

# SNiPAcord

## Block annotations

### Block info

genomic range	chr13:92,554,173-92,604,445 <i>e!</i>
block size	50,273 bp
variant count	13 variants

### Basic features

Conservation/deleteriousness		Linked genes	
phyloP	$\mu = -0.557$ [-2.987 – 0.88]	gene(s) hit or close-by	GPC5 <i>e!</i>
phastCons	$\mu = 0.073$ [0 – 0.849]	eQTL gene(s)	GPC5 <i>e!</i>
GERP++	$\mu = -1.026$ [-5.52 – 1.62]	potentially regulated gene(s)	-
CADD score	$\mu = 2.599$ [0.117 – 5.609]	disease gene(s)	-

## Direct effect on regulation

### cis-eQTL

gene	transcript	probe	tissue	min(statistic) (type)	source	variant(s)
GPC5 <i>e!</i>	?	ENSG00000179399 <i>e!</i>	subcutaneous adipocytes	1.66×10 <sup>-5</sup> (p-value)	GTEx Portal V6 <i>!m</i>	3
GPC5 <i>e!</i>	ENST00000377067 <i>e!</i>	ILMN_1688886 <i>e!</i>	adipocyte	3.94×10 <sup>-7</sup> (p-value)	MuTHER consortium <i>!m</i>	5

## Putative effect on transcript

### Intron variant

gene	affected transcript	RefSeq id	protein	variant(s)
GPC5 <i>e!</i>	ENST00000377067 <i>e!</i>	NM_004466.4	ENSP00000366267 <i>e!</i>	13

