## Starling-May18 Projects/Katarina Stuart/KStuart.Starling-Aug18/Sv10\_NZstarlings/Analysis/2024-06-12.Sexing

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2024-06-12.Sexing



## **Private alleles**

## Use the final VCF as this will ensure no siblings used

```
cd /nesi/nobackup/uoa02613/kstuart_projects/Sv10_NZstarlings/analysis/sexing
module load VCFtools/0.1.15-GCC-9.2.0-Perl-5.30.1
VCF=/nesi/nobackup/uoa02613/kstuart\_projects/Sv10\_NZstarlings/data/processing\_rawdata/BCFtools/final\_filtering/starling\_noduprel\_qual\_miss\_filt.recode.vcf
VCF=/nesi/nobackup/uoa02613/kstuart\_projects/Sv10\_NZstarlings/data/processing\_rawdata/BCFtools/variant\_calls\_annotate.vcf.gz
vcftools --vcf $VCF --chr SV_vAU_seq31 --het --out sexchrom_het
module load R/4.1.0-gimkl-2020a
library(ggplot2)
library(data.table)
library(tidyr)
library(dplyr)
setwd("/nesi/nobackup/uoa02613/kstuart_projects/Sv10_NZstarlings/analysis/sexing")
chrom <- fread("sexchrom het.het")
chrom_sorted <- chrom[order(chrom$F), ]
chrom sorted <- chrom sorted %>% mutate(order=row number())
metanames <-
read.table ("/nesi/nobackup/uoa02613/kstuart\_projects/Sv10\_NZstarlings/data/processing\_rawdata/BCFtools/Metadata\_NZ\_AU\_UK\_BE\_ReplicatesSibRemoved2.csv", header=T, september 2012 ("/nesi/nobackup/uoa02613/kstuart\_projects/Sv10\_NZstarlings/data/processing\_rawdata/BCFtools/Metadata_NZstarlings/data/processing\_rawdata/BCFtools/Metadata_NZstarlings/data/processing\_rawdata/BCFtools/Metadata_NZstarlings/data/processing\_rawdata/BCFtools/Metadata_NZstarlings/data/processing\_rawdata/BCFtools/Metadata_NZstarlings/data/processing\_rawdata/BCFtools/Metadata_NZstarlings/data/processing\_rawdata/BCFtools/Metadata_NZstarlings/data/processing_rawdata/processing_rawdata/processing_rawdata/processing_rawdata/processing_rawdata/processing_rawdata/processing_rawdata/processing_rawdata/processing_rawdata/processing_rawdata/processing_rawdata/processing_rawdata/processing_rawdata/processing_rawdata/processing_rawdata/processing_rawdata/processing_rawdata/processing_rawdata/processing_rawdata/processing_rawdata/processing_rawdata/processing_rawdata/processing_rawdata/processing_rawdata/processing_rawdata/processing_rawdata/processing_rawdata/processing_rawdata/processing_rawdata/processing_rawdata/processing_rawdata
metanames <- read.table("/nesi/nobackup/uoa02613/kstuart_projects/Sv10_NZstarlings/data/processing_rawdata/BCFtools_old/Metadata_NZ_AU_UK_BE.csv",header=T,sep =",")
data <- merge(chrom_sorted, metanames, by.x = "INDV", by.y = "id")
pdf("Sv10_sexing.pdf", width=8.5, height=5.0)
ggplot(data, aes(x=order, y=F, fill=pop2)) + geom_bar(stat = "identity")+
scale_fill_manual(values=c("blue","#4CBB17","#80ff80","#C9CC3F","#800080","#ff6600","#C9EC3F","#ffc000","#06600","#9FE2BF")) +theme_classic(base_size = 18)
dev.off()
data <- data %>% mutate(bioinfo_sex= if_else(F > 0.25, "F", "M"))
write.table(data, "sexing.txt", row.names=FALSE, sep="\t", quote = FALSE, col.names=TRUE)
write.table(data, "sexing_all.txt",row.names=FALSE,sep="\t", quote = FALSE,col.names=TRUE)
```

