Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 23:29:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524339.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_SRR10524339 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524339.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 23:29:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524339.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,020,972
Mapped reads	1,831,431 / 90.62%
Unmapped reads	189,541 / 9.38%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,789 / 0.43%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	64,564 / 3.19%
Duplication rate	2.42%
Clipped reads	1,834,749 / 90.79%

2.2. ACGT Content

Number/percentage of A's	24,577,994 / 23.36%
Number/percentage of C's	20,598,764 / 19.57%
Number/percentage of T's	34,734,302 / 33.01%
Number/percentage of G's	25,306,587 / 24.05%
Number/percentage of N's	14,218 / 0.01%
GC Percentage	43.62%

2.3. Coverage

Mean	0.034

Standard Deviation	0.3229

2.4. Mapping Quality

Mean Mapping Quality	43.21

2.5. Mismatches and indels

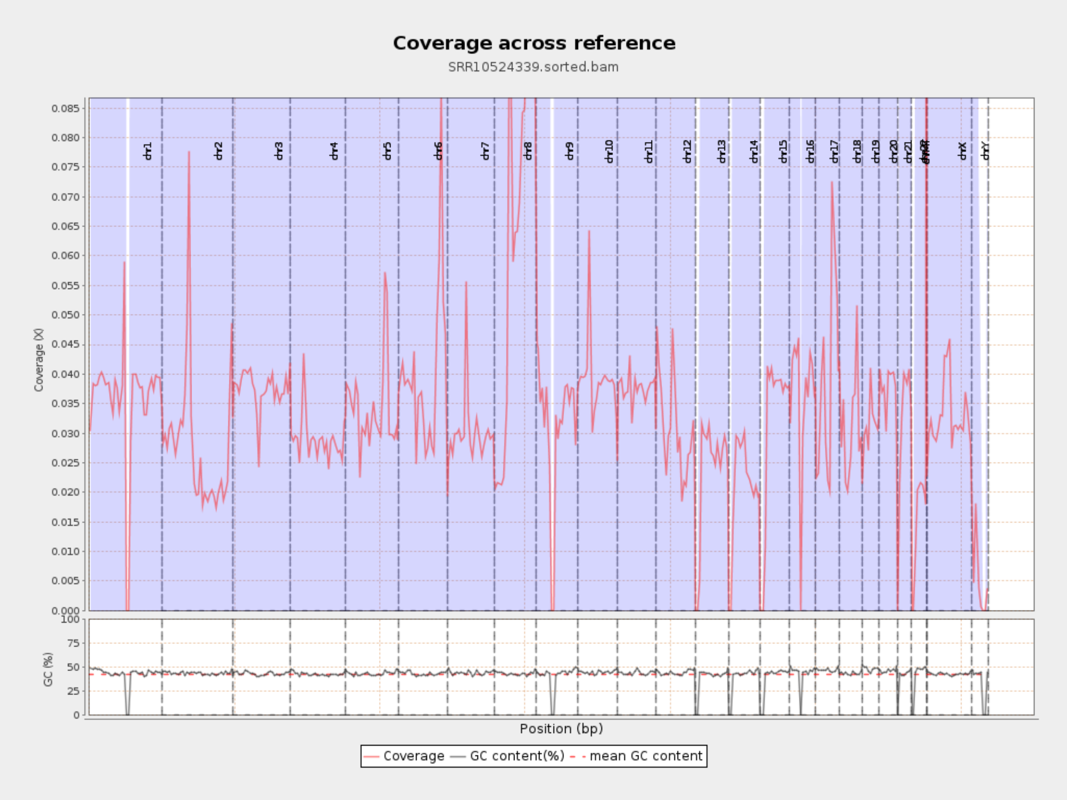
General error rate	0.53%
Mismatches	546,890
Insertions	7,086
Mapped reads with at least one insertion	0.38%
Deletions	18,150
Mapped reads with at least one deletion	0.98%
Homopolymer indels	42.99%

2.6. Chromosome stats

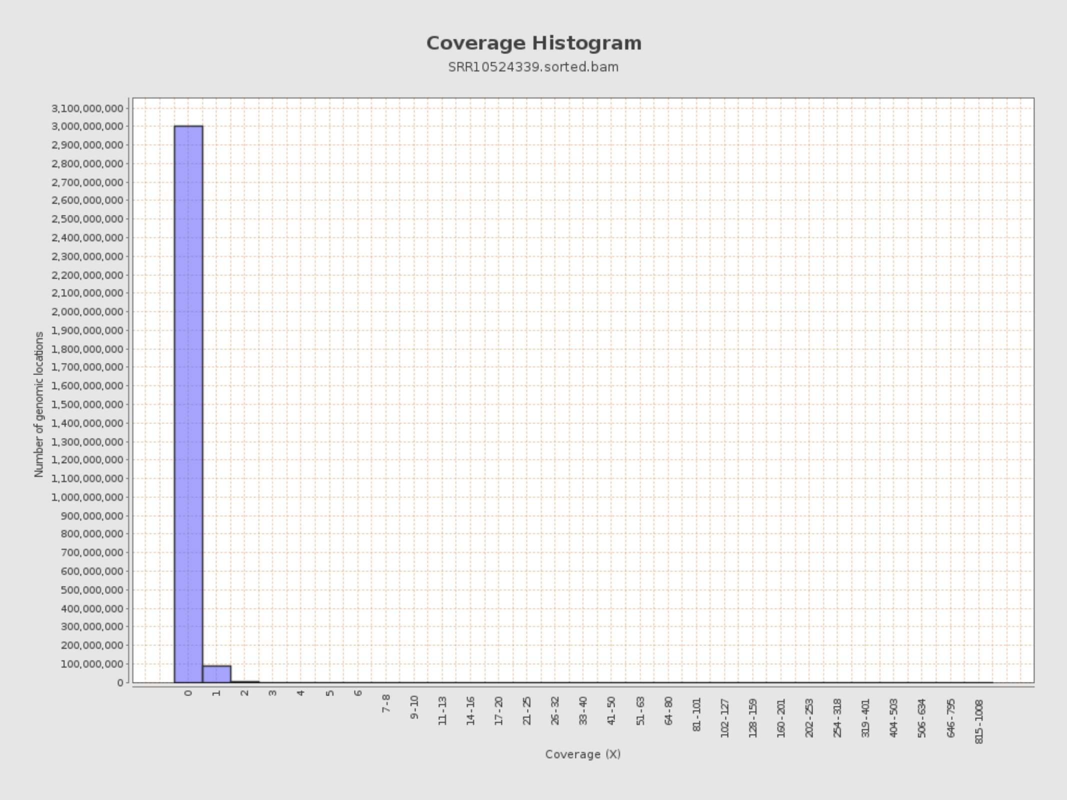
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8869357	0.0356	0.612
chr2	243199373	6774528	0.0279	0.4503
chr3	198022430	7396929	0.0374	0.2136
chr4	191154276	5518865	0.0289	0.2069
chr5	180915260	6216723	0.0344	0.2033
chr6	171115067	6784684	0.0396	0.2401
chr7	159138663	4833981	0.0304	0.4041

chr8	146364022	11025037	0.0753	0.3859
chr9	141213431	4344716	0.0308	0.2473
chr10	135534747	5331656	0.0393	0.3056
chr11	135006516	5049422	0.0374	0.2699
chr12	133851895	4138193	0.0309	0.1976
chr13	115169878	2690735	0.0234	0.1679
chr14	107349540	2229920	0.0208	0.1699
chr15	102531392	3210904	0.0313	0.1979
chr16	90354753	3292775	0.0364	0.2249
chr17	81195210	3166373	0.039	0.2426
chr18	78077248	2476789	0.0317	0.4564
chr19	59128983	1869699	0.0316	0.412
chr20	63025520	2365875	0.0375	0.2149
chr21	48129895	1512757	0.0314	0.2063
chr22	51304566	750234	0.0146	0.1322
chrMT	16571	6742	0.4069	0.6585
chrX	155270560	5098270	0.0328	0.2287
chrY	59373566	305278	0.0051	0.1365

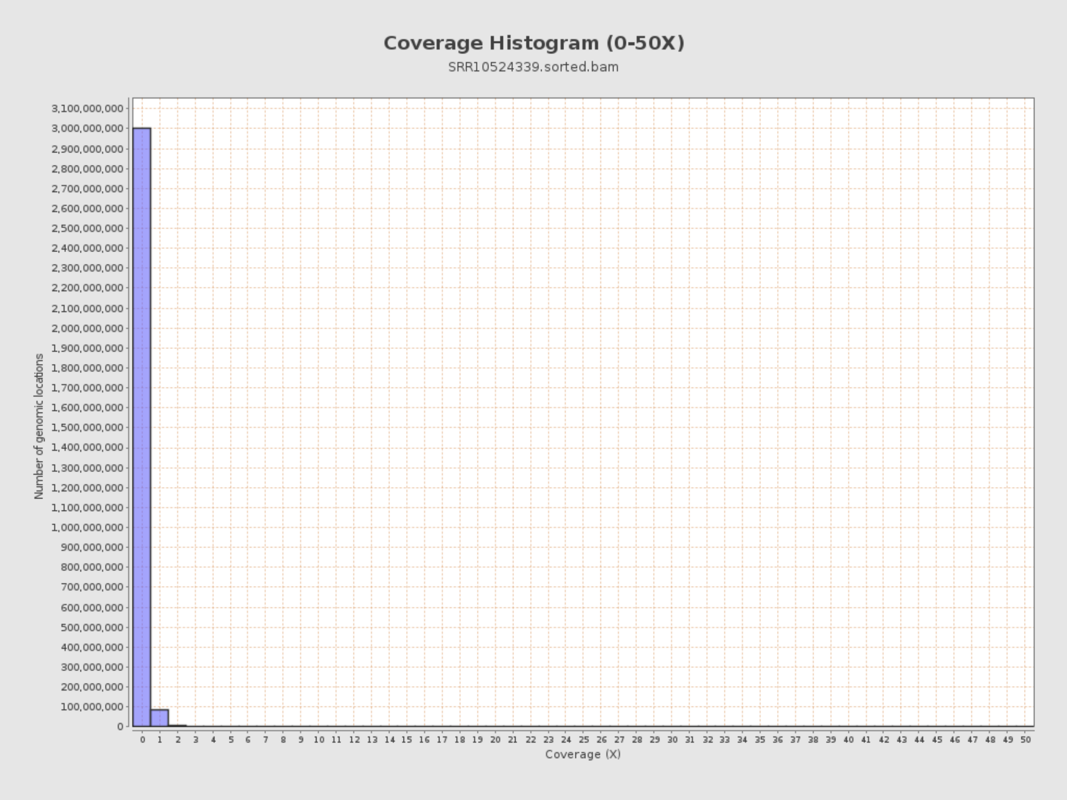
3. Results : Coverage across reference



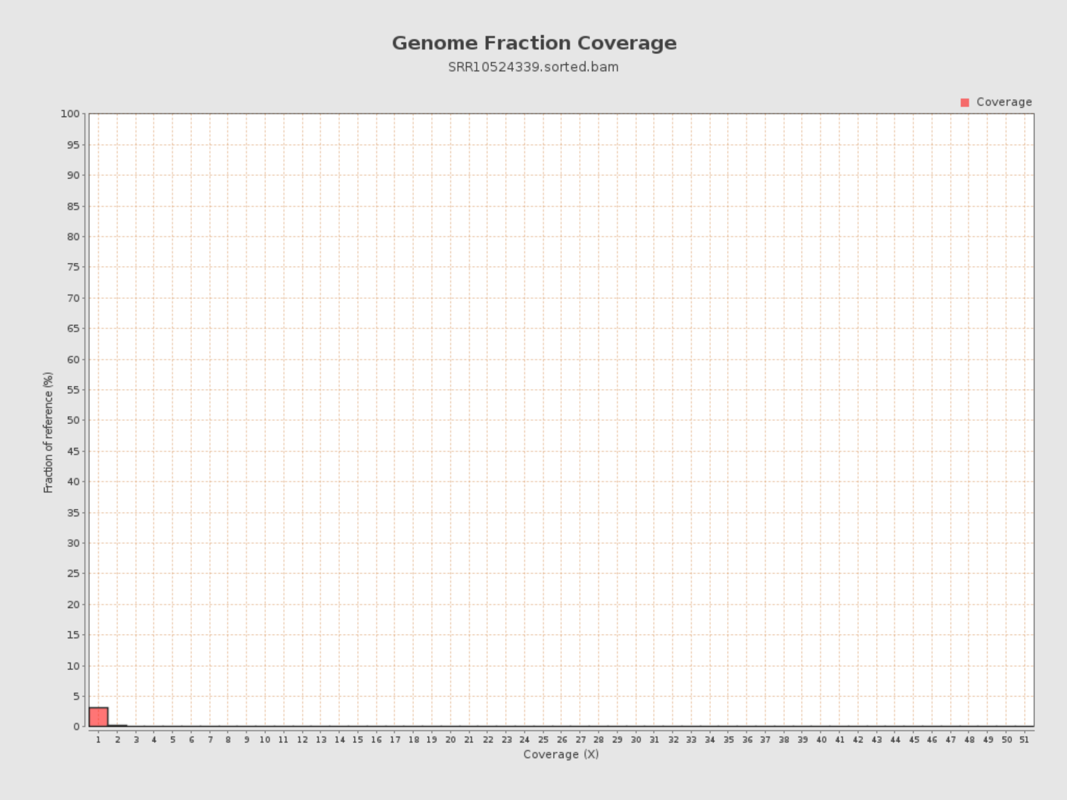
4. Results : Coverage Histogram



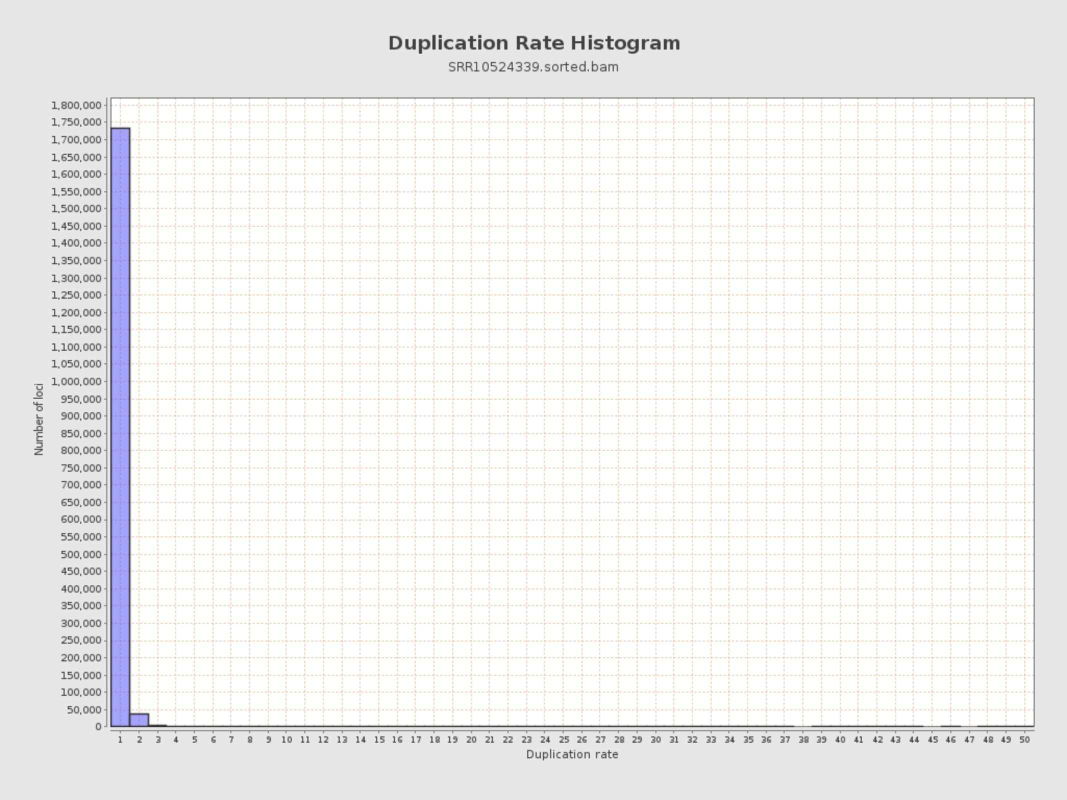
5. Results : Coverage Histogram (0-50X)



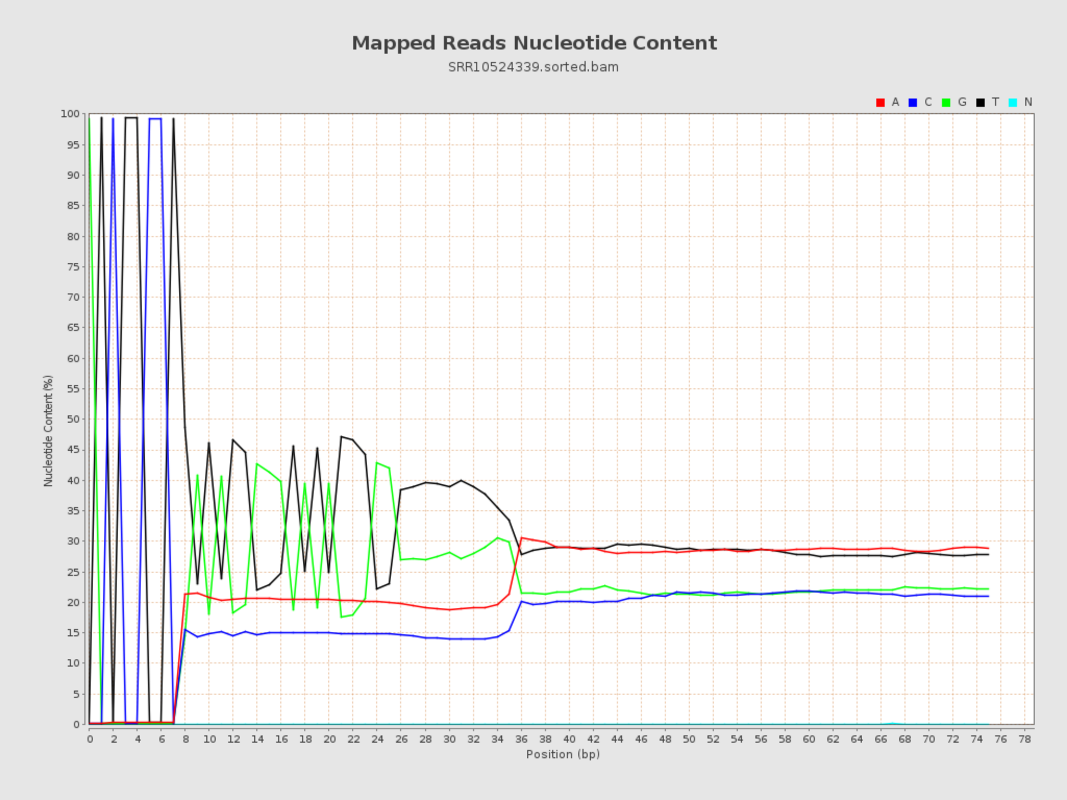
6. Results : Genome Fraction Coverage



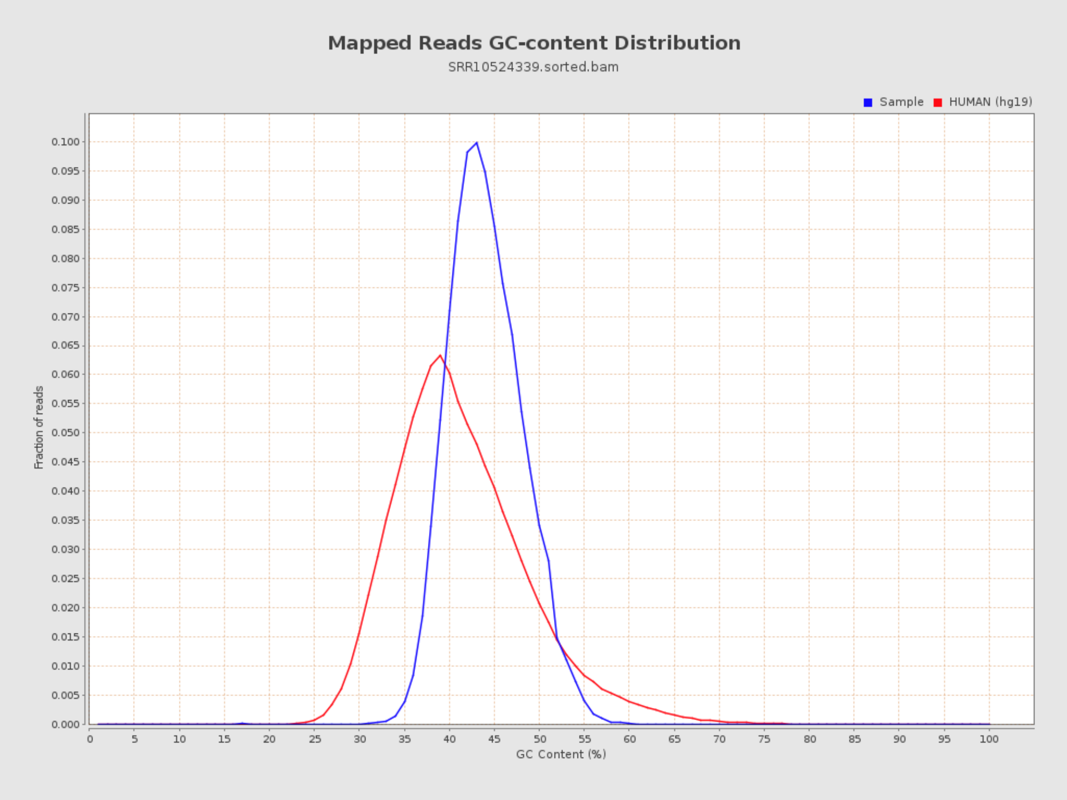
7. Results : Duplication Rate Histogram



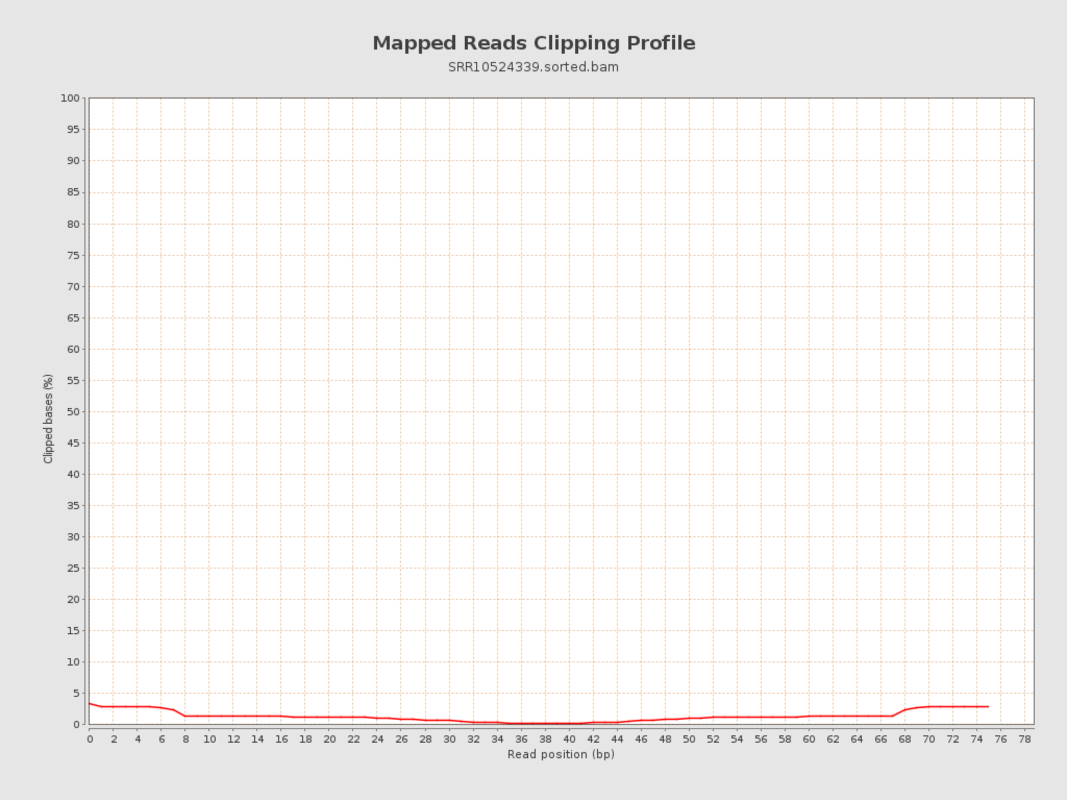
8. Results : Mapped Reads Nucleotide Content



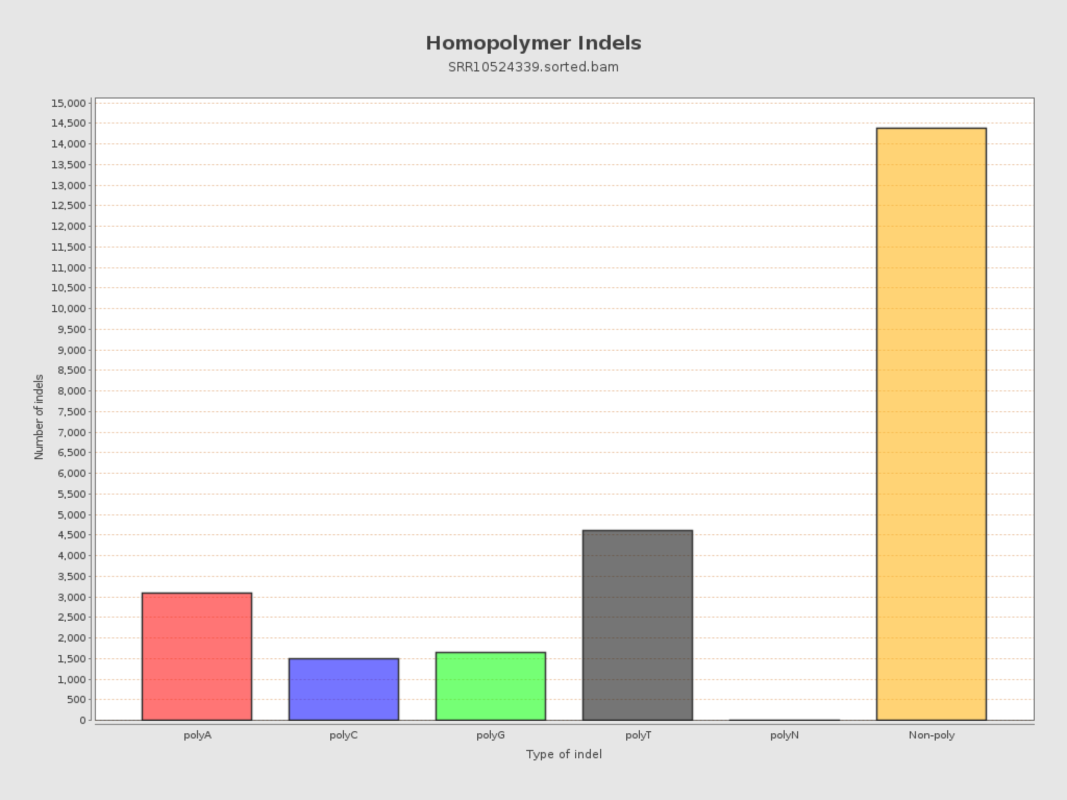
9. Results : Mapped Reads GC-content Distribution



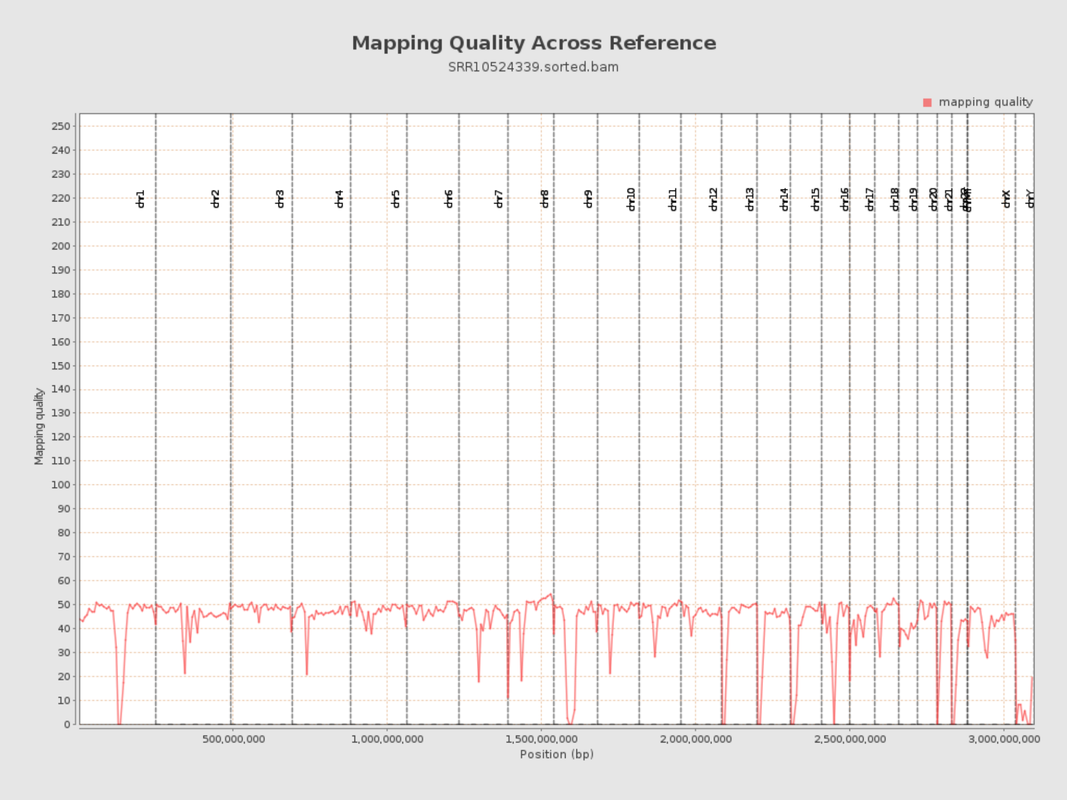
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram