Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/13 23:26:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004062.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_SRR6004062 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004062.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 13 23:26:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004062.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,306,937
Mapped reads	998,761 / 43.29%
Unmapped reads	1,308,176 / 56.71%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,636 / 0.5%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	168,548 / 7.31%
Duplication rate	12.53%
Clipped reads	637,067 / 27.62%

2.2. ACGT Content

Number/percentage of A's	17,162,031 / 27.74%
Number/percentage of C's	11,020,532 / 17.82%
Number/percentage of T's	20,033,725 / 32.39%
Number/percentage of G's	13,605,736 / 21.99%
Number/percentage of N's	38,909 / 0.06%
GC Percentage	39.81%

2.3. Coverage

Mean	0.02

Standard Deviation	0.2965

2.4. Mapping Quality

Mean Mapping Quality	45.59

2.5. Mismatches and indels

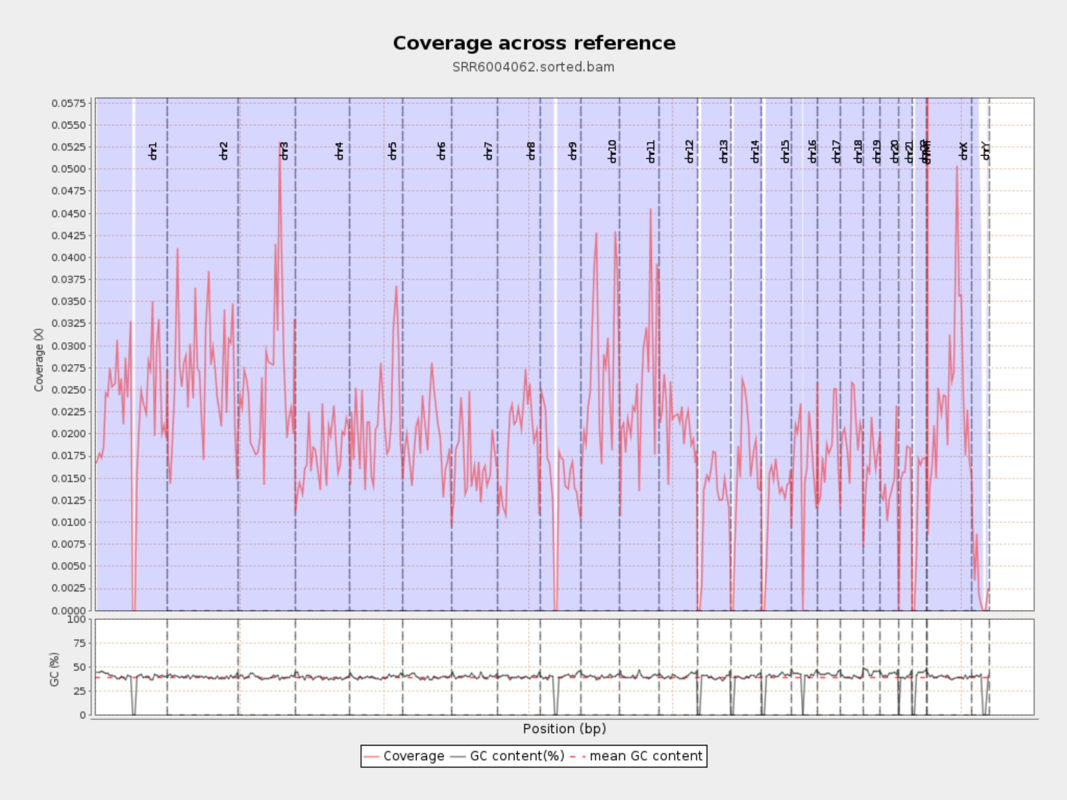
General error rate	0.96%
Mismatches	585,376
Insertions	4,482
Mapped reads with at least one insertion	0.44%
Deletions	21,161
Mapped reads with at least one deletion	2.09%
Homopolymer indels	44.64%

2.6. Chromosome stats

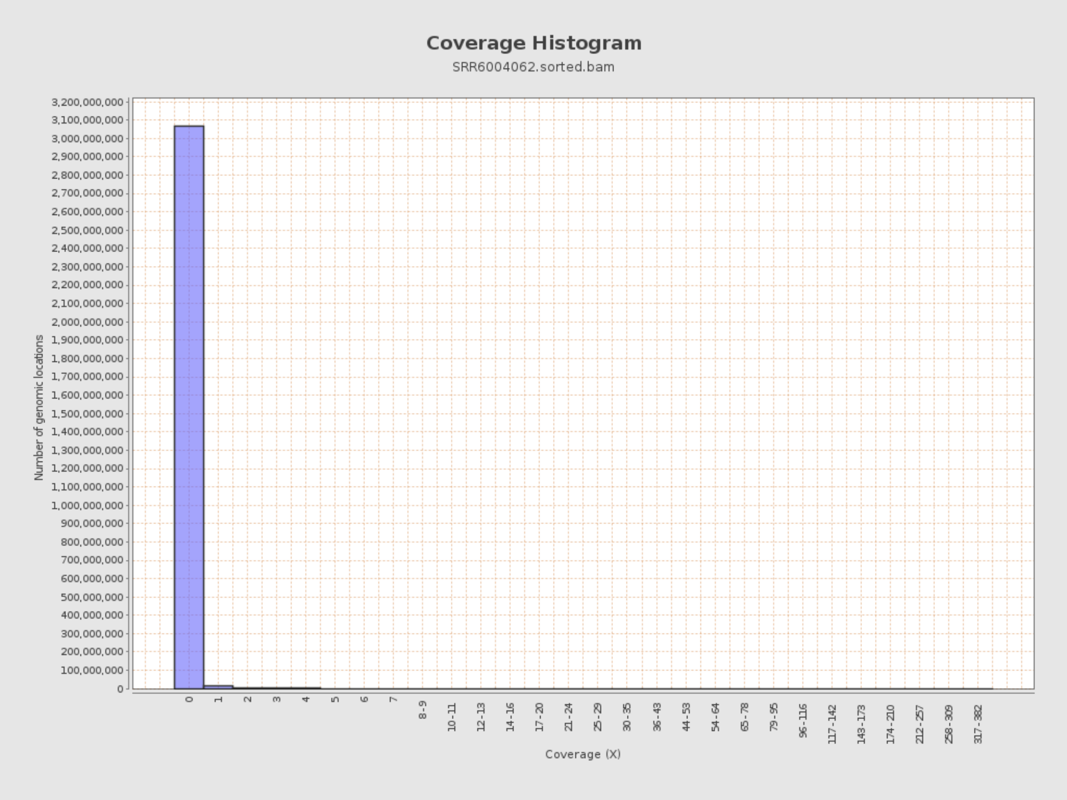
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5672496	0.0228	0.3876
chr2	243199373	6468462	0.0266	0.3527
chr3	198022430	5146731	0.026	0.291
chr4	191154276	3386112	0.0177	0.2503
chr5	180915260	3927529	0.0217	0.2672
chr6	171115067	3344570	0.0195	0.2681
chr7	159138663	2648315	0.0166	0.2506

chr8	146364022	2857994	0.0195	0.3132
chr9	141213431	2117907	0.015	0.2357
chr10	135534747	3720380	0.0274	0.314
chr11	135006516	3398422	0.0252	0.3016
chr12	133851895	2848819	0.0213	0.2602
chr13	115169878	1384547	0.012	0.1904
chr14	107349540	1705016	0.0159	0.2561
chr15	102531392	1224370	0.0119	0.2512
chr16	90354753	1464858	0.0162	0.2321
chr17	81195210	1427386	0.0176	0.2407
chr18	78077248	1594091	0.0204	0.3266
chr19	59128983	992085	0.0168	0.2658
chr20	63025520	893323	0.0142	0.2093
chr21	48129895	713986	0.0148	0.2203
chr22	51304566	595834	0.0116	0.1854
chrMT	16571	462972	27.9387	24.6435
chrX	155270560	3717611	0.0239	0.2924
chrY	59373566	182687	0.0031	0.1035

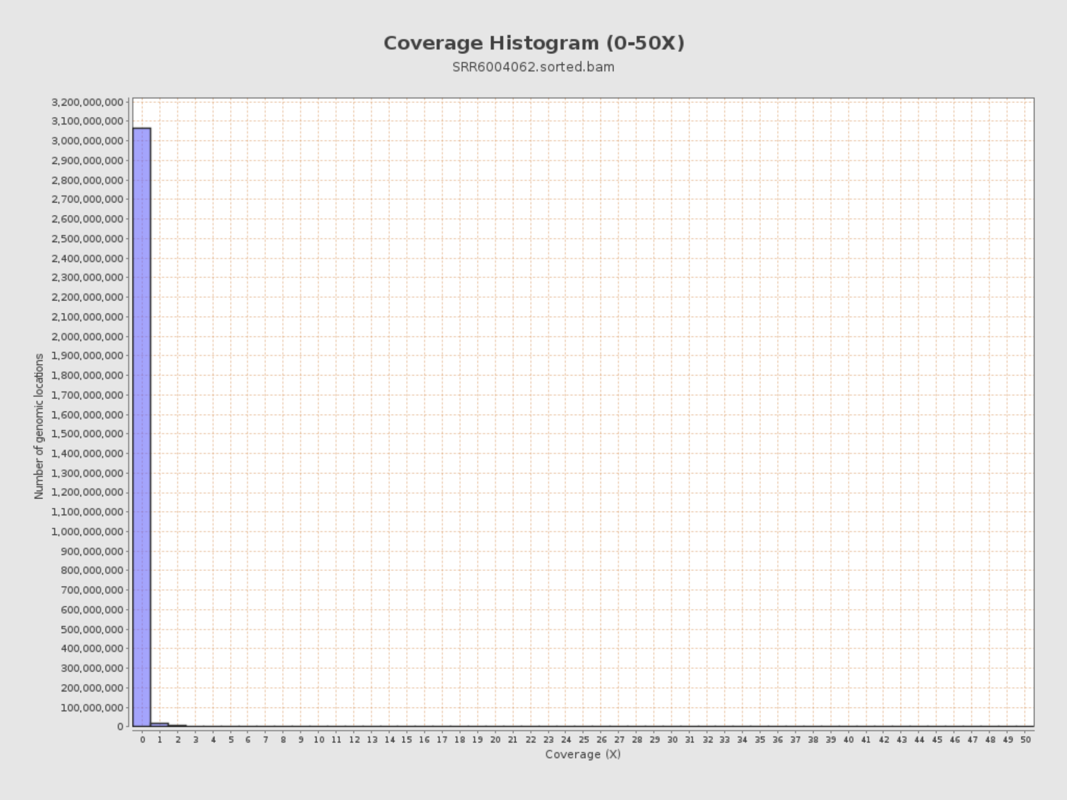
3. Results : Coverage across reference



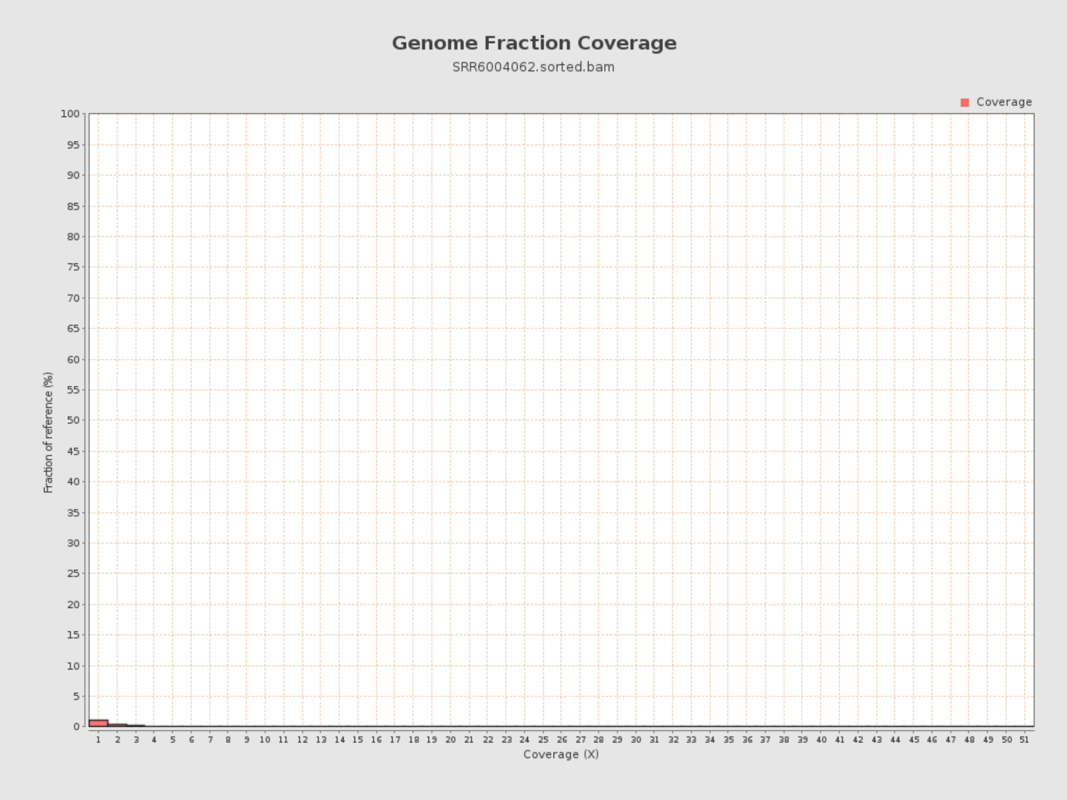
4. Results : Coverage Histogram



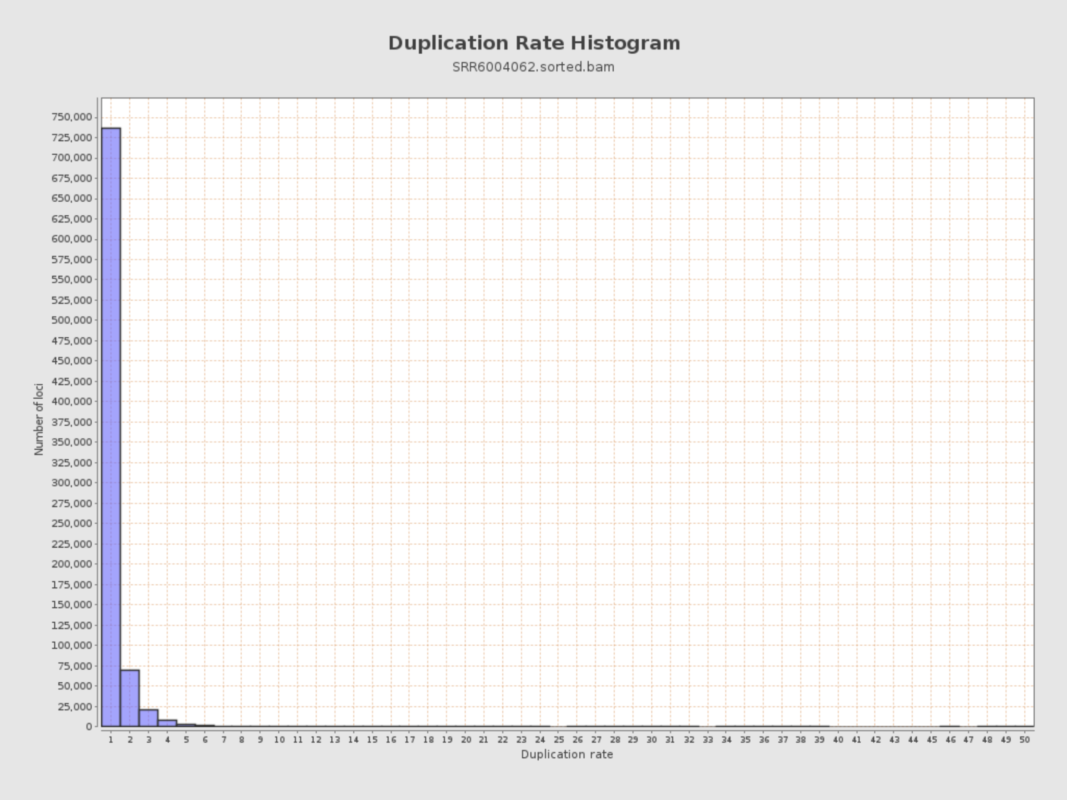
5. Results : Coverage Histogram (0-50X)



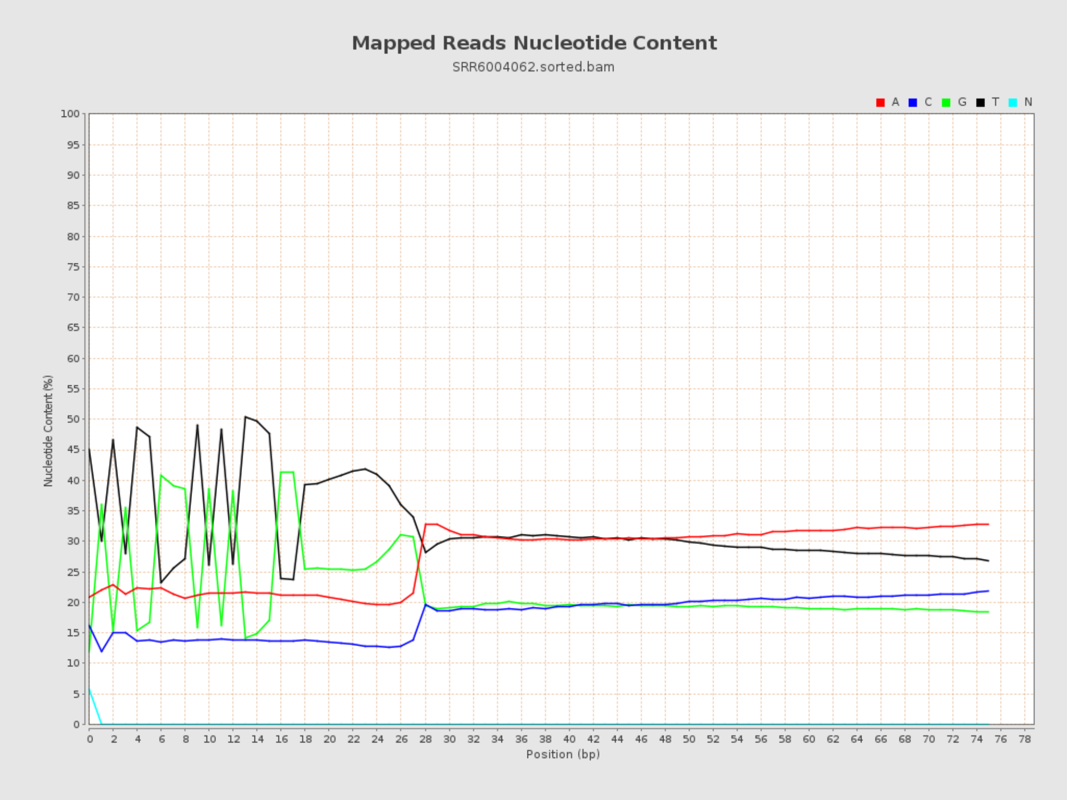
6. Results : Genome Fraction Coverage



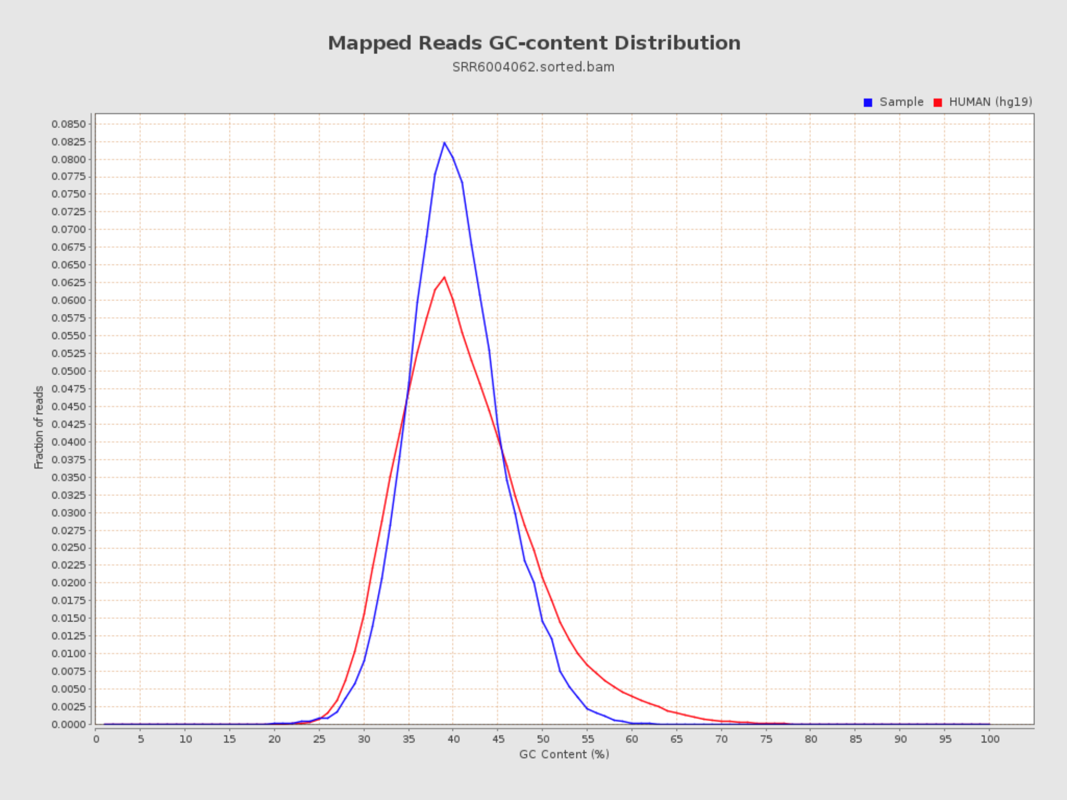
7. Results : Duplication Rate Histogram



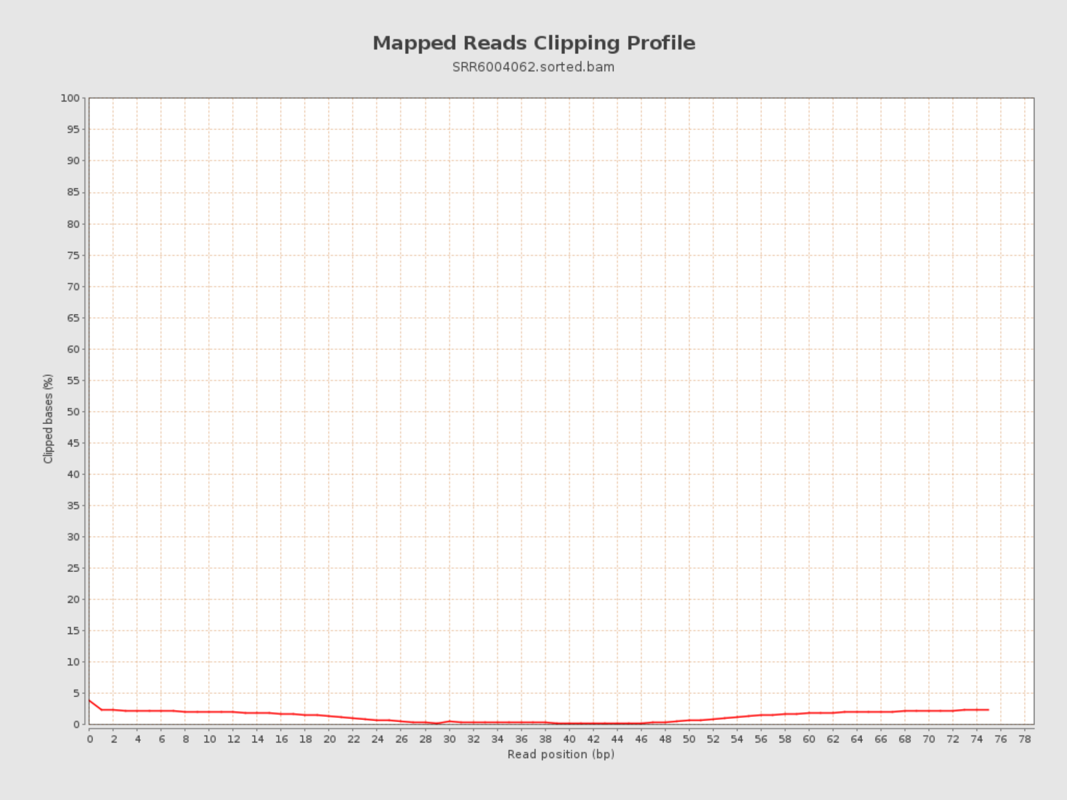
8. Results : Mapped Reads Nucleotide Content



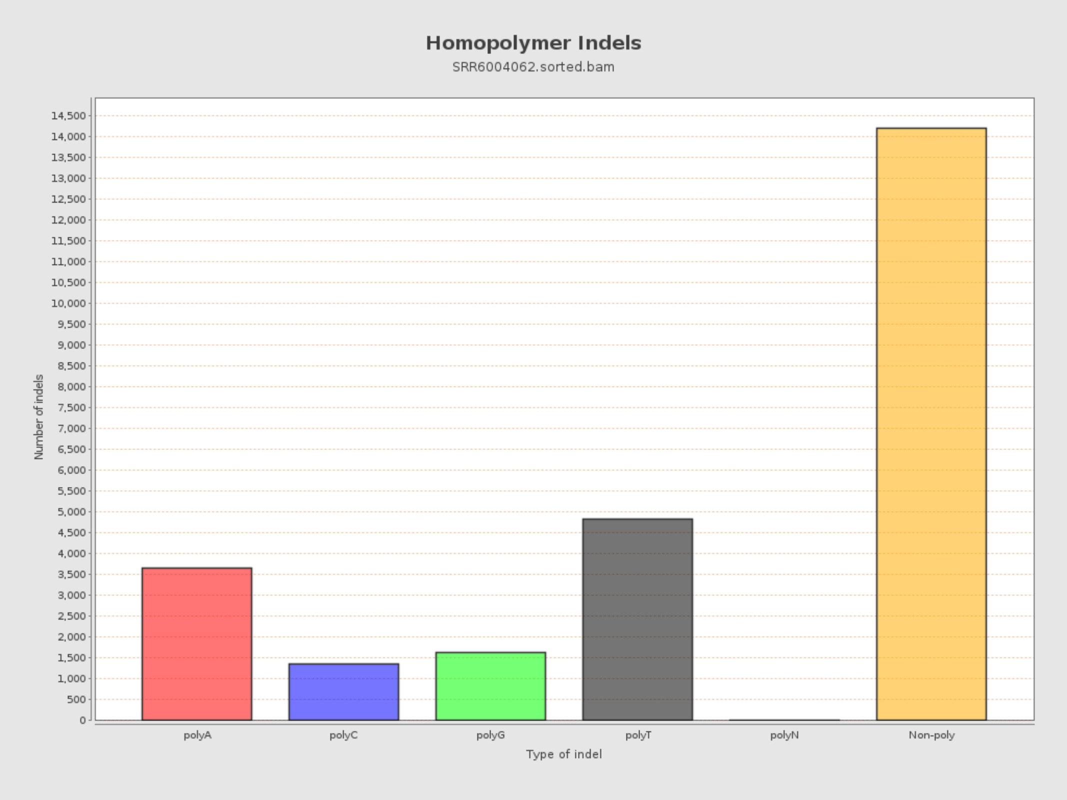
9. Results : Mapped Reads GC-content Distribution



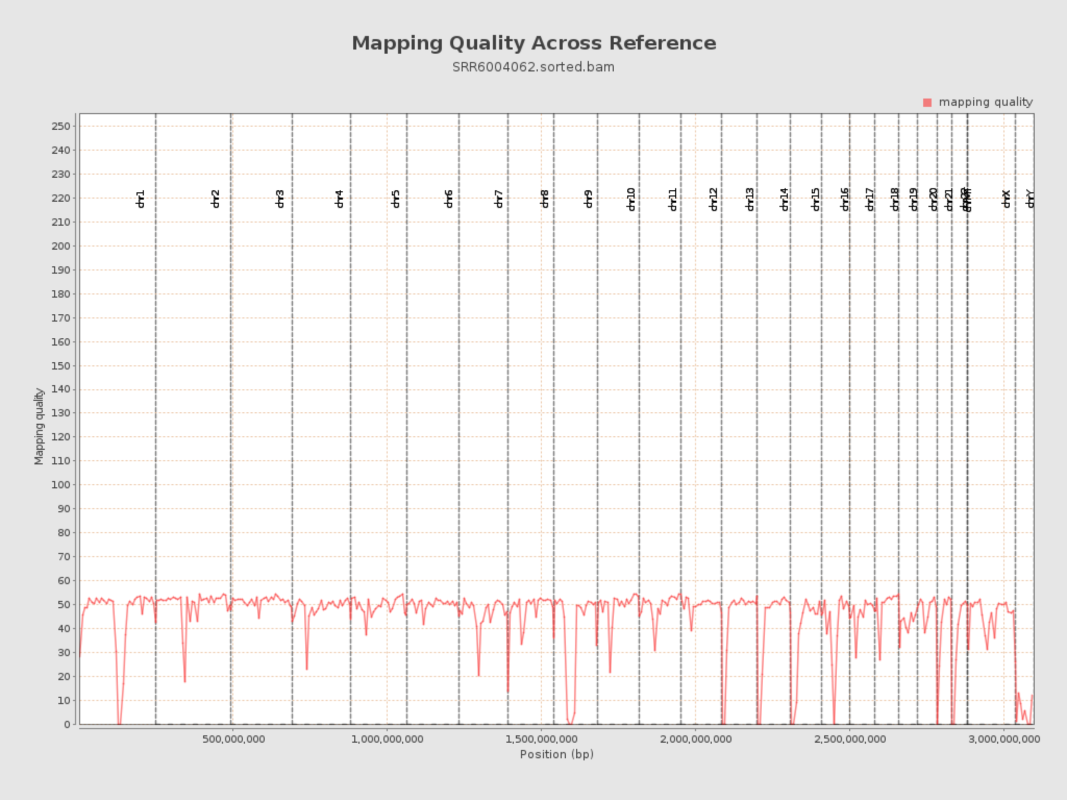
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram