Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 09:41:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524535.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_SRR10524535 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524535.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 09:41:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524535.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,483,577
Mapped reads	1,367,051 / 92.15%
Unmapped reads	116,526 / 7.85%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,649 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	62,012 / 4.18%
Duplication rate	3.47%
Clipped reads	1,367,154 / 92.15%

2.2. ACGT Content

Number/percentage of A's	20,936,610 / 25.89%
Number/percentage of C's	16,128,348 / 19.94%
Number/percentage of T's	25,021,063 / 30.94%
Number/percentage of G's	18,789,222 / 23.23%
Number/percentage of N's	1,251 / 0%
GC Percentage	43.17%

2.3. Coverage

Mean	0.0261

Standard Deviation	0.2555

2.4. Mapping Quality

Mean Mapping Quality	45.56

2.5. Mismatches and indels

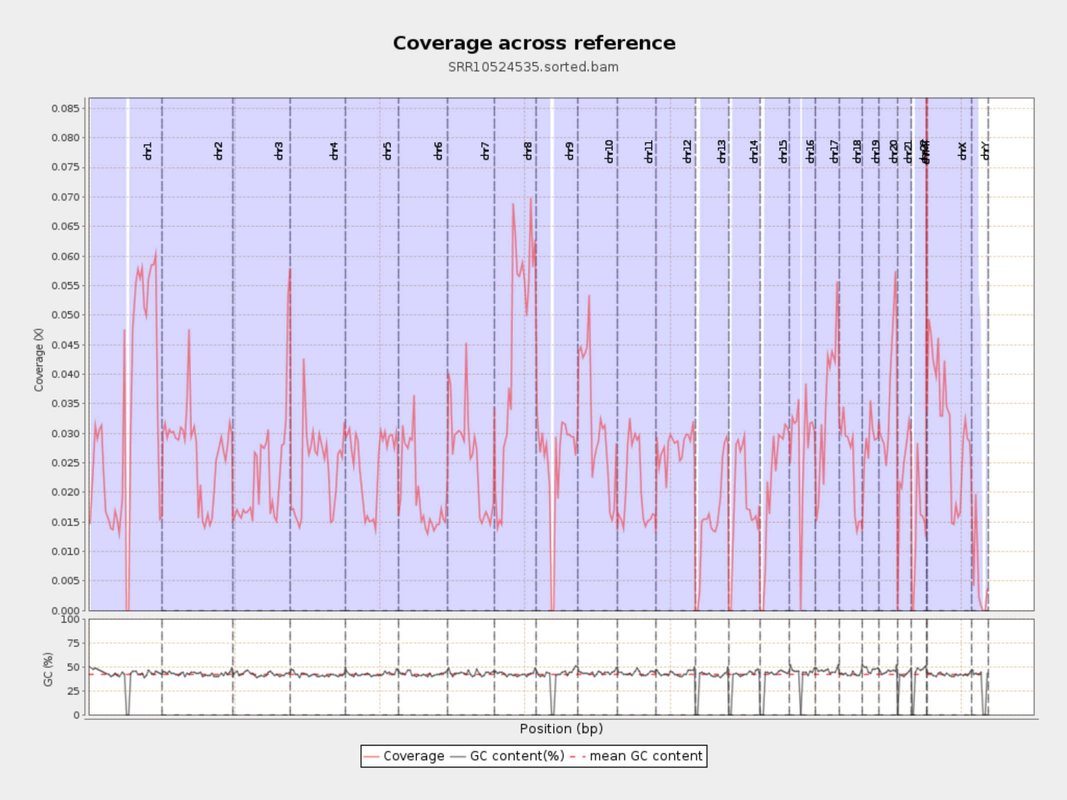
General error rate	0.52%
Mismatches	409,260
Insertions	6,525
Mapped reads with at least one insertion	0.47%
Deletions	15,701
Mapped reads with at least one deletion	1.14%
Homopolymer indels	41.46%

2.6. Chromosome stats

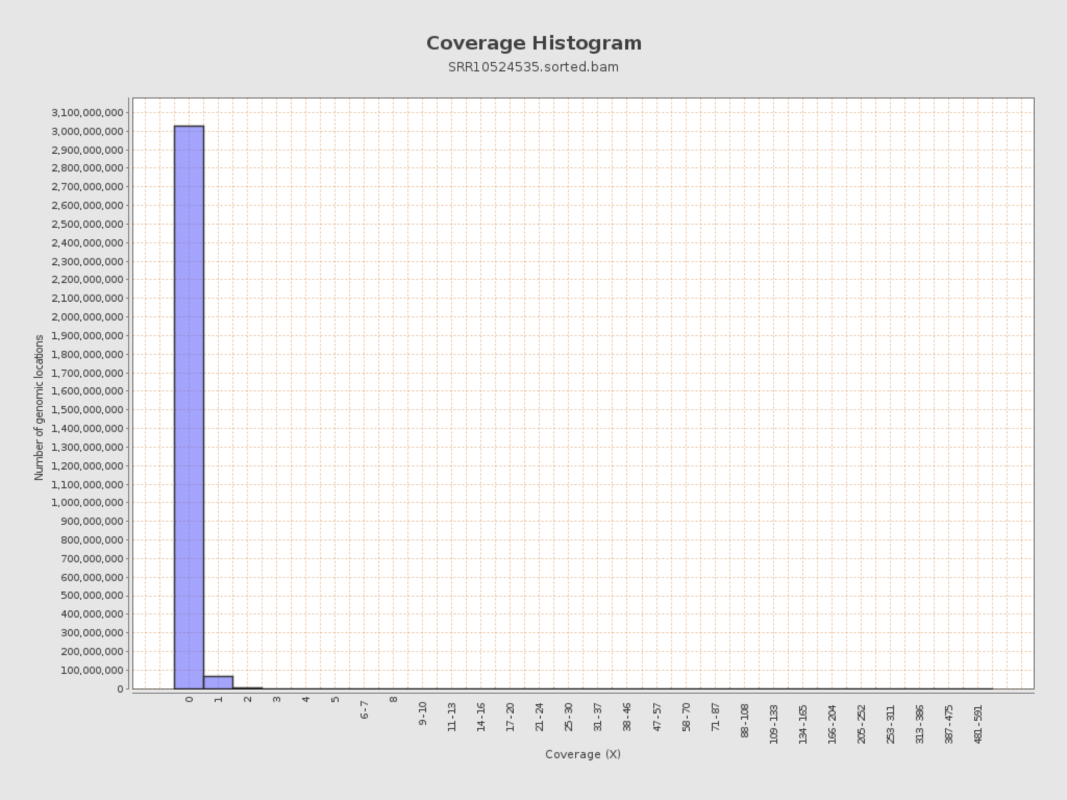
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8103714	0.0325	0.4706
chr2	243199373	6514747	0.0268	0.284
chr3	198022430	4492834	0.0227	0.1667
chr4	191154276	4607348	0.0241	0.2031
chr5	180915260	4464060	0.0247	0.1747
chr6	171115067	3391261	0.0198	0.1903
chr7	159138663	4134219	0.026	0.3001

chr8	146364022	6523930	0.0446	0.2862
chr9	141213431	3525655	0.025	0.2195
chr10	135534747	4307679	0.0318	0.2741
chr11	135006516	2789731	0.0207	0.2171
chr12	133851895	3717009	0.0278	0.1842
chr13	115169878	1793408	0.0156	0.1377
chr14	107349540	1938882	0.0181	0.1524
chr15	102531392	2196162	0.0214	0.1633
chr16	90354753	2549412	0.0282	0.1999
chr17	81195210	2886424	0.0355	0.2222
chr18	78077248	1929598	0.0247	0.3934
chr19	59128983	1689127	0.0286	0.3186
chr20	63025520	2326479	0.0369	0.2157
chr21	48129895	1138485	0.0237	0.1958
chr22	51304566	679666	0.0132	0.1263
chrMT	16571	2826	0.1705	0.4385
chrX	155270560	4897171	0.0315	0.2145
chrY	59373566	302835	0.0051	0.1772

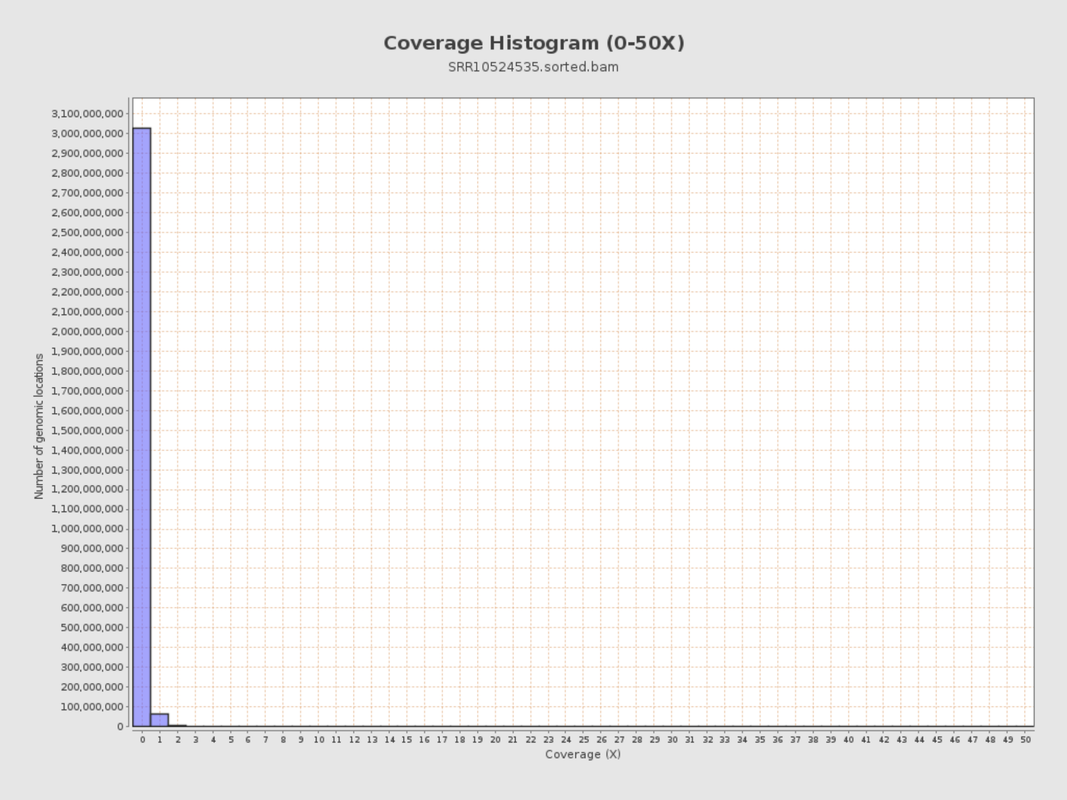
3. Results : Coverage across reference



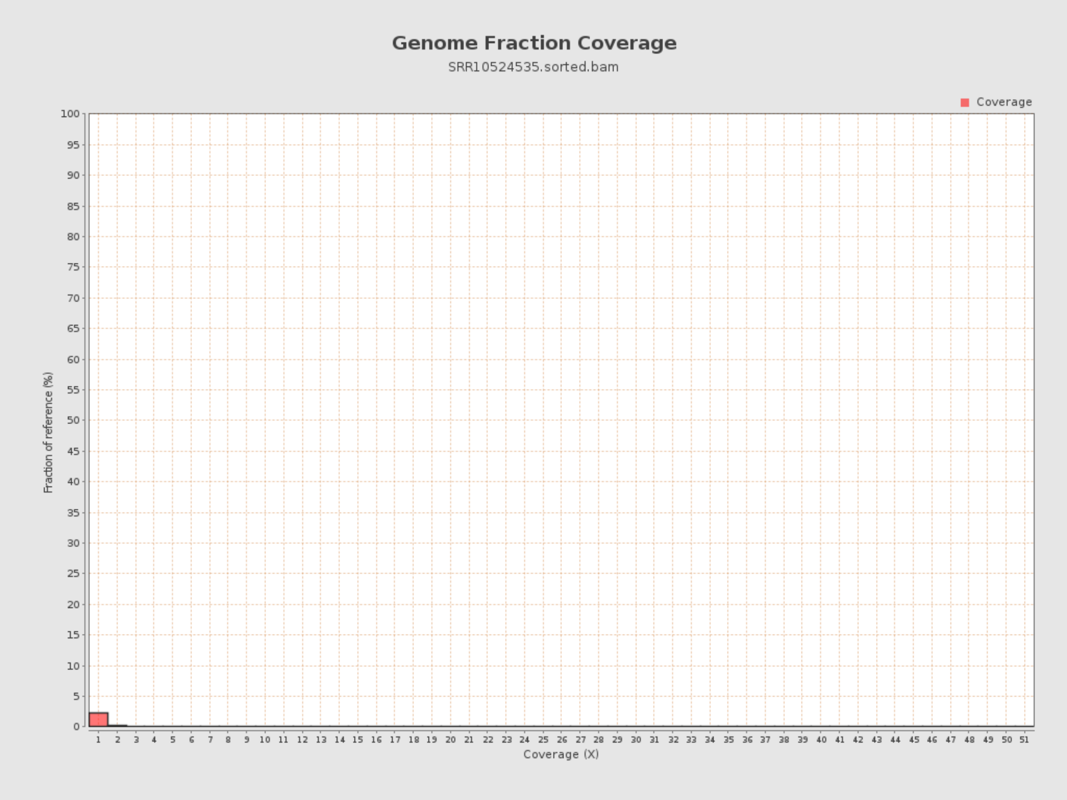
4. Results : Coverage Histogram



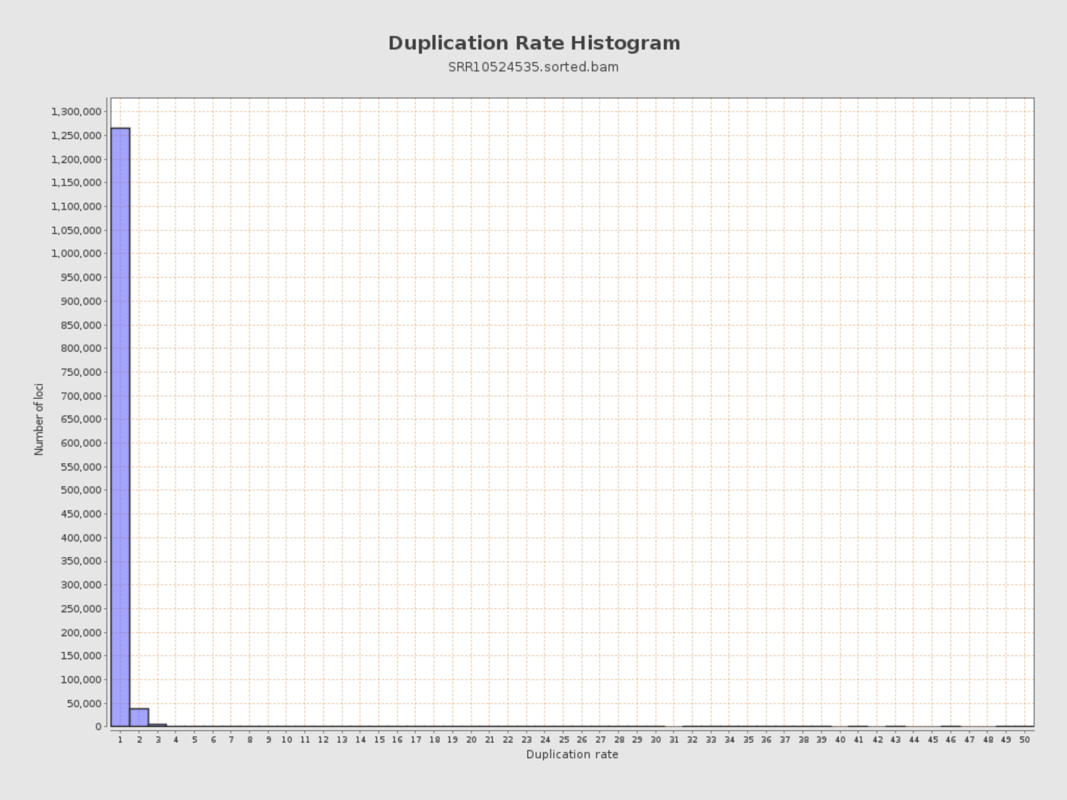
5. Results : Coverage Histogram (0-50X)



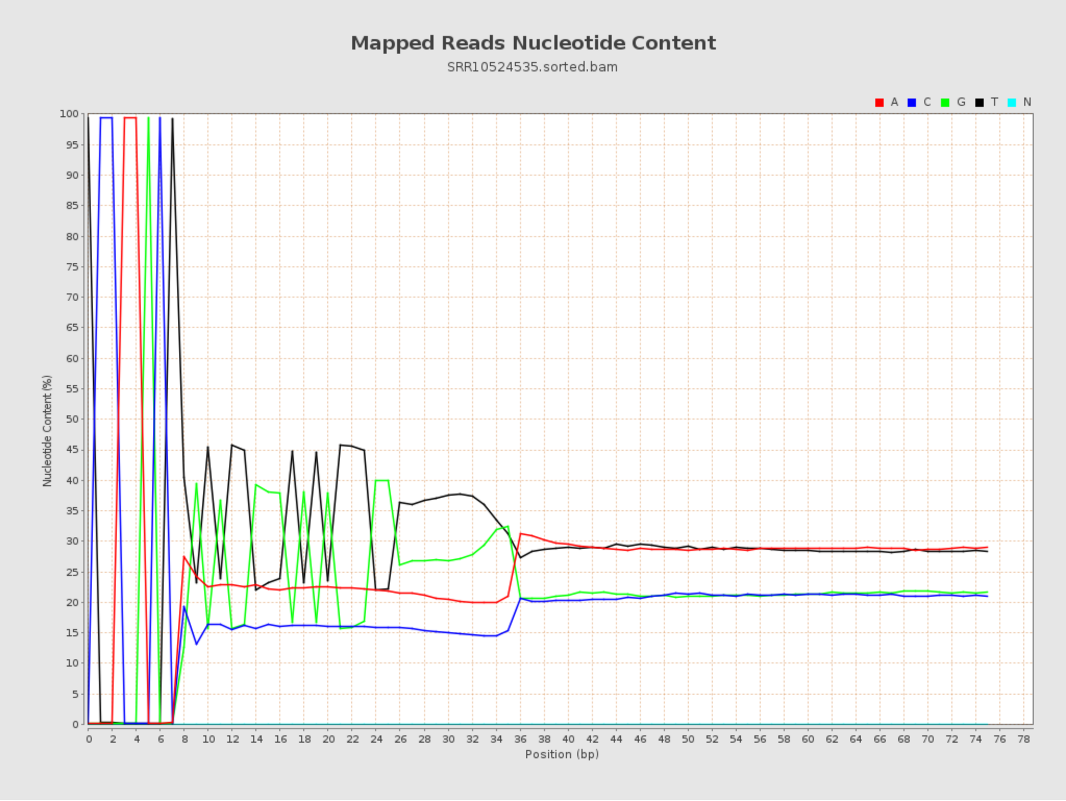
6. Results : Genome Fraction Coverage



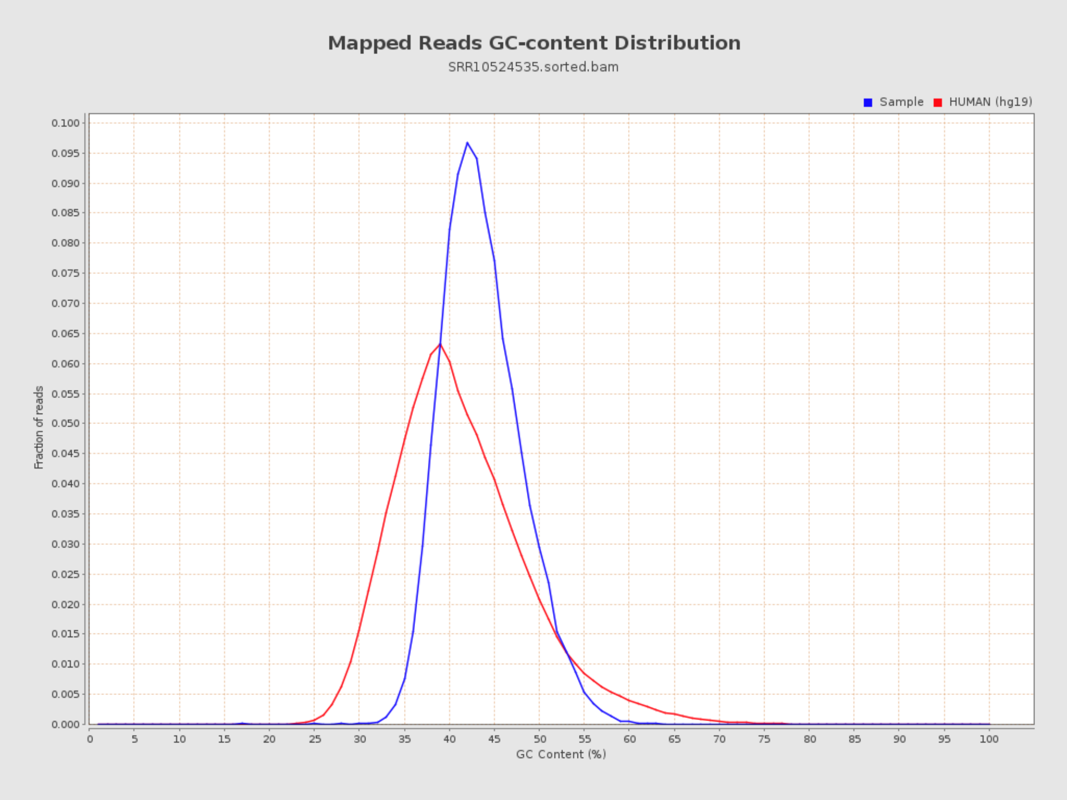
7. Results : Duplication Rate Histogram



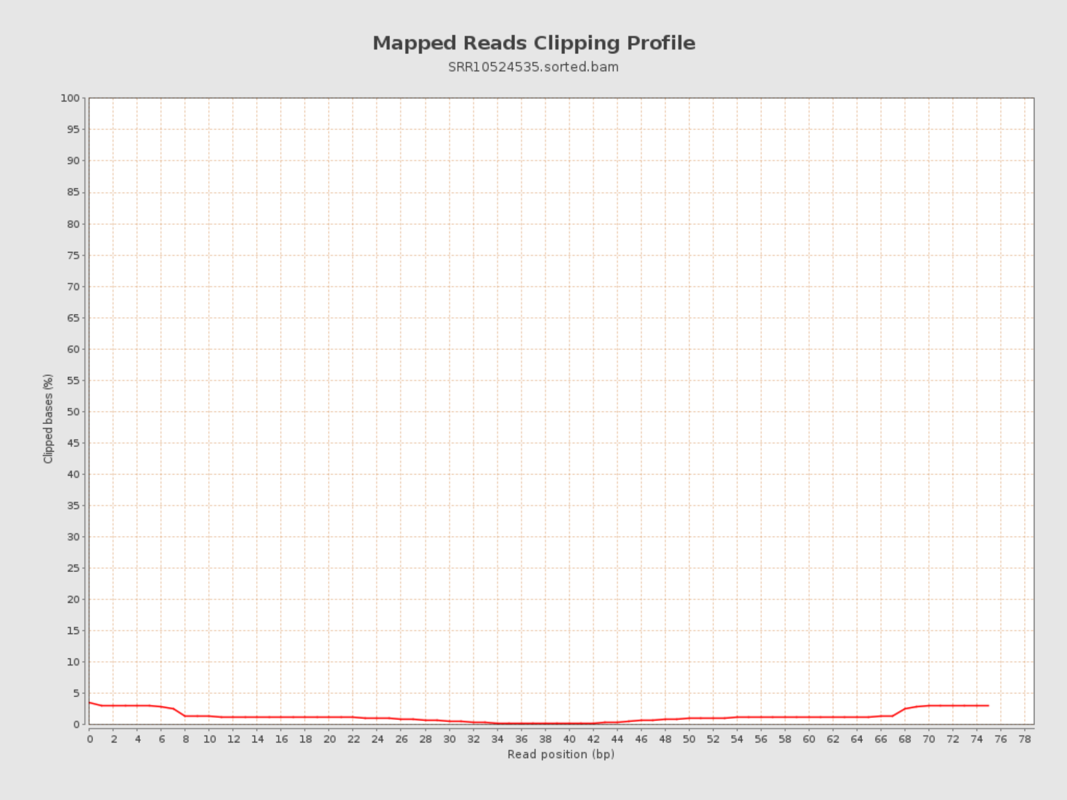
8. Results : Mapped Reads Nucleotide Content



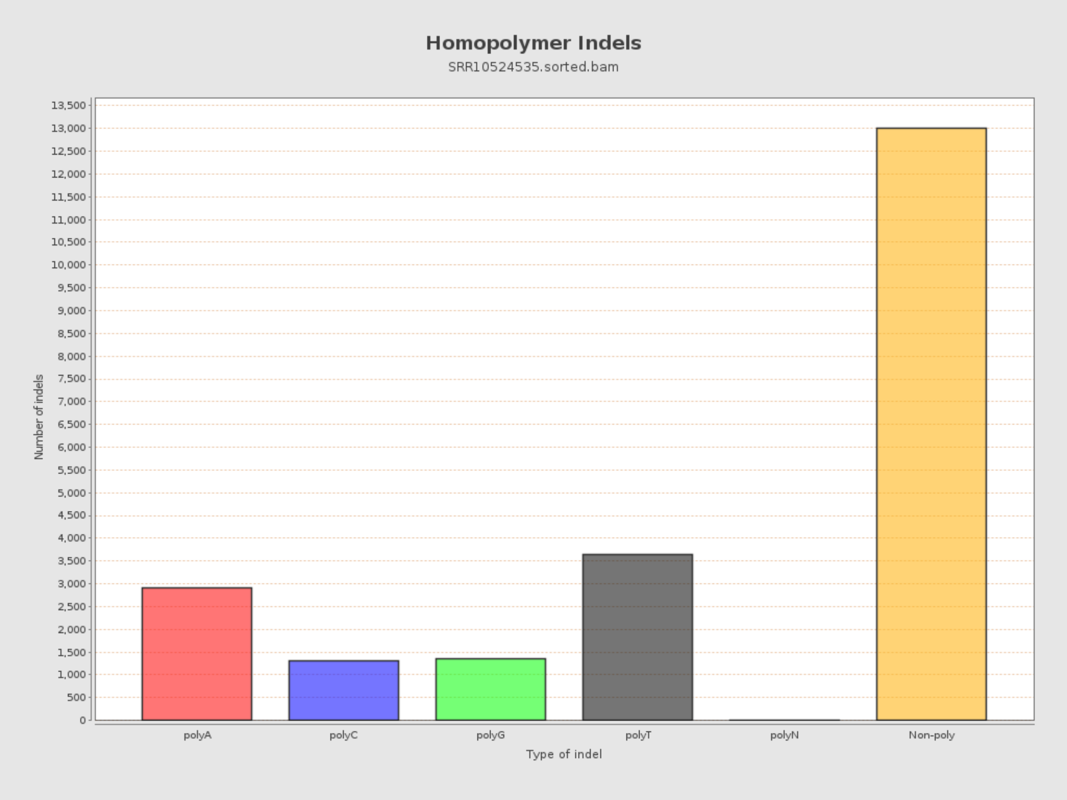
9. Results : Mapped Reads GC-content Distribution



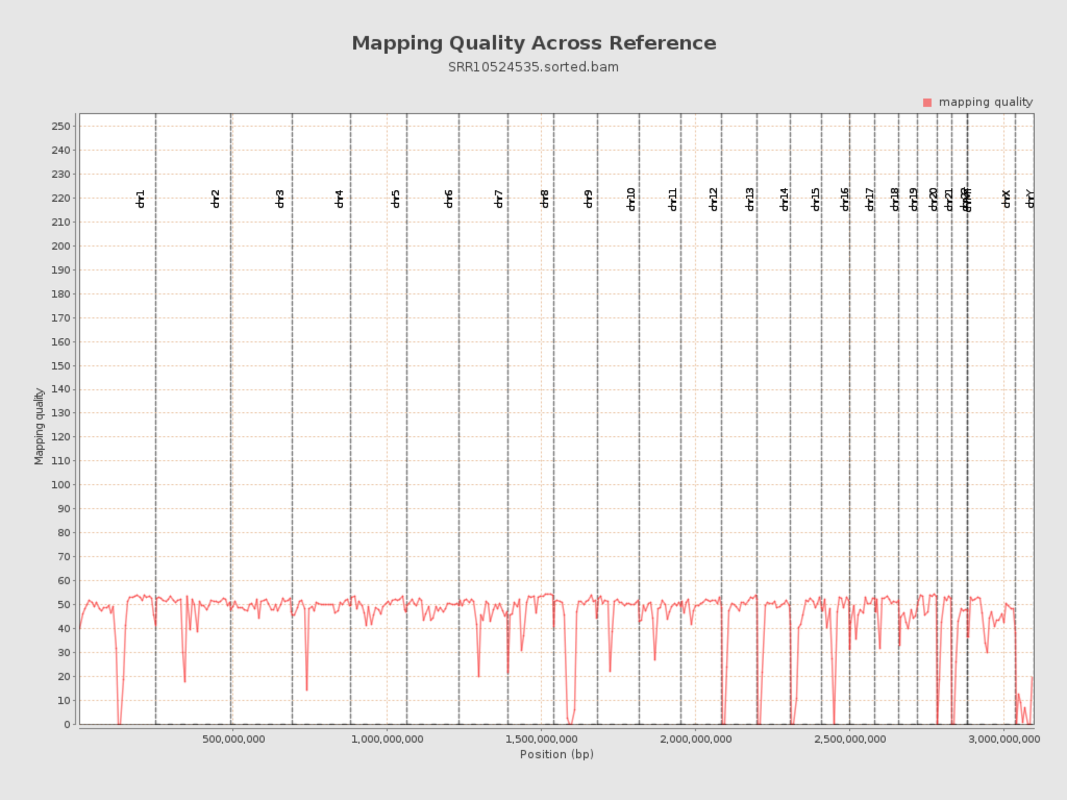
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram