Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/20 04:30:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1506339.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_SRR1506339 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1506339.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Dec 20 04:30:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1506339.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,705,953
Mapped reads	5,458,496 / 70.83%
Unmapped reads	2,247,457 / 29.17%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	79,624 / 1.03%
Read min/max/mean length	30 / 94 / 94.37
Duplicated reads (estimated)	834,772 / 10.83%
Duplication rate	11.51%
Clipped reads	3,702,204 / 48.04%

2.2. ACGT Content

Number/percentage of A's	116,414,592 / 28.09%
Number/percentage of C's	76,814,513 / 18.54%
Number/percentage of T's	120,024,351 / 28.96%
Number/percentage of G's	101,019,466 / 24.38%
Number/percentage of N's	105,562 / 0.03%
GC Percentage	42.92%

2.3. Coverage

Mean	0.1339

Standard Deviation	0.9173

2.4. Mapping Quality

Mean Mapping Quality	47.39

2.5. Mismatches and indels

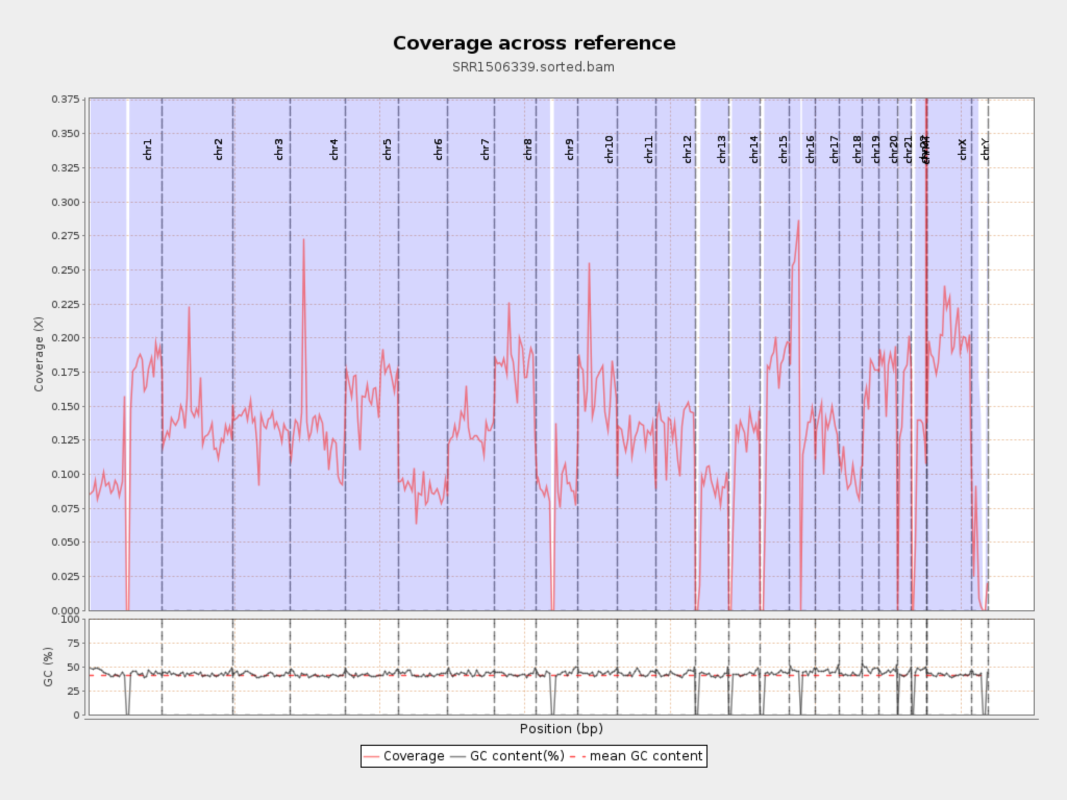
General error rate	0.74%
Mismatches	2,997,293
Insertions	33,509
Mapped reads with at least one insertion	0.6%
Deletions	85,799
Mapped reads with at least one deletion	1.54%
Homopolymer indels	44.73%

2.6. Chromosome stats

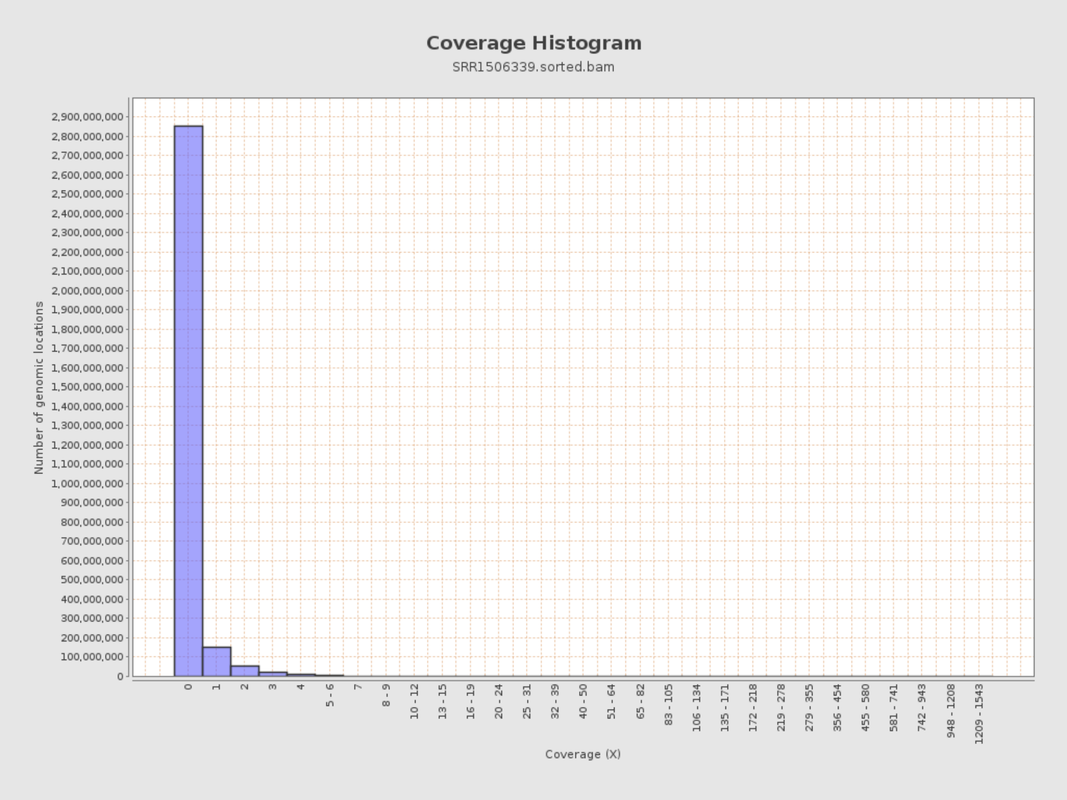
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	31322550	0.1257	1.4653
chr2	243199373	33473835	0.1376	1.0153
chr3	198022430	27093067	0.1368	0.5893
chr4	191154276	25143198	0.1315	0.8249
chr5	180915260	29565759	0.1634	0.6388
chr6	171115067	15097935	0.0882	0.5153
chr7	159138663	21004372	0.132	1.1083

chr8	146364022	26456192	0.1808	1.2391
chr9	141213431	11638851	0.0824	0.8659
chr10	135534747	22880674	0.1688	1.0373
chr11	135006516	17214480	0.1275	0.8513
chr12	133851895	17999489	0.1345	0.6786
chr13	115169878	9029546	0.0784	0.4321
chr14	107349540	11913253	0.111	0.6113
chr15	102531392	15461242	0.1508	0.6449
chr16	90354753	15407655	0.1705	0.8118
chr17	81195210	10915947	0.1344	0.6975
chr18	78077248	7707174	0.0987	1.4644
chr19	59128983	9827704	0.1662	1.1697
chr20	63025520	11198492	0.1777	0.7343
chr21	48129895	7198558	0.1496	0.7828
chr22	51304566	4772400	0.093	0.5002
chrMT	16571	69866	4.2162	3.4994
chrX	155270560	30695439	0.1977	0.8108
chrY	59373566	1459287	0.0246	0.7734

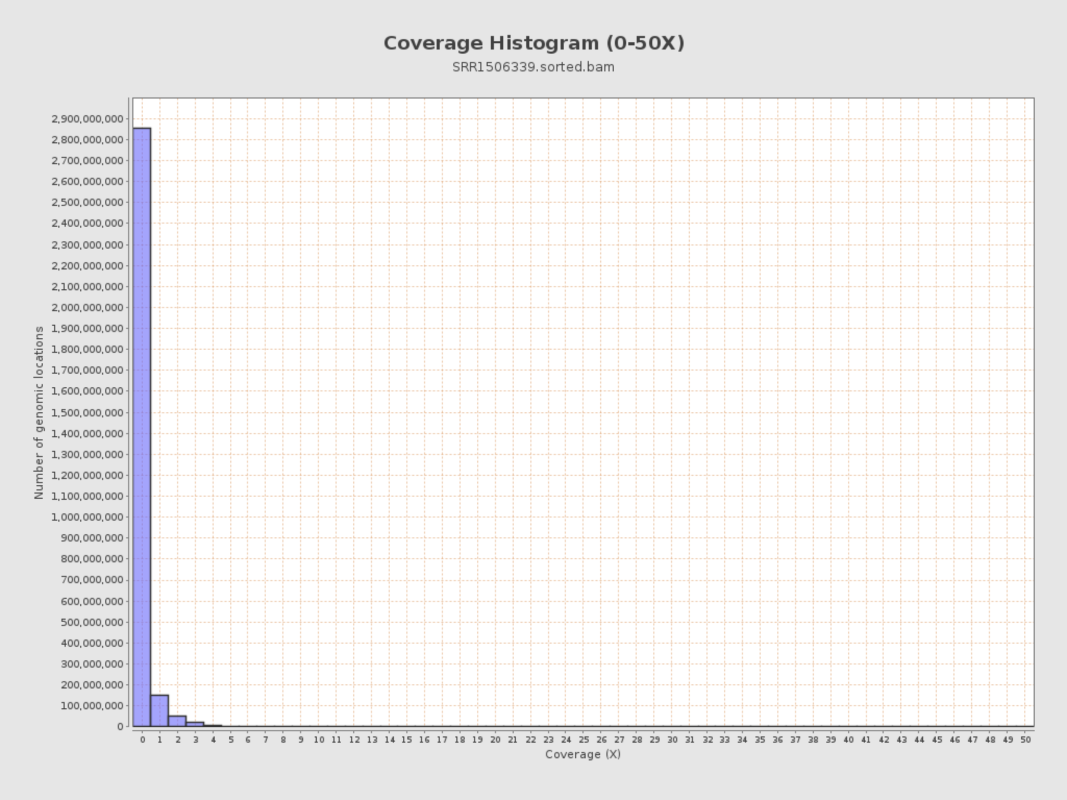
3. Results : Coverage across reference



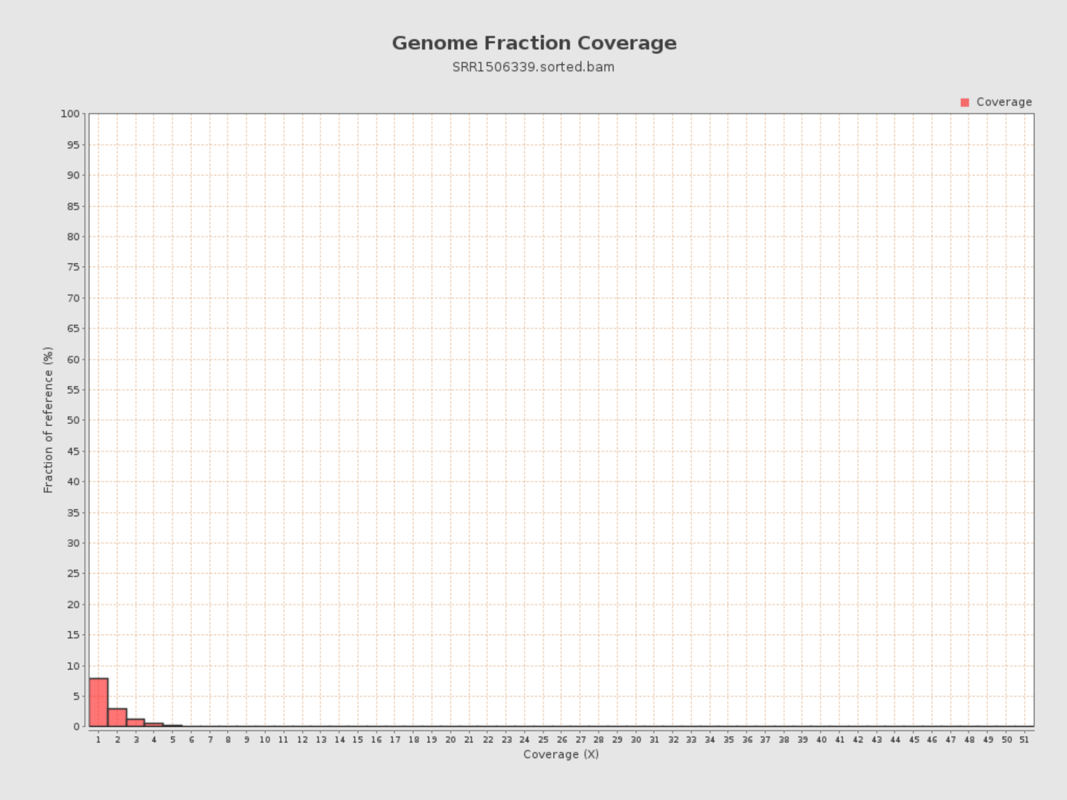
4. Results : Coverage Histogram



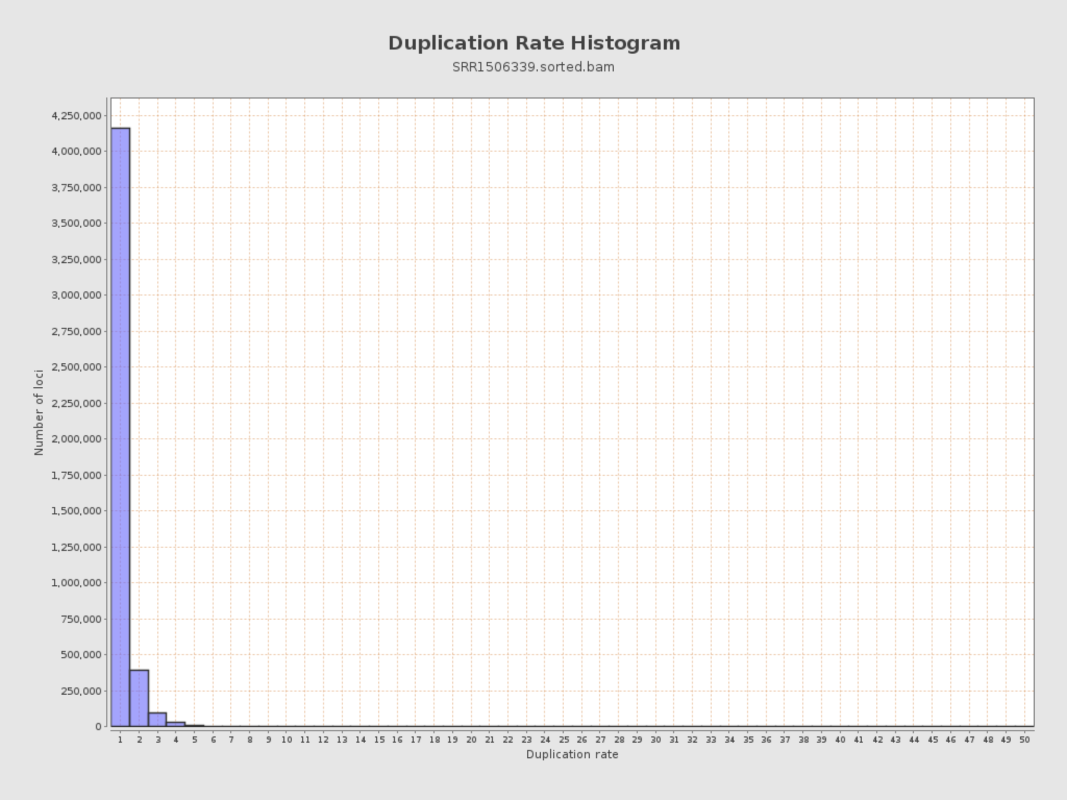
5. Results : Coverage Histogram (0-50X)



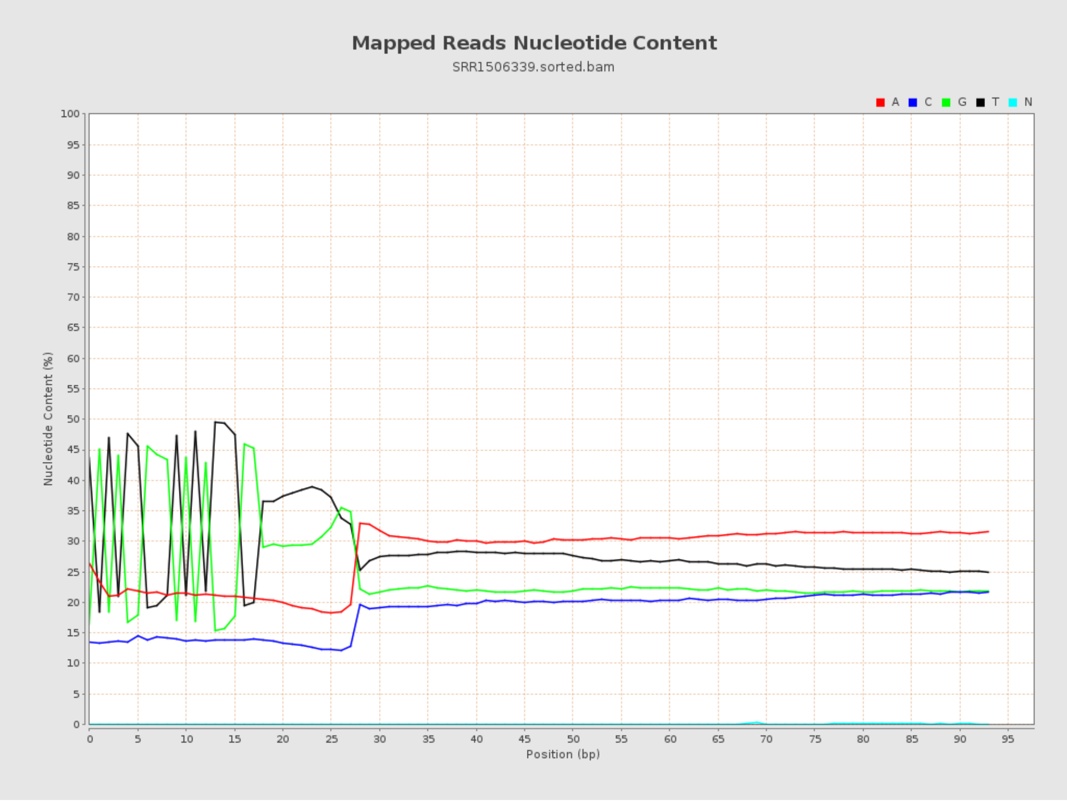
6. Results : Genome Fraction Coverage



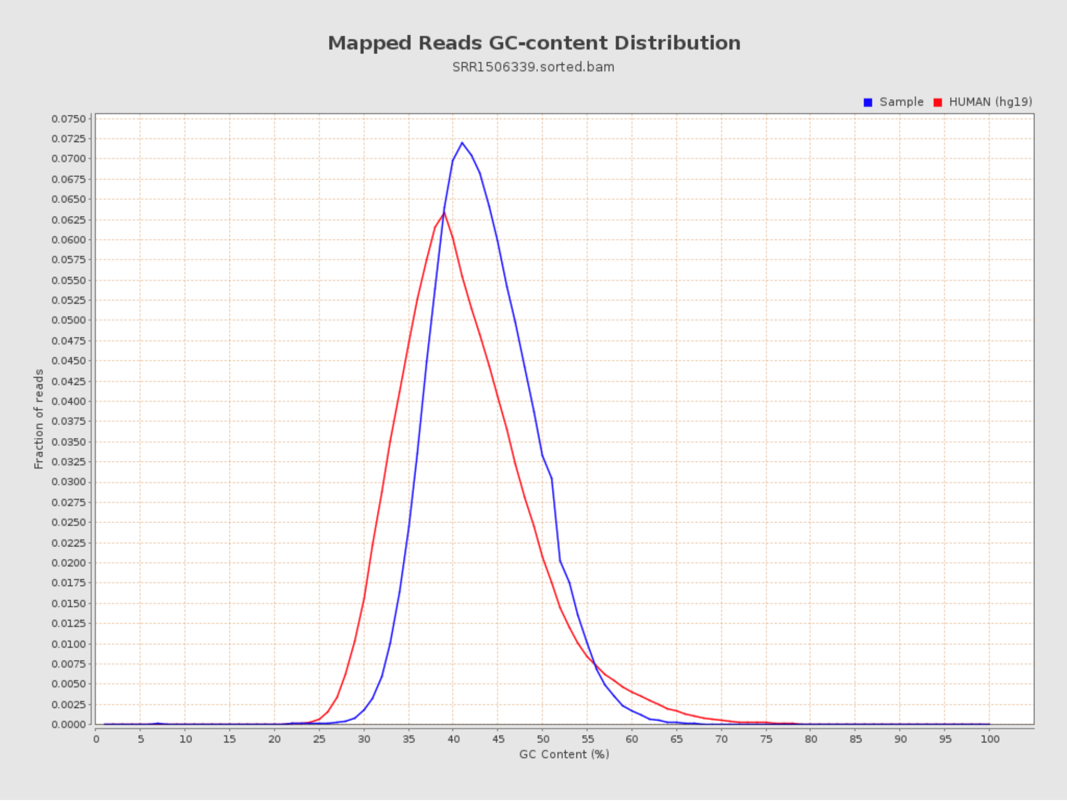
7. Results : Duplication Rate Histogram



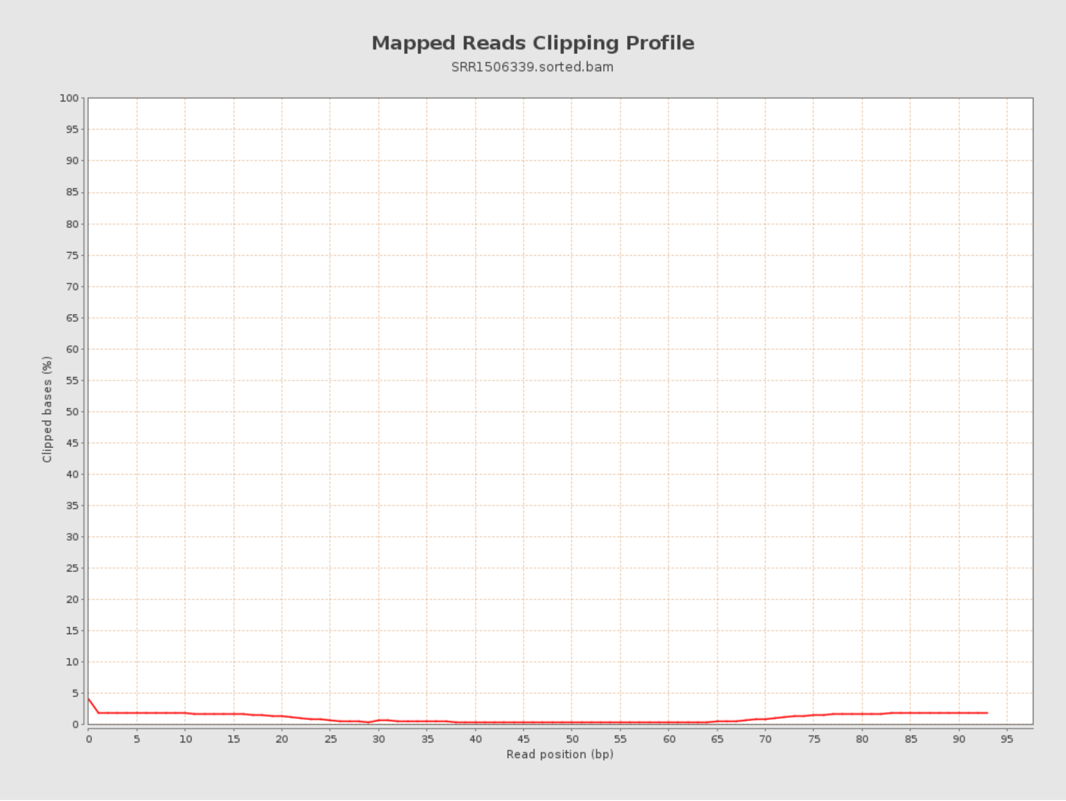
8. Results : Mapped Reads Nucleotide Content



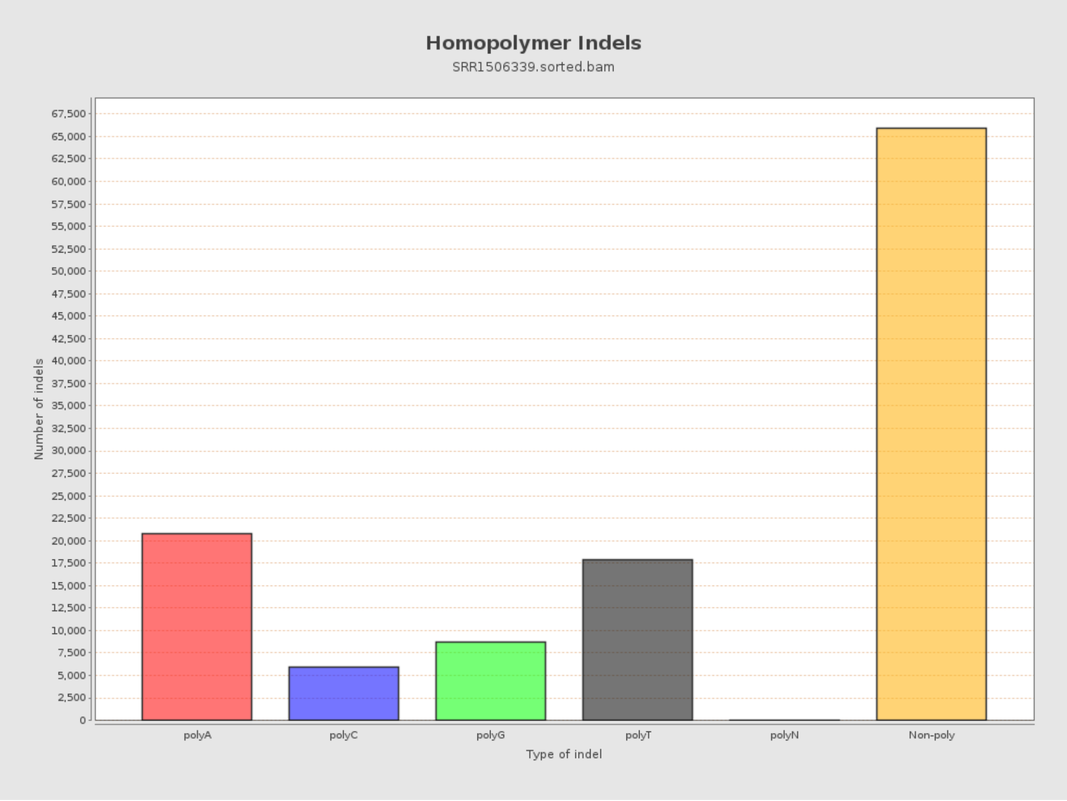
9. Results : Mapped Reads GC-content Distribution



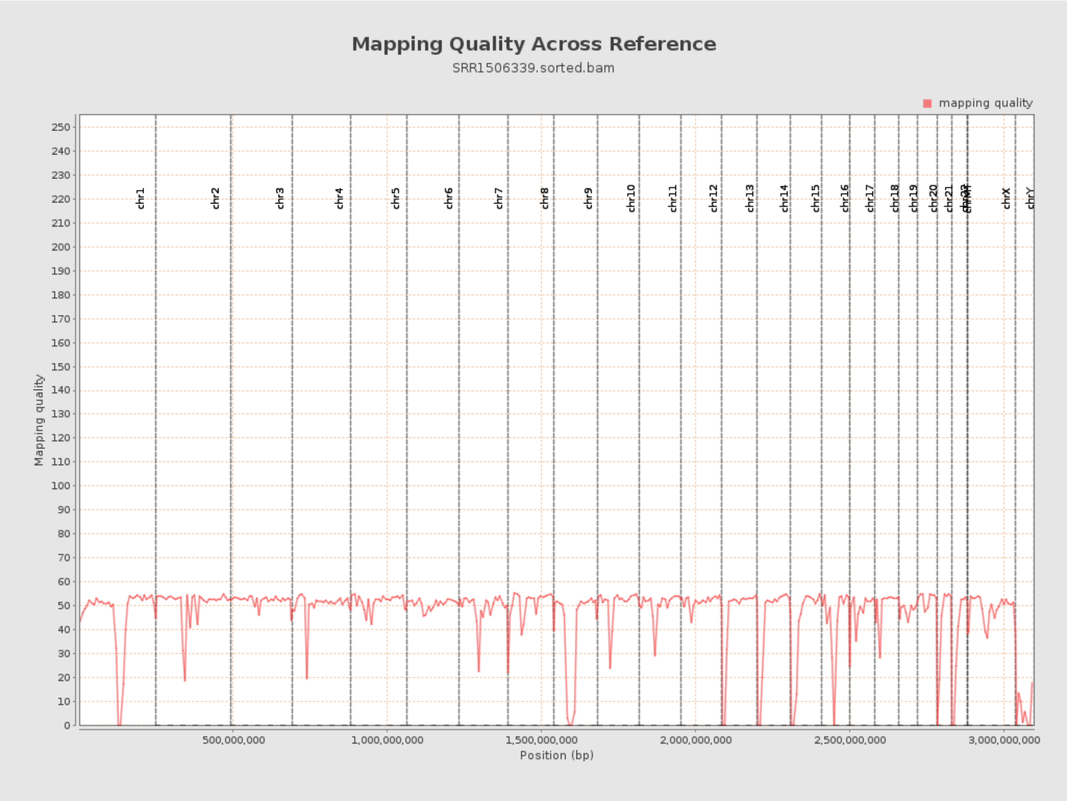
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram