Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 09:40:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084286.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_SRR3084286 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084286.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 09:40:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084286.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,470,618
Mapped reads	2,195,422 / 88.86%
Unmapped reads	275,196 / 11.14%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,805 / 0.56%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	66,906 / 2.71%
Duplication rate	2.44%
Clipped reads	1,148,970 / 46.51%

2.2. ACGT Content

Number/percentage of A's	39,515,889 / 27.59%
Number/percentage of C's	27,689,491 / 19.33%
Number/percentage of T's	43,168,153 / 30.14%
Number/percentage of G's	32,679,602 / 22.82%
Number/percentage of N's	181,897 / 0.13%
GC Percentage	42.15%

2.3. Coverage

Mean	0.0463

Standard Deviation	0.327

2.4. Mapping Quality

Mean Mapping Quality	44.23

2.5. Mismatches and indels

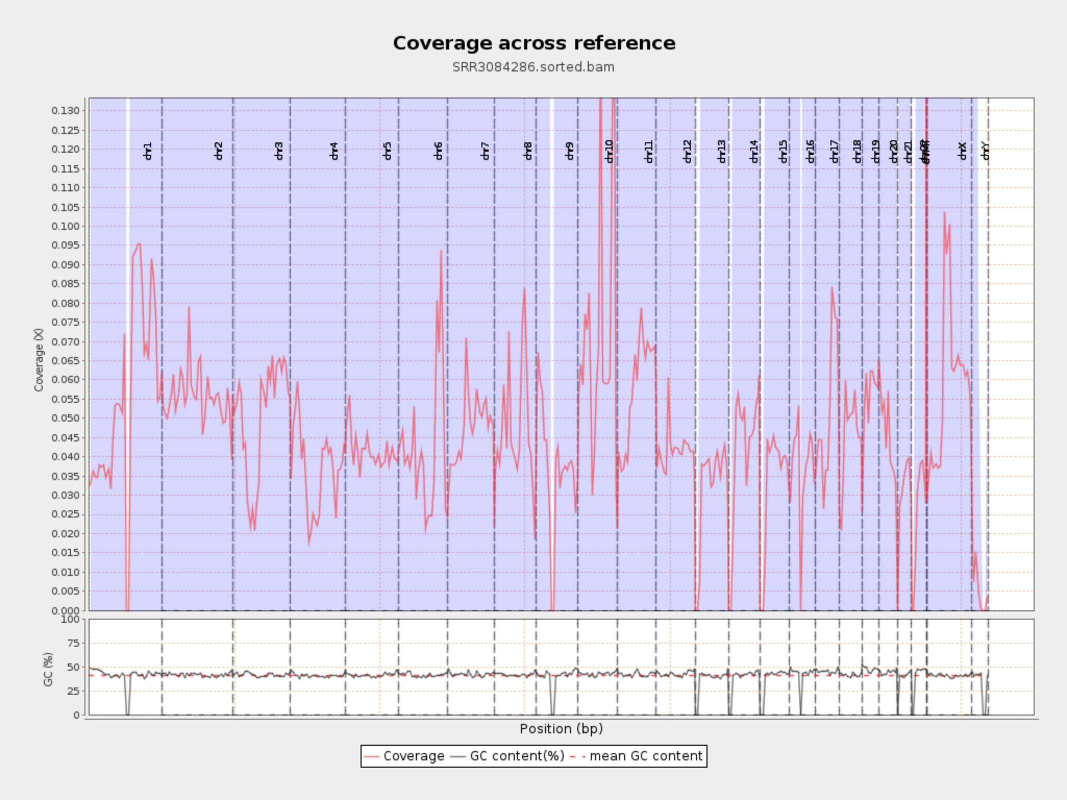
General error rate	1.06%
Mismatches	1,497,369
Insertions	11,162
Mapped reads with at least one insertion	0.5%
Deletions	30,852
Mapped reads with at least one deletion	1.39%
Homopolymer indels	45.98%

2.6. Chromosome stats

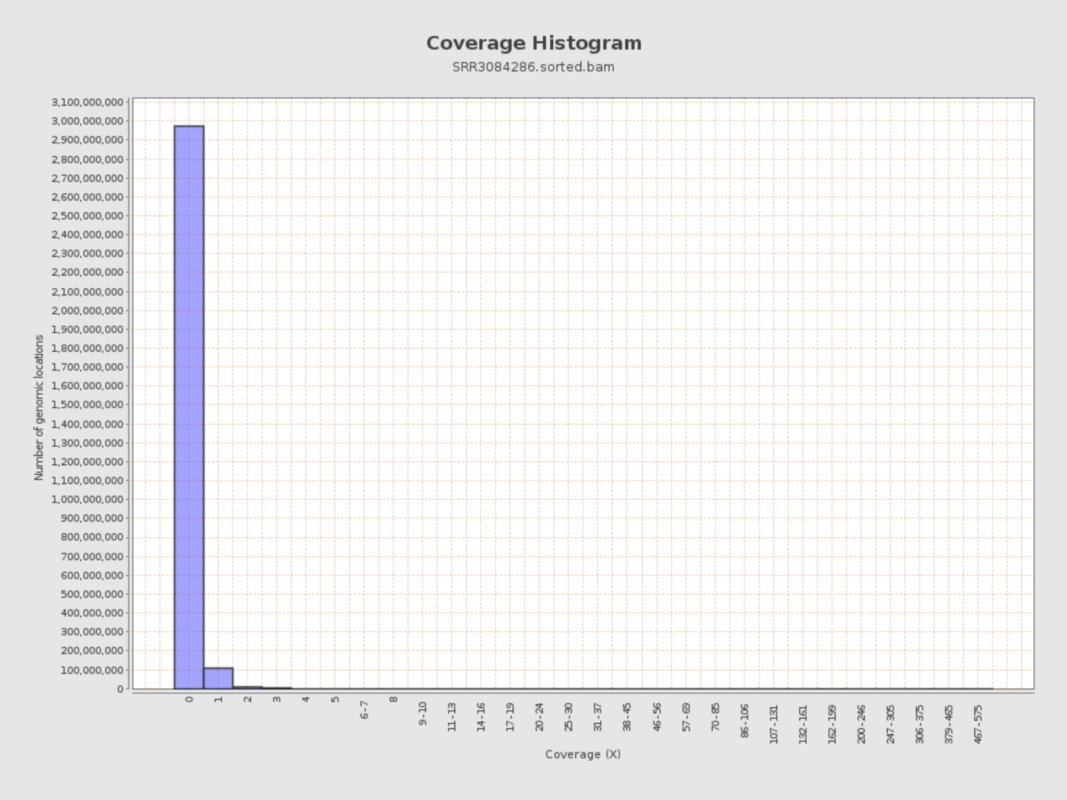
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13765359	0.0552	0.5254
chr2	243199373	13563469	0.0558	0.3855
chr3	198022430	9990453	0.0505	0.2552
chr4	191154276	7059785	0.0369	0.2248
chr5	180915260	7513304	0.0415	0.2275
chr6	171115067	7290726	0.0426	0.2637
chr7	159138663	7633641	0.048	0.4343

chr8	146364022	6924344	0.0473	0.3034
chr9	141213431	5217594	0.0369	0.27
chr10	135534747	10067638	0.0743	0.4681
chr11	135006516	7745018	0.0574	0.3361
chr12	133851895	5610769	0.0419	0.2299
chr13	115169878	3636455	0.0316	0.1988
chr14	107349540	4401945	0.041	0.2379
chr15	102531392	3403374	0.0332	0.214
chr16	90354753	3355705	0.0371	0.2398
chr17	81195210	4239056	0.0522	0.2779
chr18	78077248	3551520	0.0455	0.4742
chr19	59128983	3342829	0.0565	0.3939
chr20	63025520	2840984	0.0451	0.2441
chr21	48129895	1461312	0.0304	0.2027
chr22	51304566	1242399	0.0242	0.1721
chrMT	16571	6354	0.3834	0.6964
chrX	155270560	9093495	0.0586	0.305
chrY	59373566	327071	0.0055	0.1118

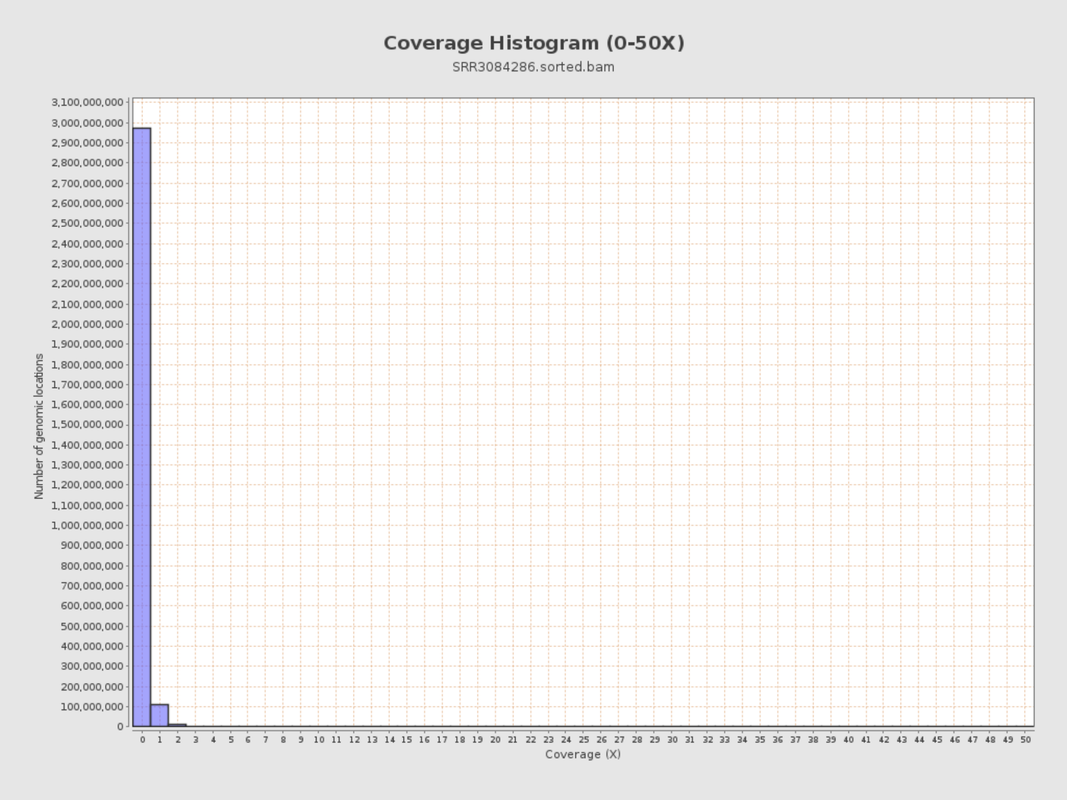
3. Results : Coverage across reference



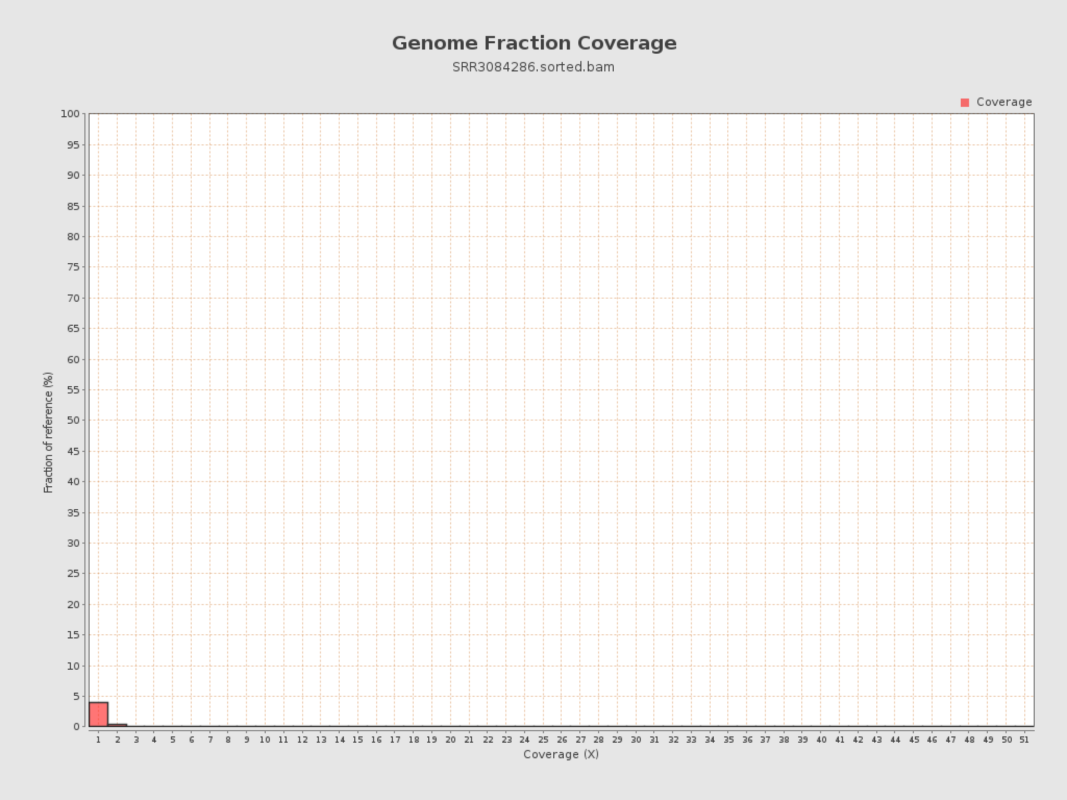
4. Results : Coverage Histogram



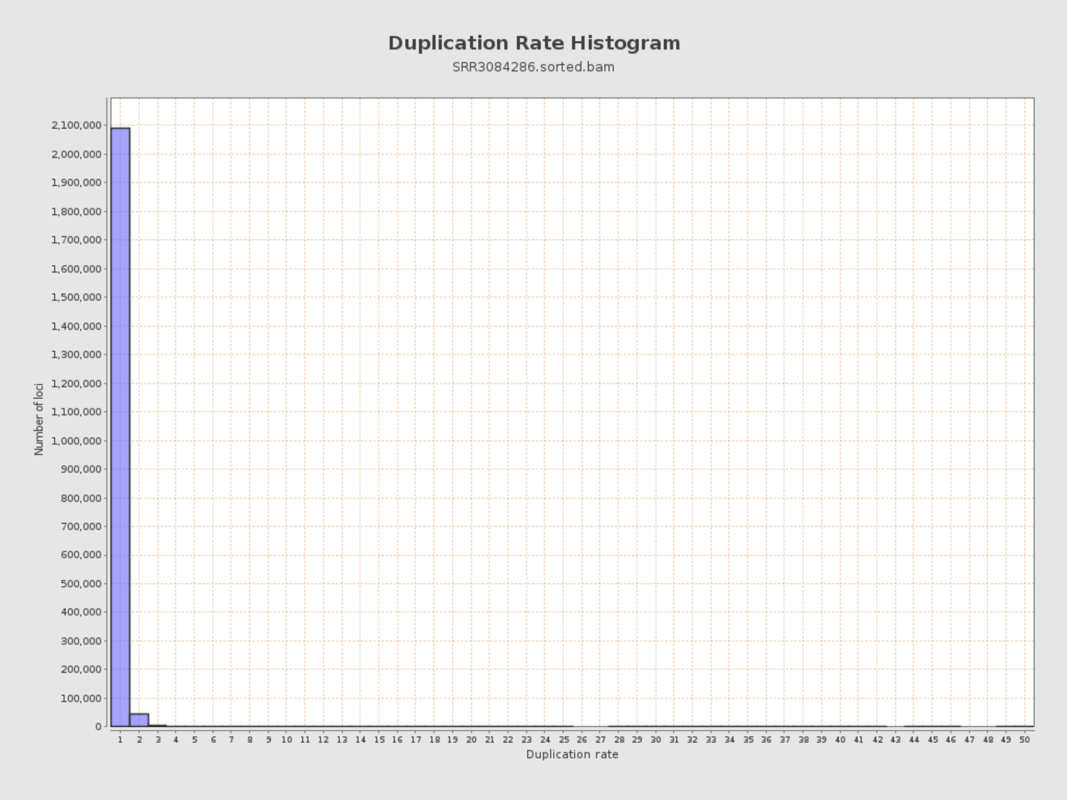
5. Results : Coverage Histogram (0-50X)



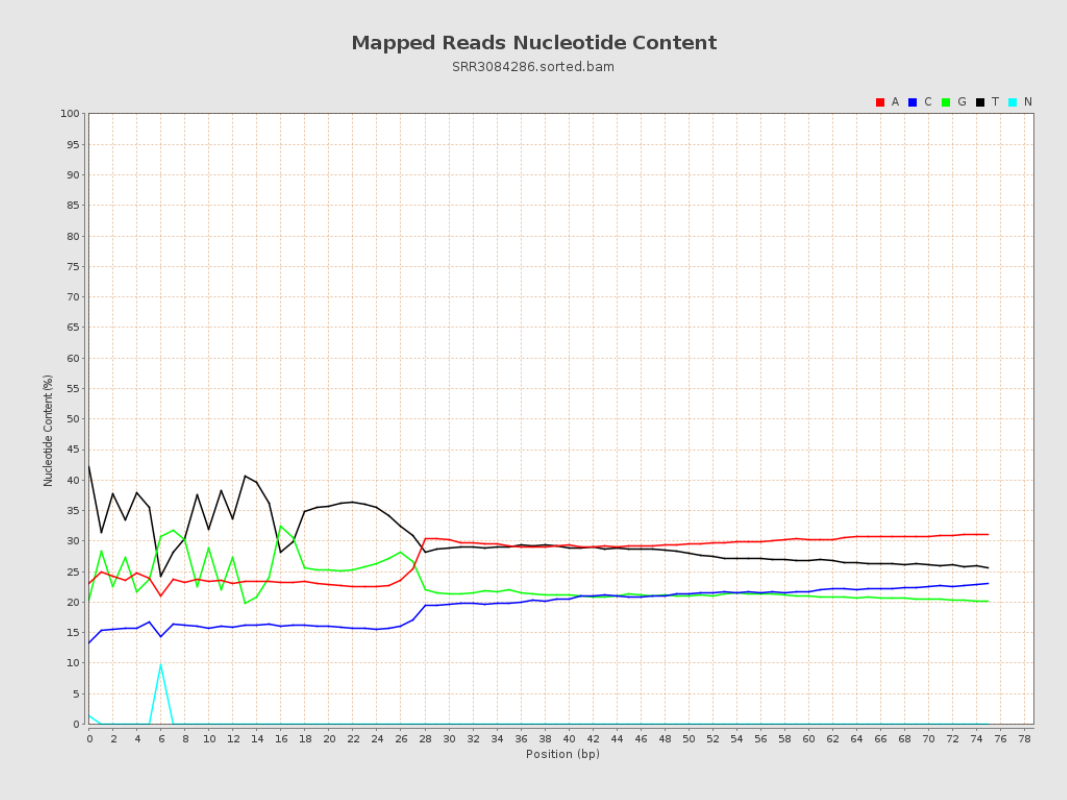
6. Results : Genome Fraction Coverage



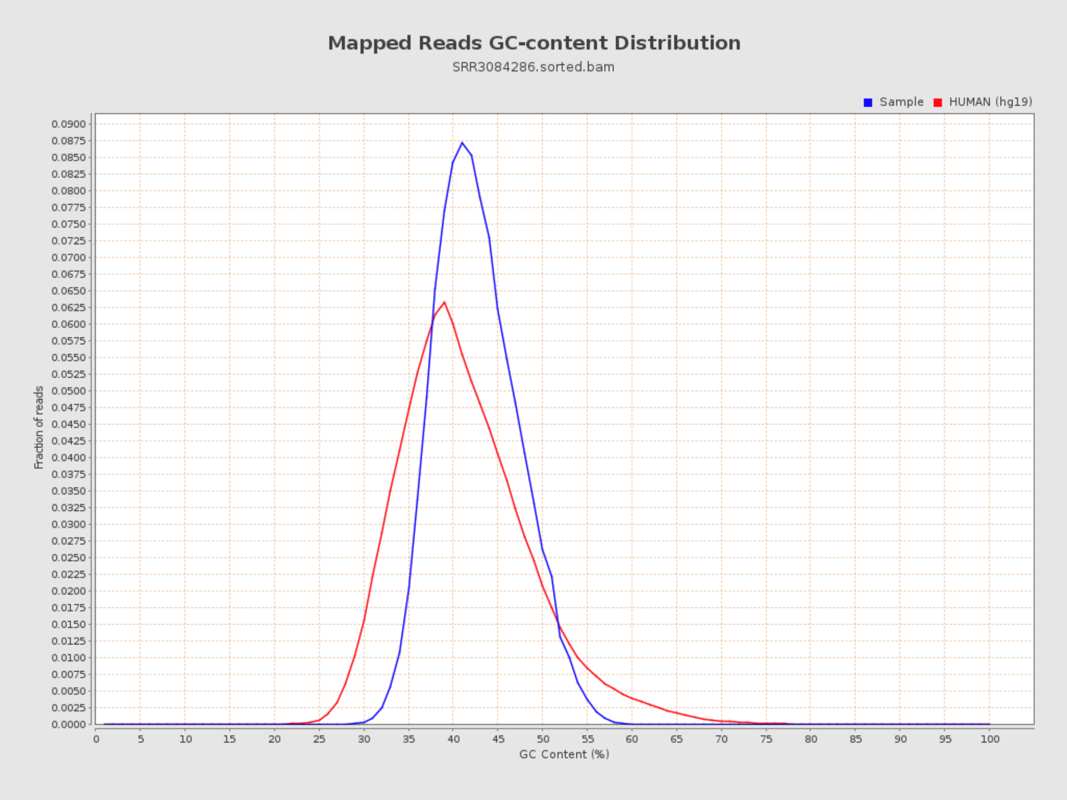
7. Results : Duplication Rate Histogram



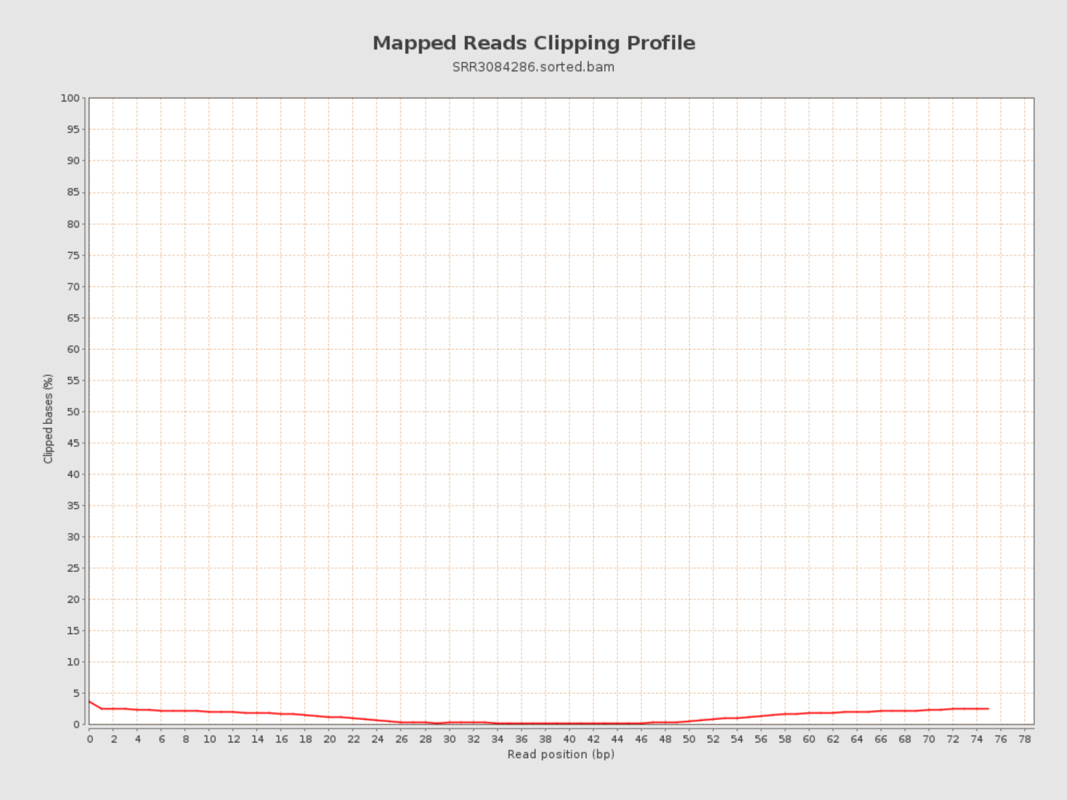
8. Results : Mapped Reads Nucleotide Content



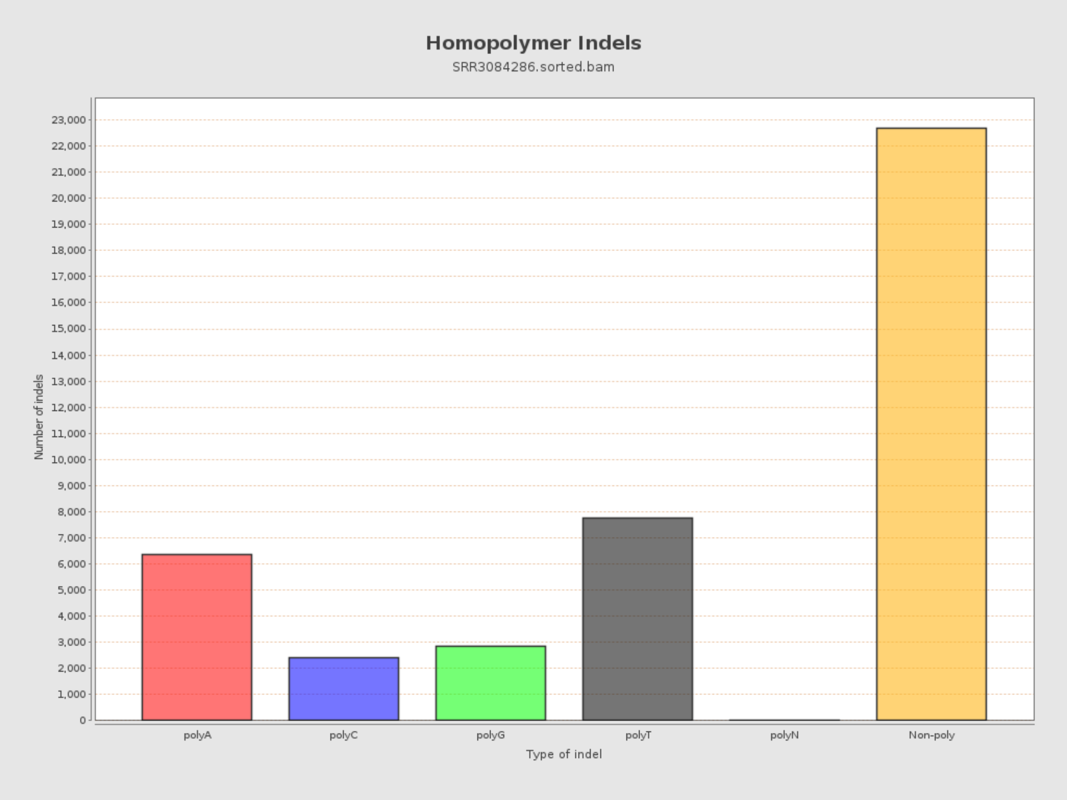
9. Results : Mapped Reads GC-content Distribution



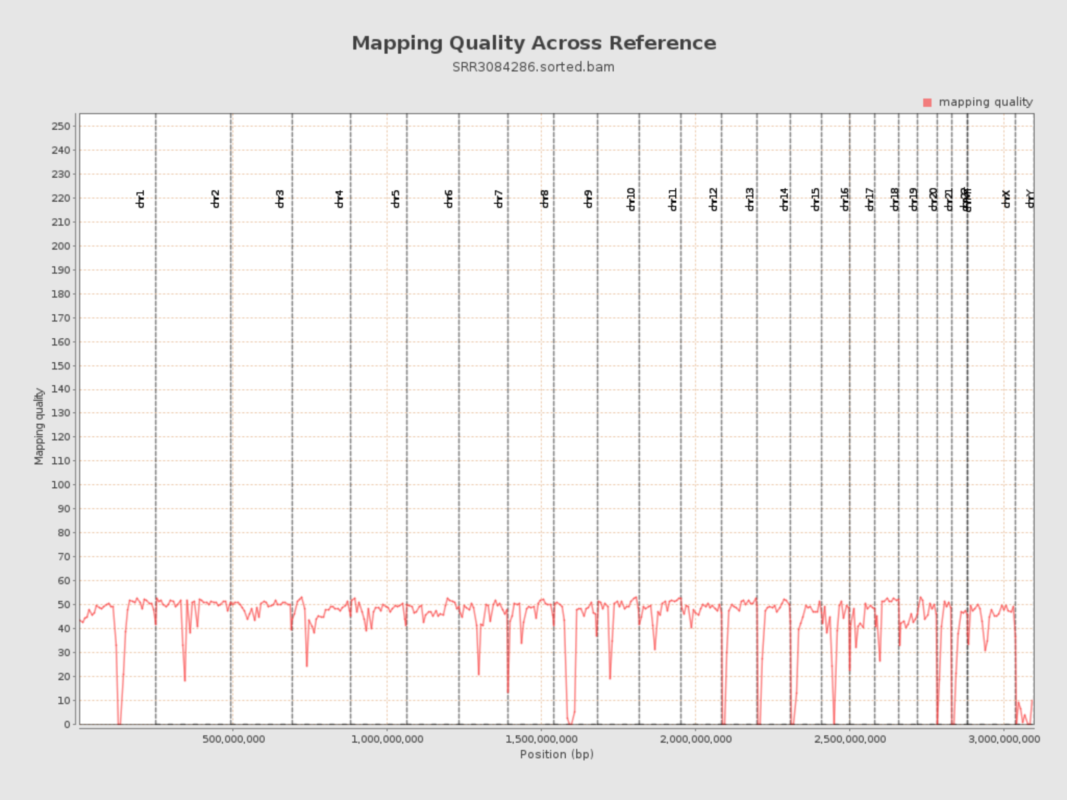
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram