ESM_4 Rare variants identified in *GABRA4* overlapping with ENCODE features from Fetal CNS

Variant	dbSNP138 ID	Functional Category	ASD Cases MAF	Controls MAF	1000 Genomes Release 3 MAF	DNAse Hypersensitivy	CTCF Binding	Putative Enhancers (H3K4me1 and/or H3K9ac)
chr4.hg19:46933966T>C	rs17641386	intronic	0.3544	0.3333	0.230631	X	X	X
chr4.hg19:46933990T>C	rs17599158	intronic	0.3563	0.3333	0.230631	X	X	X
chr4.hg19:46934014T>G	rs12508654	intronic	0.3563	0.3333	0.371206	X	X	X
chr4.hg19:46934233A>G	rs74994602	intronic	0.01829	0.009091	0.00698882	X	X	X
chr4.hg19:46936899A>G	rs6843462	intronic	0.358	0.3273	0.557308	X		
chr4.hg19:46937023C>T	rs75822667	intronic	0.03049	0.01818	0.00938498	X		
chr4.hg19:46939651C>A	rs189857459	intronic	0.03125	0.009091	0.0061901		X	
chr4.hg19:46939779T>C	.	intronic	0.00625	0	0.00159744		X	
chr4.hg19:46949319C>T	.	intronic	0.006098	0	0.00159744	X		X
chr4.hg19:46973270G>A	rs45625131	intronic	0.03659	0.05455	0.00858626	X		X
chr4.hg19:46978365C>A	rs3792210	intronic	0.006098	0	0.0940495	X		X
chr4.hg19:46981880C>T	rs149960734	intronic	0.04938	0.009091	0.0155751	X		
chr4.hg19:46981907A>G	.	intronic	0	0.009091	0.000199681	X		
chr4.hg19:46983062T>G	rs73813760	intronic	0.01235	0	0.13099	X		X
chr4.hg19:46983078C>A	rs73813761	intronic	0.01235	0	0.13099	X		X
chr4.hg19:46983118A>G	rs192188284	intronic	0.006098	0	0.000798722	X		X
chr4.hg19:46987026A>G	rs189422096	intronic	0.006098	0.009091	0.000199681	X		
chr4.hg19:46994430A>T	.	intronic	0	0.009091	0	X		
chr4.hg19:46995050G>C	rs112472467	intronic	0.0122	0.009091	0.00499201	X		
chr4.hg19:46995366G>T	rs2229940	exonic	0.4383	0.4	0.300719	X		
chr4.hg19:46995653G>T	rs13151759	UTR5	0.4321	0.4	0.326078	X		
chr4.hg19:46995660G>A	rs13151769	UTR5	0.4321	0.3909	0.325879	X		
chr4.hg19:46996824A>G	rs186233707	intergenic	0	0.009091	0.000199681	X		
chr4.hg19:47001790A>G	rs11729000	intergenic	0.006098	0.009091	0.120607	X		
chr4.hg19:47001870T>C	rs75197150	intergenic	0	0.009091	0.00239617	X		