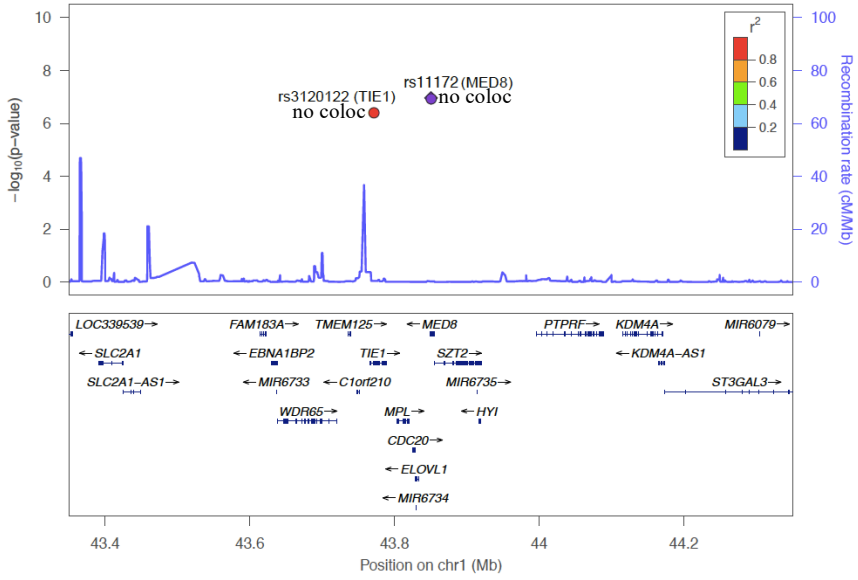
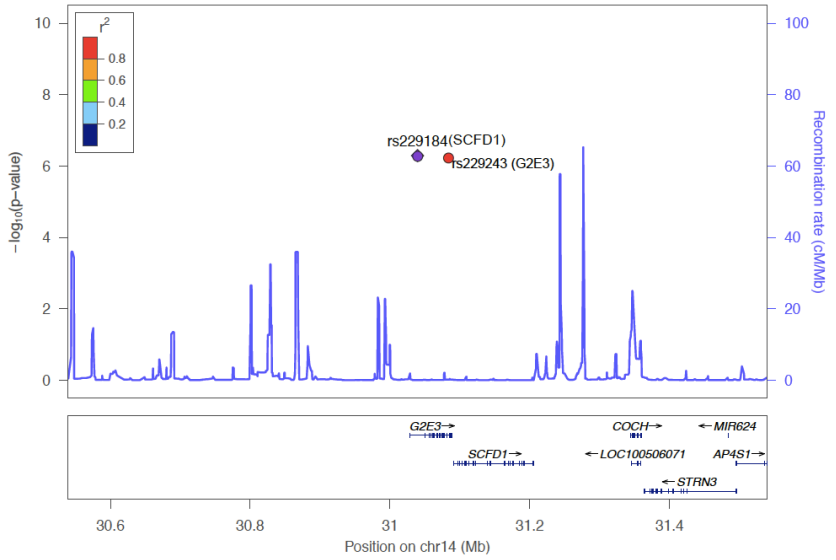
Figure 1 Genomic context and pairwise LD (r^2) for the genes associated in the main Wald Ratio analysis where the eQTL instruments resided within the same genomic location. Genes which did not colocalise with the outcome (PP_4<70%) are labelled as no coloc on the plot. Y axis on the regional association plot shows the – $\log_{10}$ scaled p-value for the Wald Ratio between the gene and trait. (a) ADHD 1p34.2 associations (b) ALS 14q12 associations (c) AD 7q22.1 associations (d) AD 16p11.2 associations (e) PD 7p15.3 associations (f) PD 16p11.2 associations (g) PD 17q21.31 associations (h) Sz 2q33.1 associations (i) Sz 3p21.1 associations (j) Sz 8p23.1 associations (k) Sz 10q 24.32 associations (l) Sz 22q13.2 associations (m) Sz 15q25.1 – 15q26.1 associations

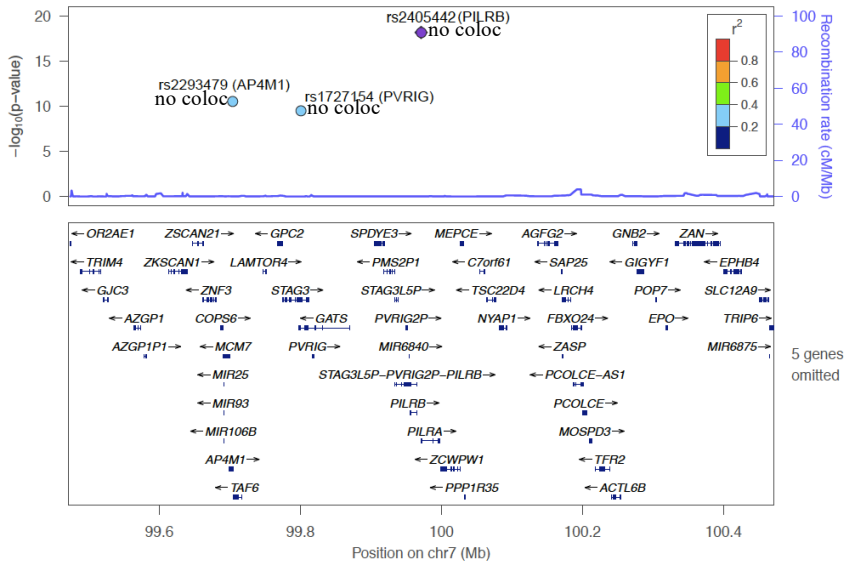
(a) ADHD 1p34.2 associations (*TIE1* and *MED8* eQTLs, r^2=0.877)



(b) ALS 14q12 associations (*SCFD1* and *G2E3* eQTLs, r^2=0.991)

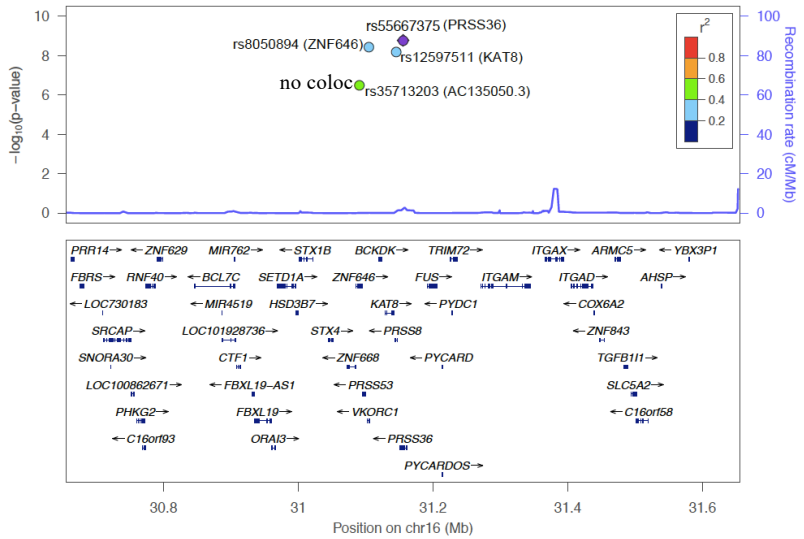


(c) AD 7q22.1 associations (*AP4M1, PVRIG* and *PILRB* eQTLs)



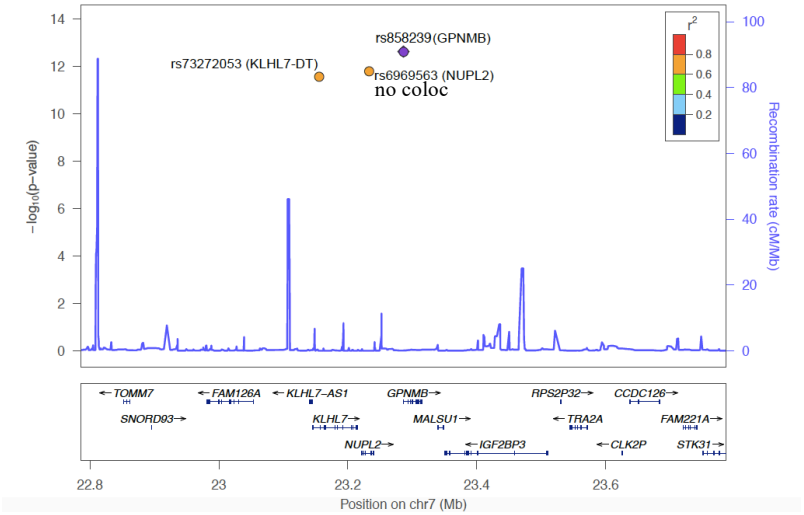
r² matrix	**rs2293479**	**rs1727145**
rs2293479 (*AP4M1*)	1	
rs1727145 (*PVRIG*)	0.273	1
rs2405442 (*PILRB*)	0.335	0.366

(d) AD 16p11.2 associations (*AC135050.3*, *ZNF646*, *KAT8*, and *PRSS36* eQTLs)



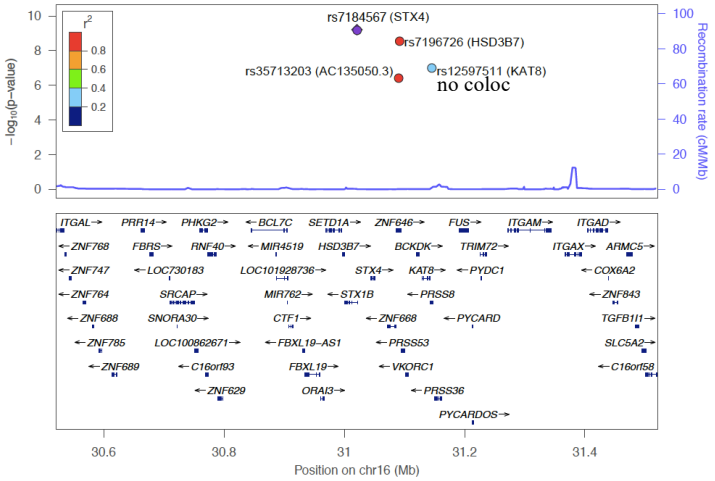
r² matrix	**rs35713203**	**rs8050894**	**rs12597511**
rs35713203 (*AC135050.3*)	1		
rs8050894 (*ZNF646*)	0.375	1	
rs12597511 (*KAT8*)	0.351	0.845	1
rs55667375 (*PRSS36*)	0.558	0.197	0.241

(e) PD 7p15.3 associations (*KLHL7-DT*, *NUPL2* and *GPNMB* eQTLs)



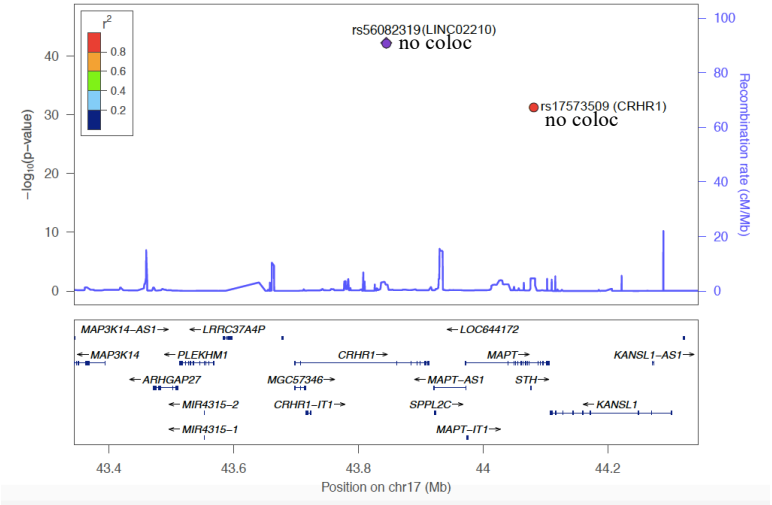
r² matrix	**rs73272053**	**rs6969563**
rs73272053 (*KLHL7-DT*)	1	
rs6969563 (*NUPL2*)	0.888	1
rs858239 (*GPNMB*)	0.641	0.65

(f) PD 16p11.2 associations (*STX4, AC135050.3, HSD3B7* and *KAT8* eQTLs)



r² matrix	**rs7184567**	**rs35713203**	**rs7196726**	**rs12597511**
rs718456 (*STX4*)	1			
rs35713203 (*AC135050.3*)	0.892	1		
rs7196726 (*HSD3B7*)	0.941	0.933	1	
rs12597511 (*KAT8*)	0.344	0.351	0.363	1

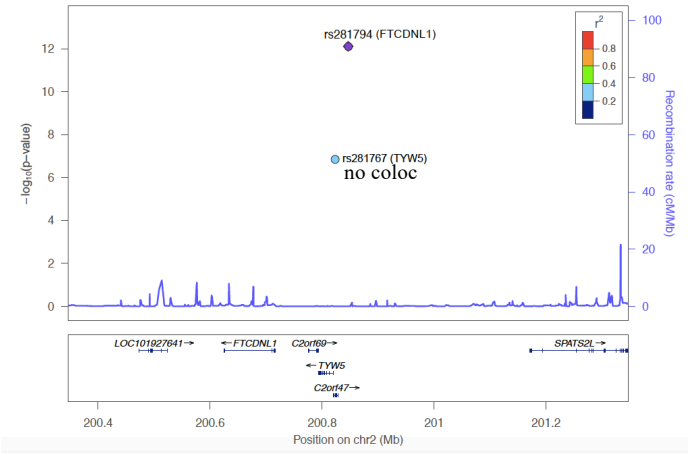
(g) PD 17q21.31 associations (*CRHR1* and *LINC02210* eQTLs)



r² matrix	rs5848	rs56082319
rs5848 (*GRN*)	1	
rs56082319 (*LINC02210*)	0.0	1
rs17573509 (*CRHR1*)	0.0	0.978

**GRN* is in the 17q21.3 arm (not plotted) as independent of the *LINC02210* and *CRHR1* instruments.

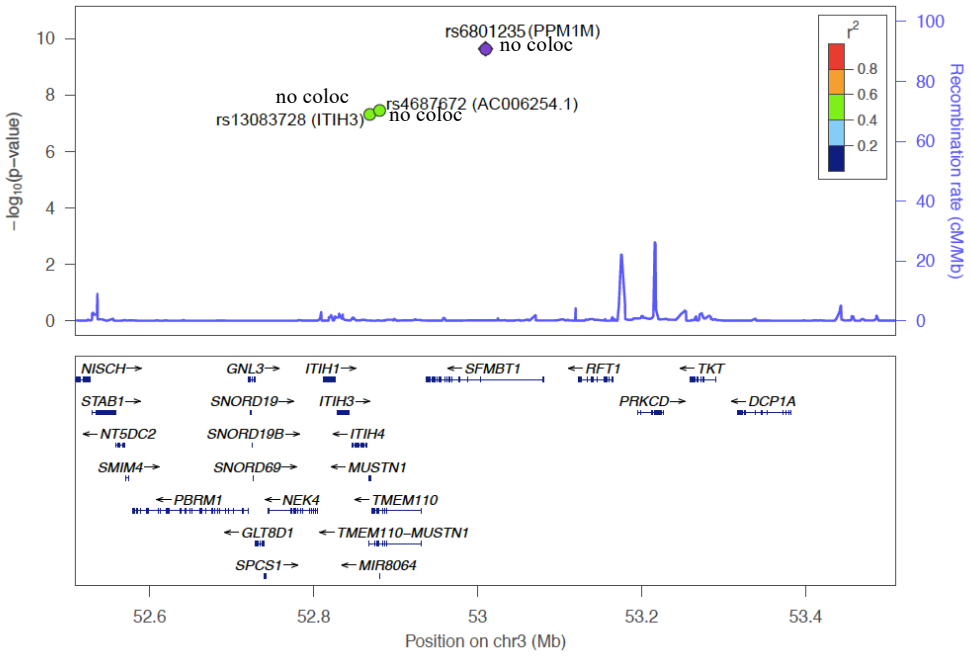
(h) Sz 2q33.1 associations (*TYW5* and *FTCDNL1* eQTLs)



r² matrix	rs2564383	rs281767
rs2564383 (*SF3B1*)	1	
rs281767 (*TYW5*)	0.001	1
rs281794 (*FTCDNL1*)	0.005	0.393

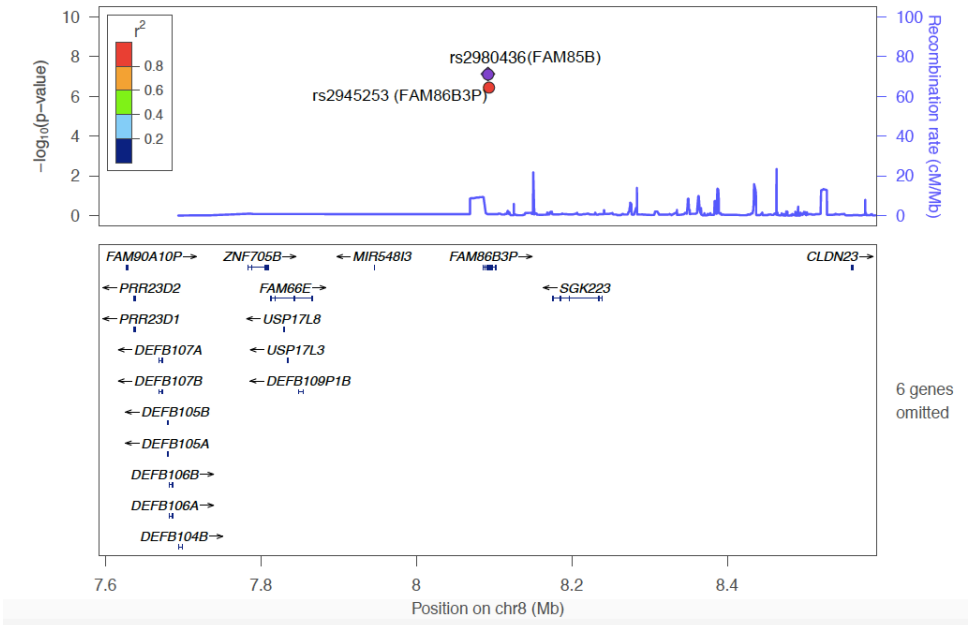
**SF3B1* is in the 2q33.1 arm (not plotted) as independent of the *TYW5* and *FTCDNL1* instruments.

(i) Sz 3p21.1 associations (*ITIH3*, *AC006254.1* and *PPM1M* eQTLs)

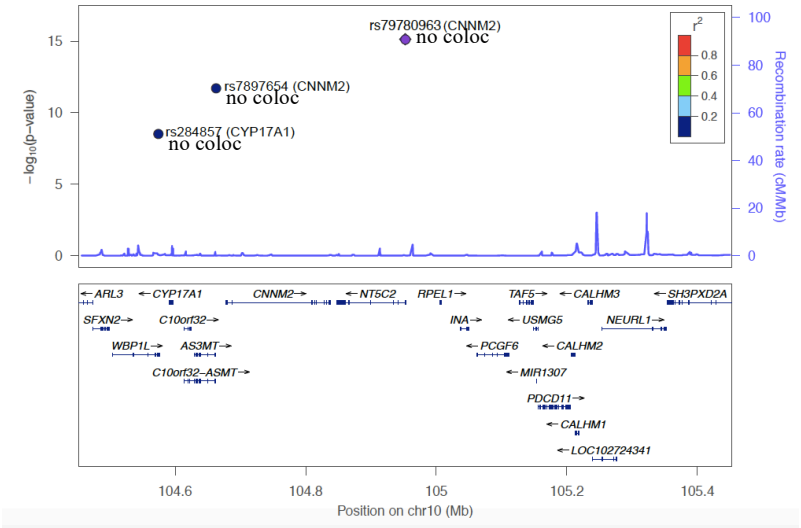


r² matrix	**rs13083728**	**rs4687672**
rs13083728 (*ITIH3*)	1	
rs4687672 (*AC006254.1*)	0.964	1
rs6801235 (*PPM1M*)	0.579	0.603

(j) Sz 8p23.1 associations (*FAM85B* and *FAM86B3P* eQTLs, r^2=0.832)

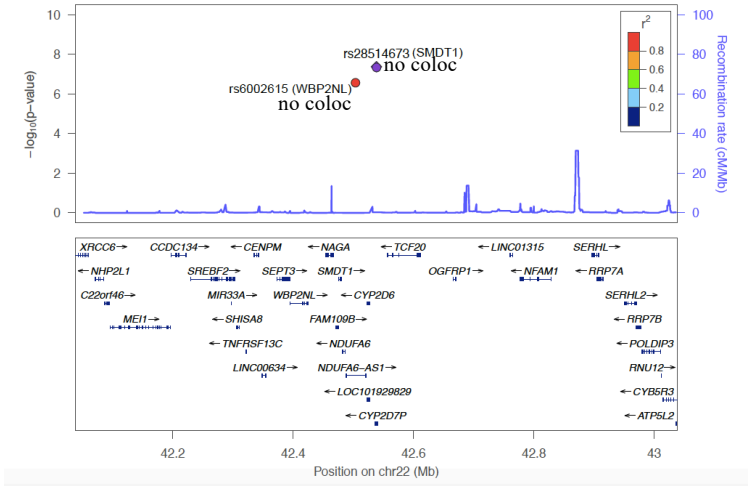


(k) Sz 10q 24.32 associations (*CYP17A1* and *CNMM2* eQTLs)



r² matrix	rs284857	rs7897654
rs284857 (*CYP17A1*)	1	
rs7897654 (*CNMM2*)	0.174	1
rs79780963 (*CNMM2*)	0.0	0.0

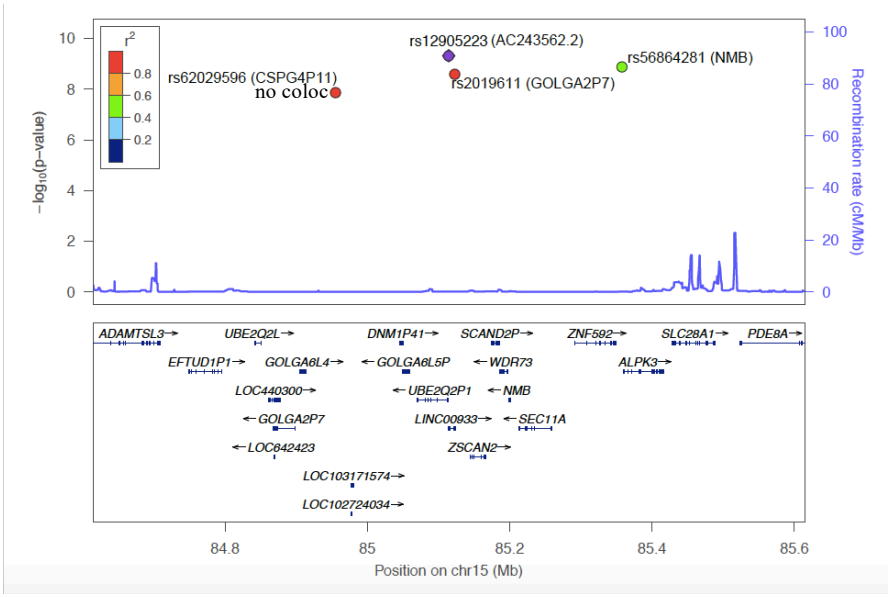
(l) Sz 22q13.2 associations (*WBP2NL* and *SMDT1* eQTLs)

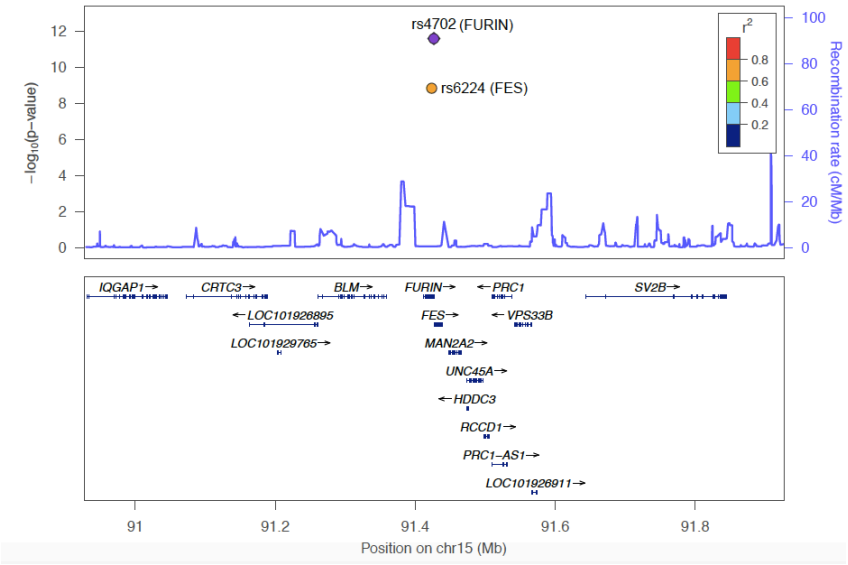


r² matrix	rs11090045	rs6002615
rs11090045 (*ZC3H7B*)	1	
rs6002615 (*WBP2NL*)	0.002	1
rs28514673 (*SMDT1*)	0.001	0.96

**ZC3H7B* is in the 2q13.2arm (not plotted) as independent of the *WBP2NL* and *SMDT1* instruments.

(m) Sz 15q25.1 – 15q26.1 associations (*CSPG4P11, AC243562.2, GOLGA2P7* and *NMB* eQTLs, *FES* and *FURIN* eQTLs)





r² matrix	rs11072763	rs62029596	rs12905223	rs2019611	rs5686428	rs6224
rs11072763 (*IREB2*)	1					
rs62029596 (*CSPG4P11*)	0.0	1				
rs12905223 (*AC243562.2*)	0.0	0.99	1			
rs2019611 (*GOLGA2P7*)	0.0	0.9	0.91	1		
rs56864281 (*NMB*)	0.001	0.579	0.58	0.552	1	
rs6224 (*FES*)	0.0	0.002	0.003	0.002	0.001	1
rs4702 (*FURIN*)	0.001	0.001	0.002	0.002	0.0	0.686

**IREB2* is in the same region (not plotted) as independent of the other gene instruments.