Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/20 07:00:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR090131.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_SRR090131 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR090131.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Apr 20 07:00:29 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR090131.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	20,904,838
Mapped reads	16,847,308 / 80.59%
Unmapped reads	4,057,530 / 19.41%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	916 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	2,539,945 / 12.15%
Duplication rate	10.32%
Clipped reads	2,602,490 / 12.45%

2.2. ACGT Content

Number/percentage of A's	254,584,342 / 32.47%
Number/percentage of C's	155,222,423 / 19.8%
Number/percentage of T's	206,156,583 / 26.3%
Number/percentage of G's	167,970,092 / 21.43%
Number/percentage of N's	56,679 / 0.01%
GC Percentage	41.22%

2.3. Coverage

Mean	0.2533

Standard Deviation	1.6862

2.4. Mapping Quality

Mean Mapping Quality	43

2.5. Mismatches and indels

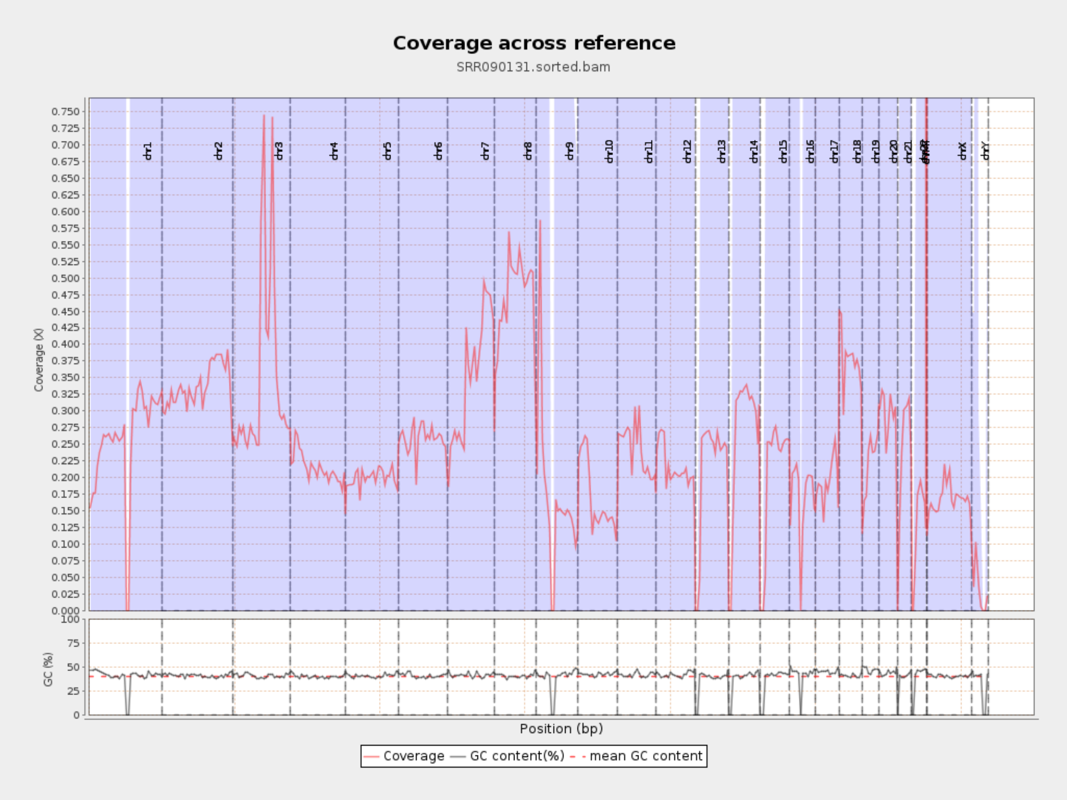
General error rate	0.46%
Mismatches	3,518,080
Insertions	35,343
Mapped reads with at least one insertion	0.21%
Deletions	105,159
Mapped reads with at least one deletion	0.62%
Homopolymer indels	44.46%

2.6. Chromosome stats

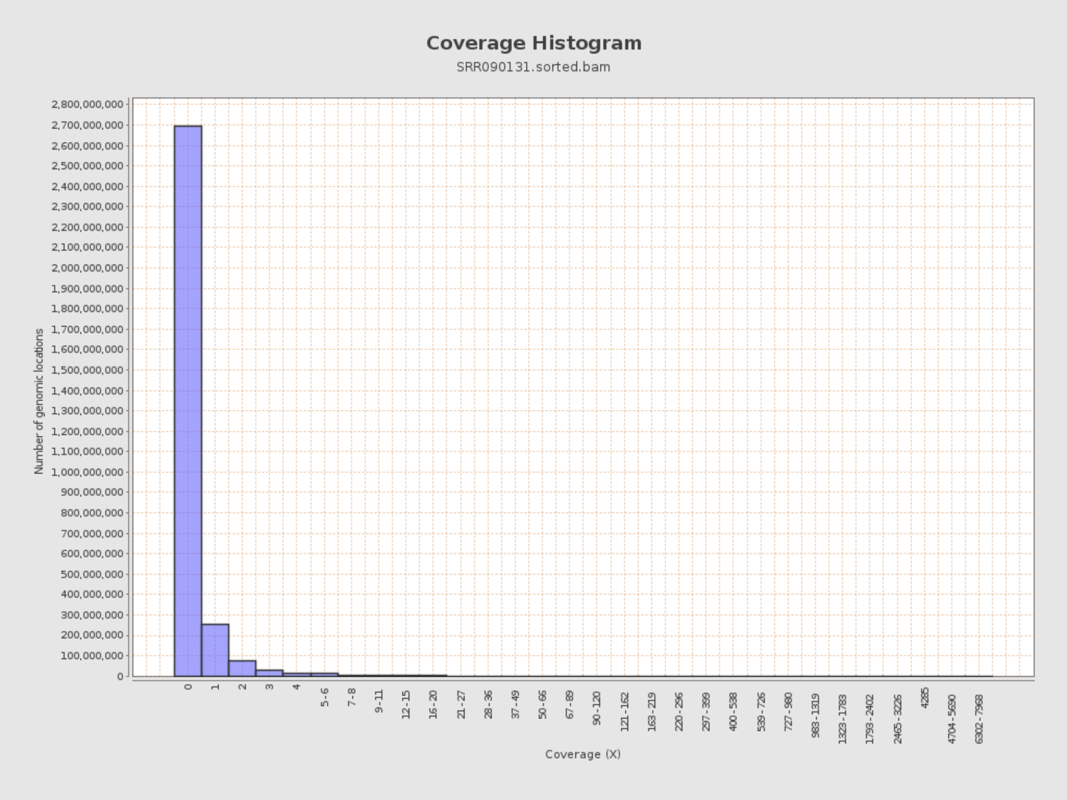
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	63535971	0.2549	1.8683
chr2	243199373	82334691	0.3385	1.6948
chr3	198022430	69427642	0.3506	1.4451
chr4	191154276	41084129	0.2149	0.9925
chr5	180915260	36092776	0.1995	0.9466
chr6	171115067	44191404	0.2583	1.1922
chr7	159138663	56681656	0.3562	2.6147

chr8	146364022	69542731	0.4751	4.6069
chr9	141213431	24729242	0.1751	1.1381
chr10	135534747	23227820	0.1714	1.0102
chr11	135006516	32588858	0.2414	1.2359
chr12	133851895	28748705	0.2148	0.9901
chr13	115169878	24374611	0.2116	0.9996
chr14	107349540	28265978	0.2633	1.1796
chr15	102531392	20868463	0.2035	0.9815
chr16	90354753	15529737	0.1719	0.916
chr17	81195210	15672816	0.193	0.9708
chr18	78077248	29461309	0.3773	1.9188
chr19	59128983	13241500	0.2239	1.5038
chr20	63025520	18465816	0.293	1.2337
chr21	48129895	11297631	0.2347	1.1872
chr22	51304566	6327692	0.1233	0.7134
chrMT	16571	558530	33.7053	30.3258
chrX	155270560	26019367	0.1676	0.92
chrY	59373566	1879334	0.0317	0.9903

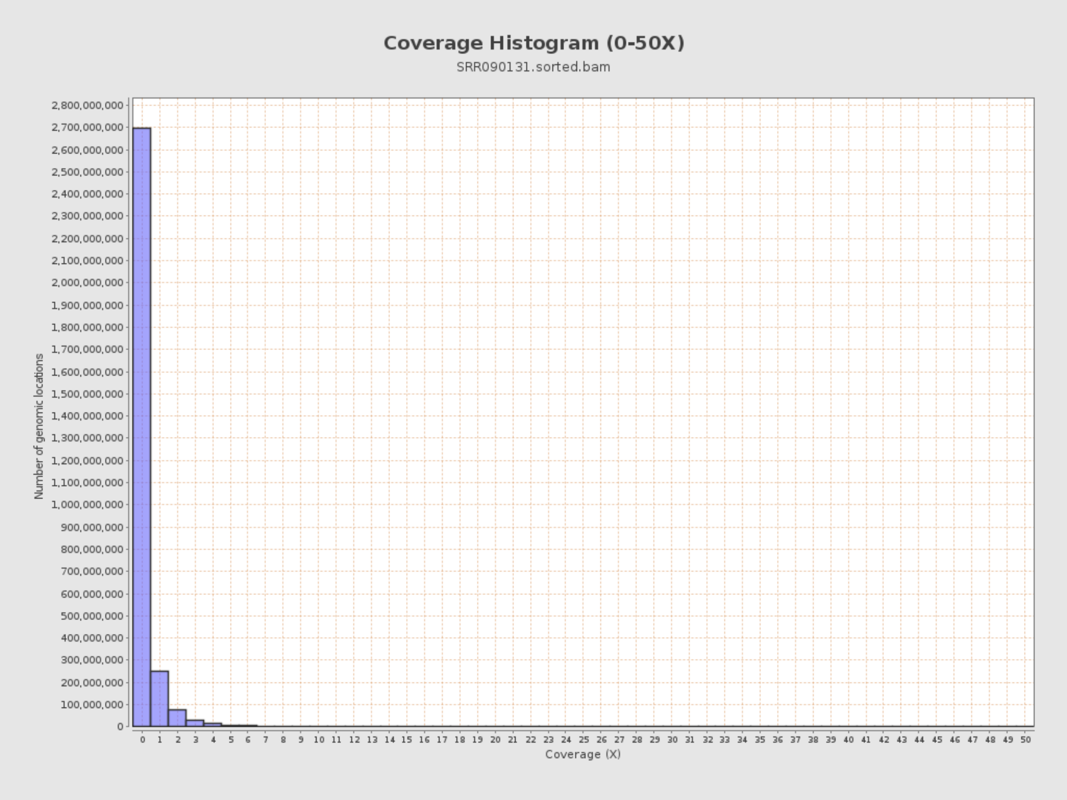
3. Results : Coverage across reference



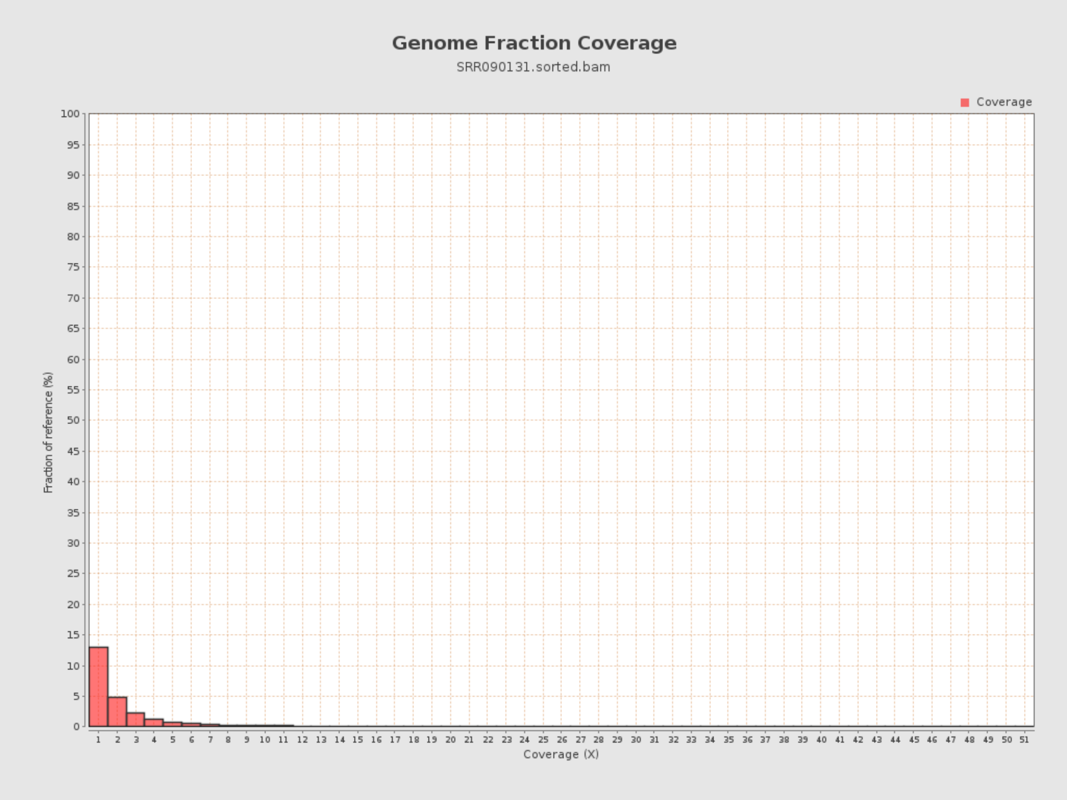
4. Results : Coverage Histogram



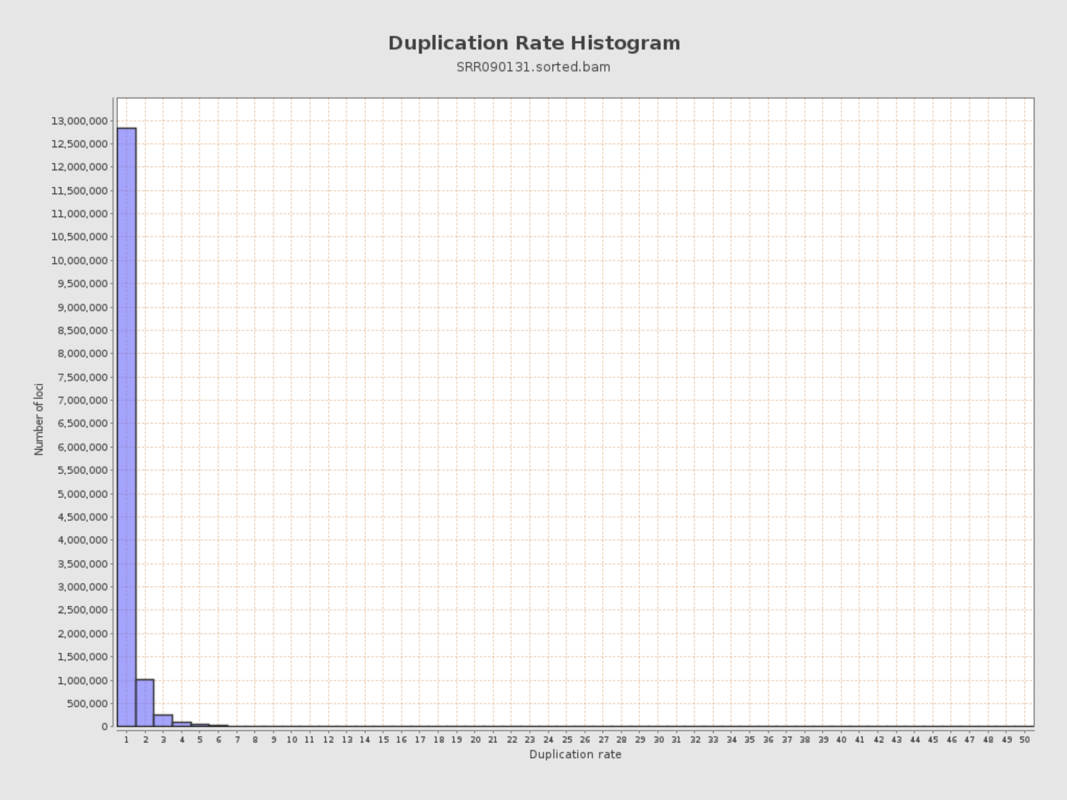
5. Results : Coverage Histogram (0-50X)



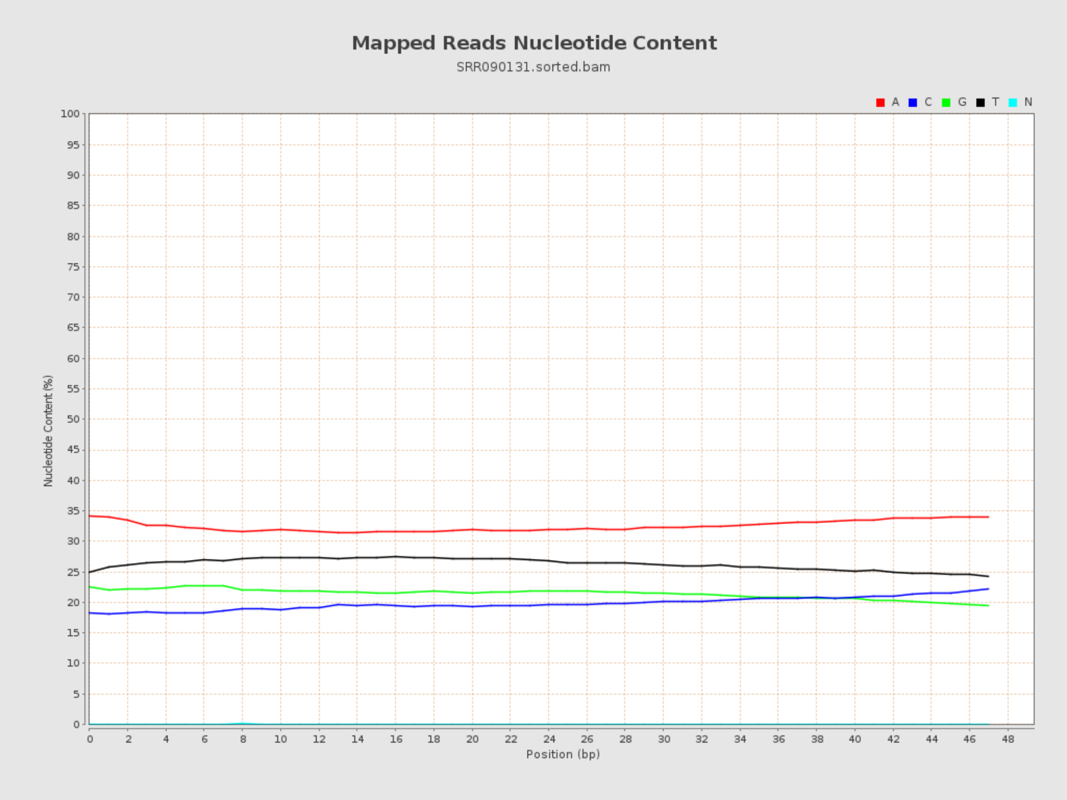
6. Results : Genome Fraction Coverage



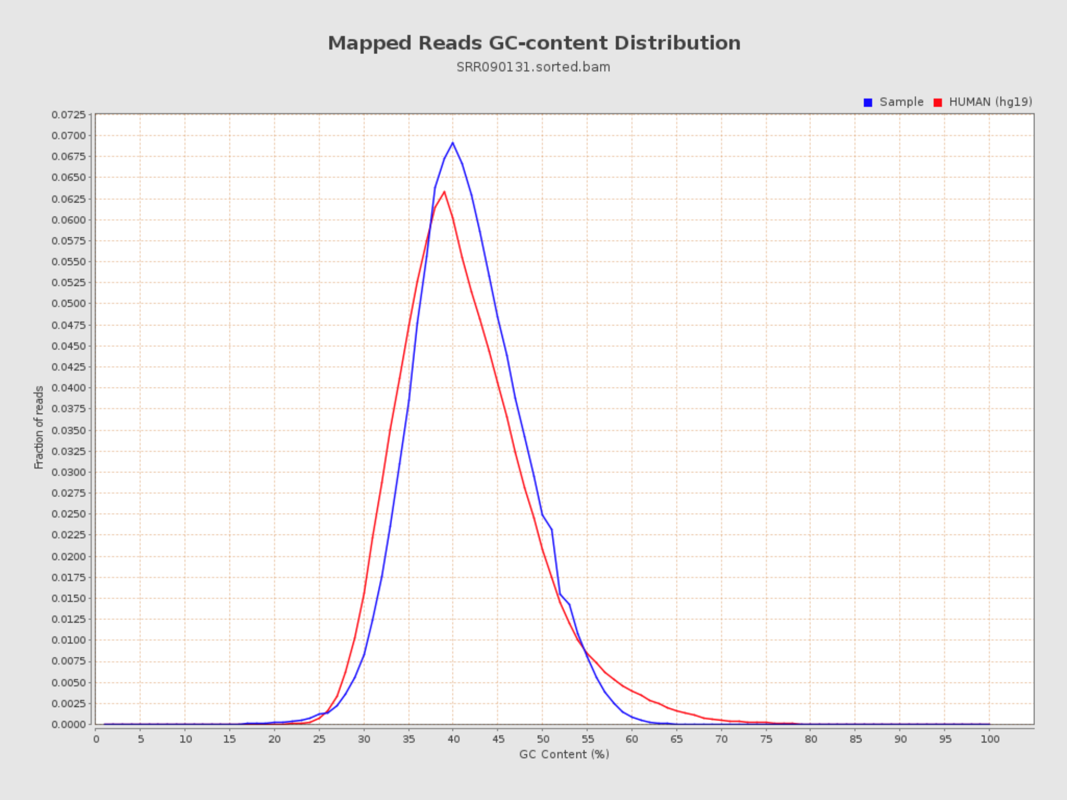
7. Results : Duplication Rate Histogram



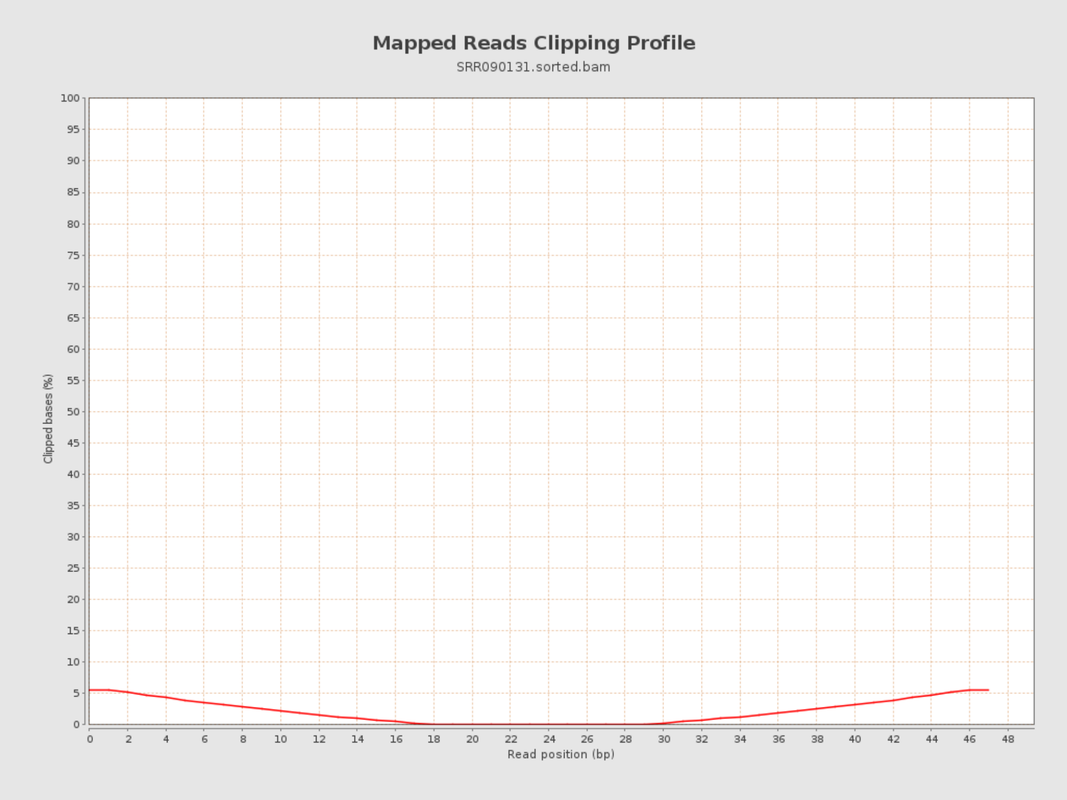
8. Results : Mapped Reads Nucleotide Content



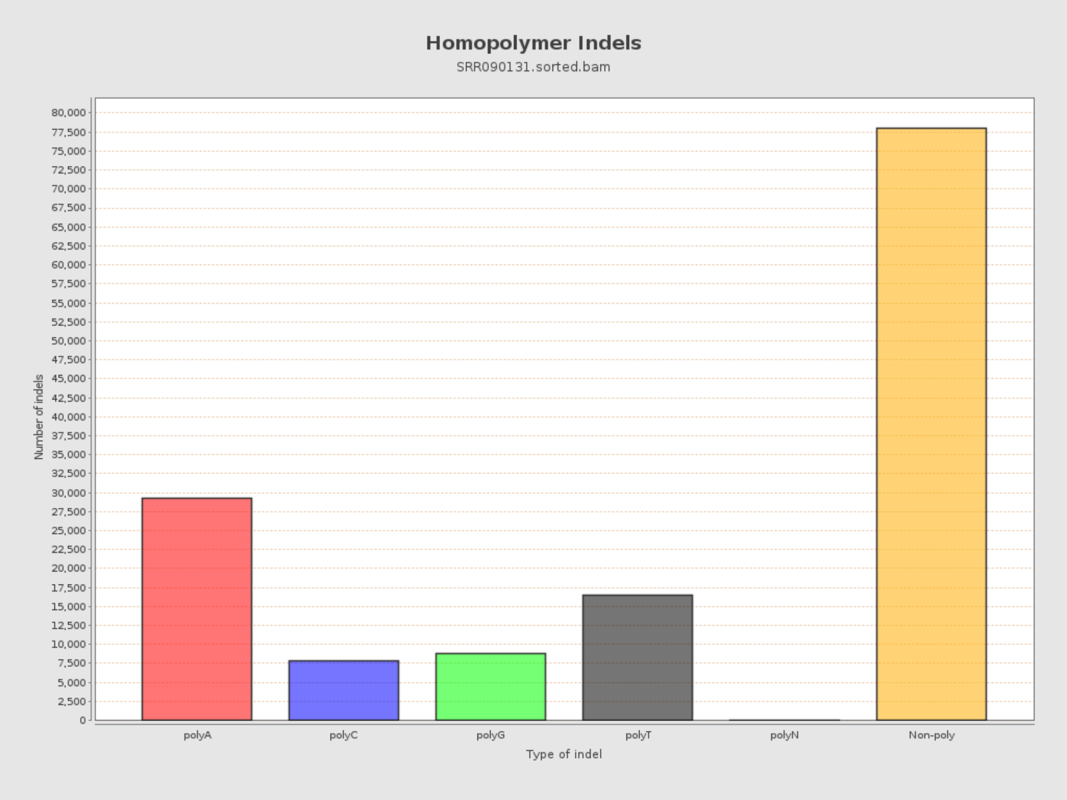
9. Results : Mapped Reads GC-content Distribution



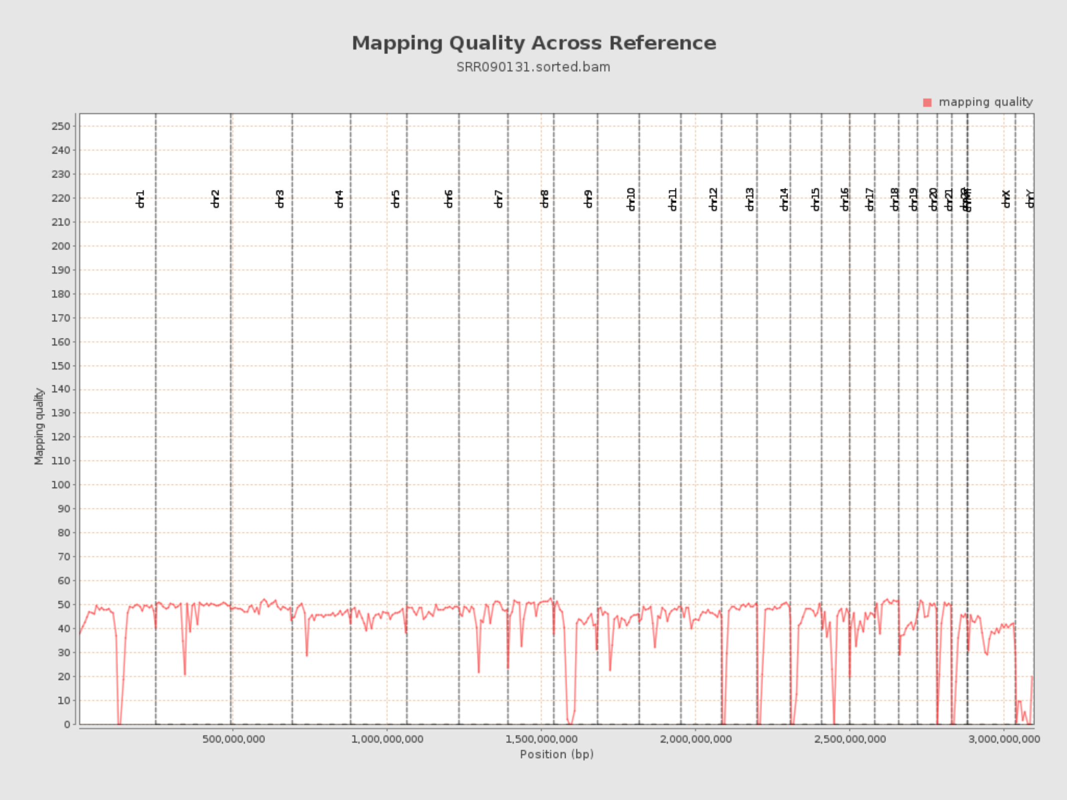
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram