Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 20:56:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082948.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_SRR3082948 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082948.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 20:56:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082948.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,832,380
Mapped reads	1,694,234 / 92.46%
Unmapped reads	138,146 / 7.54%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,165 / 0.94%
Read min/max/mean length	30 / 76 / 76.33
Duplicated reads (estimated)	75,807 / 4.14%
Duplication rate	3.76%
Clipped reads	683,677 / 37.31%

2.2. ACGT Content

Number/percentage of A's	32,097,321 / 28.03%
Number/percentage of C's	20,826,312 / 18.18%
Number/percentage of T's	36,817,394 / 32.15%
Number/percentage of G's	24,778,764 / 21.64%
Number/percentage of N's	5,655 / 0%
GC Percentage	39.82%

2.3. Coverage

Mean	0.037

Standard Deviation	0.2965

2.4. Mapping Quality

Mean Mapping Quality	46.39

2.5. Mismatches and indels

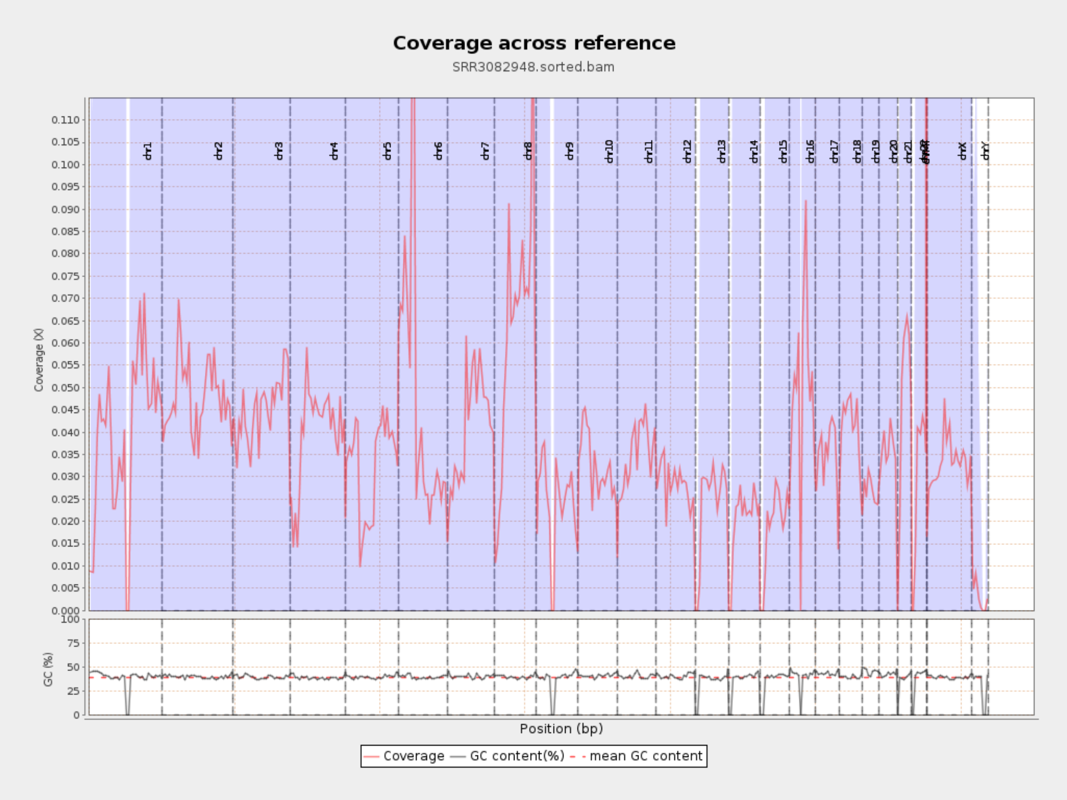
General error rate	0.72%
Mismatches	810,231
Insertions	9,581
Mapped reads with at least one insertion	0.56%
Deletions	26,671
Mapped reads with at least one deletion	1.56%
Homopolymer indels	48.81%

2.6. Chromosome stats

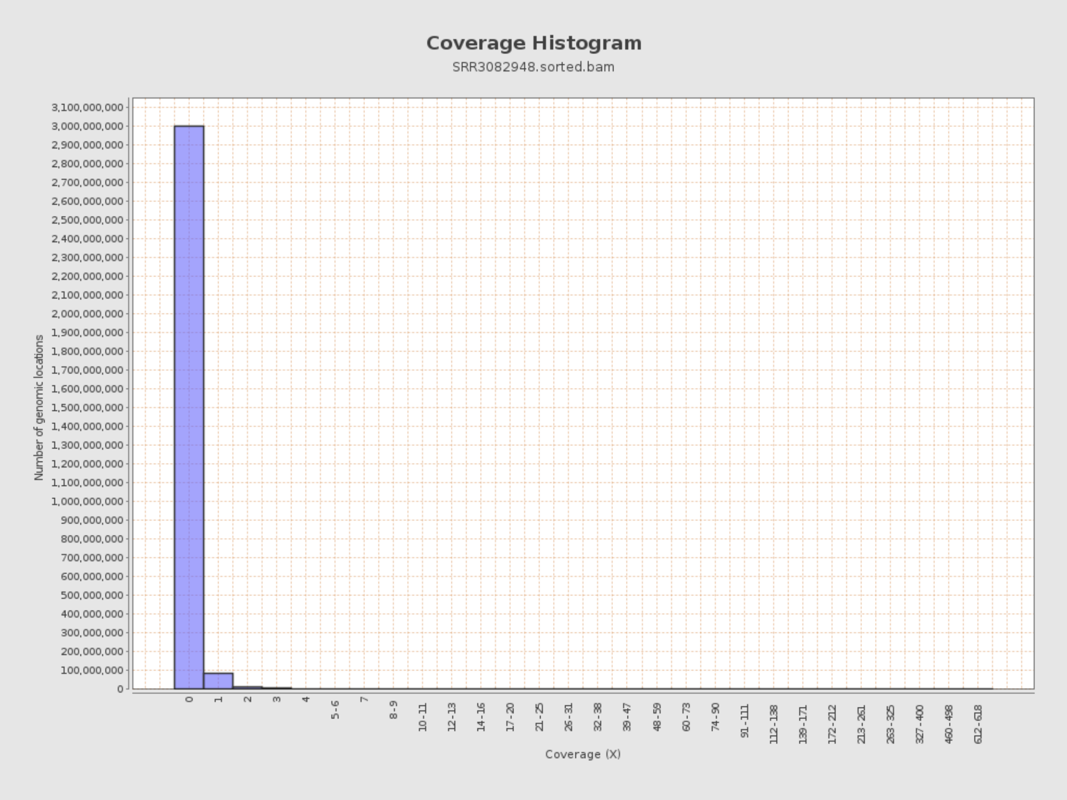
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9901281	0.0397	0.4255
chr2	243199373	11701548	0.0481	0.3985
chr3	198022430	8949531	0.0452	0.2426
chr4	191154276	7610681	0.0398	0.2301
chr5	180915260	5887380	0.0325	0.2064
chr6	171115067	8007572	0.0468	0.291
chr7	159138663	6687523	0.042	0.4427

chr8	146364022	9204403	0.0629	0.3988
chr9	141213431	3484915	0.0247	0.2454
chr10	135534747	4441232	0.0328	0.2331
chr11	135006516	4707366	0.0349	0.2731
chr12	133851895	3764327	0.0281	0.1931
chr13	115169878	2759758	0.024	0.1769
chr14	107349540	2153465	0.0201	0.1773
chr15	102531392	1899128	0.0185	0.1615
chr16	90354753	4496047	0.0498	0.2636
chr17	81195210	2801552	0.0345	0.2406
chr18	78077248	3239178	0.0415	0.4568
chr19	59128983	1601051	0.0271	0.3085
chr20	63025520	2223212	0.0353	0.2216
chr21	48129895	2247836	0.0467	0.2504
chr22	51304566	1450698	0.0283	0.1906
chrMT	16571	63335	3.822	3.1339
chrX	155270560	5096218	0.0328	0.2196
chrY	59373566	190001	0.0032	0.0677

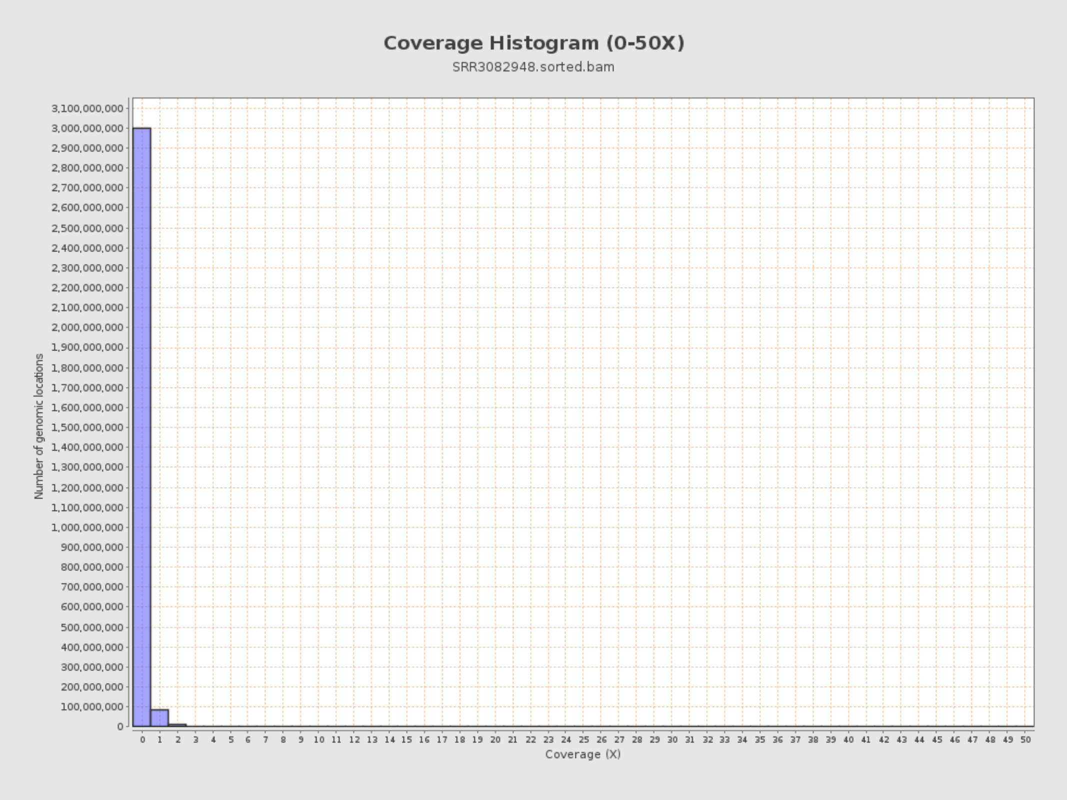
3. Results : Coverage across reference



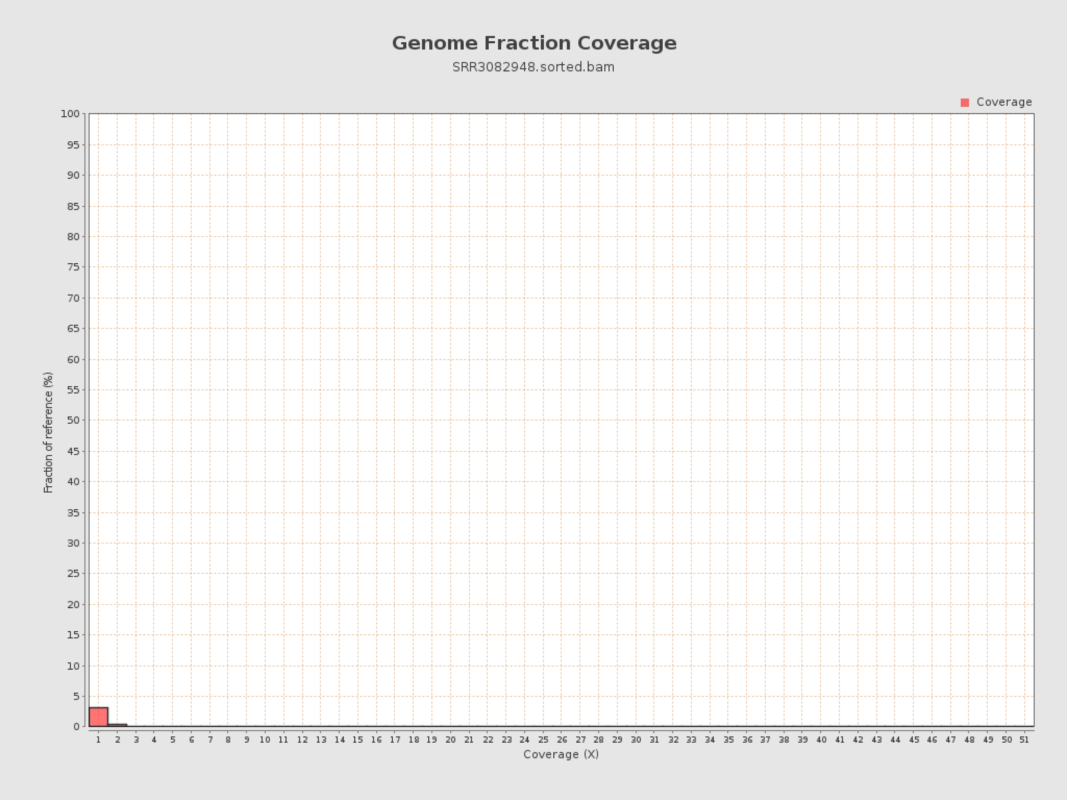
4. Results : Coverage Histogram



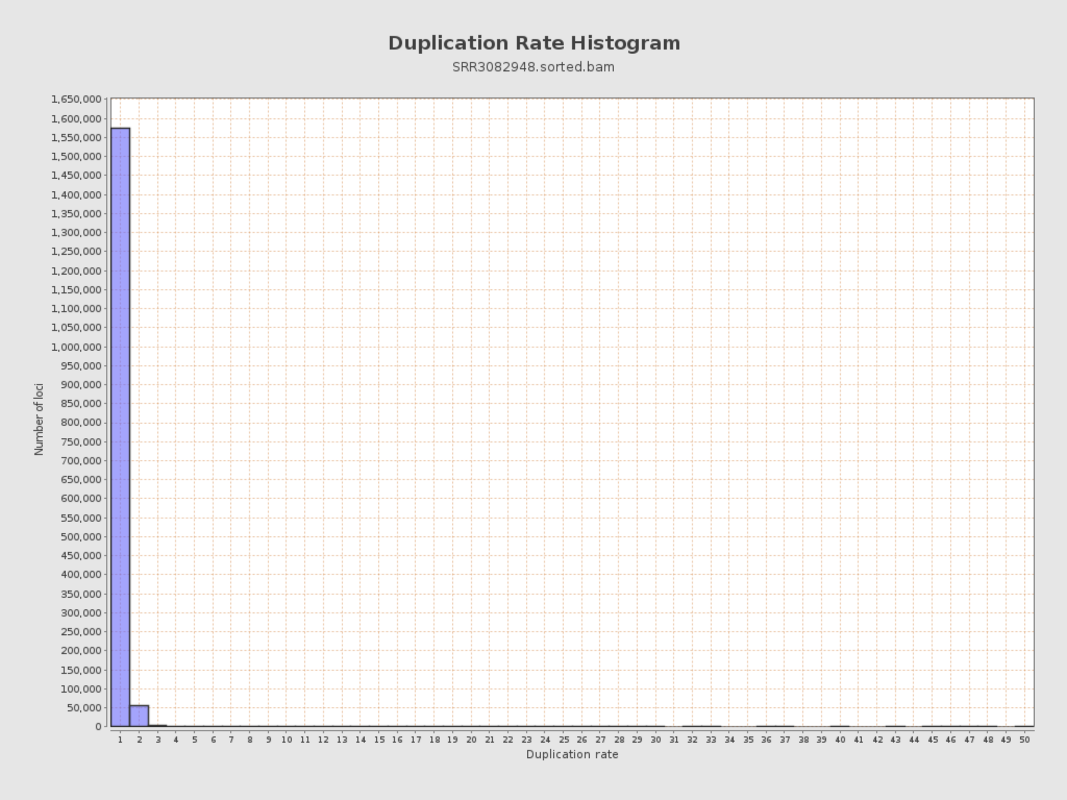
5. Results : Coverage Histogram (0-50X)



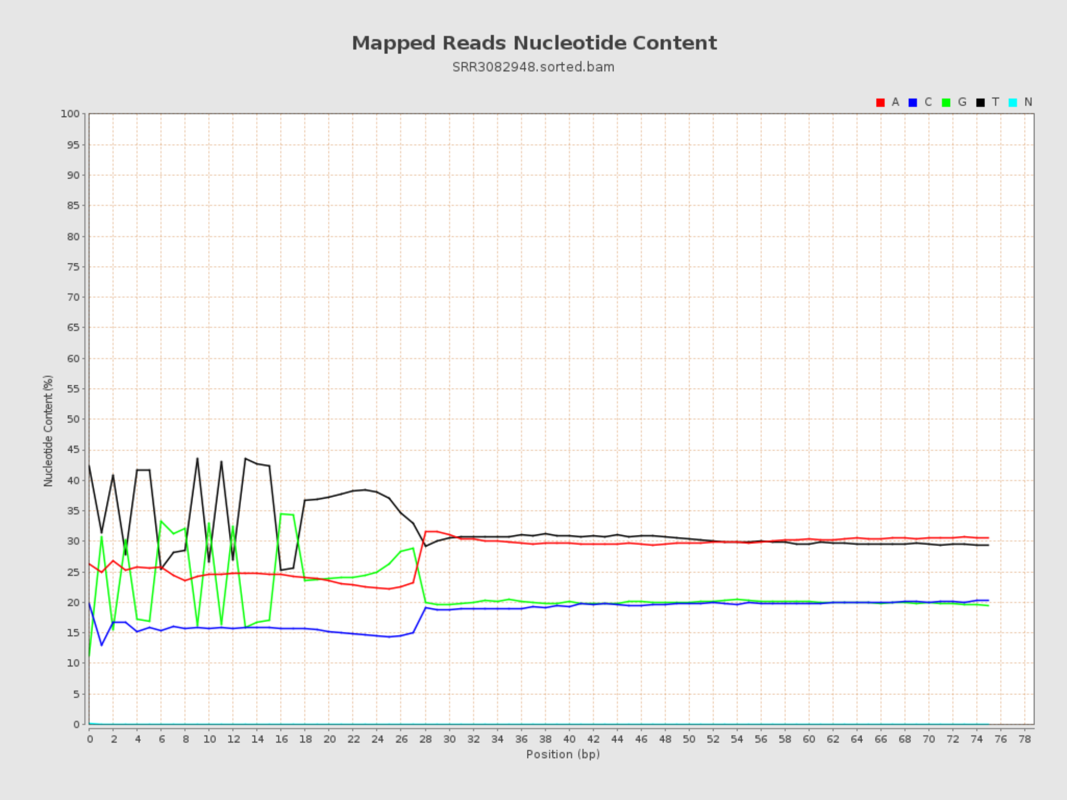
6. Results : Genome Fraction Coverage



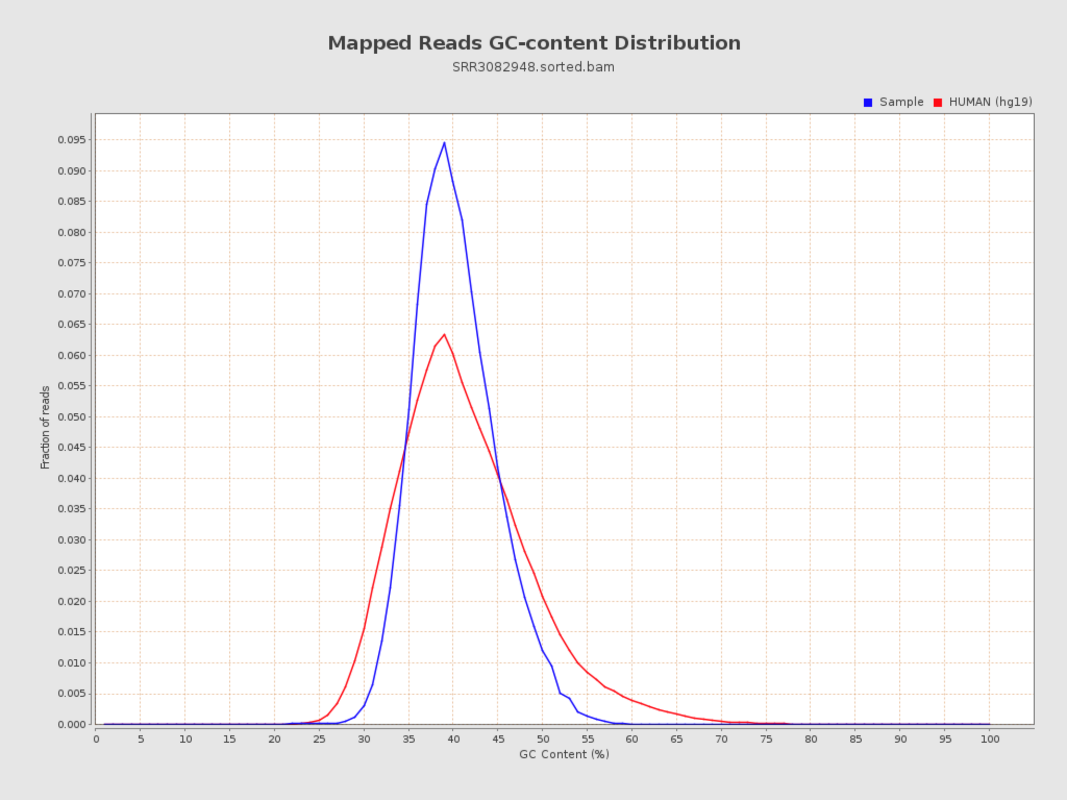
7. Results : Duplication Rate Histogram



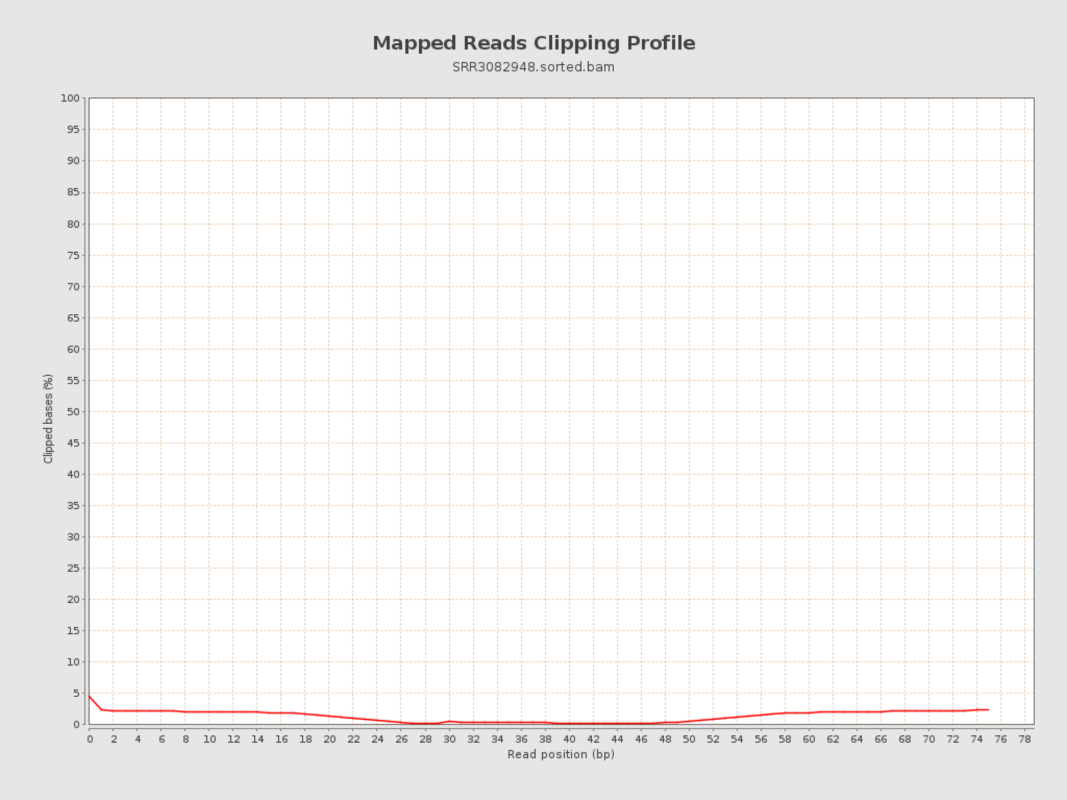
8. Results : Mapped Reads Nucleotide Content



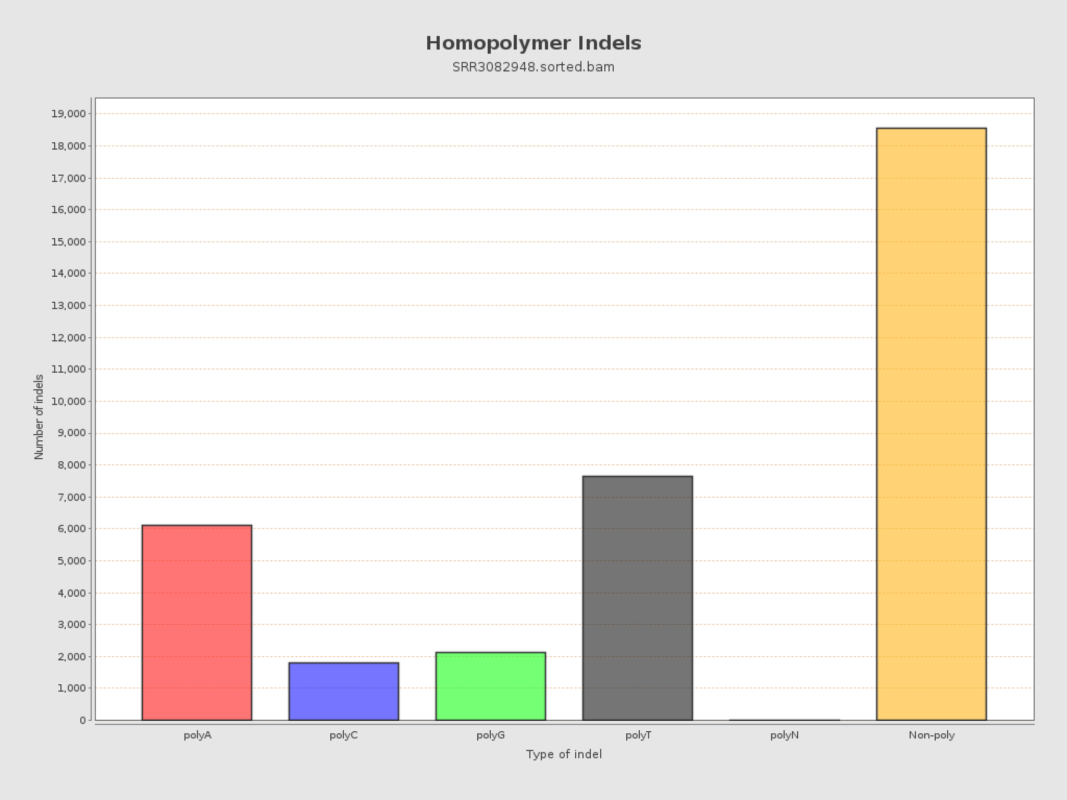
9. Results : Mapped Reads GC-content Distribution



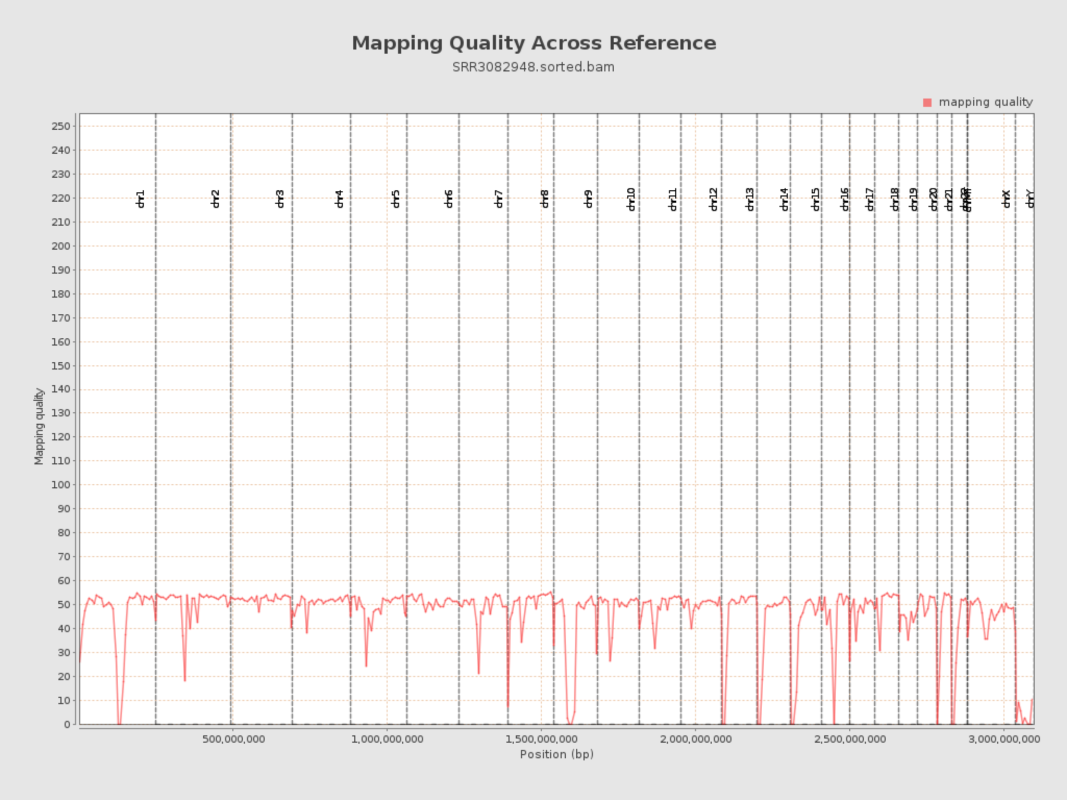
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram