Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 05:40:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081254.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_SRR3081254 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081254.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 05:40:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081254.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,096,539
Mapped reads	4,413,268 / 86.59%
Unmapped reads	683,271 / 13.41%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	48,027 / 0.94%
Read min/max/mean length	30 / 76 / 76.33
Duplicated reads (estimated)	268,072 / 5.26%
Duplication rate	4.68%
Clipped reads	1,800,491 / 35.33%

2.2. ACGT Content

Number/percentage of A's	83,059,279 / 27.83%
Number/percentage of C's	54,524,365 / 18.27%
Number/percentage of T's	95,655,768 / 32.05%
Number/percentage of G's	65,103,725 / 21.82%
Number/percentage of N's	80,558 / 0.03%
GC Percentage	40.09%

2.3. Coverage

Mean	0.0964

Standard Deviation	0.7414

2.4. Mapping Quality

Mean Mapping Quality	47.2

2.5. Mismatches and indels

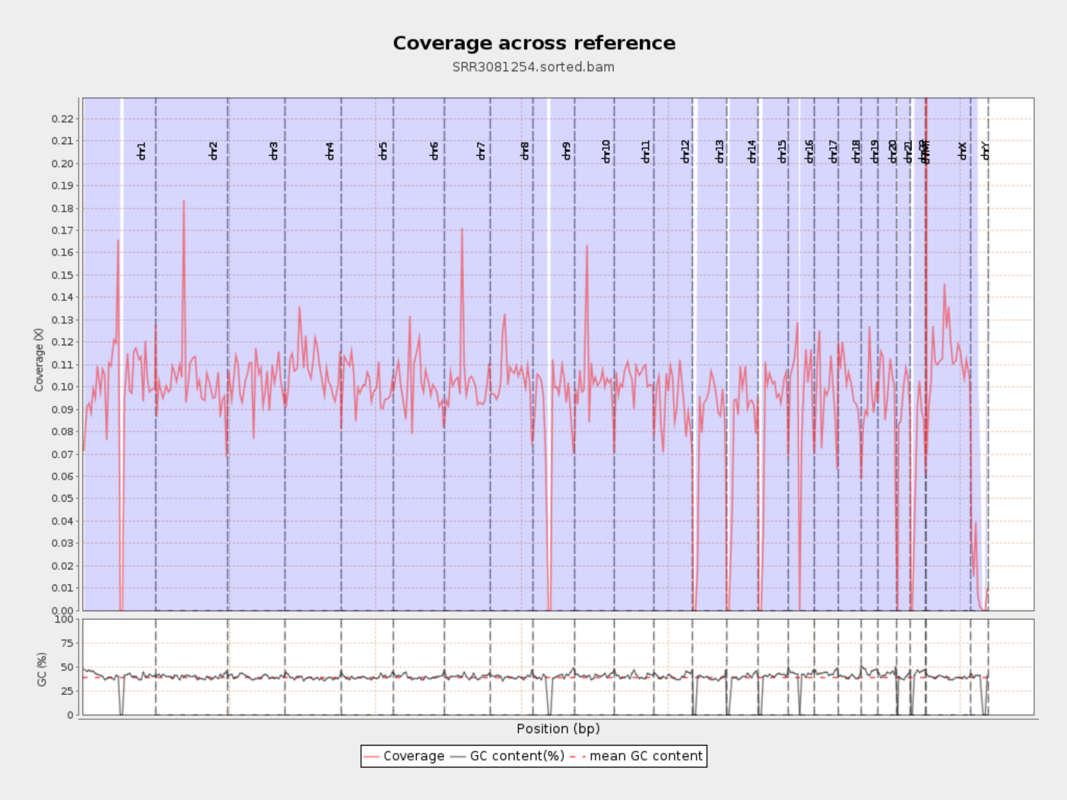
General error rate	0.87%
Mismatches	2,540,675
Insertions	25,189
Mapped reads with at least one insertion	0.57%
Deletions	71,575
Mapped reads with at least one deletion	1.6%
Homopolymer indels	48.76%

2.6. Chromosome stats

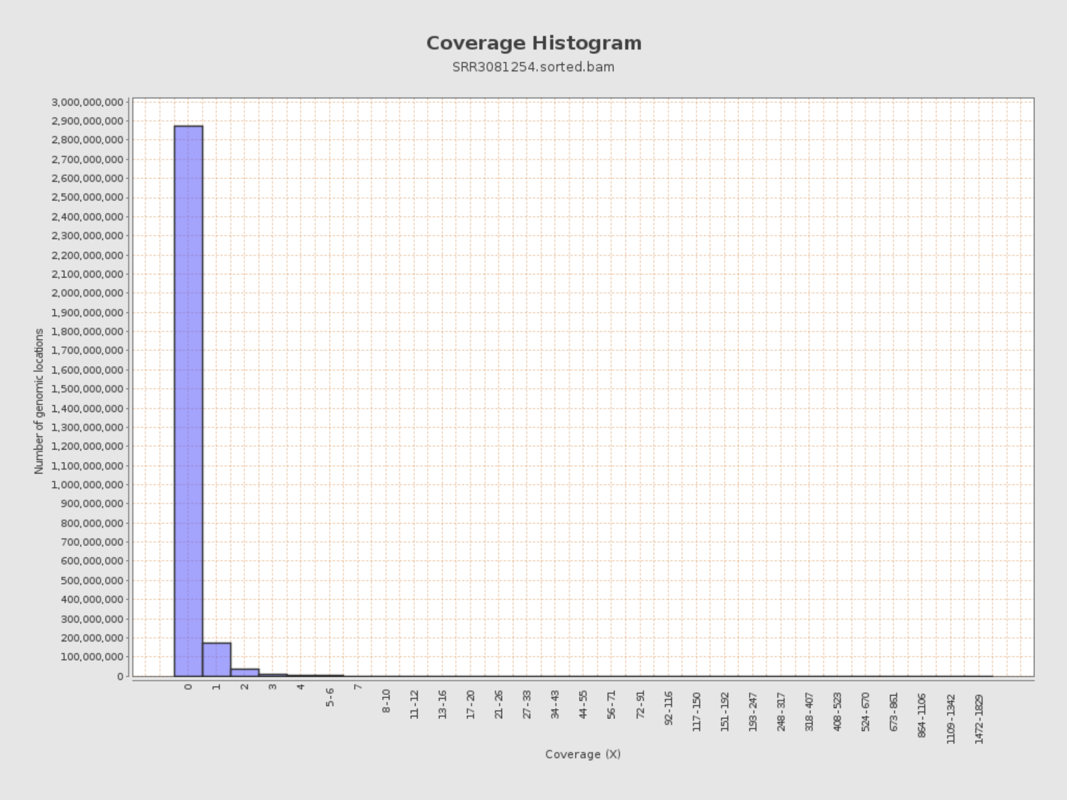
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	24514251	0.0984	1.2716
chr2	243199373	24952025	0.1026	0.7949
chr3	198022430	20373064	0.1029	0.411
chr4	191154276	20793216	0.1088	0.4576
chr5	180915260	18212910	0.1007	0.4043
chr6	171115067	17453315	0.102	0.5494
chr7	159138663	16378054	0.1029	1.0678

chr8	146364022	15285017	0.1044	1.2012
chr9	141213431	12127305	0.0859	0.661
chr10	135534747	14103334	0.1041	0.7406
chr11	135006516	13908152	0.103	0.7961
chr12	133851895	12464707	0.0931	0.403
chr13	115169878	9045388	0.0785	0.3548
chr14	107349540	8473879	0.0789	0.4057
chr15	102531392	8403476	0.082	0.3642
chr16	90354753	8467781	0.0937	0.4552
chr17	81195210	7890283	0.0972	0.5681
chr18	78077248	7960140	0.102	1.3261
chr19	59128983	5597365	0.0947	0.9758
chr20	63025520	6360848	0.1009	0.4301
chr21	48129895	4166417	0.0866	0.4313
chr22	51304566	3234811	0.0631	0.3162
chrMT	16571	159282	9.6121	5.7947
chrX	155270560	17493322	0.1127	0.4922
chrY	59373566	722322	0.0122	0.2549

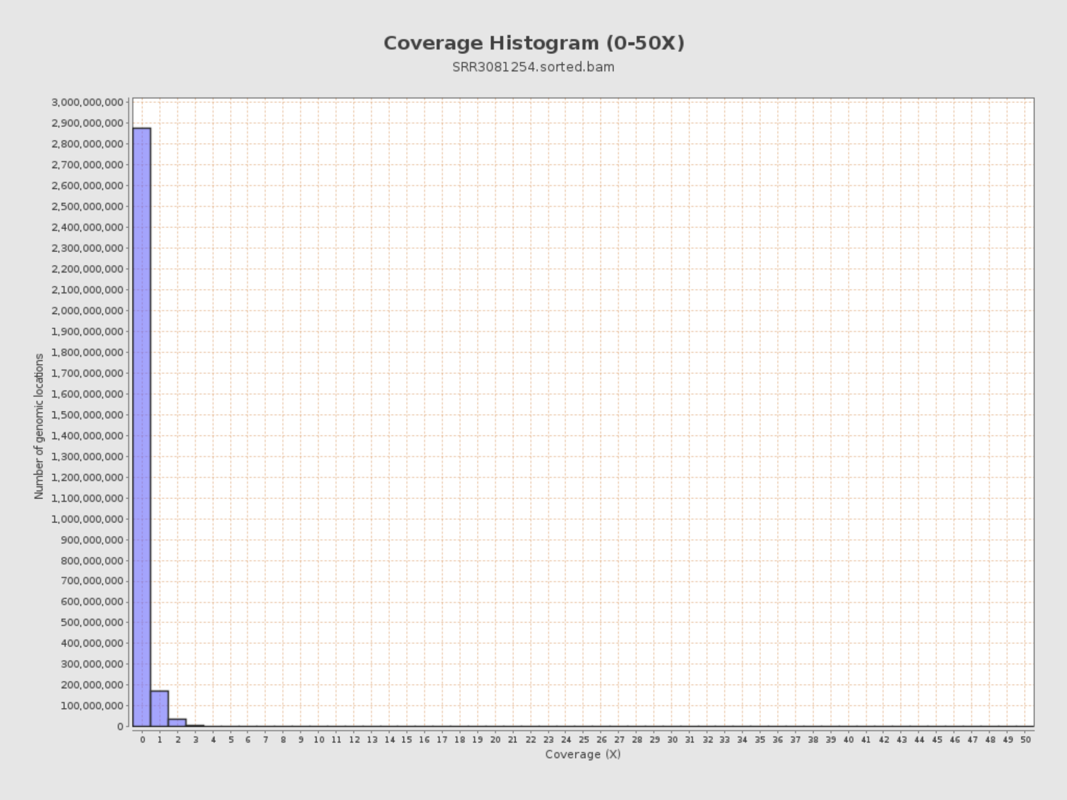
3. Results : Coverage across reference



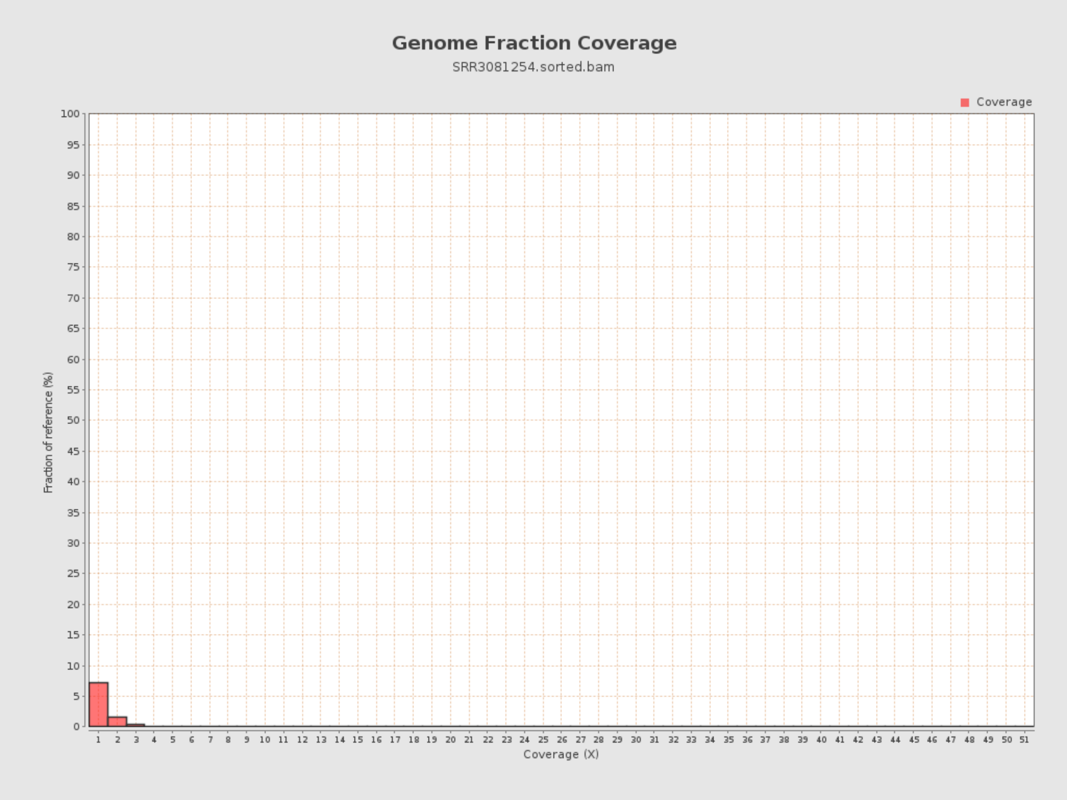
4. Results : Coverage Histogram



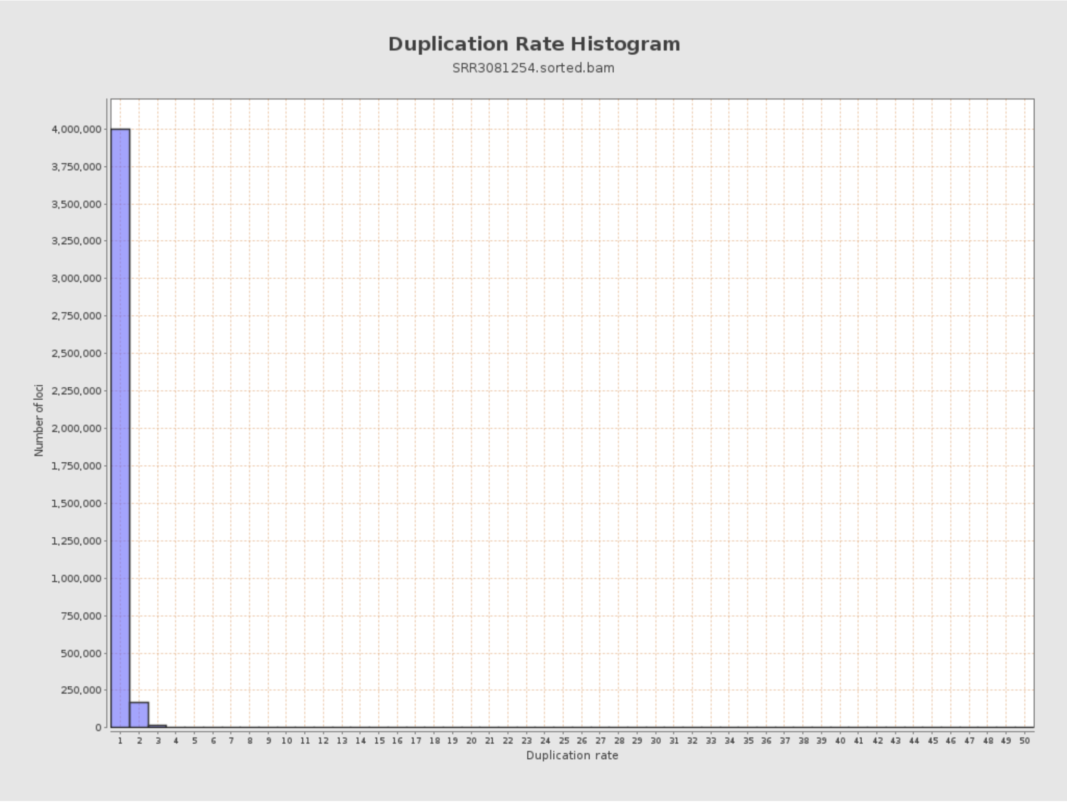
5. Results : Coverage Histogram (0-50X)



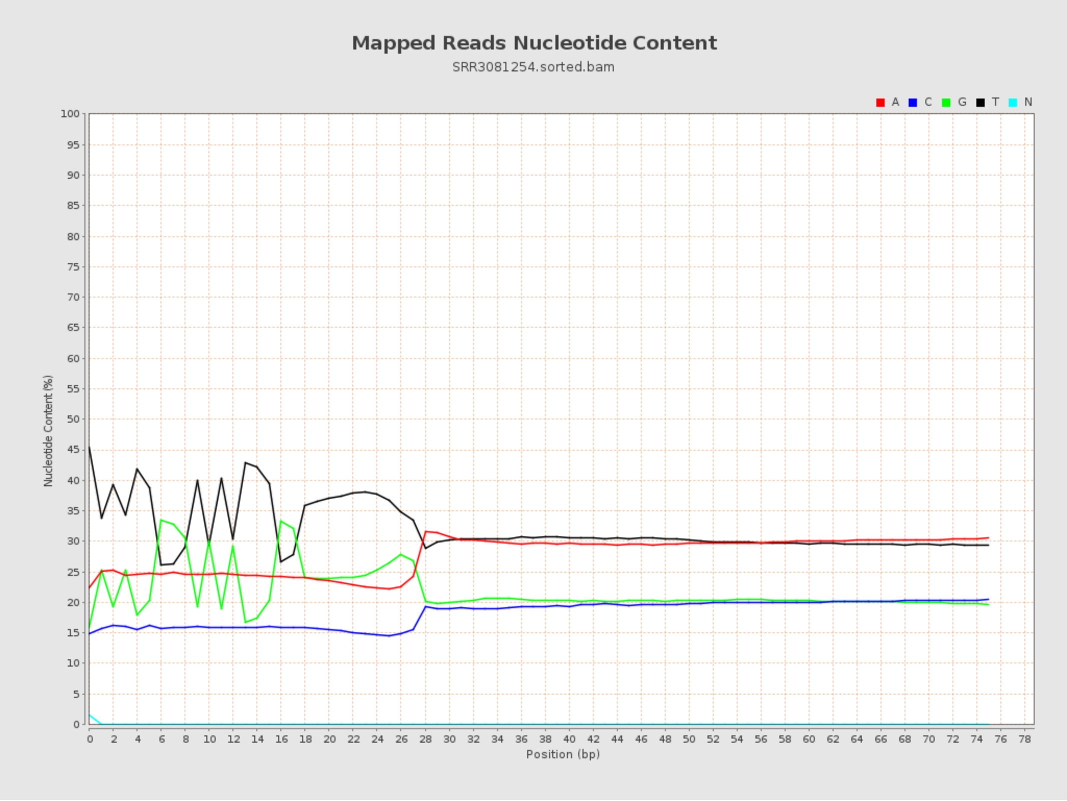
6. Results : Genome Fraction Coverage



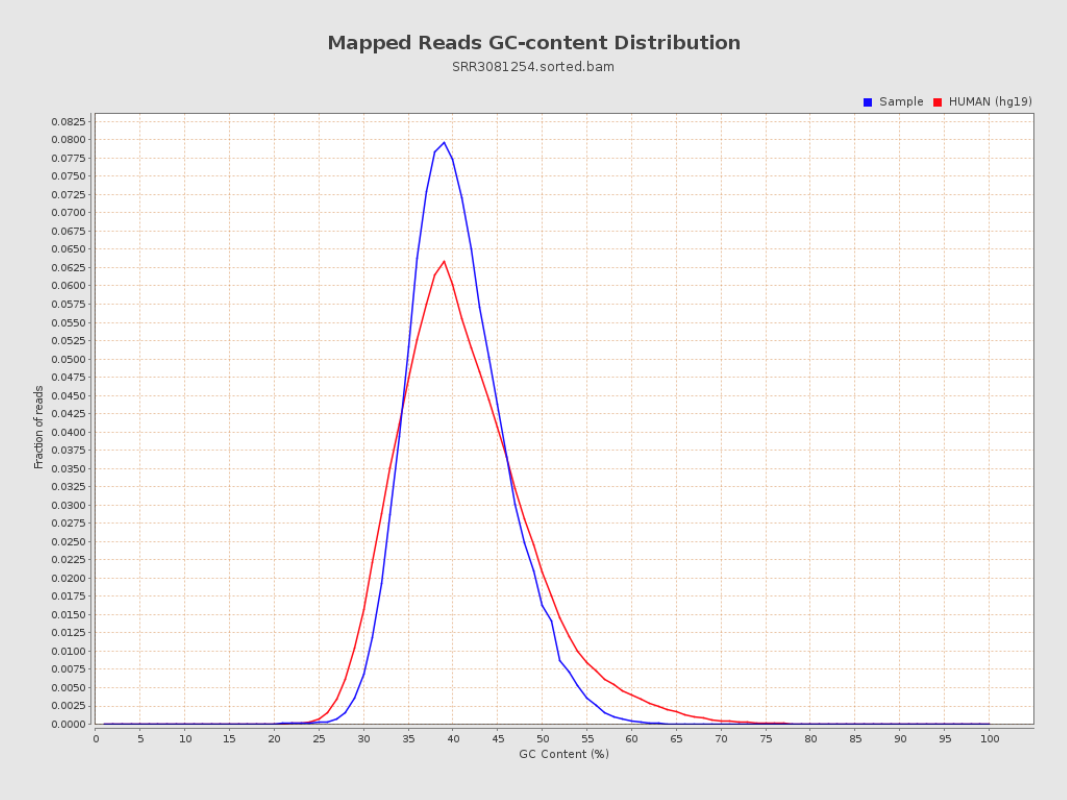
7. Results : Duplication Rate Histogram



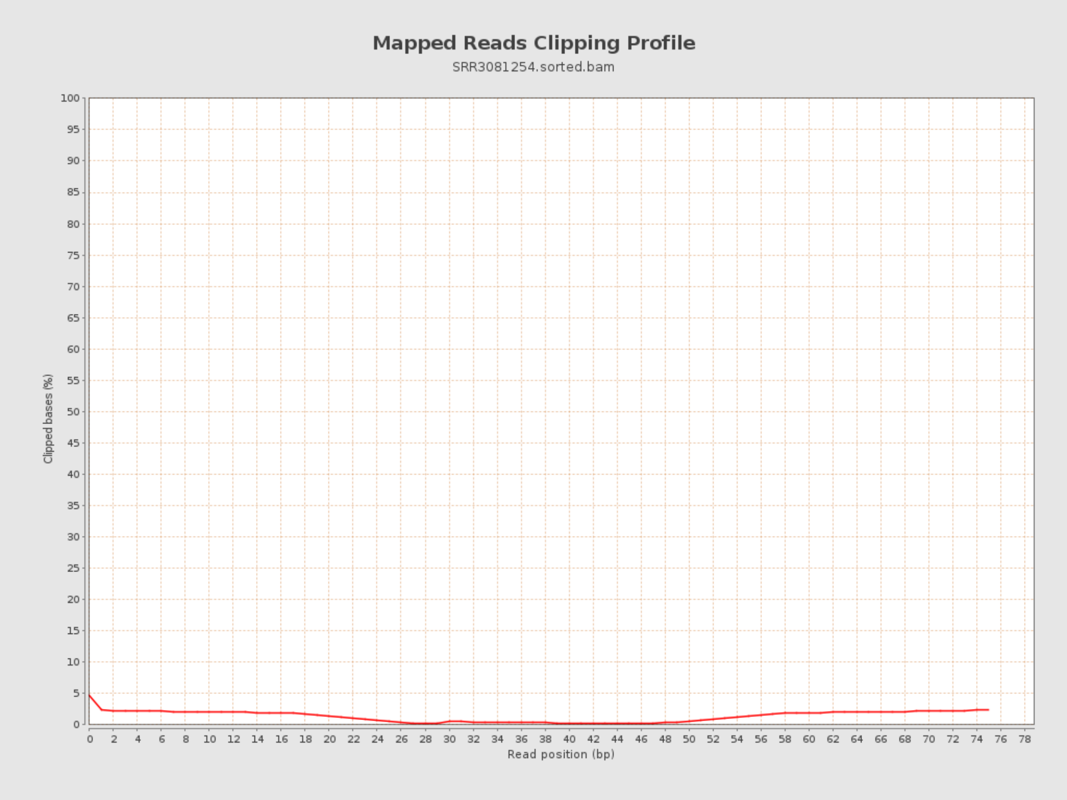
8. Results : Mapped Reads Nucleotide Content



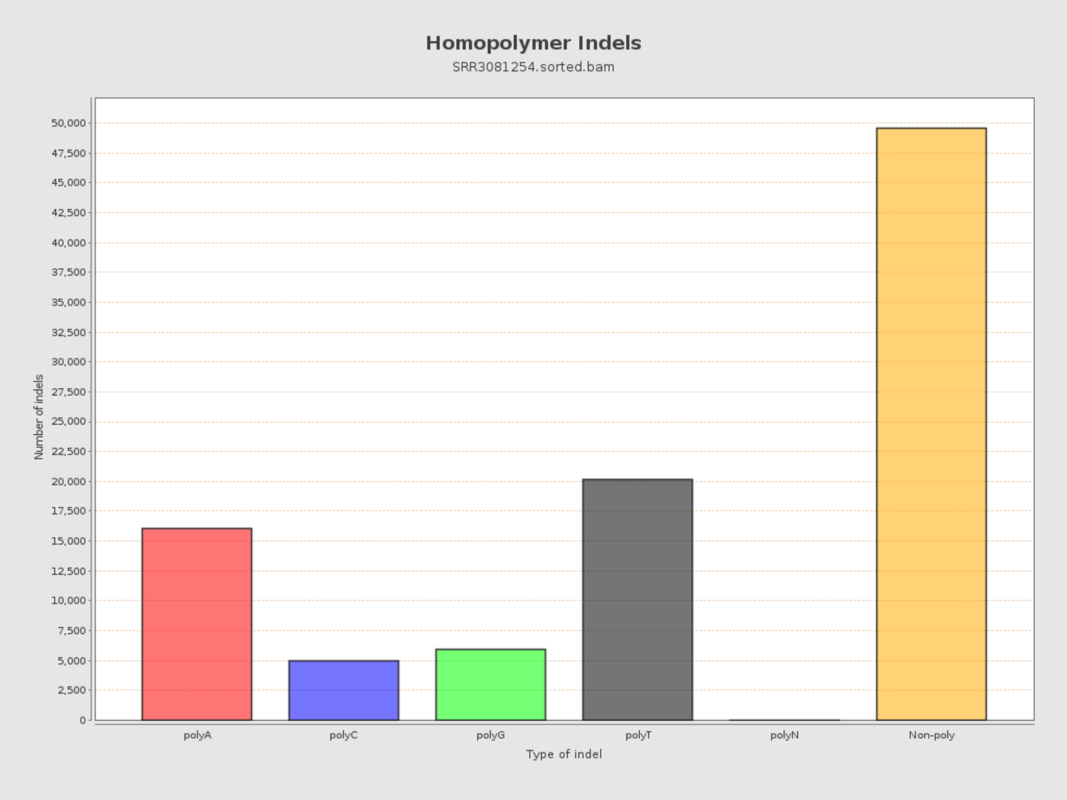
9. Results : Mapped Reads GC-content Distribution



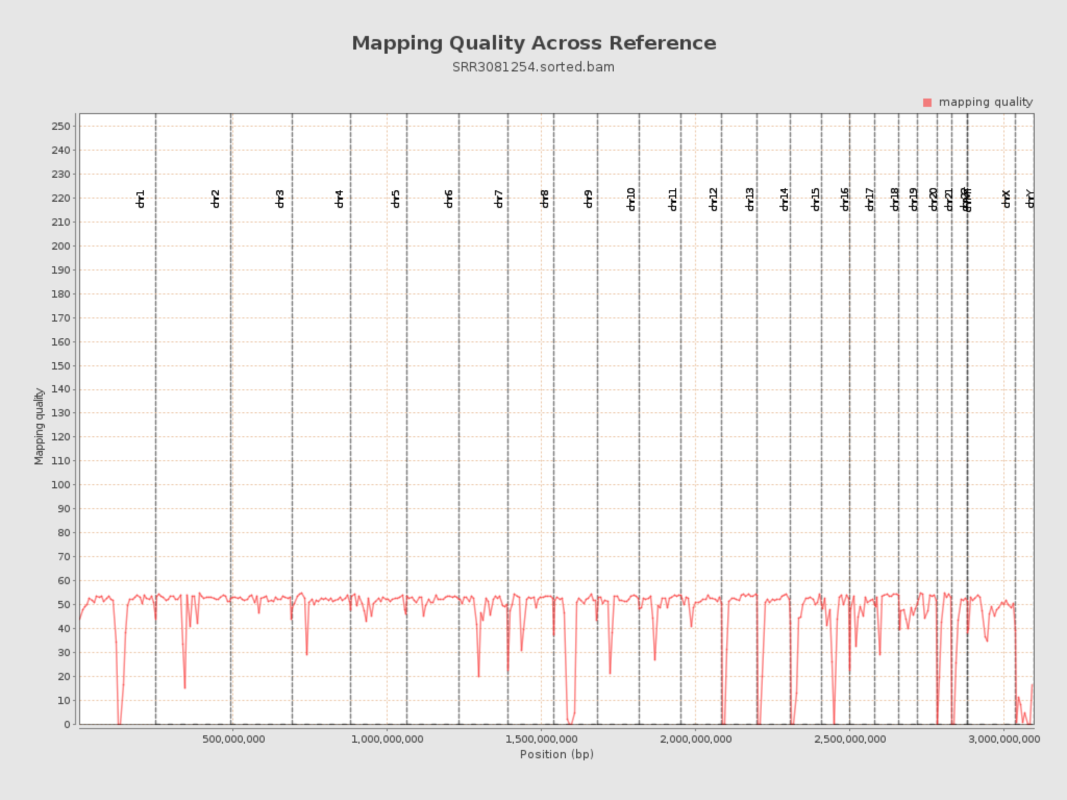
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram