Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 03:49:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6063584.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_SRR6063584 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6063584.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 03:49:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6063584.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,103,042
Mapped reads	2,683,573 / 86.48%
Unmapped reads	419,469 / 13.52%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	25,301 / 0.82%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	195,350 / 6.3%
Duplication rate	5.78%
Clipped reads	1,387,817 / 44.72%

2.2. ACGT Content

Number/percentage of A's	46,339,074 / 26.48%
Number/percentage of C's	33,045,415 / 18.89%
Number/percentage of T's	54,580,344 / 31.19%
Number/percentage of G's	40,998,636 / 23.43%
Number/percentage of N's	4,437 / 0%
GC Percentage	42.32%

2.3. Coverage

Mean	0.0565

Standard Deviation	0.5299

2.4. Mapping Quality

Mean Mapping Quality	45.14

2.5. Mismatches and indels

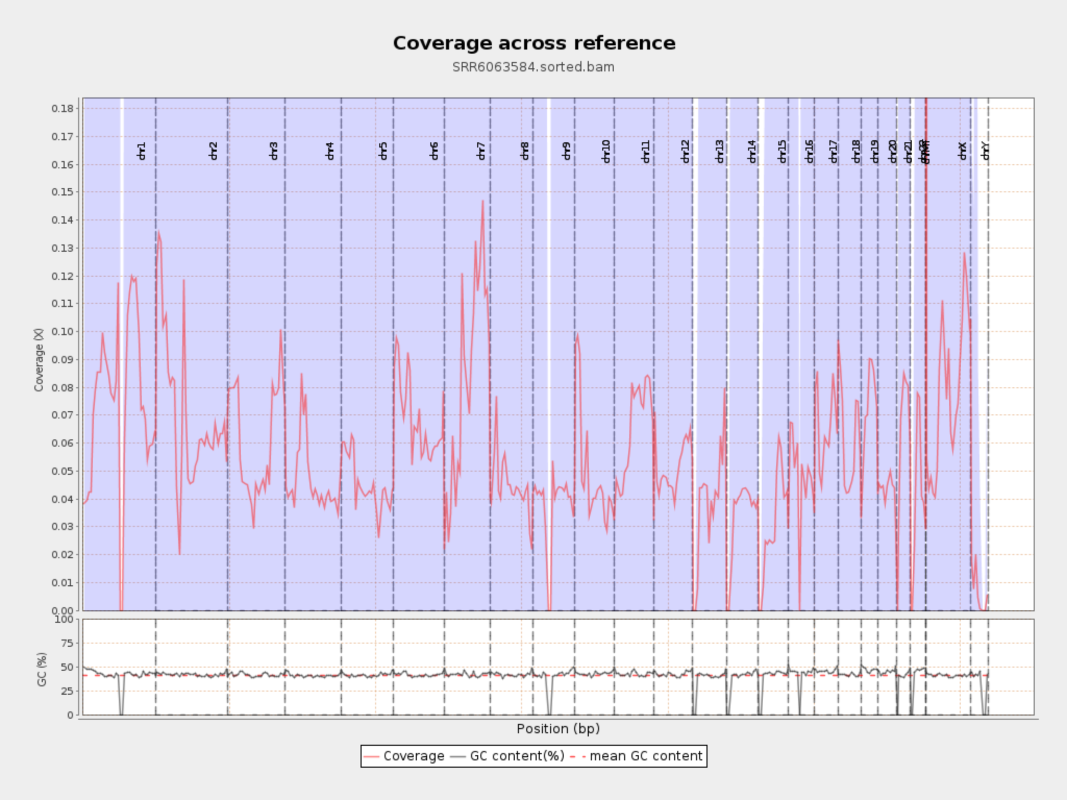
General error rate	0.82%
Mismatches	1,416,025
Insertions	12,460
Mapped reads with at least one insertion	0.46%
Deletions	43,132
Mapped reads with at least one deletion	1.59%
Homopolymer indels	46.11%

