Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 11:49:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524981.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_SRR10524981 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524981.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 11:49:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524981.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,269,611
Mapped reads	2,094,206 / 92.27%
Unmapped reads	175,405 / 7.73%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,696 / 0.21%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	109,914 / 4.84%
Duplication rate	4.01%
Clipped reads	2,093,290 / 92.23%

2.2. ACGT Content

Number/percentage of A's	30,723,907 / 25.48%
Number/percentage of C's	21,943,144 / 18.2%
Number/percentage of T's	39,165,081 / 32.48%
Number/percentage of G's	28,755,292 / 23.85%
Number/percentage of N's	1,204 / 0%
GC Percentage	42.04%

2.3. Coverage

Mean	0.039

Standard Deviation	0.3236

2.4. Mapping Quality

Mean Mapping Quality	45.66

2.5. Mismatches and indels

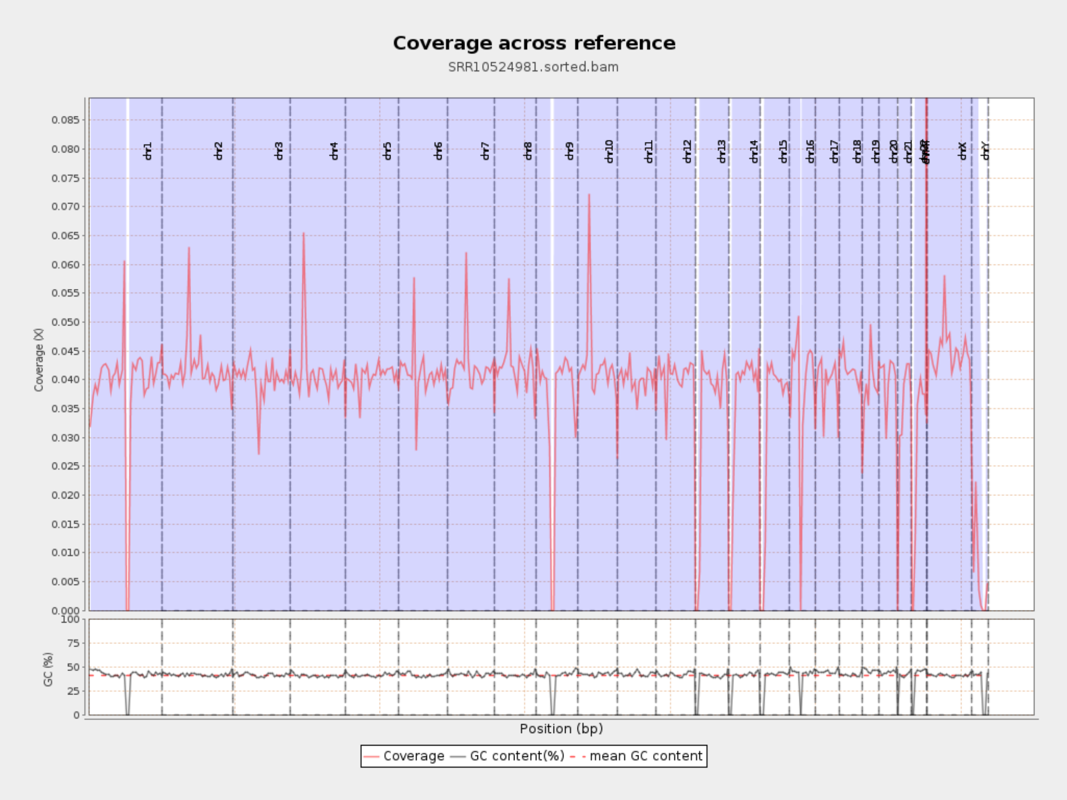
General error rate	0.5%
Mismatches	588,317
Insertions	7,676
Mapped reads with at least one insertion	0.36%
Deletions	21,756
Mapped reads with at least one deletion	1.03%
Homopolymer indels	42.21%

2.6. Chromosome stats

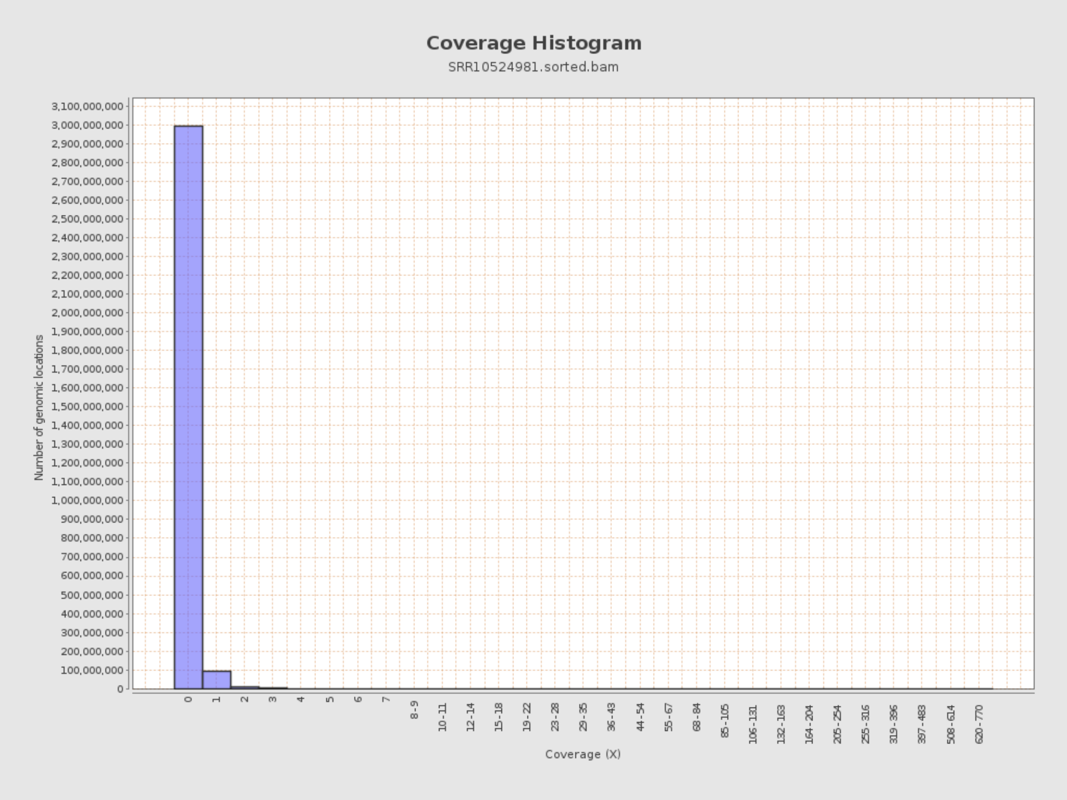
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9636998	0.0387	0.5484
chr2	243199373	10190215	0.0419	0.3772
chr3	198022430	7964376	0.0402	0.2302
chr4	191154276	7880555	0.0412	0.2694
chr5	180915260	7340959	0.0406	0.2304
chr6	171115067	7037420	0.0411	0.3035
chr7	159138663	6710331	0.0422	0.4035

chr8	146364022	6209373	0.0424	0.3481
chr9	141213431	5017272	0.0355	0.2859
chr10	135534747	5830584	0.043	0.3464
chr11	135006516	5379440	0.0398	0.31
chr12	133851895	5443989	0.0407	0.2329
chr13	115169878	3887774	0.0338	0.209
chr14	107349540	3691622	0.0344	0.2174
chr15	102531392	3328651	0.0325	0.2228
chr16	90354753	3520209	0.039	0.2395
chr17	81195210	3183834	0.0392	0.2502
chr18	78077248	3278181	0.042	0.4816
chr19	59128983	2319324	0.0392	0.3845
chr20	63025520	2501098	0.0397	0.2325
chr21	48129895	1618515	0.0336	0.2355
chr22	51304566	1338287	0.0261	0.1815
chrMT	16571	4258	0.257	0.5082
chrX	155270560	6938079	0.0447	0.2685
chrY	59373566	374483	0.0063	0.1708

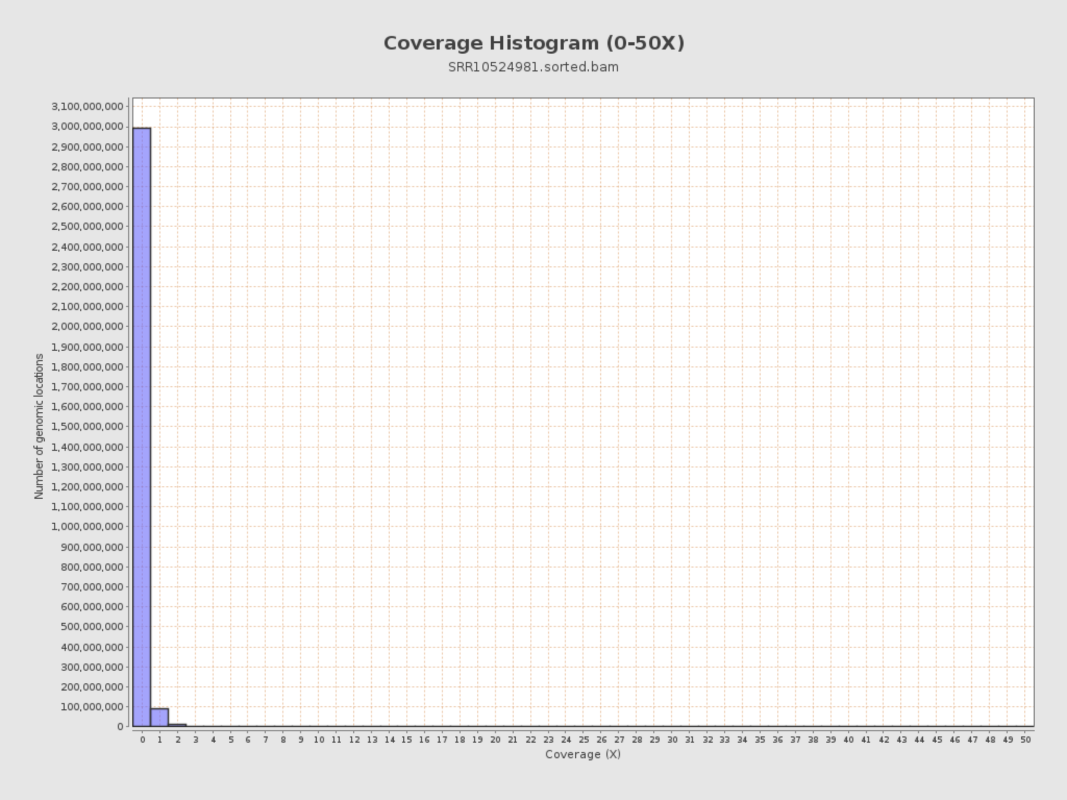
3. Results : Coverage across reference



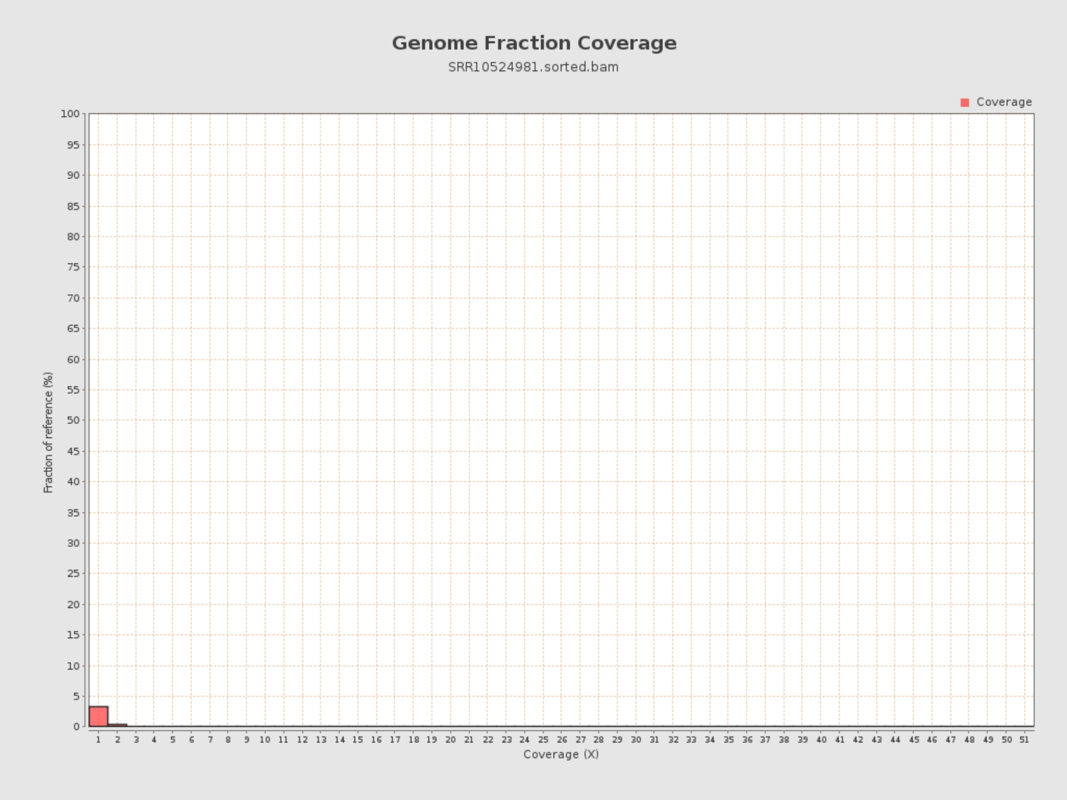
4. Results : Coverage Histogram



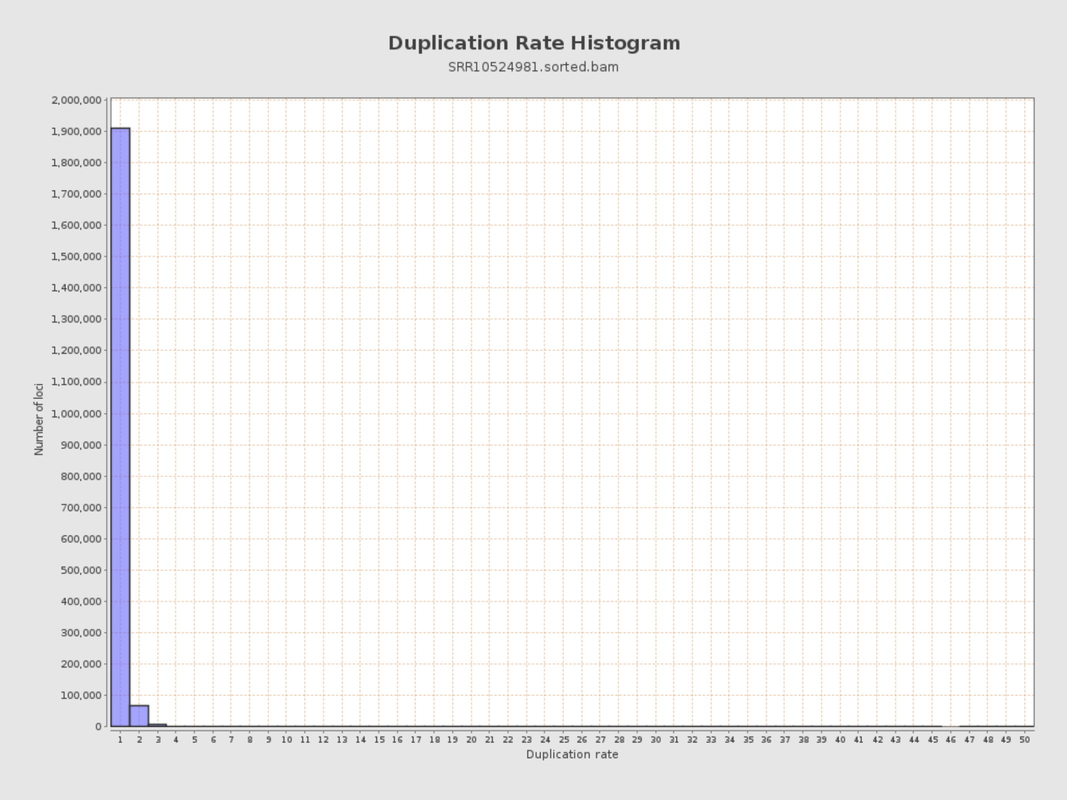
5. Results : Coverage Histogram (0-50X)



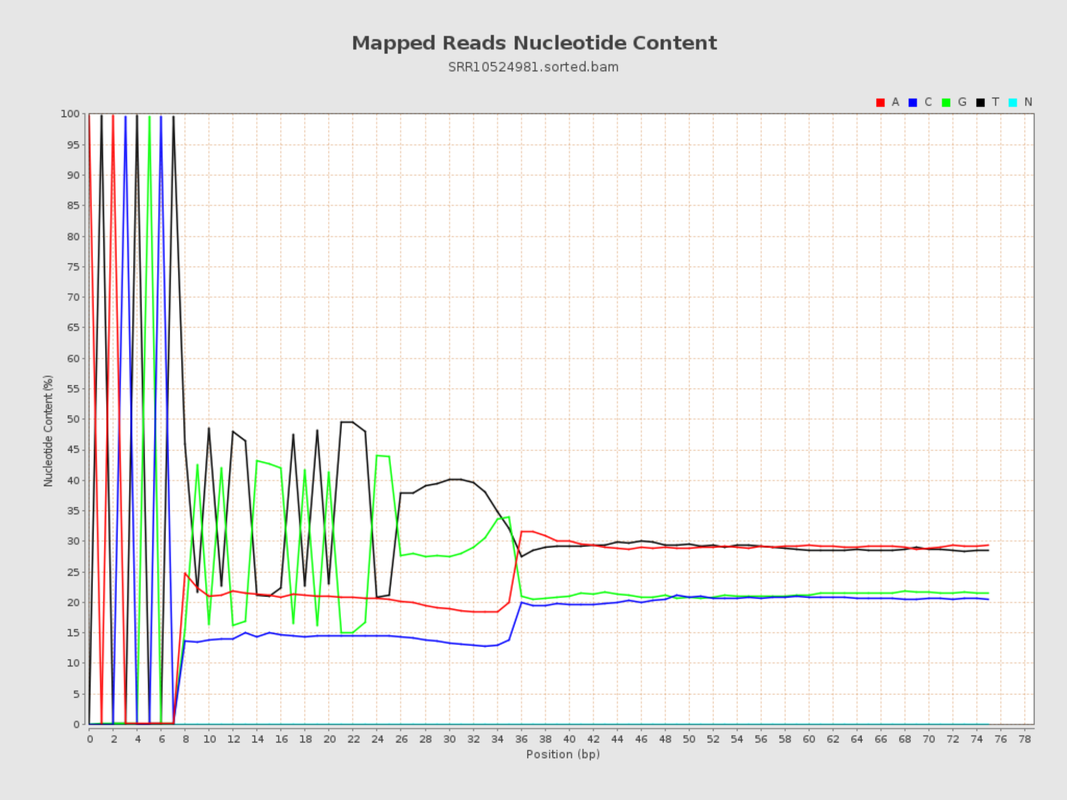
6. Results : Genome Fraction Coverage



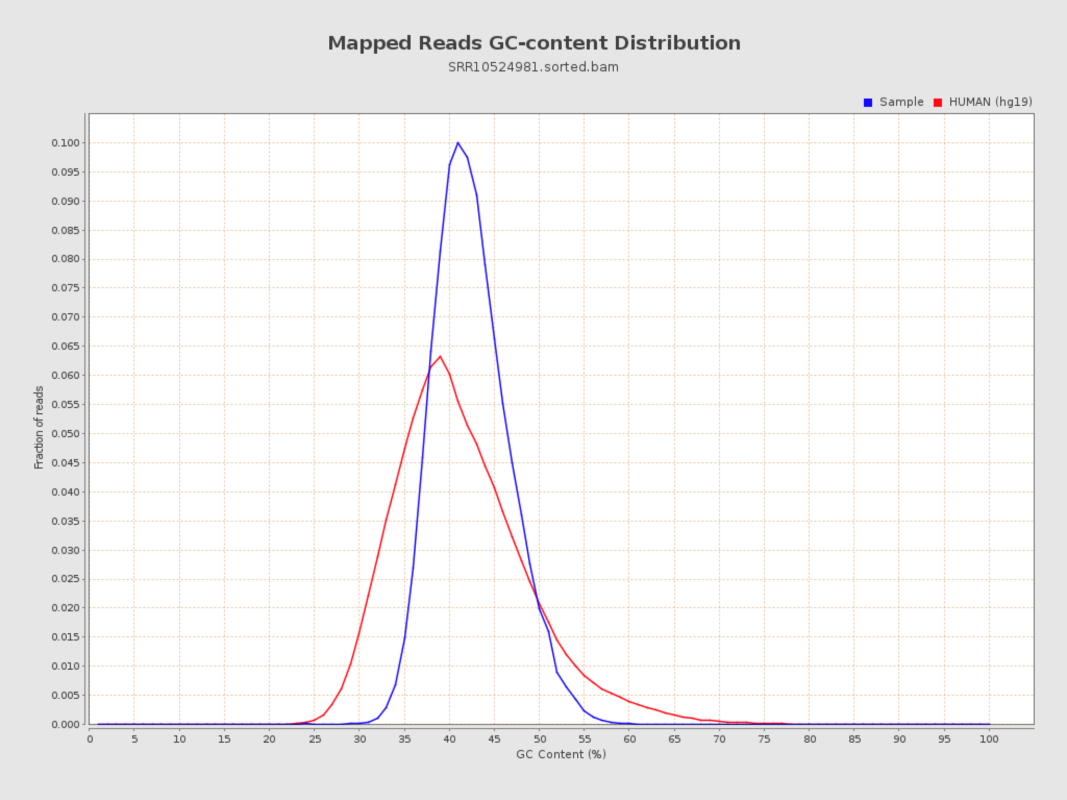
7. Results : Duplication Rate Histogram



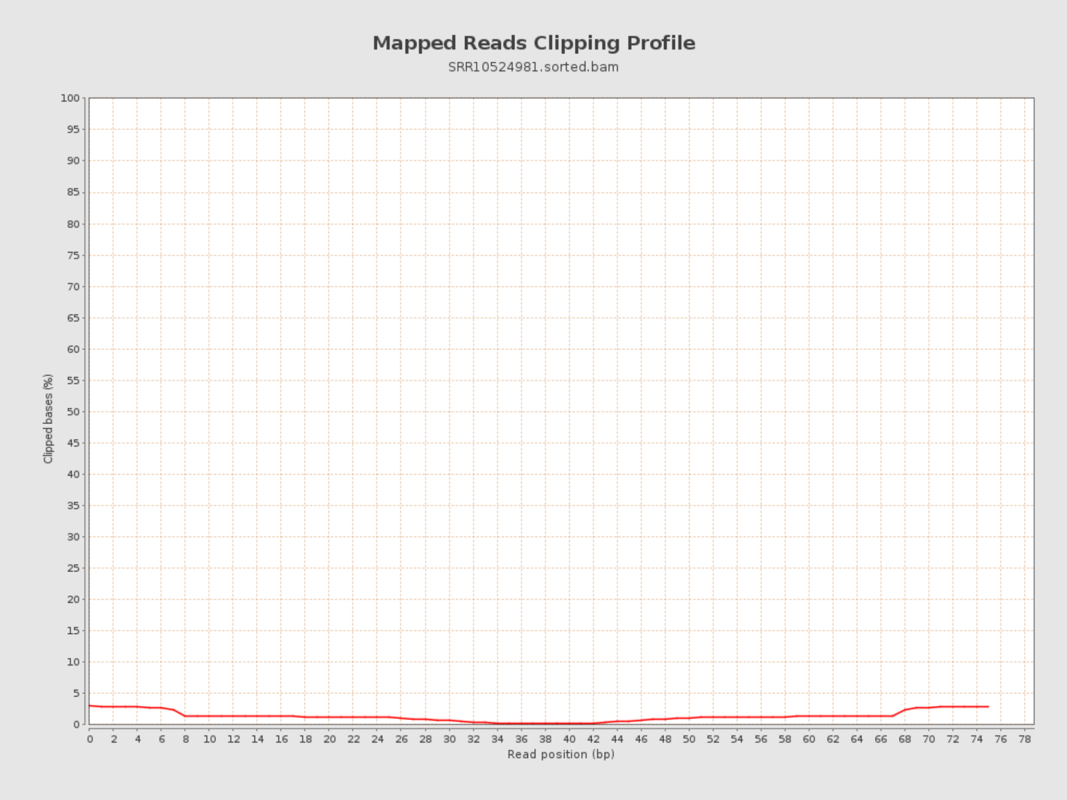
8. Results : Mapped Reads Nucleotide Content



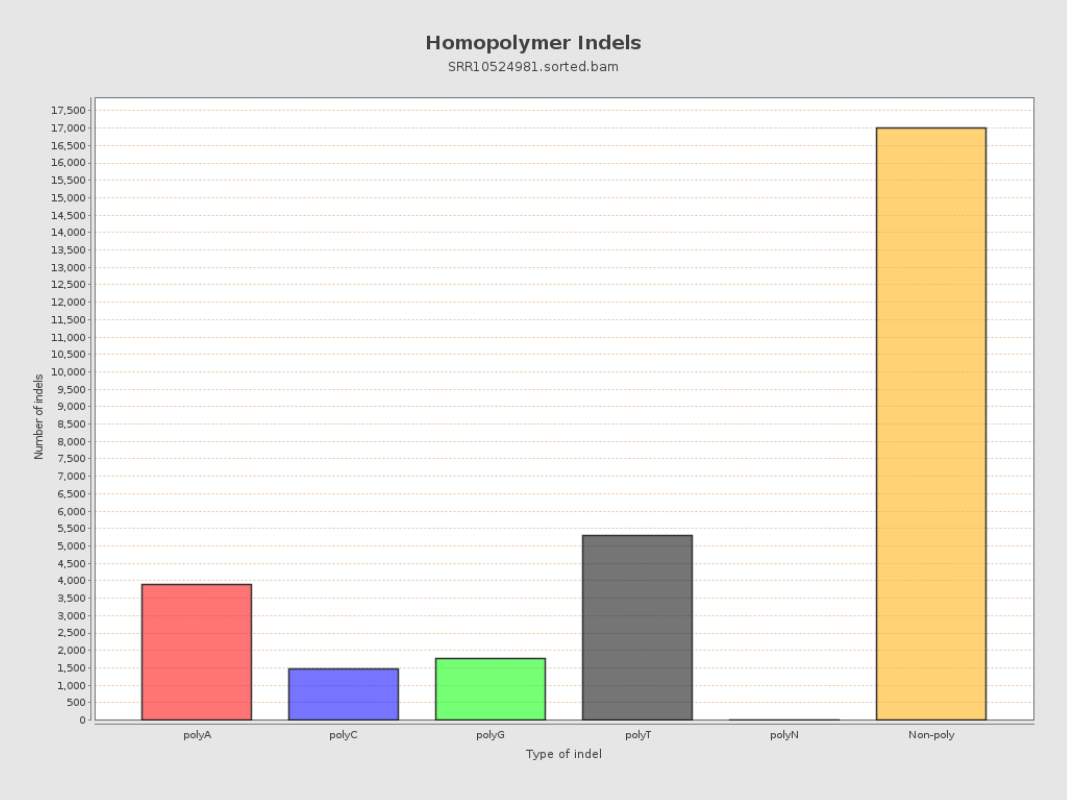
9. Results : Mapped Reads GC-content Distribution



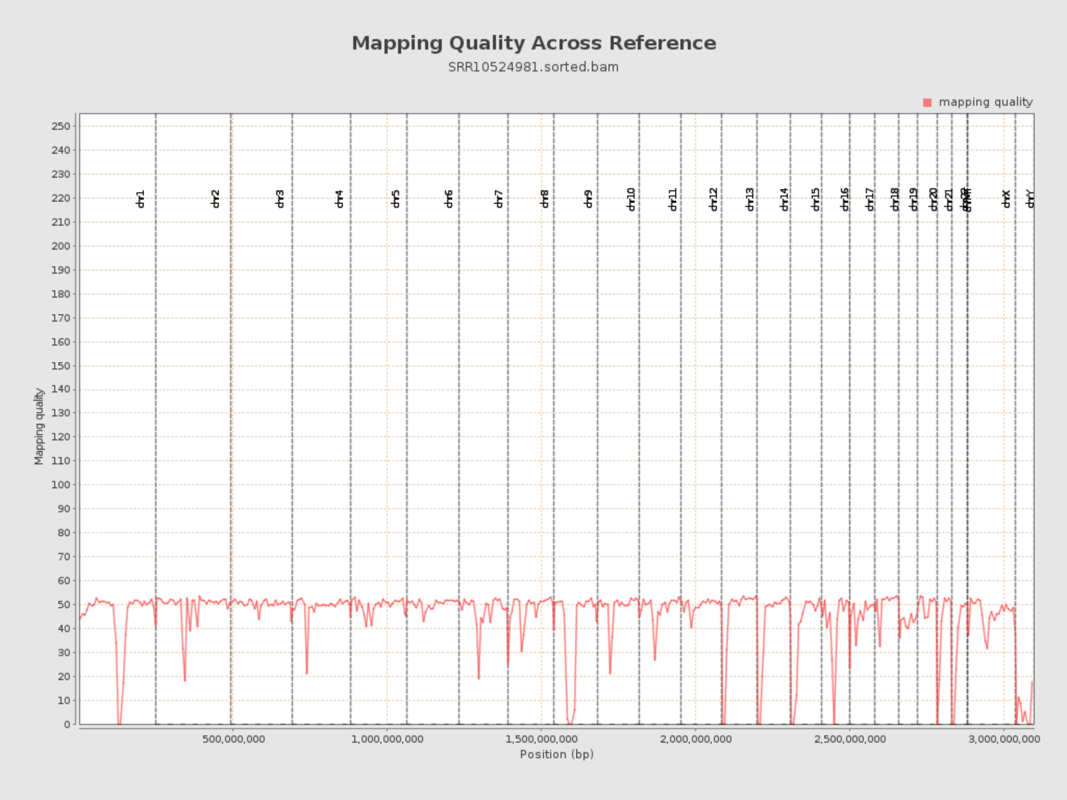
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram