60972E-06	0.031540386
	rs149718569	-0.13992187	0.015052994	-0.068690832	2.57914E-05	0.03321176
	rs17154394	-0.061894688	0.026254847	-0.056287633	0.000567597	0.017942518
	rs147809952	-0.102232743	0.014846399	-0.057489013	0.000431014	0.02901472
STX3 threshold = 0.05	rs78578195	0.151545603	0.026644268	0.078284099	1.60972E-06	0.031540386
	rs149718569	-0.13992187	0.015052994	-0.068690832	2.57914E-05	0.03321176
	rs17154394	-0.061894688	0.026254847	-0.056287633	0.000567597	0.017942518
	rs147809952	-0.102232743	0.014846399	-0.057489013	0.000431014	0.02901472
	rs143663006	-0.075705096	0.009639971	-0.040827239	0.012453667	0.030279237
	rs12277676	0.036821622	-0.025930443	0.03836352	0.018869268	0.015674609
	rs76109966	-0.06894834	0.013049753	-0.044388437	0.006583522	0.025360497
	rs2123679	0.034582052	-0.023550138	0.035891996	0.02803981	0.015736398
	rs12791616	-0.059144916	0.01310472	-0.040781375	0.012552751	0.023682426
SREBF2 threshold = 0.001	rs41311445	0.094166654	-0.047038834	0.096667938	3.05838E-09	0.015845577
	rs742086	-0.037289623	0.021740667	-0.057365217	0.00044352	0.010606099
	rs9607850	-0.033116235	0.029783394	-0.055897126	0.000620038	0.009667274
SREBF2 threshold = 0.05	rs41311445	0.094166654	-0.047038834	0.096667938	3.05838E-09	0.015845577
	rs742086	-0.037289623	0.021740667	-0.057365217	0.00044352	0.010606099
	rs9607850	-0.033116235	0.029783394	-0.055897126	0.000620038	0.009667274
	rs34344173	-0.03716766	0.005655517	-0.033535031	0.04013182	0.018103154

The models generated for STX3 and SREBF2 by the method using the series of single linear regressions. The Index indicates the performed run giving the gene for which the Cis-eQTL SNPs were identified and the p-value threshold used during the run. The columns give in order: **SNP**, the code of the Cis-eQTL SNP; **Slope**, the slope of the variable of the model. **Intercept**, the intercept of the SNP model; **rvalue**, the Pearson rank correlation between the prediction made by the model of the SNP and the measurements; **pvalue**, the probability that the slope of the model is not zero and that there is an association between the x (genotype of SNP) and y-value (gene expression) of the model. Each SNP given a linear regression model in which the genotype of that SNP was the single variable, which is why the method is said to use a series of single linear regressions)

	Component	Intercept	Coefficients
STX3 threshold = 0.001	Intercept	0.088529045	
	rs147809952		-0.104819748
	rs149718569		-0.160029855
	rs17154394		-0.065419598
	rs78578195		0.136937191
STX3 threshold = 0.05	Intercept	0.041955264	
	rs112505206		0.057106107
	rs12277676		0.074728256
	rs12791616		-0.139459696
	rs143663006		-0.128140354
	rs147809952		-0.103219982
	rs149718569		-0.152626459
	rs17154394		-0.058852962
	rs2123679		0.050493793

	rs61903579		0.151421807
	rs72927436		-0.173251409
	rs76109966		-0.113988964
	rs78578195		0.146416274
SREBF2 threshold = 0.001	Intercept	-0.026927554	
	rs41311445		0.107012117
	rs742086		-0.039182549
SREBF2 threshold = 0.05	Intercept	0.001278249	
	rs132762		-0.036332815
	rs41311445		0.096244168
	rs742086		-0.044903286

The models generated for STX3 and SREBF2 by the method using the Multivariate linear regressions. The Index indicates the performed run giving the gene for which the Cis-eQTL SNPs were indentified and the p-value threshold used during the run. The columns give in order: **Component**, the component of the model which is either the intercept or a SNP which is a variable in the model; **Intercept**, the value of the intercept of the model (only for intercept component); **Coefficients**, the coefficient value of a variable of the model (only for SNP components of the model).

	Component	Intercept	Coefficients	p-values
SREBF2 using eQTLgen pipeline Cis-eQTL SNPs	Intercept	0.016156718		0.482818201
	rs133369		-0.149103191	0.550295359
	rs6002546		0.003845065	0.793049334
	rs133368		0.099871739	0.682020291
	rs5758566		-0.296581338	0.170939631
	rs2301521		-0.055643674	0.818235464
	rs133350		-0.056466394	0.840562837
	rs2854837		0.424876835	0.073535754
STX3 using eQTLgen pipeline Cis-eQTL SNPs	Intercept	0.0342839		0.012007981
	rs11607283		-0.390075416	0.12490411
	rs11230061		0.061634533	0.001425332
	rs147809952		-0.130659698	0.292174027
	rs74559732		0.36116189	0.15620291
	rs61901646		0.082722411	0.399972674

	rs77558100		-0.00560233	0.933328484
SREBF2 using toRegressOut.log.gz Cis-eQTL SNPs	Intercept	-0.013339186		0.429310109
	rs133367		-0.046914384	1.58435E-06
	rs2076198		0.041592903	1.52652E-05
STX3 using toRegressOut.log.gz Cis-eQTL SNPs	Intercept	0.007547396		0.536464098
	rs77952732		0.15485743	1.07225E-06
	rs118030976		0.100602523	9.28034E-05

The models generated for STX3 and SREBF2 using SNP identified by external methods. The Index indicates the gene of the model as well as the external method used to obtain the Cis-eQTL SNPs of that gene. The columns give in order: **Component**, the component of the model which is either the intercept or a SNP which is a variable in the model; **Intercept**, the value of the intercept of the model (only for intercept component); **Coefficients**, the coefficient value of a variable of the model (only for SNP components of the model); **p-values**, gives the p-value of the component of the model (indicates the probability that any association between that component and the gene expression is due to random chance).

	Component	Intercept	Coefficients	p-values
NOD2 using eQTLgen pipeline Cis-eQTL SNPs for STX3, initialization using predicted values of STX3	Intercept	-0.469642175		1.6148E-301
	rs1981760		0.97762827	0
	ENSG00000166900		-0.061765056	0.709068745
	rs1981760 * ENSG00000166900		0.031532872	0.882010185
FADS2 using eQTLgen pipeline Cis-eQTL SNPs for SREBF2, initialization using predicted values of SREBF2	Intercept	-1.146713678		0
	rs968567		3.231339464	0
	ENSG00000198911		-0.348737453	0.509034818
	rs968567 * ENSG00000198911		2.036018994	0.015369611
NOD2 using toRegressOut.log.gz Cis-eQTL SNPs for STX3, initialization using predicted values of STX3	Intercept	-0.482088554		0
	rs1981760		0.981937345	0
	ENSG00000166900		0.223776898	0.107519563
	rs1981760 * ENSG00000166900		-0.072683895	0.678446514
FADS2 using toRegressOut.log.gz Cis-eQTL SNPs for	Intercept	-1.139895126		0
	rs968567		3.178320361	0

STX3, initialization using predicted values of STX3	ENSG00000198911		-0.105031956	0.734113509
	rs968567 * ENSG00000198911		0.122903176	0.806800686
NOD2 initialization using measured values of STX3	Intercept	-0.469506786		0
	rs1981760		0.971215722	0
	ENSG00000166900		-0.046452912	0.000705546
	rs1981760 * ENSG00000166900		0.118318389	6.20247E-12
FADS2 initialization using measured values of SREBF2	Intercept	-1.105159287		0
	rs968567		3.143690481	0
	ENSG00000198911		0.740127852	8.5968E-123
	rs968567 * ENSG00000198911		-0.370642814	2.68643E-13

The Interactions models generated for NOD2 and FADS2 . The Index indicates the gene of the model, the external method used to obtain the Cis-eQTL SNPs of that gene and whether or not the model was initialized using the predicted or the measured values of the TF gene (STX3 or SREBF2). The columns give in order: **Component**, the component of the model which is either the intercept or a SNP which is a variable in the model; **Intercept**, the value of the intercept of the model (only for intercept component); **Coefficients**, the coefficient value of a variable of the model (only for SNP components of the model); **p-values**, gives the p-value of the component of the model (indicates the probability that any association between that component and the gene expression is due to random chance).