Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 04:04:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524432.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_SRR10524432 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524432.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 04:04:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524432.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	388,625
Mapped reads	354,216 / 91.15%
Unmapped reads	34,409 / 8.85%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,530 / 0.39%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	7,329 / 1.89%
Duplication rate	1.6%
Clipped reads	354,782 / 91.29%

2.2. ACGT Content

Number/percentage of A's	5,176,201 / 25.01%
Number/percentage of C's	3,983,631 / 19.25%
Number/percentage of T's	6,572,914 / 31.76%
Number/percentage of G's	4,957,568 / 23.96%
Number/percentage of N's	2,213 / 0.01%
GC Percentage	43.21%

2.3. Coverage

Mean	0.0067

Standard Deviation	0.0995

2.4. Mapping Quality

Mean Mapping Quality	44.49

2.5. Mismatches and indels

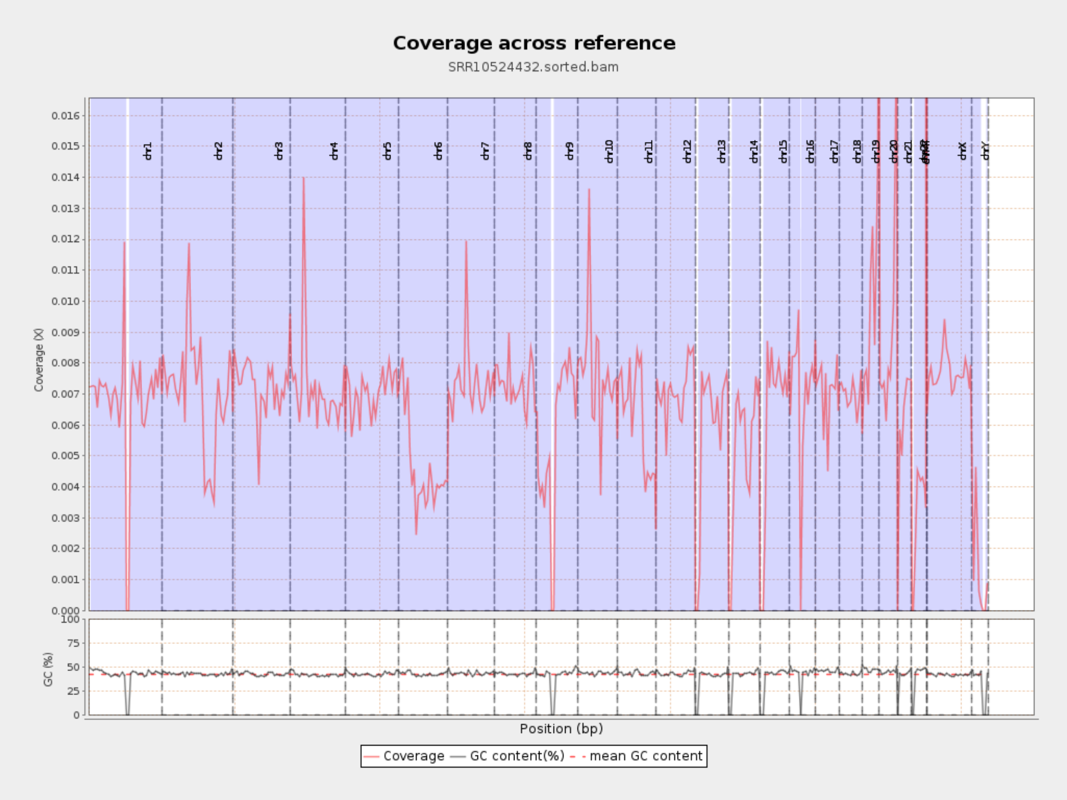
General error rate	0.52%
Mismatches	105,308
Insertions	1,554
Mapped reads with at least one insertion	0.44%
Deletions	3,550
Mapped reads with at least one deletion	0.99%
Homopolymer indels	39.03%

2.6. Chromosome stats

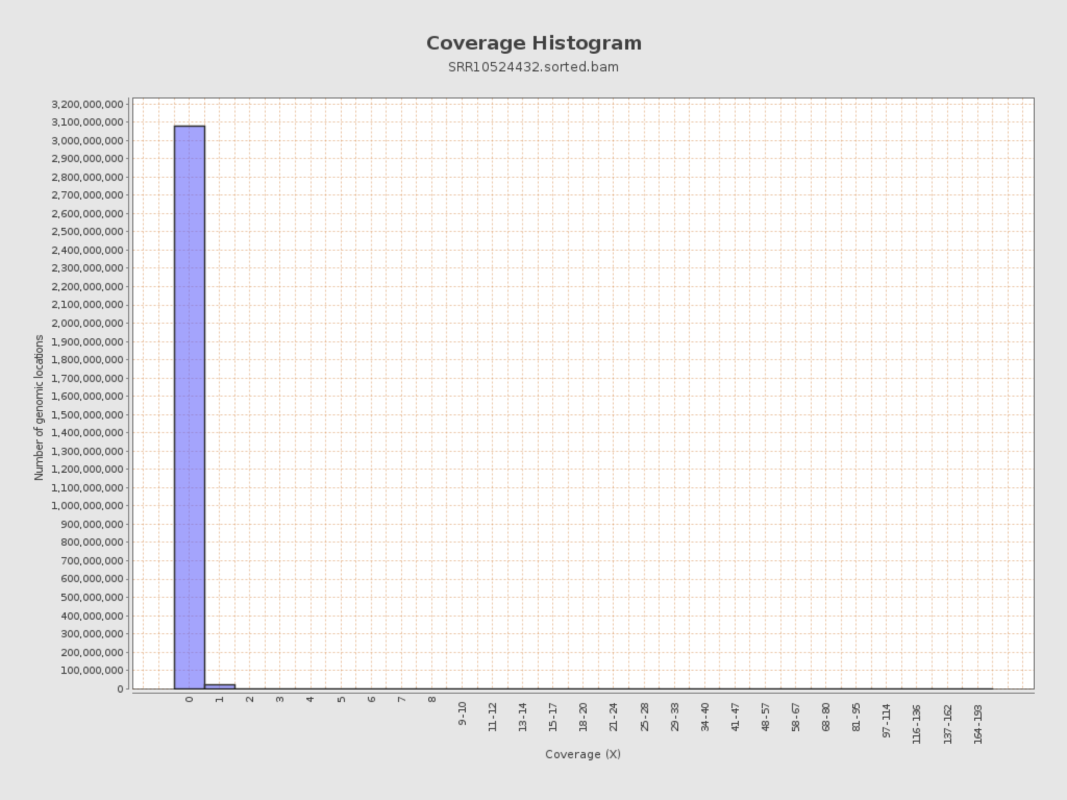
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1689618	0.0068	0.1502
chr2	243199373	1716478	0.0071	0.121
chr3	198022430	1431367	0.0072	0.0881
chr4	191154276	1366832	0.0072	0.0936
chr5	180915260	1274895	0.007	0.0869
chr6	171115067	802893	0.0047	0.0735
chr7	159138663	1178930	0.0074	0.1166

chr8	146364022	1071719	0.0073	0.0922
chr9	141213431	781652	0.0055	0.0803
chr10	135534747	1048511	0.0077	0.1039
chr11	135006516	846877	0.0063	0.0868
chr12	133851895	951617	0.0071	0.0874
chr13	115169878	665828	0.0058	0.0784
chr14	107349540	554379	0.0052	0.0746
chr15	102531392	635840	0.0062	0.0814
chr16	90354753	629940	0.007	0.0877
chr17	81195210	569526	0.007	0.0883
chr18	78077248	546660	0.007	0.105
chr19	59128983	601339	0.0102	0.1361
chr20	63025520	584056	0.0093	0.1007
chr21	48129895	287920	0.006	0.0858
chr22	51304566	154018	0.003	0.0566
chrMT	16571	40655	2.4534	2.3897
chrX	155270560	1193976	0.0077	0.0927
chrY	59373566	72728	0.0012	0.0514

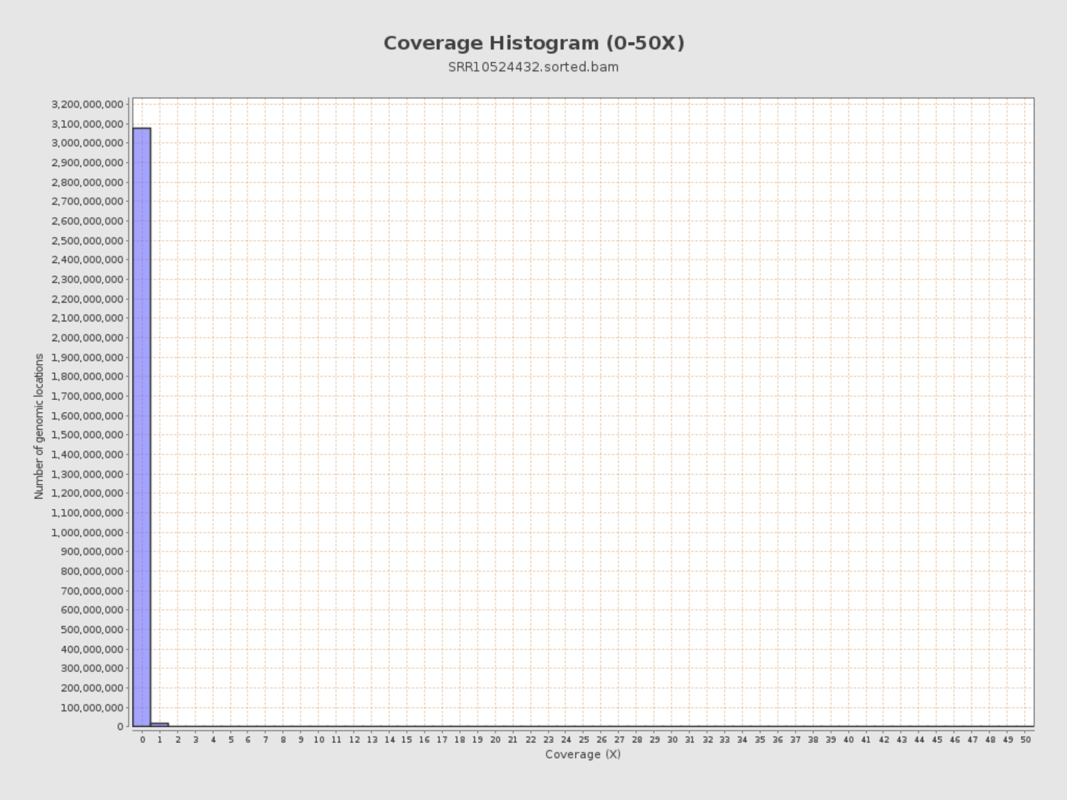
3. Results : Coverage across reference



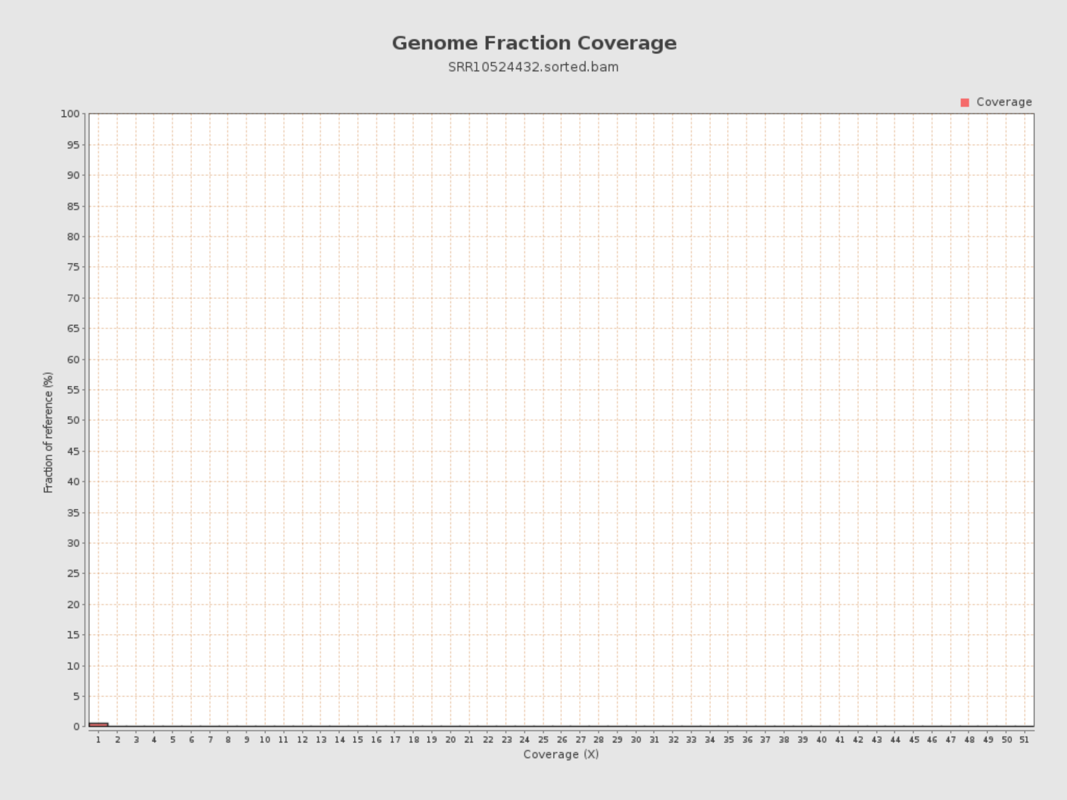
4. Results : Coverage Histogram



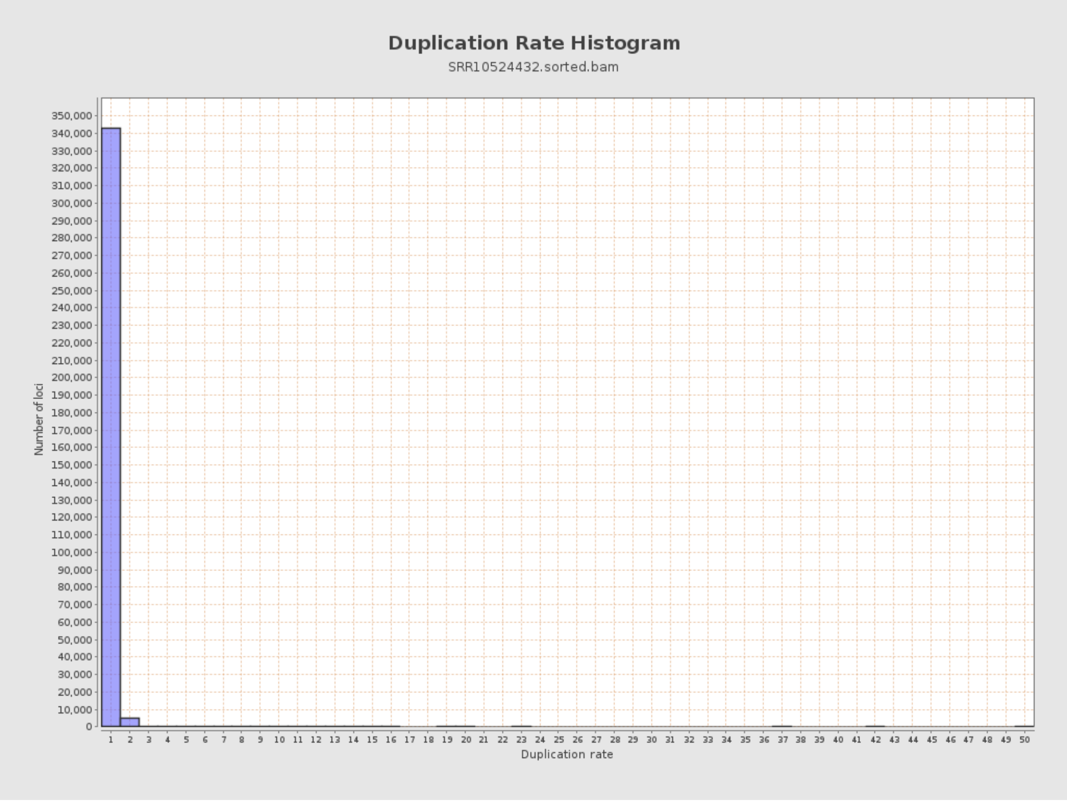
5. Results : Coverage Histogram (0-50X)



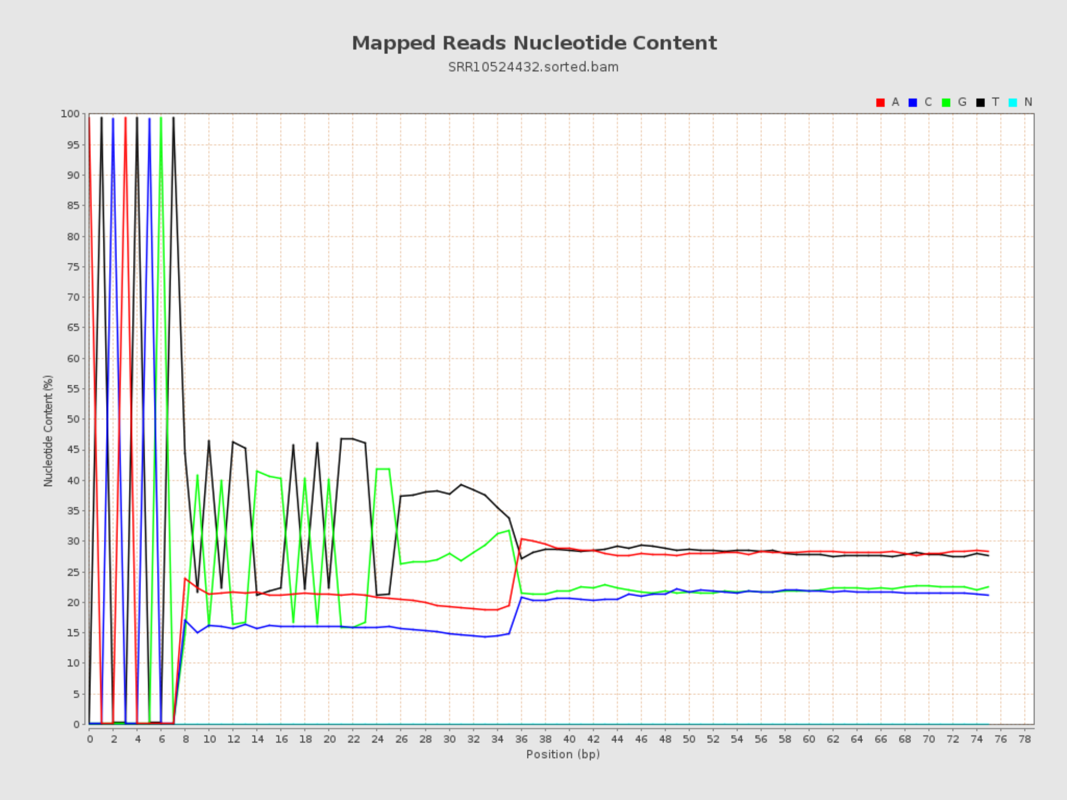
6. Results : Genome Fraction Coverage



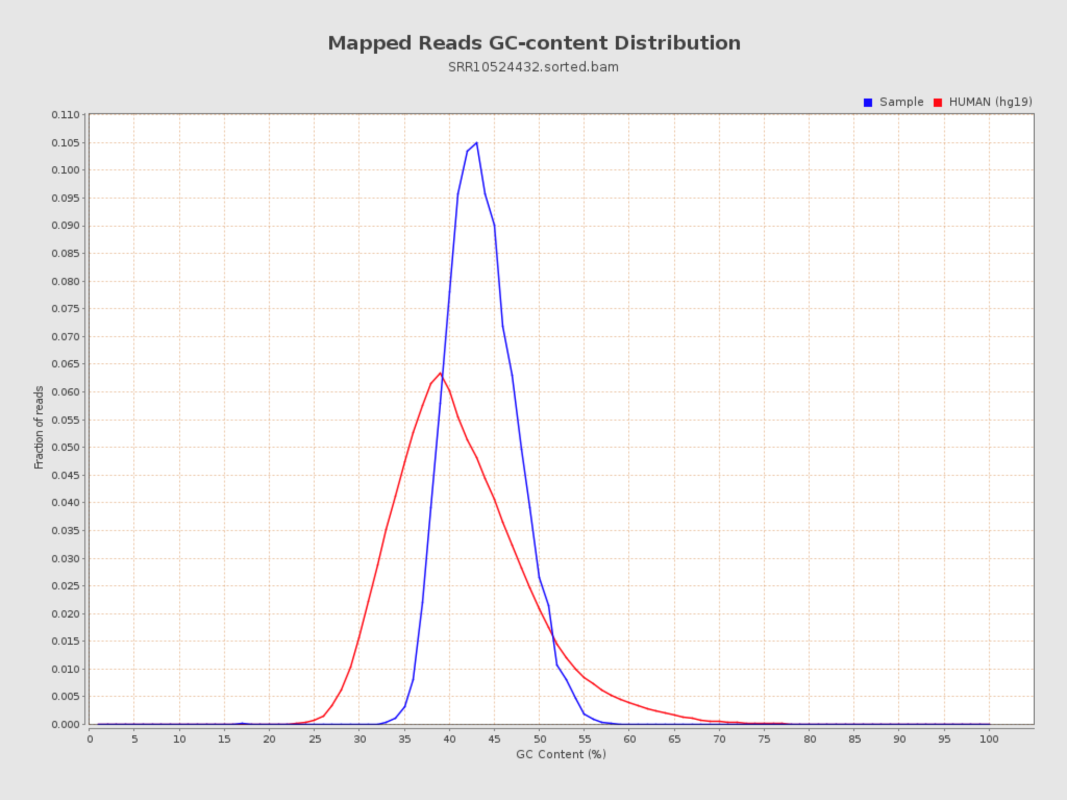
7. Results : Duplication Rate Histogram



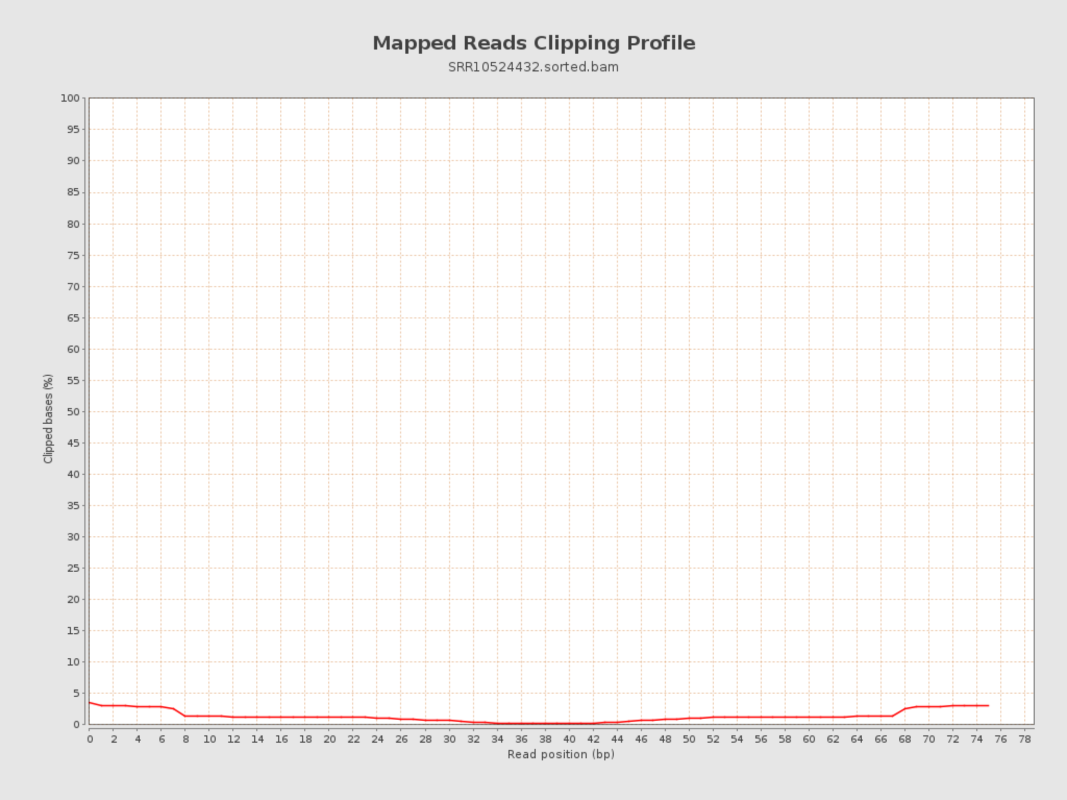
8. Results : Mapped Reads Nucleotide Content



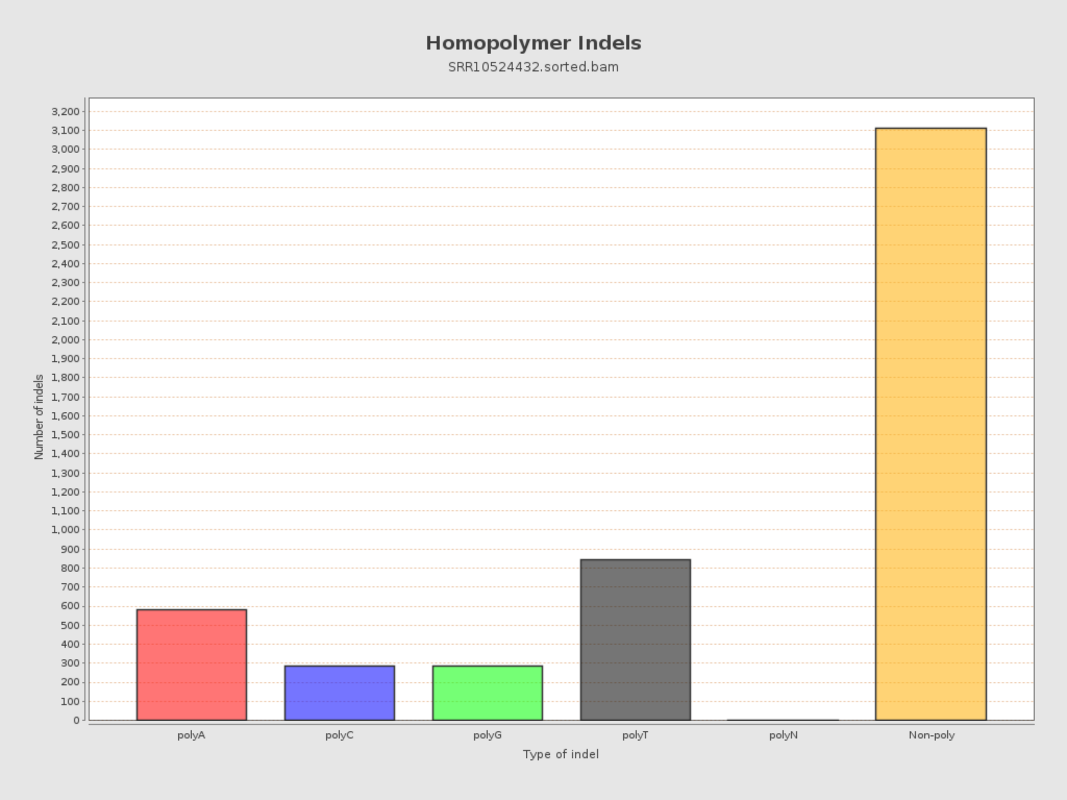
9. Results : Mapped Reads GC-content Distribution



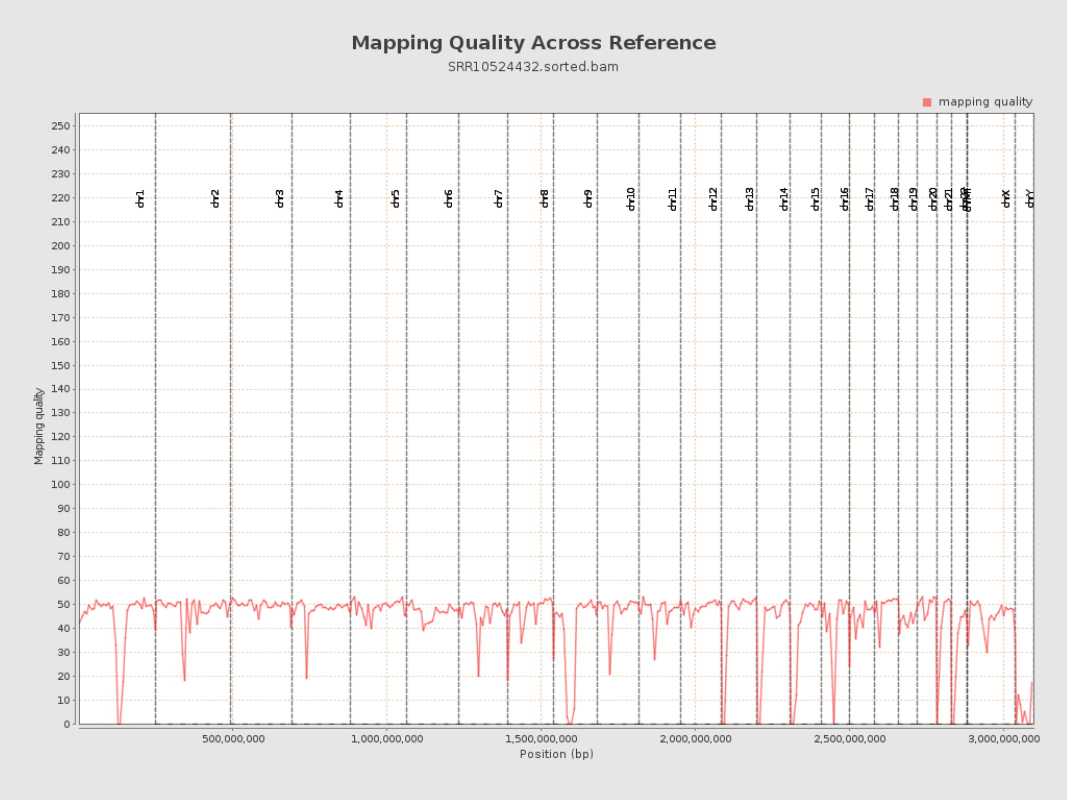
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram