Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 08:35:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524520.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_SRR10524520 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524520.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 08:35:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524520.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	580,369
Mapped reads	506,072 / 87.2%
Unmapped reads	74,297 / 12.8%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,824 / 0.66%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	10,771 / 1.86%
Duplication rate	1.24%
Clipped reads	507,911 / 87.52%

2.2. ACGT Content

Number/percentage of A's	7,653,629 / 26.33%
Number/percentage of C's	5,330,351 / 18.34%
Number/percentage of T's	8,936,593 / 30.75%
Number/percentage of G's	7,144,300 / 24.58%
Number/percentage of N's	346 / 0%
GC Percentage	42.92%

2.3. Coverage

Mean	0.0094

Standard Deviation	0.1512

2.4. Mapping Quality

Mean Mapping Quality	40.74

2.5. Mismatches and indels

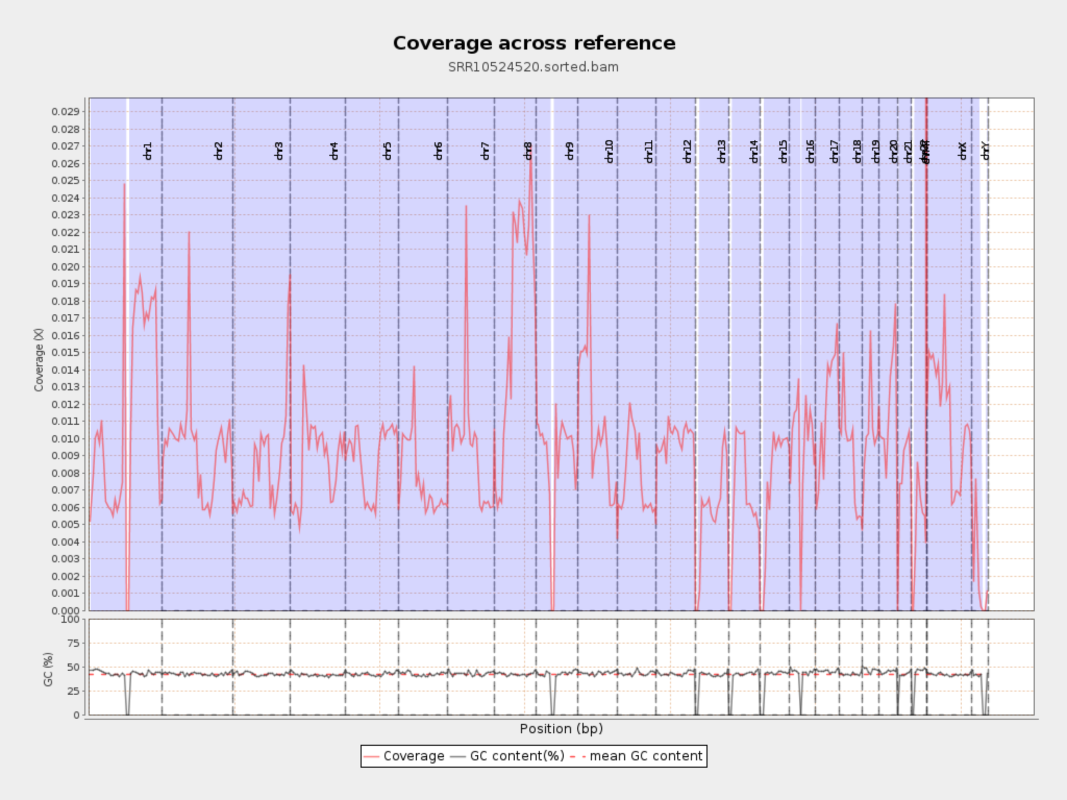
General error rate	0.55%
Mismatches	153,373
Insertions	2,627
Mapped reads with at least one insertion	0.52%
Deletions	4,867
Mapped reads with at least one deletion	0.95%
Homopolymer indels	38.83%

2.6. Chromosome stats

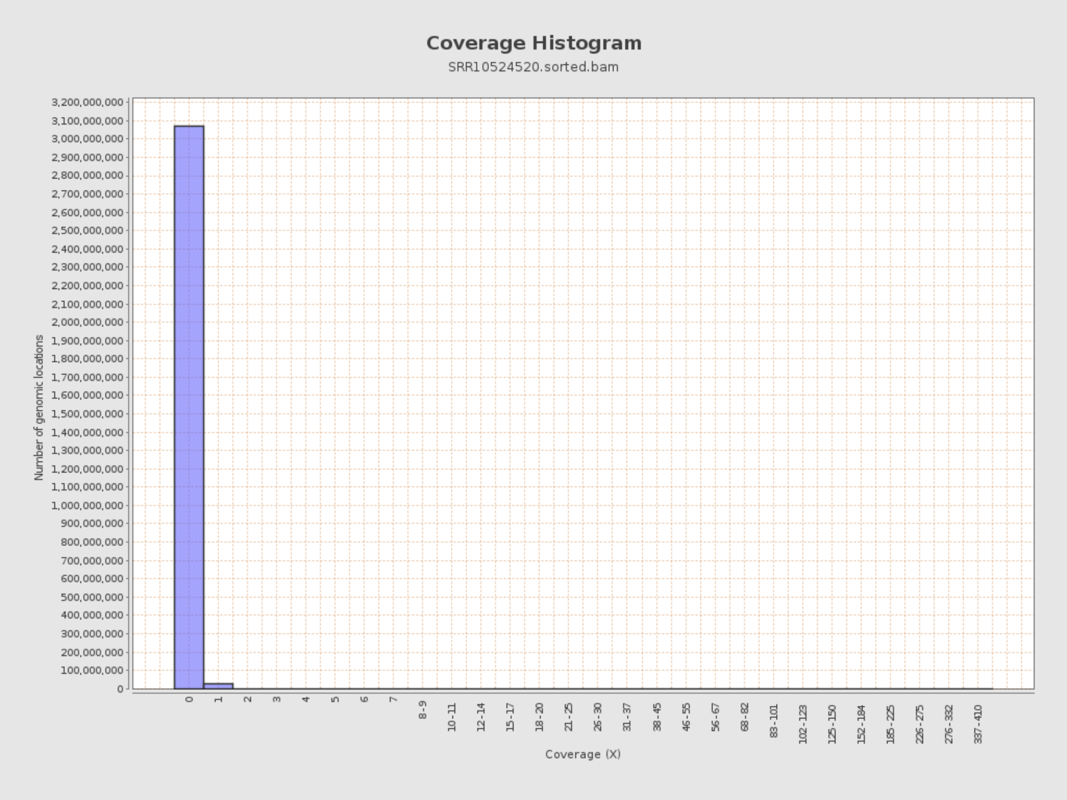
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2813699	0.0113	0.3221
chr2	243199373	2320673	0.0095	0.1431
chr3	198022430	1640330	0.0083	0.0937
chr4	191154276	1668954	0.0087	0.1025
chr5	180915260	1615981	0.0089	0.0979
chr6	171115067	1313256	0.0077	0.1036
chr7	159138663	1530706	0.0096	0.196

chr8	146364022	2490050	0.017	0.1577
chr9	141213431	1220312	0.0086	0.1225
chr10	135534747	1515811	0.0112	0.1416
chr11	135006516	1042705	0.0077	0.1189
chr12	133851895	1344824	0.01	0.1037
chr13	115169878	662557	0.0058	0.0781
chr14	107349540	709801	0.0066	0.0857
chr15	102531392	752310	0.0073	0.0894
chr16	90354753	874764	0.0097	0.1077
chr17	81195210	958833	0.0118	0.1155
chr18	78077248	707559	0.0091	0.2079
chr19	59128983	624082	0.0106	0.212
chr20	63025520	750934	0.0119	0.1132
chr21	48129895	380144	0.0079	0.096
chr22	51304566	237941	0.0046	0.0697
chrMT	16571	18262	1.102	1.1976
chrX	155270560	1762912	0.0114	0.1207
chrY	59373566	116091	0.002	0.077

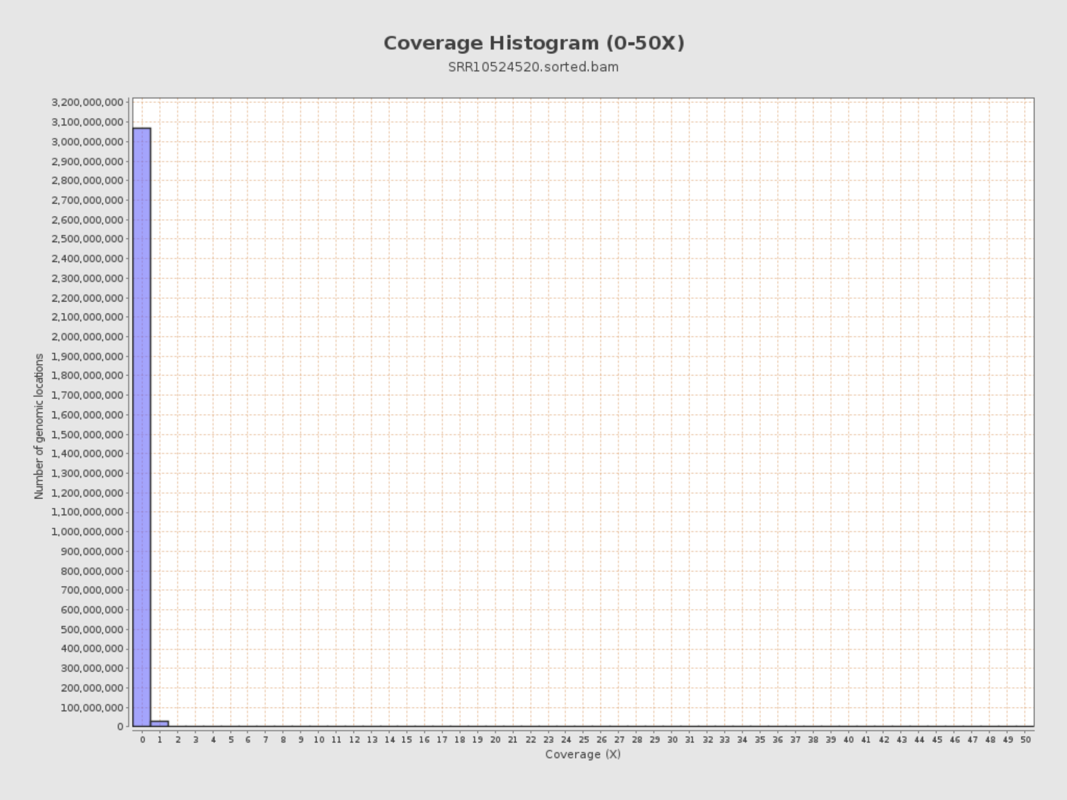
3. Results : Coverage across reference



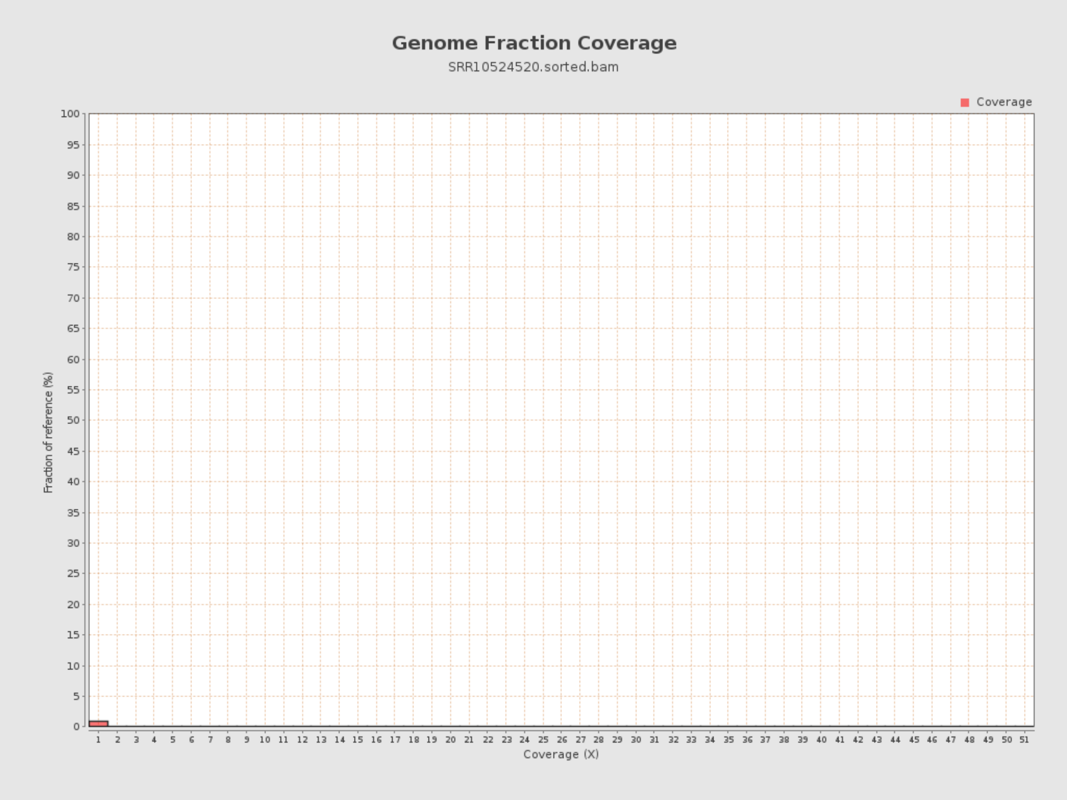
4. Results : Coverage Histogram



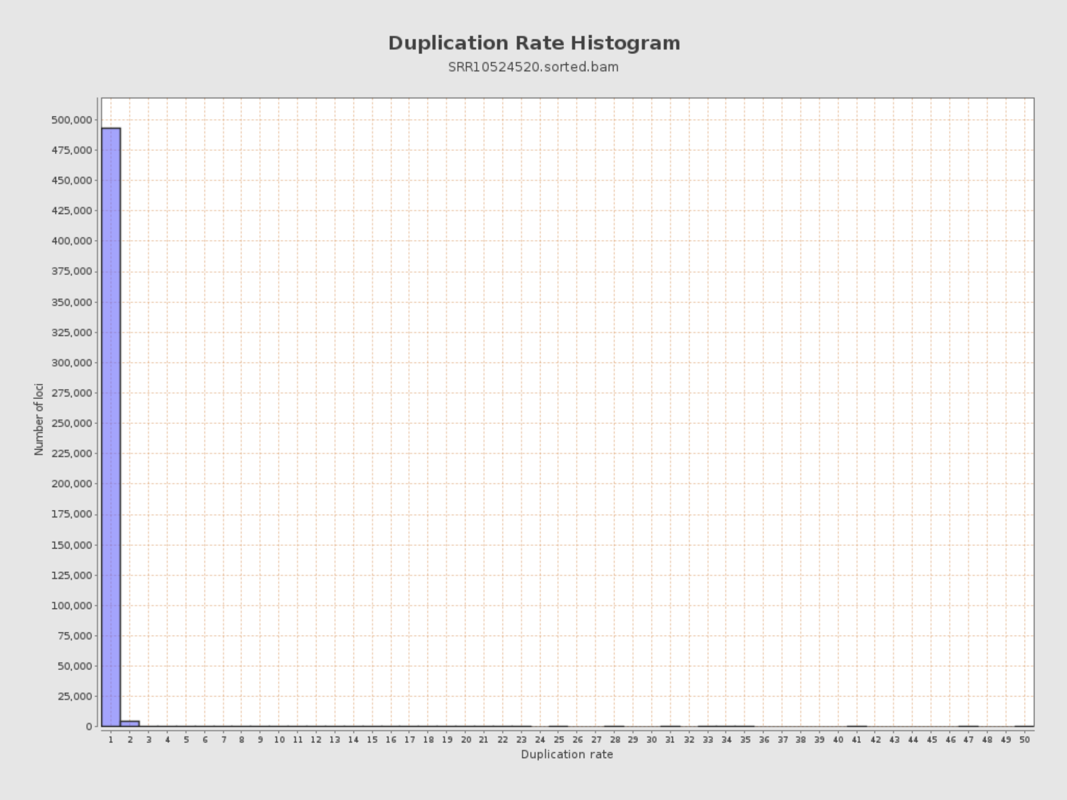
5. Results : Coverage Histogram (0-50X)



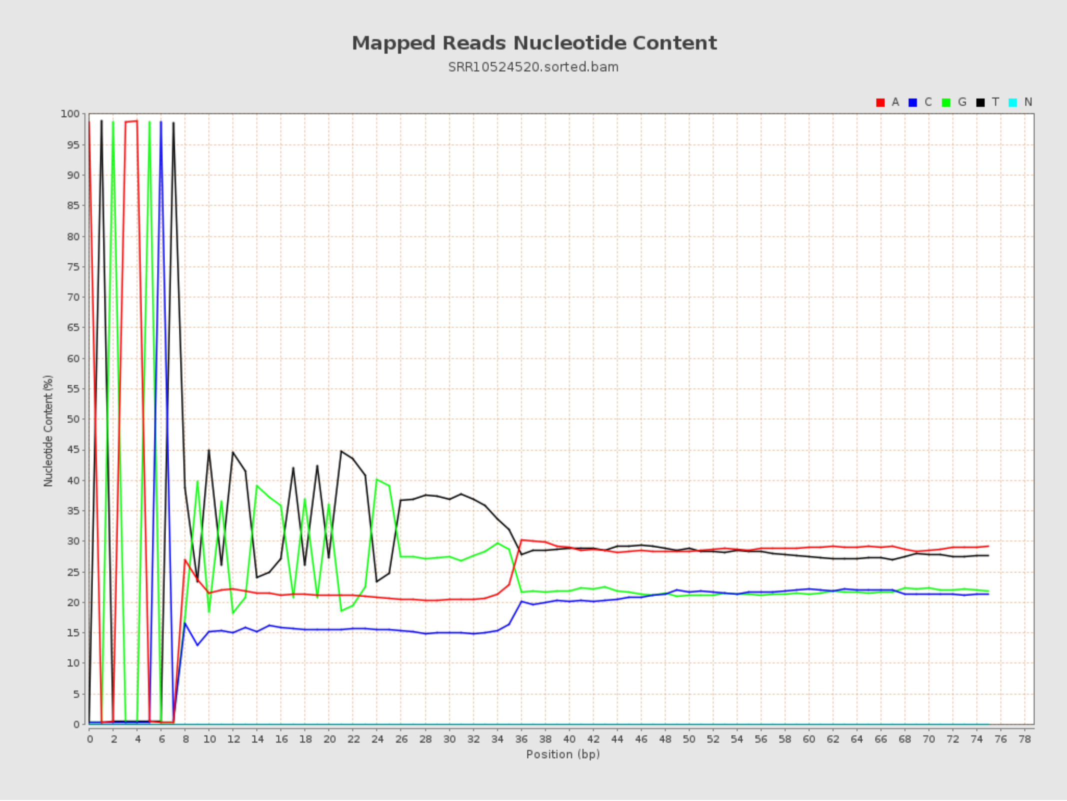
6. Results : Genome Fraction Coverage



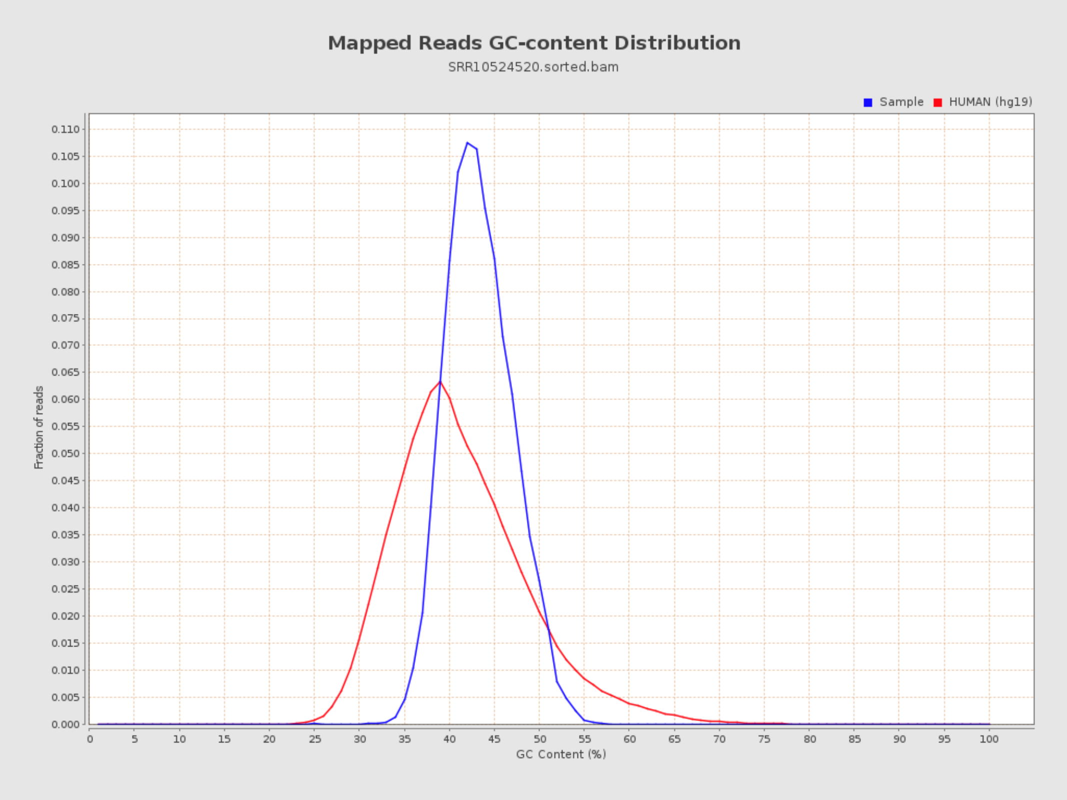
7. Results : Duplication Rate Histogram



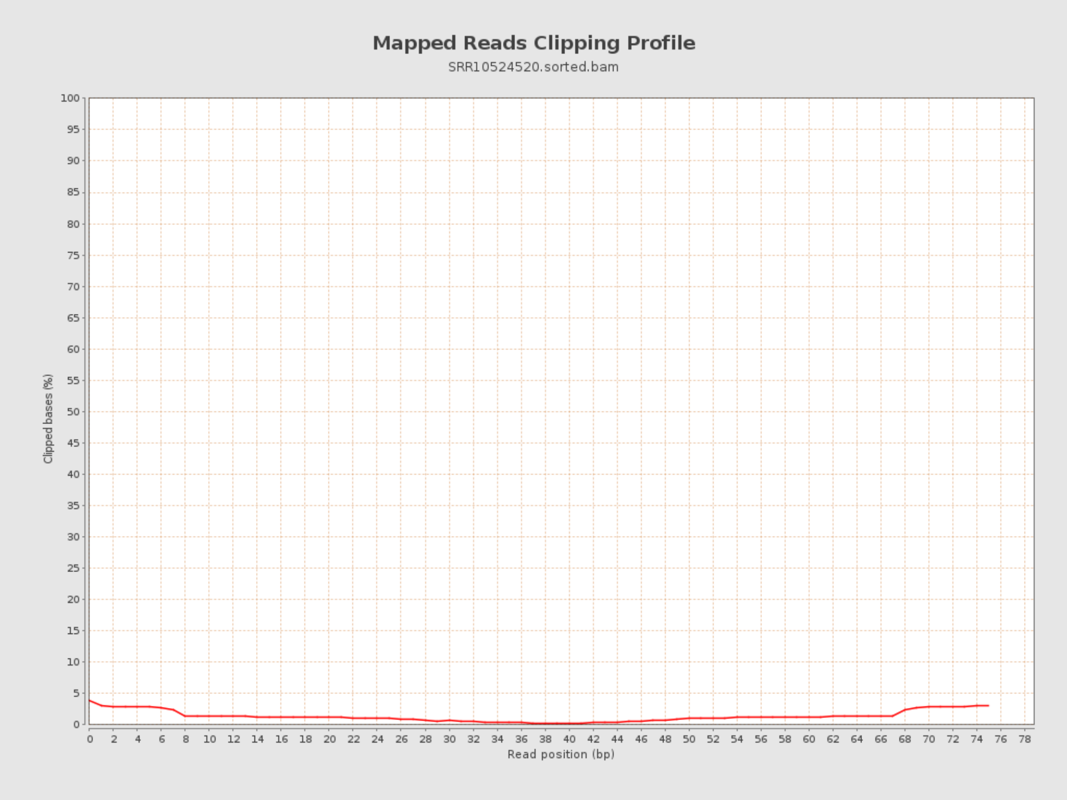
8. Results : Mapped Reads Nucleotide Content



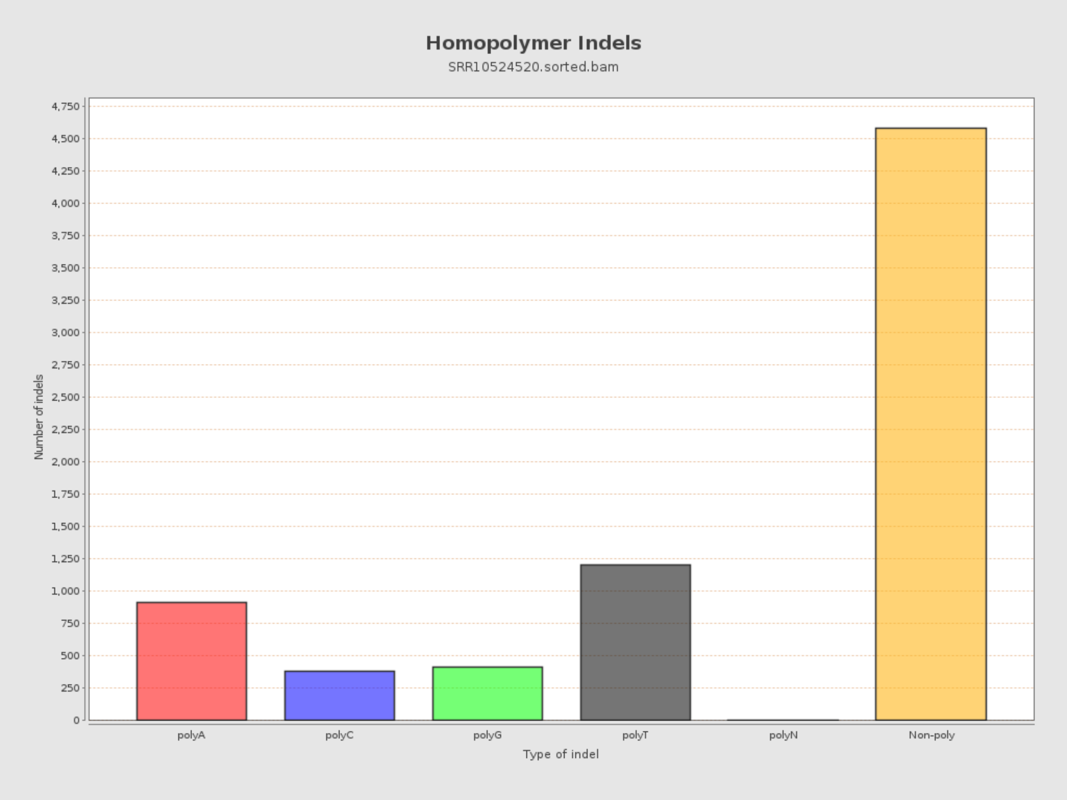
9. Results : Mapped Reads GC-content Distribution



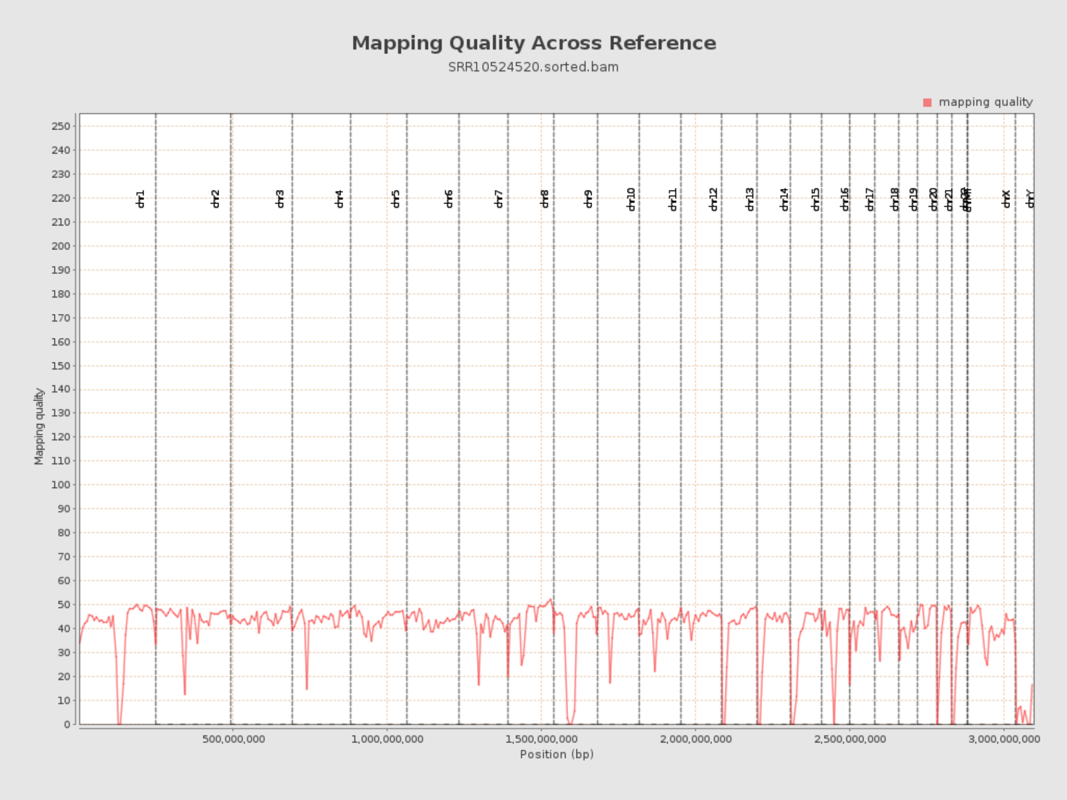
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram