Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 23:08:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524331.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_SRR10524331 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524331.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 23:08:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524331.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,331,797
Mapped reads	3,039,249 / 91.22%
Unmapped reads	292,548 / 8.78%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,938 / 0.45%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	139,112 / 4.18%
Duplication rate	3.19%
Clipped reads	3,045,930 / 91.42%

2.2. ACGT Content

Number/percentage of A's	43,320,631 / 24.52%
Number/percentage of C's	31,790,998 / 18%
Number/percentage of T's	58,034,513 / 32.85%
Number/percentage of G's	43,478,386 / 24.61%
Number/percentage of N's	23,785 / 0.01%
GC Percentage	42.61%

2.3. Coverage

Mean	0.0571

Standard Deviation	0.498

2.4. Mapping Quality

Mean Mapping Quality	43.99

2.5. Mismatches and indels

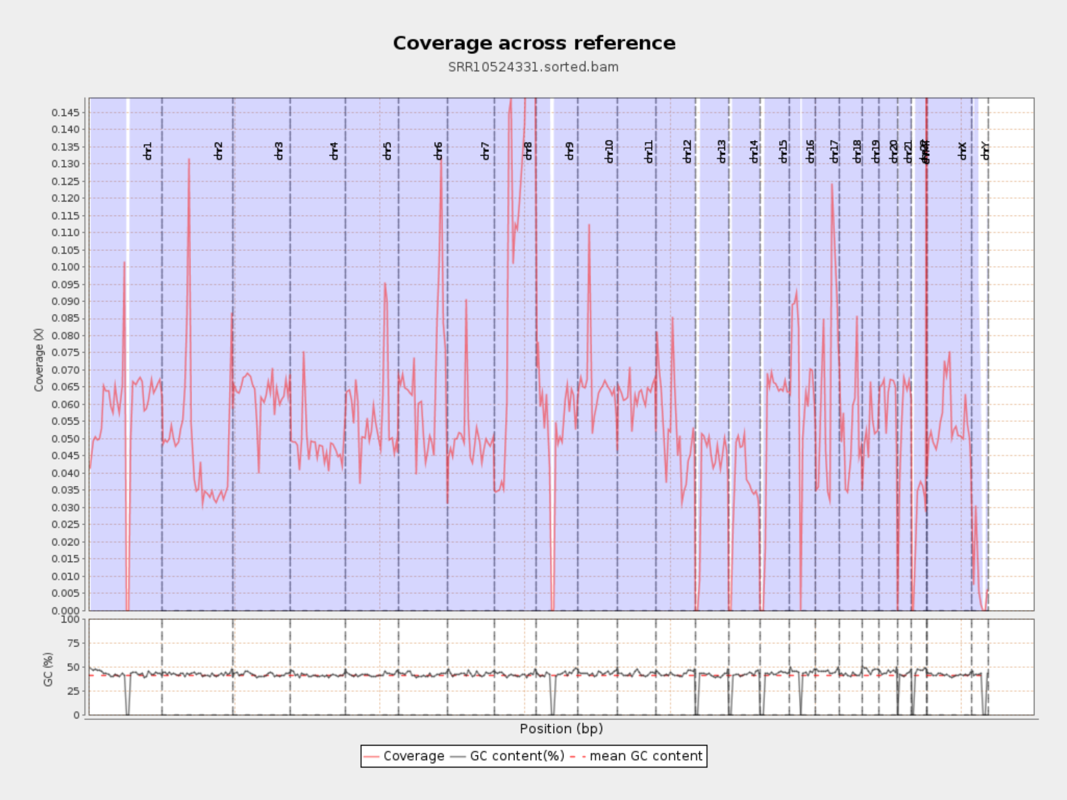
General error rate	0.53%
Mismatches	908,352
Insertions	12,238
Mapped reads with at least one insertion	0.4%
Deletions	30,580
Mapped reads with at least one deletion	1%
Homopolymer indels	42.42%

2.6. Chromosome stats

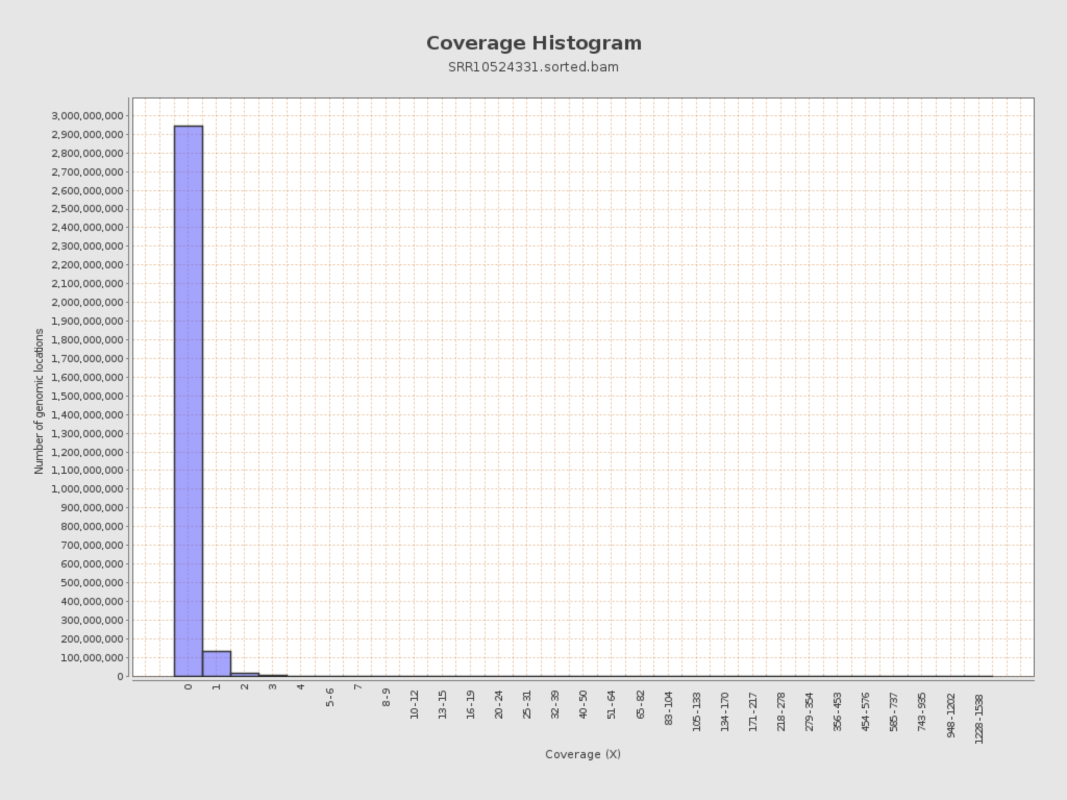
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14388540	0.0577	1.0159
chr2	243199373	11624403	0.0478	0.6853
chr3	198022430	12487197	0.0631	0.2904
chr4	191154276	9187548	0.0481	0.2963
chr5	180915260	10367477	0.0573	0.2737
chr6	171115067	11200661	0.0655	0.3314
chr7	159138663	8044645	0.0506	0.6319

chr8	146364022	18615782	0.1272	0.59
chr9	141213431	7299229	0.0517	0.3659
chr10	135534747	8934152	0.0659	0.4881
chr11	135006516	8444681	0.0626	0.3927
chr12	133851895	7053002	0.0527	0.2688
chr13	115169878	4495841	0.039	0.2252
chr14	107349540	3759008	0.035	0.2282
chr15	102531392	5417497	0.0528	0.2679
chr16	90354753	5955511	0.0659	0.3298
chr17	81195210	5361429	0.066	0.3387
chr18	78077248	4144608	0.0531	0.6944
chr19	59128983	3100505	0.0524	0.6863
chr20	63025520	3978660	0.0631	0.2944
chr21	48129895	2564759	0.0533	0.3001
chr22	51304566	1281302	0.025	0.1777
chrMT	16571	6780	0.4091	0.7433
chrX	155270560	8483302	0.0546	0.3122
chrY	59373566	500008	0.0084	0.2291

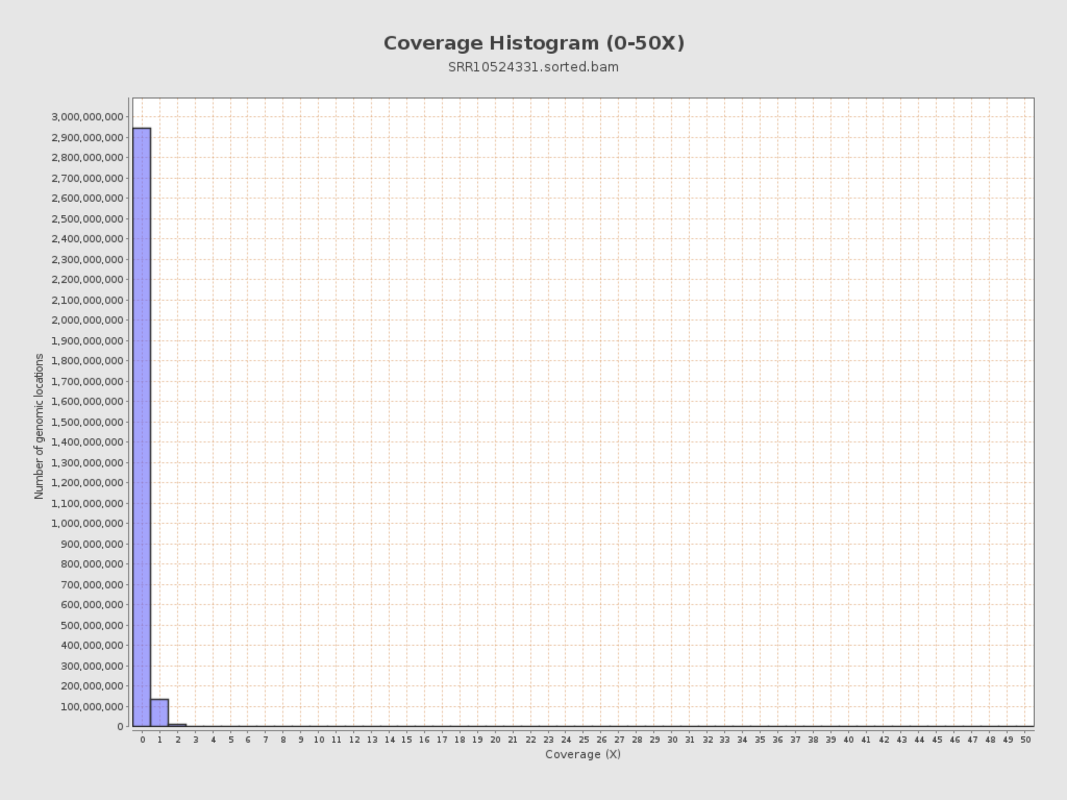
3. Results : Coverage across reference



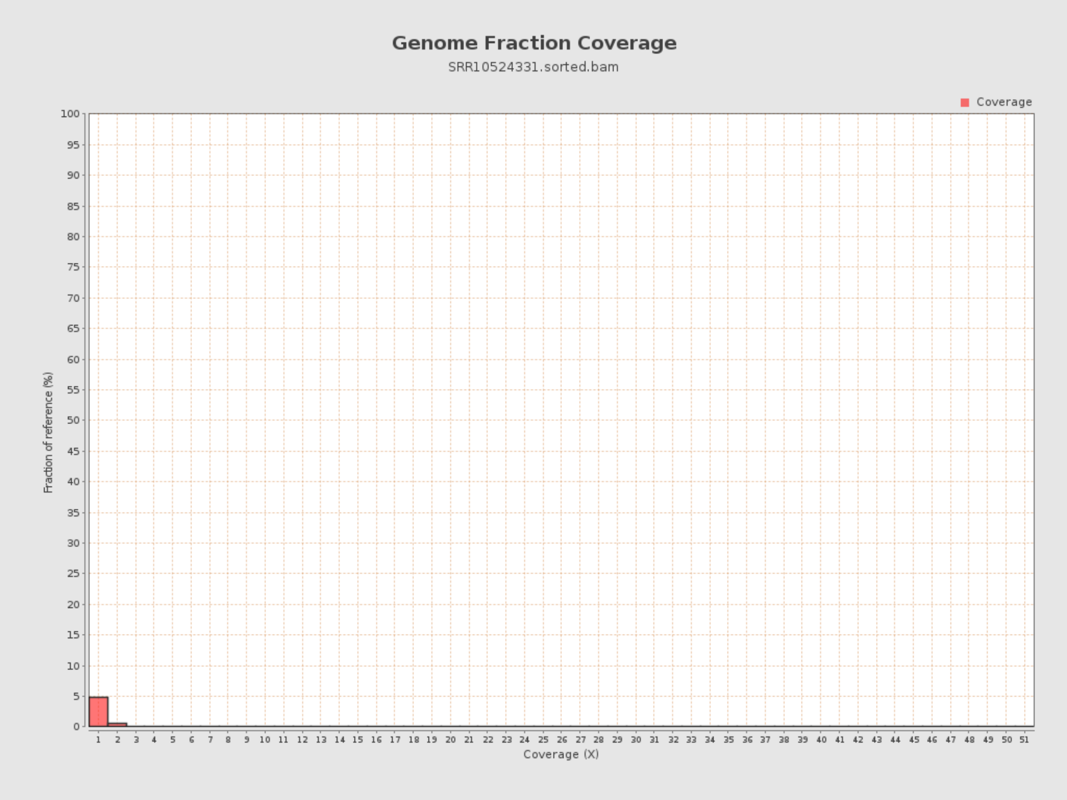
4. Results : Coverage Histogram



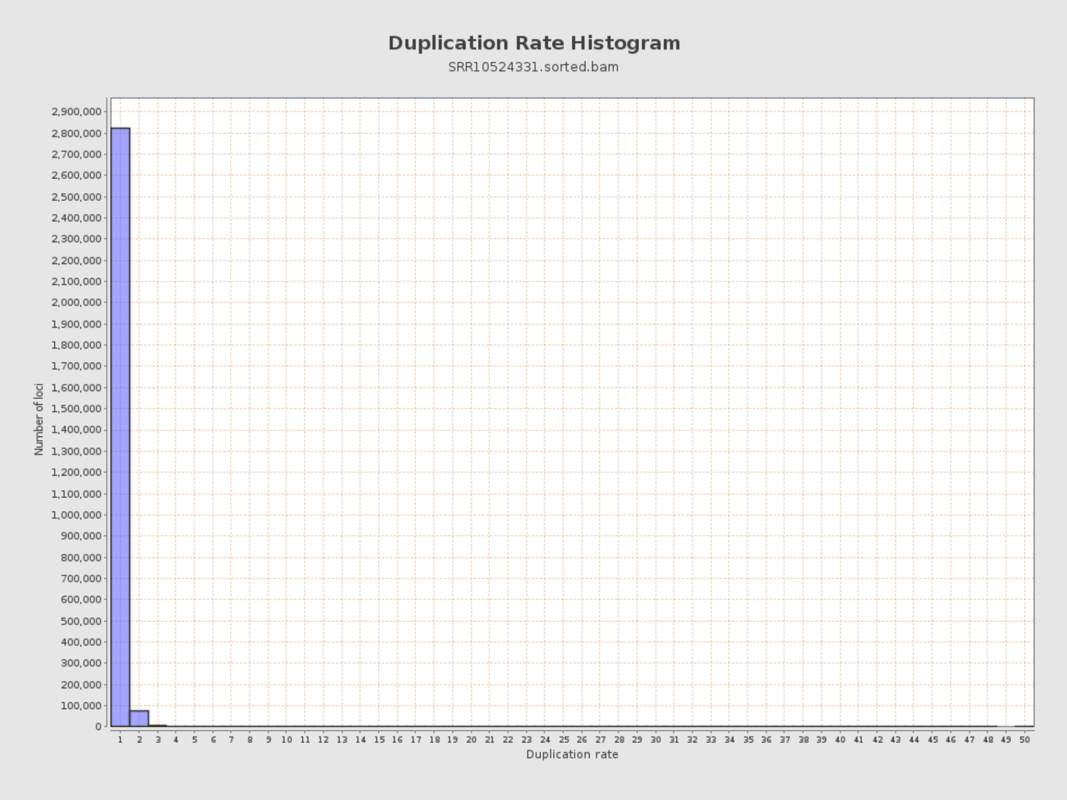
5. Results : Coverage Histogram (0-50X)



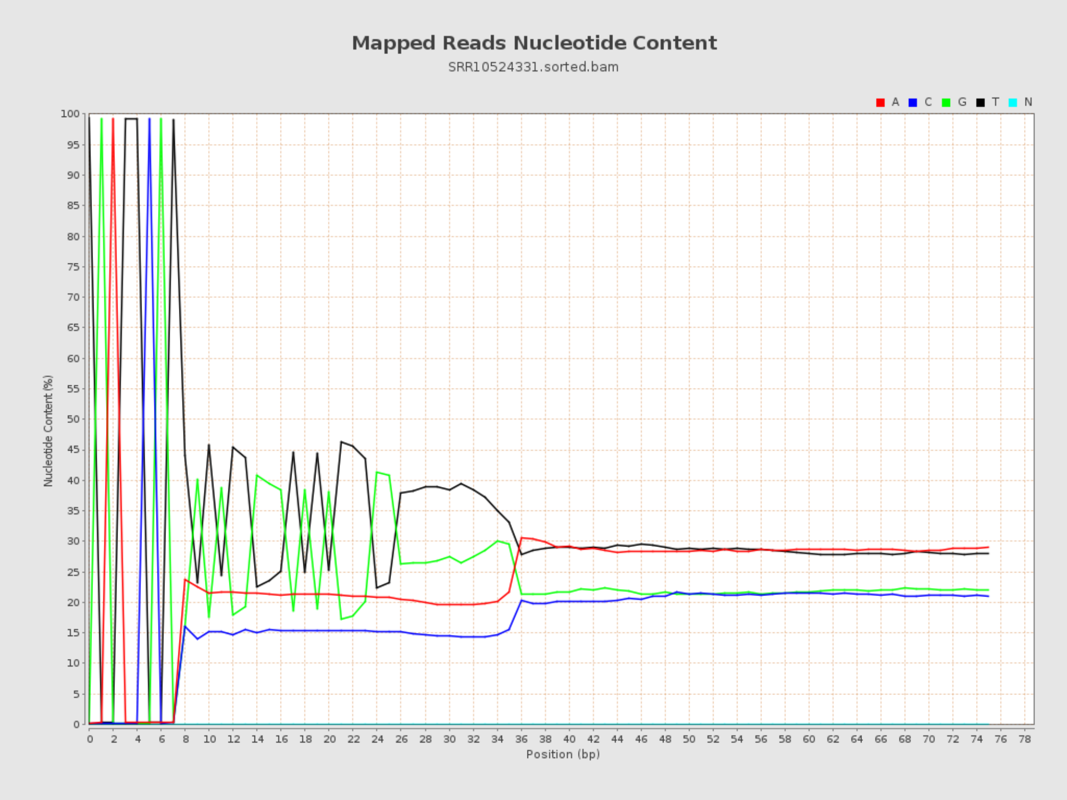
6. Results : Genome Fraction Coverage



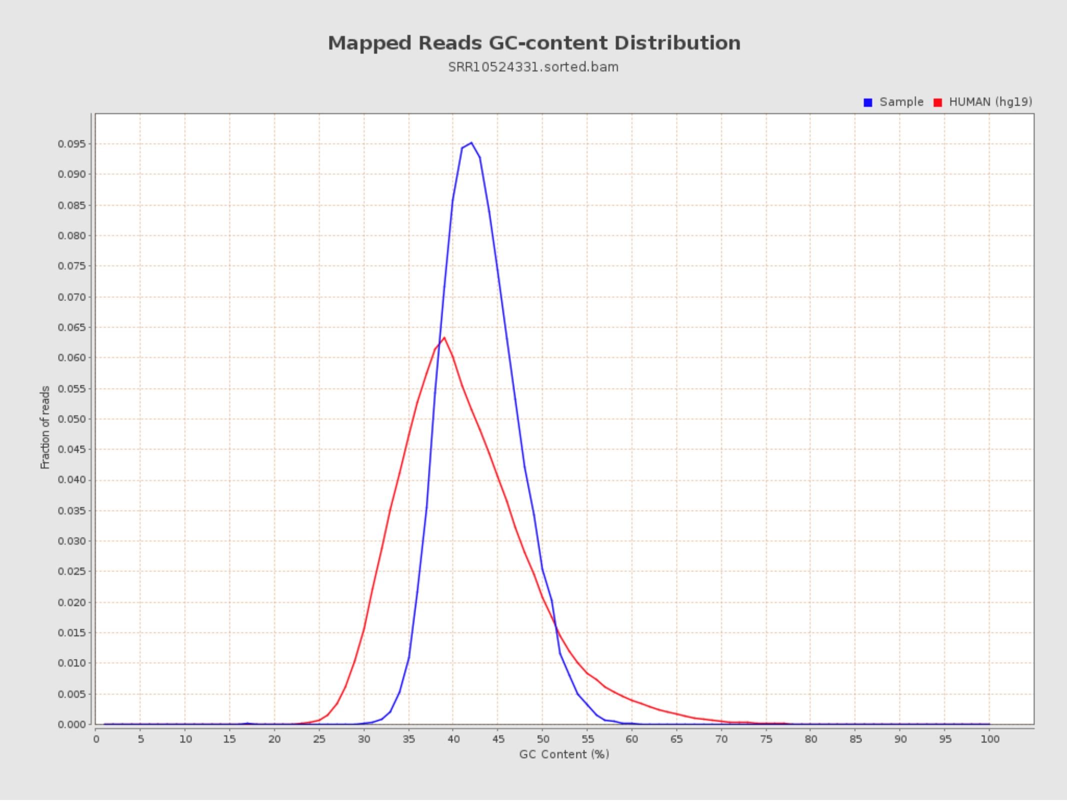
7. Results : Duplication Rate Histogram



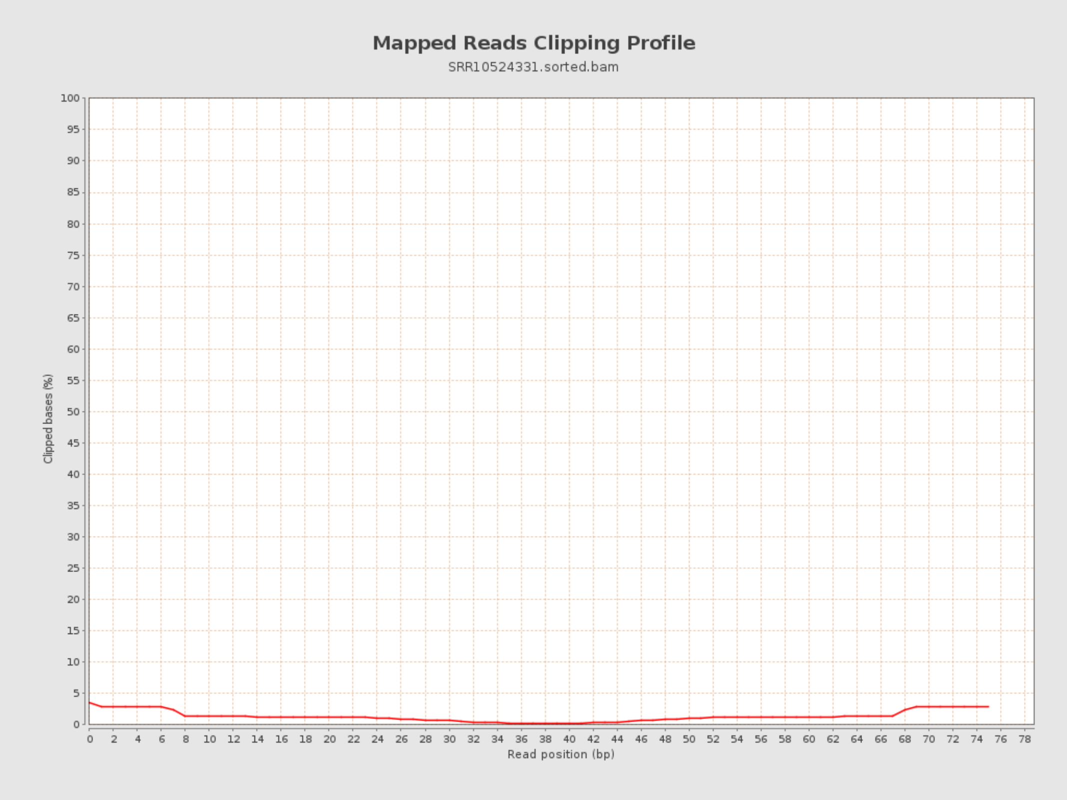
8. Results : Mapped Reads Nucleotide Content



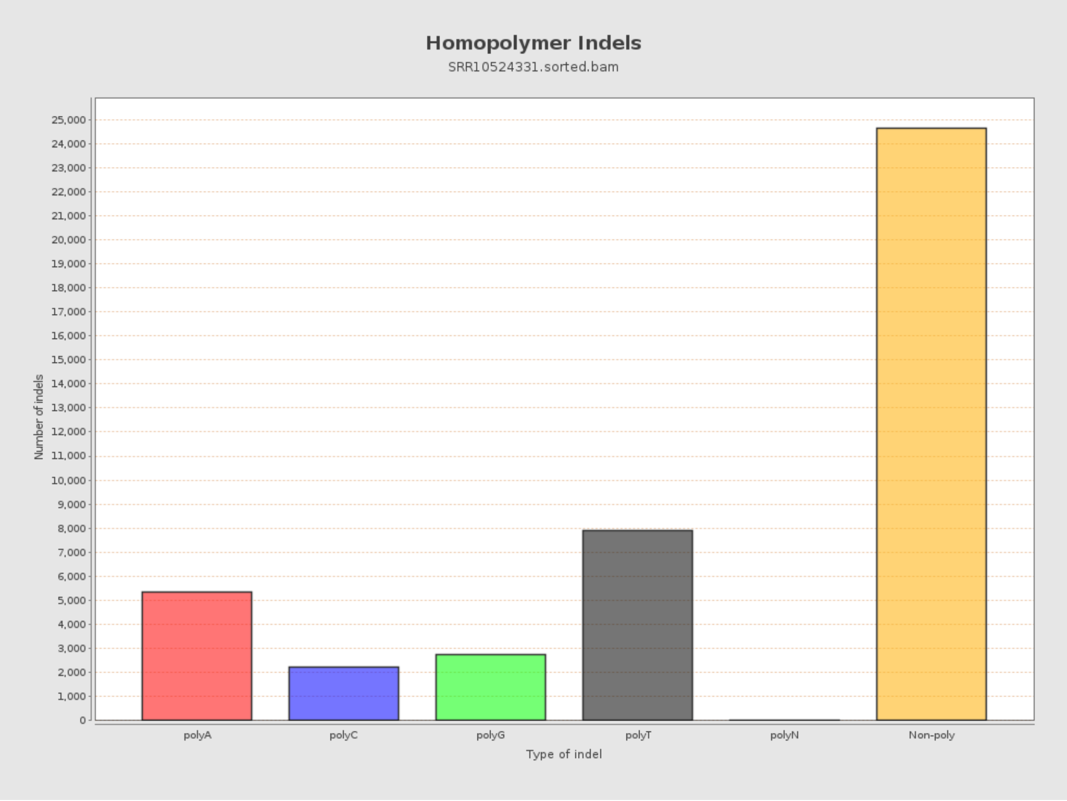
9. Results : Mapped Reads GC-content Distribution



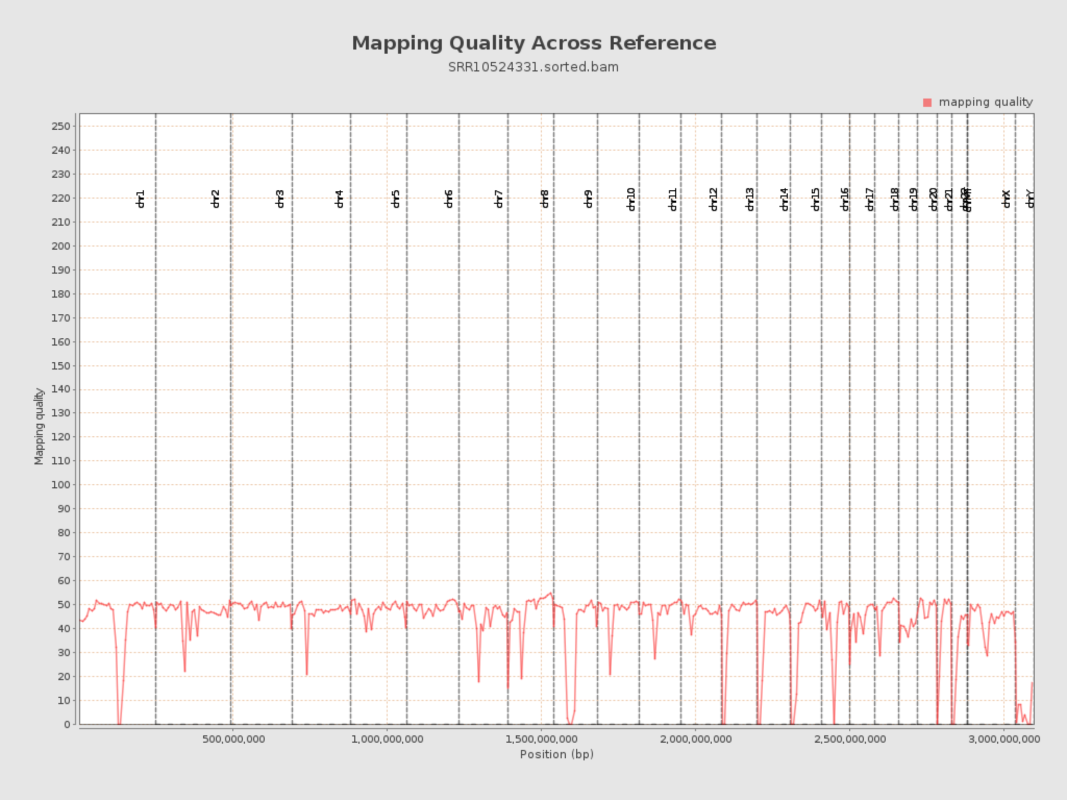
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram