Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 11:58:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524590.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_SRR10524590 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524590.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 11:58:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524590.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,445,513
Mapped reads	1,351,269 / 93.48%
Unmapped reads	94,244 / 6.52%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,003 / 0.21%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	52,253 / 3.61%
Duplication rate	3.01%
Clipped reads	1,350,219 / 93.41%

2.2. ACGT Content

Number/percentage of A's	20,110,851 / 25.26%
Number/percentage of C's	14,805,579 / 18.6%
Number/percentage of T's	25,511,587 / 32.04%
Number/percentage of G's	19,183,423 / 24.1%
Number/percentage of N's	521 / 0%
GC Percentage	42.69%

2.3. Coverage

Mean	0.0257

Standard Deviation	0.2382

2.4. Mapping Quality

Mean Mapping Quality	45.58

2.5. Mismatches and indels

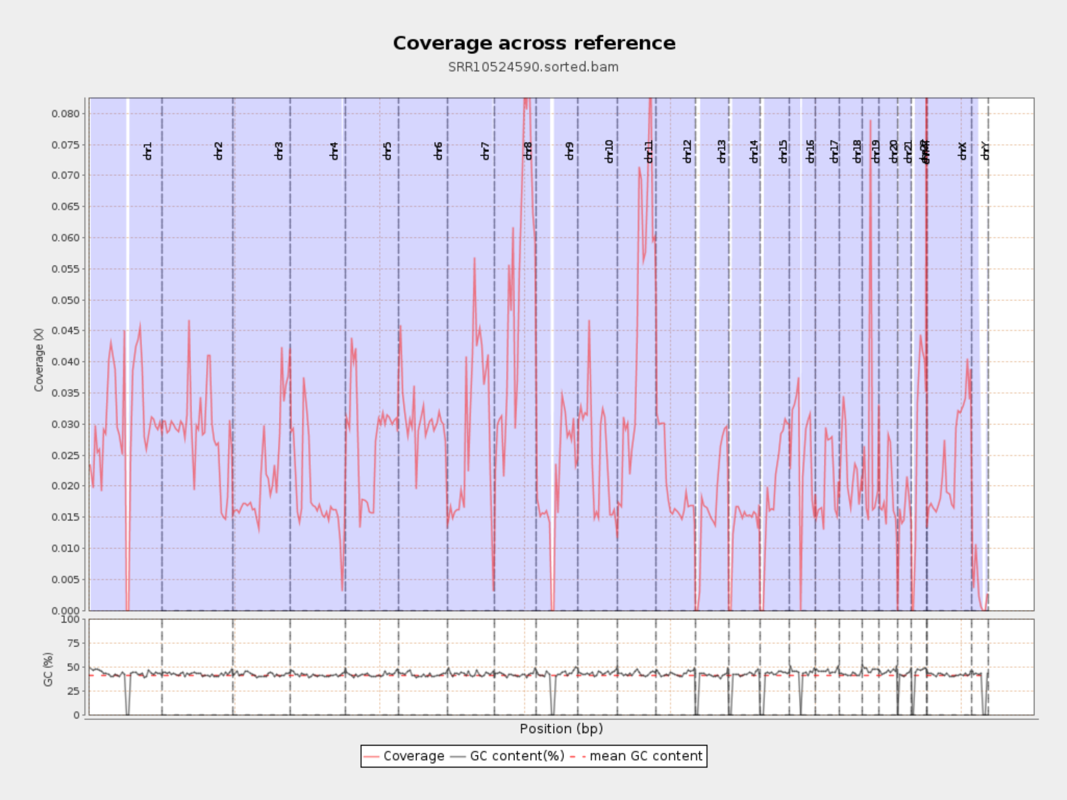
General error rate	0.47%
Mismatches	365,661
Insertions	6,033
Mapped reads with at least one insertion	0.44%
Deletions	14,745
Mapped reads with at least one deletion	1.08%
Homopolymer indels	41.22%

2.6. Chromosome stats

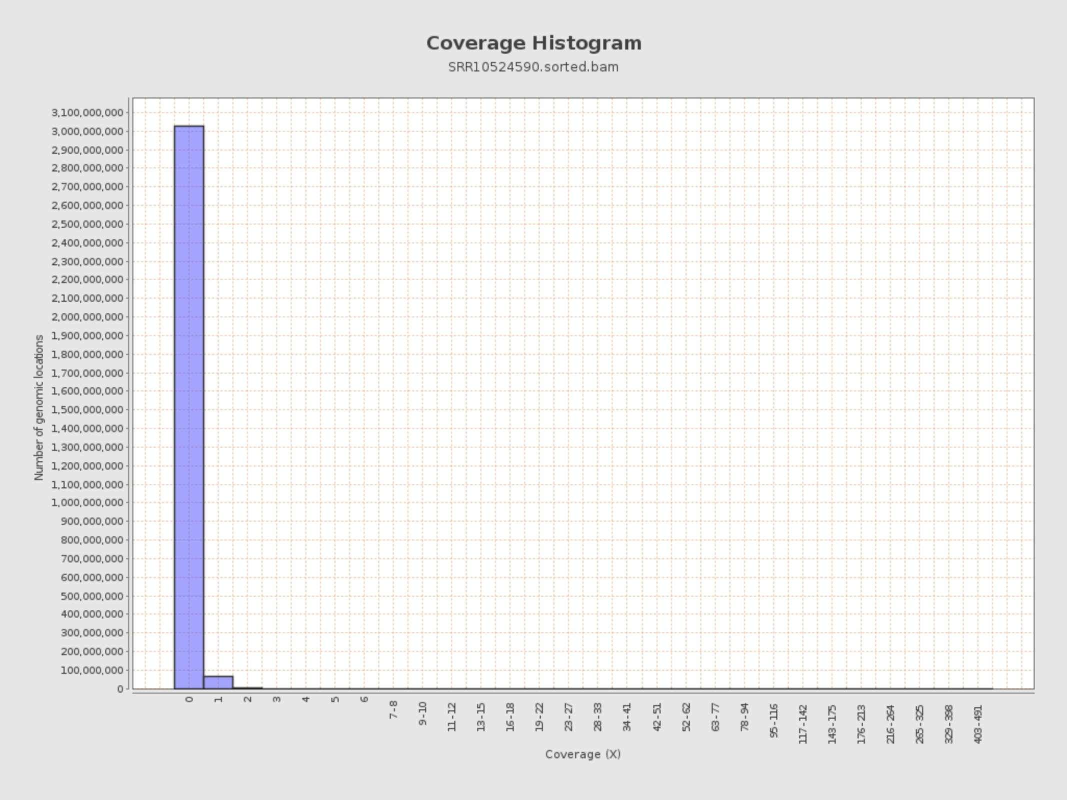
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	7483277	0.03	0.4068
chr2	243199373	6979091	0.0287	0.2683
chr3	198022430	4358966	0.022	0.1634
chr4	191154276	3517621	0.0184	0.1648
chr5	180915260	4980225	0.0275	0.1814
chr6	171115067	5264869	0.0308	0.2063
chr7	159138663	4575615	0.0288	0.2998

chr8	146364022	7544255	0.0515	0.3315
chr9	141213431	2859727	0.0203	0.204
chr10	135534747	3413364	0.0252	0.2355
chr11	135006516	6081267	0.045	0.2685
chr12	133851895	2651328	0.0198	0.1608
chr13	115169878	1956821	0.017	0.145
chr14	107349540	1431259	0.0133	0.131
chr15	102531392	1980891	0.0193	0.1577
chr16	90354753	2312604	0.0256	0.1814
chr17	81195210	1664989	0.0205	0.1619
chr18	78077248	1815328	0.0233	0.3235
chr19	59128983	1583550	0.0268	0.3092
chr20	63025520	1169593	0.0186	0.1519
chr21	48129895	725388	0.0151	0.1455
chr22	51304566	1385396	0.027	0.1793
chrMT	16571	3373	0.2035	0.5591
chrX	155270560	3710863	0.0239	0.1892
chrY	59373566	187482	0.0032	0.0906

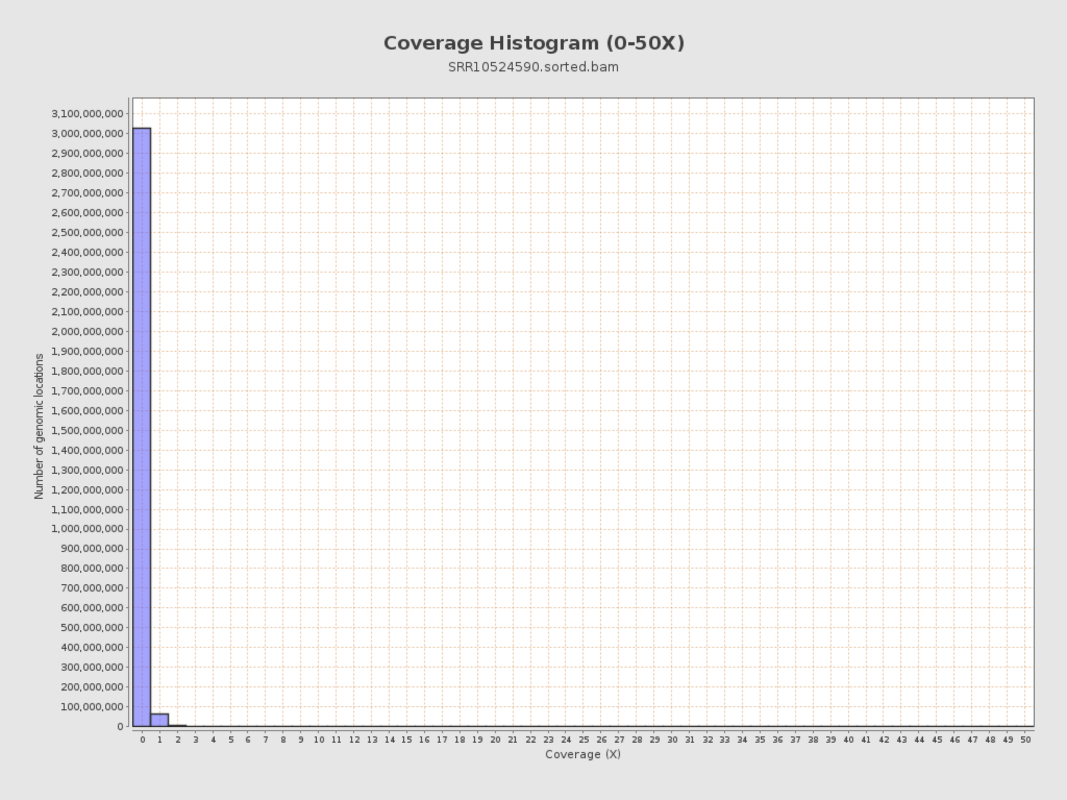
3. Results : Coverage across reference



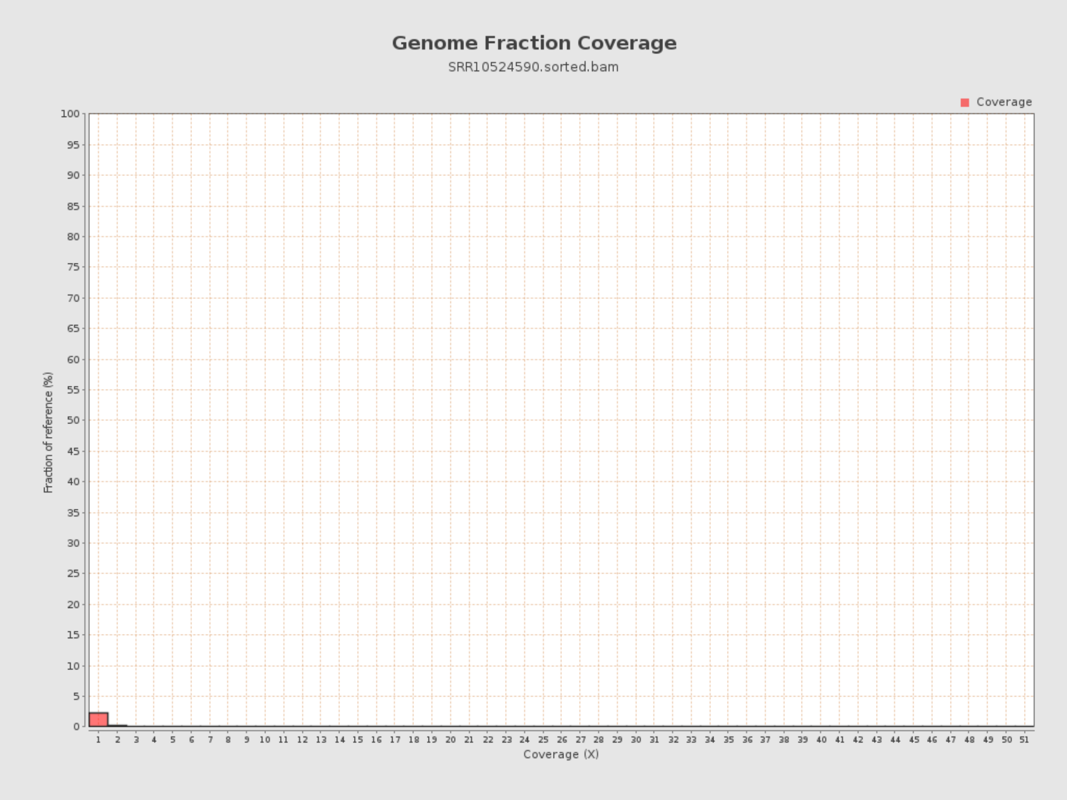
4. Results : Coverage Histogram



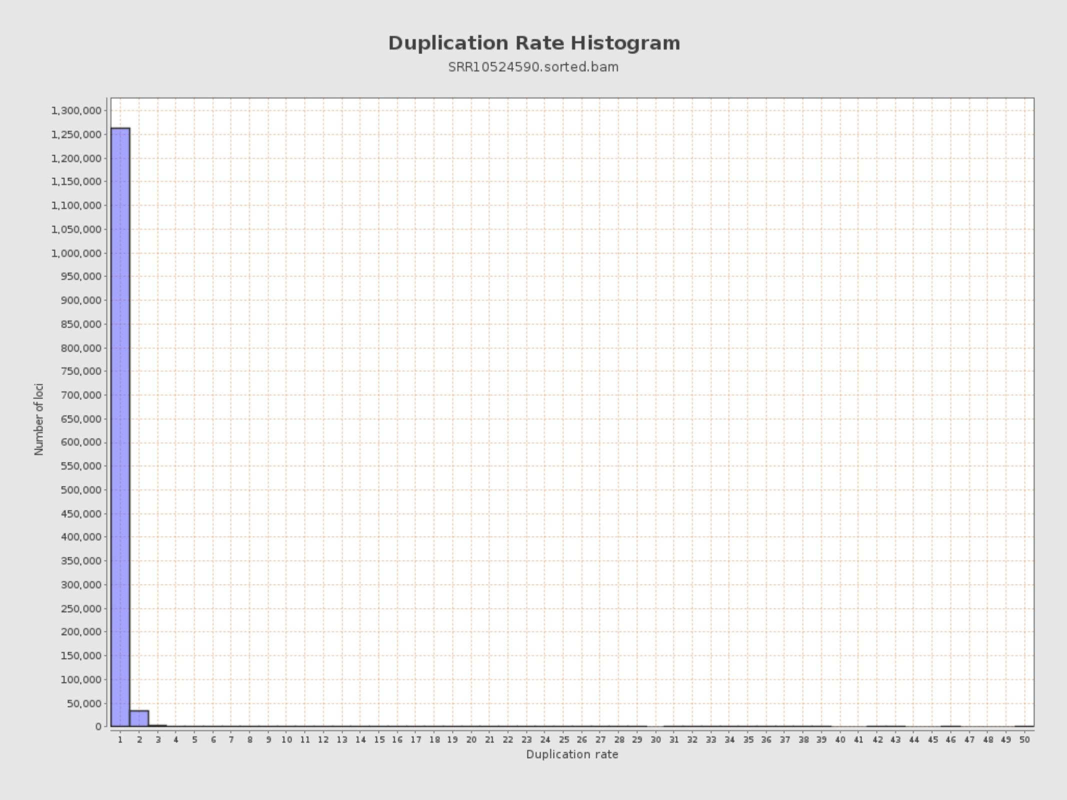
5. Results : Coverage Histogram (0-50X)



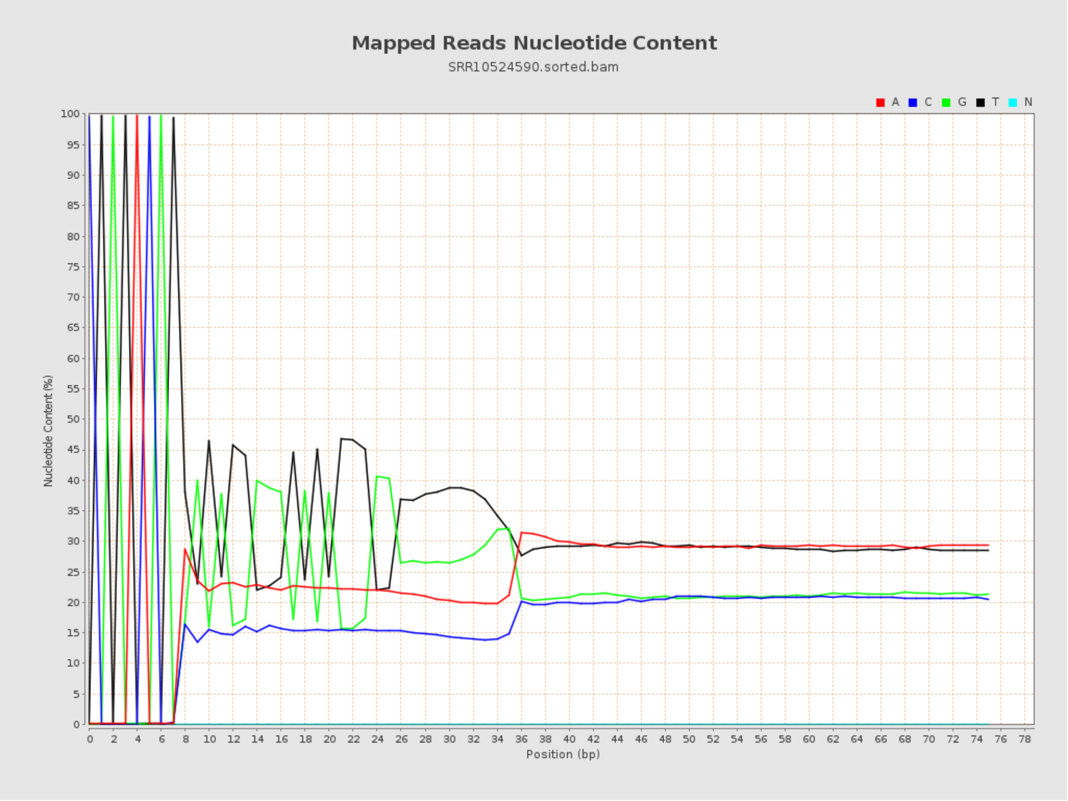
6. Results : Genome Fraction Coverage



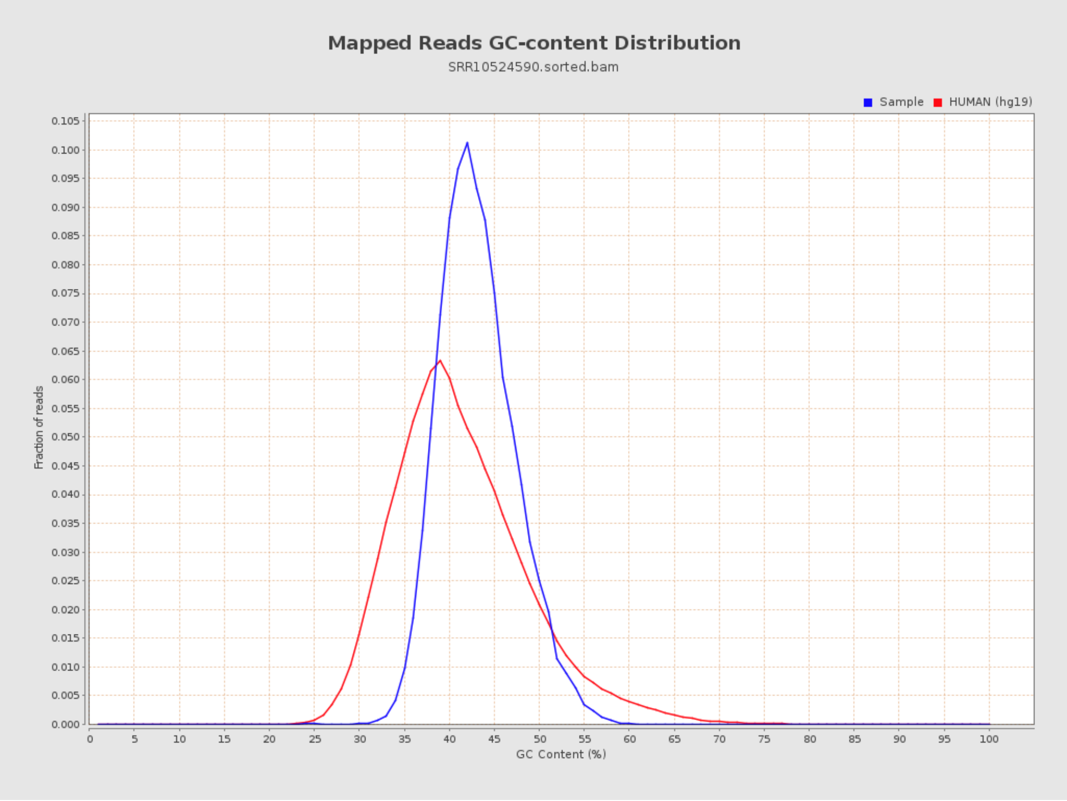
7. Results : Duplication Rate Histogram



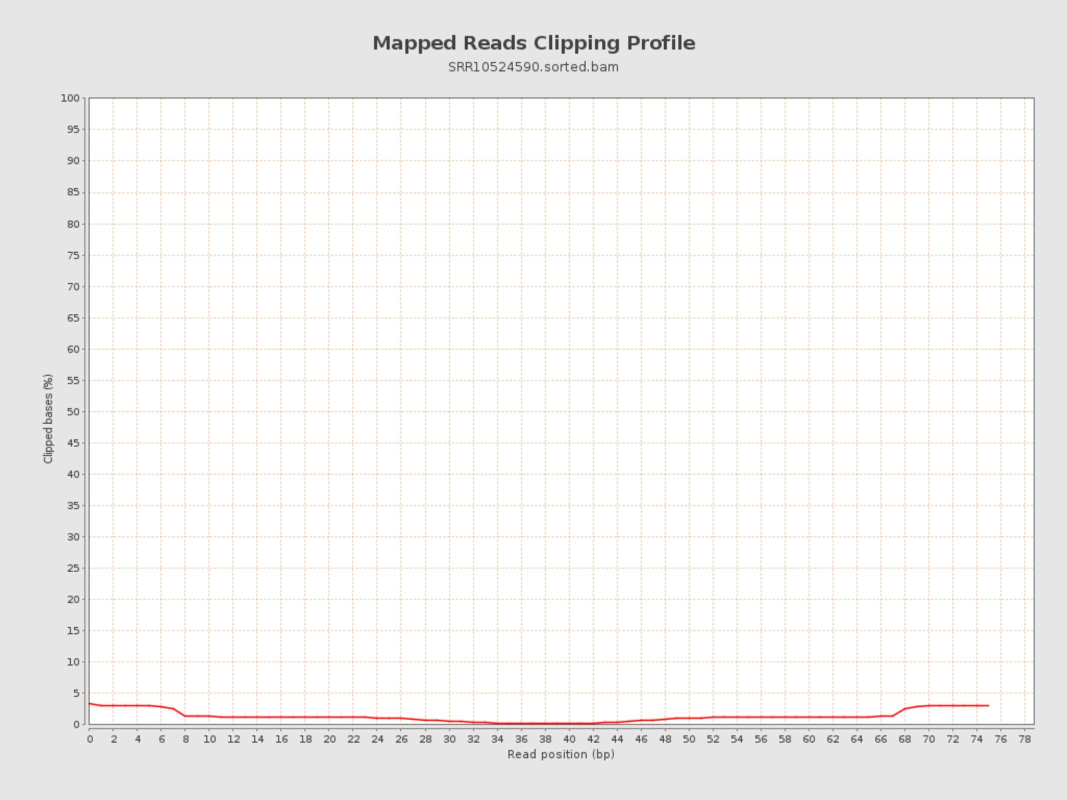
8. Results : Mapped Reads Nucleotide Content



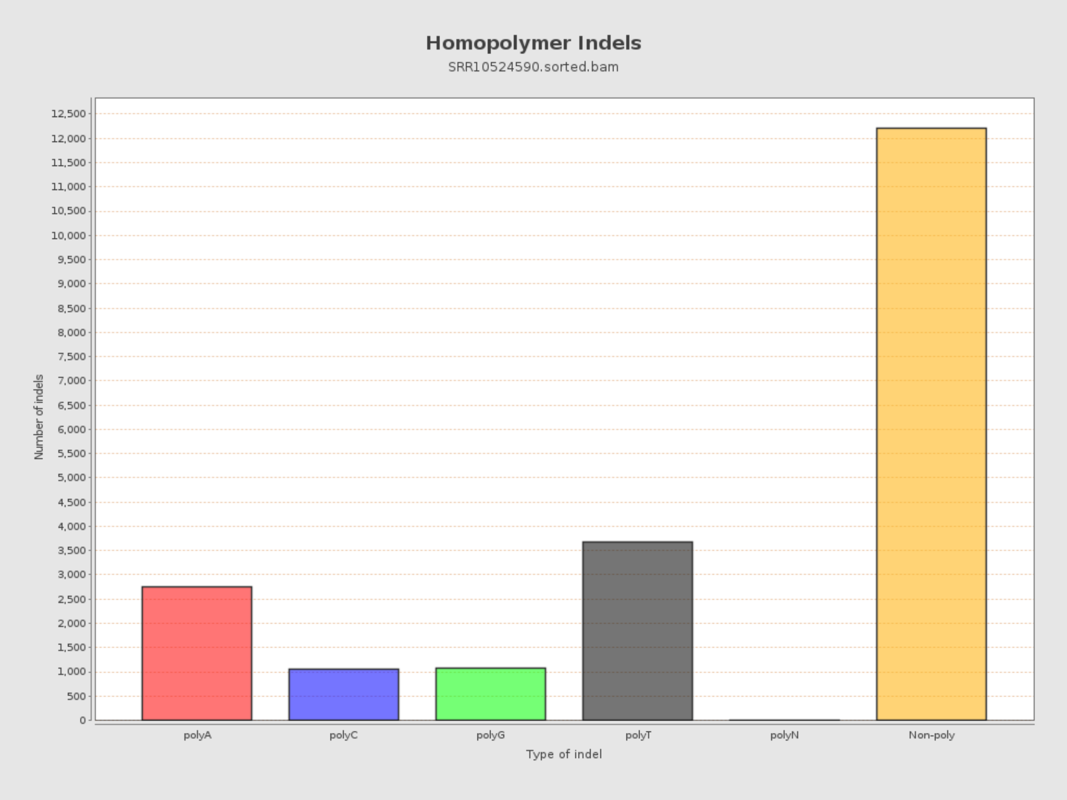
9. Results : Mapped Reads GC-content Distribution



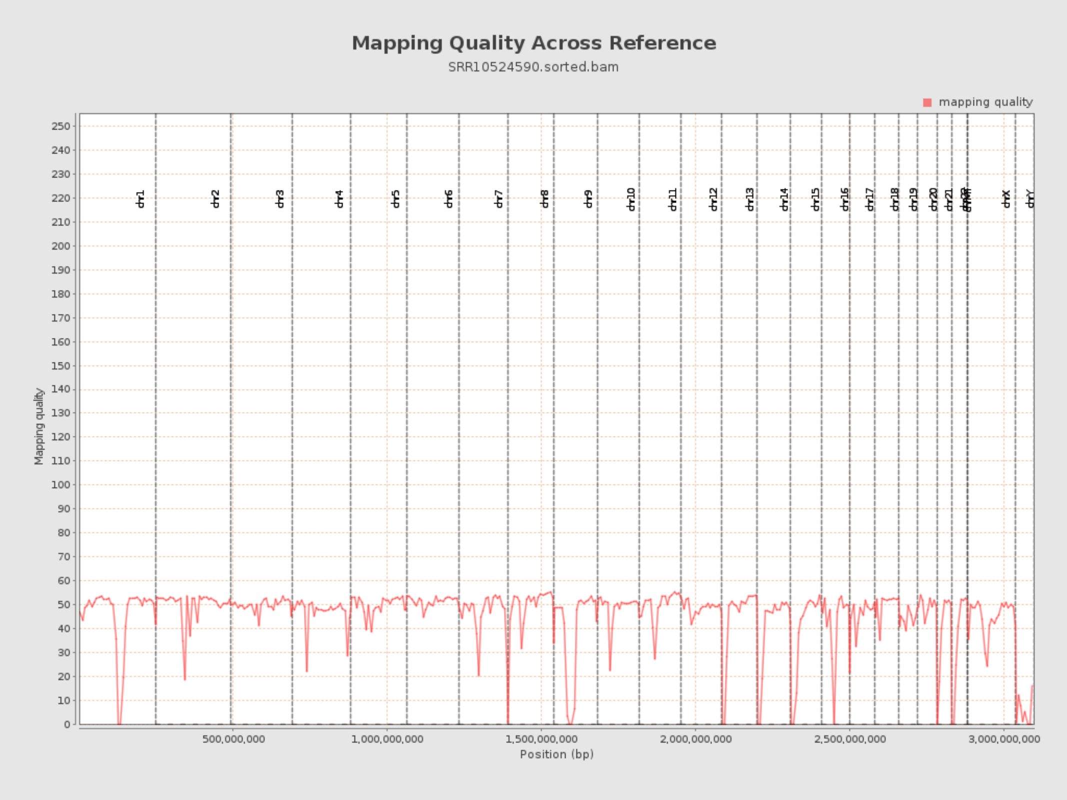
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram