Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 23:25:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524337.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_SRR10524337 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524337.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 23:25:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524337.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	455,297
Mapped reads	414,924 / 91.13%
Unmapped reads	40,373 / 8.87%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,090 / 0.46%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	6,030 / 1.32%
Duplication rate	1%
Clipped reads	416,768 / 91.54%

2.2. ACGT Content

Number/percentage of A's	5,759,494 / 23.91%
Number/percentage of C's	4,534,365 / 18.83%
Number/percentage of T's	7,707,294 / 32%
Number/percentage of G's	6,080,517 / 25.25%
Number/percentage of N's	3,410 / 0.01%
GC Percentage	44.07%

2.3. Coverage

Mean	0.0078

Standard Deviation	0.108

2.4. Mapping Quality

Mean Mapping Quality	43.25

2.5. Mismatches and indels

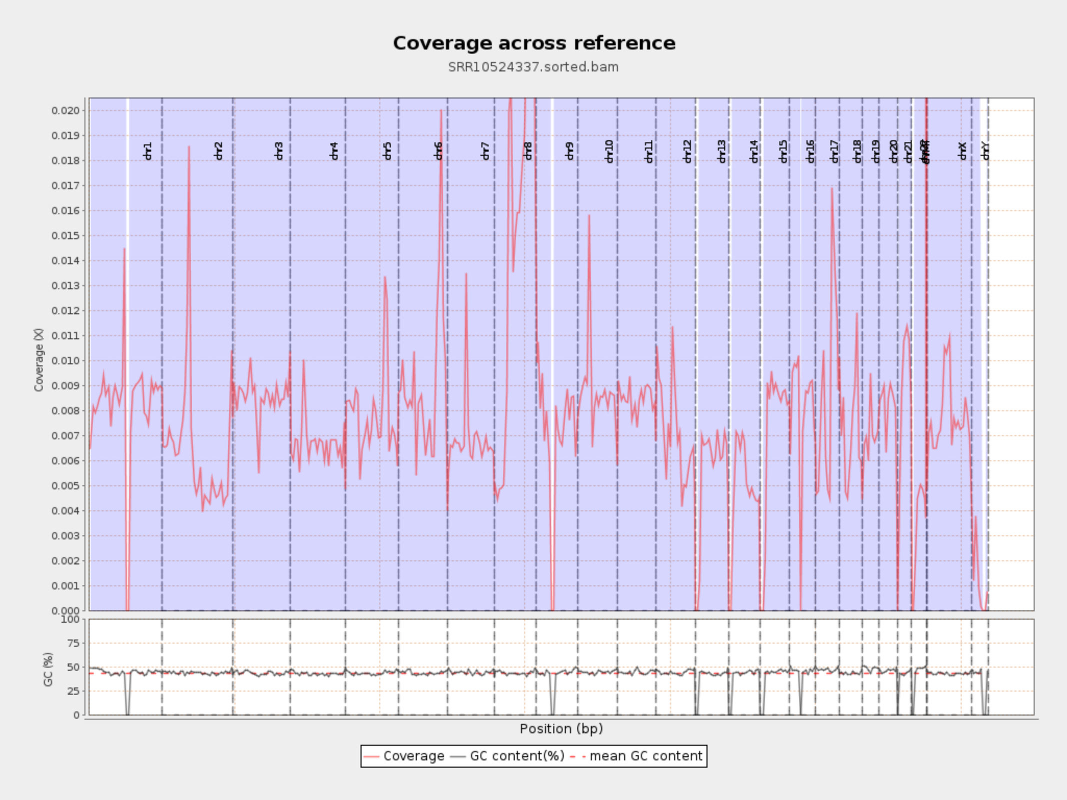
General error rate	0.52%
Mismatches	122,553
Insertions	1,356
Mapped reads with at least one insertion	0.32%
Deletions	4,066
Mapped reads with at least one deletion	0.97%
Homopolymer indels	45.59%

2.6. Chromosome stats

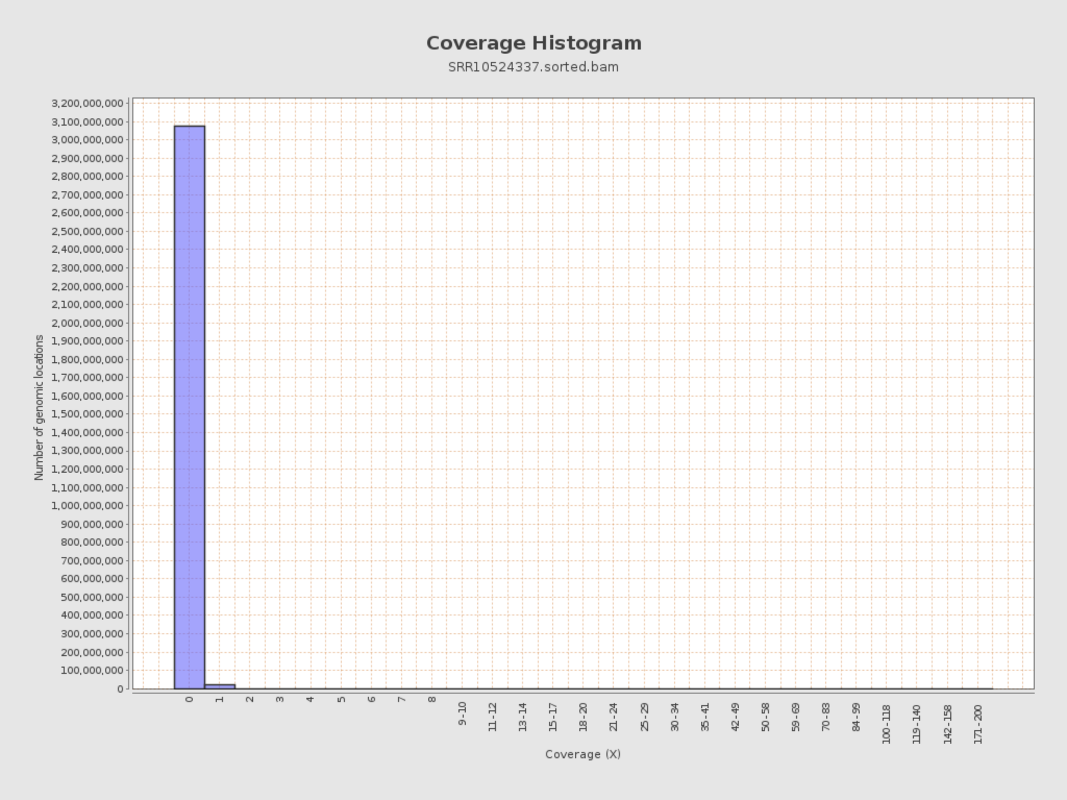
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2034295	0.0082	0.1667
chr2	243199373	1564257	0.0064	0.1173
chr3	198022430	1685939	0.0085	0.0945
chr4	191154276	1279365	0.0067	0.0855
chr5	180915260	1433739	0.0079	0.091
chr6	171115067	1556474	0.0091	0.1003
chr7	159138663	1103551	0.0069	0.1221

chr8	146364022	2506235	0.0171	0.1474
chr9	141213431	990463	0.007	0.0946
chr10	135534747	1199930	0.0089	0.112
chr11	135006516	1138025	0.0084	0.1033
chr12	133851895	952548	0.0071	0.0868
chr13	115169878	627681	0.0055	0.0755
chr14	107349540	516221	0.0048	0.0724
chr15	102531392	720984	0.007	0.0863
chr16	90354753	726148	0.008	0.0938
chr17	81195210	701045	0.0086	0.0974
chr18	78077248	576855	0.0074	0.1335
chr19	59128983	416517	0.007	0.1236
chr20	63025520	514666	0.0082	0.0928
chr21	48129895	401768	0.0083	0.0951
chr22	51304566	168634	0.0033	0.0587
chrMT	16571	13089	0.7899	0.9784
chrX	155270560	1196157	0.0077	0.0936
chrY	59373566	67033	0.0011	0.0416

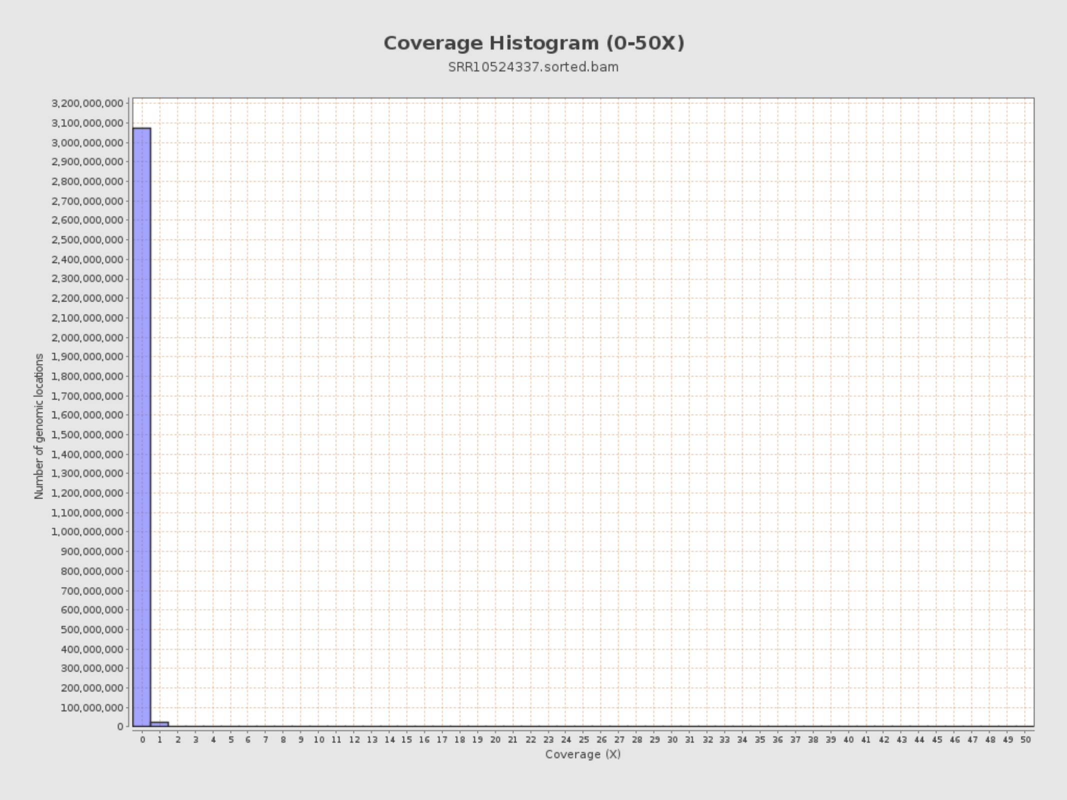
3. Results : Coverage across reference



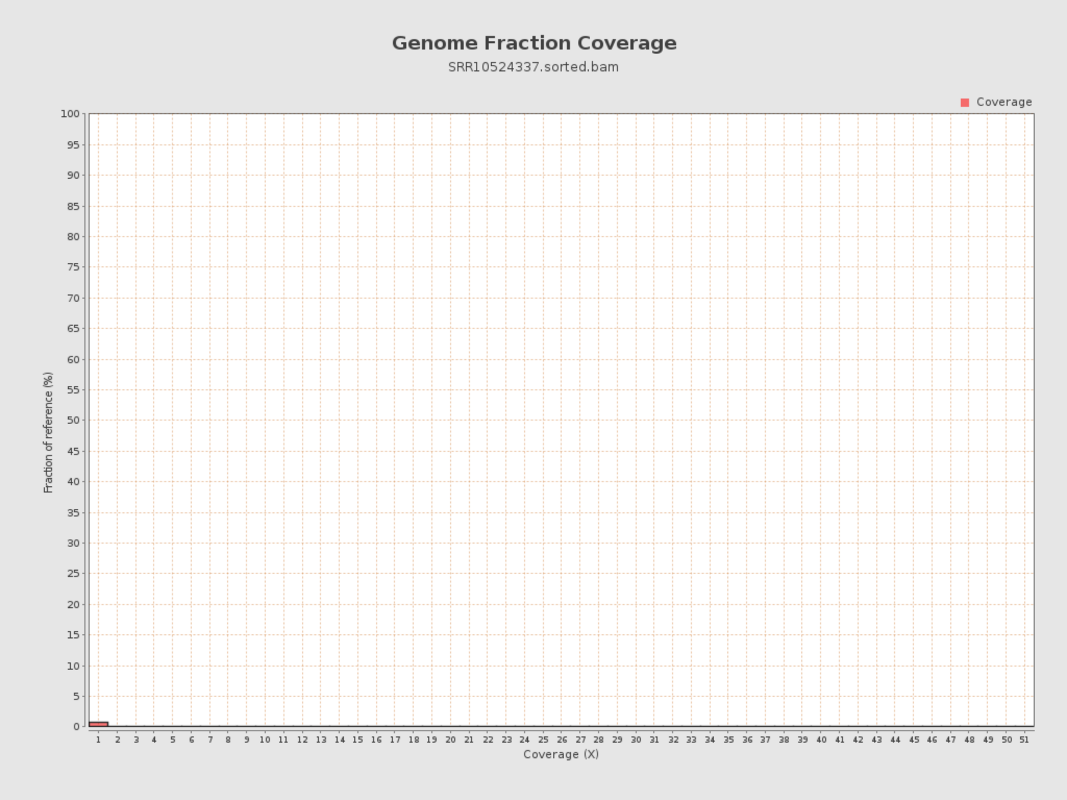
4. Results : Coverage Histogram



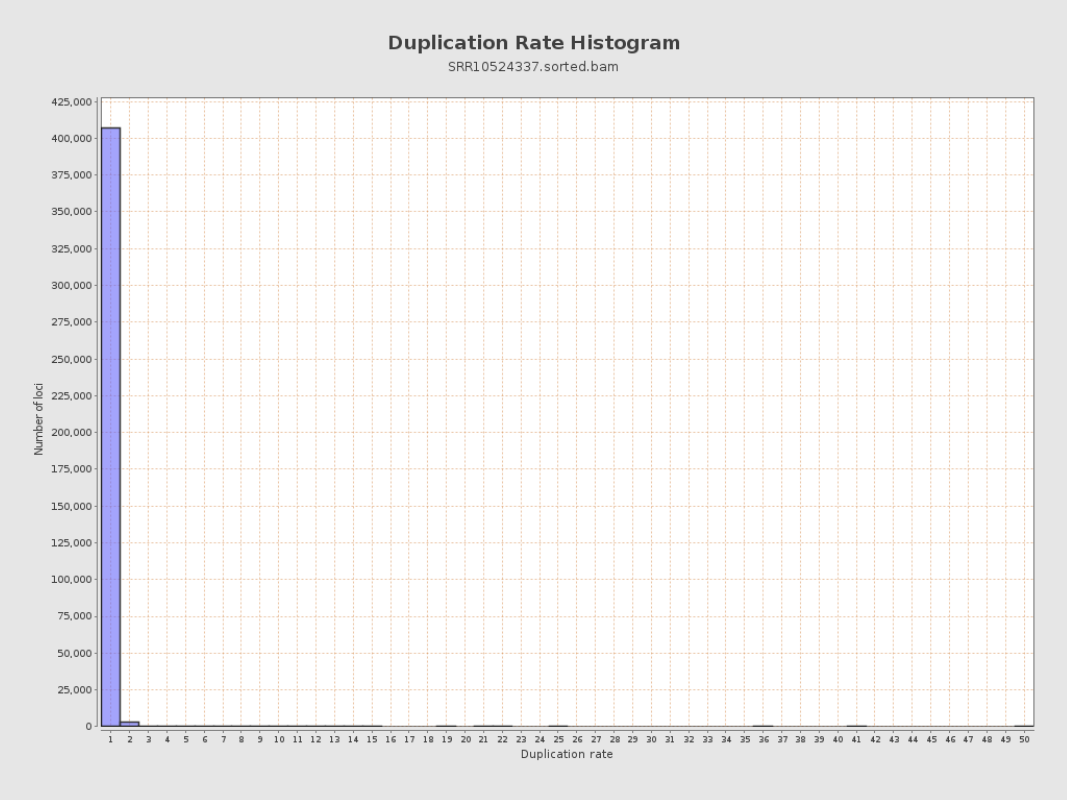
5. Results : Coverage Histogram (0-50X)



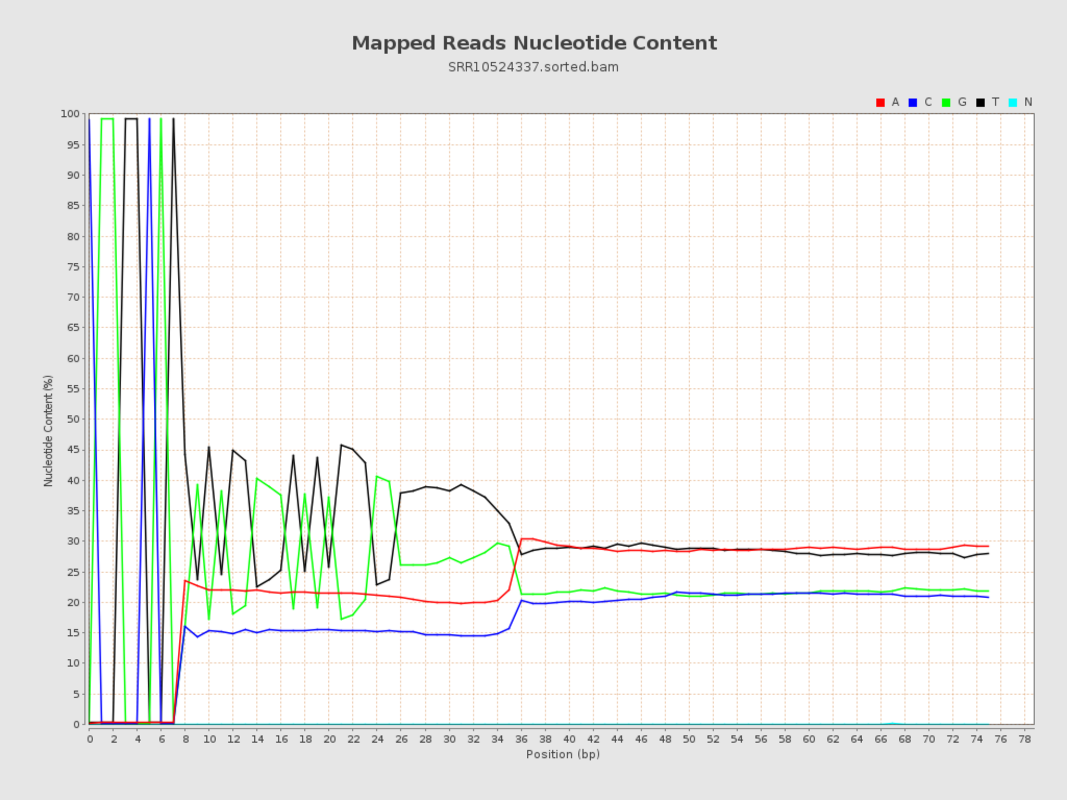
6. Results : Genome Fraction Coverage



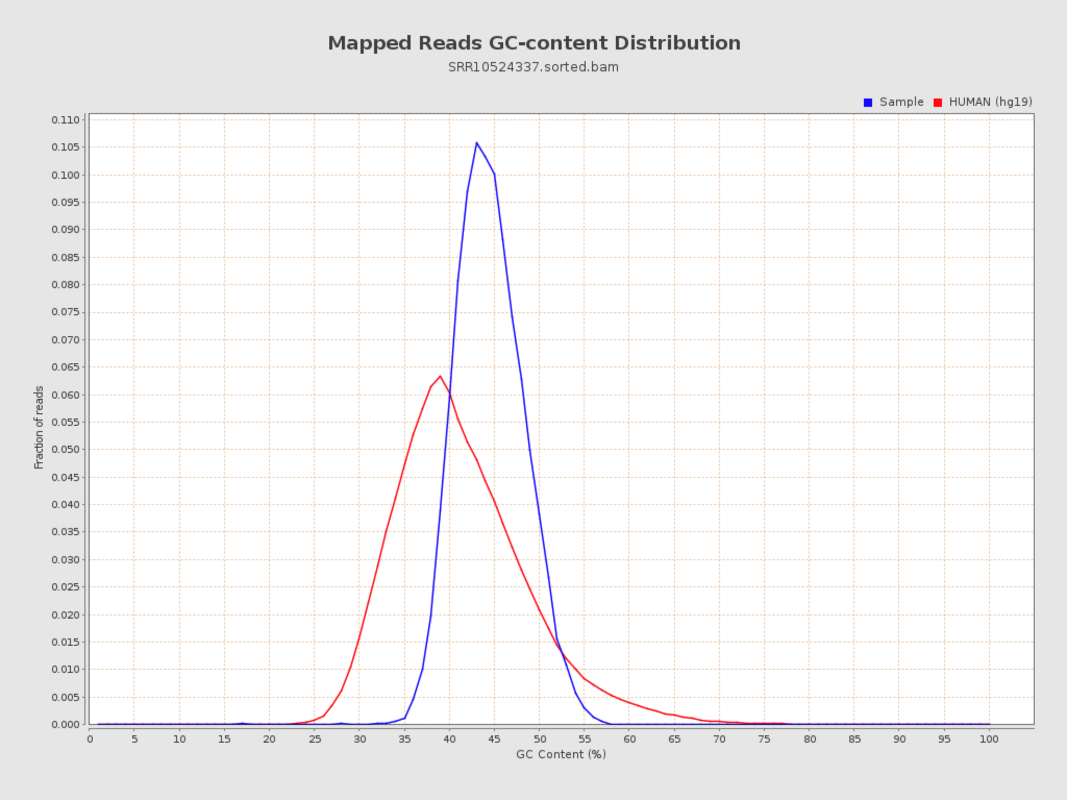
7. Results : Duplication Rate Histogram



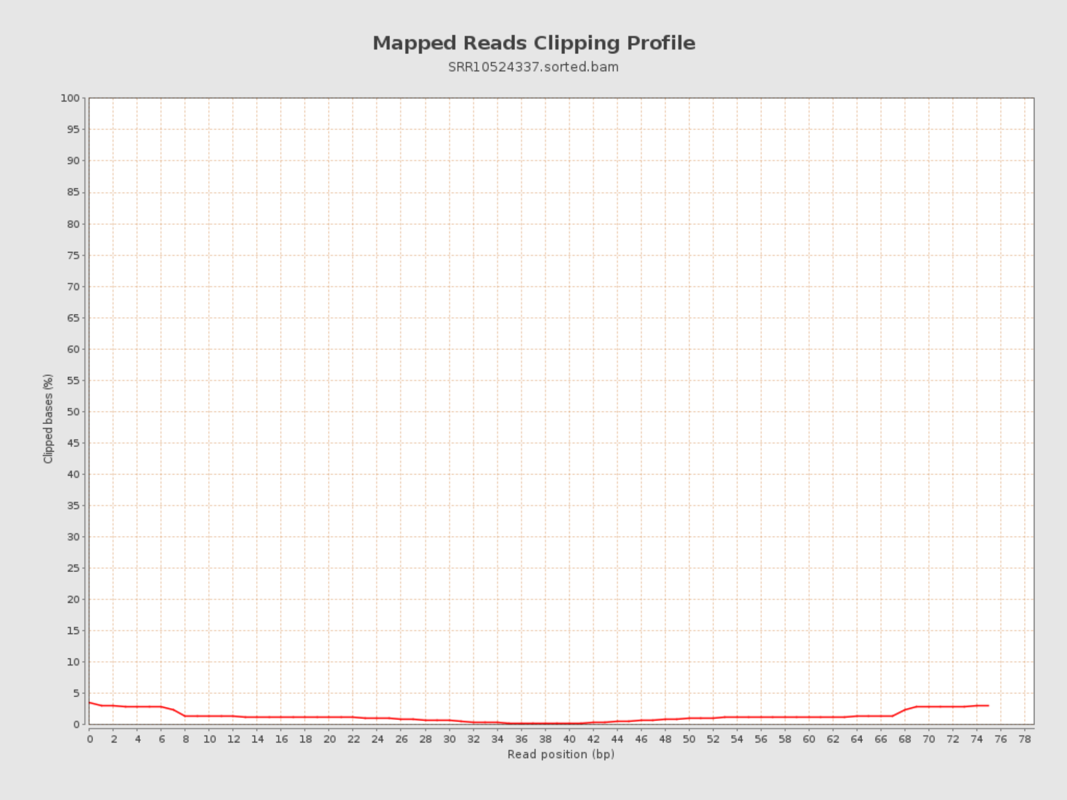
8. Results : Mapped Reads Nucleotide Content



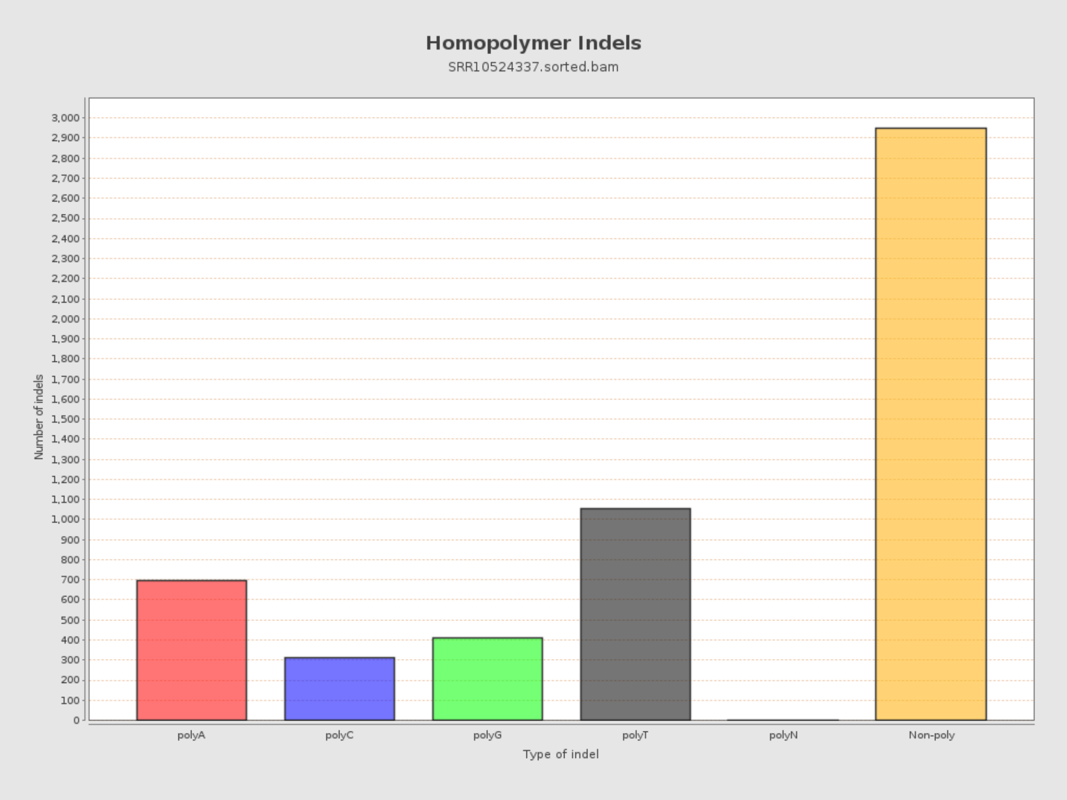
9. Results : Mapped Reads GC-content Distribution



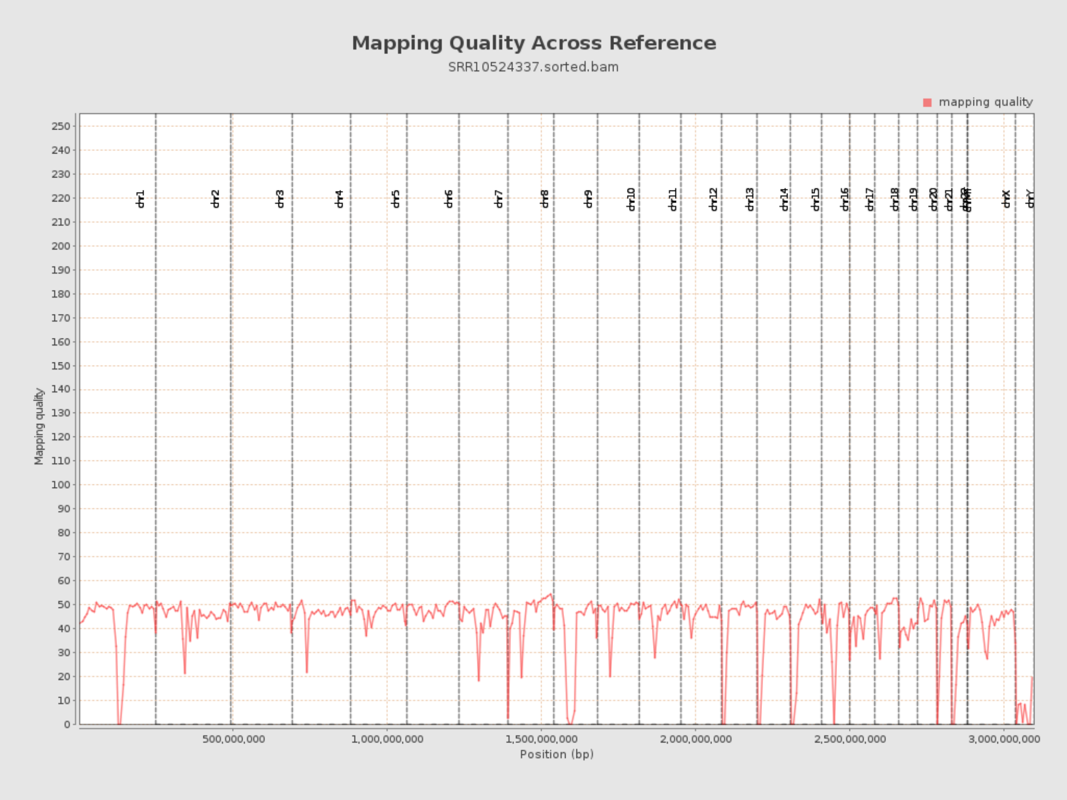
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram