Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 06:00:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524487.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_SRR10524487 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524487.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 06:00:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524487.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,812,879
Mapped reads	1,672,637 / 92.26%
Unmapped reads	140,242 / 7.74%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,154 / 0.23%
Read min/max/mean length	30 / 76 / 76.08
Duplicated reads (estimated)	96,577 / 5.33%
Duplication rate	4.5%
Clipped reads	1,672,149 / 92.24%

2.2. ACGT Content

Number/percentage of A's	25,070,687 / 25.66%
Number/percentage of C's	18,944,381 / 19.39%
Number/percentage of T's	30,564,229 / 31.29%
Number/percentage of G's	23,110,804 / 23.66%
Number/percentage of N's	1,879 / 0%
GC Percentage	43.05%

2.3. Coverage

Mean	0.0316

Standard Deviation	0.3016

2.4. Mapping Quality

Mean Mapping Quality	45.43

2.5. Mismatches and indels

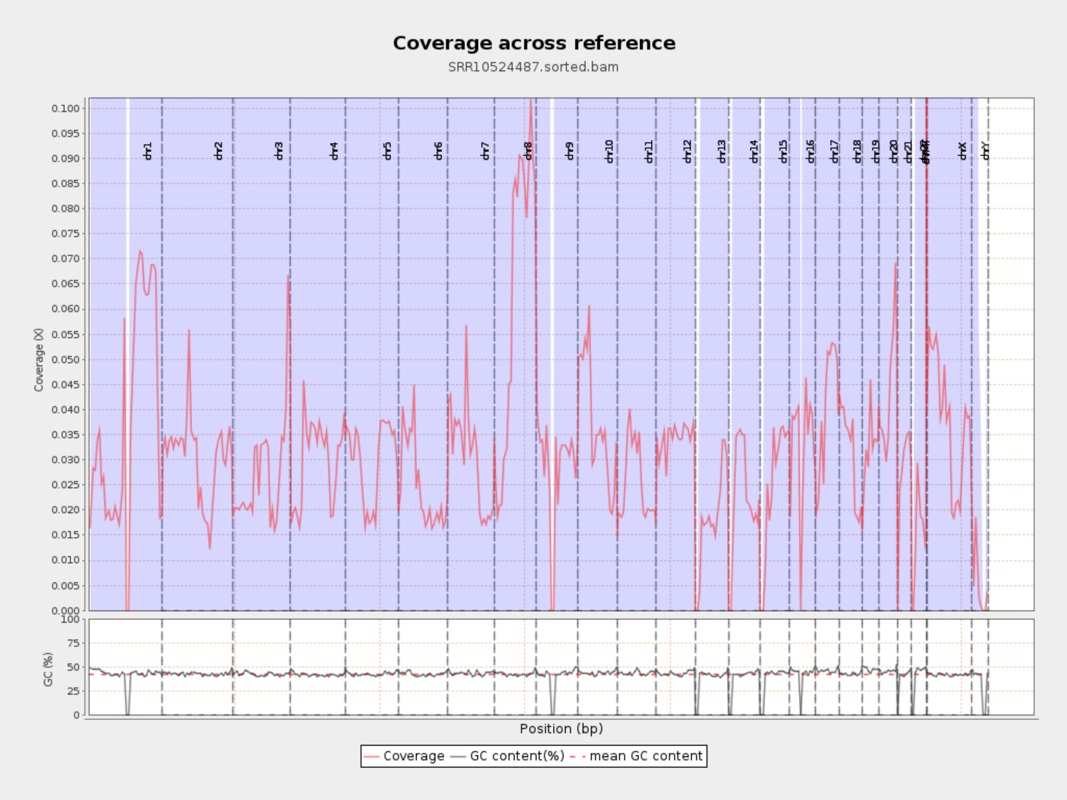
General error rate	0.48%
Mismatches	455,476
Insertions	6,731
Mapped reads with at least one insertion	0.4%
Deletions	17,230
Mapped reads with at least one deletion	1.02%
Homopolymer indels	42.69%

2.6. Chromosome stats

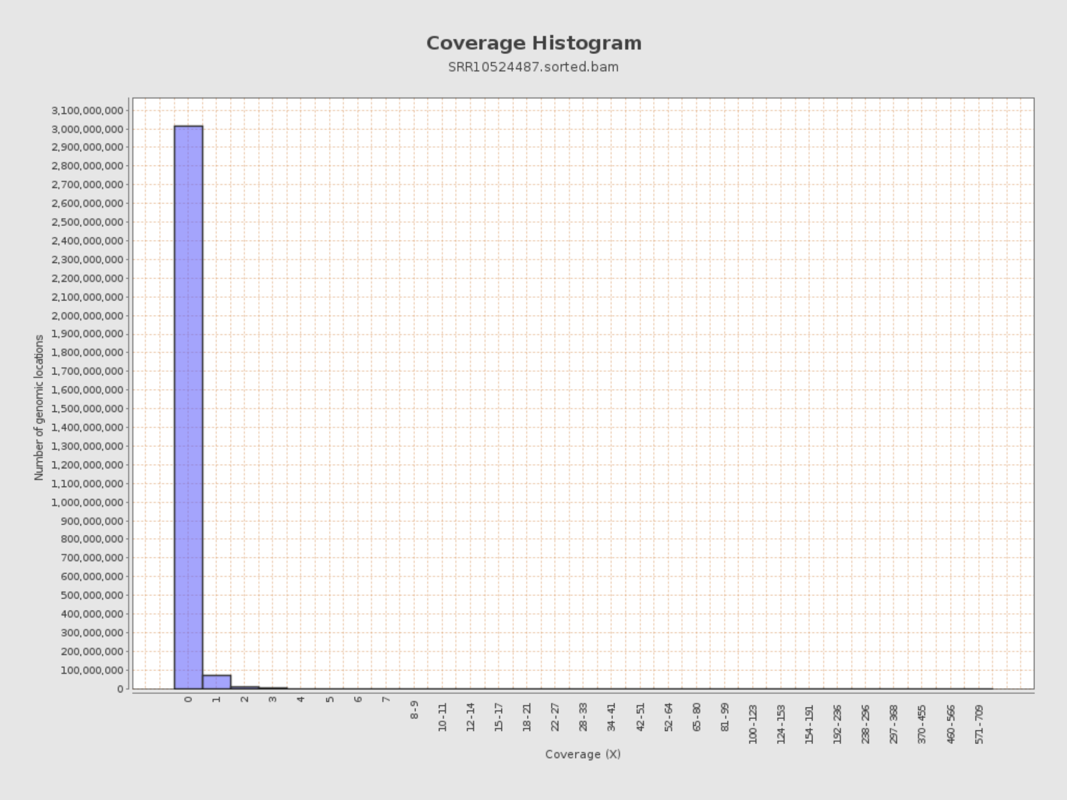
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9496692	0.0381	0.5633
chr2	243199373	7448124	0.0306	0.3376
chr3	198022430	5400512	0.0273	0.1889
chr4	191154276	5703316	0.0298	0.2223
chr5	180915260	5433419	0.03	0.1975
chr6	171115067	4230492	0.0247	0.234
chr7	159138663	4903683	0.0308	0.3979

chr8	146364022	9223553	0.063	0.3387
chr9	141213431	3947114	0.028	0.2561
chr10	135534747	5086300	0.0375	0.3051
chr11	135006516	3458888	0.0256	0.2713
chr12	133851895	4605776	0.0344	0.2119
chr13	115169878	2111725	0.0183	0.1558
chr14	107349540	2398286	0.0223	0.174
chr15	102531392	2541606	0.0248	0.1866
chr16	90354753	2983226	0.033	0.2181
chr17	81195210	3305212	0.0407	0.2451
chr18	78077248	2436249	0.0312	0.4559
chr19	59128983	1931425	0.0327	0.394
chr20	63025520	2771825	0.044	0.2435
chr21	48129895	1334901	0.0277	0.2033
chr22	51304566	733605	0.0143	0.1349
chrMT	16571	4927	0.2973	0.5783
chrX	155270560	5919264	0.0381	0.2483
chrY	59373566	311836	0.0053	0.1505

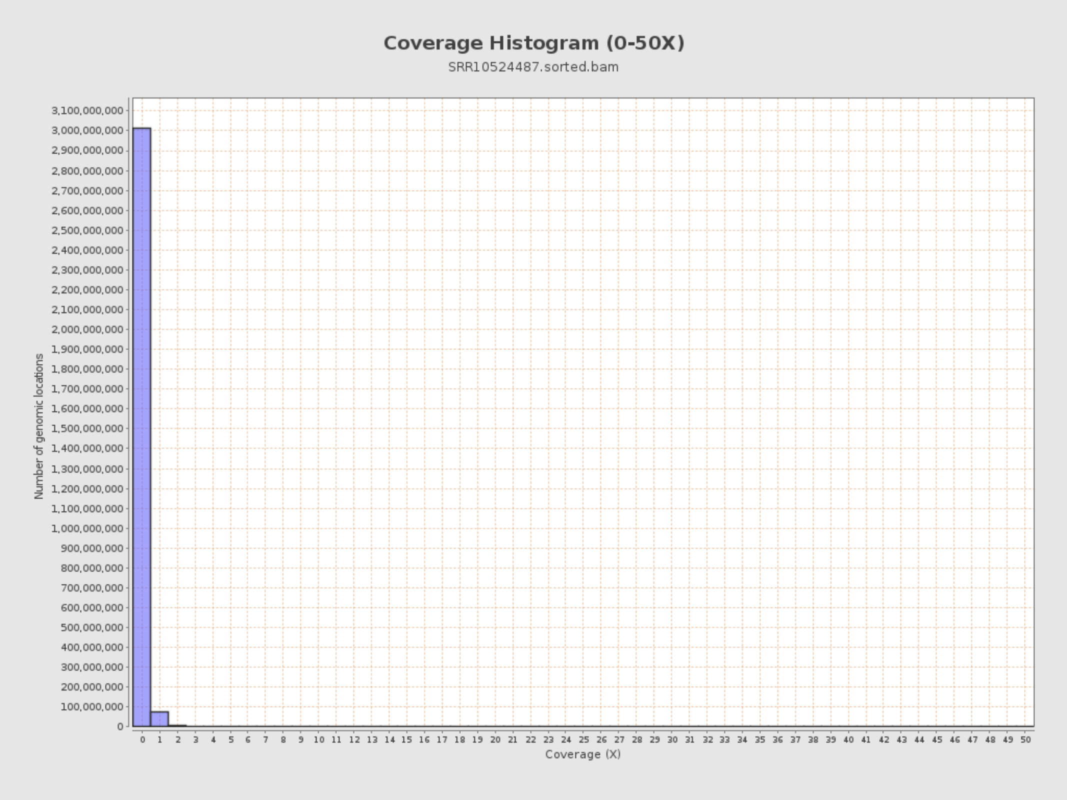
3. Results : Coverage across reference



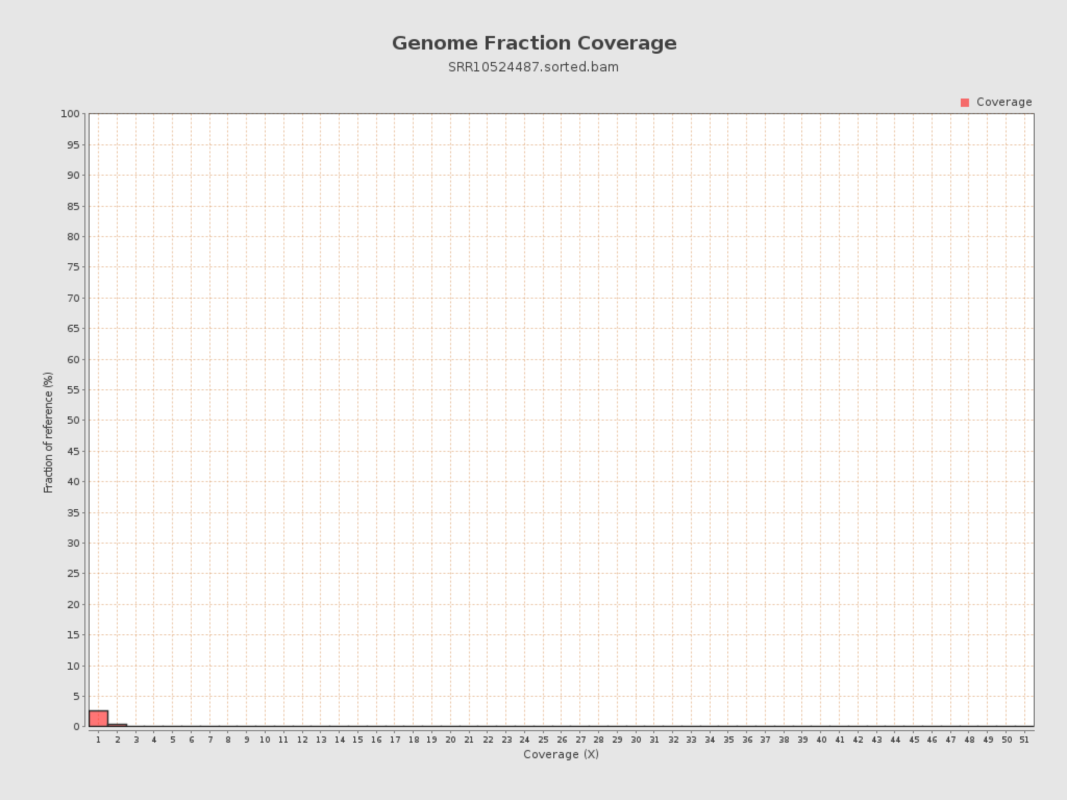
4. Results : Coverage Histogram



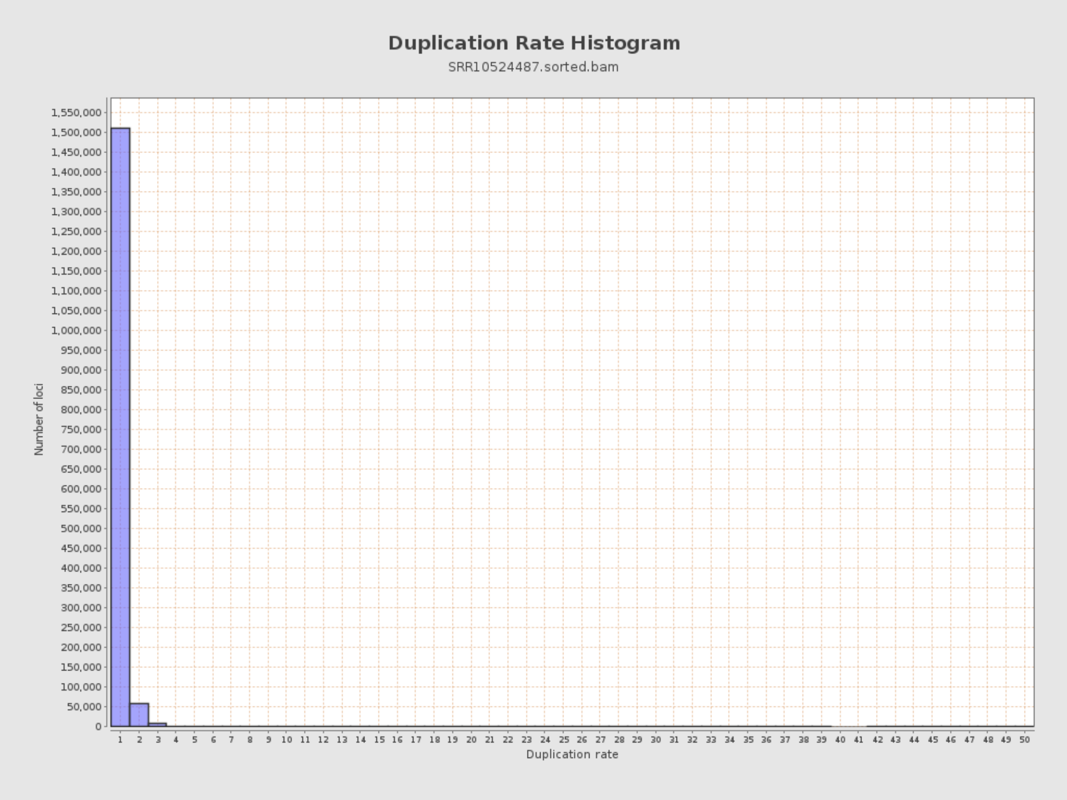
5. Results : Coverage Histogram (0-50X)



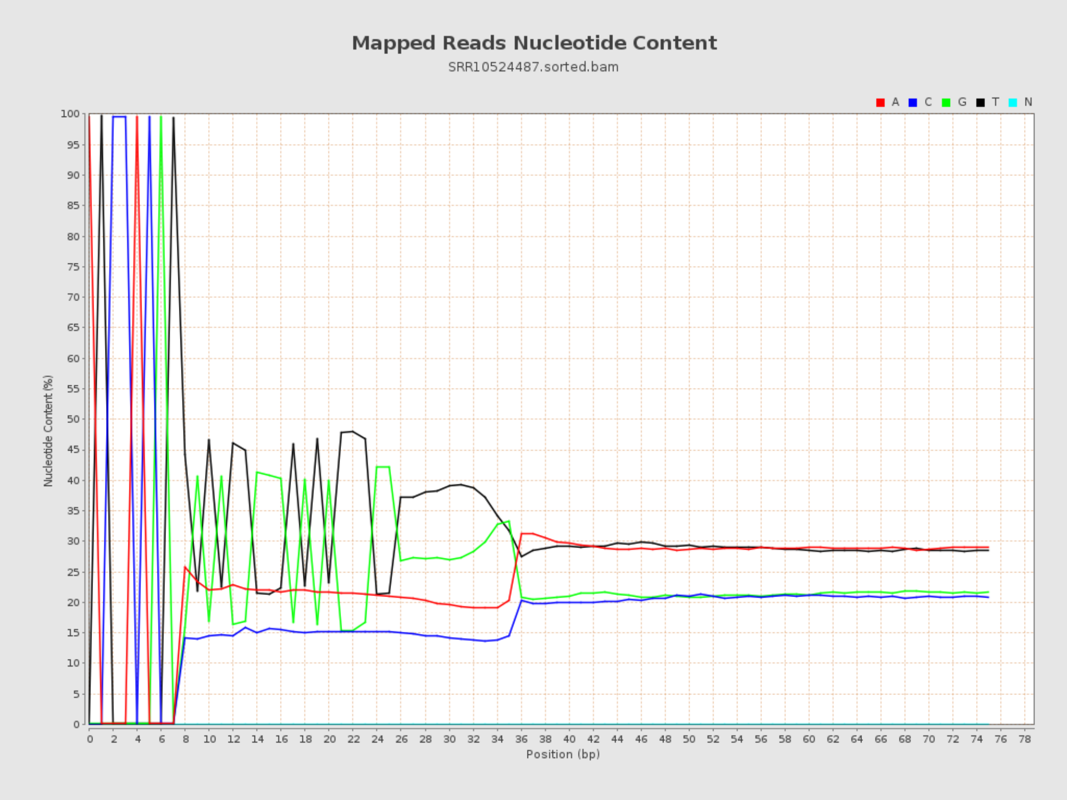
6. Results : Genome Fraction Coverage



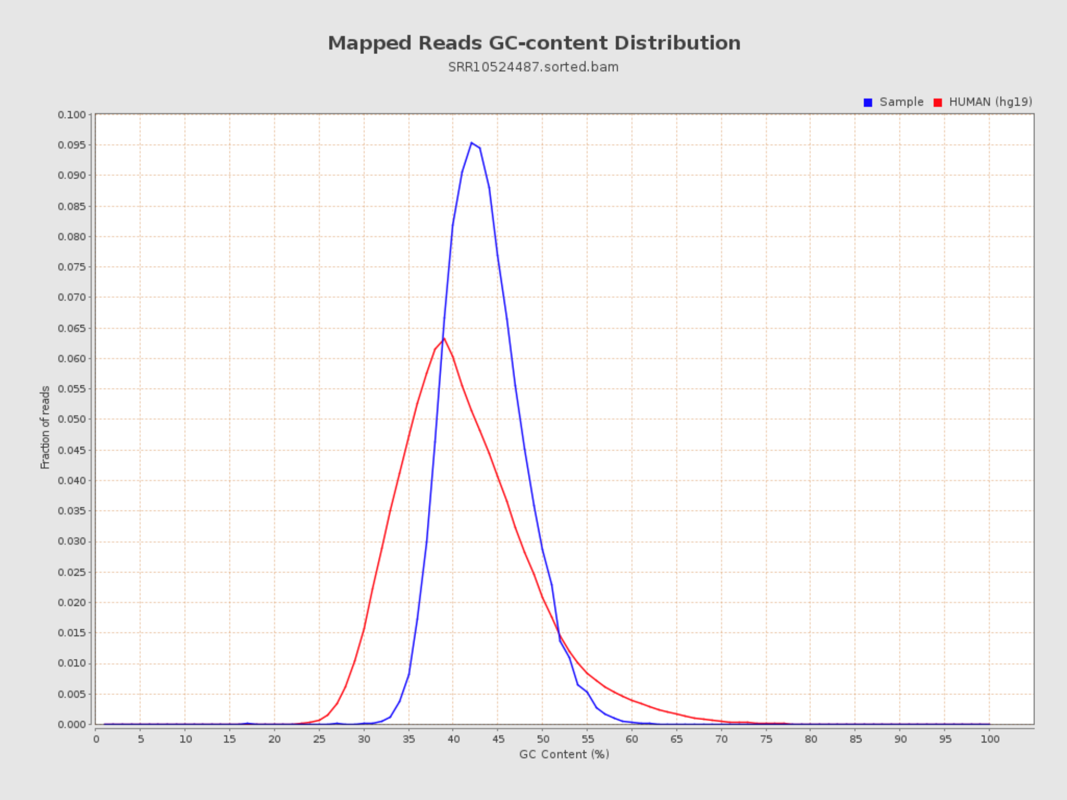
7. Results : Duplication Rate Histogram



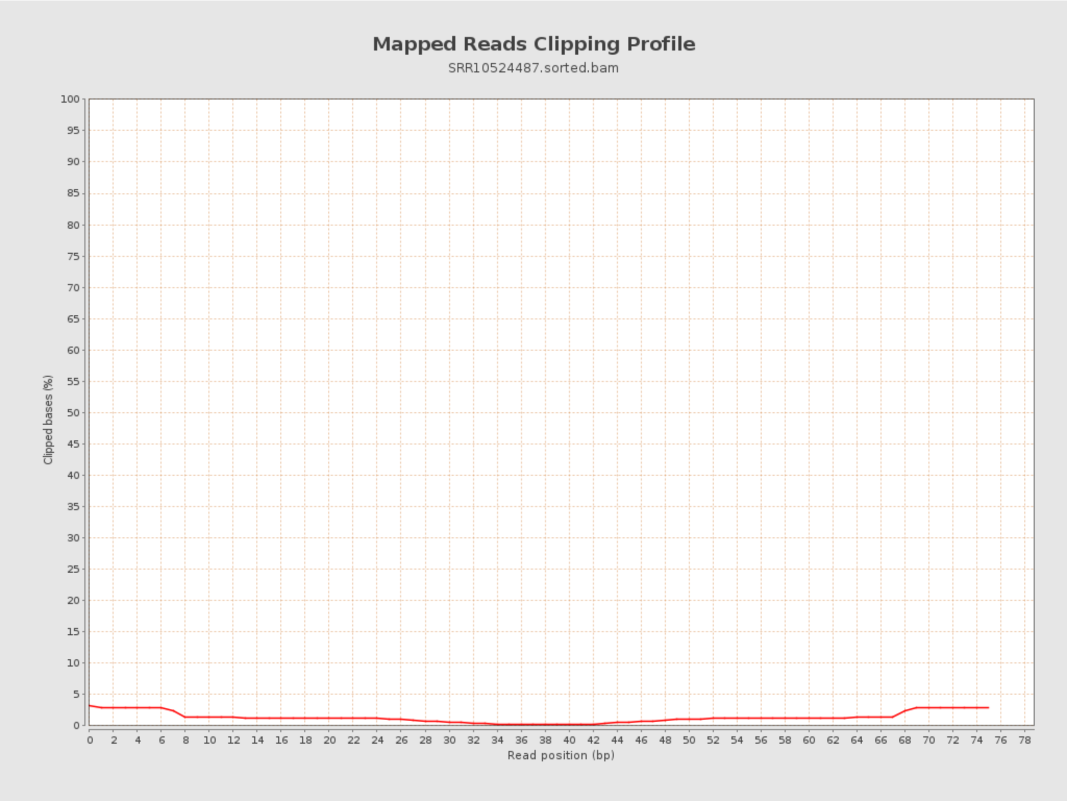
8. Results : Mapped Reads Nucleotide Content



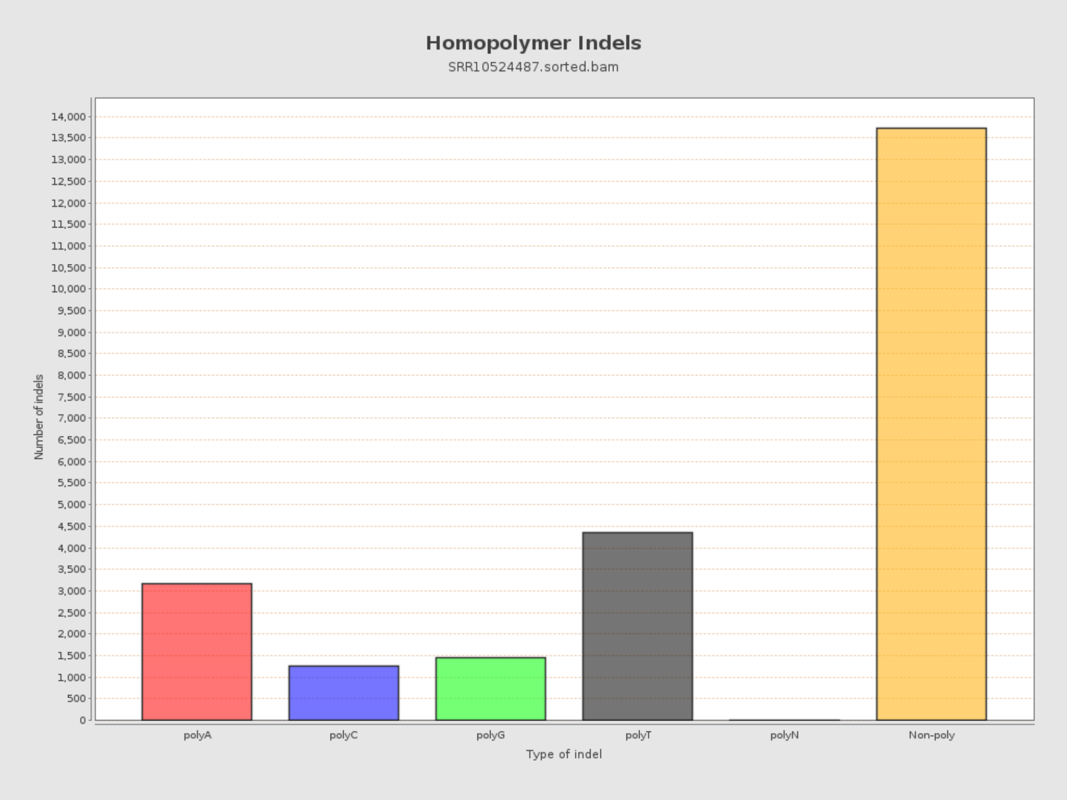
9. Results : Mapped Reads GC-content Distribution



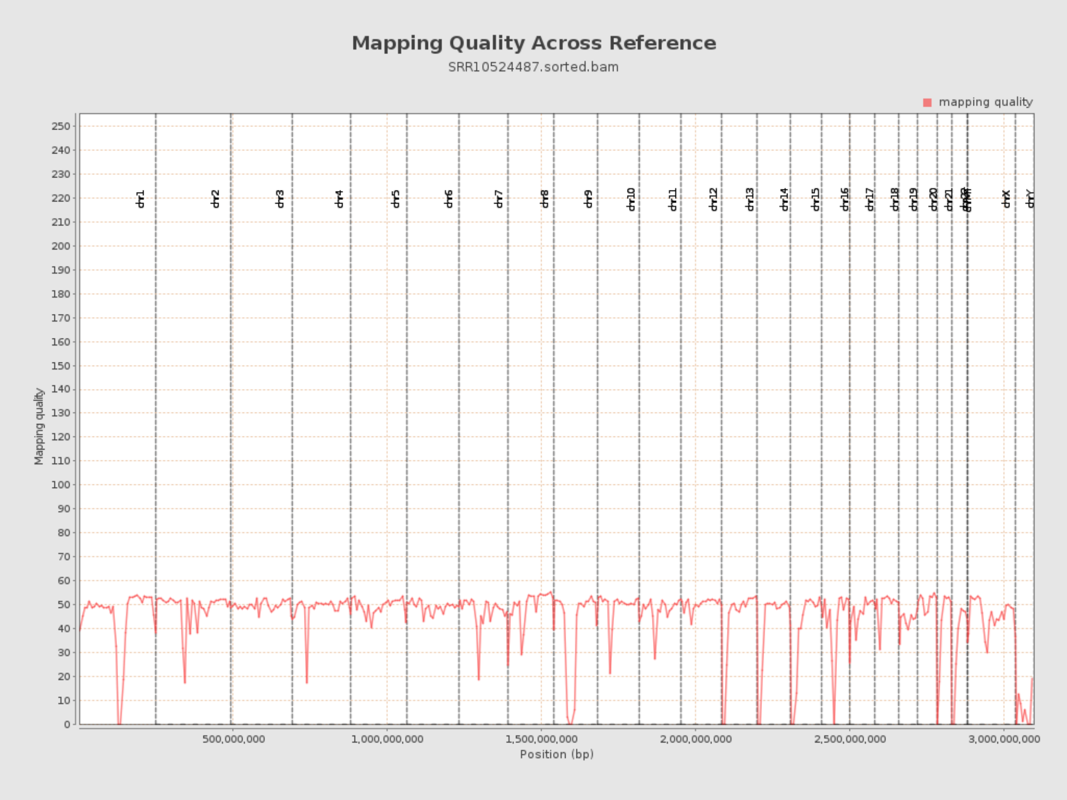
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram