Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 02:16:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524405.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_SRR10524405 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524405.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 02:16:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524405.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	857,216
Mapped reads	793,950 / 92.62%
Unmapped reads	63,266 / 7.38%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,995 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	21,996 / 2.57%
Duplication rate	2.13%
Clipped reads	796,746 / 92.95%

2.2. ACGT Content

Number/percentage of A's	11,153,002 / 24.02%
Number/percentage of C's	9,067,620 / 19.53%
Number/percentage of T's	14,414,575 / 31.05%
Number/percentage of G's	11,789,438 / 25.39%
Number/percentage of N's	5,883 / 0.01%
GC Percentage	44.92%

2.3. Coverage

Mean	0.015

Standard Deviation	0.1654

2.4. Mapping Quality

Mean Mapping Quality	45.93

2.5. Mismatches and indels

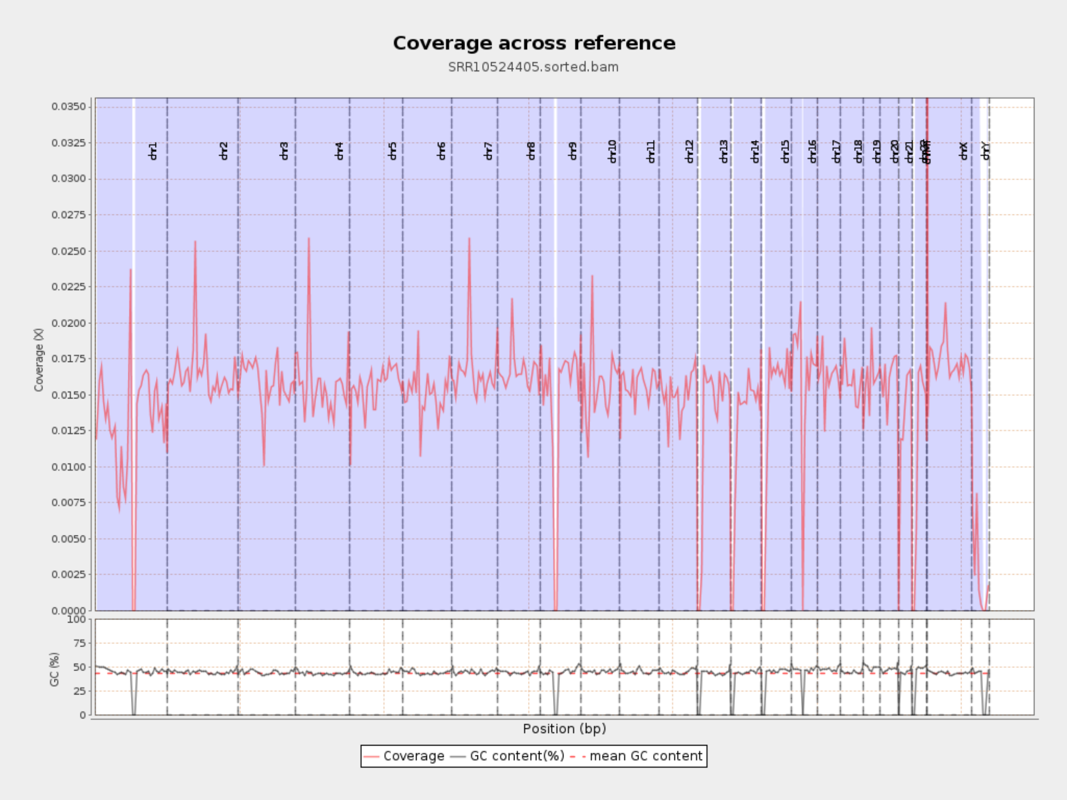
General error rate	0.49%
Mismatches	224,641
Insertions	2,653
Mapped reads with at least one insertion	0.33%
Deletions	7,992
Mapped reads with at least one deletion	1%
Homopolymer indels	43.35%

2.6. Chromosome stats

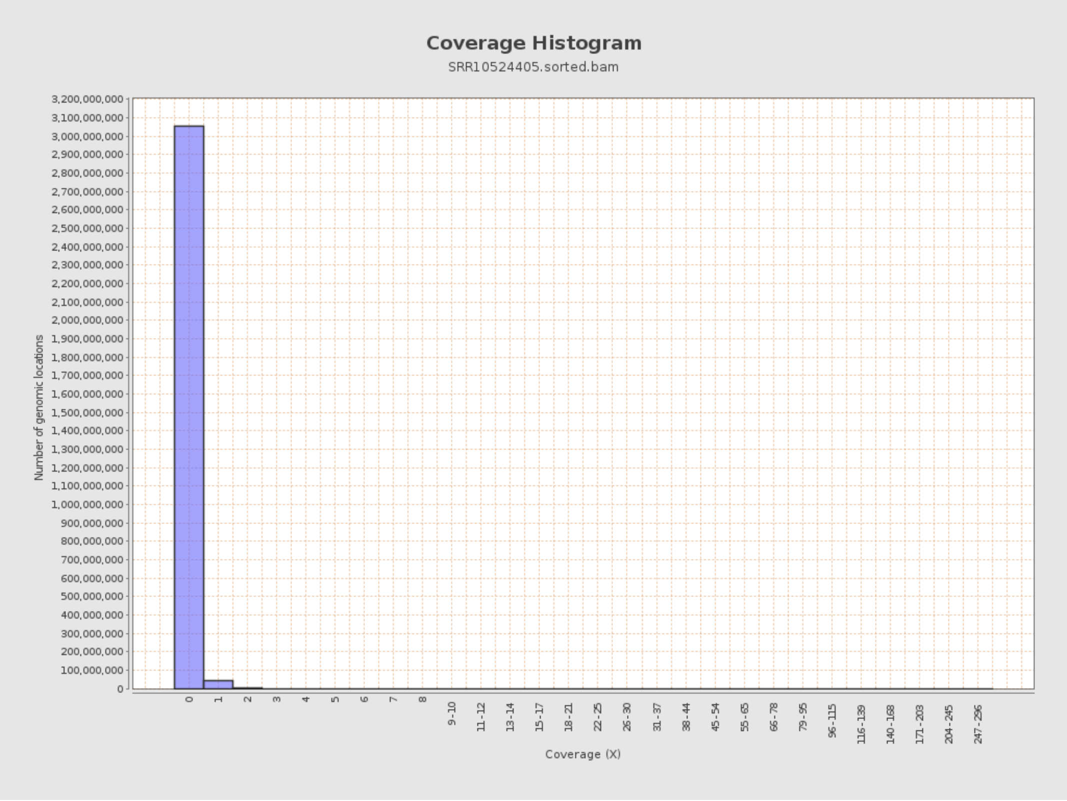
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3166272	0.0127	0.2705
chr2	243199373	4007105	0.0165	0.1898
chr3	198022430	3142664	0.0159	0.132
chr4	191154276	3030284	0.0159	0.1436
chr5	180915260	2845608	0.0157	0.1321
chr6	171115067	2591593	0.0151	0.137
chr7	159138663	2654060	0.0167	0.2103

chr8	146364022	2435741	0.0166	0.1625
chr9	141213431	2054115	0.0145	0.1507
chr10	135534747	2111203	0.0156	0.1545
chr11	135006516	2121242	0.0157	0.1557
chr12	133851895	2019790	0.0151	0.1309
chr13	115169878	1499109	0.013	0.1203
chr14	107349540	1347077	0.0125	0.1205
chr15	102531392	1409971	0.0138	0.123
chr16	90354753	1445516	0.016	0.1371
chr17	81195210	1317799	0.0162	0.1409
chr18	78077248	1243387	0.0159	0.2405
chr19	59128983	954142	0.0161	0.1921
chr20	63025520	1018012	0.0162	0.1362
chr21	48129895	625997	0.013	0.129
chr22	51304566	567007	0.0111	0.1106
chrMT	16571	4069	0.2455	0.5821
chrX	155270560	2686378	0.0173	0.1459
chrY	59373566	144765	0.0024	0.0732

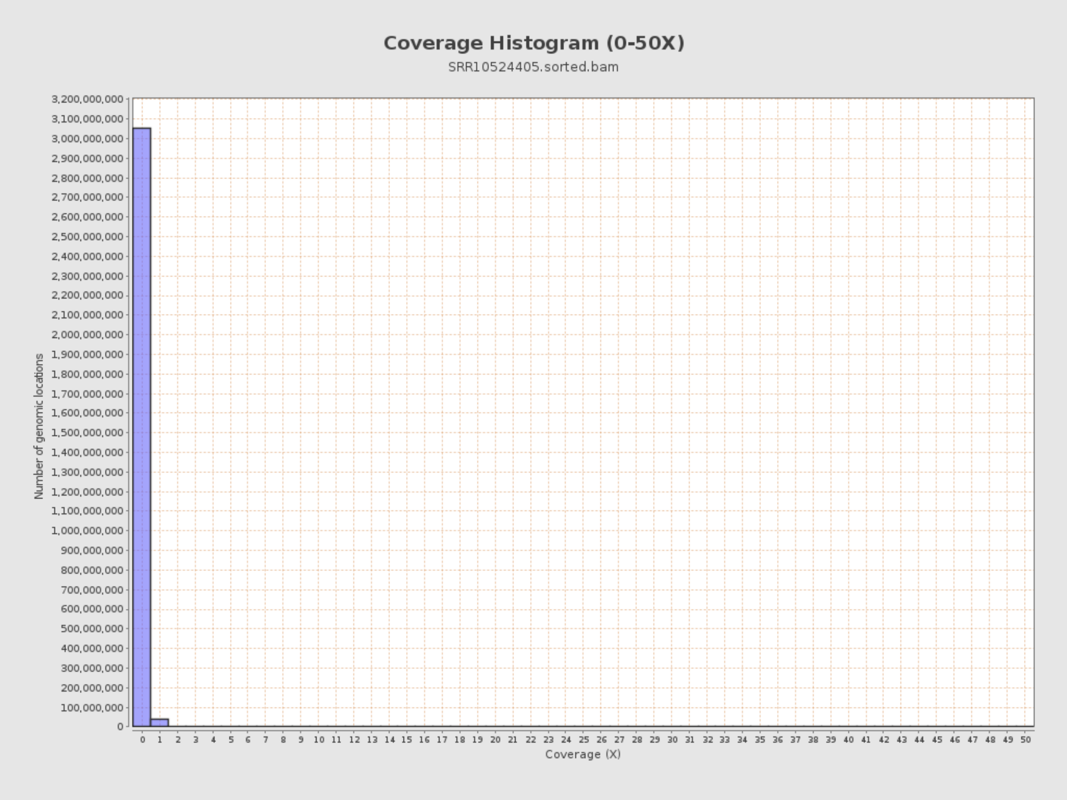
3. Results : Coverage across reference



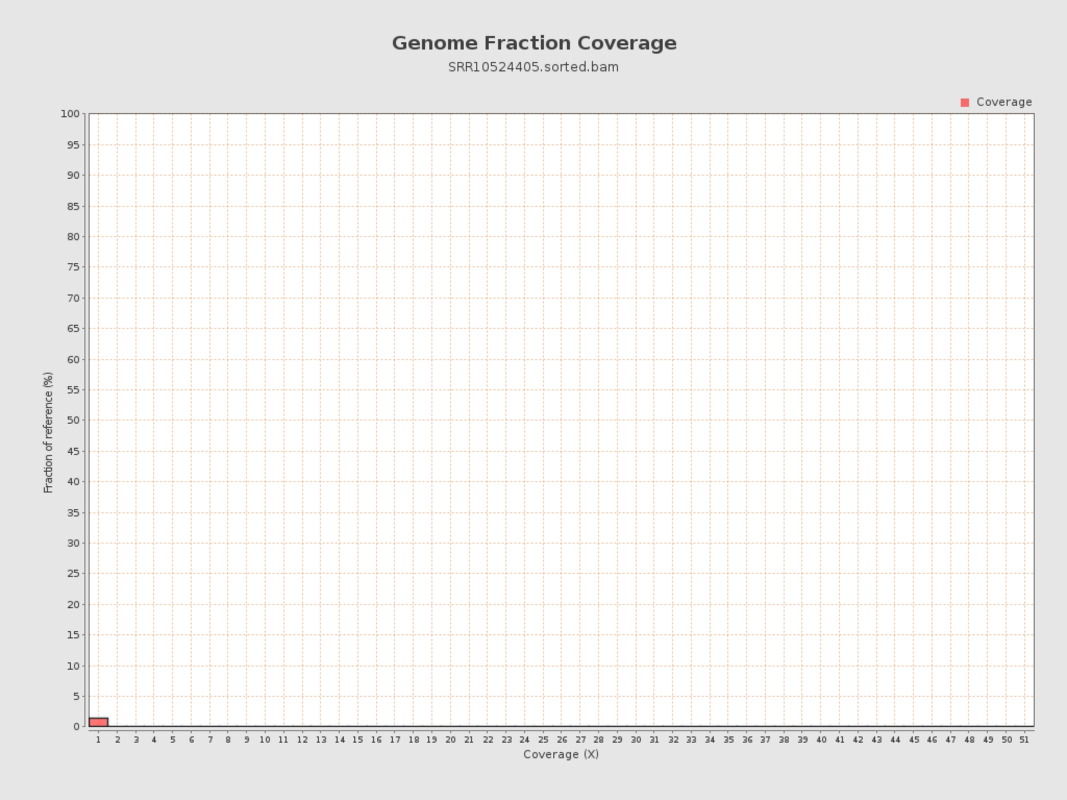
4. Results : Coverage Histogram



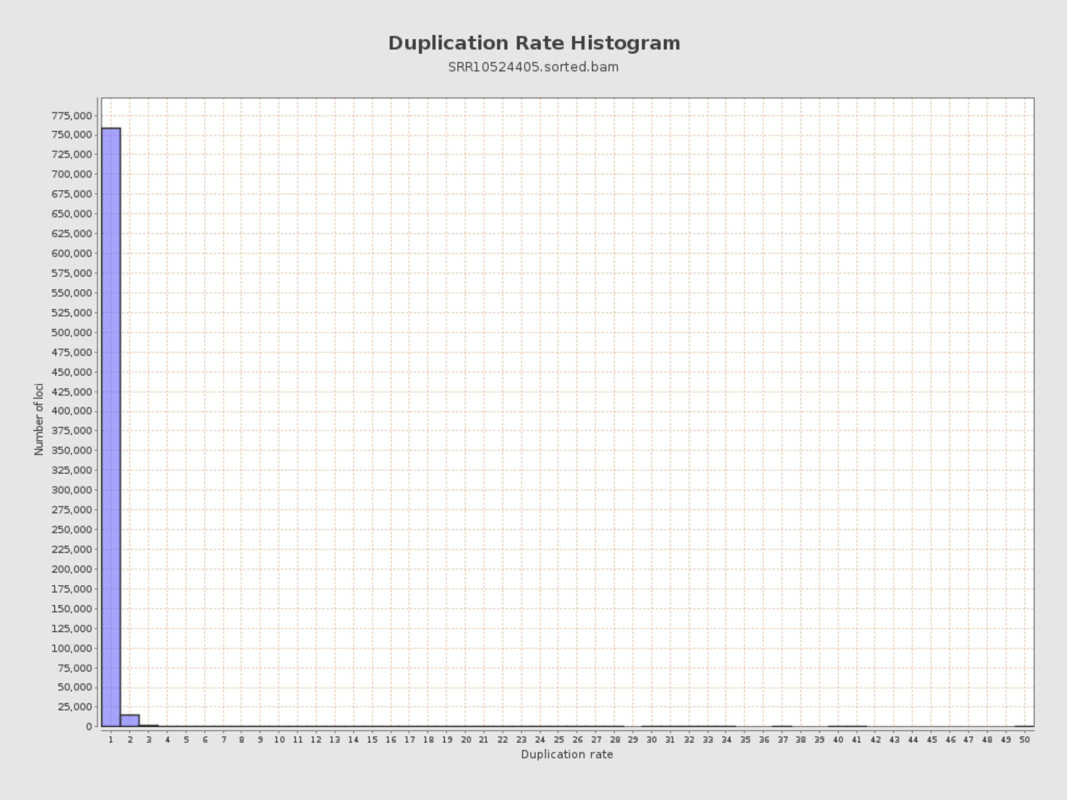
5. Results : Coverage Histogram (0-50X)



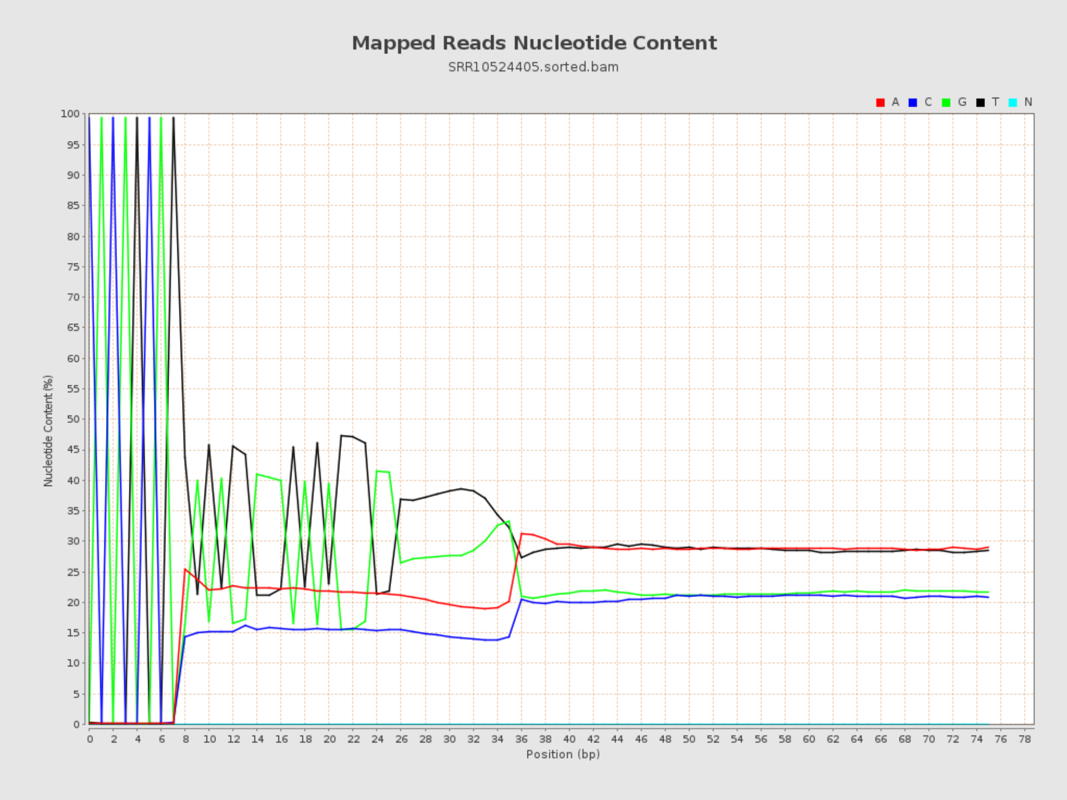
6. Results : Genome Fraction Coverage



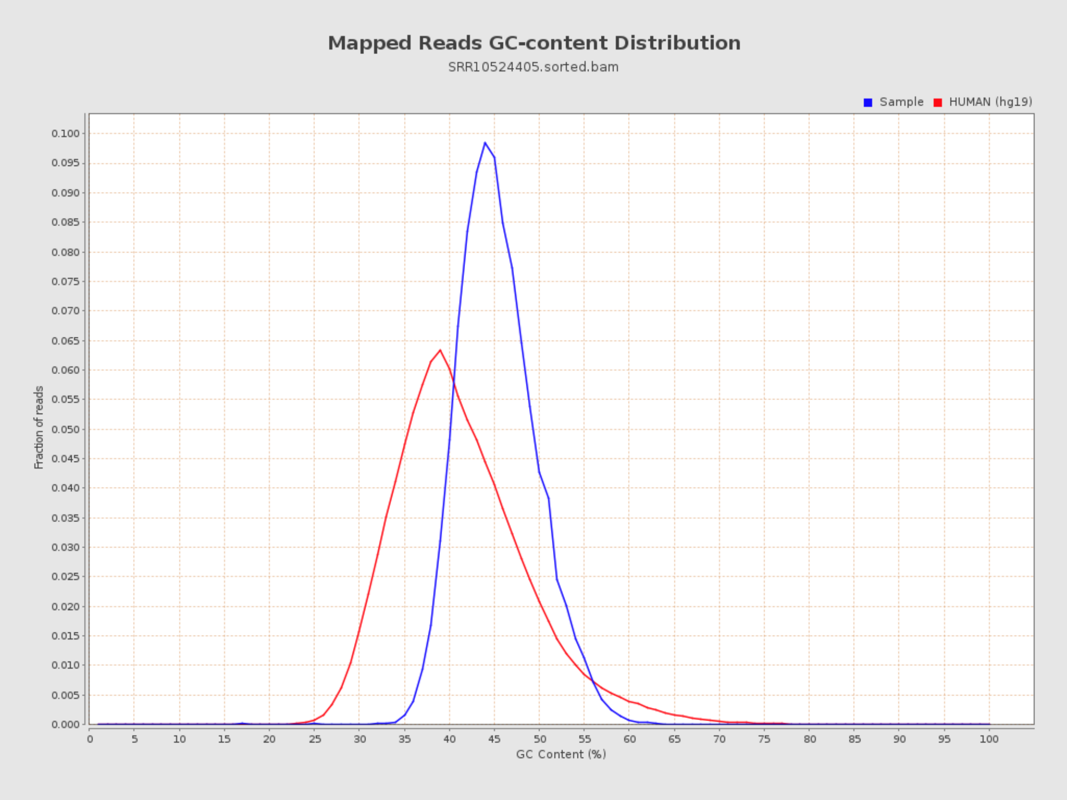
7. Results : Duplication Rate Histogram



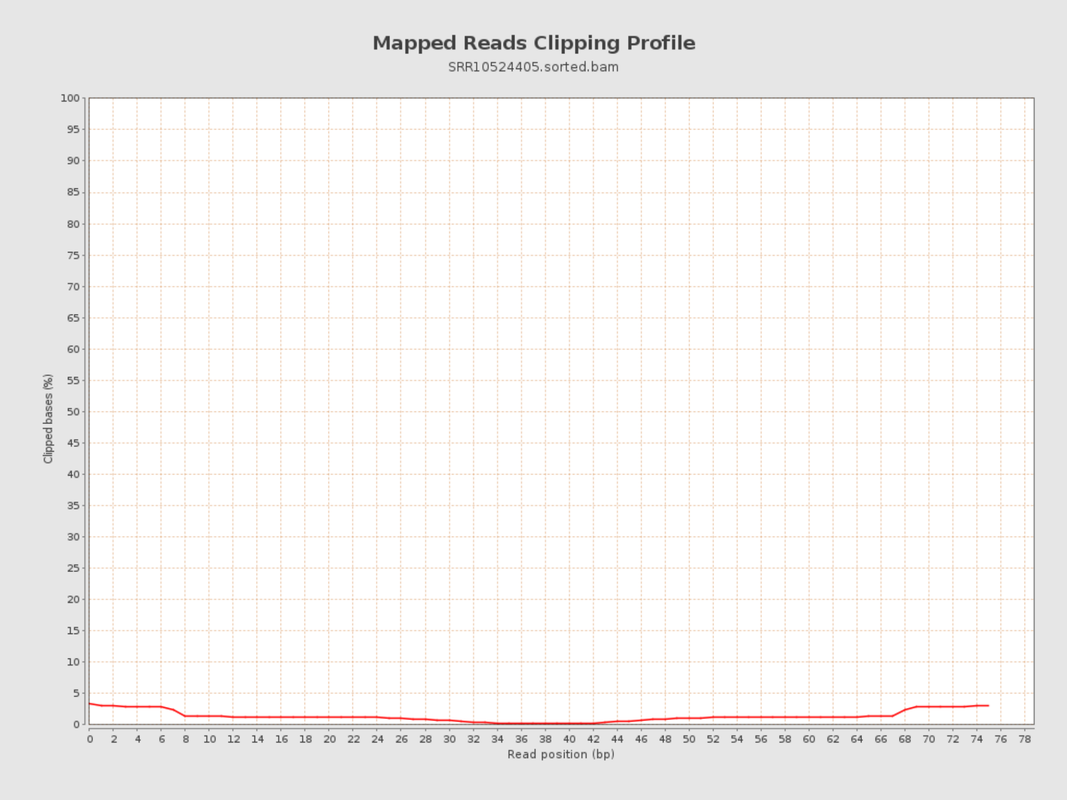
8. Results : Mapped Reads Nucleotide Content



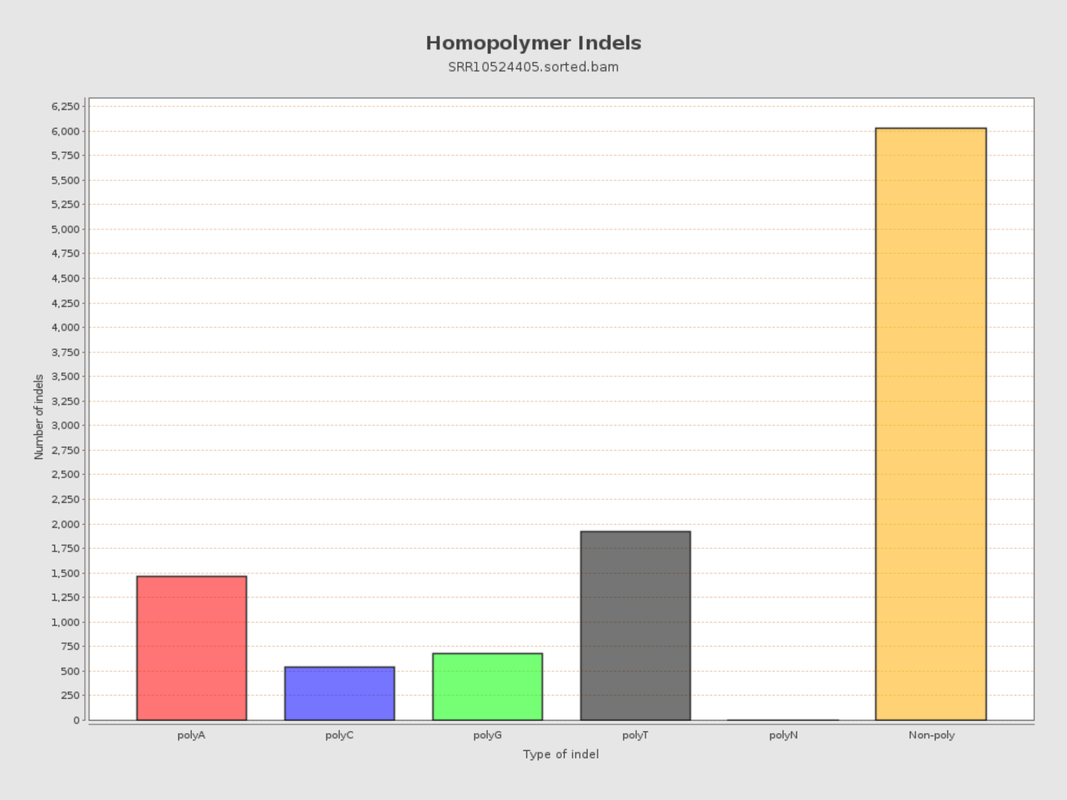
9. Results : Mapped Reads GC-content Distribution



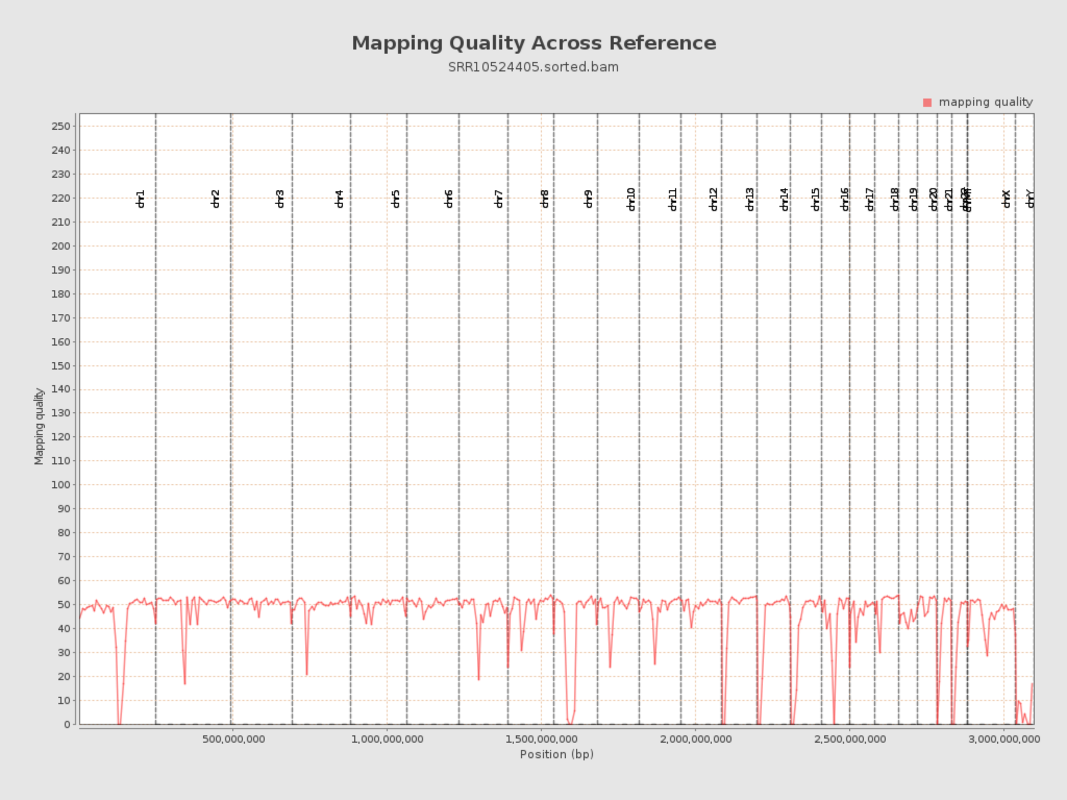
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram