

Supplementary Table S5: Summary of information in the GTEx eQTL server regarding transcriptional downregulation of *UNG* in 16 different tissues when rs34259 is present

Gene	^a p-Value	rs34259 Effect Size	T-Statistic	Standard Error	Tissue
<i>UNG</i>	0.004	-0.33	-3.0	0.11	Liver
<i>UNG</i>	0.059	-0.30	-1.9	0.15	Esophagus - Gastroesophageal Junction
<i>UNG</i>	0.070	-0.28	-1.8	0.15	Pituitary
<i>UNG</i>	0.030	-0.24	-2.2	0.11	Pancreas
<i>UNG</i>	0.021	-0.20	-2.3	0.09	Skin - Not Sun Exposed (Suprapubic)
<i>UNG</i>	0.005	-0.17	-2.8	0.06	Skin - Sun Exposed (Lower leg)
<i>UNG</i>	0.016	-0.15	-2.4	0.06	Lung
<i>UNG</i>	0.054	-0.16	-1.9	0.08	Artery - Coronary
<i>UNG</i>	0.035	-0.16	-2.1	0.08	Adipose - Visceral (Omentum)
<i>UNG</i>	0.360	-0.13	-0.9	0.14	Colon - Sigmoid
<i>UNG</i>	0.044	-0.09	-2.0	0.04	Muscle - Skeletal
<i>UNG</i>	0.023	-0.17	-2.3	0.07	Breast - Mammary Tissue
<i>UNG</i>	0.590	-0.10	-0.5	0.19	Uterus
<i>UNG</i>	0.220	-0.15	-1.2	0.12	Vagina
<i>UNG</i>	0.140	-0.16	-1.5	0.11	Ovary
<i>UNG</i>	2.5e-7	-0.19	-5.3	0.04	Whole Blood

^aNominal eQTL p-values were generated for each SNP-gene pair using a two-tailed t test, testing the alternative hypothesis that β (slope of the linear regression model) deviates from the null hypothesis of $\beta=0$.