Github personal access token for Salmonallw:

ghp\_UVWya3qkVmSr4OtbYyKzWuweqy0NUj250AVe

git config credential.helper store

git config --global credential.helper 'cache --timeout 7200'

<https://stackoverflow.com/questions/6565357/git-push-requires-username-and-password>

------------------------------------------------------------------------------------------------------

grep -v POS hg38/COVID\*2021\*txt | awk -F \':\' \'{print $2}\' | awk \'{print "chr"$1"\\t"$2-1"\\t"$2+1"\\t"$1":"$2}\' | sort -k1,1 -k2,2n | uniq > hg38/COVID19\_HGI\_2021.bed

/exports/igmm/eddie/taylor-lab/rob/bin/liftOver hg38/COVID19\_HGI\_2021.bed /exports/igmm/datastore/taylor-lab/genomes/hg19/hg19ToHg38.over.chain.gz hg19/COVID19\_HGI\_2021.bed hg19/COVID19\_HGI\_2021.unMapped

LiftOver website:

<http://genome-euro.ucsc.edu/cgi-bin/hgLiftOver>

grep -v POS COVID\*2021\*txt | awk -F ':' '{print $2}' | awk '{print "chr"$1"\t"$2-1"\t"$2+1"\t"$1":"$2}' | sort -k1,1 -k2,2n | uniq | grep '9:133270637'

#----------------------------------#

# ENSEMBL VARIANT EFFECT PREDICTOR #

#----------------------------------#

Versions:

ensembl-vep : 97.3

Help: dev@ensembl.org , helpdesk@ensembl.org

Twitter: @ensembl

http://www.ensembl.org/info/docs/tools/vep/script/index.html

Usage:

./vep [--cache|--offline|--database] [arguments]

Basic options

=============

--help Display this message and quit

-i | --input\_file Input file

-o | --output\_file Output file

--force\_overwrite Force overwriting of output file

--species [species] Species to use [default: "human"]

--everything Shortcut switch to turn on commonly used options. See web

documentation for details [default: off]

--fork [num\_forks] Use forking to improve script runtime

For full option documentation see:

<http://www.ensembl.org/info/docs/tools/vep/script/vep_options.html>

**Default VEP input**

The default format is a simple **whitespace-separated** format (columns may be separated by space or tab characters), containing five required columns plus an optional identifier column:

1. **chromosome** - just the name or number, with no 'chr' prefix
2. **start**
3. **end**
4. **allele** - pair of alleles separated by a '/', with the reference allele first
5. **strand** - defined as + (forward) or - (reverse).
6. **identifier** - this identifier will be used in VEP's output. If not provided, VEP will construct an identifier from the given coordinates and alleles.

1 881907 881906 -/C +

5 140532 140532 T/C +

12 1017956 1017956 T/A +

2 946507 946507 G/C +

14 19584687 19584687 C/T -

19 66520 66520 G/A + var1

8 150029 150029 A/T + var2

An insertion (of any size) is indicated by start coordinate = end coordinate + 1. For example, an insertion of 'C' between nucleotides 12600 and 12601 on the forward strand of chromosome 8 is indicated as follows:

8 12601 12600 -/C +

A deletion is indicated by the exact nucleotide coordinates. For example, a three base pair deletion of nucleotides 12600, 12601, and 12602 of the reverse strand of chromosome 8 will be:

8 12600 12602 CGT/- -

WARNING: Length of reference allele (G length 1) does not match co-ordinates 45834967-45834966 on line 207

WARNING: Length of reference allele (T length 1) does not match co-ordinates 133257521-133257520 on line 280

WARNING: Length of reference allele (G length 1) does not match co-ordinates 56054302-56054301 on line 440

WARNING: Length of reference allele (G length 1) does not match co-ordinates 68791128-68791127 on line 576

[s1544765@node2c11(eddie) vep\_input]$ wc -l ../GWASdata/\*

1059 ../GWASdata/COVID19\_HGI\_A2\_ALL\_eur\_leave\_23andme\_20210107.txt.gz\_1.0E-5.txt

981 ../GWASdata/COVID19\_HGI\_A2\_ALL\_eur\_leave\_ukbb\_23andme\_20210107.txt.gz\_1.0E-5.txt

1010 ../GWASdata/COVID19\_HGI\_A2\_ALL\_leave\_23andme\_20210107.txt.gz\_1.0E-5.txt

983 ../GWASdata/COVID19\_HGI\_A2\_ALL\_leave\_UKBB\_23andme\_20210107.txt.gz\_1.0E-5.txt

320 ../GWASdata/COVID19\_HGI\_B1\_ALL\_eur\_leave\_23andme\_20210107.txt.gz\_1.0E-5.txt

254 ../GWASdata/COVID19\_HGI\_B1\_ALL\_eur\_leave\_ukbb\_23andme\_20210107.txt.gz\_1.0E-5.txt

304 ../GWASdata/COVID19\_HGI\_B1\_ALL\_leave\_23andme\_20210107.txt.gz\_1.0E-5.txt

268 ../GWASdata/COVID19\_HGI\_B1\_ALL\_leave\_UKBB\_23andme\_20210107.txt.gz\_1.0E-5.txt

2796 ../GWASdata/COVID19\_HGI\_B2\_ALL\_eur\_leave\_23andme\_20210107.txt.gz\_1.0E-5.txt

1031 ../GWASdata/COVID19\_HGI\_B2\_ALL\_eur\_leave\_ukbb\_23andme\_20210107.txt.gz\_1.0E-5.txt

3393 ../GWASdata/COVID19\_HGI\_B2\_ALL\_leave\_23andme\_20210107.txt.gz\_1.0E-5.txt

974 ../GWASdata/COVID19\_HGI\_B2\_ALL\_leave\_UKBB\_23andme\_20210107.txt.gz\_1.0E-5.txt

866 ../GWASdata/COVID19\_HGI\_C2\_ALL\_eur\_leave\_23andme\_20210107.txt.gz\_1.0E-5.txt

618 ../GWASdata/COVID19\_HGI\_C2\_ALL\_eur\_leave\_ukbb\_23andme\_20210107.txt.gz\_1.0E-5.txt

888 ../GWASdata/COVID19\_HGI\_C2\_ALL\_leave\_23andme\_20210107.txt.gz\_1.0E-5.txt

651 ../GWASdata/COVID19\_HGI\_C2\_ALL\_leave\_UKBB\_23andme\_20210107.txt.gz\_1.0E-5.txt

16396 total

[s1544765@node2c11(eddie) vep\_input]$ wc -l \*

1057 A2\_ALL\_eur\_leave\_23andme\_vep\_input.txt ['9 133270497 133270498 GA/G']

980 A2\_ALL\_eur\_leave\_ukbb\_23andme\_vep\_input.txt

1009 A2\_ALL\_leave\_23andme\_vep\_input.txt

982 A2\_ALL\_leave\_UKBB\_23andme\_vep\_input.txt

319 B1\_ALL\_eur\_leave\_23andme\_vep\_input.txt

253 B1\_ALL\_eur\_leave\_ukbb\_23andme\_vep\_input.txt

303 B1\_ALL\_leave\_23andme\_vep\_input.txt

267 B1\_ALL\_leave\_UKBB\_23andme\_vep\_input.txt

2794 B2\_ALL\_eur\_leave\_23andme\_vep\_input.txt ['9 133270637 133270638 AT/A']

1029 B2\_ALL\_eur\_leave\_ukbb\_23andme\_vep\_input.txt ['9 133270637 133270638 AT/A']

3390 B2\_ALL\_leave\_23andme\_vep\_input.txt ['9 133270497 133270498 GA/G', '9 133270637 133270638 AT/A']

973 B2\_ALL\_leave\_UKBB\_23andme\_vep\_input.txt

863 C2\_ALL\_eur\_leave\_23andme\_vep\_input.txt ['9 133270497 133270498 GA/G', '9 133270637 133270638 AT/A']

615 C2\_ALL\_eur\_leave\_ukbb\_23andme\_vep\_input.txt ['9 133270497 133270498 GA/G', '9 133270637 133270638 AT/A']

885 C2\_ALL\_leave\_23andme\_vep\_input.txt ['9 133270497 133270498 GA/G', '9 133270637 133270638 AT/A']

648 C2\_ALL\_leave\_UKBB\_23andme\_vep\_input.txt ['9 133270497 133270498 GA/G', '9 133270637 133270638 AT/A']

16367 total

['9 133270497 133270498 GA/G', '9 133270637 133270638 AT/A']

------------------------------------------------------------------------------------------------------

grep -v '#' VEP\_C2\_eu.txt | awk '{print $7}' | sort | uniq -c | sort -nr | head

grep -v '#' VEP\_C2\_eu.txt | awk '{print $NF}' | awk -F ';' '{print $1}' | awk -F '=' '{print $2}' | sort | uniq -c

grep -v '#' A2\_ALL\_eur\_leave\_23andme\_output.txt | awk '{print $NF}' | awk -F ';' '{print $1}' | awk -F '=' '{print $2}' | sort | uniq -c

halLiftover = '/exports/cmvm/eddie/sbms/groups/young-lab/rob/scripts/hal/halLiftover /exports/cmvm/eddie/sbms/groups/young-lab/rob/genomes/1509\_outgroups.hal ' + hal\_genome + ' temp/' + str(job\_id) + '\_temp.bed ' + target\_genome + ' ' + output\_dir + '/' + str(job\_id) + '\_' + target\_genome + '\_temp.bed'

**zgrep '46353198' \*.bed.gz | sort | uniq (27 results)**

**Cow Jun.2014(bosTau8)**

2\_bosTau8.bed.gz:chr23 27614167 27614169 chr3:46353198-46353200 0 .

Hg38 hit: chr3:46311708-46311710 (chr3:46353199-46353201)

2\_bosTau8.bed.gz:chr25 19861309 19861311 chr3:46353198-46353200 0 .

chr16:21957538-21957540 (chr16:21968859-21968861)

2\_bosTau8.bed.gz:chr9 18474121 18474123 chr3:46353198-46353200 0 .

chr3:46311708-46311710 (chr3:46353199-46353201)

2\_C57B6J.bed.gz:7 120637969 120637971 chr3:46353198-46353200 0 .

**Dog Sep.2011(canFam3)**

2\_canFam3.bed.gz:chr6 23650087 23650089 chr3:46353198-46353200 0 .

Hg19 hit: chr16:21968860-21968862

2\_canFam3.bed.gz:chrX 47261247 47261249 chr3:46353198-46353200 0 .

chr3:46353199-46353201

2\_felCat8.bed.gz:chrE3 23944473 23944475 chr3:46353198-46353200 0 .

2\_gorGor3.bed.gz:chr3 47536766 47536768 chr3:46353198-46353200 0 .

2\_hg19.bed.gz:chr3 46353198 46353200 chr3:46353198-46353200 0 .

2\_jacJac1.bed.gz:JH725446 9847800 9847802 chr3:46353198-46353200 0 .

2\_jacJac1.bed.gz:JH725550 1911898 1911900 chr3:46353198-46353200 0 .

2\_jacJac1.bed.gz:JH725581 3930357 3930359 chr3:46353198-46353200 0 .

2\_loxAfr3.bed.gz:scaffold\_65 3931319 3931321 chr3:46353198-46353200 0 .

2\_micOch1.bed.gz:chr8 15005027 15005029 chr3:46353198-46353200 0 .

**Rabbit Apr.2009(oryCun2)**

2\_oryCun2.bed.gz:chr13 29951883 29951885 chr3:46353198-46353200 0 .

Hg19 hit: chr3:46353199-46353201

2\_oryCun2.bed.gz:chr1 38595449 38595451 chr3:46353198-46353200 0 .

chr3:46353198-46353200

2\_oryCun2.bed.gz:chr14 14596441 14596443 chr3:46353198-46353200 0 .

chr3:46353198-46353200

2\_oryCun2.bed.gz:chr6 12721377 12721379 chr3:46353198-46353200 0 .

chr16:21968859-21968861

2\_oryCun2.bed.gz:chr9 70844463 70844465 chr3:46353198-46353200 0 .

chr3:46353199-46353201

2\_oviAri3.bed.gz:chr24 19689926 19689928 chr3:46353198-46353200 0 .

2\_oviBos.bed.gz:Anc06refChr6719 31191 31193 chr3:46353198-46353200 0 .

2\_panTro4.bed.gz:chr3 47013203 47013205 chr3:46353198-46353200 0 .

2\_ponAbe2.bed.gz:chr3 100247316 100247318 chr3:46353198-46353200 0 .

2\_Rattus.bed.gz:1 197483403 197483405 chr3:46353198-46353200 0 .

2\_rheMac3.bed.gz:chr20 20433336 20433338 chr3:46353198-46353200 0 .

2\_rheMac3.bed.gz:chr2 91565785 91565787 chr3:46353198-46353200 0 .

2\_rheMac3.bed.gz:chrUn\_JH290361 299832 299834 chr3:46353198-46353200 0 .

/exports/igmm/eddie/taylor-lab/rob/scripts/hal/halStats /exports/igmm/eddie/taylor-lab/rob/genomes/1509\_outgroups.hal --tree

((((((((((SPRET\_EiJ:0.002,(PWK\_PhJ:0.001,(CAST\_EiJ:0.001,(WSB\_EiJ:1e-05,(((NZO\_HlLtJ:1e-06,(C57BL\_6NJ:1e-06,C57B6J:1e-06)Anc23:1e-06)Anc21:1e-06,((NOD\_ShiLtJ:1e-06,FVB\_NJ:1e-06)Anc24:1e-06,(((DBA\_2J:1e-06,(CBA\_J:1e-06,C3H\_HeJ:1e-06)Anc29:1e-06)Anc28:1e-06,AKR\_J:1e-06)Anc26:1e-06,(BALB\_cJ:1e-06,A\_J:1e-06)Anc27:1e-06)Anc25:1e-06)Anc22:1e-06)Anc19:1e-06,(LP\_J:1e-06,129S1\_SvImJ:1e-06)Anc20:1e-06)Anc18:1e-06)Anc17:0.0001)Anc16:1e-06)splitPoint:1e-06)Anc14:0.015,CAROLI\_EiJ:0.02)Anc13:0.01,Pahari\_EiJ:0.03)Anc12:0.02,Rattus:0.013)msca\_root:0.065,micOch1:0.15)stitch1:0.117,jacJac1:0.1859)stitch2:0.07,oryCun2:0.21)stitch3:0.01,((((hg19:0.00642915,panTro4:0.00638042)Anc11:0.00217637,gorGor3:0.00882142)Anc10:0.00935116,ponAbe2:0.0185056)Anc08:0.00440069,rheMac3:0.007)primates:0.1)stitch4:0.02,((oviAri3:0.019,bosTau8:0.0506)oviBos:0.17,(canFam3:0.11,felCat8:0.08)stitch5:0.06)stitch6:0.02)stitch7:0.02,loxAfr3:0.15)stitch8;

<http://etetoolkit.org/treeview/?treeid=ba058a1d98cab8ebd792cfeb05d2d6b0&algid=>

Diagram

Description automatically generated

**<https://www.nih.gov/news-events/news-releases/nih-funded-scientists-publish-orangutan-genome-sequence>**

The researchers catalogued one type of large structural rearrangement called segmental duplications that have played a major role in restructuring other primate genomes. These large, almost identical copies of DNA are present in at least two locations of the genome and known to be associated with human diseases. Segmental **duplications** make up about **5 percent of human and chimpanzee genomes** but are present in only about **3.8 percent of the orangutan genome.**

<https://www.nature.com/articles/nature09687> paper by Devin Locke

To explain why the ponAbe2(Orangutan) have greater >1 ratio (more multiple hits) than other primate species.

The paper seems to show an opposite trend comparing to the result here.



[s1544765@node2c10(eddie) xiawen]$ shuf --help

Usage: shuf [OPTION]... [FILE]

or: shuf -e [OPTION]... [ARG]...

or: shuf -i LO-HI [OPTION]...

Write a random permutation of the input lines to standard output.

Mandatory arguments to long options are mandatory for short options too.

-e, --echo treat each ARG as an input line

-i, --input-range=LO-HI treat each number LO through HI as an input line

-n, --head-count=COUNT output at most COUNT lines

-o, --output=FILE write result to FILE instead of standard output

--random-source=FILE get random bytes from FILE

-r, --repeat output lines can be repeated

-z, --zero-terminated end lines with 0 byte, not newline

--help display this help and exit

--version output version information and exit

With no FILE, or when FILE is -, read standard input.

GNU coreutils online help: <http://www.gnu.org/software/coreutils/>

For complete documentation, run: info coreutils 'shuf invocation'

grep -v '#' A2\_ALL\_eur\_leave\_23andme\_output.txt | wc -l

grep -v '#' A2\_ALL\_eur\_leave\_23andme\_output.txt | shuf -n 4819 -r -o shuf/A2\_ALL\_eur\_leave\_23andme\_shuf.txt

cat A2\_ALL\_eur\_leave\_23andme\_shuf.txt | awk '{print $NF}' | awk -F ';' '{print $1}' | awk -F '=' '{print $2}' | sort | uniq -c

vep\_output\_v2/B1\_ALL\_eur\_leave\_23andme\_output.txt

1138

/home/s1544765/.local/lib/python3.7/site-packages/numpy/core/fromnumeric.py:3420: RuntimeWarning: Mean of empty slice.

out=out, \*\*kwargs)

/home/s1544765/.local/lib/python3.7/site-packages/numpy/core/\_methods.py:188: RuntimeWarning: invalid value encountered in double\_scalars

ret = ret.dtype.type(ret / rcount)

/home/s1544765/.local/lib/python3.7/site-packages/numpy/core/\_methods.py:262: RuntimeWarning: Degrees of freedom <= 0 for slice

keepdims=keepdims, where=where)

/home/s1544765/.local/lib/python3.7/site-packages/numpy/core/\_methods.py:222: RuntimeWarning: invalid value encountered in true\_divide

subok=False)

/home/s1544765/.local/lib/python3.7/site-packages/numpy/core/\_methods.py:253: RuntimeWarning: invalid value encountered in double\_scalars

ret = ret.dtype.type(ret / rcount)

{'A2\_ALL\_eur\_leave\_23andme': {'high\_ci': (1.2313759176509398, 1.610729345506955), 'low\_ci': (11.554980640112205, 12.805019359887794), 'moderate\_ci': (35.56569709272033, 37.854302907279674), 'modifier\_ci': (4768.132133614484, 4770.467866385517)}, 'A2\_ALL\_eur\_leave\_ukbb\_23andme': {'high\_ci': (1.9552681508621979, 2.4992773036832565), 'low\_ci': (22.12620319331147, 23.81379680668853), 'moderate\_ci': (38.17037730059286, 40.66962269940714), 'modifier\_ci': (4168.108892924597, 4171.191107075402)}, 'A2\_ALL\_leave\_23andme': {'high\_ci': (1.4209064190934186, 1.9228435809065814), 'low\_ci': (13.806666271507236, 15.393333728492763), 'moderate\_ci': (45.16328932548097, 47.51671067451904), 'modifier\_ci': (4459.436824332567, 4462.5431756674325)}, 'A2\_ALL\_leave\_UKBB\_23andme': {'high\_ci': (2.046556729246836, 2.563199368314139), 'low\_ci': (17.023956395049424, 18.736043604950574), 'moderate\_ci': (38.33032214987309, 40.4896778501269), 'modifier\_ci': (4158.4999498932975, 4161.140050106702)}, 'B1\_ALL\_eur\_leave\_23andme': {'high\_ci': (nan, nan), 'low\_ci': (16.39152236833592, 18.20847763166408), 'moderate\_ci': (5.550269874888369, 6.409326084707591), 'modifier\_ci': (1113.7753517613423, 1115.7846482386576)}, 'B1\_ALL\_eur\_leave\_ukbb\_23andme': {'high\_ci': (nan, nan), 'low\_ci': (4.511710687511705, 5.326673150872134), 'moderate\_ci': (10.360578986483121, 11.61942101351688), 'modifier\_ci': (769.3862853357296, 770.8937146642704)}, 'B1\_ALL\_leave\_23andme': {'high\_ci': (nan, nan), 'low\_ci': (4.499513494080568, 5.35907236450529), 'moderate\_ci': (5.644554408833191, 6.5954455911668095), 'modifier\_ci': (957.3496550942616, 958.6503449057384)}, 'B1\_ALL\_leave\_UKBB\_23andme': {'high\_ci': (nan, nan), 'low\_ci': (4.528240959761065, 5.431759040238936), 'moderate\_ci': (5.592850139740386, 6.568766021875775), 'modifier\_ci': (823.3556491844114, 824.6443508155886)}, 'B2\_ALL\_eur\_leave\_23andme': {'high\_ci': (4.813200793668577, 5.651445670977888), 'low\_ci': (119.99519920856295, 124.32480079143704), 'moderate\_ci': (128.6422821201319, 133.25771787986807), 'modifier\_ci': (20481.766387810887, 20487.65361218911)}, 'B2\_ALL\_eur\_leave\_ukbb\_23andme': {'high\_ci': (3.6089141032500045, 4.37067773348469), 'low\_ci': (18.660639994188145, 20.419360005811853), 'moderate\_ci': (48.20655720530181, 50.99344279469819), 'modifier\_ci': (4479.070404024777, 4482.829595975222)}, 'B2\_ALL\_leave\_23andme': {'high\_ci': (4.488734288236482, 5.451265711763518), 'low\_ci': (137.43356998824913, 141.48643001175088), 'moderate\_ci': (93.88426483045141, 97.89573516954859), 'modifier\_ci': (27441.77692667839, 27447.58307332161)}, 'B2\_ALL\_leave\_UKBB\_23andme': {'high\_ci': (3.6369423861943595, 4.52632291992809), 'low\_ci': (10.578110027892524, 11.961889972107475), 'moderate\_ci': (49.73053939074763, 52.369460609252364), 'modifier\_ci': (4267.003696863636, 4270.356303136365)}, 'C2\_ALL\_eur\_leave\_23andme': {'high\_ci': (3.5202791863624596, 4.27563918098448), 'low\_ci': (12.863432010841443, 14.176567989158556), 'moderate\_ci': (39.12056019783941, 41.59943980216059), 'modifier\_ci': (3975.9136762684075, 3978.686323731593)}, 'C2\_ALL\_eur\_leave\_ukbb\_23andme': {'high\_ci': (3.758432872557685, 4.6052034910786785), 'low\_ci': (11.365357473094004, 12.634642526905996), 'moderate\_ci': (18.11527234677146, 19.68472765322854), 'modifier\_ci': (2489.9274140432067, 2491.9925859567934)}, 'C2\_ALL\_leave\_23andme': {'high\_ci': (3.7055429176812353, 4.496477284338967), 'low\_ci': (14.442455210037355, 16.217544789962645), 'moderate\_ci': (35.6500506427097, 38.009949357290296), 'modifier\_ci': (4129.24616018038, 4132.31383981962)}, 'C2\_ALL\_leave\_UKBB\_23andme': {'high\_ci': (2.6499681685820176, 3.3074786399286205), 'low\_ci': (8.591578319828054, 9.808421680171945), 'moderate\_ci': (28.82424037831277, 30.93575962168723), 'modifier\_ci': (2920.7563143418242, 2923.4836856581755)}}

[s1544765@node2c10(eddie) GWAS\_library]$ cat gwas\_library\_v2.bed |awk '{print $4}'| sort |uniq -c | wc -l

25085

[s1544765@node2c10(eddie) GWAS\_library]$ wc -l gwas\_library\_v2.bed

192145

2021-06-11 22:27:31.790352

/exports/cmvm/eddie/sbms/groups/young-lab/rob/scripts/hal/halLiftover /exports/cmvm/eddie/sbms/groups/young-lab/rob/genomes/1509\_outgroups.hal hg19 GWAS\_library/liftOver\_input/temp/temp\_1.bed C57B6J GWAS\_library/liftOver\_output/split\_output/hg19\_C57B6J\_1.bed

HDF5-DIAG: Error detected in HDF5 (1.8.9) thread 0:

#000: H5Dio.c line 174 in H5Dread(): can't read data

major: Dataset

minor: Read failed

#001: H5Dio.c line 449 in H5D\_read(): can't read data

major: Dataset

minor: Read failed

#002: H5Dchunk.c line 1729 in H5D\_chunk\_read(): unable to read raw data chunk

major: Low-level I/O

minor: Read failed

#003: H5Dchunk.c line 2760 in H5D\_chunk\_lock(): data pipeline read failed

major: Data filters

minor: Filter operation failed

#004: H5Z.c line 1120 in H5Z\_pipeline(): filter returned failure during read

major: Data filters

minor: Read failed

#005: H5Zdeflate.c line 136 in H5Z\_filter\_deflate(): memory allocation failed for deflate uncompression

major: Resource unavailable

minor: No space available for allocation

terminate called after throwing an instance of 'H5::DataSetIException'

-6

0

C57B6J

2021-06-11 22:31:09.518007

/exports/cmvm/eddie/sbms/groups/young-lab/rob/scripts/hal/halLiftover /exports/cmvm/eddie/sbms/groups/young-lab/rob/genomes/1509\_outgroups.hal hg19 GWAS\_library/liftOver\_input/temp/temp\_10.bed C57B6J GWAS\_library/liftOver\_output/split\_output/hg19\_C57B6J\_2.bed

HDF5-DIAG: Error detected in HDF5 (1.8.9) thread 0:

#000: H5Dio.c line 174 in H5Dread(): can't read data

major: Dataset

minor: Read failed

#001: H5Dio.c line 449 in H5D\_read(): can't read data

major: Dataset

minor: Read failed

#002: H5Dchunk.c line 1729 in H5D\_chunk\_read(): unable to read raw data chunk

major: Low-level I/O

minor: Read failed

#003: H5Dchunk.c line 2760 in H5D\_chunk\_lock(): data pipeline read failed

major: Data filters

minor: Filter operation failed

#004: H5Z.c line 1120 in H5Z\_pipeline(): filter returned failure during read

major: Data filters

minor: Read failed

#005: H5Zdeflate.c line 136 in H5Z\_filter\_deflate(): memory allocation failed for deflate uncompression

major: Resource unavailable

minor: No space available for allocation

terminate called after throwing an instance of 'H5::DataSetIException'

-6

0

C57B6J

2021-06-11 22:34:57.056022

/exports/cmvm/eddie/sbms/groups/young-lab/rob/scripts/hal/halLiftover /exports/cmvm/eddie/sbms/groups/young-lab/rob/genomes/1509\_outgroups.hal hg19 GWAS\_library/liftOver\_input/temp/temp\_2.bed C57B6J GWAS\_library/liftOver\_output/split\_output/hg19\_C57B6J\_3.bed