Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 08:36:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080797.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_SRR3080797 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080797.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 08:36:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080797.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,186,155
Mapped reads	1,978,947 / 90.52%
Unmapped reads	207,208 / 9.48%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,551 / 0.76%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	122,377 / 5.6%
Duplication rate	5.34%
Clipped reads	808,902 / 37%

2.2. ACGT Content

Number/percentage of A's	37,761,285 / 28.22%
Number/percentage of C's	24,579,848 / 18.37%
Number/percentage of T's	42,740,071 / 31.94%
Number/percentage of G's	28,708,197 / 21.45%
Number/percentage of N's	17,964 / 0.01%
GC Percentage	39.82%

2.3. Coverage

Mean	0.0432

Standard Deviation	0.3232

2.4. Mapping Quality

Mean Mapping Quality	46.81

2.5. Mismatches and indels

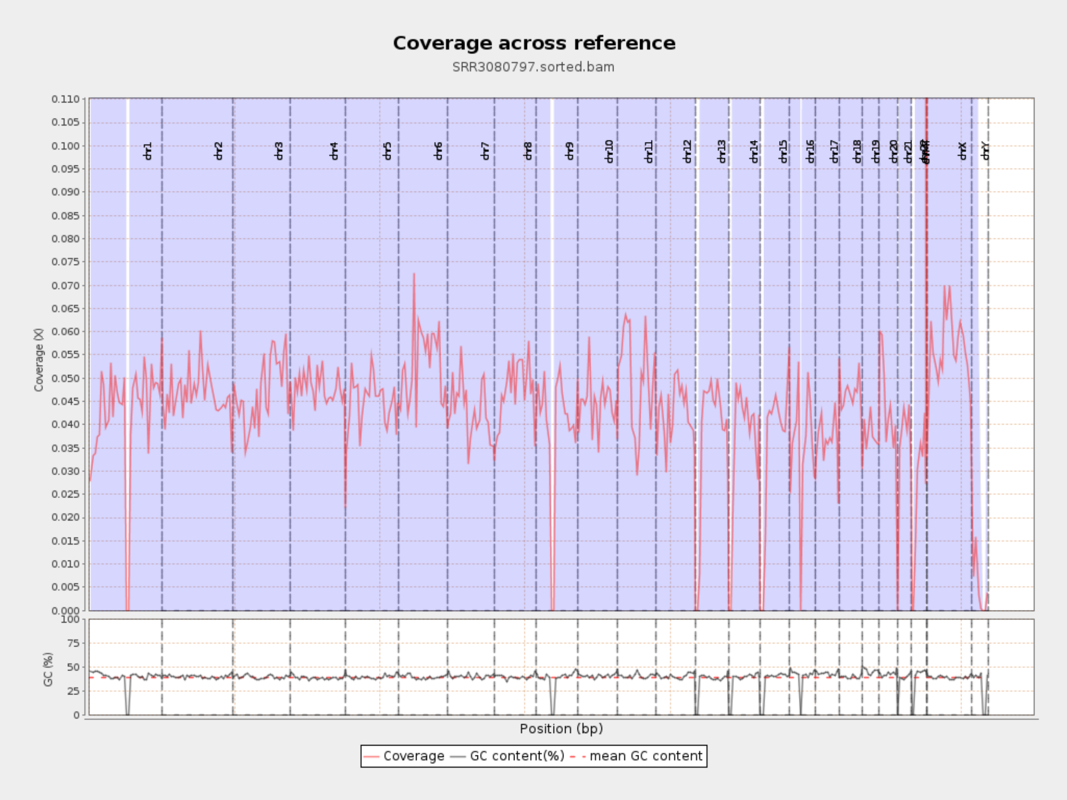
General error rate	0.82%
Mismatches	1,076,666
Insertions	9,690
Mapped reads with at least one insertion	0.49%
Deletions	27,669
Mapped reads with at least one deletion	1.38%
Homopolymer indels	47.94%

2.6. Chromosome stats

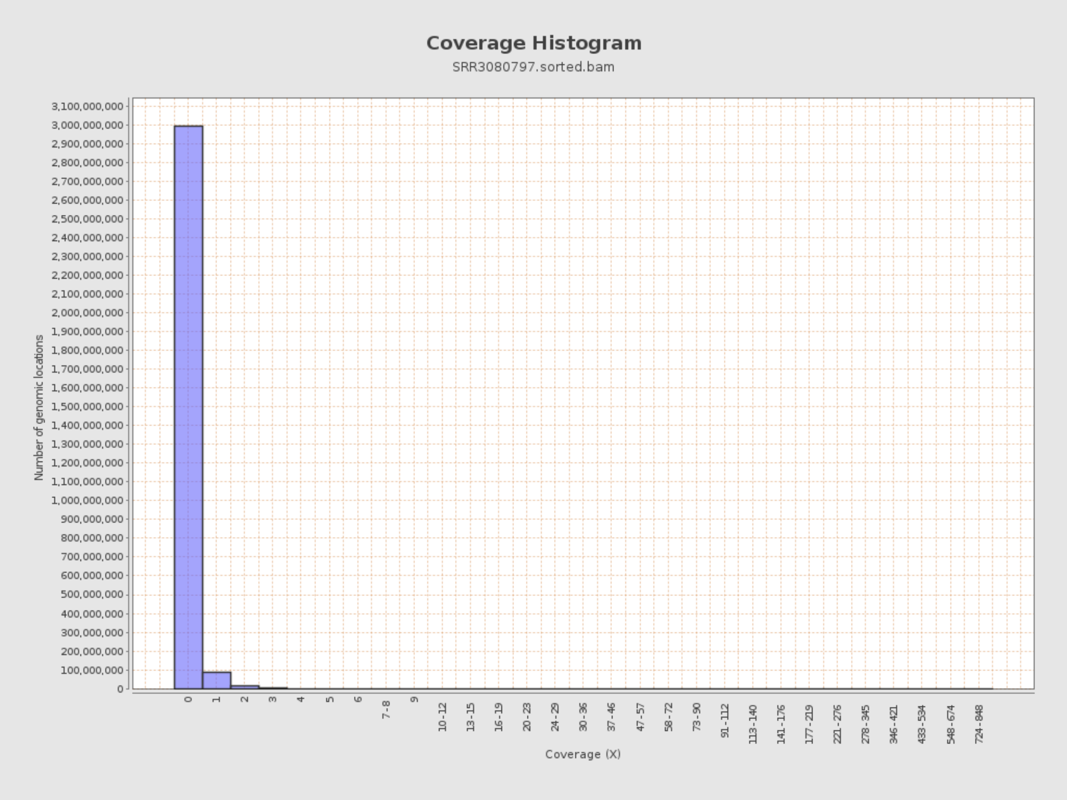
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10444509	0.0419	0.3903
chr2	243199373	11356102	0.0467	0.3656
chr3	198022430	9314544	0.047	0.2642
chr4	191154276	9147315	0.0479	0.2734
chr5	180915260	8154204	0.0451	0.2591
chr6	171115067	9039969	0.0528	0.3547
chr7	159138663	6861336	0.0431	0.3089

chr8	146364022	6926706	0.0473	0.569
chr9	141213431	5508503	0.039	0.295
chr10	135534747	6055666	0.0447	0.3357
chr11	135006516	6768284	0.0501	0.3073
chr12	133851895	5668788	0.0424	0.2532
chr13	115169878	4249832	0.0369	0.2337
chr14	107349540	3763807	0.0351	0.2379
chr15	102531392	3571055	0.0348	0.2277
chr16	90354753	3225031	0.0357	0.2482
chr17	81195210	2970905	0.0366	0.2396
chr18	78077248	3664137	0.0469	0.4839
chr19	59128983	2240428	0.0379	0.323
chr20	63025520	2781870	0.0441	0.2599
chr21	48129895	1700474	0.0353	0.2408
chr22	51304566	1258937	0.0245	0.1888
chrMT	16571	197555	11.9217	6.6042
chrX	155270560	8668035	0.0558	0.3044
chrY	59373566	318017	0.0054	0.1159

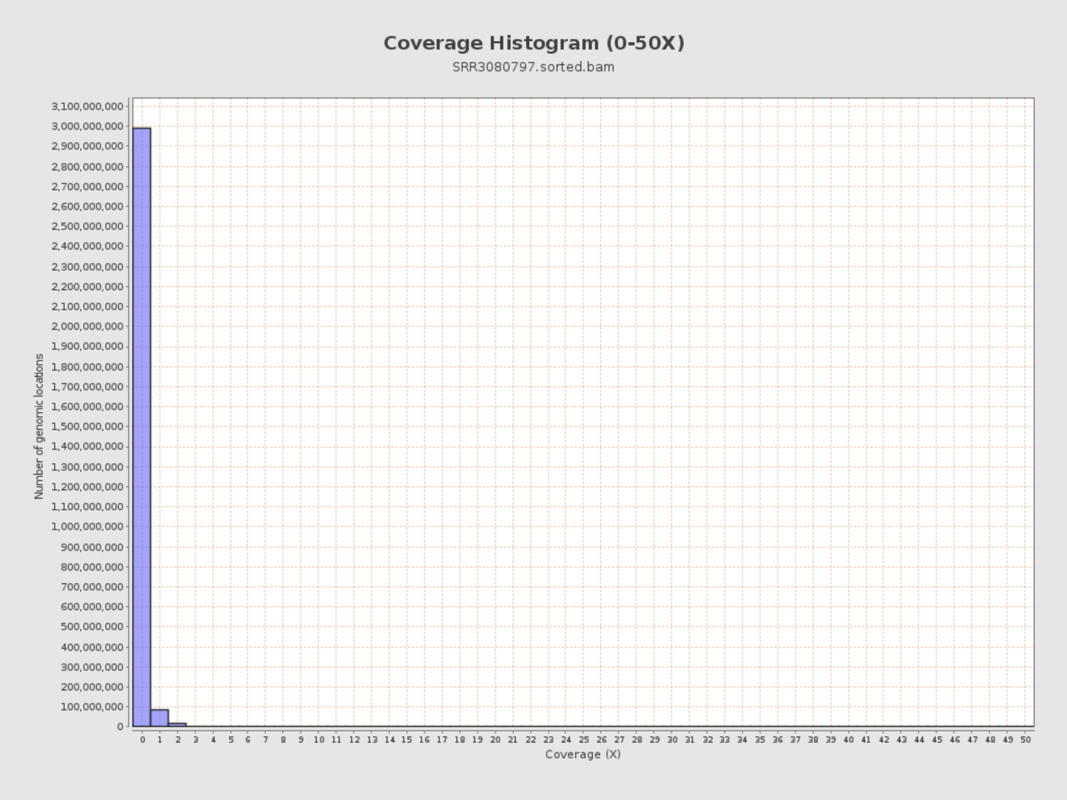
3. Results : Coverage across reference



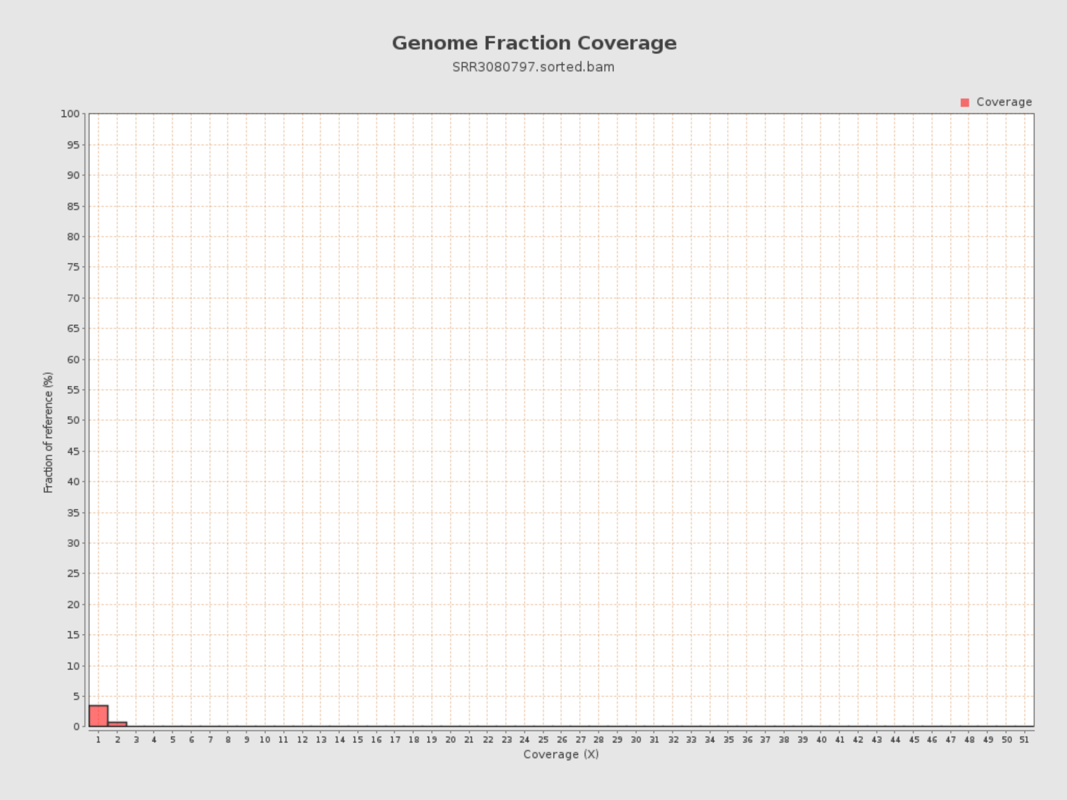
4. Results : Coverage Histogram



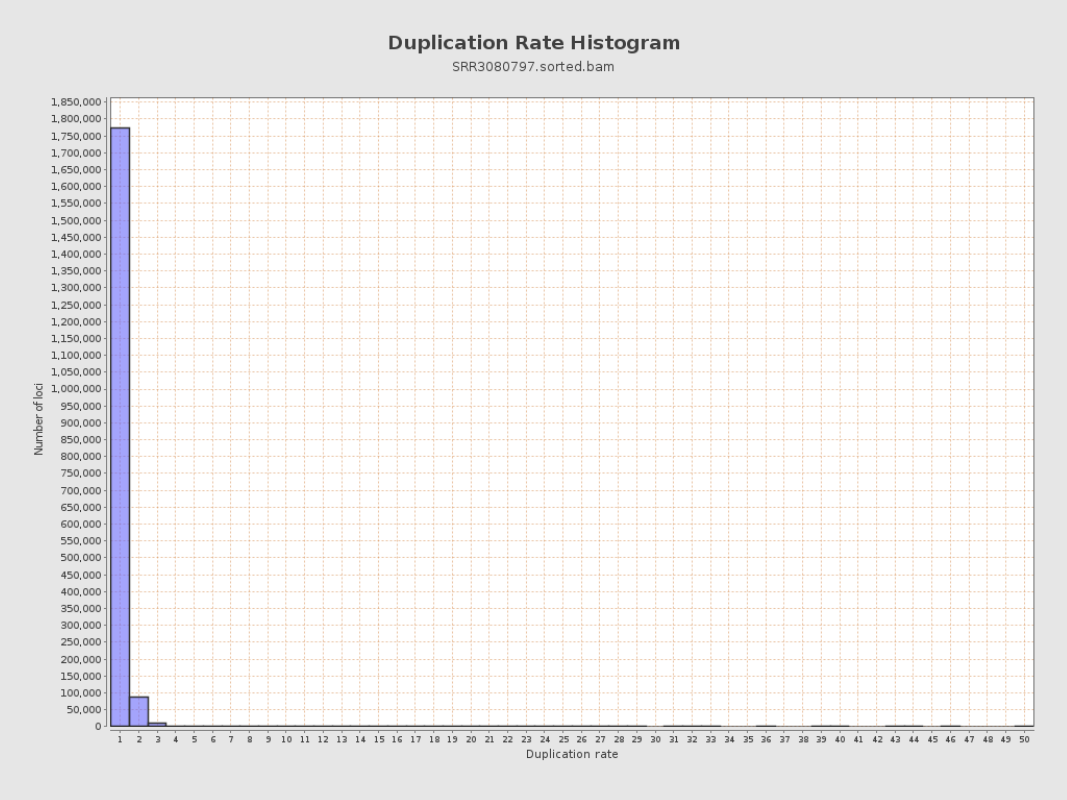
5. Results : Coverage Histogram (0-50X)



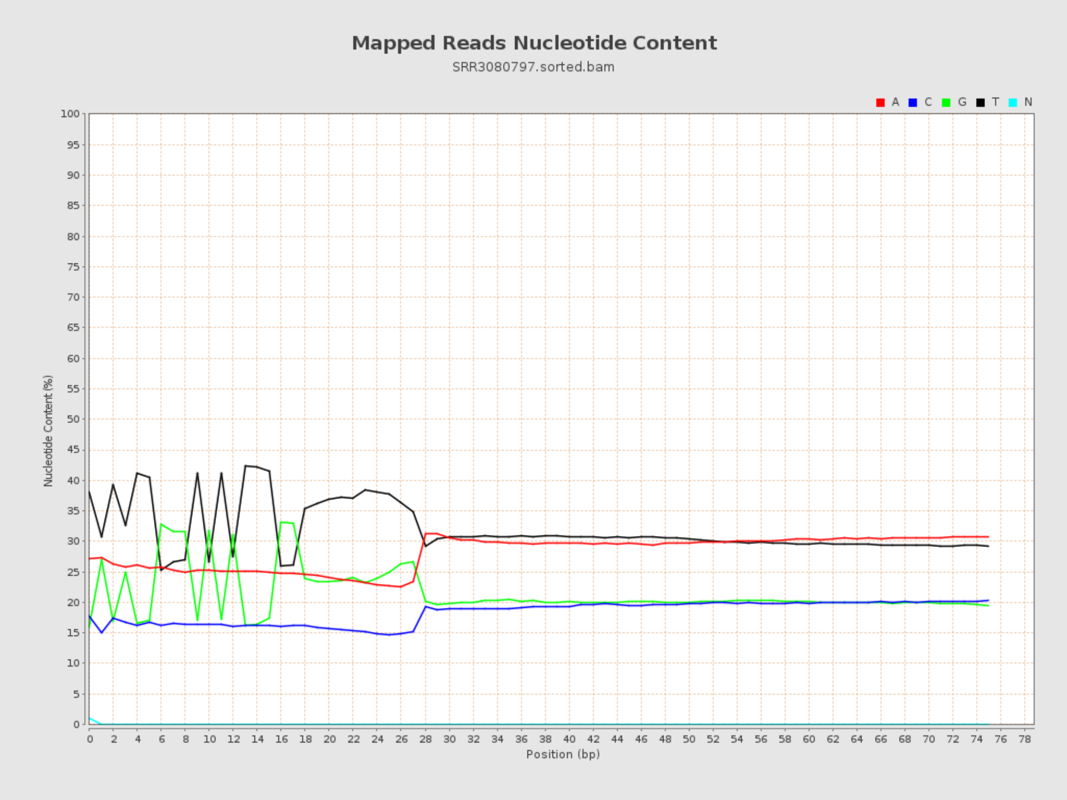
6. Results : Genome Fraction Coverage



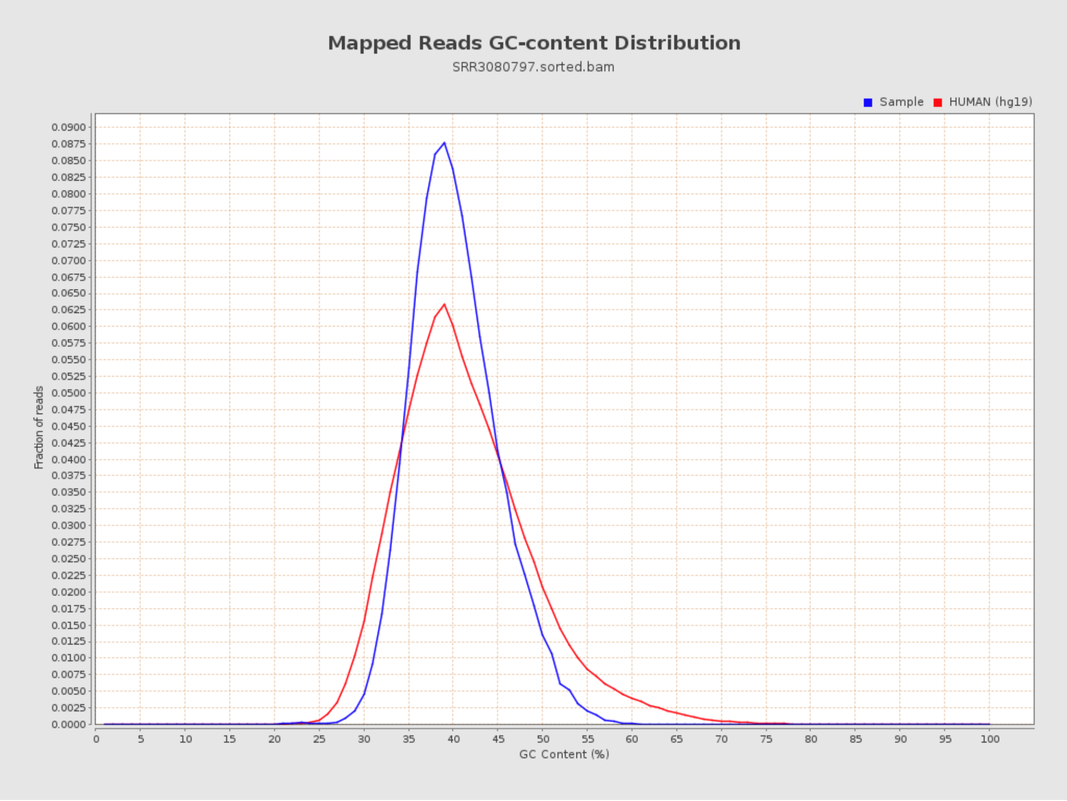
7. Results : Duplication Rate Histogram



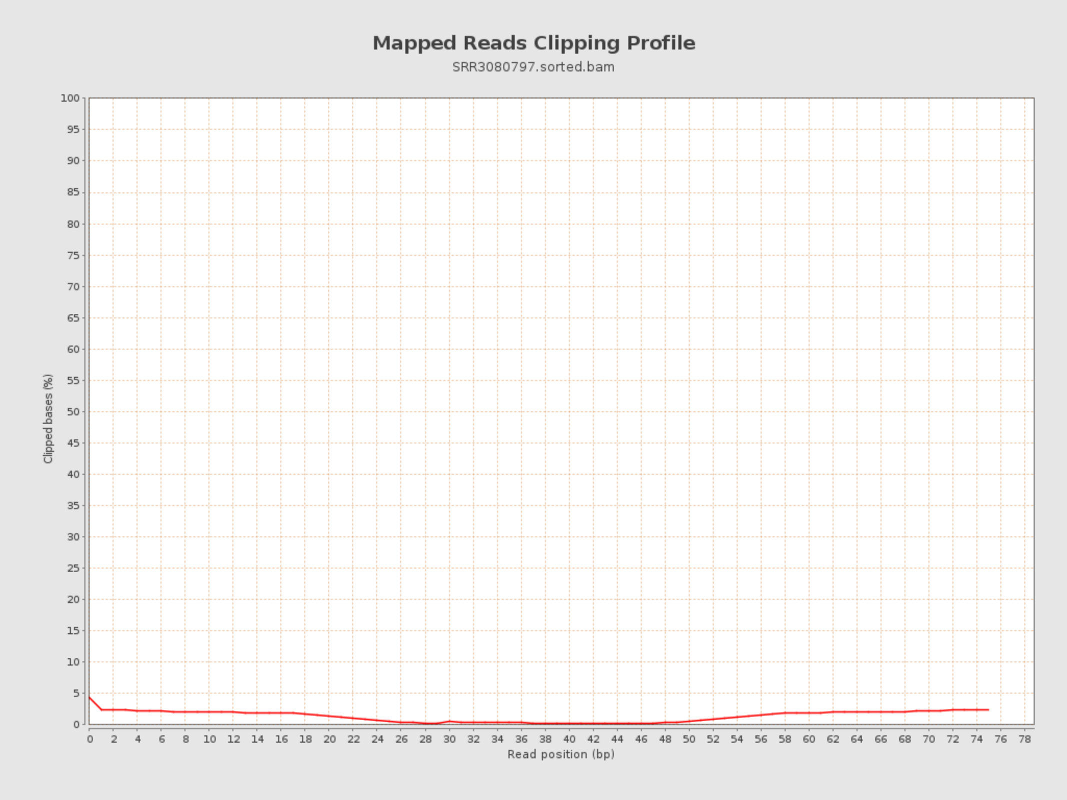
8. Results : Mapped Reads Nucleotide Content



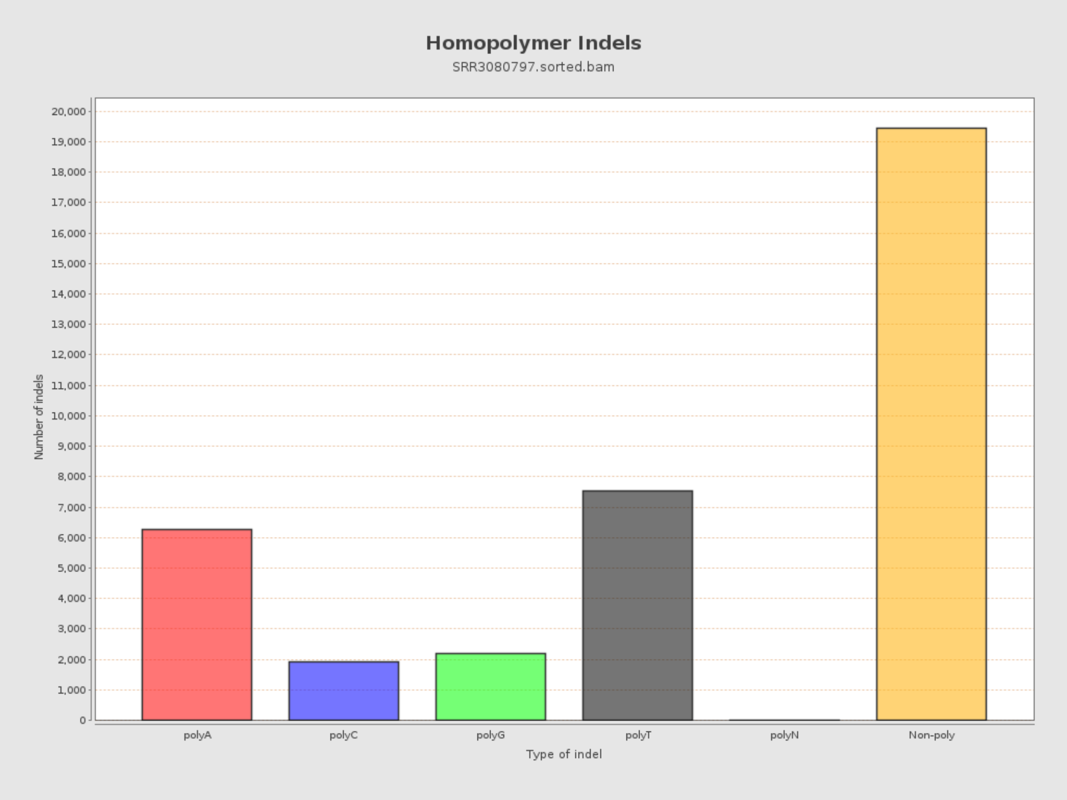
9. Results : Mapped Reads GC-content Distribution



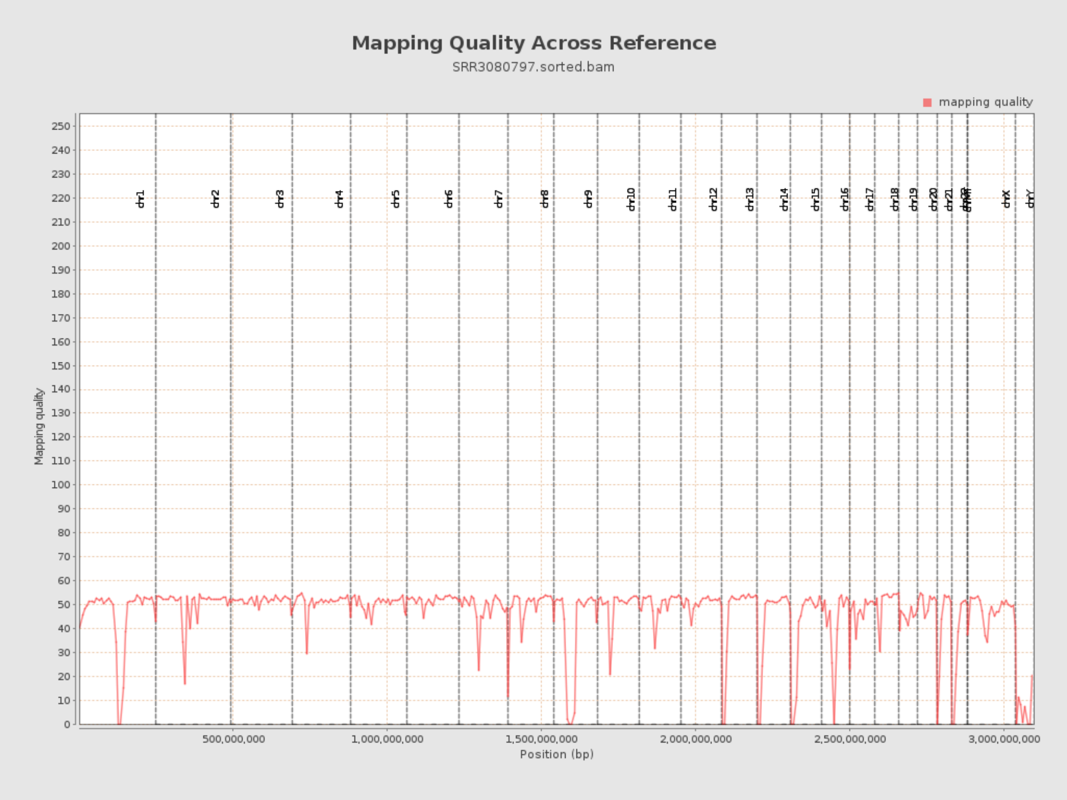
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram