Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 18:51:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082897.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_SRR3082897 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082897.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 18:51:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082897.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,841,701
Mapped reads	4,214,147 / 87.04%
Unmapped reads	627,554 / 12.96%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	41,178 / 0.85%
Read min/max/mean length	30 / 76 / 76.3
Duplicated reads (estimated)	230,485 / 4.76%
Duplication rate	4.37%
Clipped reads	1,756,746 / 36.28%

2.2. ACGT Content

Number/percentage of A's	82,722,624 / 28.84%
Number/percentage of C's	53,428,488 / 18.63%
Number/percentage of T's	91,494,219 / 31.9%
Number/percentage of G's	59,175,703 / 20.63%
Number/percentage of N's	16,109 / 0.01%
GC Percentage	39.26%

2.3. Coverage

Mean	0.0927

Standard Deviation	0.6246

2.4. Mapping Quality

Mean Mapping Quality	46.47

2.5. Mismatches and indels

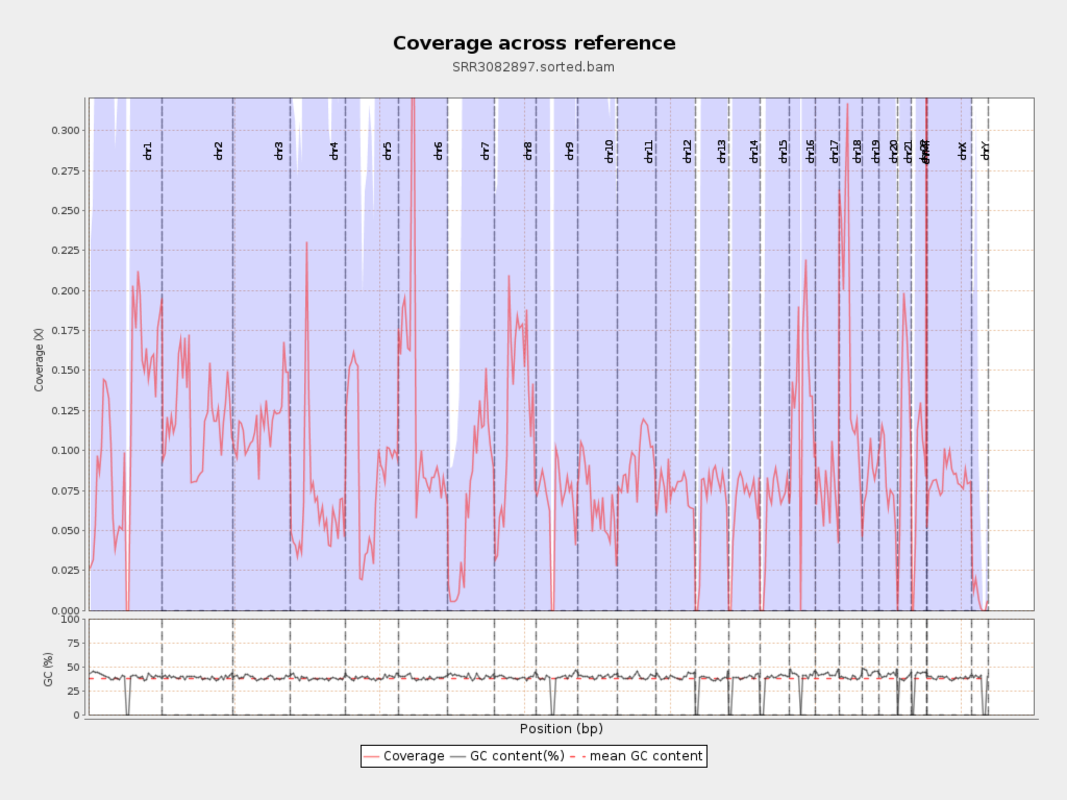
General error rate	0.91%
Mismatches	2,559,406
Insertions	23,403
Mapped reads with at least one insertion	0.55%
Deletions	61,947
Mapped reads with at least one deletion	1.46%
Homopolymer indels	47.97%

2.6. Chromosome stats

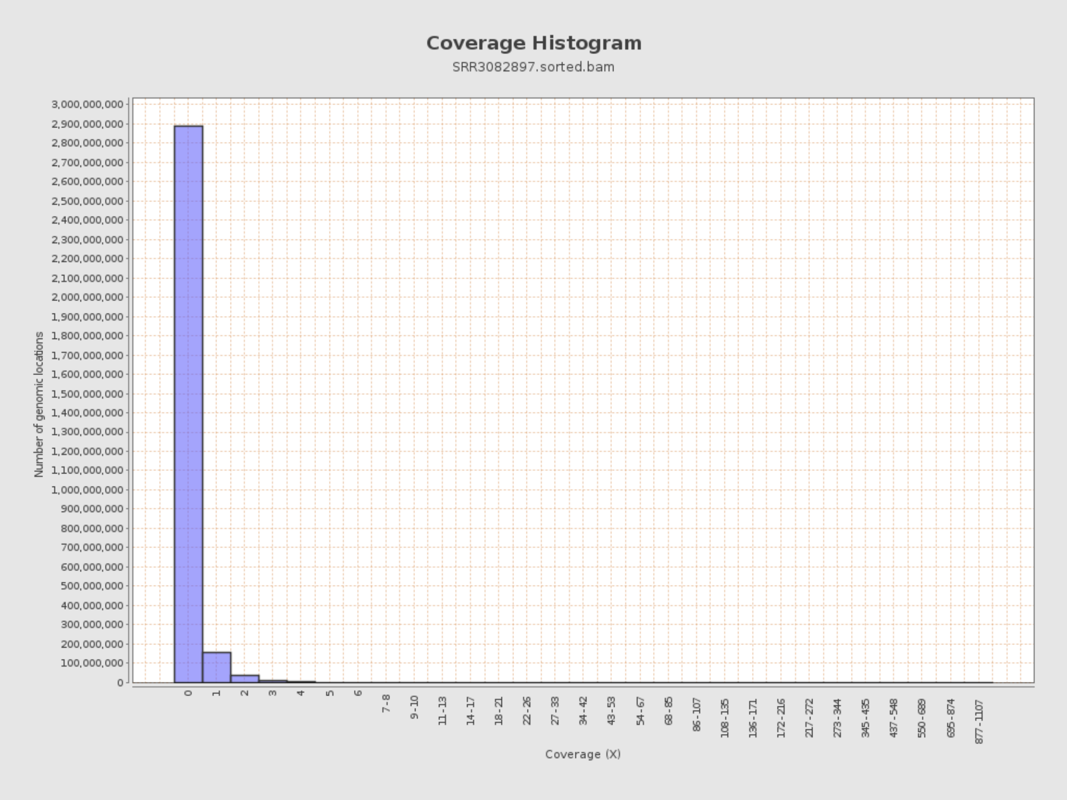
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	27988164	0.1123	1.1156
chr2	243199373	29330454	0.1206	0.8754
chr3	198022430	23234953	0.1173	0.4435
chr4	191154276	12470175	0.0652	0.344
chr5	180915260	16163465	0.0893	0.3922
chr6	171115067	21679591	0.1267	0.6573
chr7	159138663	11024058	0.0693	0.5212

chr8	146364022	18281991	0.1249	0.7131
chr9	141213431	9590981	0.0679	0.578
chr10	135534747	9267249	0.0684	0.4363
chr11	135006516	12589653	0.0933	0.536
chr12	133851895	10016164	0.0748	0.3663
chr13	115169878	7632483	0.0663	0.3358
chr14	107349540	6838732	0.0637	0.3556
chr15	102531392	6305289	0.0615	0.3188
chr16	90354753	12171845	0.1347	0.5328
chr17	81195210	5826254	0.0718	0.4044
chr18	78077248	13529106	0.1733	1.2682
chr19	59128983	4997925	0.0845	0.8142
chr20	63025520	5034675	0.0799	0.3813
chr21	48129895	5885568	0.1223	0.4735
chr22	51304566	3940997	0.0768	0.3576
chrMT	16571	13591	0.8202	1.1027
chrX	155270560	12669947	0.0816	0.4352
chrY	59373566	460478	0.0078	0.1463

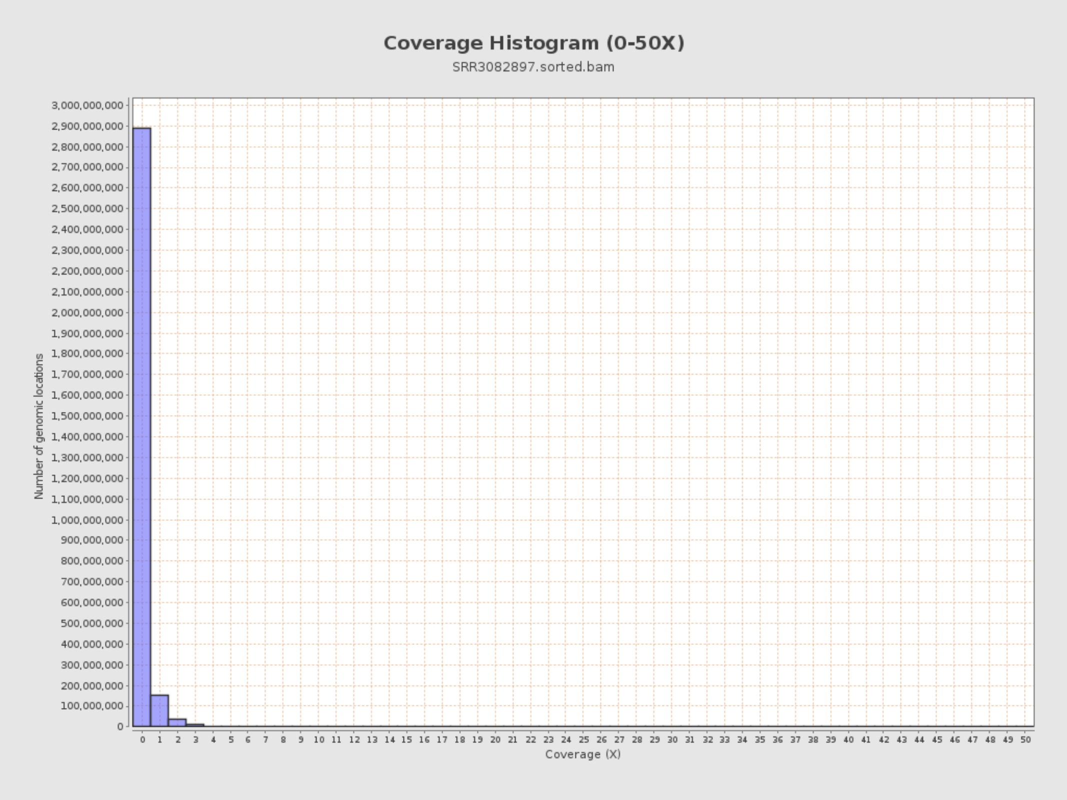
3. Results : Coverage across reference



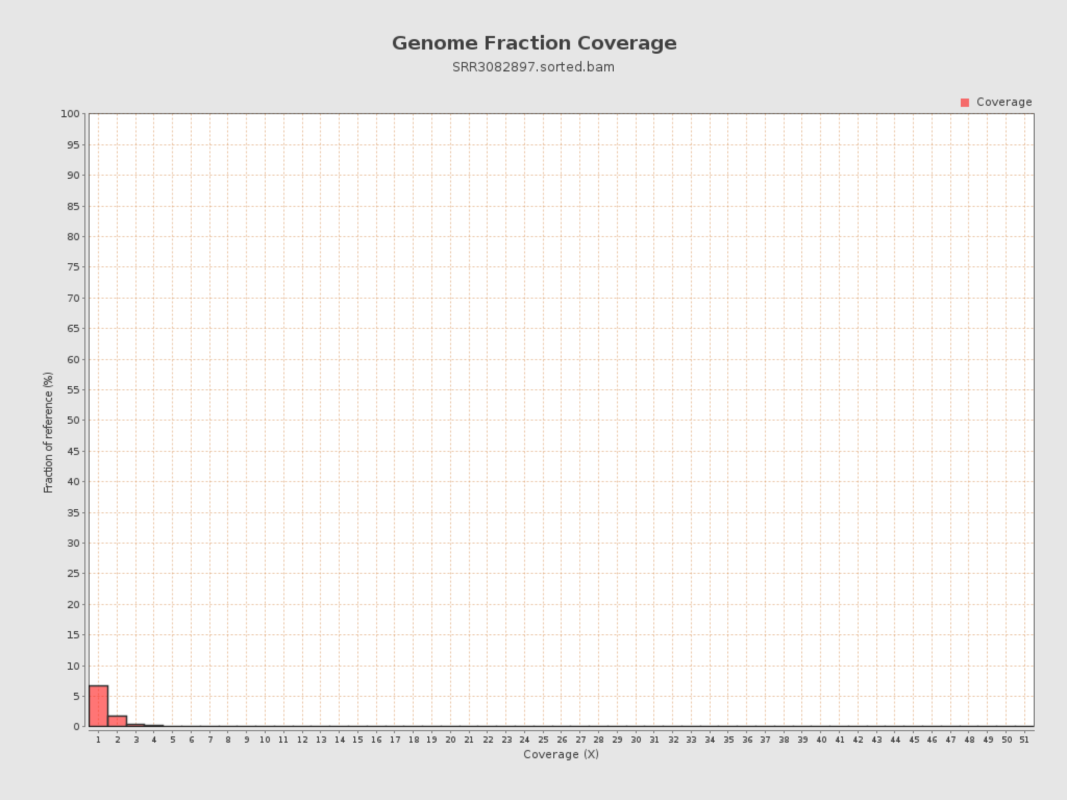
4. Results : Coverage Histogram



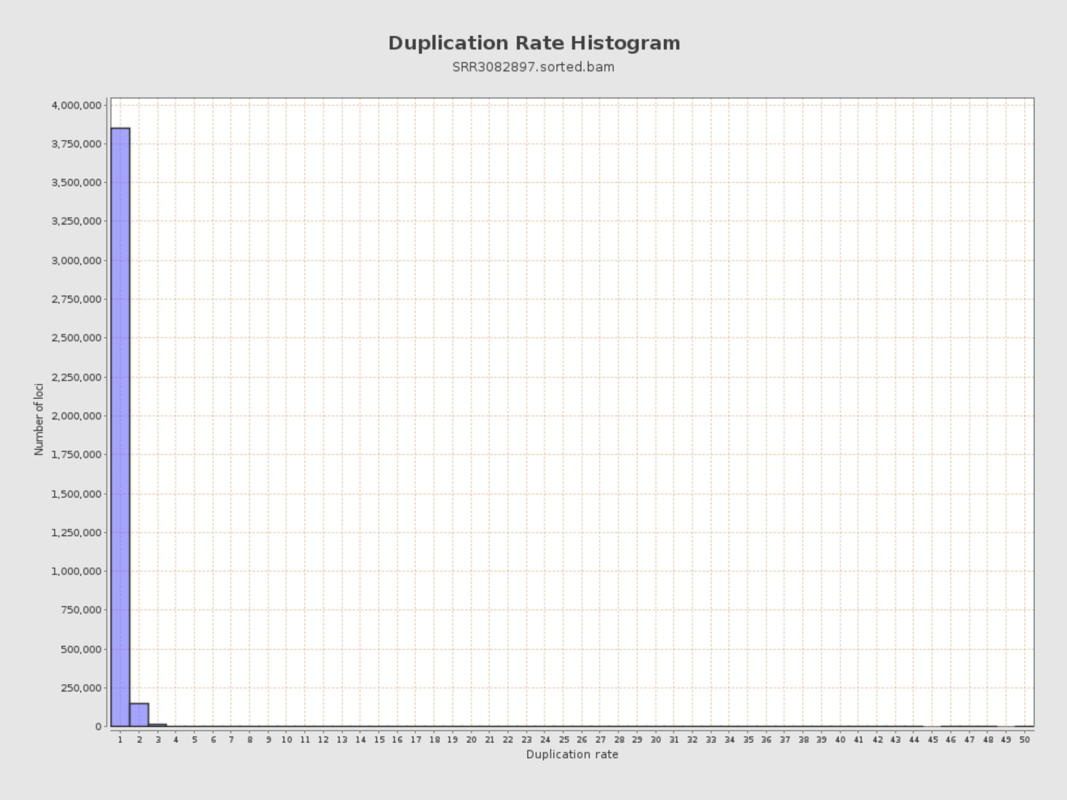
5. Results : Coverage Histogram (0-50X)



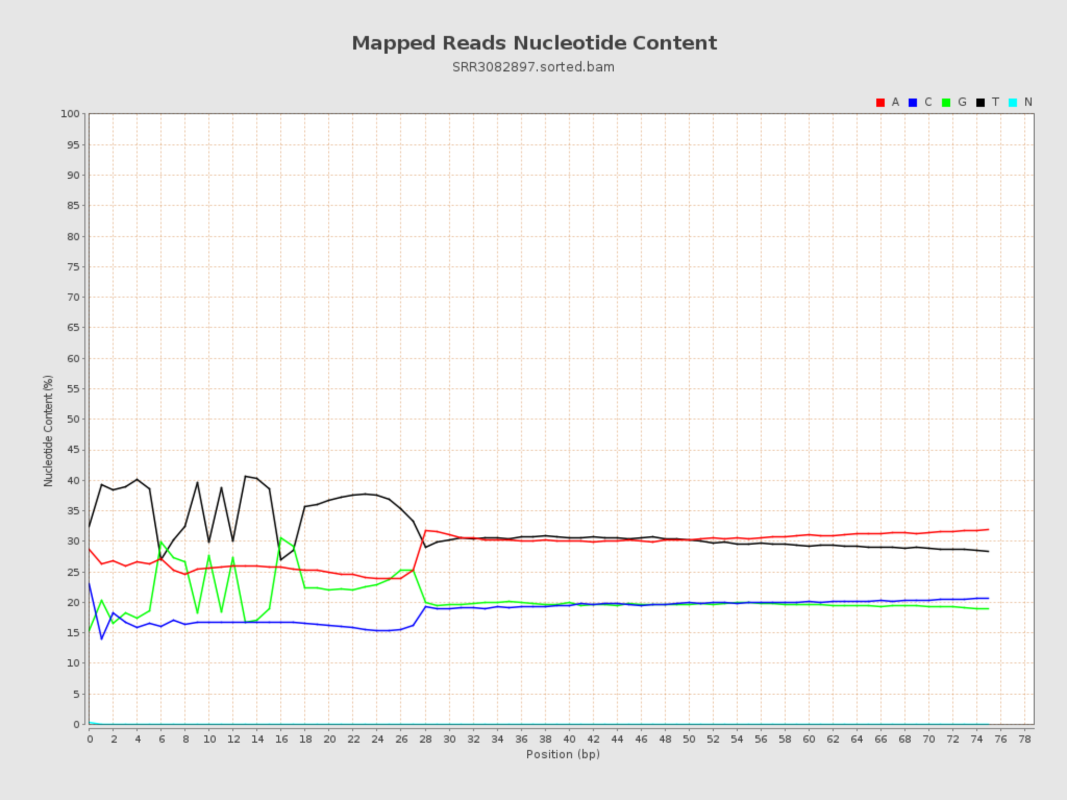
6. Results : Genome Fraction Coverage



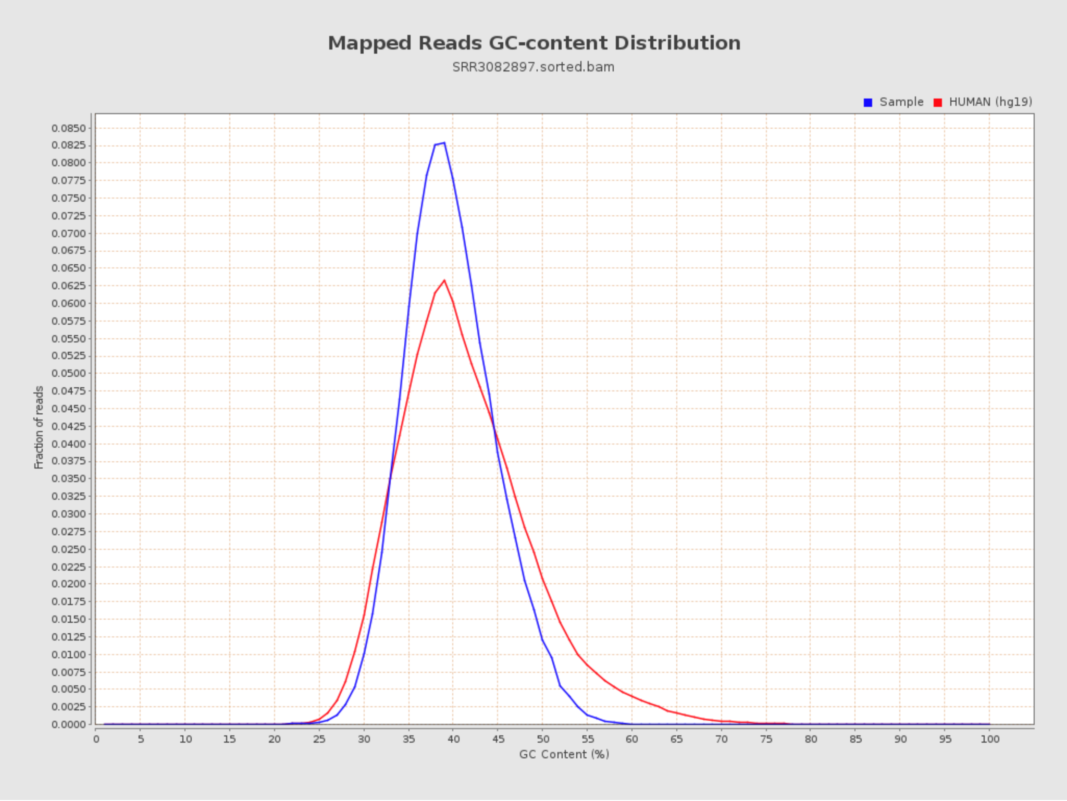
7. Results : Duplication Rate Histogram



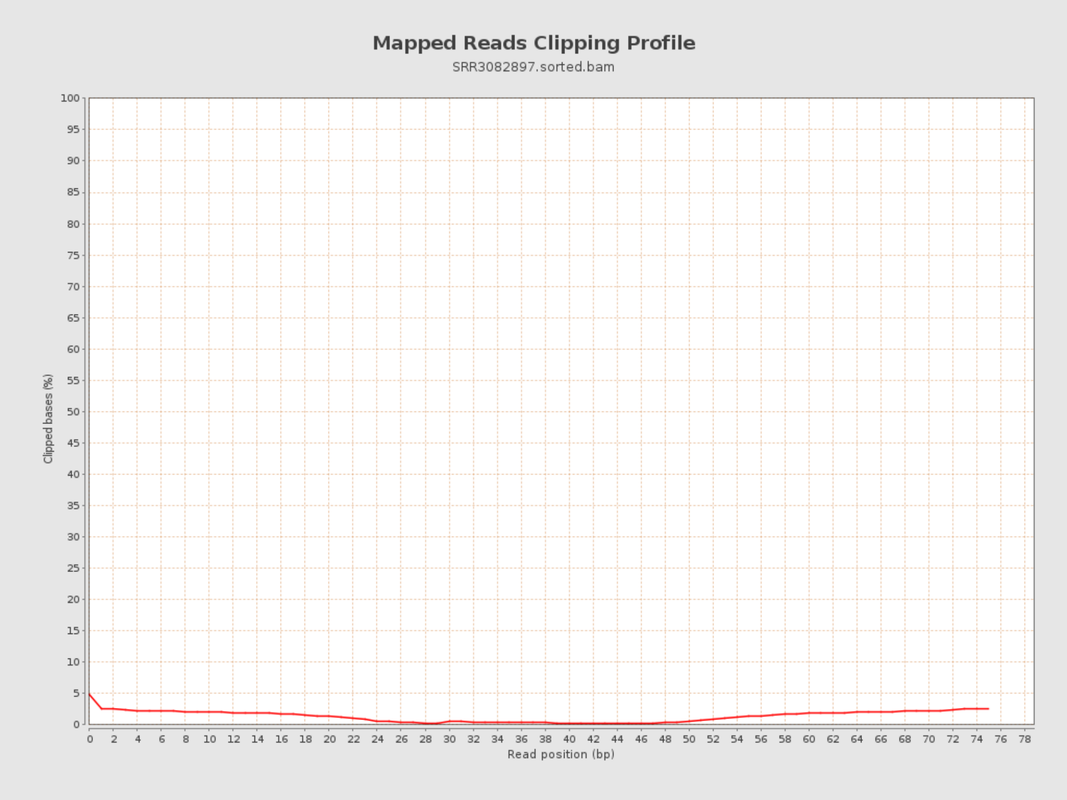
8. Results : Mapped Reads Nucleotide Content



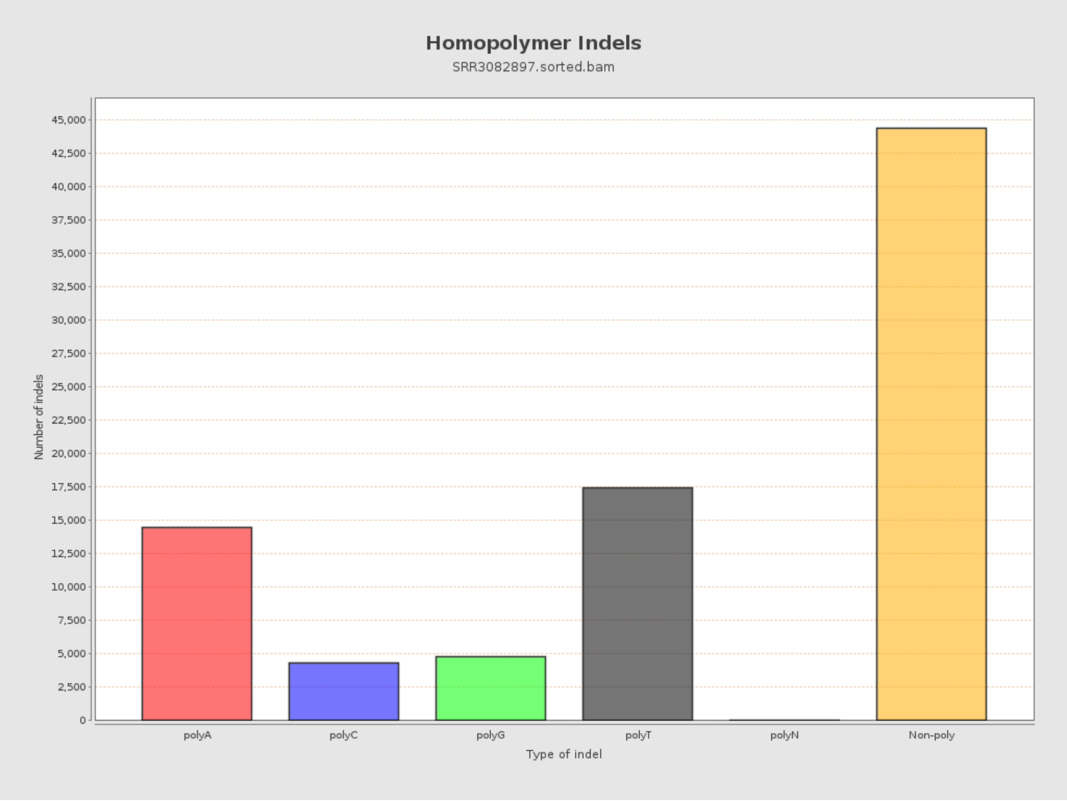
9. Results : Mapped Reads GC-content Distribution



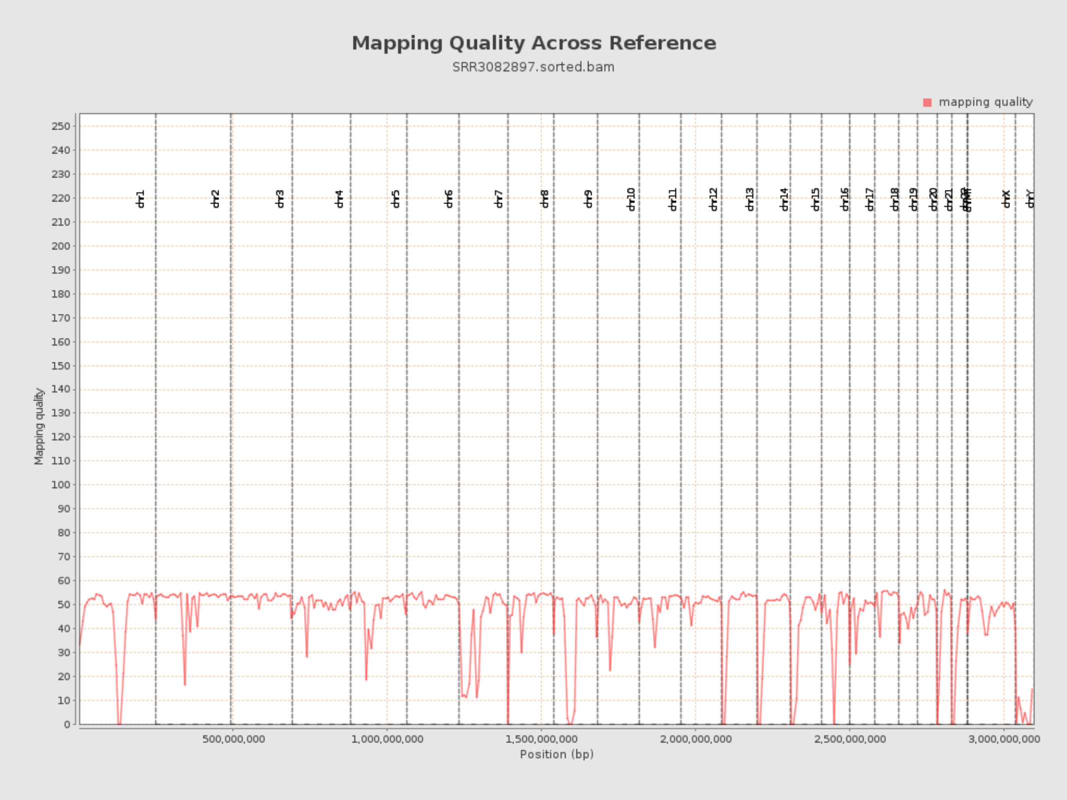
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram