

ESM Table 10. eQTL analysis showing evidence suggesting of cis-association ($p < 0.05$) between identified variant rs10229583 or its proxy rs1440971 and expression of genes within 1Mb of the SNP using data from the MuTHER Consortium. The A1 allele listed in the table is the reference/effect allele. The last 3 columns refer to the peak eQTL SNP in the corresponding tissue showing suggestive association (highlighted in bold) and r^2 between the peak eQTL SNP and rs10229583.

PROBE	GENE	Position	A1	Freq1	Adipose			LCL			Skin			Peak eQTL SNP		
					Beta	SE	P_{eQTL}	Beta	SE	P_{eQTL}	Beta	SE	P_{eQTL}	ID	r^2	P_{eQTL}
rs10229583																
ILMN_1655961	<i>C7orf54</i>	127034139	G	0.75	-0.0091	0.0143	0.5248	-0.0348	0.0172	0.0426	-0.0232	0.0175	0.1855	rs322812	0.56	3.66x10⁻⁵
ILMN_1659990	<i>C7orf68</i>	127034139	G	0.75	-0.042	0.0207	0.0415	-0.0028	0.0299	0.9248	0.0008	0.0174	0.9618	rs10229583	1	0.0415
ILMN_1752340	<i>ARF5</i>	127034139	G	0.75	-0.011	0.0121	0.3502	-0.0239	0.0101	0.0185	-0.0066	0.0176	0.7065	rs806179	1	0.0042
rs1440971																
ILMN_1655961	<i>C7orf54</i>	127059636	G	0.182	0.0161	0.0165	0.3285	0.0651	0.0199	0.001	0.0098	0.0202	0.627	rs322812	0.56	3.66x10⁻⁵
ILMN_1752340	<i>ARF5</i>	127059636	G	0.182	0.0039	0.0140	0.779	0.0283	0.0117	0.0161	-0.0089	0.0202	0.661	rs806179	1	0.0042