Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 09:58:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524541.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_SRR10524541 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524541.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 09:58:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524541.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,841,610
Mapped reads	1,685,771 / 91.54%
Unmapped reads	155,839 / 8.46%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,060 / 0.33%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	77,879 / 4.23%
Duplication rate	3.43%
Clipped reads	1,688,686 / 91.7%

2.2. ACGT Content

Number/percentage of A's	23,154,218 / 23.7%
Number/percentage of C's	18,271,226 / 18.7%
Number/percentage of T's	31,404,648 / 32.14%
Number/percentage of G's	24,867,974 / 25.45%
Number/percentage of N's	1,552 / 0%
GC Percentage	44.15%

2.3. Coverage

Mean	0.0316

Standard Deviation	0.3011

2.4. Mapping Quality

Mean Mapping Quality	44.73

2.5. Mismatches and indels

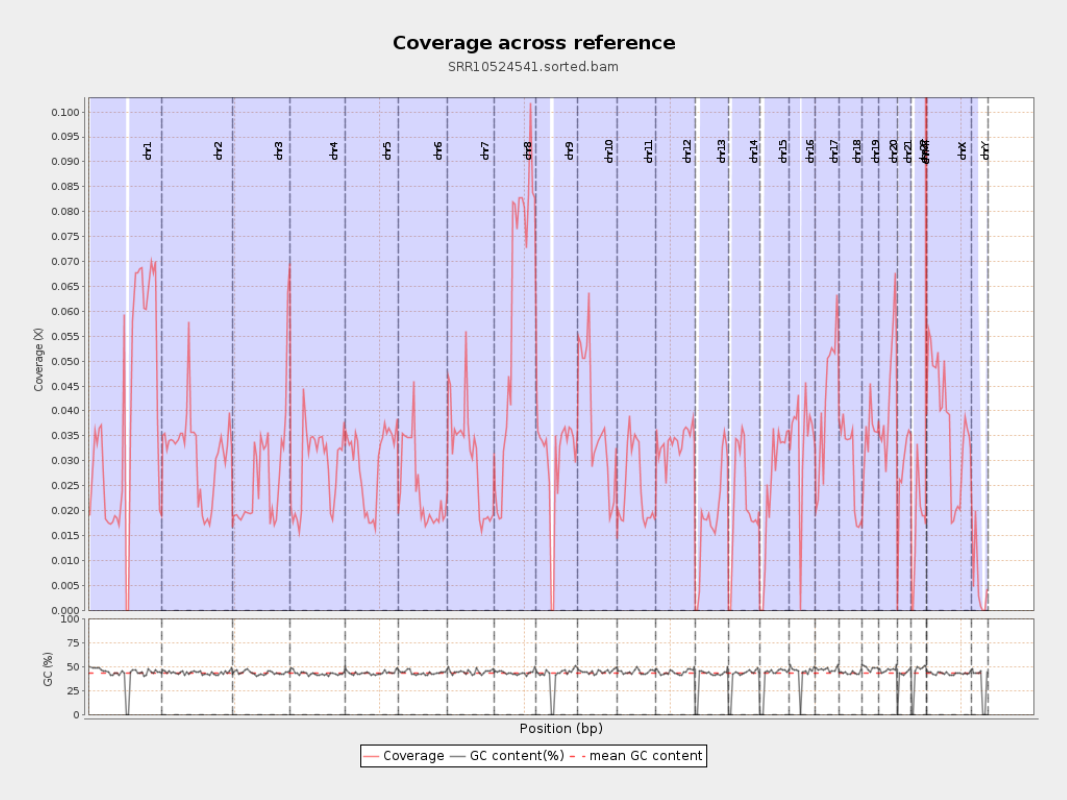
General error rate	0.51%
Mismatches	488,354
Insertions	5,772
Mapped reads with at least one insertion	0.34%
Deletions	18,480
Mapped reads with at least one deletion	1.09%
Homopolymer indels	43.25%

2.6. Chromosome stats

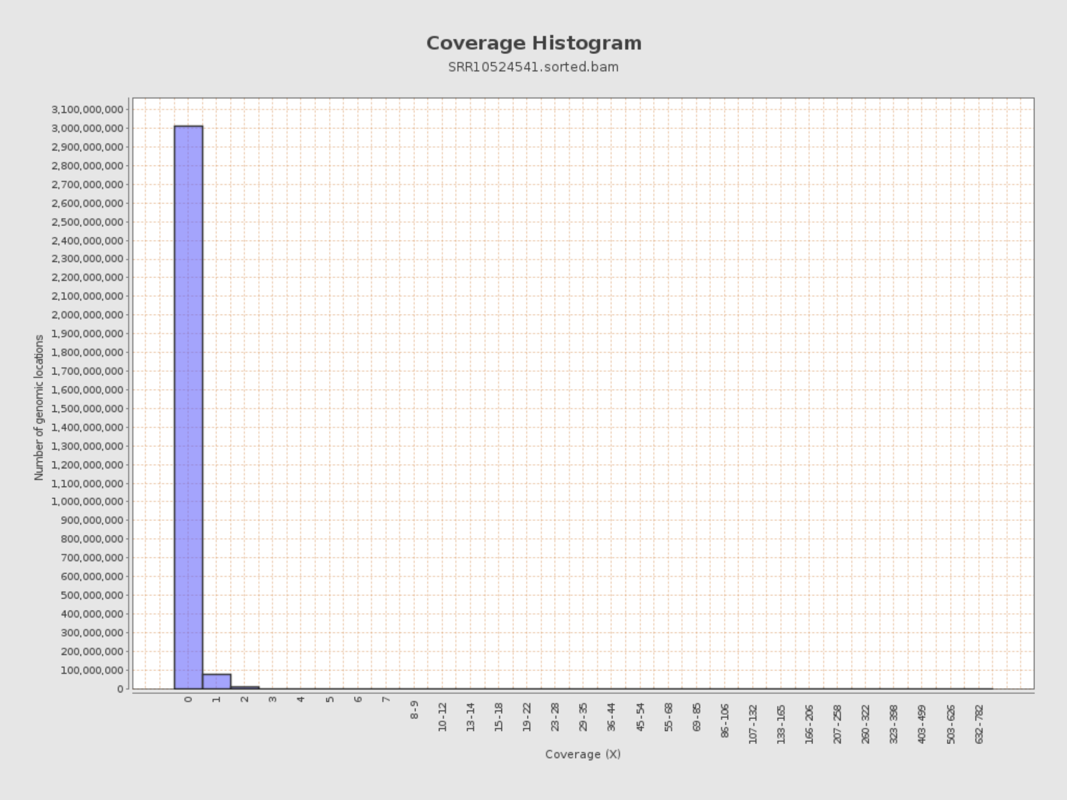
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9655437	0.0387	0.581
chr2	243199373	7640247	0.0314	0.3484
chr3	198022430	5313722	0.0268	0.1834
chr4	191154276	5500881	0.0288	0.2151
chr5	180915260	5348934	0.0296	0.1922
chr6	171115067	4194811	0.0245	0.2215
chr7	159138663	4889249	0.0307	0.3718

chr8	146364022	8817333	0.0602	0.3271
chr9	141213431	4198433	0.0297	0.2445
chr10	135534747	5132005	0.0379	0.3108
chr11	135006516	3328808	0.0247	0.2698
chr12	133851895	4531092	0.0339	0.2052
chr13	115169878	2164002	0.0188	0.1522
chr14	107349540	2313432	0.0216	0.1676
chr15	102531392	2547137	0.0248	0.1791
chr16	90354753	3097840	0.0343	0.2236
chr17	81195210	3475140	0.0428	0.2437
chr18	78077248	2298457	0.0294	0.444
chr19	59128983	2072182	0.035	0.3979
chr20	63025520	2755199	0.0437	0.2339
chr21	48129895	1353627	0.0281	0.2059
chr22	51304566	836161	0.0163	0.141
chrMT	16571	131009	7.9059	5.2352
chrX	155270560	5806218	0.0374	0.2383
chrY	59373566	329018	0.0055	0.1647

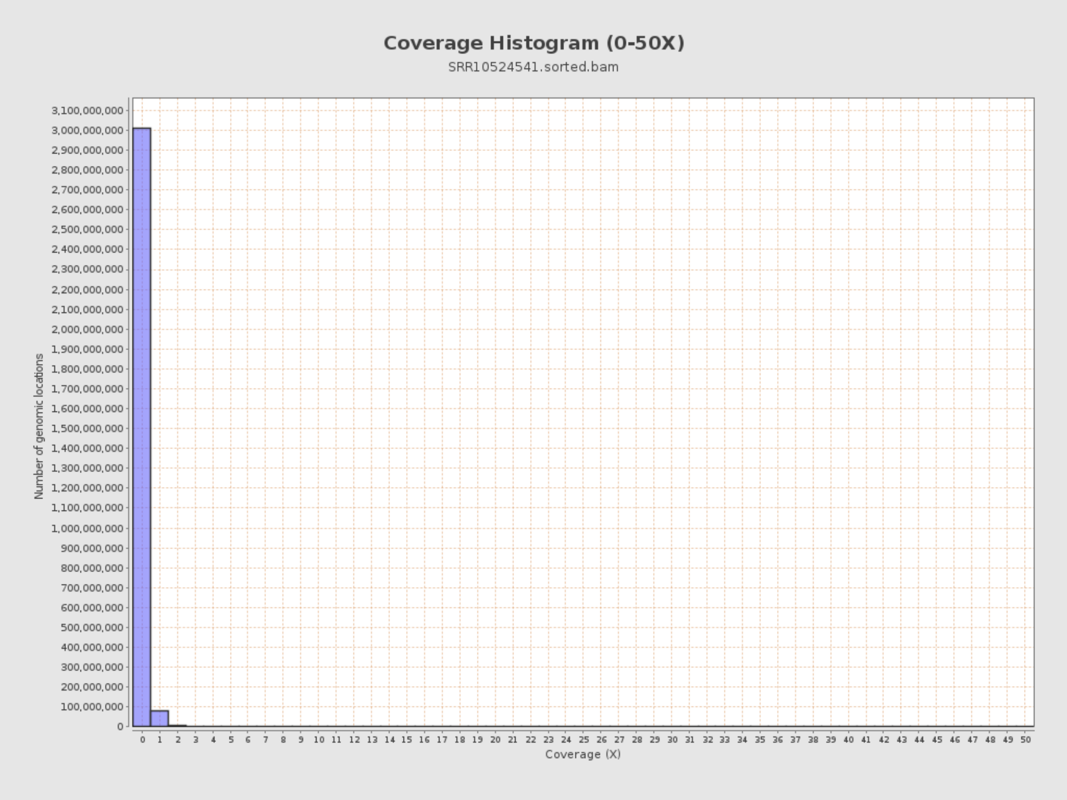
3. Results : Coverage across reference



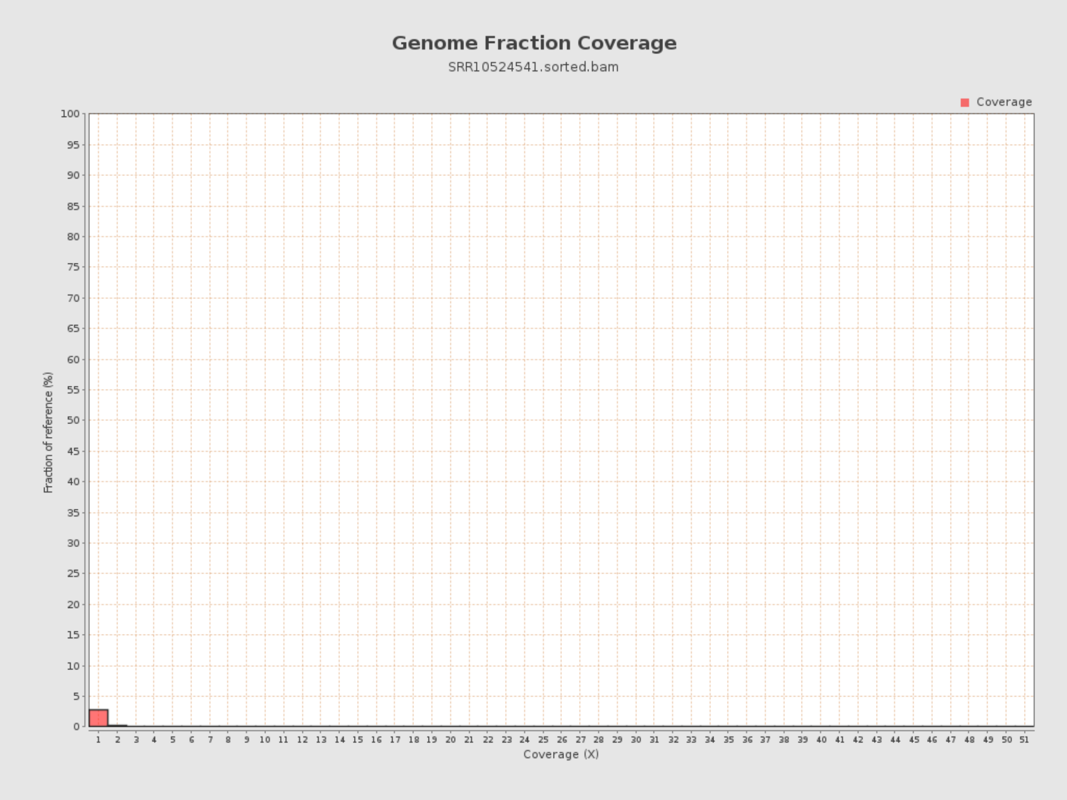
4. Results : Coverage Histogram



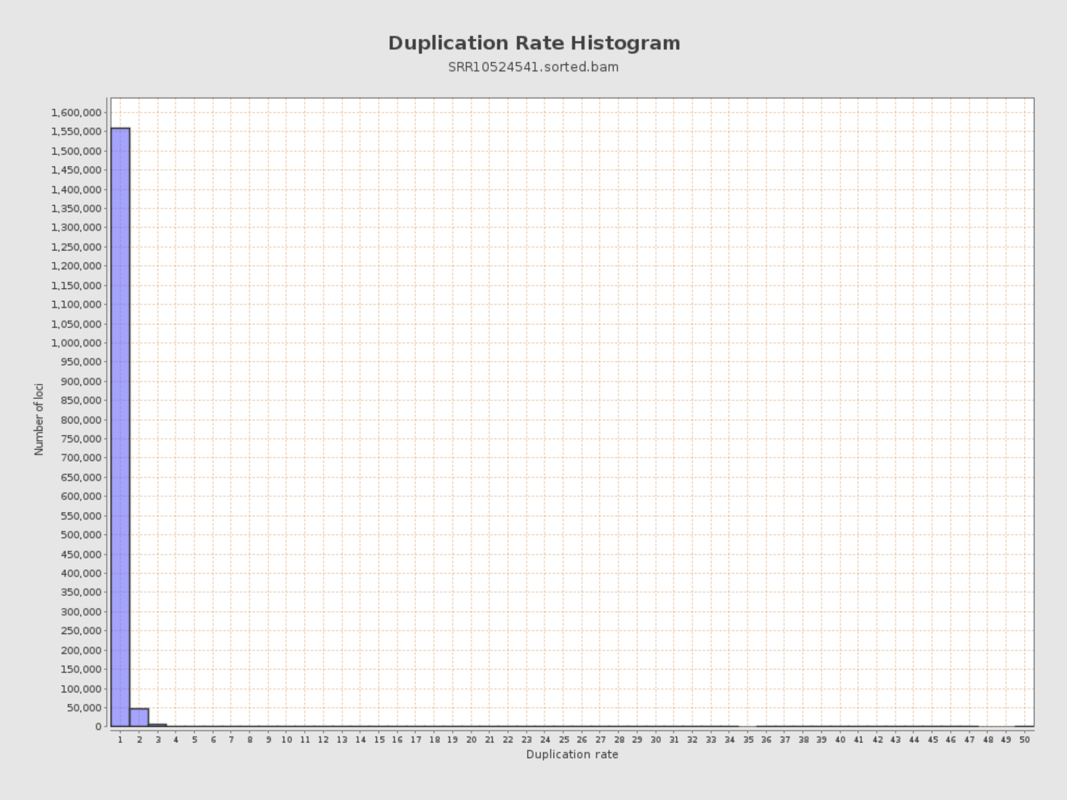
5. Results : Coverage Histogram (0-50X)



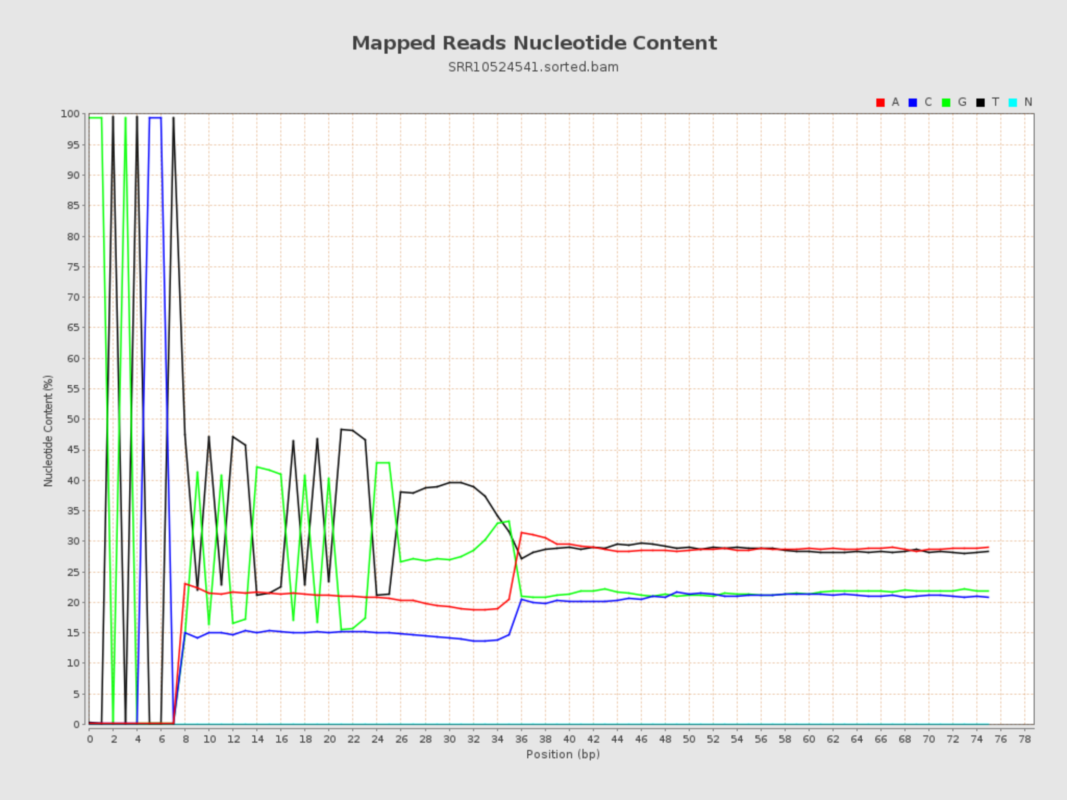
6. Results : Genome Fraction Coverage



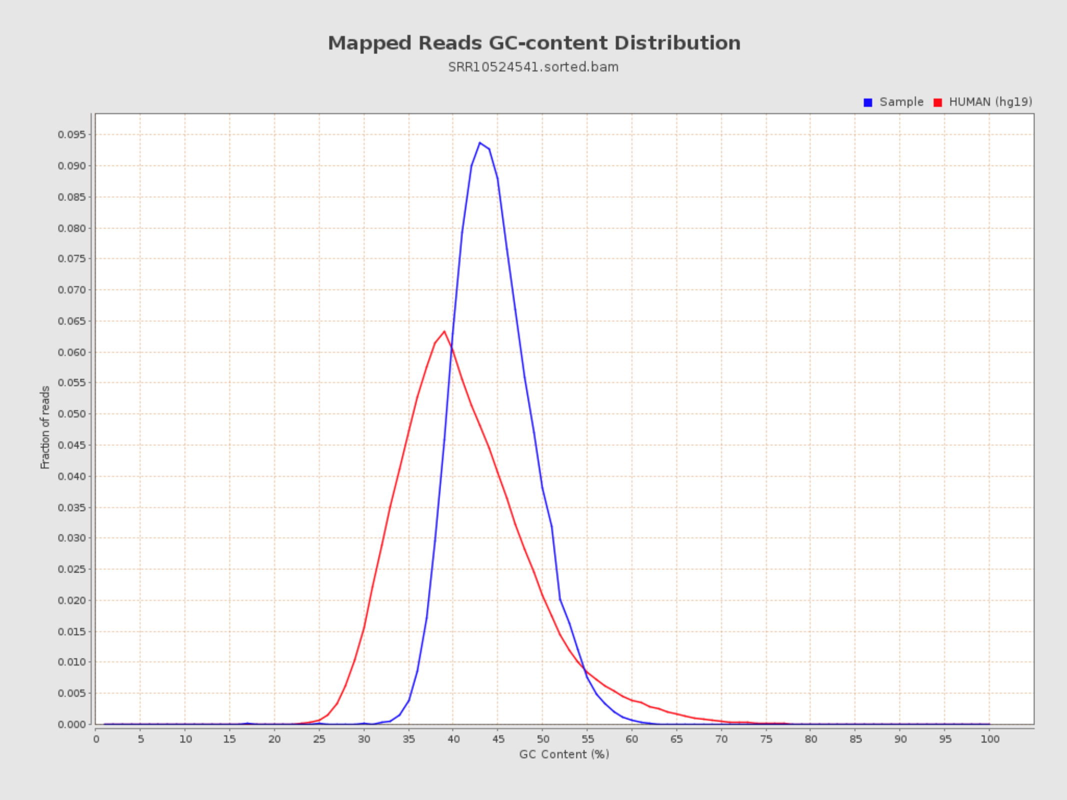
7. Results : Duplication Rate Histogram



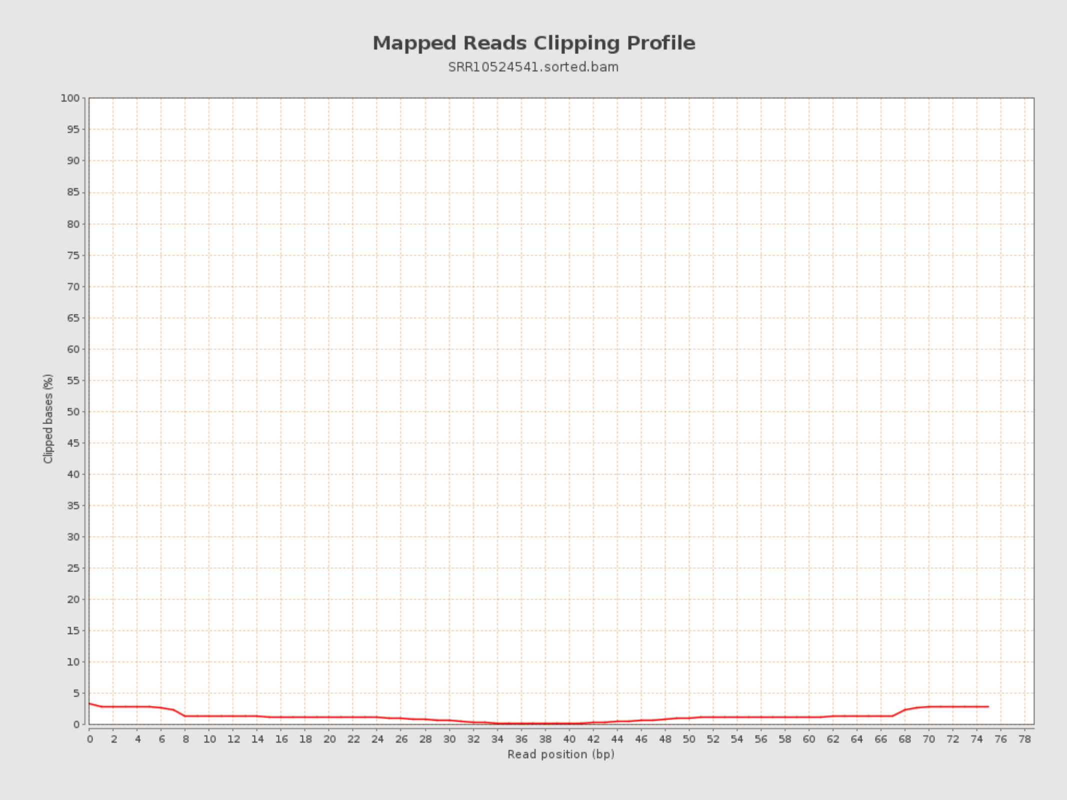
8. Results : Mapped Reads Nucleotide Content



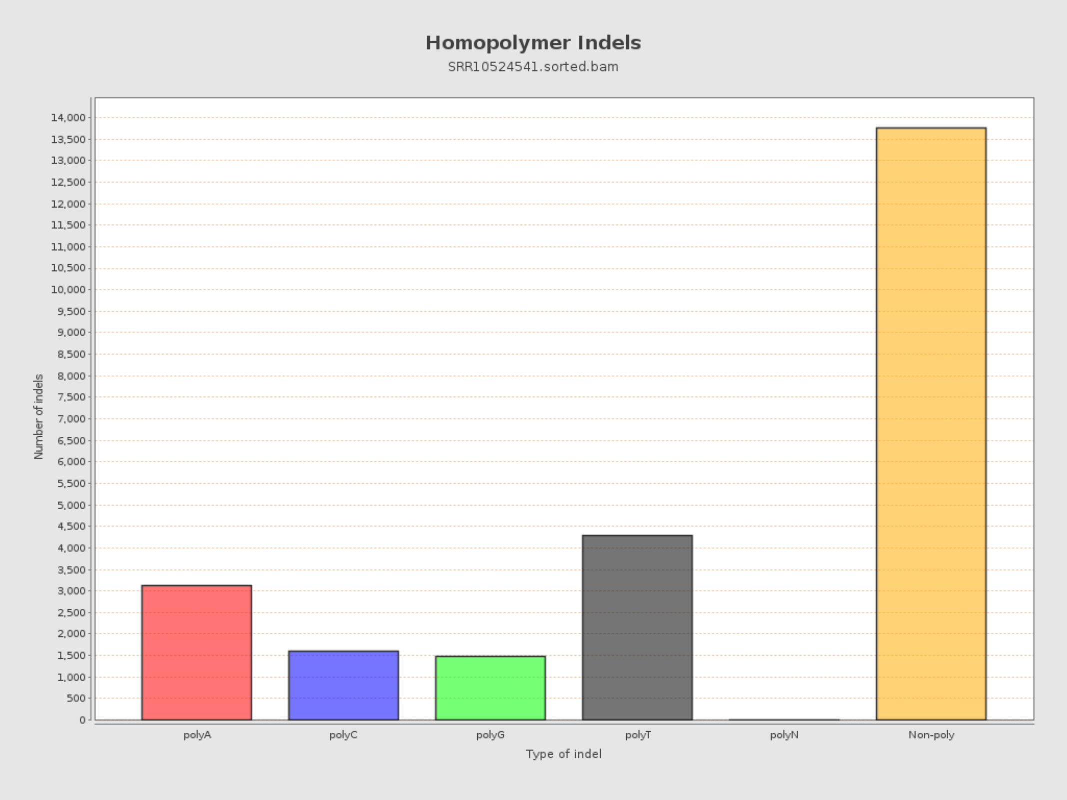
9. Results : Mapped Reads GC-content Distribution



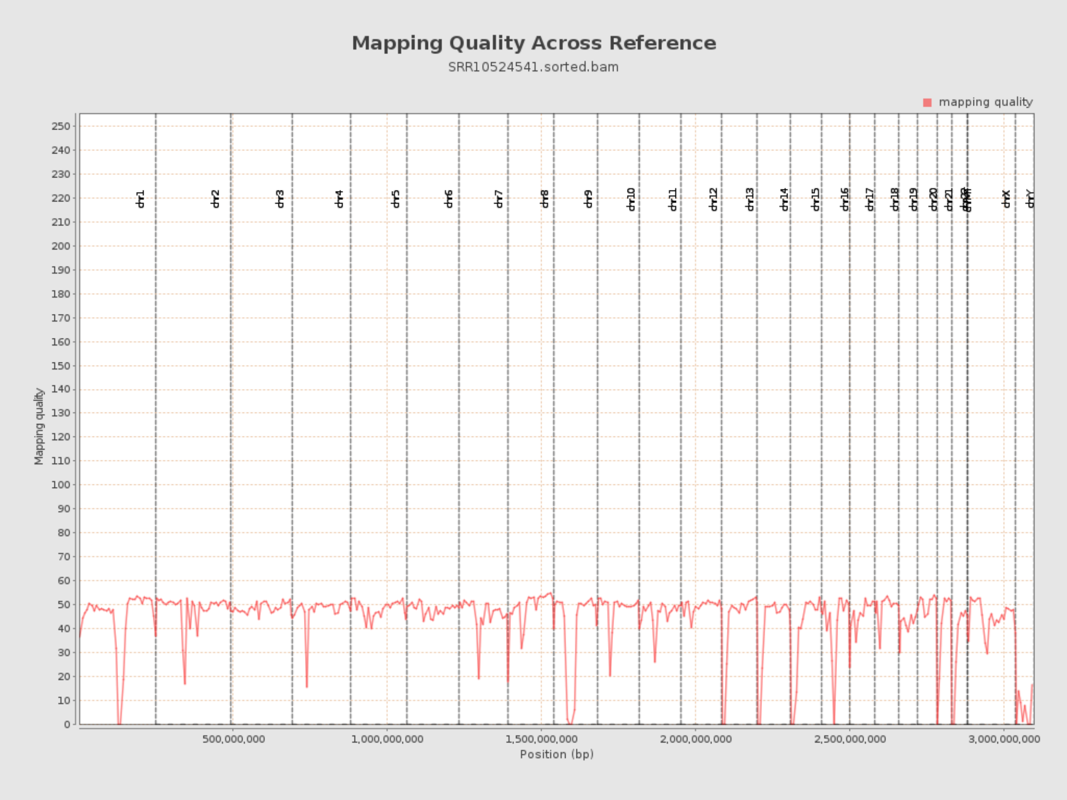
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram