Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/01 08:22:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472820.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_SRR3472820 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472820.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 01 08:22:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472820.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,650,039
Mapped reads	1,971,586 / 74.4%
Unmapped reads	678,453 / 25.6%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,285 / 0.73%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	128,551 / 4.85%
Duplication rate	4.53%
Clipped reads	1,223,284 / 46.16%

2.2. ACGT Content

Number/percentage of A's	32,784,093 / 26.7%
Number/percentage of C's	24,907,526 / 20.28%
Number/percentage of T's	35,804,470 / 29.16%
Number/percentage of G's	29,292,777 / 23.86%
Number/percentage of N's	2,235 / 0%
GC Percentage	44.14%

2.3. Coverage

Mean	0.0397

Standard Deviation	0.3444

2.4. Mapping Quality

Mean Mapping Quality	42.24

2.5. Mismatches and indels

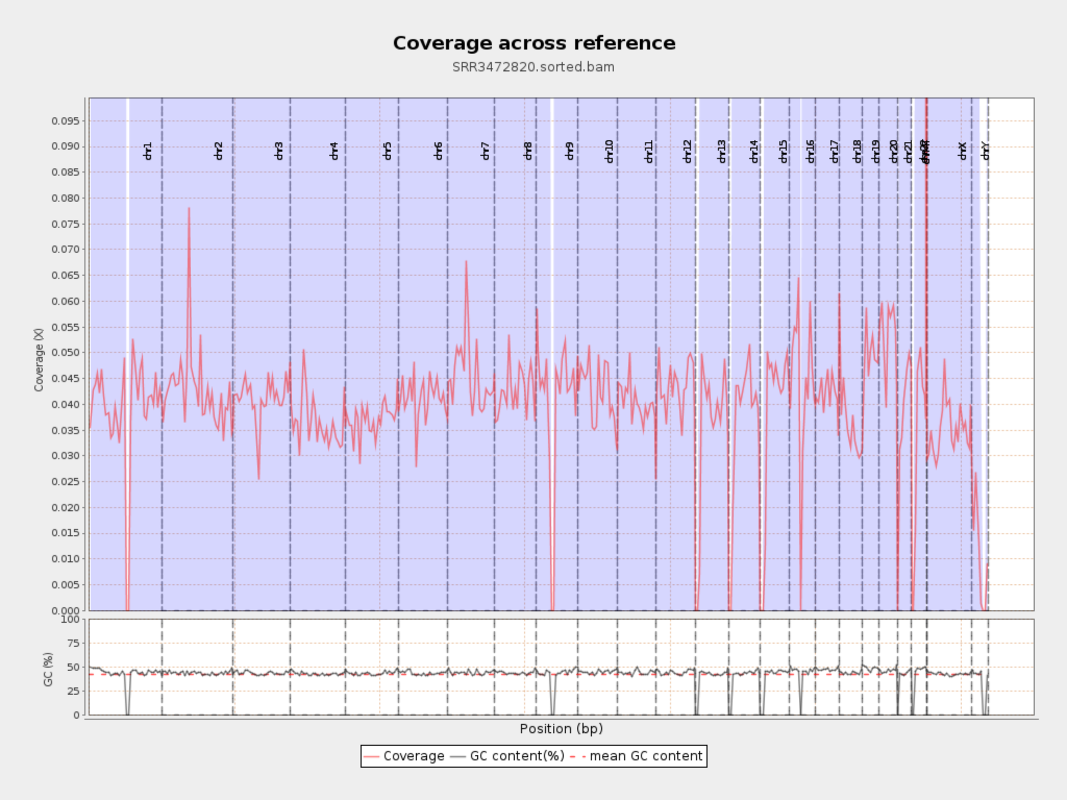
General error rate	0.92%
Mismatches	1,111,559
Insertions	9,342
Mapped reads with at least one insertion	0.47%
Deletions	31,312
Mapped reads with at least one deletion	1.57%
Homopolymer indels	45.15%

2.6. Chromosome stats

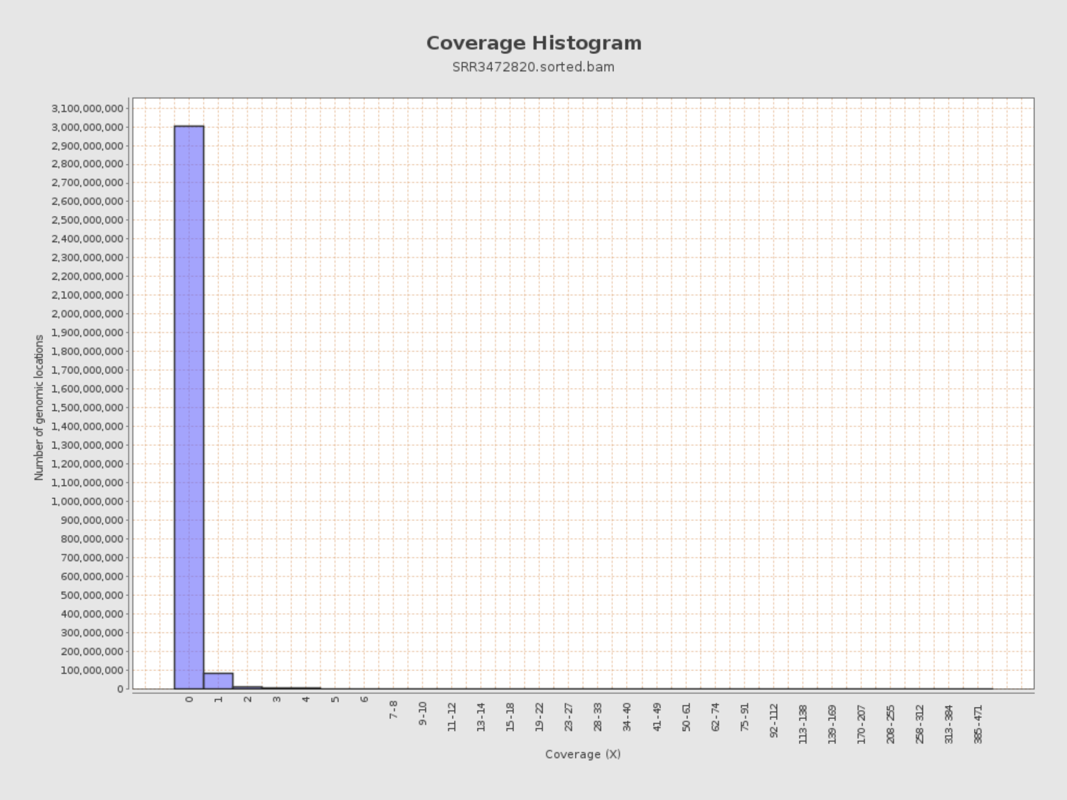
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9670335	0.0388	0.4233
chr2	243199373	10430418	0.0429	0.4417
chr3	198022430	8116939	0.041	0.2686
chr4	191154276	6945107	0.0363	0.2713
chr5	180915260	6685893	0.037	0.2627
chr6	171115067	7052667	0.0412	0.2948
chr7	159138663	7287413	0.0458	0.4683

chr8	146364022	6215600	0.0425	0.3301
chr9	141213431	5583283	0.0395	0.36
chr10	135534747	5757595	0.0425	0.3329
chr11	135006516	5436660	0.0403	0.3749
chr12	133851895	5832509	0.0436	0.2977
chr13	115169878	3992704	0.0347	0.26
chr14	107349540	3858881	0.0359	0.2941
chr15	102531392	3813487	0.0372	0.2916
chr16	90354753	3996237	0.0442	0.3044
chr17	81195210	3413129	0.042	0.3002
chr18	78077248	2849034	0.0365	0.5538
chr19	59128983	2916808	0.0493	0.3805
chr20	63025520	3386000	0.0537	0.3309
chr21	48129895	1801543	0.0374	0.2817
chr22	51304566	1607821	0.0313	0.2481
chrMT	16571	157066	9.4784	7.04
chrX	155270560	5427869	0.035	0.2861
chrY	59373566	612825	0.0103	0.1578

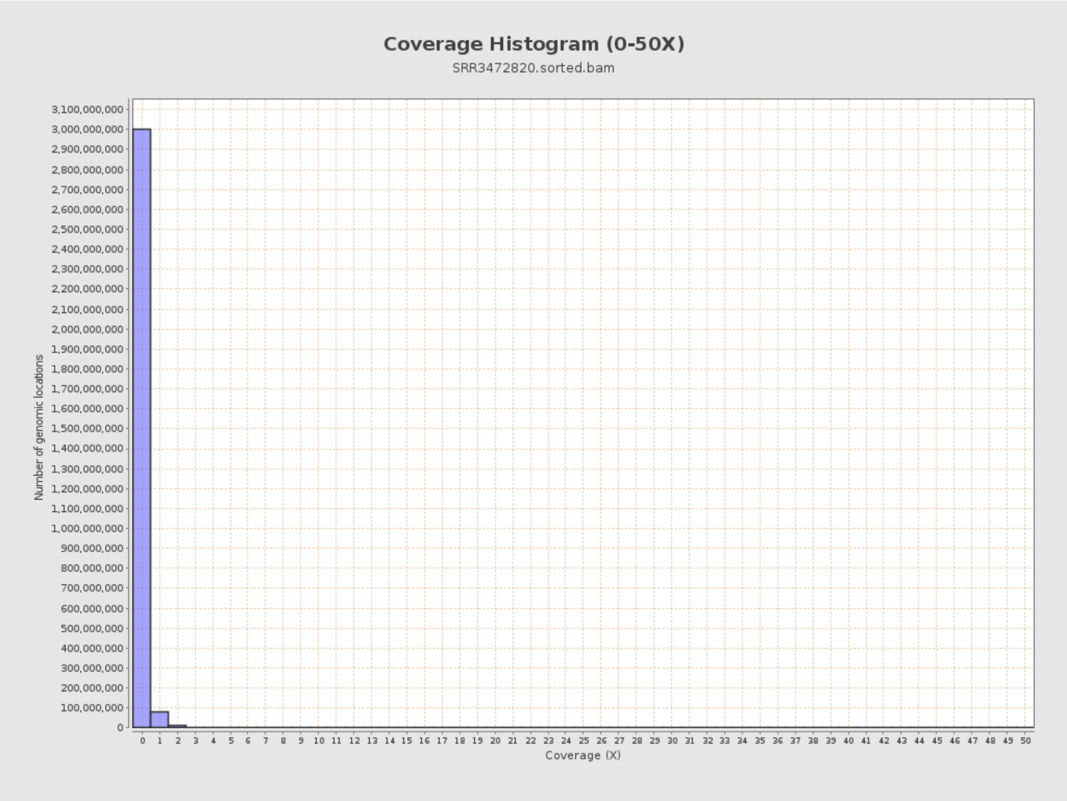
3. Results : Coverage across reference



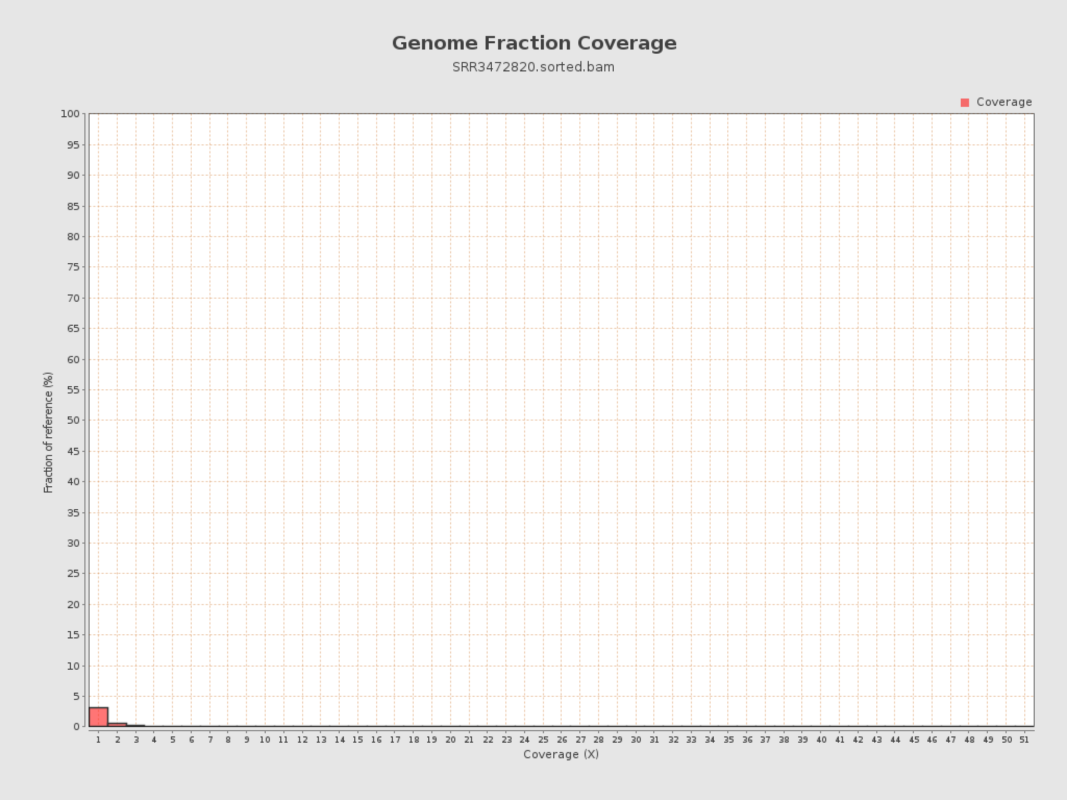
4. Results : Coverage Histogram



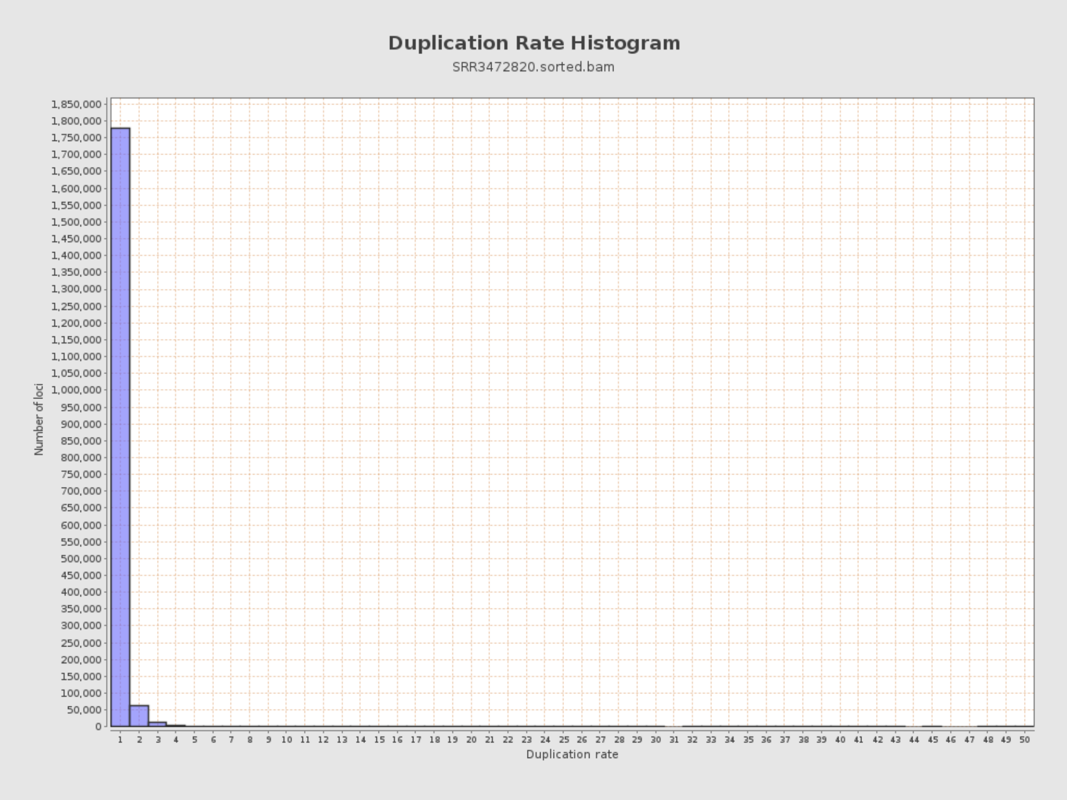
5. Results : Coverage Histogram (0-50X)



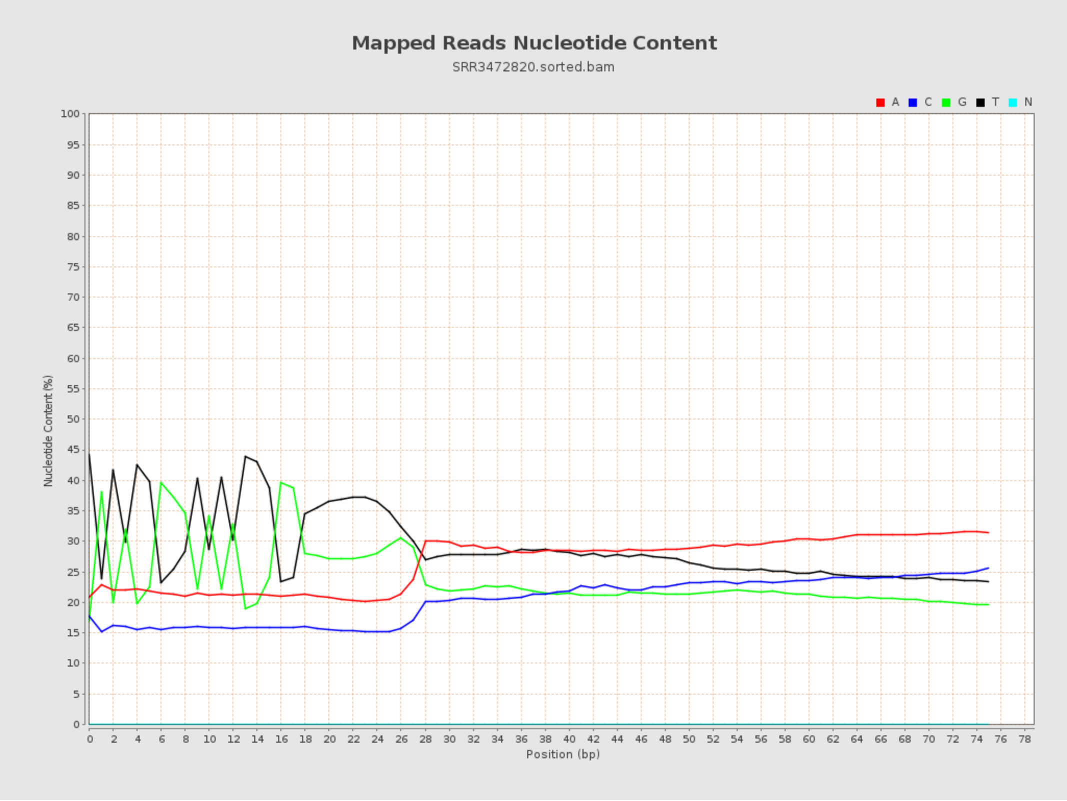
6. Results : Genome Fraction Coverage



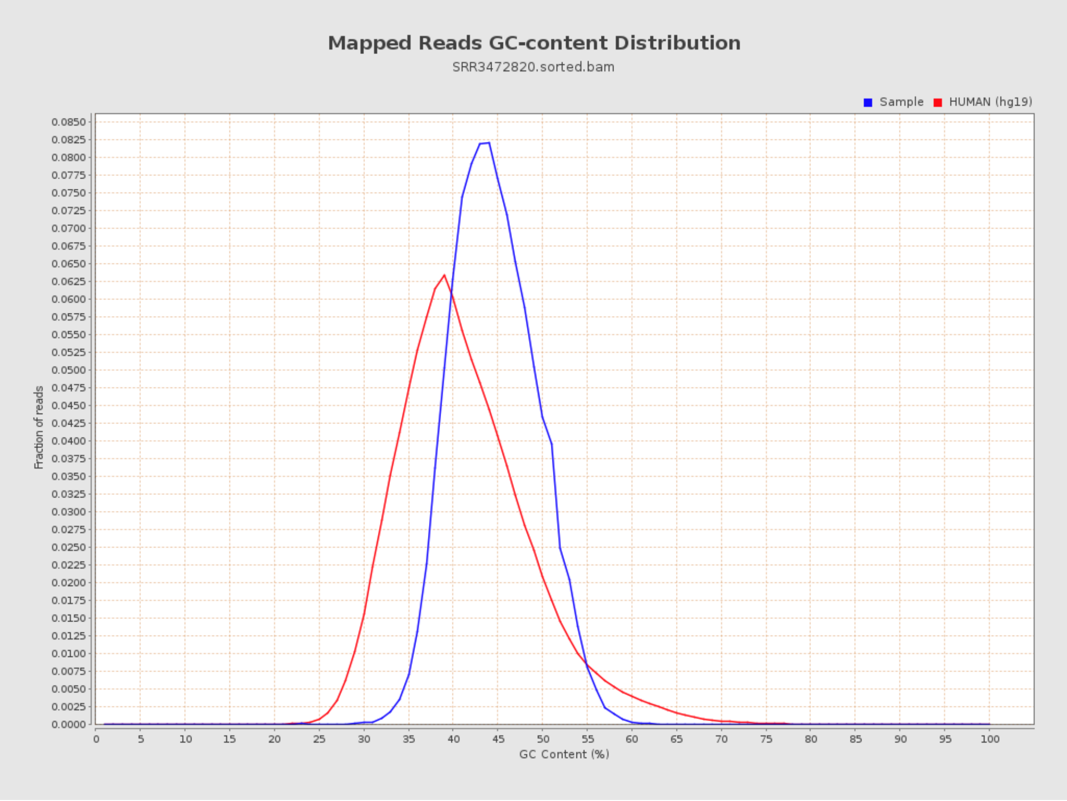
7. Results : Duplication Rate Histogram



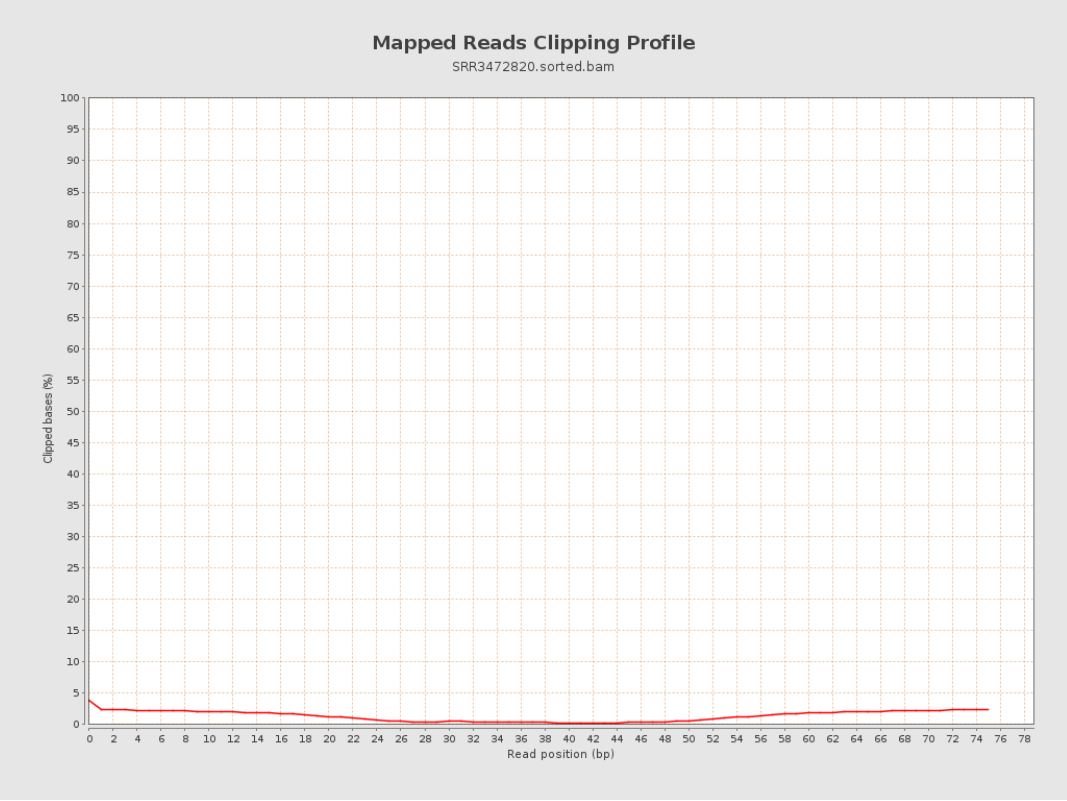
8. Results : Mapped Reads Nucleotide Content



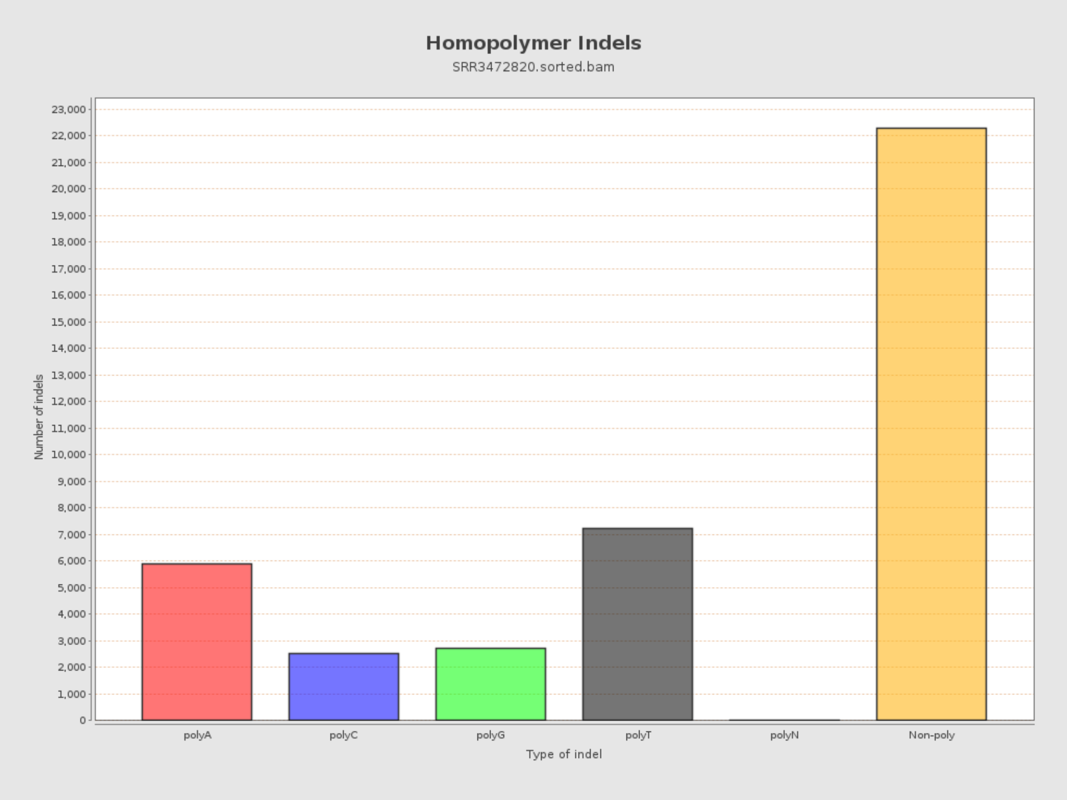
9. Results : Mapped Reads GC-content Distribution



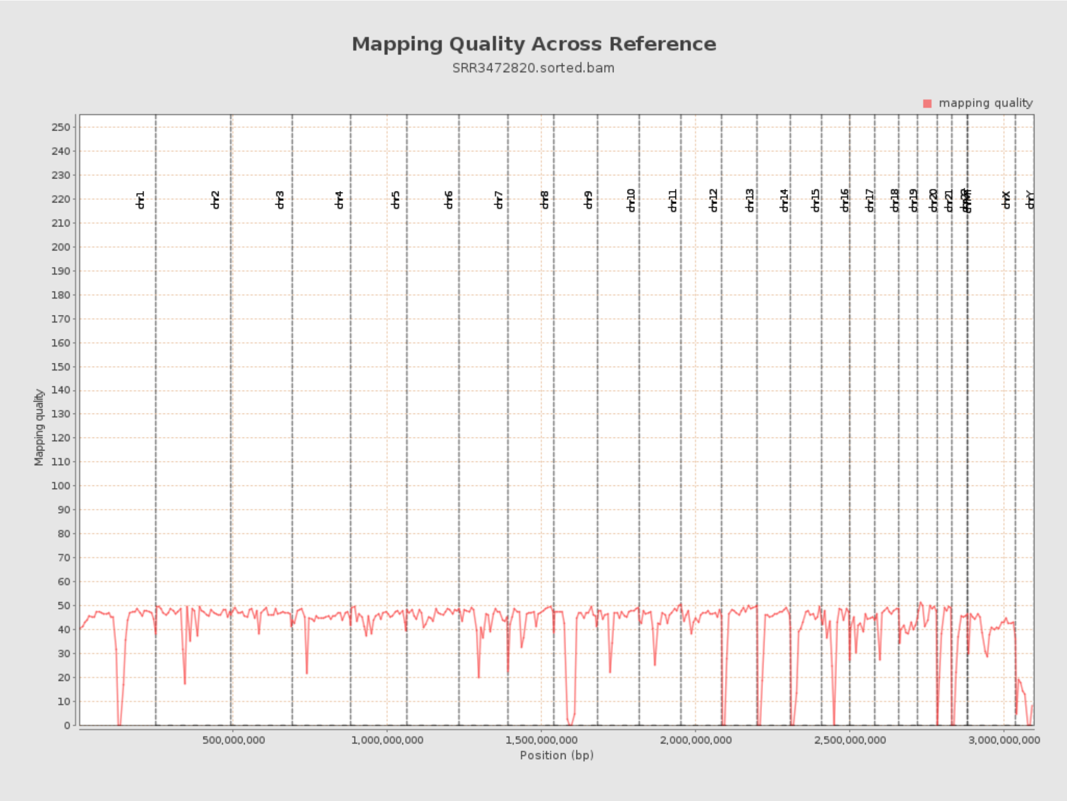
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram