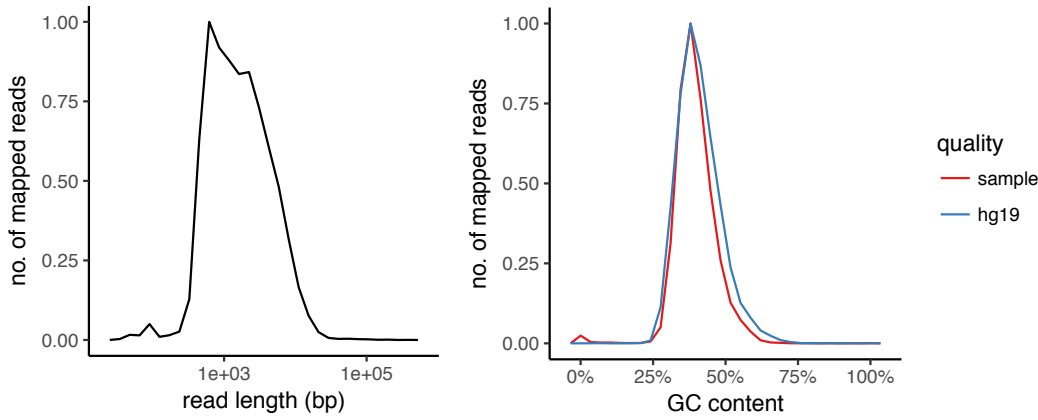


## Supplementary Figures S1 – S3

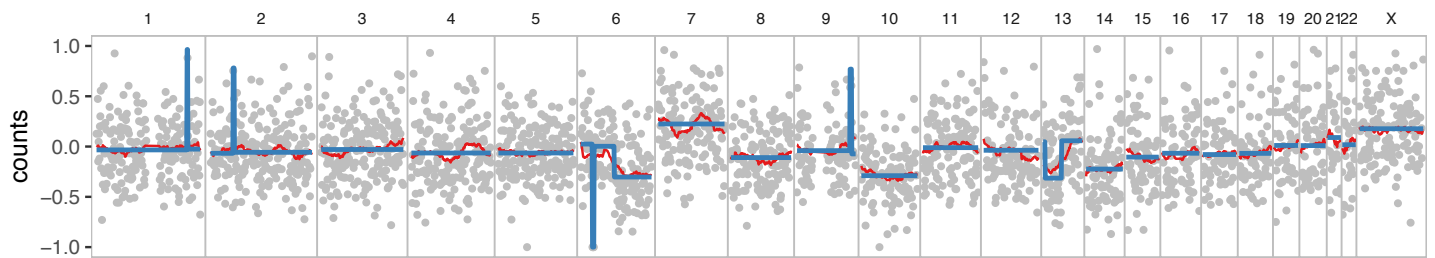
**Fig. S1: Sequencing reports for nanopore whole genome sequencing.** For each sample that underwent whole genome sequencing, basic quality metrics (read length and GC distribution), the copy number profile and the result of methylation-based pan-cancer random forest classification are shown.

# 2197T

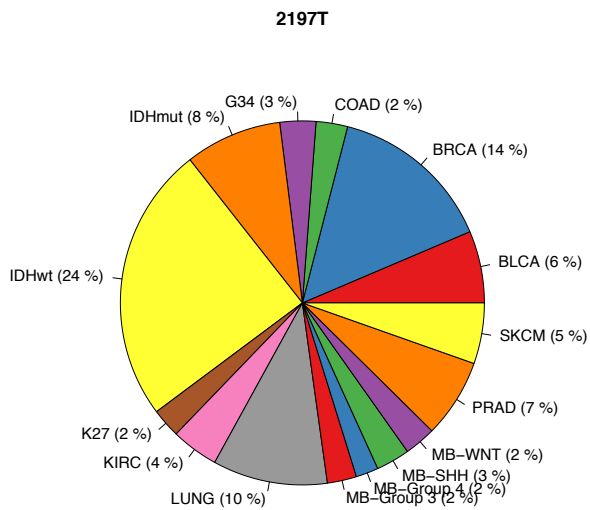
## Quality control metrics



## Copy number profile

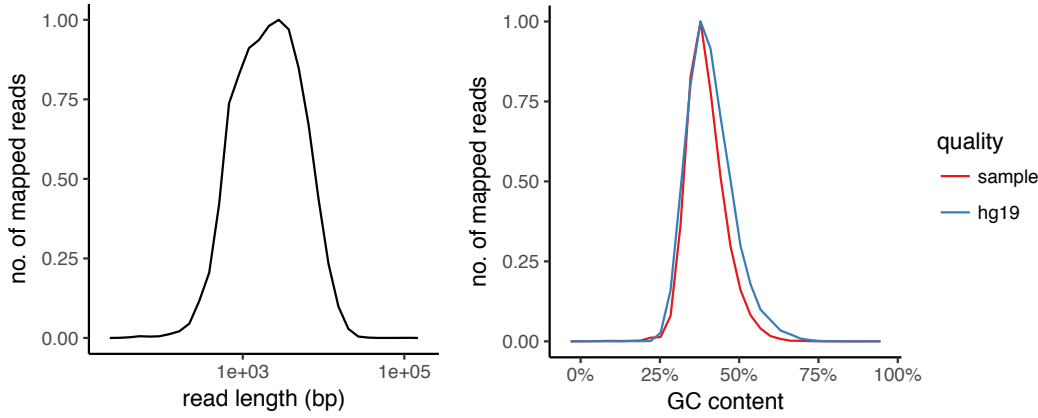


## Methylation based classification

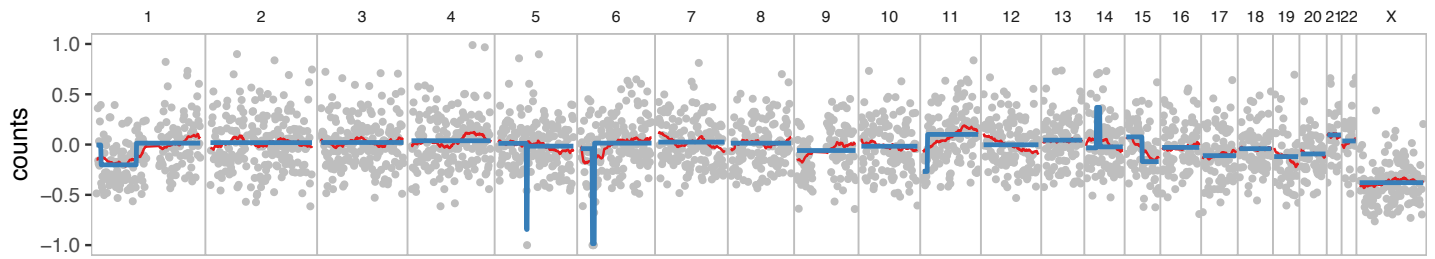


# 2402T

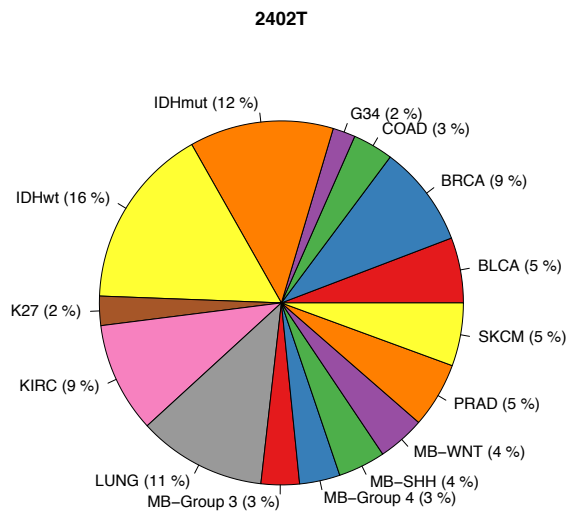
## Quality control metrics



## Copy number profile

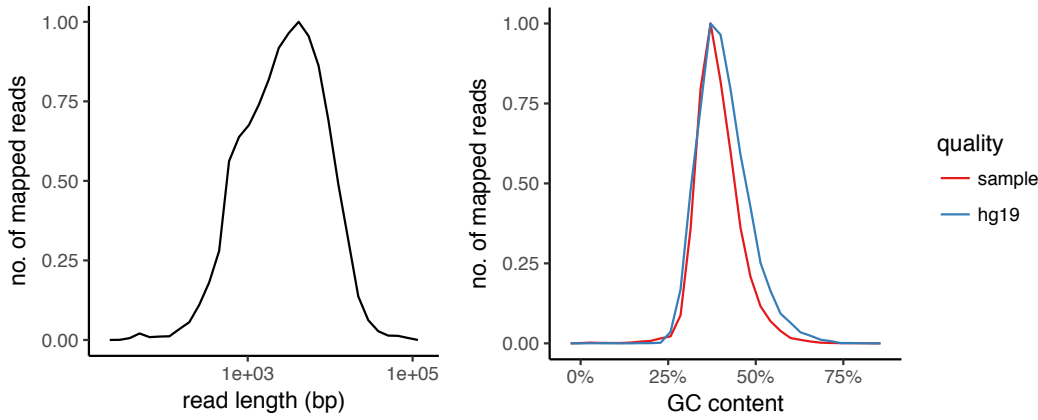


## Methylation based classification

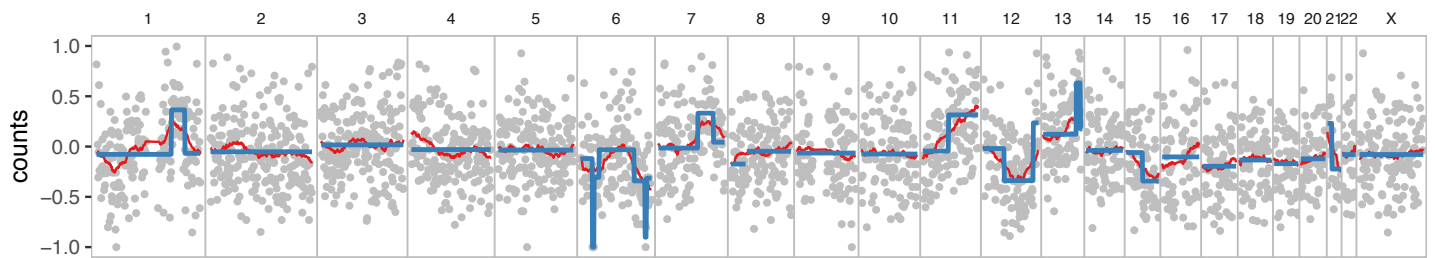


# 2483T

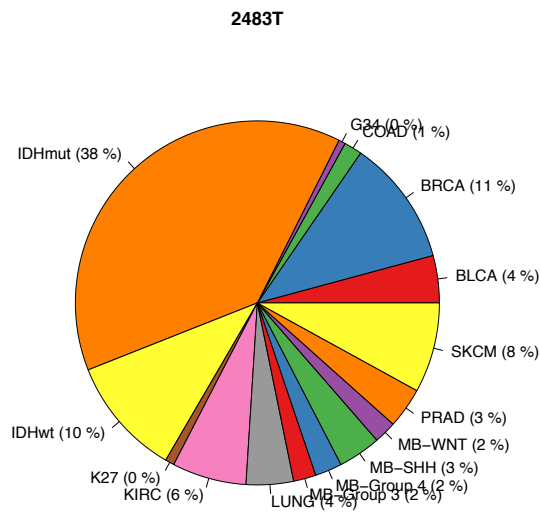
## Quality control metrics



## Copy number profile

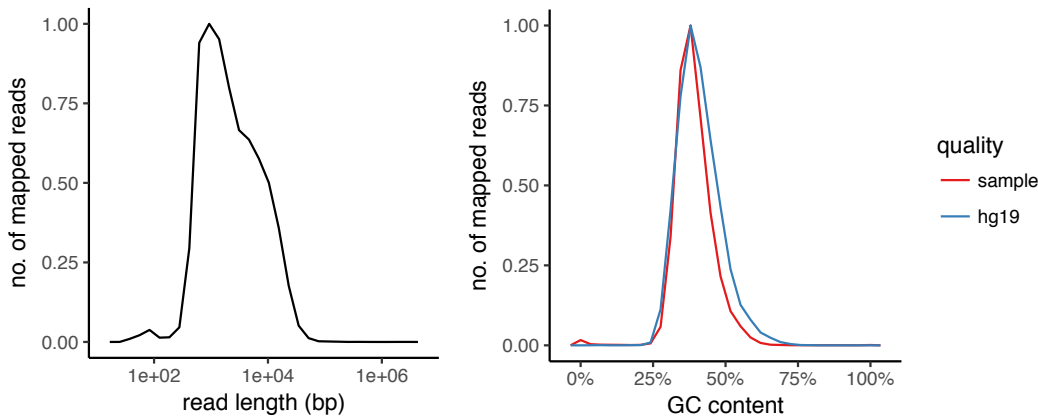


## Methylation based classification

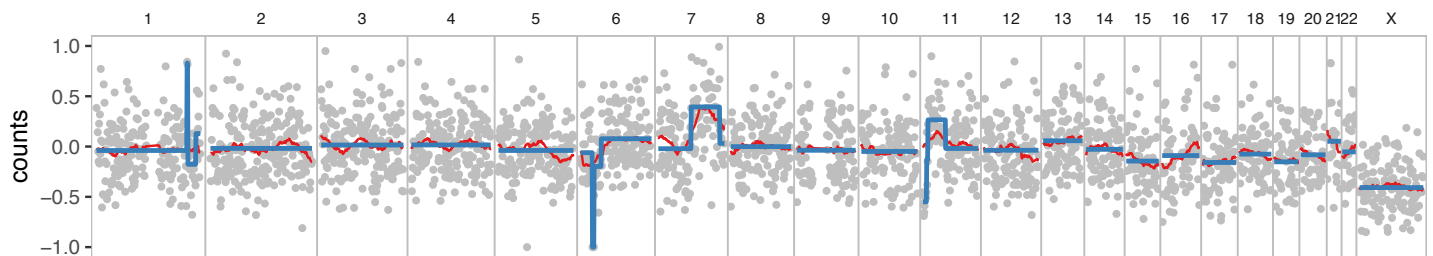


# 2922T

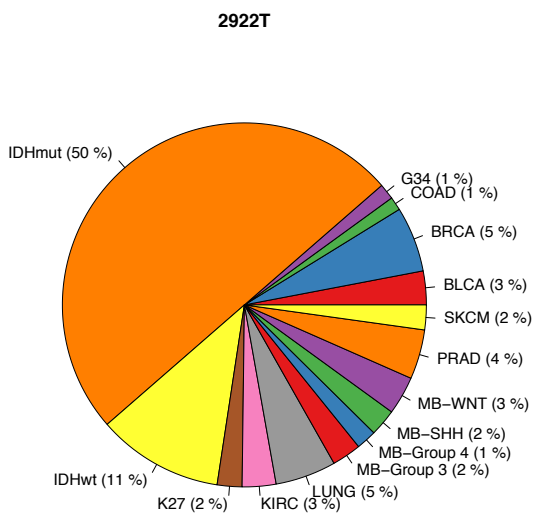
## Quality control metrics



## Copy number profile

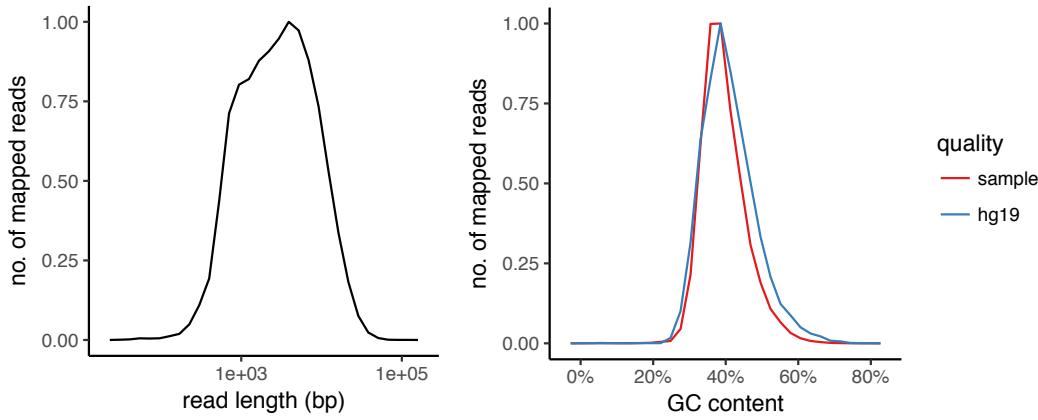


## Methylation based classification

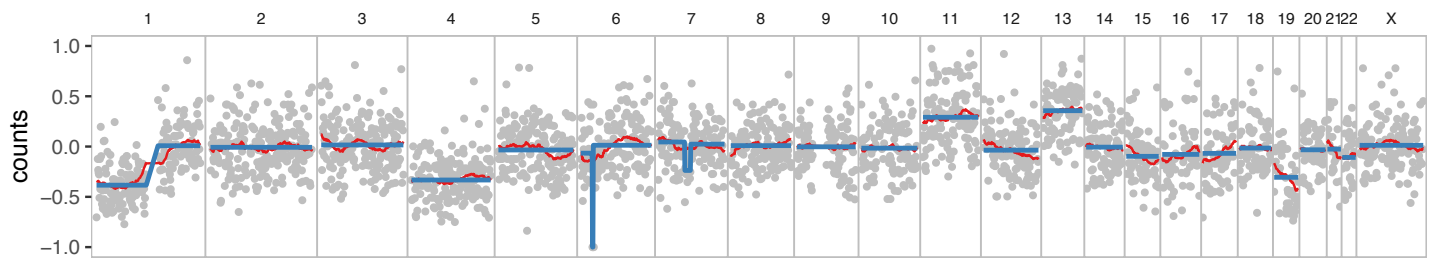


# 2965T

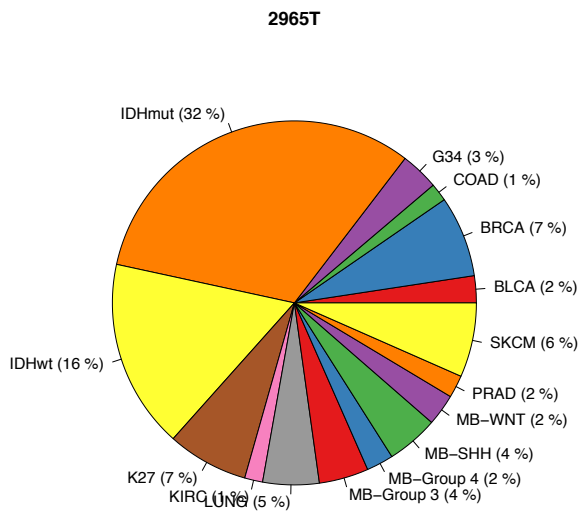
## Quality control metrics



## Copy number profile

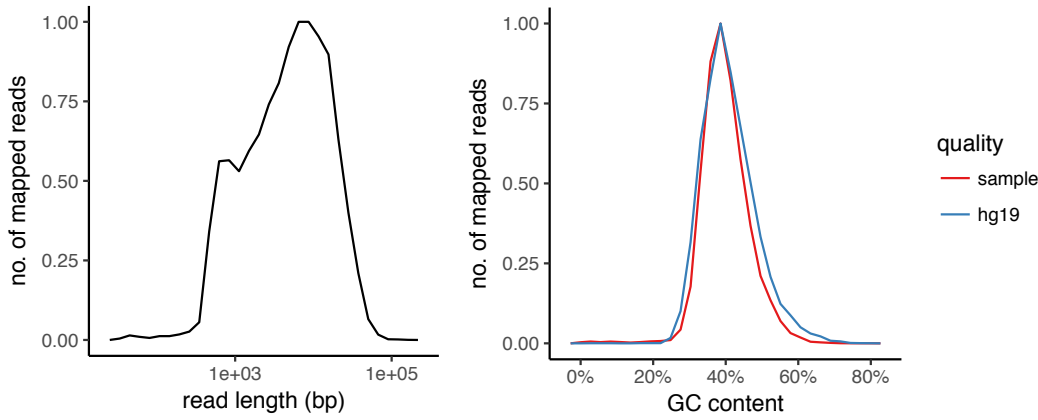


## Methylation based classification

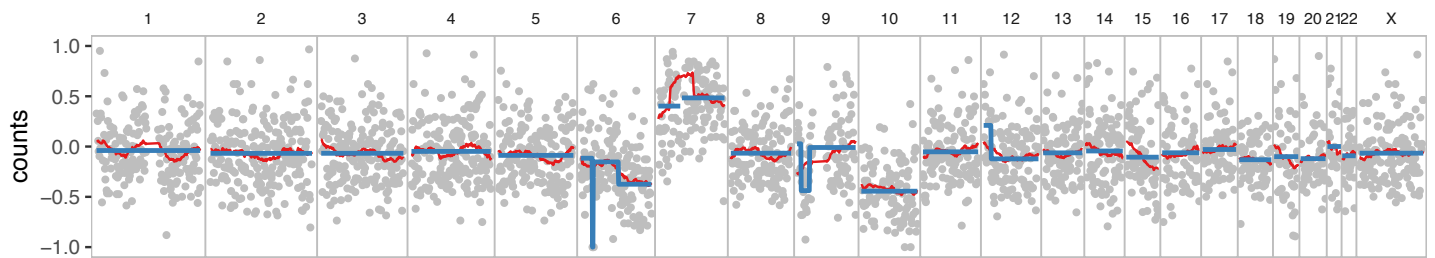


# 3427T

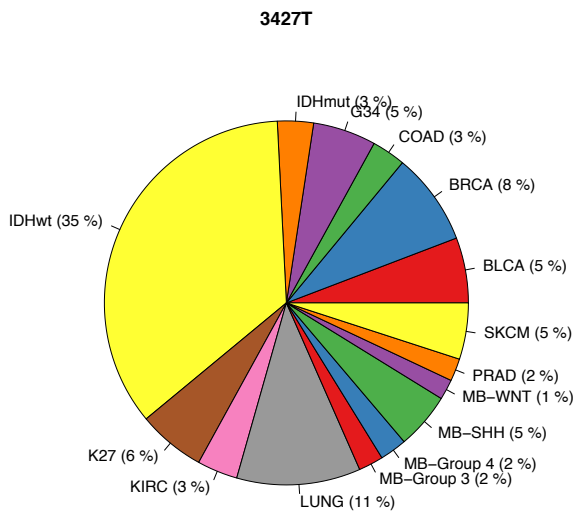
## Quality control metrics



## Copy number profile

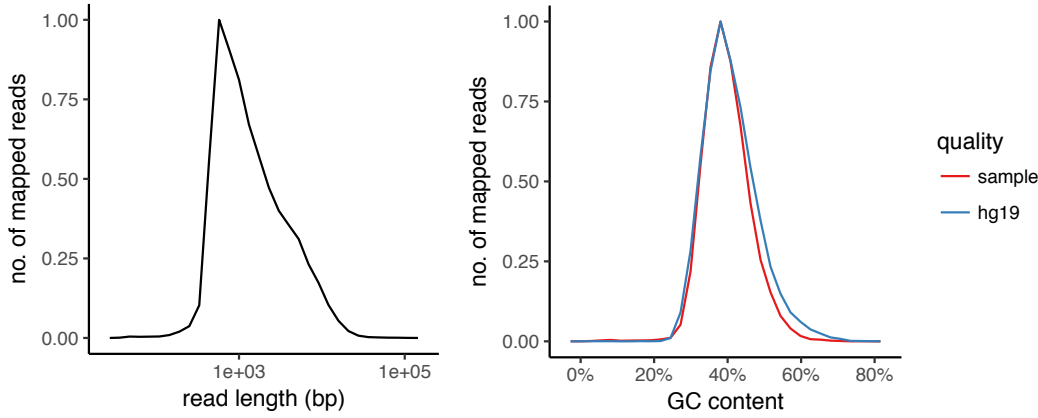


## Methylation based classification

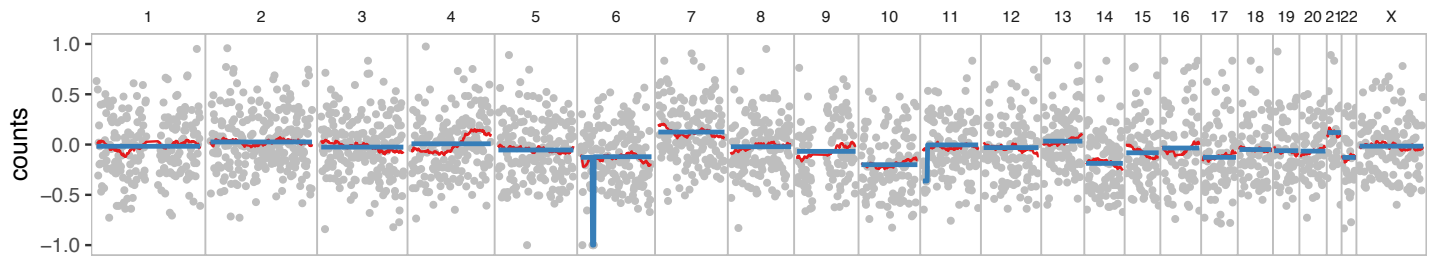


# 3523T

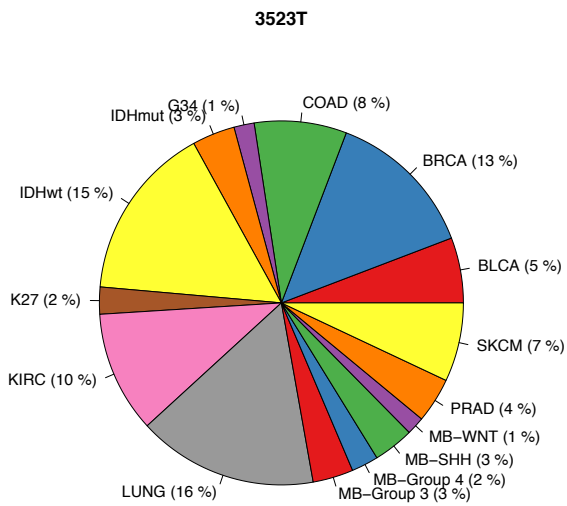
## Quality control metrics



## Copy number profile



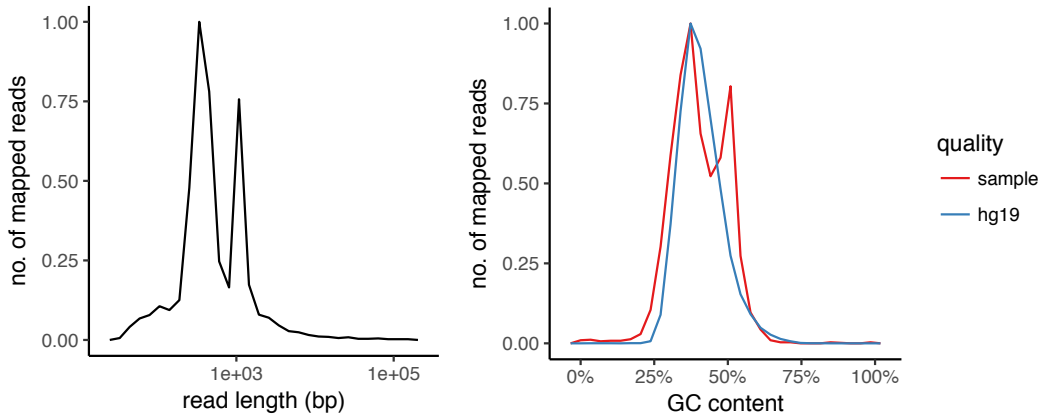
## Methylation based classification



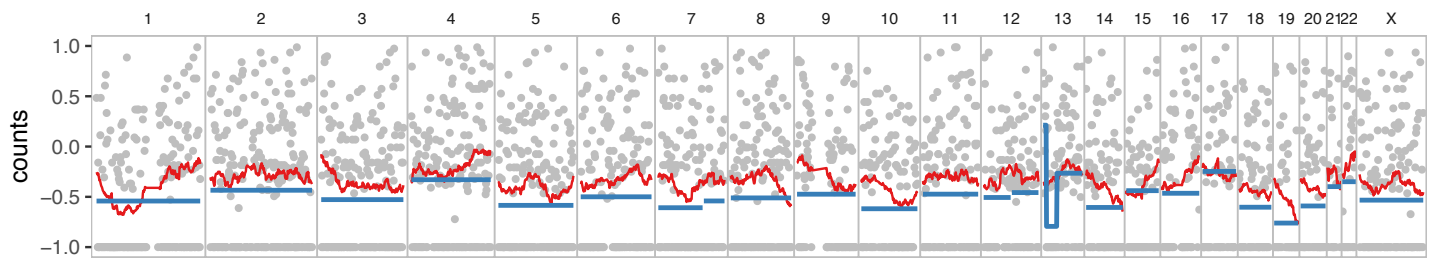


# 4596TP

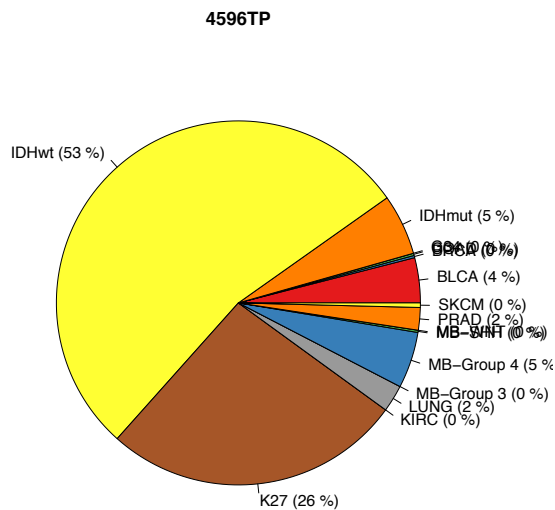
## Quality control metrics



## Copy number profile

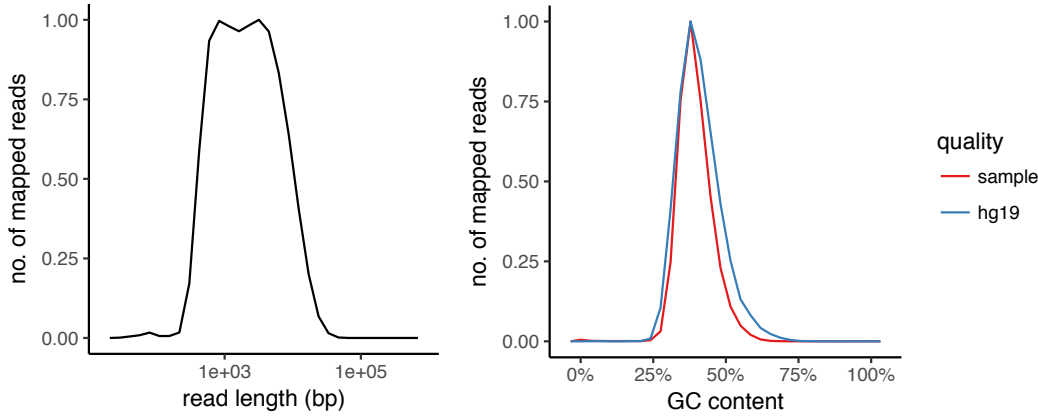


## Methylation based classification

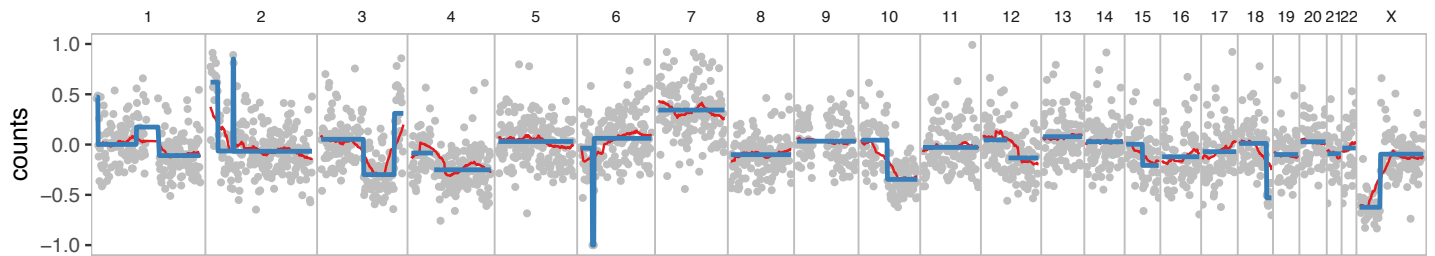


# 5337T

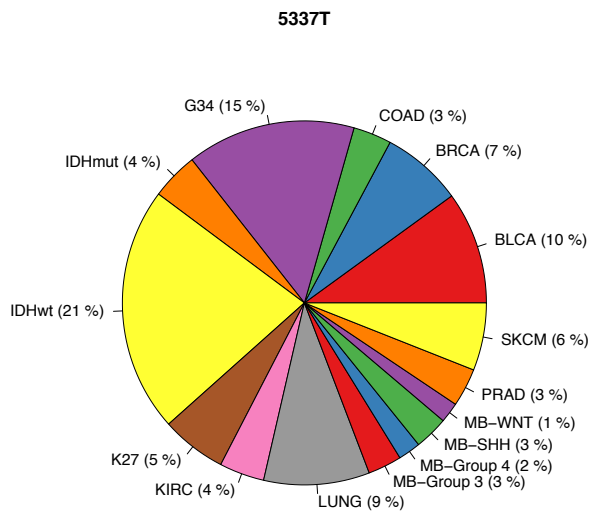
## Quality control metrics



## Copy number profile

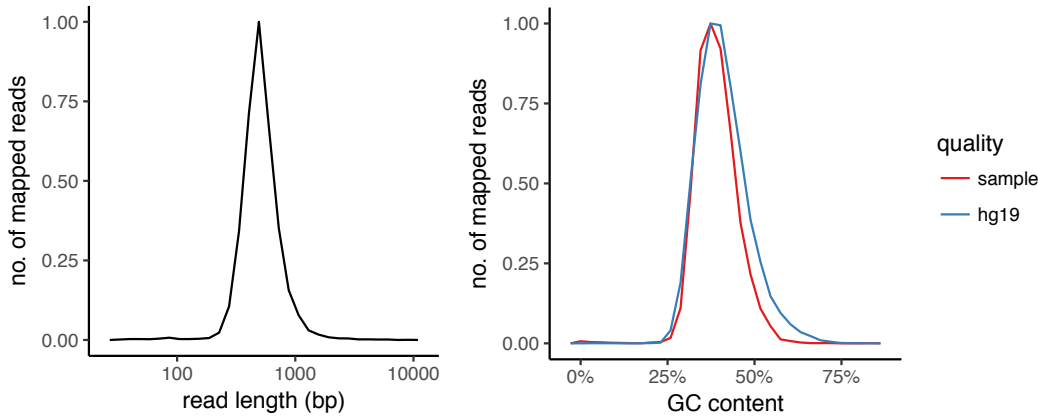


## Methylation based classification

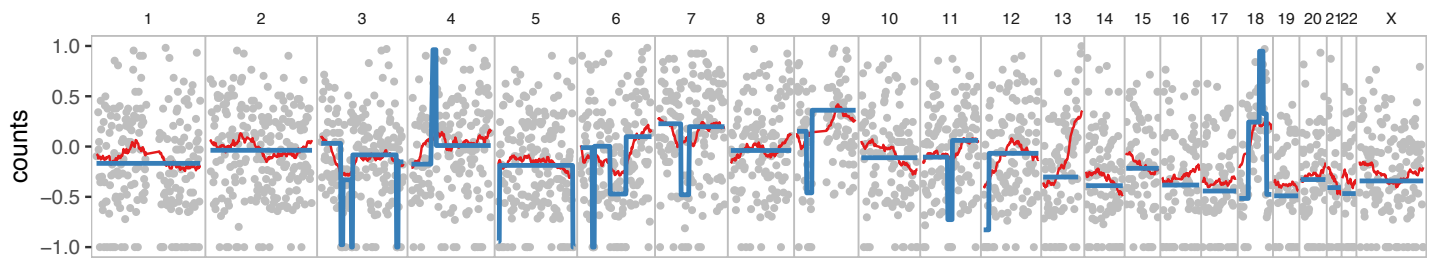


# 6228T

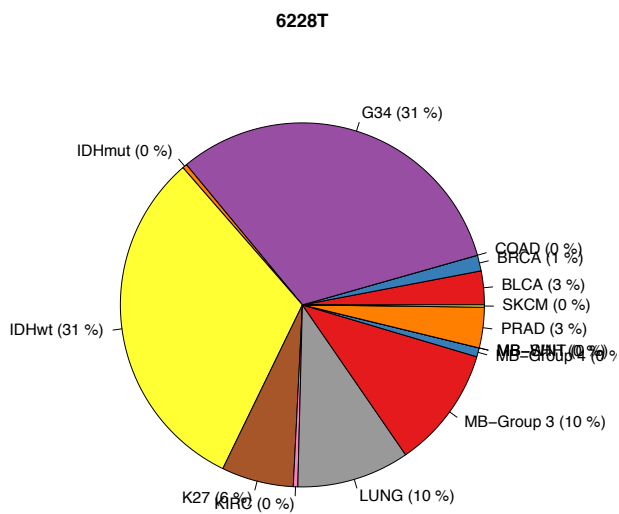
## Quality control metrics



## Copy number profile

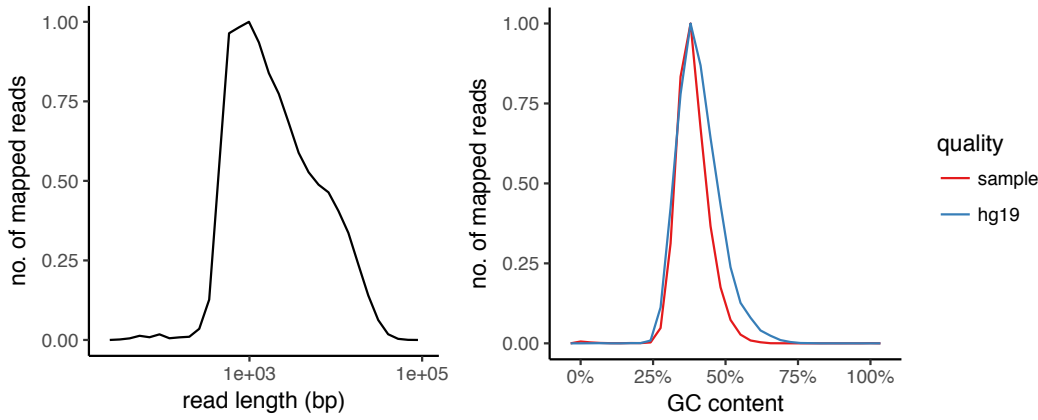


## Methylation based classification

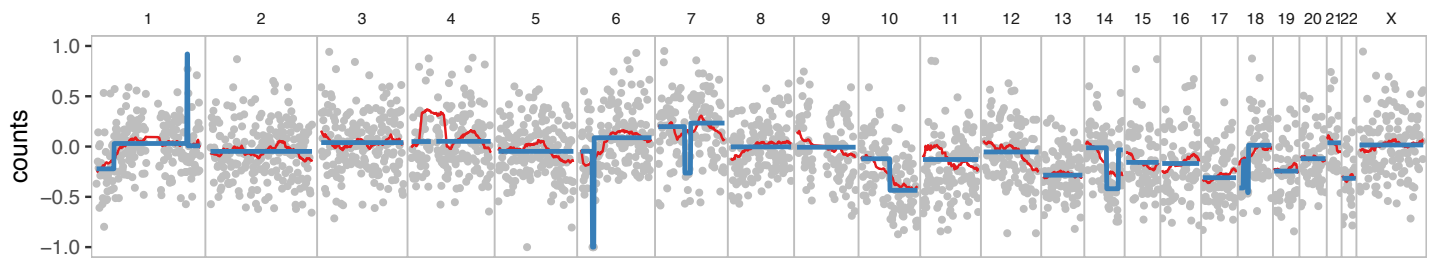


# 7382T

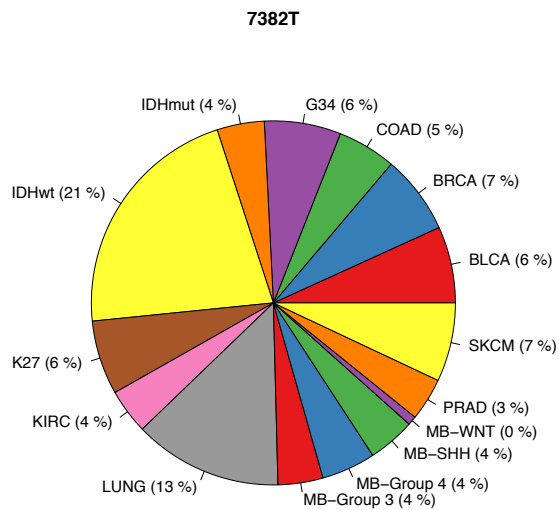
## Quality control metrics



## Copy number profile

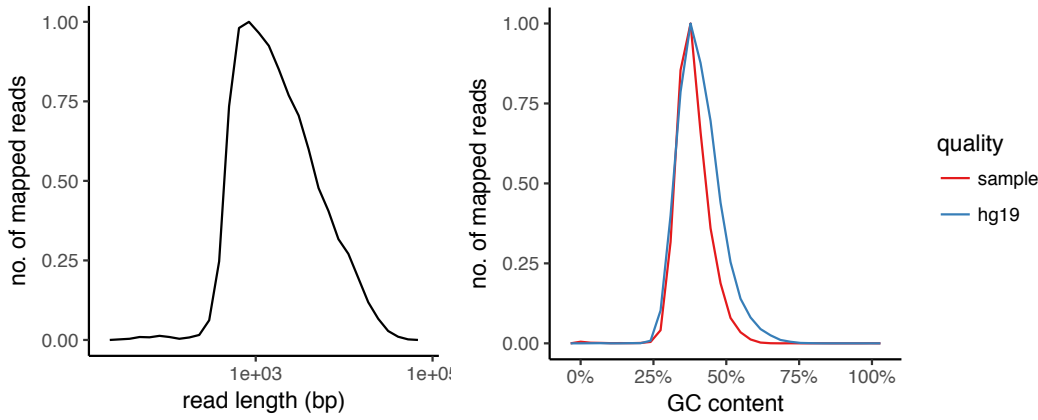


## Methylation based classification

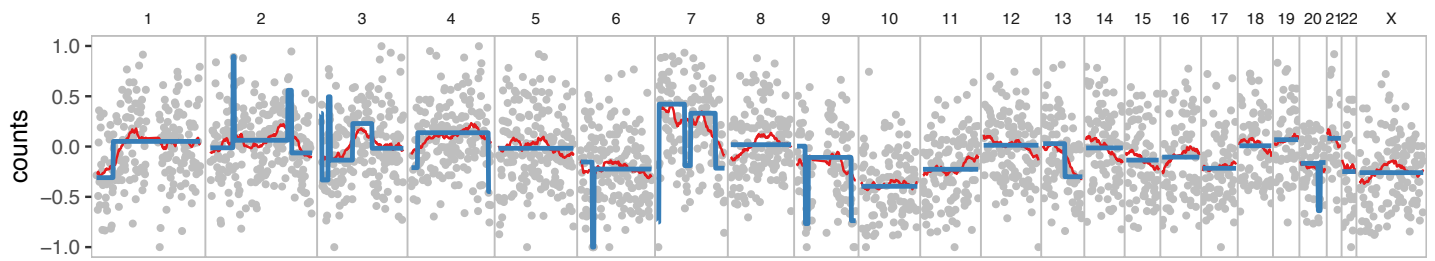


# 7455T

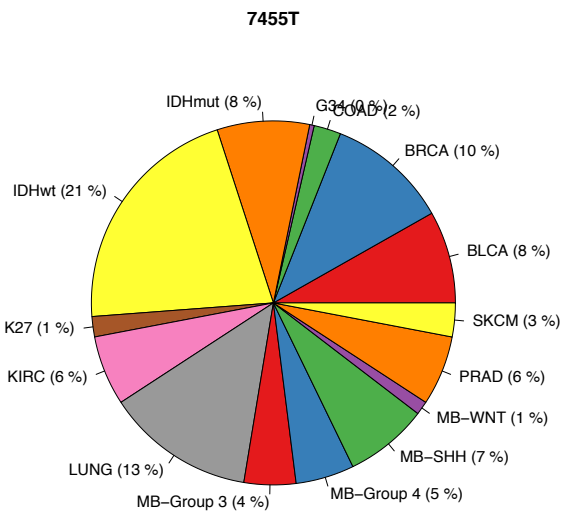
## Quality control metrics



## Copy number profile

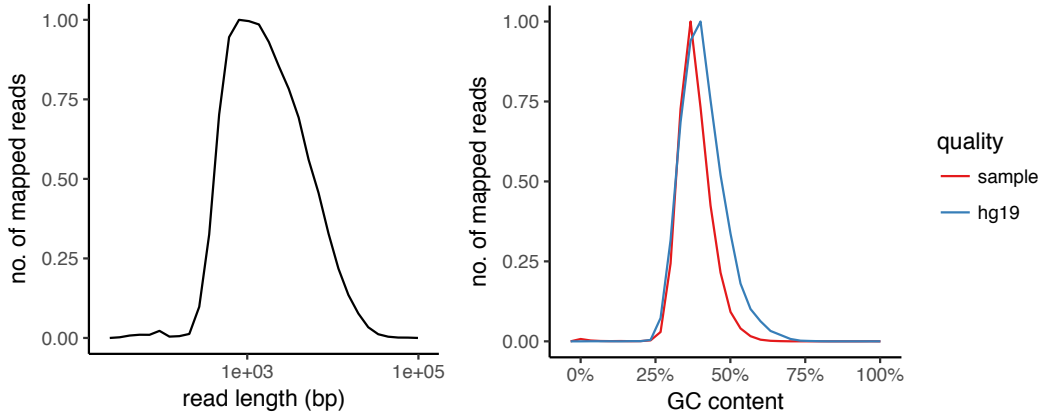


## Methylation based classification

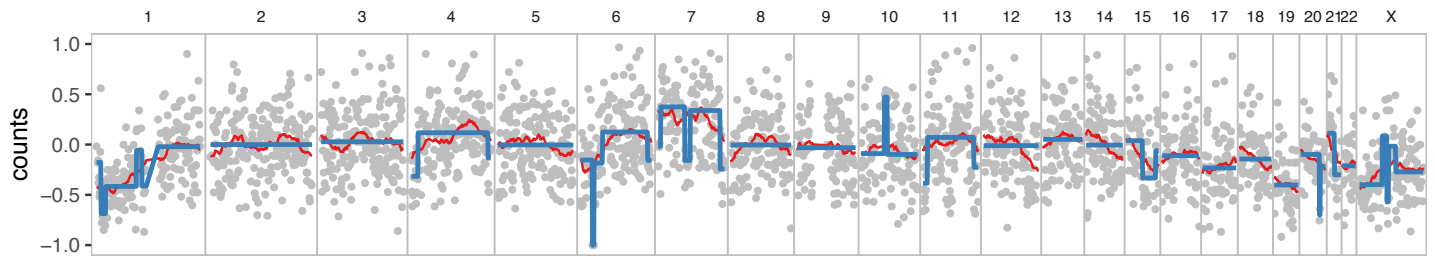


# 8137T

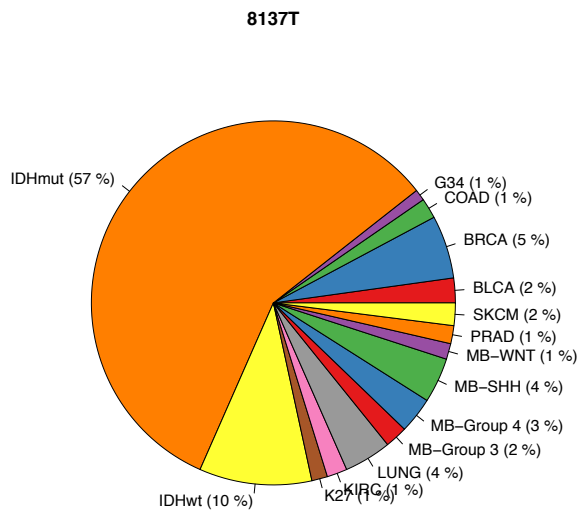
## Quality control metrics



## Copy number profile

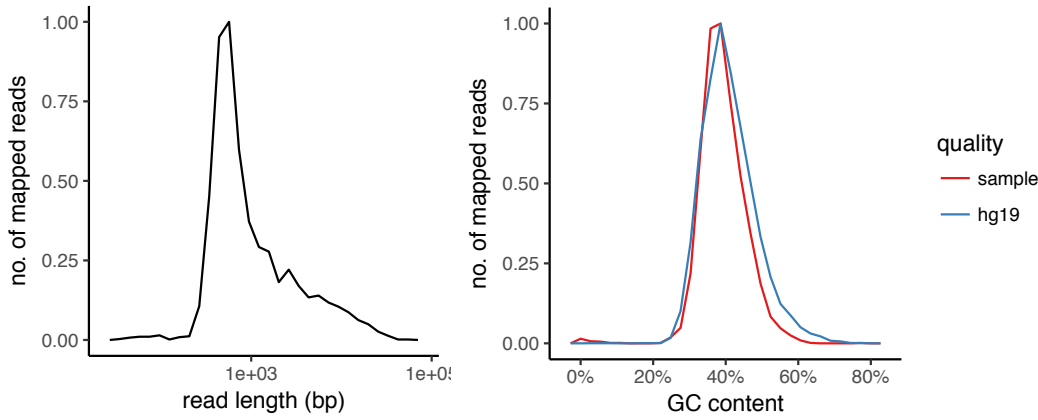


## Methylation based classification

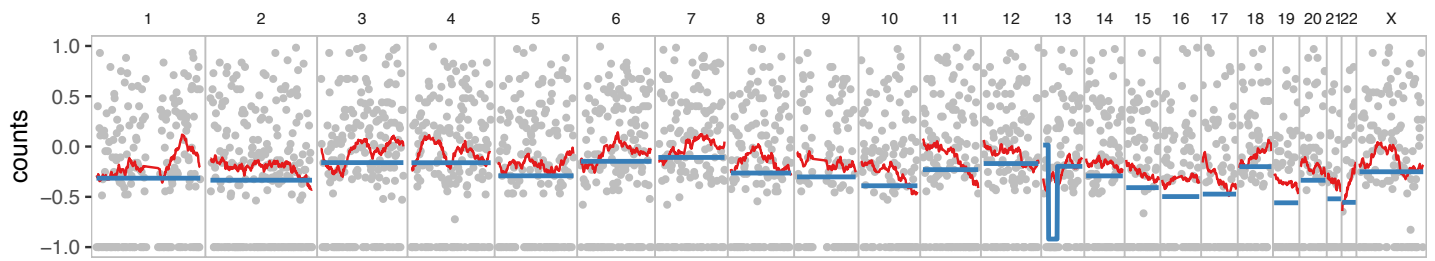


# 8146T

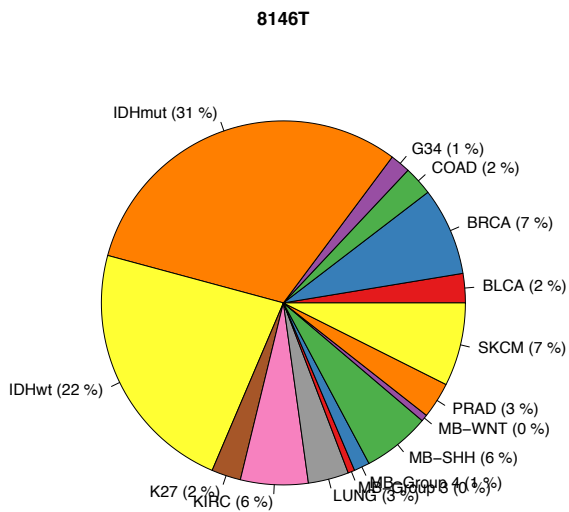
## Quality control metrics



## Copy number profile

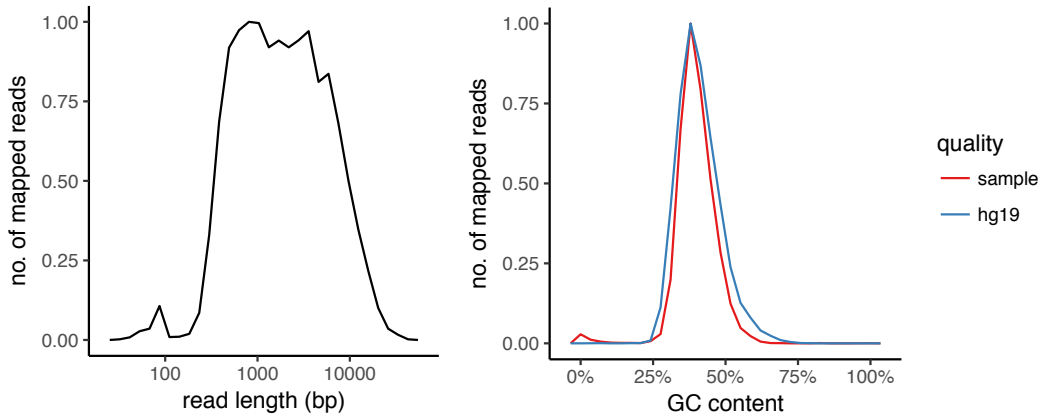


## Methylation based classification

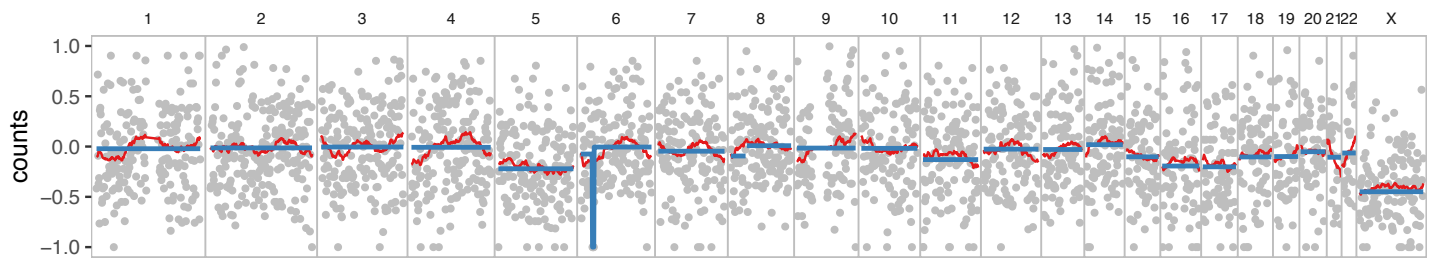


# 8355T

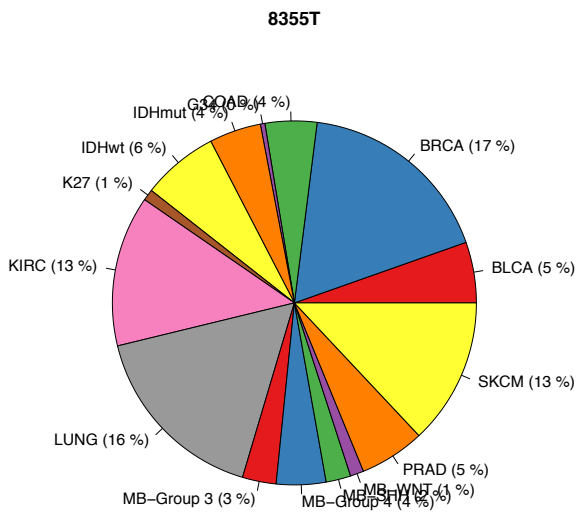
## Quality control metrics



## Copy number profile



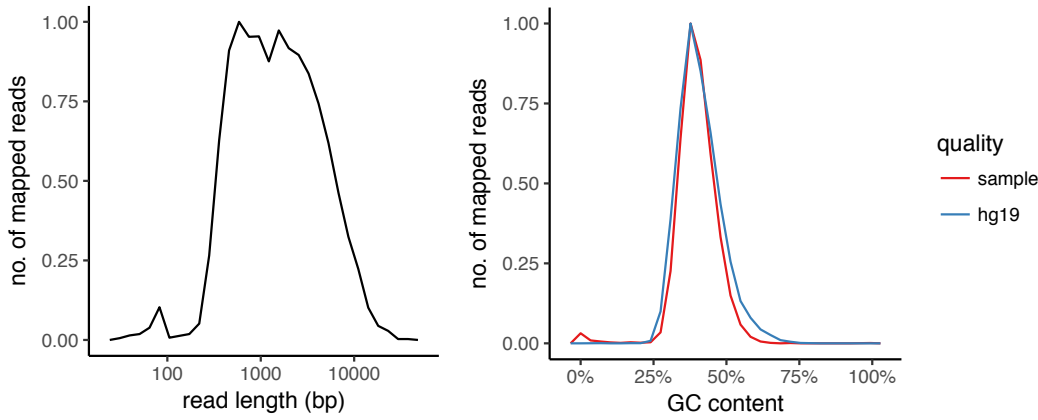
## Methylation based classification



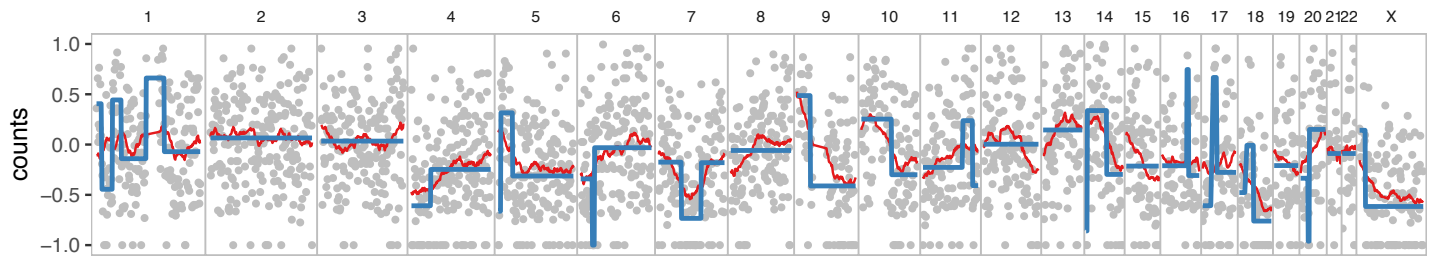


# 8356T

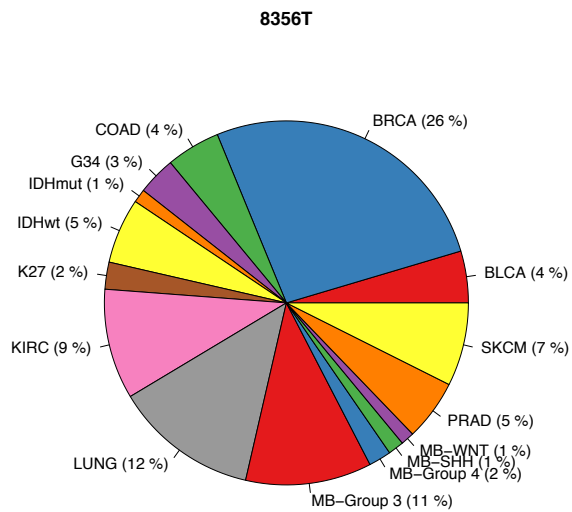
## Quality control metrics



## Copy number profile

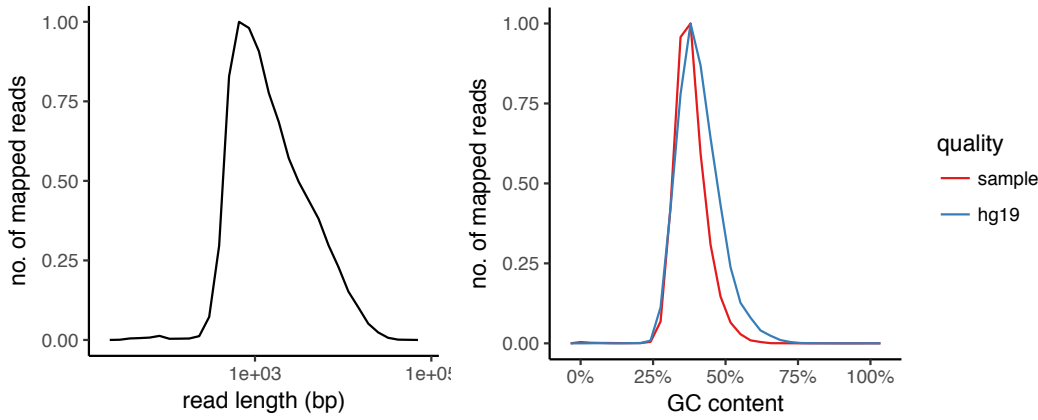


## Methylation based classification

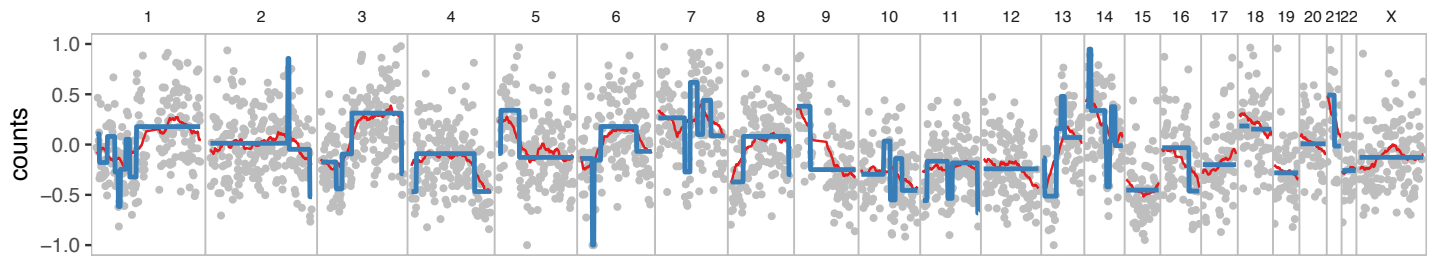


8357T

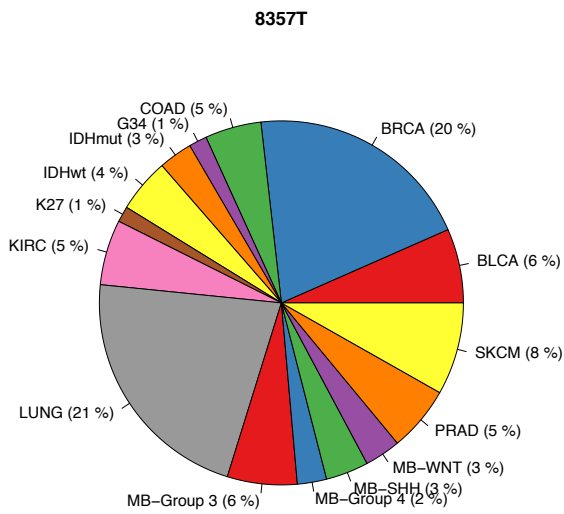
### Quality control metrics



### Copy number profile

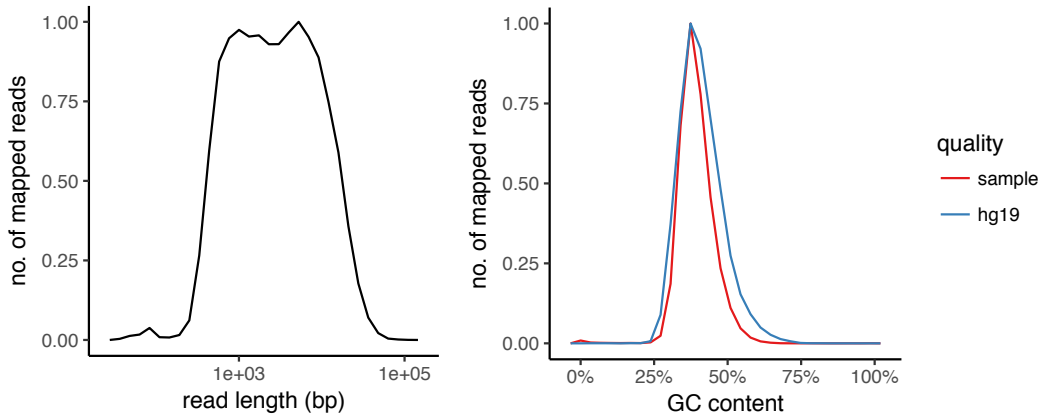


### Methylation based classification

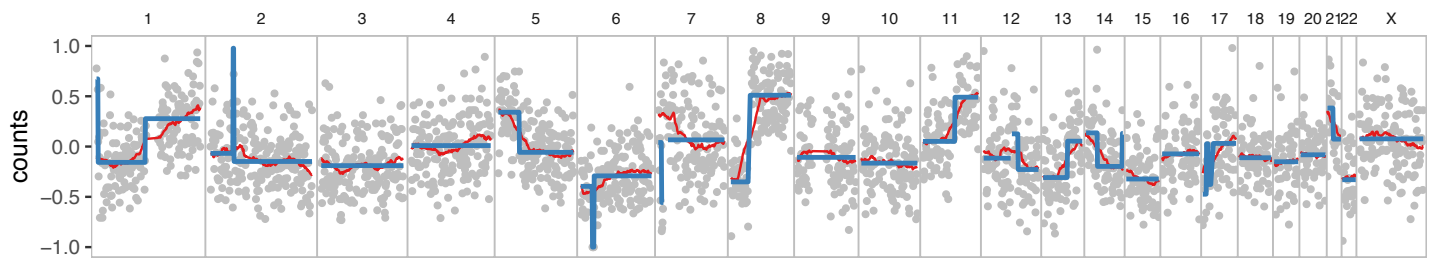


# 8358T

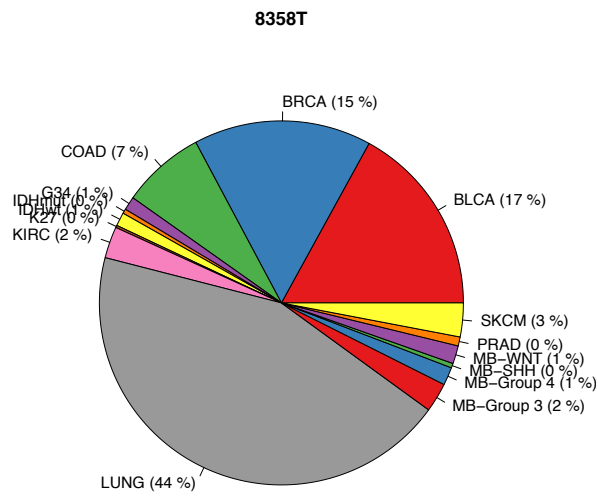
## Quality control metrics



## Copy number profile

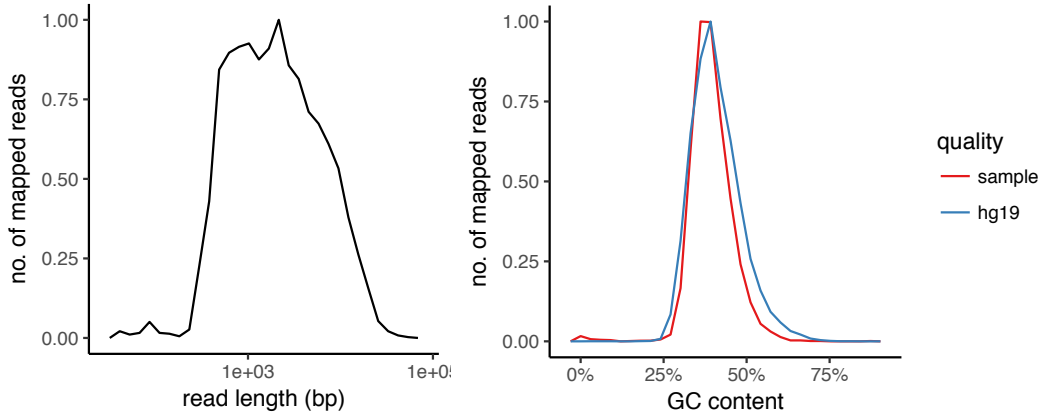


## Methylation based classification

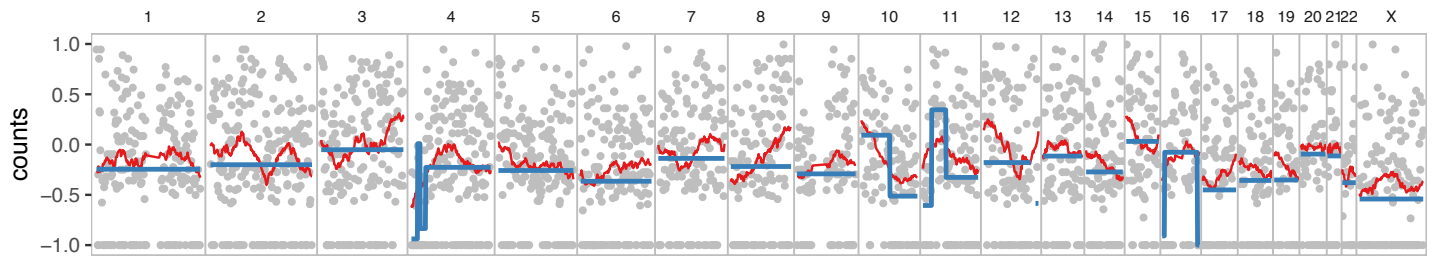


# 8359T

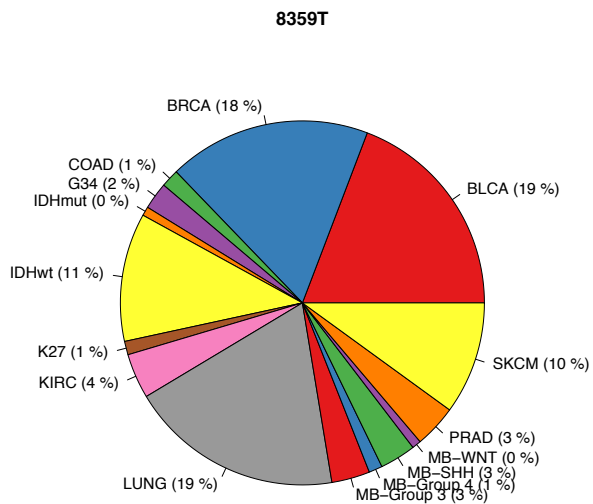
## Quality control metrics



## Copy number profile

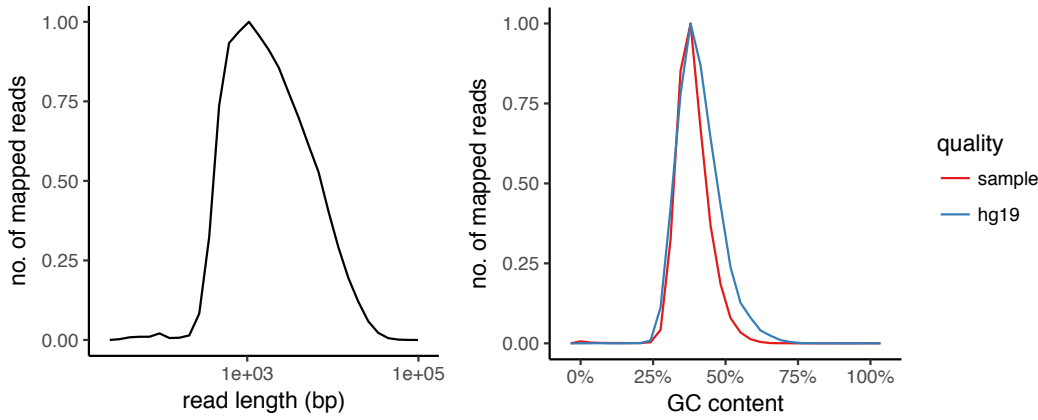


## Methylation based classification

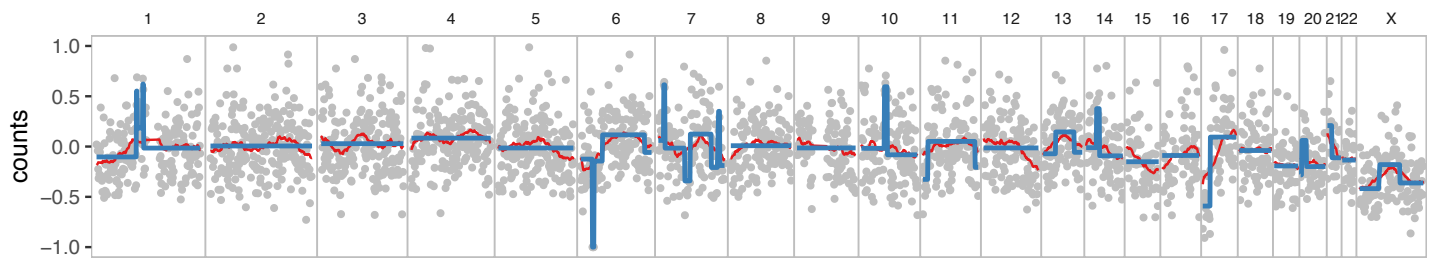


# 8372T

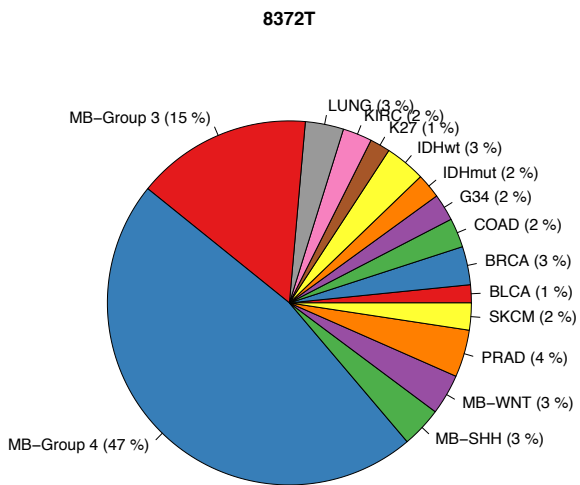
## Quality control metrics



## Copy number profile

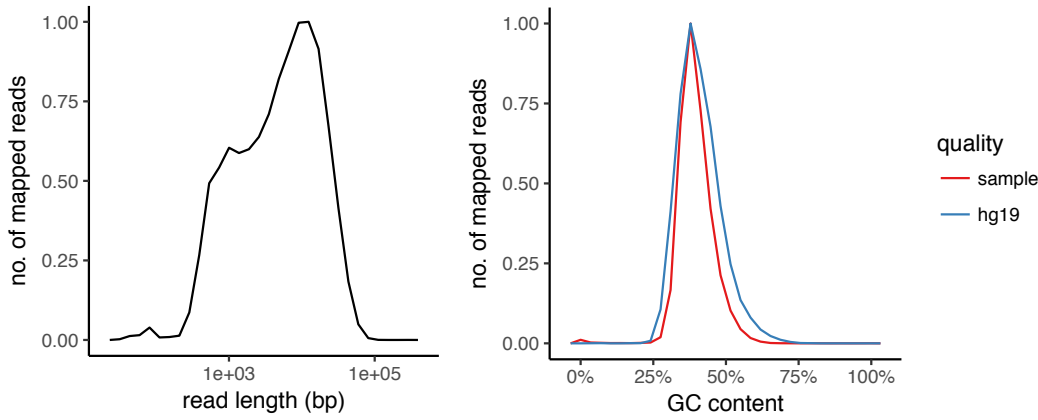


## Methylation based classification

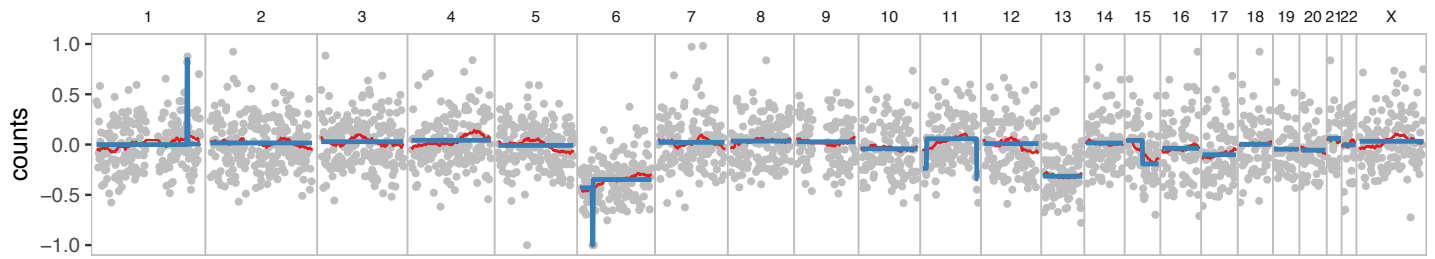


# MB683

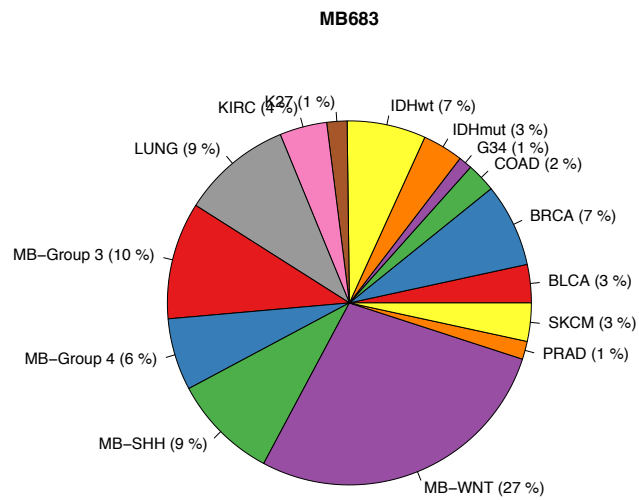
## Quality control metrics

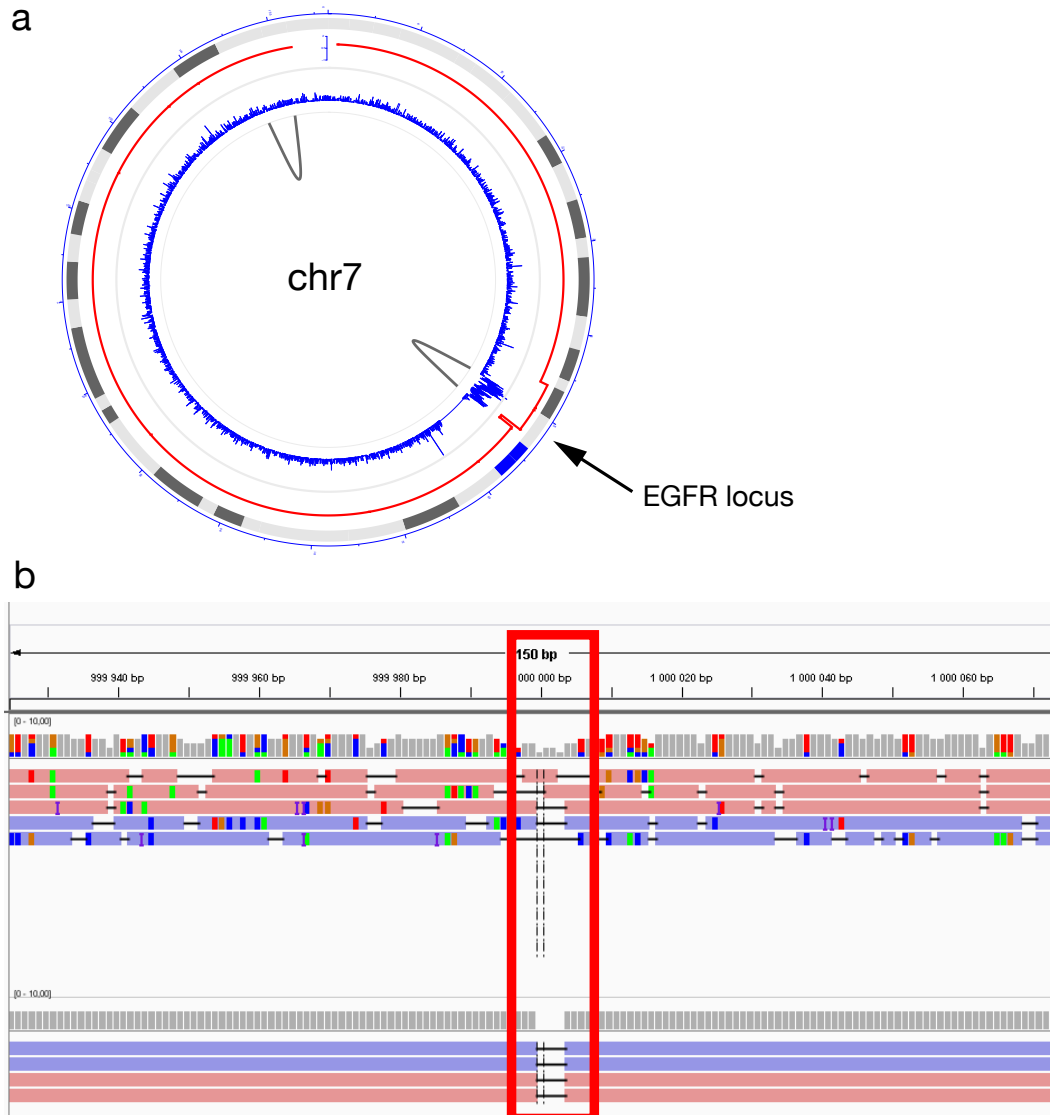


## Copy number profile

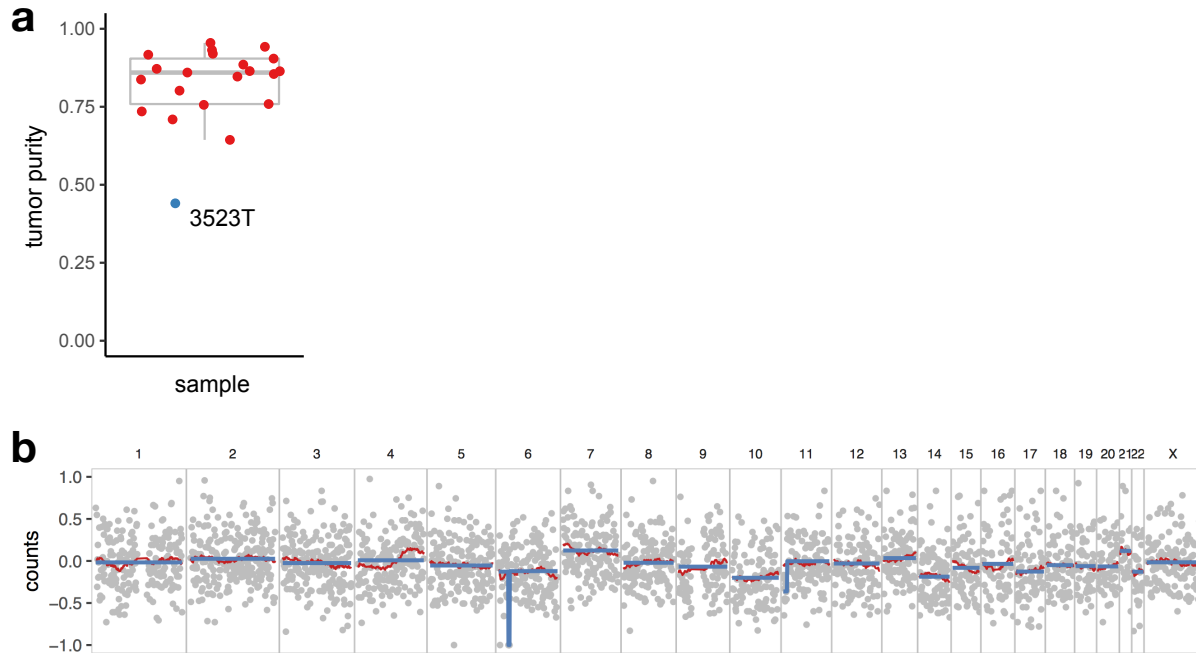


## Methylation based classification





**Fig. S2: Breakpoint identification for an EGFR double minute.** (a) Circular plot of CNV and structural alteration on chromosome 7 in a glioblastoma (3427T) sample identified by NanoSV. Only CNVs larger than 1000bp are shown. Circular tracks from outside to inside: chromosome 7 cytobands (*black, grey*) with centromeric region (*blue*), CNVs log ratio values (*red line*), depth of coverage (*blue*), intrachromosomal structural alterations (*grey*). (b) Sanger sequencing of a PCR amplicon designed to circularization site confirms the predicted breakpoint (highlighted in *red*).



**Fig. S3: Tumor purity estimation and influence on copy number profiling. (a)** Tumor purity estimates from matched RNA-seq gene expression data using ESTIMATE (12) identifies low purity for sample 3523T in comparison to a series of GBM from the same institution (7). **(b)** CN profile for sample 3523T shows correct segmentation (blue) but low amplitude of log ratios. Automatic CN calling using fixed thresholds thus missed chromosome 7 gain and chromosome 10 loss. Red lines indicate running mean of log ratios.

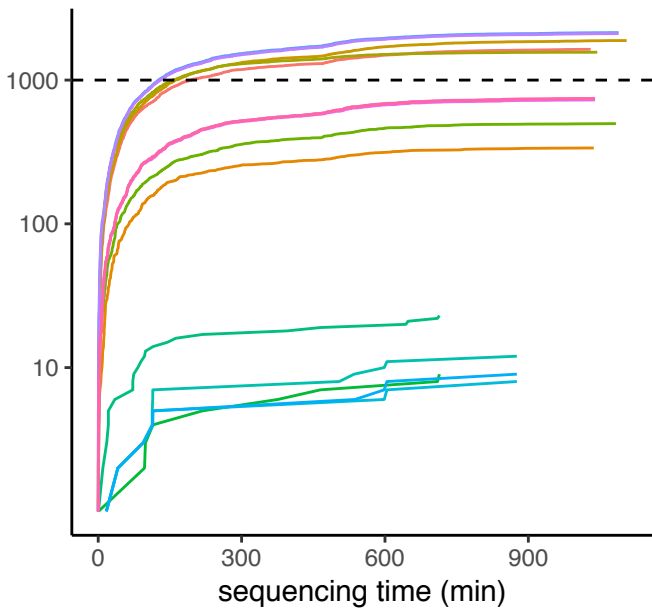


**Fig. S4: Sequencing reports for nanopore amplicon sequencing.** For each sample, we report read depth (no. of reads) per targeted genomic region (*colored*) over the time frame of the entire sequencing run. When minimum coverage of 1000X in all amplicons could be achieved, the time to reach 1000X depth is indicated.



# 8360T

no. of reads per target



H3F3A exon 2

IDH1 exon 4

IDH2 exon 4

TERT promoter

TP53 exon 1

TP53 exon 10

TP53 exon 11

TP53 exon 2

TP53 exon 3

TP53 exon 4

TP53 exon 5

TP53 exon 6

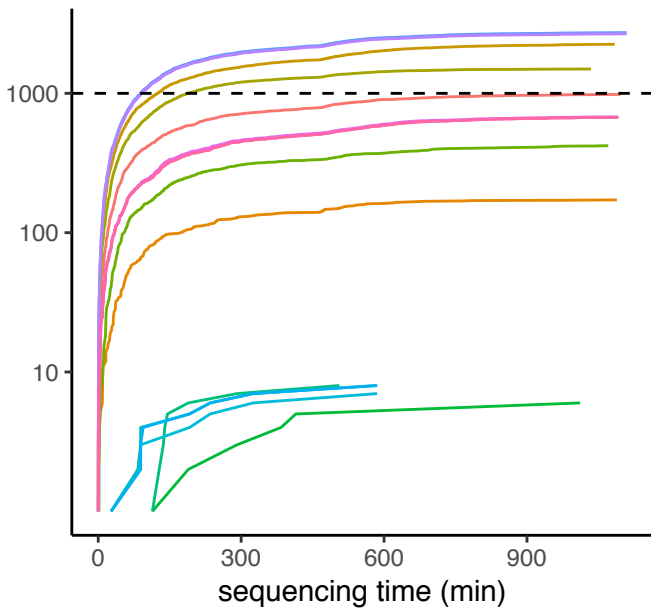
TP53 exon 7

TP53 exon 8

TP53 exon 9

# 8359T

no. of reads per target



H3F3A exon 2

IDH1 exon 4

IDH2 exon 4

TERT promoter

TP53 exon 1

TP53 exon 10

TP53 exon 11

TP53 exon 2

TP53 exon 3

TP53 exon 4

TP53 exon 5

TP53 exon 6

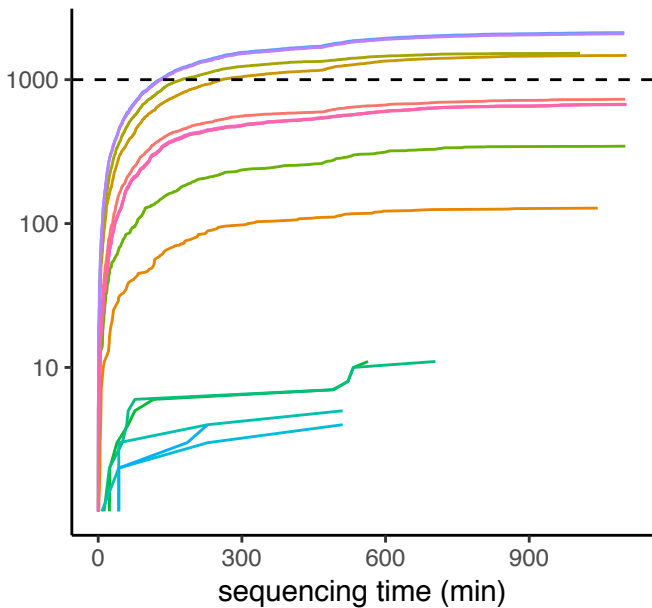
TP53 exon 7

TP53 exon 8

TP53 exon 9

# 8347T

no. of reads per target



H3F3A exon 2

IDH1 exon 4

IDH2 exon 4

TERT promoter

TP53 exon 1

TP53 exon 10

TP53 exon 11

TP53 exon 2

TP53 exon 3

TP53 exon 4

TP53 exon 5

TP53 exon 6

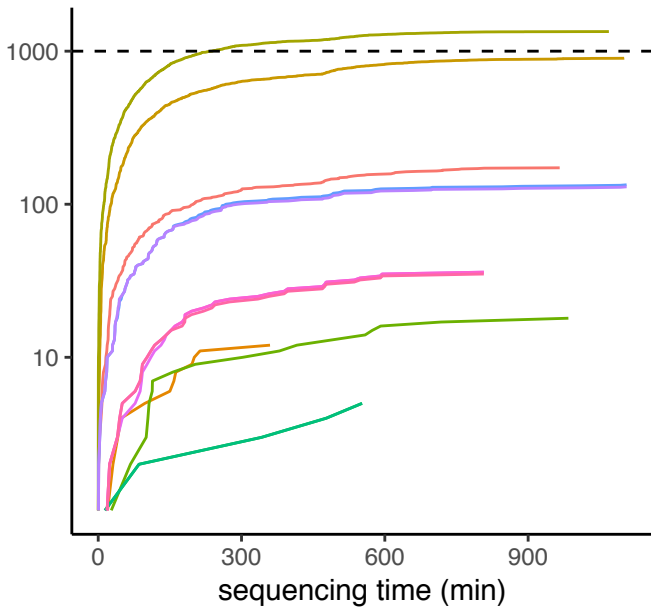
TP53 exon 7

TP53 exon 8

TP53 exon 9

# 8146T

no. of reads per target



H3F3A exon 2

IDH1 exon 4

IDH2 exon 4

TERT promoter

TP53 exon 1

TP53 exon 10

TP53 exon 11

TP53 exon 2

TP53 exon 3

TP53 exon 4

TP53 exon 5

TP53 exon 6

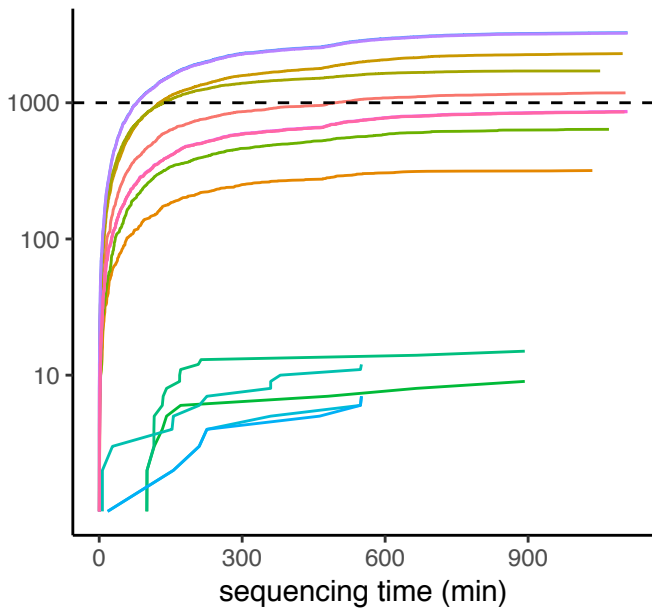
TP53 exon 7

TP53 exon 8

TP53 exon 9

# 8137T

no. of reads per target



H3F3A exon 2

IDH1 exon 4

IDH2 exon 4

TERT promoter

TP53 exon 1

TP53 exon 10

TP53 exon 11

TP53 exon 2

TP53 exon 3

TP53 exon 4

TP53 exon 5

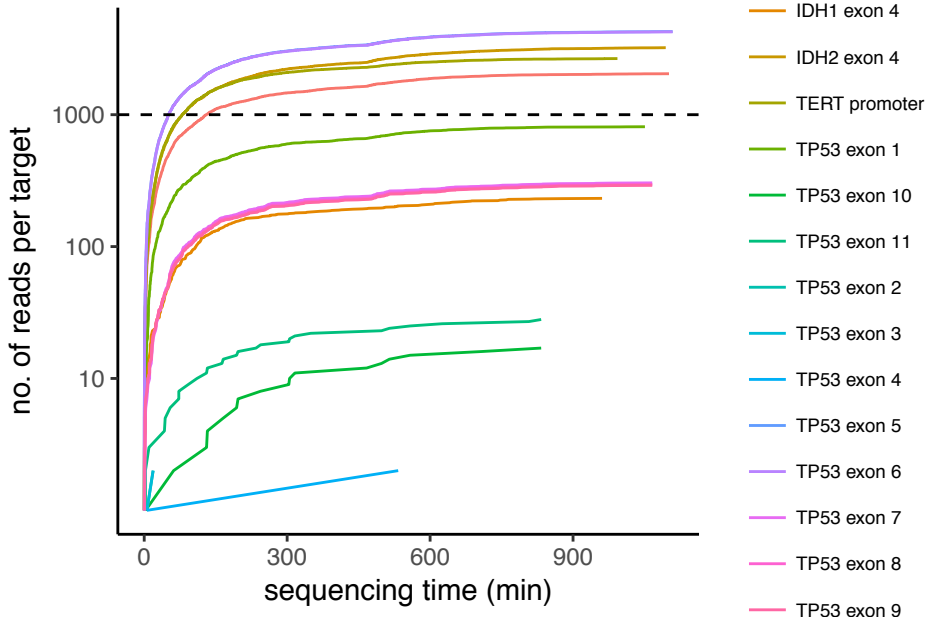
TP53 exon 6

TP53 exon 7

TP53 exon 8

TP53 exon 9

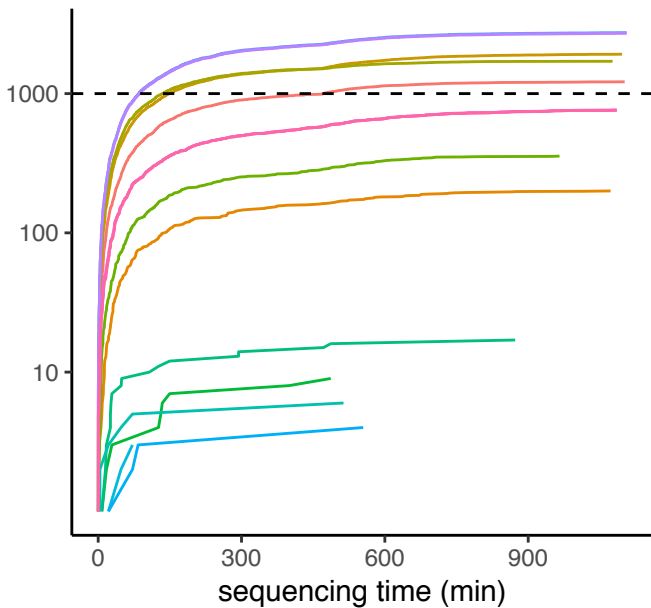
# 7455T





# 7382T

no. of reads per target



H3F3A exon 2

IDH1 exon 4

IDH2 exon 4

TERT promoter

TP53 exon 1

TP53 exon 10

TP53 exon 11

TP53 exon 2

TP53 exon 3

TP53 exon 4

TP53 exon 5

TP53 exon 6

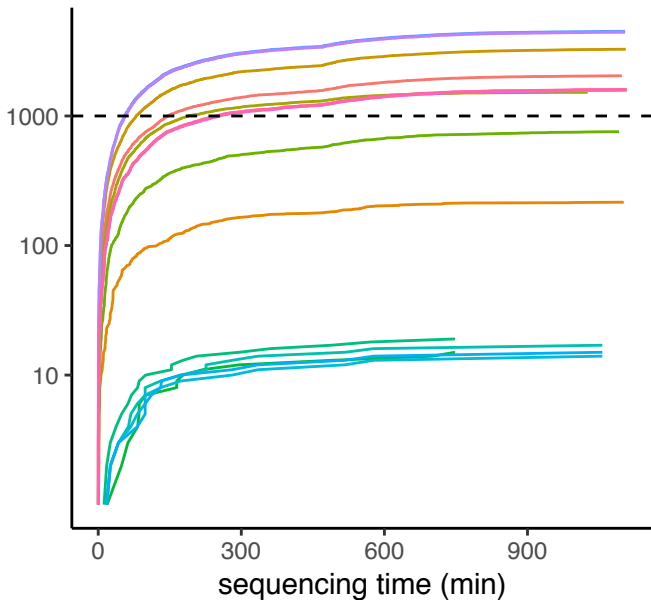
TP53 exon 7

TP53 exon 8

TP53 exon 9

# 5337T (255 min for 1000X)

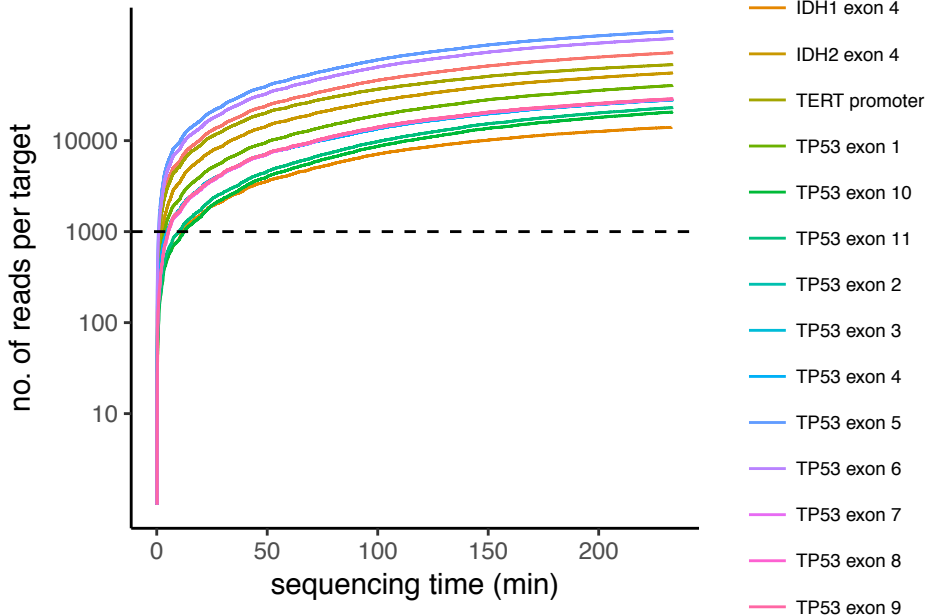
no. of reads per target



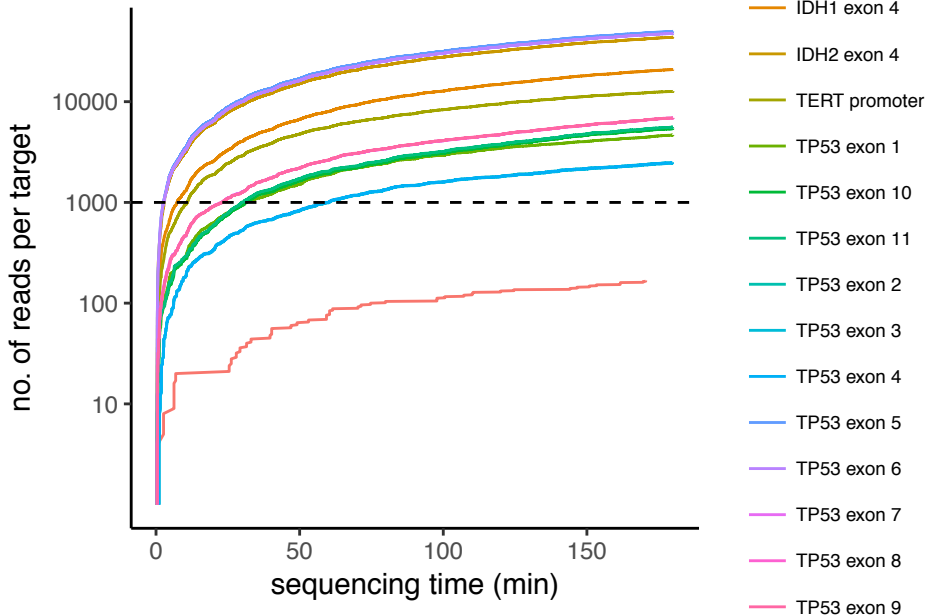
- H3F3A exon 2
- IDH1 exon 4
- IDH2 exon 4
- TERT promoter
- TP53 exon 1
- TP53 exon 10
- TP53 exon 11
- TP53 exon 2
- TP53 exon 3
- TP53 exon 4
- TP53 exon 5
- TP53 exon 6
- TP53 exon 7
- TP53 exon 8
- TP53 exon 9



# 3427T-amplicon (12 min for 1000X)

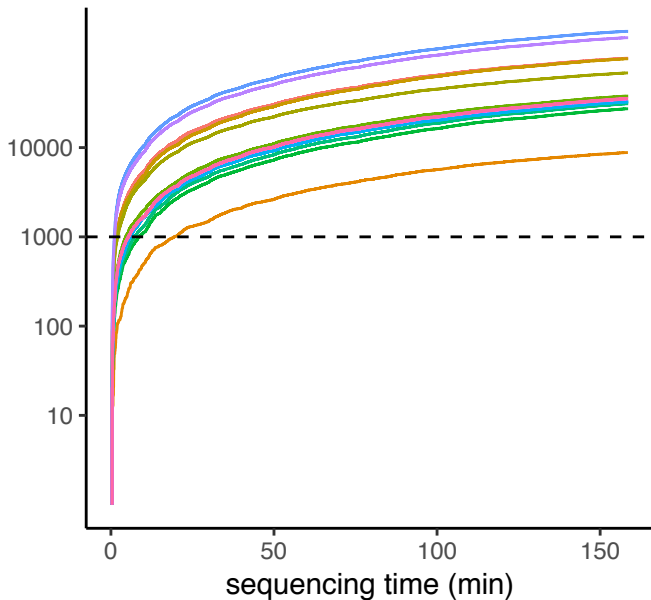


# 2965T-amplicon



# 2483T-amplicon (20 min for 1000X)

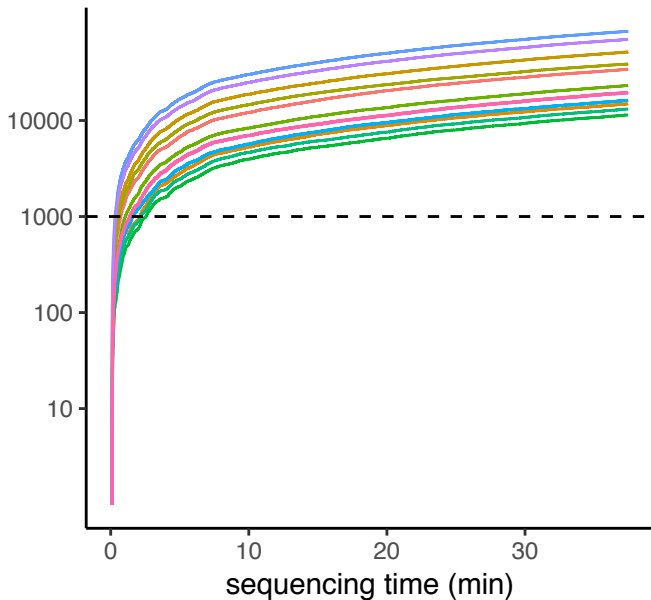
no. of reads per target



- H3F3A exon 2
- IDH1 exon 4
- IDH2 exon 4
- TERT promoter
- TP53 exon 1
- TP53 exon 10
- TP53 exon 11
- TP53 exon 2
- TP53 exon 3
- TP53 exon 4
- TP53 exon 5
- TP53 exon 6
- TP53 exon 7
- TP53 exon 8
- TP53 exon 9

# 2402T-amplicon (3 min for 1000X)

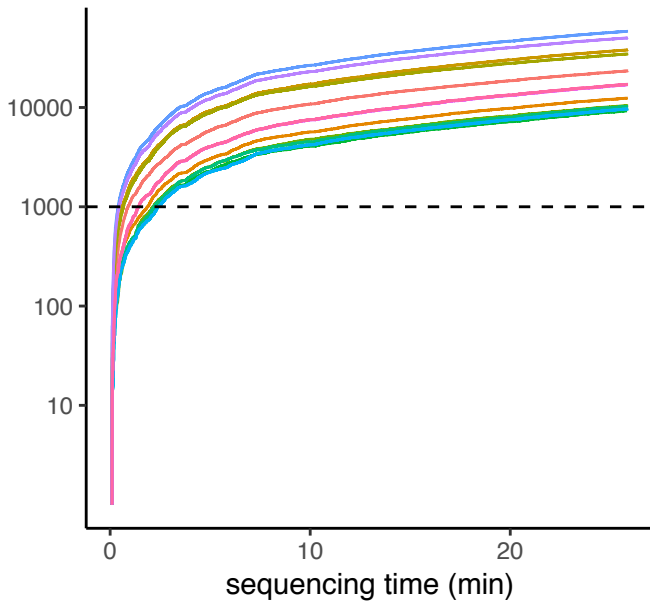
no. of reads per target



- H3F3A exon 2
- IDH1 exon 4
- IDH2 exon 4
- TERT promoter
- TP53 exon 1
- TP53 exon 10
- TP53 exon 11
- TP53 exon 2
- TP53 exon 3
- TP53 exon 4
- TP53 exon 5
- TP53 exon 6
- TP53 exon 7
- TP53 exon 8
- TP53 exon 9

# 2197T-amplicon (2 min for 1000X)

no. of reads per target



H3F3A exon 2

IDH1 exon 4

IDH2 exon 4

TERT promoter

TP53 exon 1

TP53 exon 10

TP53 exon 11

TP53 exon 2

TP53 exon 3

TP53 exon 4

TP53 exon 5

TP53 exon 6

TP53 exon 7

TP53 exon 8

TP53 exon 9