VCF Compare Script

Files

 $[1]\ "03_RET6b.txt.Q40.vcf.gz"\ "03_RET6.txt.Q40.vcf.gz"\ [3]\ "03_RET6a.txt.Q40.vcf.gz"$

Individual VCF Results

03_RET6.040

03_RET6.Q40_03_RET6a.Q40

03_RET6.Q40__03_RET6a.Q40

03_RET6a.Q40

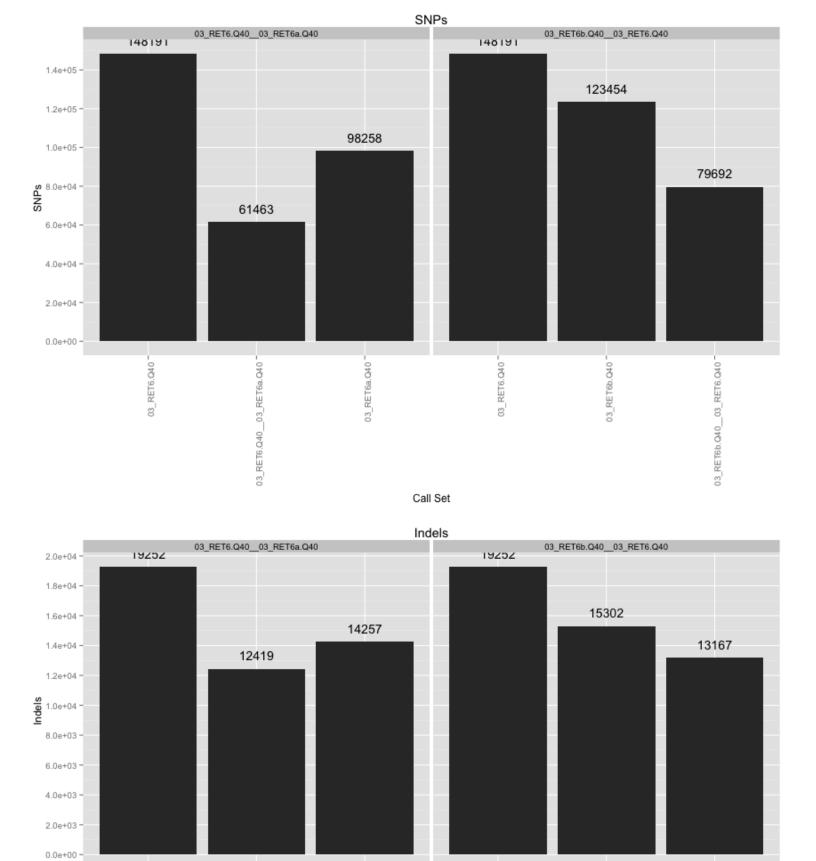
Call Set

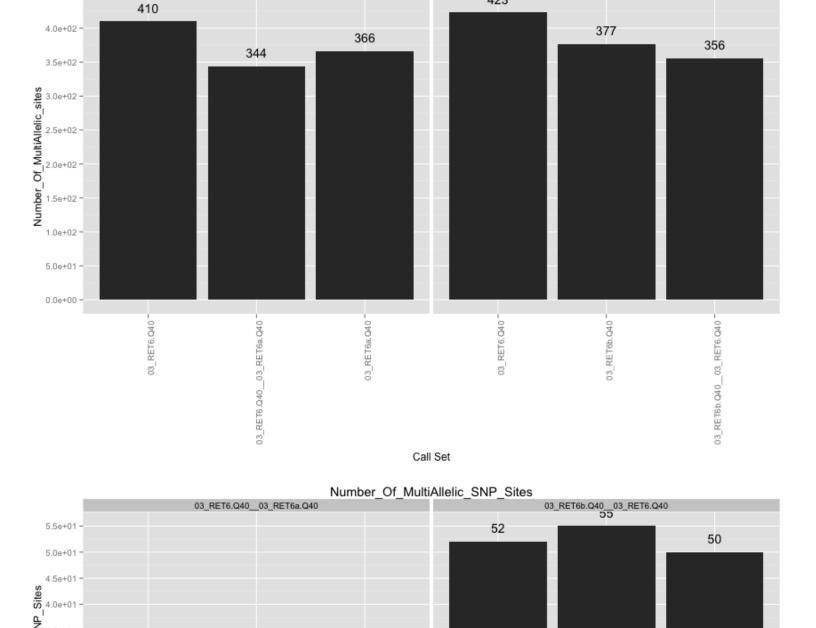
Number_Of_MultiAllelic_sites

03 RET6.040

03_RET6b.Q40

03_RET6b.Q40__03_RET6.Q40

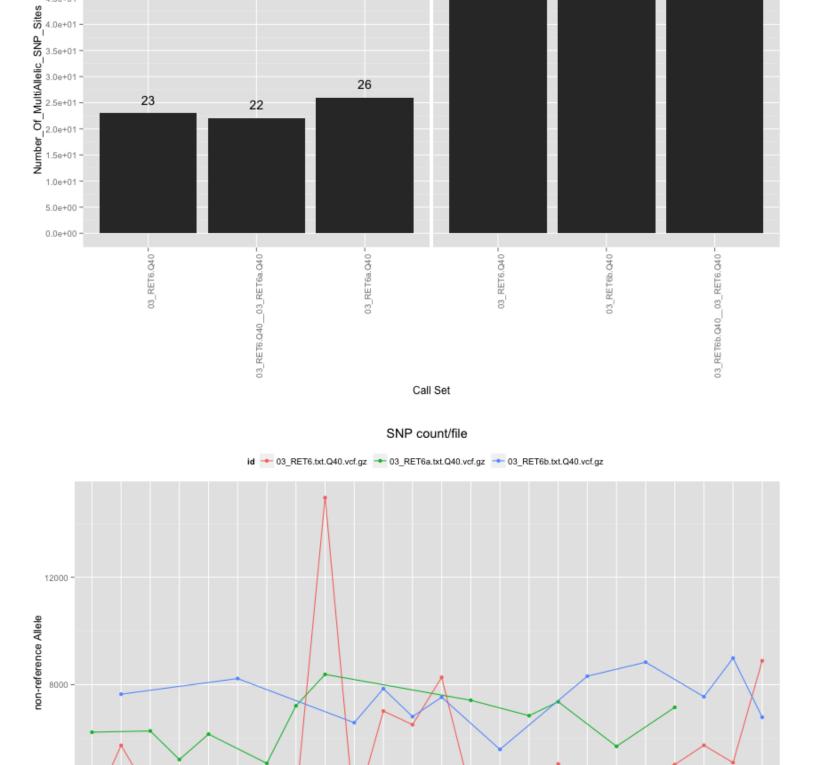




03_RET6b.Q40__03_RET6.Q40_

OX1214

WN2001



JU1581

JU2001

JU393

Strain Name

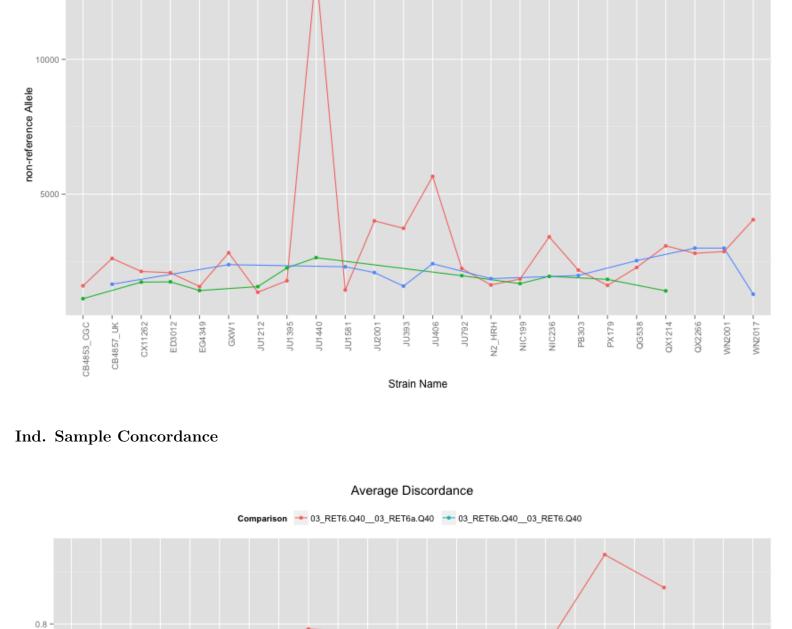
SNP count/file

id - 03_RET6.txt.Q40.vcf.gz - 03_RET6a.txt.Q40.vcf.gz - 03_RET6b.txt.Q40.vcf.gz

JU792

N2_HRH

NIC236



EG4349

GXW1

ED3012

CB4857_UK

Average Discordance (%) 0.4 ED3012 E64349 JU1581 N2_HRH NIC236 CB4857_UK GXW1 QX2266 Sample Name Figure 1: plot of chunk ind_conc Pairwise Concordance 03_RET6b.Q40__03_RET6.Q40 WN2017 -WN2001 QX2266 QG538 PB303 -

JU2001

JU1581

GXW1

JU406

Query

Concordance 0.0 0.2 0.4 0.6

N2_HRH

0.6538

QX2266

WN2001

Sample

N2_HRH =

JU406 -

JU393 -

JU2001 ·

JU1581 ·

GXW1-

CB4857_UK -

03_RET6.Q40__03_RET6a.Q40 QX1214 -PX179 -NIC236 -NIC199 -JU792 -Sample JU1440 -JU1395 -JU1212 -EG4349 -ED3012 -CX11262 -CB4853_CGC -QX1214 -ED3012 = JU1212 ⁻ EG4349 -NIC236 " CB4853_CGC Query Concordance 0.00 0.25 0.50 0.75 [[2]]