Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 06:45:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524933.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_SRR10524933 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524933.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 06:45:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524933.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,993,175
Mapped reads	1,820,921 / 91.36%
Unmapped reads	172,254 / 8.64%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,559 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	61,870 / 3.1%
Duplication rate	2.44%
Clipped reads	1,823,944 / 91.51%

2.2. ACGT Content

Number/percentage of A's	27,017,838 / 25.75%
Number/percentage of C's	20,527,441 / 19.56%
Number/percentage of T's	32,715,356 / 31.18%
Number/percentage of G's	24,667,171 / 23.51%
Number/percentage of N's	3,297 / 0%
GC Percentage	43.07%

2.3. Coverage

Mean	0.0339

Standard Deviation	0.3001

2.4. Mapping Quality

Mean Mapping Quality	45.21

2.5. Mismatches and indels

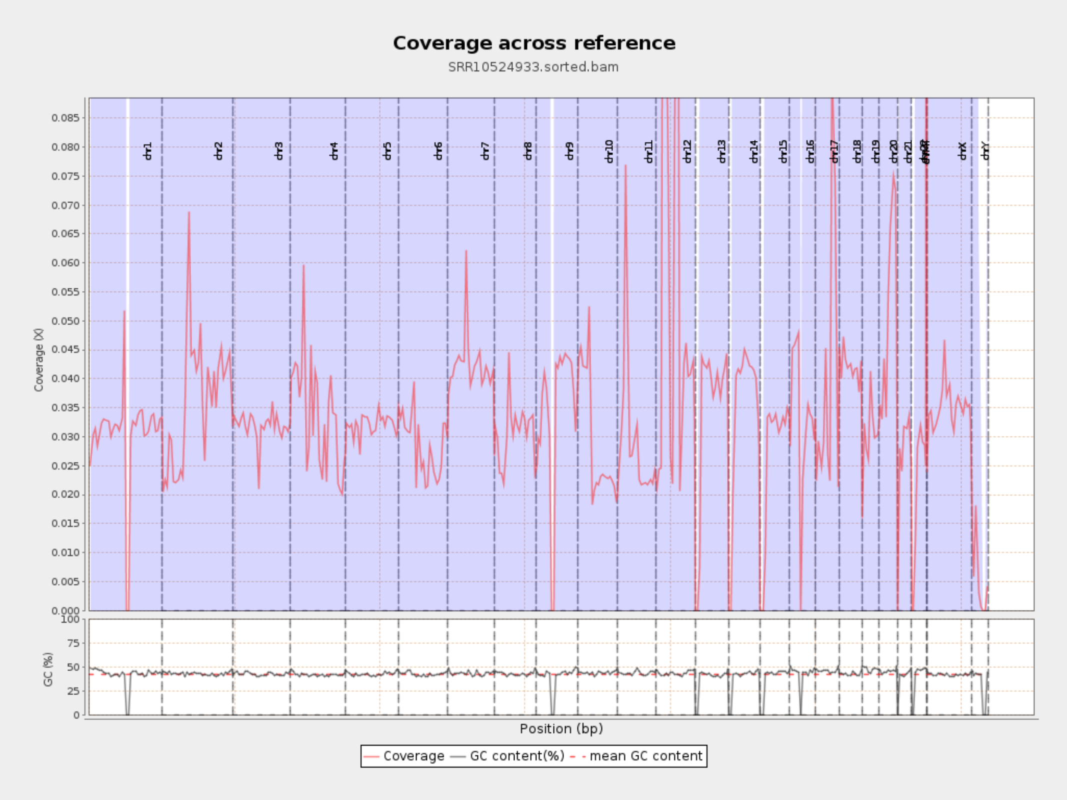
General error rate	0.49%
Mismatches	504,914
Insertions	6,347
Mapped reads with at least one insertion	0.35%
Deletions	16,956
Mapped reads with at least one deletion	0.93%
Homopolymer indels	42.61%

2.6. Chromosome stats

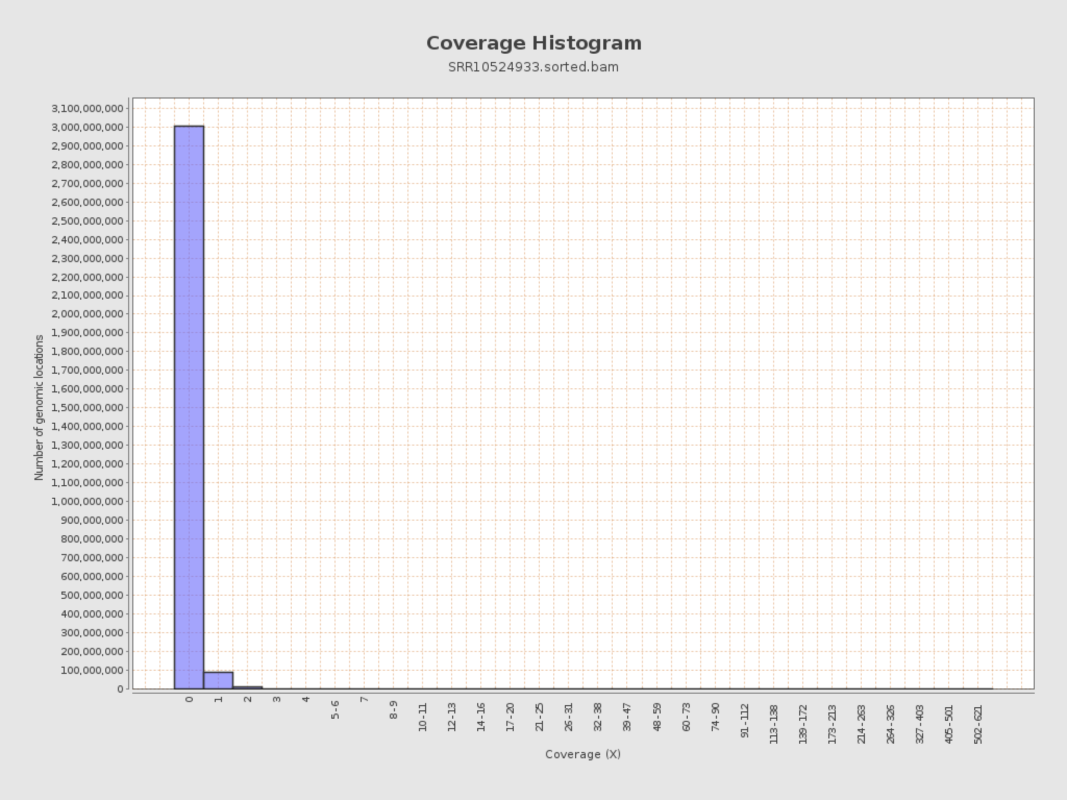
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7557629	0.0303	0.5147
chr2	243199373	8863305	0.0364	0.3354
chr3	198022430	6296473	0.0318	0.1941
chr4	191154276	6481219	0.0339	0.2266
chr5	180915260	5789996	0.032	0.1957
chr6	171115067	4888074	0.0286	0.2058
chr7	159138663	6784310	0.0426	0.4168

chr8	146364022	4520276	0.0309	0.2853
chr9	141213431	4858407	0.0344	0.2925
chr10	135534747	3999340	0.0295	0.28
chr11	135006516	4033659	0.0299	0.2526
chr12	133851895	7820419	0.0584	0.2986
chr13	115169878	3926744	0.0341	0.2009
chr14	107349540	3707465	0.0345	0.2185
chr15	102531392	2724328	0.0266	0.1779
chr16	90354753	3027406	0.0335	0.2162
chr17	81195210	3199236	0.0394	0.2272
chr18	78077248	3287193	0.0421	0.5422
chr19	59128983	1824224	0.0309	0.3952
chr20	63025520	3288269	0.0522	0.2579
chr21	48129895	1279008	0.0266	0.2055
chr22	51304566	1054735	0.0206	0.1547
chrMT	16571	7968	0.4808	0.7869
chrX	155270560	5435272	0.035	0.2384
chrY	59373566	303956	0.0051	0.1313

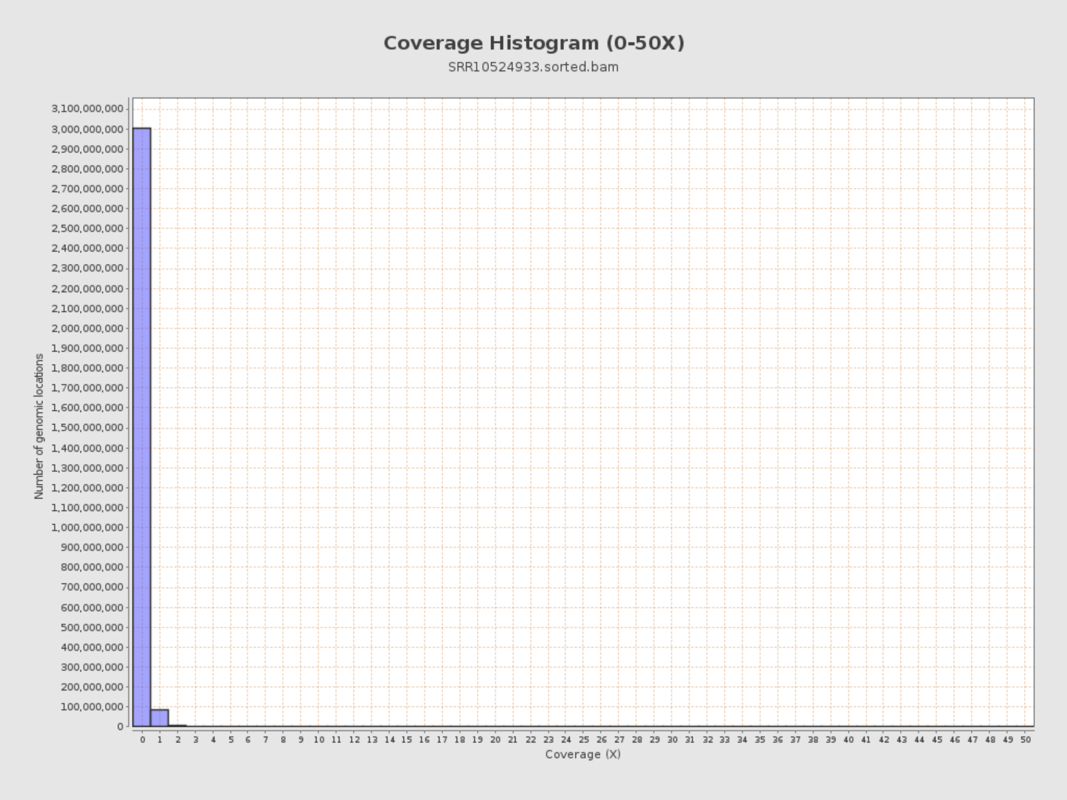
3. Results : Coverage across reference



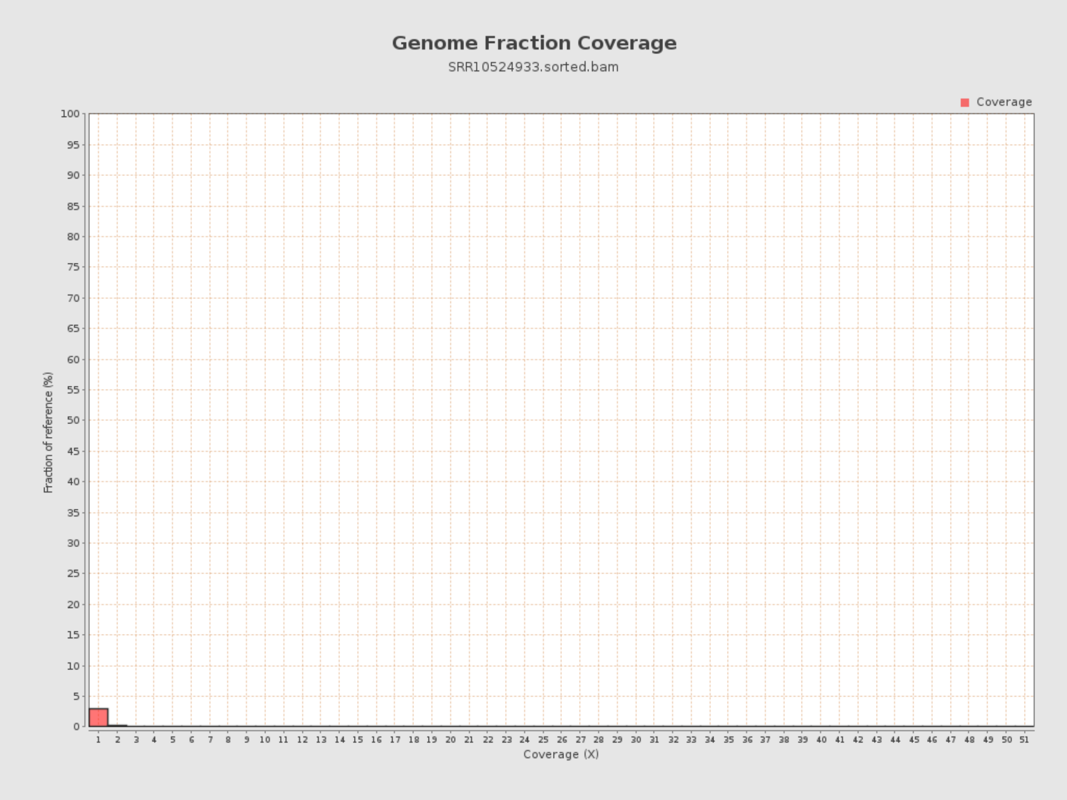
4. Results : Coverage Histogram



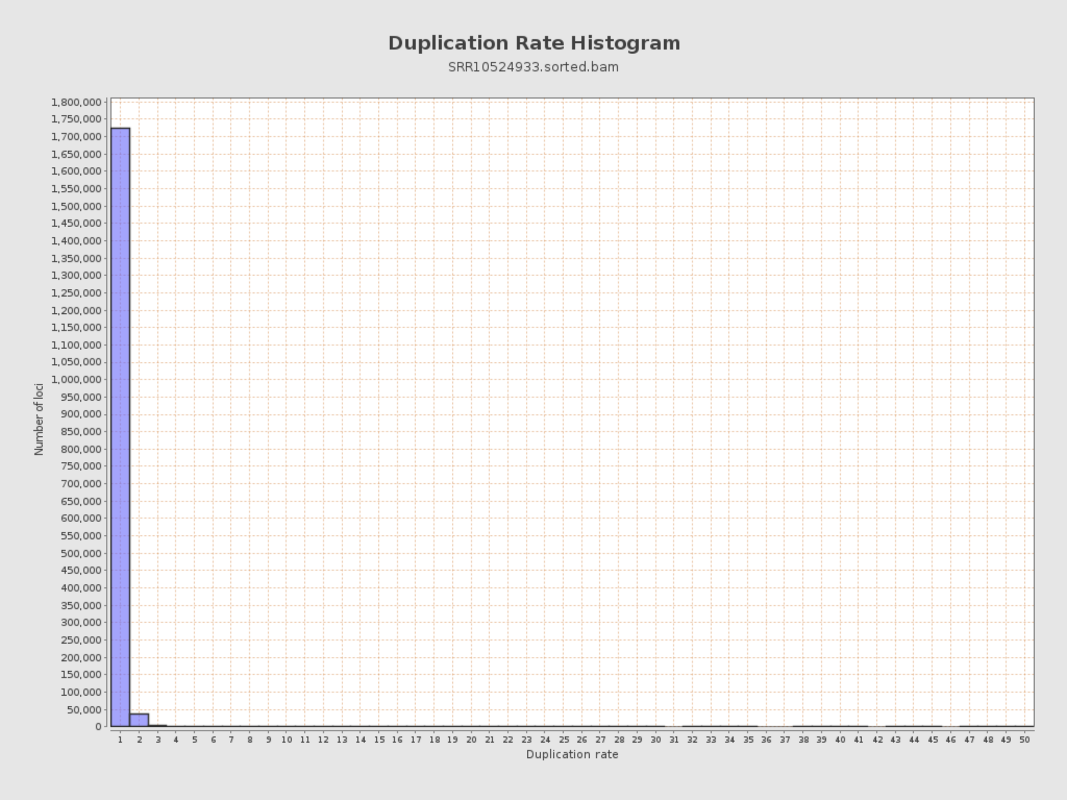
5. Results : Coverage Histogram (0-50X)



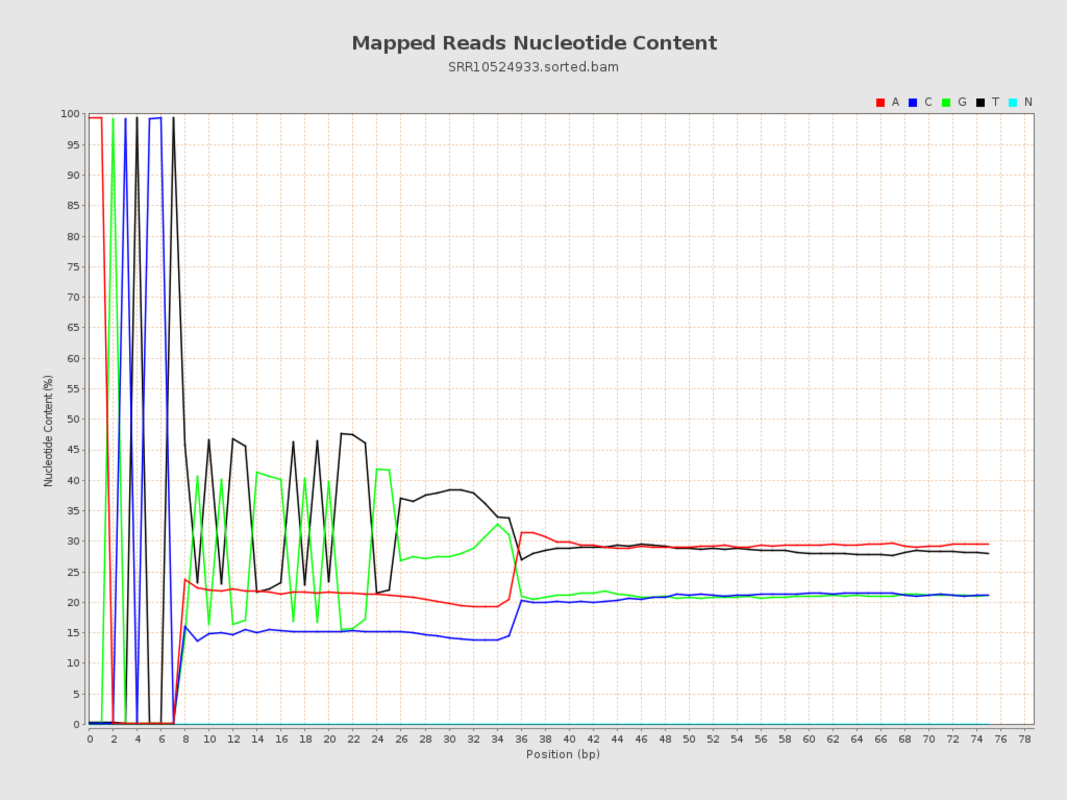
6. Results : Genome Fraction Coverage



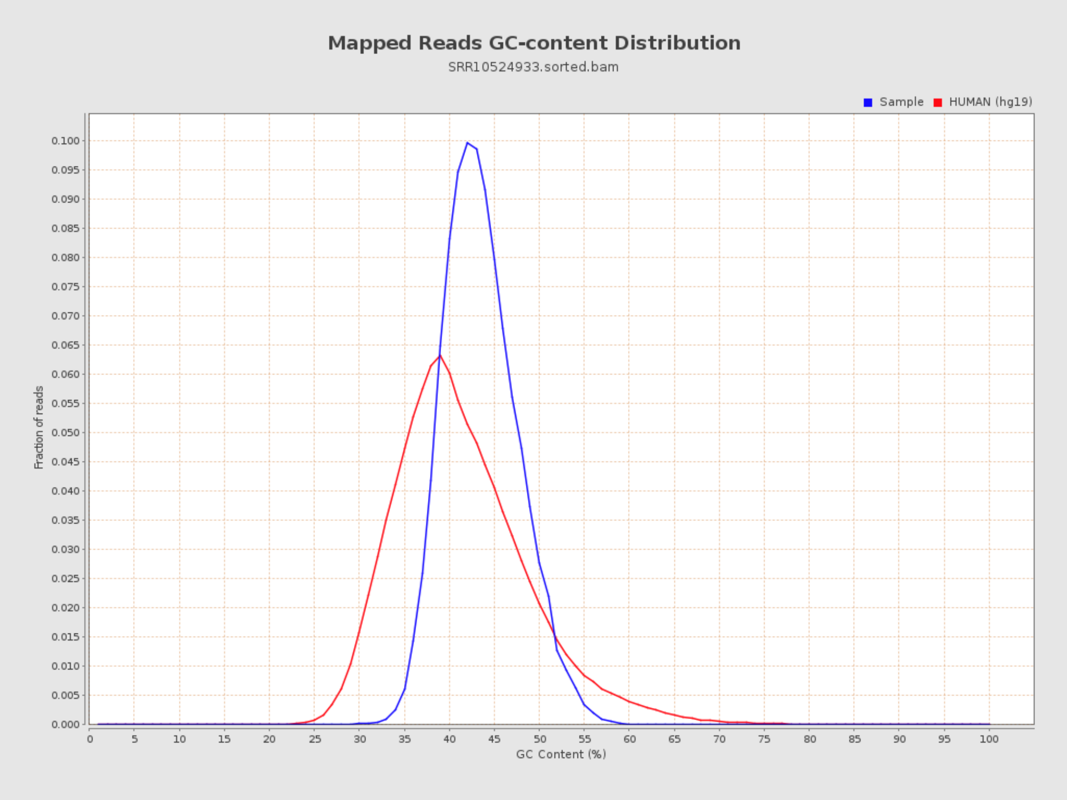
7. Results : Duplication Rate Histogram



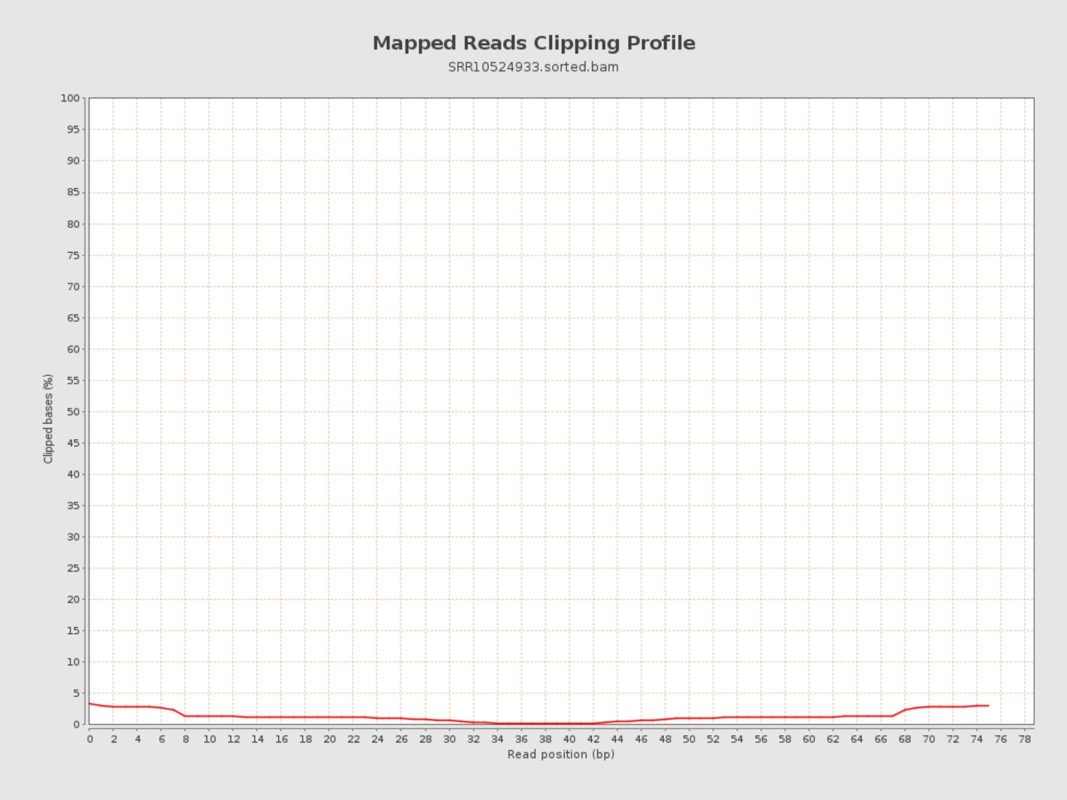
8. Results : Mapped Reads Nucleotide Content



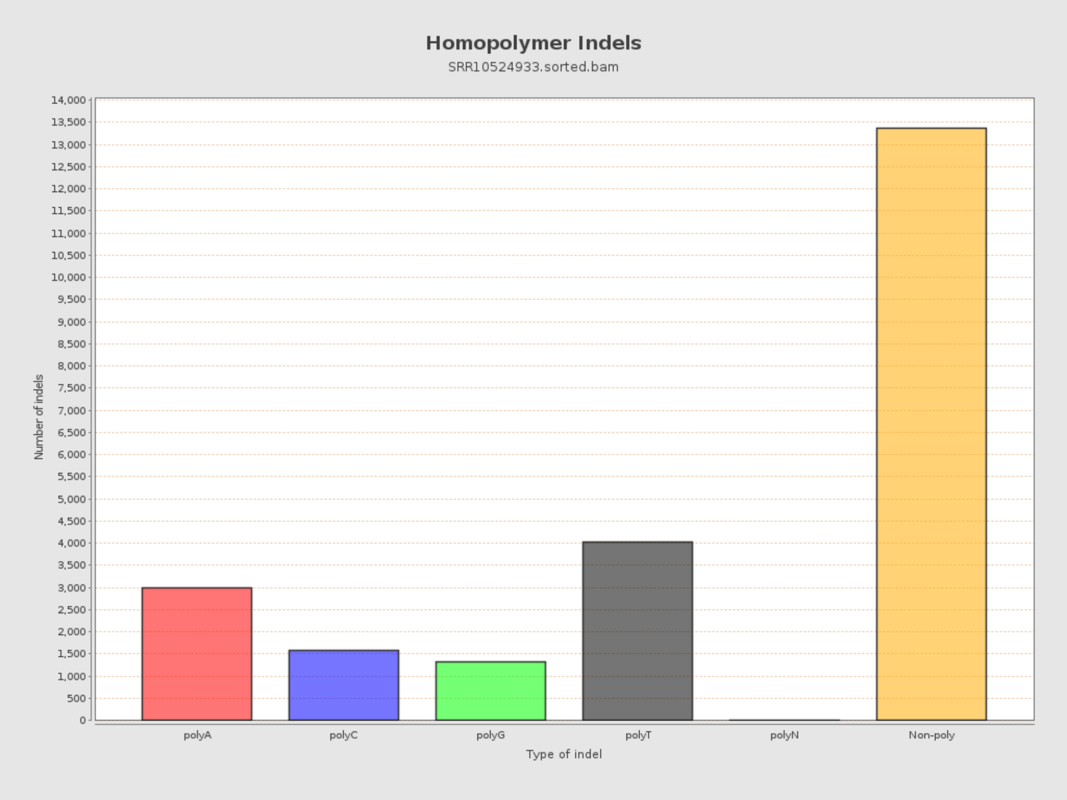
9. Results : Mapped Reads GC-content Distribution



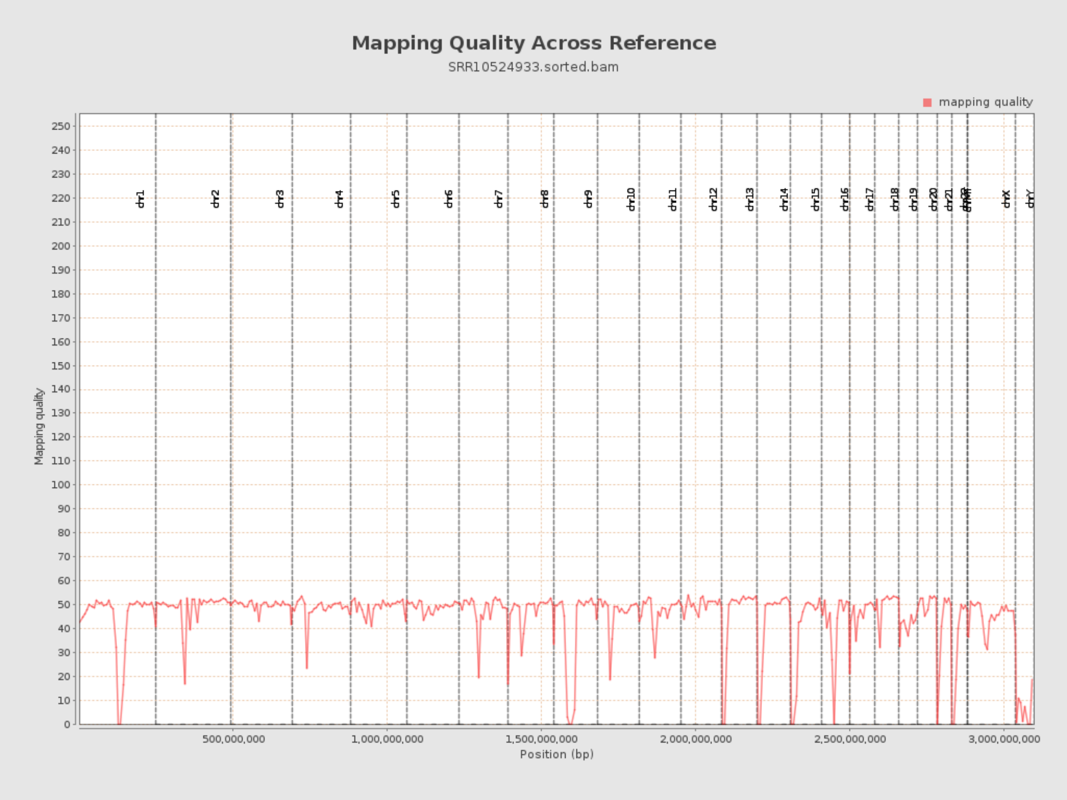
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram