Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 15:36:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082497.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_SRR3082497 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082497.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 15:36:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082497.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,296,230
Mapped reads	1,161,629 / 89.62%
Unmapped reads	134,601 / 10.38%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,161 / 0.78%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	29,865 / 2.3%
Duplication rate	2.01%
Clipped reads	462,012 / 35.64%

2.2. ACGT Content

Number/percentage of A's	23,281,140 / 29.25%
Number/percentage of C's	14,977,493 / 18.82%
Number/percentage of T's	24,129,349 / 30.31%
Number/percentage of G's	17,206,187 / 21.62%
Number/percentage of N's	1,669 / 0%
GC Percentage	40.43%

2.3. Coverage

Mean	0.0257

Standard Deviation	0.2396

2.4. Mapping Quality

Mean Mapping Quality	46.58

2.5. Mismatches and indels

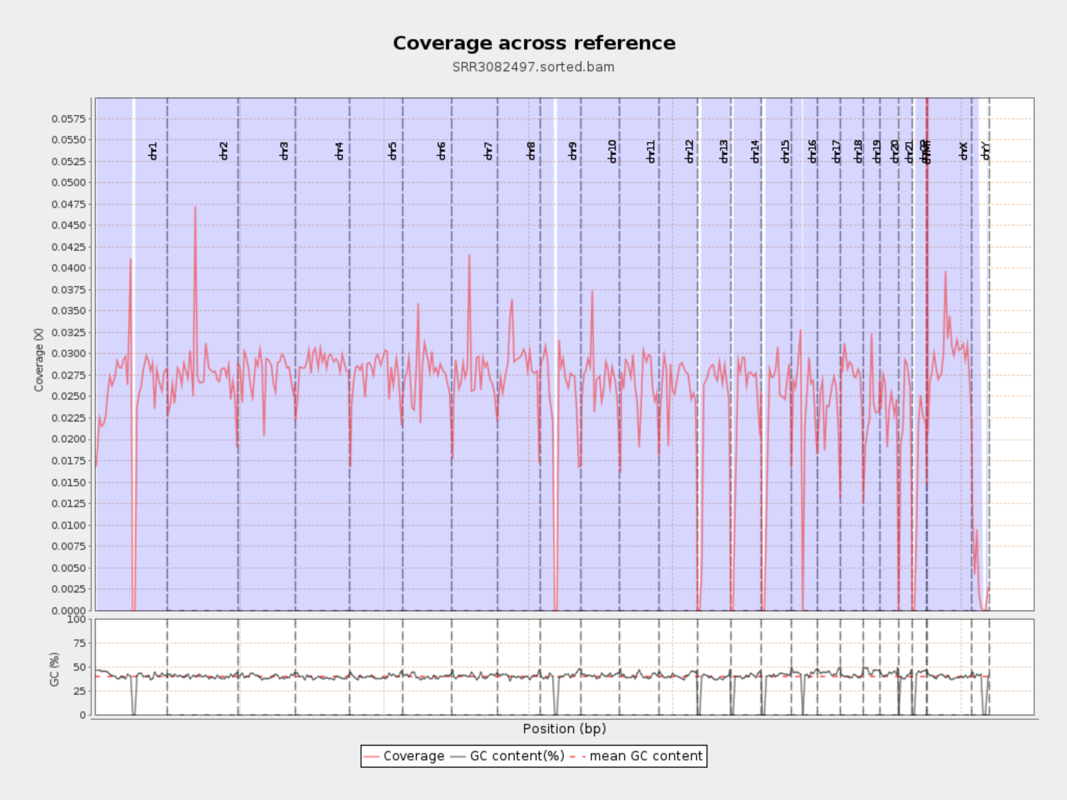
General error rate	0.88%
Mismatches	685,304
Insertions	6,526
Mapped reads with at least one insertion	0.56%
Deletions	17,159
Mapped reads with at least one deletion	1.46%
Homopolymer indels	46.76%

2.6. Chromosome stats

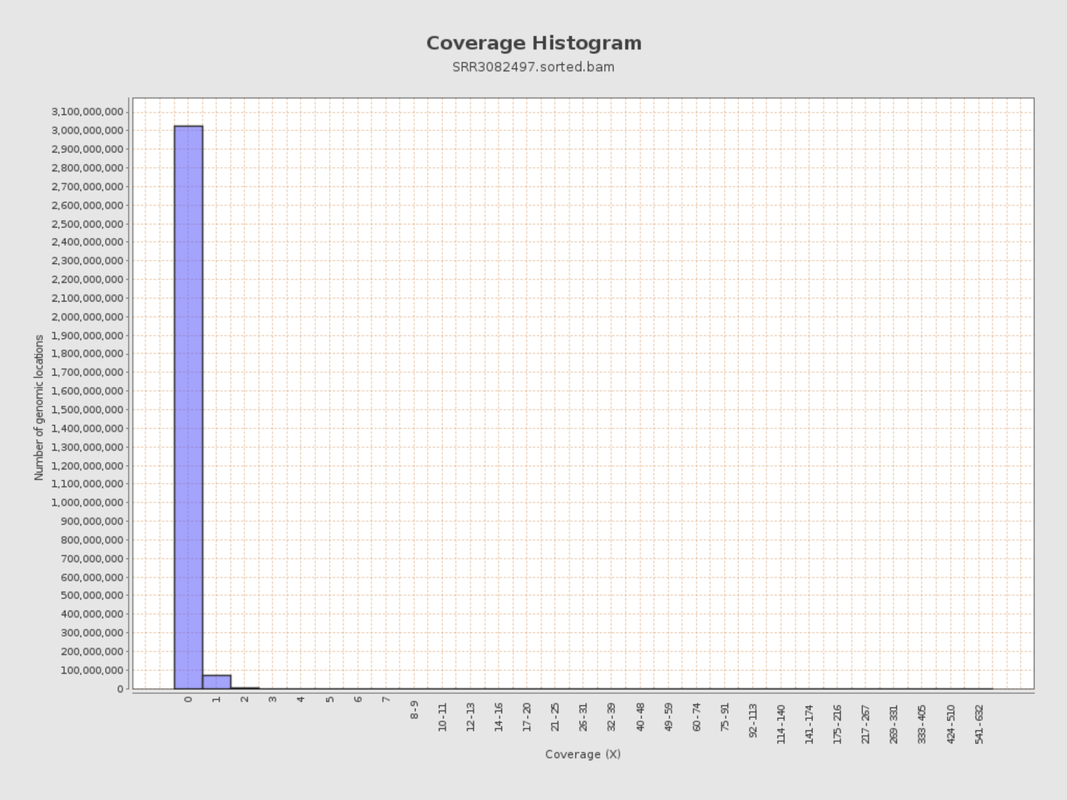
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6269048	0.0252	0.374
chr2	243199373	6724254	0.0276	0.2726
chr3	198022430	5513705	0.0278	0.1769
chr4	191154276	5486651	0.0287	0.1822
chr5	180915260	5027604	0.0278	0.177
chr6	171115067	4731512	0.0277	0.1937
chr7	159138663	4396898	0.0276	0.2836

chr8	146364022	4186769	0.0286	0.4218
chr9	141213431	3384091	0.024	0.2174
chr10	135534747	3681358	0.0272	0.2181
chr11	135006516	3603361	0.0267	0.2013
chr12	133851895	3523053	0.0263	0.1722
chr13	115169878	2612050	0.0227	0.1587
chr14	107349540	2421719	0.0226	0.1679
chr15	102531392	2266032	0.0221	0.1575
chr16	90354753	2127772	0.0235	0.1724
chr17	81195210	1912224	0.0236	0.17
chr18	78077248	2195011	0.0281	0.3559
chr19	59128983	1373704	0.0232	0.2953
chr20	63025520	1490549	0.0236	0.1643
chr21	48129895	1055029	0.0219	0.1616
chr22	51304566	802775	0.0156	0.1317
chrMT	16571	6880	0.4152	0.687
chrX	155270560	4629391	0.0298	0.1948
chrY	59373566	202577	0.0034	0.0822

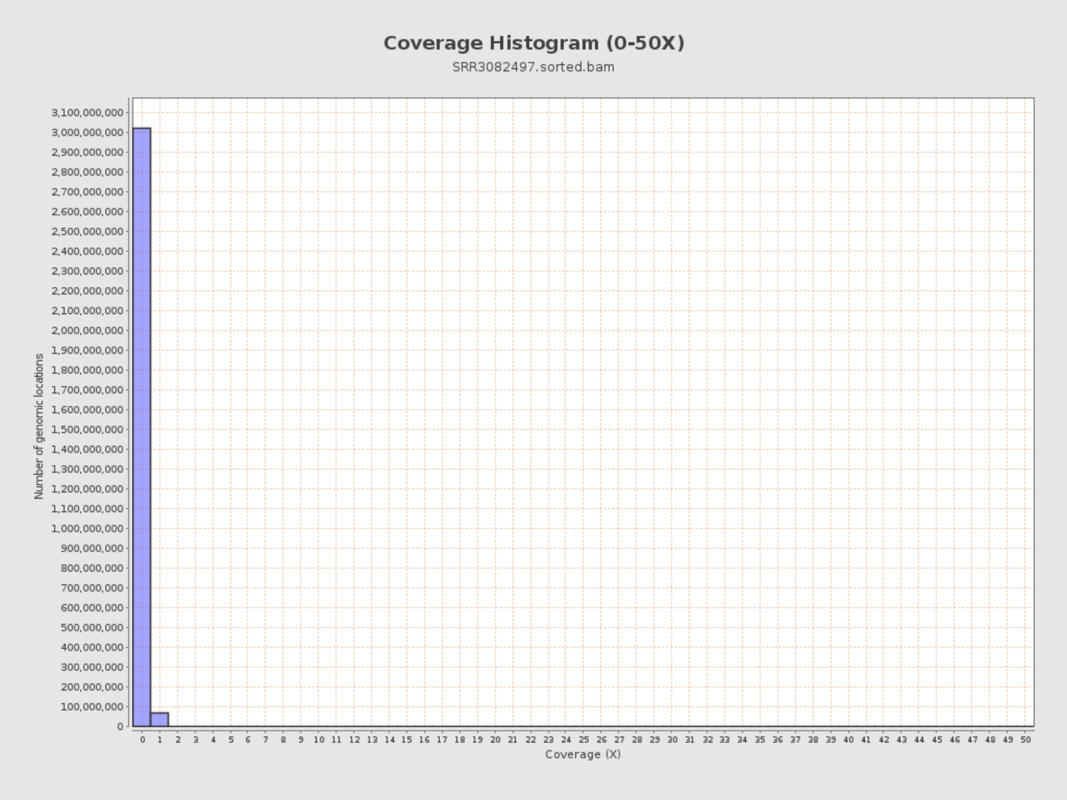
3. Results : Coverage across reference



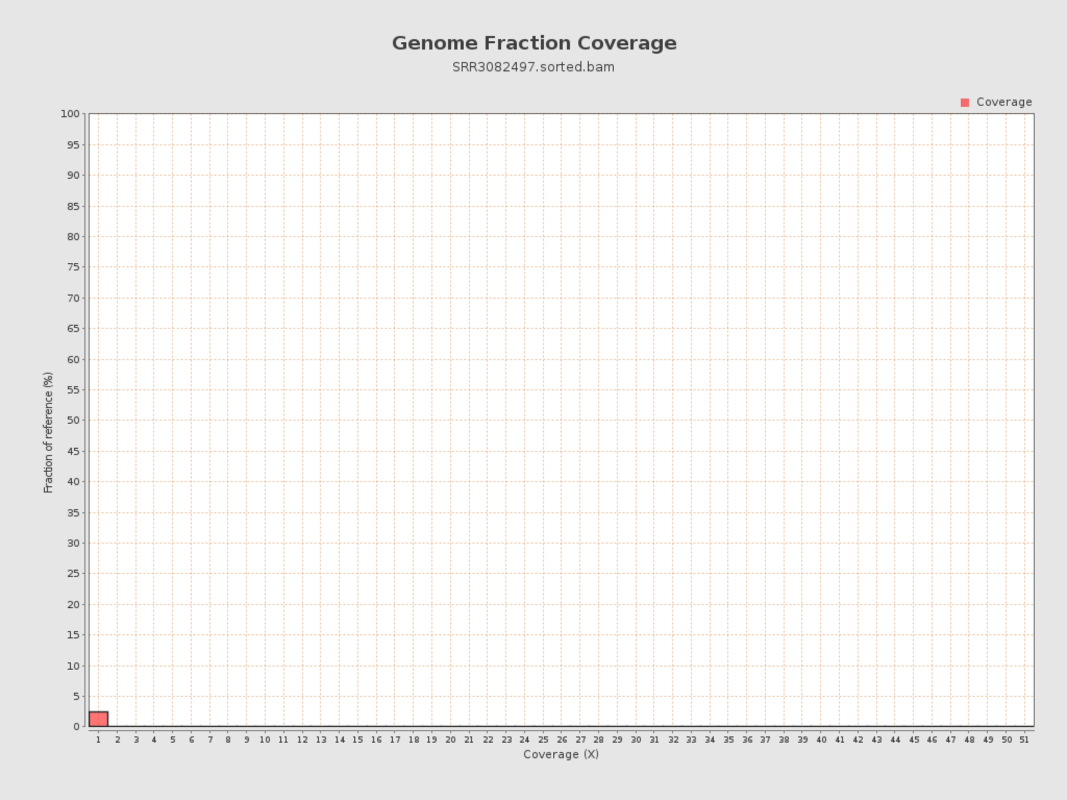
4. Results : Coverage Histogram



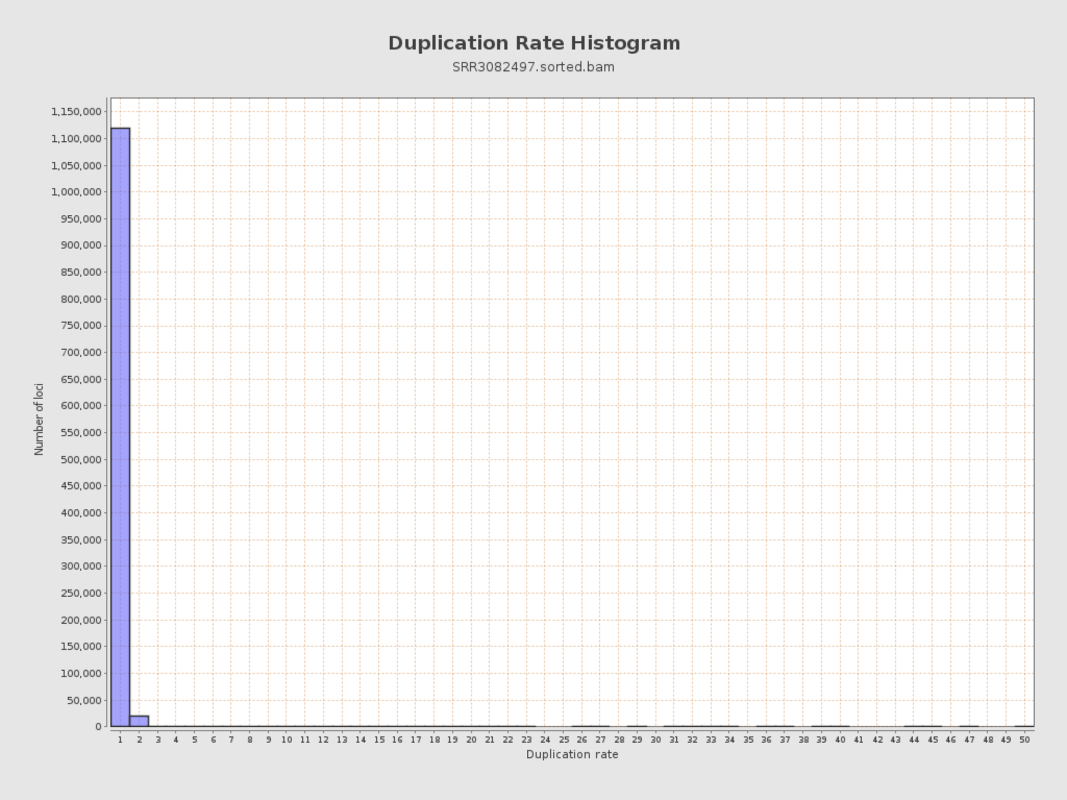
5. Results : Coverage Histogram (0-50X)



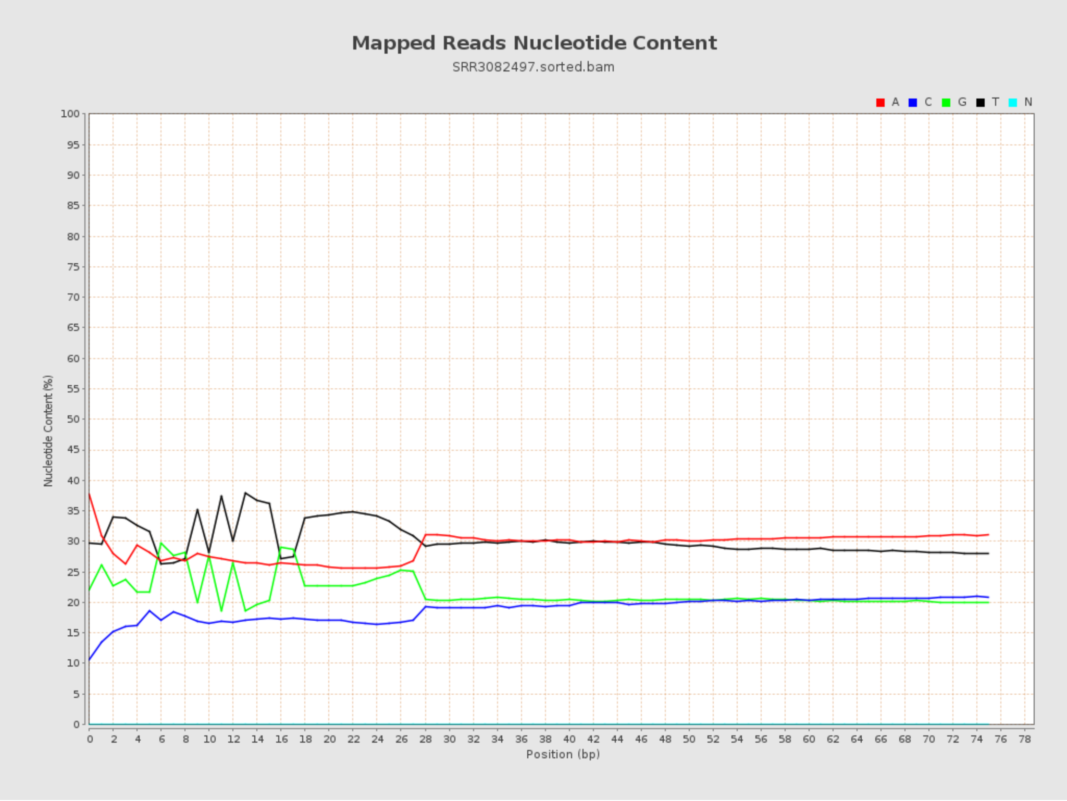
6. Results : Genome Fraction Coverage



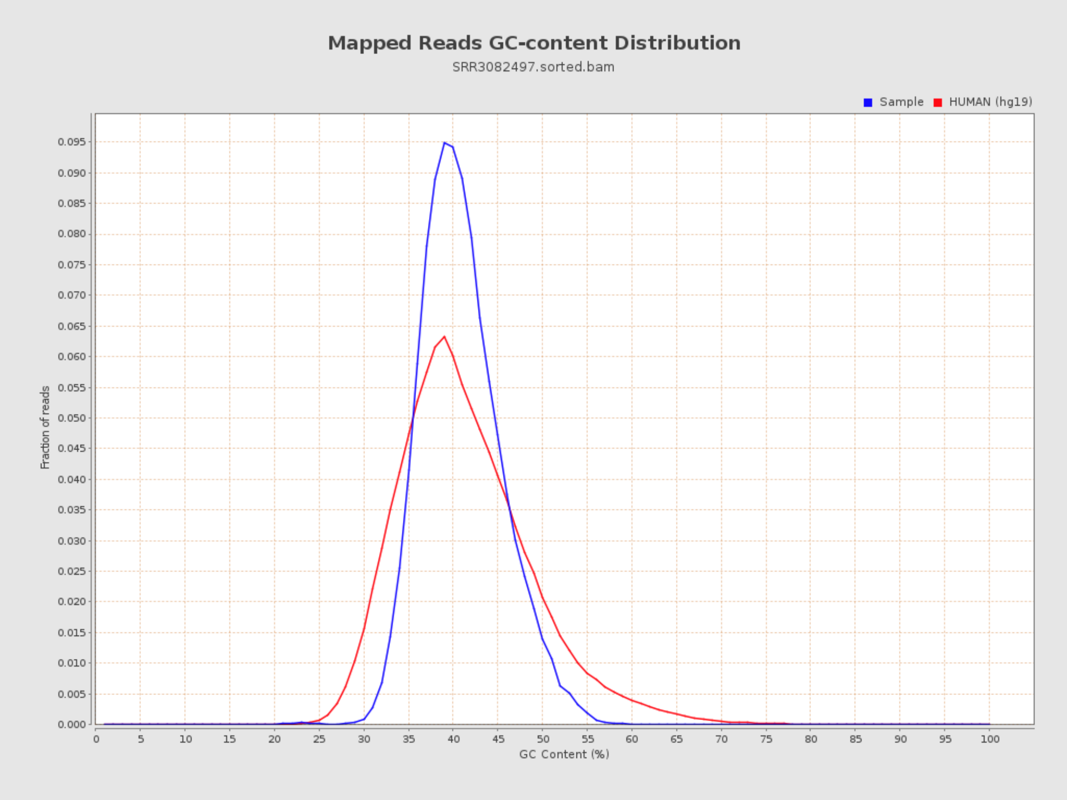
7. Results : Duplication Rate Histogram



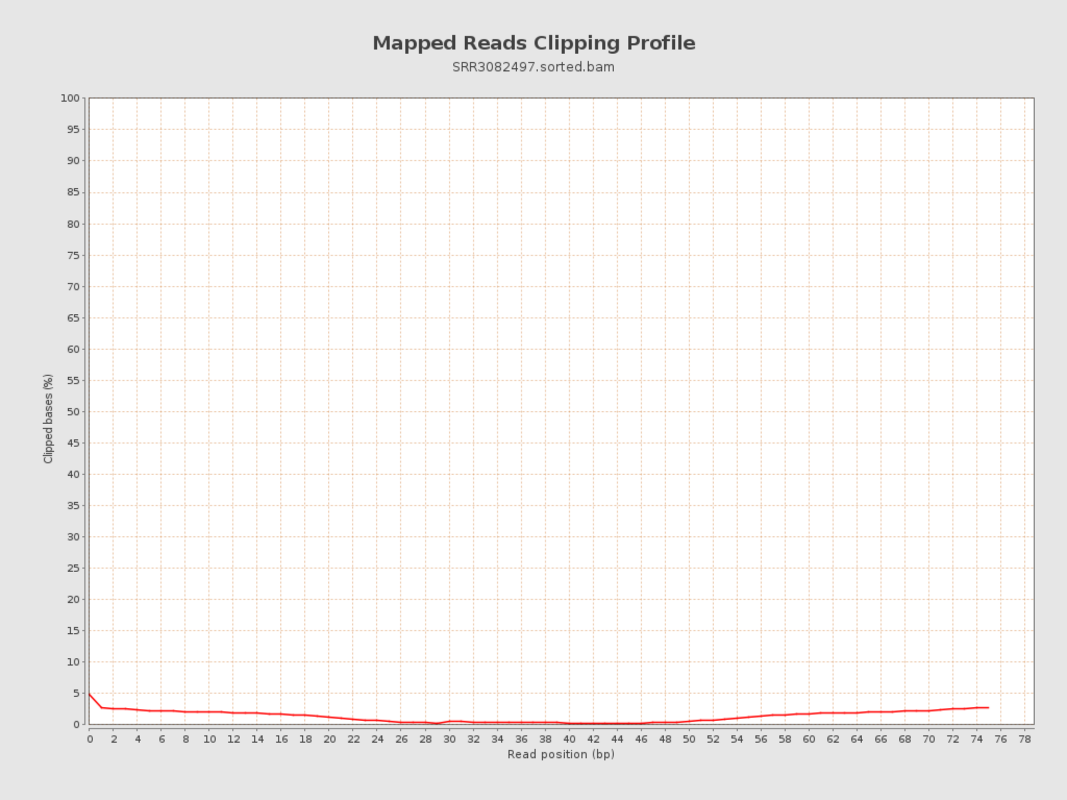
8. Results : Mapped Reads Nucleotide Content



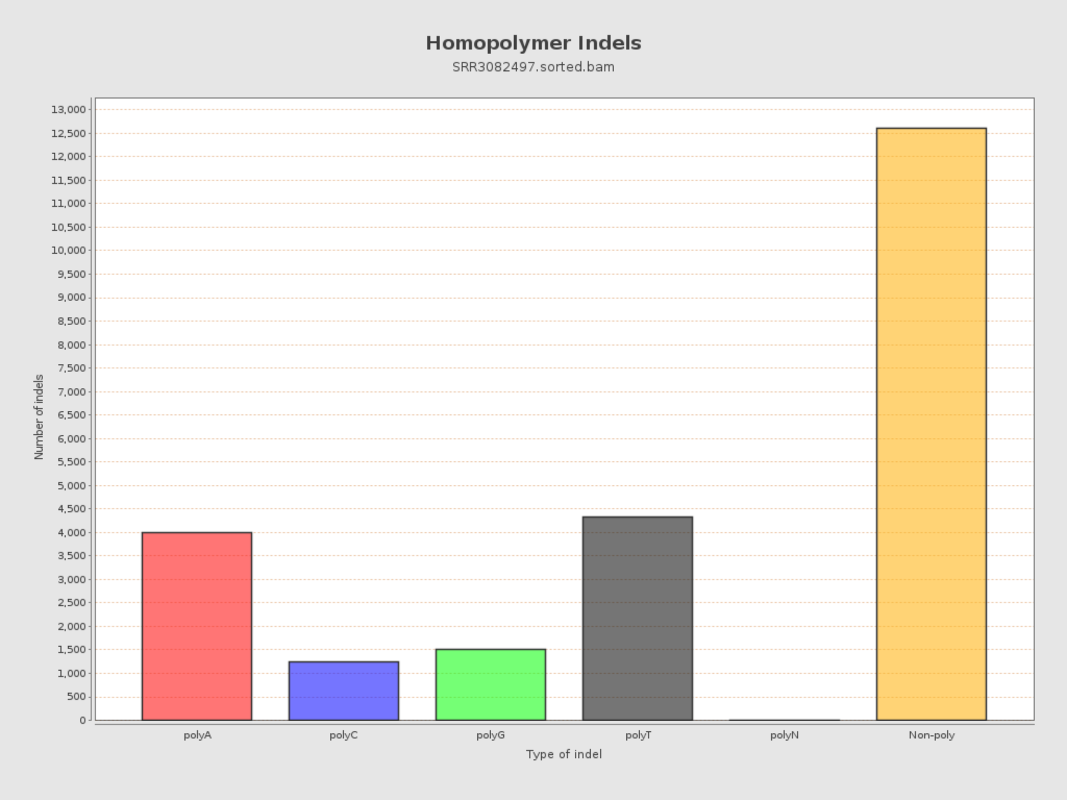
9. Results : Mapped Reads GC-content Distribution



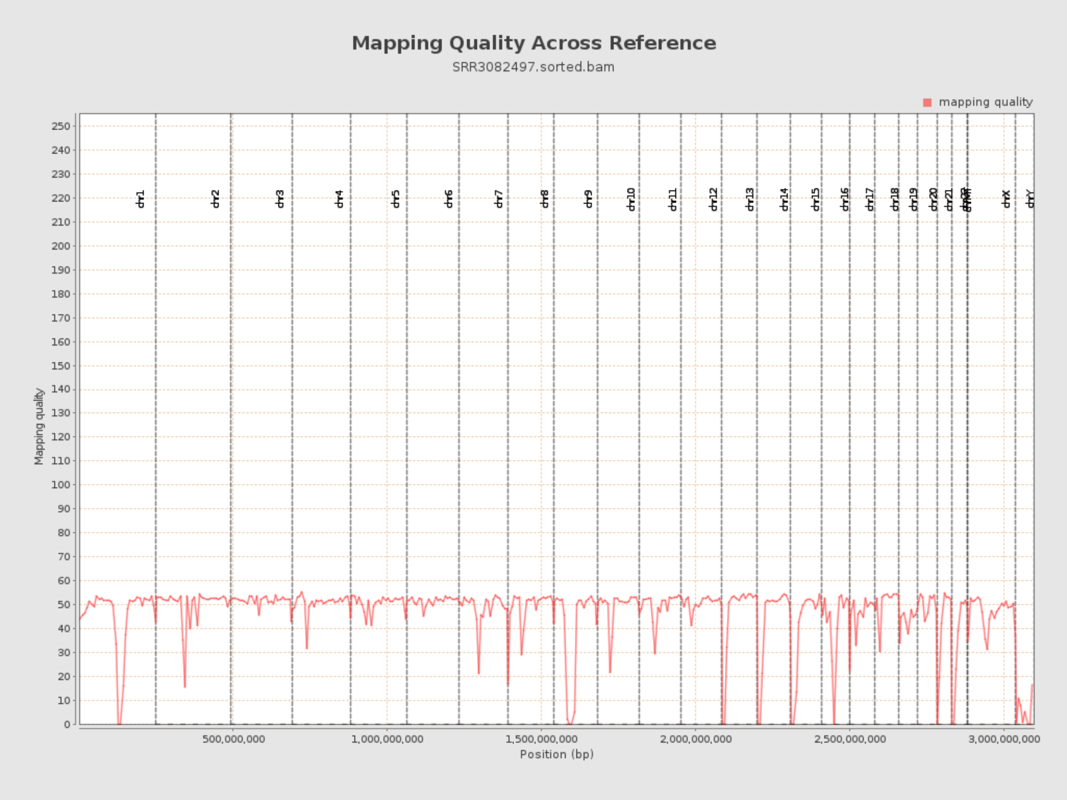
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram