Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 01:33:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524887.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_SRR10524887 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524887.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 01:33:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524887.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,489,502
Mapped reads	2,295,109 / 92.19%
Unmapped reads	194,393 / 7.81%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,080 / 0.36%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	110,025 / 4.42%
Duplication rate	3.49%
Clipped reads	2,302,921 / 92.51%

2.2. ACGT Content

Number/percentage of A's	33,654,690 / 25.09%
Number/percentage of C's	25,910,428 / 19.32%
Number/percentage of T's	42,077,225 / 31.37%
Number/percentage of G's	32,466,832 / 24.21%
Number/percentage of N's	18,155 / 0.01%
GC Percentage	43.52%

2.3. Coverage

Mean	0.0433

Standard Deviation	0.4079

2.4. Mapping Quality

Mean Mapping Quality	46.11

2.5. Mismatches and indels

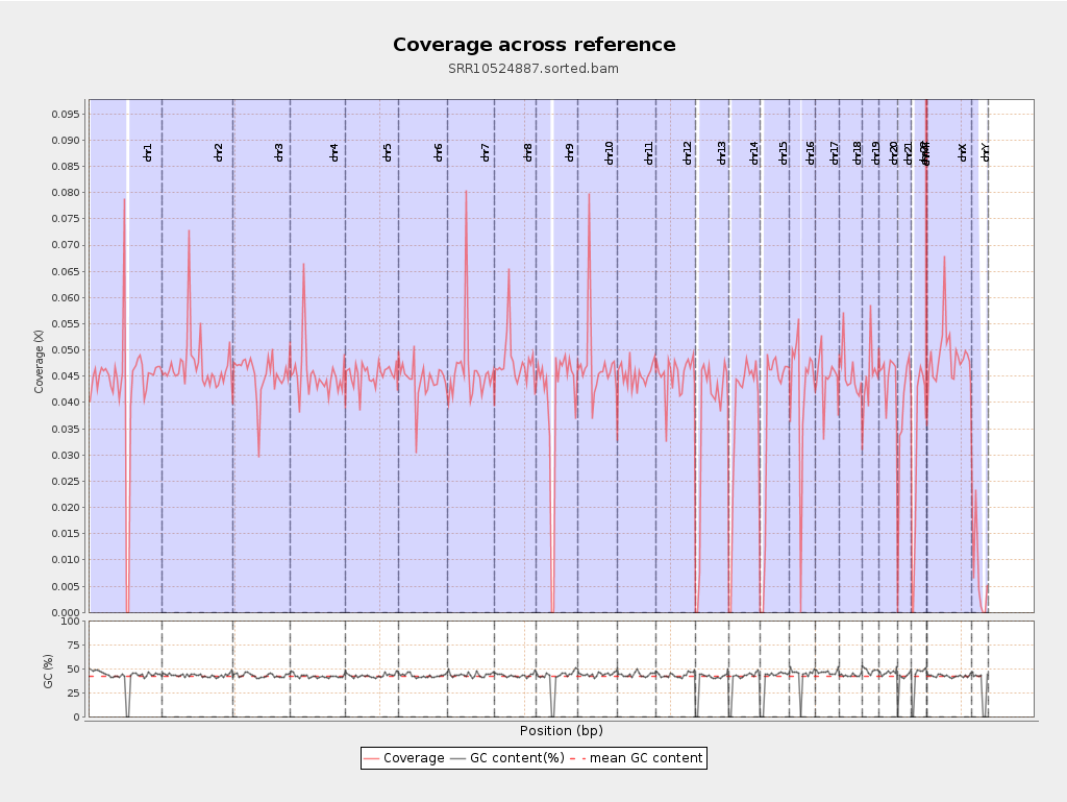
General error rate	0.5%
Mismatches	657,664
Insertions	7,902
Mapped reads with at least one insertion	0.34%
Deletions	25,340
Mapped reads with at least one deletion	1.1%
Homopolymer indels	44.38%

2.6. Chromosome stats

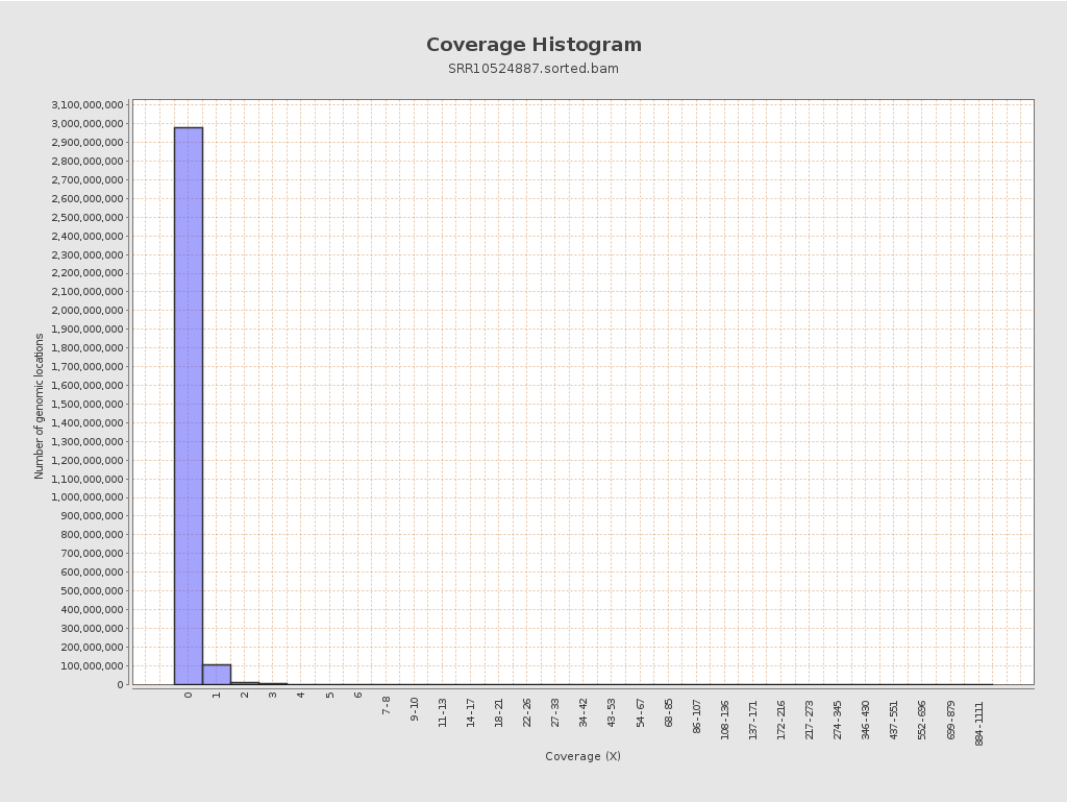
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	10767685	0.0432	0.8345
chr2	243199373	11446380	0.0471	0.4467
chr3	198022430	8961588	0.0453	0.2369
chr4	191154276	8647950	0.0452	0.2655
chr5	180915260	8196636	0.0453	0.2398
chr6	171115067	7589976	0.0444	0.2628
chr7	159138663	7374349	0.0463	0.5788

chr8	146364022	6985788	0.0477	0.3878
chr9	141213431	5646049	0.04	0.3577
chr10	135534747	6391231	0.0472	0.3806
chr11	135006516	6096989	0.0452	0.3571
chr12	133851895	6045239	0.0452	0.245
chr13	115169878	4212793	0.0366	0.2125
chr14	107349540	4031815	0.0376	0.2292
chr15	102531392	3839402	0.0374	0.2168
chr16	90354753	3859403	0.0427	0.2582
chr17	81195210	3610984	0.0445	0.2614
chr18	78077248	3561085	0.0456	0.7094
chr19	59128983	2679409	0.0453	0.5349
chr20	63025520	2835106	0.045	0.2425
chr21	48129895	1795092	0.0373	0.2473
chr22	51304566	1584549	0.0309	0.1956
chrMT	16571	42831	2.5847	2.051
chrX	155270560	7565593	0.0487	0.2973
chrY	59373566	399886	0.0067	0.1729

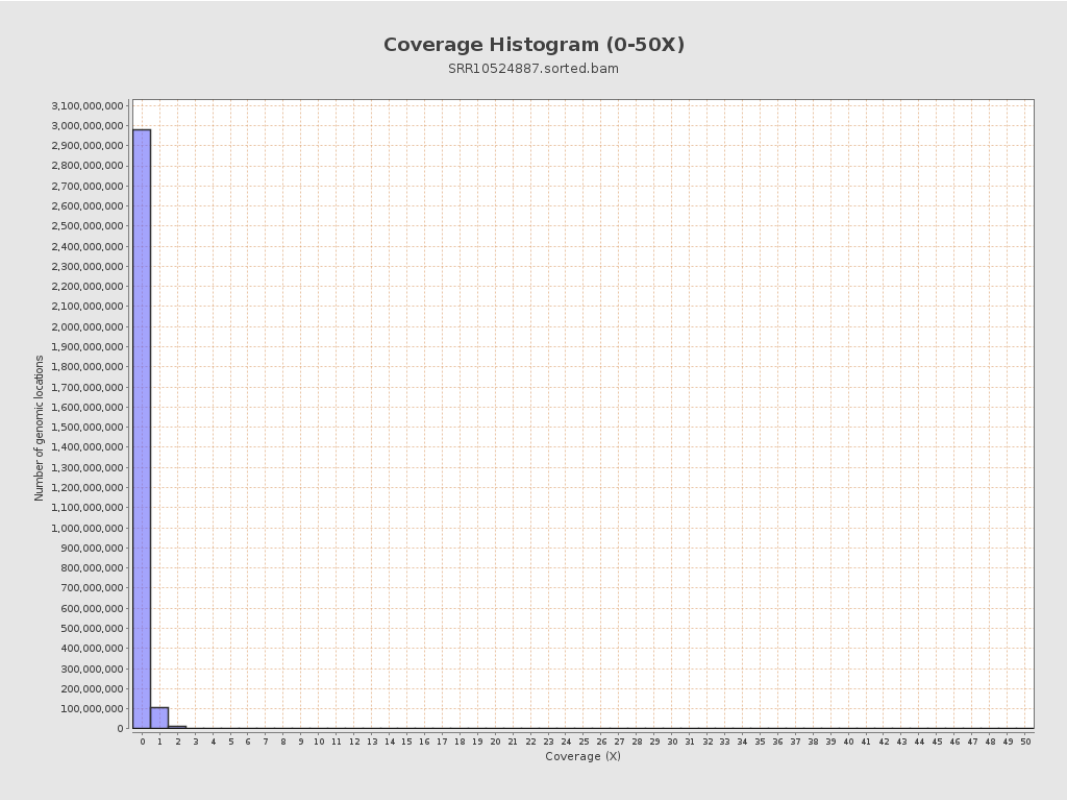
3. Results : Coverage across reference



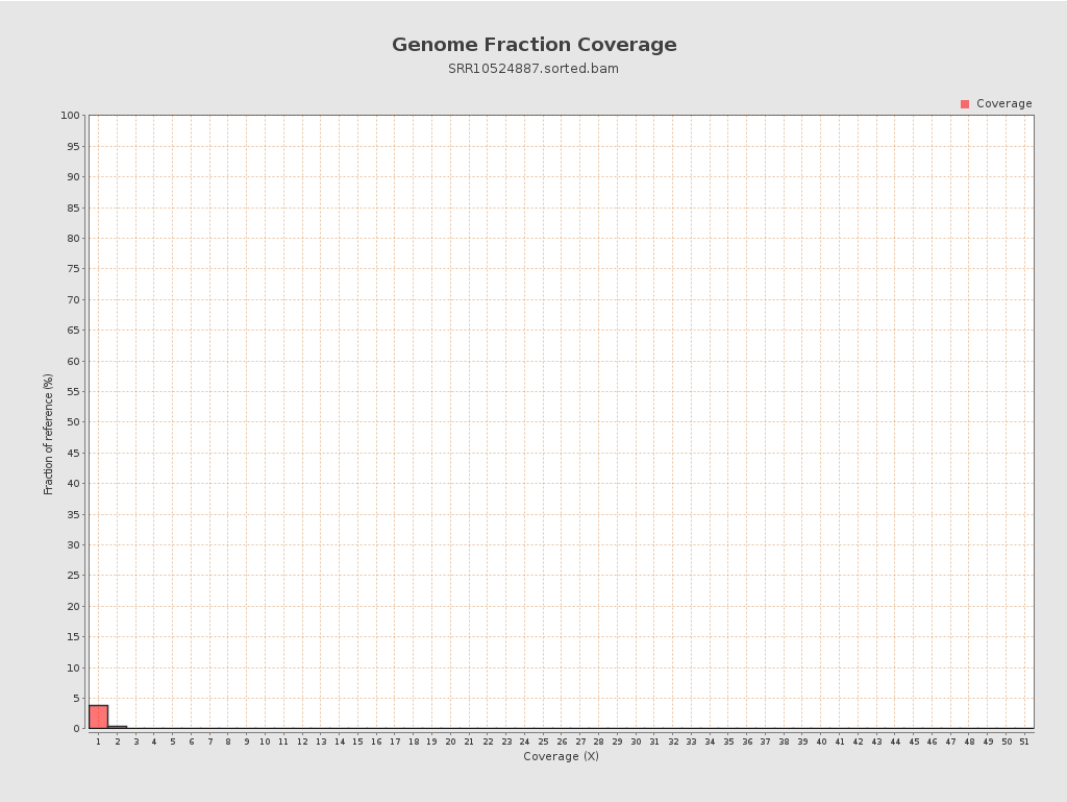
4. Results : Coverage Histogram



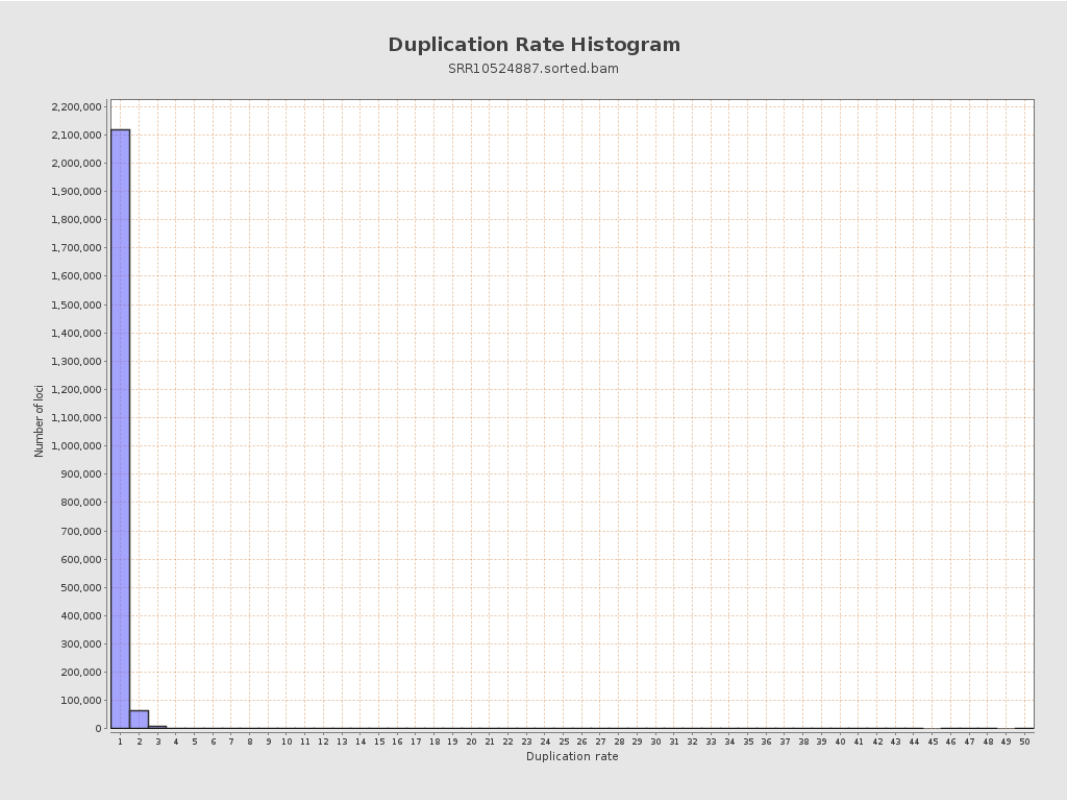
5. Results : Coverage Histogram (0-50X)



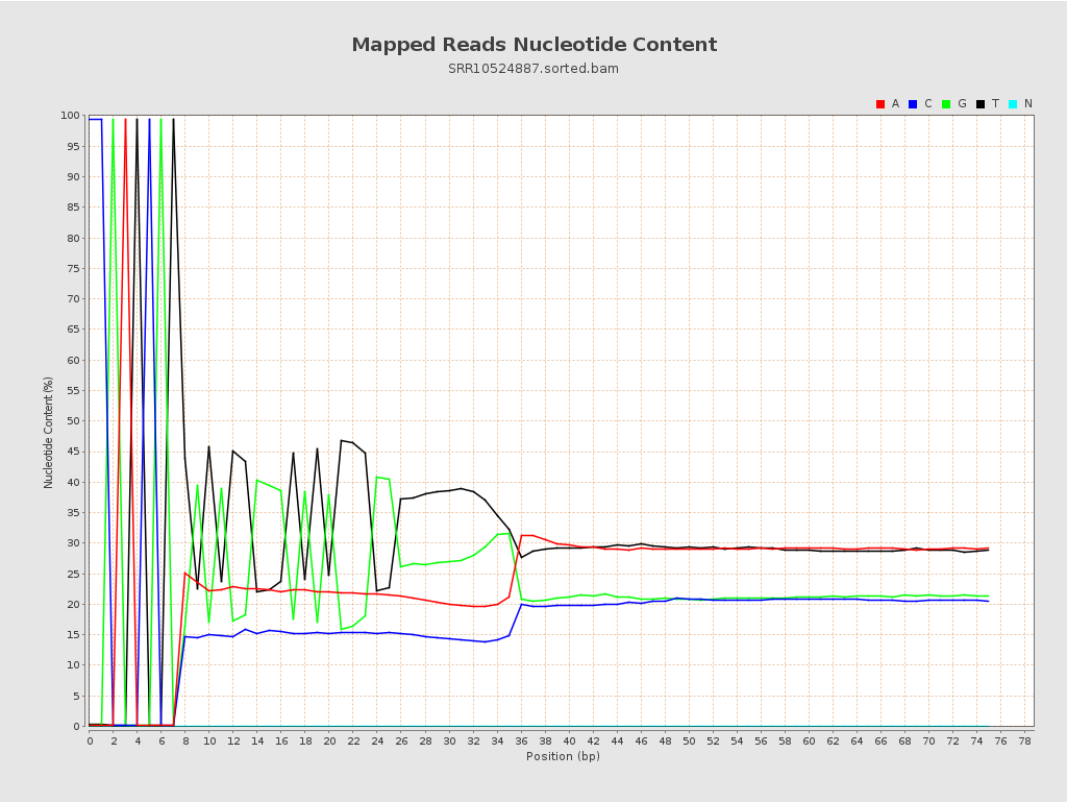
6. Results : Genome Fraction Coverage



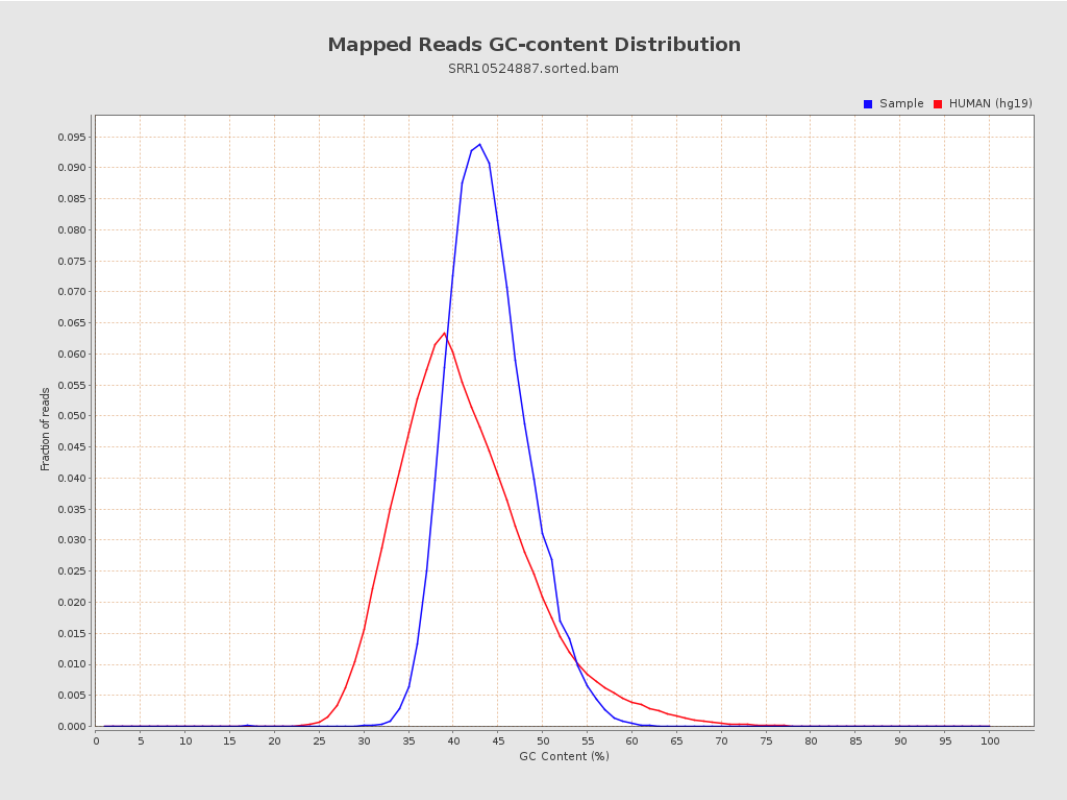
7. Results : Duplication Rate Histogram



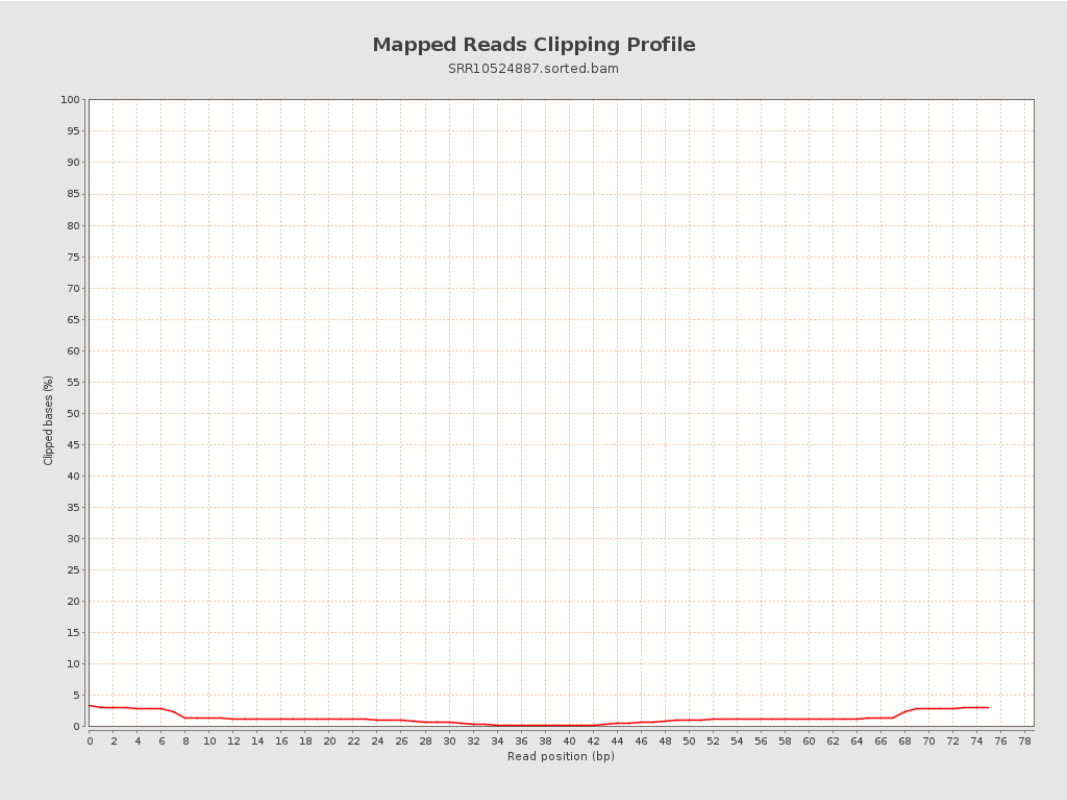
8. Results : Mapped Reads Nucleotide Content



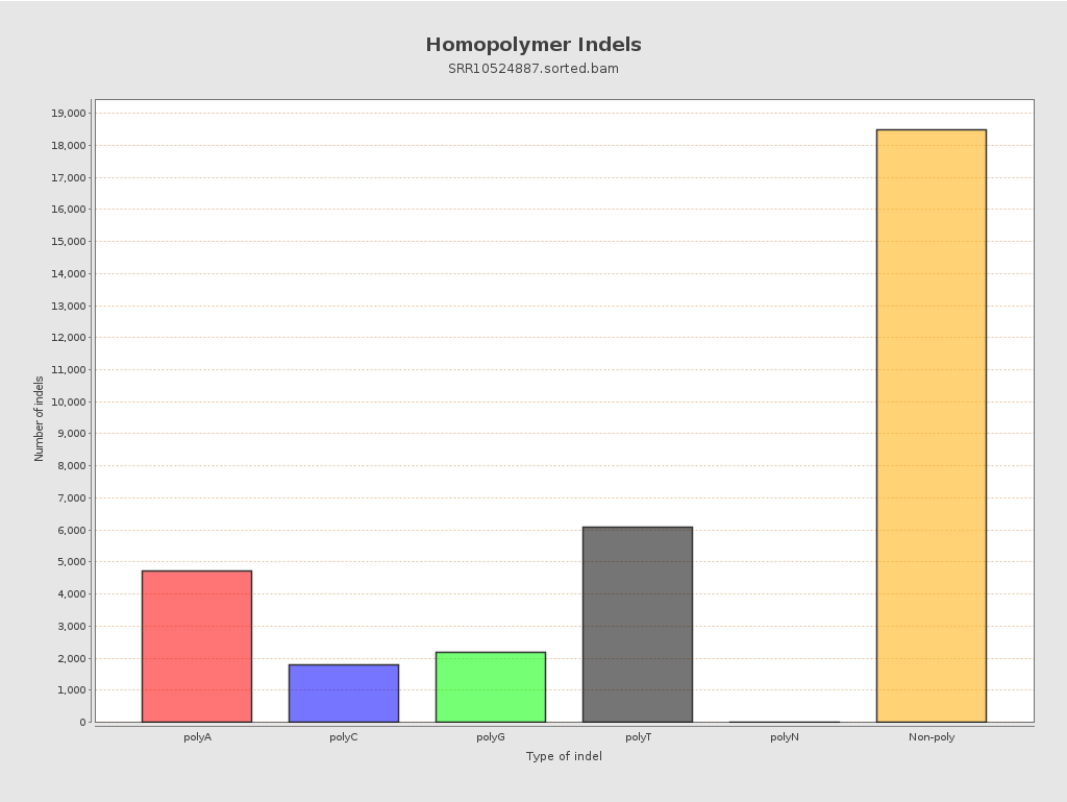
9. Results : Mapped Reads GC-content Distribution



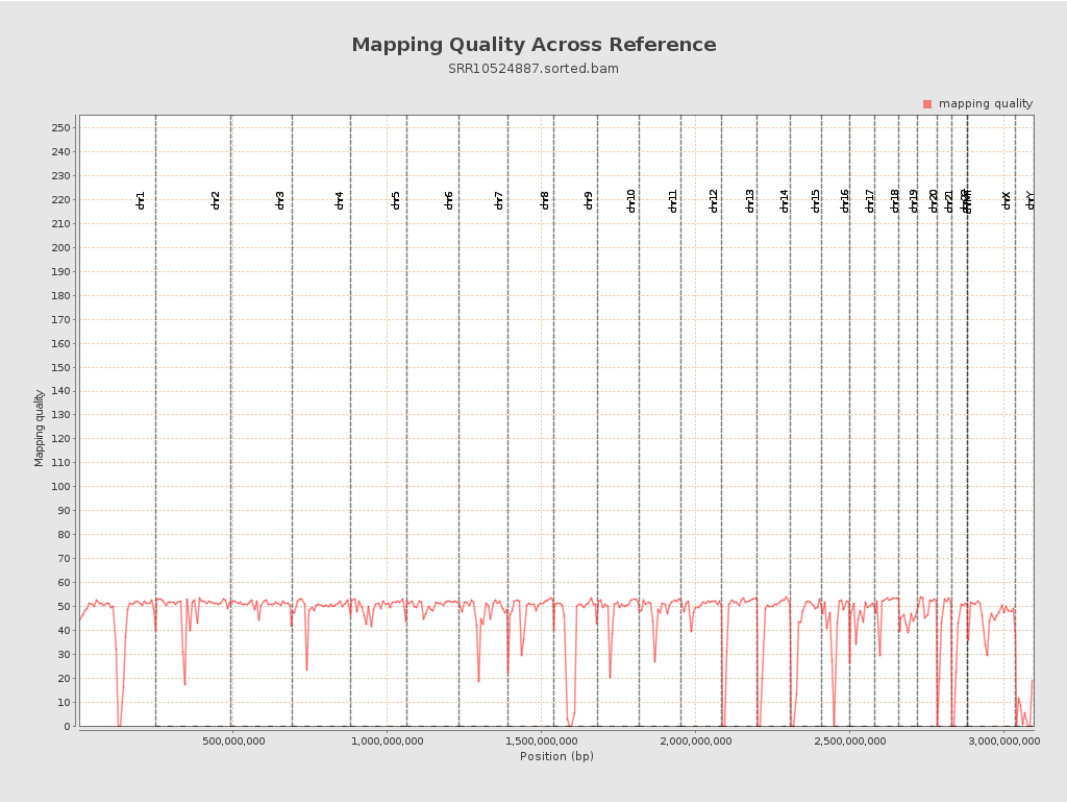
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram