Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 21:01:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524284.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_SRR10524284 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524284.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 21:01:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524284.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,602,914
Mapped reads	3,345,824 / 92.86%
Unmapped reads	257,090 / 7.14%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,435 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	226,310 / 6.28%
Duplication rate	4.99%
Clipped reads	3,353,930 / 93.09%

2.2. ACGT Content

Number/percentage of A's	49,214,606 / 25.09%
Number/percentage of C's	38,079,763 / 19.41%
Number/percentage of T's	61,444,537 / 31.32%
Number/percentage of G's	47,417,228 / 24.17%
Number/percentage of N's	24,559 / 0.01%
GC Percentage	43.58%

2.3. Coverage

Mean	0.0634

Standard Deviation	0.5902

2.4. Mapping Quality

Mean Mapping Quality	46.22

2.5. Mismatches and indels

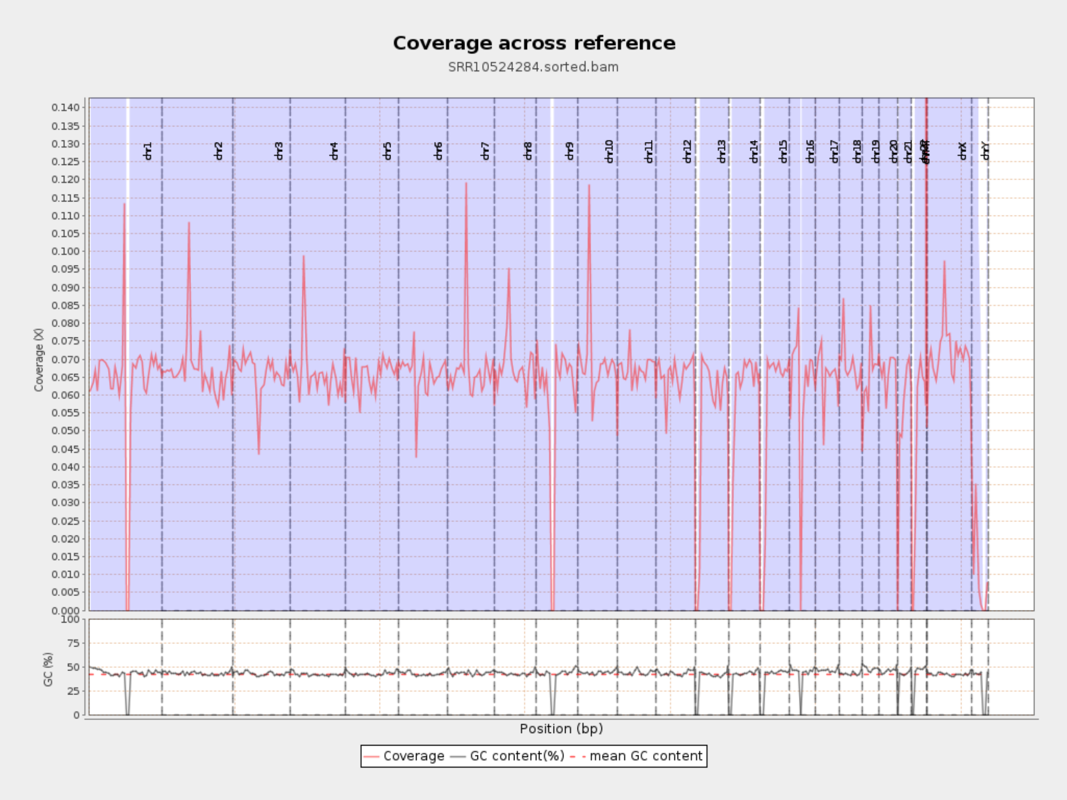
General error rate	0.49%
Mismatches	946,830
Insertions	11,985
Mapped reads with at least one insertion	0.36%
Deletions	36,569
Mapped reads with at least one deletion	1.08%
Homopolymer indels	44.96%

2.6. Chromosome stats

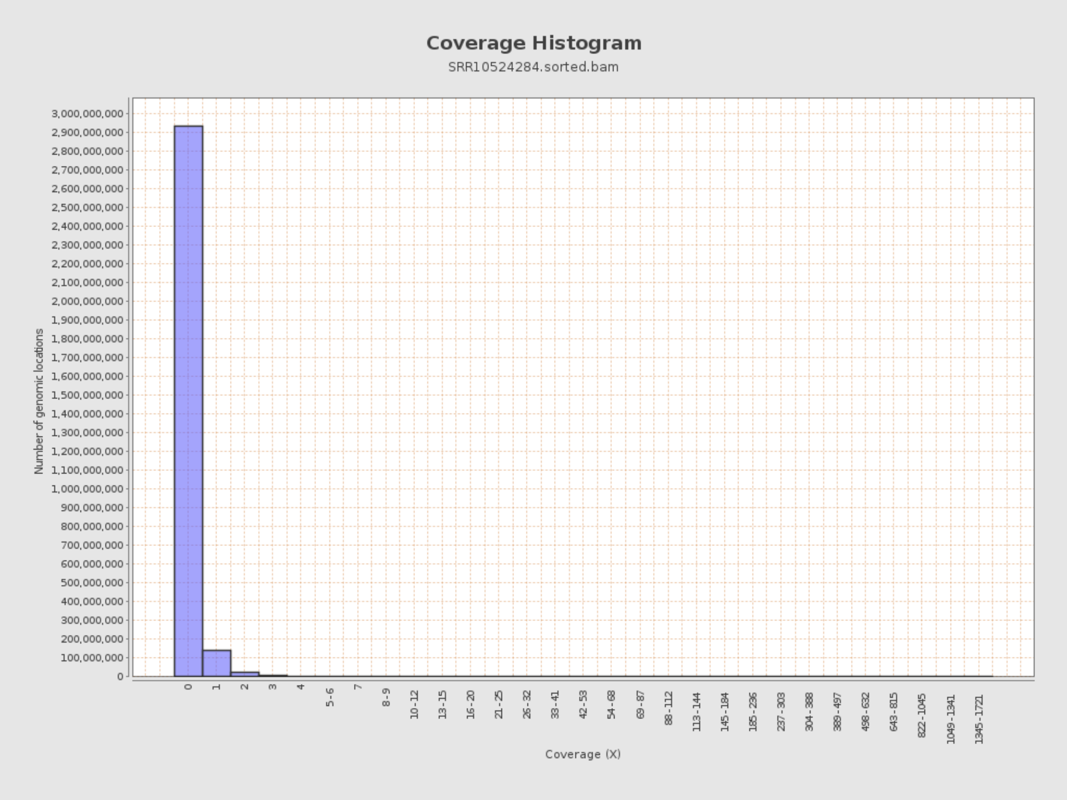
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15834569	0.0635	1.2621
chr2	243199373	16381049	0.0674	0.6054
chr3	198022430	13066701	0.066	0.3011
chr4	191154276	12652780	0.0662	0.358
chr5	180915260	11957022	0.0661	0.3068
chr6	171115067	11276993	0.0659	0.3481
chr7	159138663	10815633	0.068	0.8816

chr8	146364022	9977321	0.0682	0.5468
chr9	141213431	8216090	0.0582	0.5136
chr10	135534747	9429441	0.0696	0.5168
chr11	135006516	9047936	0.067	0.5272
chr12	133851895	8774514	0.0656	0.3155
chr13	115169878	6169954	0.0536	0.2723
chr14	107349540	5996751	0.0559	0.3101
chr15	102531392	5587981	0.0545	0.2739
chr16	90354753	5624245	0.0622	0.3406
chr17	81195210	5279367	0.065	0.342
chr18	78077248	5376294	0.0689	1.1005
chr19	59128983	3896995	0.0659	0.7818
chr20	63025520	4171360	0.0662	0.3145
chr21	48129895	2592109	0.0539	0.3257
chr22	51304566	2329589	0.0454	0.2476
chrMT	16571	65598	3.9586	2.866
chrX	155270560	11121404	0.0716	0.3962
chrY	59373566	596970	0.0101	0.2444

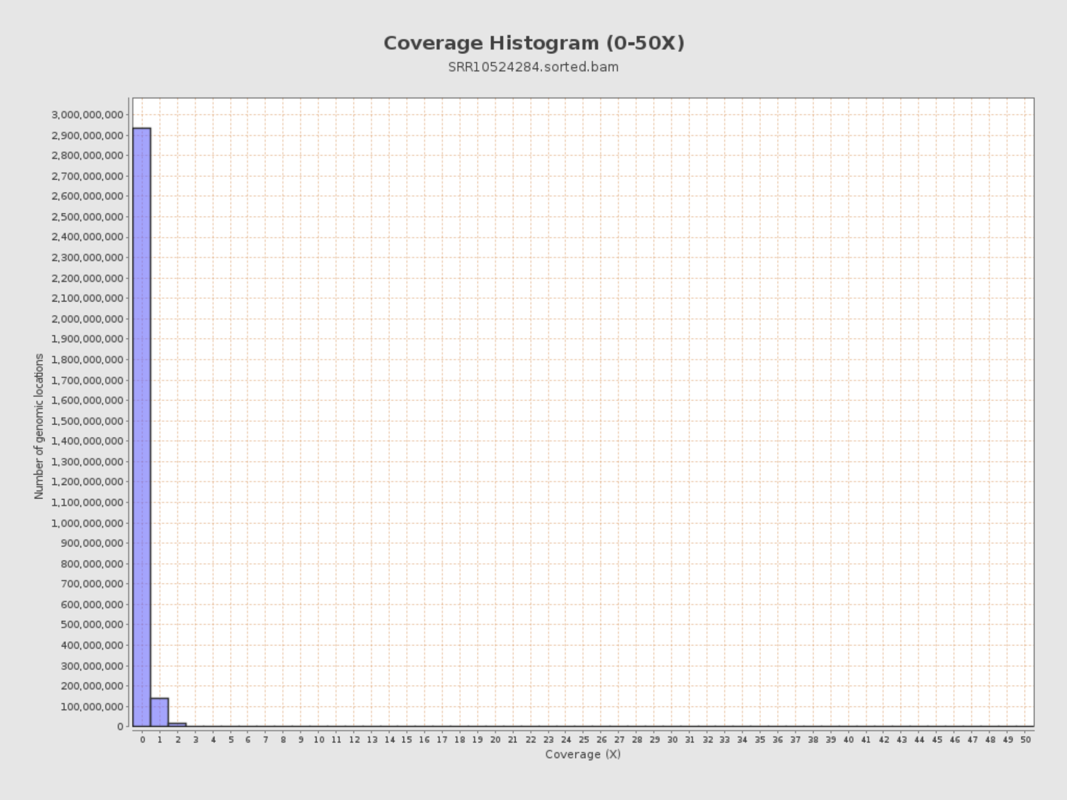
3. Results : Coverage across reference



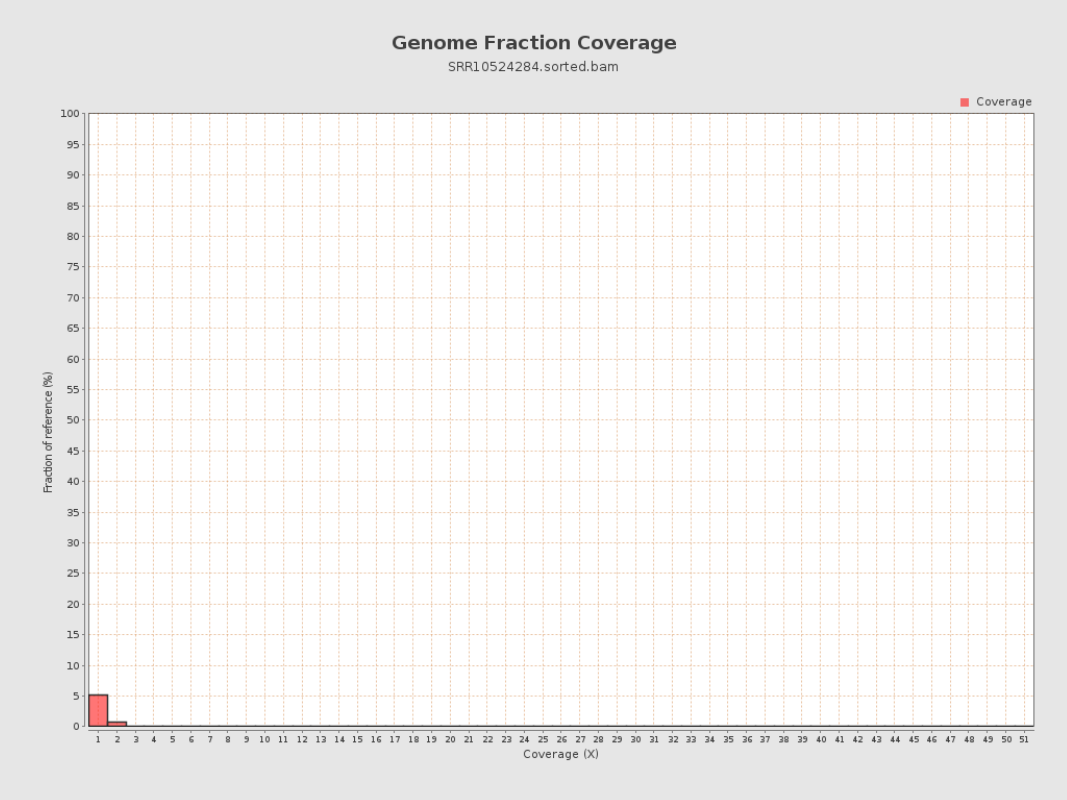
4. Results : Coverage Histogram



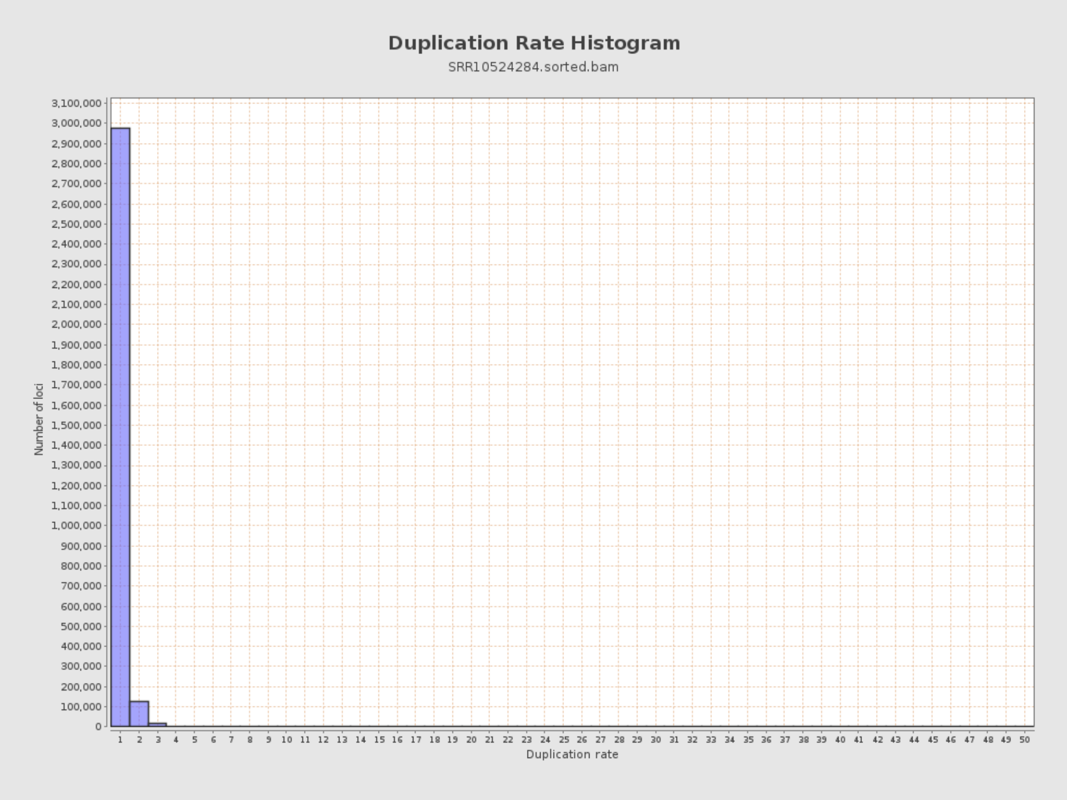
5. Results : Coverage Histogram (0-50X)



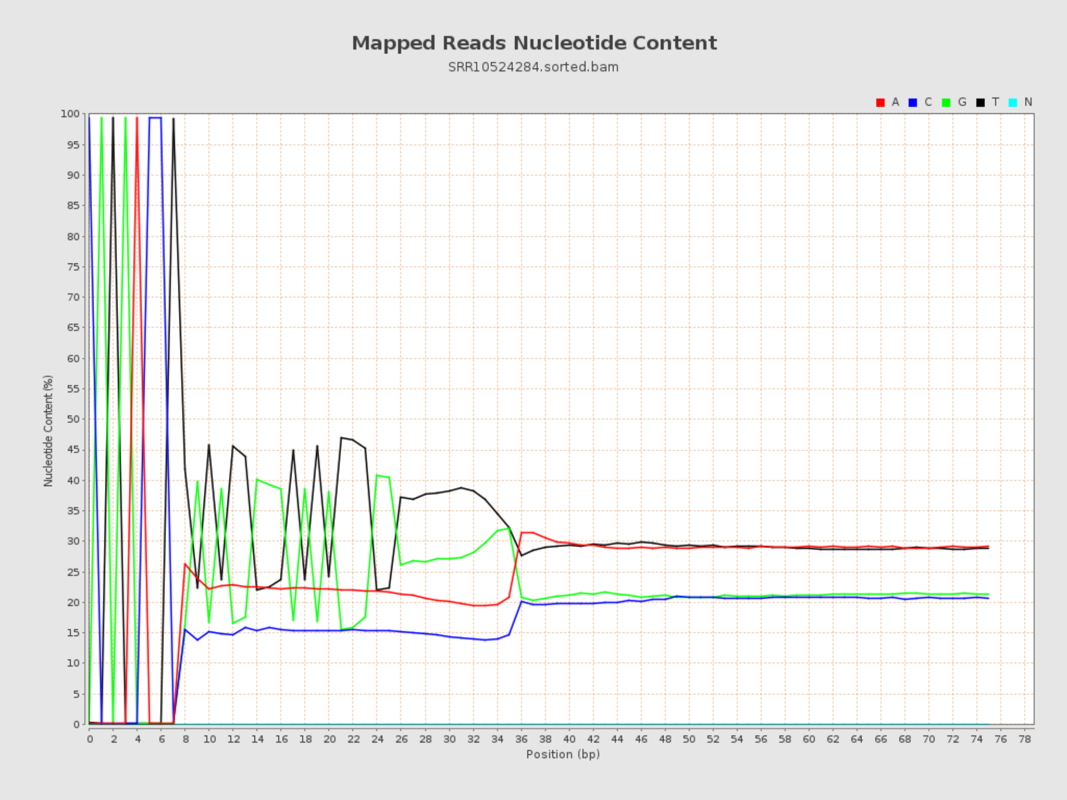
6. Results : Genome Fraction Coverage



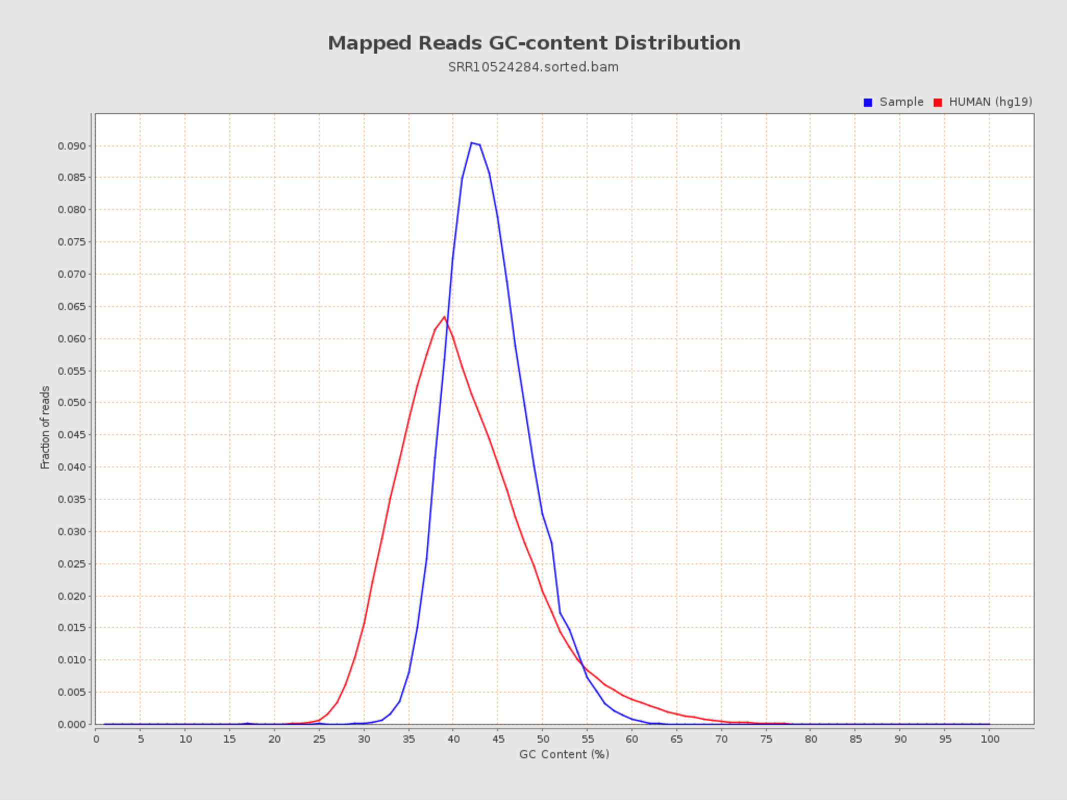
7. Results : Duplication Rate Histogram



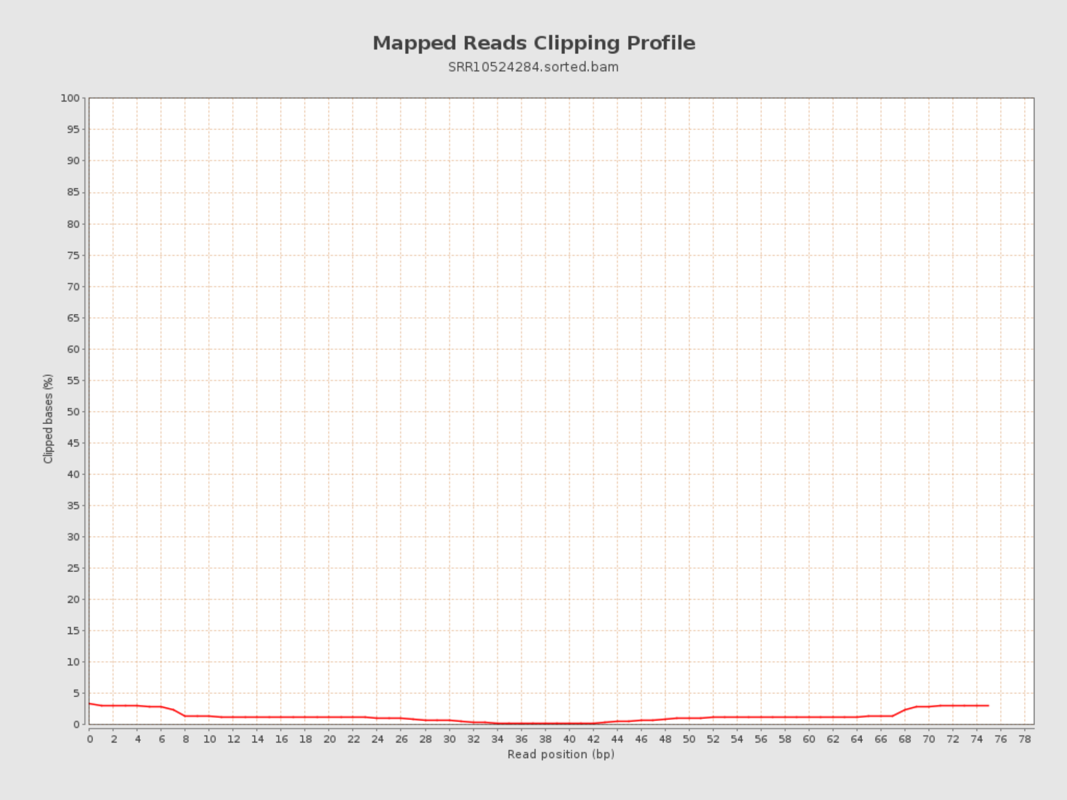
8. Results : Mapped Reads Nucleotide Content



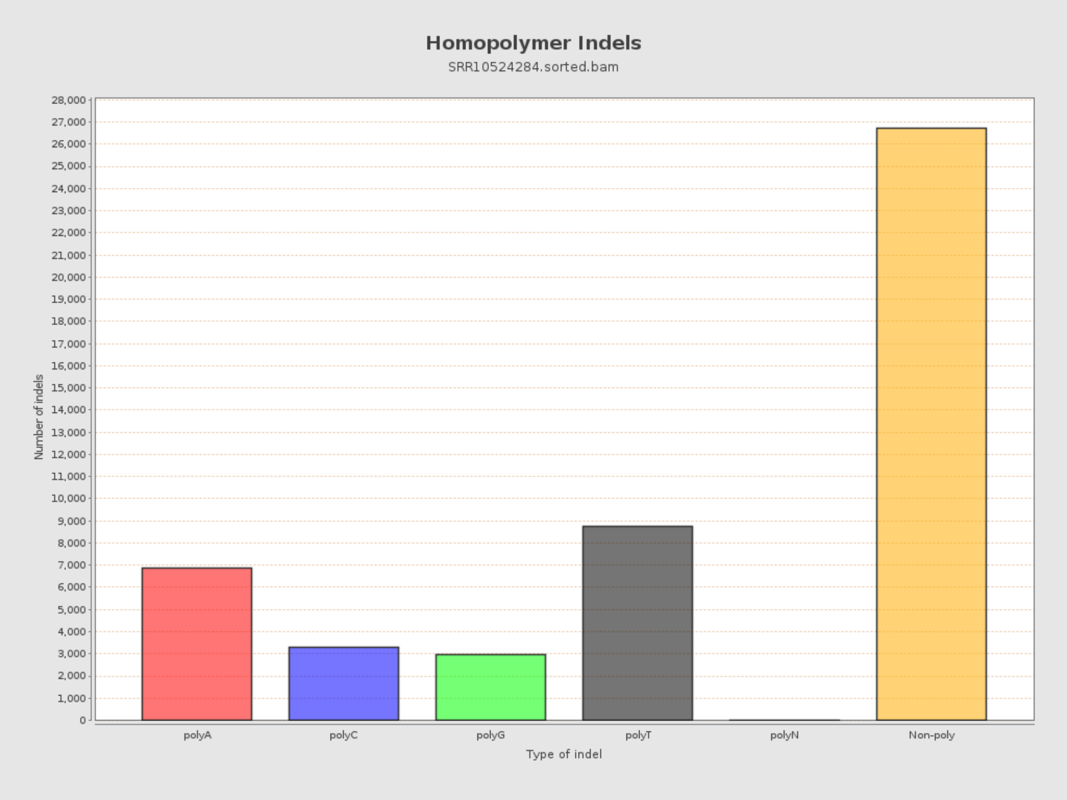
9. Results : Mapped Reads GC-content Distribution



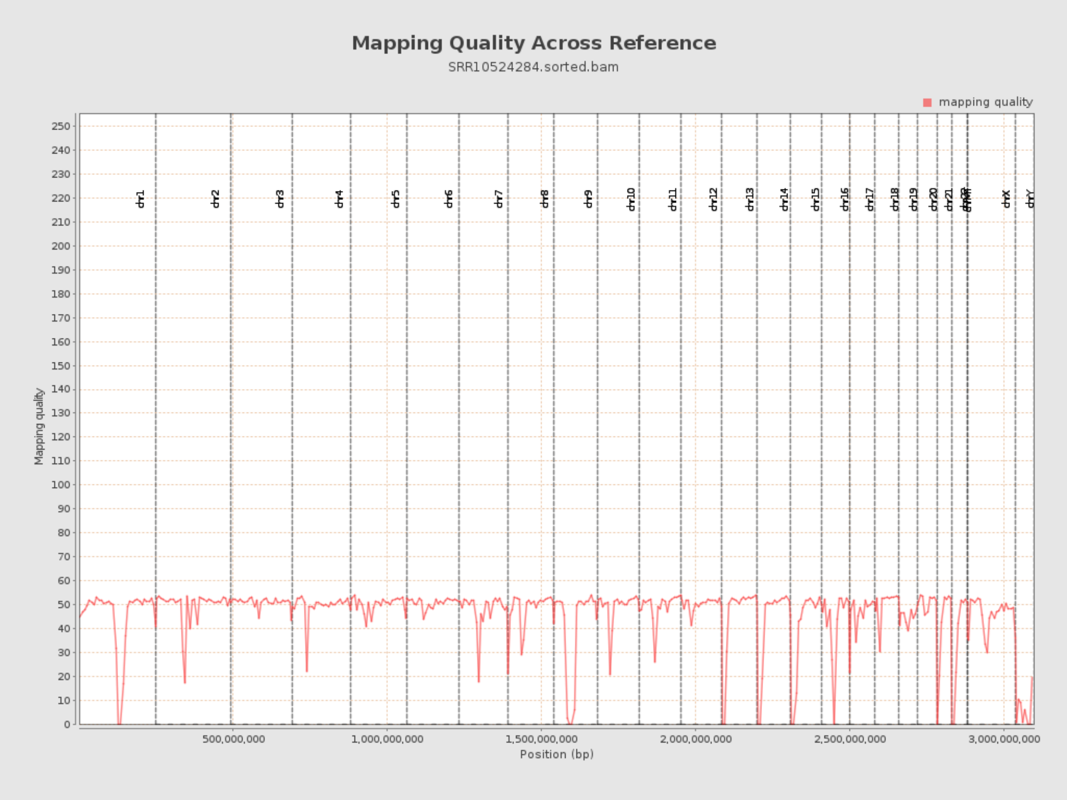
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram