Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/20 03:31:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1506331.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_SRR1506331 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1506331.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Dec 20 03:31:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1506331.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,509,331
Mapped reads	2,341,478 / 66.72%
Unmapped reads	1,167,853 / 33.28%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	35,885 / 1.02%
Read min/max/mean length	30 / 94 / 94.37
Duplicated reads (estimated)	177,752 / 5.07%
Duplication rate	6.15%
Clipped reads	1,512,450 / 43.1%

2.2. ACGT Content

Number/percentage of A's	49,514,770 / 27.03%
Number/percentage of C's	33,432,087 / 18.25%
Number/percentage of T's	56,255,306 / 30.71%
Number/percentage of G's	43,920,117 / 23.98%
Number/percentage of N's	42,791 / 0.02%
GC Percentage	42.23%

2.3. Coverage

Mean	0.0592

Standard Deviation	0.4591

2.4. Mapping Quality

Mean Mapping Quality	48.01

2.5. Mismatches and indels

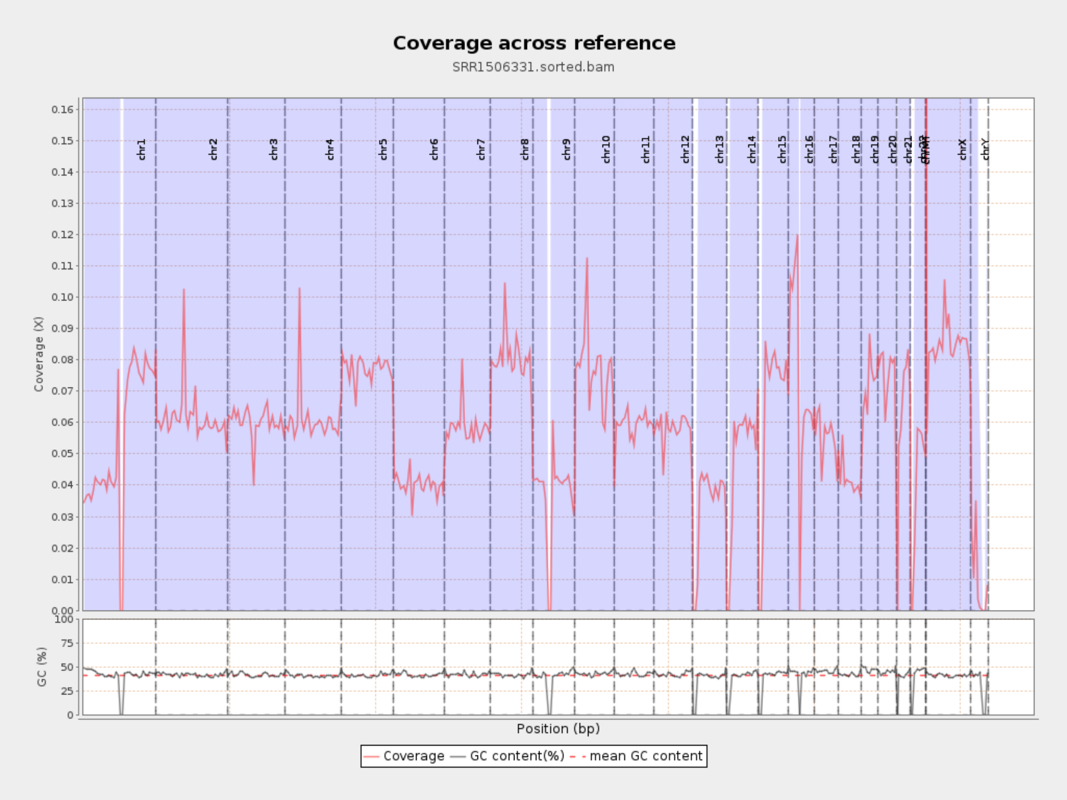
General error rate	0.81%
Mismatches	1,442,267
Insertions	14,741
Mapped reads with at least one insertion	0.62%
Deletions	40,179
Mapped reads with at least one deletion	1.69%
Homopolymer indels	45.82%

2.6. Chromosome stats

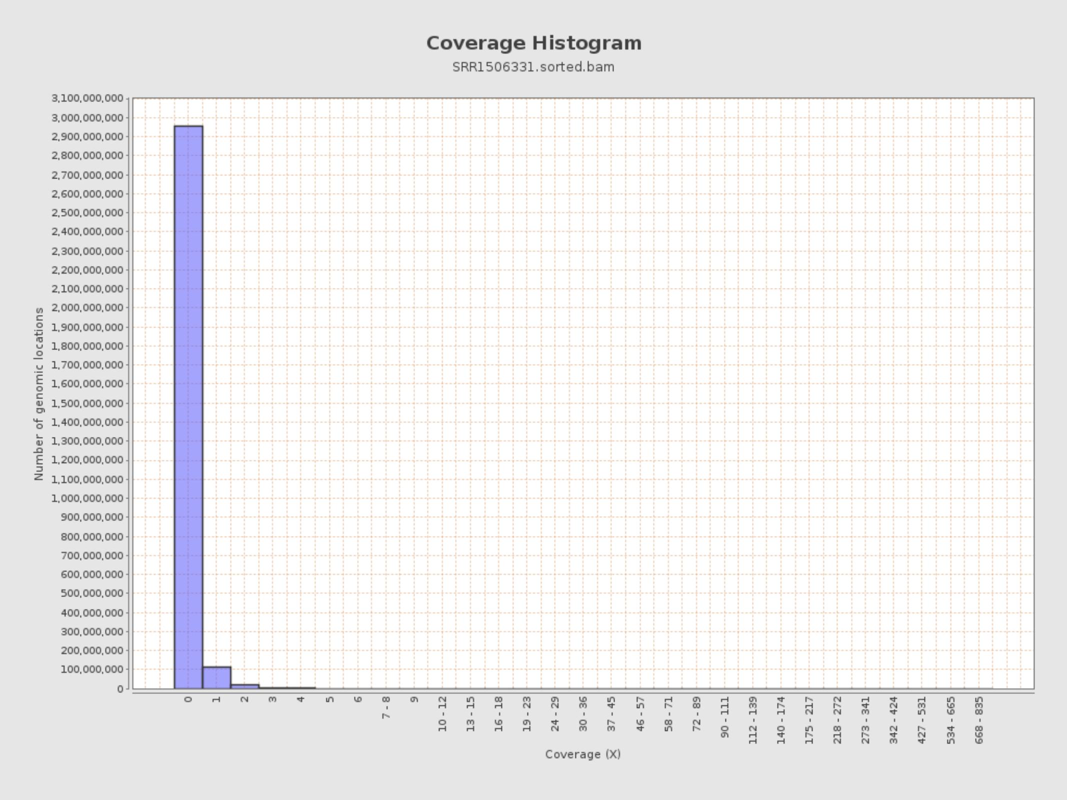
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13635393	0.0547	0.7654
chr2	243199373	14979513	0.0616	0.5016
chr3	198022430	11913983	0.0602	0.2987
chr4	191154276	11693173	0.0612	0.3657
chr5	180915260	13938745	0.077	0.3436
chr6	171115067	6877167	0.0402	0.2855
chr7	159138663	9310404	0.0585	0.5556

chr8	146364022	11775979	0.0805	0.6268
chr9	141213431	5239070	0.0371	0.4357
chr10	135534747	10429963	0.077	0.5032
chr11	135006516	8015575	0.0594	0.4388
chr12	133851895	7776298	0.0581	0.2995
chr13	115169878	3843262	0.0334	0.2198
chr14	107349540	5221644	0.0486	0.3103
chr15	102531392	6534562	0.0637	0.3129
chr16	90354753	6531004	0.0723	0.369
chr17	81195210	4524771	0.0557	0.3315
chr18	78077248	3275927	0.042	0.7486
chr19	59128983	4241472	0.0717	0.5941
chr20	63025520	4748553	0.0753	0.3506
chr21	48129895	3029368	0.0629	0.3743
chr22	51304566	1976073	0.0385	0.2426
chrMT	16571	15564	0.9392	1.2078
chrX	155270560	13132602	0.0846	0.4088
chrY	59373566	582496	0.0098	0.2927

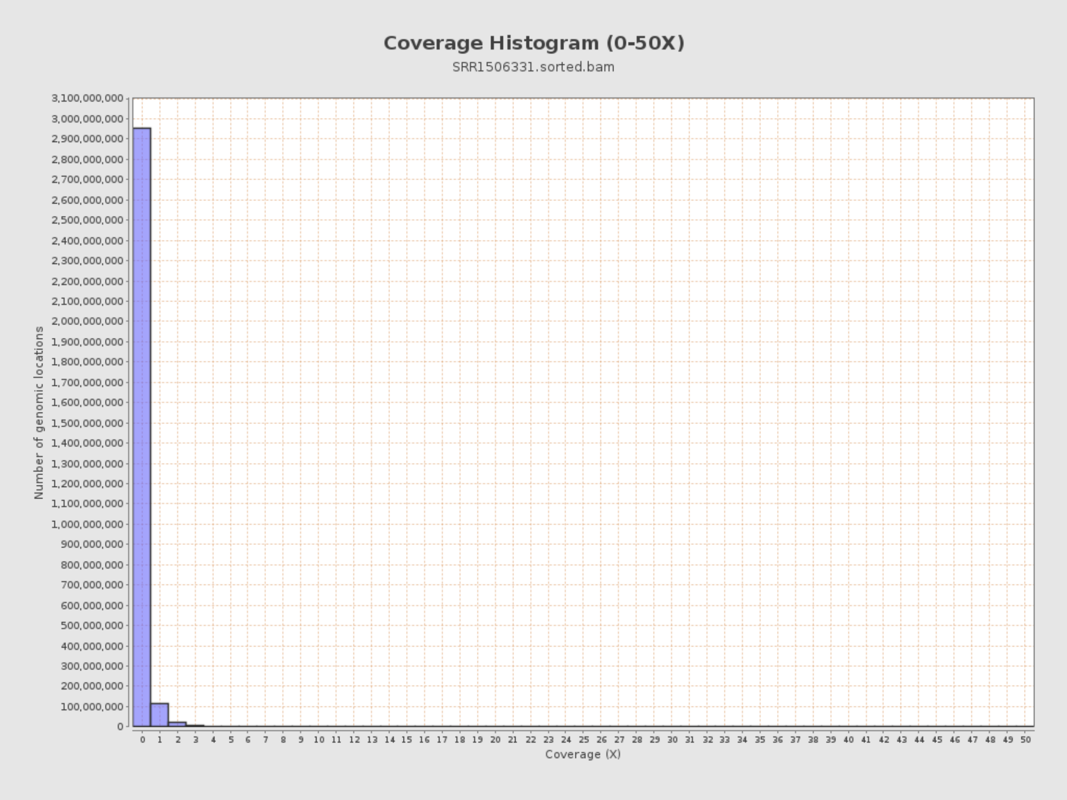
3. Results : Coverage across reference



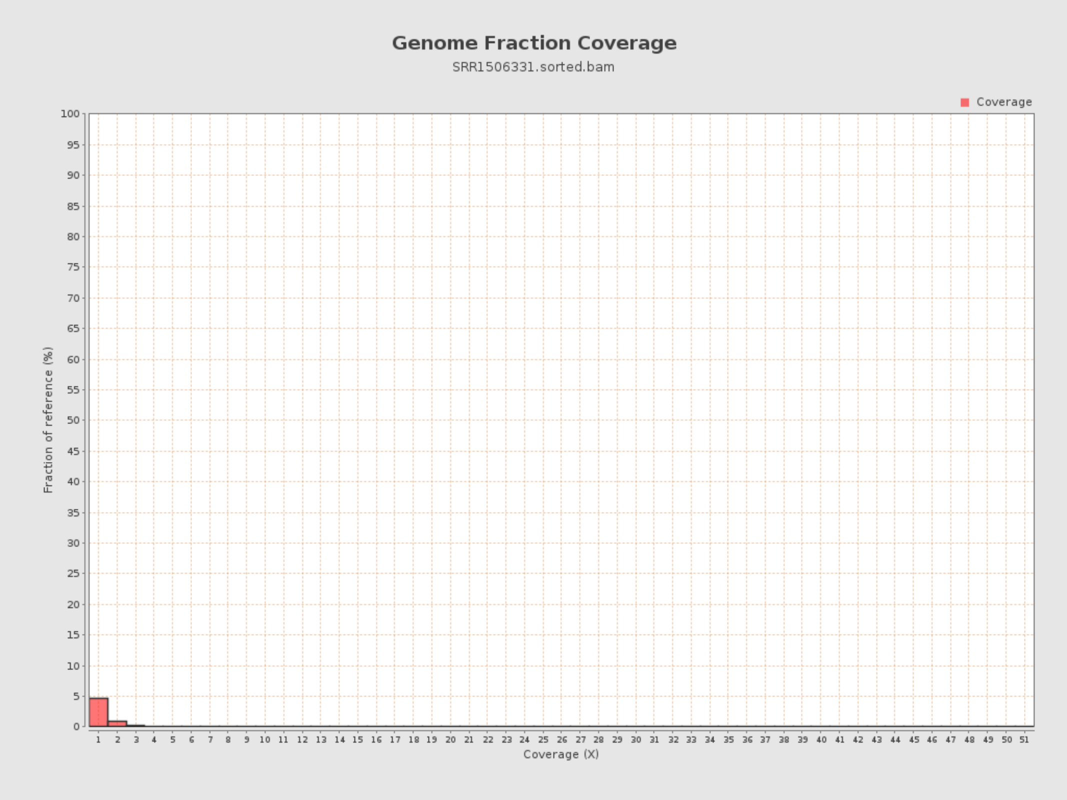
4. Results : Coverage Histogram



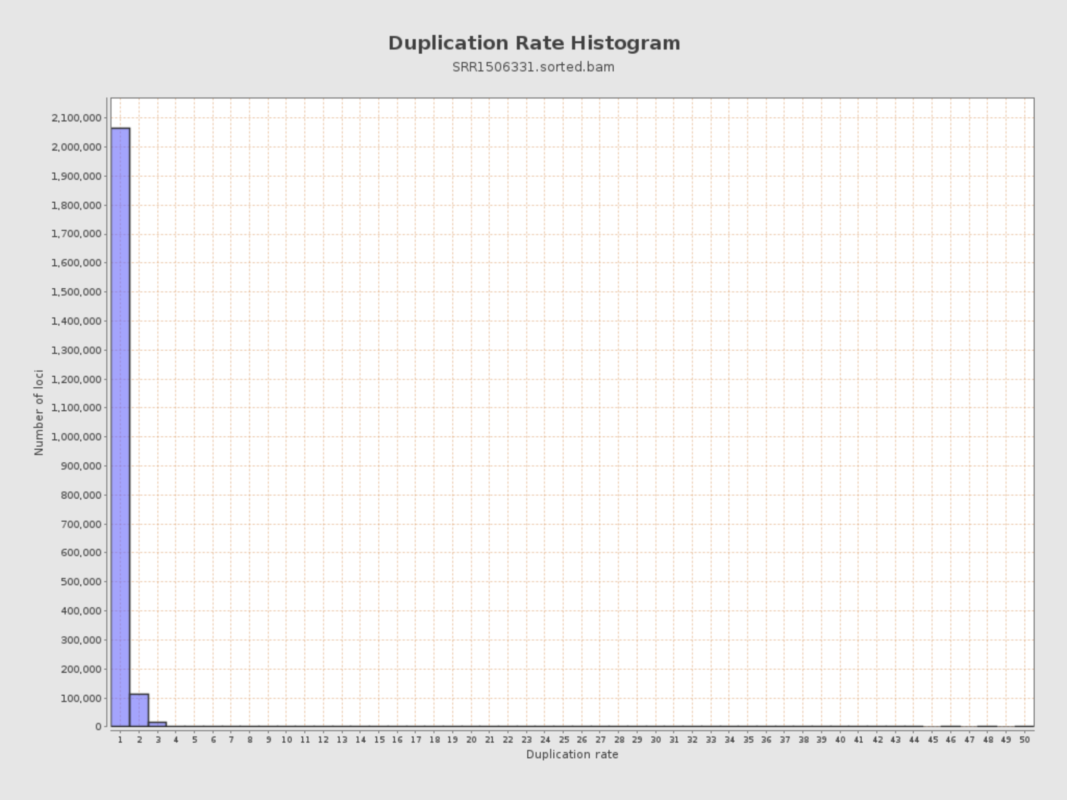
5. Results : Coverage Histogram (0-50X)



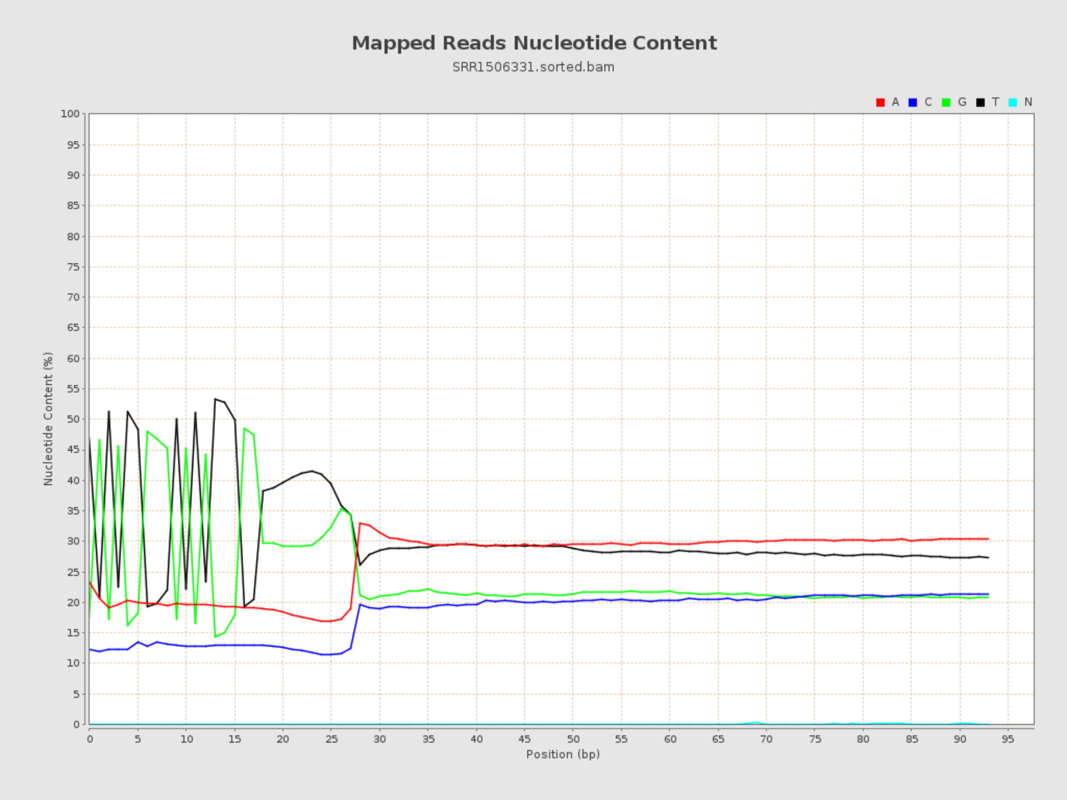
6. Results : Genome Fraction Coverage



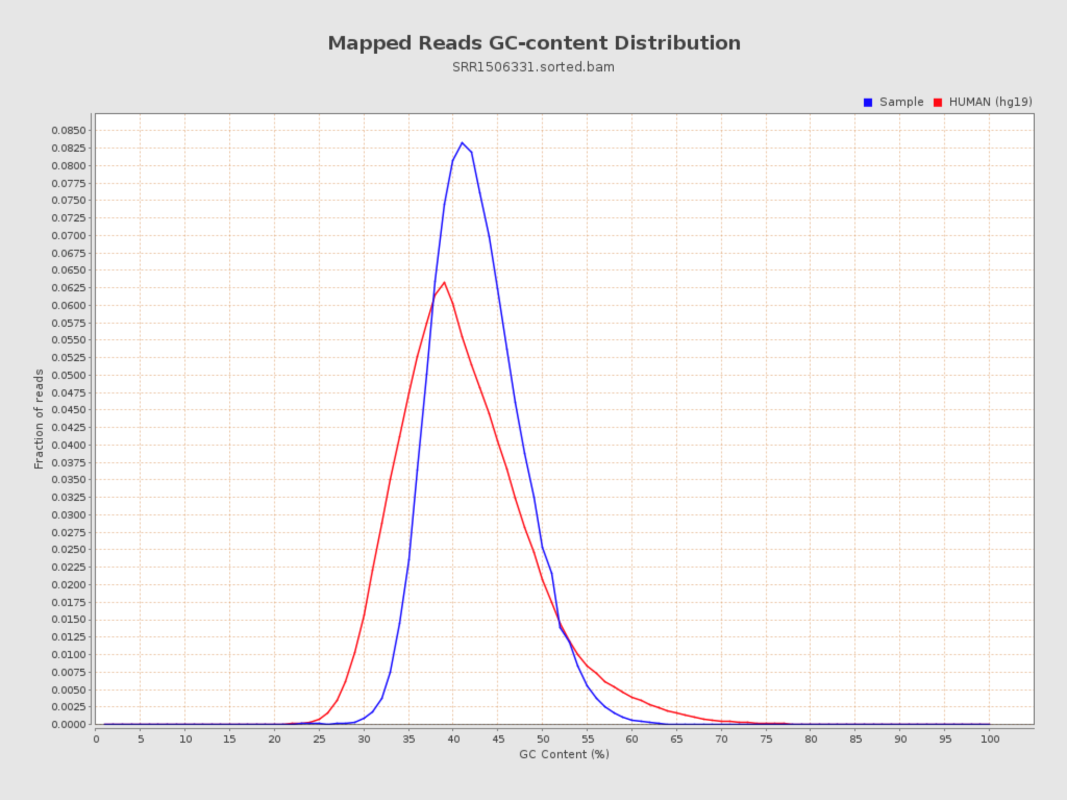
7. Results : Duplication Rate Histogram



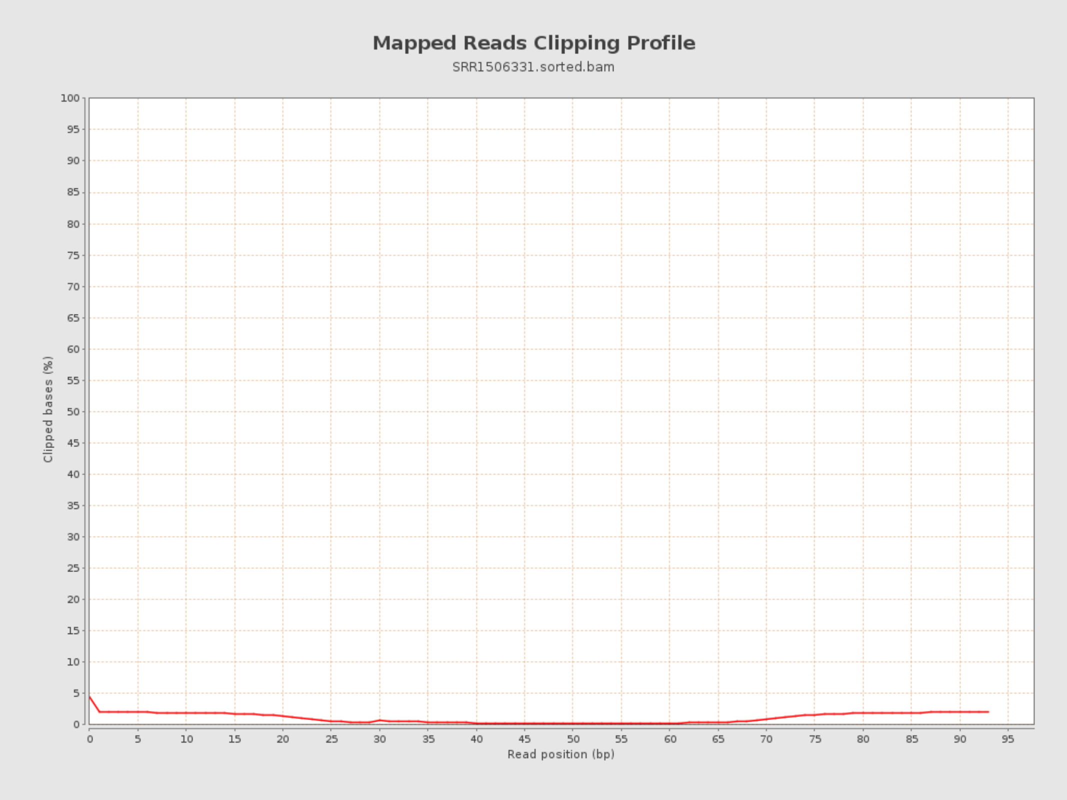
8. Results : Mapped Reads Nucleotide Content



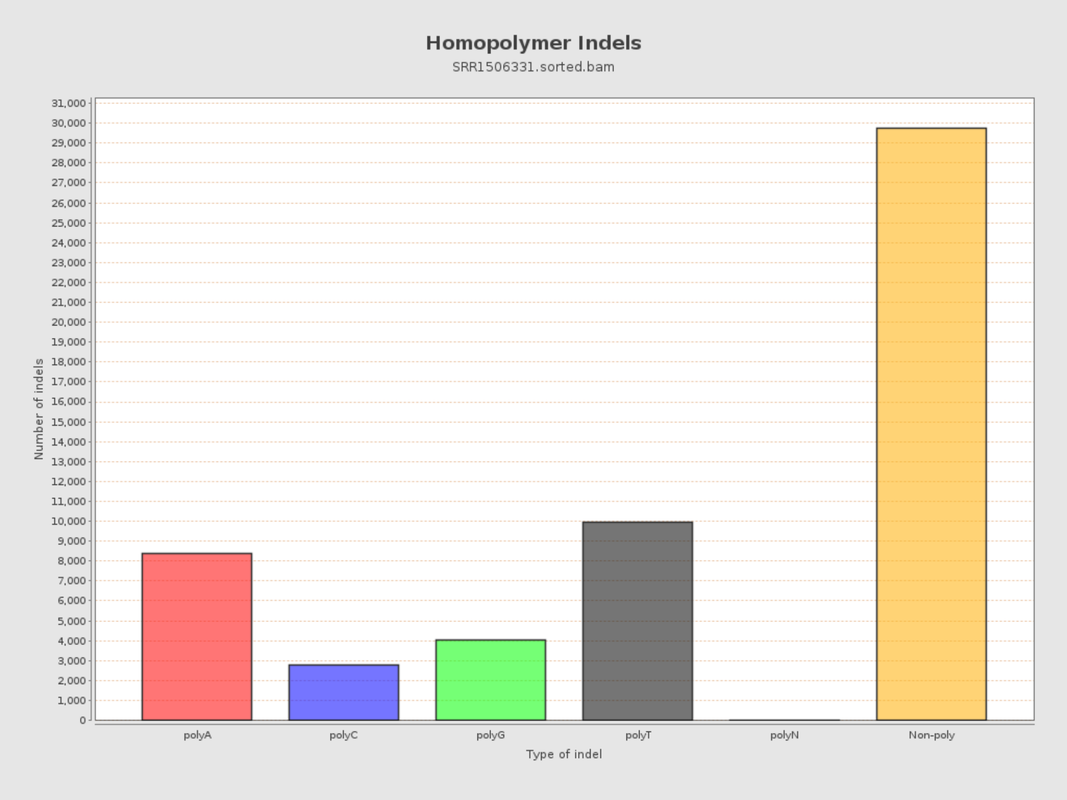
9. Results : Mapped Reads GC-content Distribution



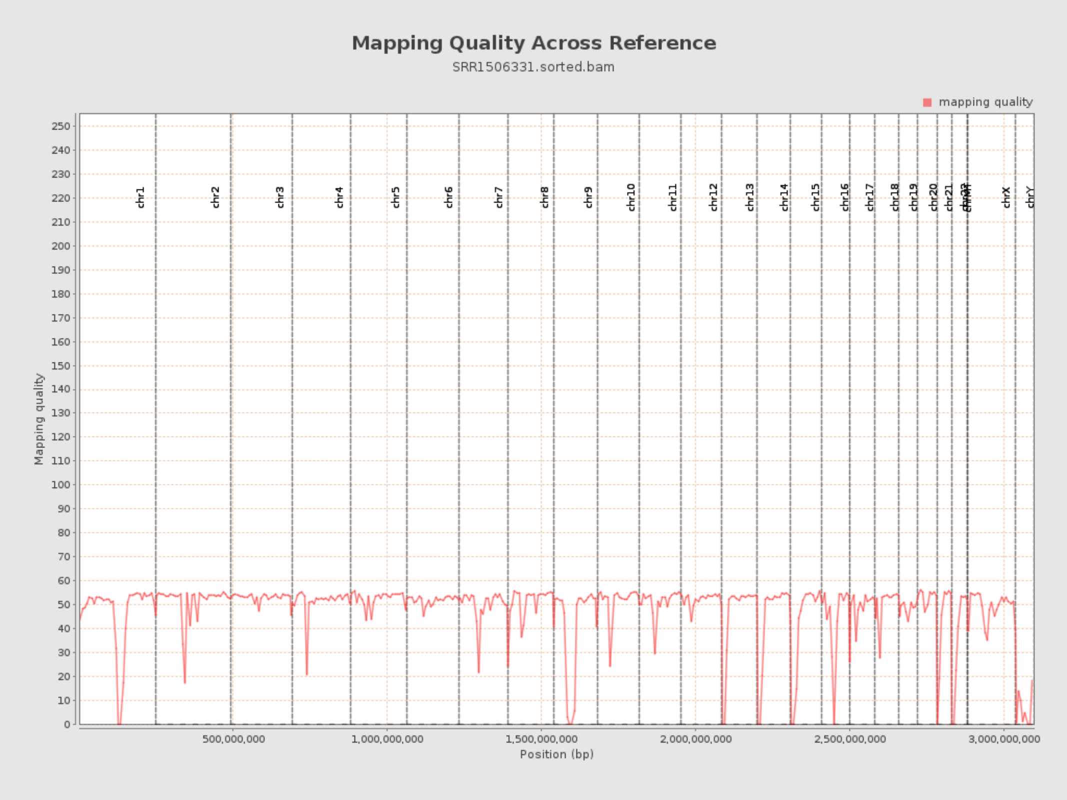
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram