Codes Used for Bedtools Intersect:

[jfisher@int0001 ~]$ cat -t Hereditary\_Cancer\_Coordinates\_for\_Filters.bed #reads each file parameter in sequence and writes it to standard output

[jfisher@int0001 ~]$ less CCI\_VCFs.patient.txt #allows you to look inside the file

[jfisher@int0001 ~]$ cp /cluster/projects/csl\_public/WGS\_processing/ss\_pipeline/variant\_calls/sentieon-201808.07/strelka-2.9.10/HALB3013059.vcf.gz CCI\_VCFs #allows you to see in the patient list. Select on line per run.

[jfisher@int0001 ~]$ cd CCI\_VCFs/ #change directory to folder you want information to go into

[jfisher@int0001 CCI\_VCFs]$ gunzip HALB3013059.vcf.gz #unzips the file

[jfisher@int0001 CCI\_VCFs]$ cd #change directory

[jfisher@int0001 ~]$ bedtools intersect -a CCI\_VCFs/HALB3013059.vcf -b Hereditary\_Cancer\_Coordinates\_for\_Filters.bed | head #intersects the two files

[jfisher@int0001 ~]$ bedtools intersect -a /cluster/home/jfisher/CCI\_VCFs/HALB3005276.vcf -b /cluster/home/jfisher/Hereditary\_Cancer\_Coordinates\_for\_Filters.bed > /cluster/home/jfisher/CCI\_VCFs/HALB3005276\_cancer\_intesect.vcf #filter the files in CCI\_VCF

HAIB0804:Desktop biotrain$ scp -r jfisher\@login01.cluster.haib.org:~/CCI\_VCFs /Users/biotrain/Desktop #shows that all the intersected files are unzipped and in the CCI\_VCFs folder