VCF Coverage Stats

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Calculating median depth for callableLoci maxcov filter using FreeBayes vcf files. Downloaded vcf files from DNAnexus. Generated *.ldepth files using vcftools and bash script get_depth.sh.

```
library(tidyverse); packageVersion("tidyverse")
## [1] '1.2.1'
depth files <- list.files(path = ".", pattern = "ldepth")</pre>
names(depth_files) <- depth_files %>% str_remove(".vcf.gz.ldepth")
depth_df <- depth_files %>%
   map_dfr(read_tsv, col_types = "ciic", .id = "dataset")
summary_df <- depth_df %>% group_by(dataset) %>%
    summarise(med_depth = median(SUM_DEPTH),
              min_depth = min(SUM_DEPTH),
              max depth = max(SUM DEPTH),
              mean_depth = mean(SUM_DEPTH)) %>%
   mutate(maxcov = 2*med_depth)
summary_df %>%
    mutate(dataset = str_remove(dataset, "_novoalign"))
## # A tibble: 8 x 6
##
     dataset
                              med_depth min_depth max_depth mean_depth maxcov
                                             <dbl>
                                                                  <dbl> <dbl>
##
     <chr>>
                                  <dbl>
                                                       <dbl>
## 1 HG006_1_GRCh37_6Kb_Mate~
                                                2
                                                      186310
                                                                   36.4
                                     19
                                                                            38
## 2 HG006 1 GRCh37 Hiseq100~
                                                2
                                                                   93.5
                                     91
                                                      15171
                                                                           182
## 3 HG006_1_GRCh38_6Kb_Mate~
                                     18
                                                2
                                                                   24.2
                                                                            36
                                                      22685
## 4 HG006 1 GRCh38 Hiseq100~
                                     89
                                                      455338
                                                                  112.
                                                                           178
## 5 HG007_1_GRCh37_6Kb_Mate~
                                     18
                                                 1
                                                      202736
                                                                   38.1
                                                                            36
## 6 HG007 1 GRCh37 Hiseq100~
                                     91
                                                1
                                                        7321
                                                                   94.2
                                                                           182
## 7 HG007 1 GRCh38 6Kb Mate~
                                                                   24.6
                                     17
                                                1
                                                      26551
                                                                            34
## 8 HG007_1_GRCh38_Hiseq100~
                                     90
                                                      497810
                                                                  119.
                                                                           180
write tsv(summary df, "chrom1 variant depth.tsv")
```