Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 20:04:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082921.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_SRR3082921 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082921.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 20:04:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082921.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,841,559
Mapped reads	1,677,173 / 91.07%
Unmapped reads	164,386 / 8.93%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,456 / 1.06%
Read min/max/mean length	30 / 76 / 76.37
Duplicated reads (estimated)	78,474 / 4.26%
Duplication rate	3.98%
Clipped reads	701,251 / 38.08%

2.2. ACGT Content

Number/percentage of A's	31,328,590 / 27.73%
Number/percentage of C's	20,977,068 / 18.57%
Number/percentage of T's	35,858,522 / 31.74%
Number/percentage of G's	24,799,020 / 21.95%
Number/percentage of N's	5,225 / 0%
GC Percentage	40.52%

2.3. Coverage

Mean	0.0365

Standard Deviation	0.2898

2.4. Mapping Quality

Mean Mapping Quality	46.1

2.5. Mismatches and indels

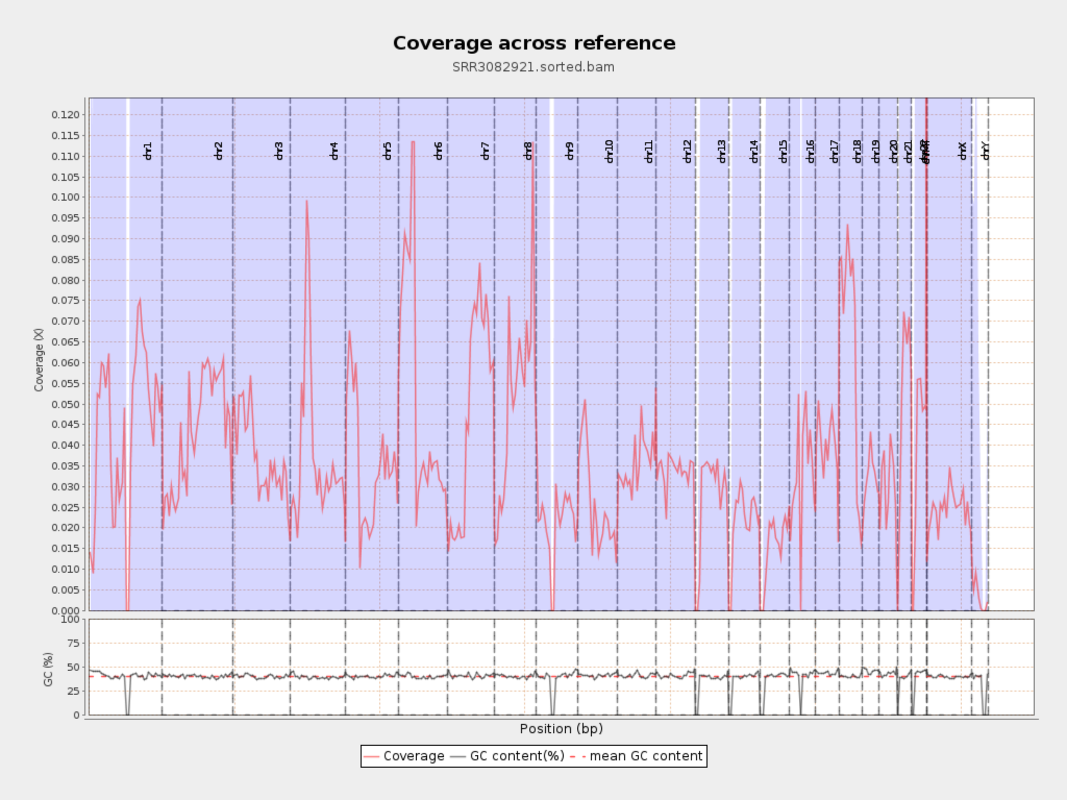
General error rate	0.74%
Mismatches	815,912
Insertions	9,234
Mapped reads with at least one insertion	0.55%
Deletions	26,764
Mapped reads with at least one deletion	1.58%
Homopolymer indels	48.67%

2.6. Chromosome stats

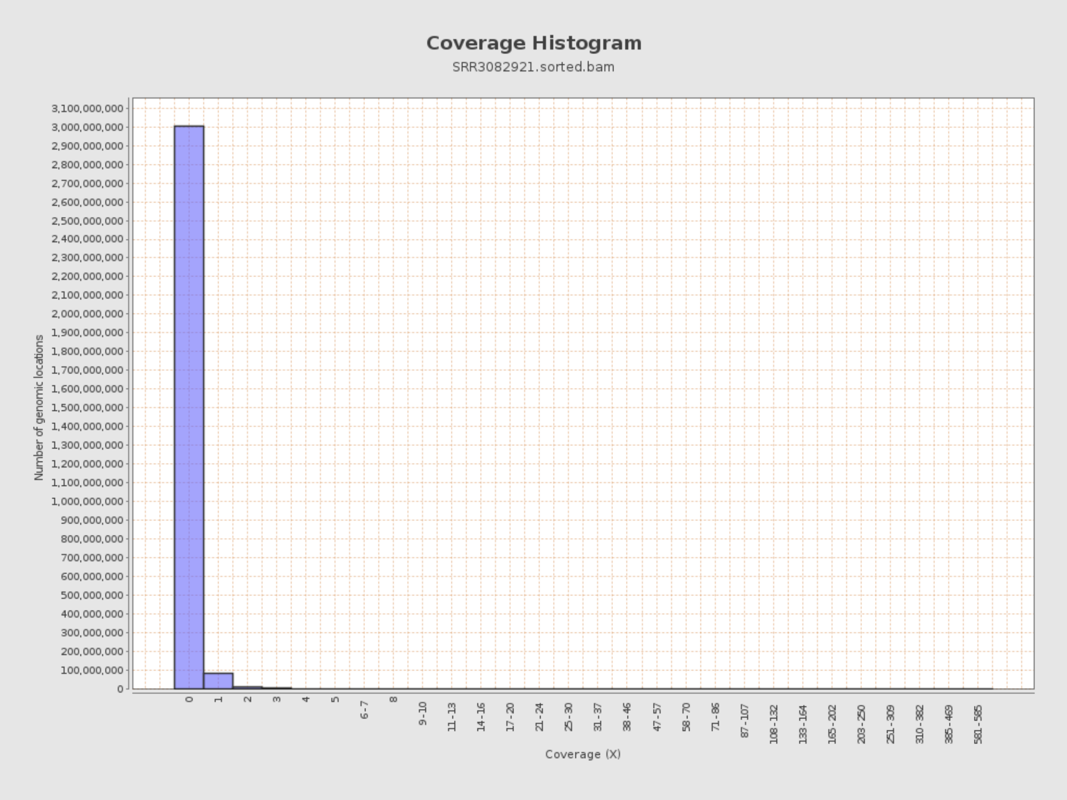
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10915634	0.0438	0.4707
chr2	243199373	10473880	0.0431	0.3726
chr3	198022430	7476759	0.0378	0.2258
chr4	191154276	7192637	0.0376	0.231
chr5	180915260	6472242	0.0358	0.2206
chr6	171115067	8829509	0.0516	0.3202
chr7	159138663	7724704	0.0485	0.3345

chr8	146364022	7561794	0.0517	0.333
chr9	141213431	2947881	0.0209	0.2274
chr10	135534747	3599573	0.0266	0.2036
chr11	135006516	4779326	0.0354	0.2505
chr12	133851895	4491990	0.0336	0.2138
chr13	115169878	3140260	0.0273	0.1933
chr14	107349540	2311417	0.0215	0.1787
chr15	102531392	1572202	0.0153	0.1489
chr16	90354753	2992625	0.0331	0.2213
chr17	81195210	3204323	0.0395	0.2446
chr18	78077248	5185930	0.0664	0.5429
chr19	59128983	1914069	0.0324	0.2969
chr20	63025520	1874757	0.0297	0.2082
chr21	48129895	2478595	0.0515	0.2696
chr22	51304566	1883063	0.0367	0.2231
chrMT	16571	6680	0.4031	0.6626
chrX	155270560	3792654	0.0244	0.1936
chrY	59373566	190292	0.0032	0.0713

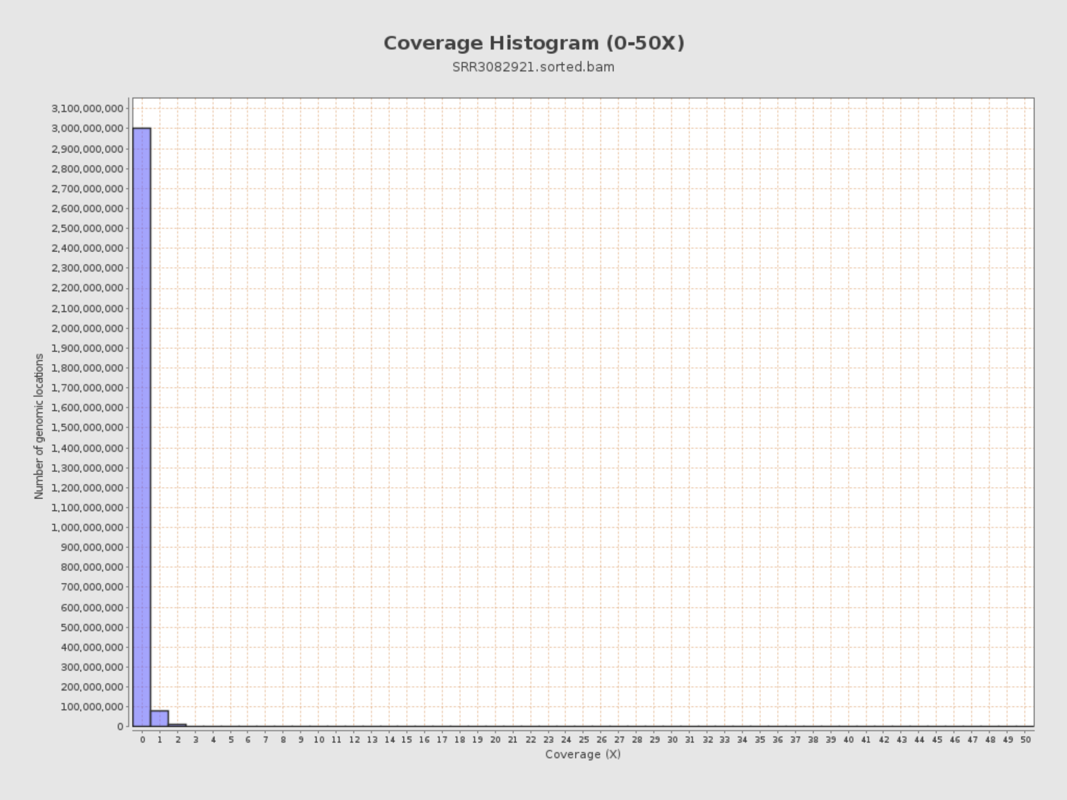
3. Results : Coverage across reference



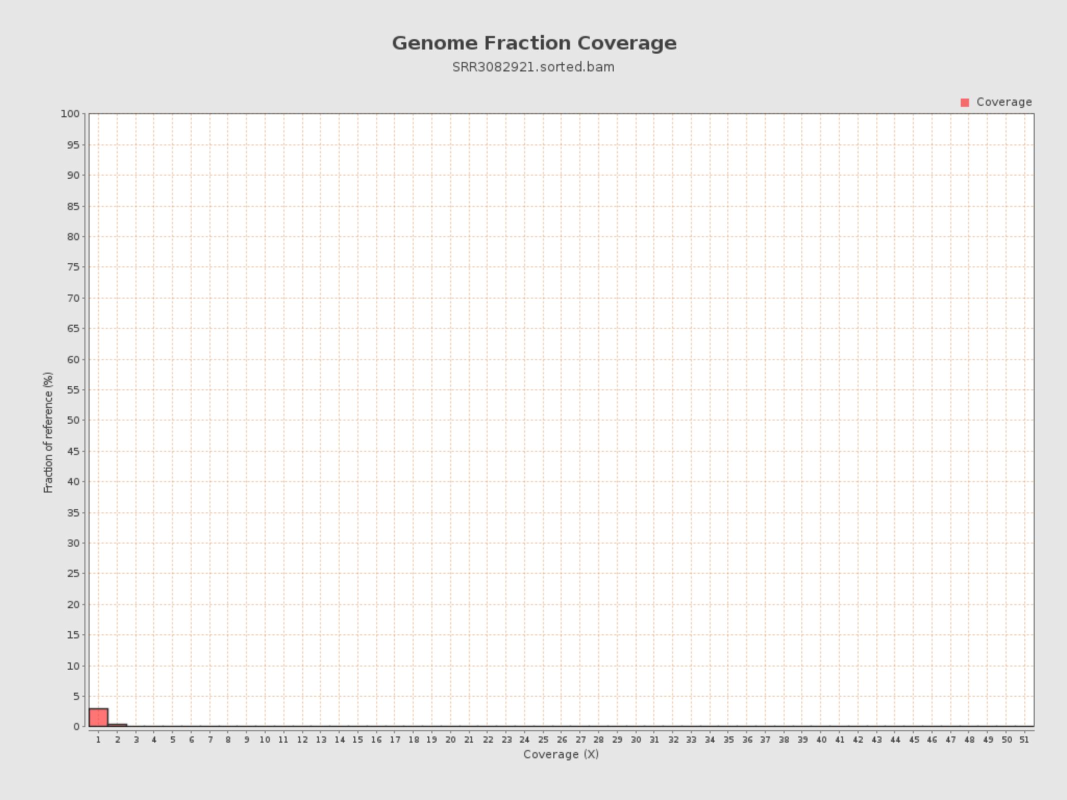
4. Results : Coverage Histogram



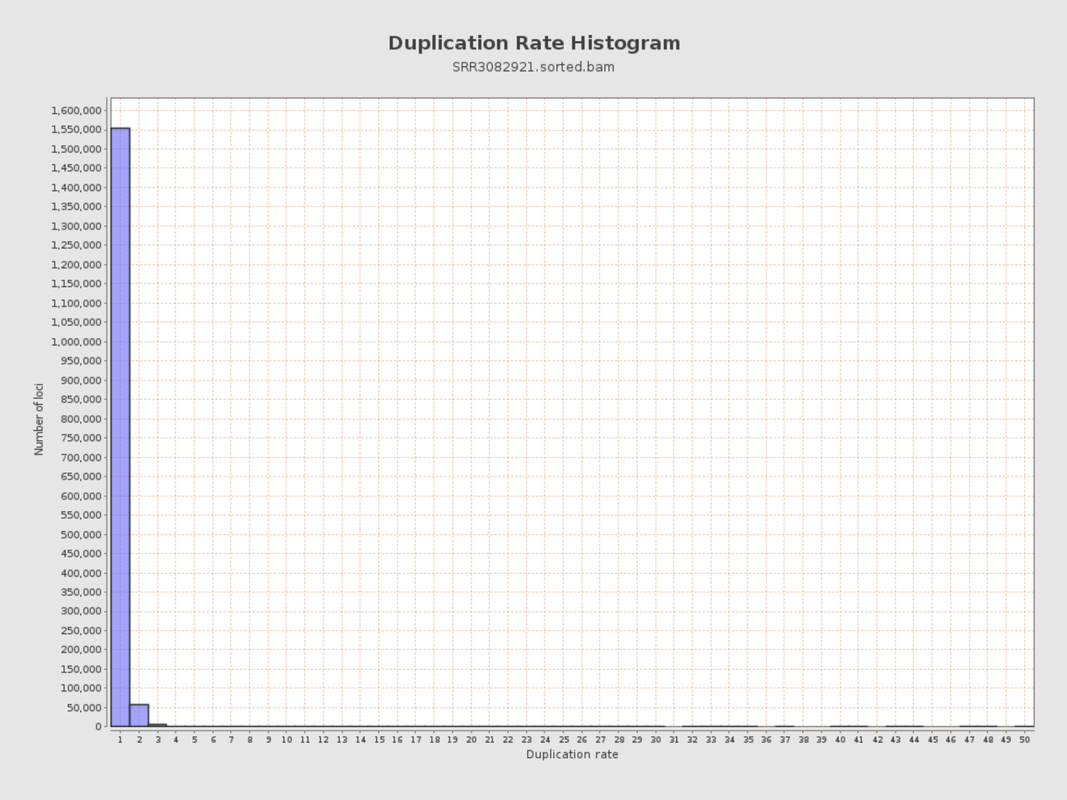
5. Results : Coverage Histogram (0-50X)



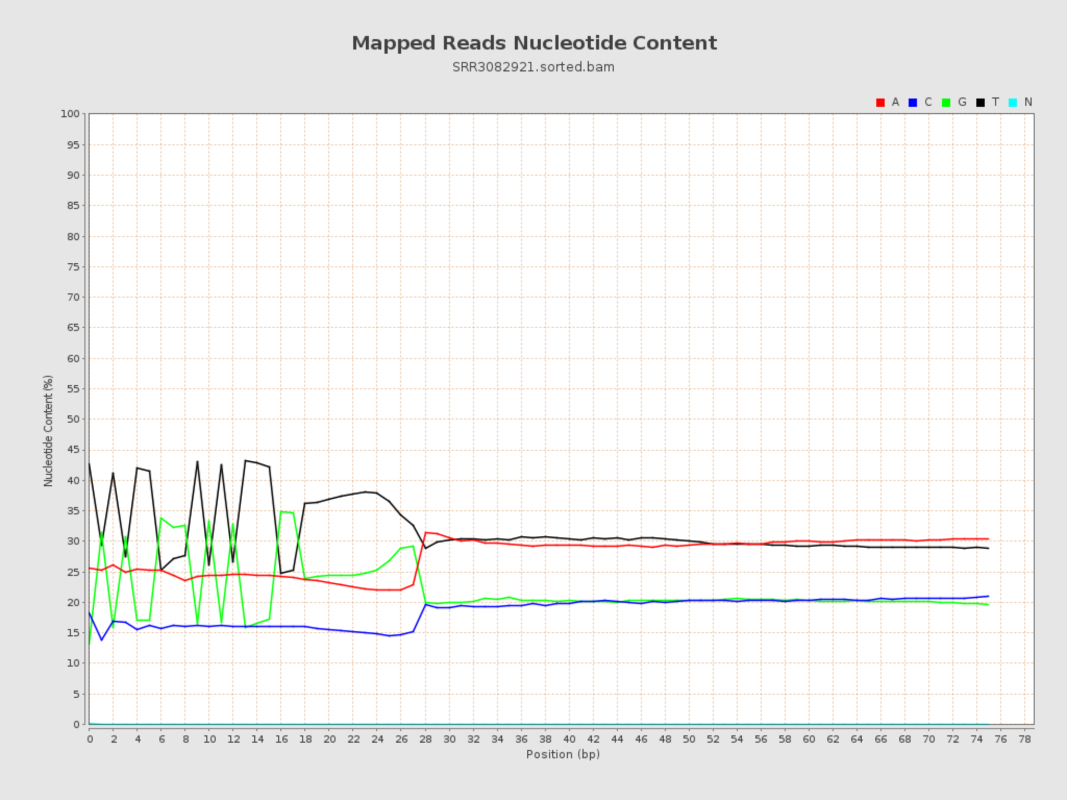
6. Results : Genome Fraction Coverage



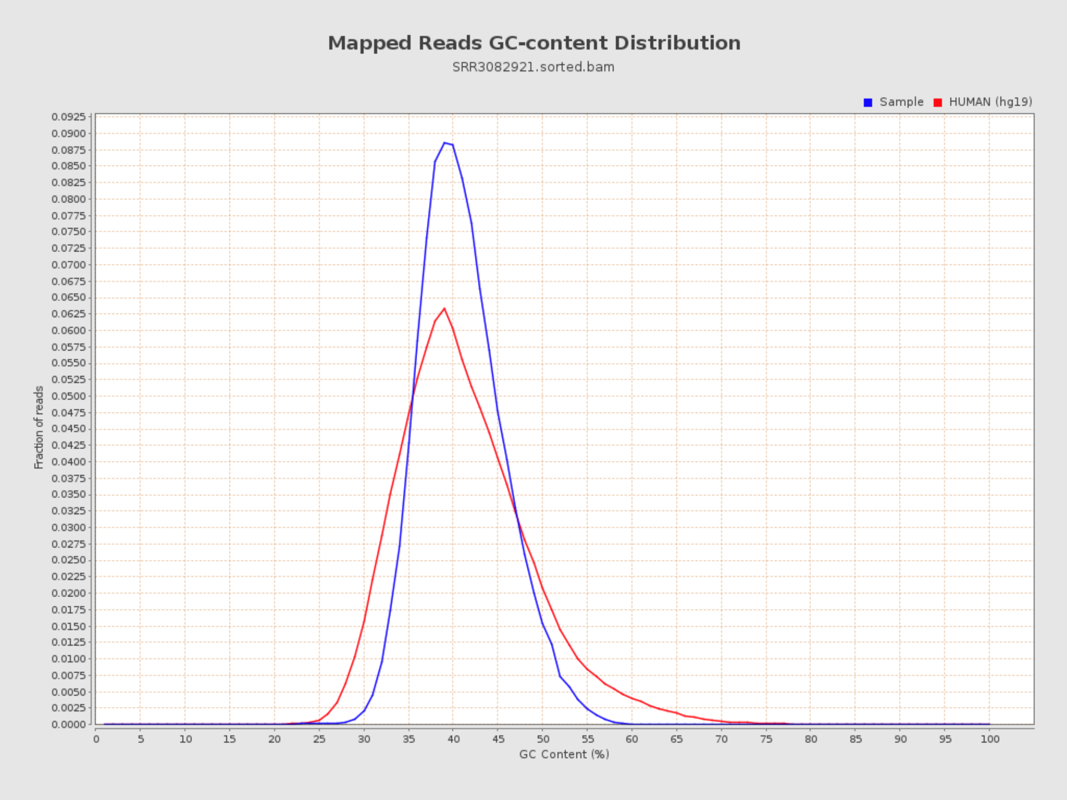
7. Results : Duplication Rate Histogram



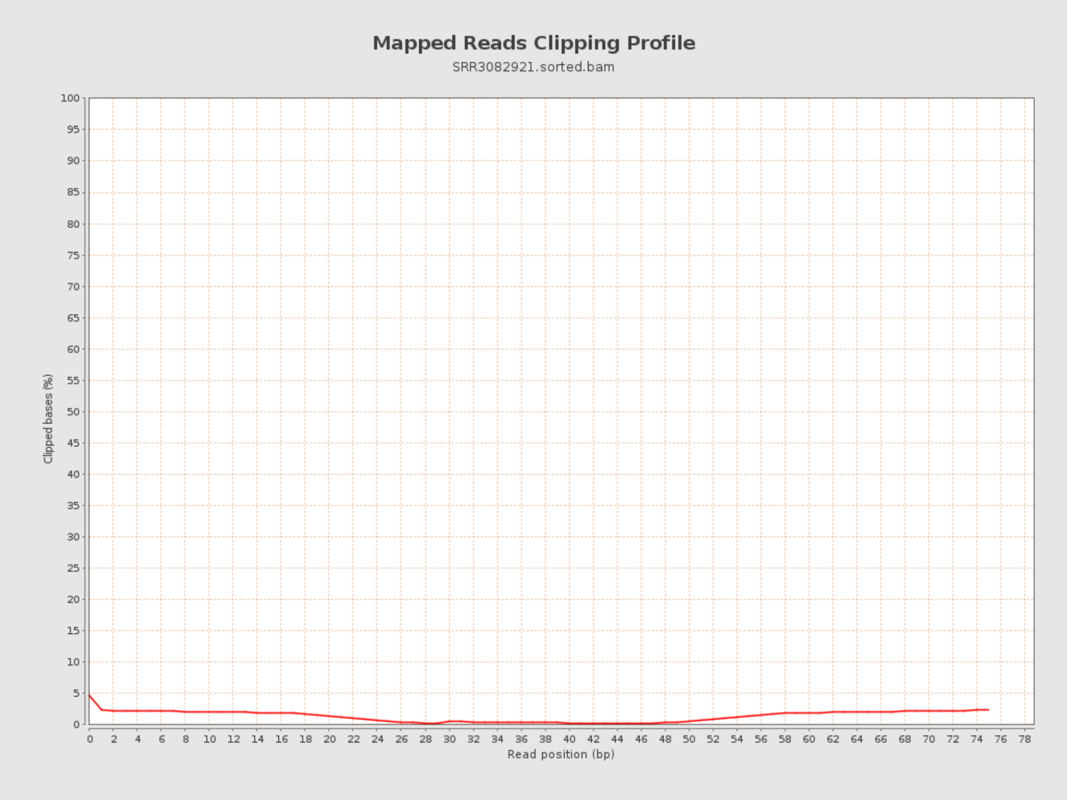
8. Results : Mapped Reads Nucleotide Content



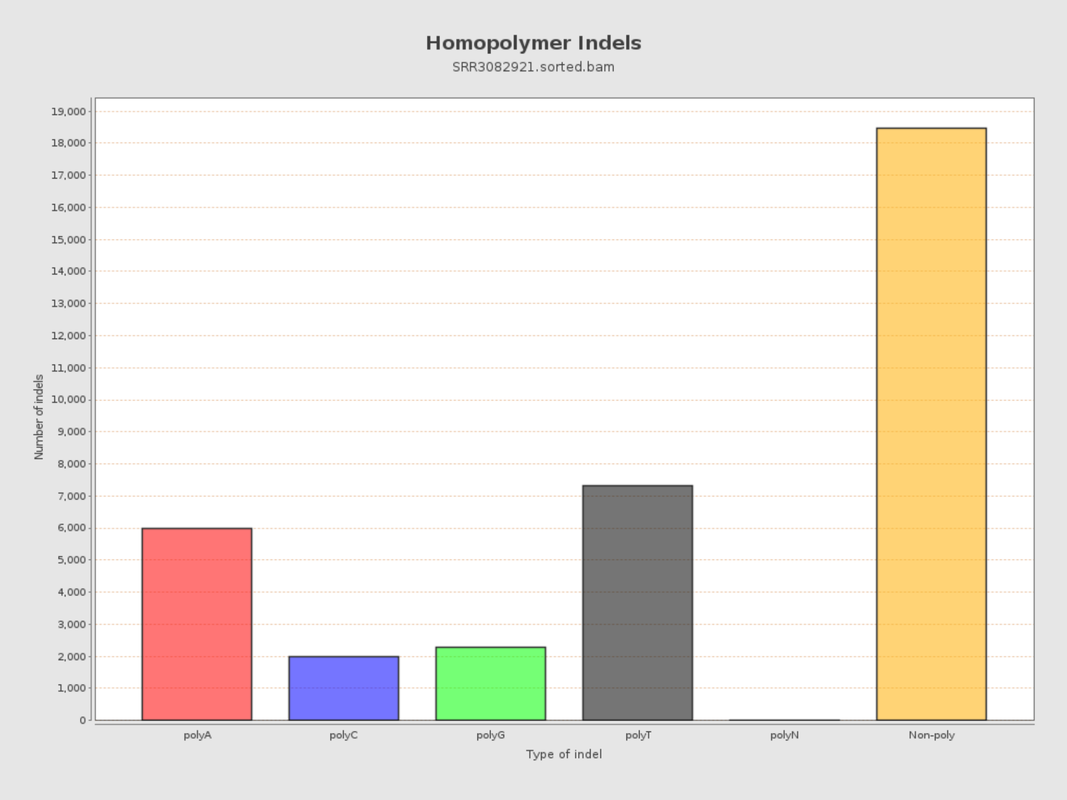
9. Results : Mapped Reads GC-content Distribution



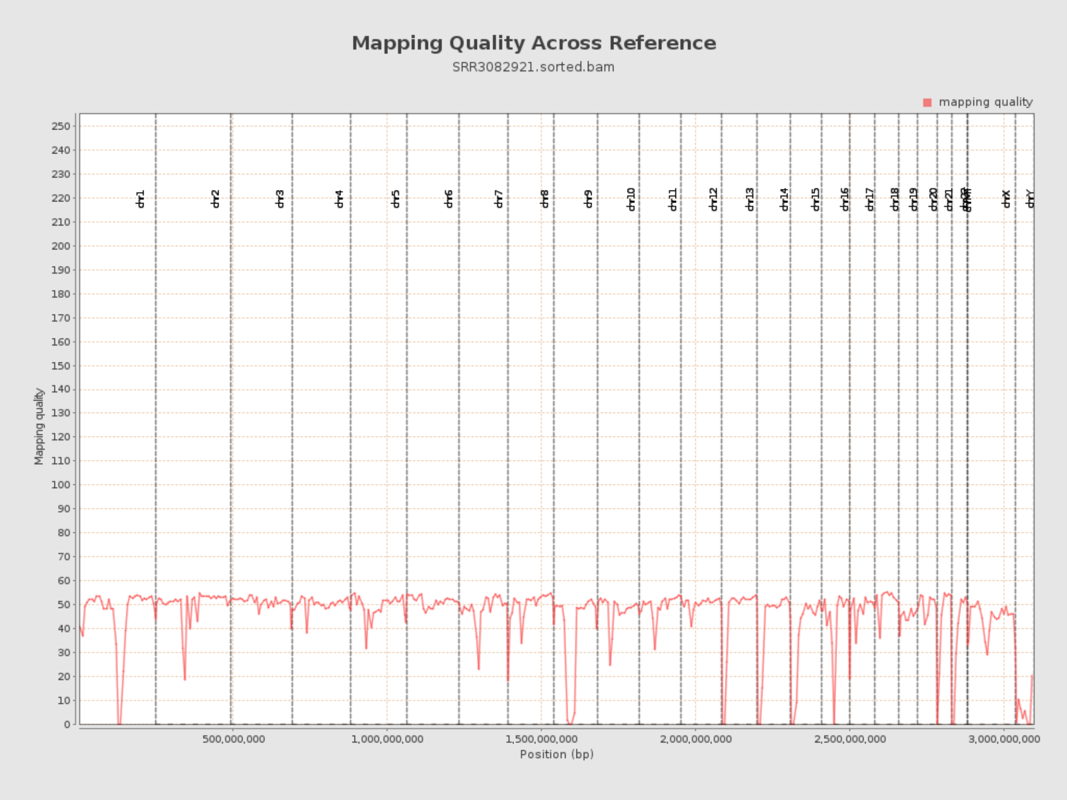
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram