Summary data on fQTLs calculated from 8 cell types

Cell_type	num_fQTls	min_bonf_corrected_p_val	max_bonf_corrected_p_val
Ex4	630	1.46E-23	0.049764449
Ex3	126	1.93E-09	0.042337565
Astrocytes	105	1.44E-07	0.048867252
Microglia	91	4.06E-07	0.048665373
Ex5	26	1.32E-10	0.045802929
Oligodendrocytes	10	1.38E-08	0.029443349
Endothelial	8	0.021597405	0.047000607
Neuron	0	--	--

Stats on fQTLs w/SNVs that coincide with trans-eQTLs

439/457 genes have all needed data (ENSG ID, TSS, etc)

Results based on using 8 cell types				
p_val_thresh	tot # matches	# unq matched SNVs	# unq fQTL SNVs	fract unq fQTL SNVs that match eSNVs
0.05	100100	**697**	726	**0.96**
0.1	113433	843	898	0.939
0.2	126070	996	1089	0.915
0.3	133431	1113	1242	0.896

* P-values are Bonferroni-corrected (for both fQTLs and trans-eQTLs)

Trans-eGenes associated with the 20 most significant fQTLs (linked through common SNV) [8 cell analysis]

ATP13A4	ATPase 13A4
CDC14A	cell division cycle 14A
CLDN11	claudin 11
CPNE4	copine 4
DPYD	dihydropyrimidine dehydrogenase
GPR153	G protein-coupled receptor 153
IL1RAP	interleukin 1 receptor accessory protein
LMO4	LIM domain only 4
LRRC38	leucine rich repeat containing 38
MAP6D1	MAP6 domain containing 1
MSX1	msh homeobox 1
PLD1	phospholipase D1
PTPRU	protein tyrosine phosphatase, receptor type U
RGS12	regulator of G protein signaling 12
SORCS2	sortilin related VPS10 domain containing receptor 2
SOX2-OT	SOX2 overlapping transcript
SST	somatostatin
STK32B	serine/threonine kinase 32B
TF	transferrin
TMCO4	transmembrane and coiled-coil domains 4

Most significant GO Processes among top 1000 fQTLs matched to trans-eQTLs [8 cell analysis]

synaptic transmission, GABAergic
forebrain neuron fate commitment
axonal fasciculation
neuron projection fasciculation
regulation of neuroblast proliferation
cardiac muscle tissue growth
negative regulation of smoothened signaling pathway
heart growth
cardiac epithelial to mesenchymal transition
detection of mechanical stimulus involved in sensory perception
ventricular cardiac muscle tissue morphogenesis
ventricular cardiac muscle tissue development
positive regulation of phospholipid metabolic process
oligodendrocyte differentiation

eGenes associated with the 20 most significant fQTLs [8 cell analysis]

CLDN11	Multiple Sclerosis
DPYD	Colorectal Neoplasms Carcinoma, Hepatocellular Neutropenia **Peripheral Nervous System Diseases** **Autistic Disorder** Head and Neck Neoplasms Lung Neoplasms Pancreatic Neoplasms **Schizophrenia** Colonic Neoplasms Leukoencephalopathies Neoplasm Metastasis Obesity **Autism Spectrum Disorder** Breast Neoplasms Nervous System Diseases Stomach Neoplasms Dihydropyrimidine Dehydrogenase Deficiency **Language Development Disorders** Purine-Pyrimidine Metabolism, Inborn Errors

eGenes associated with the 20 most significant fQTLs [8 cell anaysis]

GPR153	**Schizophrenia**
IL1RAP	Liver Diseases
MSX1	Craniofacial Abnormalities Tooth Abnormalities Wolf-Hirschhorn Syndrome Anodontia Witkop syndrome Cleft Palate Stomach Neoplasms Orofacial Cleft 5

eGenes associated with the 20 most significant fQTLs [8 cell anaysis]

PLD1	Infarction, Middle Cerebral Artery Cardiomegaly
RGS12	**Schizophrenia**
SST	Hypokalemia **Ischemia** **Mood Disorders** Vipoma Multiple Organ Failure **Seizures** Barrett Esophagus Neoplasms Abortion, Spontaneous Esophageal Neoplasms Pancreatic Neoplasms Pancreatitis Endometriosis Esophageal and Gastric Varices

eGenes associated with the 20 most significant fQTLs [8 cell anaysis]

TF	
	Adenocarcinoma of lung
	Hepatitis
	Paratuberculosis
	Anemia, hypochromic microcytic
	Iron Overload
	Mammary Neoplasms, Animal
	Alcoholism
	Carcinoma
	Congenital atransferrinemia
	Fatty Liver
	Alzheimer Disease
	Drug-Induced Liver Injury
	Echinococcosis
	Nephrotic Syndrome
	Inflammation
	Neoplasm Invasiveness
	Restless Legs Syndrome
	Autistic Disorder
	Mammary Neoplasms, Experimental
	Mesothelioma, Malignant
	Obesity

Summary data on fQTLs calculated from 24 cell types

Cell_type	num_fQTls	min_bonf_corrected_p_val	max_bonf_corrected_p_val
Ex6	15664	5.84E-23	0.049929385
Fetal-replicating	12412	2.29E-18	0.049950551
In5	9444	2.16E-29	0.049976051
In1	4701	1.02E-58	0.049933975
In4	4133	3.10E-25	0.049991607
Fetal-quiescent	3958	5.55E-13	0.049987782
In3	2482	1.01E-17	0.049816673
Ex7	2257	6.80E-21	0.049925943
Ex2	2074	2.55E-52	0.049865889
Ex8	1369	1.78E-46	0.049889222
OPC	1252	1.31E-53	0.048778289
In8	902	1.73E-19	0.049814123
Ex4	380	4.37E-22	0.04993066
In6	113	1.76E-14	0.048444104
Ex3	58	5.79E-08	0.04883592
Astrocytes	42	4.33E-06	0.042957397
Microglia	23	1.22E-05	0.048852113
Ex5	9	3.96E-09	0.047241623
Oligodendrocytes	6	4.15E-07	0.038137404
Ex1	0	--	--
In2	0	--	--
In7	0	--	--
Endothelial	0	--	--
Neuron	0	--	--

Stats on fQTLs w/SNVs that coincide with trans-eQTLs [24 cells analysis]

439/457 genes have all needed data (ENSG ID, TSS, etc)

24 cell types				
p_val_thresh	tot # matches	# unq matched SNVs	# unq fQTL SNVs	fract unq fQTL SNVs that match eSNVs
0.05	520995	**22885**	41465	**0.552**
0.1	637069	26639	47223	0.564
0.2	777733	30850	53569	0.576
0.3	873281	33529	57341	0.585

* P-values are Bonferroni-corrected (for both fQTLs and trans-eQTLs)

Trans-eGenes associated with the 20 most significant fQTLs (linked through common SNV) [24 cell analysis]

Had to take the top 53 most significant fQTLs to build a list of 20 unique genes – ie, there's considerable over-representation of certain genes among the most significant matches

ATP10A	ATPase phospholipid transporting 10A (putative)
BRIP1	BRCA1 interacting protein C-terminal helicase 1
CAMK2A	calcium/calmodulin dependent protein kinase II alpha
CENPF	centromere protein F
DPYSL3	dihydropyrimidinase like 3
ENPP2	ectonucleotide pyrophosphatase/phosphodiesterase 2
EYA1	EYA transcriptional coactivator and phosphatase 1
HAS2	hyaluronan synthase 2
MDGA1	MAM domain containing glycosylphosphatidylinositol anchor 1
MEX3A	mex-3 RNA binding family member A
MSX1	msh homeobox 1
MYB	MYB proto-oncogene, transcription factor
NMBR	neuromedin B receptor
PBK	PDZ binding kinase
PRDM8	PR/SET domain 8
RELN	reelin
SLC10A4	solute carrier family 10 member 4
STK32B	serine/threonine kinase 32B
TESC	tescalcin
VAV3	vav guanine nucleotide exchange factor 3

A general note on the number of ways to compute QTLs (at least 2^5 = 32)

normalized vs. **non-normalized** [2]

w/peer or **w/o** peer [2]

cis or **trans** [2]

calculate significance via **Bonferroni** on nominal run or FDR w/permutations [2]

significance thresholds (**.05**, .10) [2]