Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 15:51:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013205.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_SRR6013205 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013205.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 15:51:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013205.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,171,146
Mapped reads	1,946,425 / 89.65%
Unmapped reads	224,721 / 10.35%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,698 / 0.82%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	120,966 / 5.57%
Duplication rate	4.58%
Clipped reads	771,495 / 35.53%

2.2. ACGT Content

Number/percentage of A's	37,776,221 / 28.53%
Number/percentage of C's	24,391,780 / 18.42%
Number/percentage of T's	42,176,719 / 31.85%
Number/percentage of G's	28,047,264 / 21.18%
Number/percentage of N's	29,646 / 0.02%
GC Percentage	39.6%

2.3. Coverage

Mean	0.0428

Standard Deviation	0.481

2.4. Mapping Quality

Mean Mapping Quality	46.48

2.5. Mismatches and indels

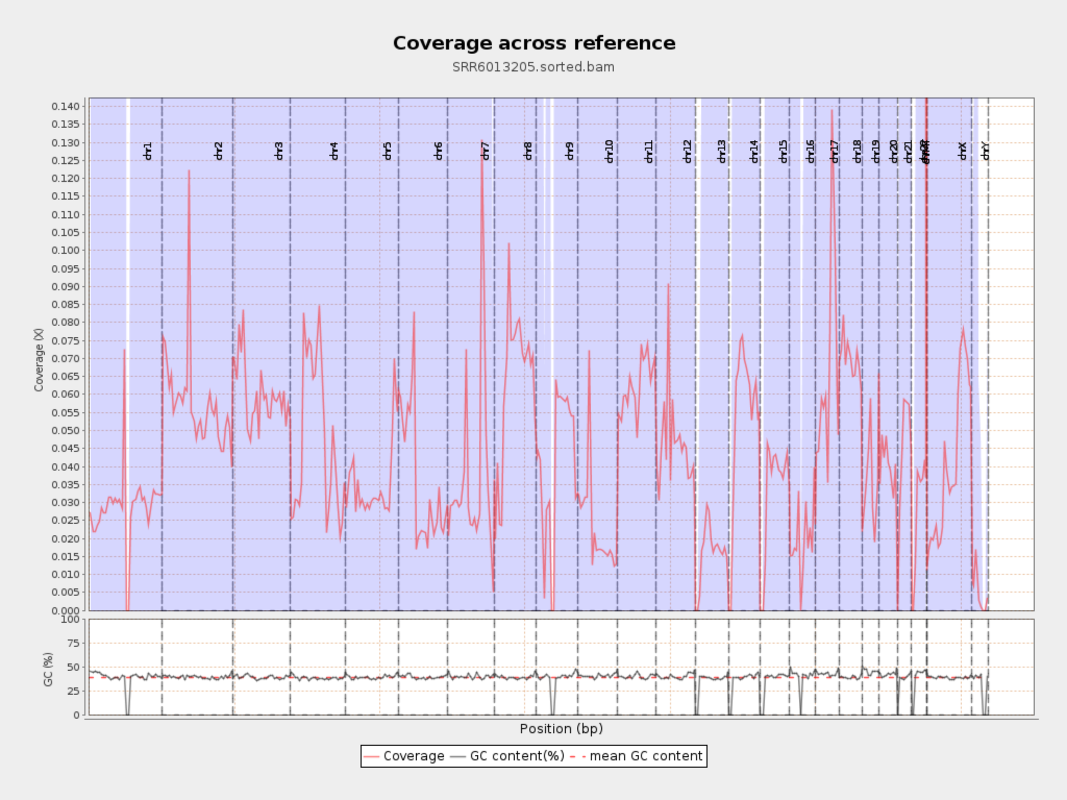
General error rate	0.82%
Mismatches	1,064,819
Insertions	10,197
Mapped reads with at least one insertion	0.52%
Deletions	29,686
Mapped reads with at least one deletion	1.51%
Homopolymer indels	47.37%

2.6. Chromosome stats

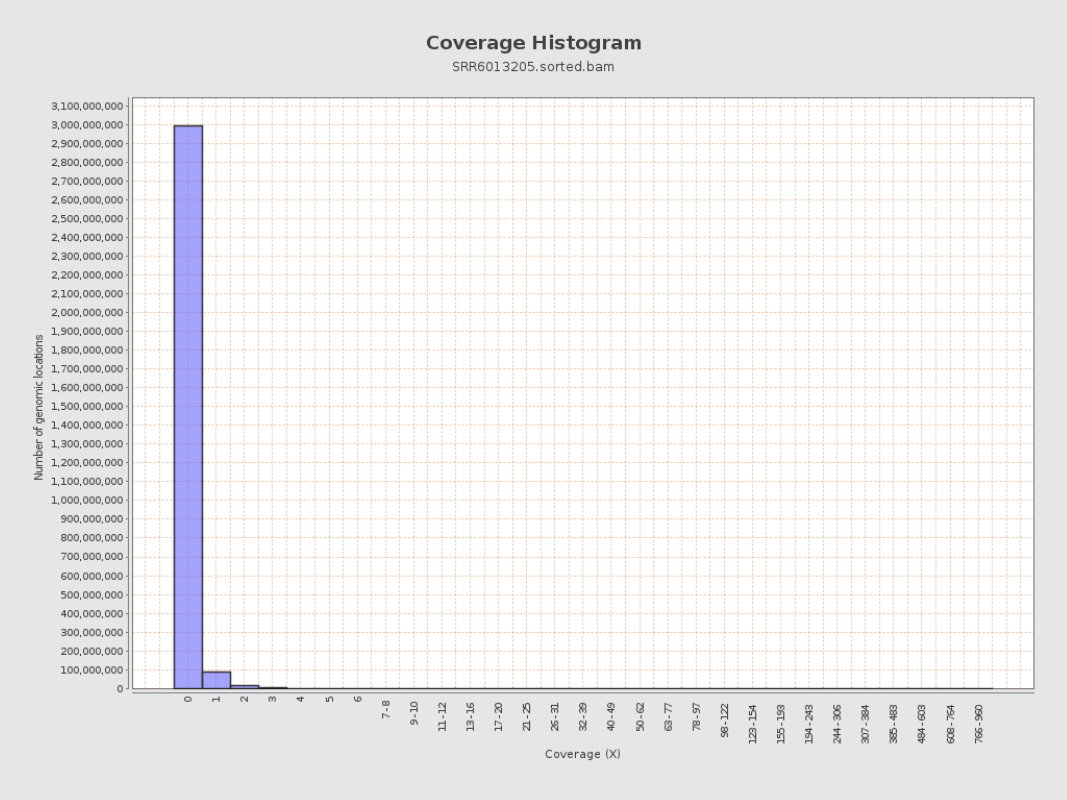
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7150268	0.0287	0.8163
chr2	243199373	14121467	0.0581	0.6149
chr3	198022430	11951087	0.0604	0.2958
chr4	191154276	8960169	0.0469	0.3123
chr5	180915260	6405052	0.0354	0.2304
chr6	171115067	6204826	0.0363	0.3249
chr7	159138663	6097898	0.0383	0.5879

chr8	146364022	9276103	0.0634	0.6437
chr9	141213431	5707796	0.0404	0.4899
chr10	135534747	3155279	0.0233	0.4899
chr11	135006516	8374835	0.062	0.4212
chr12	133851895	6196785	0.0463	0.2731
chr13	115169878	1823094	0.0158	0.151
chr14	107349540	5765047	0.0537	0.3022
chr15	102531392	3403653	0.0332	0.2176
chr16	90354753	1778248	0.0197	0.2267
chr17	81195210	5416048	0.0667	0.3558
chr18	78077248	5484491	0.0702	1.0225
chr19	59128983	2149119	0.0363	0.5716
chr20	63025520	2532052	0.0402	0.263
chr21	48129895	2108158	0.0438	0.2892
chr22	51304566	1357925	0.0265	0.1902
chrMT	16571	506593	30.5711	17.271
chrX	155270560	6266556	0.0404	0.2784
chrY	59373566	281066	0.0047	0.1792

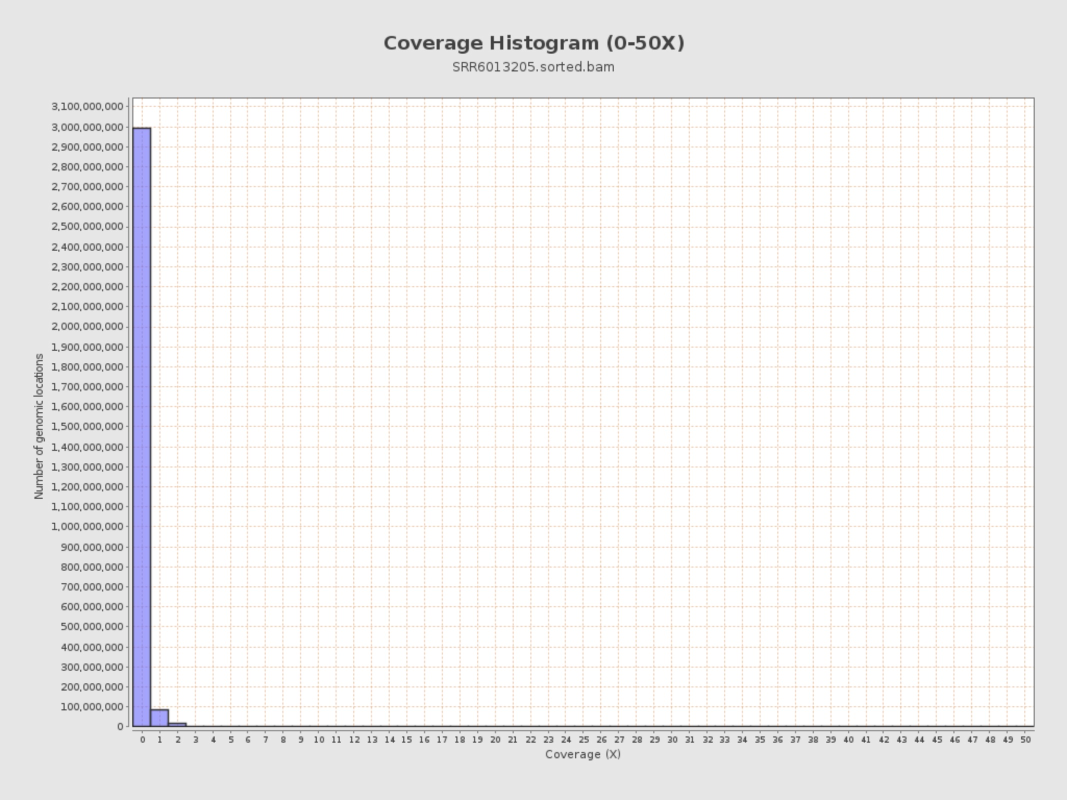
3. Results : Coverage across reference



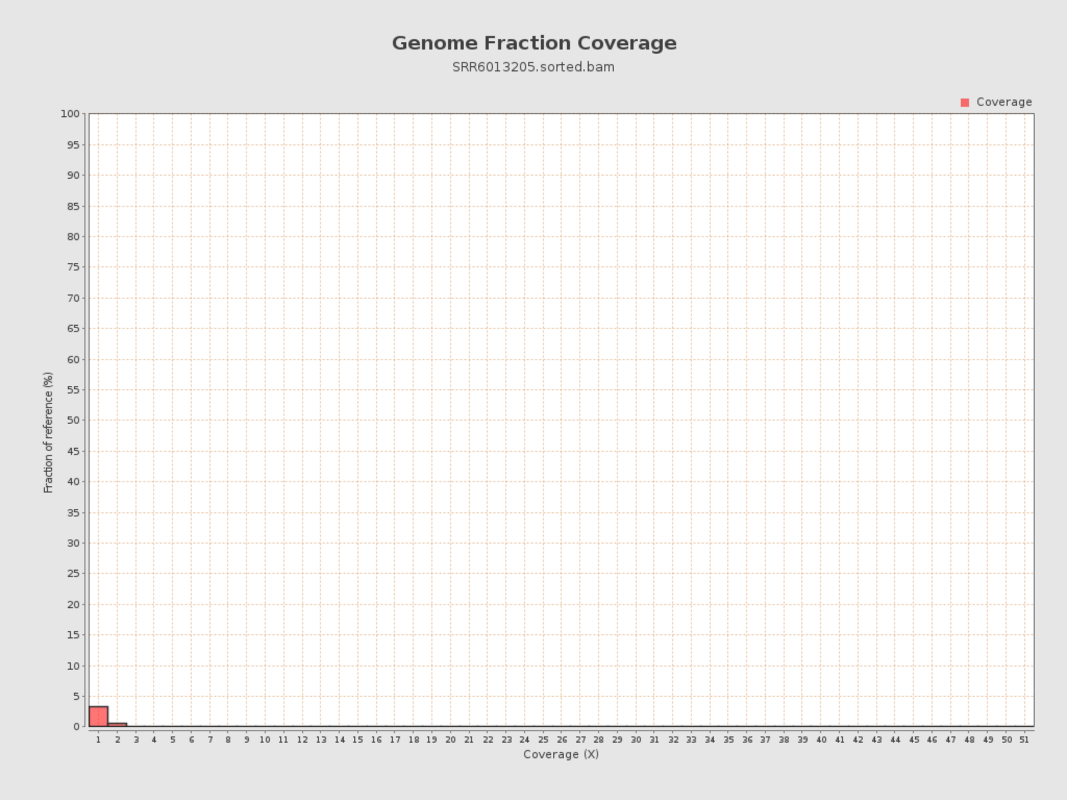
4. Results : Coverage Histogram



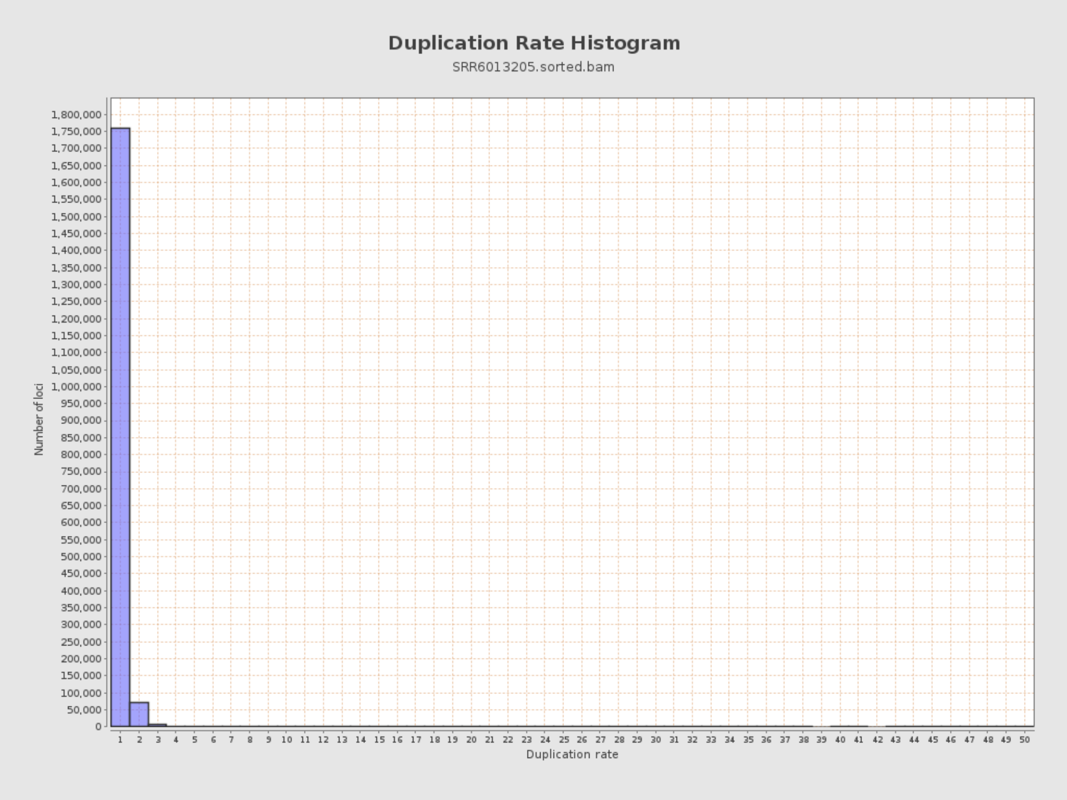
5. Results : Coverage Histogram (0-50X)



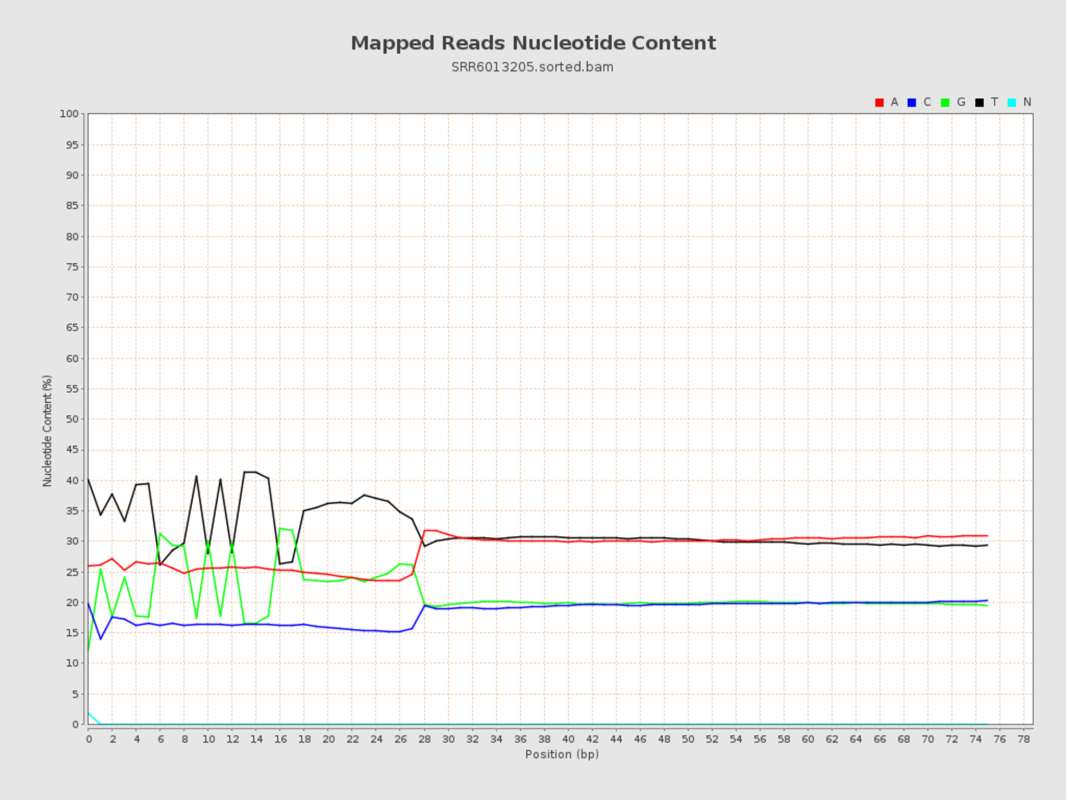
6. Results : Genome Fraction Coverage



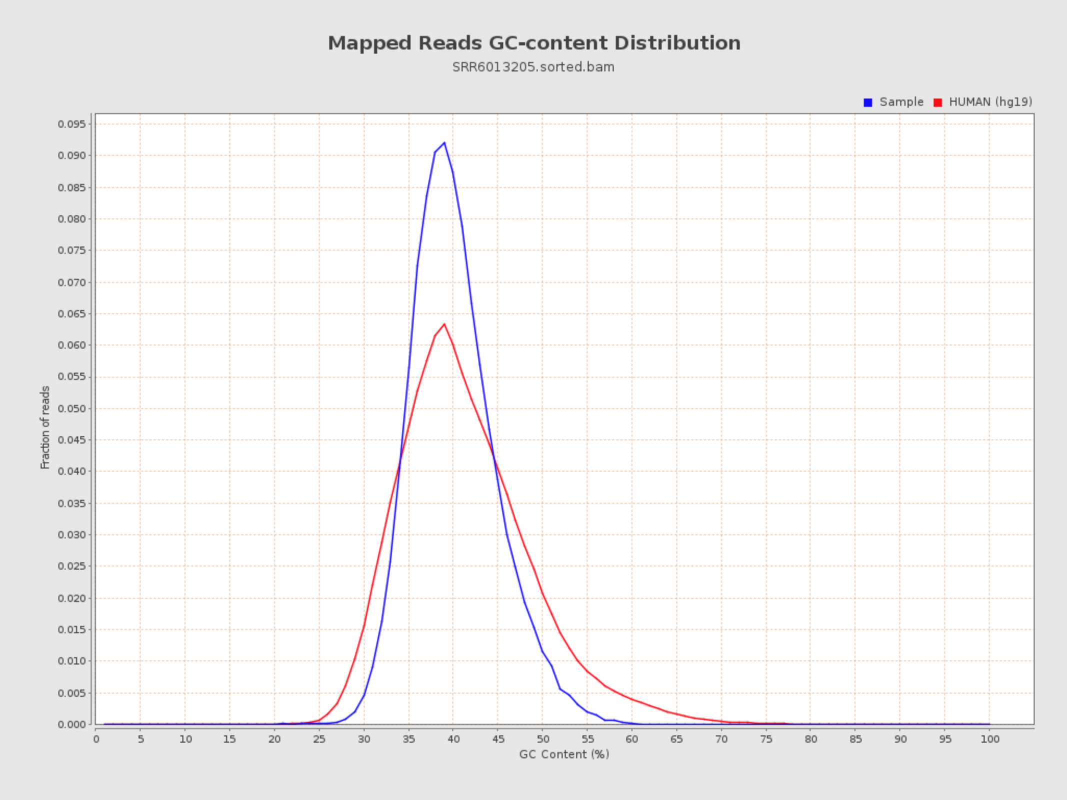
7. Results : Duplication Rate Histogram



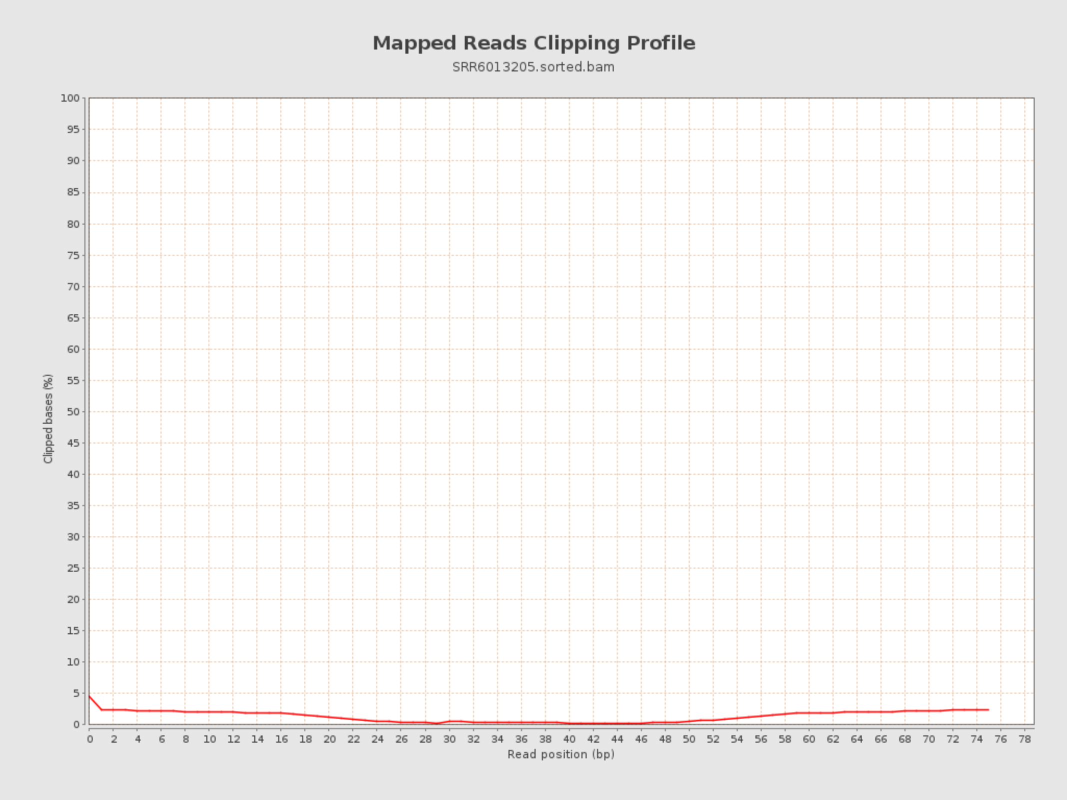
8. Results : Mapped Reads Nucleotide Content



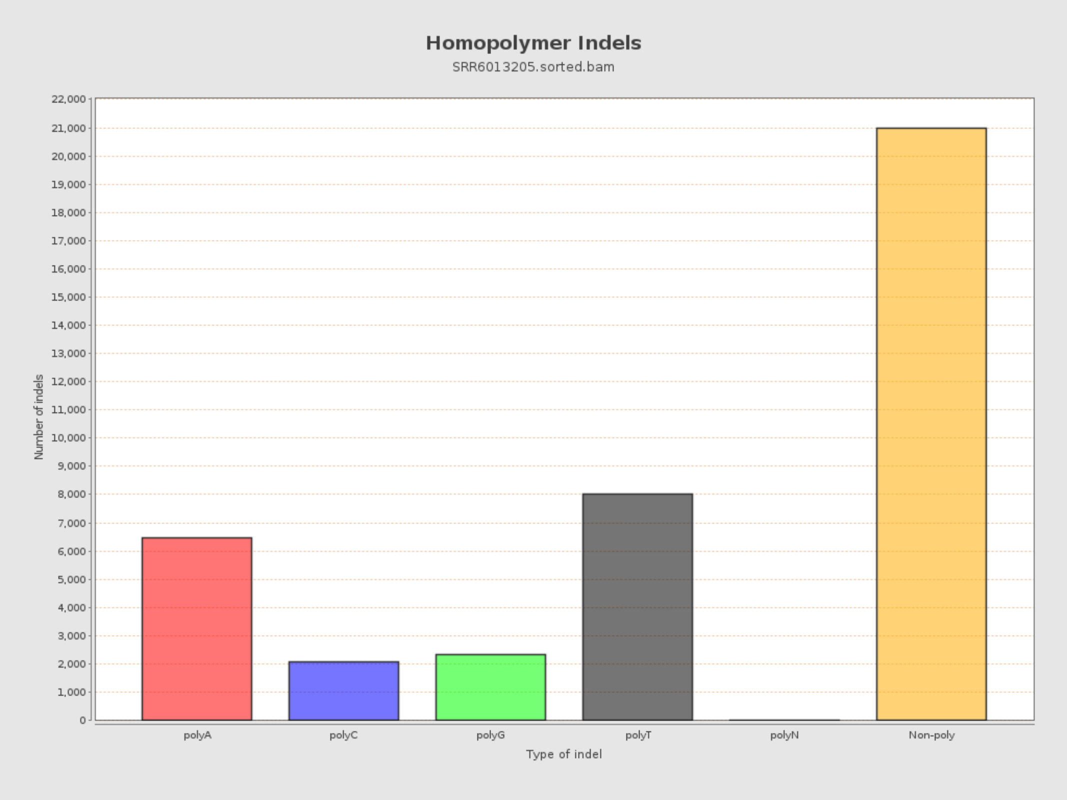
9. Results : Mapped Reads GC-content Distribution



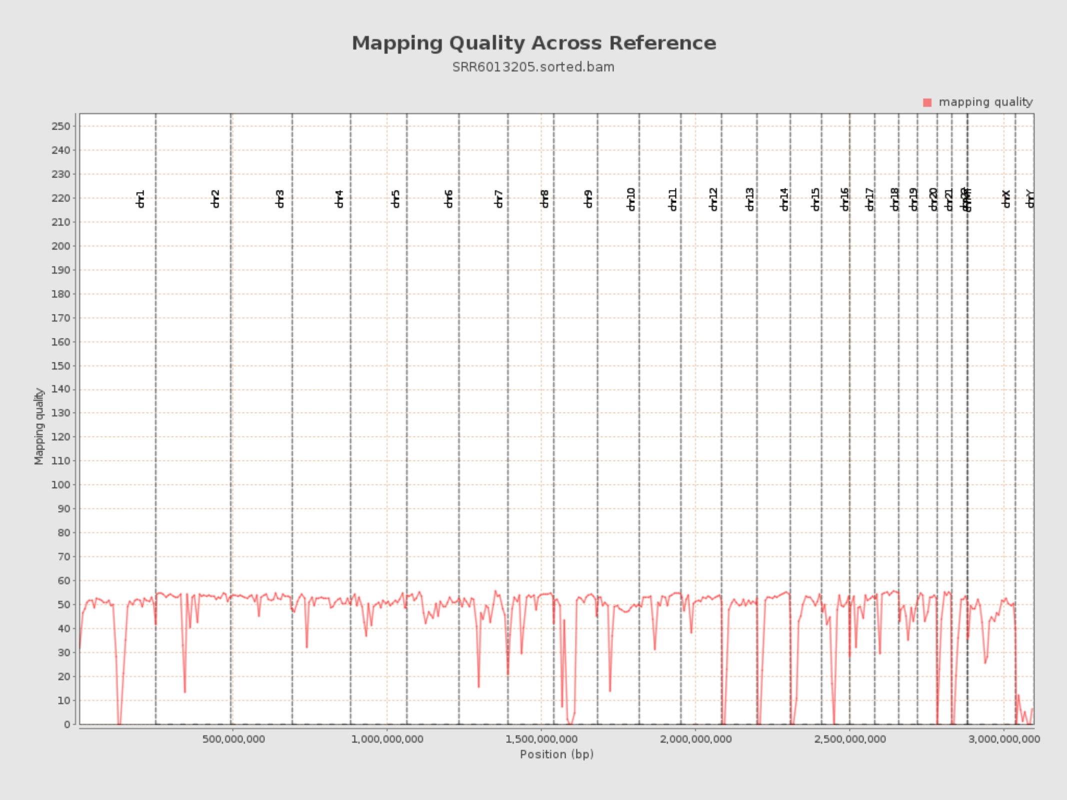
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram