Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 10:59:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080910.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_SRR3080910 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080910.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 10:59:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080910.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,895,997
Mapped reads	3,530,986 / 90.63%
Unmapped reads	365,011 / 9.37%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	36,263 / 0.93%
Read min/max/mean length	30 / 76 / 76.33
Duplicated reads (estimated)	161,549 / 4.15%
Duplication rate	3.53%
Clipped reads	1,284,454 / 32.97%

2.2. ACGT Content

Number/percentage of A's	69,740,992 / 28.81%
Number/percentage of C's	42,862,596 / 17.7%
Number/percentage of T's	77,808,544 / 32.14%
Number/percentage of G's	50,533,506 / 20.87%
Number/percentage of N's	1,159,582 / 0.48%
GC Percentage	38.58%

2.3. Coverage

Mean	0.0782

Standard Deviation	0.5859

2.4. Mapping Quality

Mean Mapping Quality	47.83

2.5. Mismatches and indels

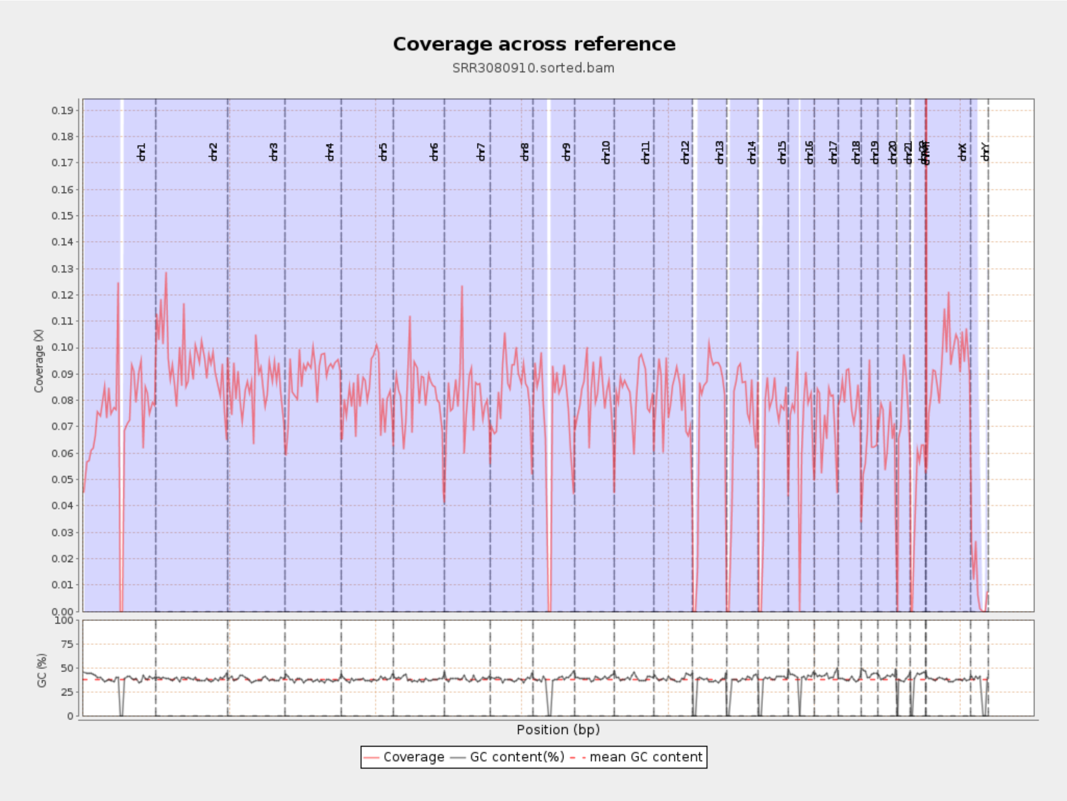
General error rate	1.18%
Mismatches	2,826,798
Insertions	19,261
Mapped reads with at least one insertion	0.54%
Deletions	55,666
Mapped reads with at least one deletion	1.56%
Homopolymer indels	50.12%

2.6. Chromosome stats

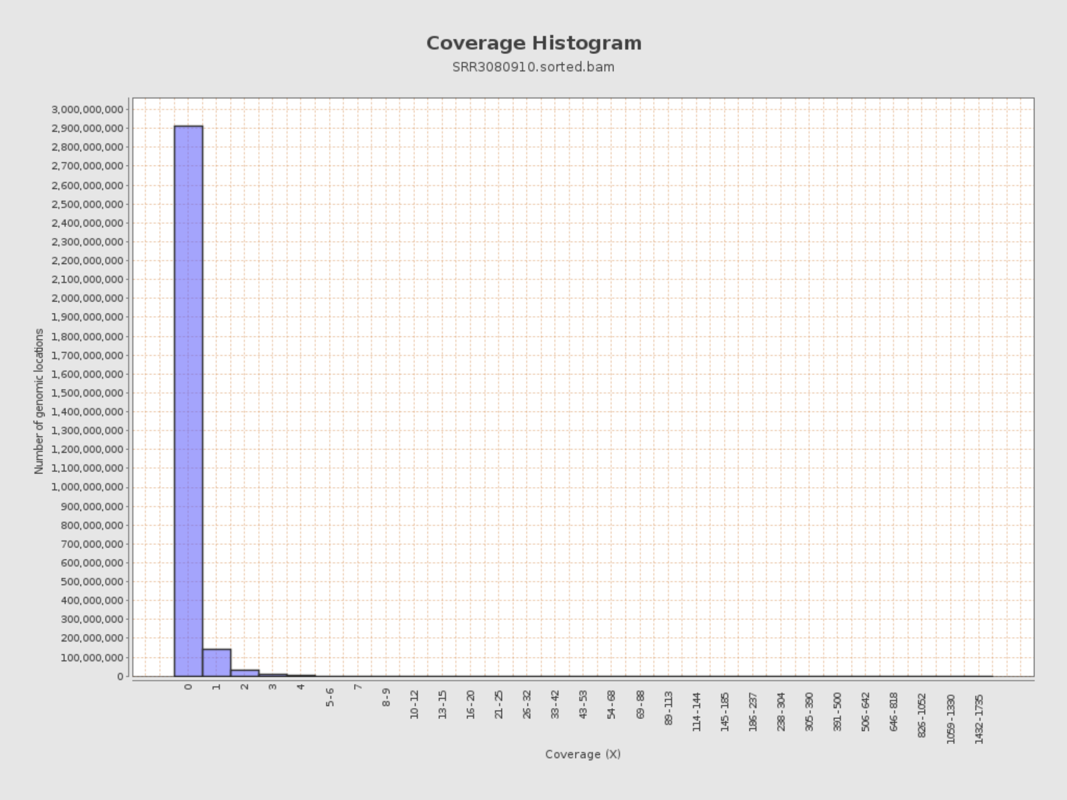
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17955163	0.072	1.0596
chr2	243199373	23056945	0.0948	0.5524
chr3	198022430	16872979	0.0852	0.3663
chr4	191154276	17150672	0.0897	0.397
chr5	180915260	14796019	0.0818	0.3622
chr6	171115067	14177254	0.0829	0.4382
chr7	159138663	12820556	0.0806	0.7962

chr8	146364022	12279101	0.0839	1.0865
chr9	141213431	10263731	0.0727	0.522
chr10	135534747	11123287	0.0821	0.4976
chr11	135006516	11160248	0.0827	0.4738
chr12	133851895	10699021	0.0799	0.3621
chr13	115169878	8602418	0.0747	0.3444
chr14	107349540	7346045	0.0684	0.3602
chr15	102531392	6624798	0.0646	0.3182
chr16	90354753	6226089	0.0689	0.3595
chr17	81195210	5852543	0.0721	0.3985
chr18	78077248	6371315	0.0816	0.9136
chr19	59128983	3804937	0.0643	0.6663
chr20	63025520	4273450	0.0678	0.3467
chr21	48129895	3388707	0.0704	0.3587
chr22	51304566	2202316	0.0429	0.2555
chrMT	16571	13948	0.8417	1.0692
chrX	155270560	14587532	0.0939	0.4256
chrY	59373566	547888	0.0092	0.1781

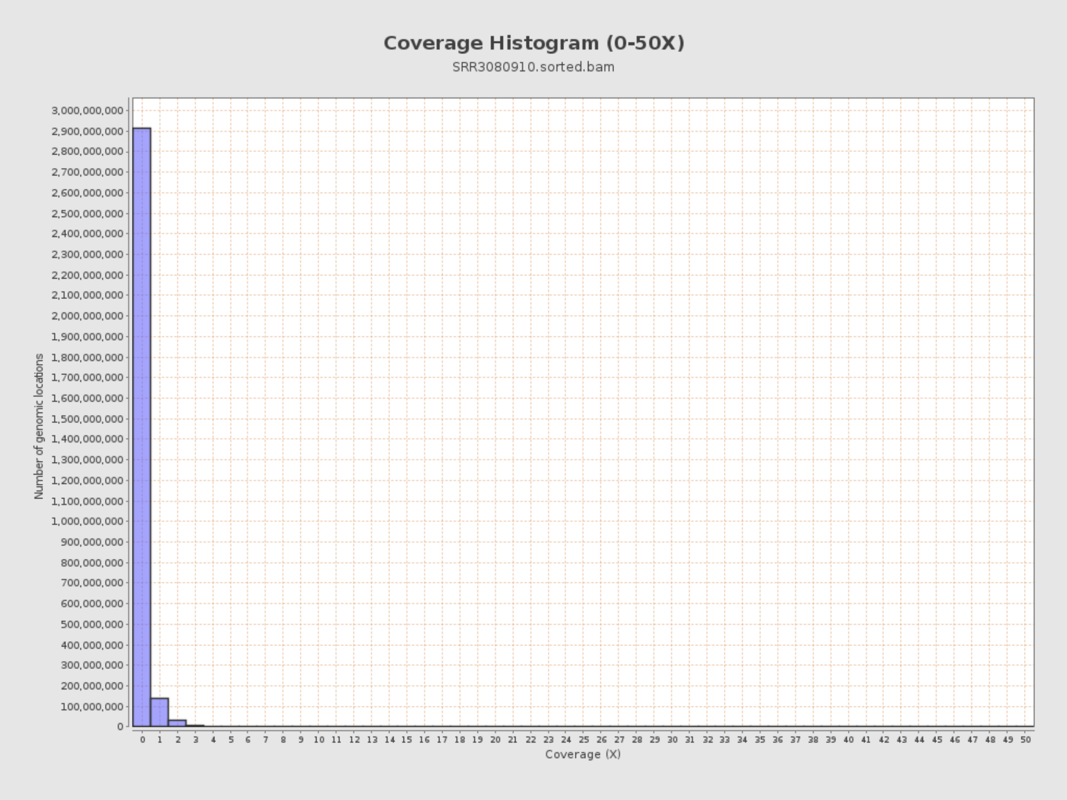
3. Results : Coverage across reference



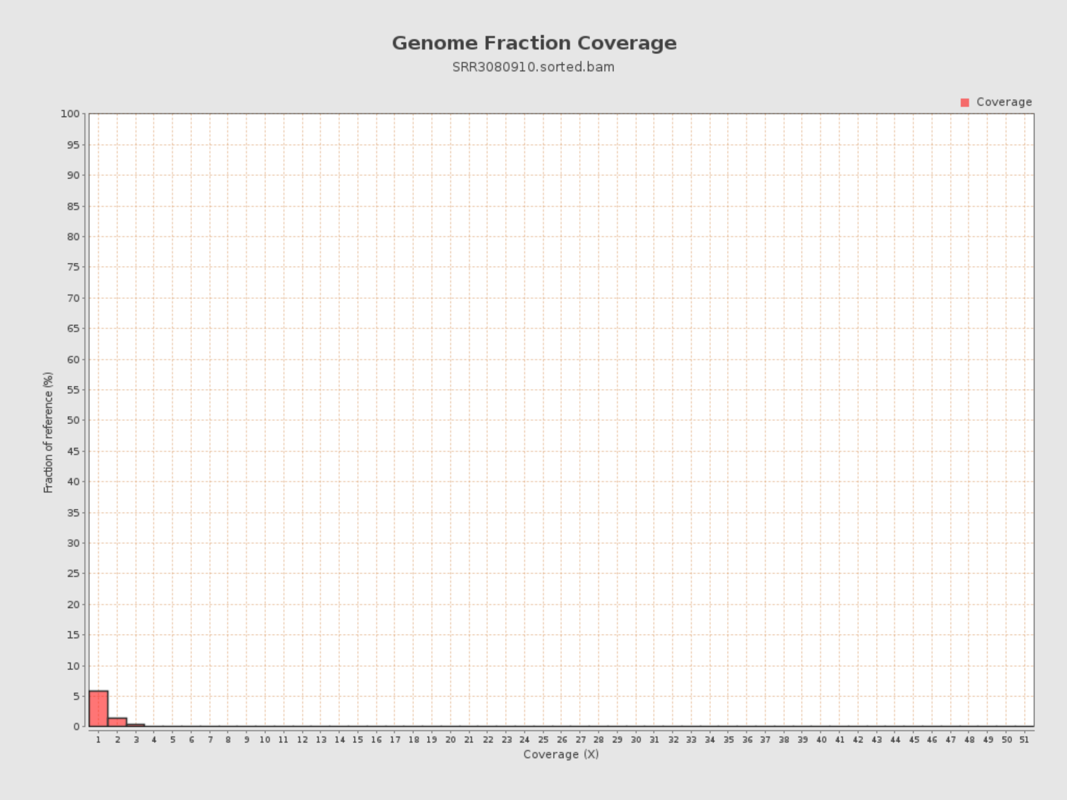
4. Results : Coverage Histogram



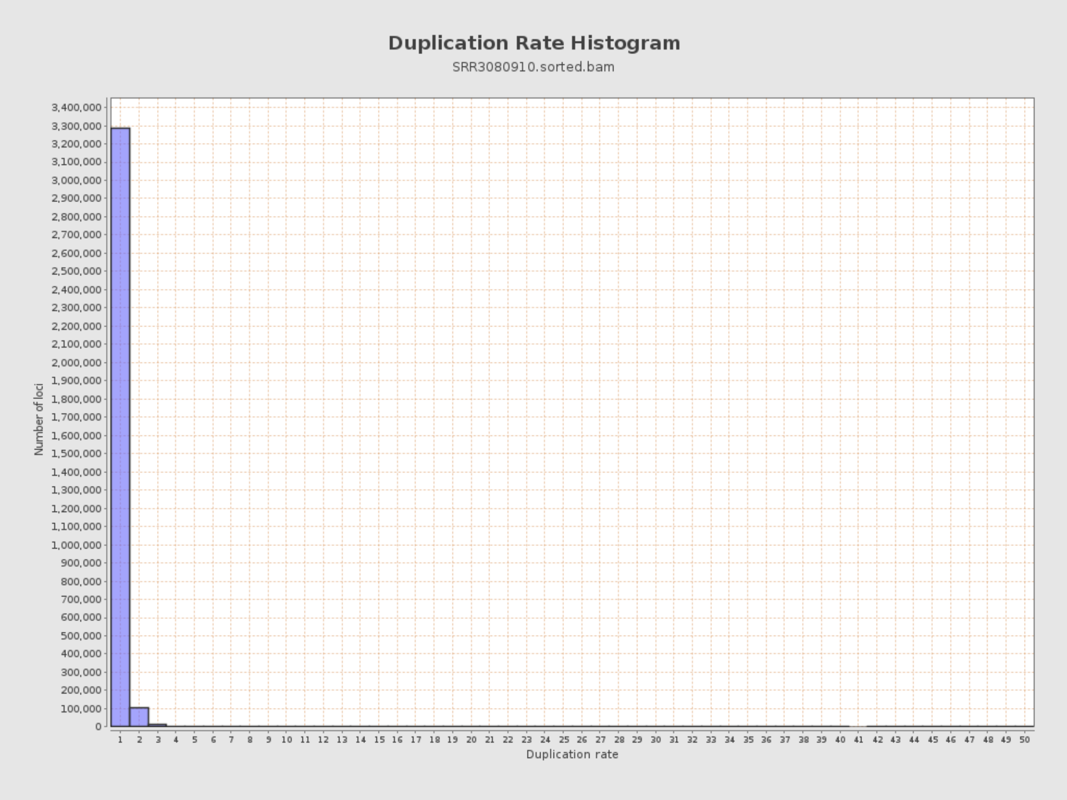
5. Results : Coverage Histogram (0-50X)



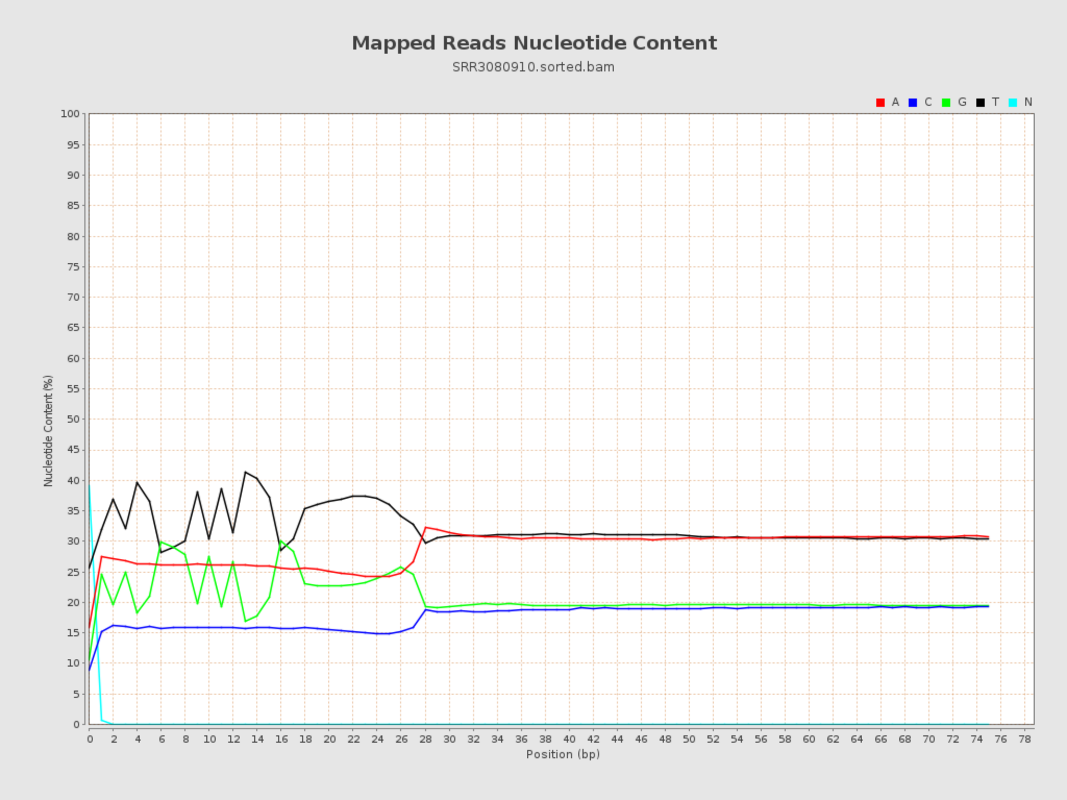
6. Results : Genome Fraction Coverage



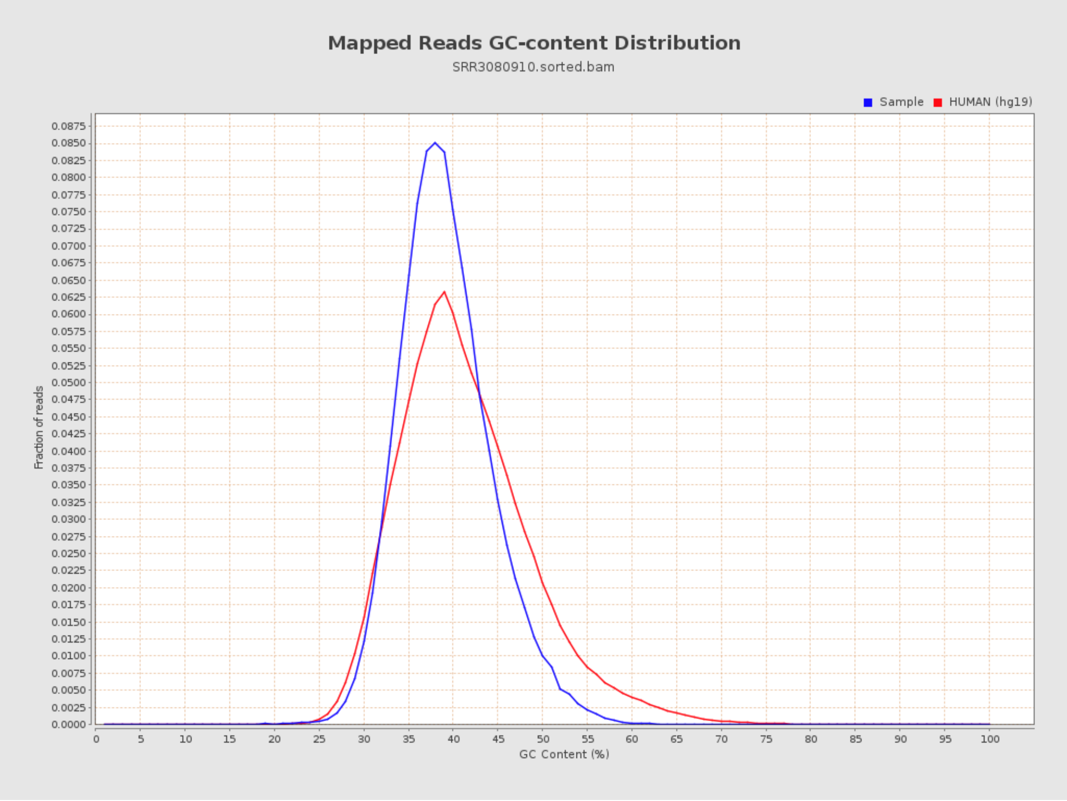
7. Results : Duplication Rate Histogram



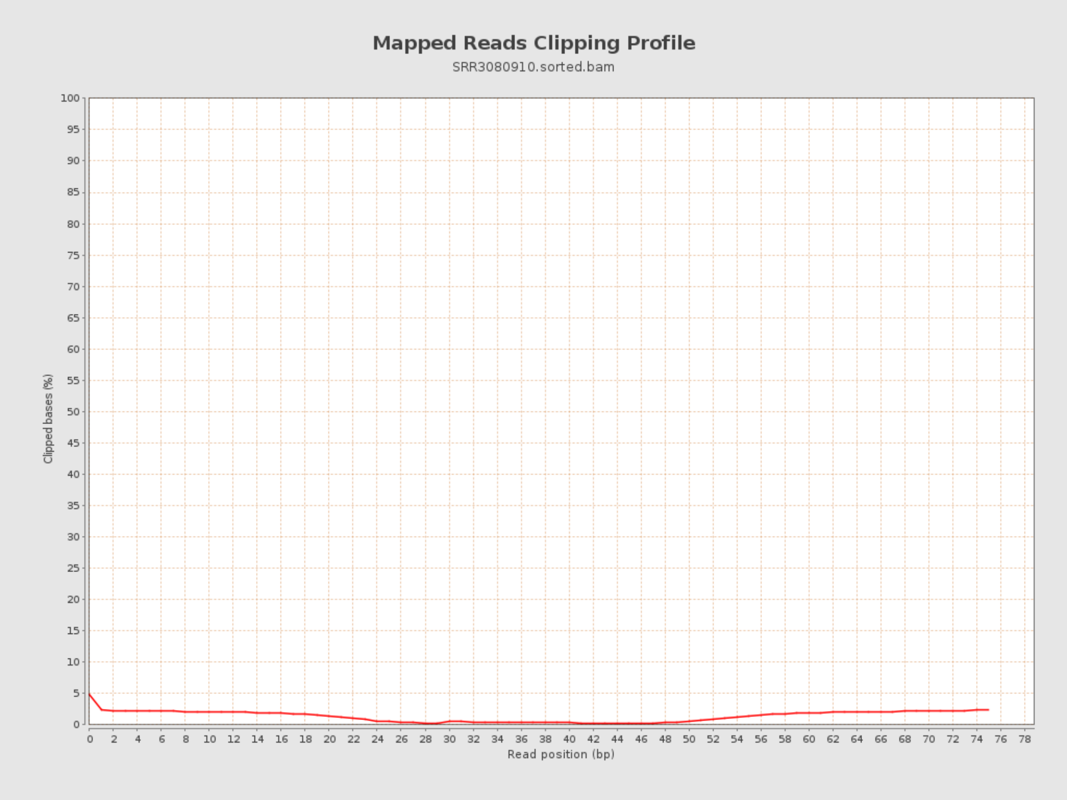
8. Results : Mapped Reads Nucleotide Content



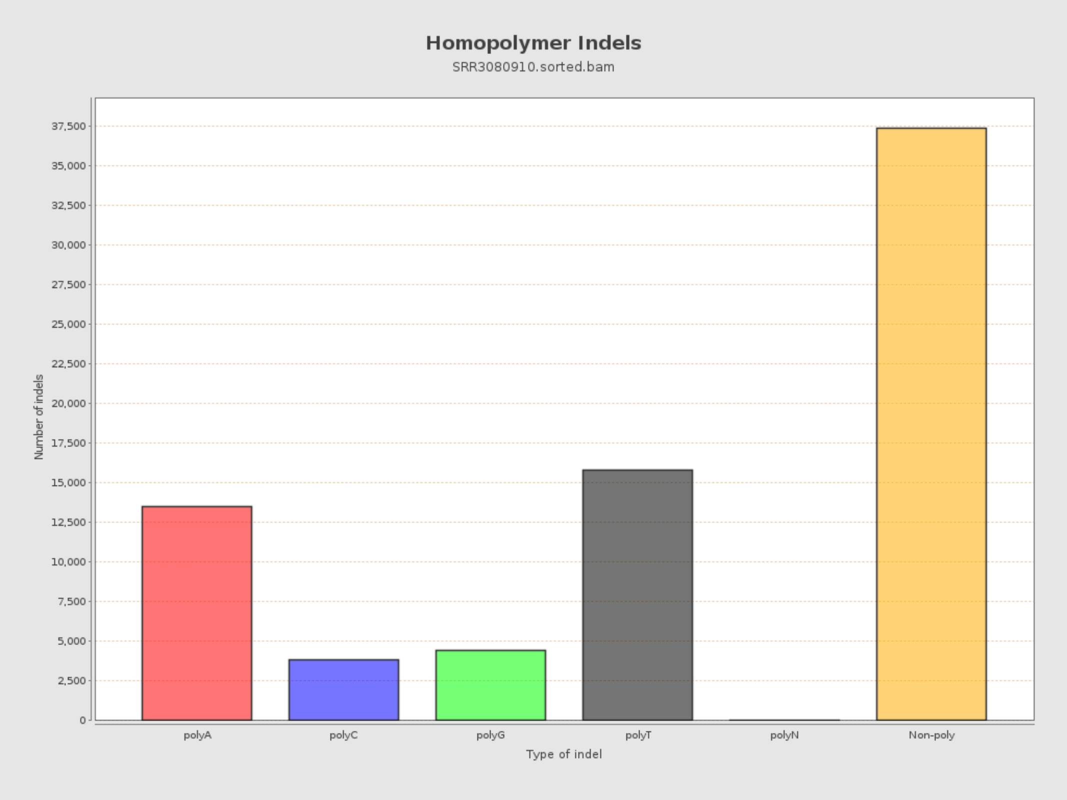
9. Results : Mapped Reads GC-content Distribution



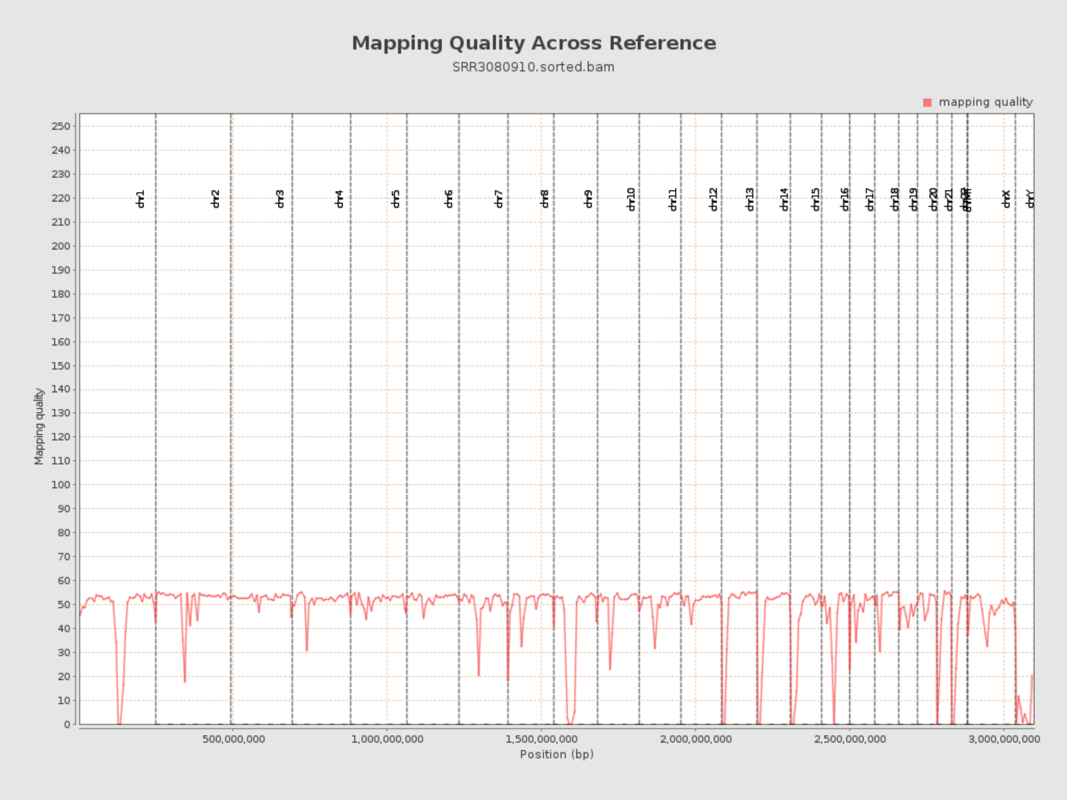
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram