Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 21:23:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524293.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_SRR10524293 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524293.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 21:23:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524293.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,642,974
Mapped reads	2,414,741 / 91.36%
Unmapped reads	228,233 / 8.64%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,222 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	108,401 / 4.1%
Duplication rate	3.17%
Clipped reads	2,417,620 / 91.47%

2.2. ACGT Content

Number/percentage of A's	33,728,030 / 24.19%
Number/percentage of C's	26,051,730 / 18.68%
Number/percentage of T's	44,974,129 / 32.25%
Number/percentage of G's	34,664,187 / 24.86%
Number/percentage of N's	19,315 / 0.01%
GC Percentage	43.54%

2.3. Coverage

Mean	0.0451

Standard Deviation	0.4113

2.4. Mapping Quality

Mean Mapping Quality	44

2.5. Mismatches and indels

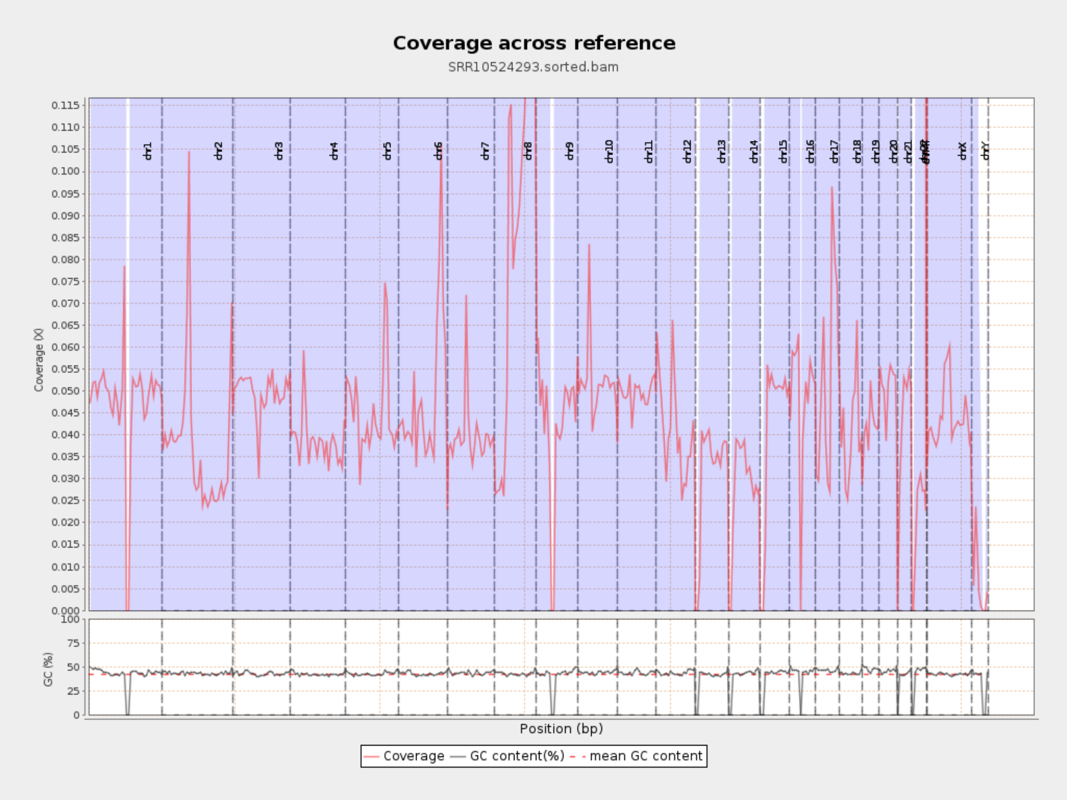
General error rate	0.53%
Mismatches	717,113
Insertions	10,733
Mapped reads with at least one insertion	0.44%
Deletions	24,330
Mapped reads with at least one deletion	1%
Homopolymer indels	40.69%

2.6. Chromosome stats

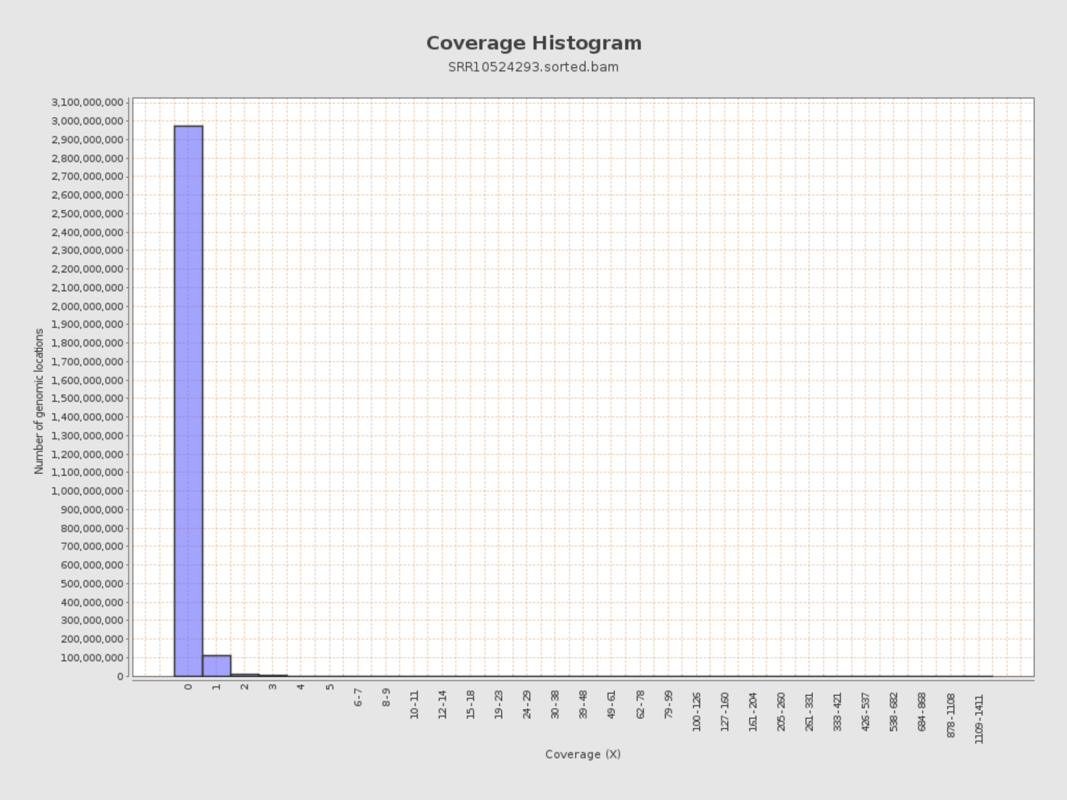
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11787132	0.0473	0.7931
chr2	243199373	9105120	0.0374	0.6101
chr3	198022430	9792335	0.0495	0.2517
chr4	191154276	7339892	0.0384	0.2553
chr5	180915260	8199766	0.0453	0.2406
chr6	171115067	8279665	0.0484	0.2868
chr7	159138663	6377635	0.0401	0.5085

chr8	146364022	14465562	0.0988	0.4908
chr9	141213431	5851425	0.0414	0.3015
chr10	135534747	7044018	0.052	0.3724
chr11	135006516	6701866	0.0496	0.3386
chr12	133851895	5535465	0.0414	0.2339
chr13	115169878	3582307	0.0311	0.198
chr14	107349540	2996992	0.0279	0.2043
chr15	102531392	4266857	0.0416	0.2362
chr16	90354753	4415712	0.0489	0.2654
chr17	81195210	4287746	0.0528	0.2906
chr18	78077248	3263676	0.0418	0.5568
chr19	59128983	2497048	0.0422	0.5134
chr20	63025520	3201346	0.0508	0.2571
chr21	48129895	2012811	0.0418	0.2593
chr22	51304566	1021926	0.0199	0.1568
chrMT	16571	250216	15.0996	9.6811
chrX	155270560	6813362	0.0439	0.2729
chrY	59373566	385714	0.0065	0.1911

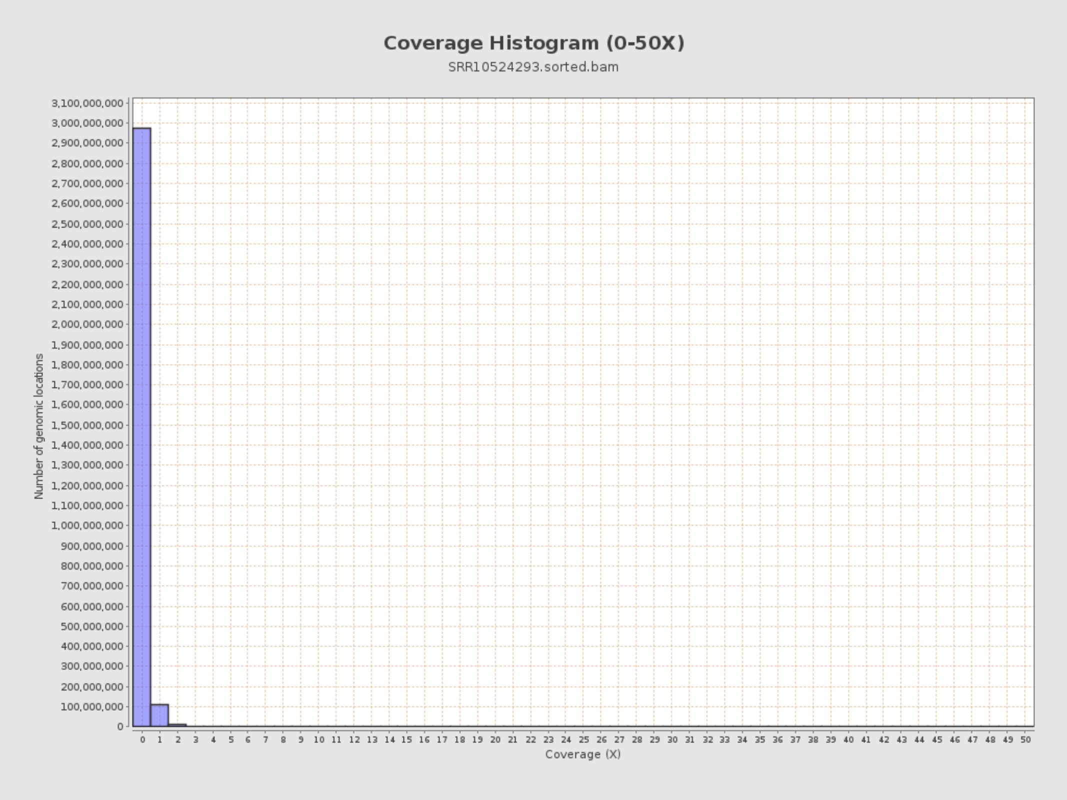
3. Results : Coverage across reference



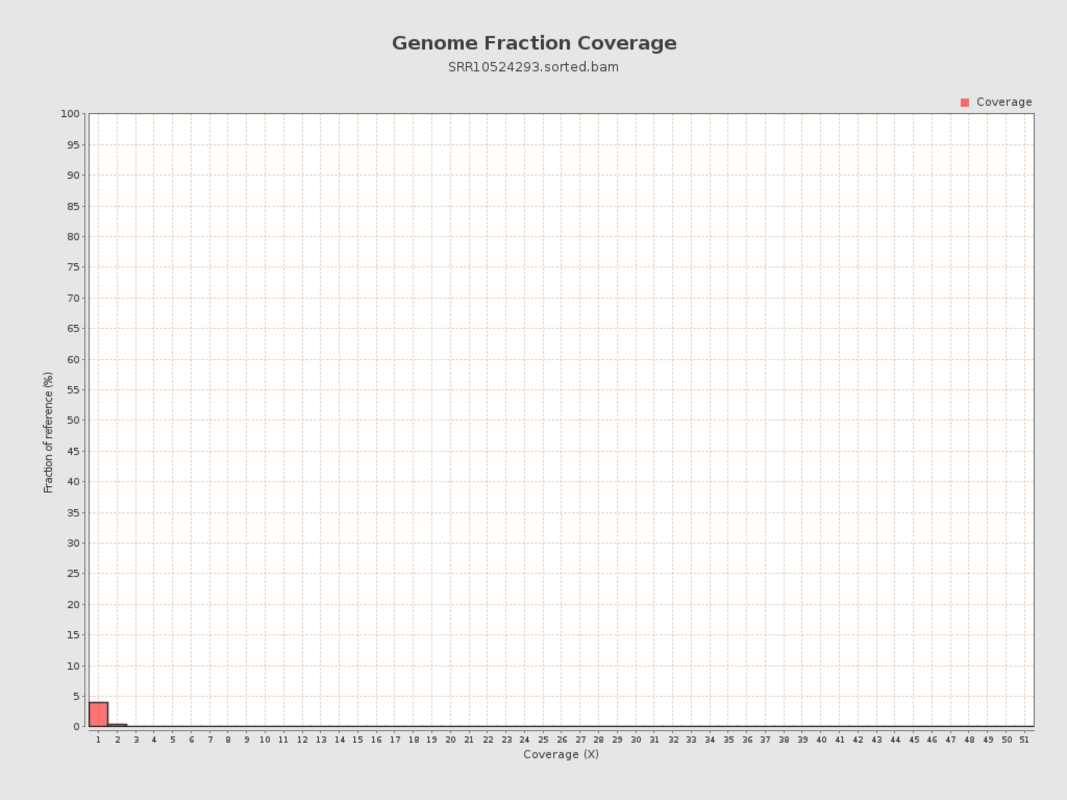
4. Results : Coverage Histogram



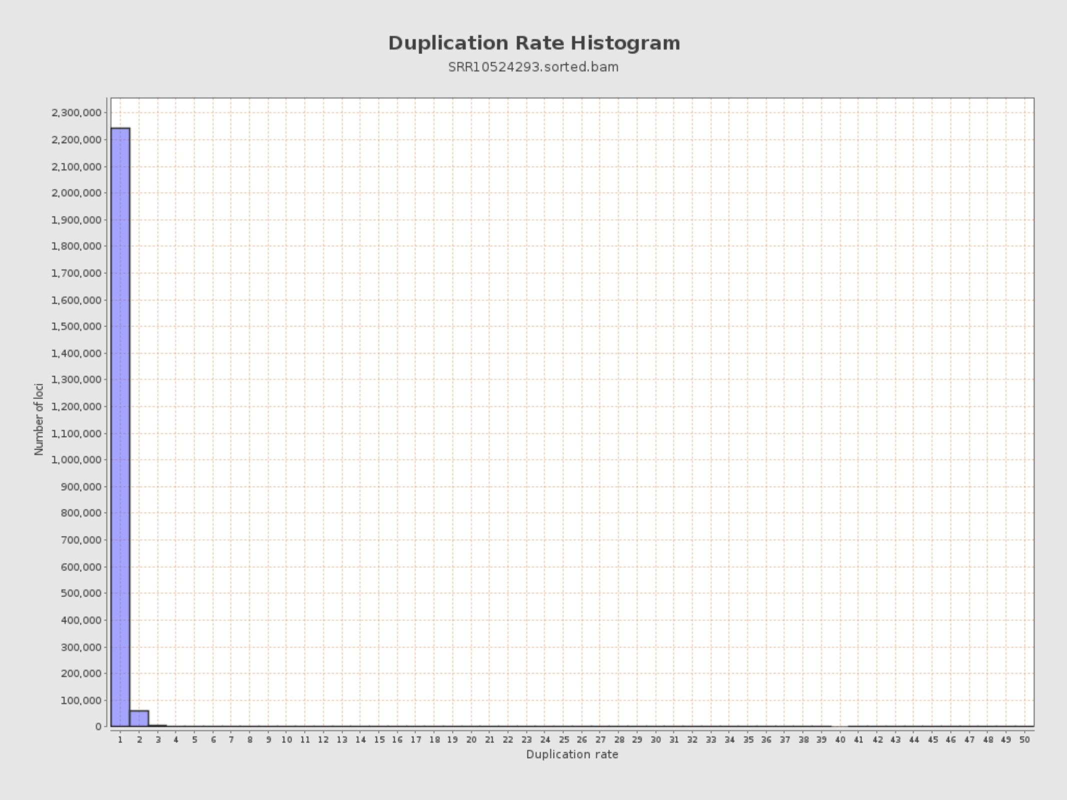
5. Results : Coverage Histogram (0-50X)



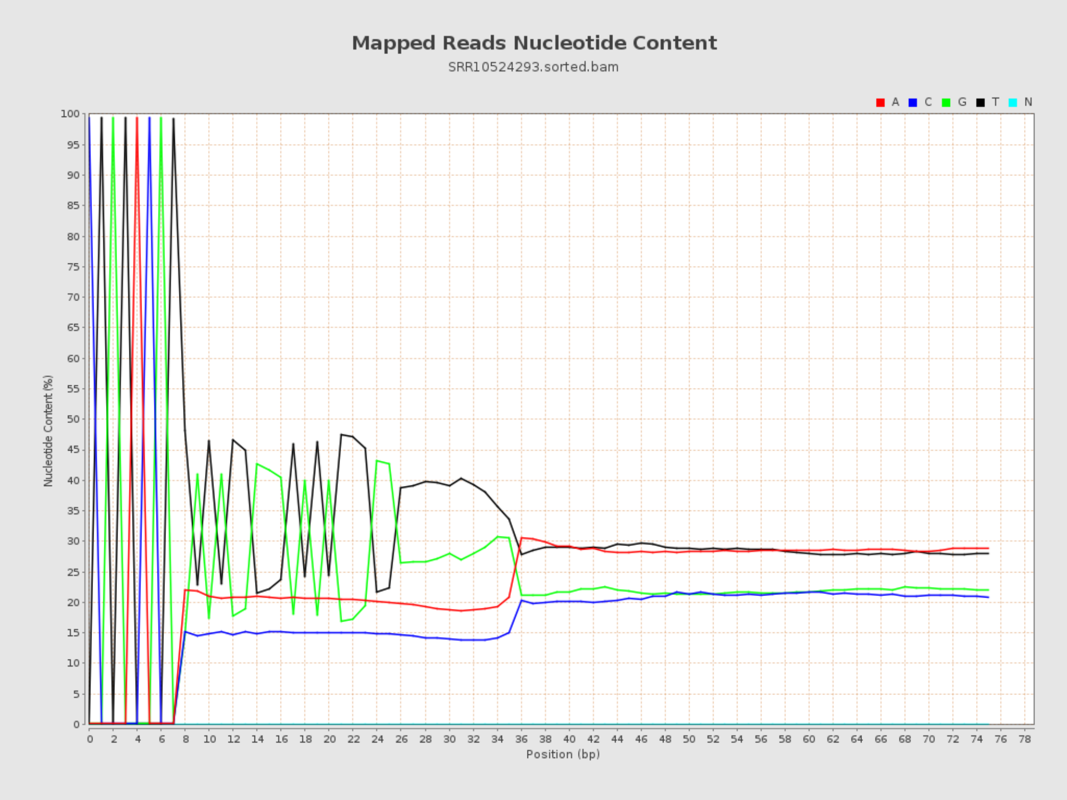
6. Results : Genome Fraction Coverage



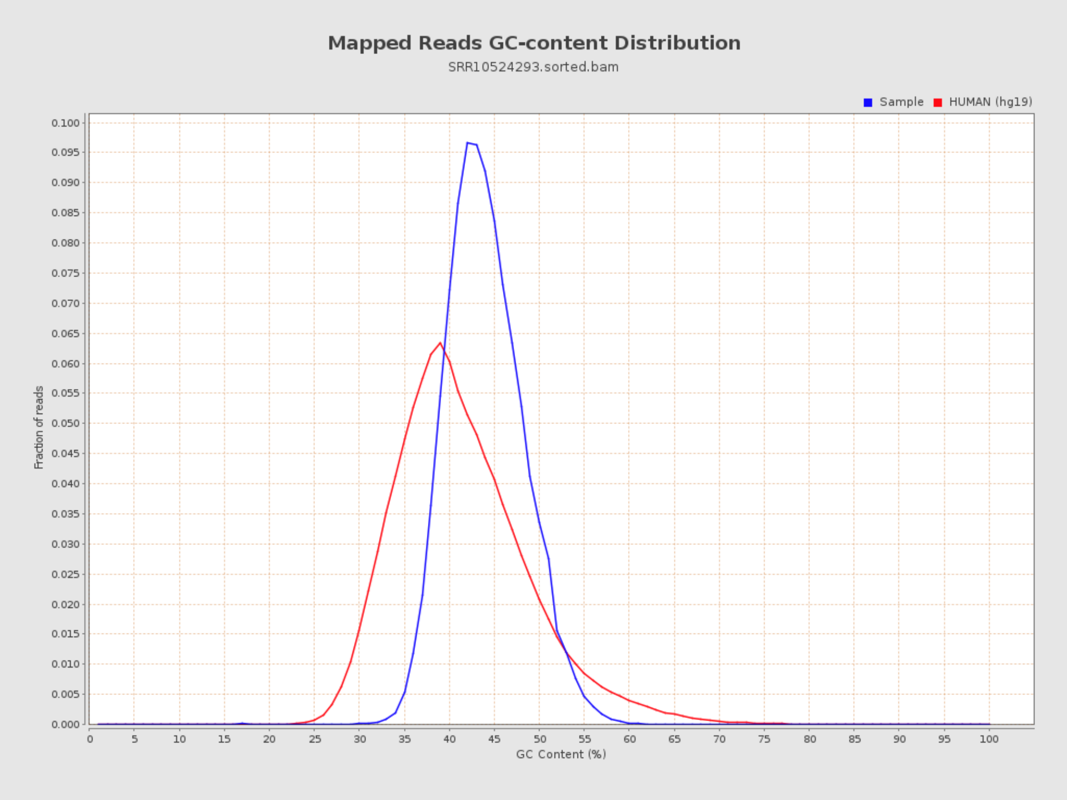
7. Results : Duplication Rate Histogram



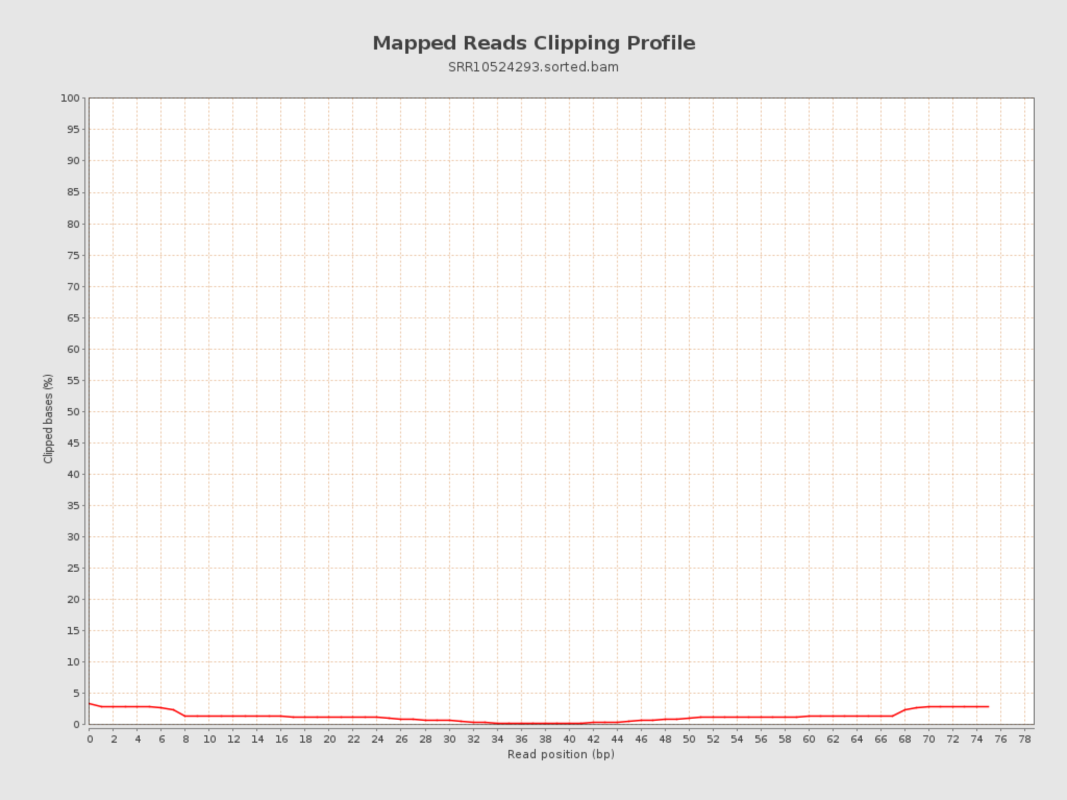
8. Results : Mapped Reads Nucleotide Content



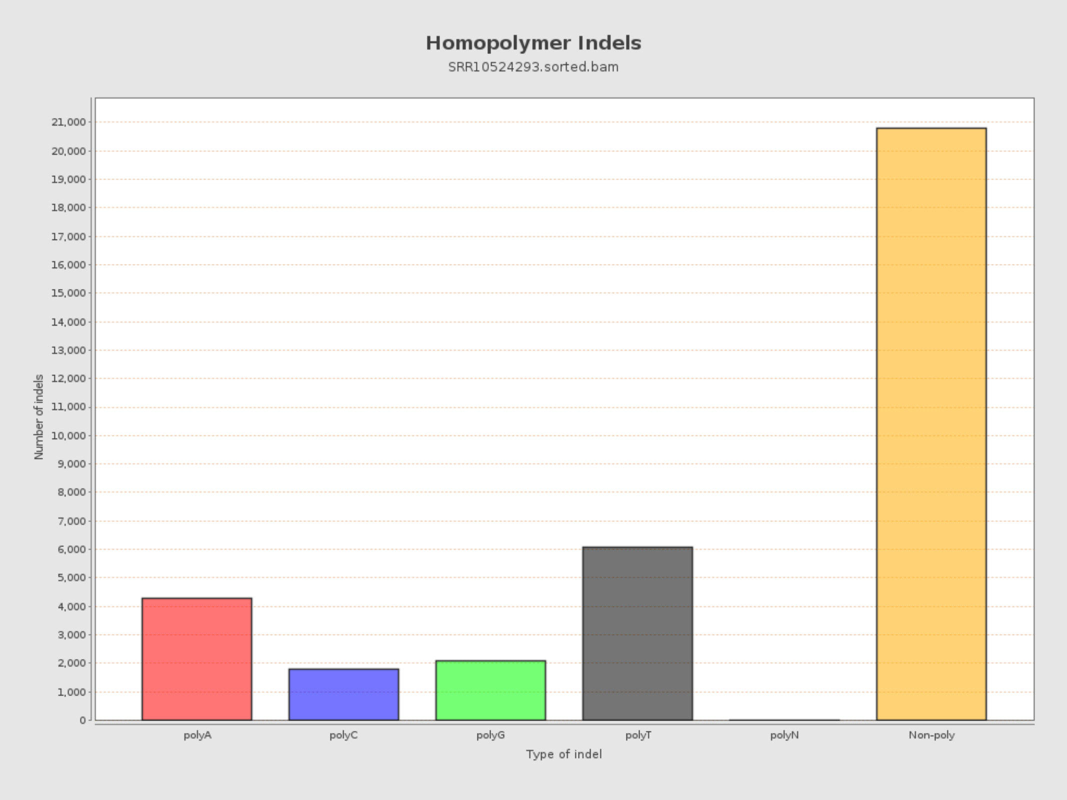
9. Results : Mapped Reads GC-content Distribution



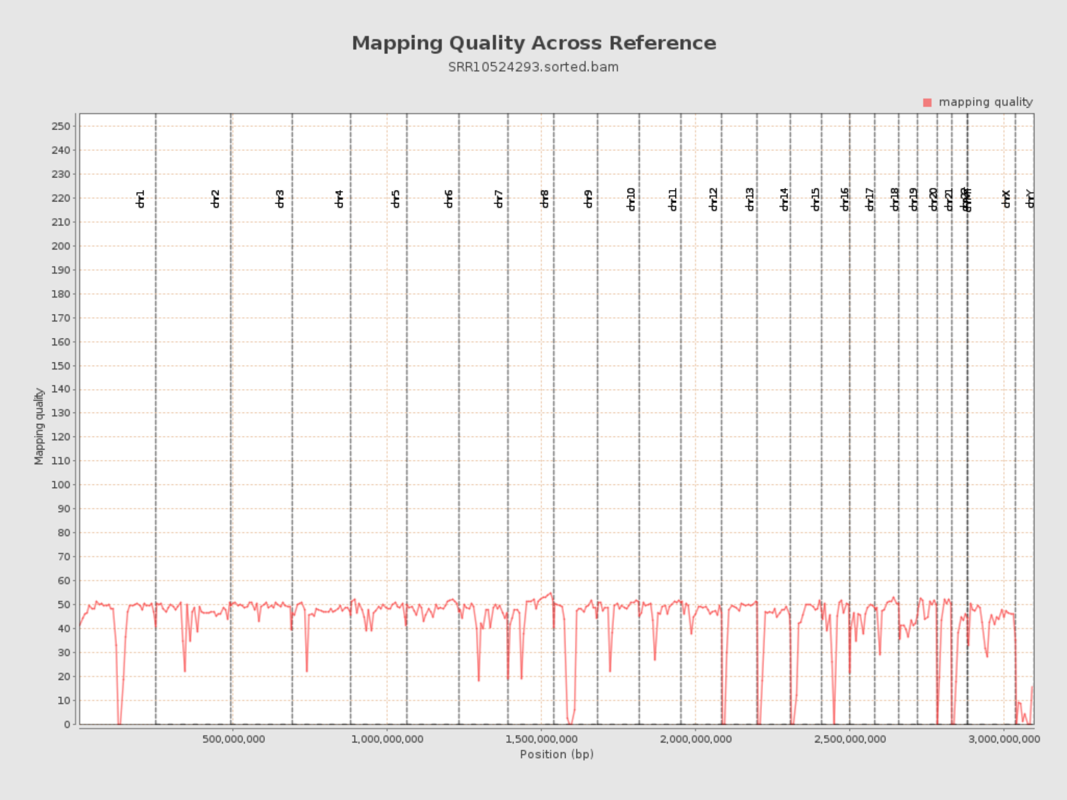
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram