

Supplementary Table 1: eQTL effects of rs7804356 on *SKAP2* and nearby genes in various tissues according to the Genotype-Tissue Expression (GTEx) Portal.

Gene Symbol	Variant ID	SNP	p-value	NES	Tstats	Tissue
<i>SKAP2</i>	chr7_26852046_T_C_b38	rs7804356	1.90E-13	0.15	7.5	Whole blood
<i>HOTAIRM1</i>	chr7_26852046_T_C_b38	rs7804356	1.90E-08	0.28	5.7	
<i>HOXA1</i>	chr7_26852046_T_C_b38	rs7804356	0.0000013	0.27	4.9	
<i>HOXA4</i>	chr7_26852046_T_C_b38	rs7804356	0.00043	0.21	3.5	
<i>HOXA2</i>	chr7_26852046_T_C_b38	rs7804356	0.00055	0.19	3.5	
<i>HOXA-AS2</i>	chr7_26852046_T_C_b38	rs7804356	0.0021	0.17	3.1	
<i>HOXA5</i>	chr7_26852046_T_C_b38	rs7804356	0.024	0.12	2.3	
<i>SKAP2</i>	chr7_26852046_T_C_b38	rs7804356	0.025	0.1	2.2	Pancreas
<i>SKAP2</i>	chr7_26852046_T_C_b38	rs7804356	0.025	0.2	2.3	EBV-transformed lymphocytes
<i>HOTAIRM1</i>	chr7_26852046_T_C_b38	rs7804356	0.0079	-0.18	-2.7	Cultured fibroblasts
<i>HOXA9</i>	chr7_26852046_T_C_b38	rs7804356	0.034	0.08	2.1	
<i>HOXA4</i>	chr7_26852046_T_C_b38	rs7804356	0.049	0.11	2	

GTEx used beta-distribution-adjusted empirical p-values from FastQTL to calculate q-values and a false discovery rate (FDR) threshold of ≤ 0.05 to identify genes with a significant eQTL. The normalized effect size (NES) of the eQTLs is defined as the slope of the linear regression and is computed as the effect of the alternative (minor) allele relative to the reference (major) allele in the human genome reference GRCh38/hg38 (i.e., the eQTL effect allele is the alternative allele). The Variant ID consists of chromosomal position followed by reference and alternative alleles and genome build, all separated by “_”.