Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 03:42:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524424.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_SRR10524424 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524424.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 03:42:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524424.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,103,927
Mapped reads	2,853,046 / 91.92%
Unmapped reads	250,881 / 8.08%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,129 / 0.39%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	199,670 / 6.43%
Duplication rate	5.05%
Clipped reads	2,858,859 / 92.1%

2.2. ACGT Content

Number/percentage of A's	41,477,109 / 24.95%
Number/percentage of C's	32,014,341 / 19.25%
Number/percentage of T's	52,825,988 / 31.77%
Number/percentage of G's	39,937,441 / 24.02%
Number/percentage of N's	17,007 / 0.01%
GC Percentage	43.27%

2.3. Coverage

Mean	0.0537

Standard Deviation	0.5183

2.4. Mapping Quality

Mean Mapping Quality	44.58

2.5. Mismatches and indels

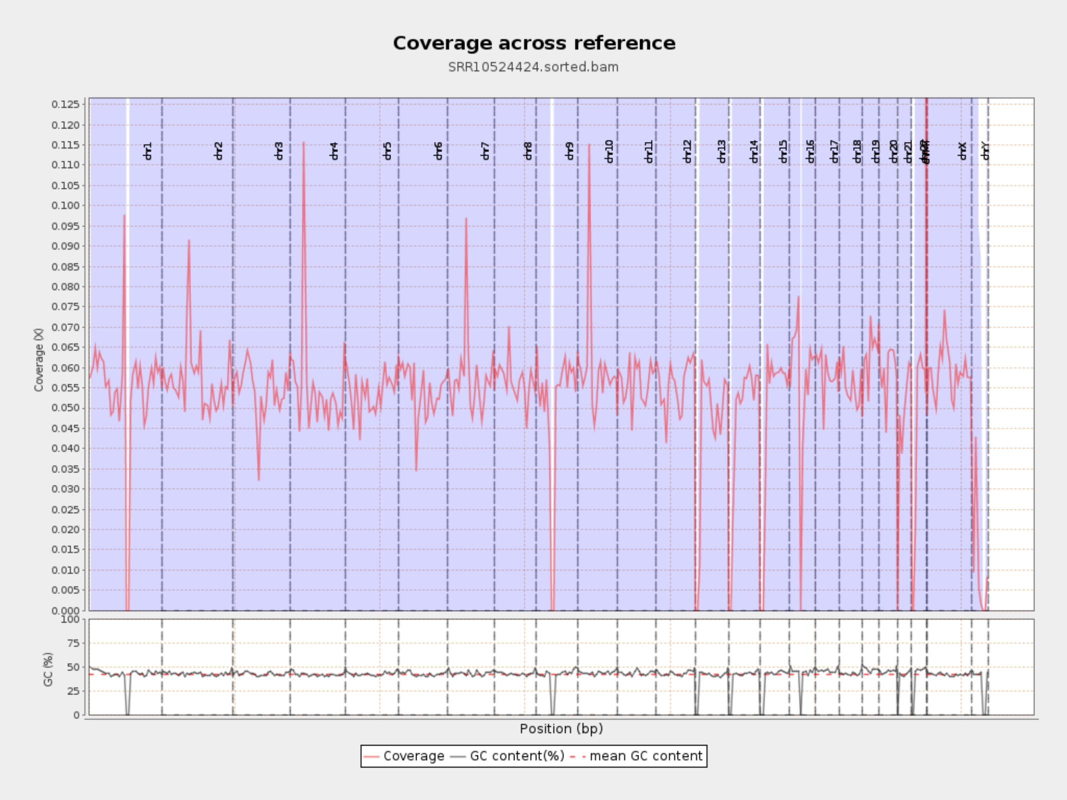
General error rate	0.52%
Mismatches	844,398
Insertions	12,522
Mapped reads with at least one insertion	0.44%
Deletions	28,921
Mapped reads with at least one deletion	1.01%
Homopolymer indels	41%

2.6. Chromosome stats

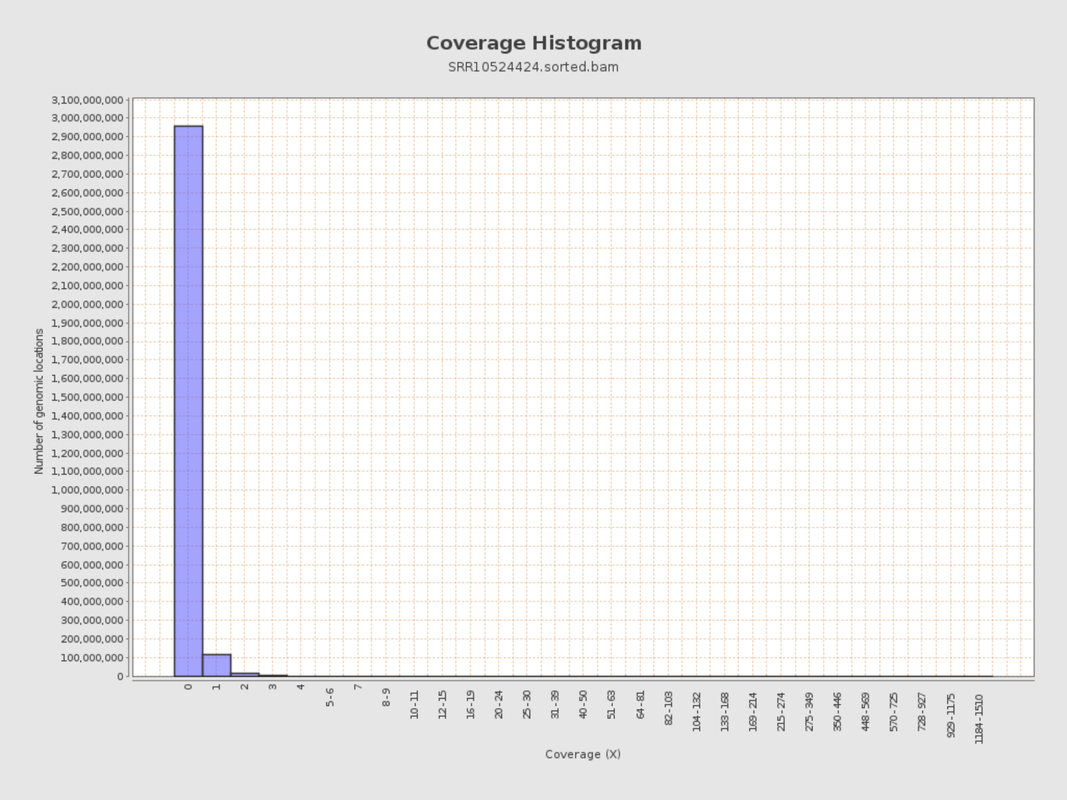
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13557177	0.0544	1.0719
chr2	243199373	13944195	0.0573	0.7329
chr3	198022430	10779461	0.0544	0.2807
chr4	191154276	10510657	0.055	0.4072
chr5	180915260	9735381	0.0538	0.2753
chr6	171115067	9297482	0.0543	0.3198
chr7	159138663	9141843	0.0574	0.6644

chr8	146364022	8303026	0.0567	0.3701
chr9	141213431	6989697	0.0495	0.3624
chr10	135534747	8117744	0.0599	0.5711
chr11	135006516	7586668	0.0562	0.3939
chr12	133851895	7478301	0.0559	0.2908
chr13	115169878	5040872	0.0438	0.2497
chr14	107349540	4960075	0.0462	0.2752
chr15	102531392	4967714	0.0485	0.2633
chr16	90354753	5125845	0.0567	0.3174
chr17	81195210	4751828	0.0585	0.3253
chr18	78077248	4369801	0.056	0.728
chr19	59128983	3741141	0.0633	0.6884
chr20	63025520	3720132	0.059	0.3135
chr21	48129895	2247897	0.0467	0.3567
chr22	51304566	2142021	0.0418	0.2479
chrMT	16571	12940	0.7809	1.0505
chrX	155270560	9136783	0.0588	0.3352
chrY	59373566	660263	0.0111	0.3724

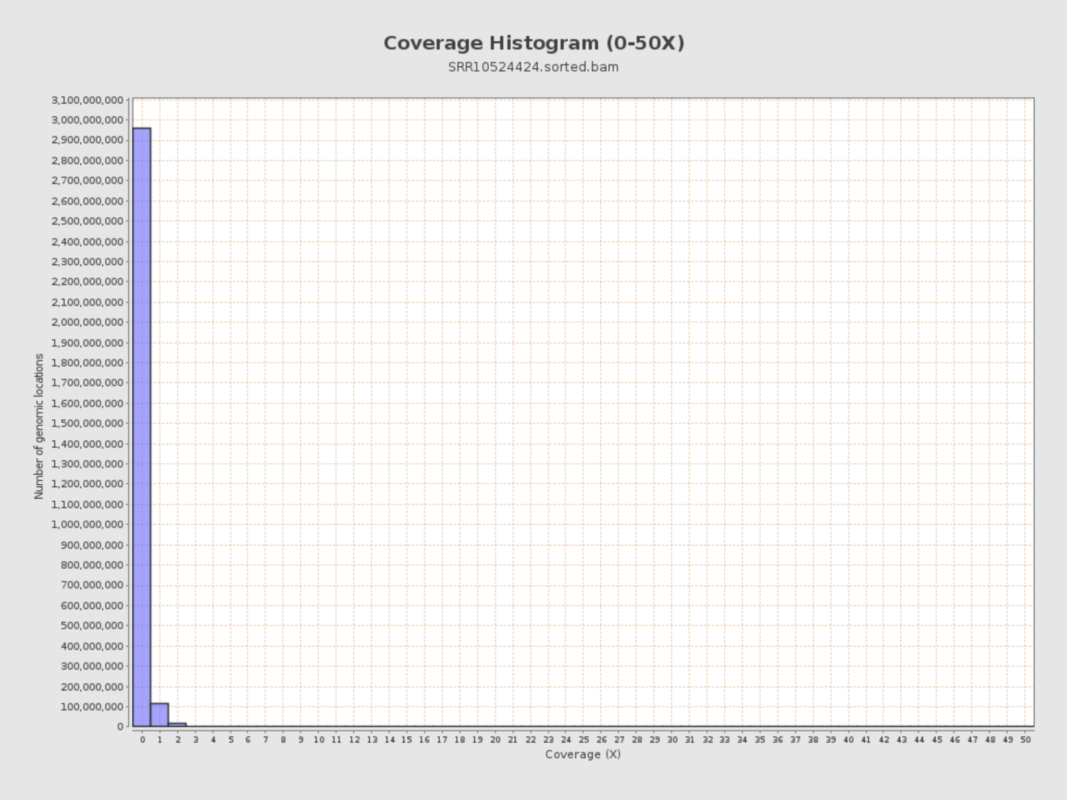
3. Results : Coverage across reference



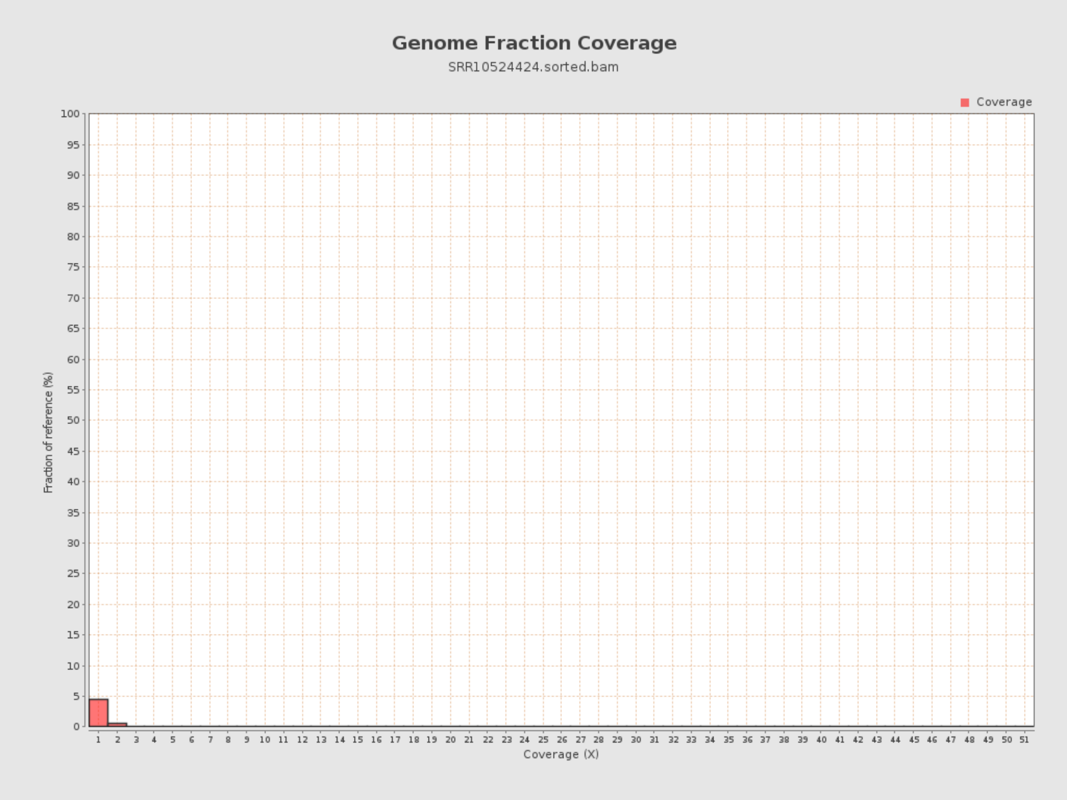
4. Results : Coverage Histogram



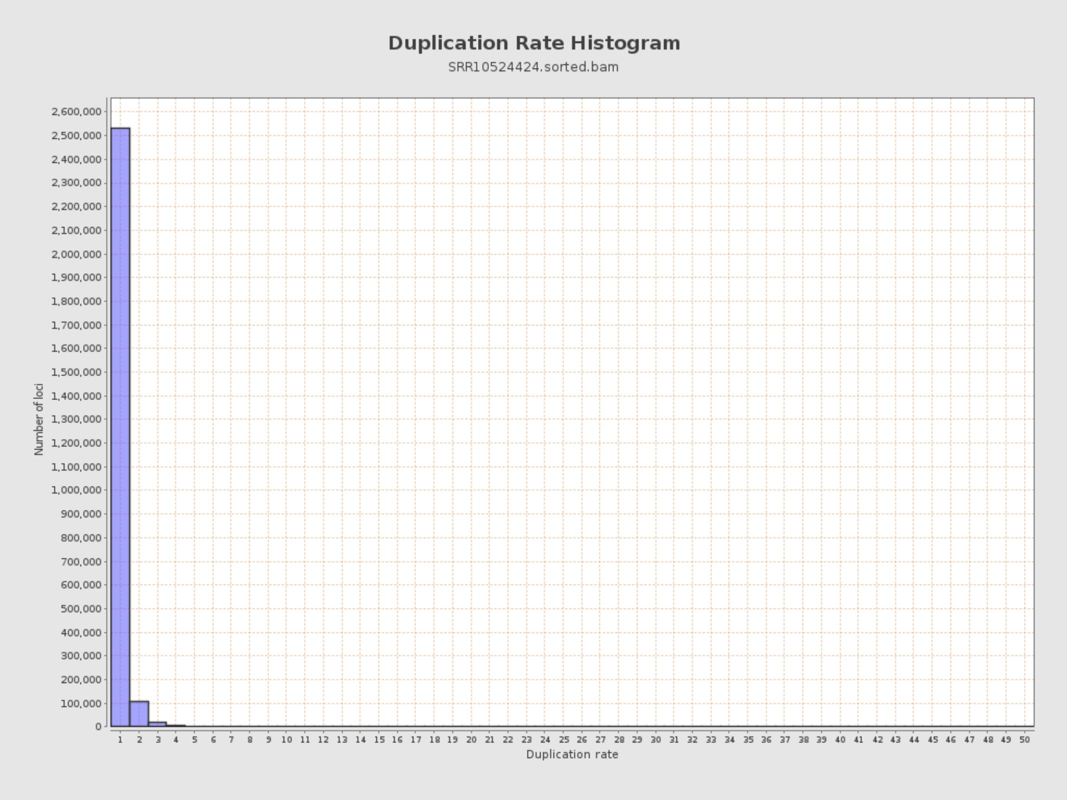
5. Results : Coverage Histogram (0-50X)



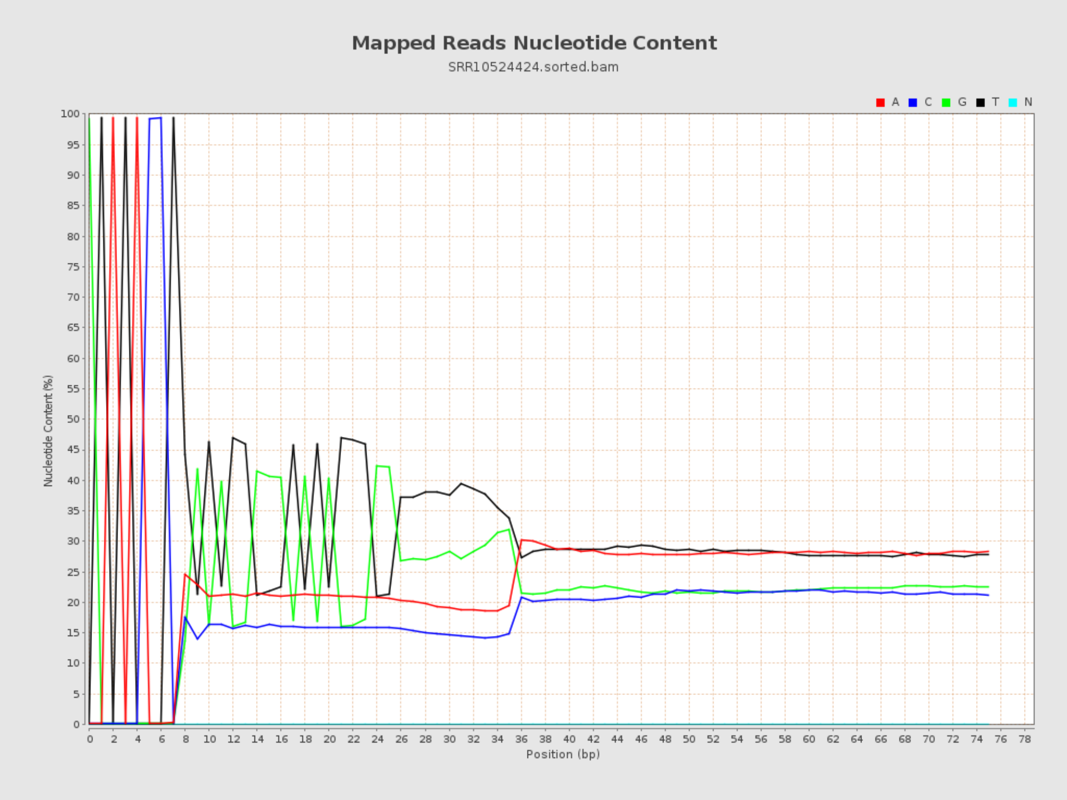
6. Results : Genome Fraction Coverage



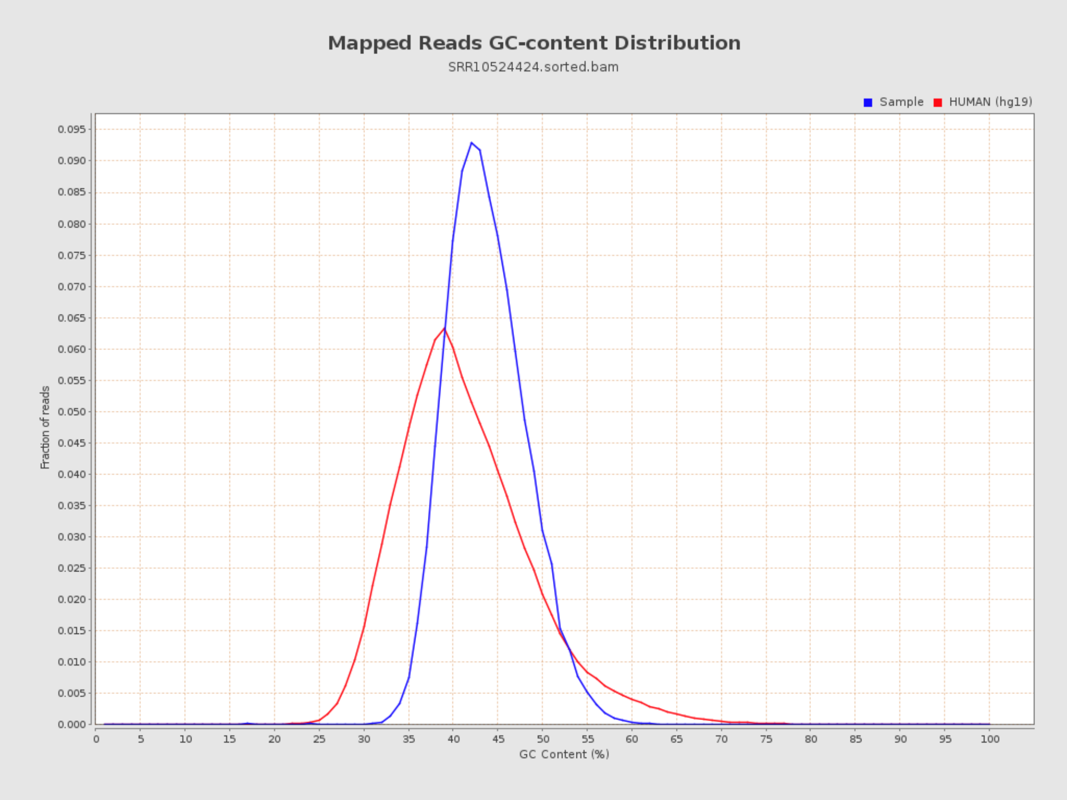
7. Results : Duplication Rate Histogram



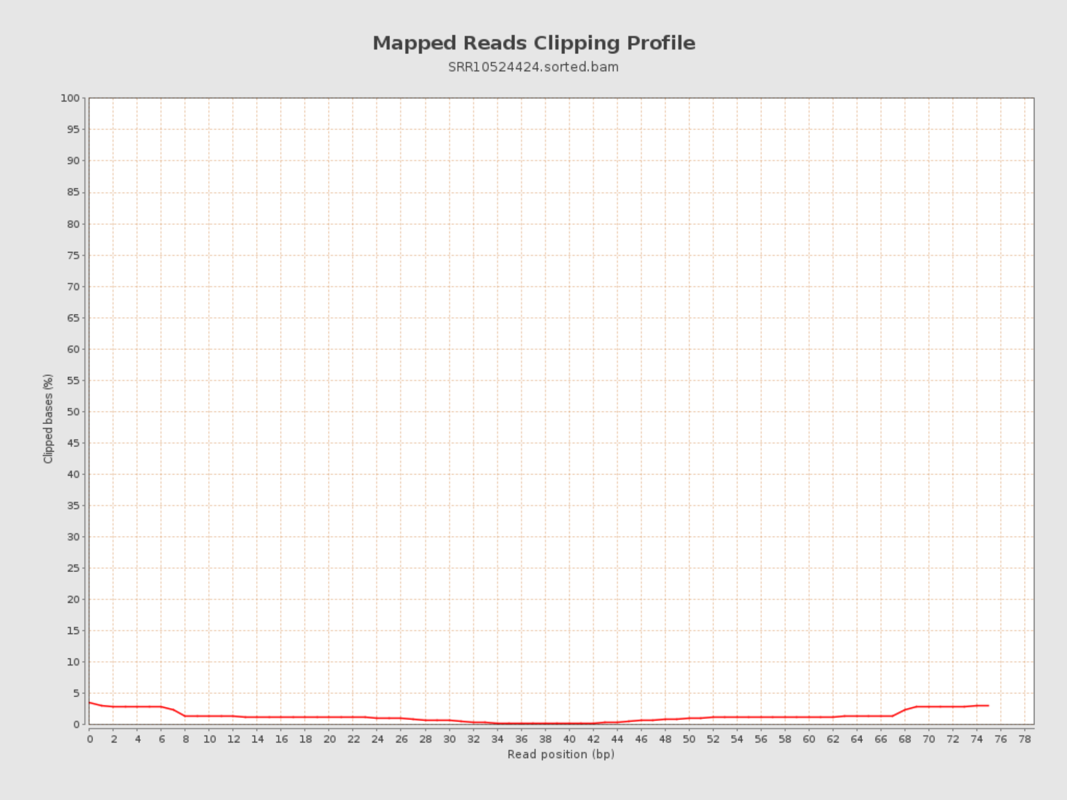
8. Results : Mapped Reads Nucleotide Content



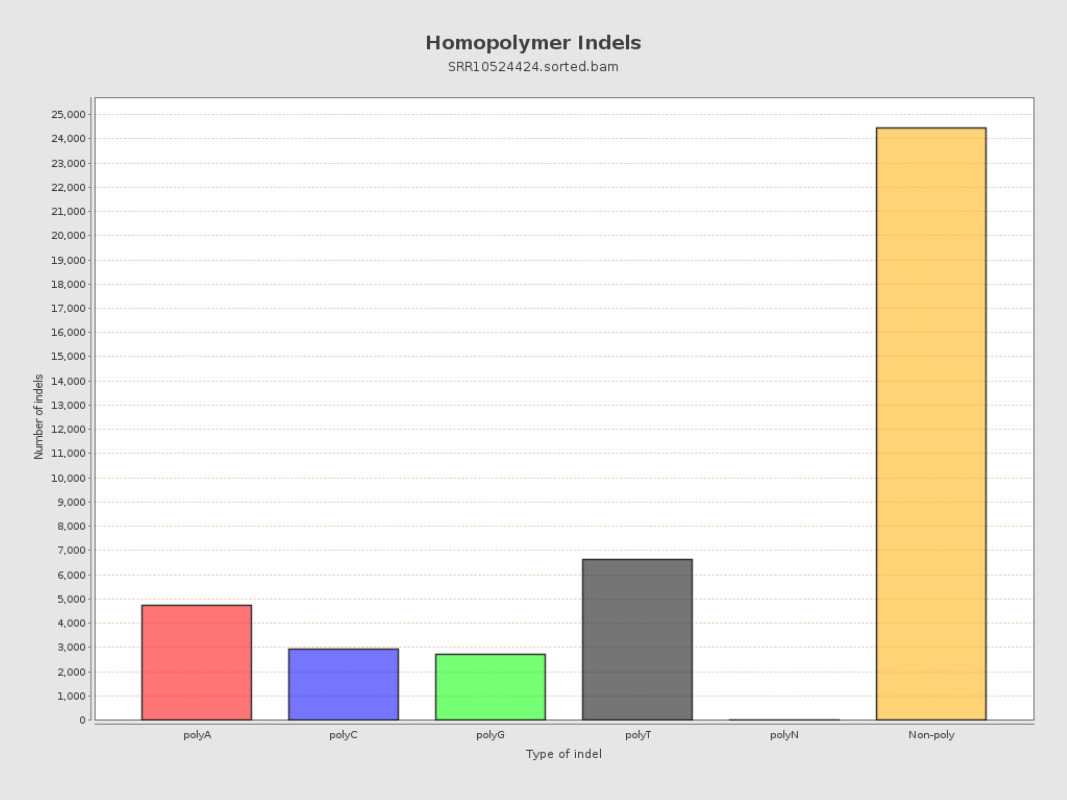
9. Results : Mapped Reads GC-content Distribution



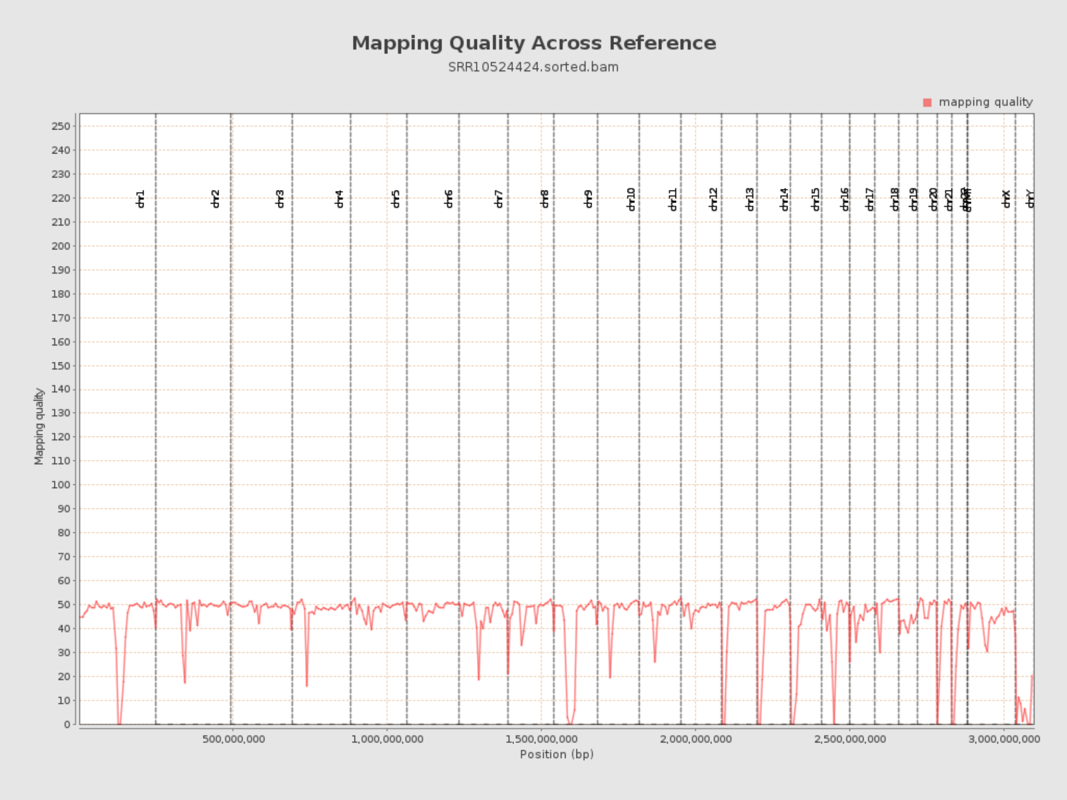
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram