Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 22:18:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013340.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_SRR6013340 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013340.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 22:18:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013340.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,637,433
Mapped reads	2,372,321 / 89.95%
Unmapped reads	265,112 / 10.05%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,062 / 0.68%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	93,302 / 3.54%
Duplication rate	2.97%
Clipped reads	1,115,158 / 42.28%

2.2. ACGT Content

Number/percentage of A's	43,040,712 / 27.38%
Number/percentage of C's	29,829,878 / 18.98%
Number/percentage of T's	48,763,398 / 31.02%
Number/percentage of G's	35,507,837 / 22.59%
Number/percentage of N's	37,887 / 0.02%
GC Percentage	41.57%

2.3. Coverage

Mean	0.0508

Standard Deviation	0.4599

2.4. Mapping Quality

Mean Mapping Quality	46.08

2.5. Mismatches and indels

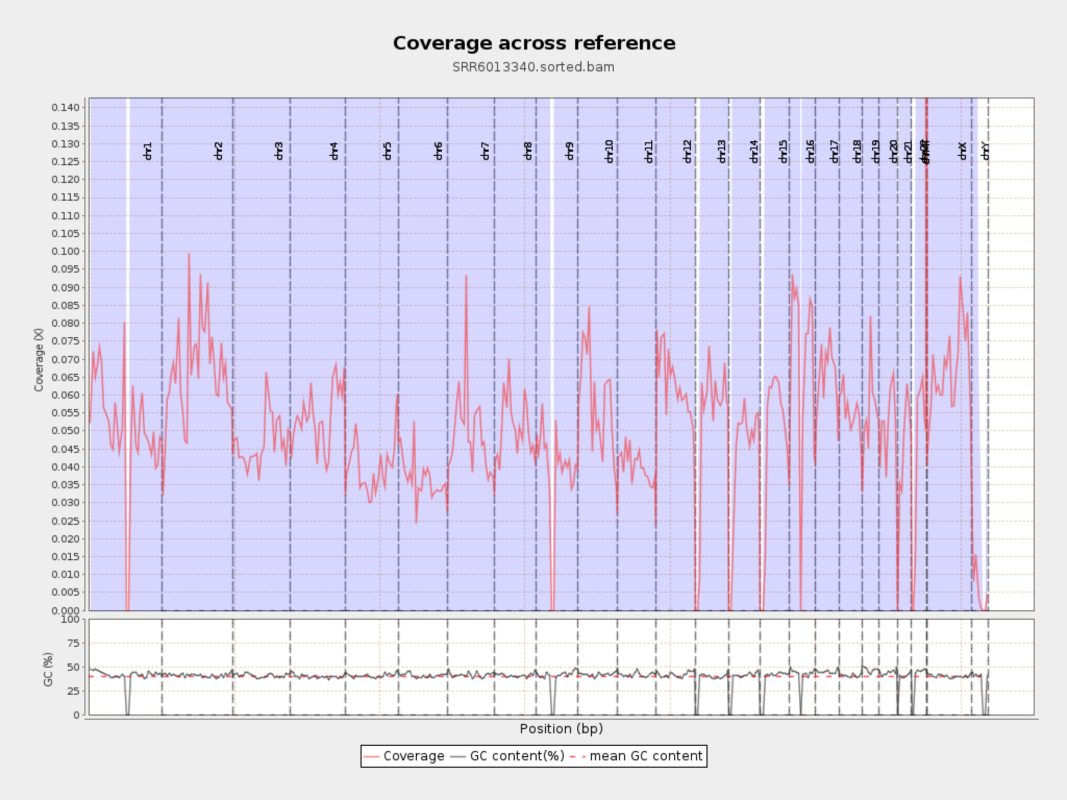
General error rate	0.8%
Mismatches	1,245,213
Insertions	10,385
Mapped reads with at least one insertion	0.43%
Deletions	34,684
Mapped reads with at least one deletion	1.45%
Homopolymer indels	45.59%

2.6. Chromosome stats

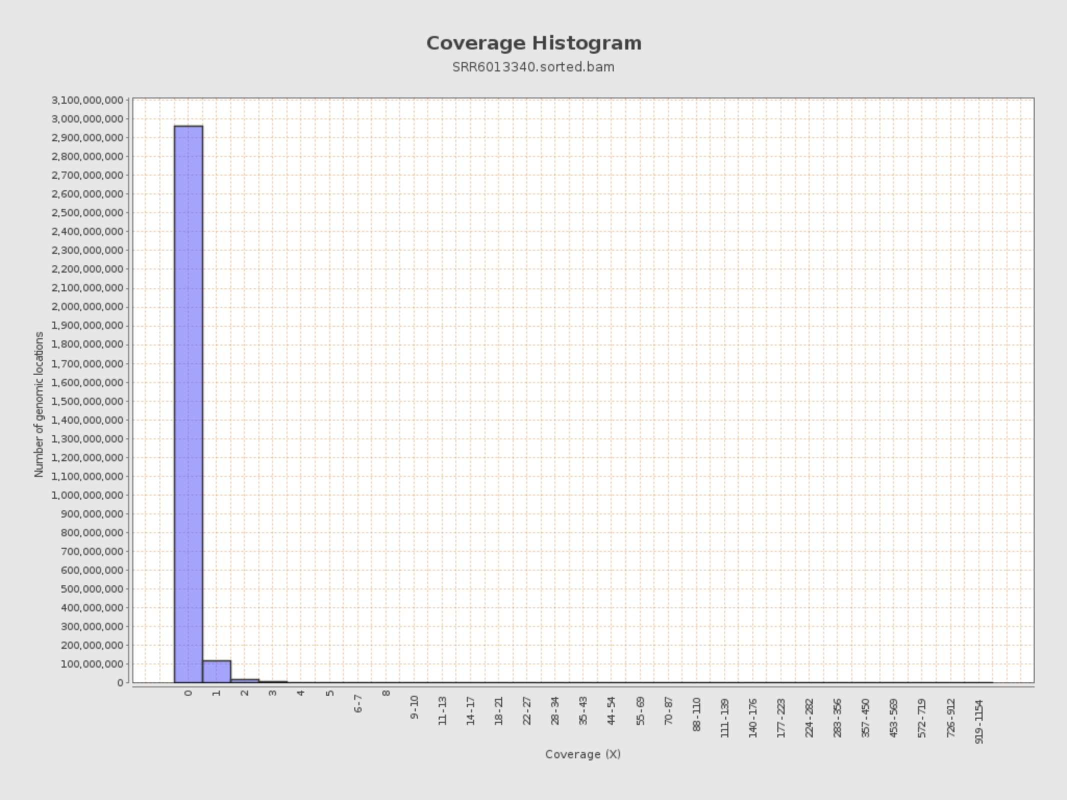
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12605557	0.0506	0.9654
chr2	243199373	16179325	0.0665	0.5095
chr3	198022430	9293459	0.0469	0.2461
chr4	191154276	10284862	0.0538	0.272
chr5	180915260	7249783	0.0401	0.2294
chr6	171115067	6318706	0.0369	0.2805
chr7	159138663	7937467	0.0499	0.7263

chr8	146364022	7443135	0.0509	0.428
chr9	141213431	5367608	0.038	0.3493
chr10	135534747	7952169	0.0587	0.4424
chr11	135006516	5406100	0.04	0.2983
chr12	133851895	8431857	0.063	0.2924
chr13	115169878	5881062	0.0511	0.261
chr14	107349540	4561912	0.0425	0.2618
chr15	102531392	4729922	0.0461	0.2442
chr16	90354753	6311229	0.0698	0.3311
chr17	81195210	5307221	0.0654	0.3369
chr18	78077248	4359063	0.0558	0.6289
chr19	59128983	3336578	0.0564	0.6942
chr20	63025520	3242540	0.0514	0.2668
chr21	48129895	2079611	0.0432	0.2532
chr22	51304566	2055068	0.0401	0.2285
chrMT	16571	238000	14.3624	8.6733
chrX	155270560	10319579	0.0665	0.3247
chrY	59373566	347102	0.0058	0.1168

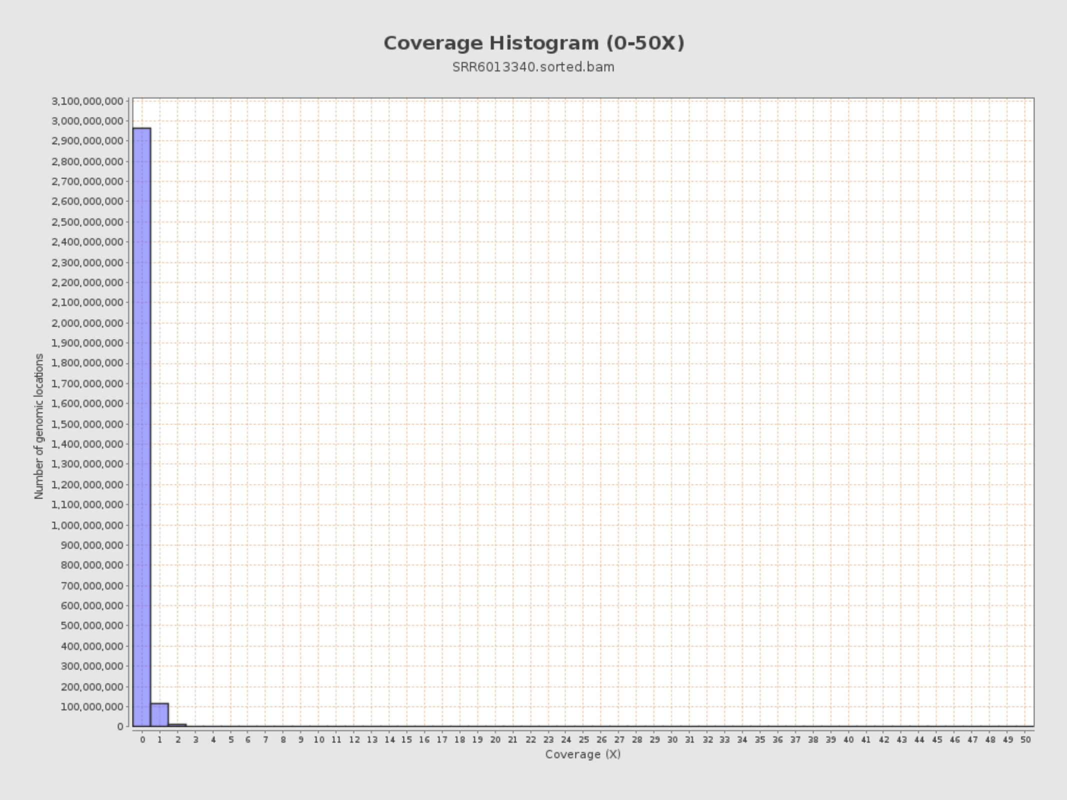
3. Results : Coverage across reference



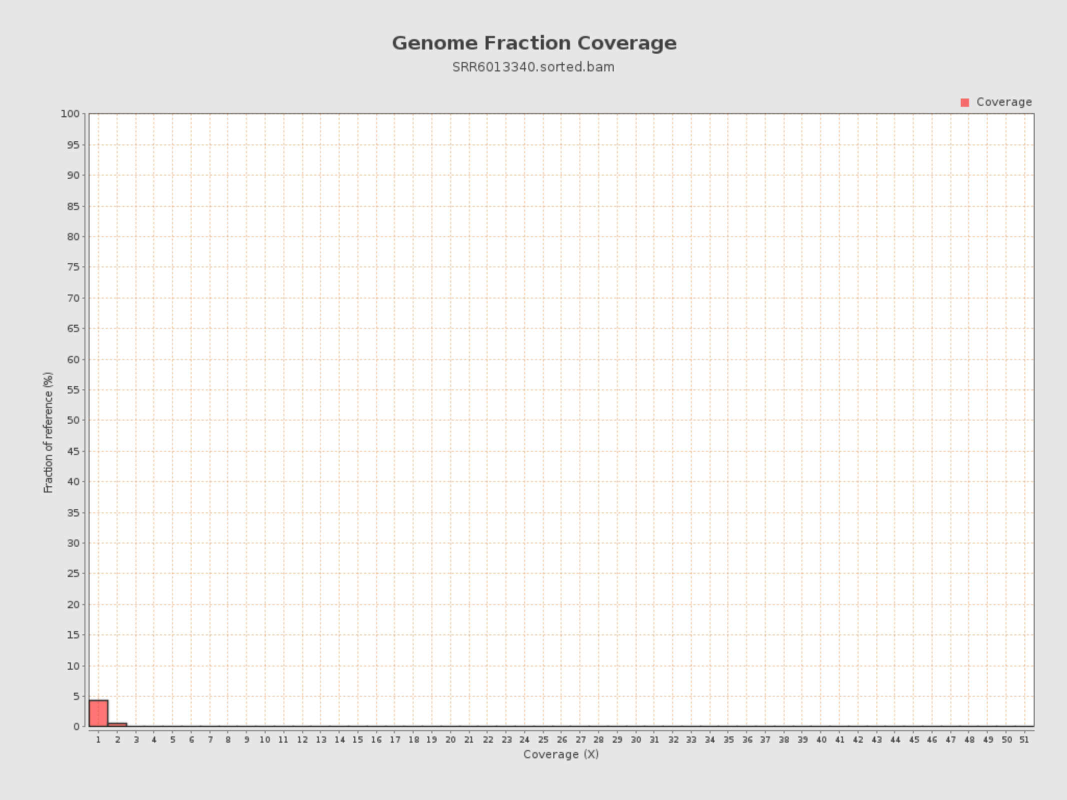
4. Results : Coverage Histogram



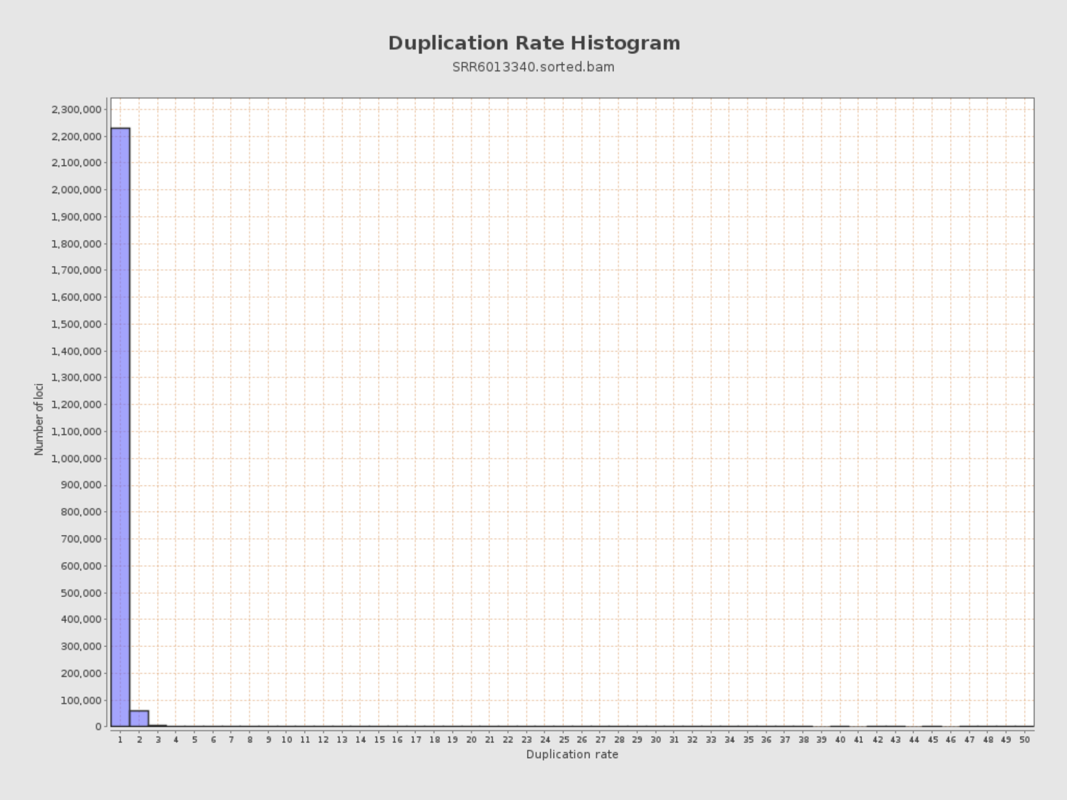
5. Results : Coverage Histogram (0-50X)



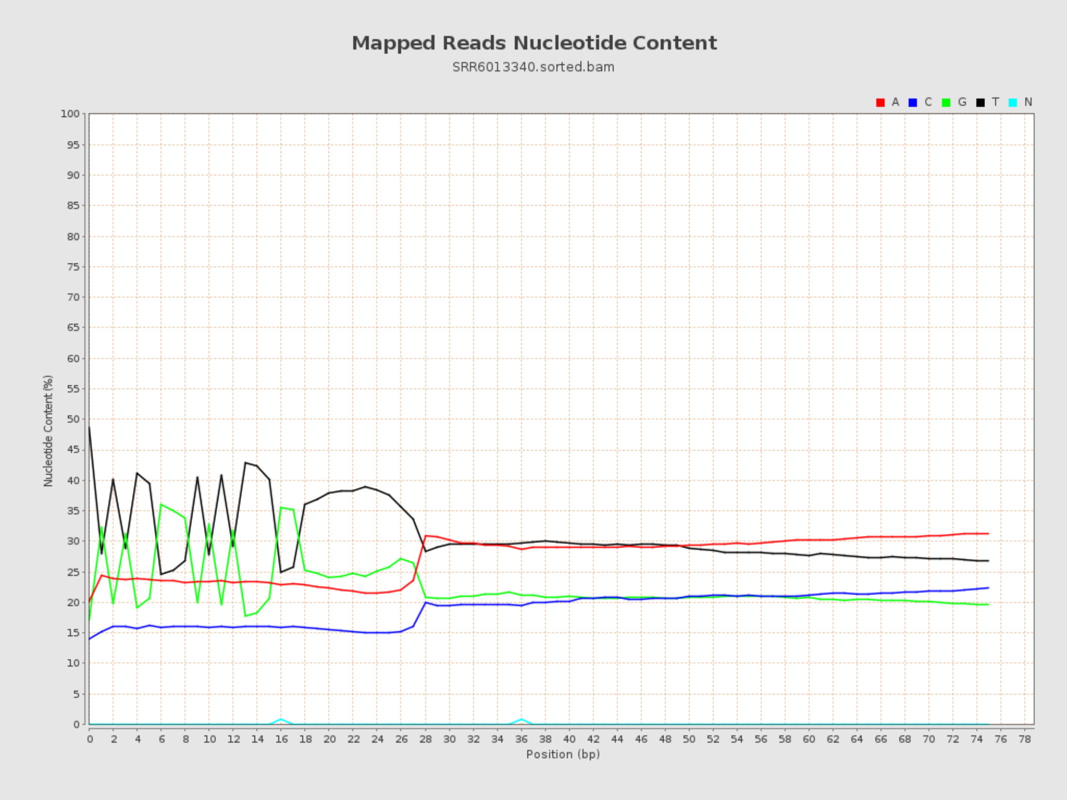
6. Results : Genome Fraction Coverage



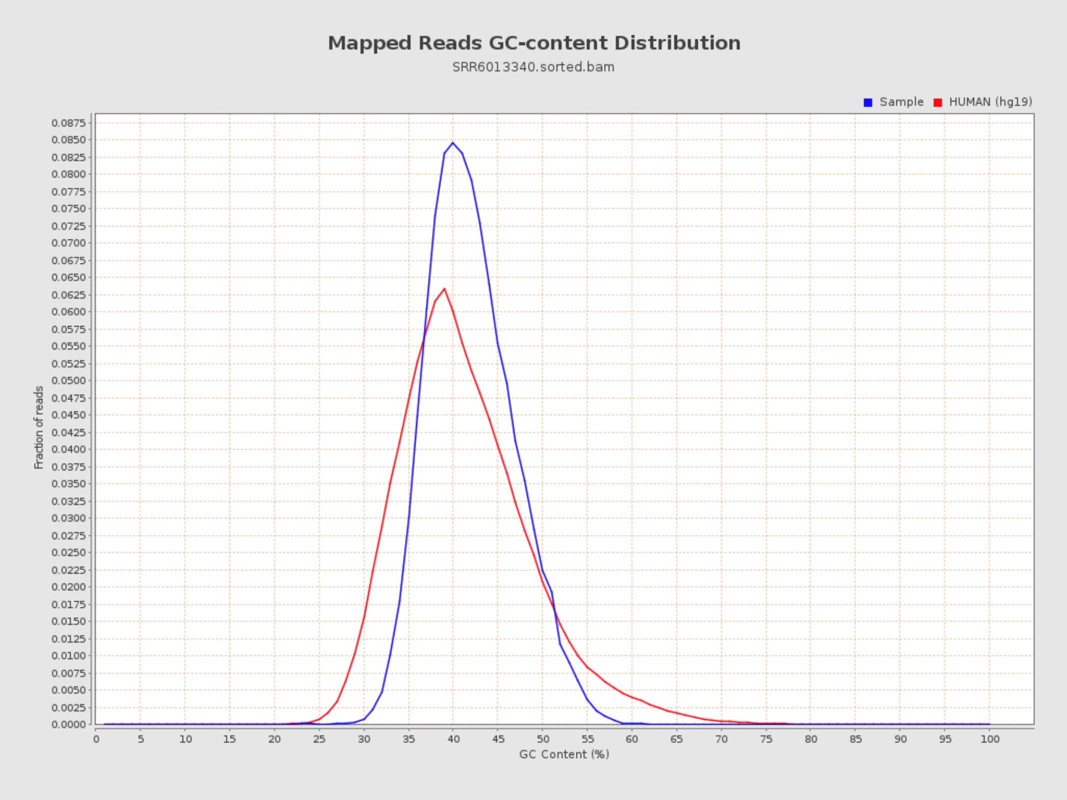
7. Results : Duplication Rate Histogram



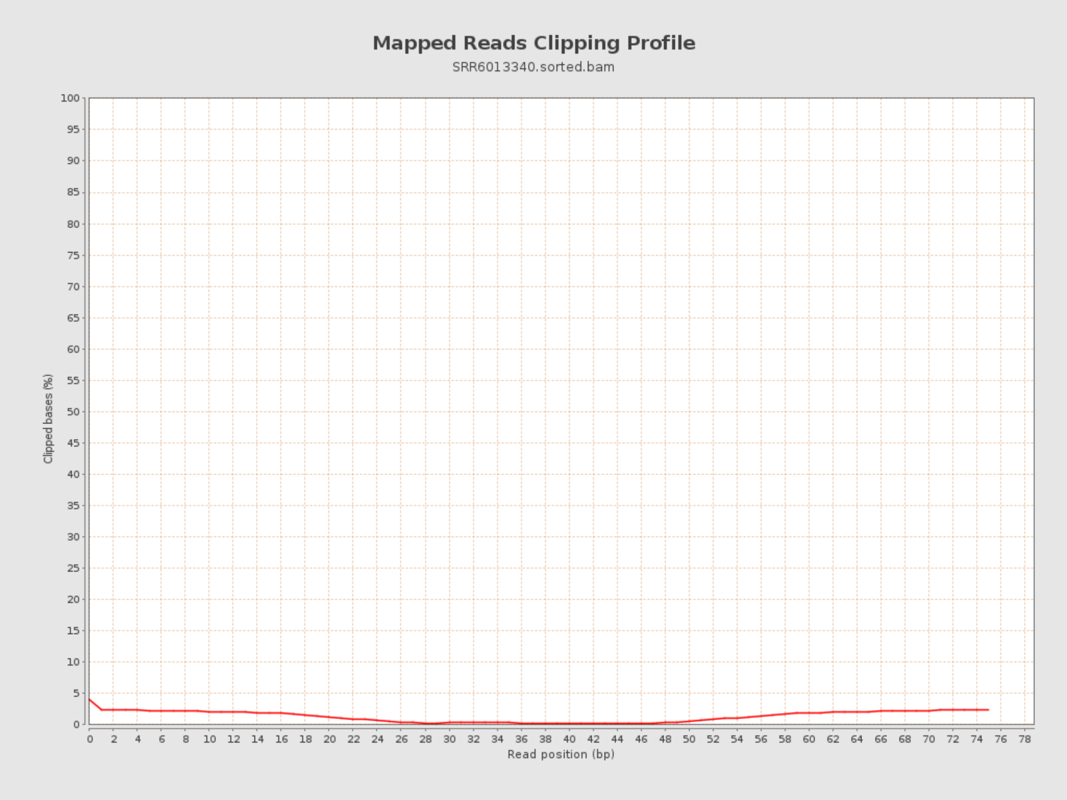
8. Results : Mapped Reads Nucleotide Content



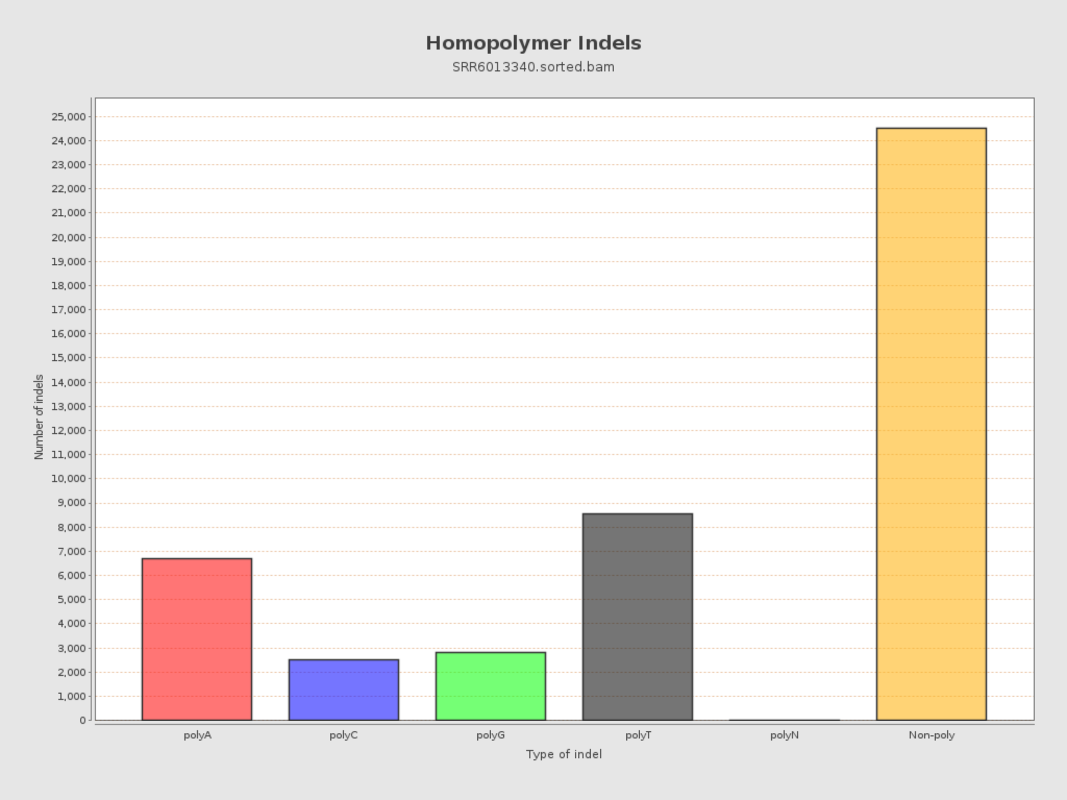
9. Results : Mapped Reads GC-content Distribution



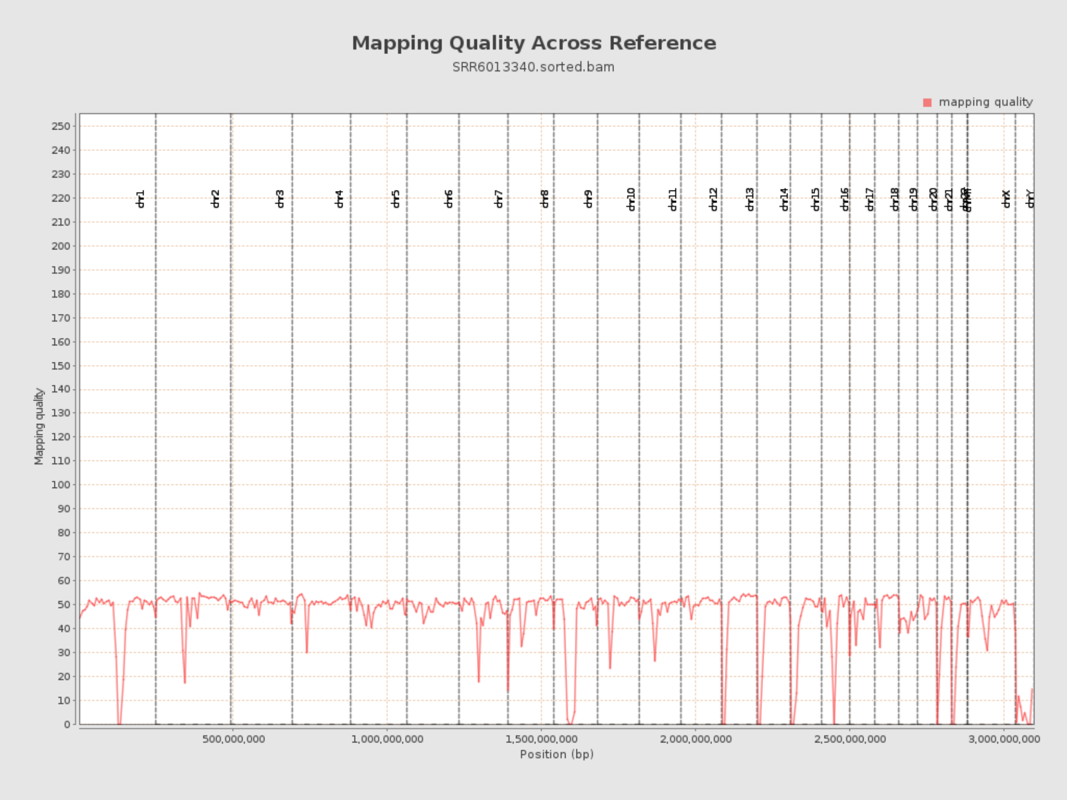
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram