Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 20:27:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013301.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_SRR6013301 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013301.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 20:27:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013301.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,591,566
Mapped reads	2,247,317 / 86.72%
Unmapped reads	344,249 / 13.28%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,719 / 0.76%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	117,302 / 4.53%
Duplication rate	4.12%
Clipped reads	1,158,684 / 44.71%

2.2. ACGT Content

Number/percentage of A's	41,272,782 / 28.05%
Number/percentage of C's	27,099,381 / 18.42%
Number/percentage of T's	46,652,501 / 31.71%
Number/percentage of G's	32,089,247 / 21.81%
Number/percentage of N's	29,944 / 0.02%
GC Percentage	40.23%

2.3. Coverage

Mean	0.0476

Standard Deviation	0.4064

2.4. Mapping Quality

Mean Mapping Quality	45.13

2.5. Mismatches and indels

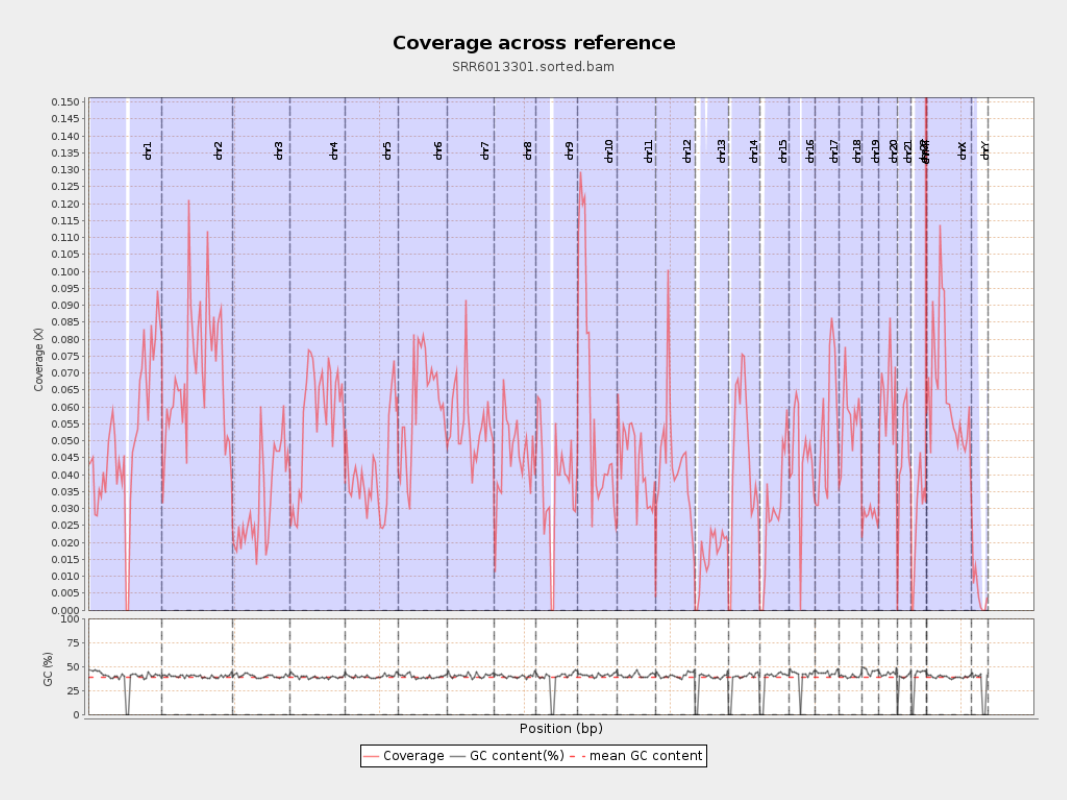
General error rate	0.86%
Mismatches	1,251,972
Insertions	11,038
Mapped reads with at least one insertion	0.49%
Deletions	35,460
Mapped reads with at least one deletion	1.56%
Homopolymer indels	46.33%

2.6. Chromosome stats

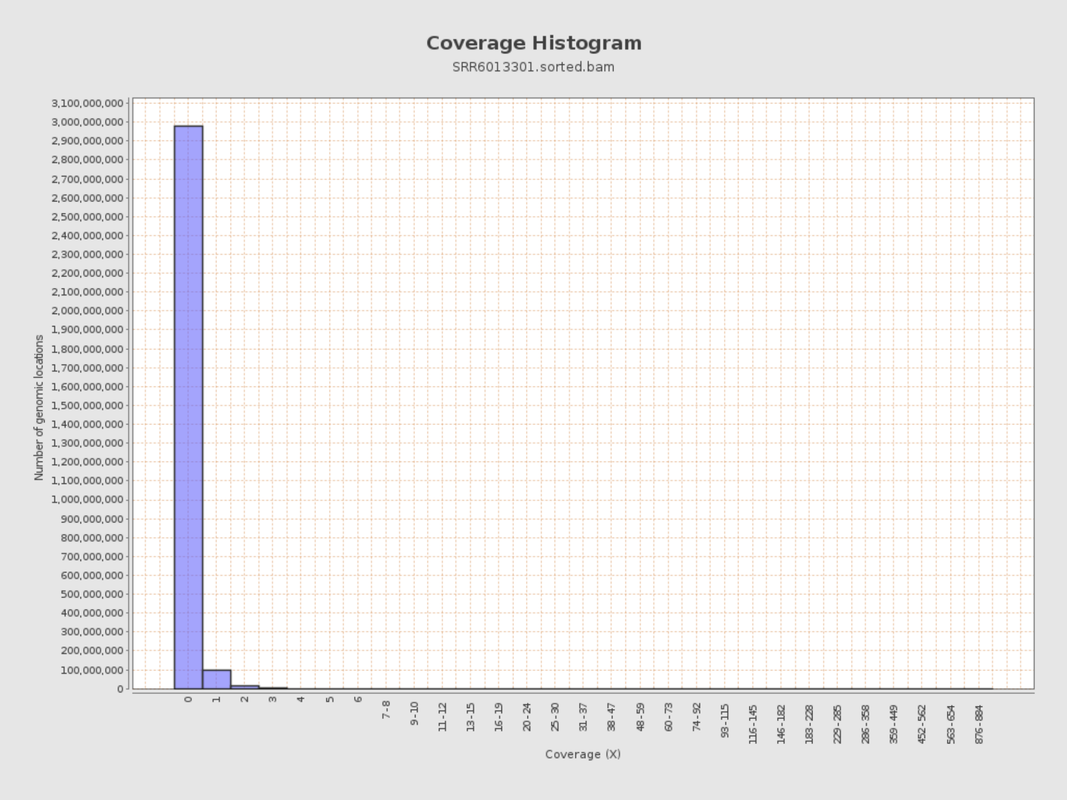
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12655655	0.0508	0.4601
chr2	243199373	16822918	0.0692	0.6307
chr3	198022430	6424986	0.0324	0.2132
chr4	191154276	10843301	0.0567	0.2877
chr5	180915260	7370391	0.0407	0.242
chr6	171115067	10373462	0.0606	0.4253
chr7	159138663	8845684	0.0556	0.6623

chr8	146364022	6549902	0.0448	0.4811
chr9	141213431	5225002	0.037	0.3972
chr10	135534747	8267587	0.061	0.4425
chr11	135006516	5859002	0.0434	0.3777
chr12	133851895	5866574	0.0438	0.2548
chr13	115169878	1878145	0.0163	0.153
chr14	107349540	4806752	0.0448	0.2765
chr15	102531392	3020154	0.0295	0.207
chr16	90354753	4006445	0.0443	0.2709
chr17	81195210	4427605	0.0545	0.3373
chr18	78077248	4413378	0.0565	0.7137
chr19	59128983	1661821	0.0281	0.404
chr20	63025520	3997917	0.0634	0.307
chr21	48129895	2152453	0.0447	0.2651
chr22	51304566	1334233	0.026	0.189
chrMT	16571	30811	1.8593	1.8874
chrX	155270560	10024420	0.0646	0.374
chrY	59373566	344409	0.0058	0.105

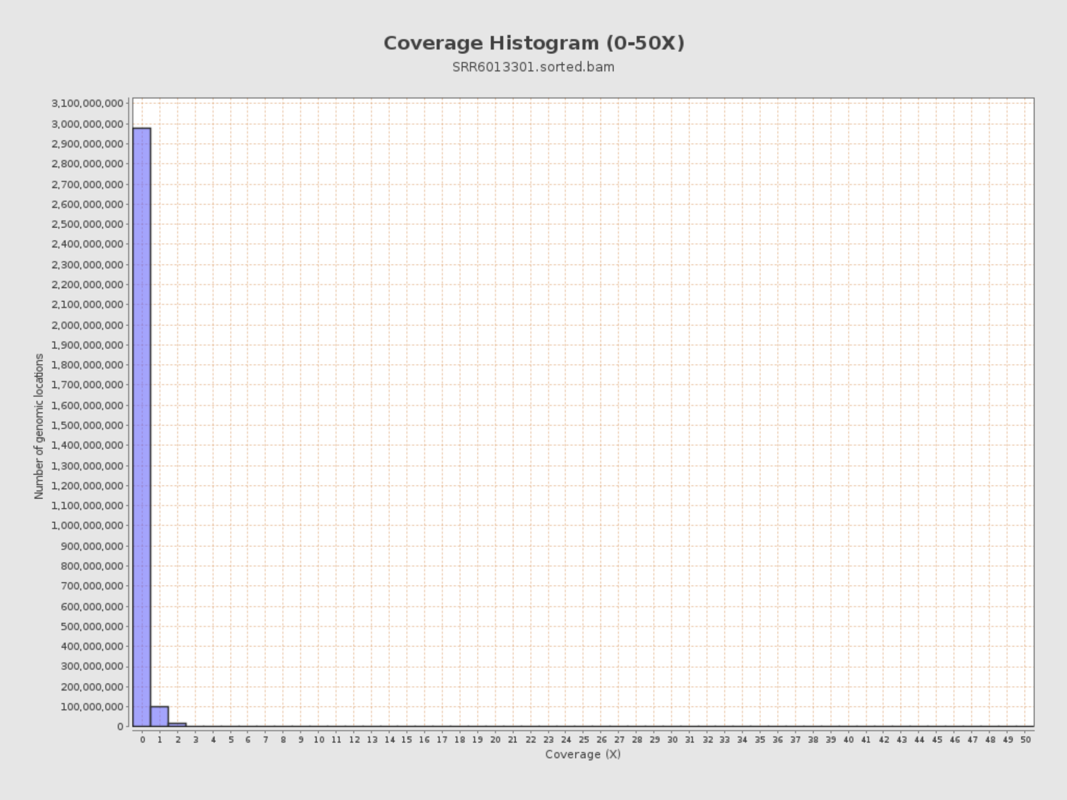
3. Results : Coverage across reference



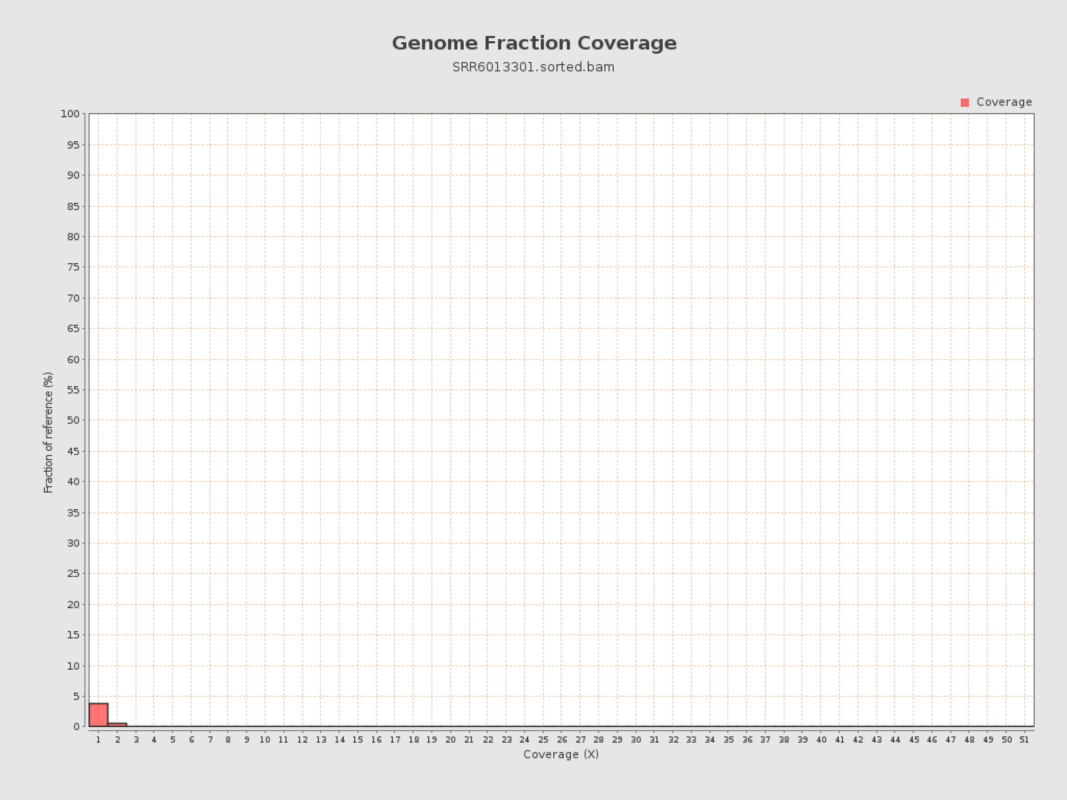
4. Results : Coverage Histogram



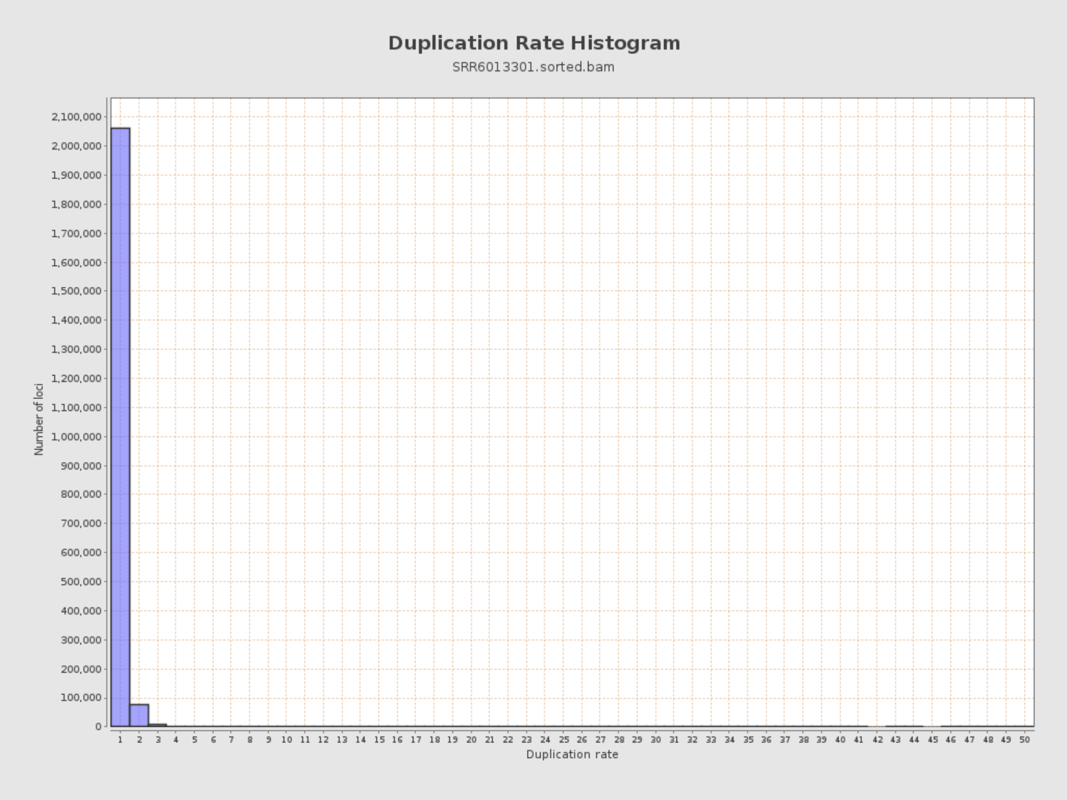
5. Results : Coverage Histogram (0-50X)



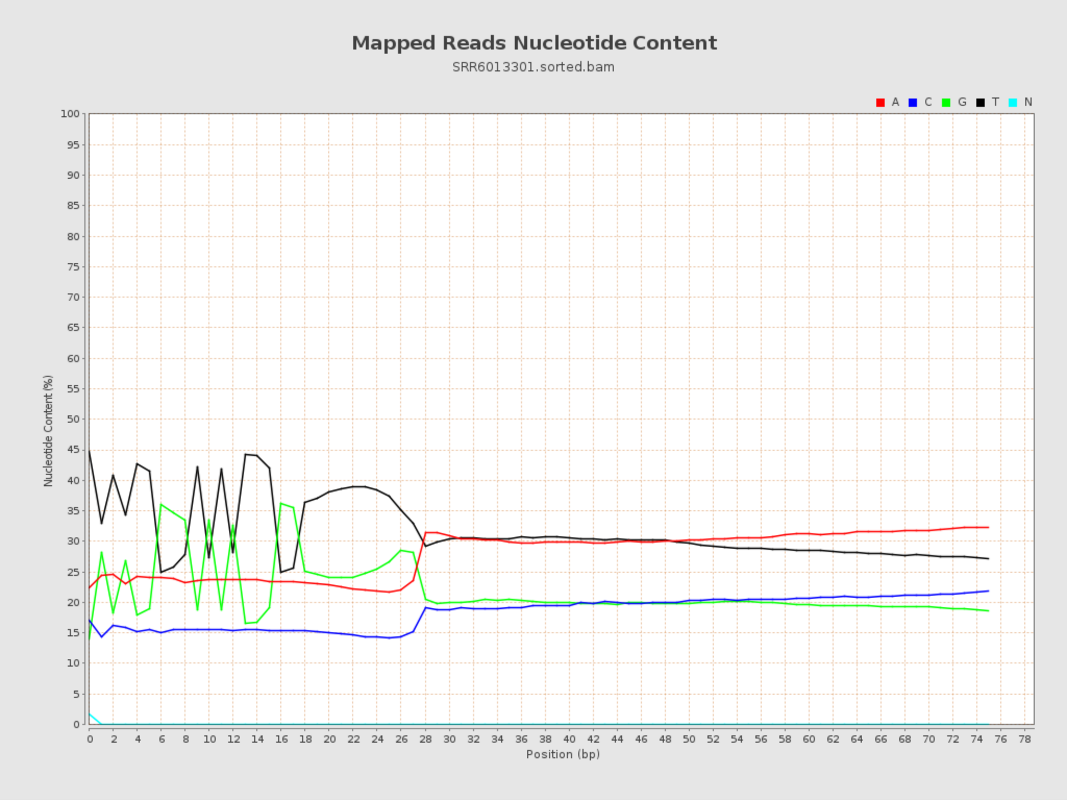
6. Results : Genome Fraction Coverage



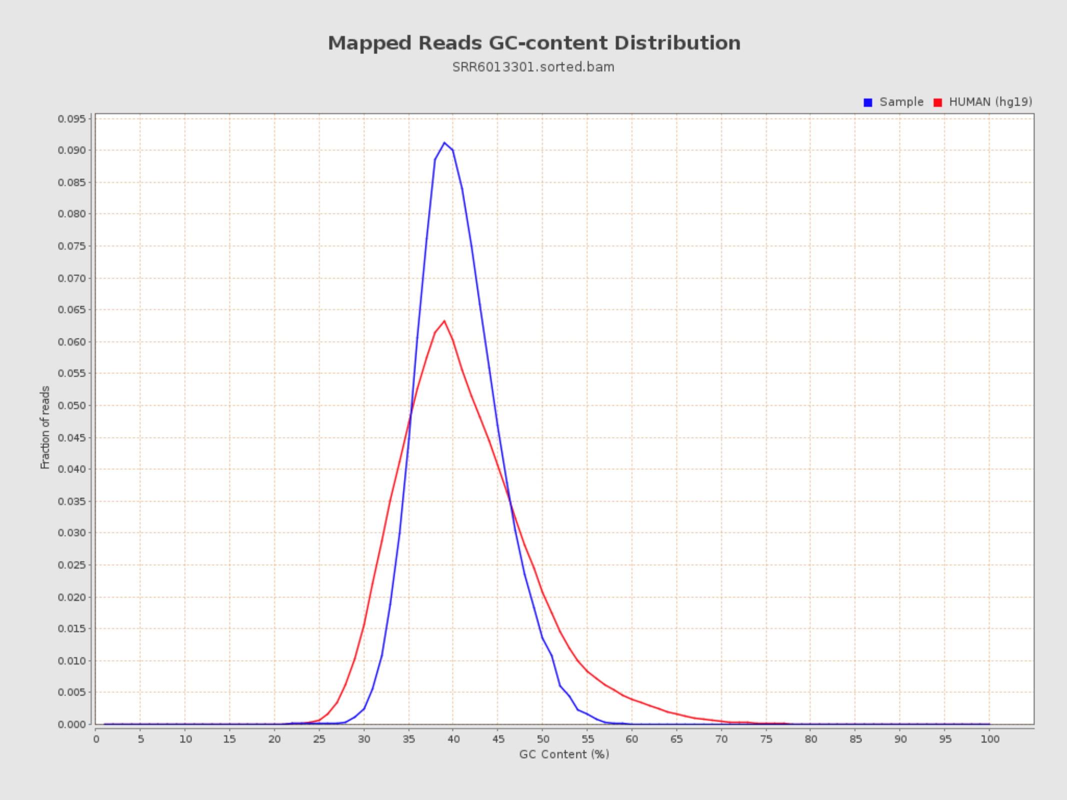
7. Results : Duplication Rate Histogram



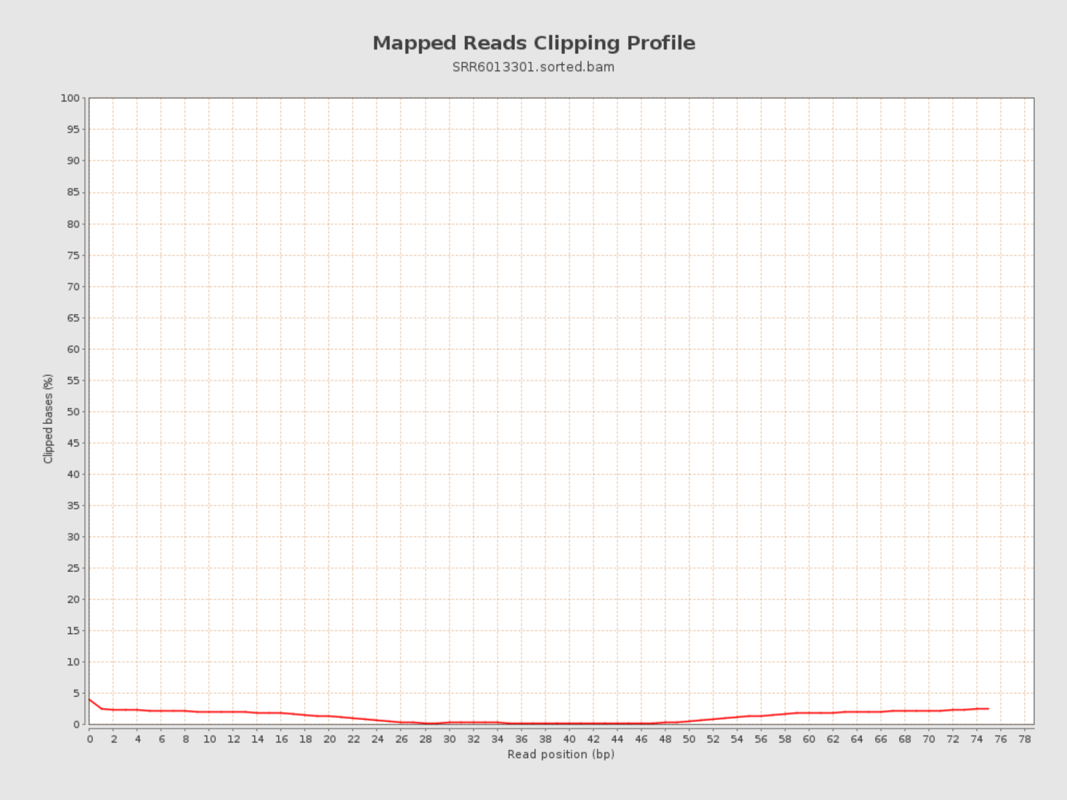
8. Results : Mapped Reads Nucleotide Content



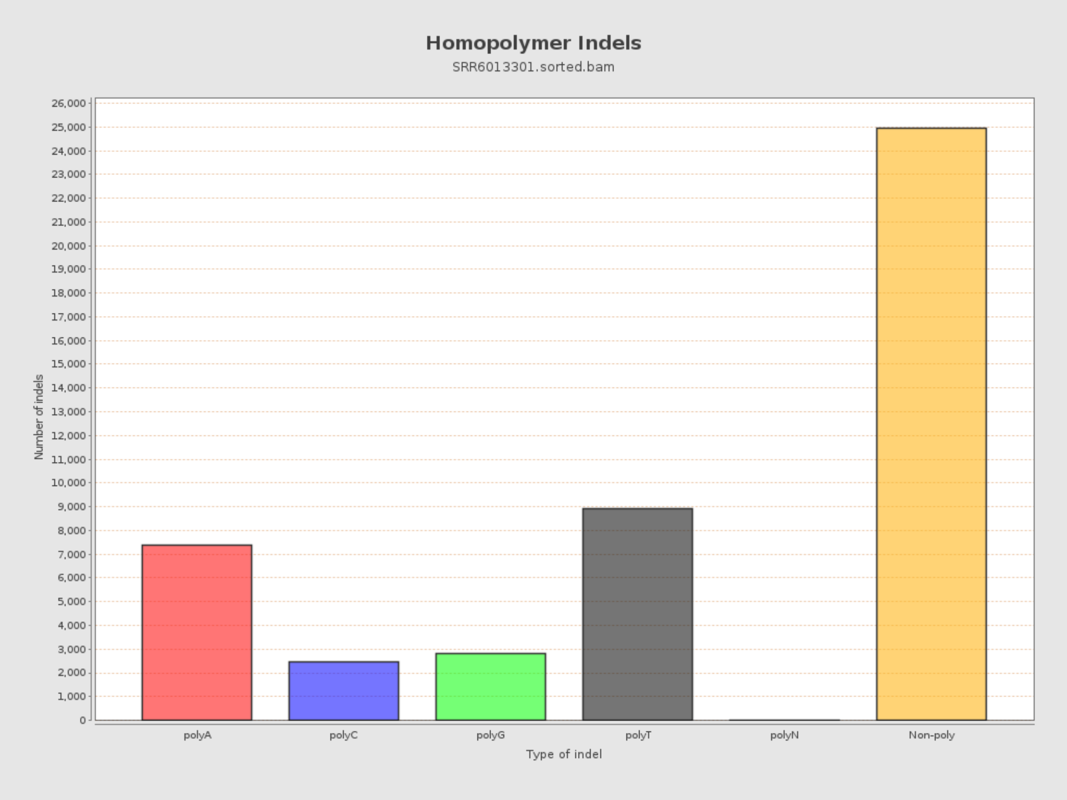
9. Results : Mapped Reads GC-content Distribution



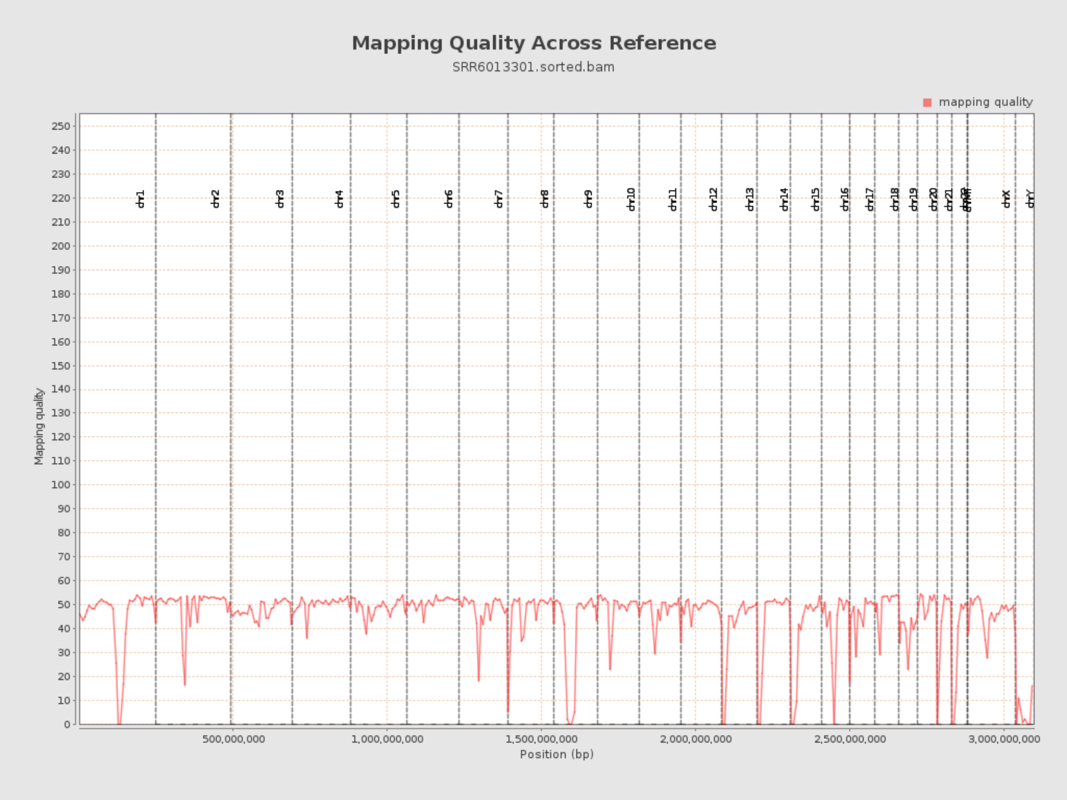
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram