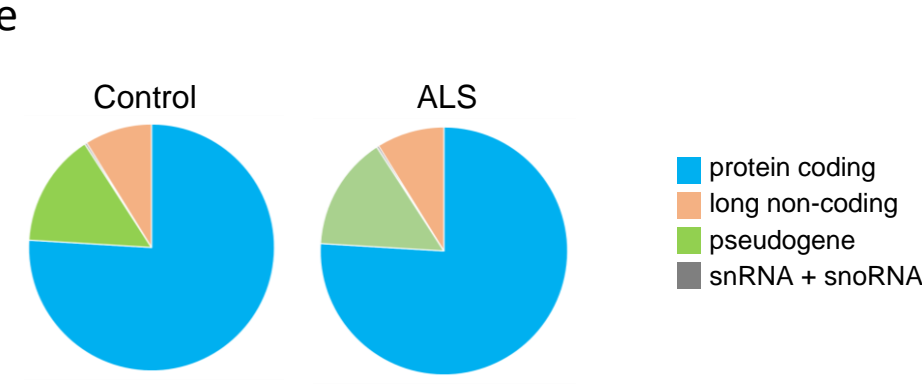
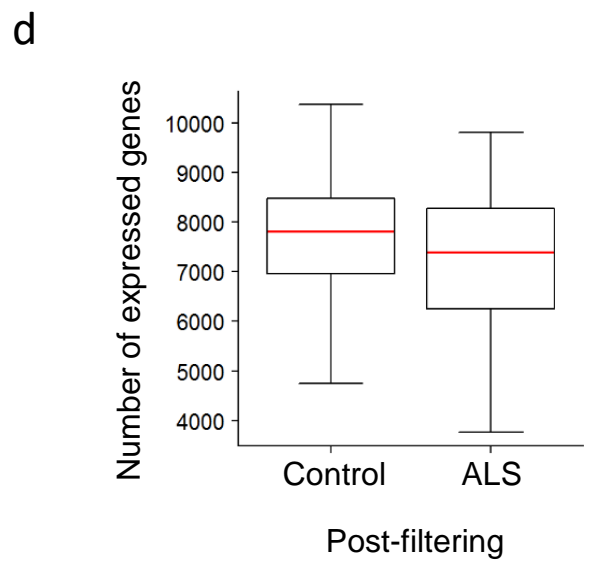
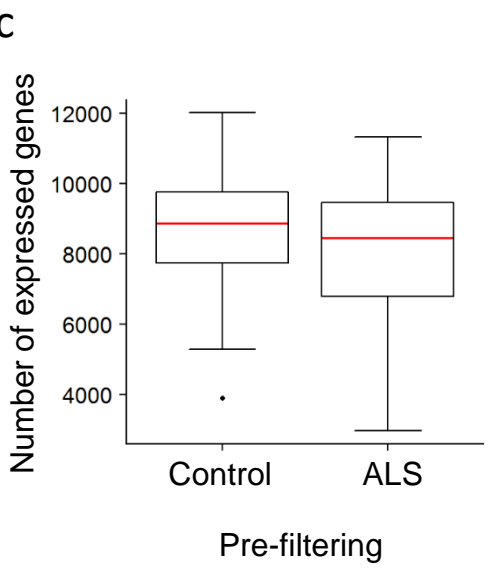
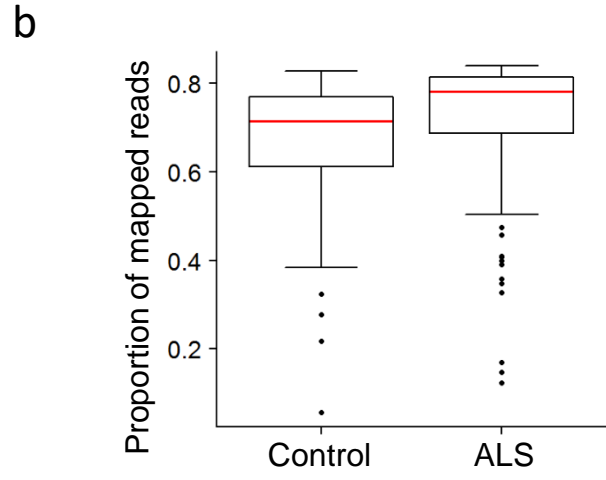
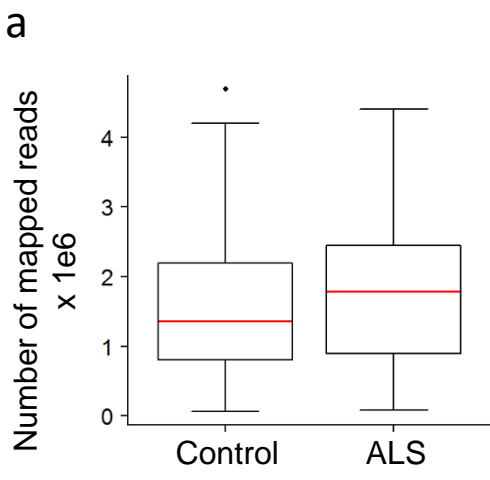


Figure S1



# Figure S2

GO term (Genes upregulated in neurons)	FDR
Postsynaptic cell membrane	8.20E-09
GABAergic synapse	1.10E-05
gamma-aminobutyric acid signaling pathway	4.70E-04
Voltage-gated channel	7.70E-04
Glutamatergic synapse	1.70E-02

GO term (Genes downregulated in neurons)	FDR
Cell cycle	3.40E-07
oligodendrocyte differentiation	5.40E-04

Figure S3

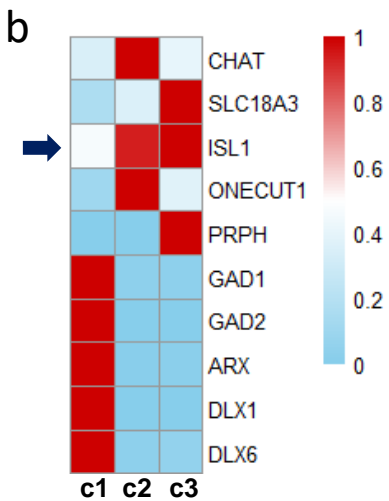
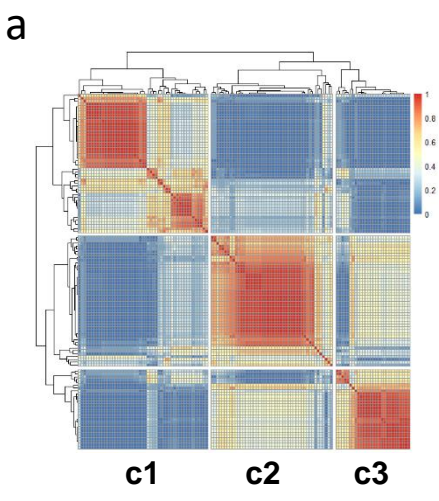


Figure S4

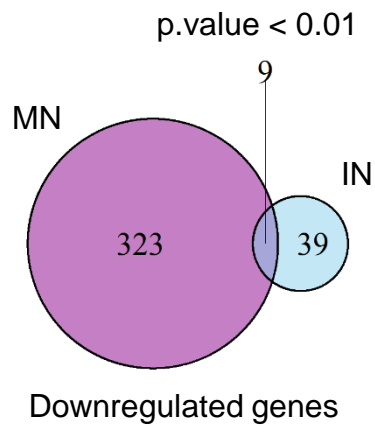
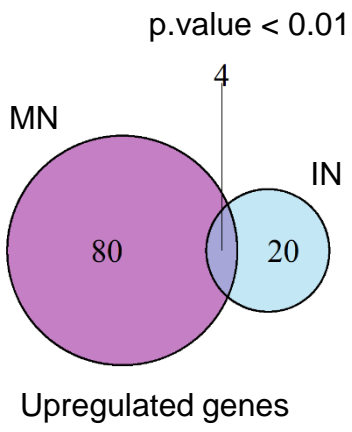
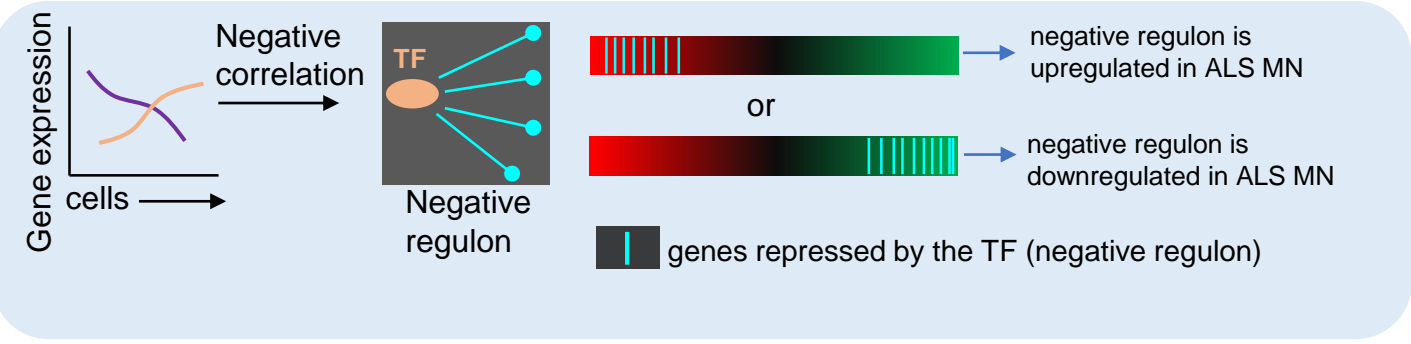
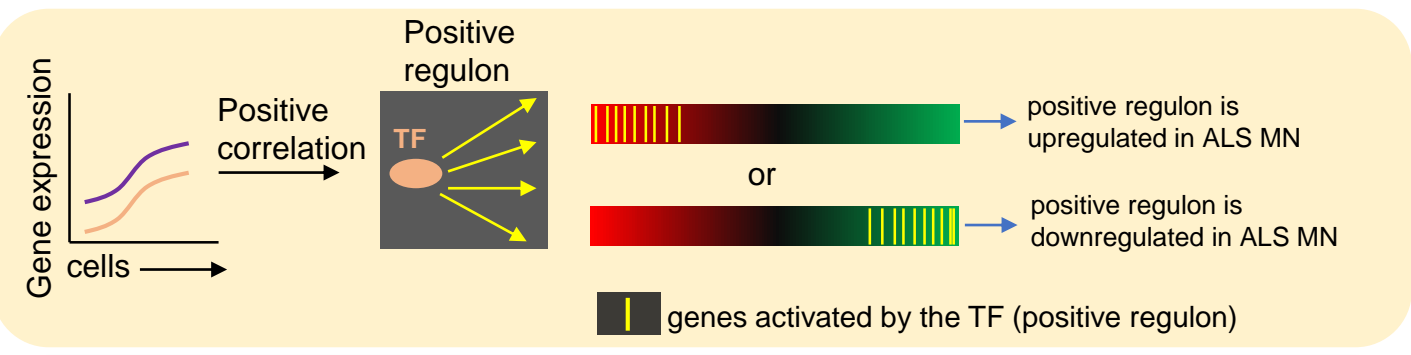


Figure S5



— Target expression  
— TF expression



**Filtering master regulators for concordance**

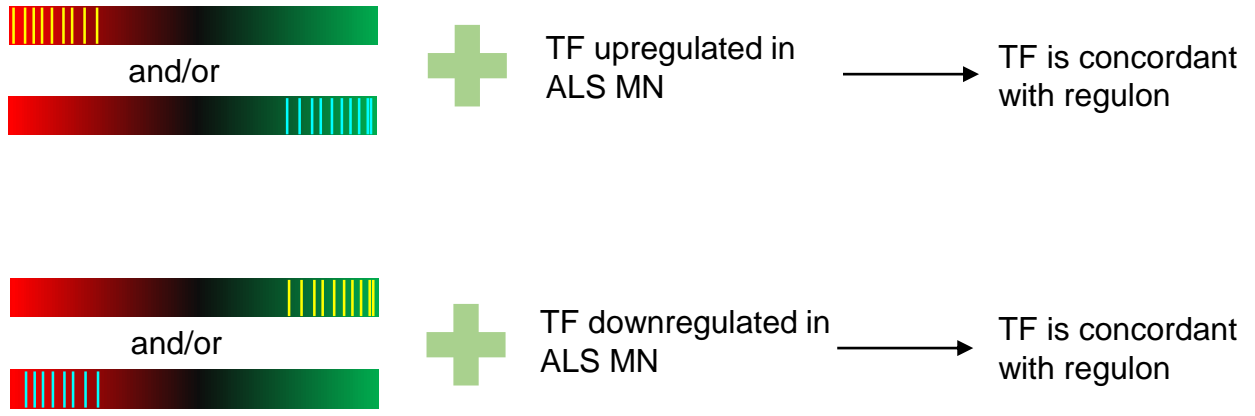


Figure S6

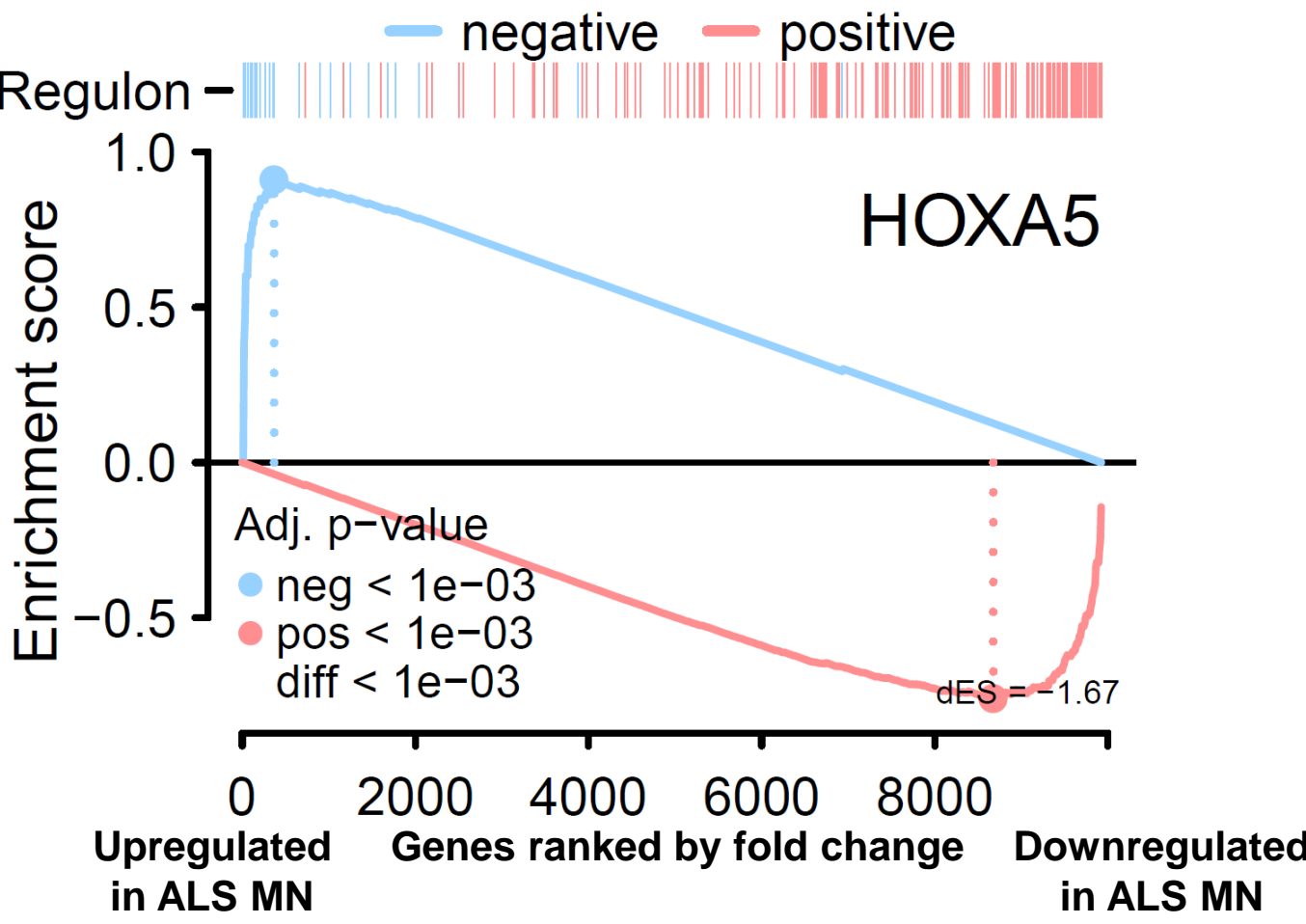


Figure S7

TF	Functional category	P-value	FDR
HOXA1	Signalling by NGF (REACTOME)	1.76E-05	0.050477
	axon	0.000199	0.05419
	synapse	0.00083	0.099058
HOXA5	regulation of actin filament organization	4.81E-06	0.016707
	adherens junction	1.09E-05	0.001891
	synapse	7.97E-05	0.006592
	postsynapse	0.000299	0.01615
HOXD1	Membrane Trafficking (REACTOME)	3.46E-05	0.099584
	synapse	2.55E-06	0.001591
	synaptic membrane	3.68E-05	0.006993
MAFG	No significant enrichment	-	-
ATF2	macroautophagy	1.05E-09	8.70E-07
	Membrane Trafficking (REACTOME)	3.70E-08	0.000106
	nucleoside-triphosphatase activity	3.40E-07	0.00047
	endosomal transport	5.67E-07	0.000256
PRDM2	mitochondrial envelope	3.66E-07	6.77E-05
	mitochondrial membrane	5.82E-06	0.000653
TSC22D2	No significant enrichment	-	-
ZMIZ1	No significant enrichment	-	-
ZNF134	No significant enrichment	-	-
ZBTB6	mitochondrial envelope	0.000301	0.052106
	mitochondrial membrane	0.00053	0.067262
HMGB2	Cell Cycle, Mitotic (REACTOME)	9.59E-05	0.068004
HOXD8	No significant enrichment	-	-
SOX4	mRNA metabolic process	3.13E-11	1.67E-07
	protein targeting to ER	3.79E-10	4.61E-07
	chromatin organization	1.45E-07	4.68E-05
	positive regulation of cell death	0.000235	0.023033
	DNA repair	0.000986	0.070476

Figure S8

