

# SNiPACard

## Block annotations

### Block info

genomic range	chr17:34,262,254-34,262,254 <i>e!</i>
block size	1 bp
variant count	1 variants

### Basic features

Conservation/deleteriousness		Linked genes	
phyloP	0.135	gene(s) hit or close-by	LYZL6 <i>e!</i> , RDM1 <i>e!</i>
phastCons	0.001	eQTL gene(s)	-
GERP++	0.799	potentially regulated gene(s)	-
CADD score	2.777	disease gene(s)	-

## Putative effect on regulation

### Variation proximal to gene

gene	variant type	min(distance)	transcript	RefSeq id	protein	variant(s)
LYZL6 <i>e!</i>	downstream gene variant	1439	ENST00000617692 <i>e!</i>	?	ENSP00000481373 <i>e!</i>	1
RDM1 <i>e!</i>	upstream gene variant	4968	ENST00000615024 <i>e!</i>	?	ENSP00000481648 <i>e!</i>	1
RDM1 <i>e!</i>	upstream gene variant	4523	ENST00000619368 <i>e!</i>	?	ENSP00000478131 <i>e!</i>	1
RDM1 <i>e!</i>	upstream gene variant	4951	ENST00000615378 <i>e!</i>	NM_001163125.1	ENSP00000480131 <i>e!</i>	1
RDM1 <i>e!</i>	upstream gene variant	4497	ENST00000619876 <i>e!</i>	?	ENSP00000483890 <i>e!</i>	1
RDM1 <i>e!</i>	upstream gene variant	4523	ENST00000612980 <i>e!</i>	NM_001163120.1	ENSP00000483387 <i>e!</i>	1
RDM1 <i>e!</i>	upstream gene variant	4968	ENST00000619828 <i>e!</i>	NM_001163122.1	ENSP00000483933 <i>e!</i>	1
RDM1 <i>e!</i>	upstream gene variant	4477	ENST00000620284 <i>e!</i>	NM_145654.3	ENSP00000483549 <i>e!</i>	1
RDM1 <i>e!</i>	upstream gene variant	4523	ENST00000615288 <i>e!</i>	?	ENSP00000477869 <i>e!</i>	1
RDM1 <i>e!</i>	upstream gene variant	4968	ENST00000617591 <i>e!</i>	NM_001163124.1	ENSP00000479622 <i>e!</i>	1
RDM1 <i>e!</i>	upstream gene variant	4968	ENST00000618511 <i>e!</i>	?	ENSP00000477995 <i>e!</i>	1
RDM1 <i>e!</i>	upstream gene variant	4523	ENST00000616596 <i>e!</i>	NM_001163121.1	ENSP00000478915 <i>e!</i>	1
RDM1 <i>e!</i>	upstream gene variant	4481	ENST00000619262 <i>e!</i>	NM_001163130.1	ENSP00000479310 <i>e!</i>	1
RDM1 <i>e!</i>	upstream gene variant	4510	ENST00000613308 <i>e!</i>	NM_001034836.1	ENSP00000482288 <i>e!</i>	1
RDM1 <i>e!</i>	upstream gene variant	4523	ENST00000619193 <i>e!</i>	?	ENSP00000482981 <i>e!</i>	1

## Putative effect on transcript

### Intron variant

gene	affected transcript	RefSeq id	protein	variant(s)
LYZL6 <i>e!</i>	ENST00000615905 <i>e!</i>	NM_020426.2	ENSP00000483897 <i>e!</i>	1
LYZL6 <i>e!</i>	ENST00000618542 <i>e!</i>	NM_001199951.1	ENSP00000482955 <i>e!</i>	1

