Response: clustered by variant (general non-clustered response> as many rows as instances, 10)
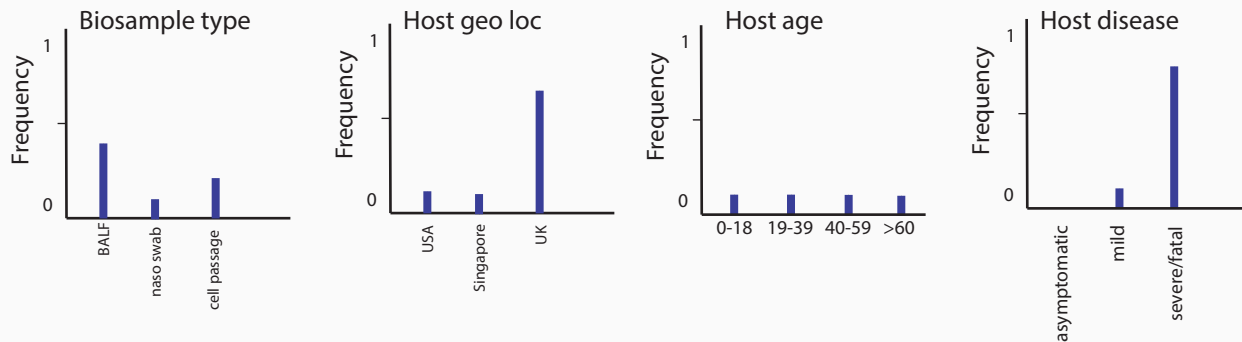
variant	alt Freq	variantType	variantEffect
1251A>T	0.0002	SNP	silent
1255A>C	0.0001	SNP	non-coding

Statistics per variant: 1251A>T

Response: clustered by sample> 8 responses

sampleID	variant	sample Freq	variantType	variantEffect	biosampleType	hostId	hostAge	hostDiseaseCourse
SAM12456	1251A>T, 1255A>C	0.0002	SNP, SNP	silent, silent	BALF	awnksojs	45	severe
SAM12457	1255A>C	0.0001	SNP, SNP	silent, silent	nasoph	awnksojs	45	severe

Response: clustered by sample> 8 responses

sampleID	variant	var Freq	variantType	variantEffect	biosampleType	hostId	hostAge	hostDiseaseCourse
SAM12456	1251A>T, 1255A>C	0.0002, 0.001	SNP, SNP	silent, silent	BALF	awnksojs	45	severe
SAM12457	1255A>C	0.0001	SNP, SNP	silent, silent	nasoph	awnksojs	45	severe