Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 01:29:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524388.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_SRR10524388 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524388.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 01:29:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524388.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	659,484
Mapped reads	610,165 / 92.52%
Unmapped reads	49,319 / 7.48%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,581 / 0.39%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	12,621 / 1.91%
Duplication rate	1.51%
Clipped reads	610,737 / 92.61%

2.2. ACGT Content

Number/percentage of A's	9,398,486 / 26.07%
Number/percentage of C's	6,777,608 / 18.8%
Number/percentage of T's	11,472,419 / 31.82%
Number/percentage of G's	8,403,516 / 23.31%
Number/percentage of N's	4,911 / 0.01%
GC Percentage	42.1%

2.3. Coverage

Mean	0.0117

Standard Deviation	0.1447

2.4. Mapping Quality

Mean Mapping Quality	46.12

2.5. Mismatches and indels

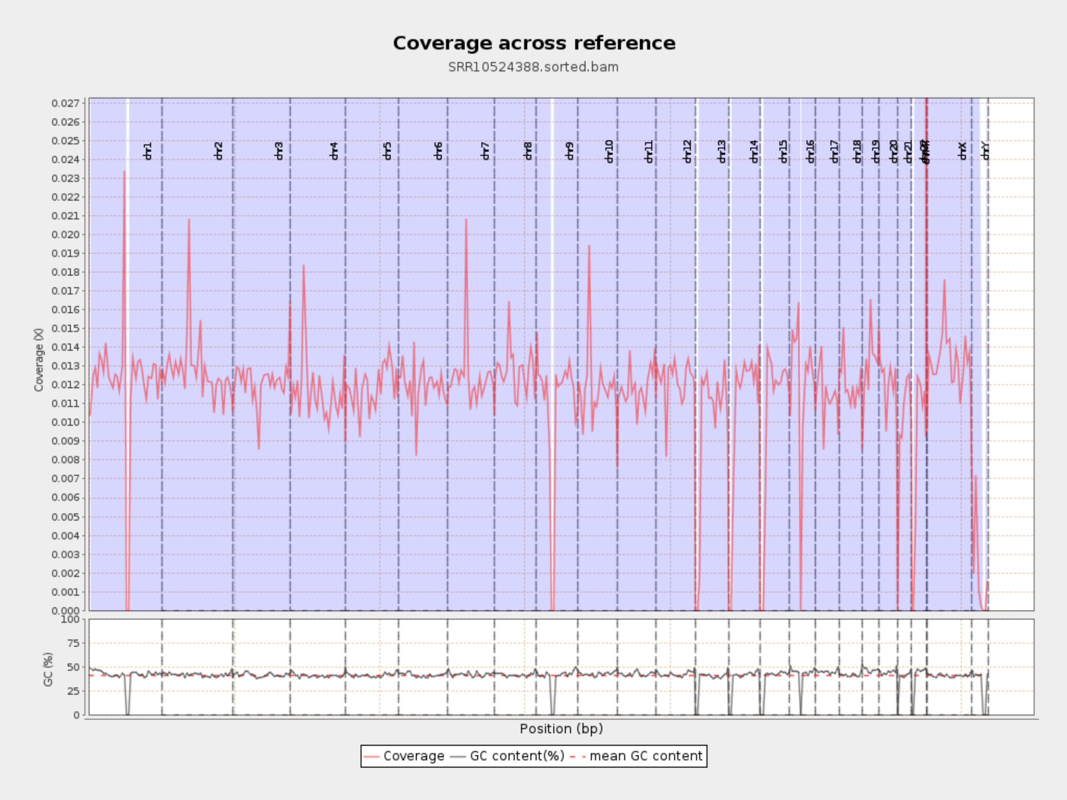
General error rate	0.5%
Mismatches	173,913
Insertions	2,524
Mapped reads with at least one insertion	0.41%
Deletions	6,499
Mapped reads with at least one deletion	1.06%
Homopolymer indels	42.2%

2.6. Chromosome stats

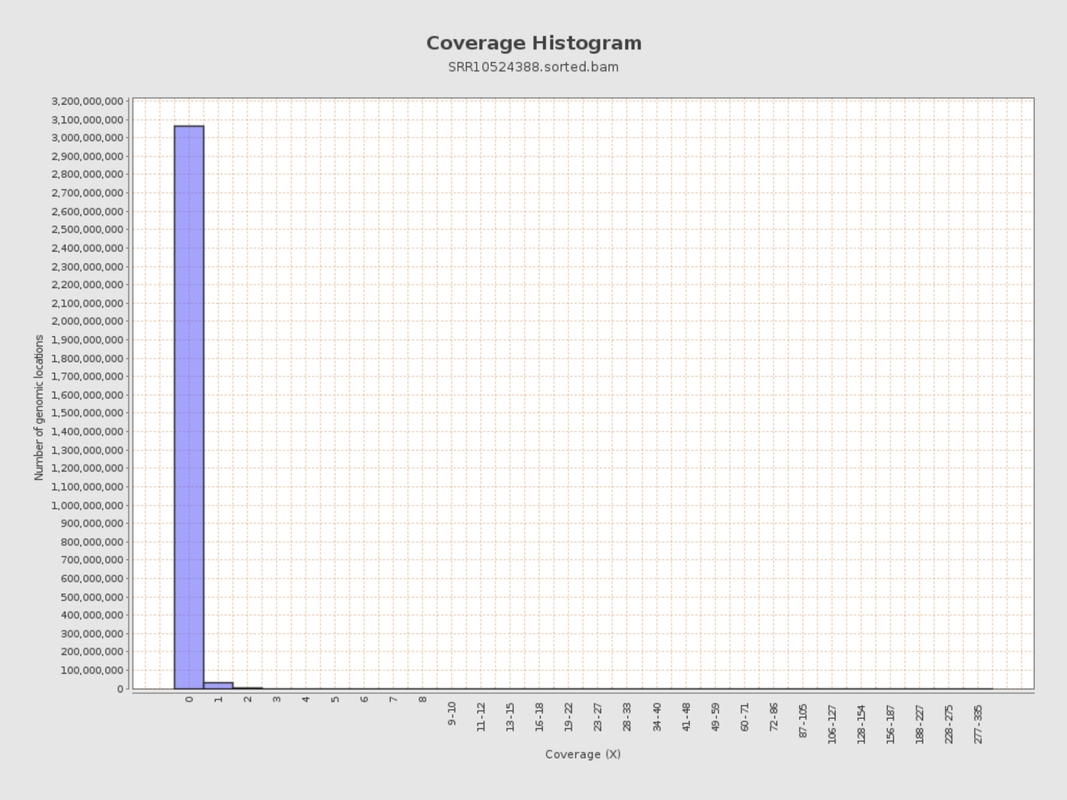
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3006571	0.0121	0.2677
chr2	243199373	3121766	0.0128	0.1492
chr3	198022430	2392228	0.0121	0.1138
chr4	191154276	2225620	0.0116	0.1184
chr5	180915260	2151352	0.0119	0.1132
chr6	171115067	2047901	0.012	0.1172
chr7	159138663	1996355	0.0125	0.1677

chr8	146364022	1870781	0.0128	0.1353
chr9	141213431	1502615	0.0106	0.1253
chr10	135534747	1622626	0.012	0.1357
chr11	135006516	1590228	0.0118	0.131
chr12	133851895	1640321	0.0123	0.1161
chr13	115169878	1112000	0.0097	0.1019
chr14	107349540	1121526	0.0104	0.1092
chr15	102531392	1059937	0.0103	0.1055
chr16	90354753	1097701	0.0121	0.1177
chr17	81195210	926566	0.0114	0.1151
chr18	78077248	945158	0.0121	0.2003
chr19	59128983	783698	0.0133	0.183
chr20	63025520	760806	0.0121	0.1149
chr21	48129895	472889	0.0098	0.1084
chr22	51304566	415340	0.0081	0.0935
chrMT	16571	16427	0.9913	1.183
chrX	155270560	2070838	0.0133	0.1246
chrY	59373566	115864	0.002	0.069

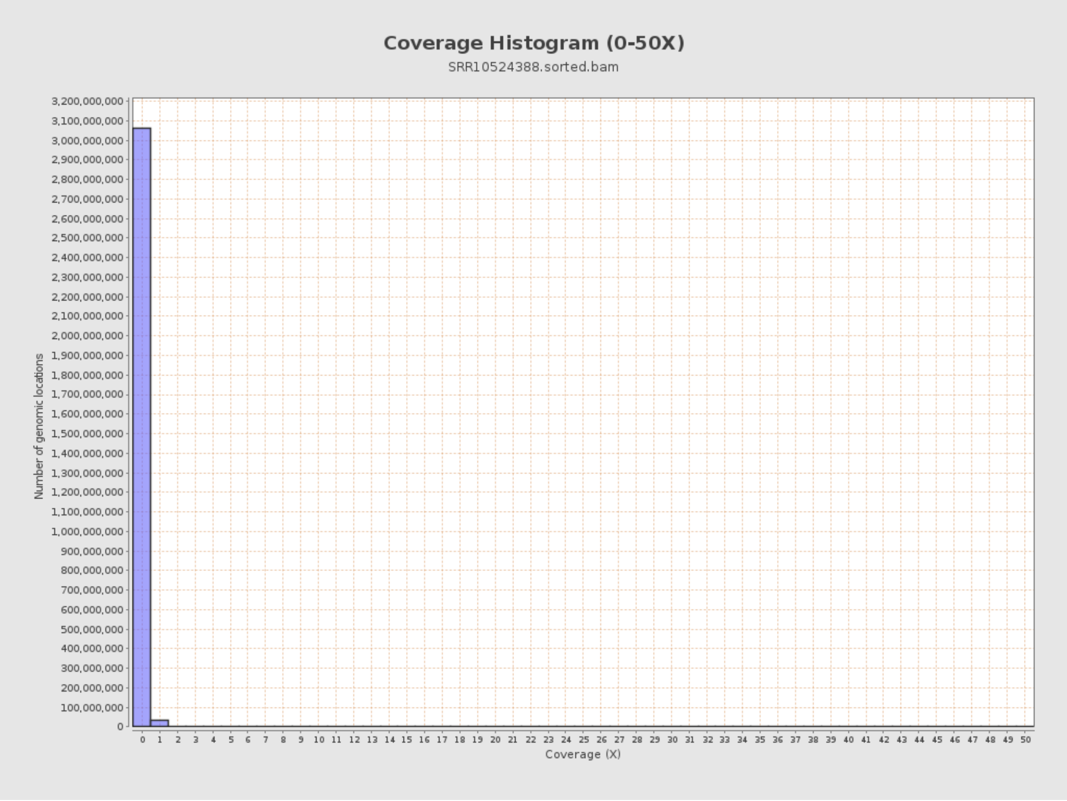
3. Results : Coverage across reference



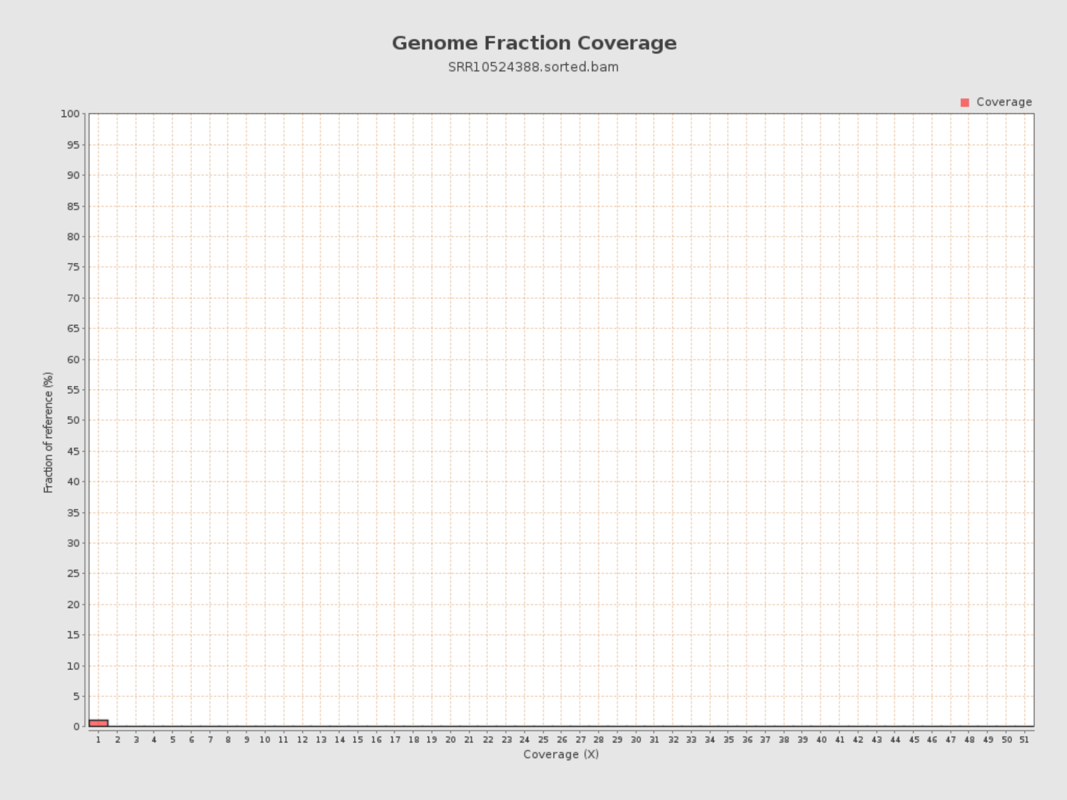
4. Results : Coverage Histogram



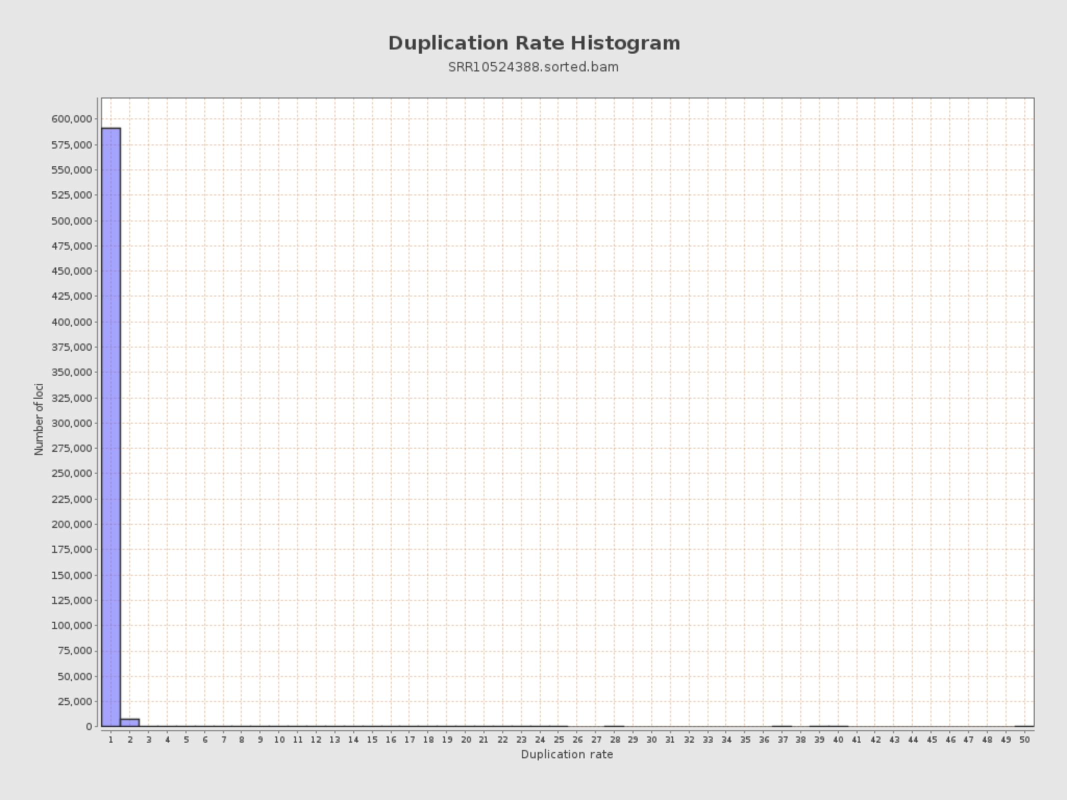
5. Results : Coverage Histogram (0-50X)



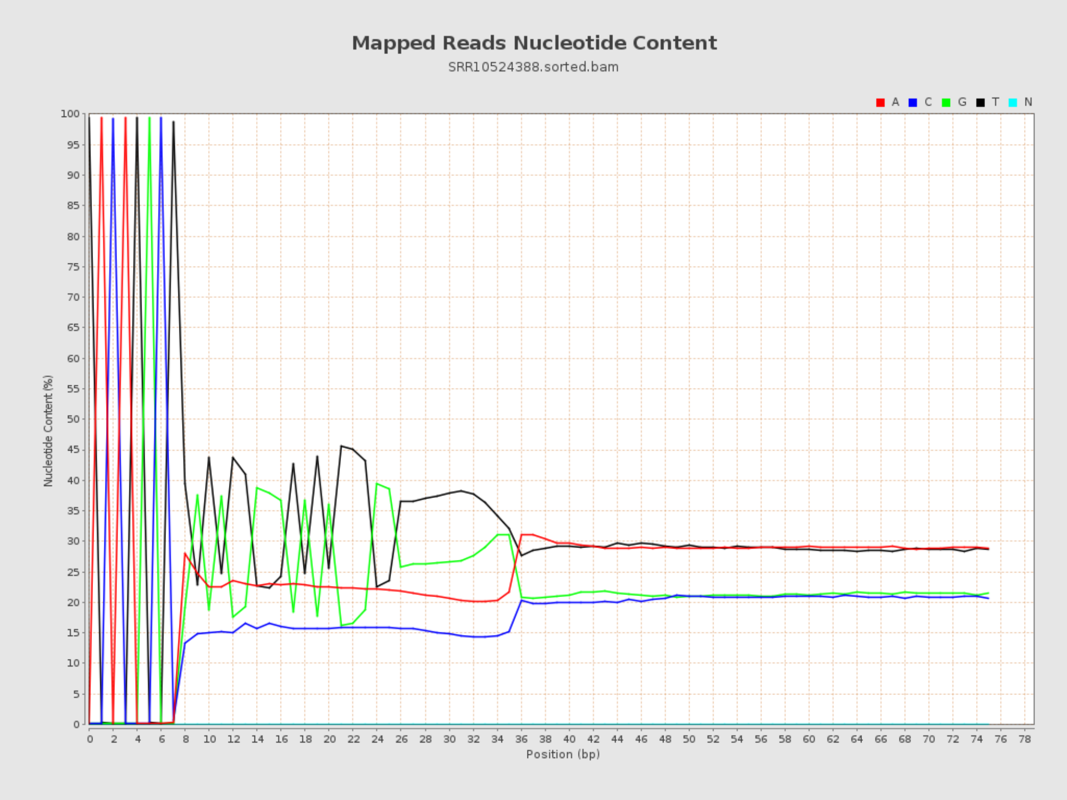
6. Results : Genome Fraction Coverage



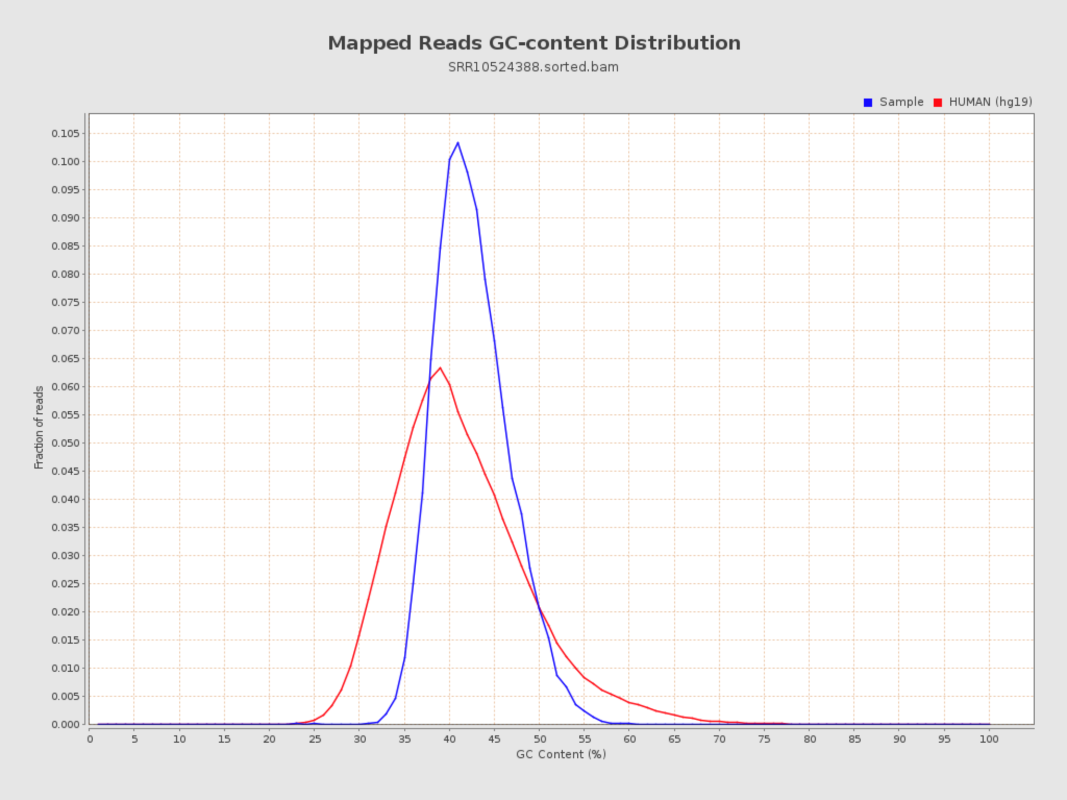
7. Results : Duplication Rate Histogram



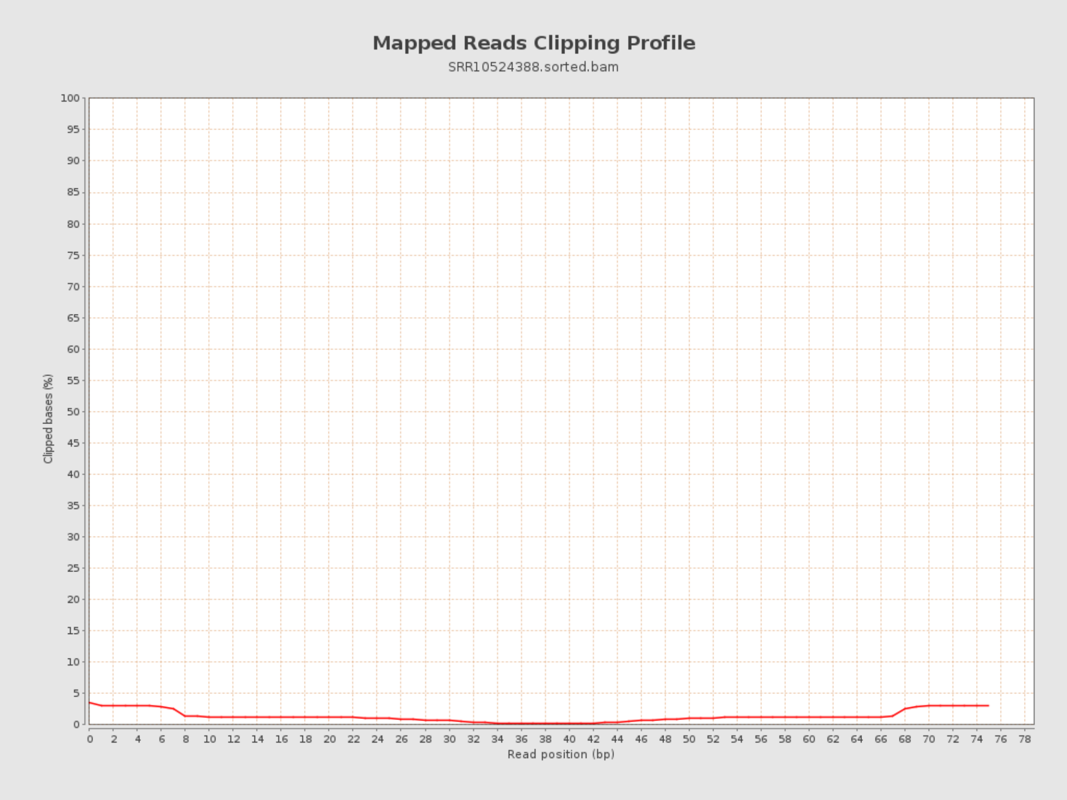
8. Results : Mapped Reads Nucleotide Content



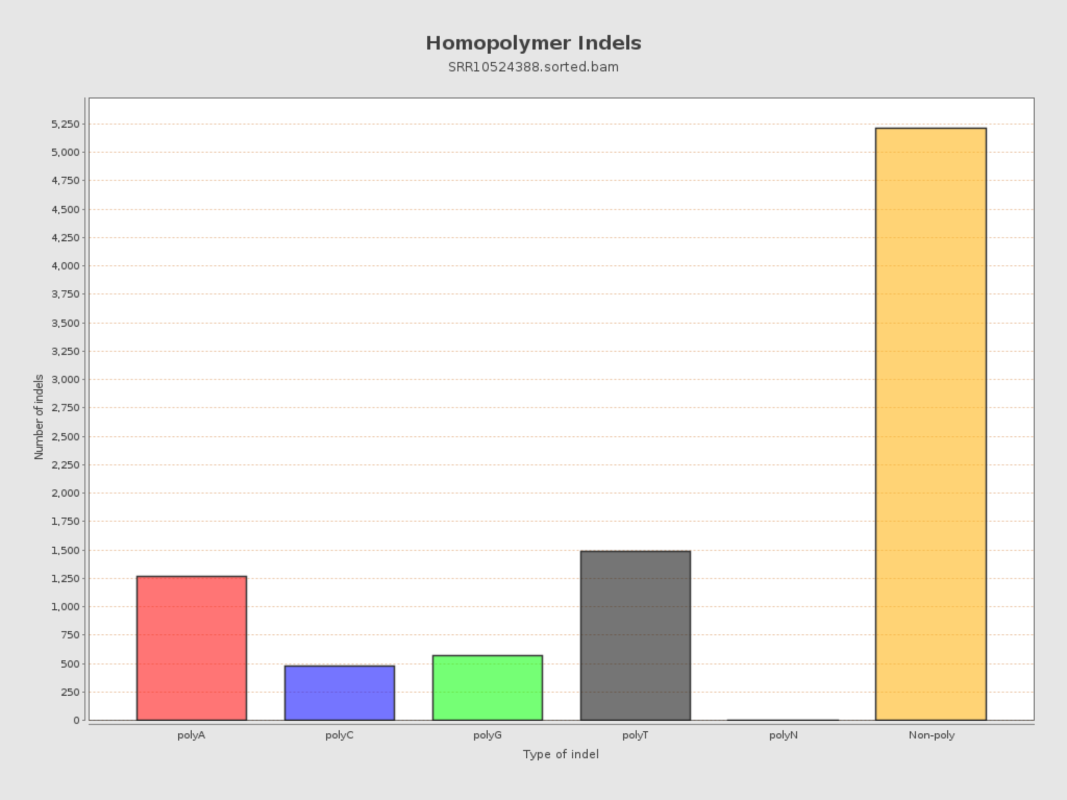
9. Results : Mapped Reads GC-content Distribution



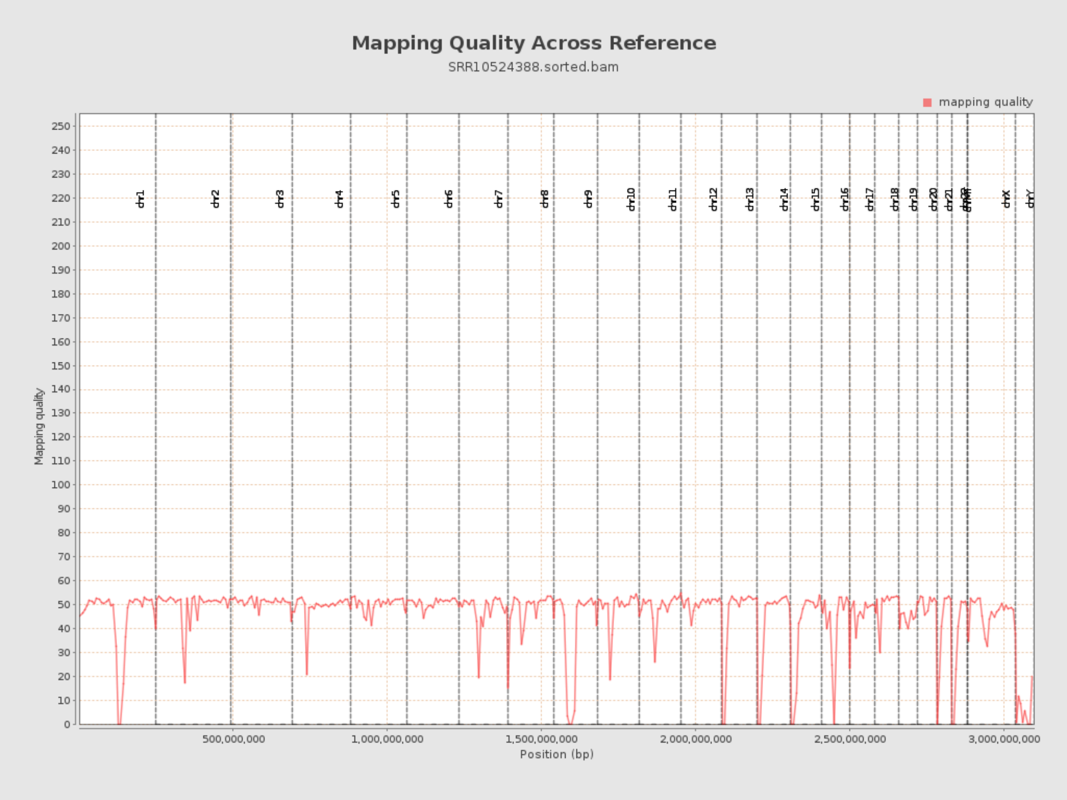
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram