Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 01:09:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524377.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_SRR10524377 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524377.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 01:09:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524377.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	429,468
Mapped reads	398,995 / 92.9%
Unmapped reads	30,473 / 7.1%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,562 / 0.36%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	6,236 / 1.45%
Duplication rate	1.17%
Clipped reads	399,514 / 93.03%

2.2. ACGT Content

Number/percentage of A's	5,832,245 / 24.9%
Number/percentage of C's	4,602,621 / 19.65%
Number/percentage of T's	7,261,272 / 31%
Number/percentage of G's	5,724,476 / 24.44%
Number/percentage of N's	3,126 / 0.01%
GC Percentage	44.09%

2.3. Coverage

Mean	0.0076

Standard Deviation	0.1053

2.4. Mapping Quality

Mean Mapping Quality	45.77

2.5. Mismatches and indels

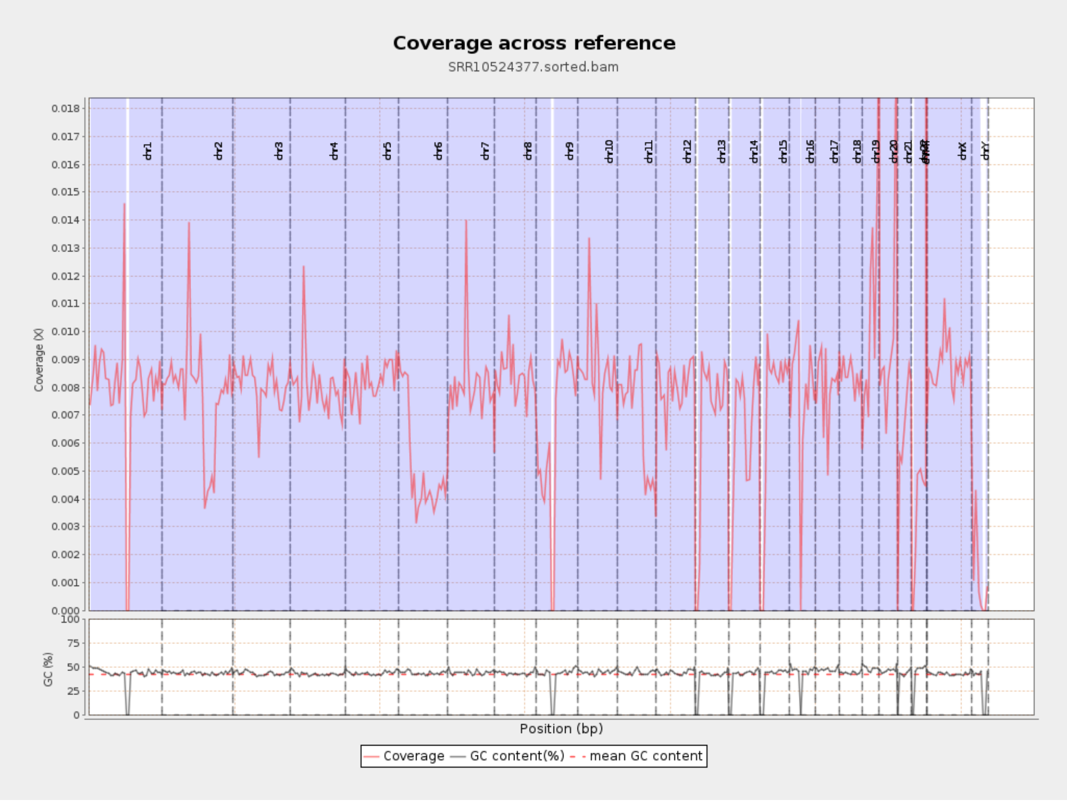
General error rate	0.5%
Mismatches	113,911
Insertions	1,610
Mapped reads with at least one insertion	0.4%
Deletions	4,254
Mapped reads with at least one deletion	1.06%
Homopolymer indels	42.38%

2.6. Chromosome stats

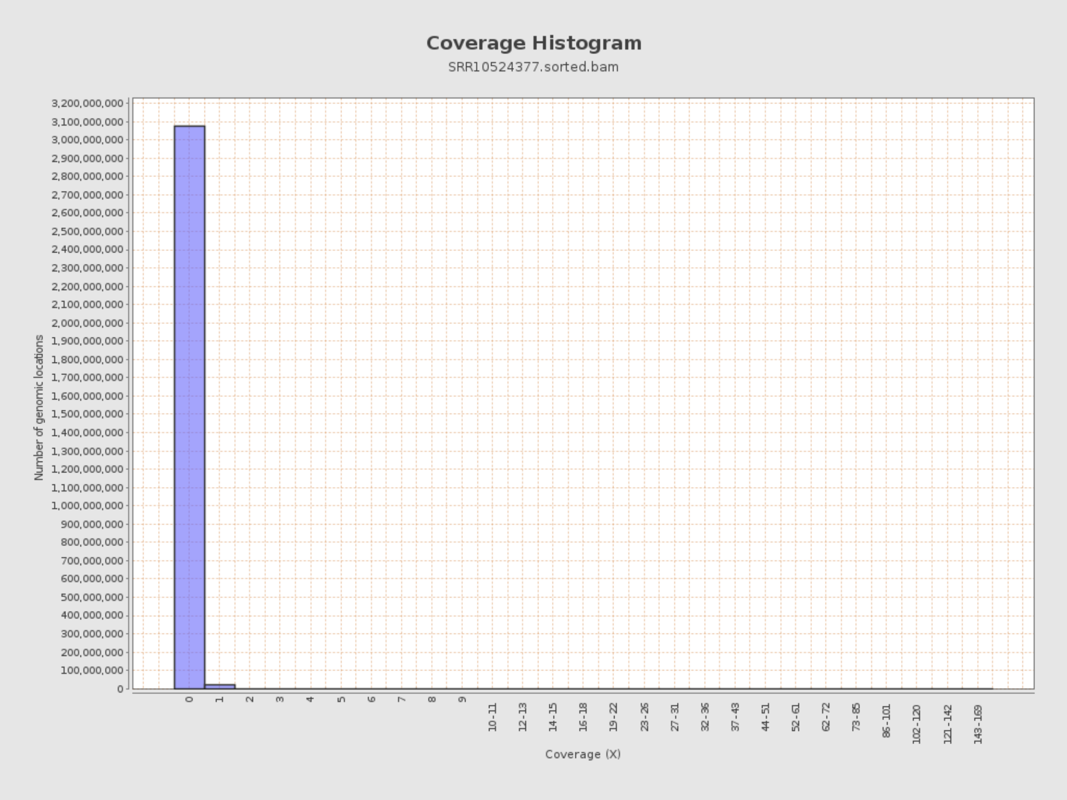
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1972008	0.0079	0.1676
chr2	243199373	1900172	0.0078	0.1113
chr3	198022430	1605578	0.0081	0.0923
chr4	191154276	1530728	0.008	0.0948
chr5	180915260	1492087	0.0082	0.093
chr6	171115067	887751	0.0052	0.0754
chr7	159138663	1303660	0.0082	0.1296

chr8	146364022	1237292	0.0085	0.1037
chr9	141213431	910292	0.0064	0.0898
chr10	135534747	1167250	0.0086	0.107
chr11	135006516	946568	0.007	0.0945
chr12	133851895	1085988	0.0081	0.0926
chr13	115169878	782099	0.0068	0.0844
chr14	107349540	666849	0.0062	0.0817
chr15	102531392	731458	0.0071	0.0863
chr16	90354753	697497	0.0077	0.0913
chr17	81195210	641203	0.0079	0.0938
chr18	78077248	659918	0.0085	0.1293
chr19	59128983	650262	0.011	0.142
chr20	63025520	639519	0.0101	0.1041
chr21	48129895	302968	0.0063	0.0836
chr22	51304566	172179	0.0034	0.059
chrMT	16571	14698	0.887	1.1135
chrX	155270560	1360619	0.0088	0.0982
chrY	59373566	71759	0.0012	0.0423

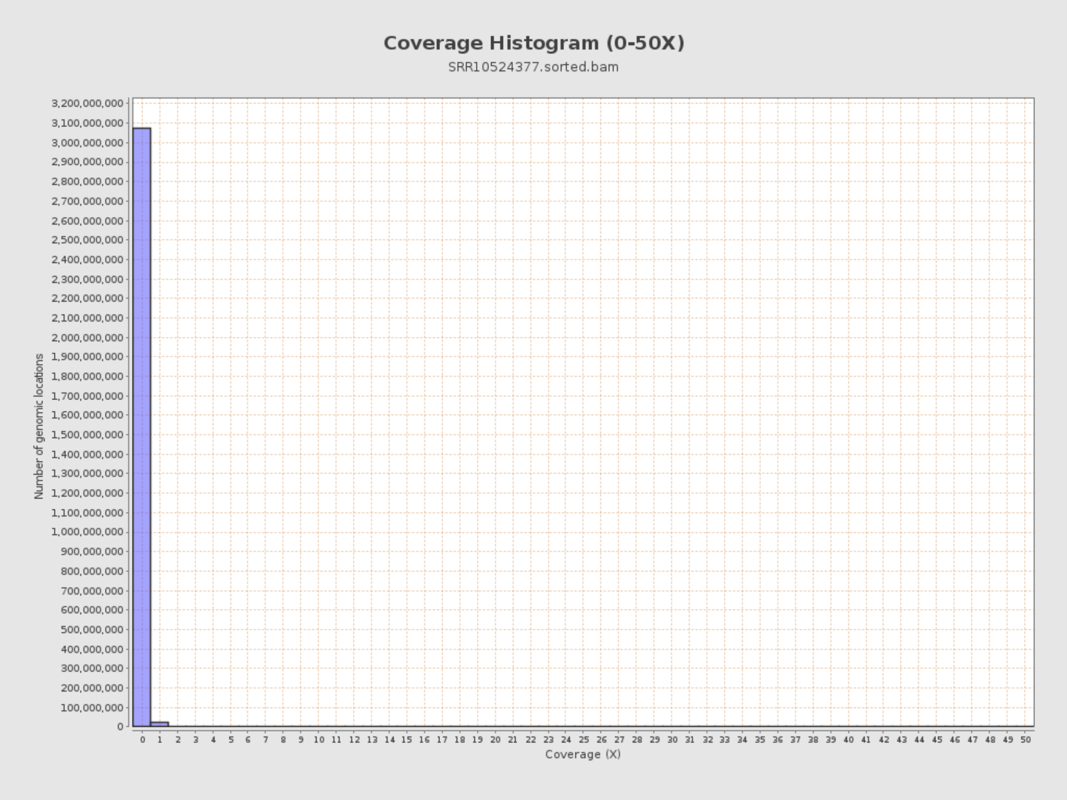
3. Results : Coverage across reference



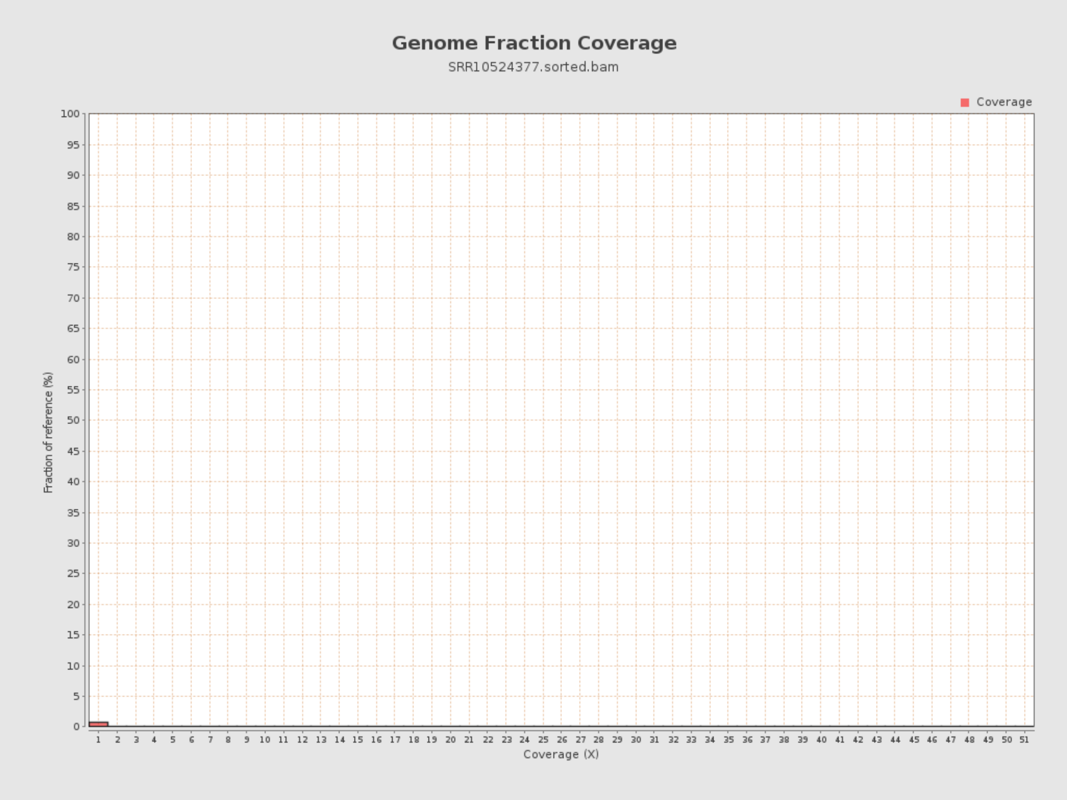
4. Results : Coverage Histogram



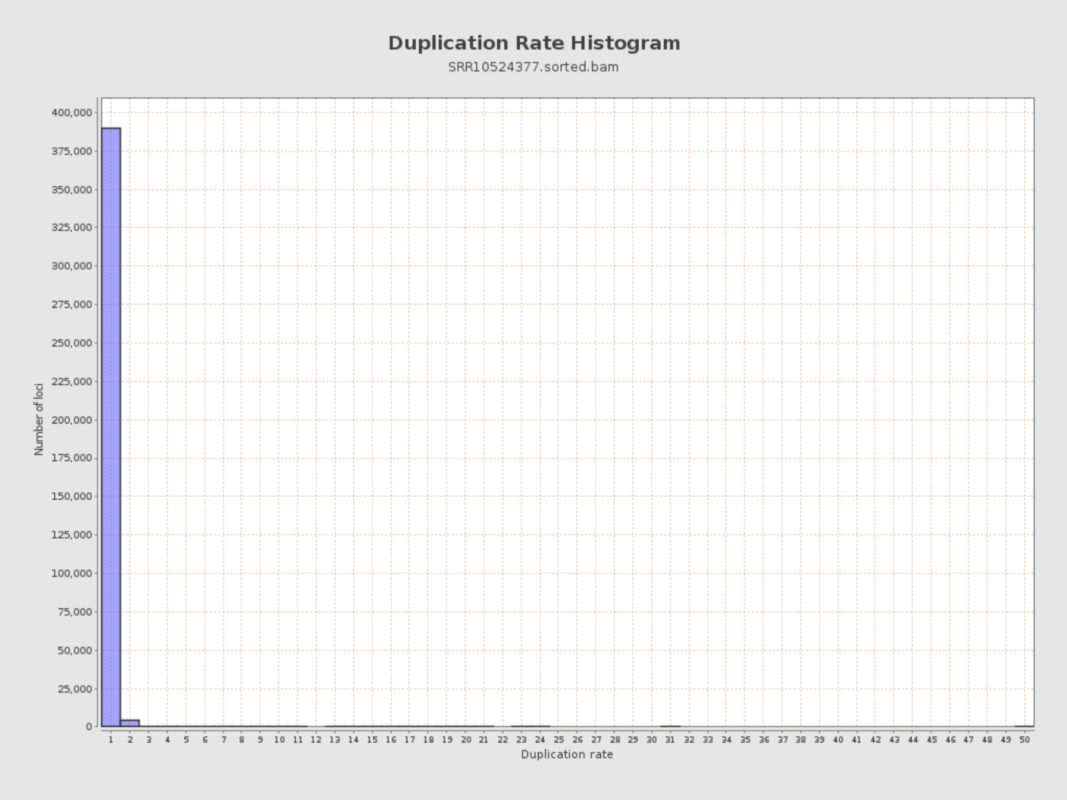
5. Results : Coverage Histogram (0-50X)



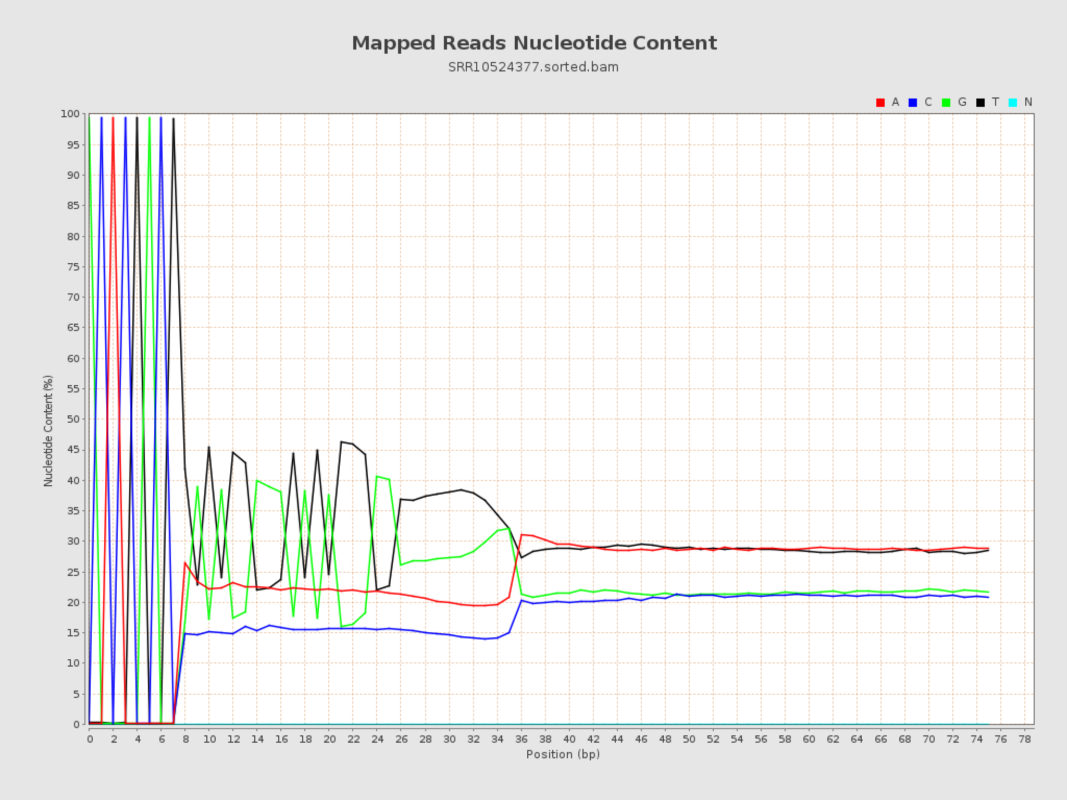
6. Results : Genome Fraction Coverage



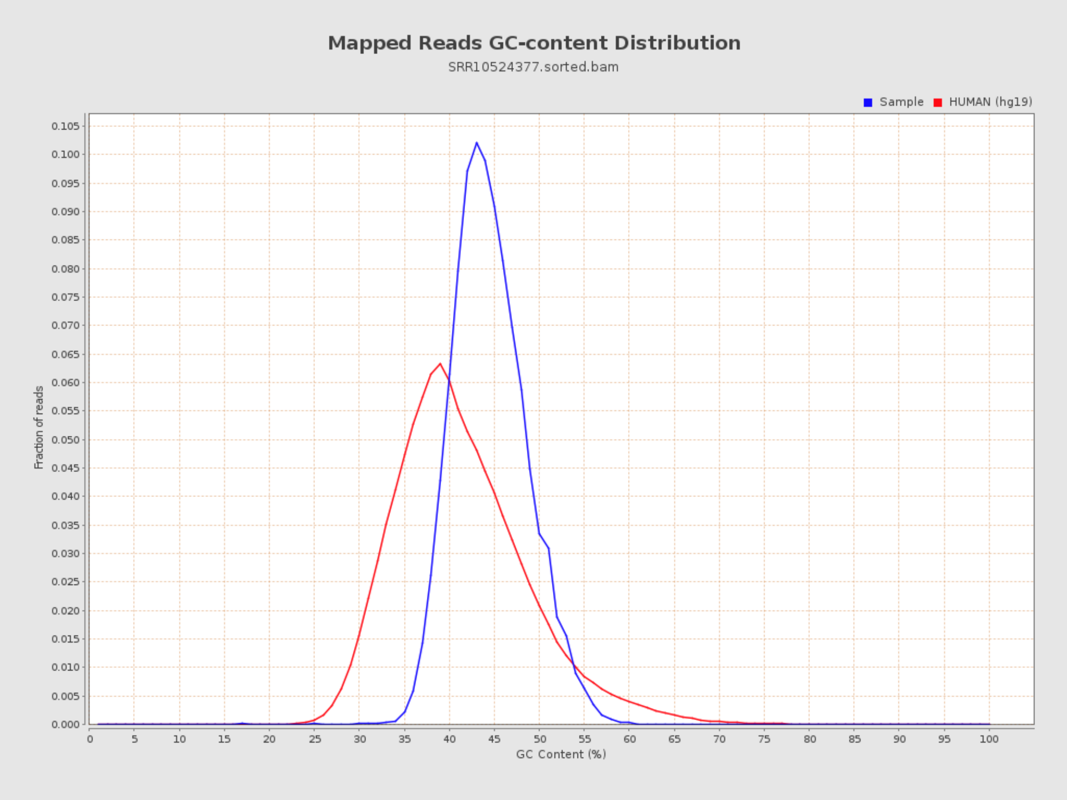
7. Results : Duplication Rate Histogram



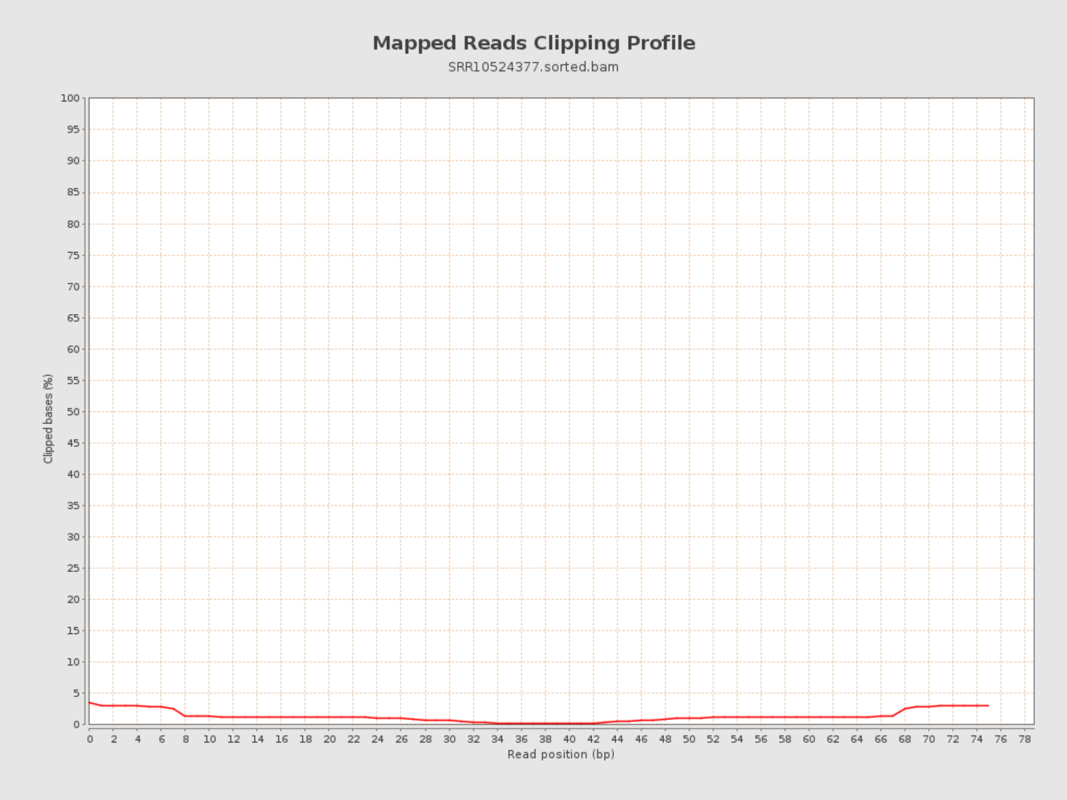
8. Results : Mapped Reads Nucleotide Content



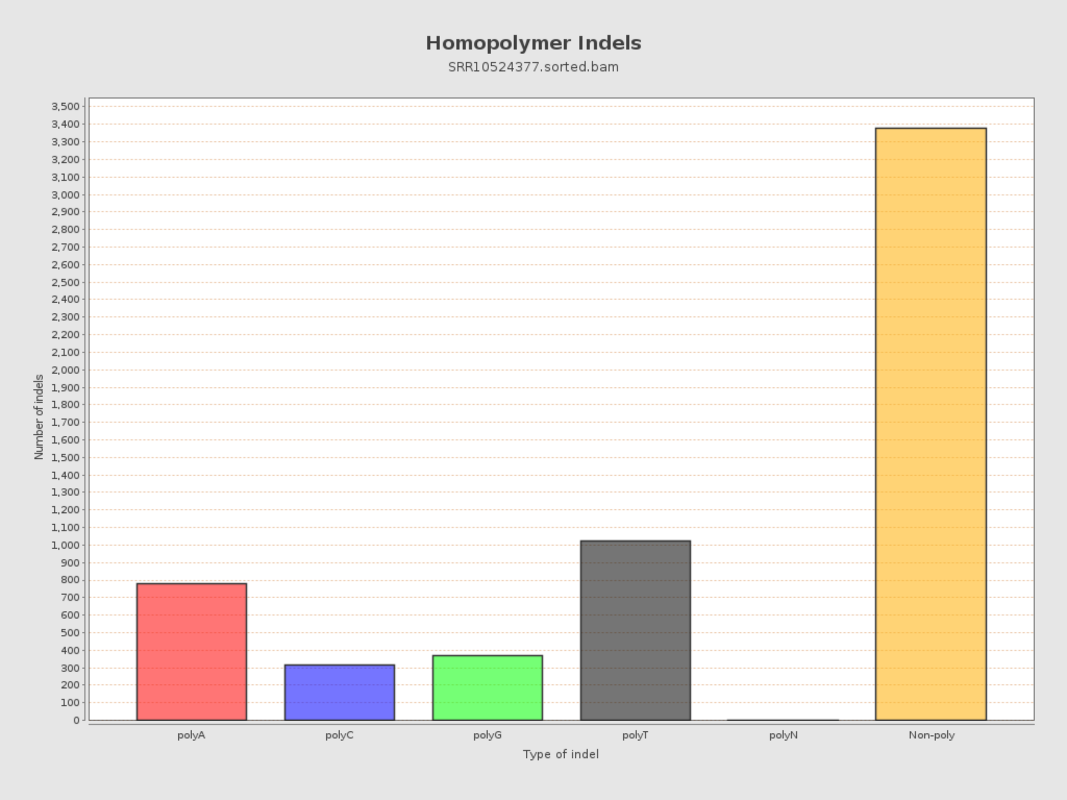
9. Results : Mapped Reads GC-content Distribution



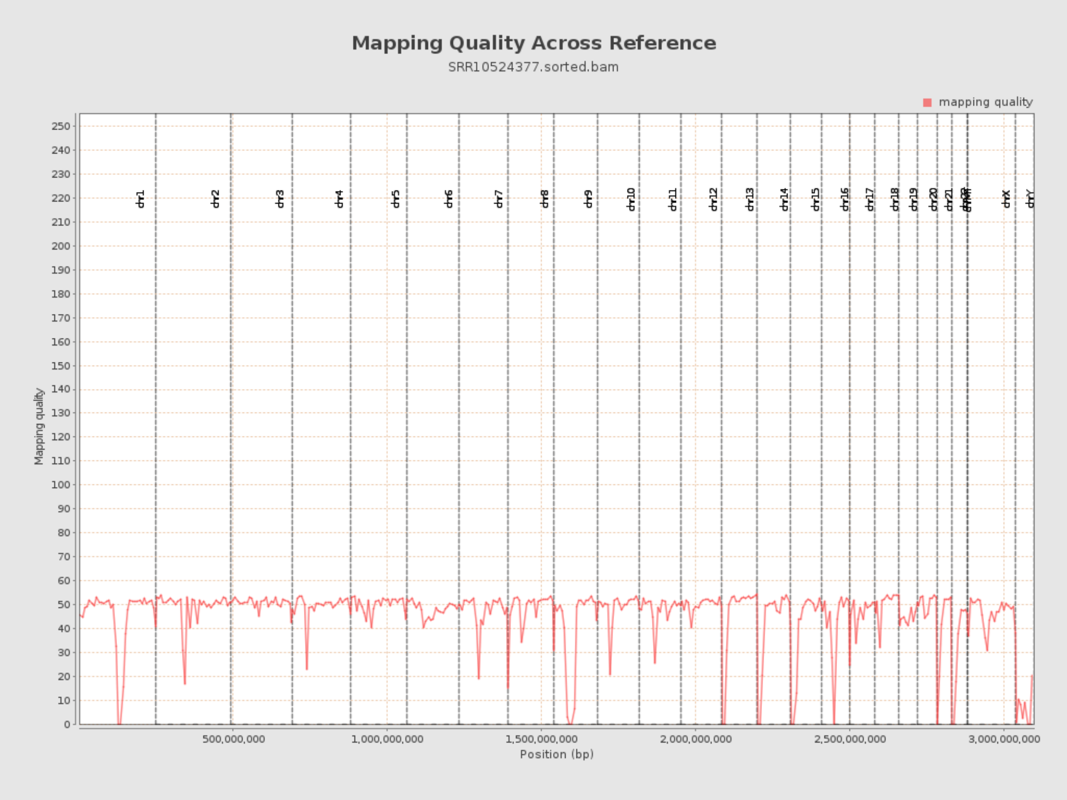
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram