Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 03:45:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6063583.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_SRR6063583 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6063583.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 03:45:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6063583.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,237,726
Mapped reads	2,848,969 / 87.99%
Unmapped reads	388,757 / 12.01%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	24,068 / 0.74%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	191,289 / 5.91%
Duplication rate	5.23%
Clipped reads	1,534,485 / 47.39%

2.2. ACGT Content

Number/percentage of A's	47,819,430 / 25.98%
Number/percentage of C's	34,254,199 / 18.61%
Number/percentage of T's	57,961,065 / 31.49%
Number/percentage of G's	44,009,785 / 23.91%
Number/percentage of N's	4,560 / 0%
GC Percentage	42.52%

2.3. Coverage

Mean	0.0595

Standard Deviation	0.5632

2.4. Mapping Quality

Mean Mapping Quality	44.4

2.5. Mismatches and indels

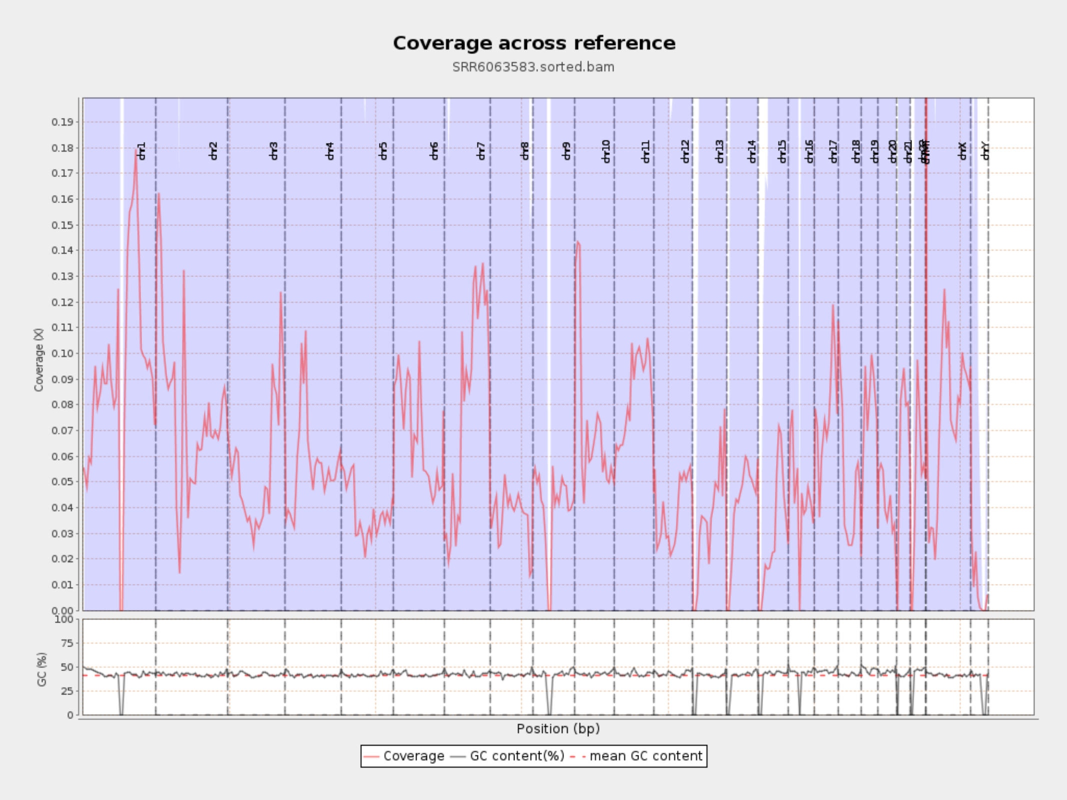
General error rate	0.83%
Mismatches	1,503,085
Insertions	13,149
Mapped reads with at least one insertion	0.46%
Deletions	45,441
Mapped reads with at least one deletion	1.58%
Homopolymer indels	45.91%

2.6. Chromosome stats

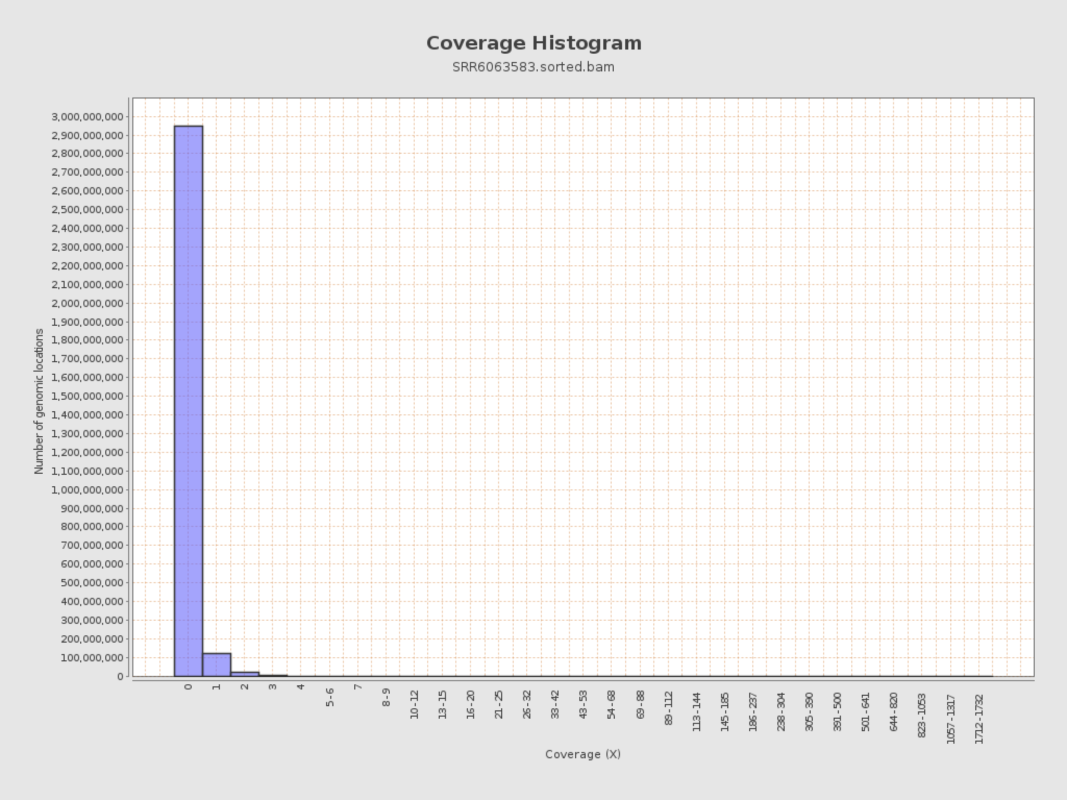
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	23118396	0.0928	1.0944
chr2	243199373	18969546	0.078	0.8609
chr3	198022430	11002664	0.0556	0.2833
chr4	191154276	11004350	0.0576	0.3391
chr5	180915260	6942061	0.0384	0.2365
chr6	171115067	11811080	0.069	0.4157
chr7	159138663	12919786	0.0812	0.8073

chr8	146364022	5355852	0.0366	0.5819
chr9	141213431	5696084	0.0403	0.4751
chr10	135534747	9899270	0.073	0.3914
chr11	135006516	11325479	0.0839	0.5242
chr12	133851895	5160575	0.0386	0.2654
chr13	115169878	4210116	0.0366	0.24
chr14	107349540	4340531	0.0404	0.2862
chr15	102531392	3003302	0.0293	0.2459
chr16	90354753	3946879	0.0437	0.2768
chr17	81195210	6261320	0.0771	0.378
chr18	78077248	3939183	0.0505	0.7995
chr19	59128983	4585990	0.0776	0.7498
chr20	63025520	2657550	0.0422	0.2783
chr21	48129895	3167838	0.0658	0.3249
chr22	51304566	2510045	0.0489	0.2635
chrMT	16571	200690	12.1109	9.5179
chrX	155270560	11590419	0.0746	0.4351
chrY	59373566	501942	0.0085	0.1776

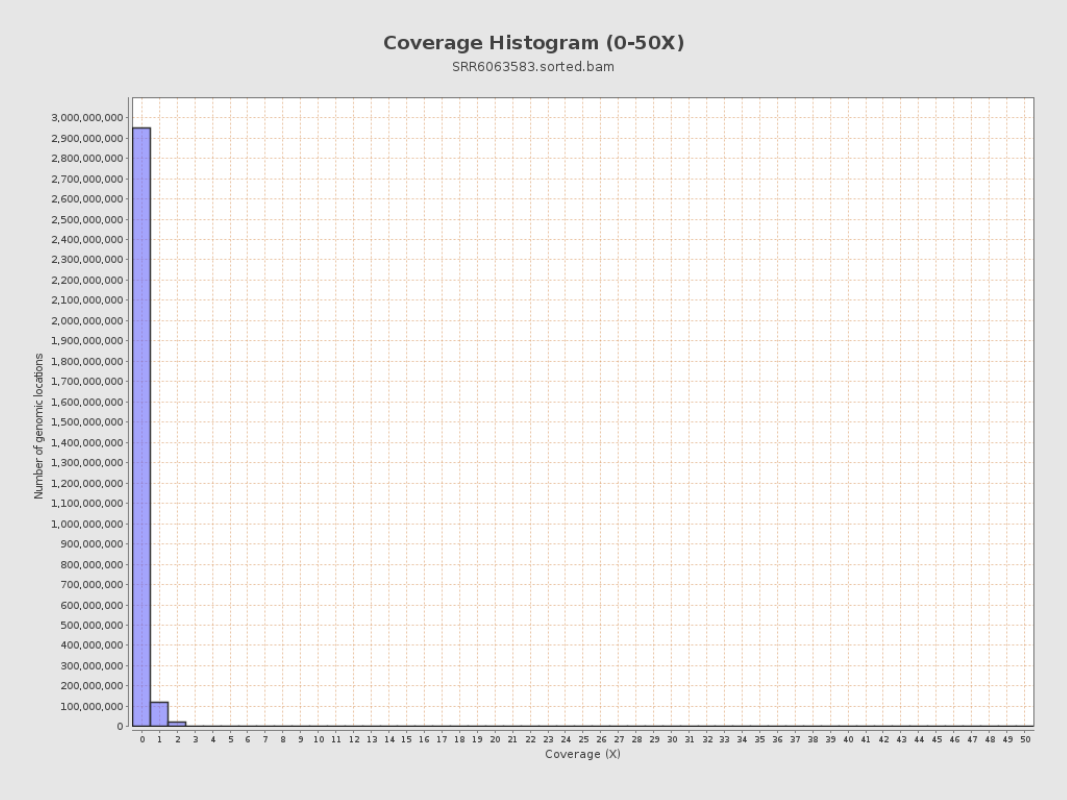
3. Results : Coverage across reference



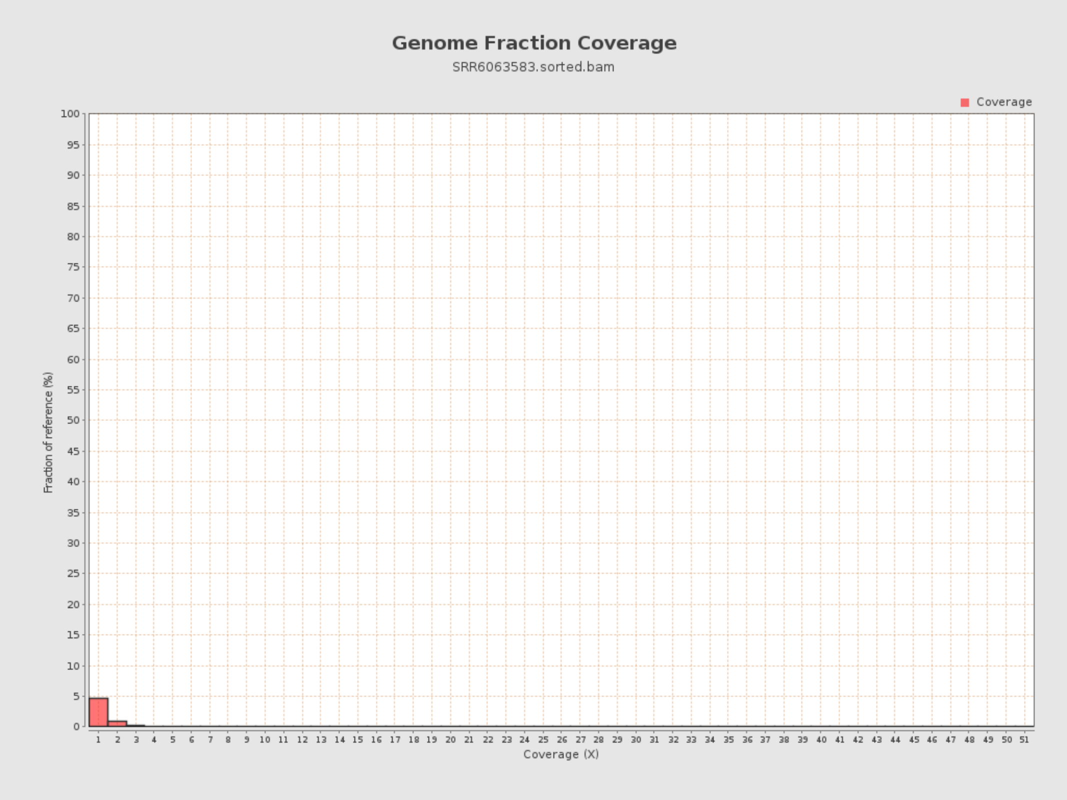
4. Results : Coverage Histogram



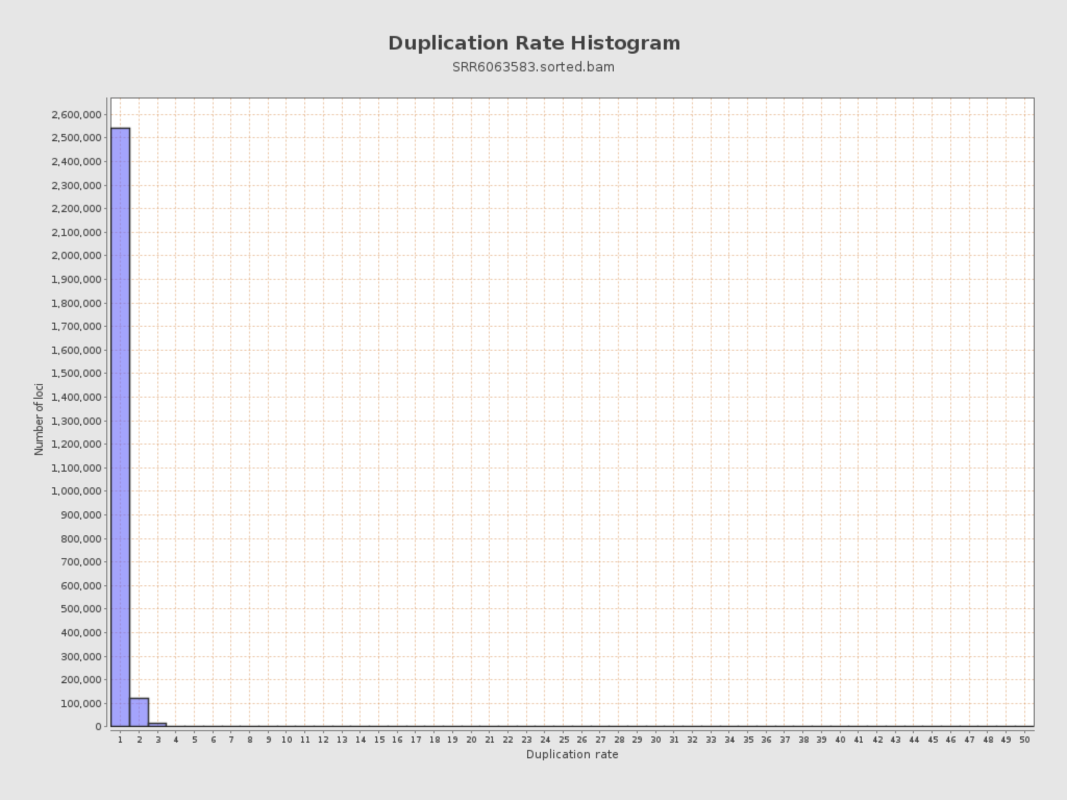
5. Results : Coverage Histogram (0-50X)



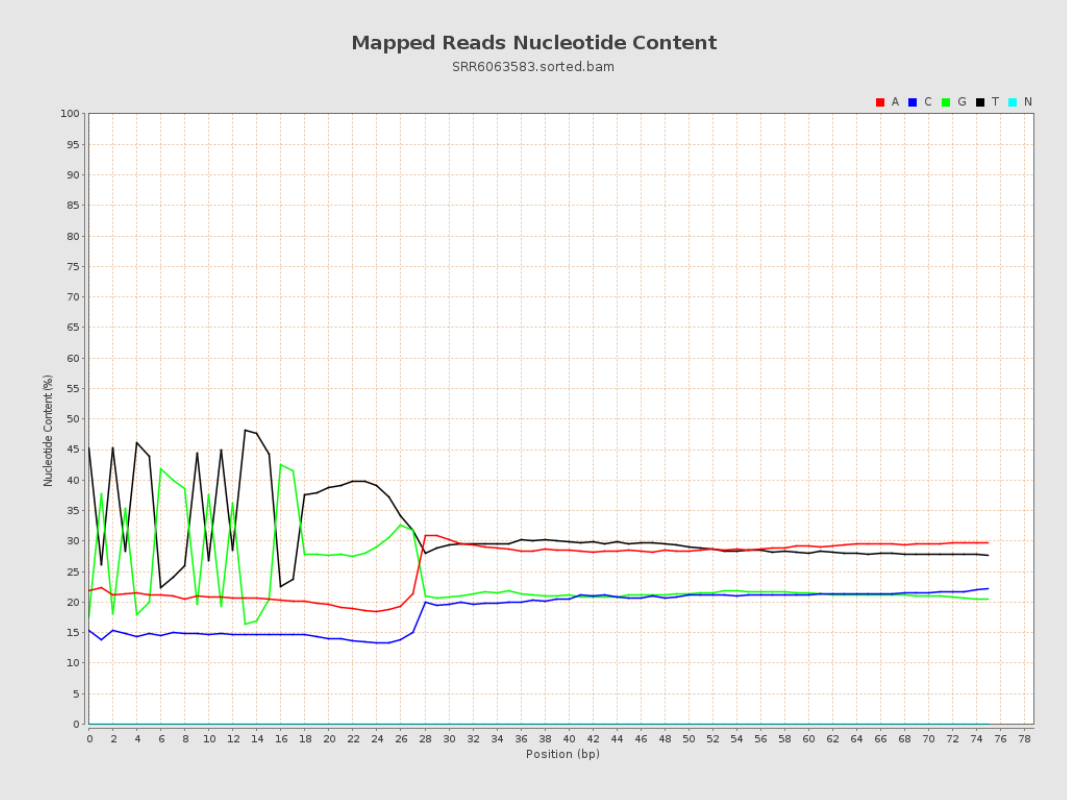
6. Results : Genome Fraction Coverage



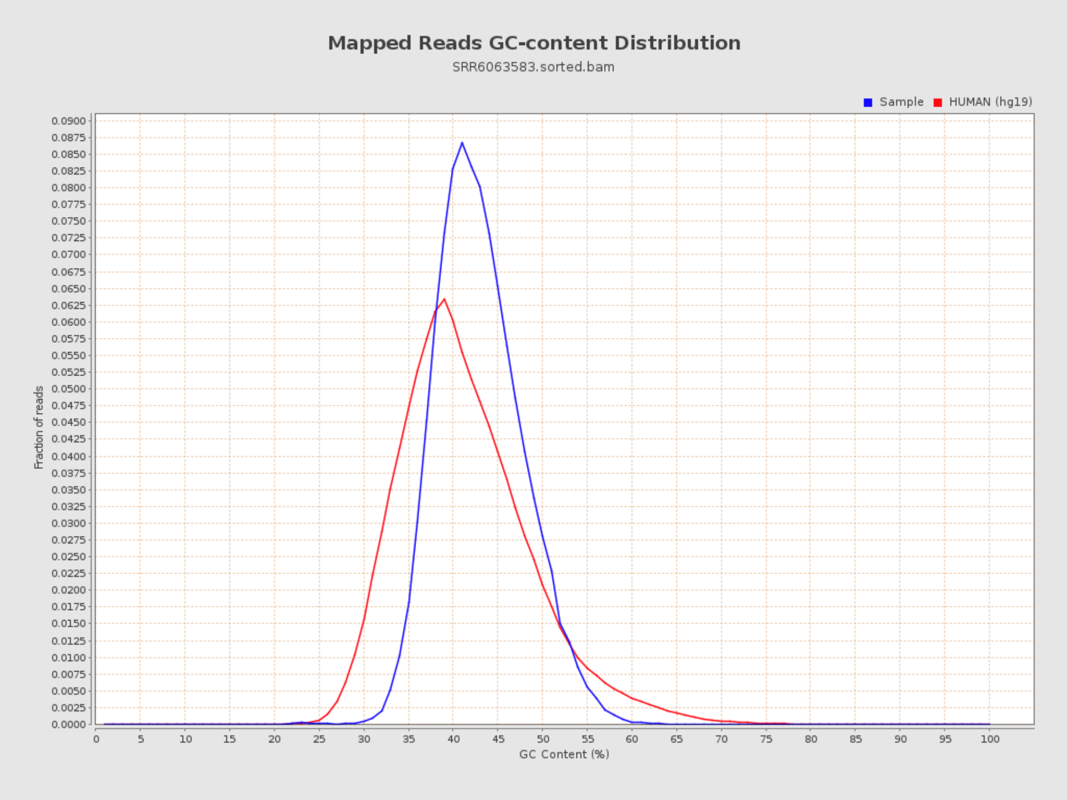
7. Results : Duplication Rate Histogram



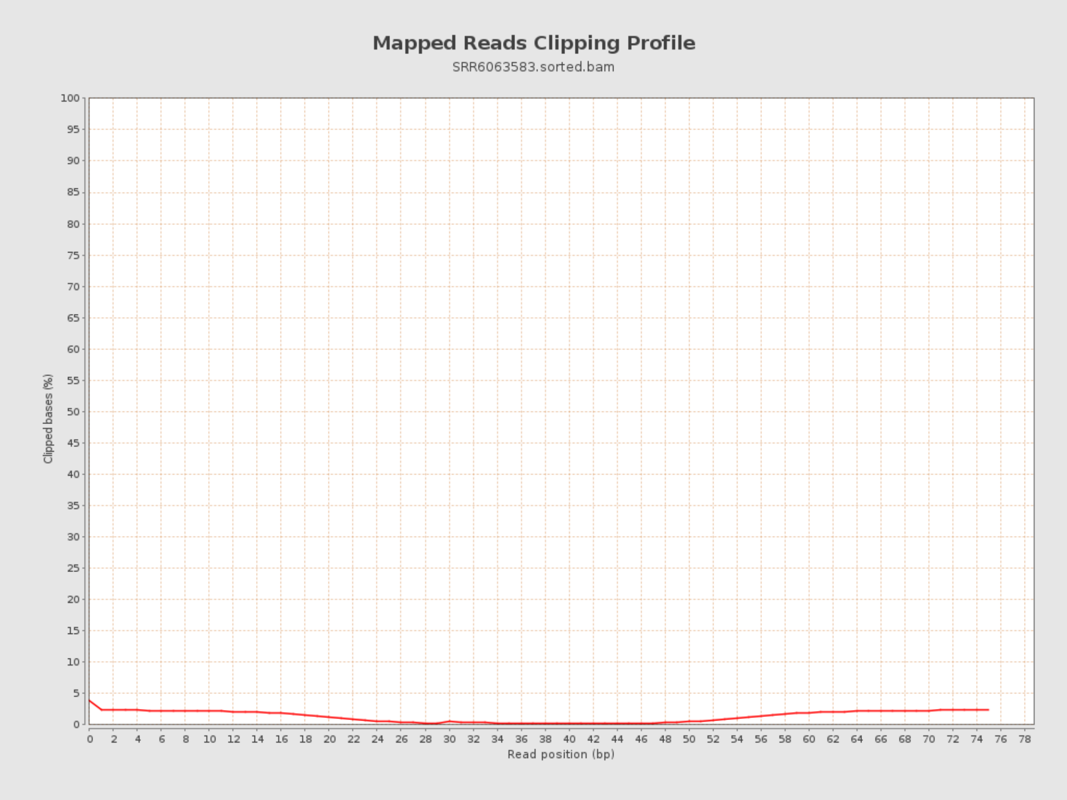
8. Results : Mapped Reads Nucleotide Content



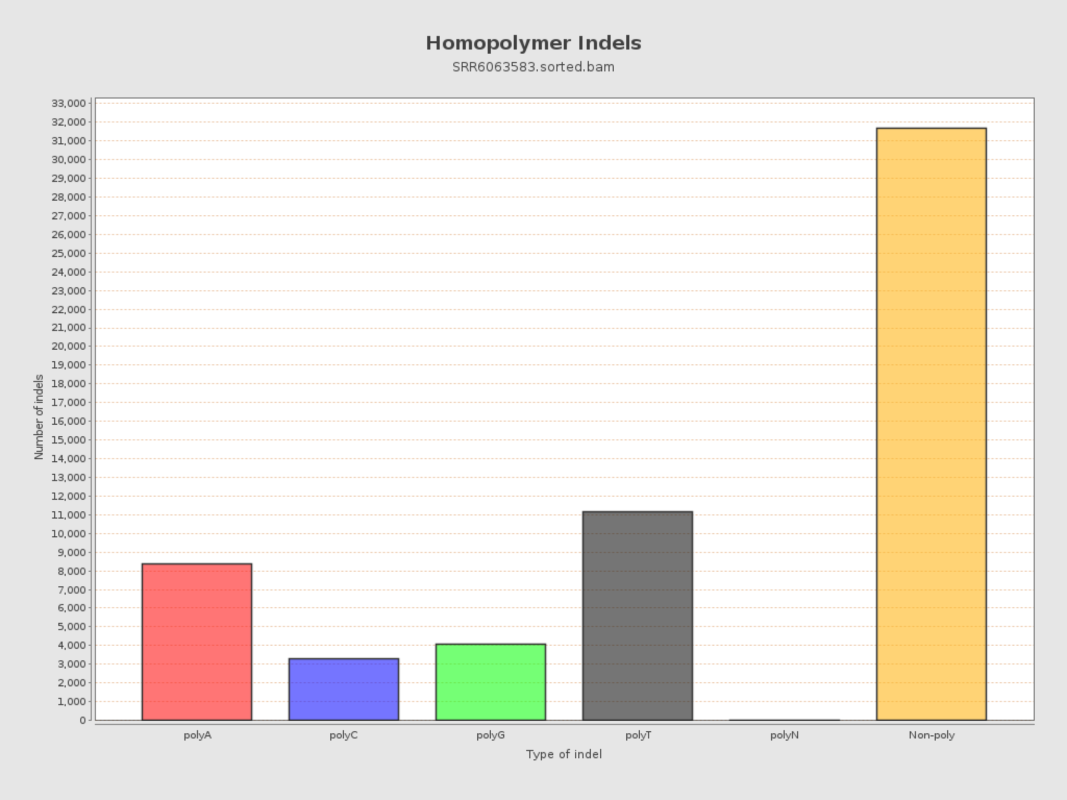
9. Results : Mapped Reads GC-content Distribution



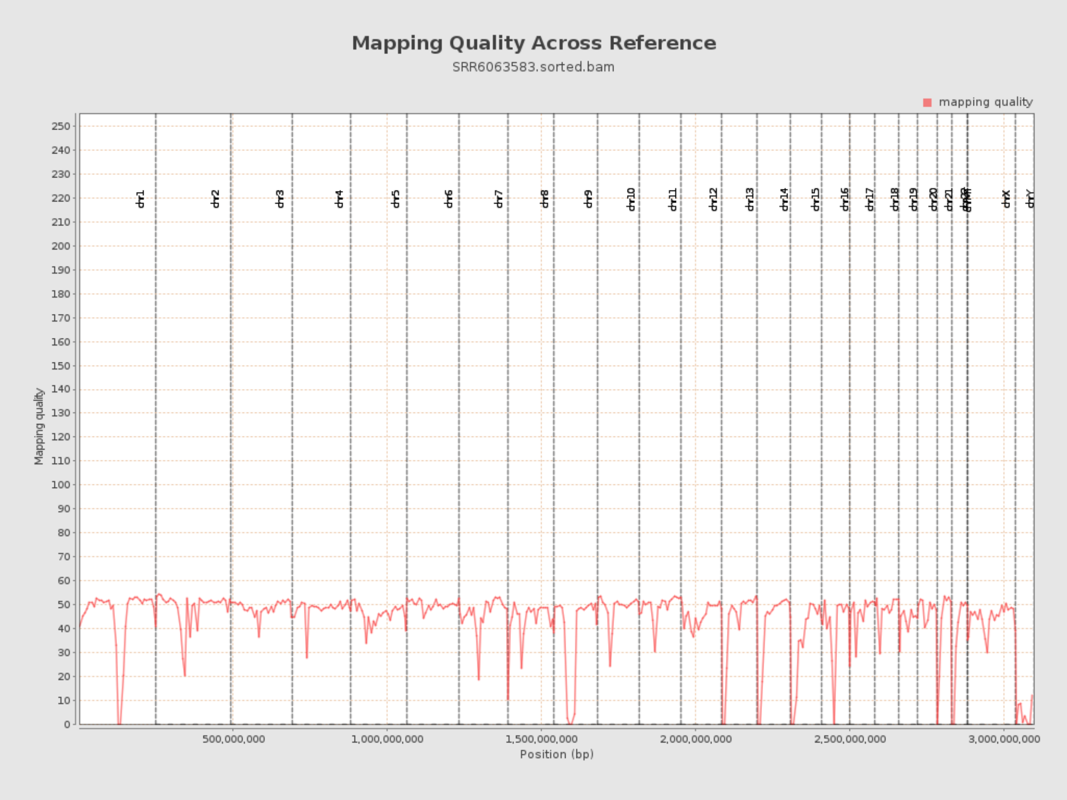
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram