Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 10:37:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818783.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR1818783 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818783.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 10:37:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818783.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,067,533
Mapped reads	2,011,507 / 97.29%
Unmapped reads	56,026 / 2.71%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,843 / 0.67%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	837,535 / 40.51%
Duplication rate	35.76%
Clipped reads	2,013,273 / 97.38%

2.2. ACGT Content

Number/percentage of A's	39,394,237 / 28.83%
Number/percentage of C's	29,913,075 / 21.89%
Number/percentage of T's	38,444,569 / 28.13%
Number/percentage of G's	28,884,632 / 21.14%
Number/percentage of N's	8,858 / 0.01%
GC Percentage	43.03%

2.3. Coverage

Mean	0.0442

Standard Deviation	0.5364

2.4. Mapping Quality

Mean Mapping Quality	47.59

2.5. Mismatches and indels

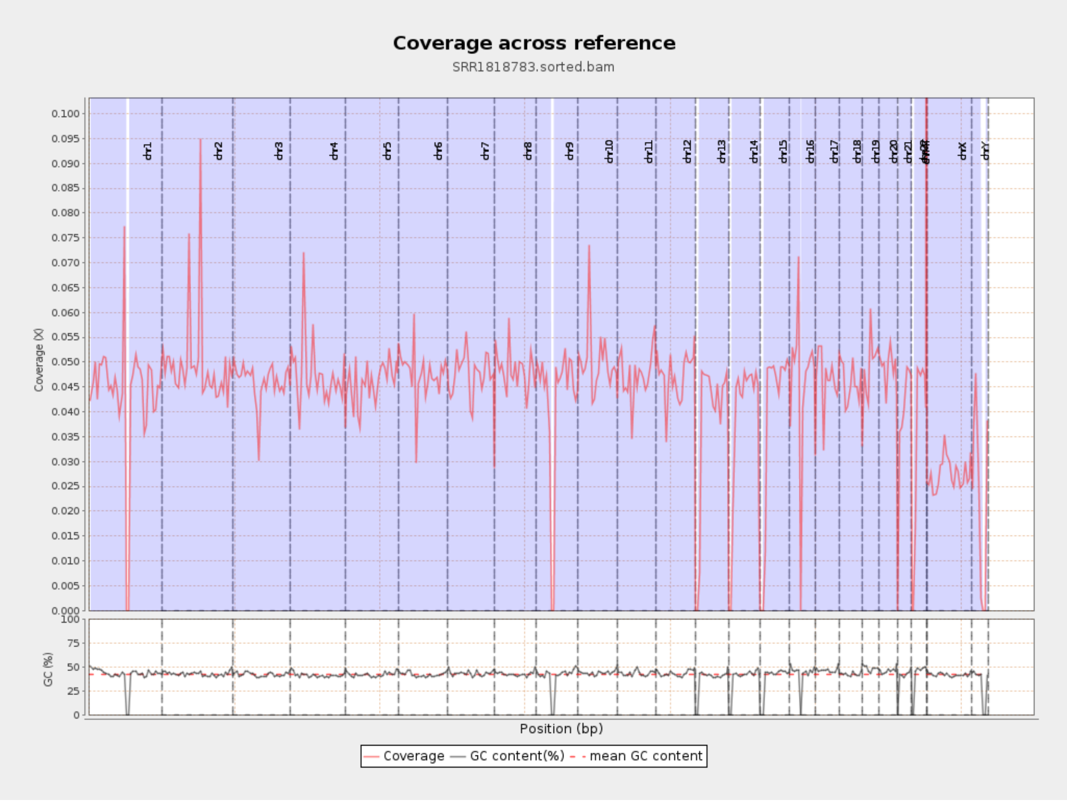
General error rate	0.54%
Mismatches	703,535
Insertions	15,576
Mapped reads with at least one insertion	0.77%
Deletions	34,089
Mapped reads with at least one deletion	1.68%
Homopolymer indels	41.22%

2.6. Chromosome stats

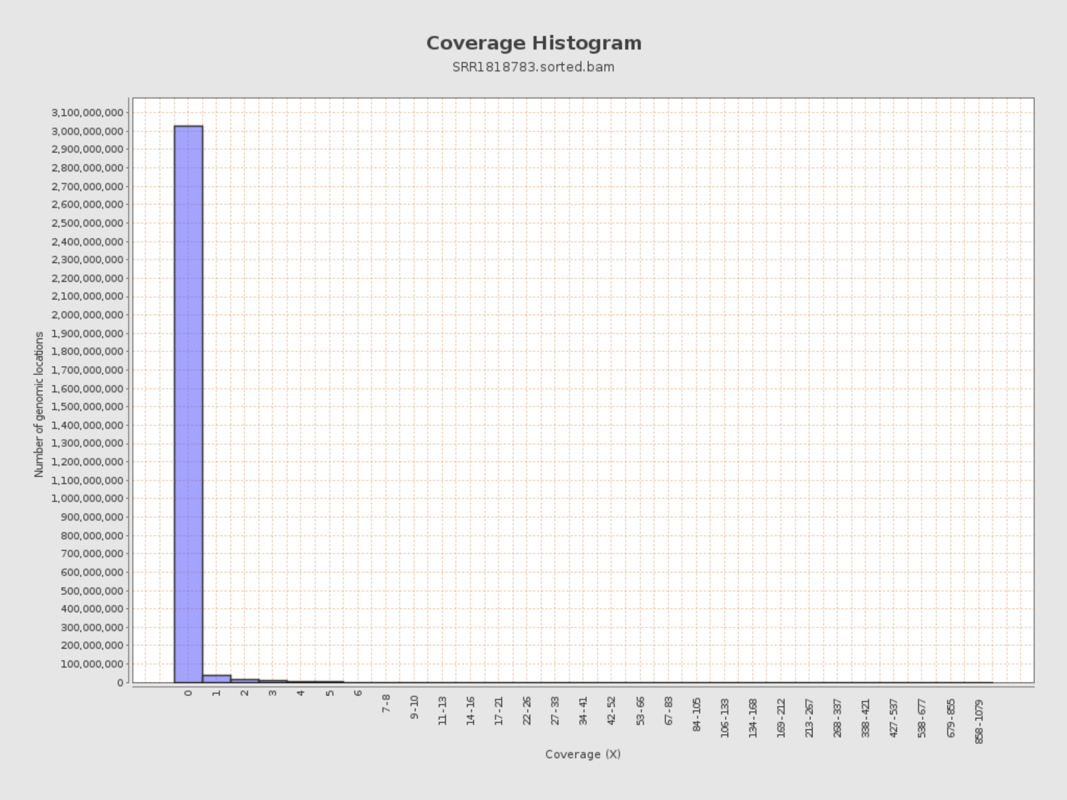
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10882539	0.0437	0.8371
chr2	243199373	12098575	0.0497	0.8421
chr3	198022430	9117026	0.046	0.3742
chr4	191154276	9055848	0.0474	0.4383
chr5	180915260	8308102	0.0459	0.3868
chr6	171115067	8149547	0.0476	0.4199
chr7	159138663	7585460	0.0477	0.4686

chr8	146364022	7091505	0.0485	0.4401
chr9	141213431	5883273	0.0417	0.4442
chr10	135534747	6778499	0.05	0.5765
chr11	135006516	6413124	0.0475	0.4423
chr12	133851895	6300968	0.0471	0.4301
chr13	115169878	4302107	0.0374	0.3361
chr14	107349540	4093502	0.0381	0.381
chr15	102531392	3978049	0.0388	0.3484
chr16	90354753	4200250	0.0465	0.5692
chr17	81195210	3769197	0.0464	0.4191
chr18	78077248	3591465	0.046	0.5924
chr19	59128983	2904374	0.0491	0.6786
chr20	63025520	3084498	0.0489	0.4145
chr21	48129895	1860952	0.0387	0.3758
chr22	51304566	1695663	0.0331	0.3529
chrMT	16571	6544	0.3949	1.081
chrX	155270560	4260358	0.0274	0.3372
chrY	59373566	1290558	0.0217	0.9481

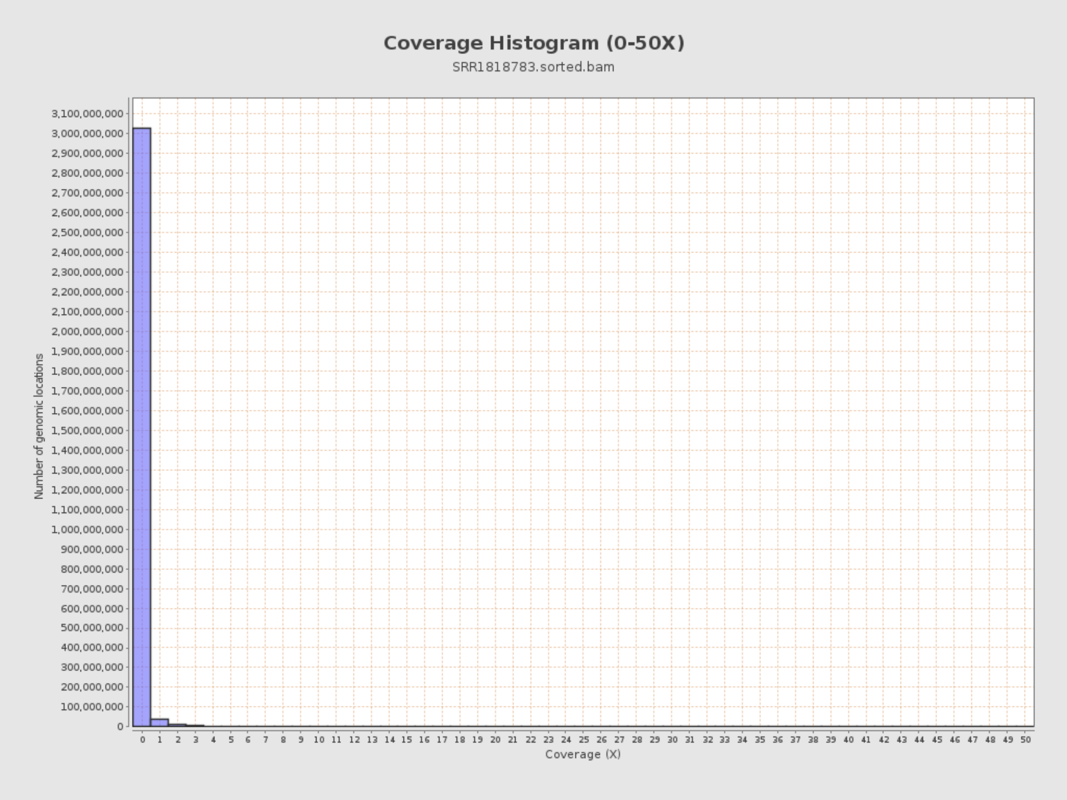
3. Results : Coverage across reference



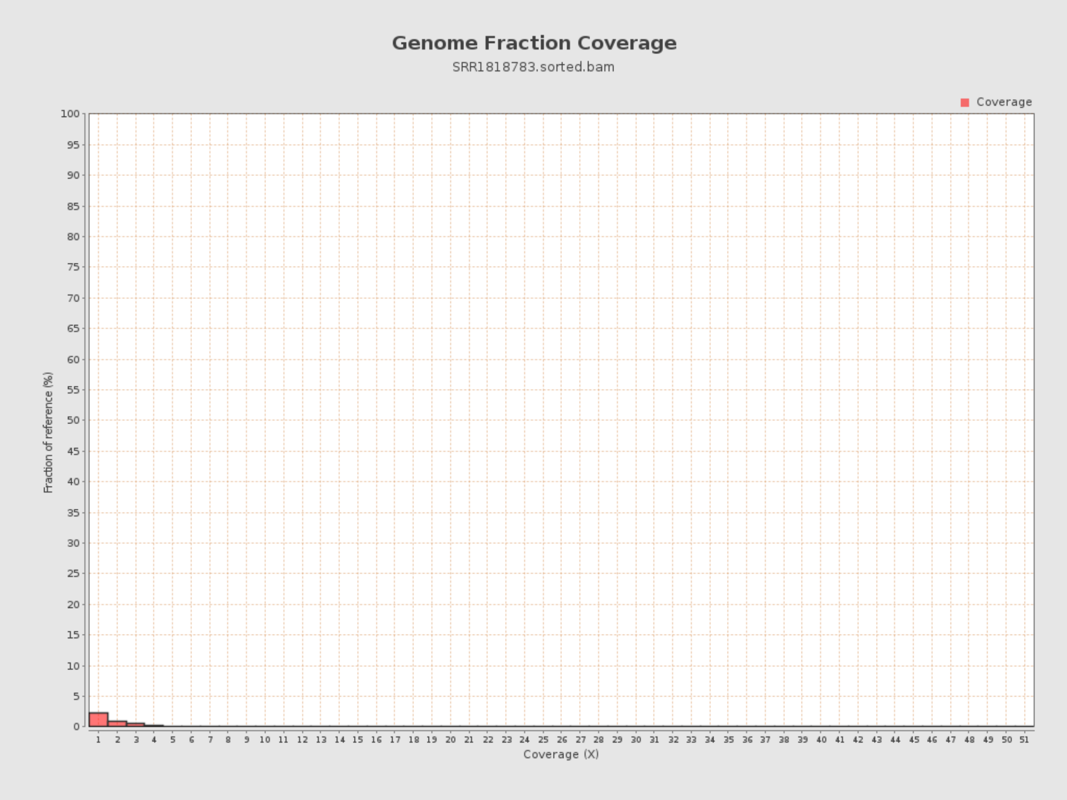
4. Results : Coverage Histogram



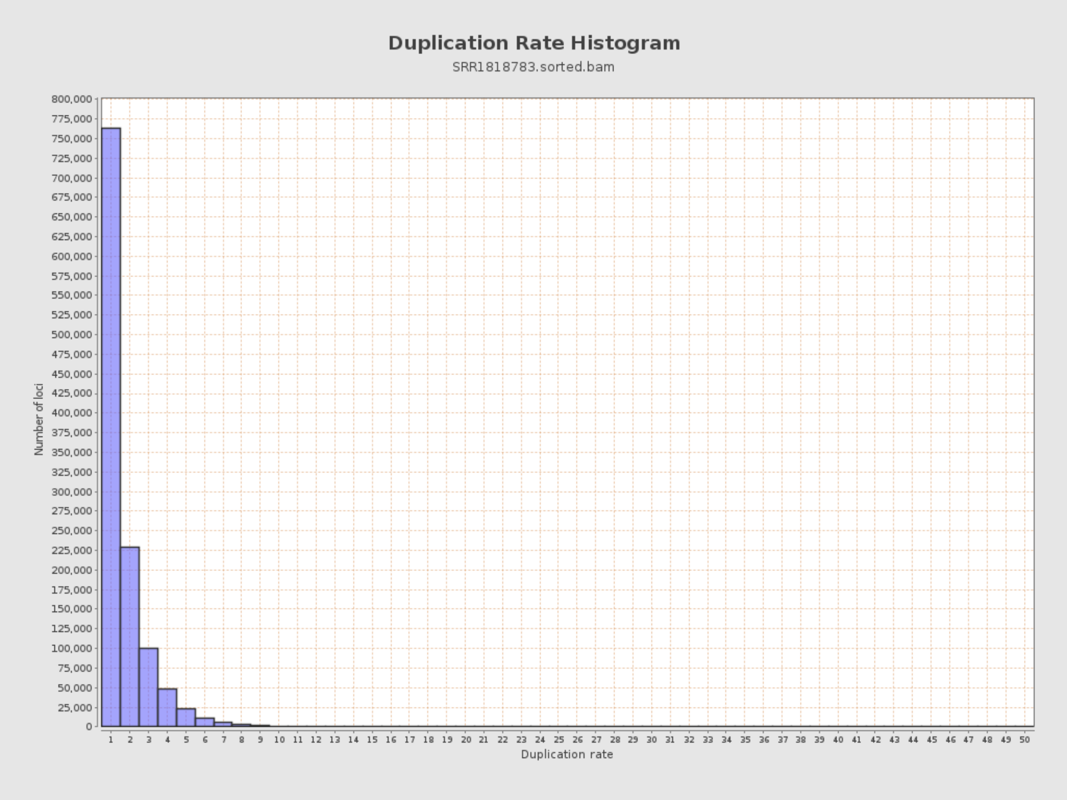
5. Results : Coverage Histogram (0-50X)



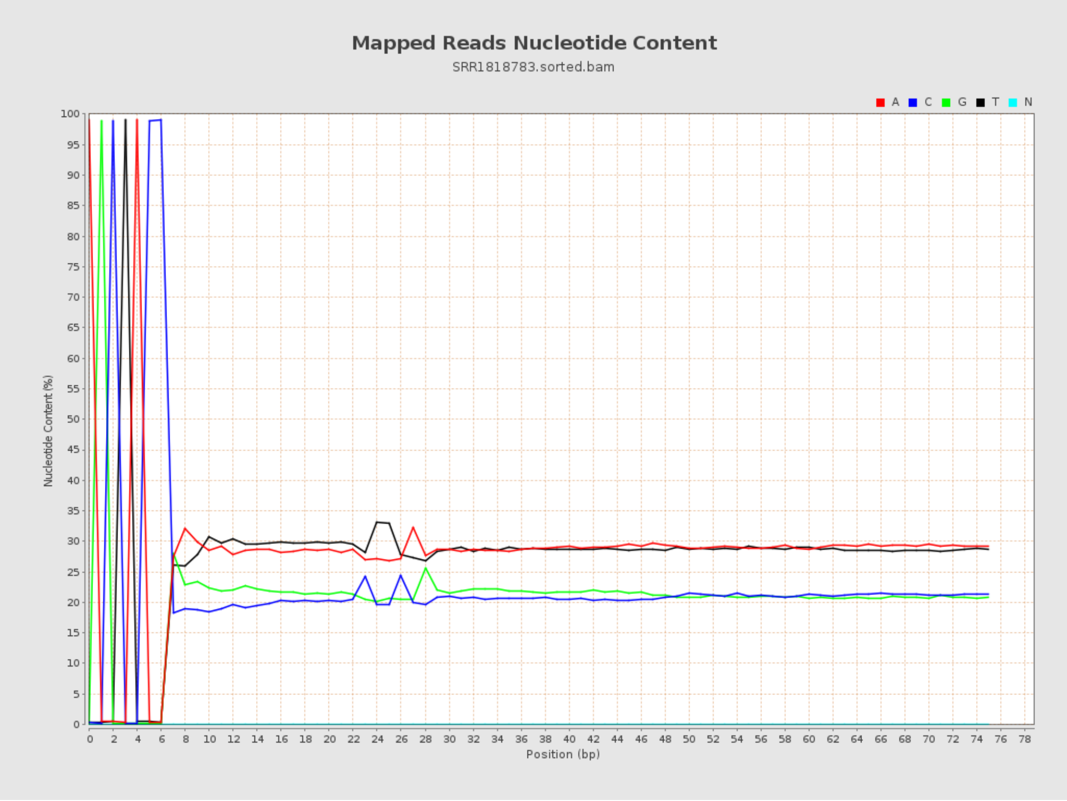
6. Results : Genome Fraction Coverage



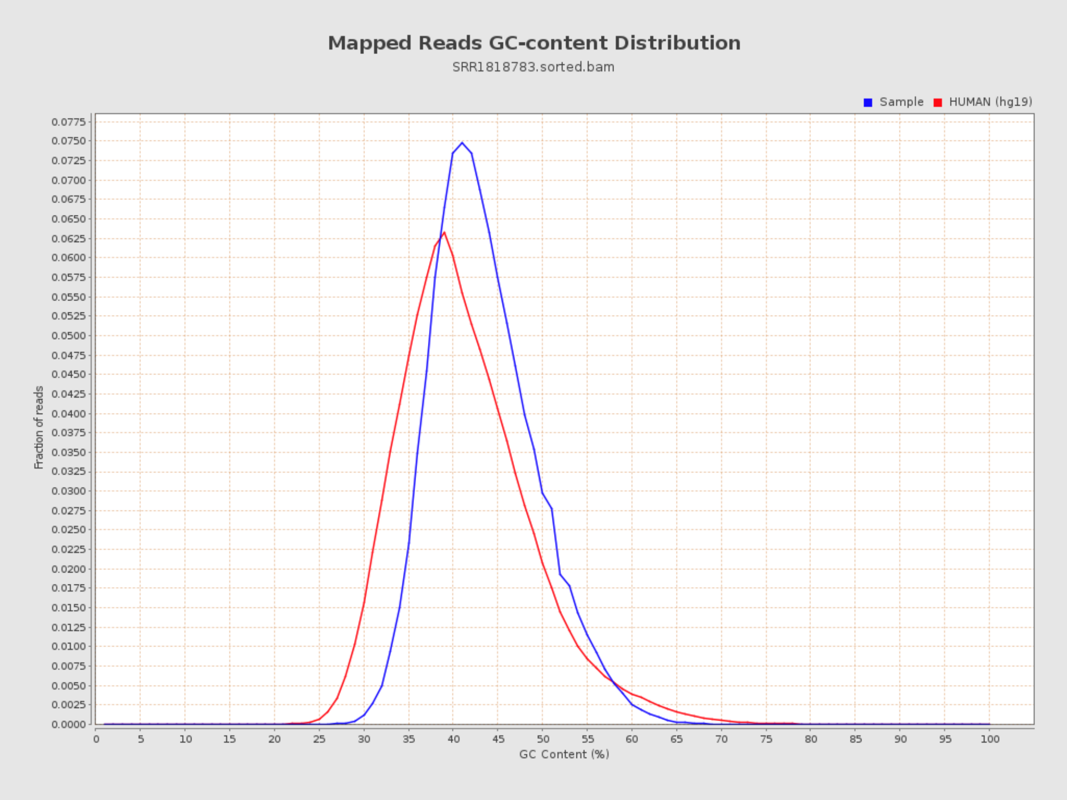
7. Results : Duplication Rate Histogram



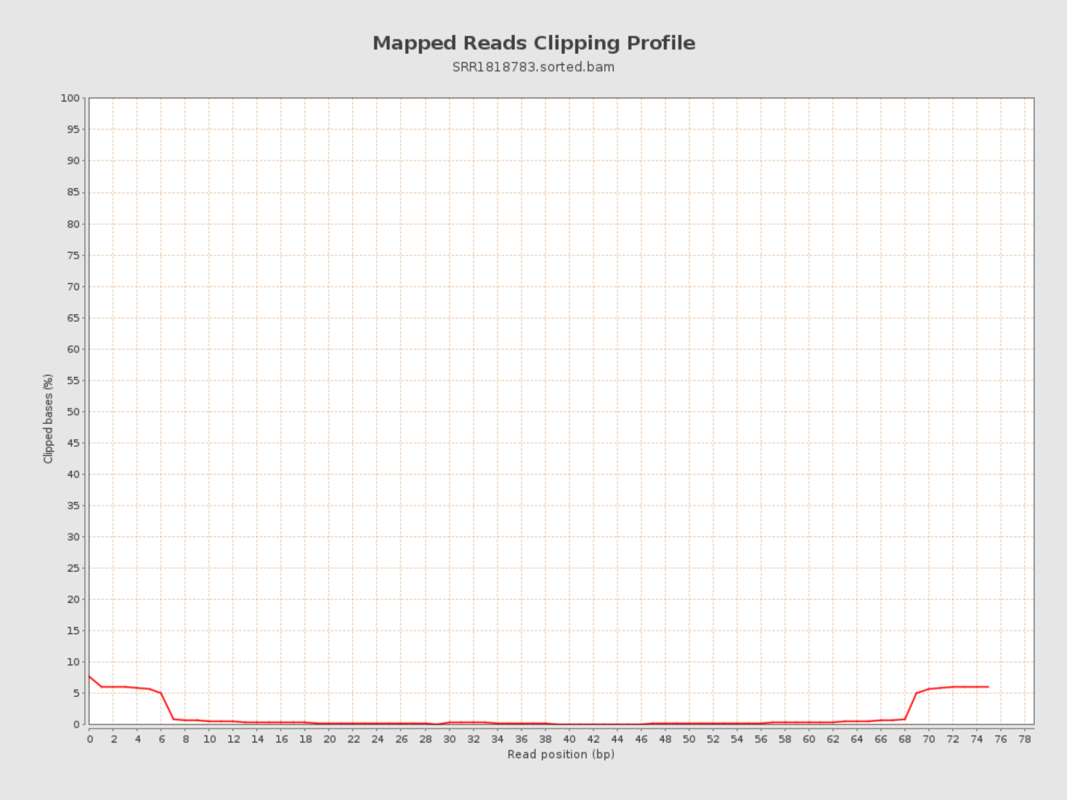
8. Results : Mapped Reads Nucleotide Content



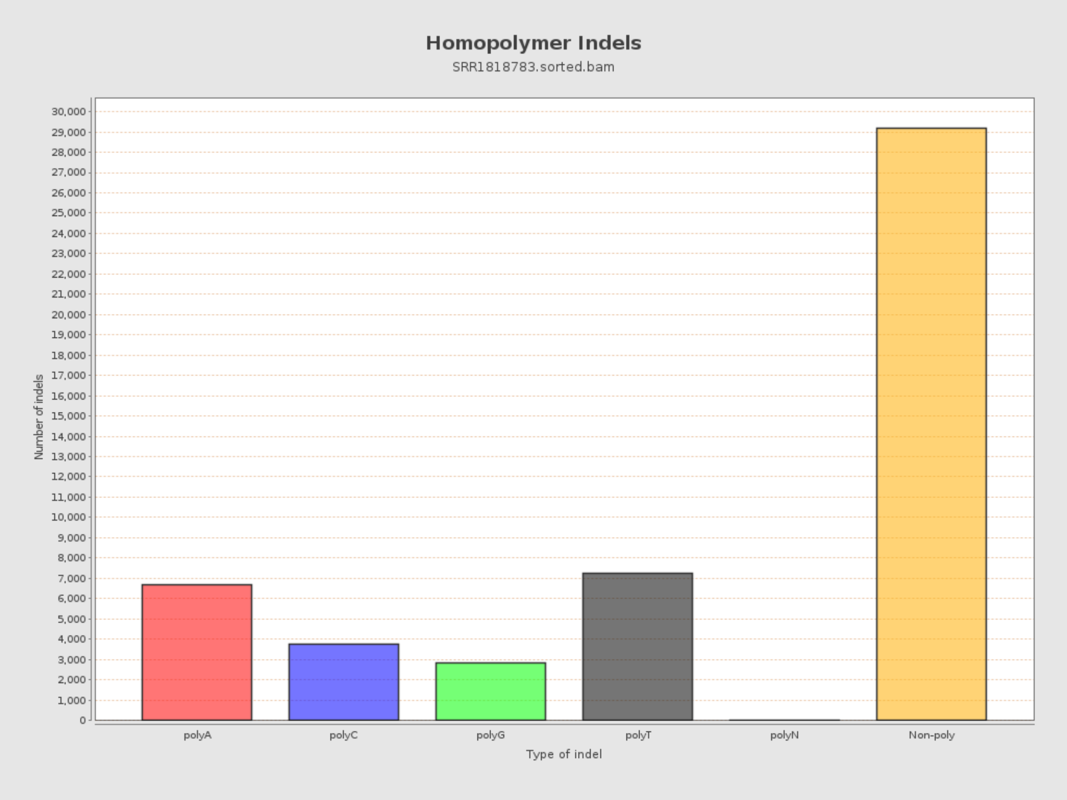
9. Results : Mapped Reads GC-content Distribution



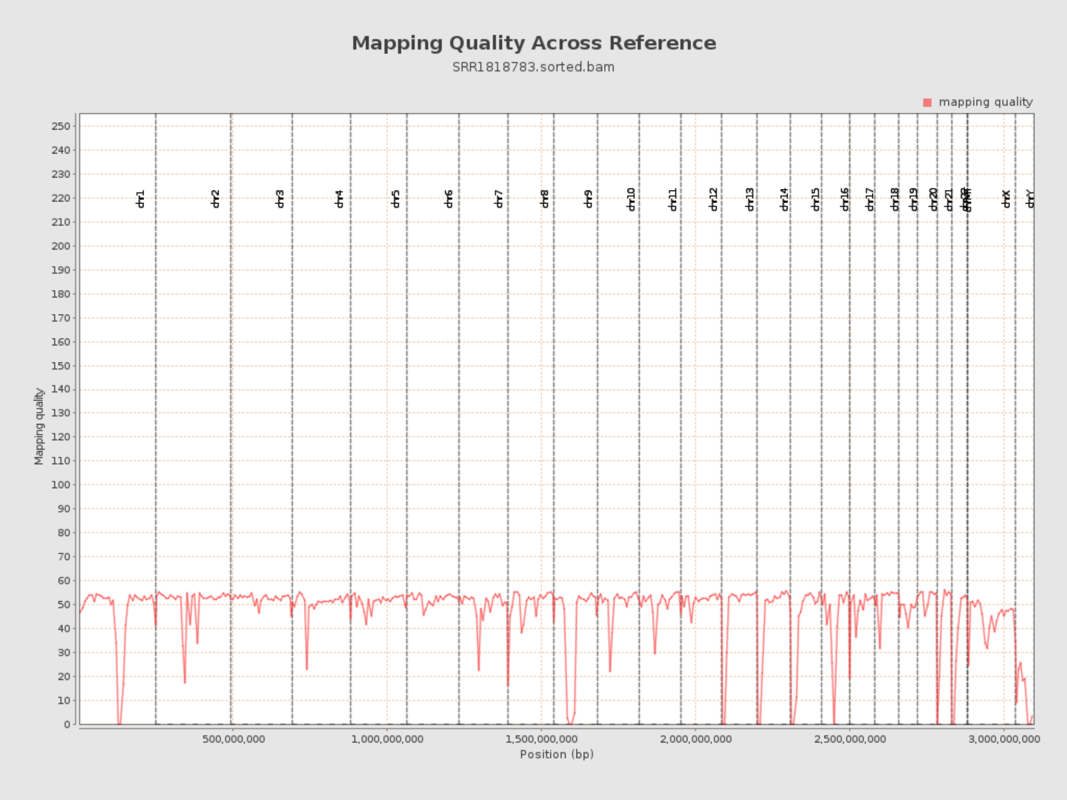
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram