Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 05:07:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524925.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_SRR10524925 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524925.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 05:07:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524925.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,608,119
Mapped reads	1,496,895 / 93.08%
Unmapped reads	111,224 / 6.92%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,841 / 0.43%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	73,989 / 4.6%
Duplication rate	3.96%
Clipped reads	1,499,498 / 93.25%

2.2. ACGT Content

Number/percentage of A's	21,449,430 / 24.49%
Number/percentage of C's	15,894,648 / 18.15%
Number/percentage of T's	28,619,833 / 32.68%
Number/percentage of G's	21,624,270 / 24.69%
Number/percentage of N's	779 / 0%
GC Percentage	42.84%

2.3. Coverage

Mean	0.0283

Standard Deviation	0.2477

2.4. Mapping Quality

Mean Mapping Quality	44.95

2.5. Mismatches and indels

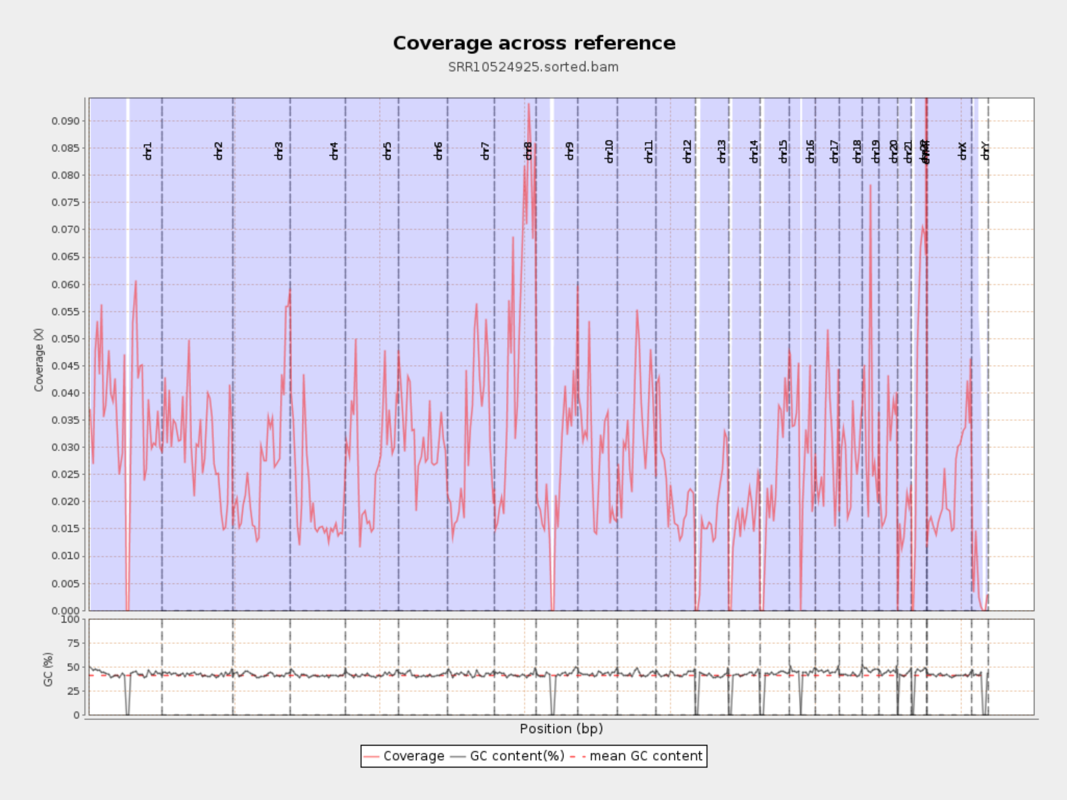
General error rate	0.5%
Mismatches	428,336
Insertions	6,631
Mapped reads with at least one insertion	0.44%
Deletions	16,832
Mapped reads with at least one deletion	1.12%
Homopolymer indels	42.5%

2.6. Chromosome stats

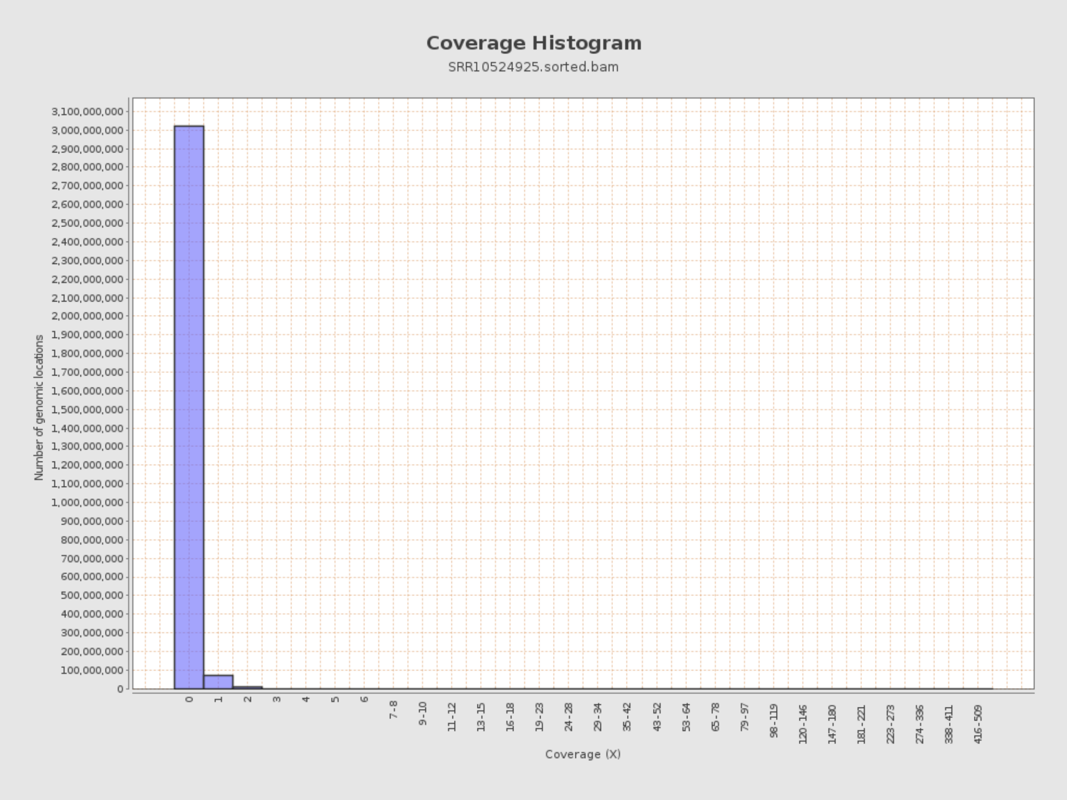
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9050776	0.0363	0.4182
chr2	243199373	7586742	0.0312	0.3119
chr3	198022430	5397440	0.0273	0.1839
chr4	191154276	3730490	0.0195	0.1847
chr5	180915260	5161216	0.0285	0.1881
chr6	171115067	5504988	0.0322	0.2084
chr7	159138663	5083429	0.0319	0.2863

chr8	146364022	7429527	0.0508	0.329
chr9	141213431	3351830	0.0237	0.2071
chr10	135534747	3795551	0.028	0.2597
chr11	135006516	4594053	0.034	0.23
chr12	133851895	2976218	0.0222	0.1699
chr13	115169878	1924783	0.0167	0.1443
chr14	107349540	1677103	0.0156	0.1432
chr15	102531392	2432785	0.0237	0.1722
chr16	90354753	2697208	0.0299	0.1981
chr17	81195210	2440599	0.0301	0.1988
chr18	78077248	2190472	0.0281	0.311
chr19	59128983	2032189	0.0344	0.3043
chr20	63025520	1785300	0.0283	0.1928
chr21	48129895	746043	0.0155	0.1606
chr22	51304566	2202002	0.0429	0.2353
chrMT	16571	7365	0.4445	0.7987
chrX	155270560	3597066	0.0232	0.1835
chrY	59373566	222263	0.0037	0.141

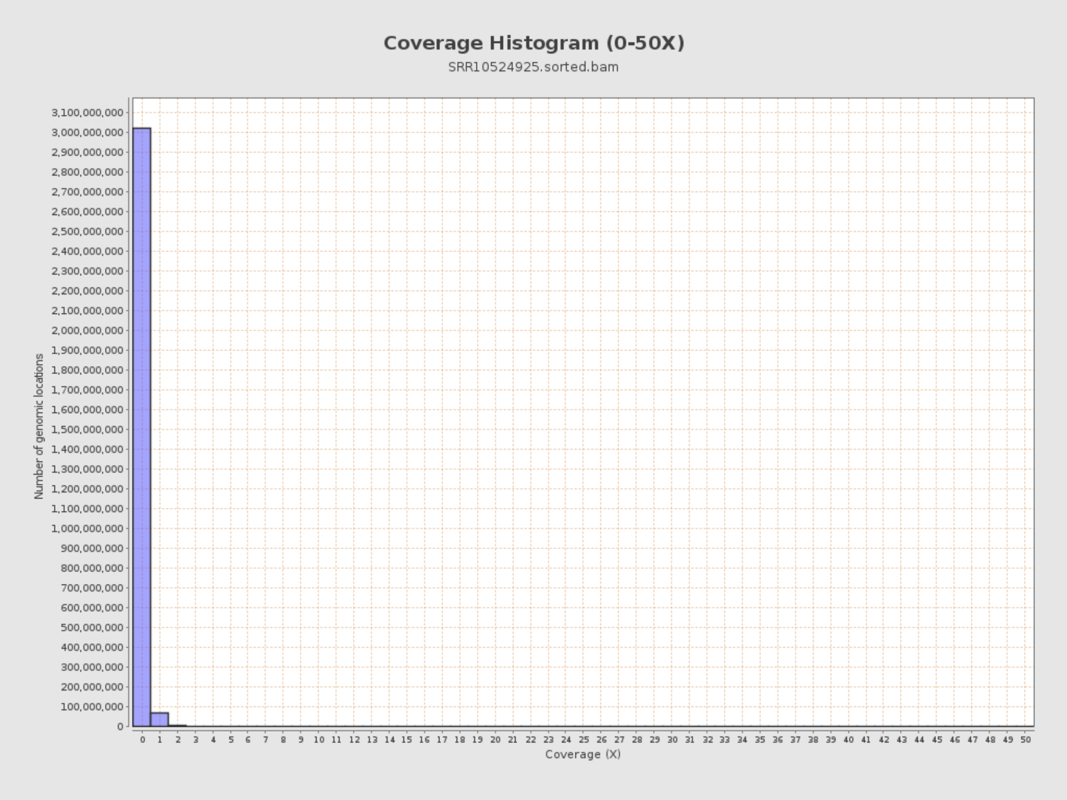
3. Results : Coverage across reference



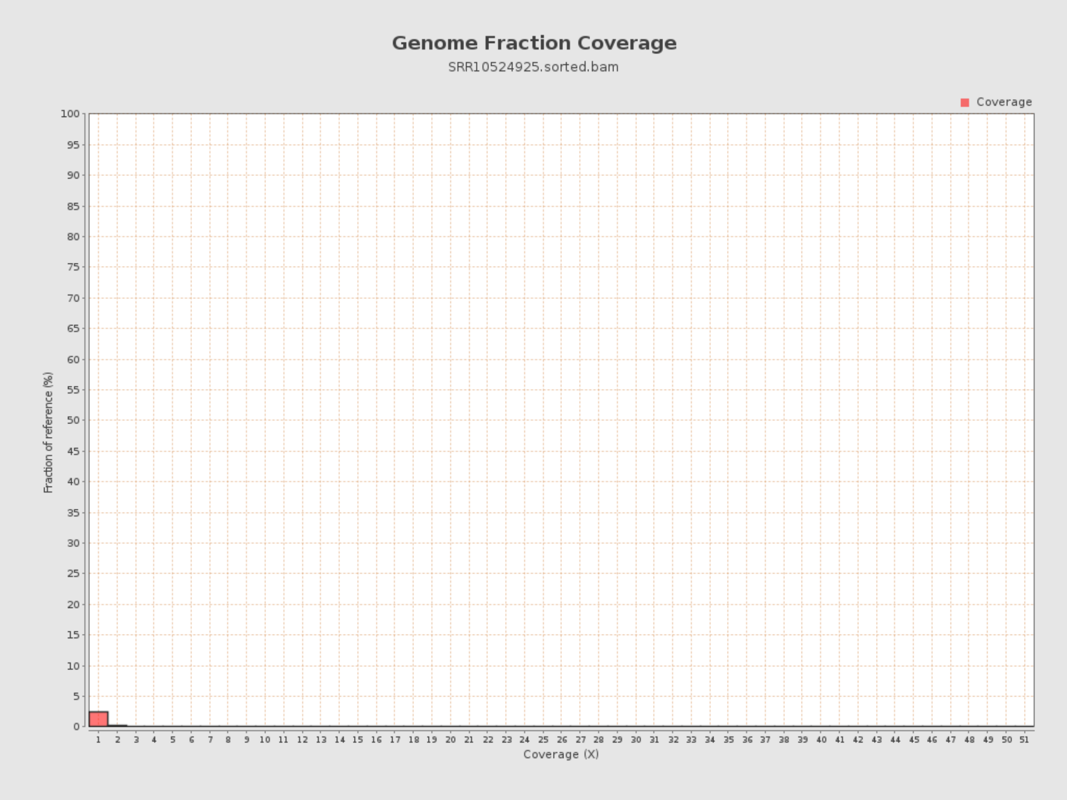
4. Results : Coverage Histogram



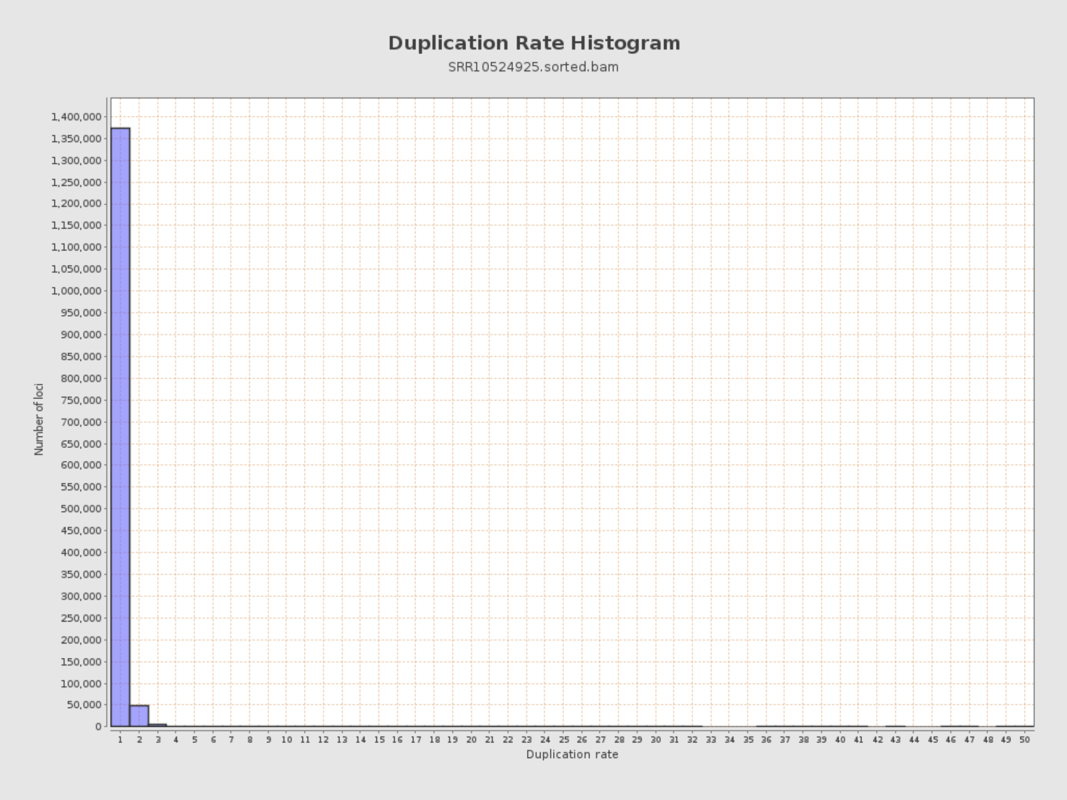
5. Results : Coverage Histogram (0-50X)



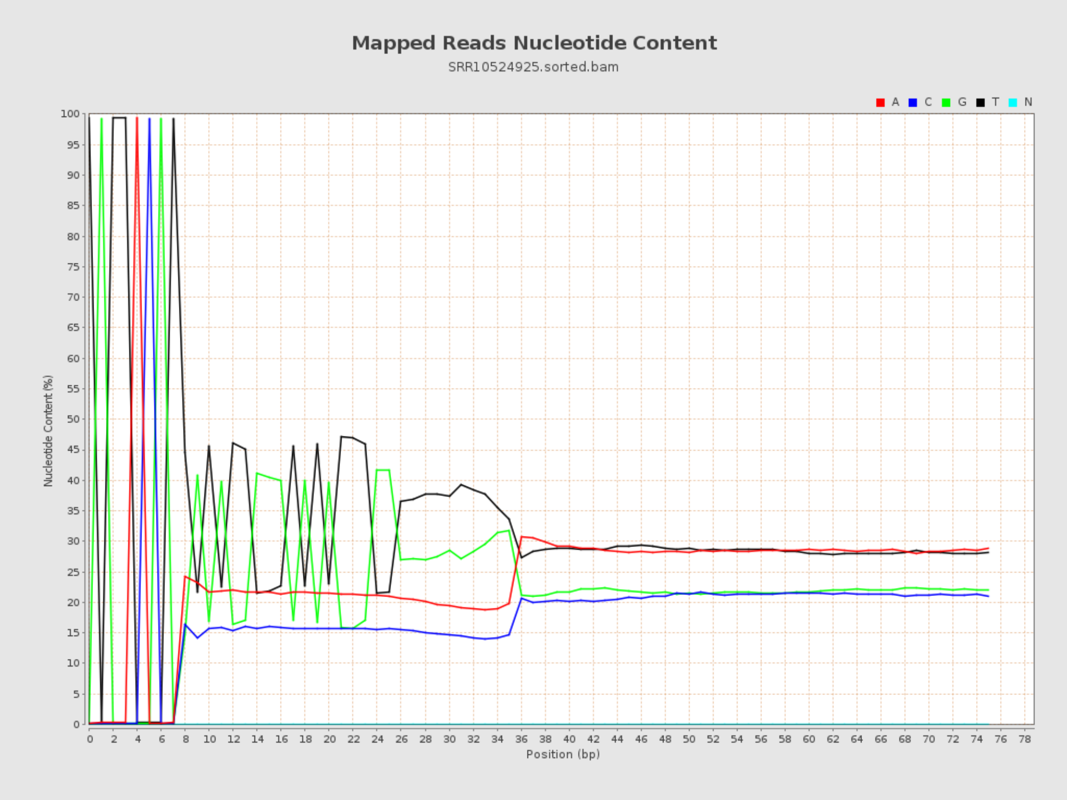
6. Results : Genome Fraction Coverage



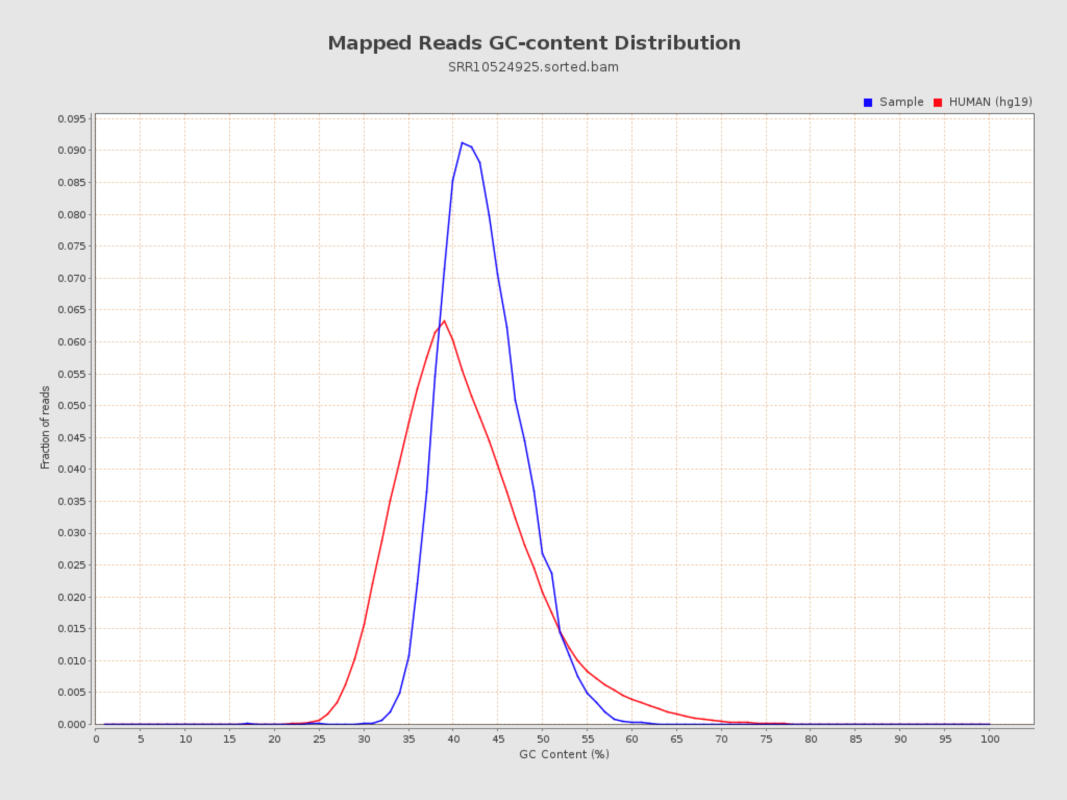
7. Results : Duplication Rate Histogram



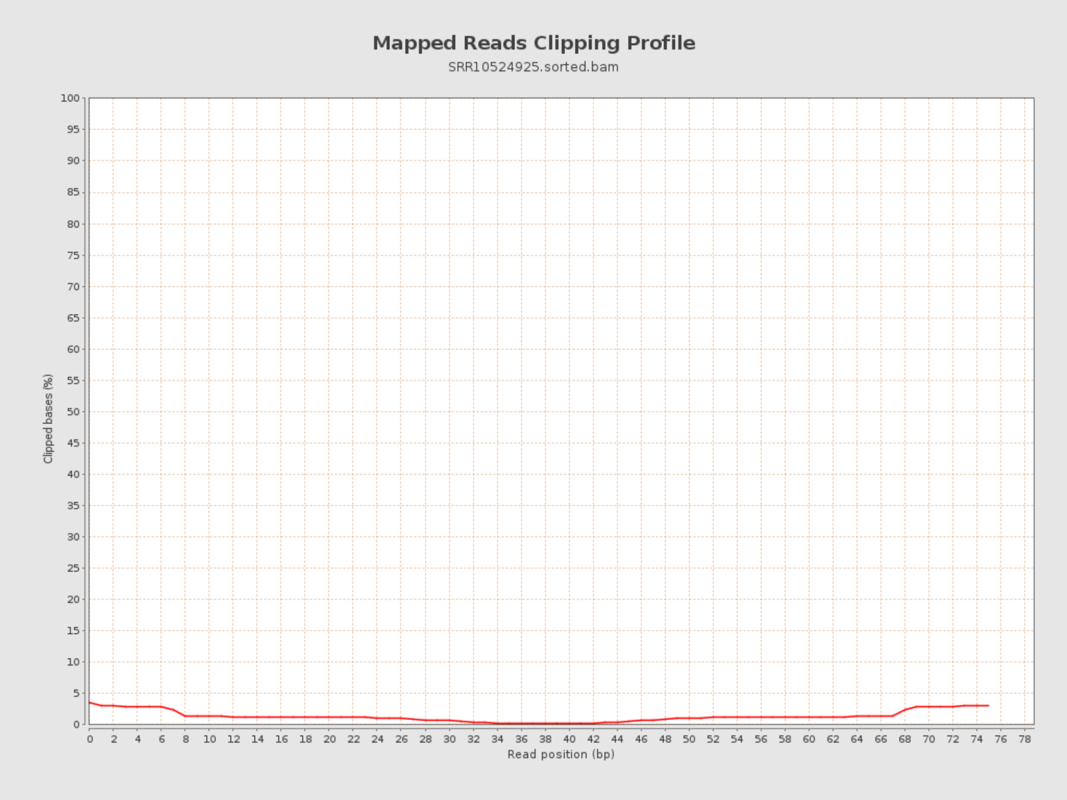
8. Results : Mapped Reads Nucleotide Content



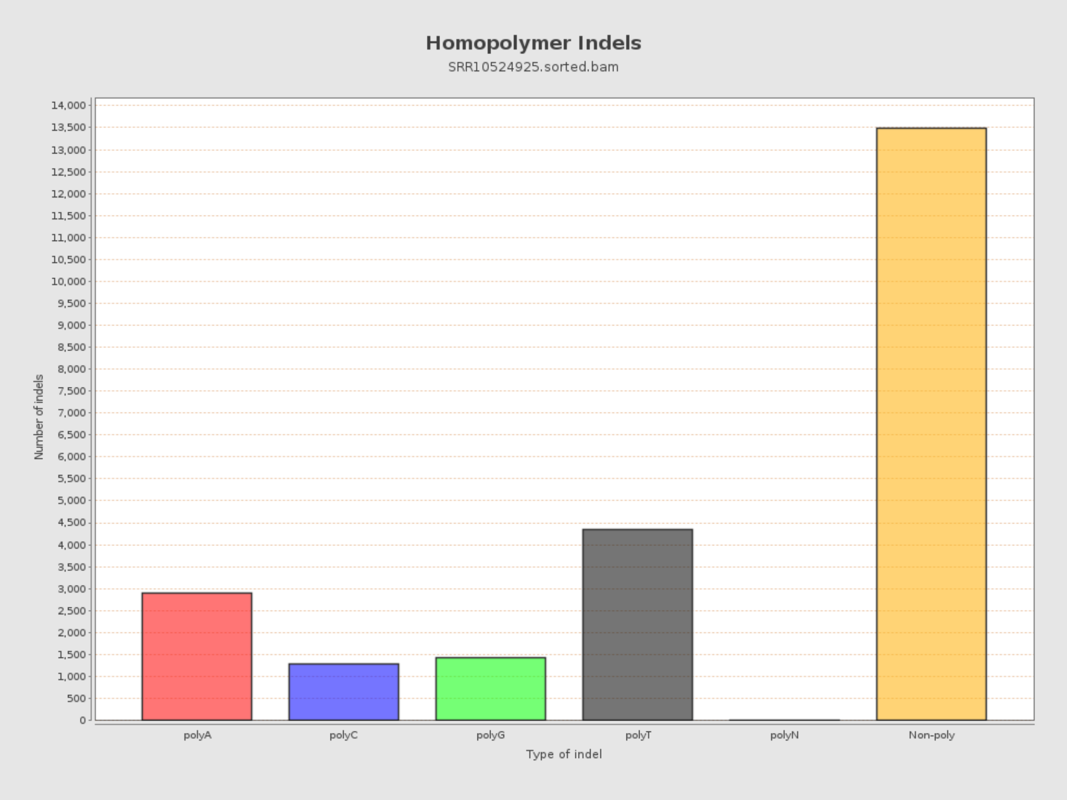
9. Results : Mapped Reads GC-content Distribution



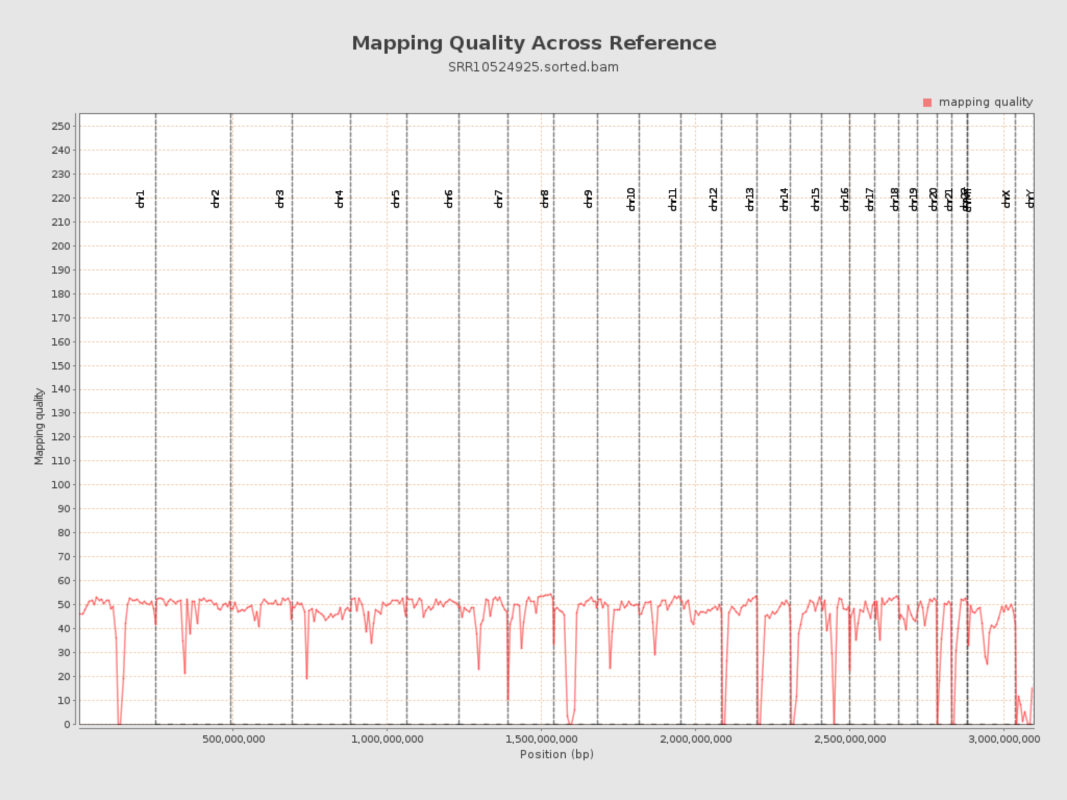
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram