Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 22:36:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013346.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_SRR6013346 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013346.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 22:36:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013346.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,898,958
Mapped reads	1,685,291 / 88.75%
Unmapped reads	213,667 / 11.25%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,458 / 0.6%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	69,985 / 3.69%
Duplication rate	3.41%
Clipped reads	757,454 / 39.89%

2.2. ACGT Content

Number/percentage of A's	30,227,465 / 27%
Number/percentage of C's	21,491,529 / 19.19%
Number/percentage of T's	34,617,247 / 30.92%
Number/percentage of G's	25,602,242 / 22.87%
Number/percentage of N's	28,954 / 0.03%
GC Percentage	42.06%

2.3. Coverage

Mean	0.0362

Standard Deviation	0.3045

2.4. Mapping Quality

Mean Mapping Quality	45.96

2.5. Mismatches and indels

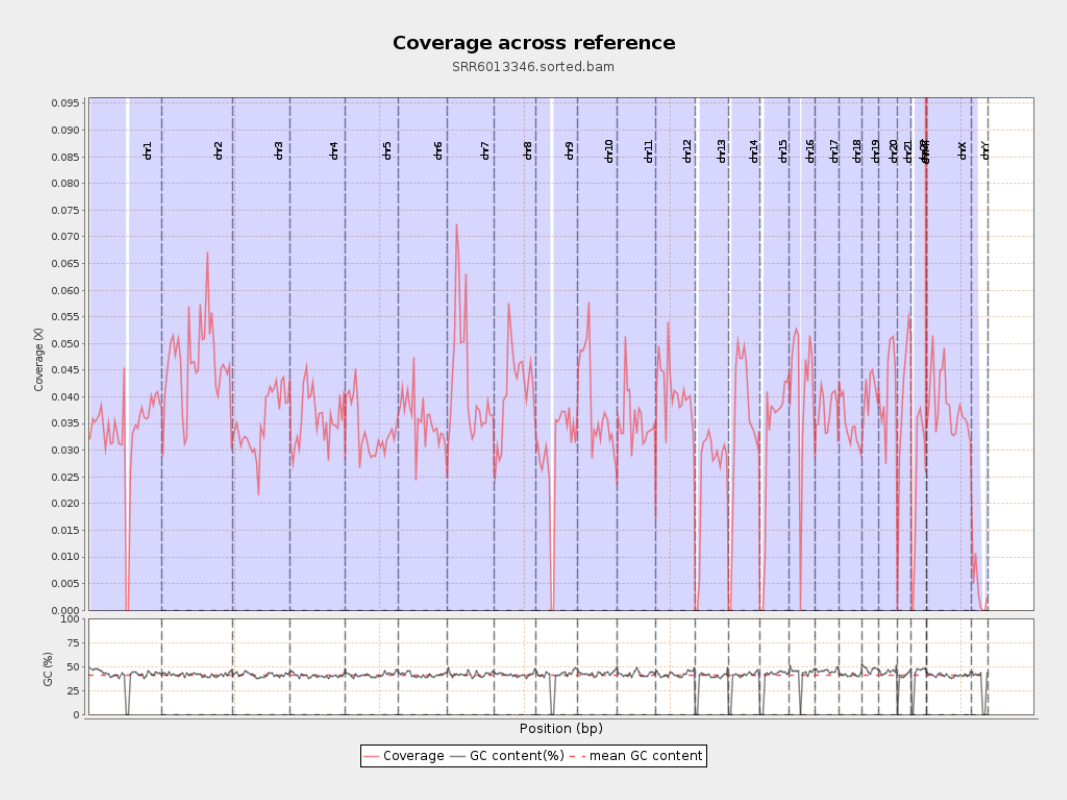
General error rate	0.81%
Mismatches	892,016
Insertions	7,587
Mapped reads with at least one insertion	0.45%
Deletions	29,386
Mapped reads with at least one deletion	1.72%
Homopolymer indels	45.25%

2.6. Chromosome stats

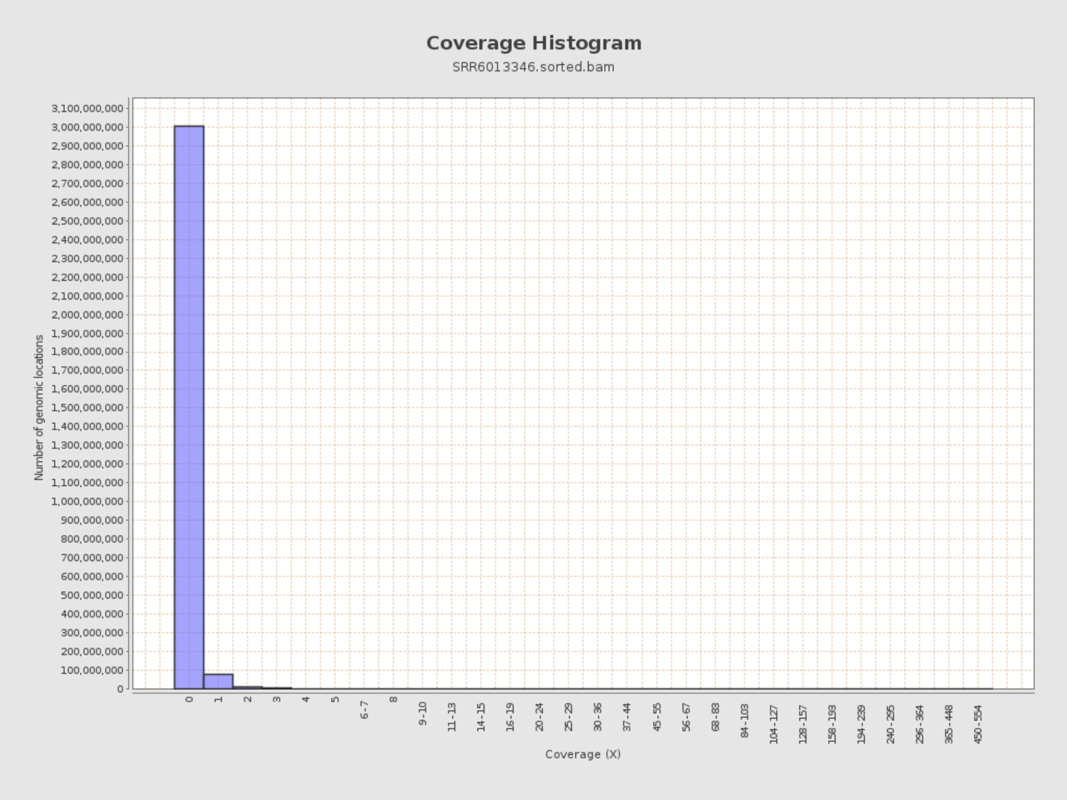
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8287576	0.0332	0.4323
chr2	243199373	11250044	0.0463	0.3899
chr3	198022430	7019522	0.0354	0.2207
chr4	191154276	6862221	0.0359	0.227
chr5	180915260	6081198	0.0336	0.2162
chr6	171115067	6091607	0.0356	0.2625
chr7	159138663	6820679	0.0429	0.4868

chr8	146364022	6035519	0.0412	0.2957
chr9	141213431	4102072	0.029	0.258
chr10	135534747	5241102	0.0387	0.3187
chr11	135006516	4795735	0.0355	0.2558
chr12	133851895	5487079	0.041	0.2395
chr13	115169878	2888650	0.0251	0.1895
chr14	107349540	3673620	0.0342	0.2273
chr15	102531392	3204073	0.0312	0.2088
chr16	90354753	3755244	0.0416	0.2577
chr17	81195210	3026647	0.0373	0.2466
chr18	78077248	2711484	0.0347	0.3992
chr19	59128983	2410486	0.0408	0.3692
chr20	63025520	2610237	0.0414	0.2429
chr21	48129895	1897594	0.0394	0.2444
chr22	51304566	1238518	0.0241	0.1834
chrMT	16571	338752	20.4425	13.1015
chrX	155270560	5955114	0.0384	0.2443
chrY	59373566	234301	0.0039	0.0923

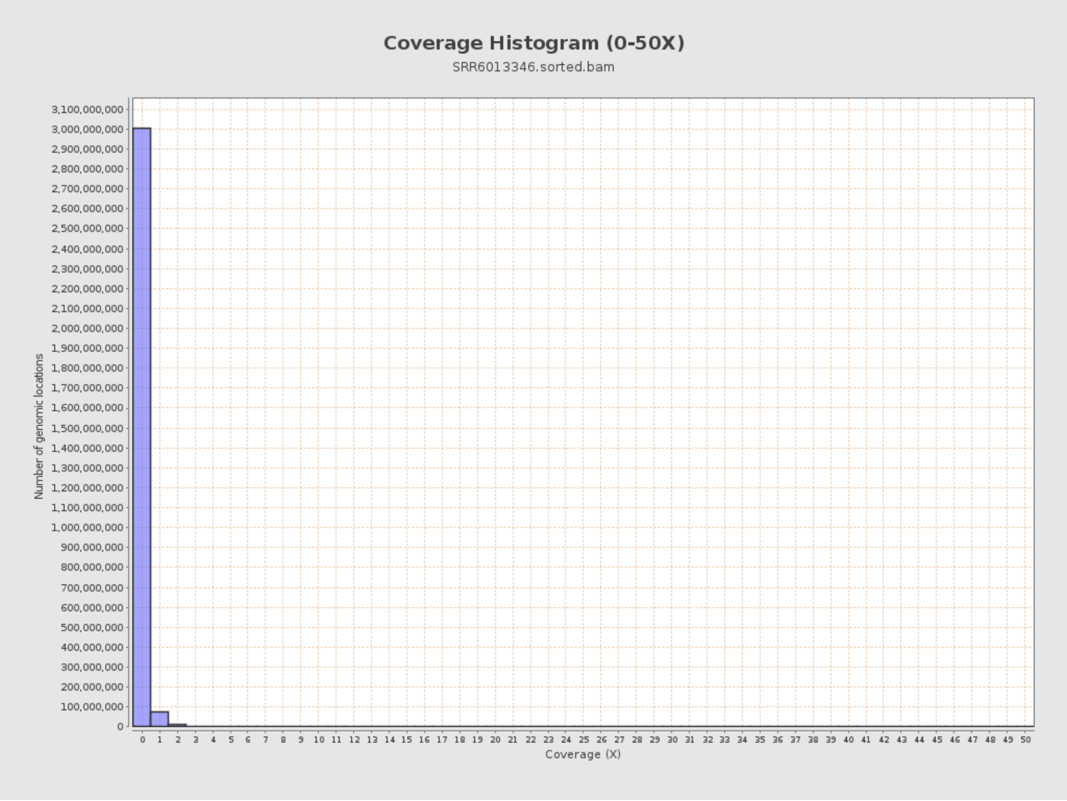
3. Results : Coverage across reference



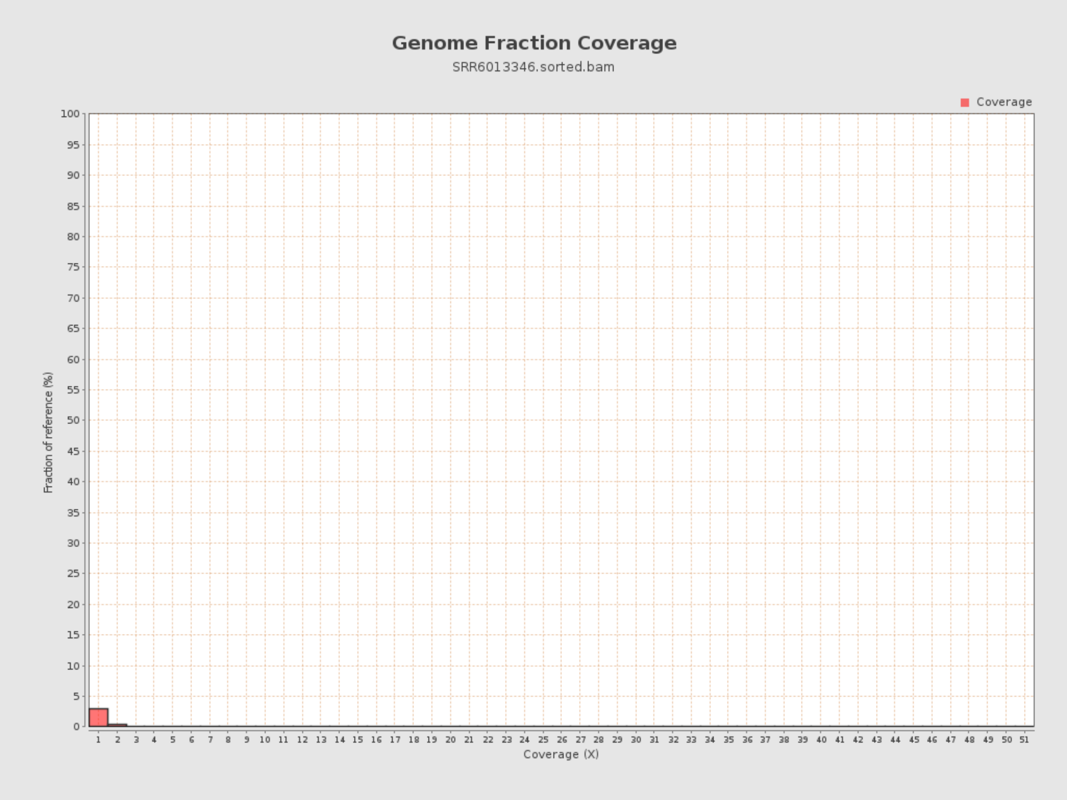
4. Results : Coverage Histogram



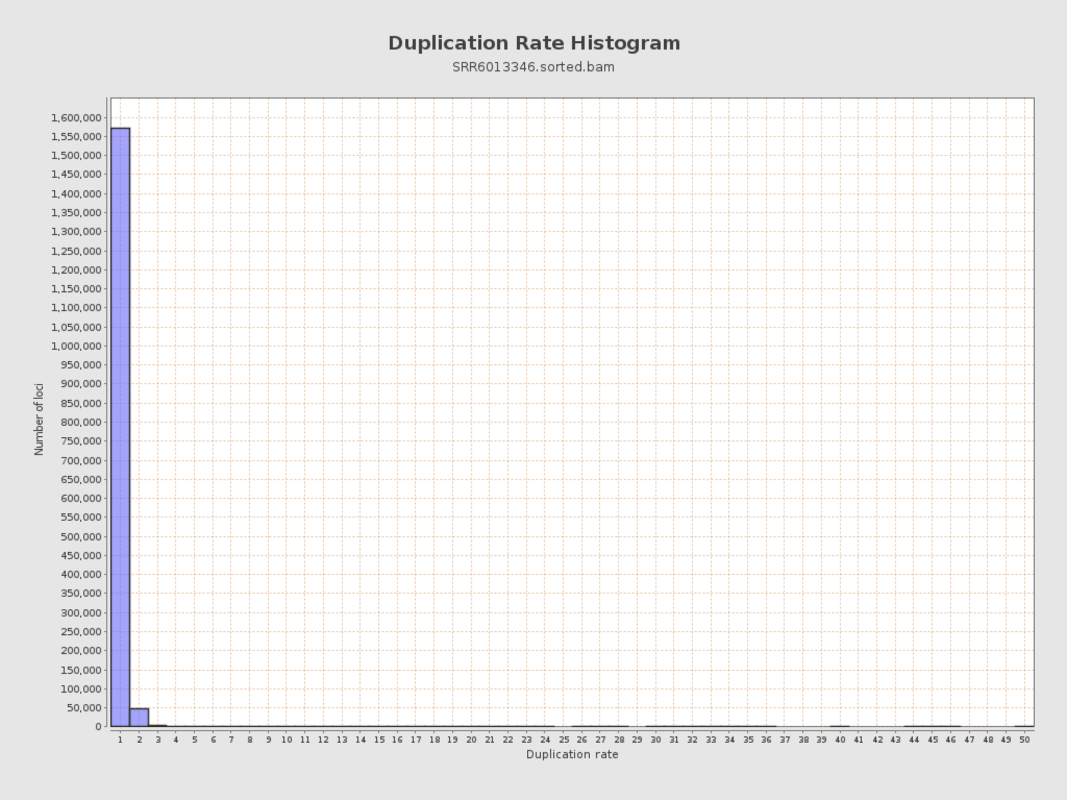
5. Results : Coverage Histogram (0-50X)



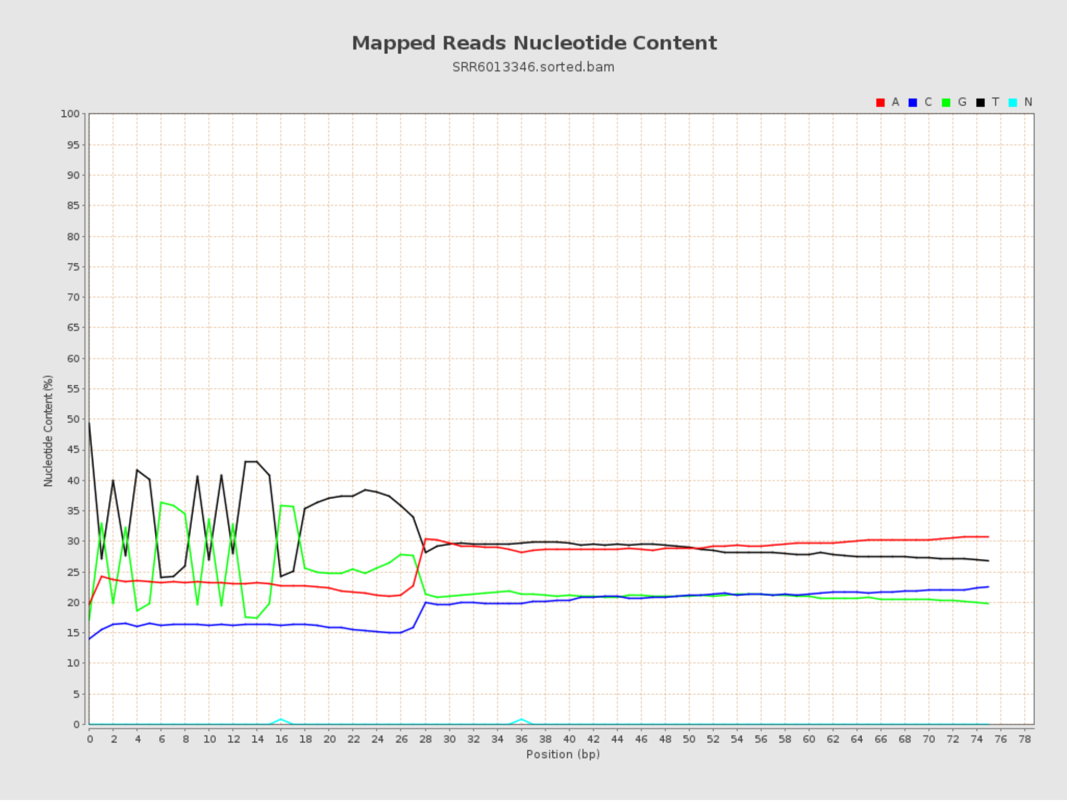
6. Results : Genome Fraction Coverage



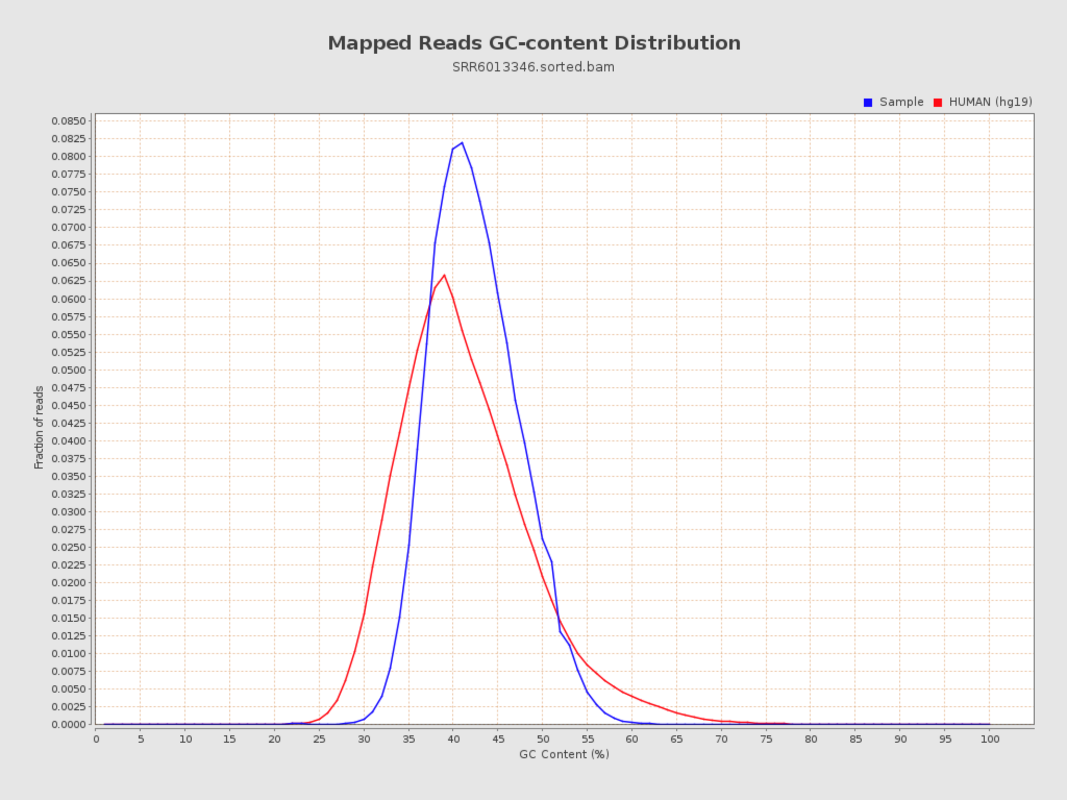
7. Results : Duplication Rate Histogram



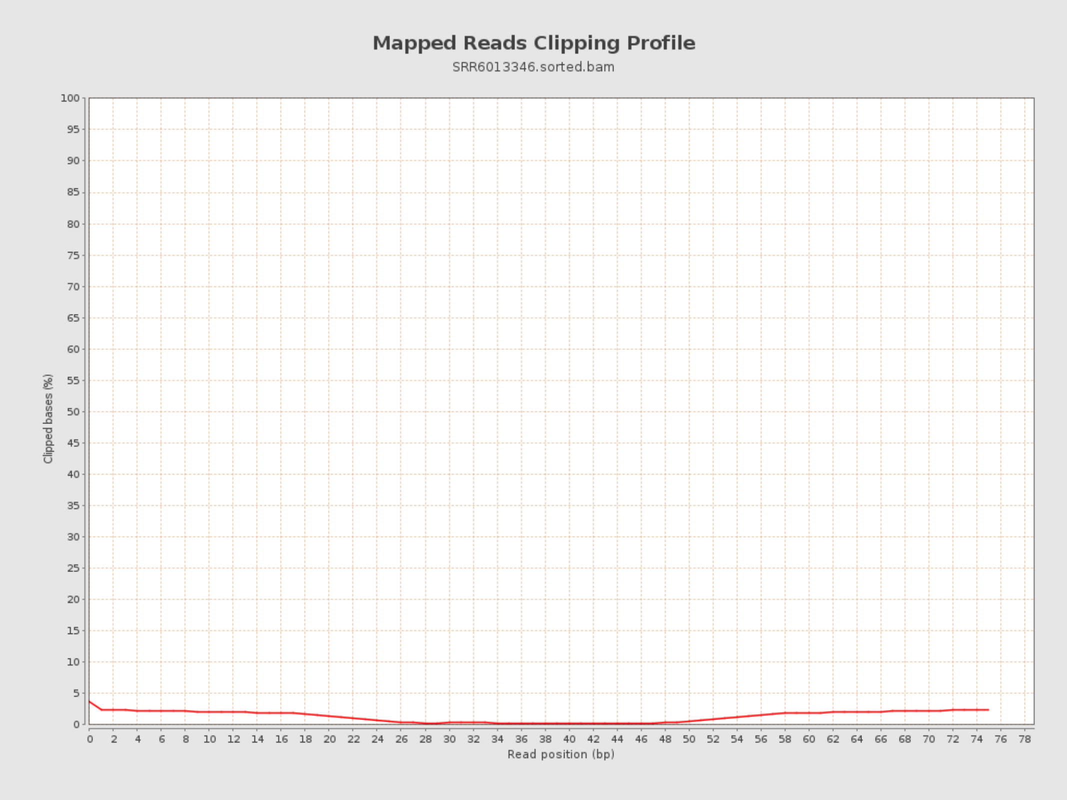
8. Results : Mapped Reads Nucleotide Content



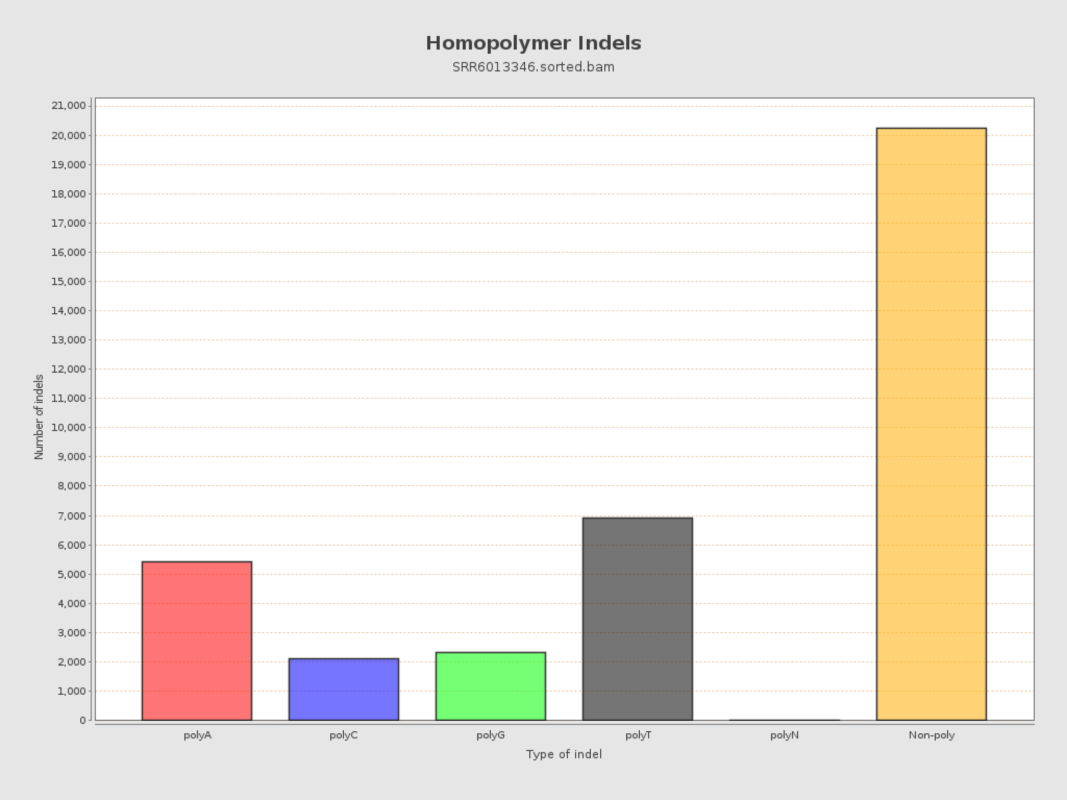
9. Results : Mapped Reads GC-content Distribution



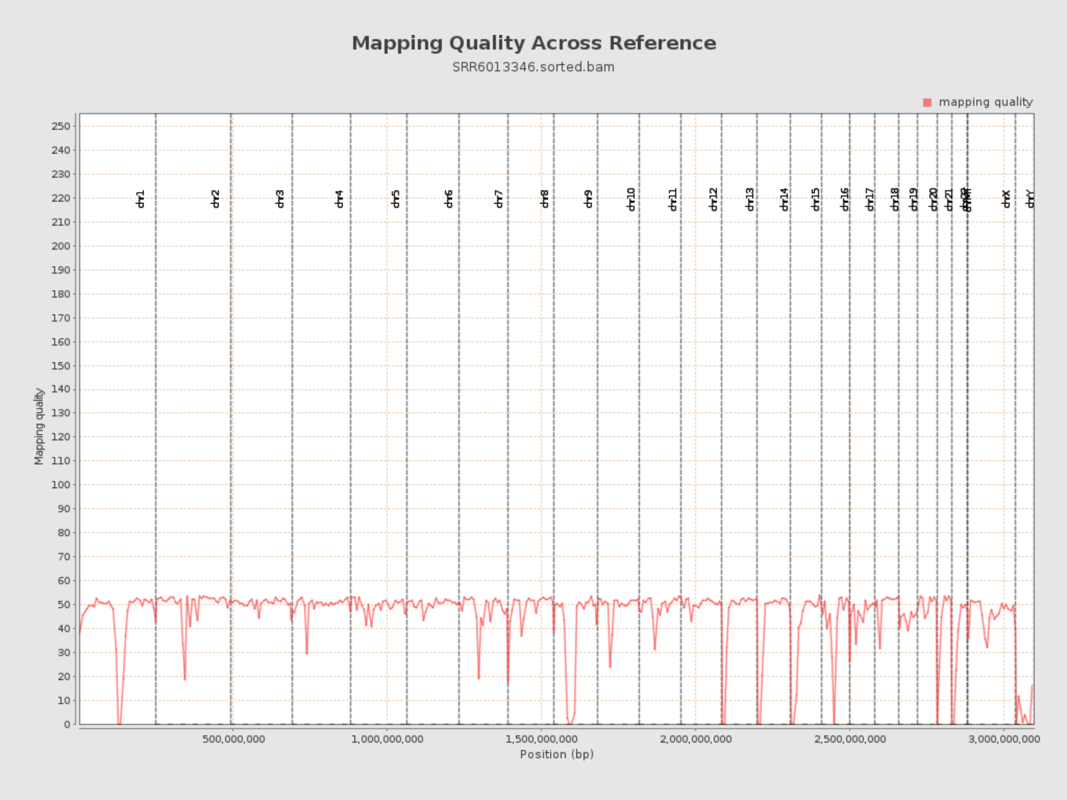
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram