Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 22:25:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082977.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_SRR3082977 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082977.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 22:25:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082977.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,014,928
Mapped reads	2,307,841 / 76.55%
Unmapped reads	707,087 / 23.45%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,259 / 0.47%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	80,461 / 2.67%
Duplication rate	2.62%
Clipped reads	918,419 / 30.46%

2.2. ACGT Content

Number/percentage of A's	44,930,596 / 28.59%
Number/percentage of C's	28,582,535 / 18.18%
Number/percentage of T's	50,144,463 / 31.9%
Number/percentage of G's	33,503,861 / 21.32%
Number/percentage of N's	15,168 / 0.01%
GC Percentage	39.5%

2.3. Coverage

Mean	0.0508

Standard Deviation	0.4057

2.4. Mapping Quality

Mean Mapping Quality	45.85

2.5. Mismatches and indels

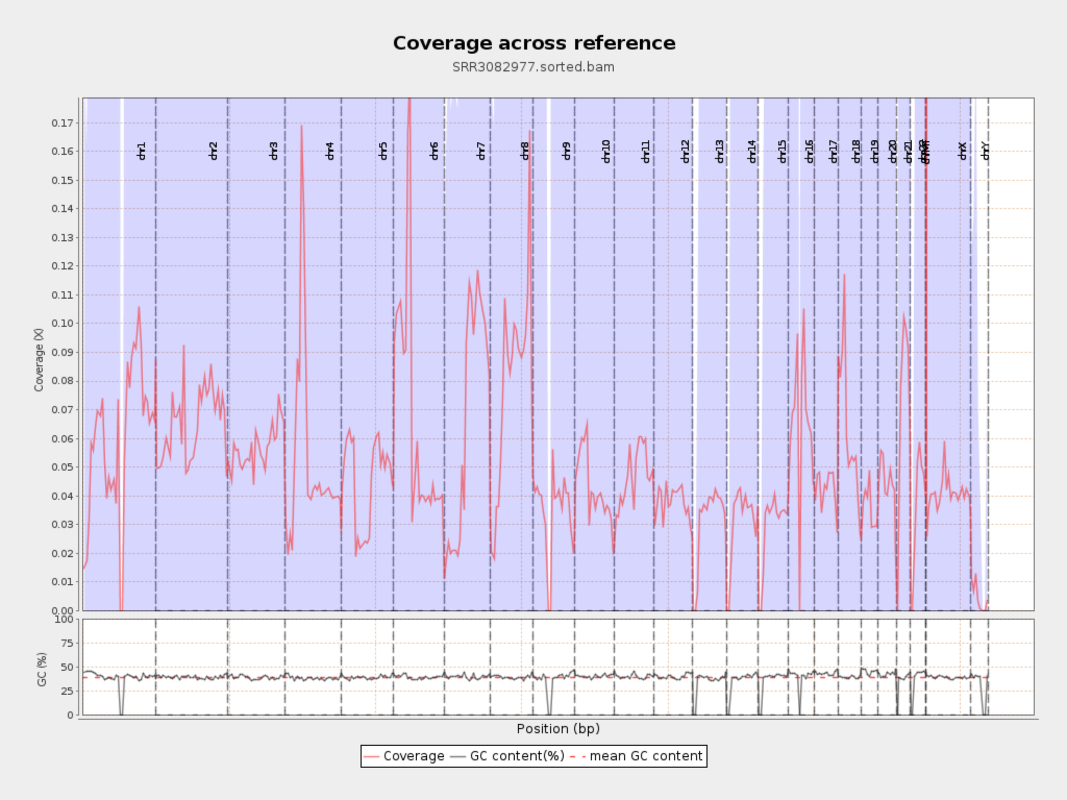
General error rate	0.98%
Mismatches	1,522,688
Insertions	14,274
Mapped reads with at least one insertion	0.61%
Deletions	37,166
Mapped reads with at least one deletion	1.59%
Homopolymer indels	47.9%

2.6. Chromosome stats

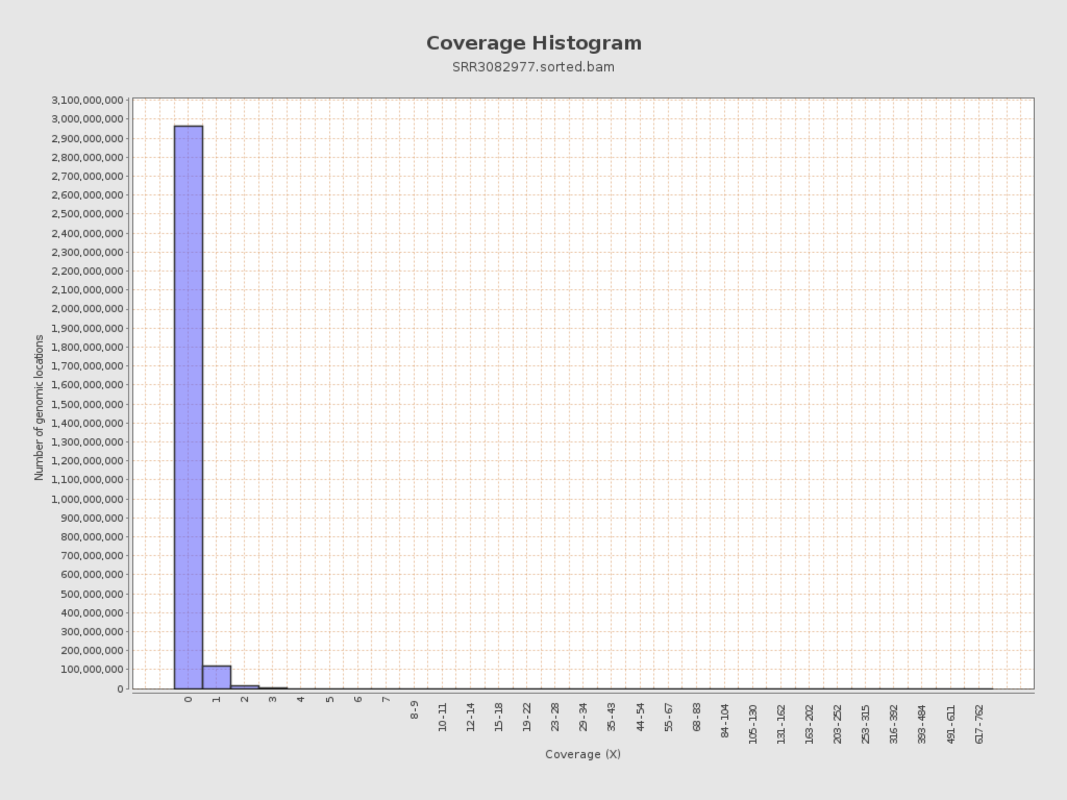
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14797567	0.0594	0.7106
chr2	243199373	15901854	0.0654	0.5005
chr3	198022430	11176194	0.0564	0.2682
chr4	191154276	10216964	0.0534	0.2702
chr5	180915260	8098548	0.0448	0.24
chr6	171115067	11575248	0.0676	0.4871
chr7	159138663	10565305	0.0664	0.3919

chr8	146364022	11703413	0.08	0.5796
chr9	141213431	4875048	0.0345	0.3704
chr10	135534747	5795921	0.0428	0.3133
chr11	135006516	6292208	0.0466	0.3325
chr12	133851895	5042428	0.0377	0.2275
chr13	115169878	3593595	0.0312	0.1967
chr14	107349540	3320686	0.0309	0.2367
chr15	102531392	2918582	0.0285	0.1901
chr16	90354753	5816426	0.0644	0.3266
chr17	81195210	3488459	0.043	0.2643
chr18	78077248	5076300	0.065	0.76
chr19	59128983	2124376	0.0359	0.5101
chr20	63025520	2848191	0.0452	0.2562
chr21	48129895	3390785	0.0705	0.311
chr22	51304566	1850663	0.0361	0.2136
chrMT	16571	171627	10.3571	7.1966
chrX	155270560	6328337	0.0408	0.2579
chrY	59373566	272573	0.0046	0.0978

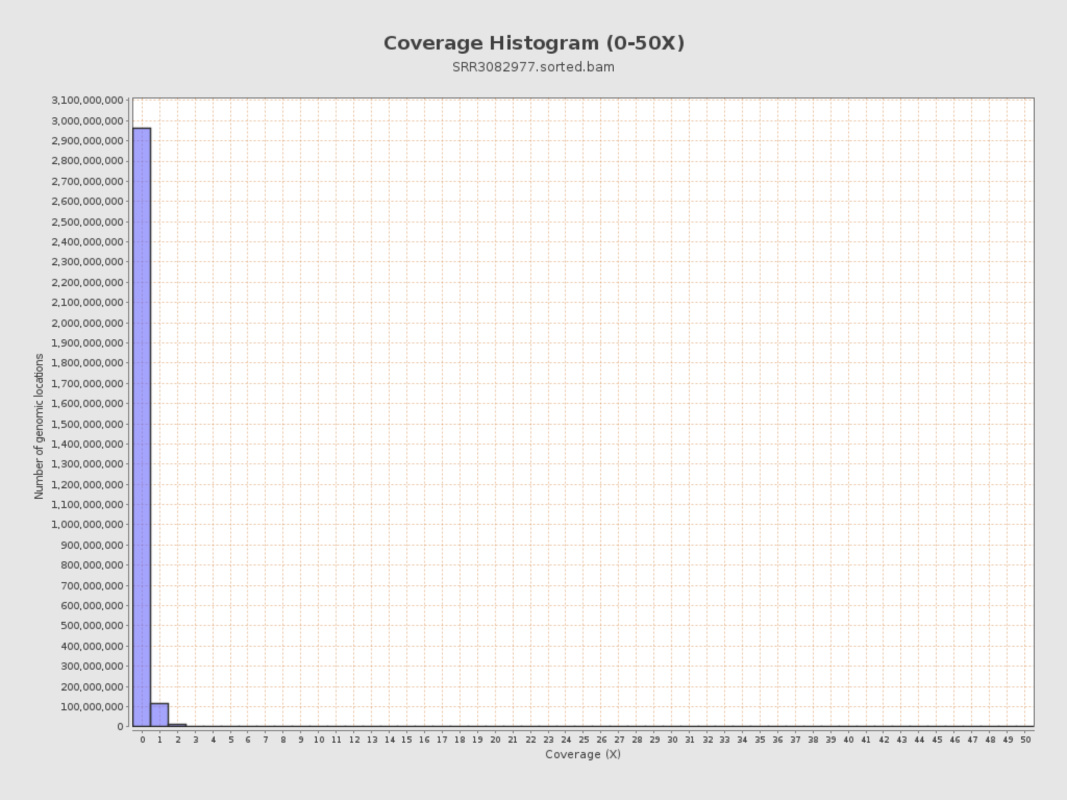
3. Results : Coverage across reference



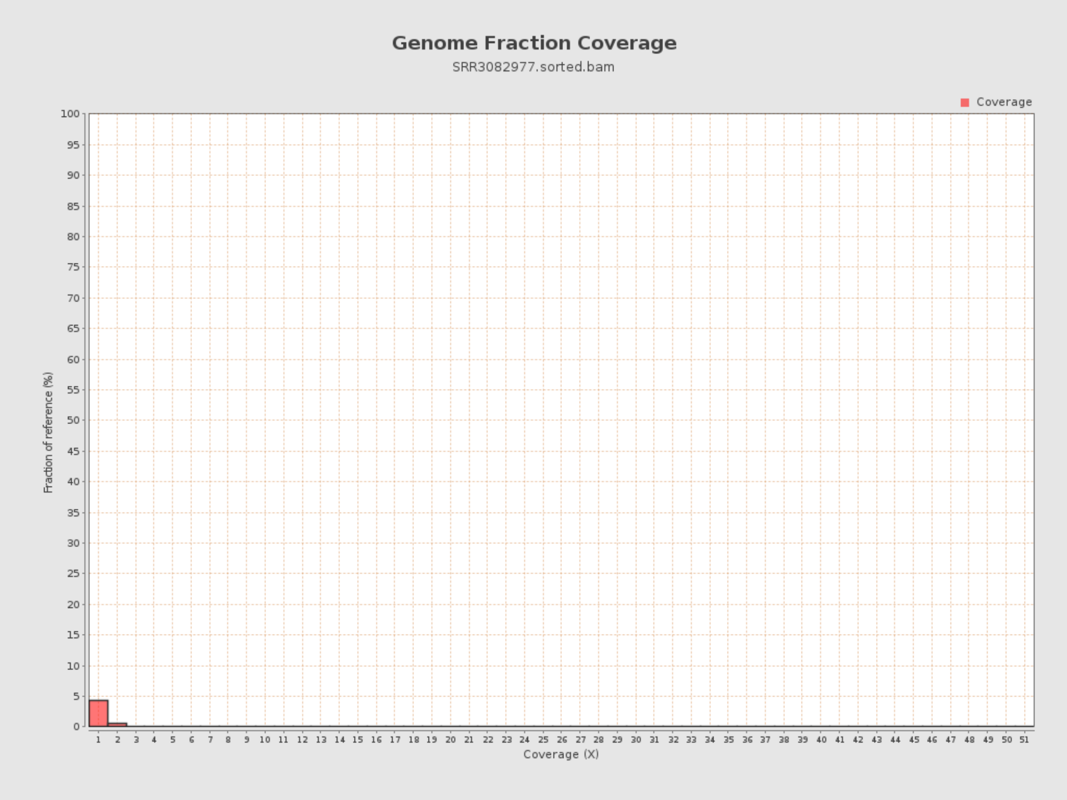
4. Results : Coverage Histogram



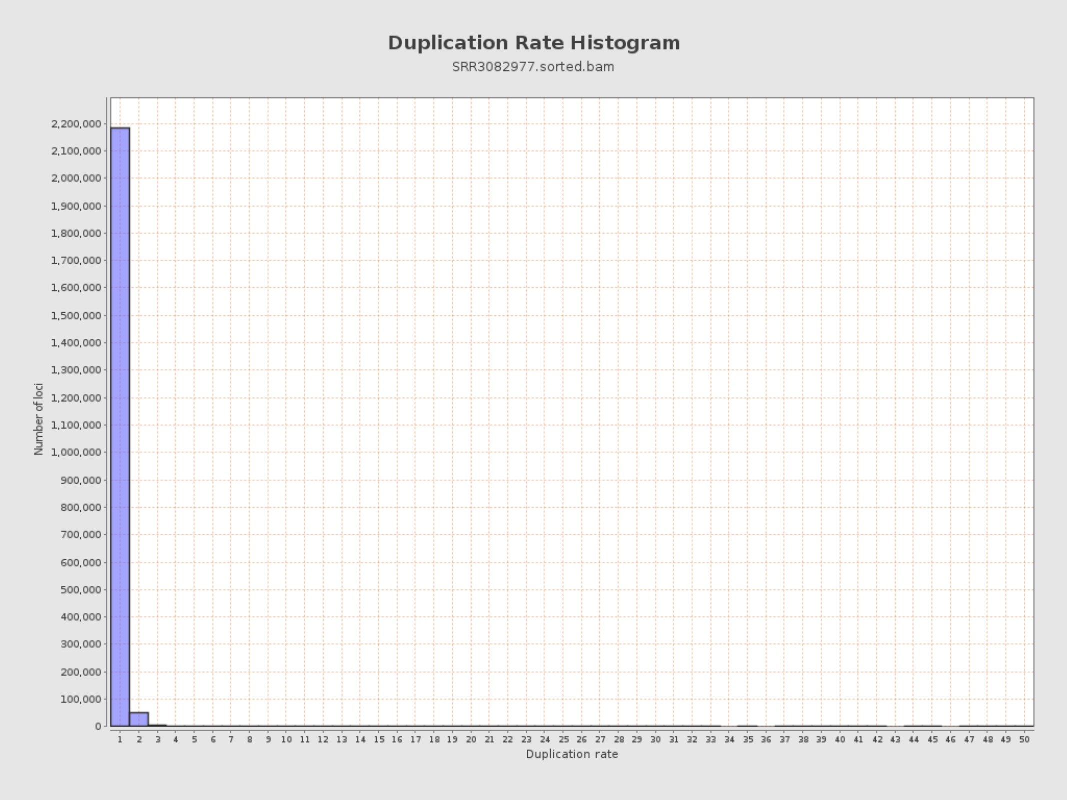
5. Results : Coverage Histogram (0-50X)



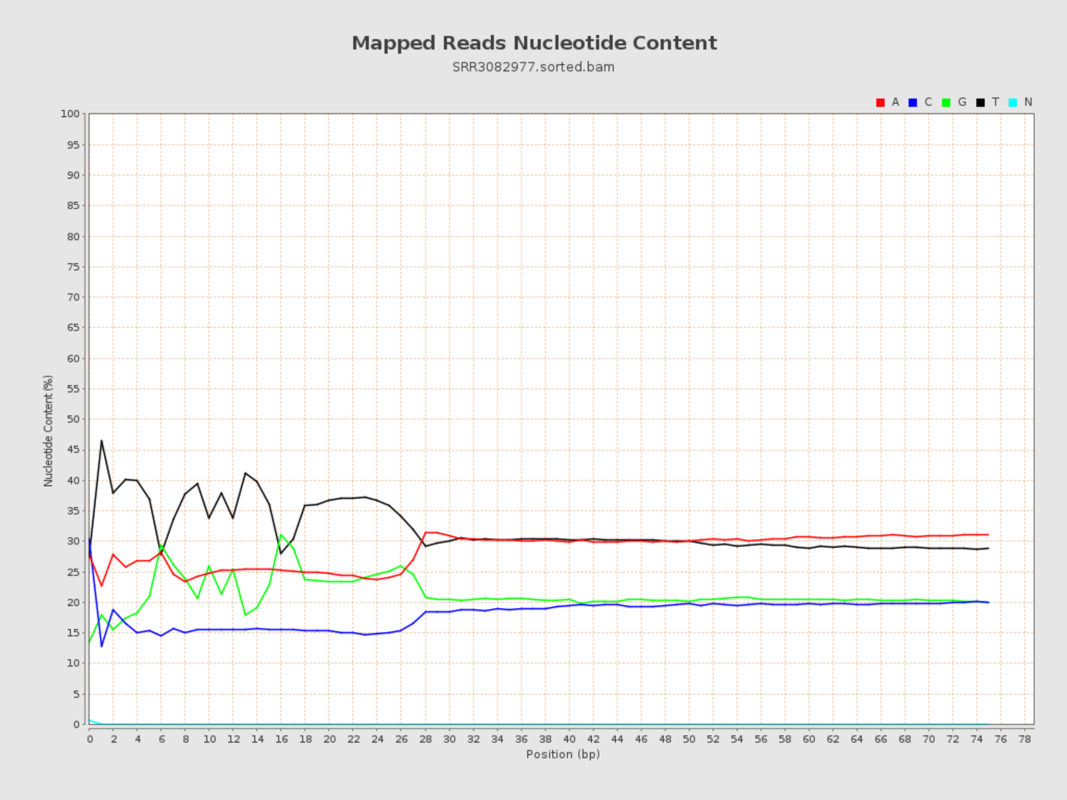
6. Results : Genome Fraction Coverage



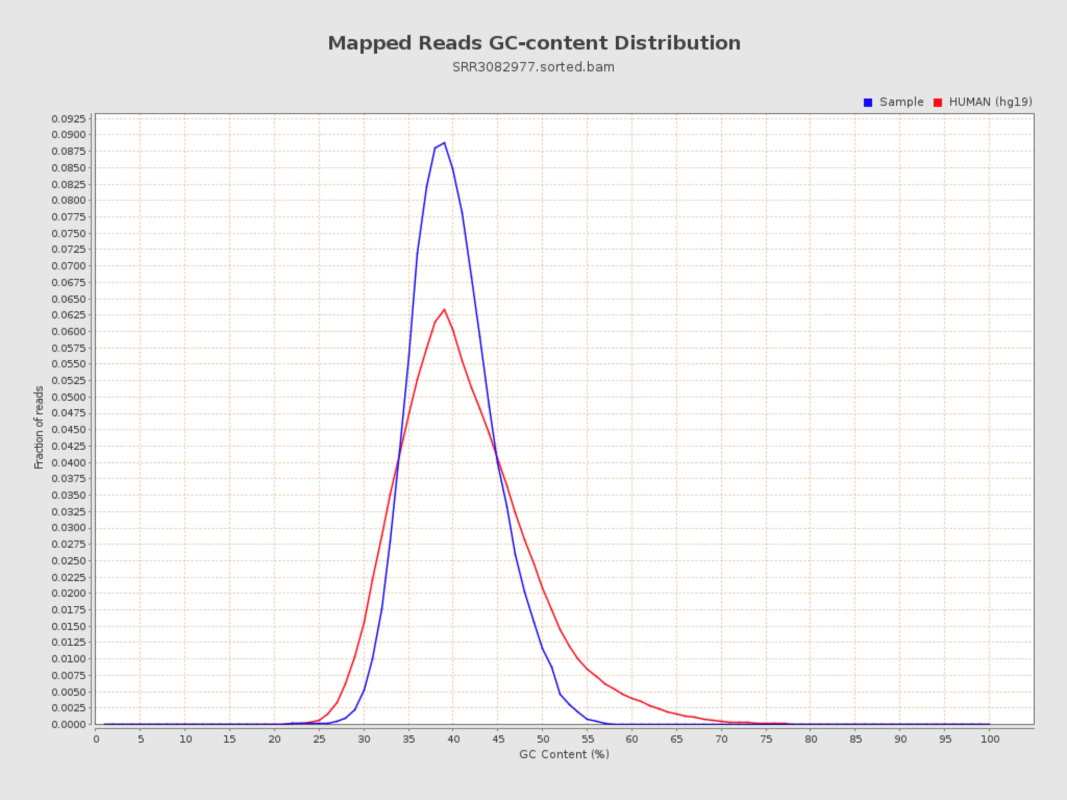
7. Results : Duplication Rate Histogram



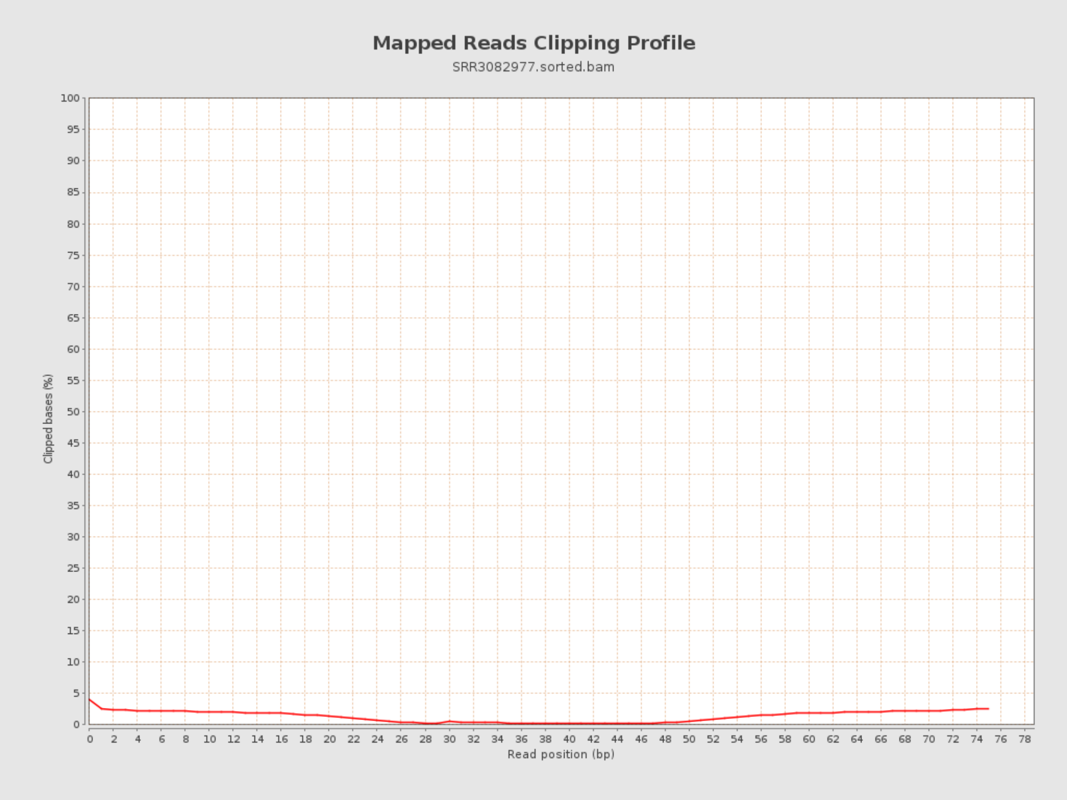
8. Results : Mapped Reads Nucleotide Content



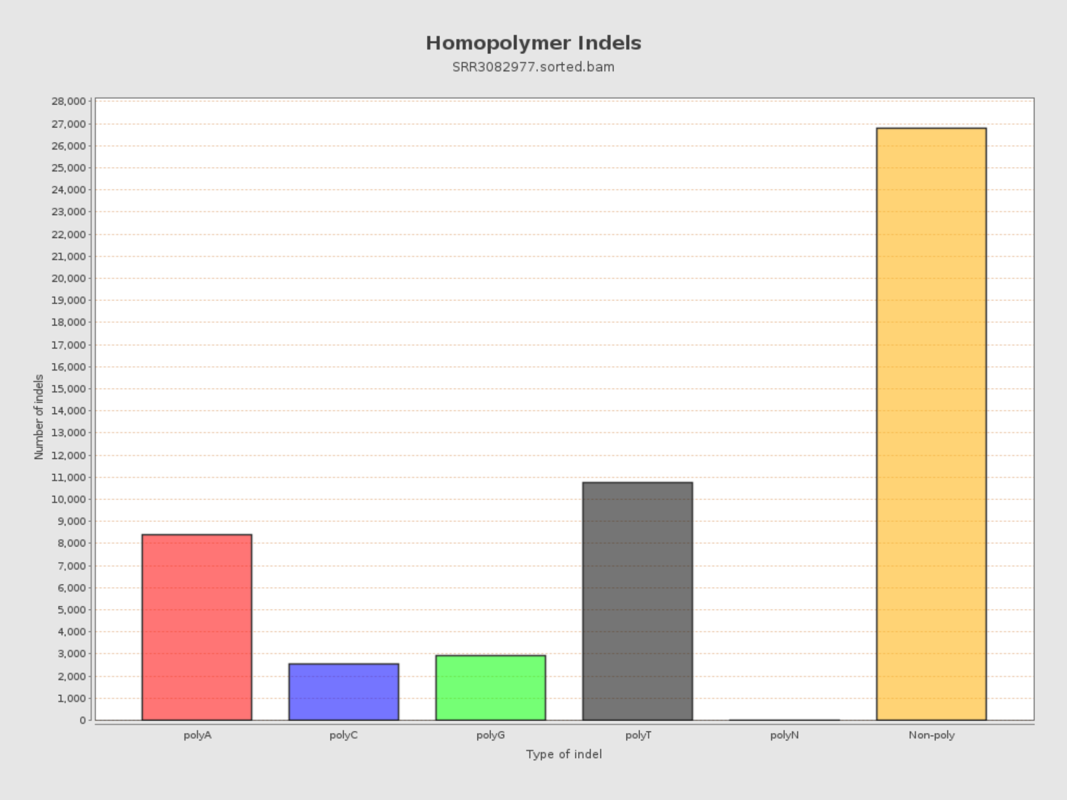
9. Results : Mapped Reads GC-content Distribution



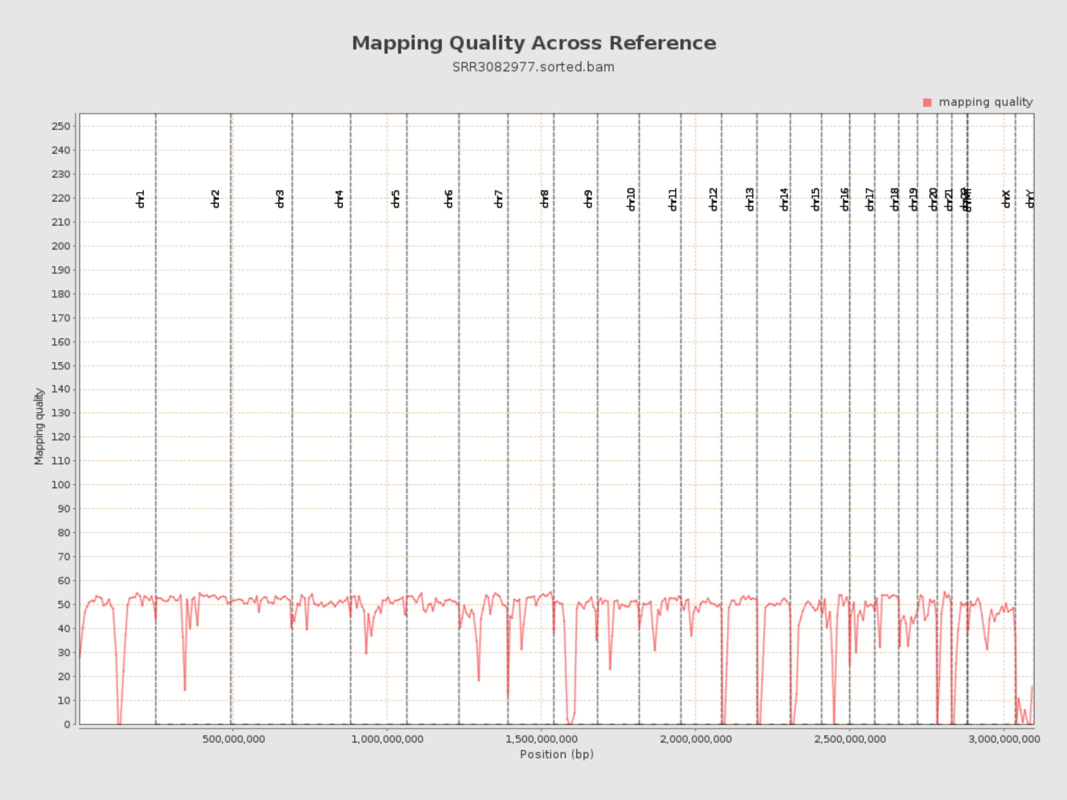
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram