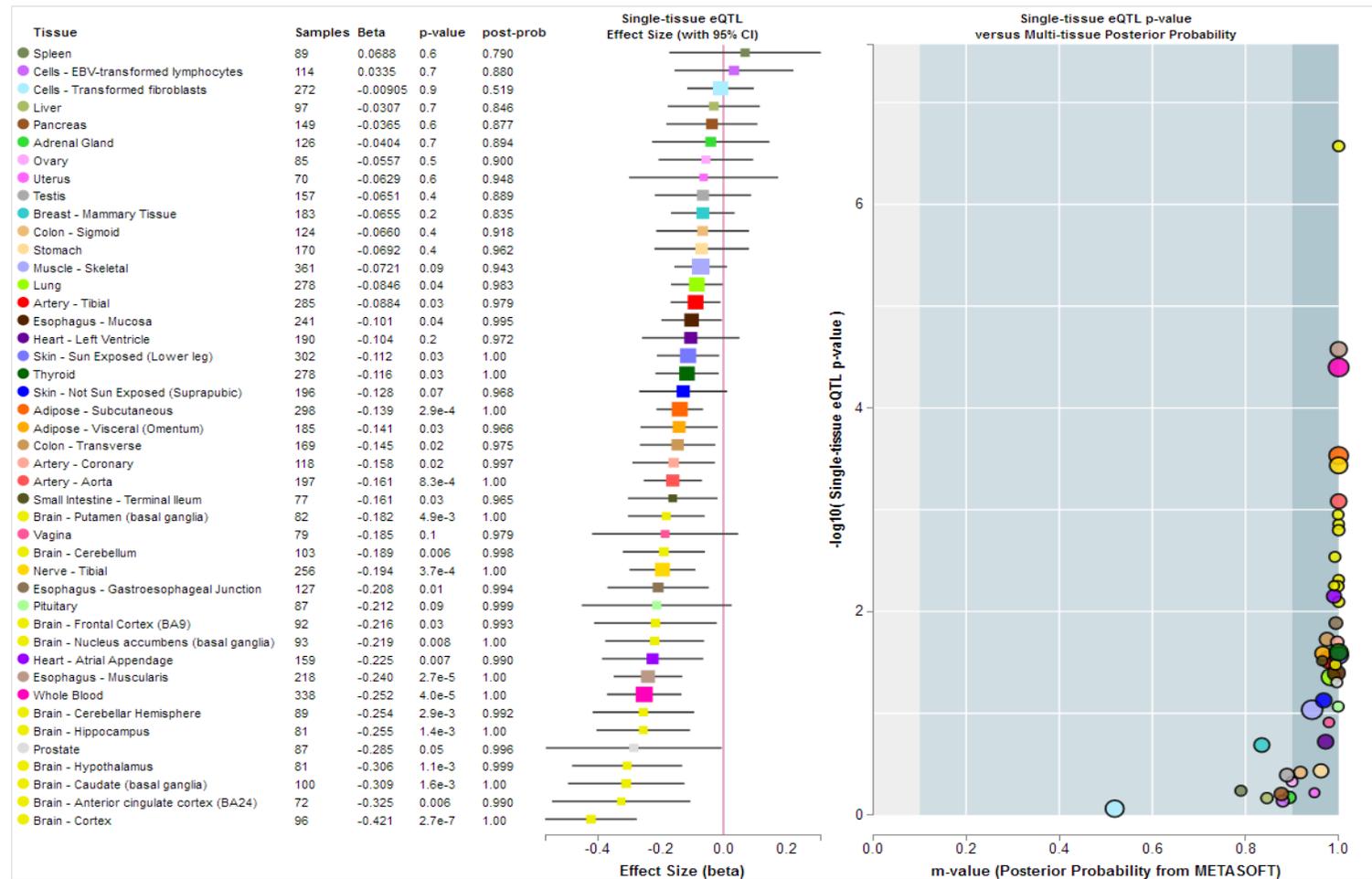


Multi-tissue eQTL Comparison

ENSG00000197461.9 PDGFA and rs9690350 eQTL (Meta Analysis RE2 P-Value: 9.80909e-45)



Supplementary Figure 1. SNP rs9690350 played as an expression quantitative locus (eQTL) with *PDGFA* across different tissues in human, especially in Central nervous system using GTEX tool (<https://www.gtexportal.org/home/>).

Supplementary Table 1. The detailed clinical information of the subjects in this study

Variable	Cases (n=506)	%	Controls (n=1473)	%
Age (Months)	2.088±1.934		18.61±19.75	
≤3	470	92.89%	521	35.37%
>3	36	7.11%	952	64.63%
Gender				
Females	214	42.29%	506	34.35%
Males	292	57.71%	967	65.65%
Clinical manifestation				
Cystic biliary atresia (CBA)	44	8.70%		
non-CBA	462	91.30%		

Supplementary Table 2. The functional annotation of candidate SNP rs9690350 by SCAN (http://www.scandb.org/newinterface/index_v1.html) and Regulome DB (<http://regulomedb.org/>)

SNP	CHR	A1/A2	SCAN				Regulome DB	
			gene	feature	left_gene	right_gene	hits	score
rs9690350	7	C/G	PDGFA	intron[NM_033023.3]	<i>LOC100132080</i>	<i>PRKAR1B</i>	TF binding + any motif + DNase Footprint + DNase peak	2b*