Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 23:17:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013360.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_SRR6013360 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013360.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 23:17:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013360.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,022,918
Mapped reads	1,834,210 / 90.67%
Unmapped reads	188,708 / 9.33%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,309 / 0.56%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	82,903 / 4.1%
Duplication rate	3.27%
Clipped reads	740,624 / 36.61%

2.2. ACGT Content

Number/percentage of A's	35,476,115 / 28.53%
Number/percentage of C's	22,699,438 / 18.25%
Number/percentage of T's	39,707,226 / 31.93%
Number/percentage of G's	26,452,068 / 21.27%
Number/percentage of N's	27,129 / 0.02%
GC Percentage	39.52%

2.3. Coverage

Mean	0.0402

Standard Deviation	0.439

2.4. Mapping Quality

Mean Mapping Quality	46.42

2.5. Mismatches and indels

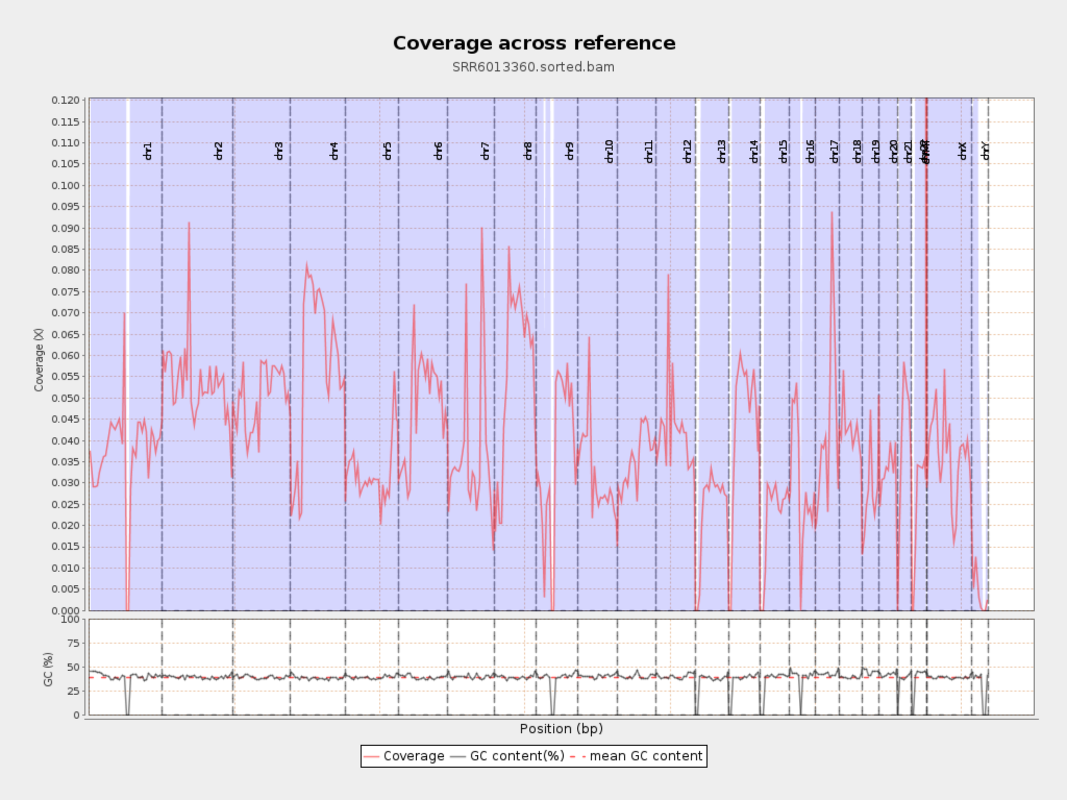
General error rate	0.8%
Mismatches	971,432
Insertions	9,493
Mapped reads with at least one insertion	0.51%
Deletions	27,931
Mapped reads with at least one deletion	1.51%
Homopolymer indels	47.4%

2.6. Chromosome stats

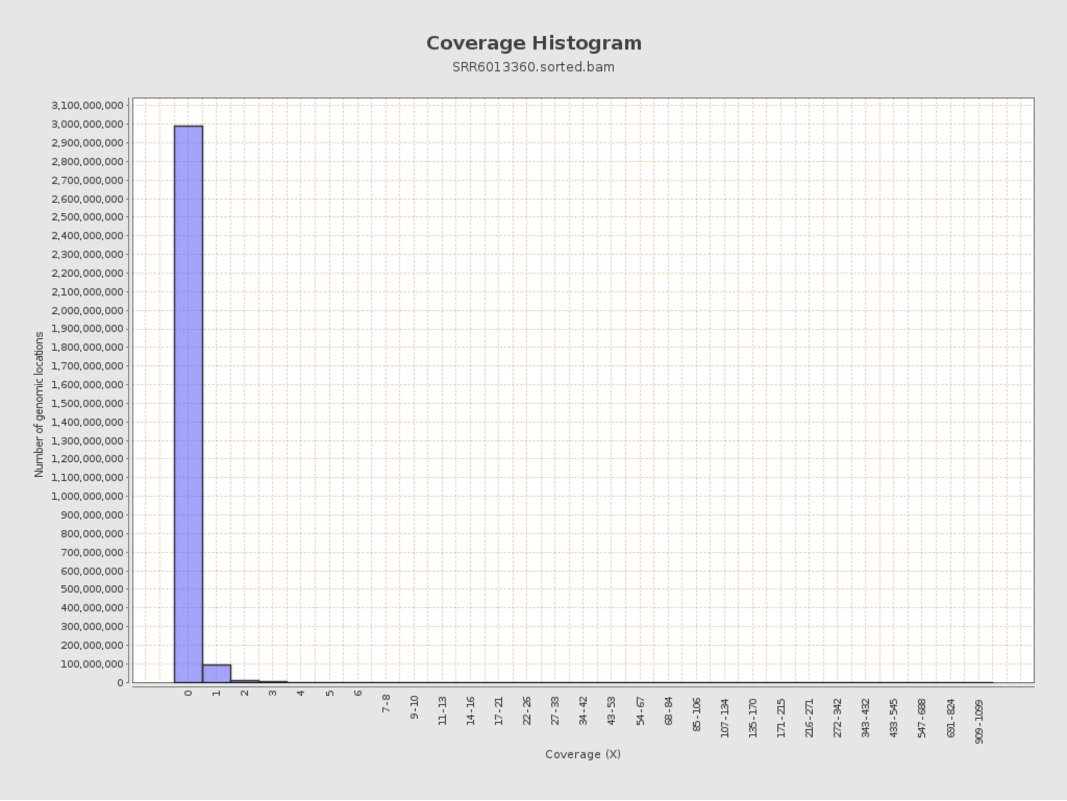
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9257215	0.0371	0.704
chr2	243199373	13076163	0.0538	0.493
chr3	198022430	9986018	0.0504	0.2509
chr4	191154276	10940648	0.0572	0.2891
chr5	180915260	5905845	0.0326	0.2049
chr6	171115067	8268616	0.0483	0.317
chr7	159138663	6018289	0.0378	0.6605

chr8	146364022	8334209	0.0569	0.6999
chr9	141213431	5016741	0.0355	0.4038
chr10	135534747	4373861	0.0323	0.3708
chr11	135006516	4787417	0.0355	0.2958
chr12	133851895	5698986	0.0426	0.2407
chr13	115169878	2702447	0.0235	0.174
chr14	107349540	4743775	0.0442	0.2593
chr15	102531392	2239702	0.0218	0.1694
chr16	90354753	2727059	0.0302	0.2252
chr17	81195210	3442259	0.0424	0.2479
chr18	78077248	3327885	0.0426	0.8112
chr19	59128983	1658742	0.0281	0.476
chr20	63025520	2059607	0.0327	0.2155
chr21	48129895	1899757	0.0395	0.2384
chr22	51304566	1232582	0.024	0.1712
chrMT	16571	819811	49.4726	27.2099
chrX	155270560	5653731	0.0364	0.2424
chrY	59373566	239496	0.004	0.1216

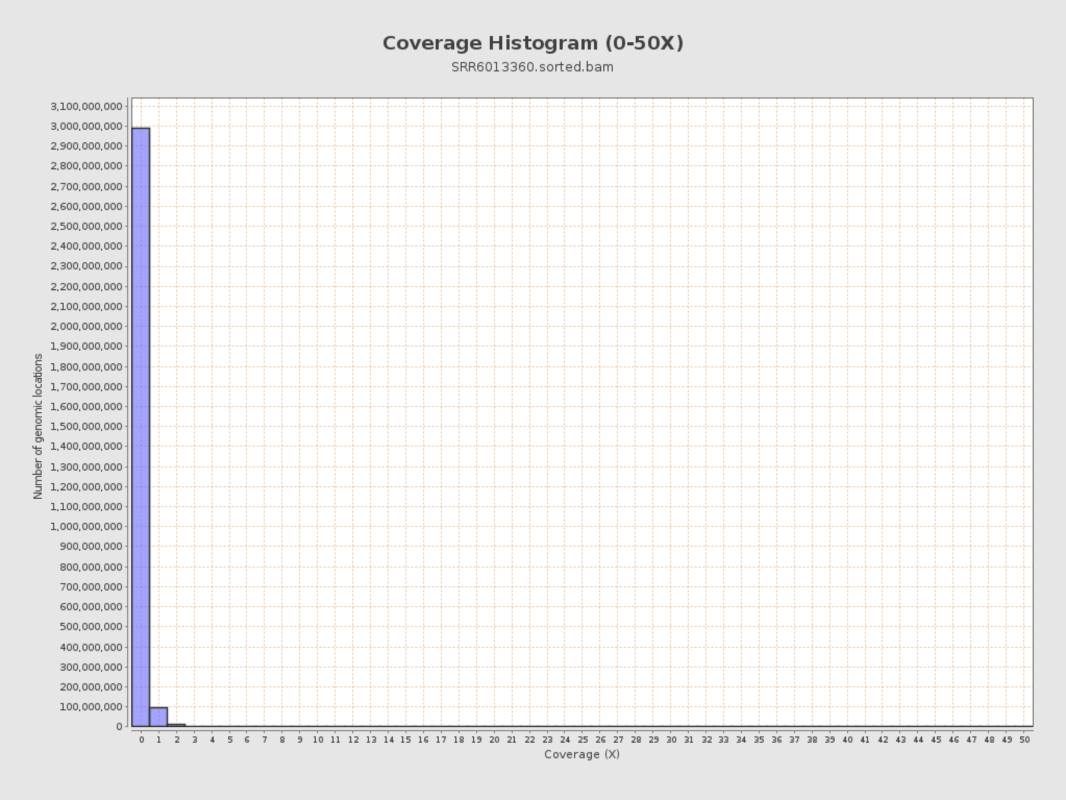
3. Results : Coverage across reference



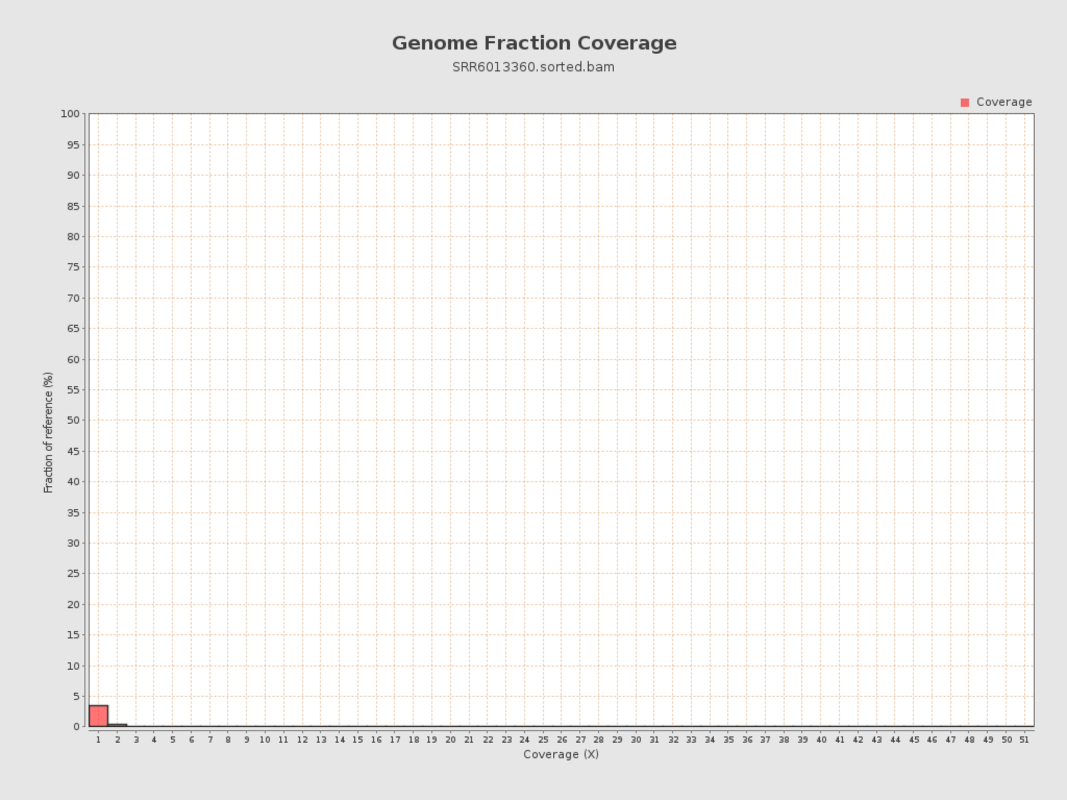
4. Results : Coverage Histogram



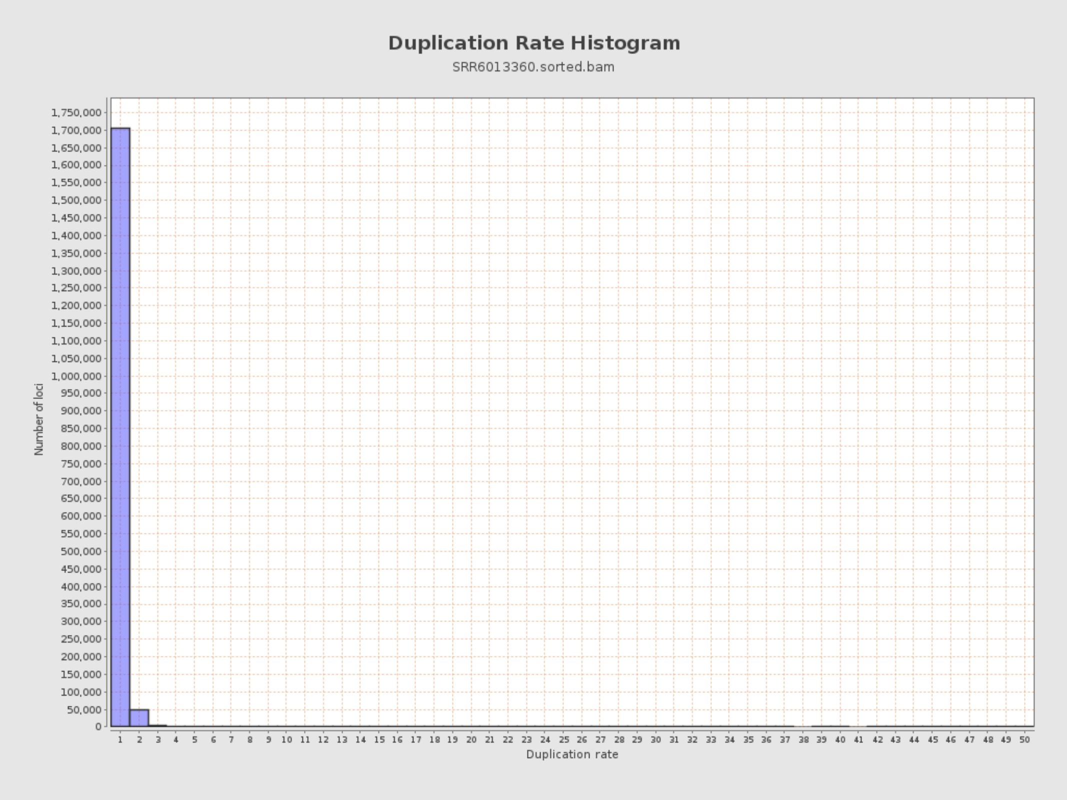
5. Results : Coverage Histogram (0-50X)



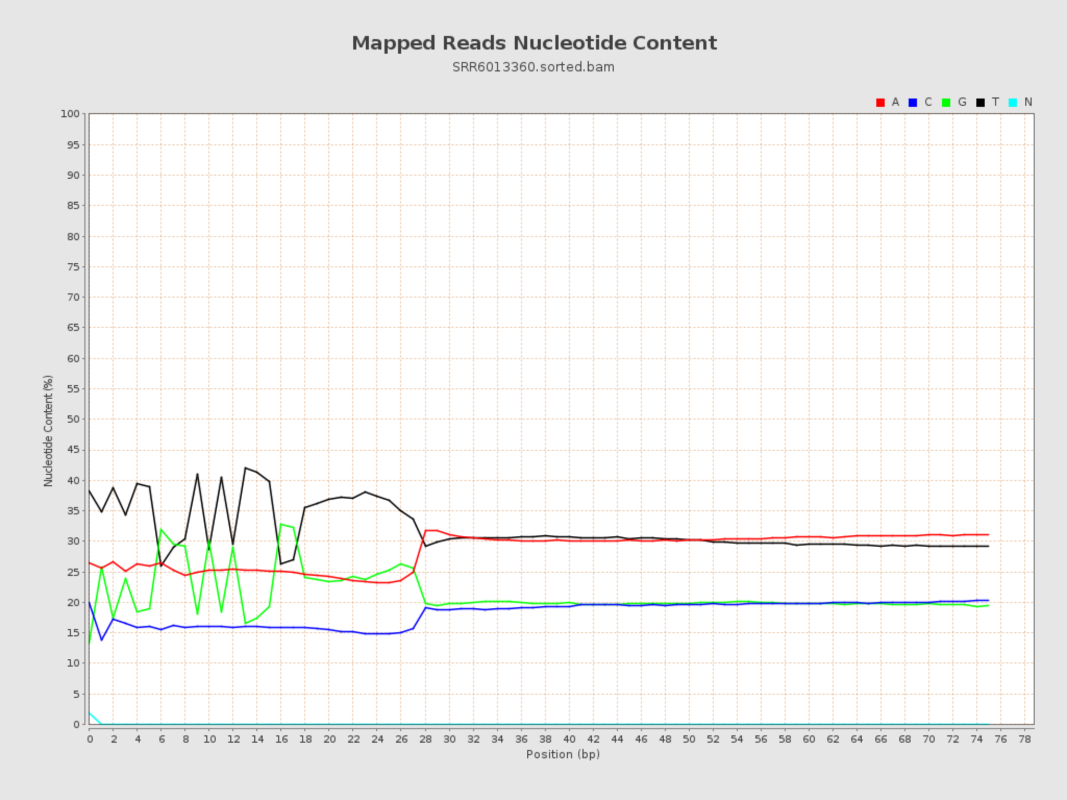
6. Results : Genome Fraction Coverage



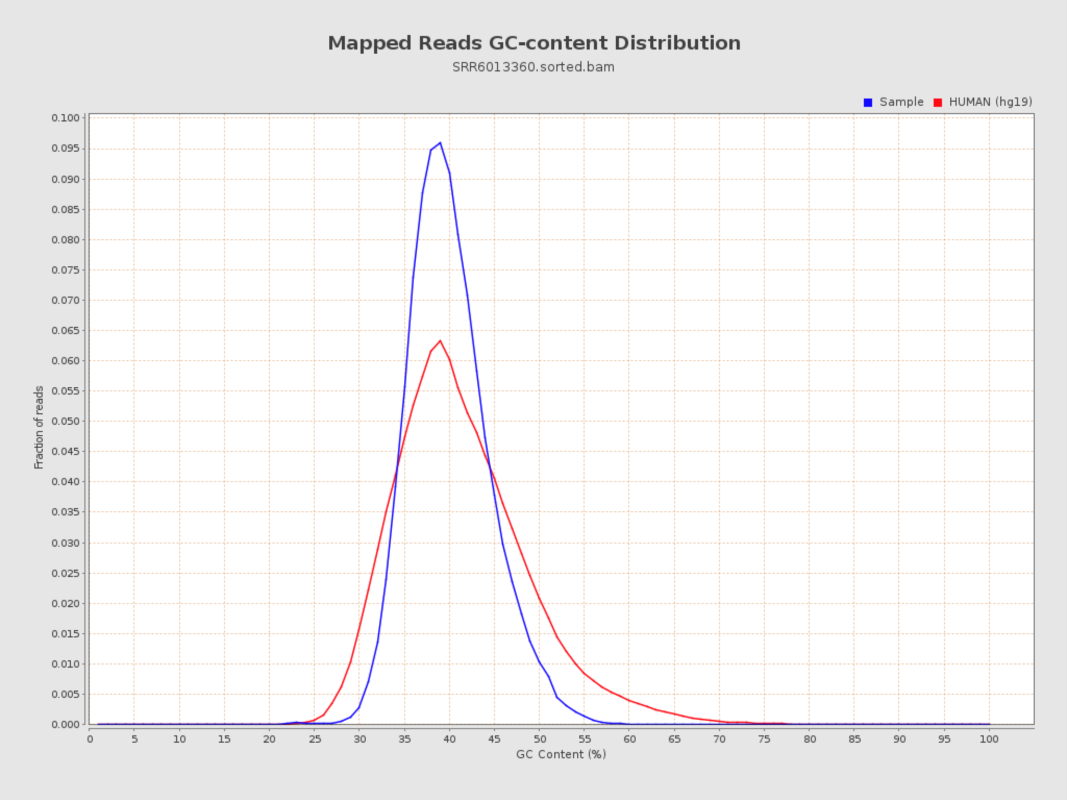
7. Results : Duplication Rate Histogram



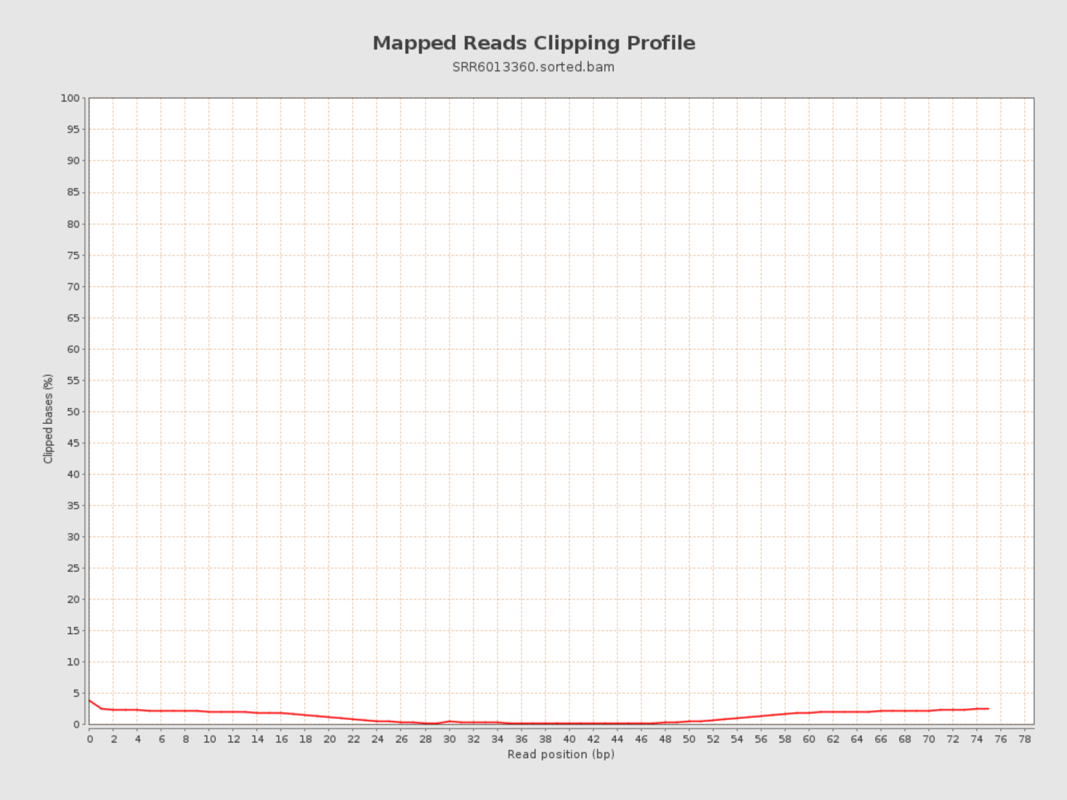
8. Results : Mapped Reads Nucleotide Content



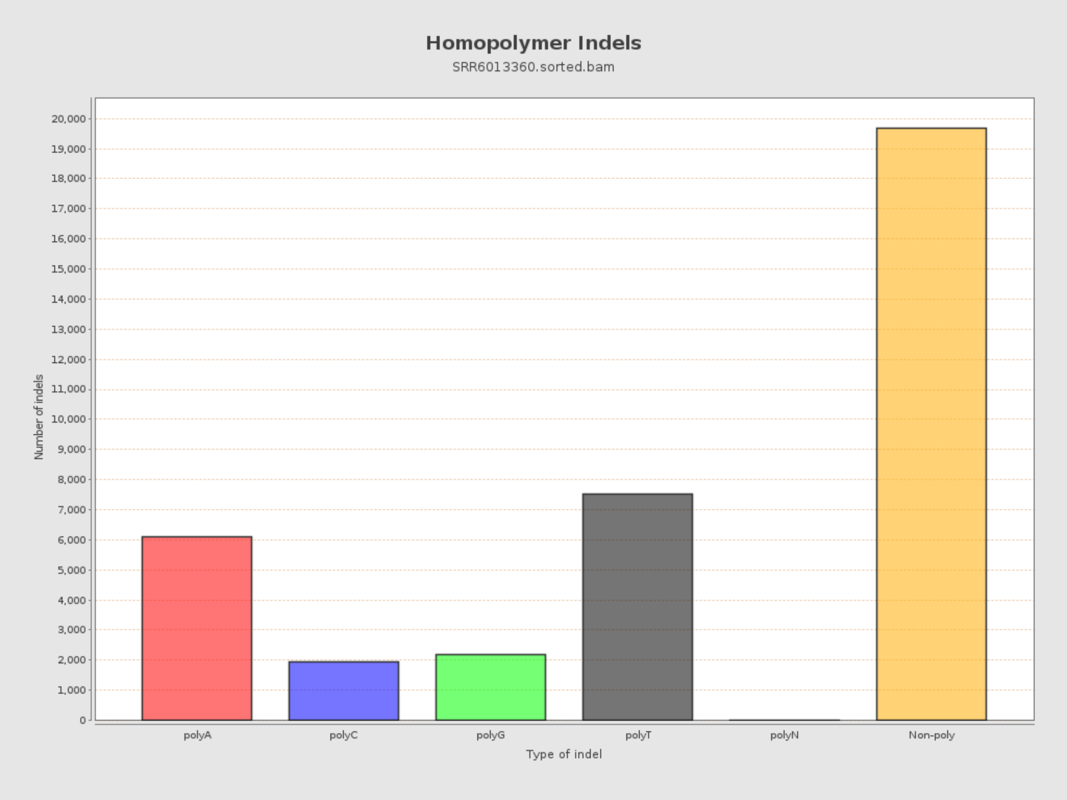
9. Results : Mapped Reads GC-content Distribution



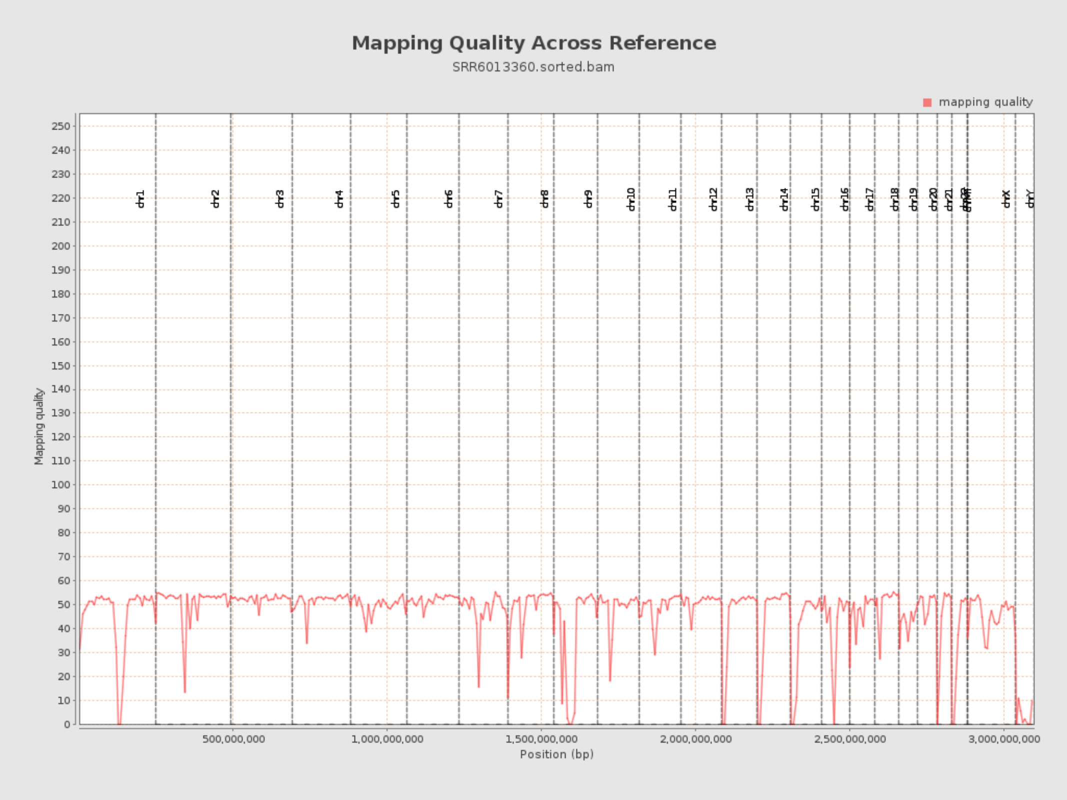
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram