Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 21:27:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524294.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_SRR10524294 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524294.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 21:27:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524294.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,993,617
Mapped reads	1,827,138 / 91.65%
Unmapped reads	166,479 / 8.35%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,410 / 0.37%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	60,299 / 3.02%
Duplication rate	2.27%
Clipped reads	1,828,240 / 91.7%

2.2. ACGT Content

Number/percentage of A's	27,016,016 / 25.41%
Number/percentage of C's	19,100,971 / 17.96%
Number/percentage of T's	33,312,118 / 31.33%
Number/percentage of G's	26,881,183 / 25.28%
Number/percentage of N's	15,079 / 0.01%
GC Percentage	43.25%

2.3. Coverage

Mean	0.0344

Standard Deviation	0.3214

2.4. Mapping Quality

Mean Mapping Quality	44.08

2.5. Mismatches and indels

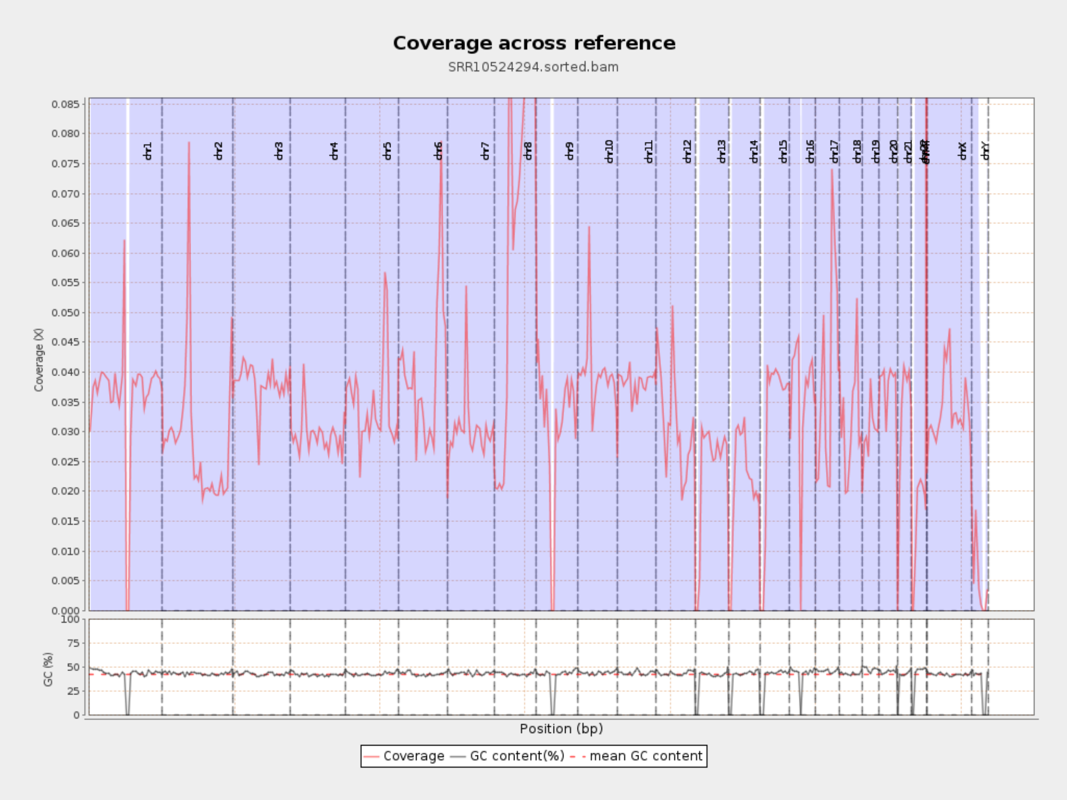
General error rate	0.52%
Mismatches	538,244
Insertions	8,454
Mapped reads with at least one insertion	0.46%
Deletions	18,821
Mapped reads with at least one deletion	1.02%
Homopolymer indels	40.02%

2.6. Chromosome stats

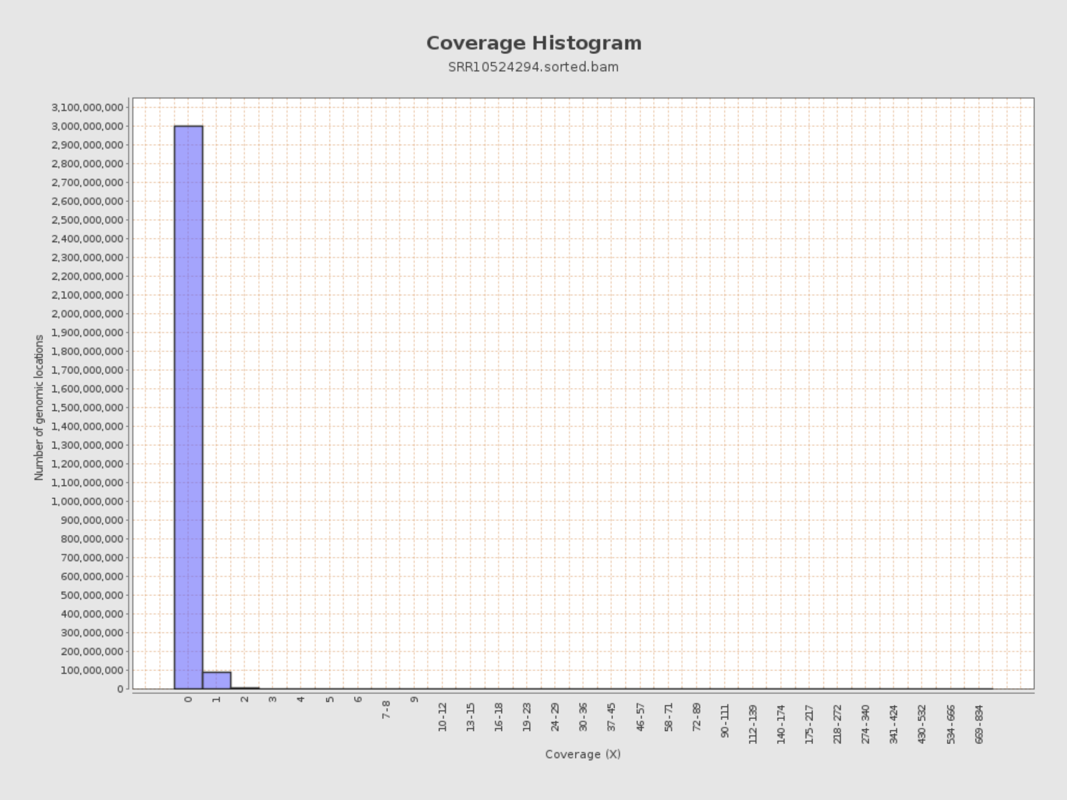
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8947310	0.0359	0.6429
chr2	243199373	6888487	0.0283	0.3936
chr3	198022430	7545320	0.0381	0.2139
chr4	191154276	5608394	0.0293	0.2024
chr5	180915260	6290565	0.0348	0.2032
chr6	171115067	6780338	0.0396	0.2375
chr7	159138663	4884152	0.0307	0.3939

chr8	146364022	11188503	0.0764	0.3902
chr9	141213431	4345163	0.0308	0.2402
chr10	135534747	5419448	0.04	0.3111
chr11	135006516	5140065	0.0381	0.2725
chr12	133851895	4213862	0.0315	0.197
chr13	115169878	2682076	0.0233	0.1667
chr14	107349540	2284455	0.0213	0.1712
chr15	102531392	3209901	0.0313	0.1972
chr16	90354753	3262532	0.0361	0.2221
chr17	81195210	3164199	0.039	0.2351
chr18	78077248	2522432	0.0323	0.4507
chr19	59128983	1792282	0.0303	0.4388
chr20	63025520	2386631	0.0379	0.2132
chr21	48129895	1532399	0.0318	0.2069
chr22	51304566	748595	0.0146	0.132
chrMT	16571	7841	0.4732	0.7851
chrX	155270560	5219604	0.0336	0.2259
chrY	59373566	289626	0.0049	0.1312

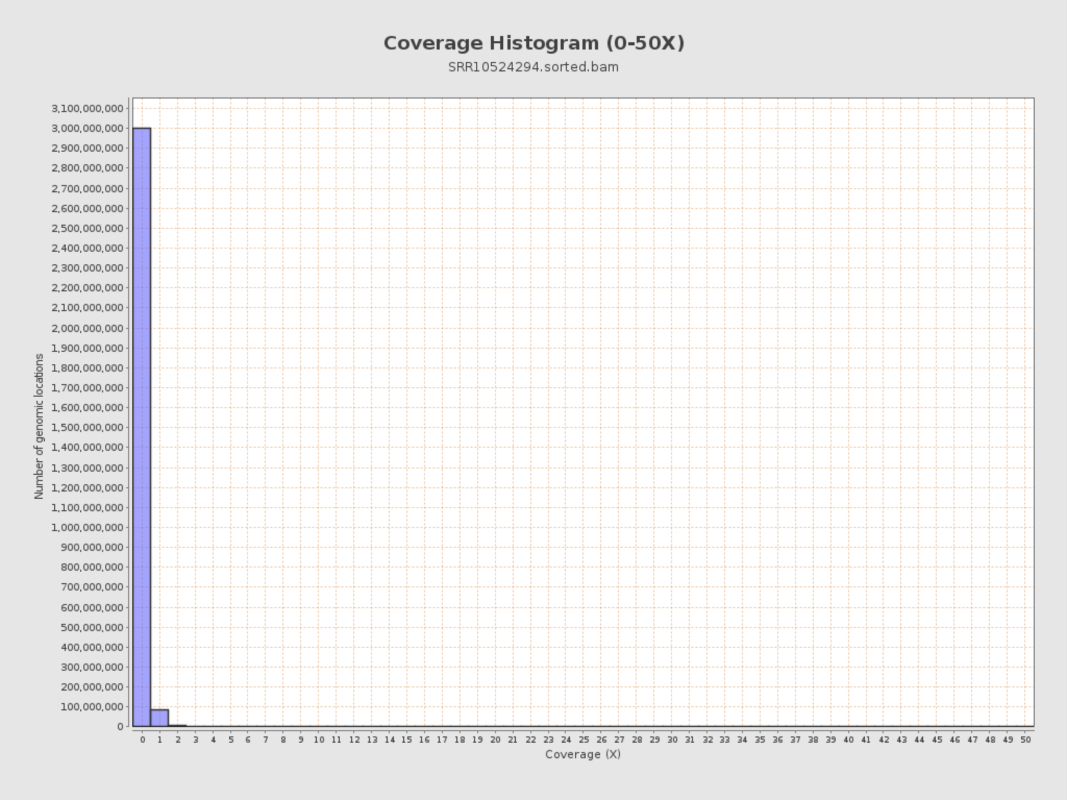
3. Results : Coverage across reference



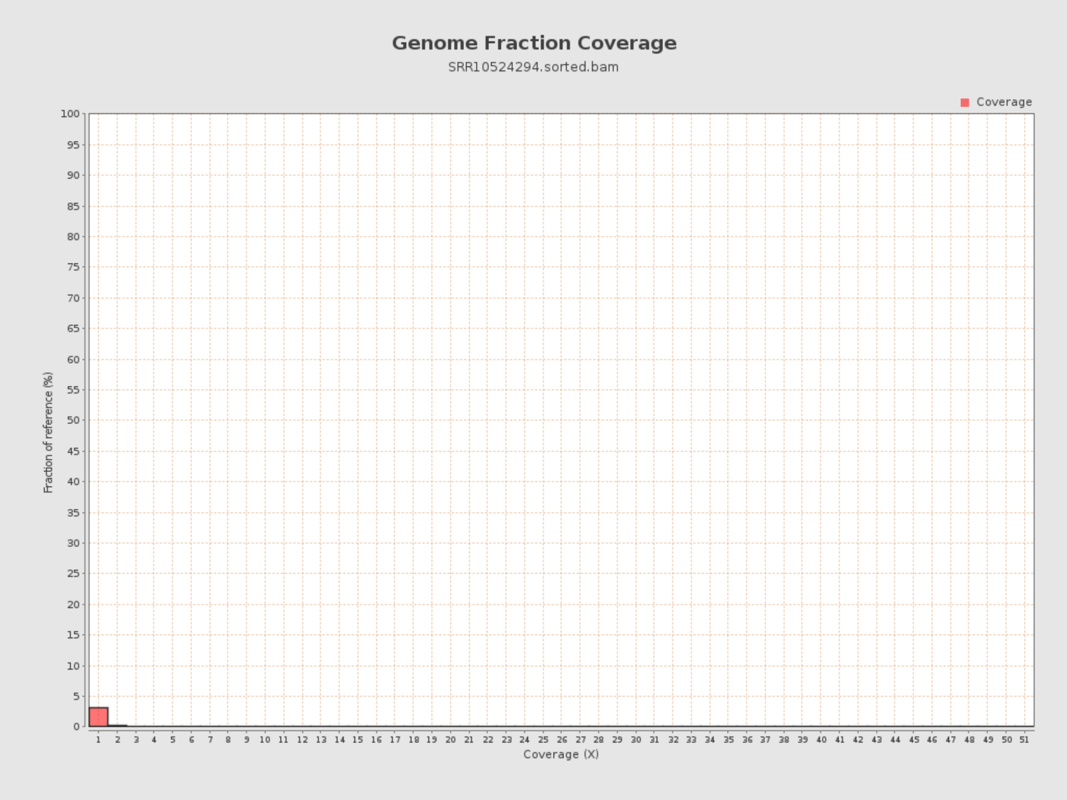
4. Results : Coverage Histogram



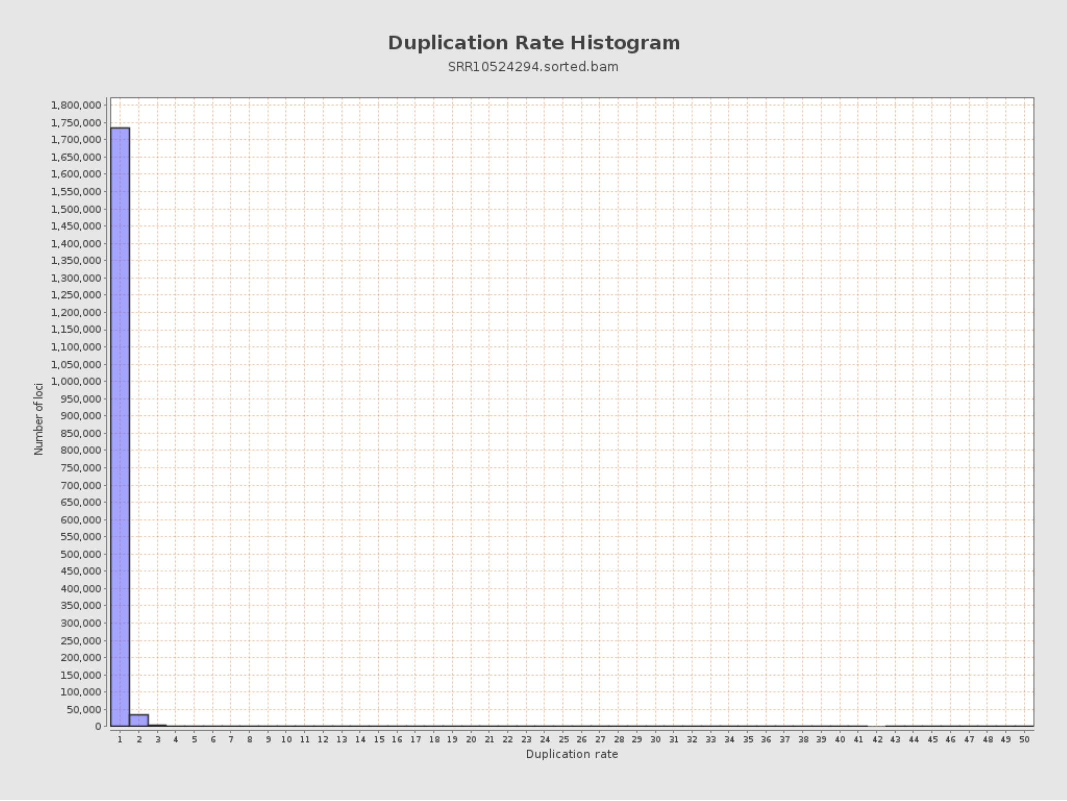
5. Results : Coverage Histogram (0-50X)



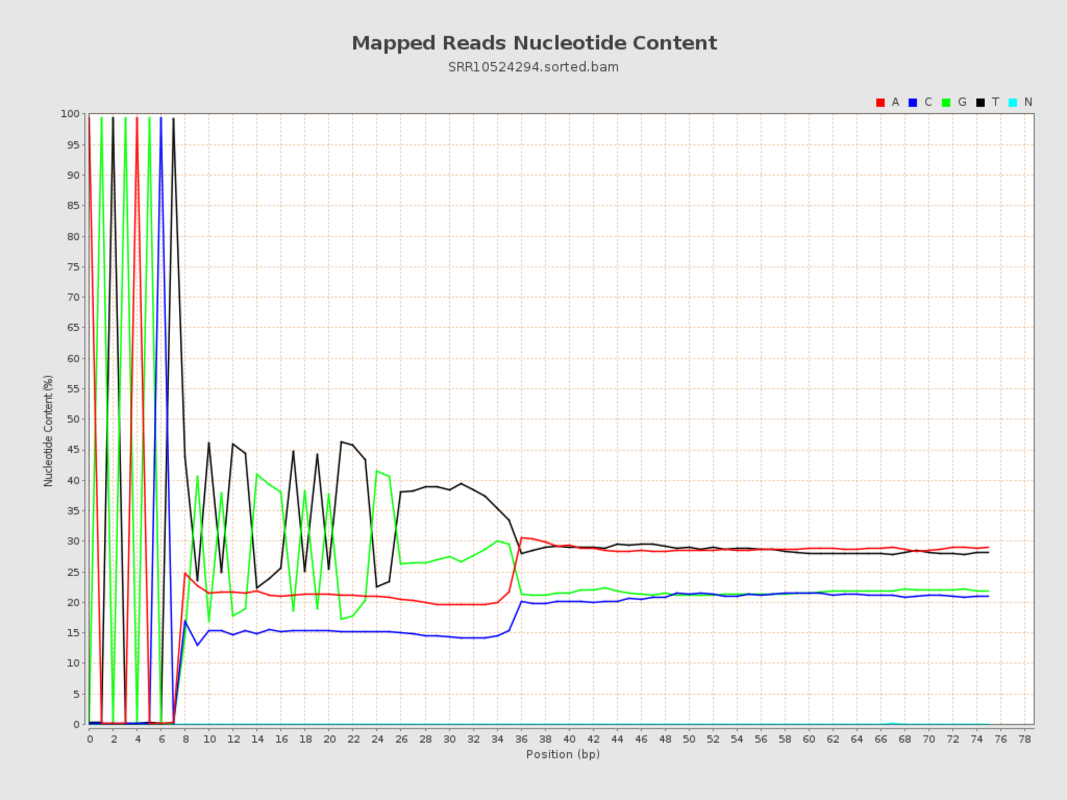
6. Results : Genome Fraction Coverage



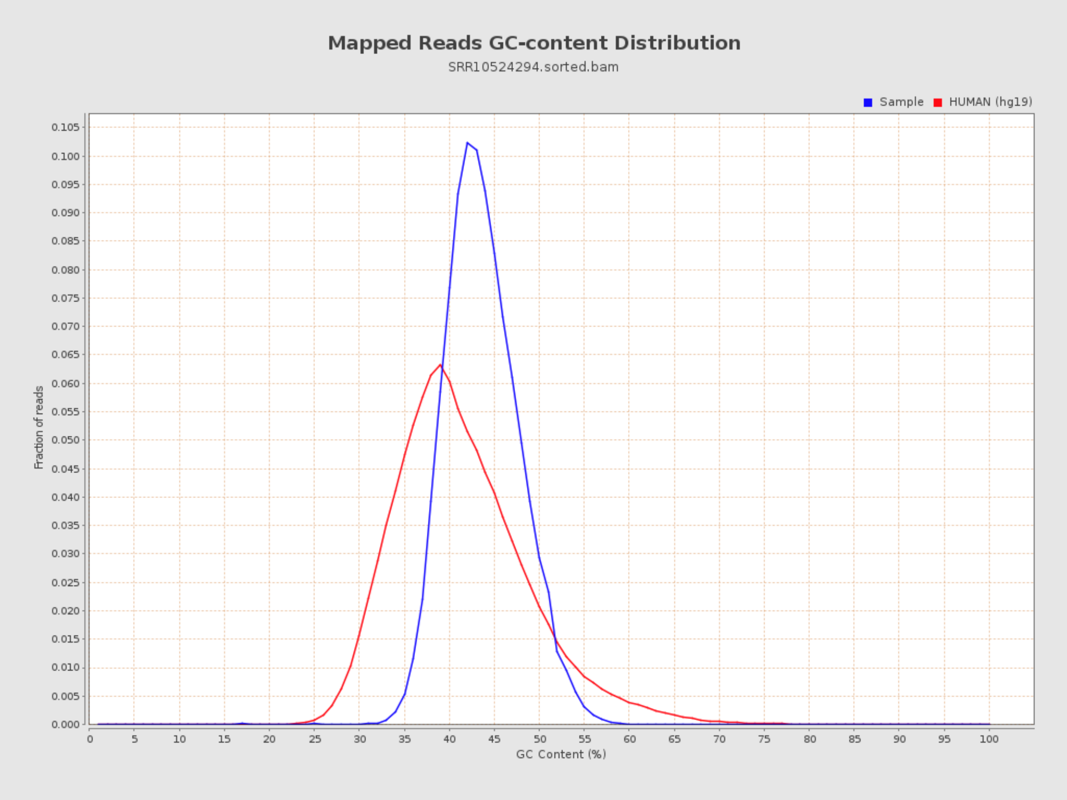
7. Results : Duplication Rate Histogram



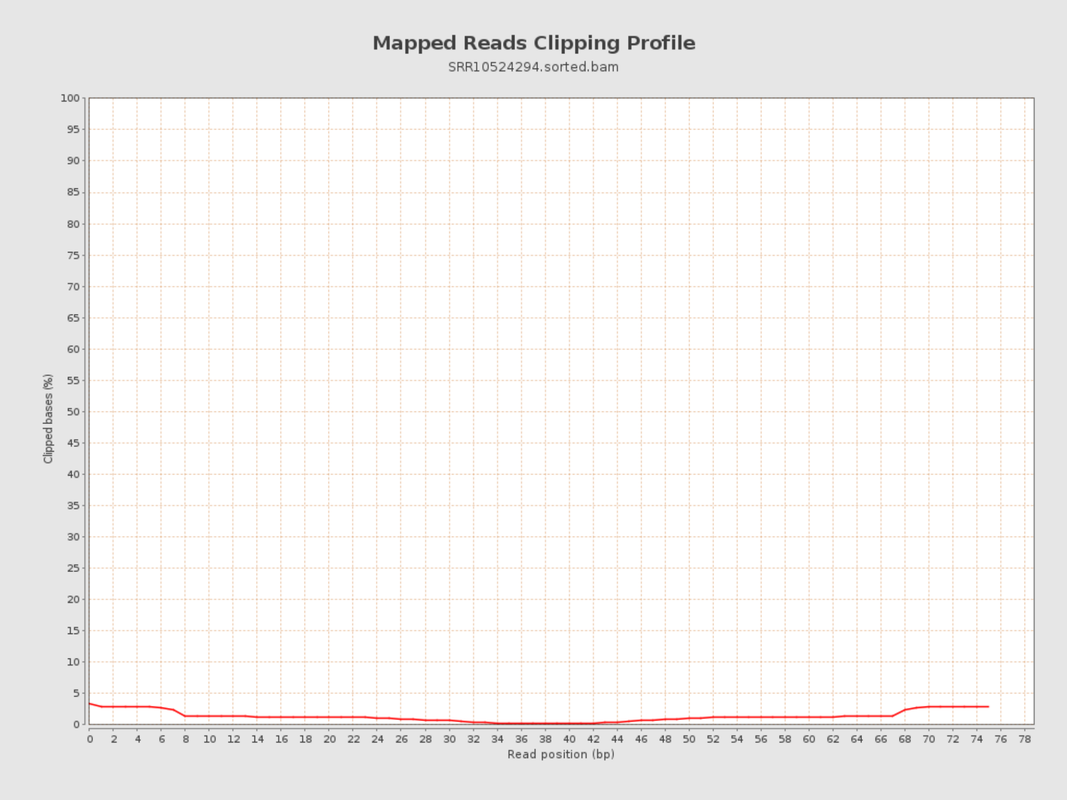
8. Results : Mapped Reads Nucleotide Content



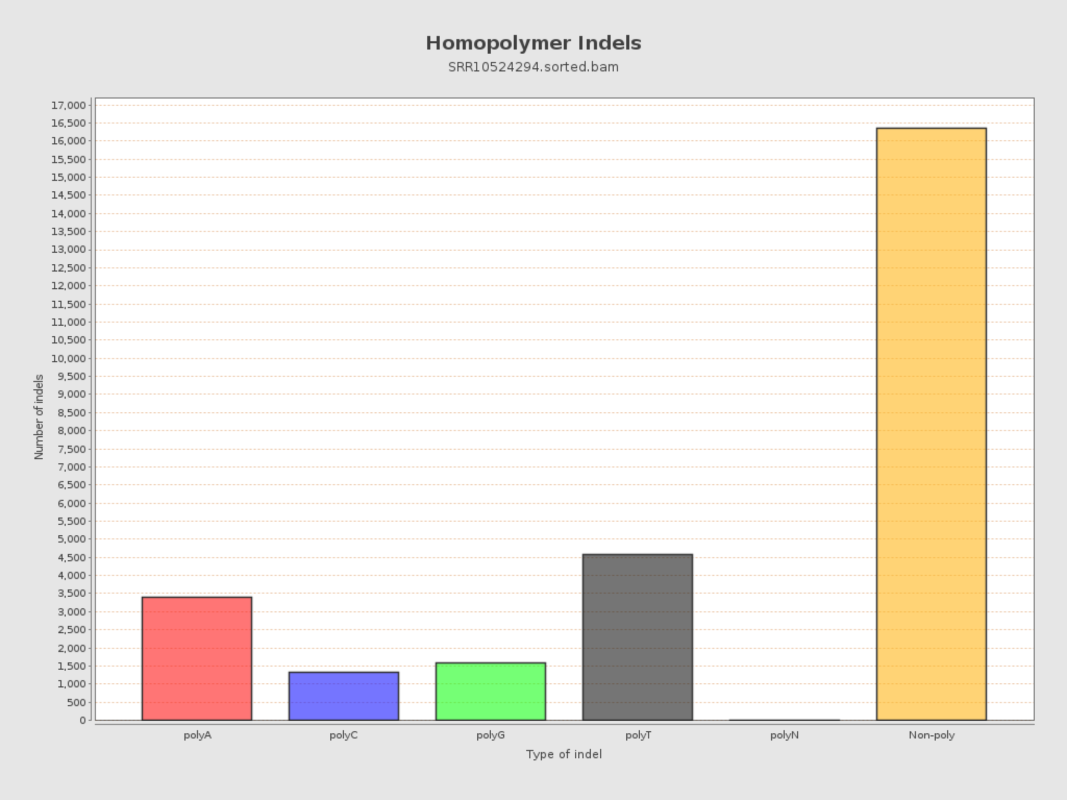
9. Results : Mapped Reads GC-content Distribution



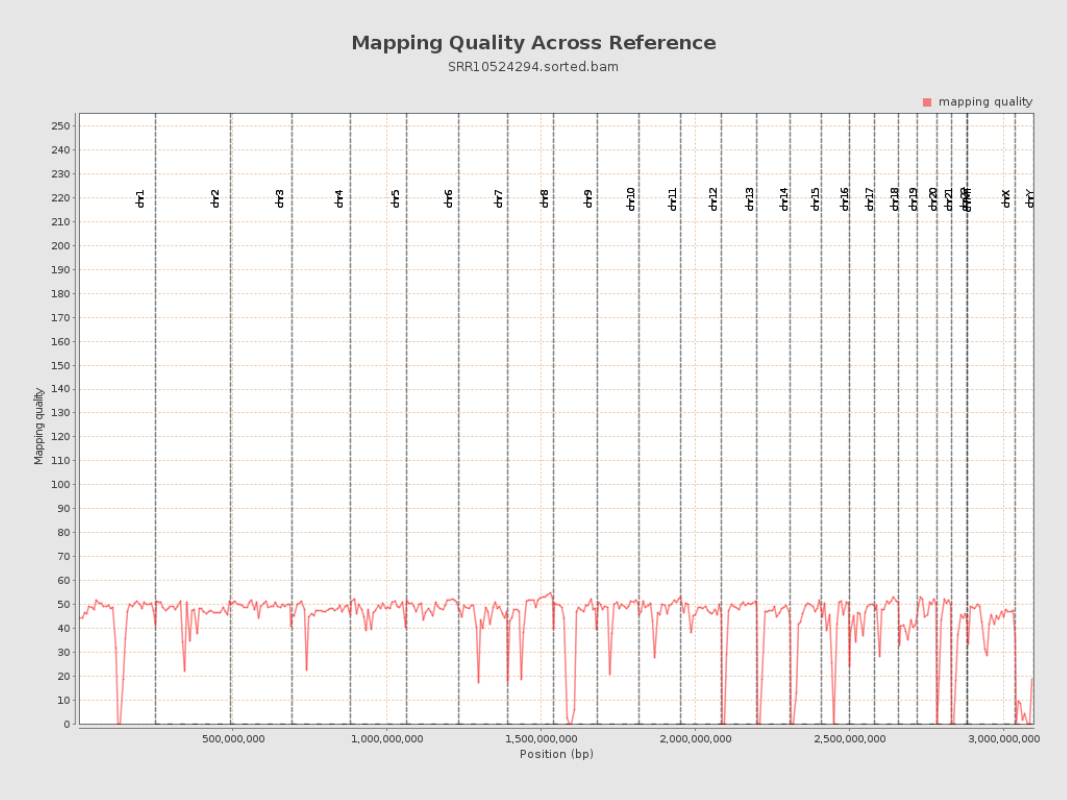
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram