Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 18:25:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524737.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_SRR10524737 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524737.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 18:25:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524737.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,048,901
Mapped reads	960,537 / 91.58%
Unmapped reads	88,364 / 8.42%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,598 / 0.34%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	24,646 / 2.35%
Duplication rate	1.91%
Clipped reads	961,270 / 91.65%

2.2. ACGT Content

Number/percentage of A's	13,760,495 / 24.69%
Number/percentage of C's	9,496,965 / 17.04%
Number/percentage of T's	17,837,585 / 32%
Number/percentage of G's	14,631,524 / 26.25%
Number/percentage of N's	7,275 / 0.01%
GC Percentage	43.29%

2.3. Coverage

Mean	0.018

Standard Deviation	0.1781

2.4. Mapping Quality

Mean Mapping Quality	45.05

2.5. Mismatches and indels

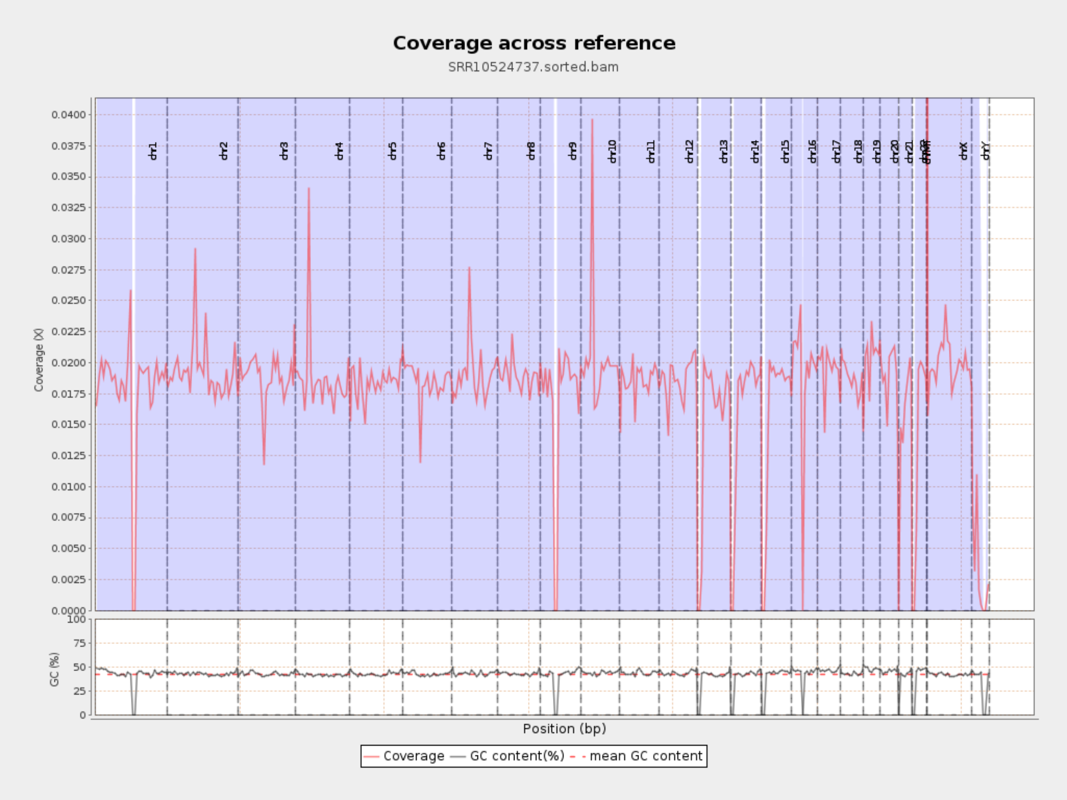
General error rate	0.52%
Mismatches	280,112
Insertions	3,937
Mapped reads with at least one insertion	0.41%
Deletions	11,443
Mapped reads with at least one deletion	1.18%
Homopolymer indels	43.06%

2.6. Chromosome stats

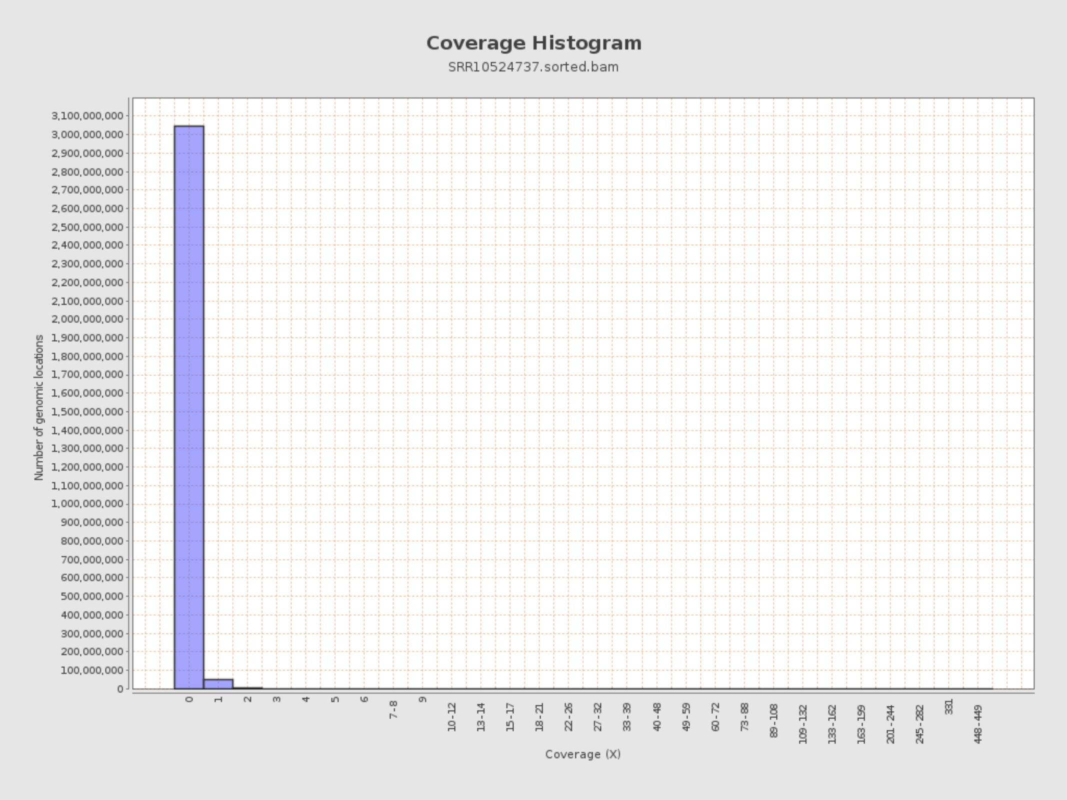
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4419994	0.0177	0.2464
chr2	243199373	4706106	0.0194	0.2496
chr3	198022430	3716088	0.0188	0.1465
chr4	191154276	3587960	0.0188	0.1593
chr5	180915260	3338631	0.0185	0.1439
chr6	171115067	3164215	0.0185	0.1507
chr7	159138663	3042864	0.0191	0.205

chr8	146364022	2771221	0.0189	0.1697
chr9	141213431	2368435	0.0168	0.16
chr10	135534747	2759596	0.0204	0.211
chr11	135006516	2518532	0.0187	0.1626
chr12	133851895	2494324	0.0186	0.1459
chr13	115169878	1725529	0.015	0.1297
chr14	107349540	1681835	0.0157	0.1362
chr15	102531392	1588042	0.0155	0.1319
chr16	90354753	1685678	0.0187	0.1567
chr17	81195210	1583791	0.0195	0.1535
chr18	78077248	1463890	0.0187	0.2347
chr19	59128983	1207279	0.0204	0.2068
chr20	63025520	1196190	0.019	0.1493
chr21	48129895	738867	0.0154	0.1398
chr22	51304566	688195	0.0134	0.1249
chrMT	16571	26296	1.5869	1.4719
chrX	155270560	3093931	0.0199	0.1567
chrY	59373566	184761	0.0031	0.0935

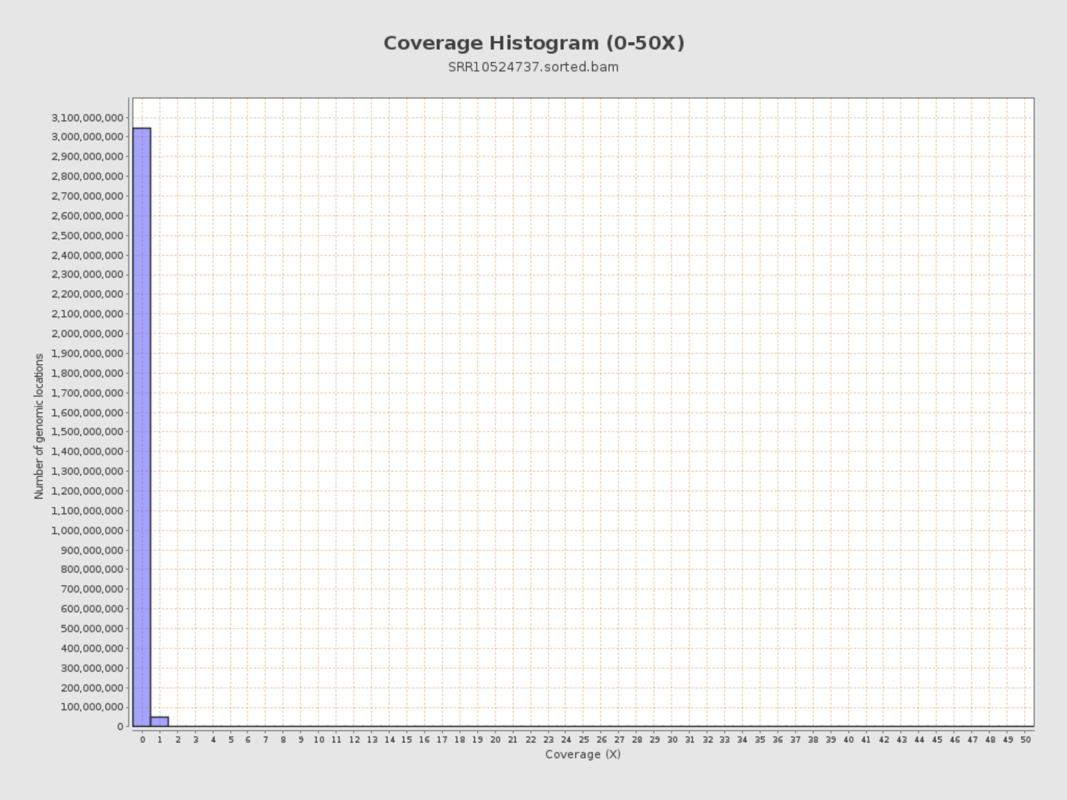
3. Results : Coverage across reference



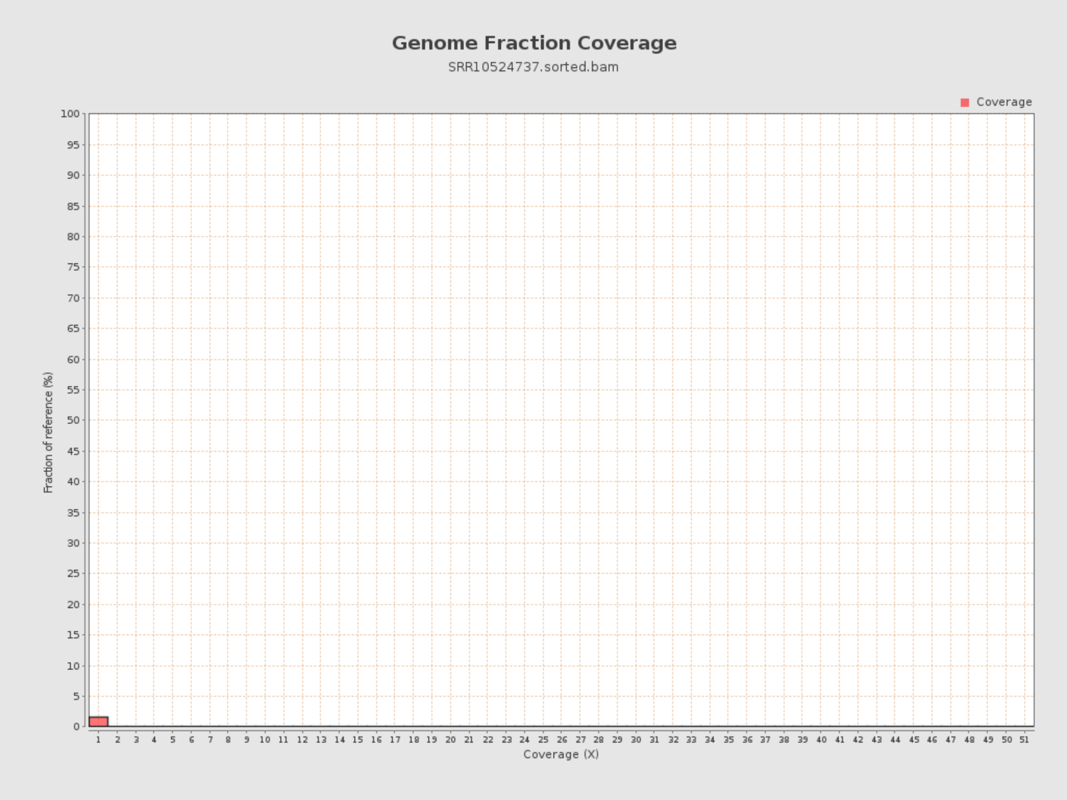
4. Results : Coverage Histogram



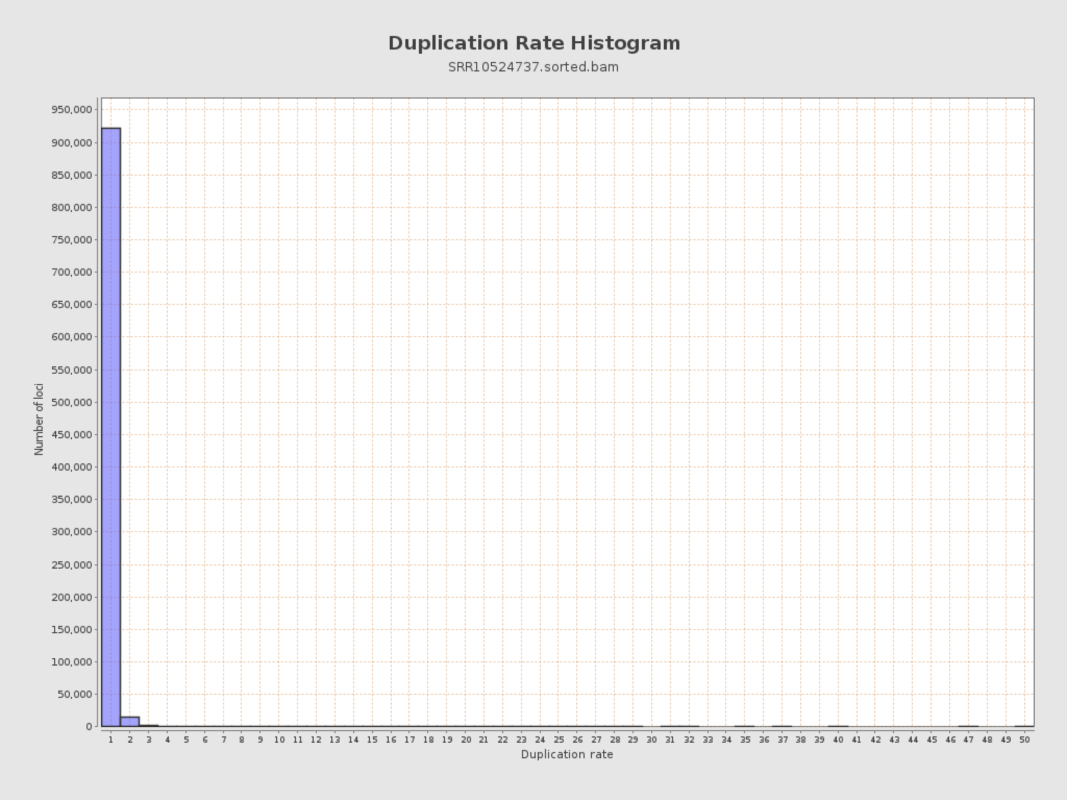
5. Results : Coverage Histogram (0-50X)



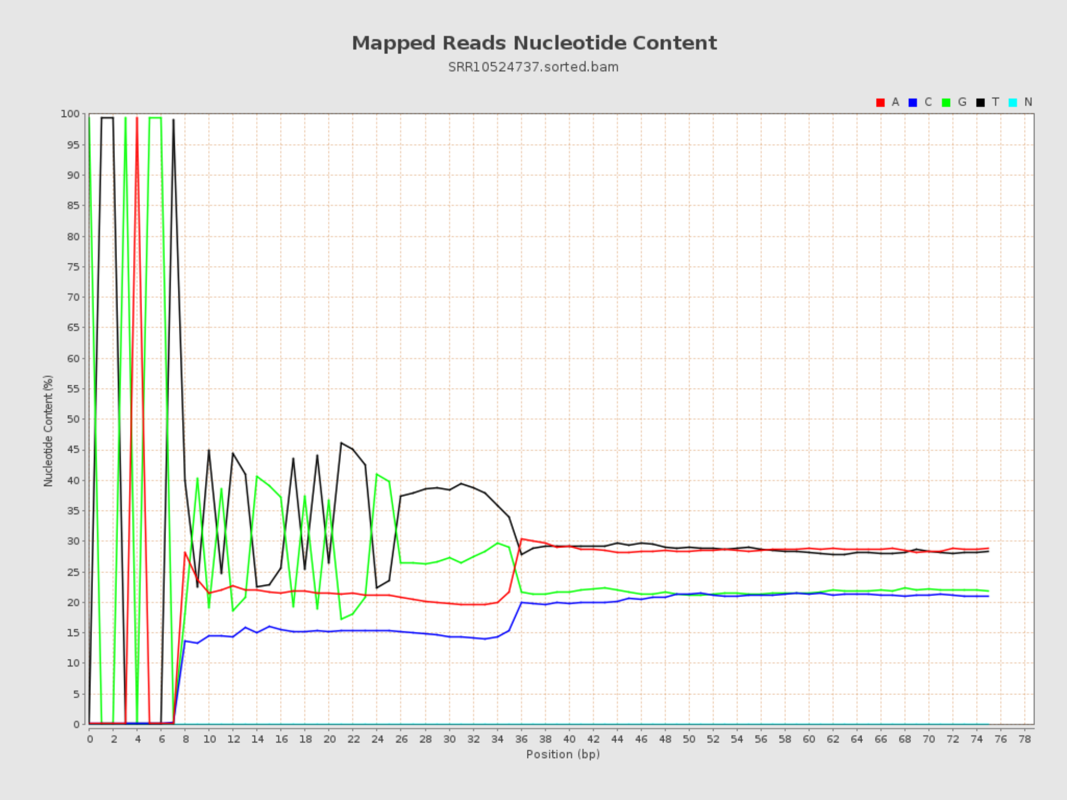
6. Results : Genome Fraction Coverage



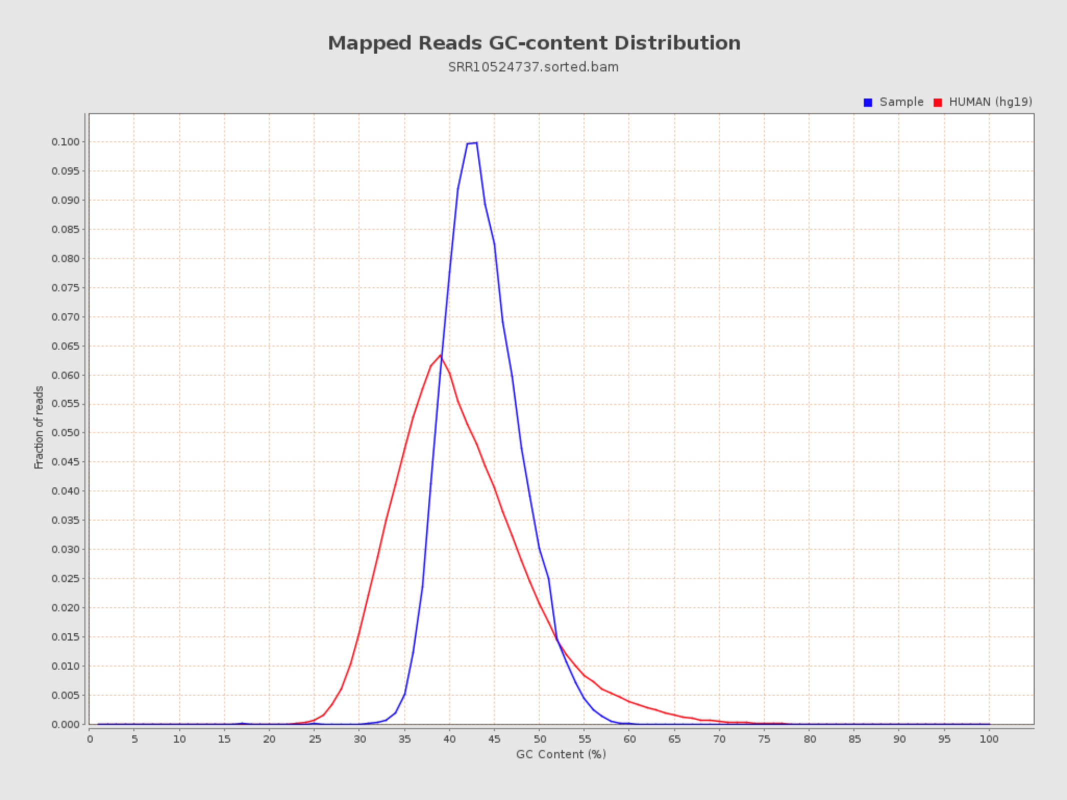
7. Results : Duplication Rate Histogram



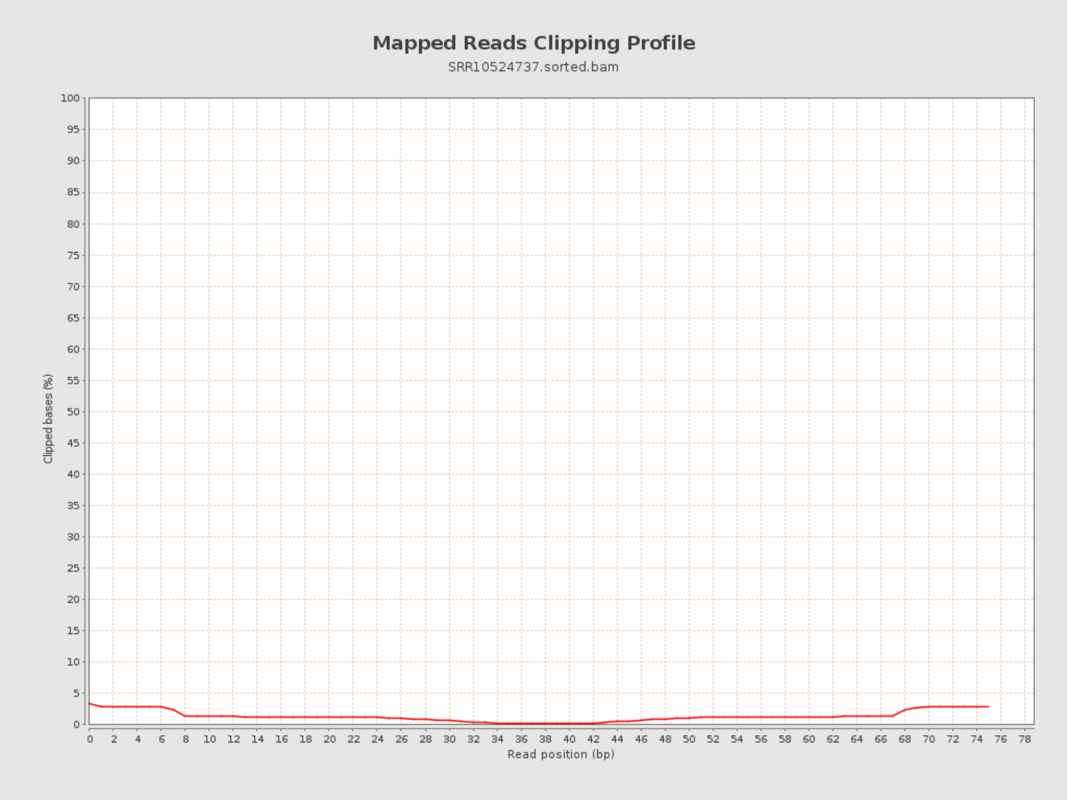
8. Results : Mapped Reads Nucleotide Content



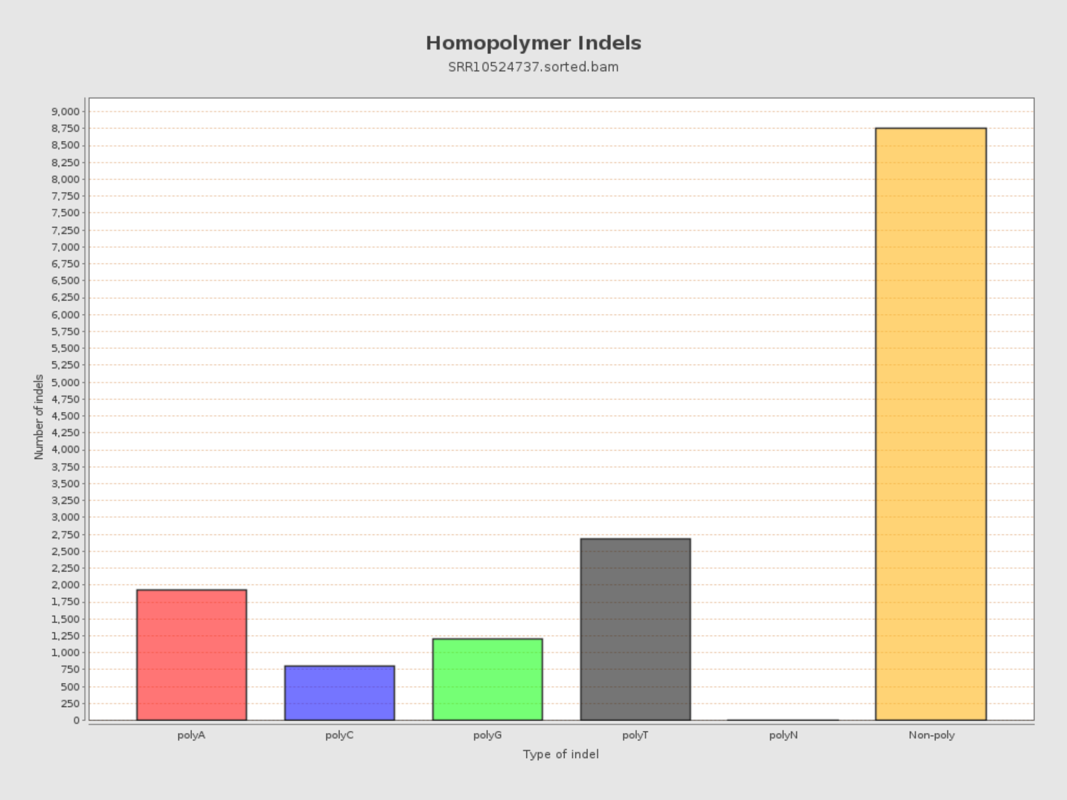
9. Results : Mapped Reads GC-content Distribution



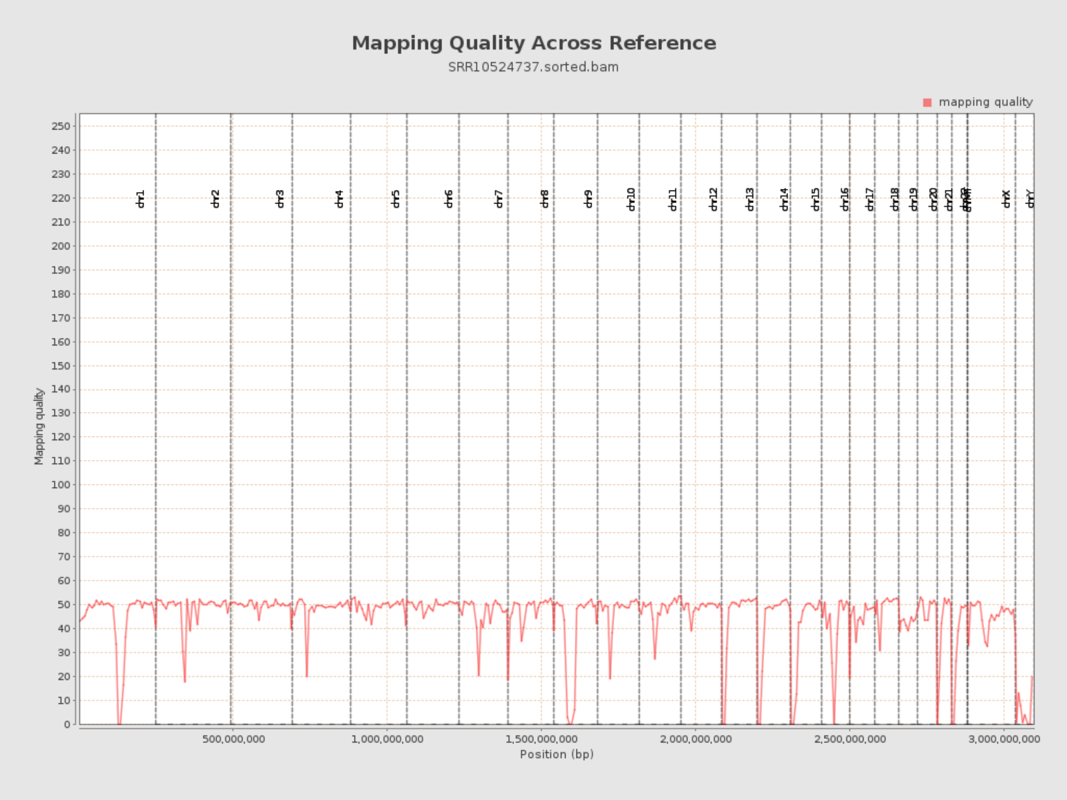
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram