Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 04:59:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524455.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_SRR10524455 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524455.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 04:59:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524455.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	402,109
Mapped reads	370,385 / 92.11%
Unmapped reads	31,724 / 7.89%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,284 / 0.32%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	6,504 / 1.62%
Duplication rate	1.34%
Clipped reads	370,582 / 92.16%

2.2. ACGT Content

Number/percentage of A's	5,623,234 / 26.03%
Number/percentage of C's	3,960,177 / 18.33%
Number/percentage of T's	6,662,161 / 30.84%
Number/percentage of G's	5,359,111 / 24.8%
Number/percentage of N's	444 / 0%
GC Percentage	43.13%

2.3. Coverage

Mean	0.007

Standard Deviation	0.0995

2.4. Mapping Quality

Mean Mapping Quality	45.8

2.5. Mismatches and indels

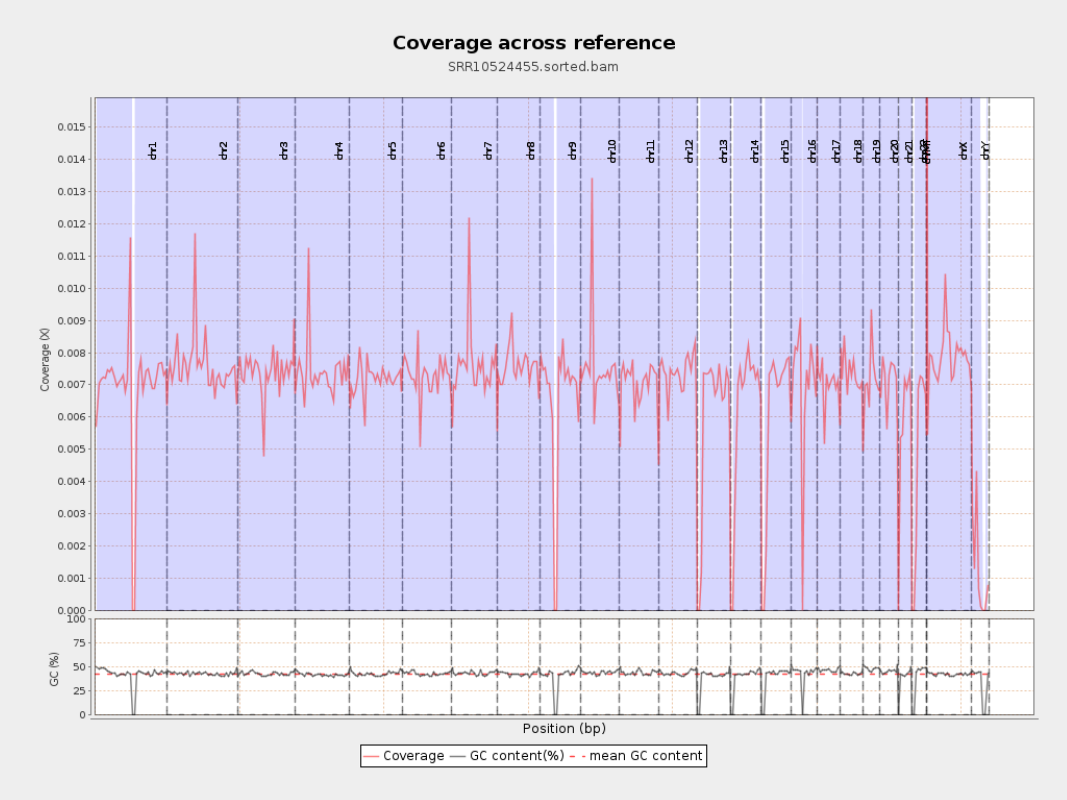
General error rate	0.52%
Mismatches	109,666
Insertions	1,624
Mapped reads with at least one insertion	0.44%
Deletions	4,538
Mapped reads with at least one deletion	1.22%
Homopolymer indels	44.24%

2.6. Chromosome stats

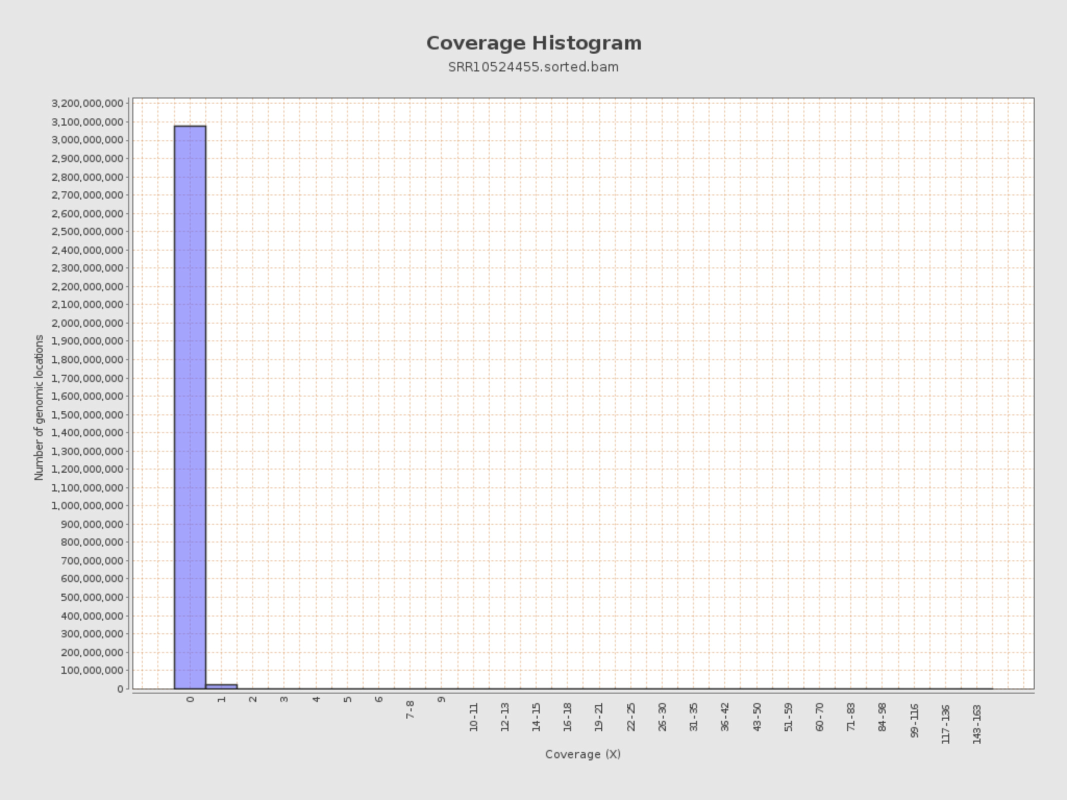
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1707225	0.0068	0.1383
chr2	243199373	1845149	0.0076	0.1152
chr3	198022430	1462212	0.0074	0.0885
chr4	191154276	1417901	0.0074	0.0902
chr5	180915260	1305267	0.0072	0.0872
chr6	171115067	1245620	0.0073	0.0901
chr7	159138663	1219111	0.0077	0.1177

chr8	146364022	1112634	0.0076	0.1107
chr9	141213431	910965	0.0065	0.091
chr10	135534747	1023841	0.0076	0.1023
chr11	135006516	961035	0.0071	0.0908
chr12	133851895	989921	0.0074	0.0889
chr13	115169878	685623	0.006	0.0792
chr14	107349540	659356	0.0061	0.0811
chr15	102531392	608898	0.0059	0.0796
chr16	90354753	618512	0.0068	0.0877
chr17	81195210	565640	0.007	0.0863
chr18	78077248	575989	0.0074	0.1317
chr19	59128983	426771	0.0072	0.1124
chr20	63025520	447679	0.0071	0.0867
chr21	48129895	282061	0.0059	0.0798
chr22	51304566	244366	0.0048	0.0709
chrMT	16571	801	0.0483	0.2145
chrX	155270560	1224044	0.0079	0.0931
chrY	59373566	71854	0.0012	0.0474

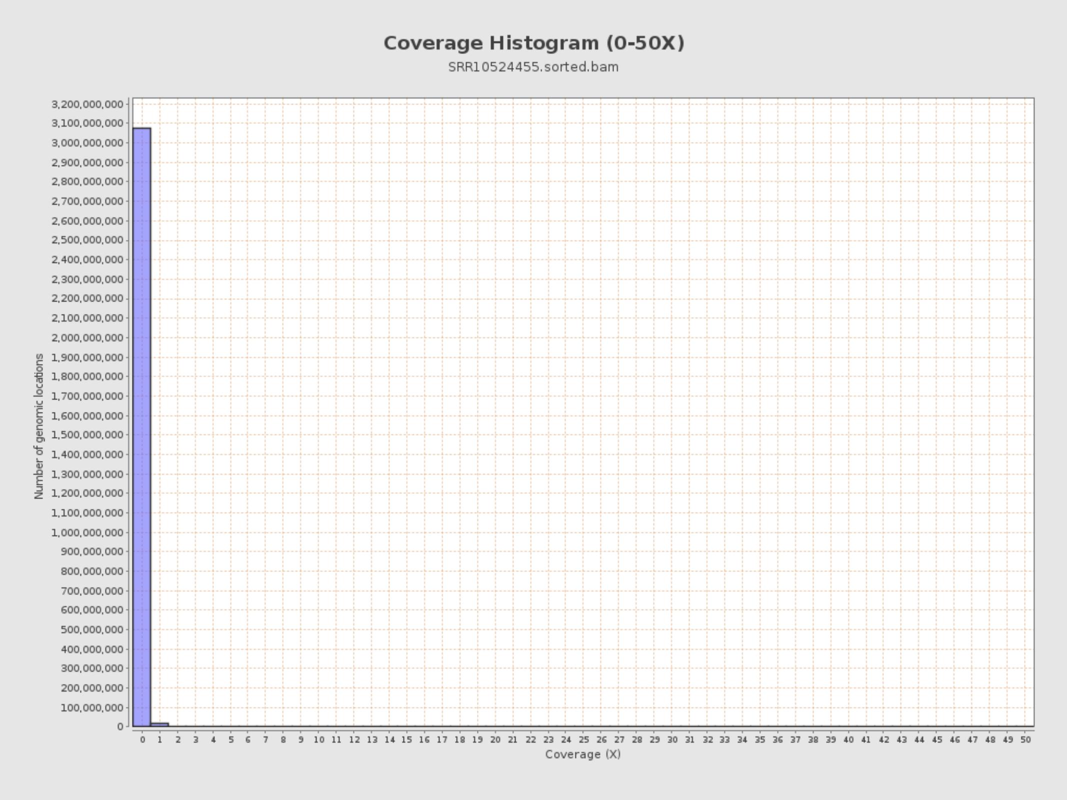
3. Results : Coverage across reference



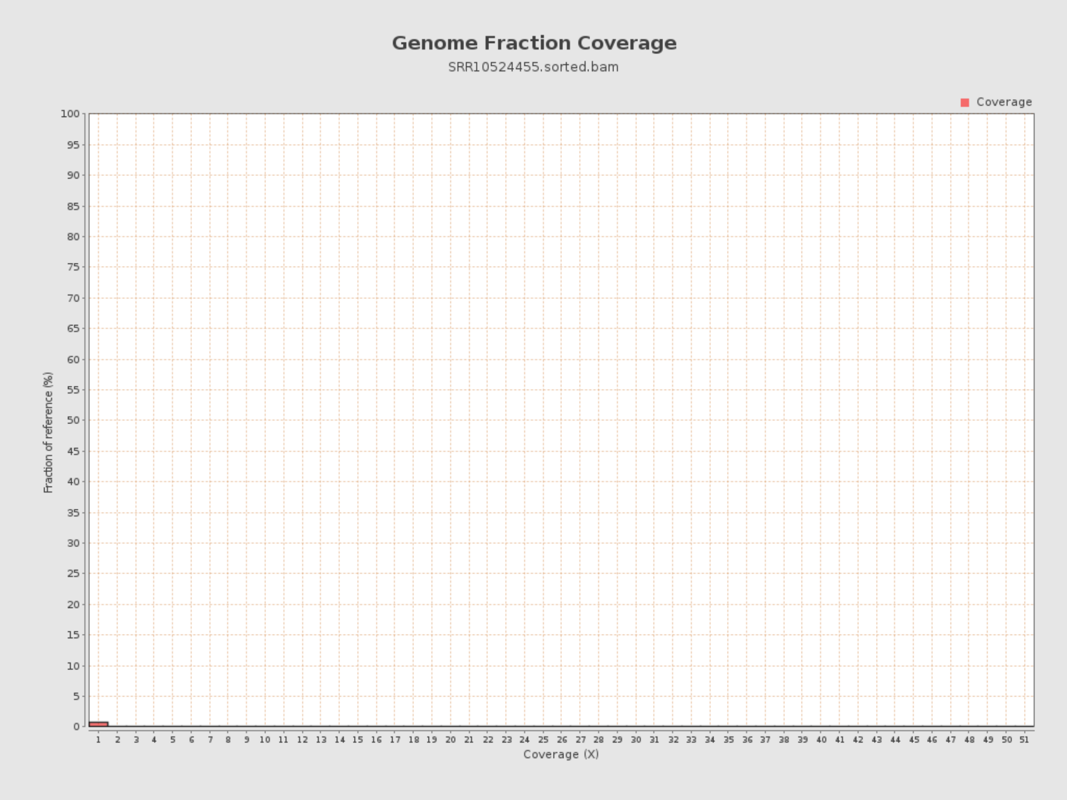
4. Results : Coverage Histogram



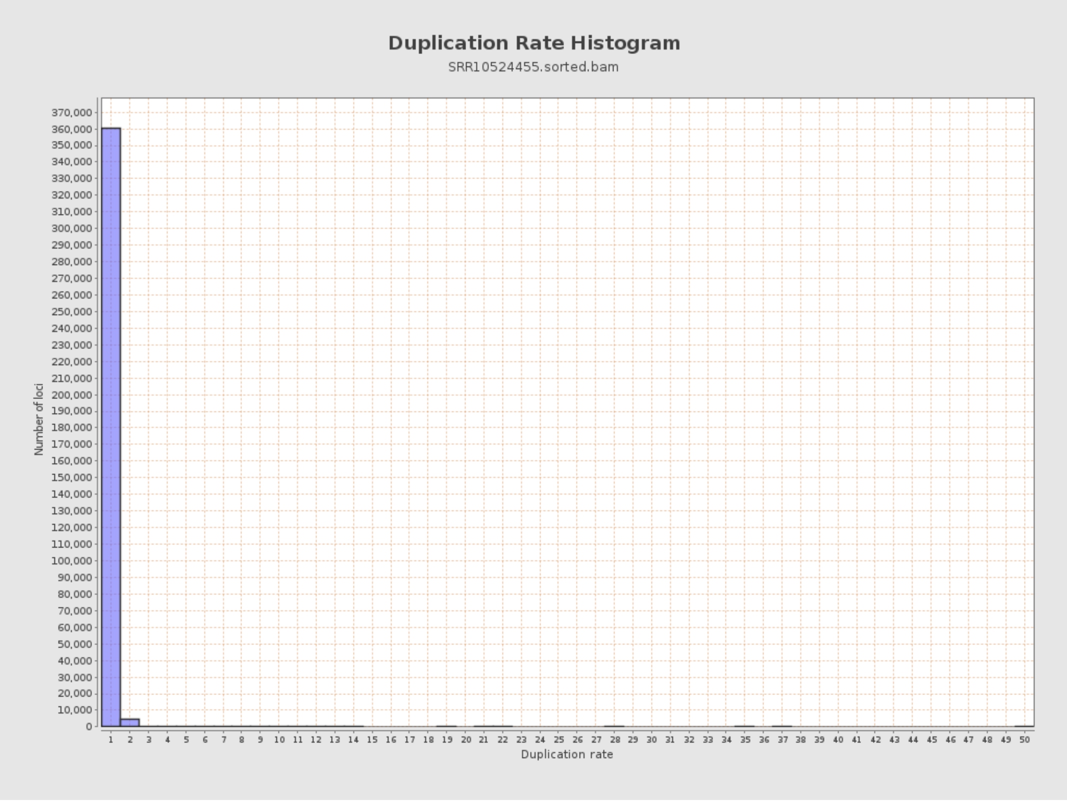
5. Results : Coverage Histogram (0-50X)



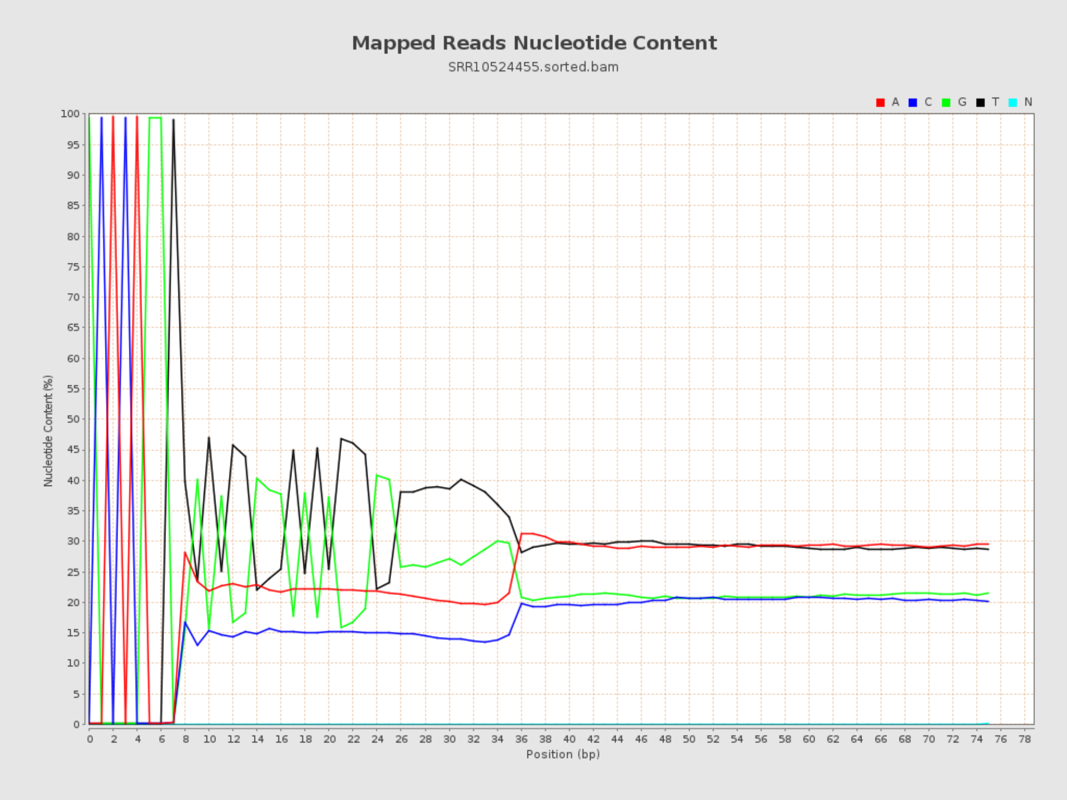
6. Results : Genome Fraction Coverage



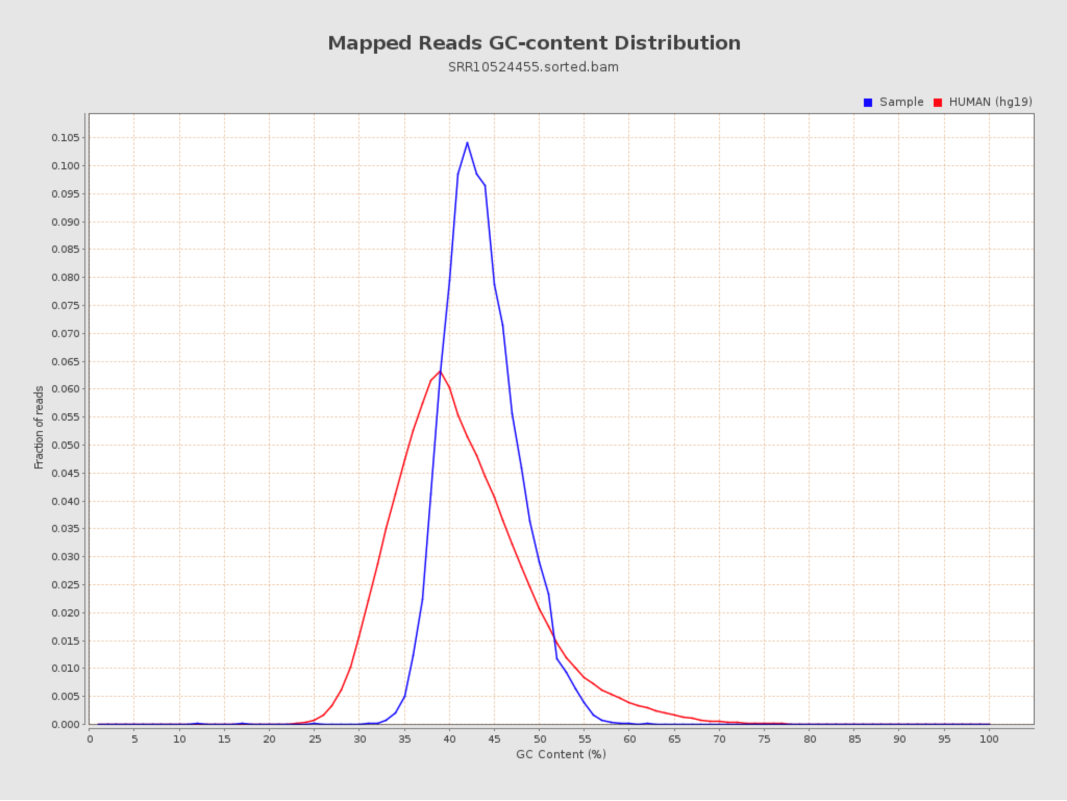
7. Results : Duplication Rate Histogram



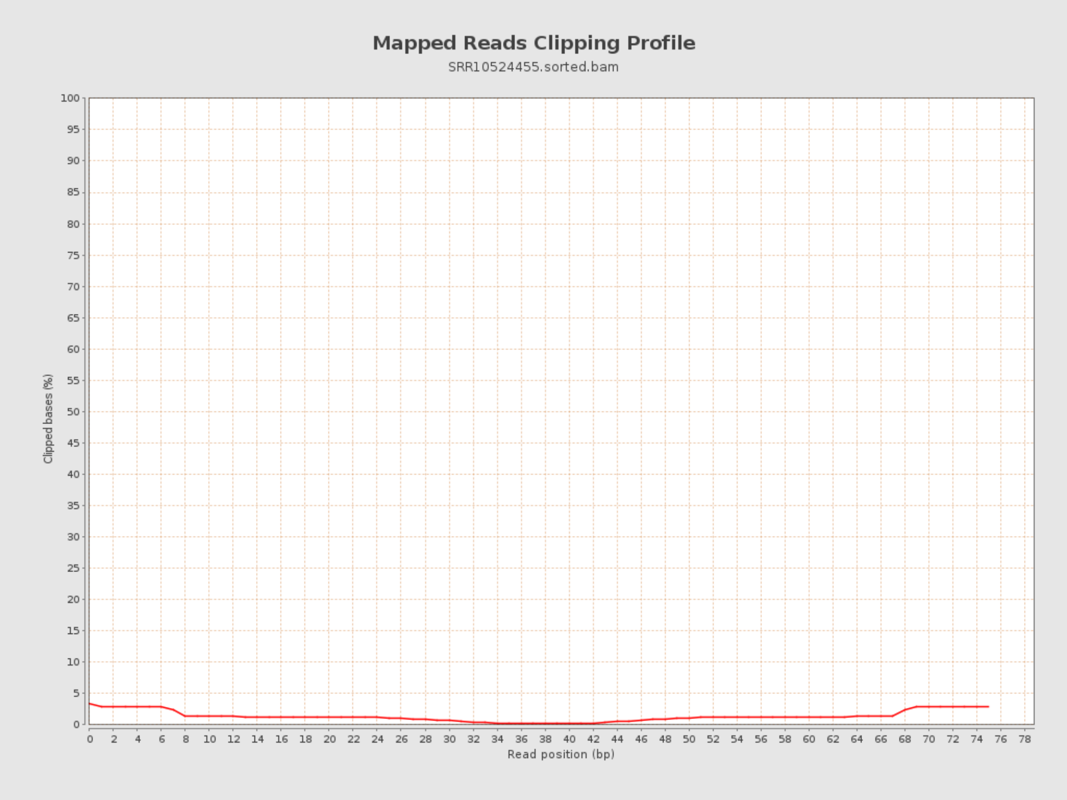
8. Results : Mapped Reads Nucleotide Content



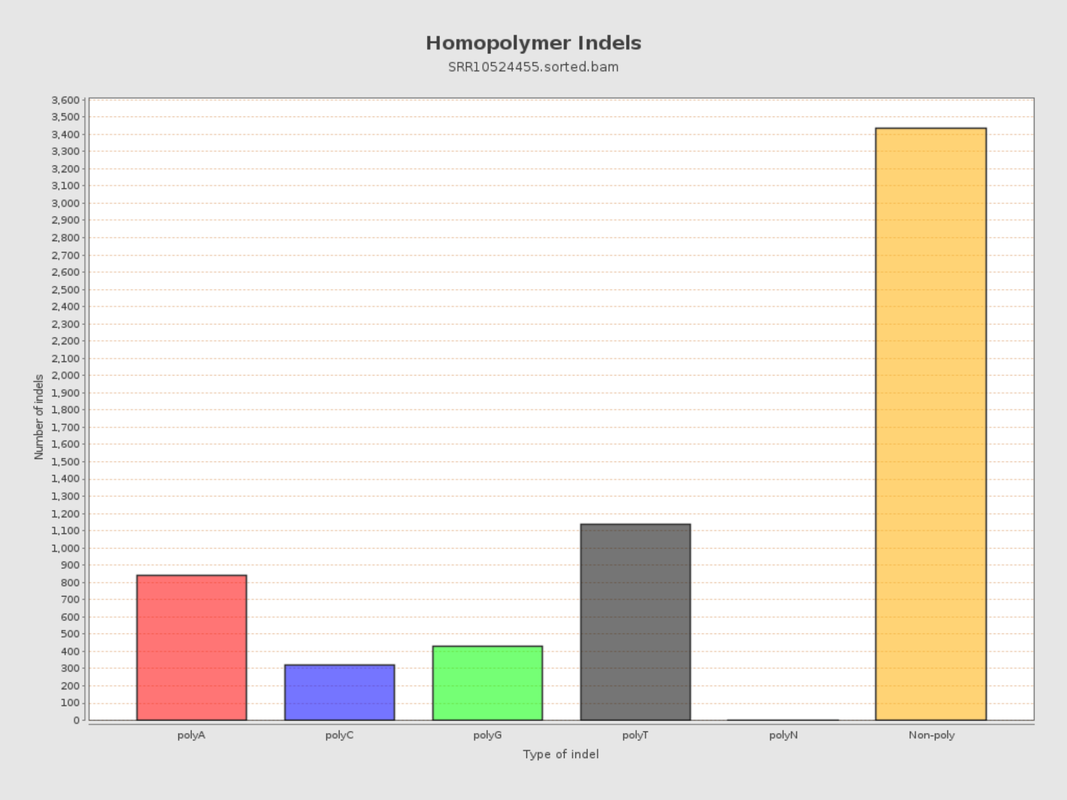
9. Results : Mapped Reads GC-content Distribution



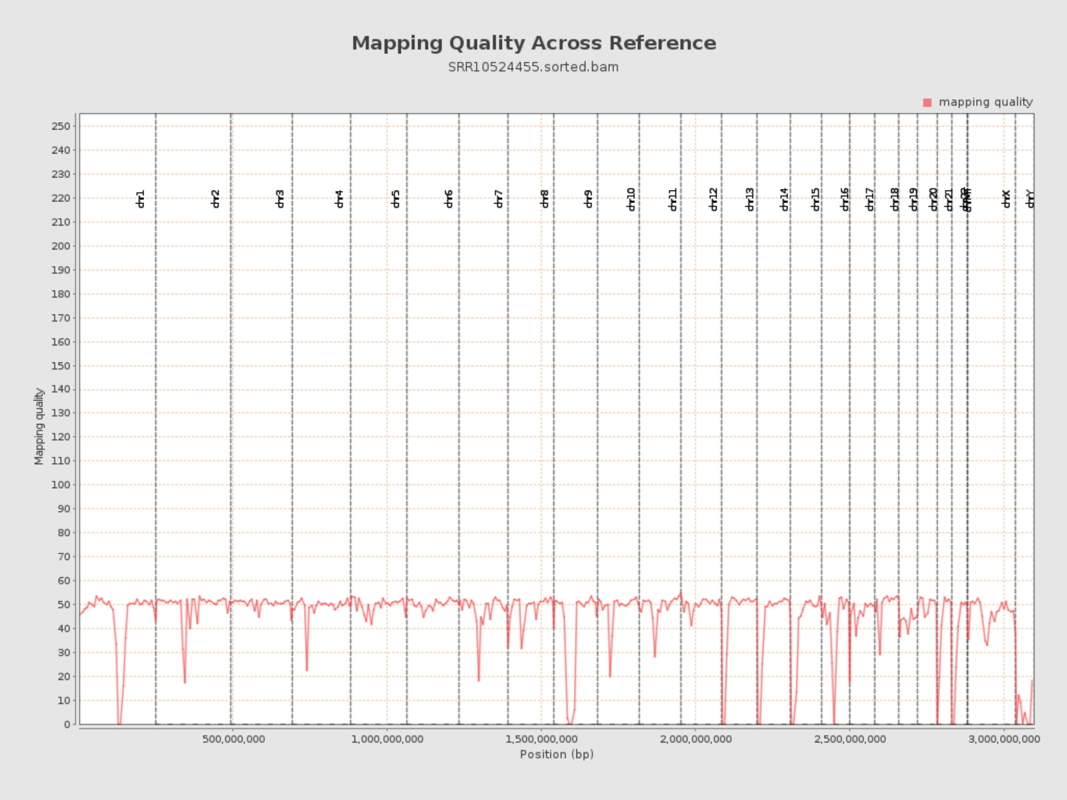
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram