Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 23:00:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013354.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_SRR6013354 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013354.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 23:00:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013354.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,196,747
Mapped reads	2,792,826 / 87.36%
Unmapped reads	403,921 / 12.64%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,375 / 0.64%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	81,613 / 2.55%
Duplication rate	2.06%
Clipped reads	1,420,941 / 44.45%

2.2. ACGT Content

Number/percentage of A's	50,657,209 / 27.88%
Number/percentage of C's	35,466,376 / 19.52%
Number/percentage of T's	54,171,916 / 29.82%
Number/percentage of G's	41,328,499 / 22.75%
Number/percentage of N's	41,375 / 0.02%
GC Percentage	42.27%

2.3. Coverage

Mean	0.0587

Standard Deviation	0.4285

2.4. Mapping Quality

Mean Mapping Quality	43.57

2.5. Mismatches and indels

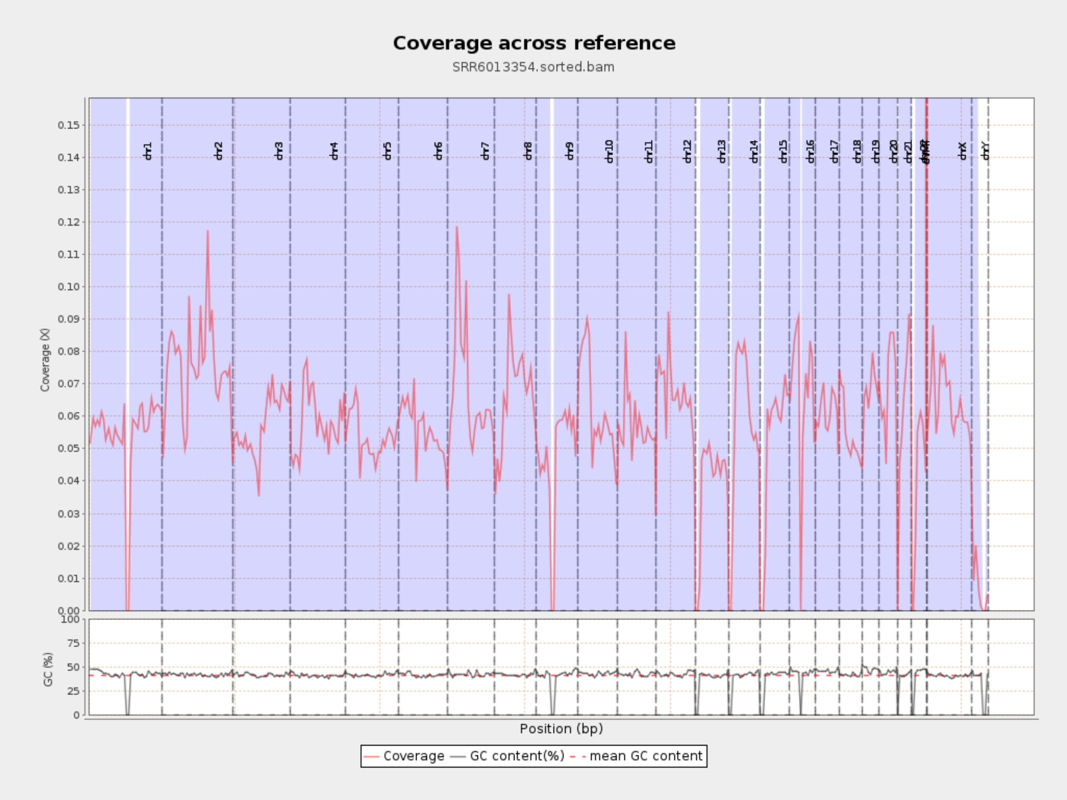
General error rate	0.79%
Mismatches	1,404,932
Insertions	13,599
Mapped reads with at least one insertion	0.48%
Deletions	38,963
Mapped reads with at least one deletion	1.38%
Homopolymer indels	45.38%

2.6. Chromosome stats

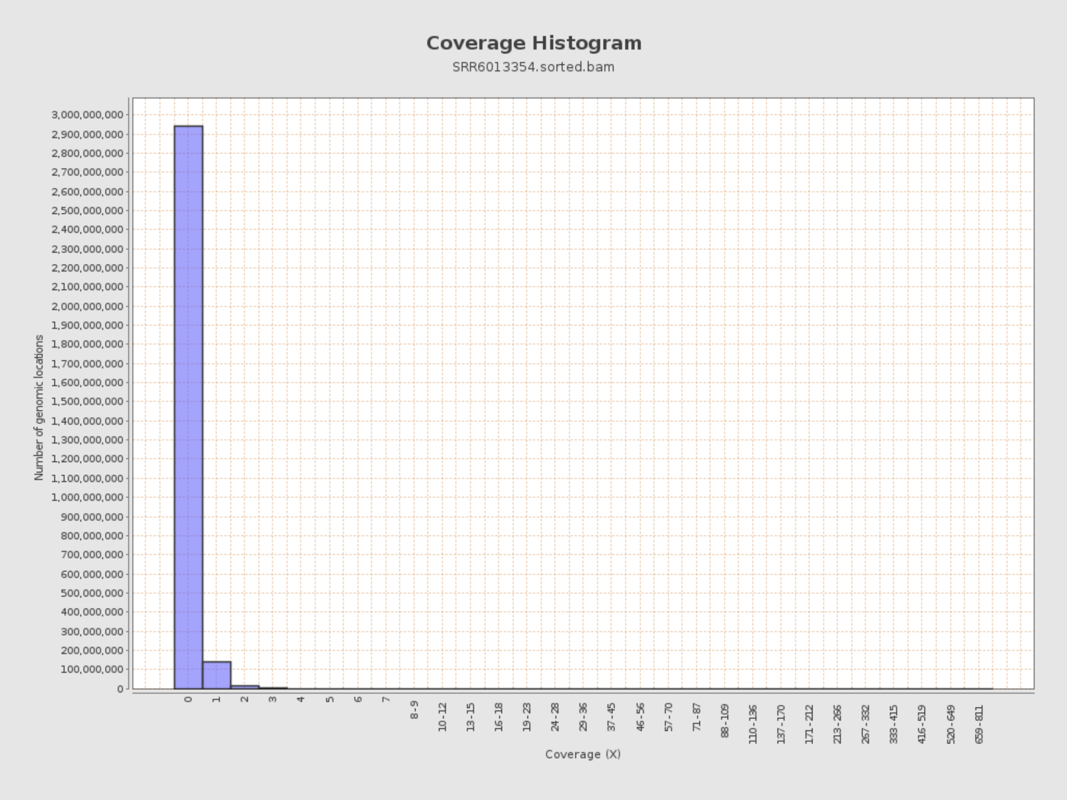
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13465284	0.054	0.5647
chr2	243199373	18409104	0.0757	0.5733
chr3	198022430	11334892	0.0572	0.2671
chr4	191154276	11062726	0.0579	0.2882
chr5	180915260	9709163	0.0537	0.2718
chr6	171115067	9578643	0.056	0.3204
chr7	159138663	10948955	0.0688	0.8047

chr8	146364022	9764502	0.0667	0.4176
chr9	141213431	6644304	0.0471	0.3676
chr10	135534747	8582498	0.0633	0.4111
chr11	135006516	7725570	0.0572	0.3485
chr12	133851895	9041120	0.0675	0.2973
chr13	115169878	4394878	0.0382	0.2295
chr14	107349540	6119639	0.057	0.294
chr15	102531392	5228020	0.051	0.2684
chr16	90354753	6097808	0.0675	0.335
chr17	81195210	4969819	0.0612	0.303
chr18	78077248	4282177	0.0548	0.6326
chr19	59128983	4033741	0.0682	0.4919
chr20	63025520	4358483	0.0692	0.3033
chr21	48129895	3000764	0.0623	0.3078
chr22	51304566	1975047	0.0385	0.2181
chrMT	16571	586285	35.3802	28.4822
chrX	155270560	9982565	0.0643	0.3084
chrY	59373566	438062	0.0074	0.1551

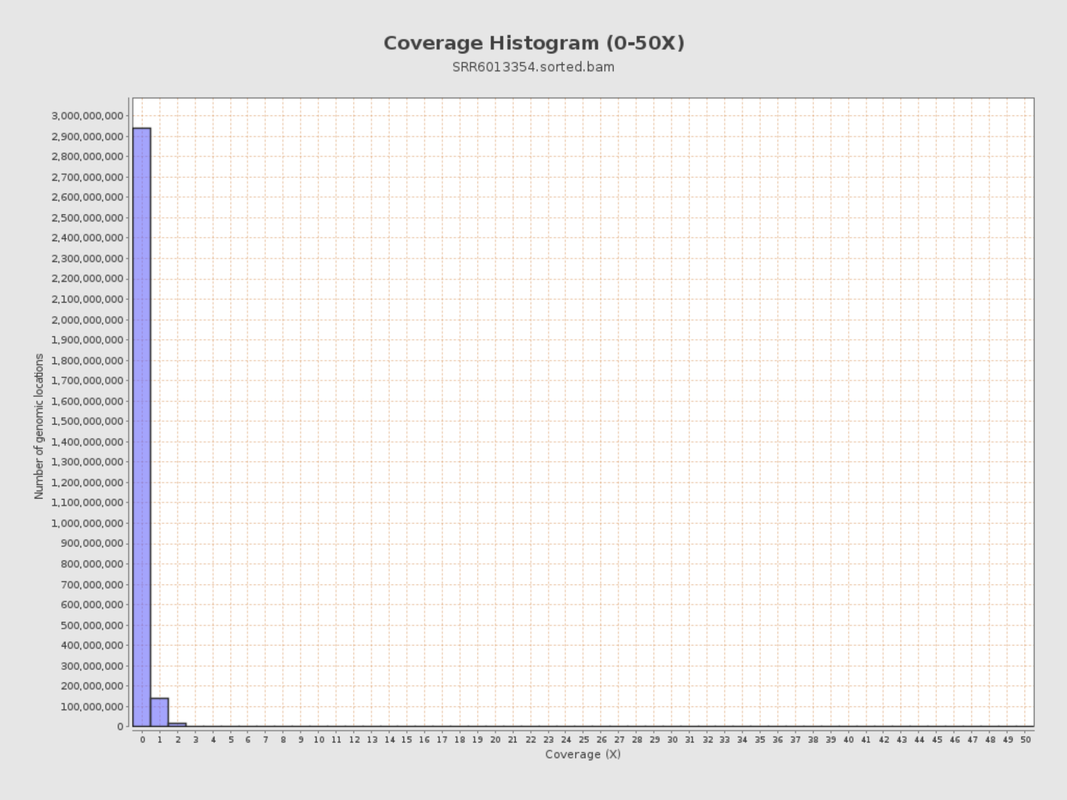
3. Results : Coverage across reference



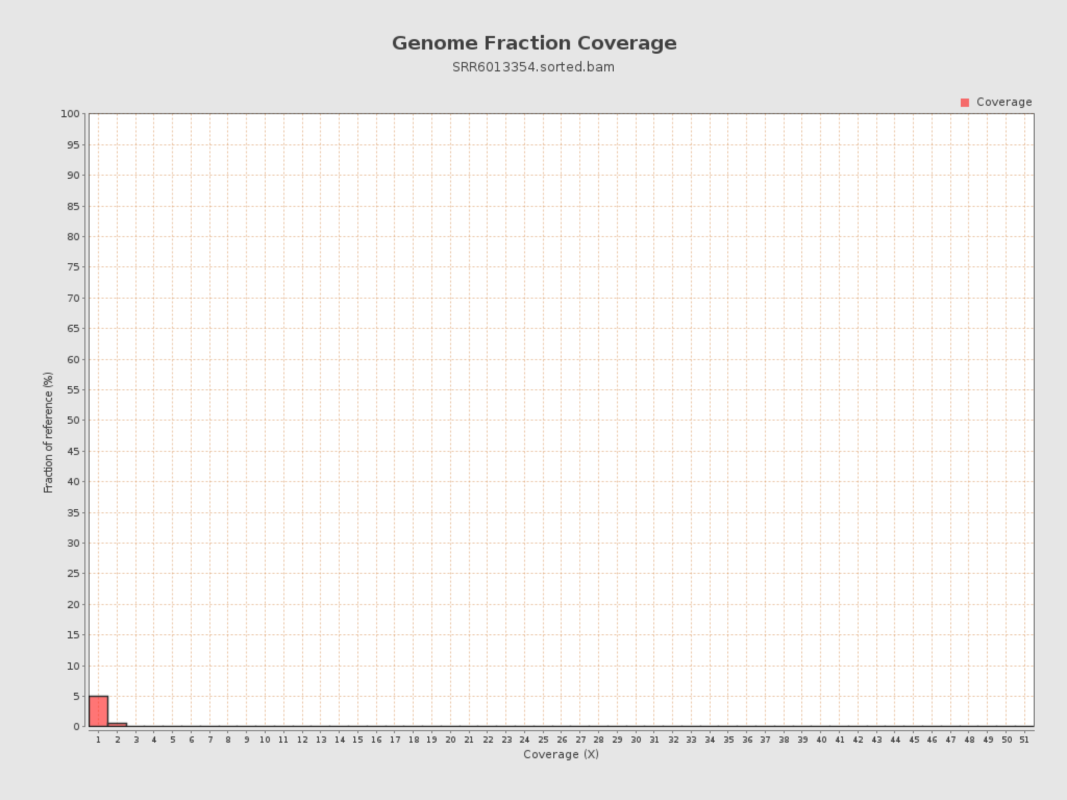
4. Results : Coverage Histogram



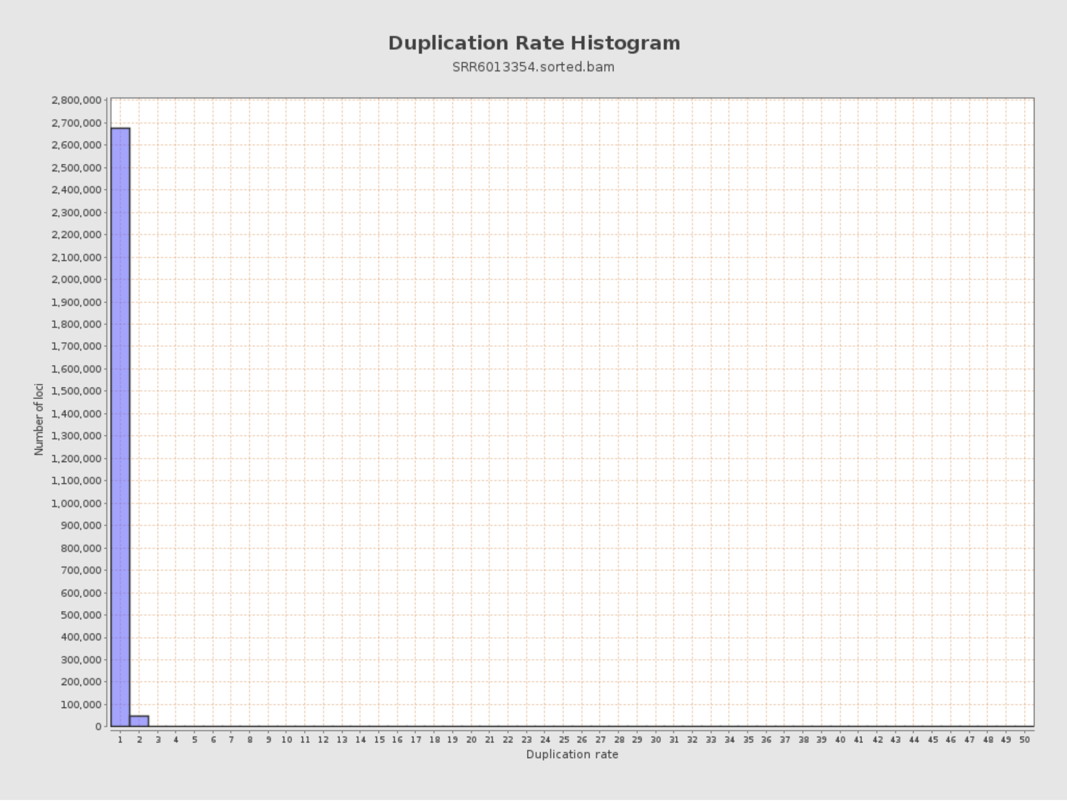
5. Results : Coverage Histogram (0-50X)



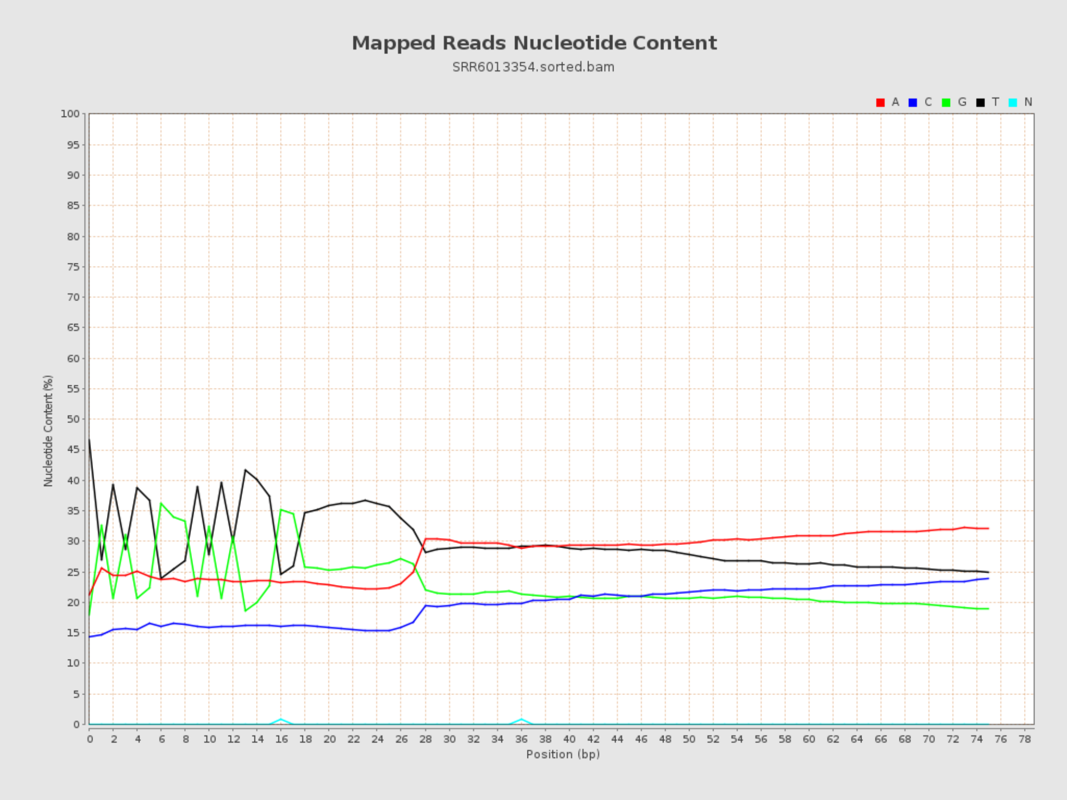
6. Results : Genome Fraction Coverage



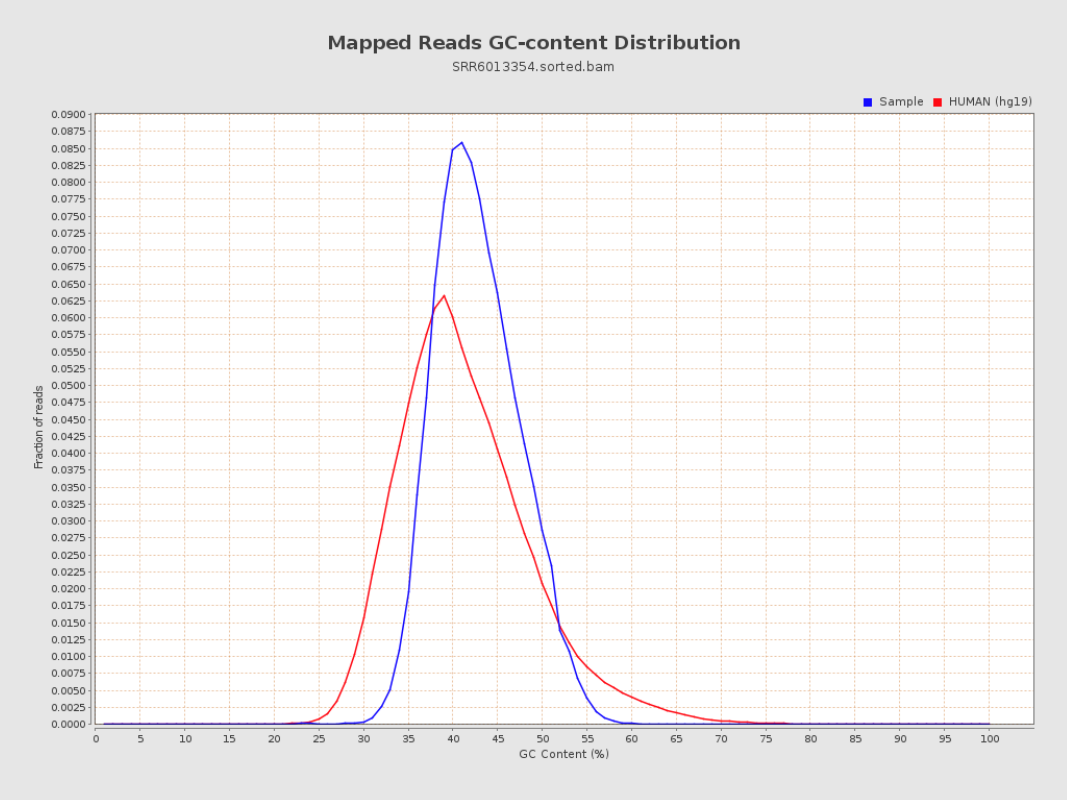
7. Results : Duplication Rate Histogram



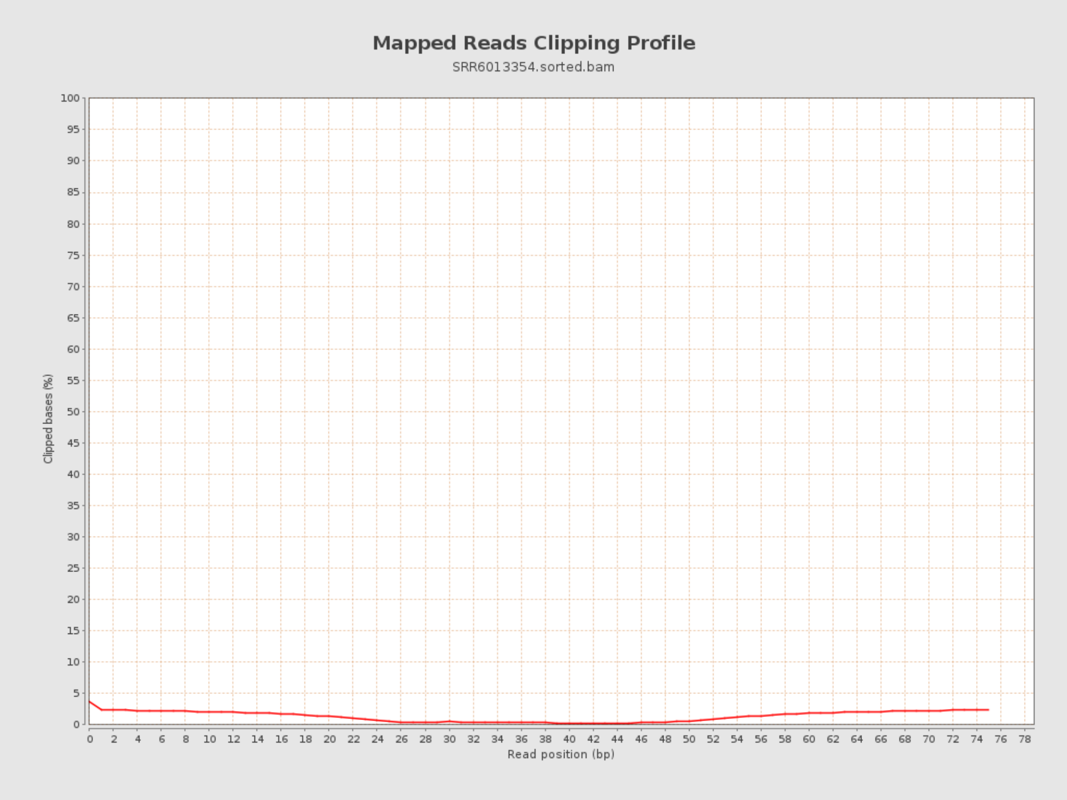
8. Results : Mapped Reads Nucleotide Content



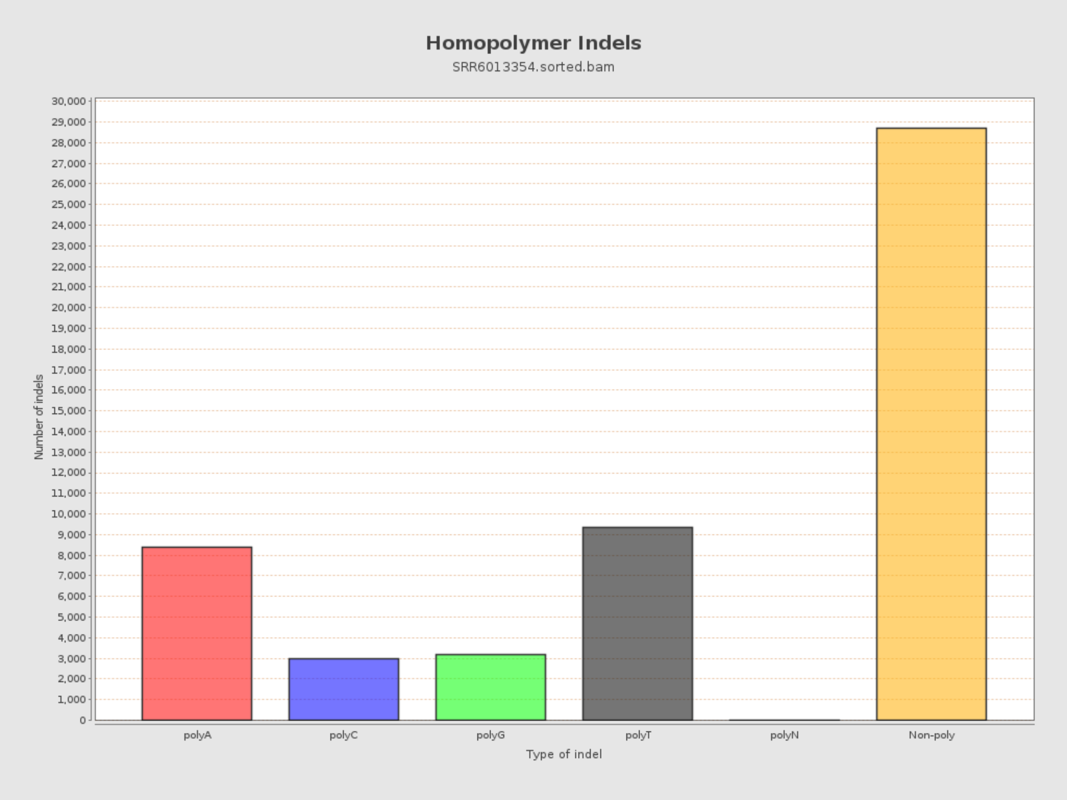
9. Results : Mapped Reads GC-content Distribution



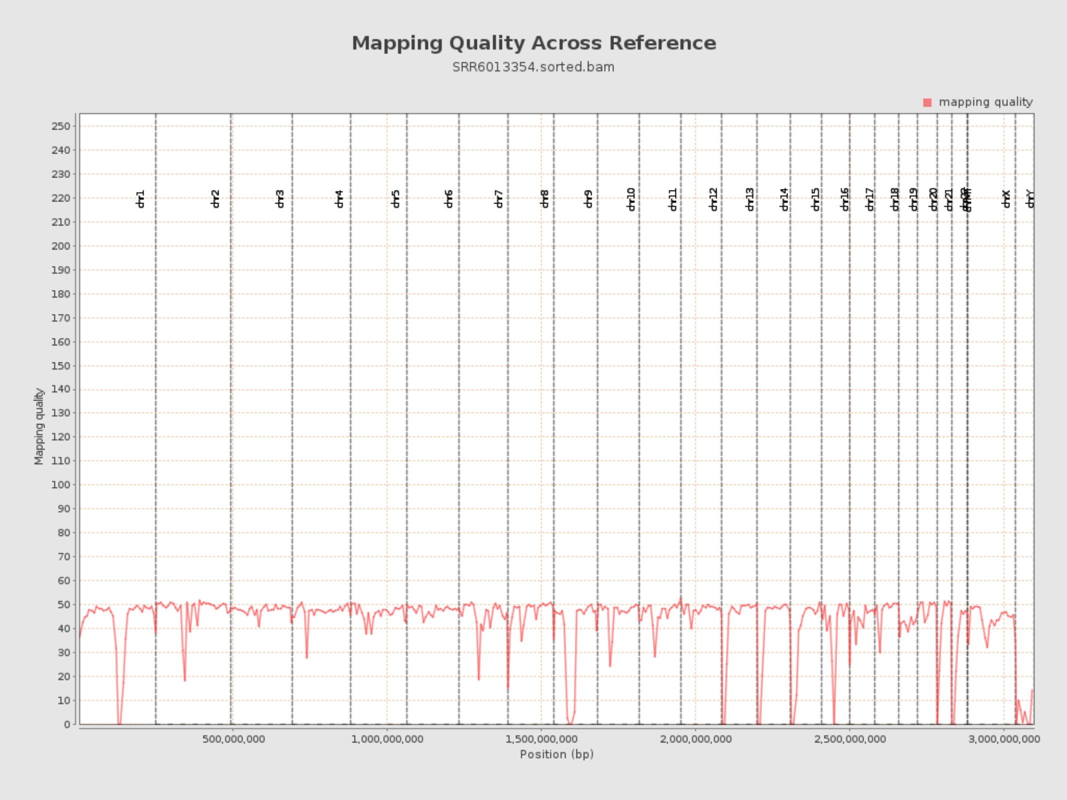
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram