

Metadata in the vcf file

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```
> library("vcf2R")
> library("trioClasses")
> library("trio")
> library("VariantAnnotation")
> data("BMP4-european-all.vcf")
> data(ped, package = "trioClasses")

> geno.mat <- geno(vcf)$GT
> save(geno.mat, file = paste0("/home/bst/student/syounkin/R/packages/vcf2R/data/",
    locus, "-european-all.geno.RData"))

> names(geno(vcf))

[1] "DNGL" "DNGT" "DNGQ" "GT"   "GQ"   "DP"   "DS"   "GL"   "FT"
[10] "DNFT" "PL"   "BA"

> table(geno(vcf)$FT)

          .          DETP20
316820          3
      HPMR5      MMQSD50
      390          821
MMQSD50;DETP20 MMQSD50;HPMR5
      1          8
MMQSD50;MQD30 MMQSD50;RLD25
      11          4
MMQSD50;RLD25;DETP20 MVC4
      1          257
      MVC4;DETP20 MVC4;MMQSD50
      7          36
MVC4;MMQSD50;MQD30 MVC4;MMQSD50;MQD30;RLD25
      5          1
      MVC4;MQD30 MVC4;MQD30;RLD25;DETP20
      5          1
      MVC4;RLD25 MVC4;RLD25;DETP20
      9          1
      NRC          PASS
      25          20043
      PB10          PB10;MVC4
      1          6
```

PB10;MVC4;DETP20	PB10;MVC4;MMQSD50
1	1
PB10;MVC4;RLD25	PB10;SB1;MVC4
1	15
RLD25	SB1
1	906
SB1;DETP20	SB1;HPMR5
1	1
SB1;MMQSD50	SB1;MMQSD50;MQD30
96	3
SB1;MMQSD50;MQD30;RLD25	SB1;MMQSD50;RLD25
2	5
SB1;MVC4	SB1;MVC4;DETP20
338	9
SB1;MVC4;MMQSD50	SB1;MVC4;MMQSD50;DETP20
20	1
SB1;MVC4;MMQSD50;MQD30	SB1;MVC4;MQD30
1	1
SB1;MVC4;RLD25	SB1;RLD25
2	1

```
> table(geno(vcf)$DNFT)
```

.	PASS	Polymutt	Denovo
2609	6	1	