

S1 Text. Supplementary Materials

Parameter adjustment details:

In this study, we examined the presence of runs of homozygosity (ROH) in Japanese individuals by using two high-coverage WGS datasets. We used BCFtools/RoH and PLINK 1.90 in which the following parameters were applied to adjust the detectability of ROH according to the different compositions in each cohort.

BCFtools/RoH:

<Extraction of data>

```
bcftools view -m2 -M2 -v snps \  
  
-g ^miss \  
  
-q 0.05 -Q 0.95 \  
  
-O b -o ${BCFFILE} ${THREADS_OPT} ${VCFFILE}
```

<Detection of ROH>

```
bcftools roh -G30 \  
  
-b 20480 \  
  
-m ${MAPFILE} \  
  
-R ${REGION} \  
  
-O r -o ${OUTFILE} ${BCFFILE}
```

PLINK:

```
plink --memory 20480 \  
  
--bcf ${BCFFILE} \  

```

--allow-extra-chr \

--keep-allele-order \

--geno 0.03 \

--homozyg-snp 50 \

--homozyg-kb 100 \

--homozyg-density 50 \

--homozyg-gap 1000 \

--homozyg-window-snp 50 \

--homozyg-window-het (1 or 2 or 3 or 4) \

--homozyg-window-missing 5 \

--out \${OUTFILE}