2.6. Chromosome stats

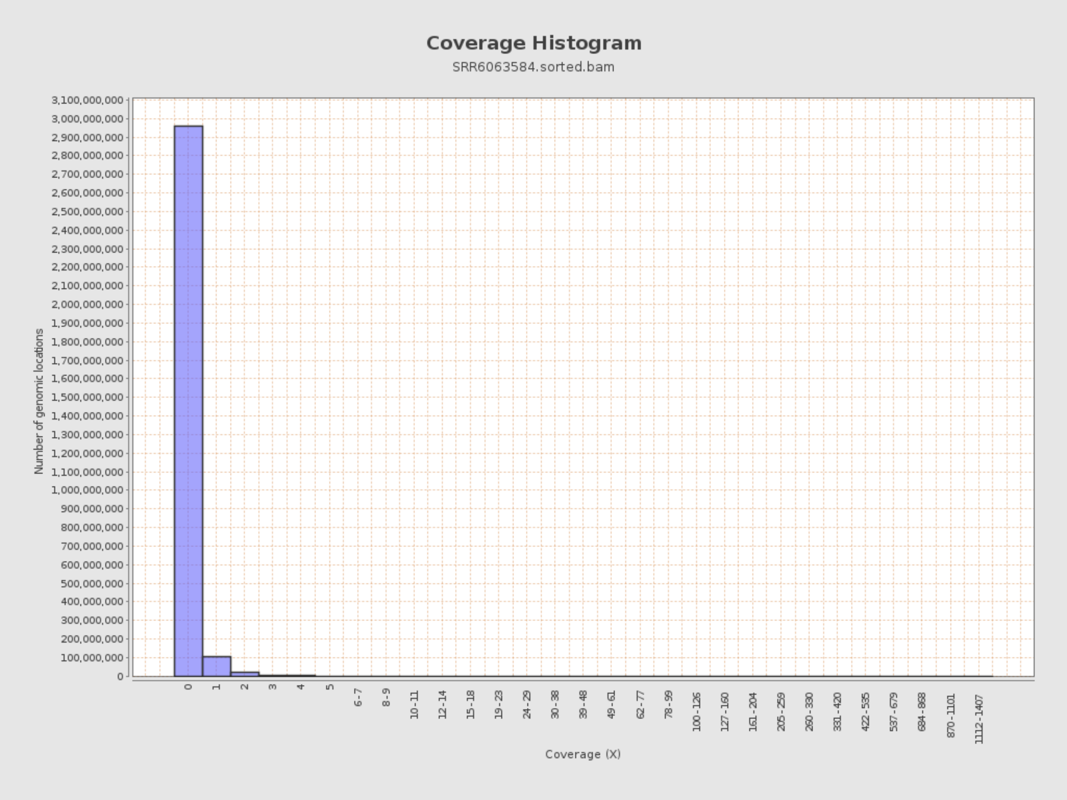
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	18582916	0.0746	1.0375
chr2	243199373	17321175	0.0712	0.7536
chr3	198022430	12082189	0.061	0.3057
chr4	191154276	9014648	0.0472	0.2966
chr5	180915260	8199516	0.0453	0.2653
chr6	171115067	11800416	0.069	0.3808
chr7	159138663	13312524	0.0837	0.8456

chr8	146364022	6525892	0.0446	0.5468
chr9	141213431	5294365	0.0375	0.4256
chr10	135534747	6754015	0.0498	0.3596
chr11	135006516	8758005	0.0649	0.4479
chr12	133851895	6927282	0.0518	0.2939
chr13	115169878	4459739	0.0387	0.2501
chr14	107349540	3623860	0.0338	0.2715
chr15	102531392	3103564	0.0303	0.2346
chr16	90354753	4230507	0.0468	0.2883
chr17	81195210	5433971	0.0669	0.3482
chr18	78077248	4794313	0.0614	0.691
chr19	59128983	4293654	0.0726	0.7167
chr20	63025520	2767608	0.0439	0.2801
chr21	48129895	2981794	0.062	0.3215
chr22	51304566	2035007	0.0397	0.243
chrMT	16571	185732	11.2083	7.827
chrX	155270560	12159626	0.0783	0.4093
chrY	59373566	394236	0.0066	0.1789

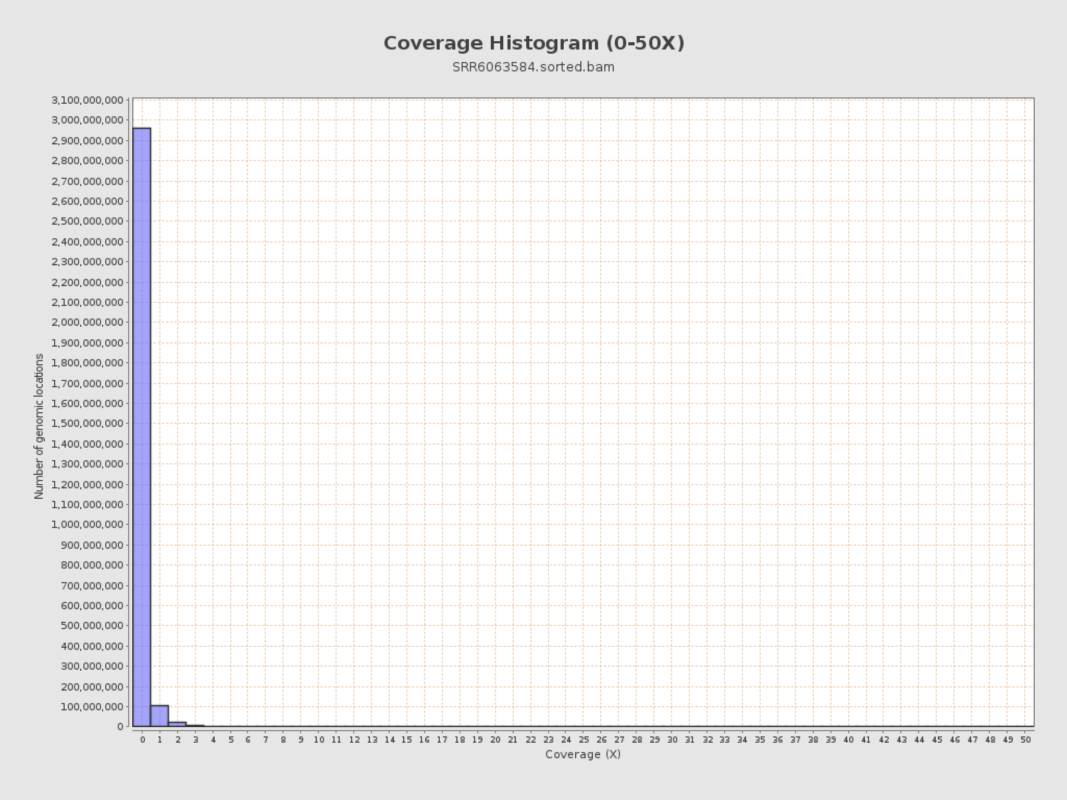
3. Results : Coverage across reference



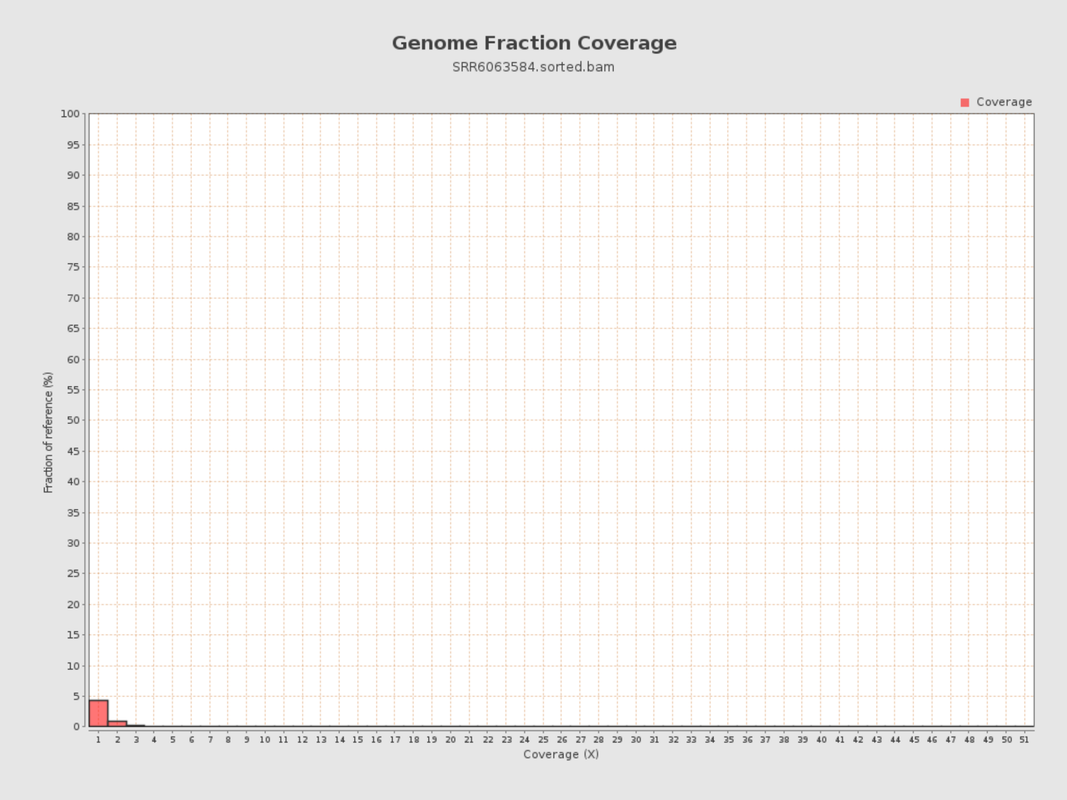
4. Results : Coverage Histogram



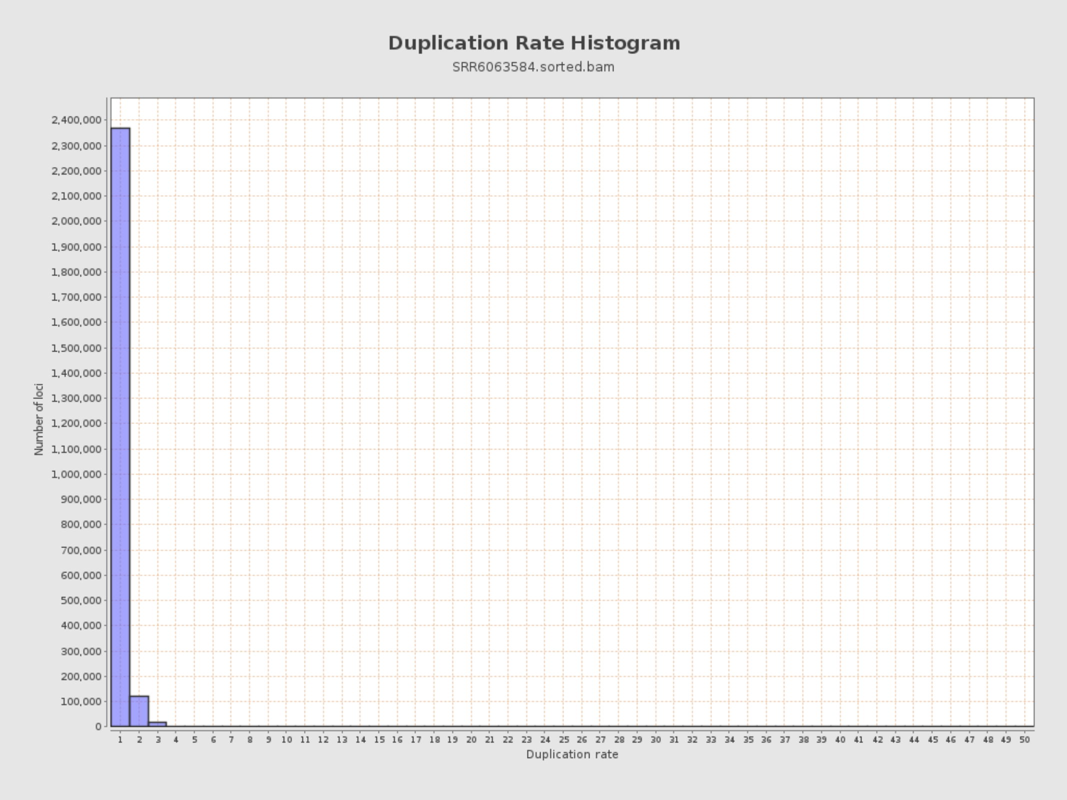
5. Results : Coverage Histogram (0-50X)



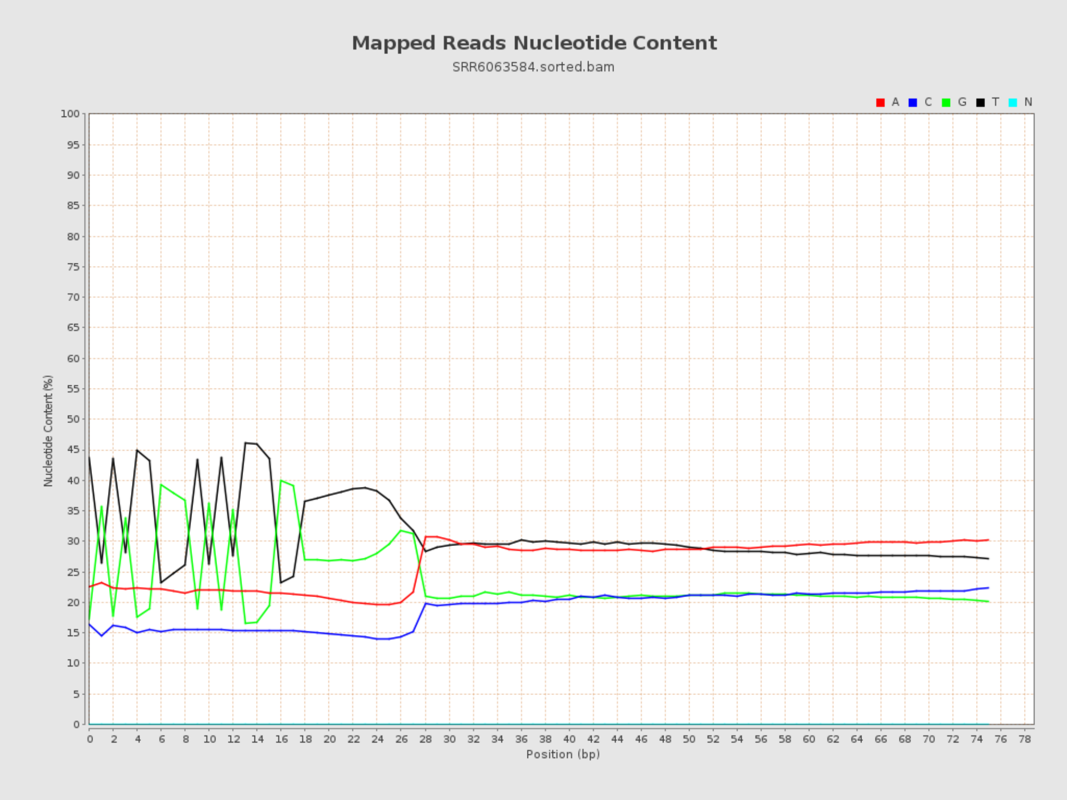
6. Results : Genome Fraction Coverage



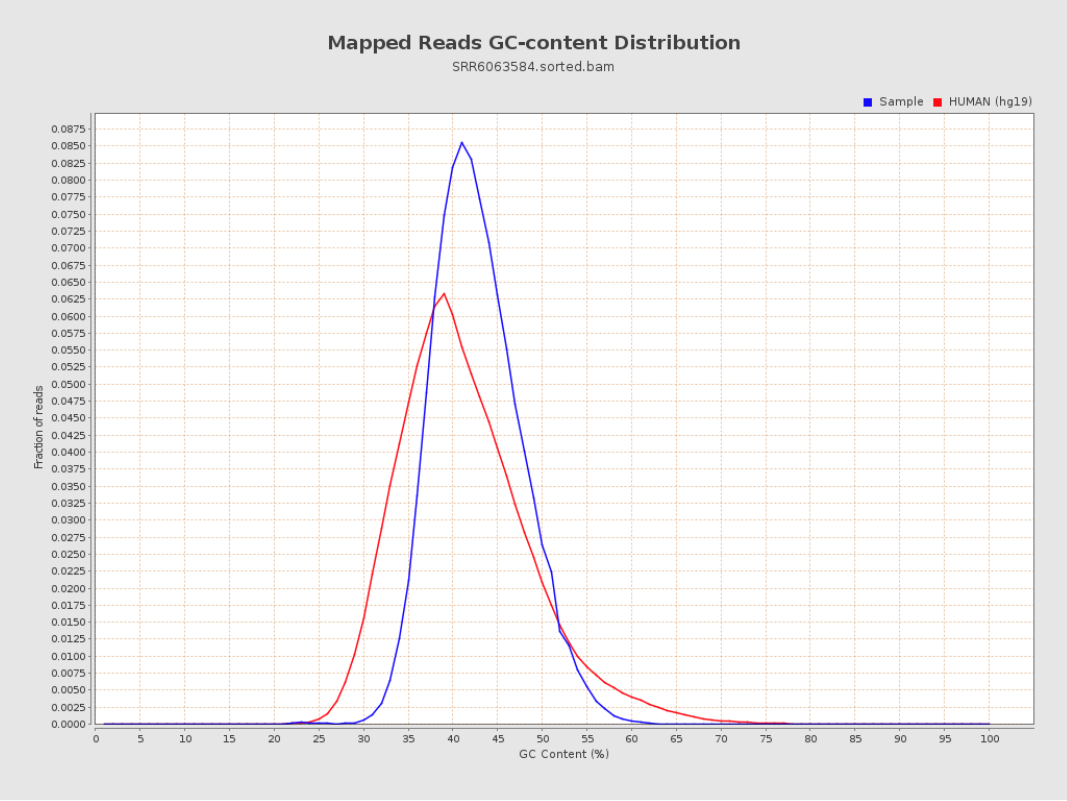
7. Results : Duplication Rate Histogram



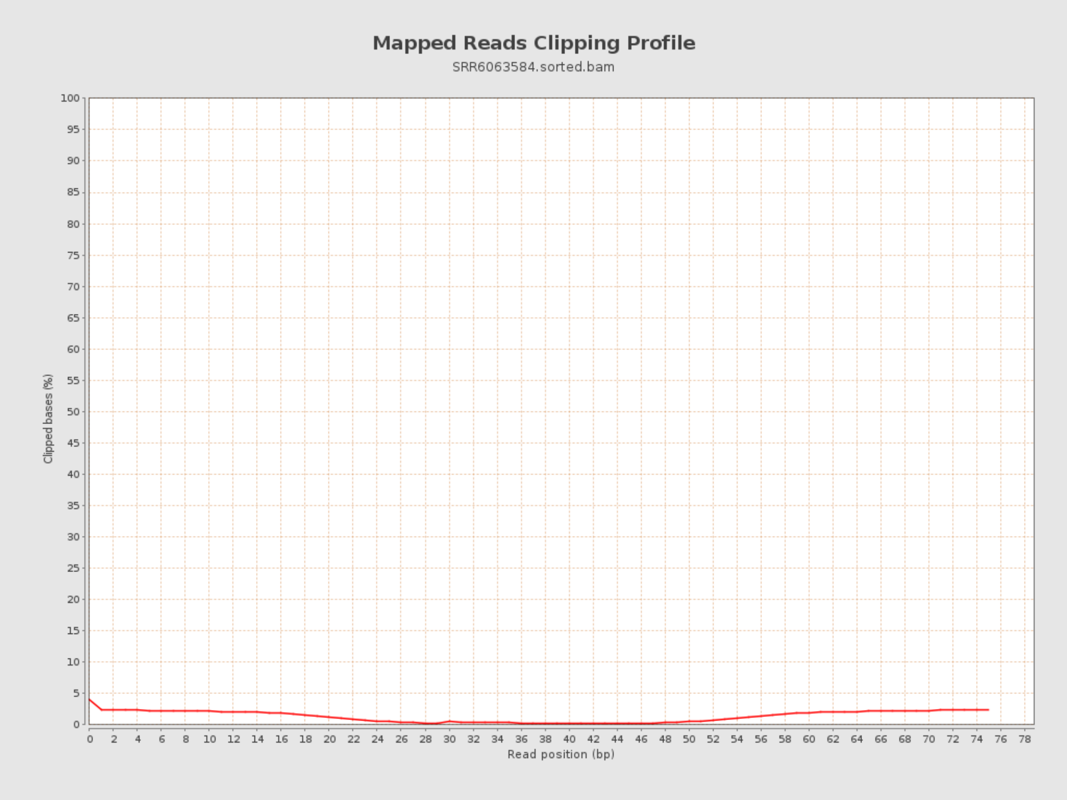
8. Results : Mapped Reads Nucleotide Content



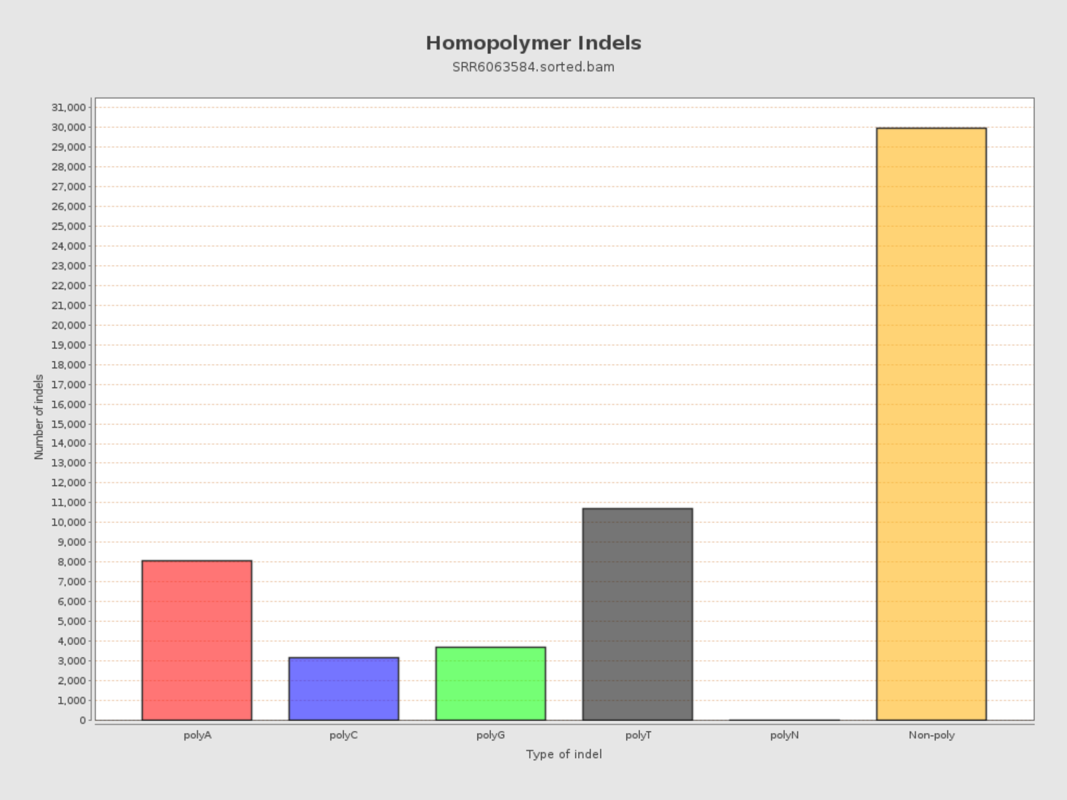
9. Results : Mapped Reads GC-content Distribution



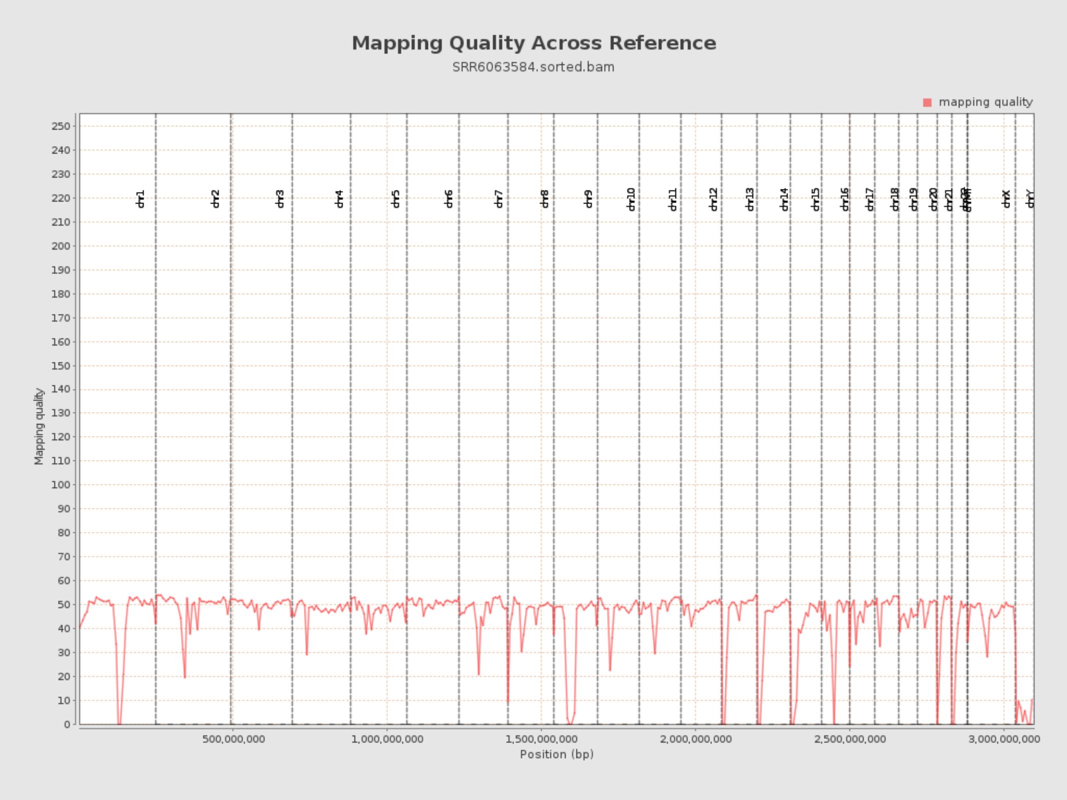
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram