

```

> library("vcf2R")
> library("snpStats")
> data("ABCA4-chinese-all.sm")
> data(ped, package = "vcf2R")

```

After loading the necessary packages and data we first make sure that the pedigree data frame contains fields F, M and O for father, mother and offspring ids. Note that these ids should match those in the vcf file.

```

> ped.df <- with(ped.df, {
  data.frame(ped = ped, id = id, father = fid, mother = mid,
    sex = sex, affected = affected + 1)
})
> pedigreeInfo <- subset(ped.df, !is.na(id))
> rownames(pedigreeInfo) <- pedigreeInfo$id

> maf <- colSums(as(sm, "numeric"), na.rm = TRUE)/colSums(!is.na(sm))/2
> maf <- ifelse(maf > 0.5, 1 - maf, maf)
> sub <- which(maf >= 0.05)

> tdt.obj <- tdt.snp(data = pedigreeInfo, snp.data = sm,
  snp.subset = sub)

```

Analysing 457 potentially complete trios in 457 different pedigrees

```
> qq.chisq(chi.squared(tdt.obj, 1), df = 1)
```

N	omitted	lambda
1018.000000	0.000000	1.696365

