Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 00:40:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6063531.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_SRR6063531 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6063531.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 00:40:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6063531.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,990,100
Mapped reads	4,713,726 / 94.46%
Unmapped reads	276,374 / 5.54%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	42,749 / 0.86%
Read min/max/mean length	30 / 76 / 76.3
Duplicated reads (estimated)	784,112 / 15.71%
Duplication rate	13.29%
Clipped reads	2,689,043 / 53.89%

2.2. ACGT Content

Number/percentage of A's	78,122,569 / 26.03%
Number/percentage of C's	54,690,122 / 18.22%
Number/percentage of T's	97,033,456 / 32.33%
Number/percentage of G's	70,236,381 / 23.4%
Number/percentage of N's	34,461 / 0.01%
GC Percentage	41.63%

2.3. Coverage

Mean	0.097

Standard Deviation	0.9919

2.4. Mapping Quality

Mean Mapping Quality	45.38

2.5. Mismatches and indels

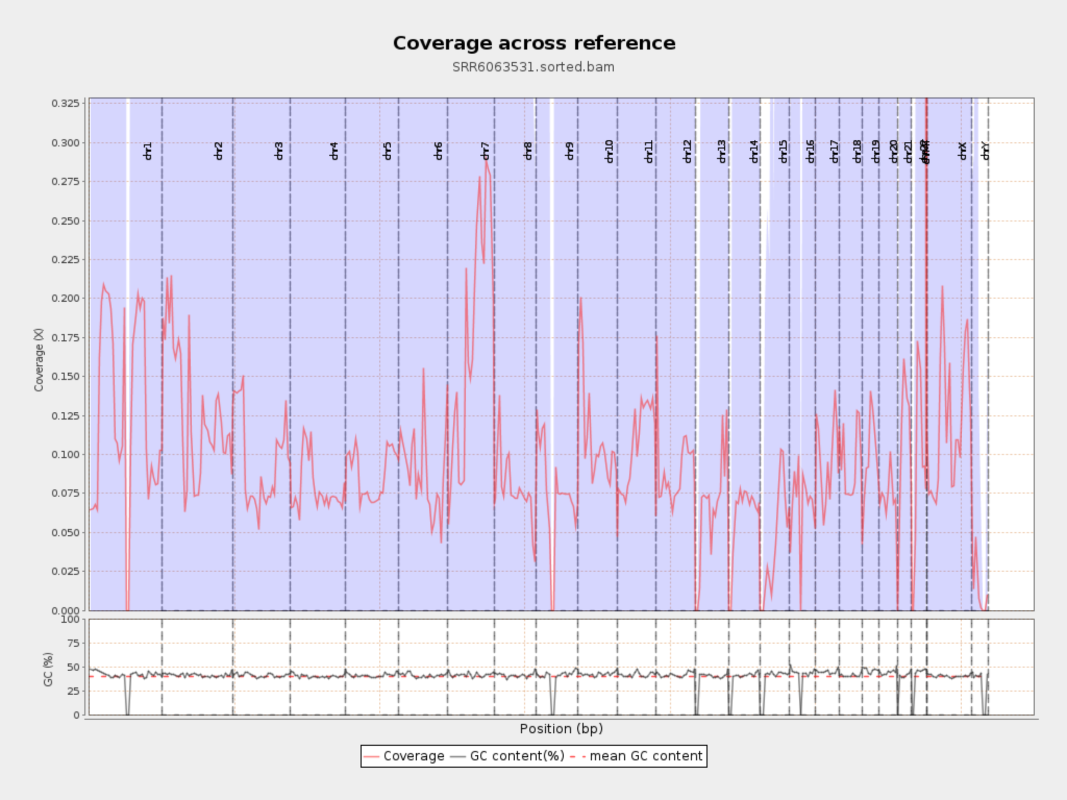
General error rate	0.55%
Mismatches	1,627,535
Insertions	18,871
Mapped reads with at least one insertion	0.4%
Deletions	61,927
Mapped reads with at least one deletion	1.3%
Homopolymer indels	43.75%

2.6. Chromosome stats

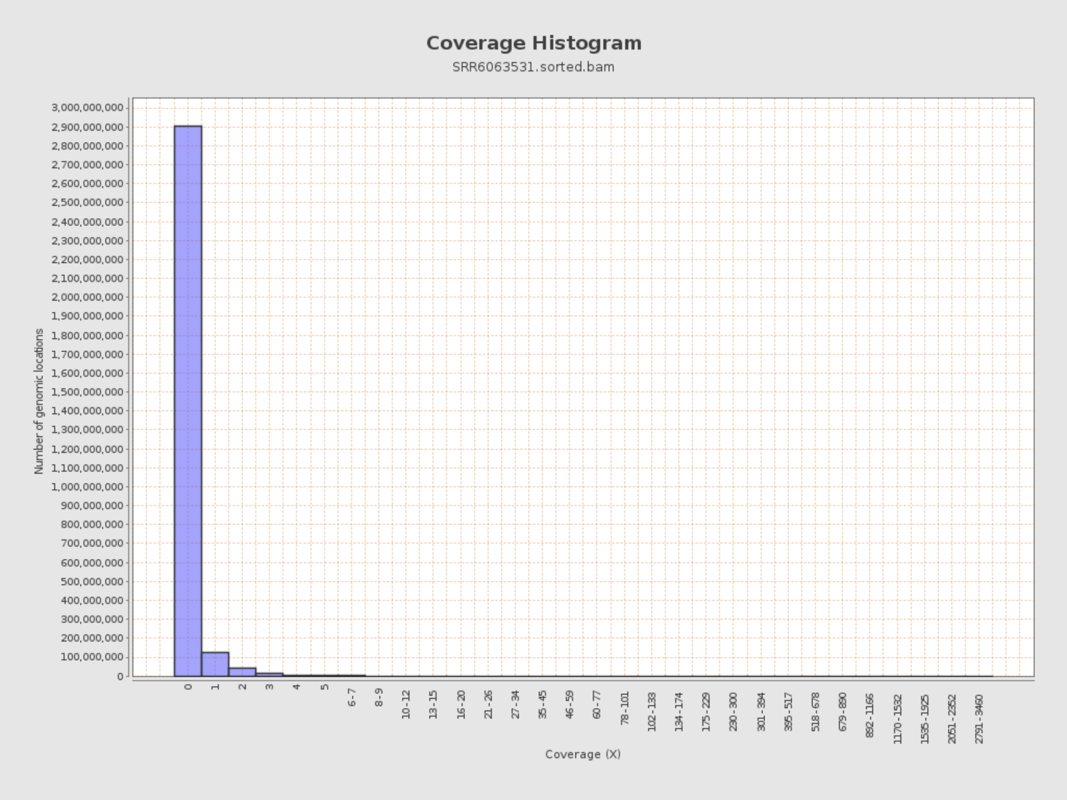
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	31873825	0.1279	1.9169
chr2	243199373	31191302	0.1283	1.6958
chr3	198022430	18954684	0.0957	0.4516
chr4	191154276	14958360	0.0783	0.4881
chr5	180915260	15832977	0.0875	0.4382
chr6	171115067	15318210	0.0895	0.6587
chr7	159138663	28249857	0.1775	1.5137

chr8	146364022	11413041	0.078	1.1738
chr9	141213431	10394766	0.0736	0.6821
chr10	135534747	15321016	0.113	0.6763
chr11	135006516	14281706	0.1058	0.6691
chr12	133851895	12228031	0.0914	0.4795
chr13	115169878	7548811	0.0655	0.4402
chr14	107349540	6393634	0.0596	0.4319
chr15	102531392	4464210	0.0435	0.3639
chr16	90354753	6143333	0.068	0.4315
chr17	81195210	7818402	0.0963	0.5026
chr18	78077248	7415920	0.095	1.2835
chr19	59128983	5940379	0.1005	1.2805
chr20	63025520	4613904	0.0732	0.4443
chr21	48129895	5173423	0.1075	0.5147
chr22	51304566	4466898	0.0871	0.4256
chrMT	16571	448260	27.0509	17.7933
chrX	155270560	18982112	0.1223	0.6427
chrY	59373566	797299	0.0134	0.459

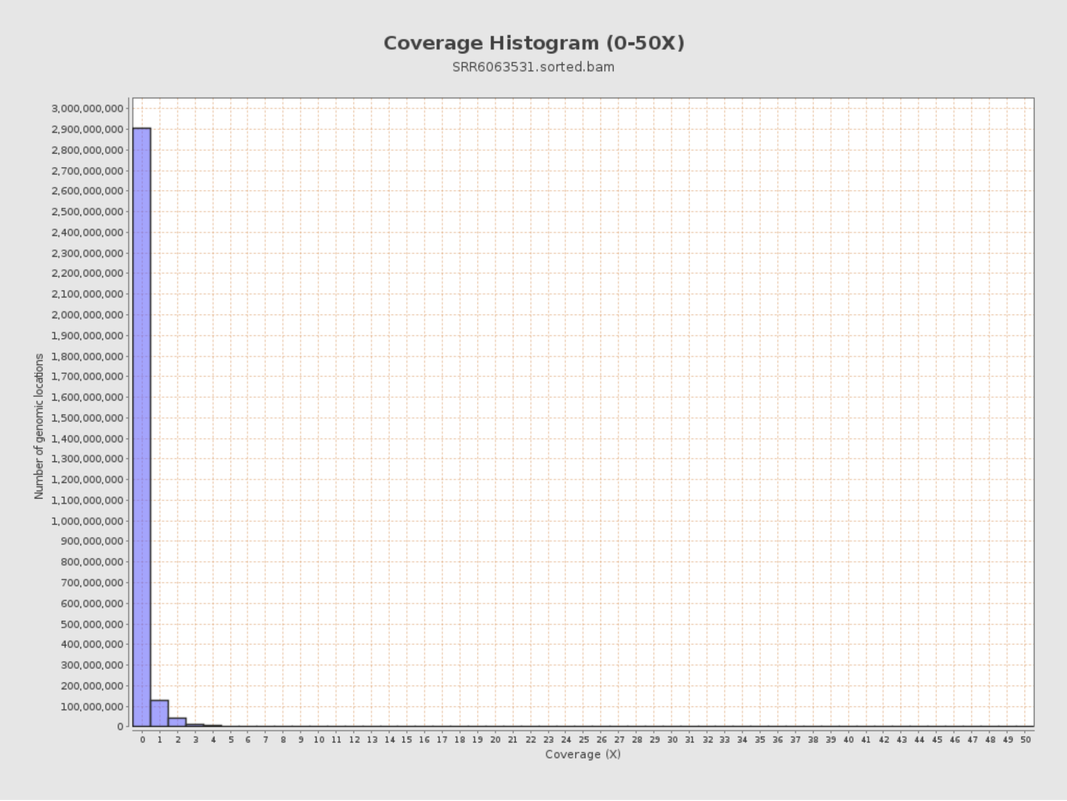
3. Results : Coverage across reference



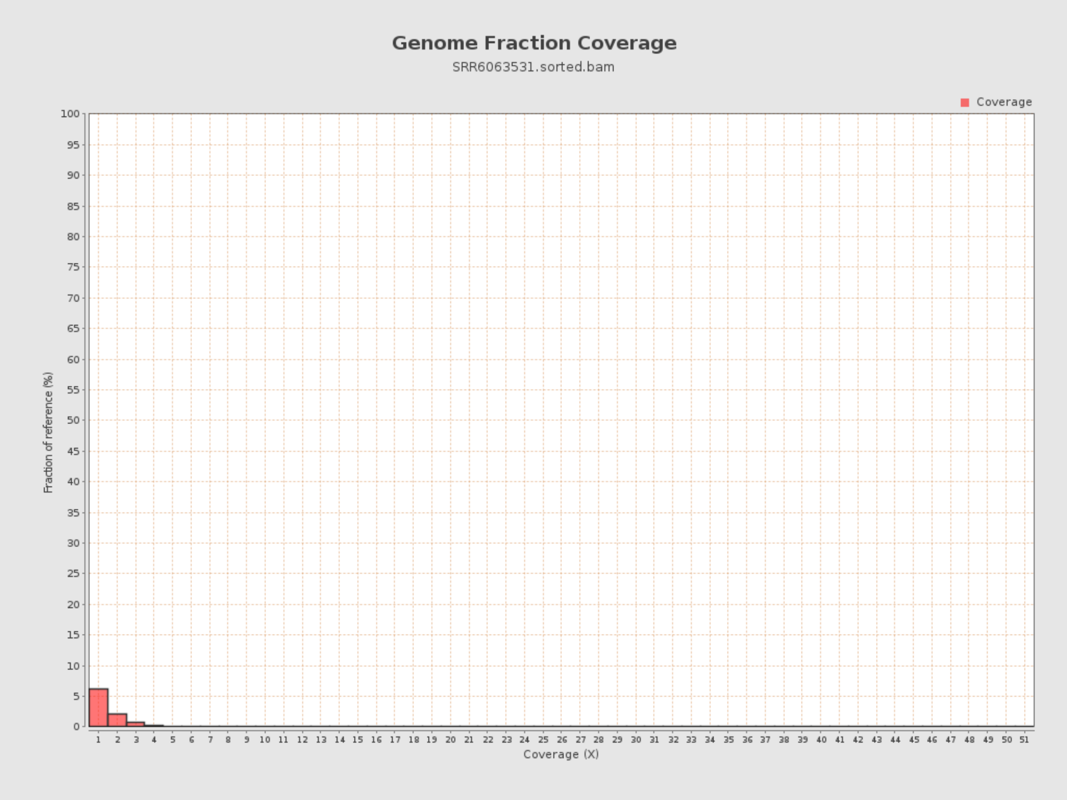
4. Results : Coverage Histogram



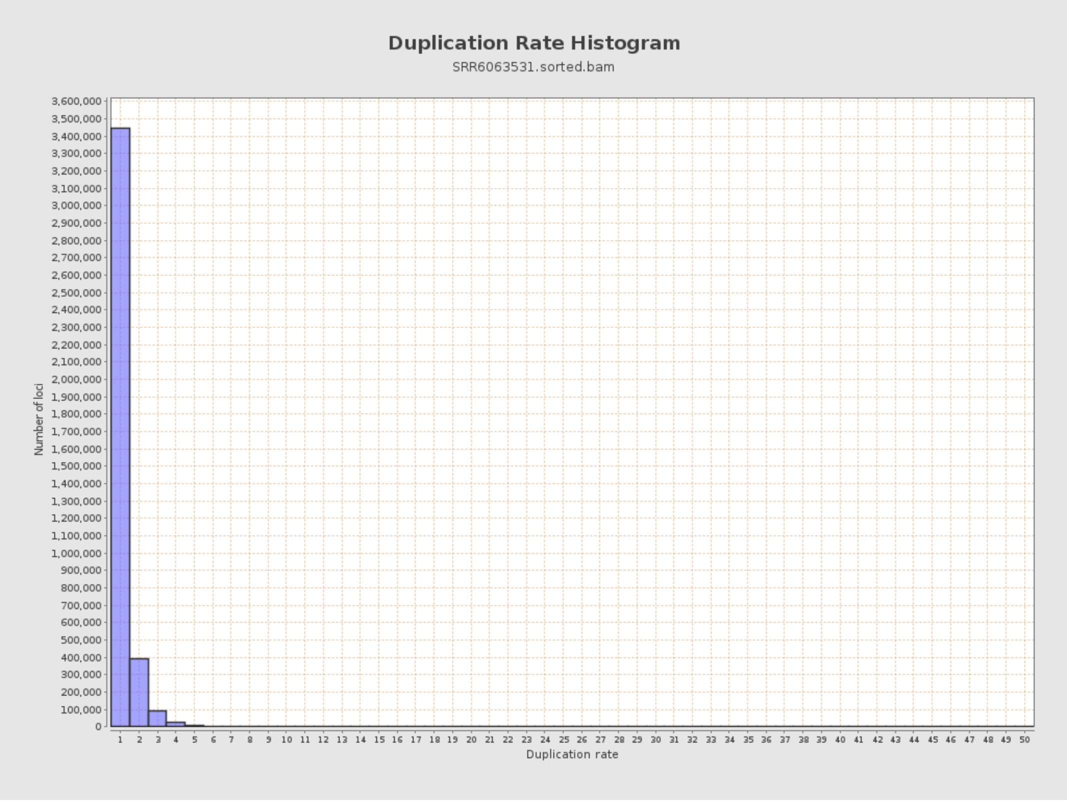
5. Results : Coverage Histogram (0-50X)



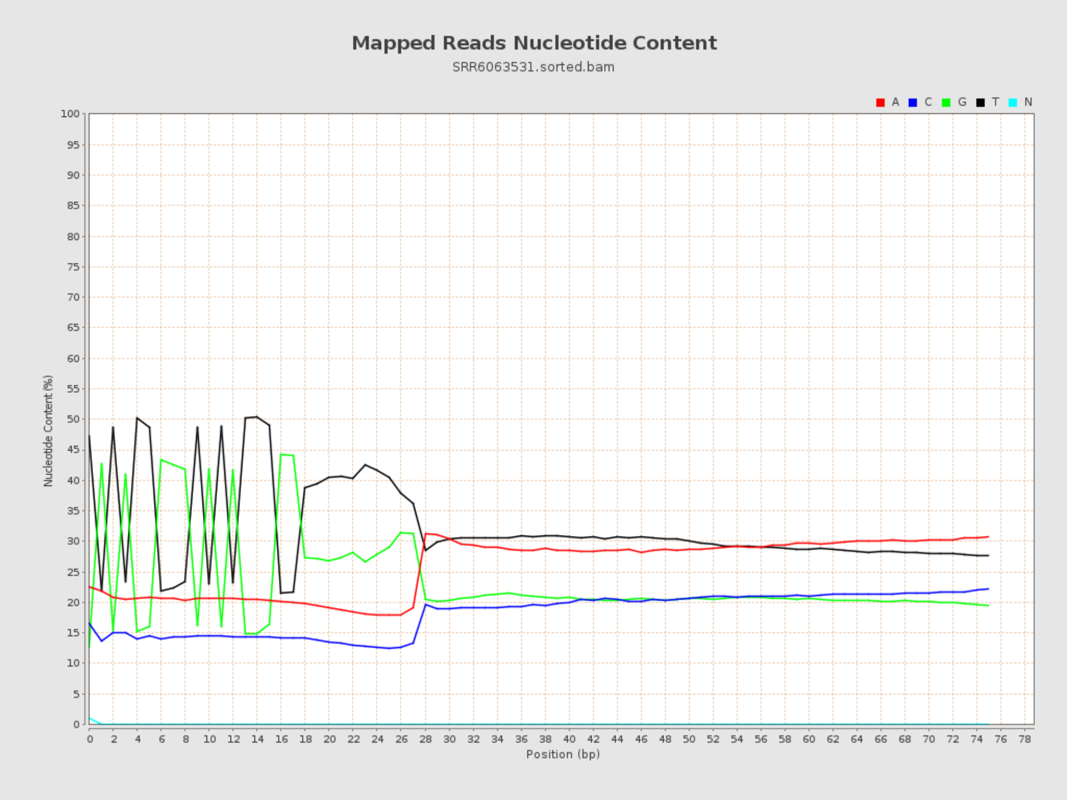
6. Results : Genome Fraction Coverage



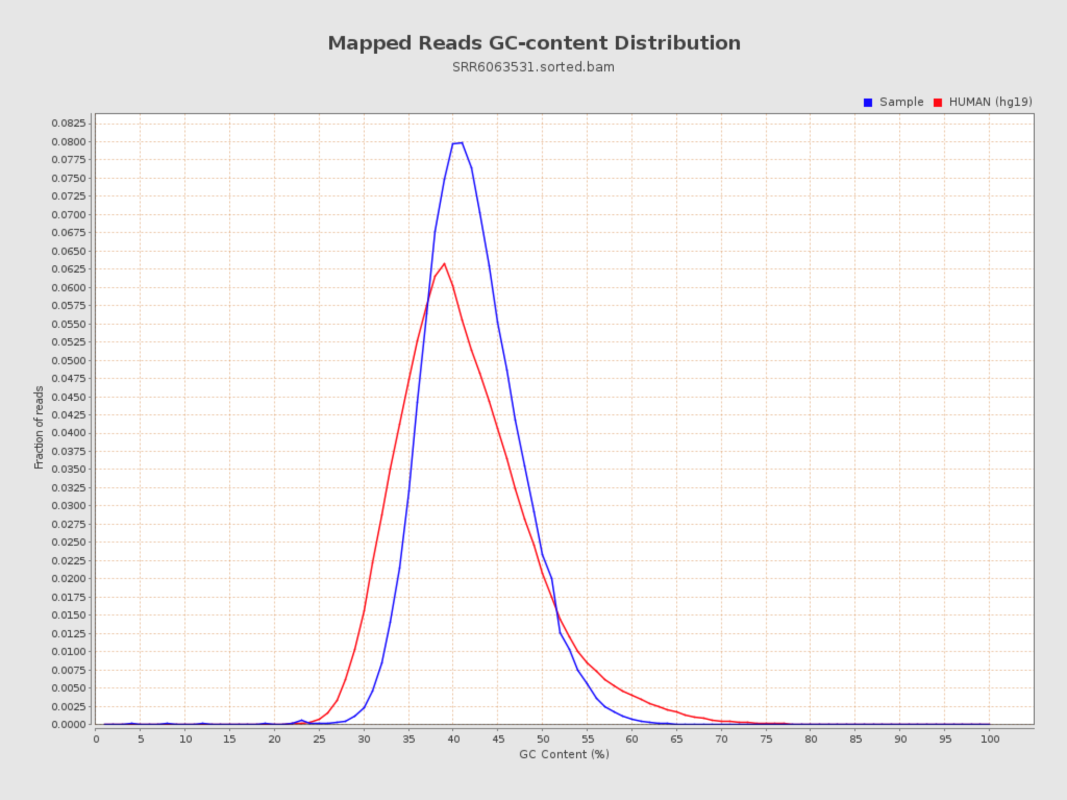
7. Results : Duplication Rate Histogram



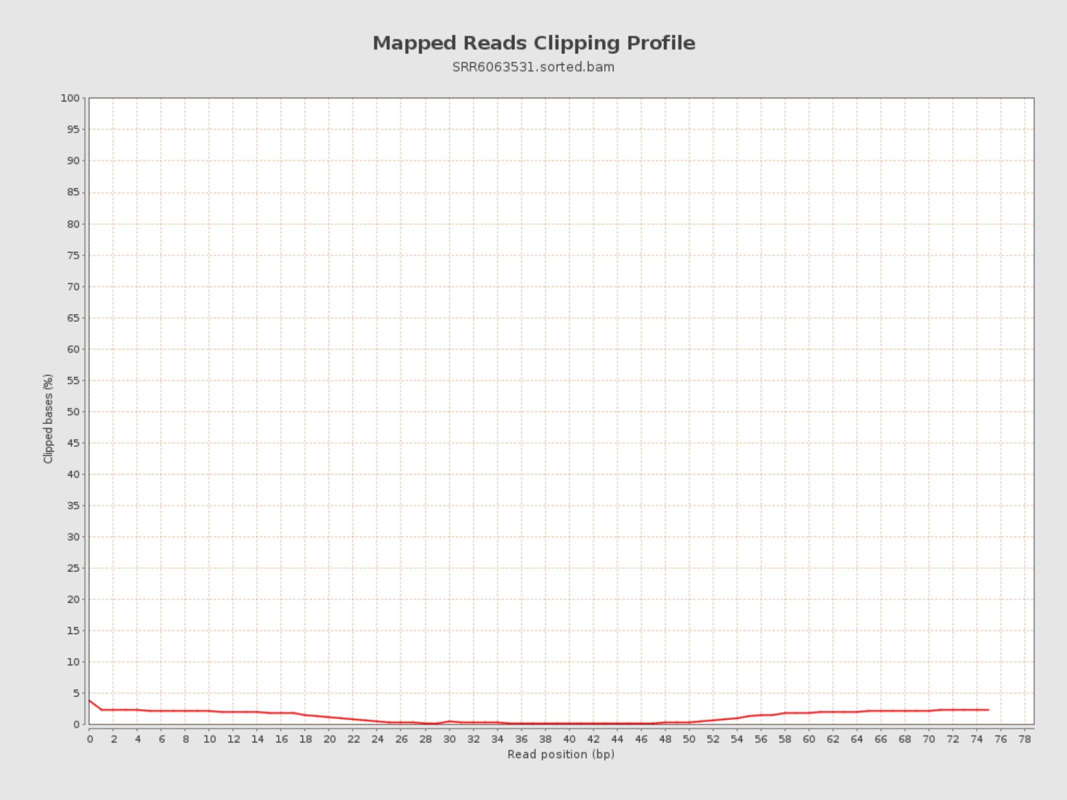
8. Results : Mapped Reads Nucleotide Content



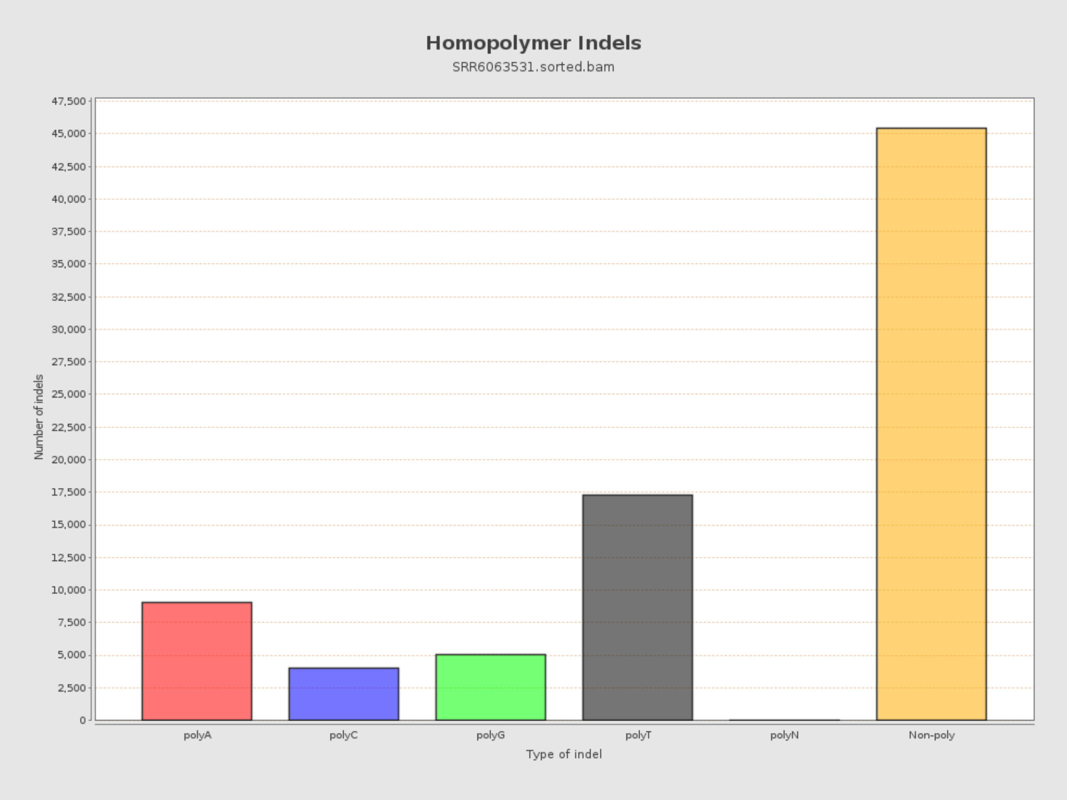
9. Results : Mapped Reads GC-content Distribution



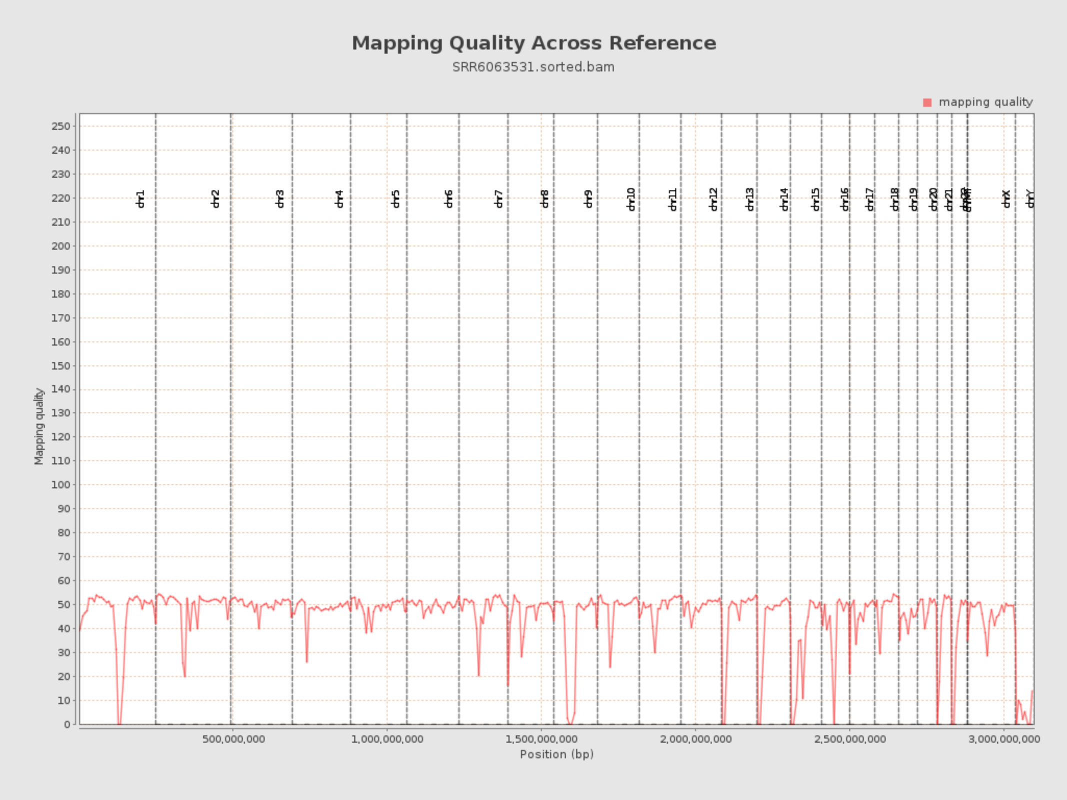
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram