Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 12:06:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080953.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_SRR3080953 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080953.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 12:06:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080953.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,543,359
Mapped reads	4,130,080 / 90.9%
Unmapped reads	413,279 / 9.1%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	53,667 / 1.18%
Read min/max/mean length	30 / 76 / 76.42
Duplicated reads (estimated)	224,728 / 4.95%
Duplication rate	3.87%
Clipped reads	1,424,876 / 31.36%

2.2. ACGT Content

Number/percentage of A's	82,804,906 / 28.98%
Number/percentage of C's	51,595,098 / 18.06%
Number/percentage of T's	90,267,630 / 31.6%
Number/percentage of G's	59,642,551 / 20.88%
Number/percentage of N's	1,390,560 / 0.49%
GC Percentage	38.94%

2.3. Coverage

Mean	0.0923

Standard Deviation	0.8471

2.4. Mapping Quality

Mean Mapping Quality	46.93

2.5. Mismatches and indels

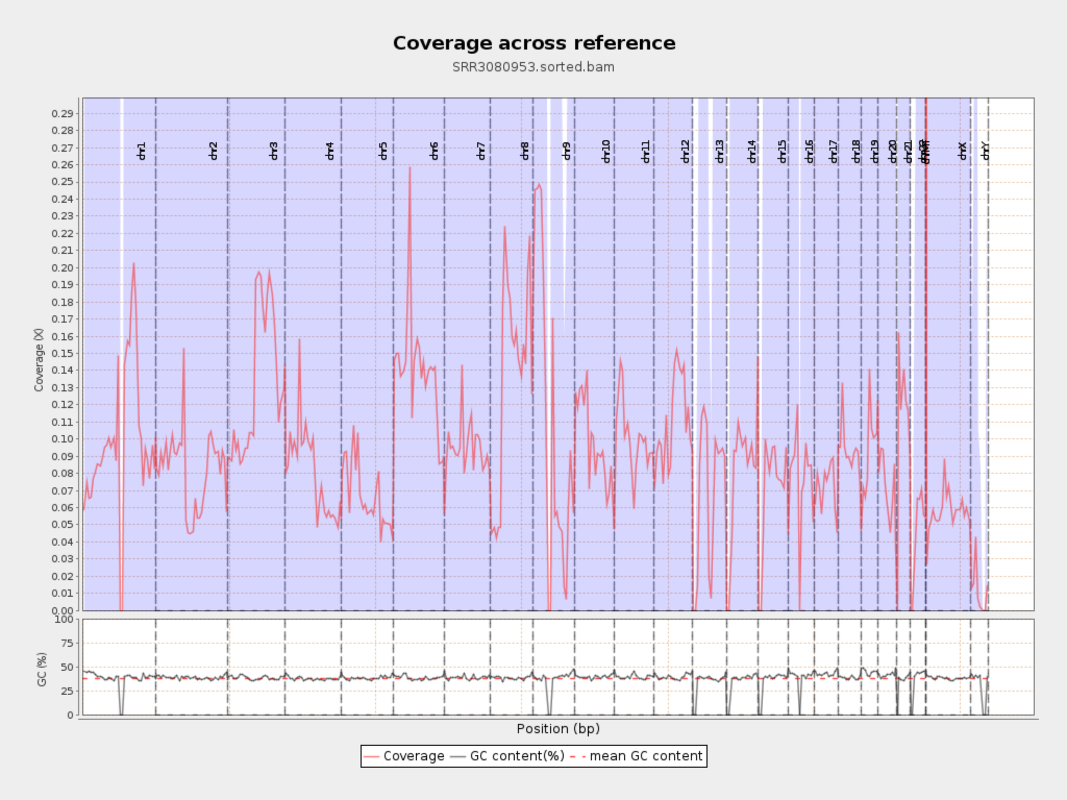
General error rate	1.18%
Mismatches	3,342,999
Insertions	22,955
Mapped reads with at least one insertion	0.55%
Deletions	65,717
Mapped reads with at least one deletion	1.57%
Homopolymer indels	48.94%

2.6. Chromosome stats

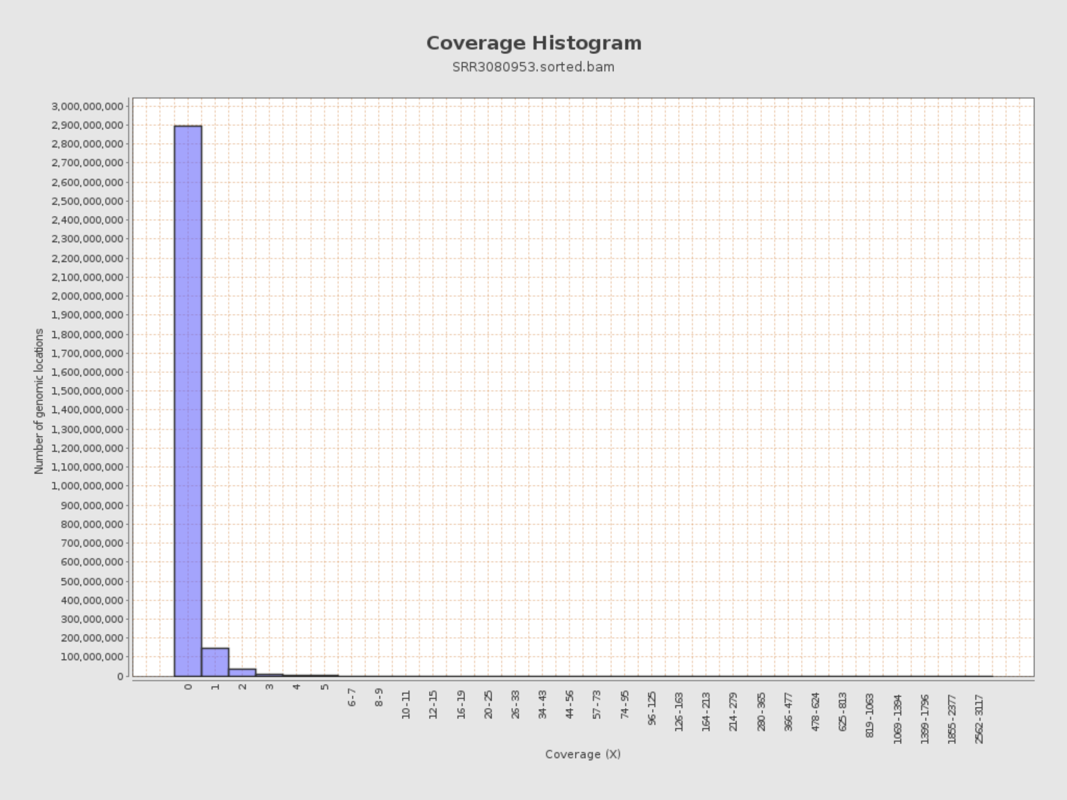
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	24534223	0.0984	1.2851
chr2	243199373	19992271	0.0822	0.7351
chr3	198022430	26054105	0.1316	0.4852
chr4	191154276	15412867	0.0806	0.436
chr5	180915260	12299993	0.068	0.358
chr6	171115067	24307858	0.1421	0.8814
chr7	159138663	15104194	0.0949	0.8437

chr8	146364022	20095042	0.1373	1.9971
chr9	141213431	15138091	0.1072	0.9578
chr10	135534747	13250695	0.0978	0.686
chr11	135006516	13553862	0.1004	0.6463
chr12	133851895	14766333	0.1103	0.4791
chr13	115169878	7771674	0.0675	0.3434
chr14	107349540	8494287	0.0791	0.5382
chr15	102531392	7236387	0.0706	0.3503
chr16	90354753	6771481	0.0749	0.5173
chr17	81195210	5921336	0.0729	0.4038
chr18	78077248	7393670	0.0947	1.8178
chr19	59128983	5538570	0.0937	0.9163
chr20	63025520	4592137	0.0729	0.4053
chr21	48129895	5538107	0.1151	0.5914
chr22	51304566	2294969	0.0447	0.272
chrMT	16571	58915	3.5553	3.0789
chrX	155270560	8977165	0.0578	0.376
chrY	59373566	711645	0.012	0.2669

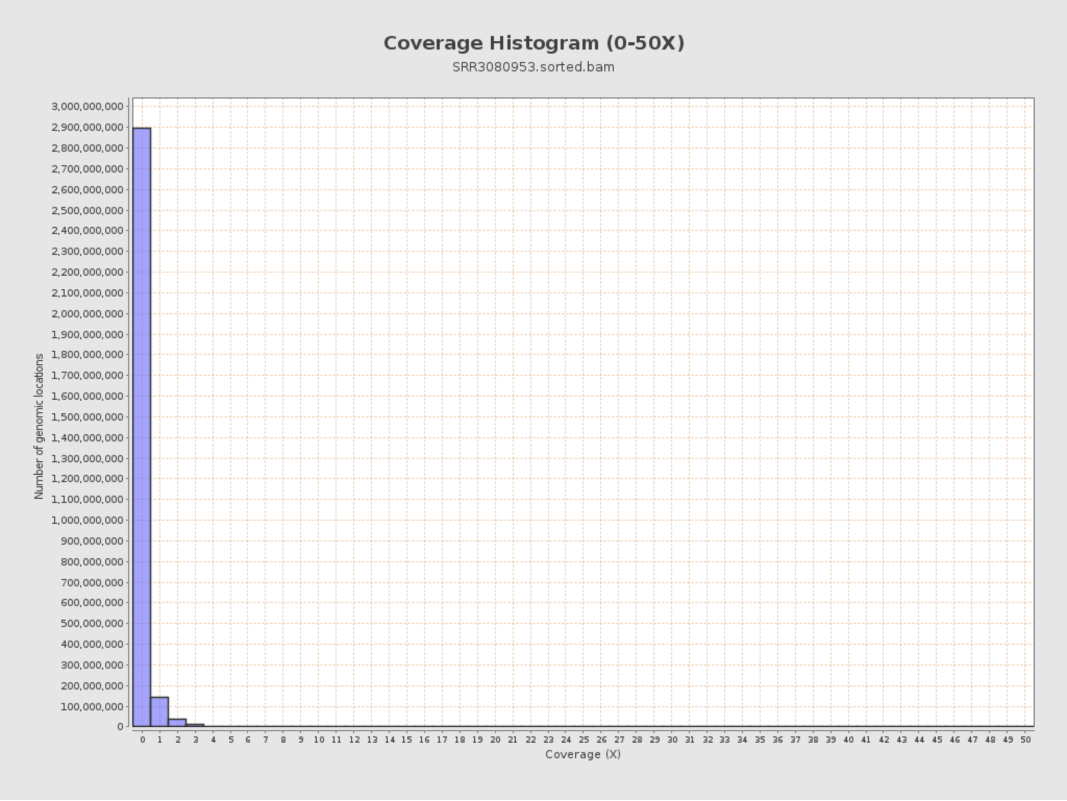
3. Results : Coverage across reference



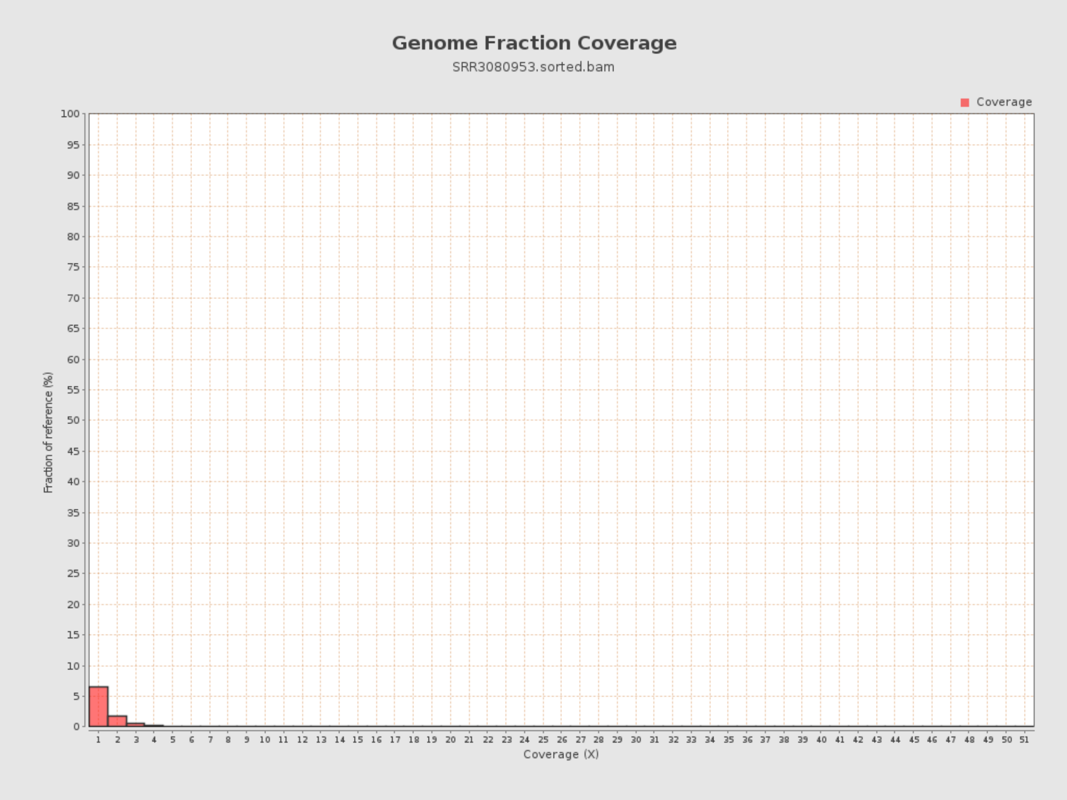
4. Results : Coverage Histogram



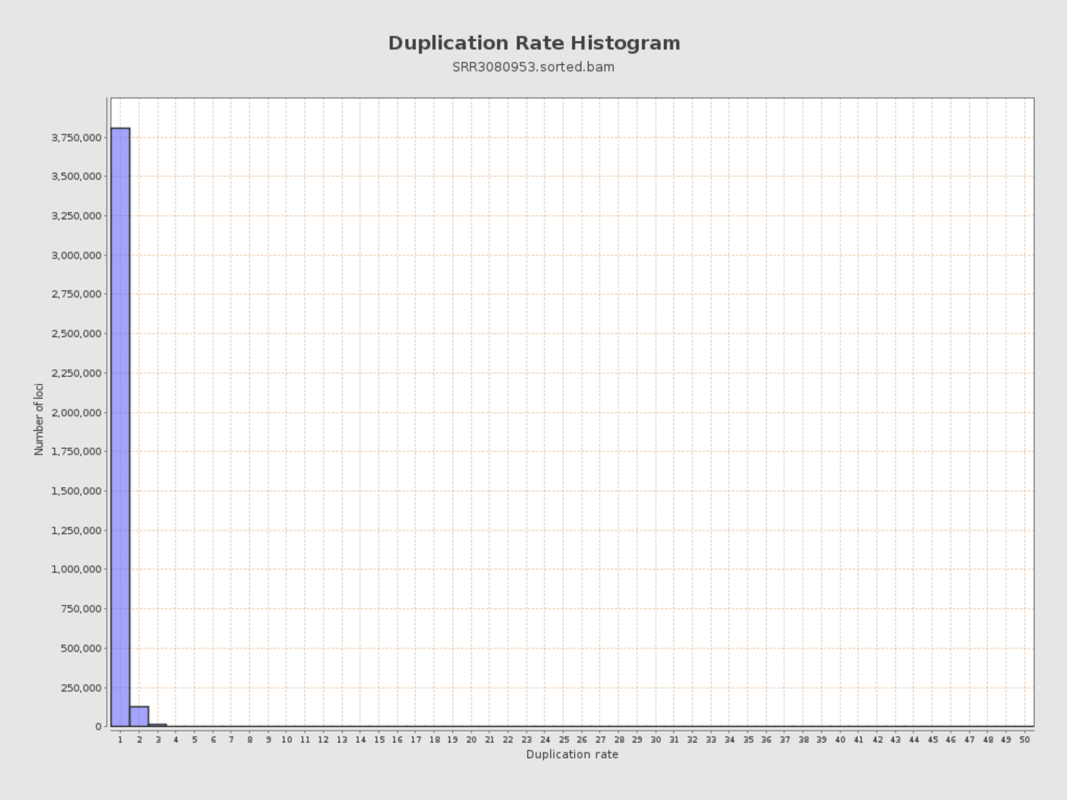
5. Results : Coverage Histogram (0-50X)



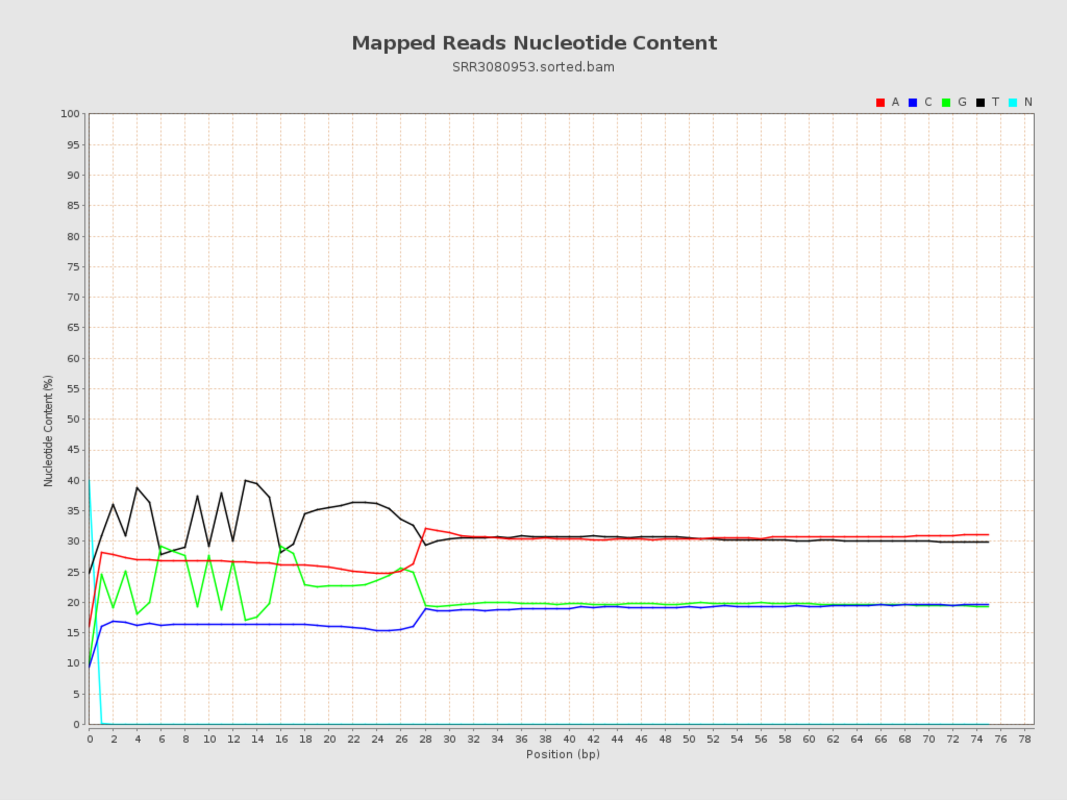
6. Results : Genome Fraction Coverage



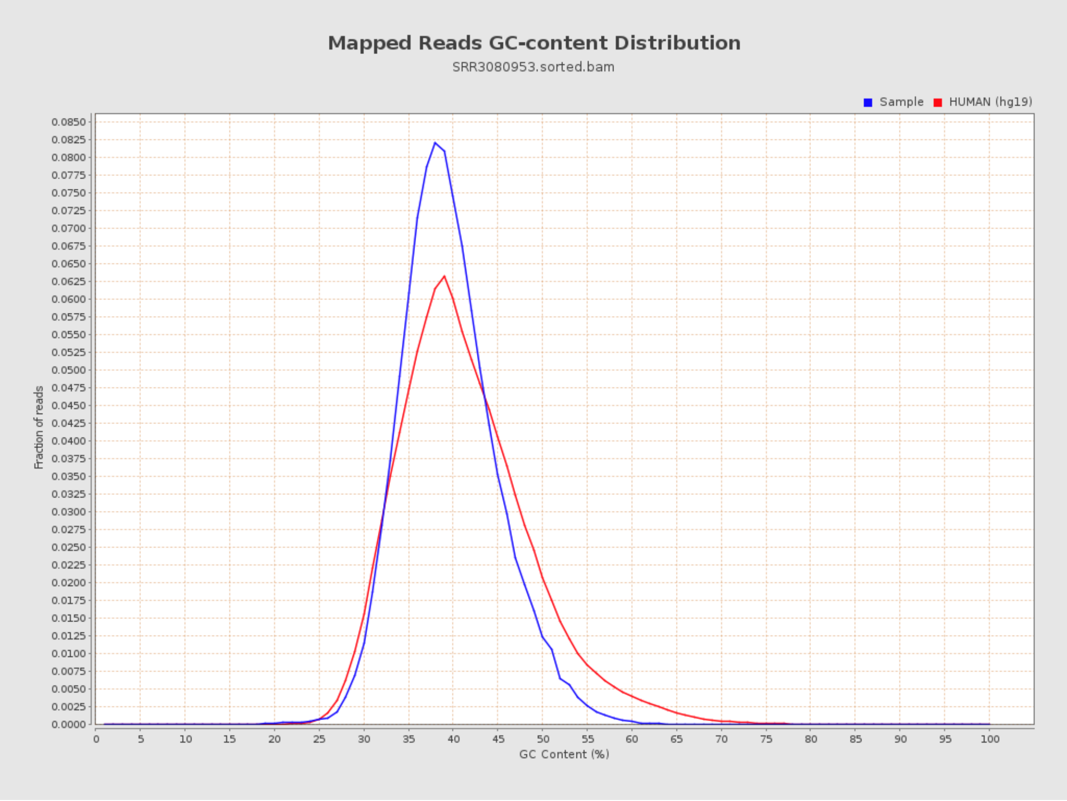
7. Results : Duplication Rate Histogram



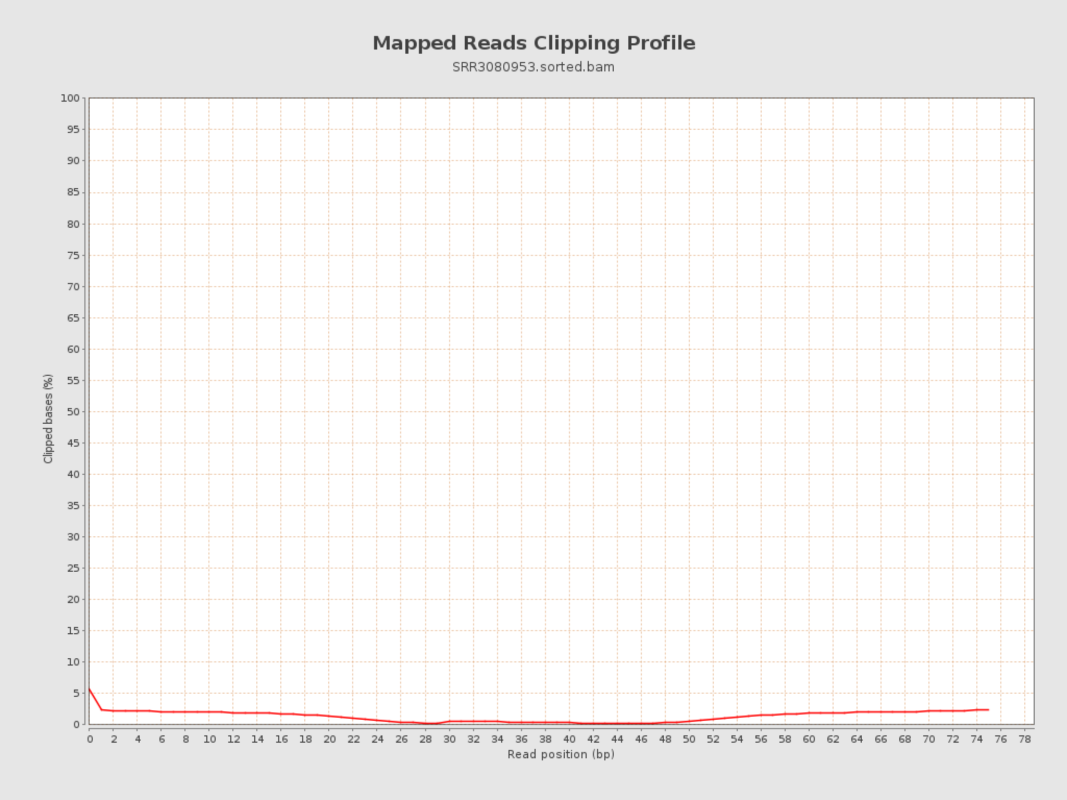
8. Results : Mapped Reads Nucleotide Content



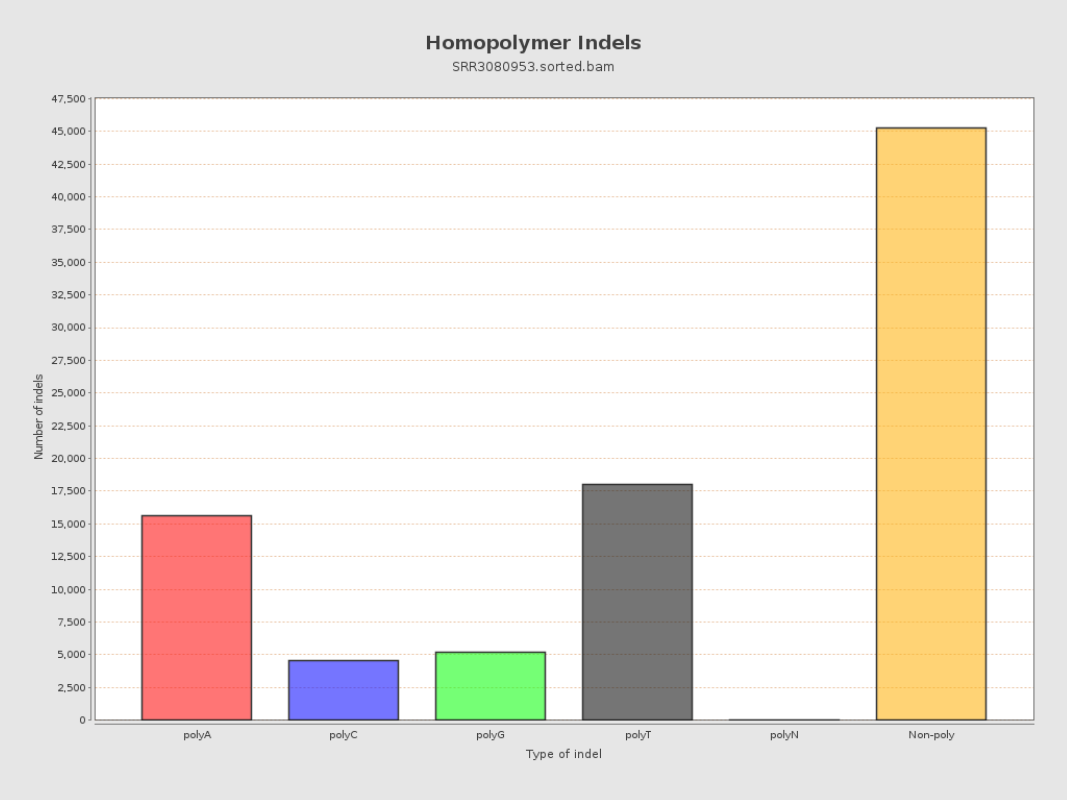
9. Results : Mapped Reads GC-content Distribution



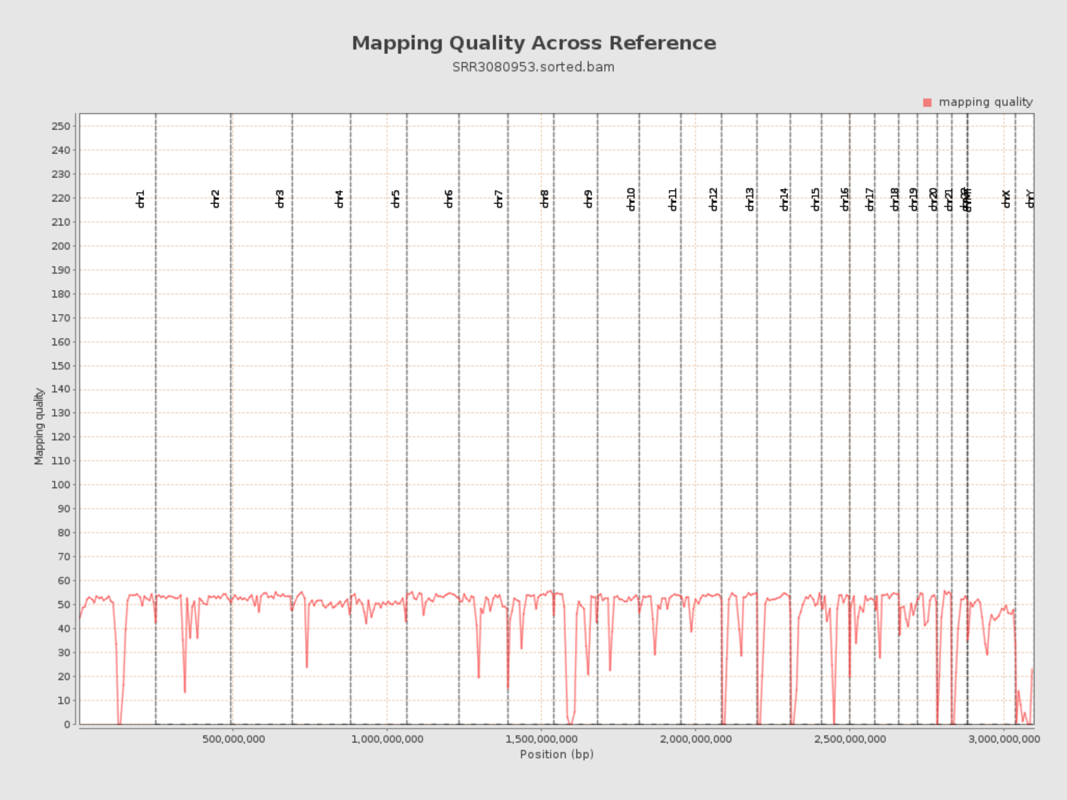
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram