Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 20:59:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082949.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_SRR3082949 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082949.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 20:59:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082949.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,954,094
Mapped reads	1,790,943 / 91.65%
Unmapped reads	163,151 / 8.35%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,001 / 0.87%
Read min/max/mean length	30 / 76 / 76.3
Duplicated reads (estimated)	96,364 / 4.93%
Duplication rate	4.44%
Clipped reads	757,280 / 38.75%

2.2. ACGT Content

Number/percentage of A's	33,414,050 / 27.8%
Number/percentage of C's	21,808,687 / 18.14%
Number/percentage of T's	38,700,969 / 32.2%
Number/percentage of G's	26,267,691 / 21.85%
Number/percentage of N's	5,666 / 0%
GC Percentage	40%

2.3. Coverage

Mean	0.0388

Standard Deviation	0.3317

2.4. Mapping Quality

Mean Mapping Quality	46.01

2.5. Mismatches and indels

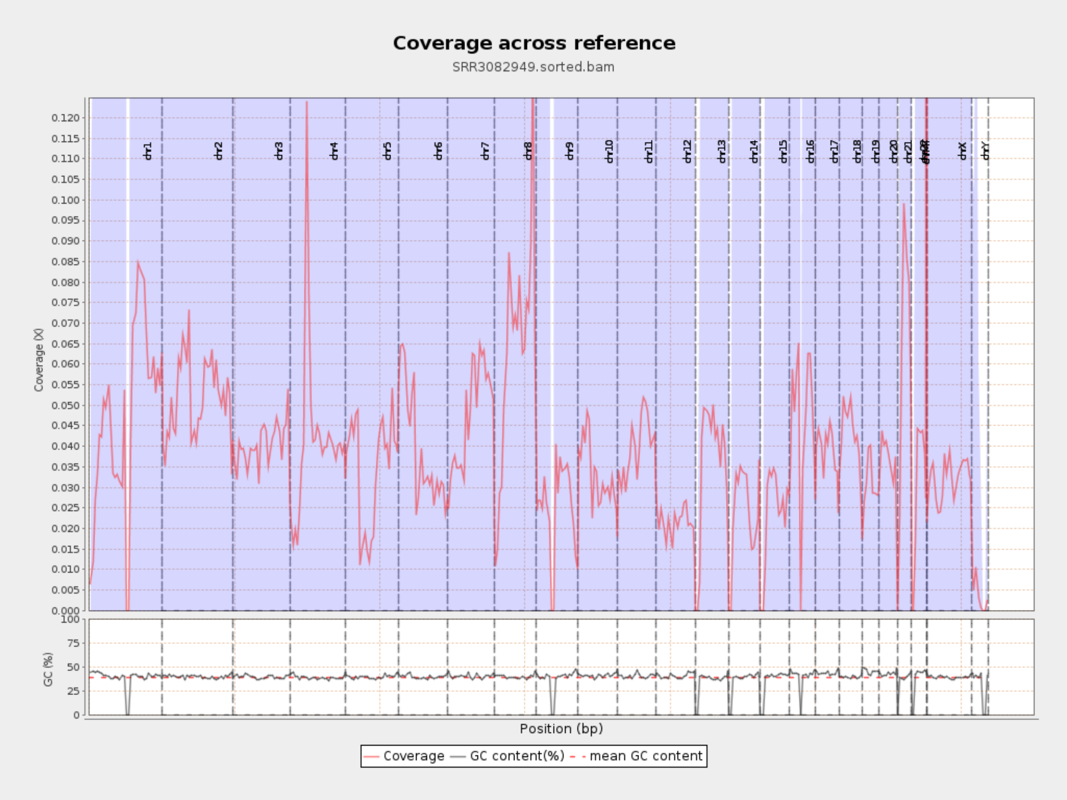
General error rate	0.74%
Mismatches	873,099
Insertions	10,130
Mapped reads with at least one insertion	0.56%
Deletions	28,011
Mapped reads with at least one deletion	1.55%
Homopolymer indels	48.52%

2.6. Chromosome stats

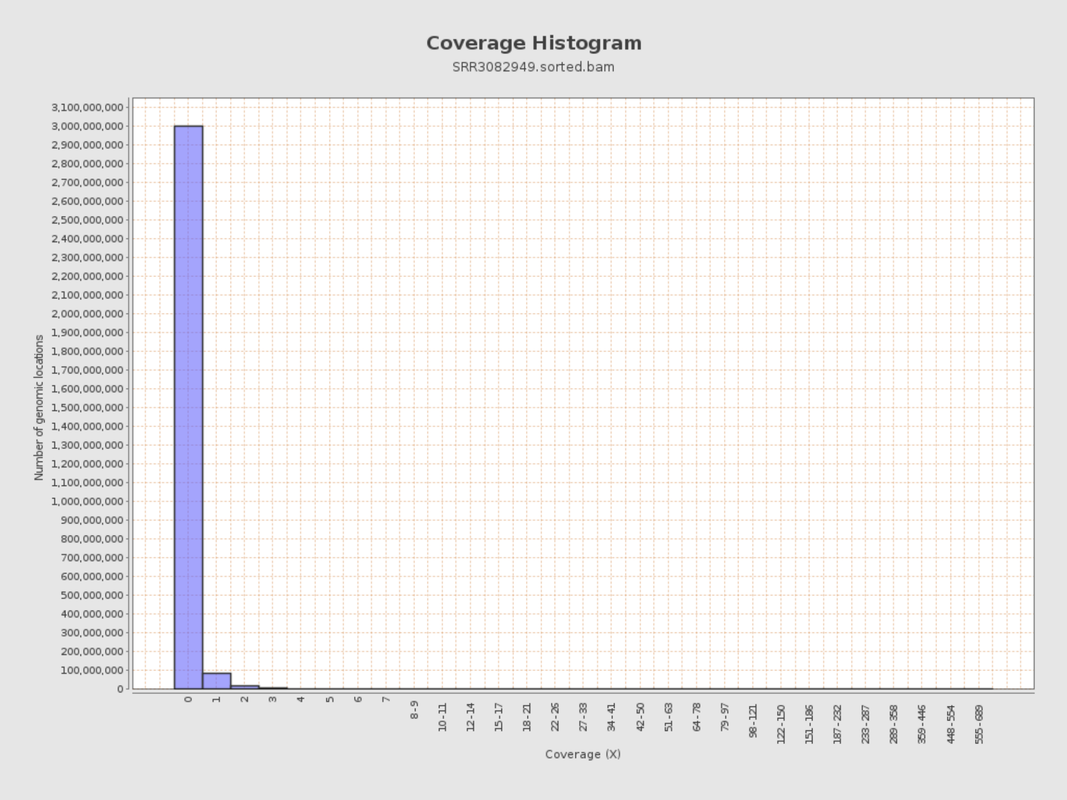
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11735255	0.0471	0.4877
chr2	243199373	12699438	0.0522	0.454
chr3	198022430	7996152	0.0404	0.2369
chr4	191154276	7937715	0.0415	0.2503
chr5	180915260	6211172	0.0343	0.2206
chr6	171115067	6701661	0.0392	0.2792
chr7	159138663	7627758	0.0479	0.4171

chr8	146364022	9366165	0.064	0.4614
chr9	141213431	3613447	0.0256	0.3143
chr10	135534747	4556611	0.0336	0.2493
chr11	135006516	5324017	0.0394	0.3103
chr12	133851895	2866107	0.0214	0.1774
chr13	115169878	4109154	0.0357	0.2261
chr14	107349540	2459230	0.0229	0.2028
chr15	102531392	2414536	0.0235	0.1919
chr16	90354753	4263257	0.0472	0.2701
chr17	81195210	3167193	0.039	0.272
chr18	78077248	3394422	0.0435	0.6556
chr19	59128983	1836083	0.0311	0.3631
chr20	63025520	2319546	0.0368	0.2394
chr21	48129895	2970508	0.0617	0.3037
chr22	51304566	1497135	0.0292	0.1996
chrMT	16571	14027	0.8465	1.1139
chrX	155270560	4952132	0.0319	0.2337
chrY	59373566	210379	0.0035	0.083

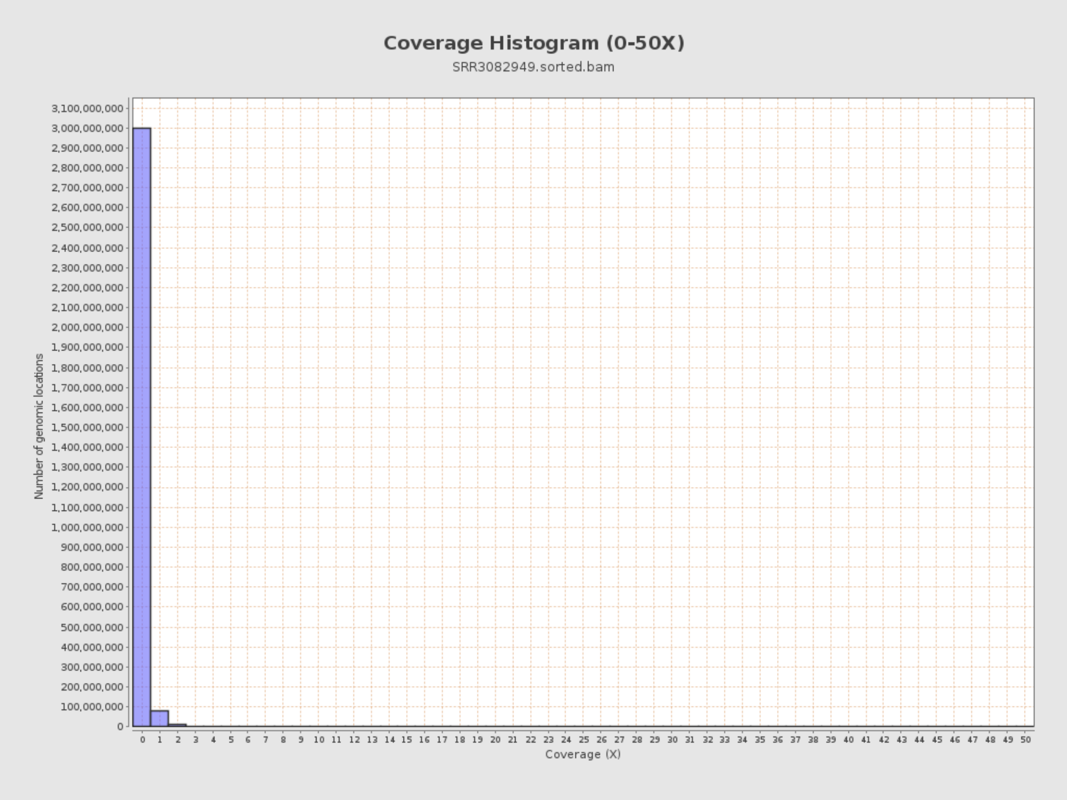
3. Results : Coverage across reference



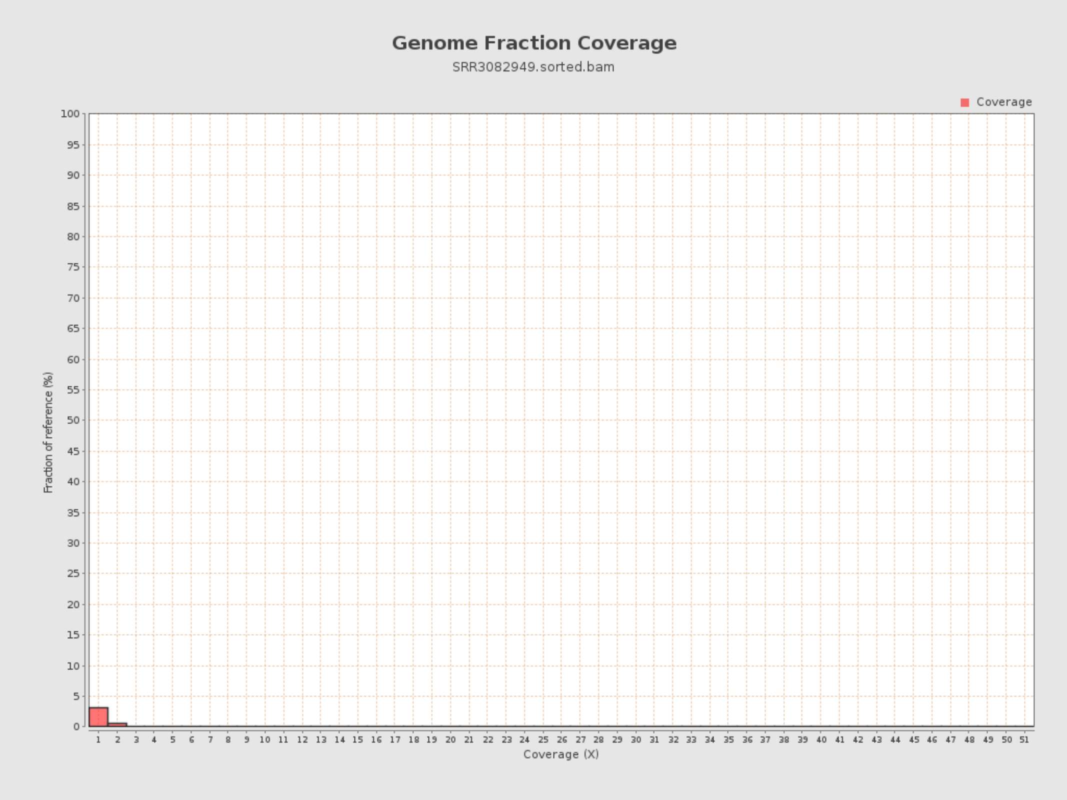
4. Results : Coverage Histogram



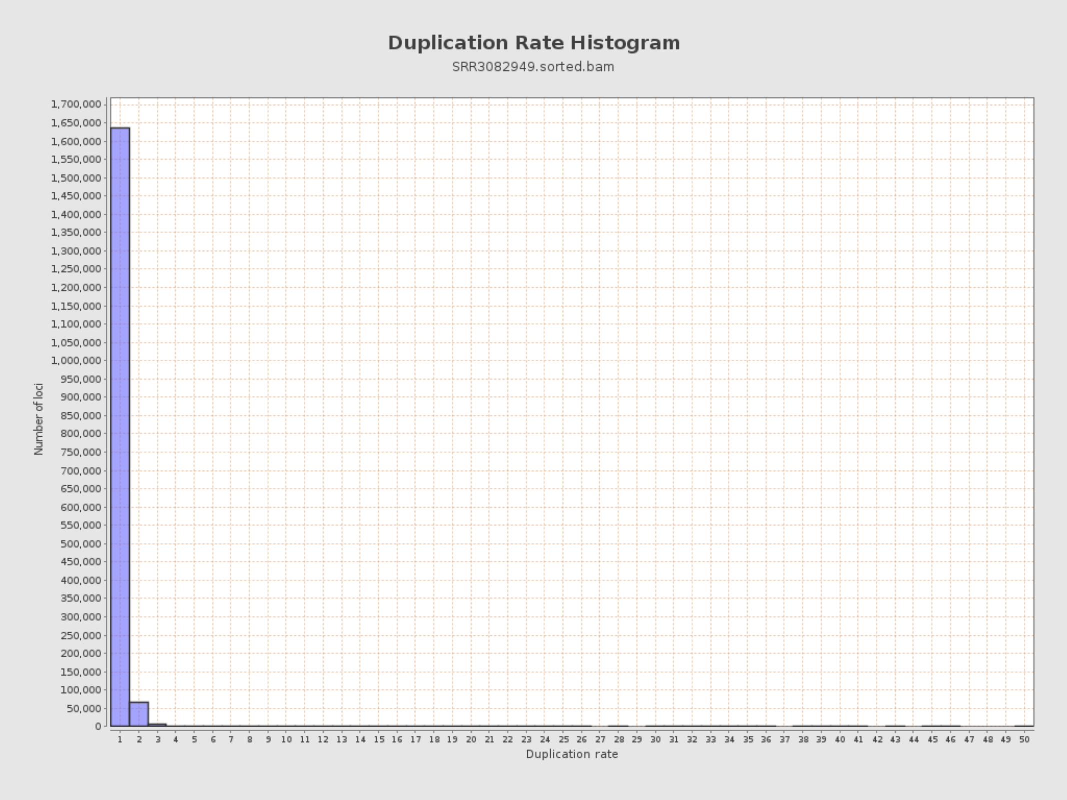
5. Results : Coverage Histogram (0-50X)



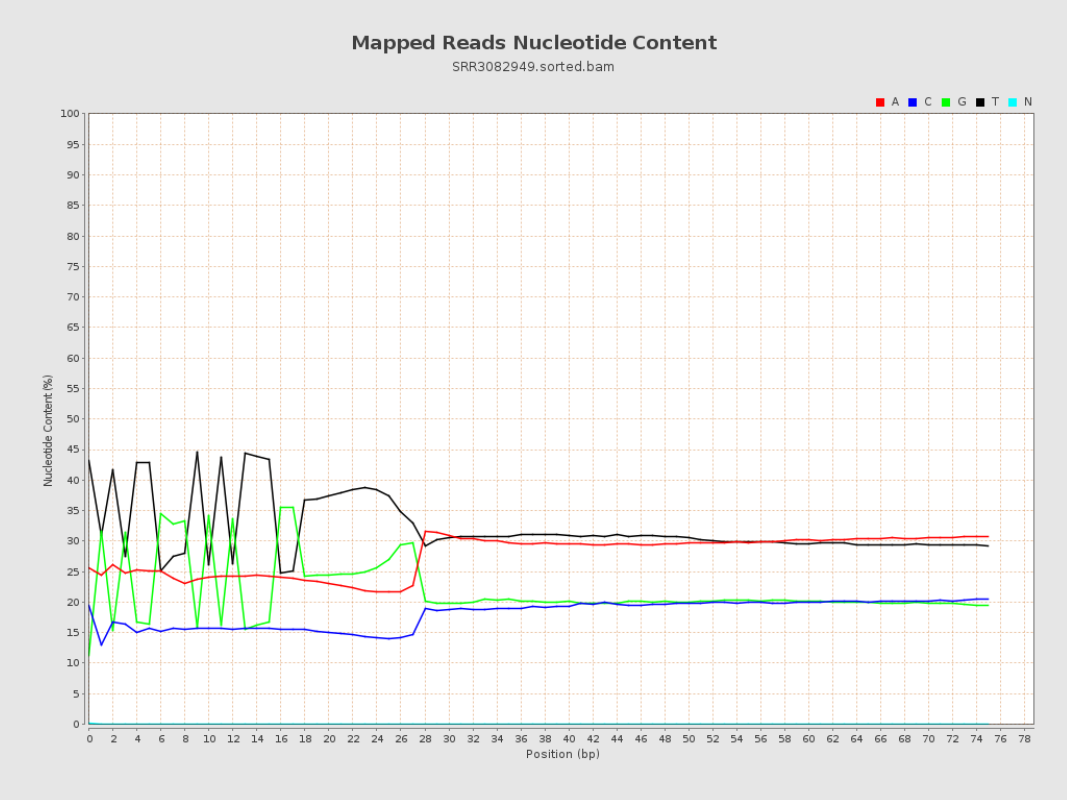
6. Results : Genome Fraction Coverage



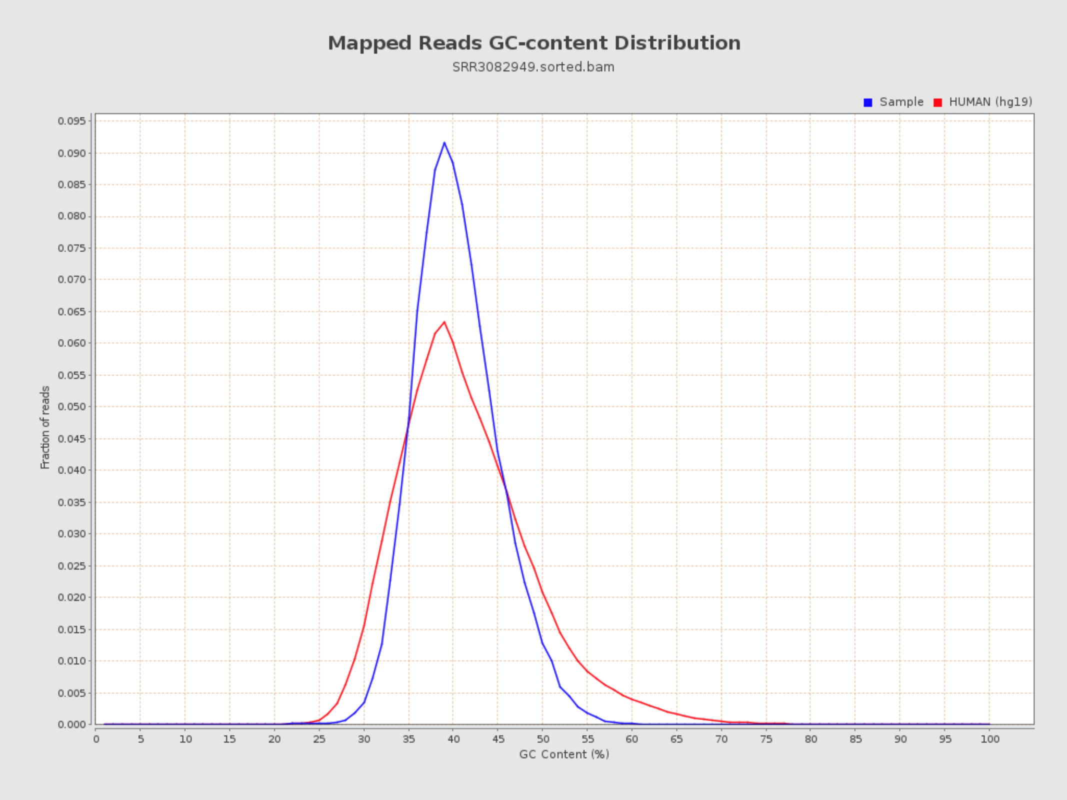
7. Results : Duplication Rate Histogram



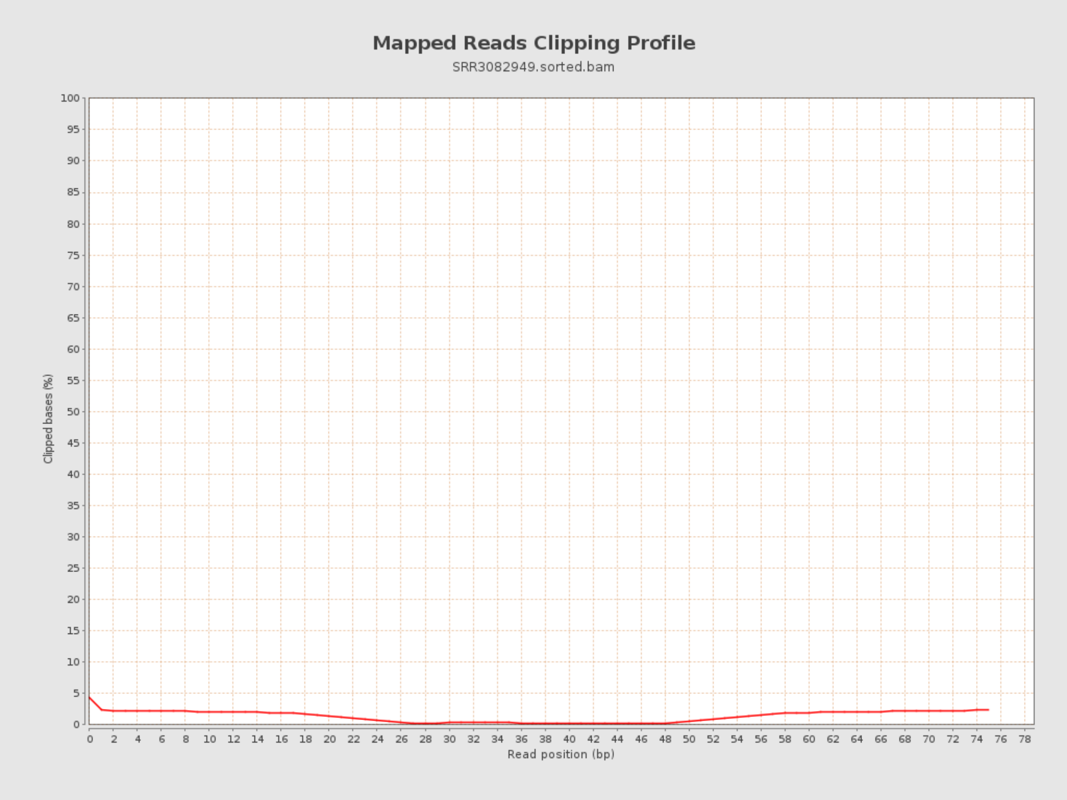
8. Results : Mapped Reads Nucleotide Content



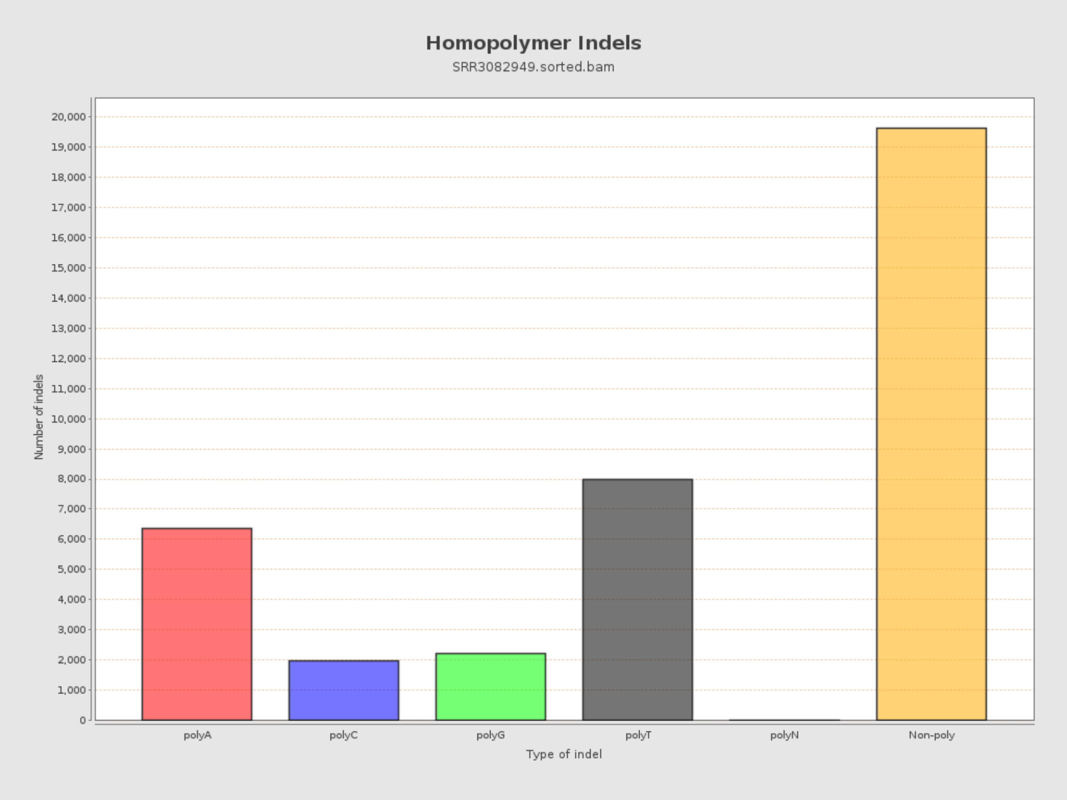
9. Results : Mapped Reads GC-content Distribution



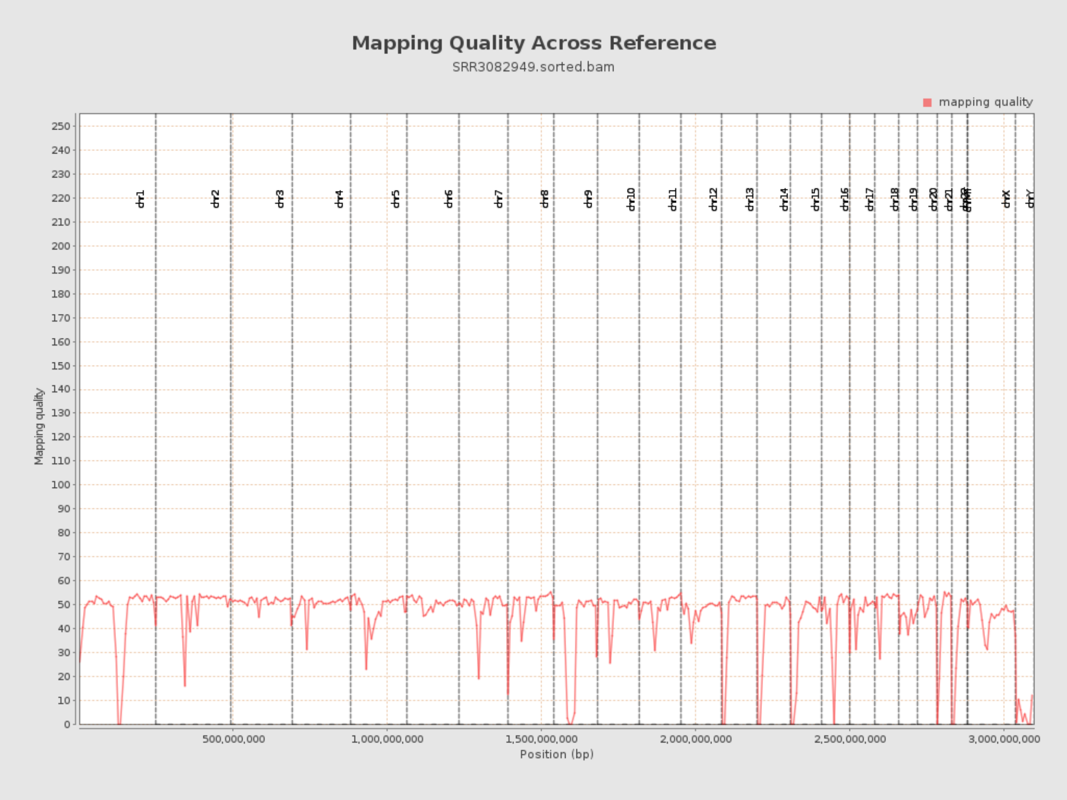
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram