

Exome report

Exome variant calling report

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library(knitr)
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Quality Control

Min length Max length Average length Min base quality Number of reads before in 1 Number of reads after in 1 Number of reads before in 2 Number of reads after in 2

	Min length	Max length	Min base quality	# reads in R1	# reads in R2
R1	100	150	30	1546792374	134892437
R2	100	150	30	1546792374	134892437

Targeted info

Num of regions Num of bases Average coverage

Alignment

Number base aligned Number reads aligned % reads aligned

Calling

SNPs: Number, Ts/tv ratio, indels: Number, Max lenght, min length, average length,

Variants