Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 02:24:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524904.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_SRR10524904 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524904.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 02:24:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524904.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,208,112
Mapped reads	1,106,732 / 91.61%
Unmapped reads	101,380 / 8.39%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,199 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	53,756 / 4.45%
Duplication rate	3.85%
Clipped reads	1,108,008 / 91.71%

2.2. ACGT Content

Number/percentage of A's	16,168,276 / 25.23%
Number/percentage of C's	12,464,541 / 19.45%
Number/percentage of T's	20,205,845 / 31.53%
Number/percentage of G's	15,239,279 / 23.78%
Number/percentage of N's	543 / 0%
GC Percentage	43.23%

2.3. Coverage

Mean	0.0207

Standard Deviation	0.2139

2.4. Mapping Quality

Mean Mapping Quality	44.66

2.5. Mismatches and indels

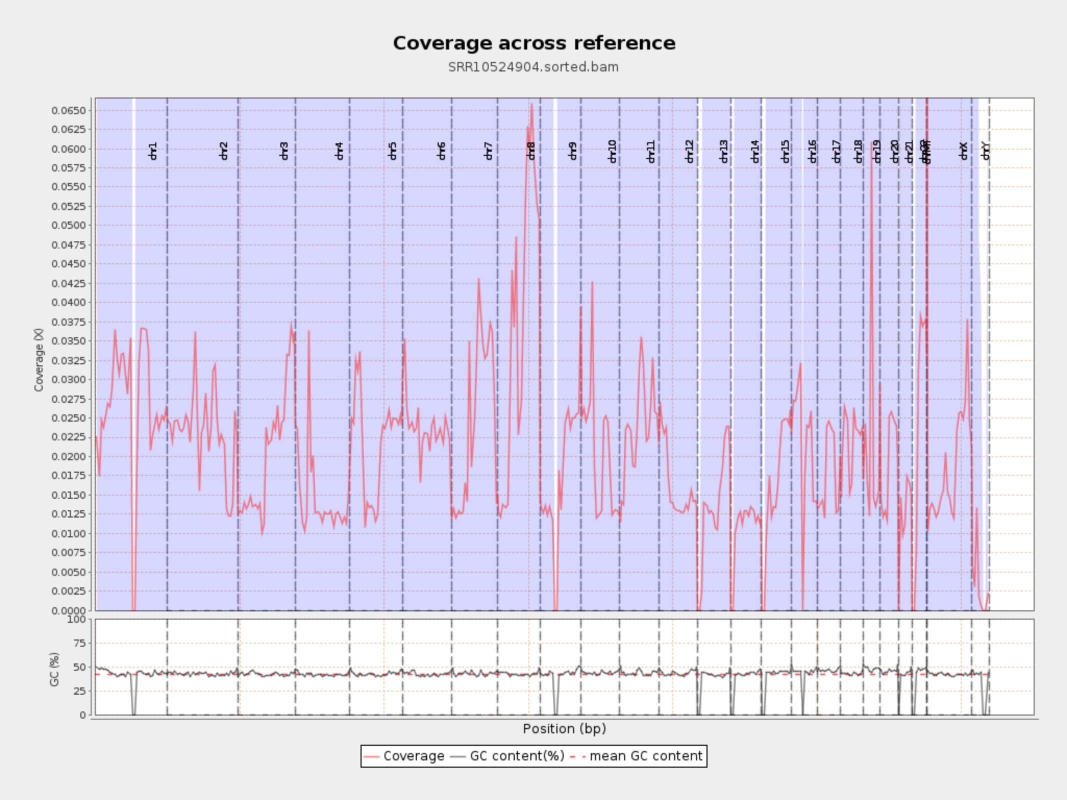
General error rate	0.53%
Mismatches	330,567
Insertions	4,214
Mapped reads with at least one insertion	0.38%
Deletions	12,237
Mapped reads with at least one deletion	1.1%
Homopolymer indels	42.5%

2.6. Chromosome stats

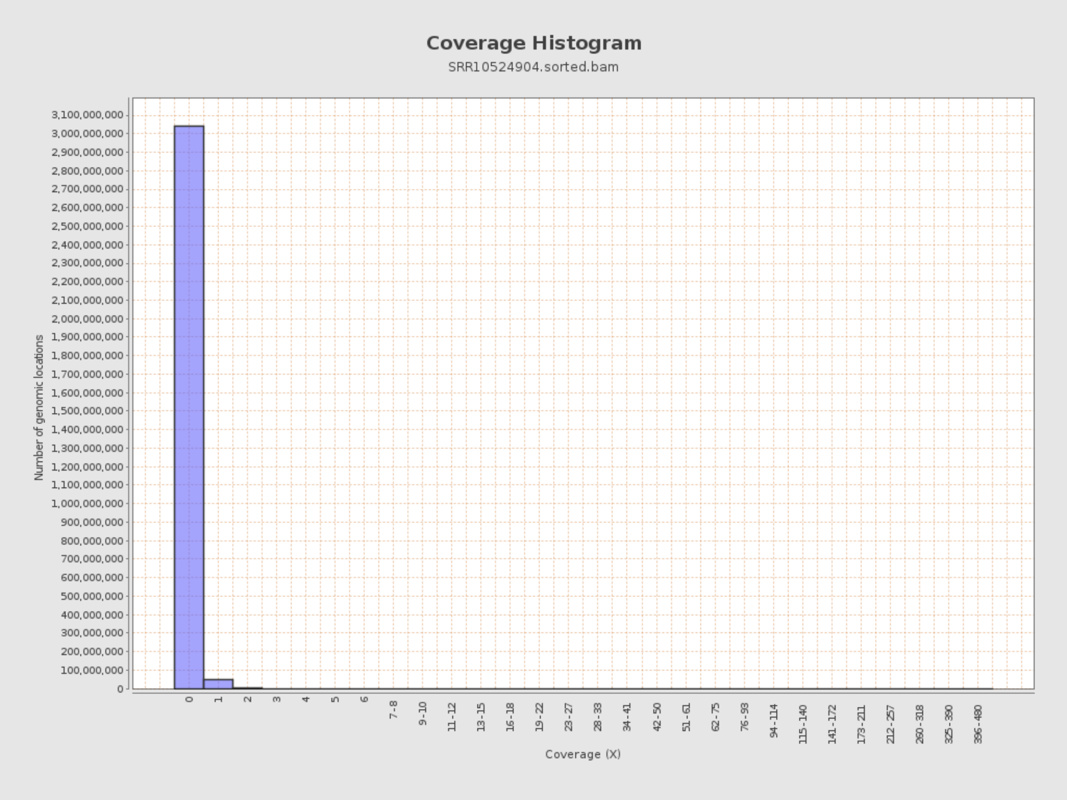
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6576850	0.0264	0.3657
chr2	243199373	5638181	0.0232	0.2667
chr3	198022430	4037398	0.0204	0.1581
chr4	191154276	2821630	0.0148	0.159
chr5	180915260	3959495	0.0219	0.1628
chr6	171115067	4062830	0.0237	0.177
chr7	159138663	3949464	0.0248	0.2592

chr8	146364022	5515426	0.0377	0.2892
chr9	141213431	2401114	0.017	0.1726
chr10	135534747	2817505	0.0208	0.2297
chr11	135006516	3250991	0.0241	0.1916
chr12	133851895	2181304	0.0163	0.1442
chr13	115169878	1543357	0.0134	0.1273
chr14	107349540	1141097	0.0106	0.118
chr15	102531392	1637763	0.016	0.1389
chr16	90354753	1937132	0.0214	0.1682
chr17	81195210	1428180	0.0176	0.1507
chr18	78077248	1713338	0.0219	0.2663
chr19	59128983	1331671	0.0225	0.2764
chr20	63025520	1202373	0.0191	0.1567
chr21	48129895	610008	0.0127	0.1451
chr22	51304566	1245681	0.0243	0.174
chrMT	16571	1641	0.099	0.3365
chrX	155270560	2900549	0.0187	0.1611
chrY	59373566	194054	0.0033	0.1268

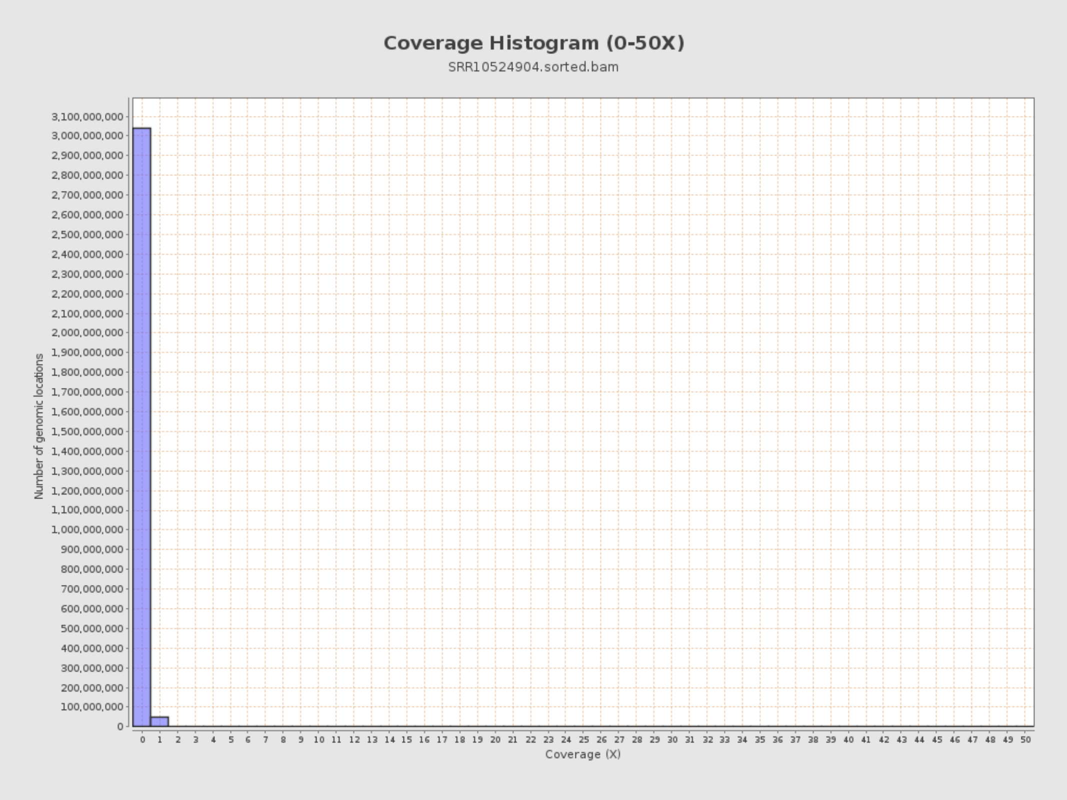
3. Results : Coverage across reference



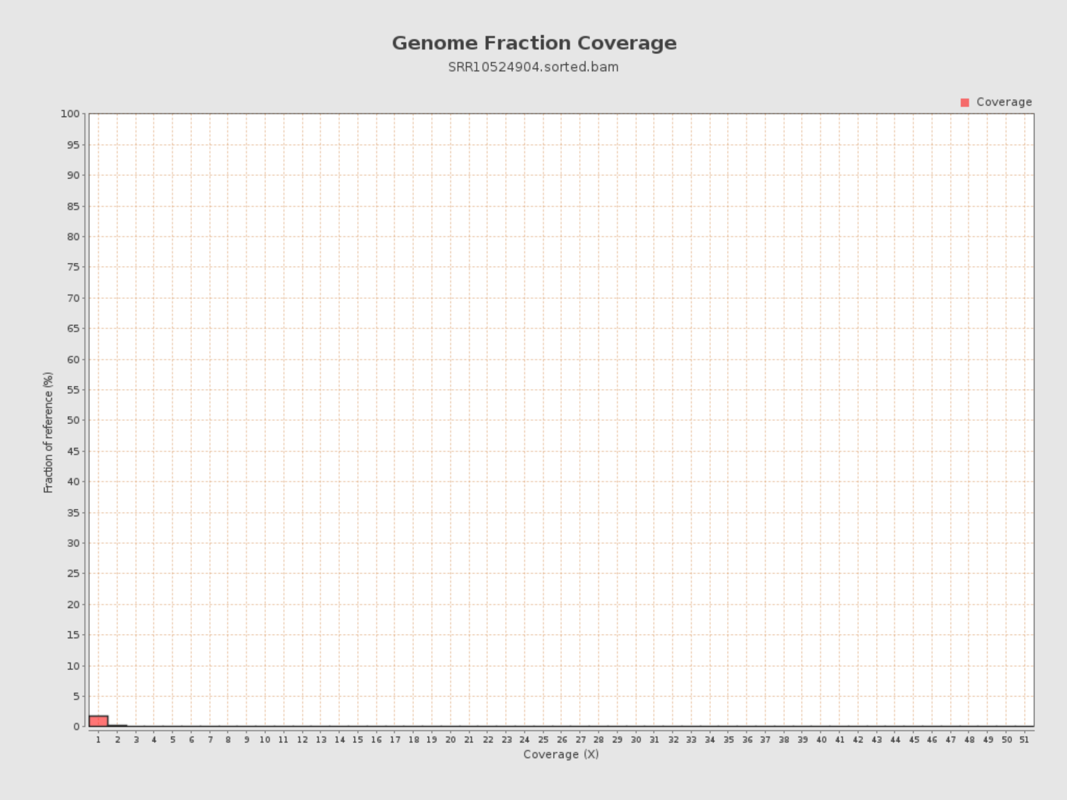
4. Results : Coverage Histogram



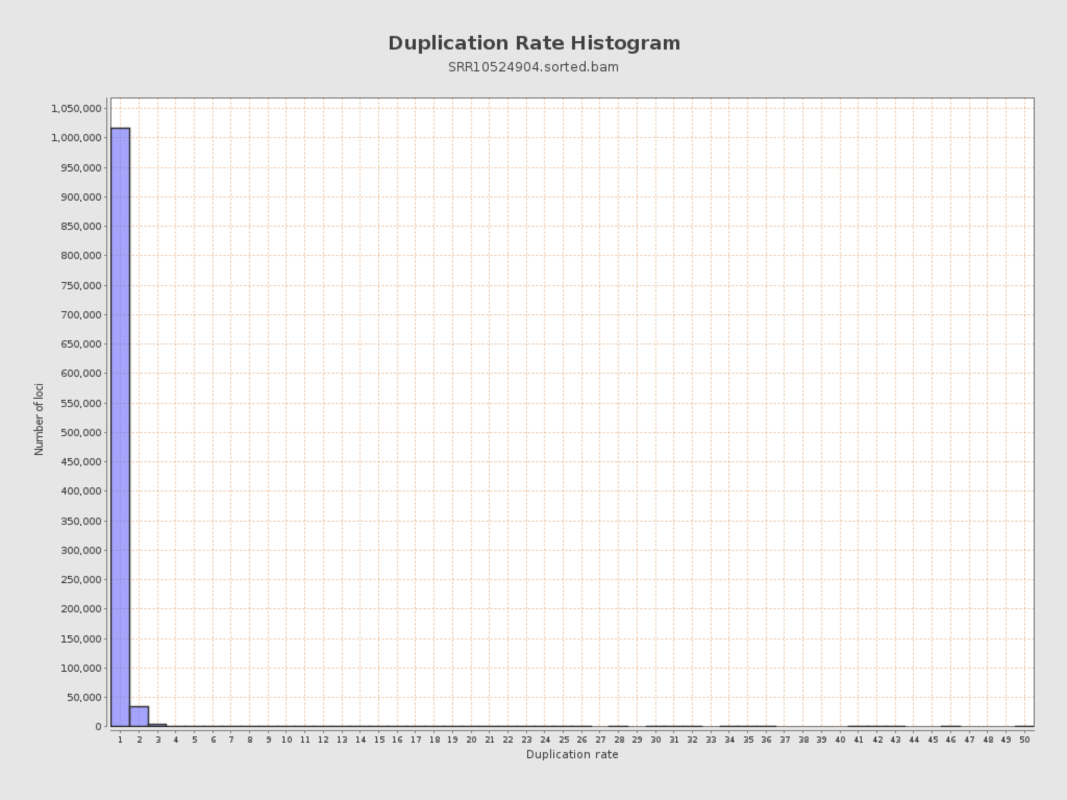
5. Results : Coverage Histogram (0-50X)



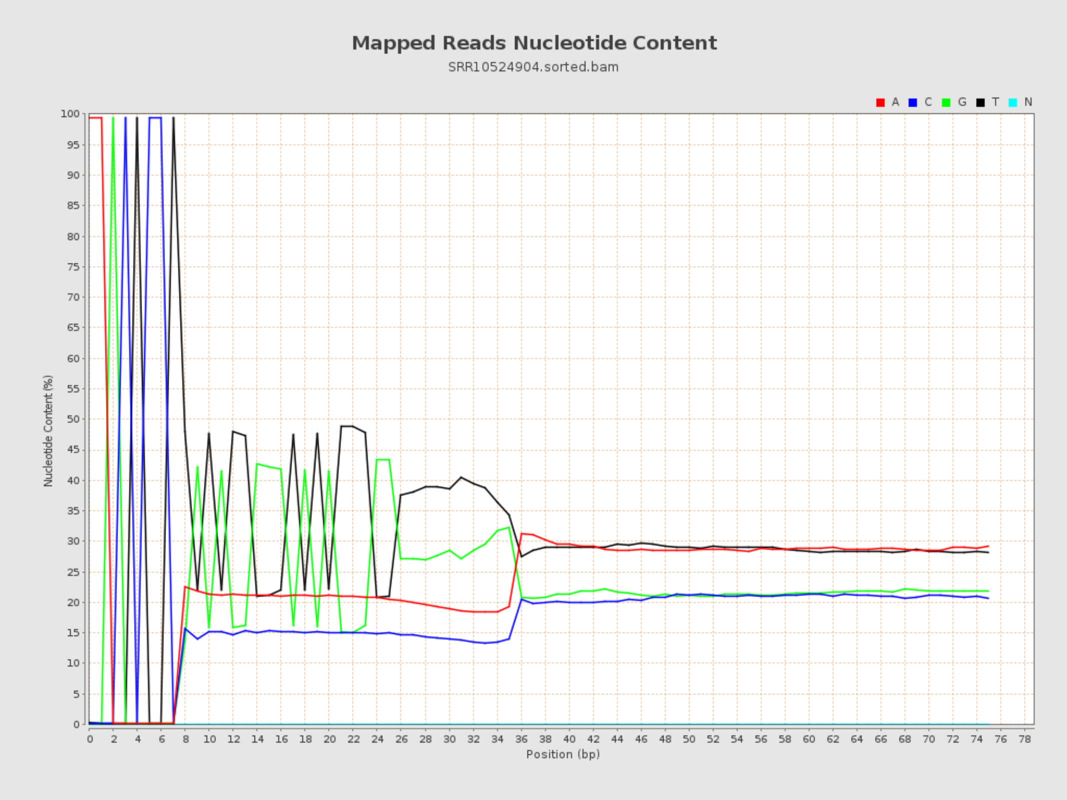
6. Results : Genome Fraction Coverage



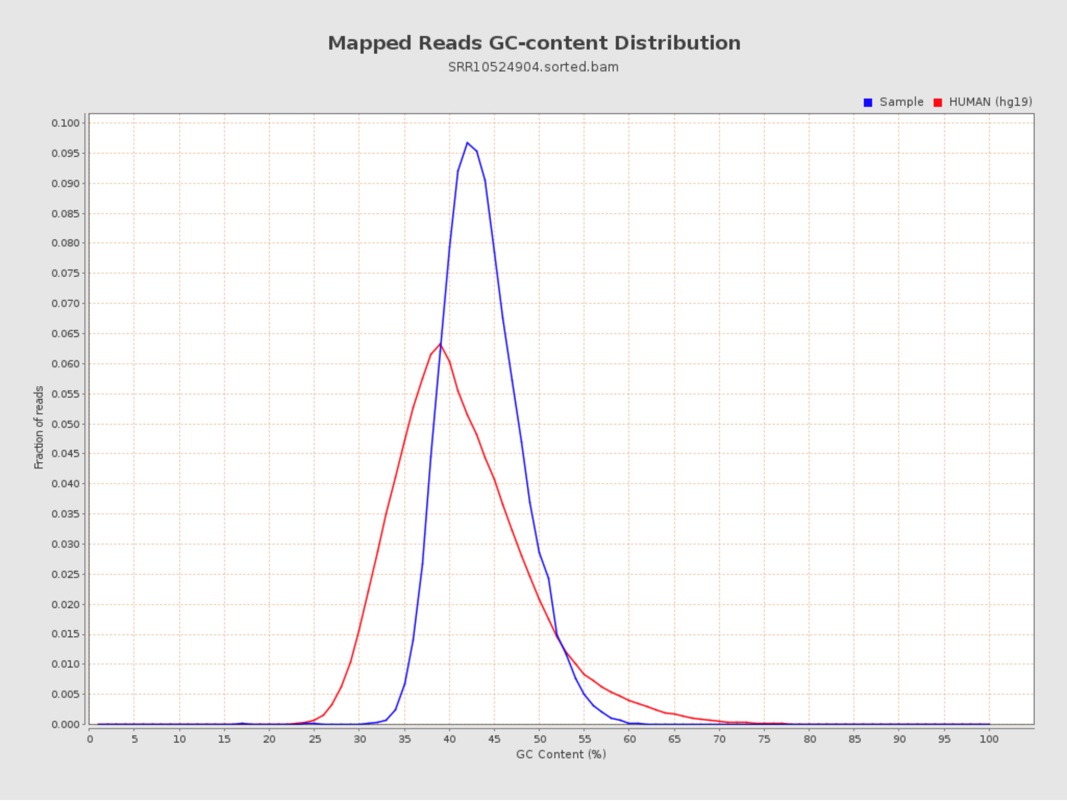
7. Results : Duplication Rate Histogram



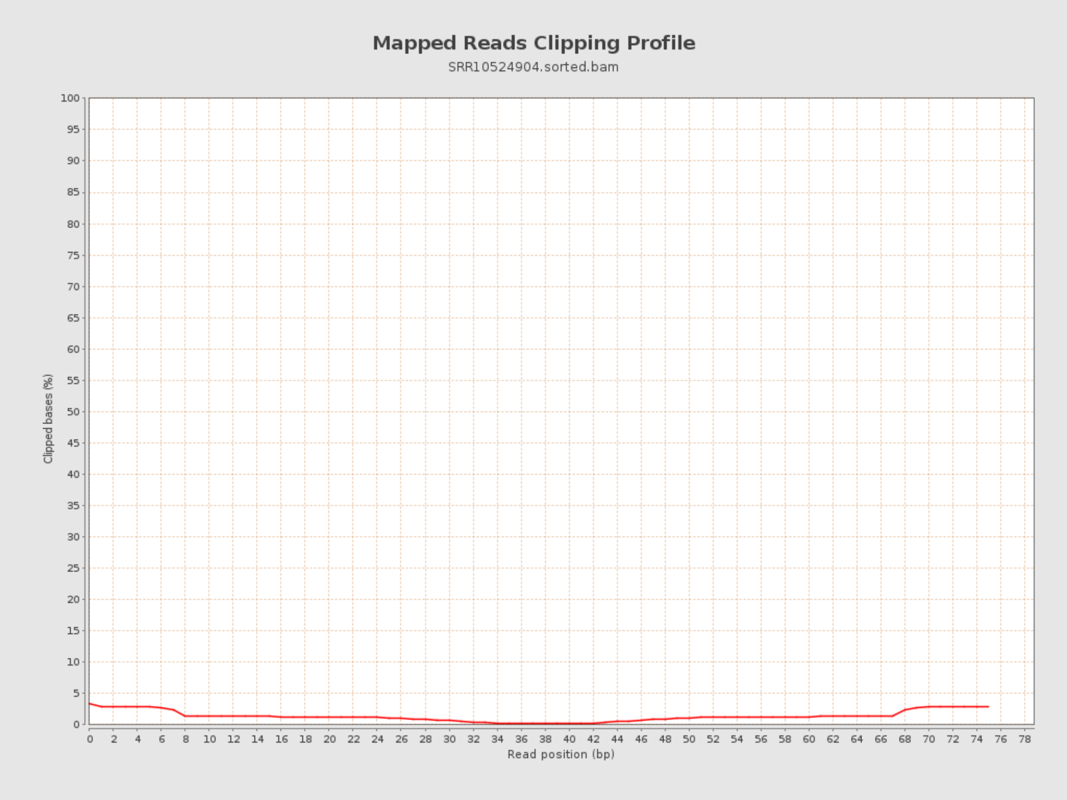
8. Results : Mapped Reads Nucleotide Content



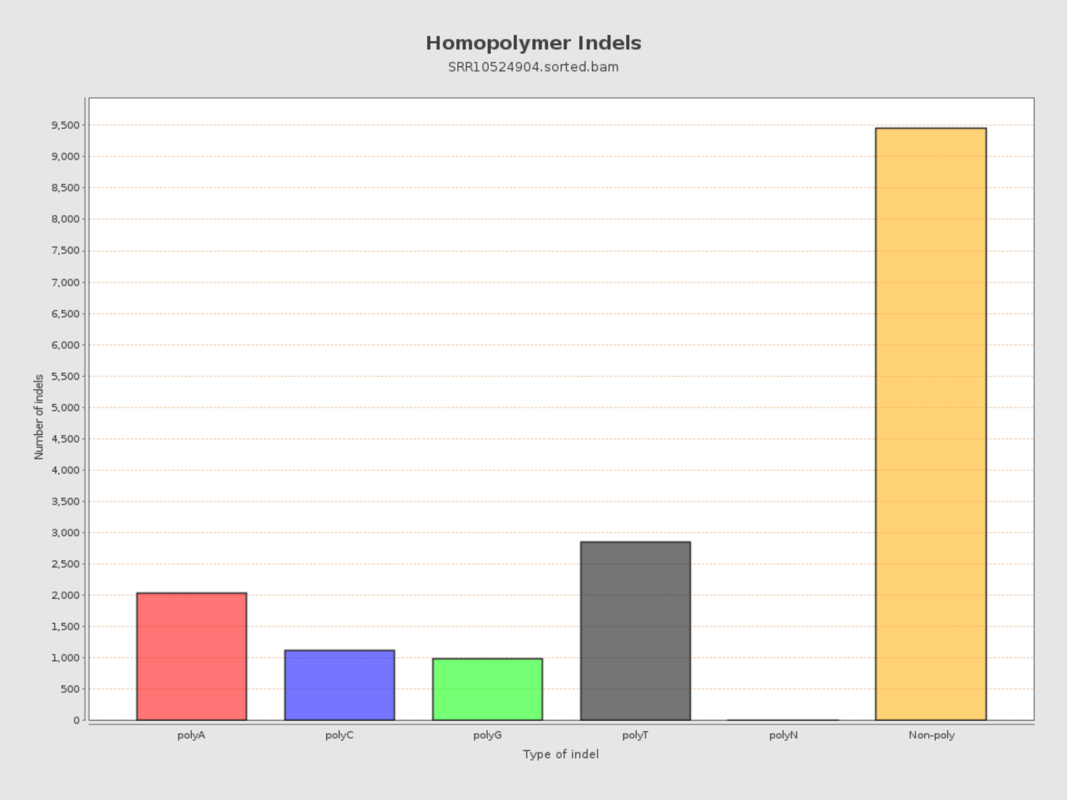
9. Results : Mapped Reads GC-content Distribution



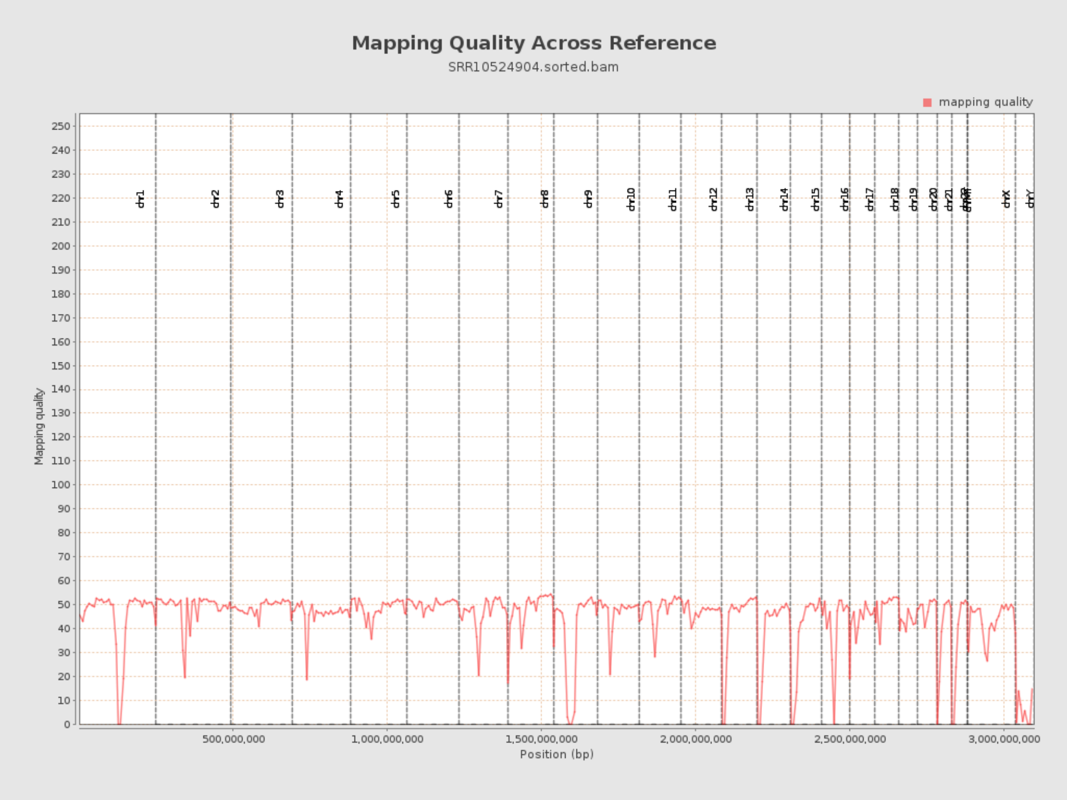
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram