Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 06:58:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524508.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_SRR10524508 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524508.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 06:58:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524508.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	807,491
Mapped reads	734,985 / 91.02%
Unmapped reads	72,506 / 8.98%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,609 / 0.2%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	33,047 / 4.09%
Duplication rate	3.65%
Clipped reads	734,114 / 90.91%

2.2. ACGT Content

Number/percentage of A's	10,424,789 / 24.99%
Number/percentage of C's	7,589,887 / 18.19%
Number/percentage of T's	13,620,458 / 32.65%
Number/percentage of G's	10,085,532 / 24.17%
Number/percentage of N's	852 / 0%
GC Percentage	42.37%

2.3. Coverage

Mean	0.0135

Standard Deviation	0.1578

2.4. Mapping Quality

Mean Mapping Quality	44.65

2.5. Mismatches and indels

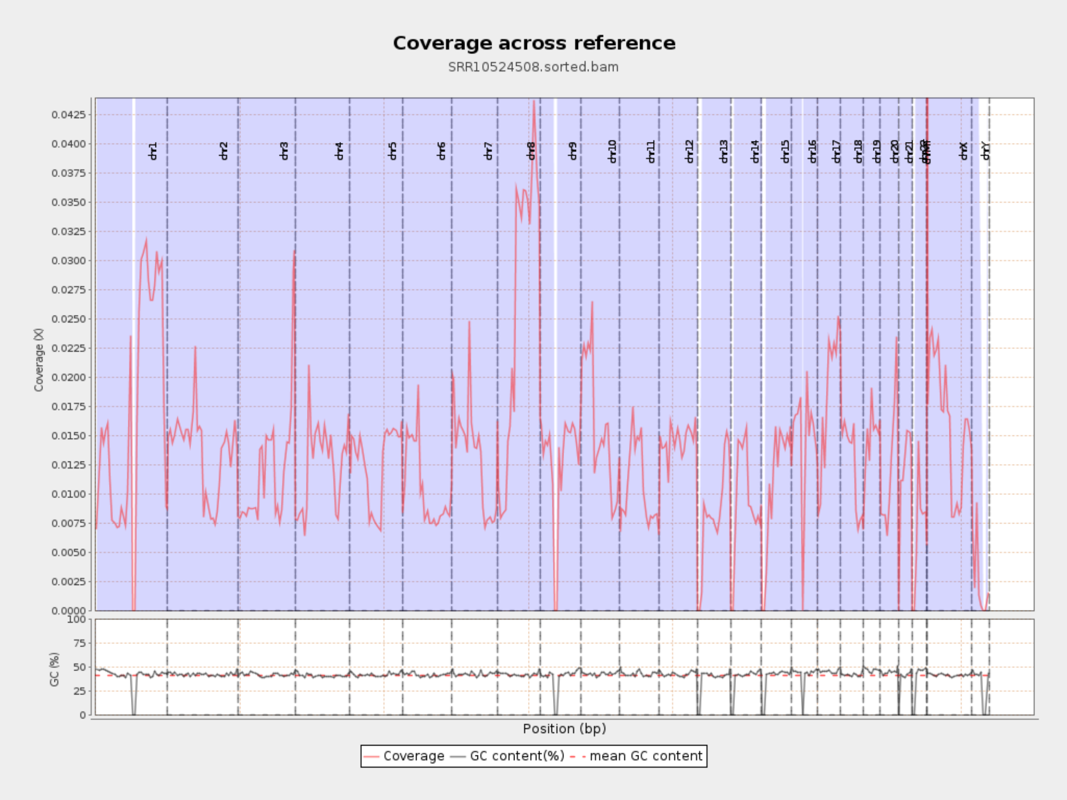
General error rate	0.5%
Mismatches	200,081
Insertions	3,036
Mapped reads with at least one insertion	0.41%
Deletions	7,869
Mapped reads with at least one deletion	1.06%
Homopolymer indels	43.37%

2.6. Chromosome stats

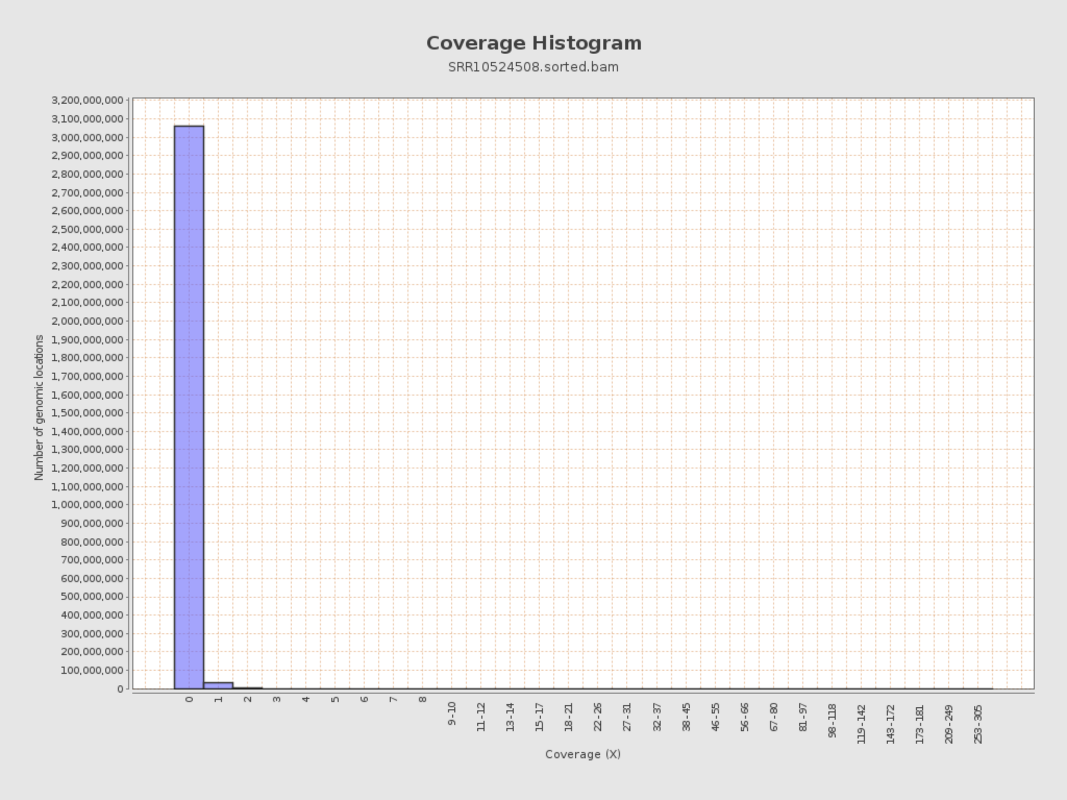
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4180963	0.0168	0.2455
chr2	243199373	3320272	0.0137	0.1875
chr3	198022430	2345218	0.0118	0.1201
chr4	191154276	2386573	0.0125	0.1308
chr5	180915260	2285193	0.0126	0.1234
chr6	171115067	1790474	0.0105	0.1292
chr7	159138663	2125041	0.0134	0.1922

chr8	146364022	3853603	0.0263	0.1935
chr9	141213431	1787751	0.0127	0.1376
chr10	135534747	2174242	0.016	0.1707
chr11	135006516	1455756	0.0108	0.1391
chr12	133851895	1949292	0.0146	0.1326
chr13	115169878	943663	0.0082	0.0997
chr14	107349540	1003666	0.0093	0.1075
chr15	102531392	1101496	0.0107	0.1158
chr16	90354753	1310671	0.0145	0.1362
chr17	81195210	1480505	0.0182	0.1514
chr18	78077248	981034	0.0126	0.2051
chr19	59128983	875239	0.0148	0.192
chr20	63025520	771979	0.0122	0.1237
chr21	48129895	580048	0.0121	0.1269
chr22	51304566	356284	0.0069	0.0918
chrMT	16571	4930	0.2975	0.6149
chrX	155270560	2523661	0.0163	0.1476
chrY	59373566	147368	0.0025	0.0842

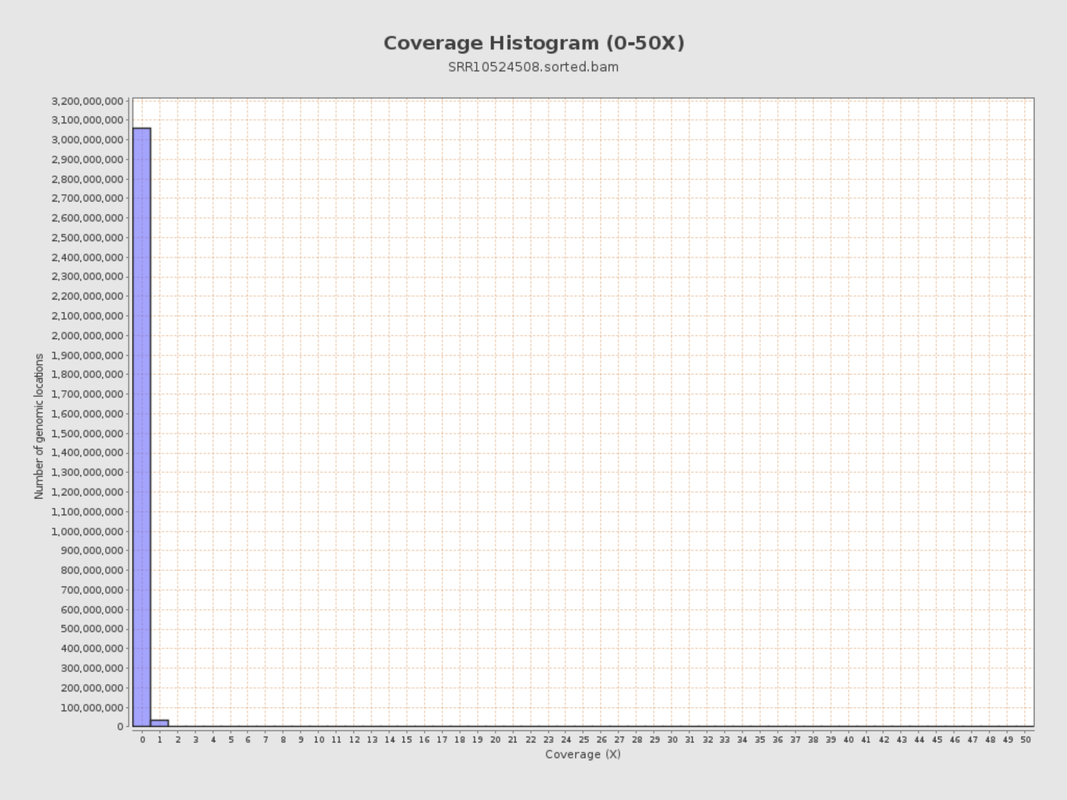
3. Results : Coverage across reference



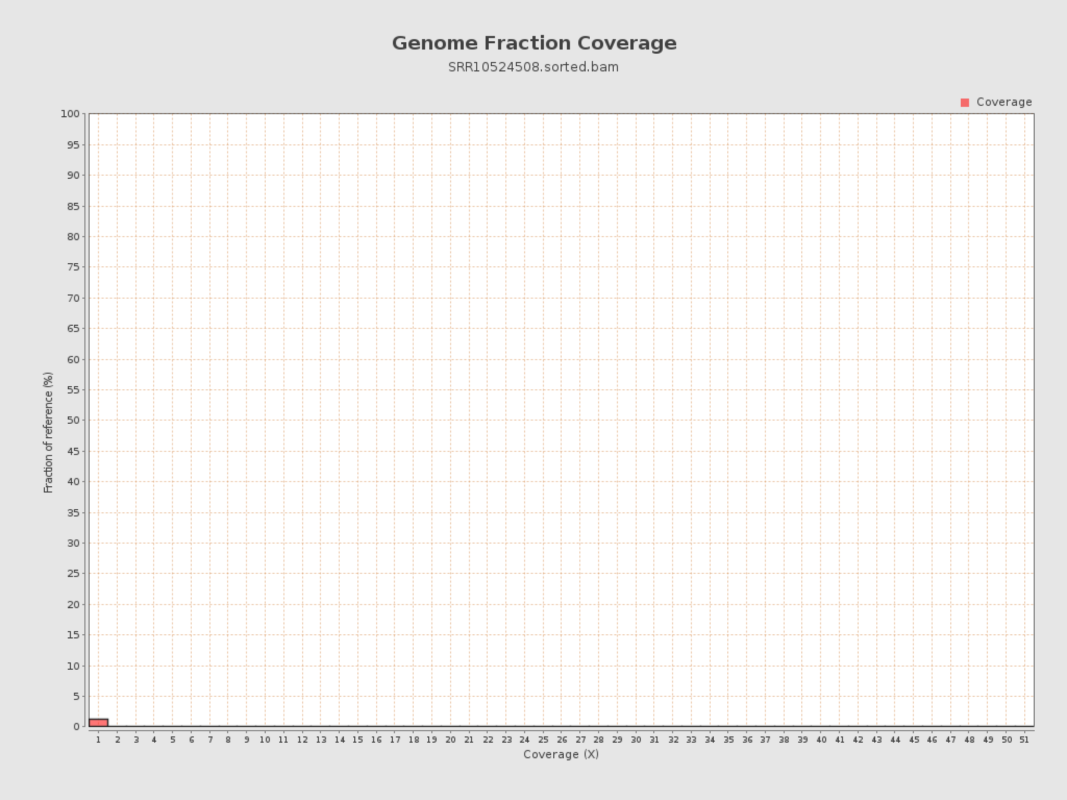
4. Results : Coverage Histogram



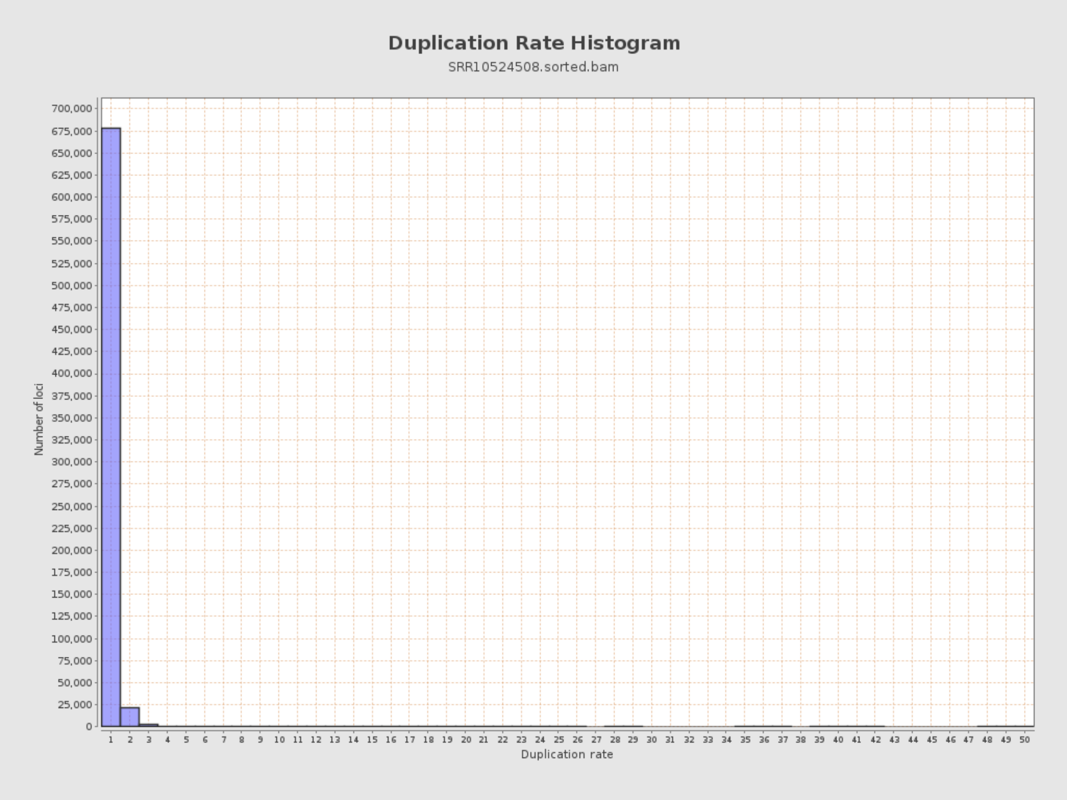
5. Results : Coverage Histogram (0-50X)



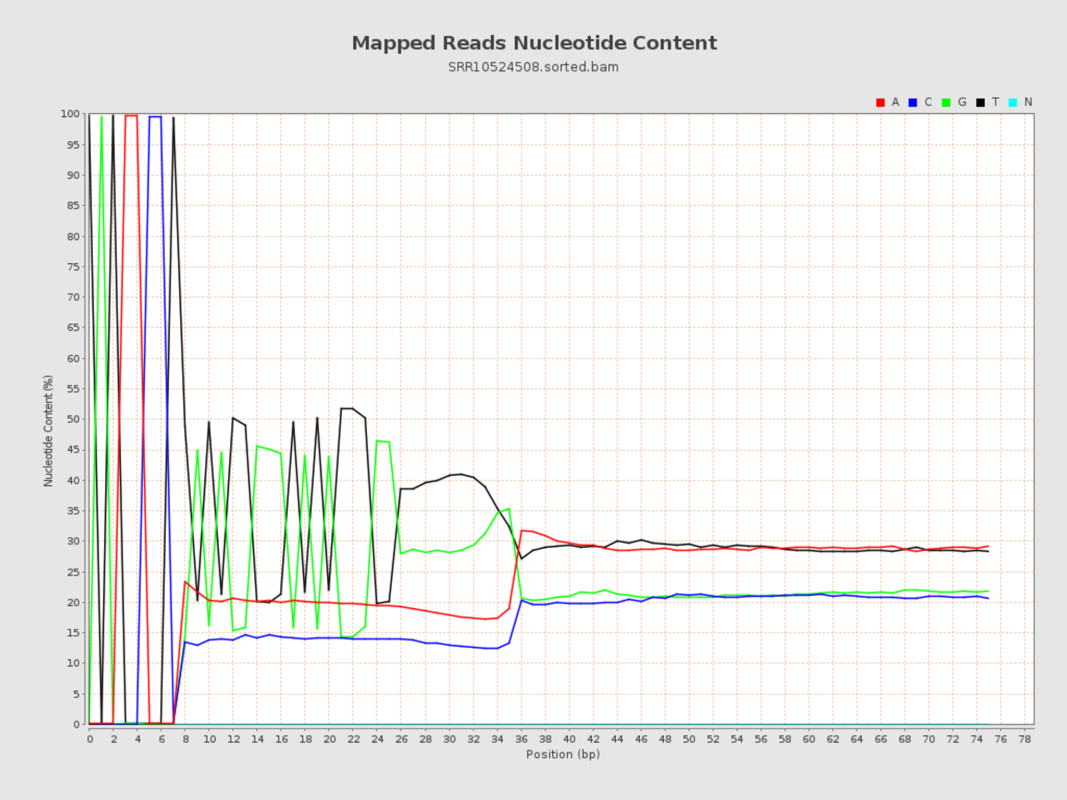
6. Results : Genome Fraction Coverage



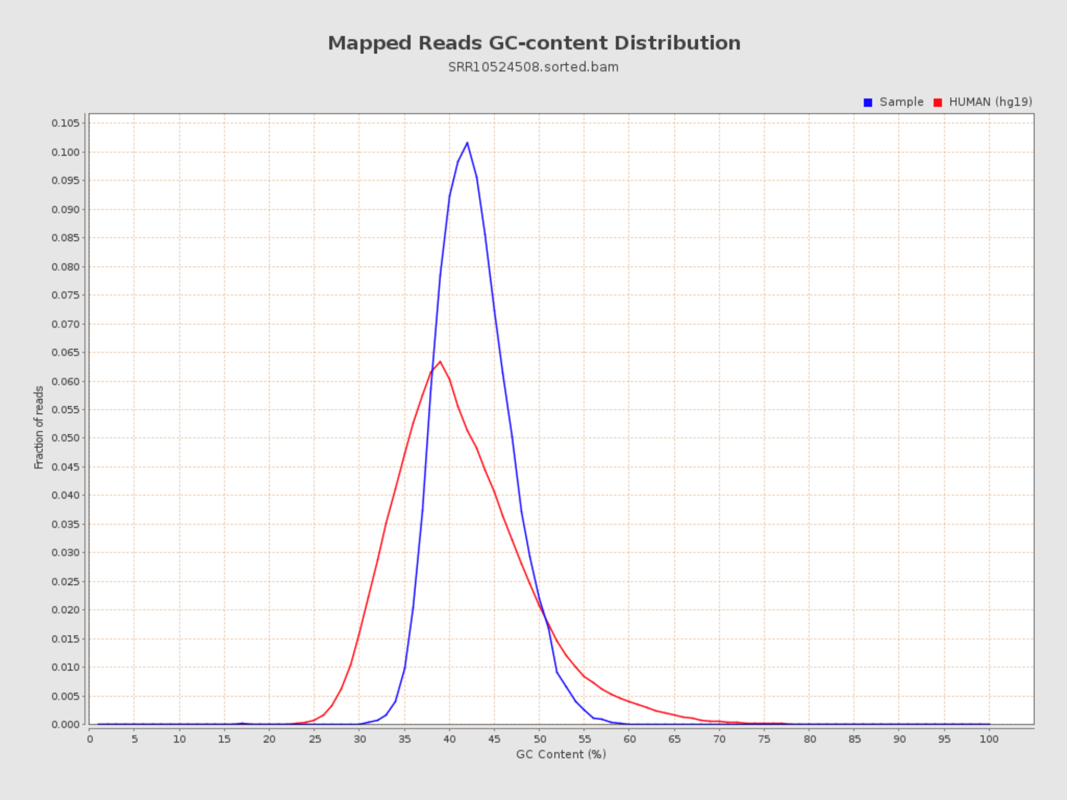
7. Results : Duplication Rate Histogram



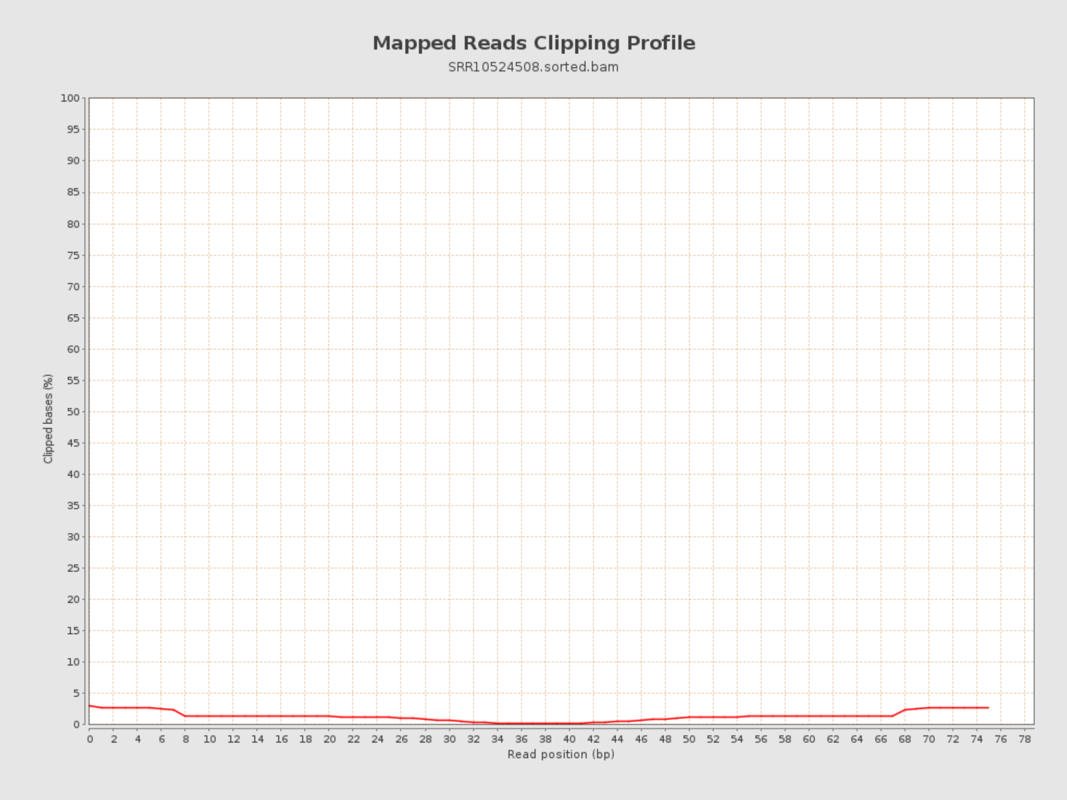
8. Results : Mapped Reads Nucleotide Content



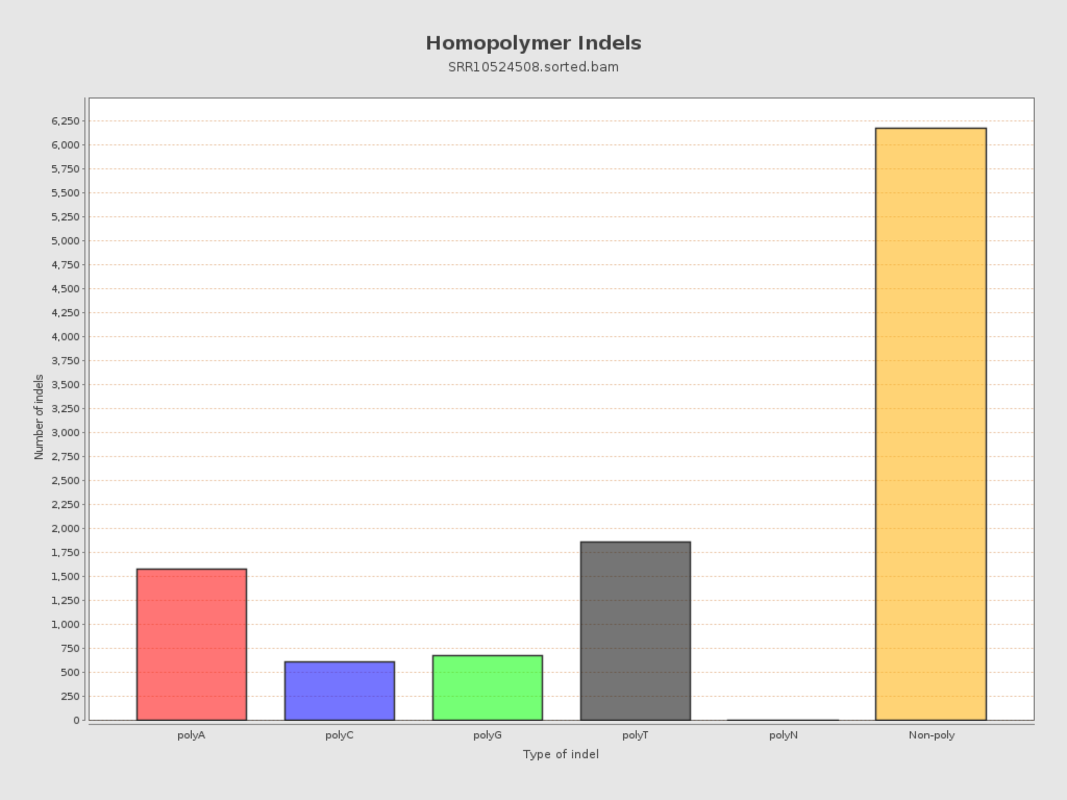
9. Results : Mapped Reads GC-content Distribution



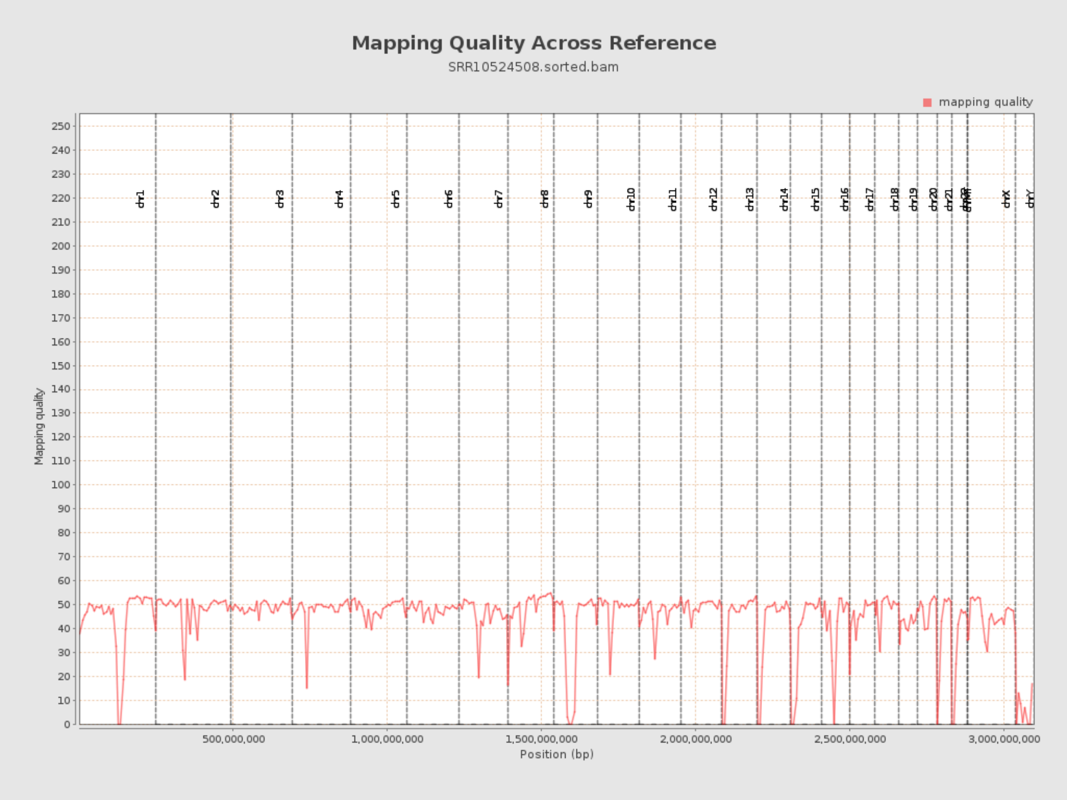
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram