





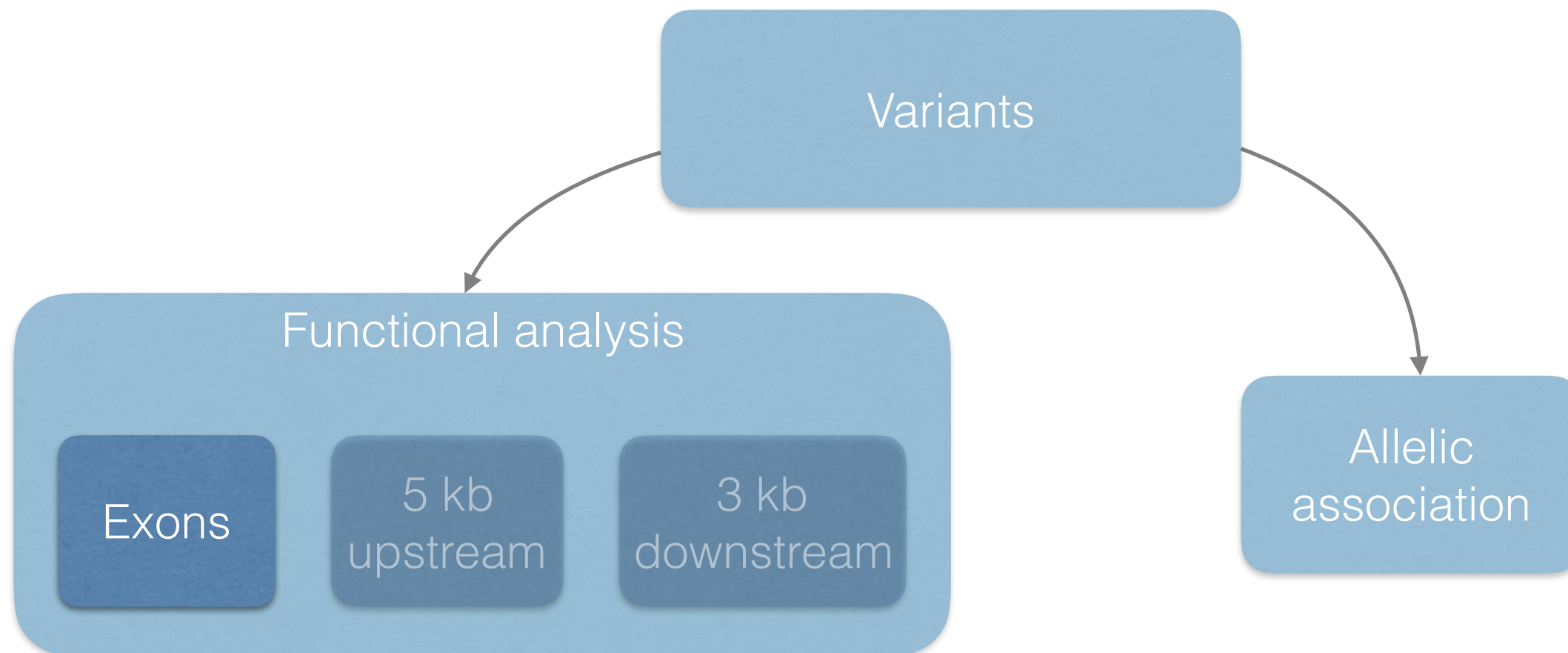
Is  $SNV$  with significant effects

Gene	Chr	Position	Ref	Alt	Protein change	Protein domain	Polyphen2 Prediction	Polyphen 2 Score	SIFT Prediction	SIFT Score
<i>FCN1</i>	11	106,827,968	C	T	Arg142Cys	FBG	probably damaging	0.986	tolerated	0.06
<i>MBL2</i>	26	6,344,919	C	A	Pro42Gln	CLD	probably damaging	0.974	deleterious	0
<i>SFTPD</i>	28	35,820,078	C	T	Pro132Ser	CLD	probably damaging	0.958	deleterious	0.05
<i>CGN</i>	28	35,598,640	G	A	Arg173His	CLD	possibly damaging	0.72	tolerated	0.16
<i>CL46</i>	28	35,675,371	C	T	Pro185Leu	CLD	possibly damaging	0.672	tolerated	0.32
<i>CL43</i>	28	35,718,034	A	G	Thr117Ala	CLD	possibly damaging	0.659	tolerated	0.9
<i>CL43</i>	28	35,718,807	G	T	Gln185His	neck region	possibly damaging	0.634	deleterious	0.01
<i>MASP2</i>	16	43,463,621	G	A	Gly102Ser	CUB domain	benign	0.191	deleterious	0.01
<i>FCN1</i>	11	106,828,710	C	T	Thr193Met	FBG	benign	0.042	deleterious	0.03
<i>CGN</i>	28	35,602,463	A	C	Glu302Asp	CRD	benign	0.036	deleterious	0.04
<i>SFTPD</i>	28	35,824,136	C	G	Ala288Gly	CRD	benign	0.002	deleterious	0.02



# Functional analysis and allelic association

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# SNVs with significant effects

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