Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 19:44:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6230367.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_SRR6230367 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6230367.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 19:44:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6230367.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,880,474
Mapped reads	2,737,193 / 95.03%
Unmapped reads	143,281 / 4.97%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,247 / 0.67%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	151,012 / 5.24%
Duplication rate	3.8%
Clipped reads	642,285 / 22.3%

2.2. ACGT Content

Number/percentage of A's	59,222,942 / 29.97%
Number/percentage of C's	40,037,288 / 20.26%
Number/percentage of T's	58,173,059 / 29.44%
Number/percentage of G's	40,080,897 / 20.28%
Number/percentage of N's	113,757 / 0.06%
GC Percentage	40.54%

2.3. Coverage

Mean	0.0639

Standard Deviation	0.8583

2.4. Mapping Quality

Mean Mapping Quality	48.11

2.5. Mismatches and indels

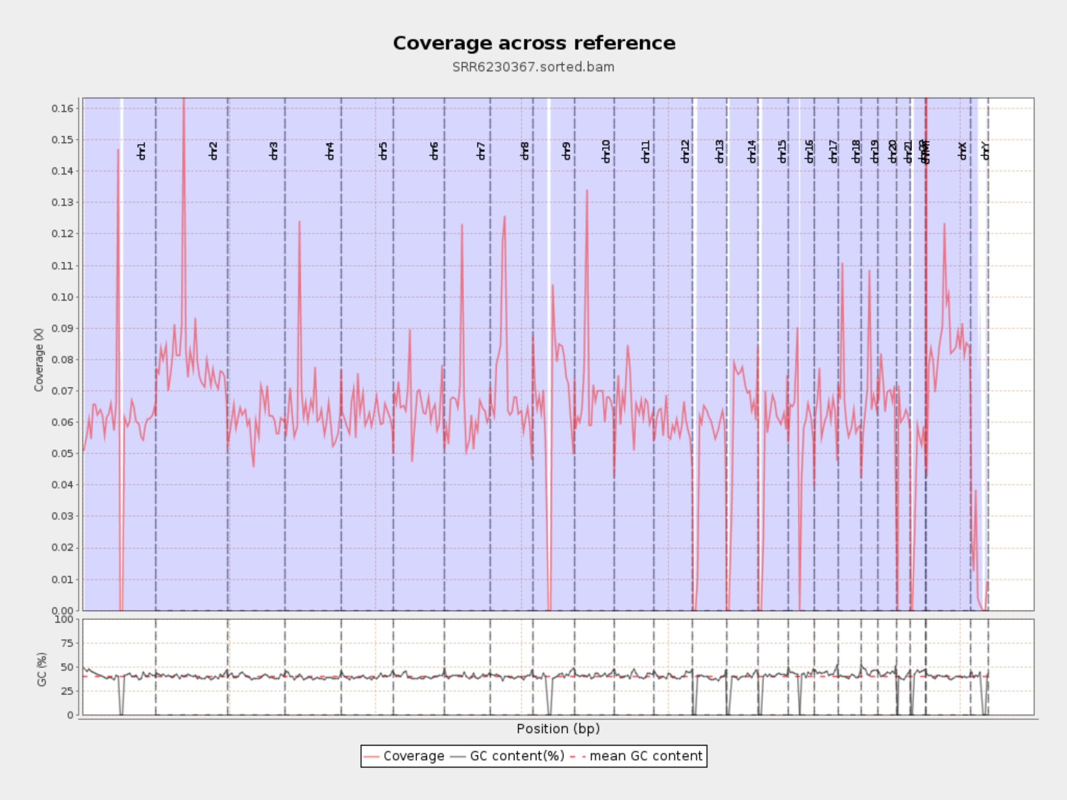
General error rate	0.88%
Mismatches	1,694,375
Insertions	17,493
Mapped reads with at least one insertion	0.63%
Deletions	45,303
Mapped reads with at least one deletion	1.63%
Homopolymer indels	48.7%

2.6. Chromosome stats

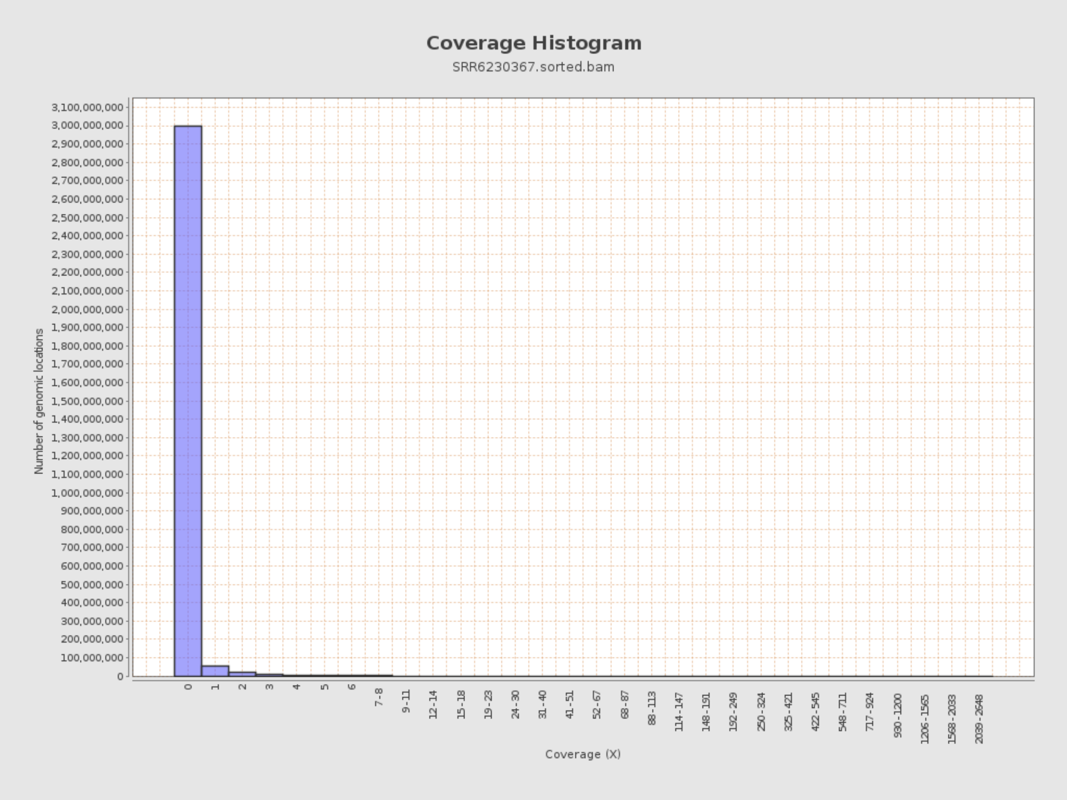
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14877288	0.0597	1.9829
chr2	243199373	19748458	0.0812	0.8552
chr3	198022430	12015935	0.0607	0.4259
chr4	191154276	12314714	0.0644	0.5136
chr5	180915260	11333428	0.0626	0.4402
chr6	171115067	11265431	0.0658	0.4998
chr7	159138663	10245368	0.0644	0.7583

chr8	146364022	10486829	0.0716	1.154
chr9	141213431	9222199	0.0653	0.7689
chr10	135534747	9412012	0.0694	0.7355
chr11	135006516	8841952	0.0655	0.6272
chr12	133851895	7916042	0.0591	0.4395
chr13	115169878	5793397	0.0503	0.3912
chr14	107349540	6438081	0.06	0.4688
chr15	102531392	5227245	0.051	0.391
chr16	90354753	5161014	0.0571	0.4997
chr17	81195210	5148188	0.0634	0.5158
chr18	78077248	5163924	0.0661	1.5026
chr19	59128983	4118747	0.0697	1.0844
chr20	63025520	4365296	0.0693	0.4915
chr21	48129895	2752843	0.0572	0.4905
chr22	51304566	1999569	0.039	0.3316
chrMT	16571	53420	3.2237	3.3721
chrX	155270560	13170949	0.0848	0.5621
chrY	59373566	631931	0.0106	0.3435

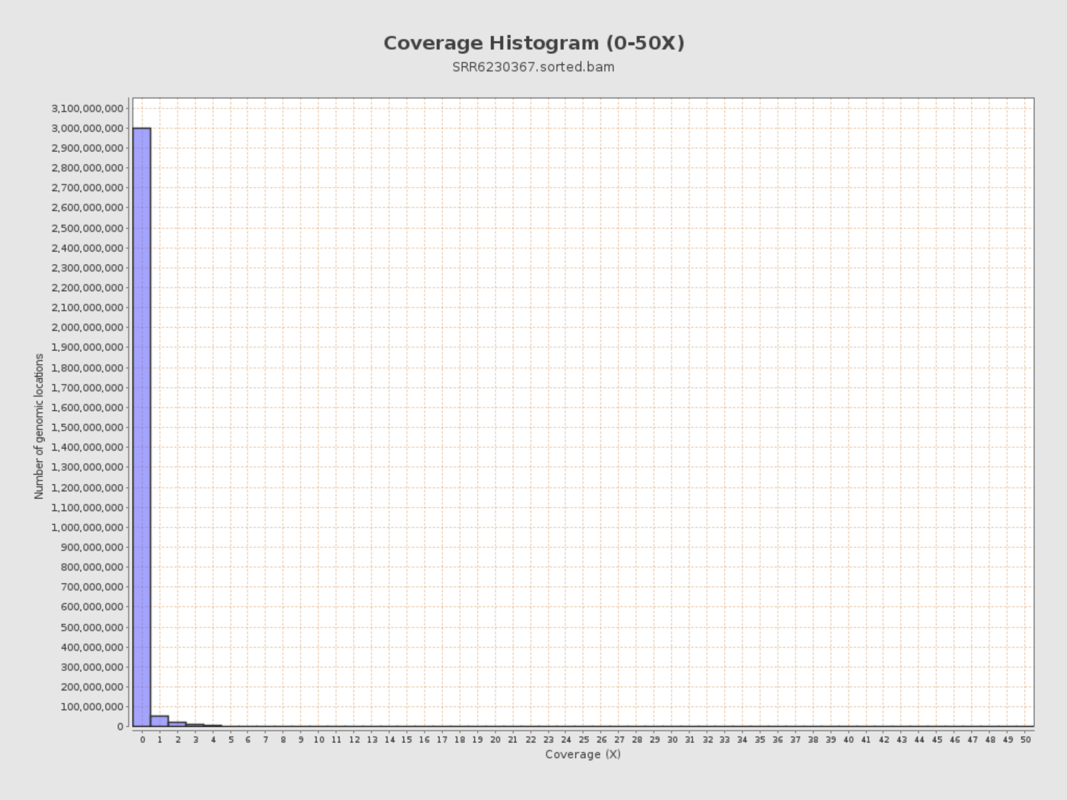
3. Results : Coverage across reference



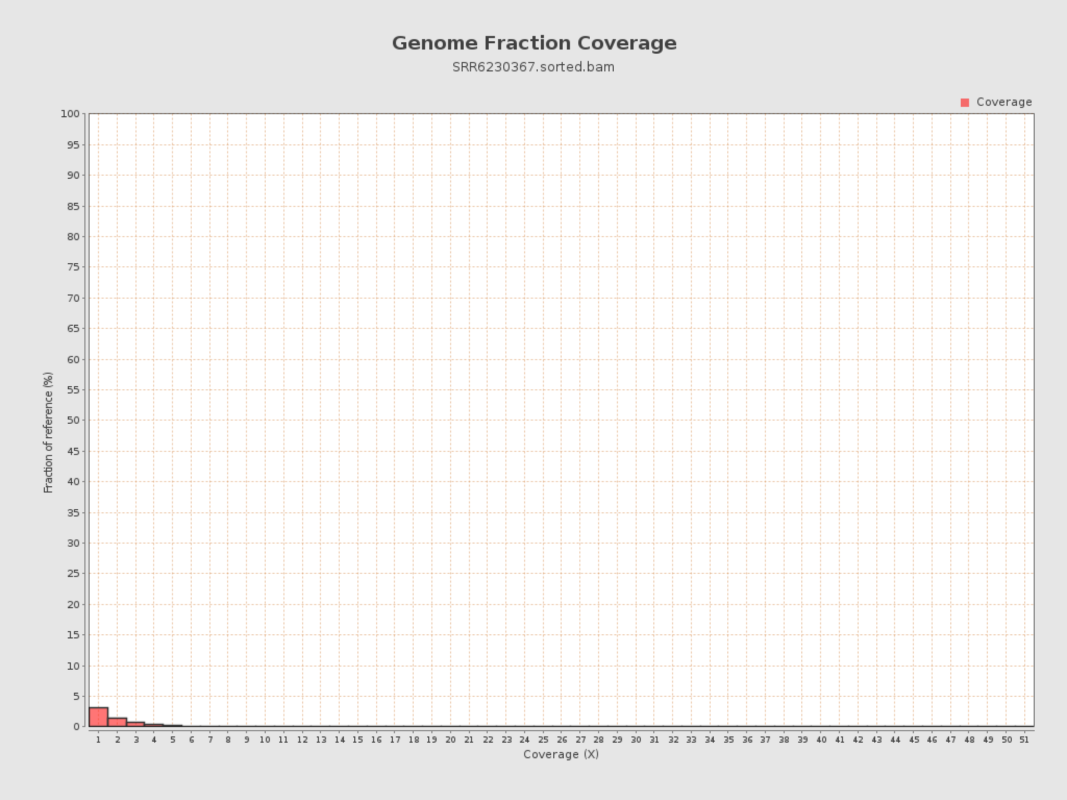
4. Results : Coverage Histogram



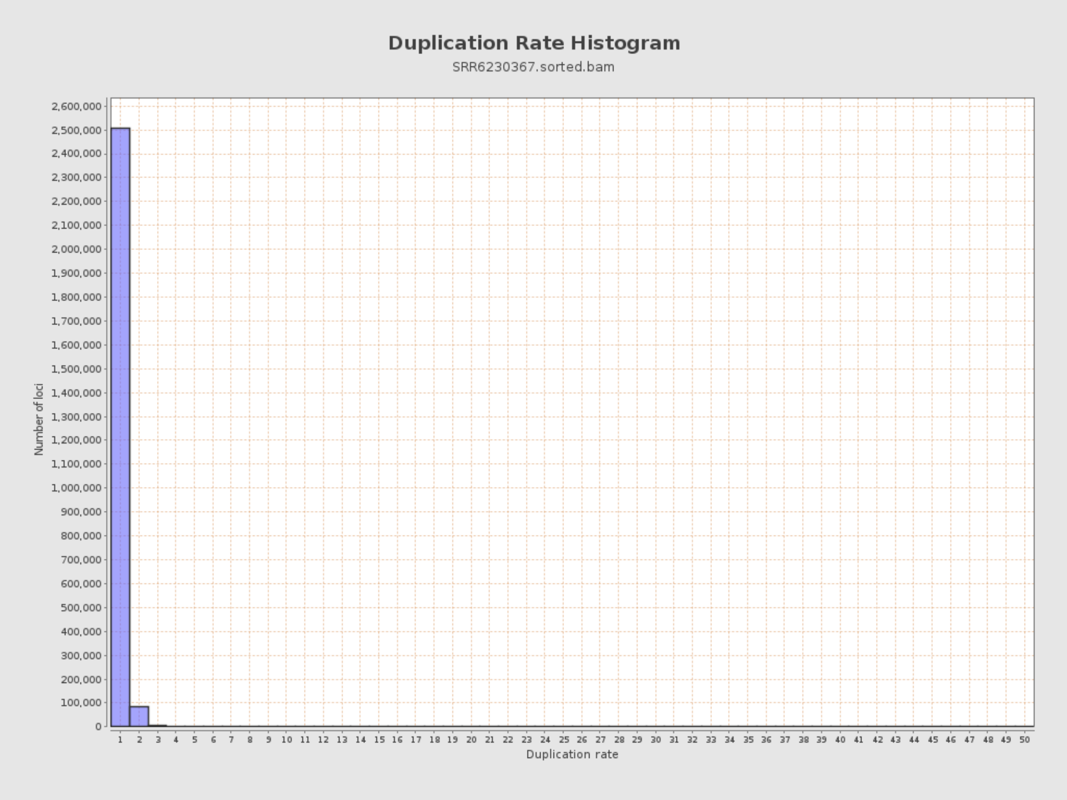
5. Results : Coverage Histogram (0-50X)



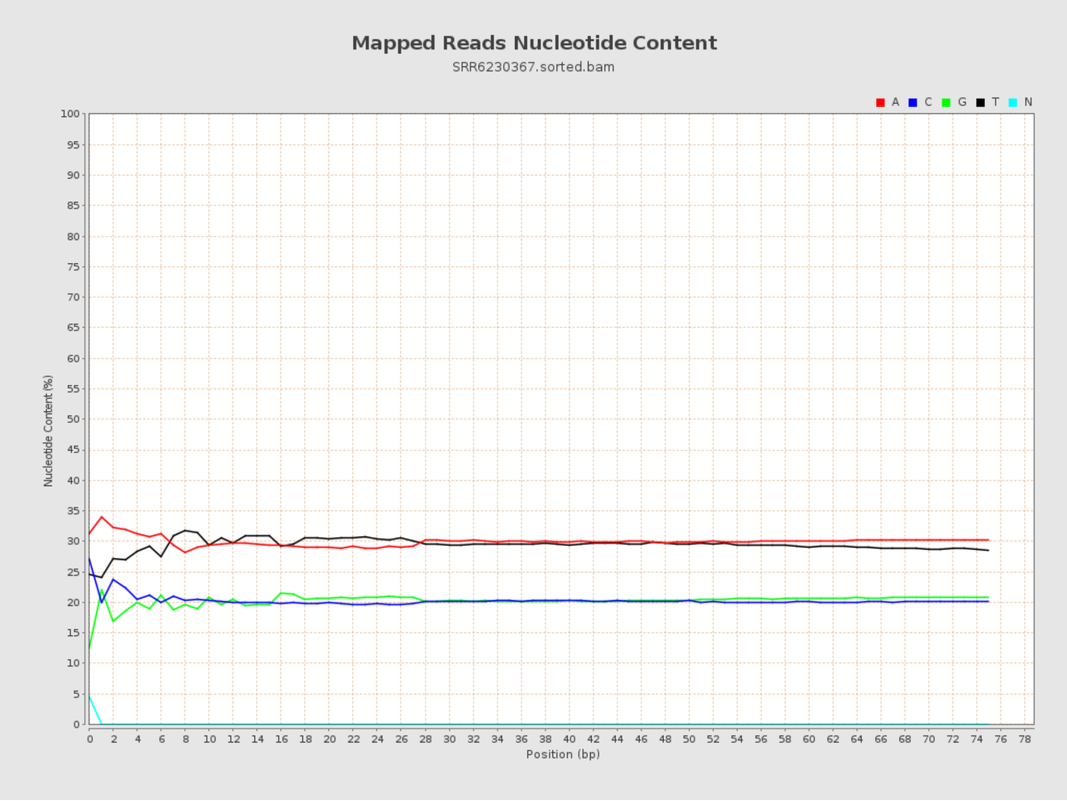
6. Results : Genome Fraction Coverage



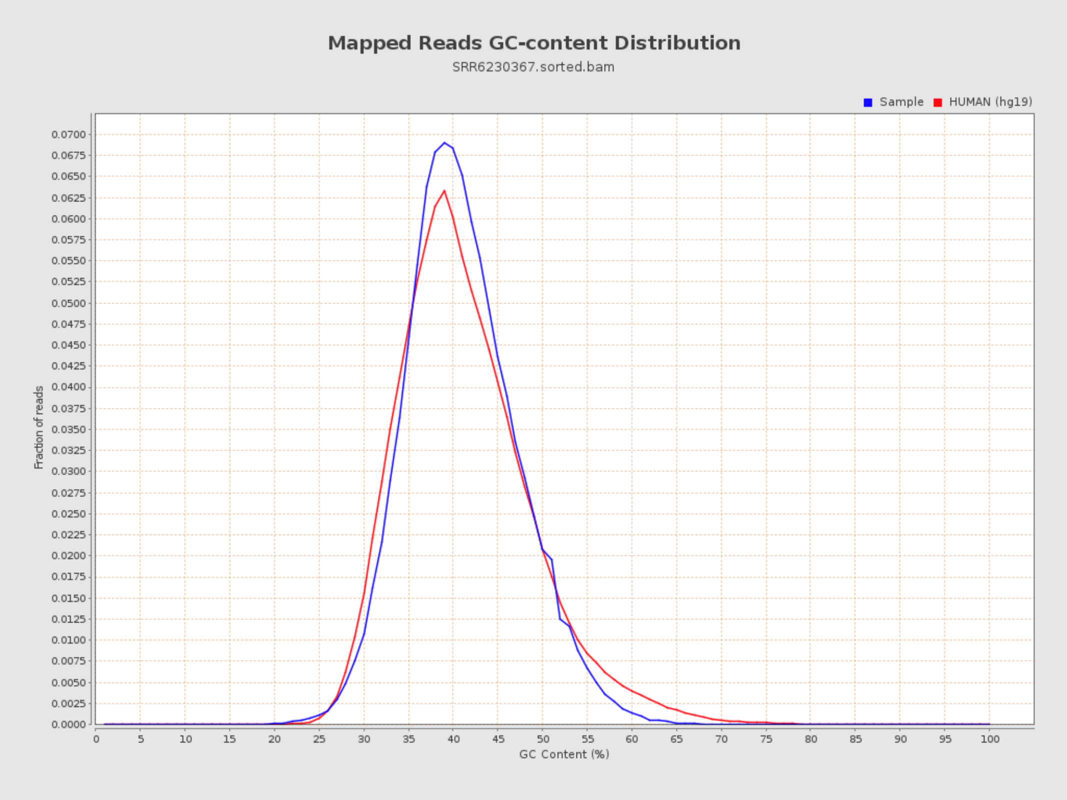
7. Results : Duplication Rate Histogram



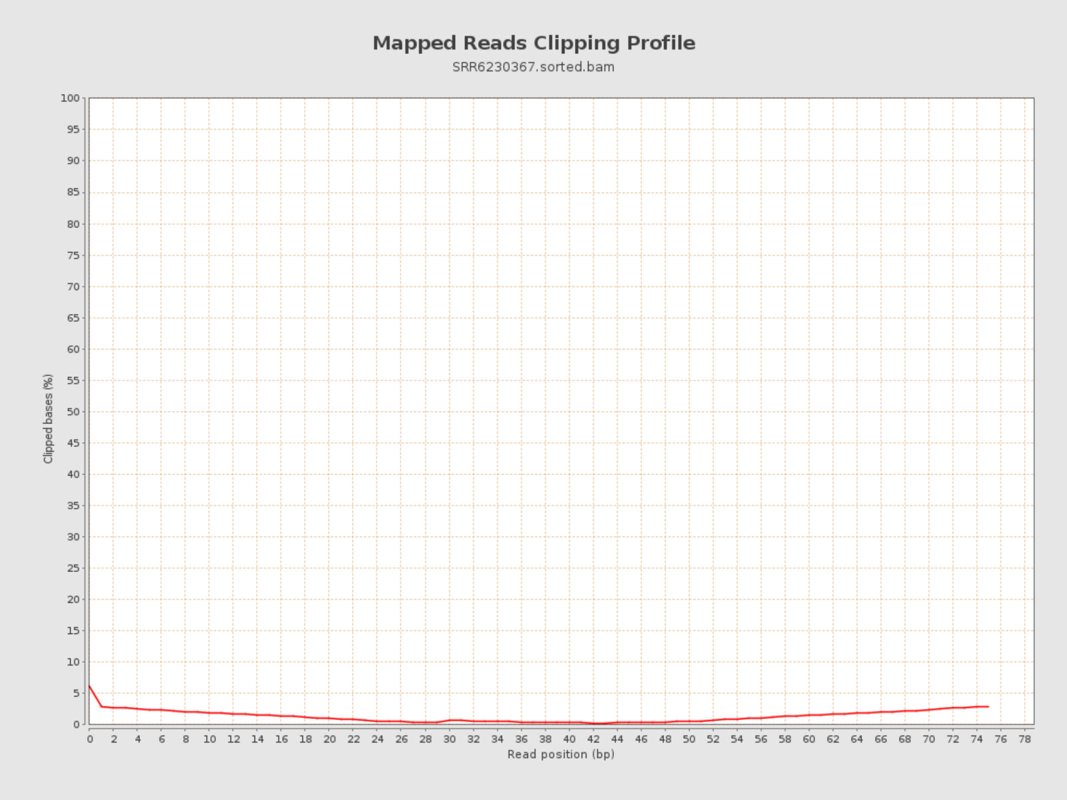
8. Results : Mapped Reads Nucleotide Content



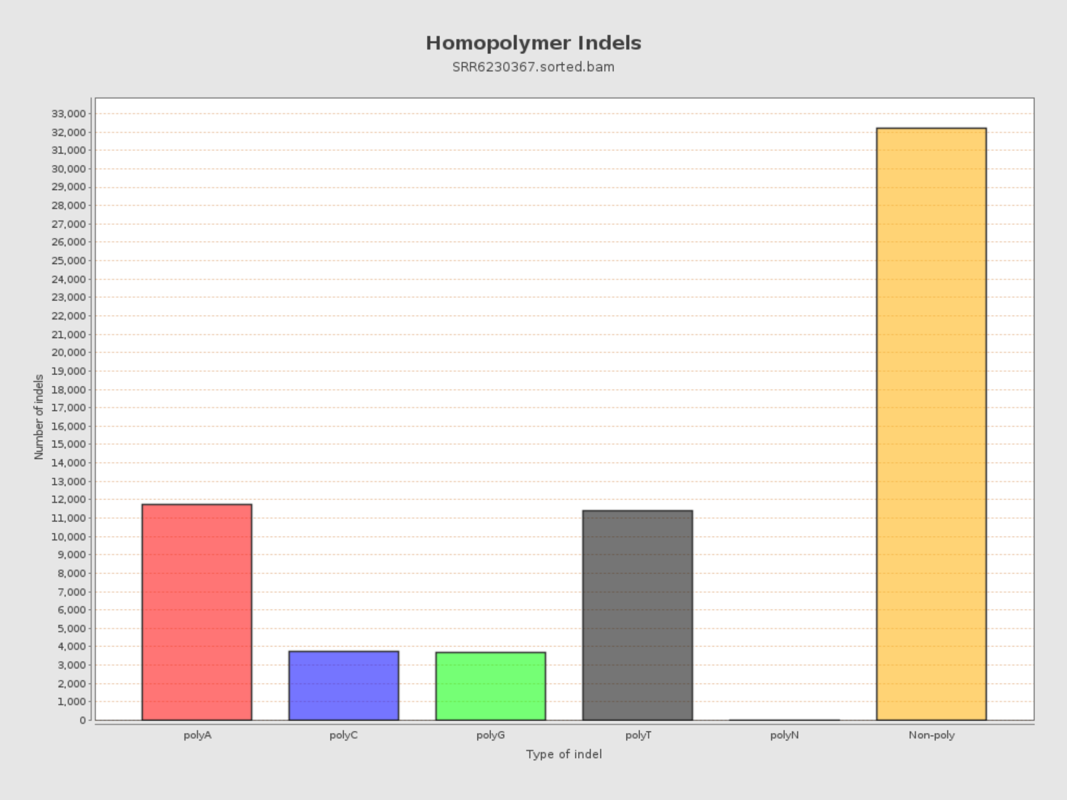
9. Results : Mapped Reads GC-content Distribution



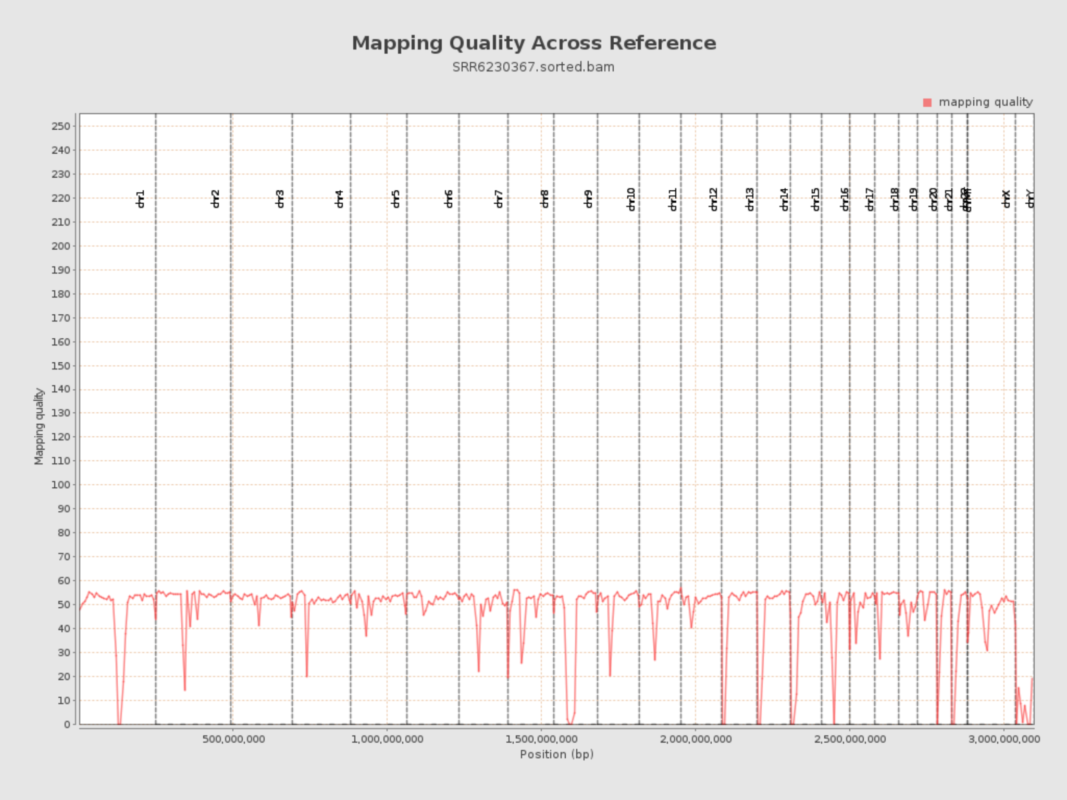
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram