Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 22:27:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013343.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_SRR6013343 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013343.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 22:27:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013343.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,223,827
Mapped reads	2,011,855 / 90.47%
Unmapped reads	211,972 / 9.53%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,639 / 0.52%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	77,188 / 3.47%
Duplication rate	2.99%
Clipped reads	889,270 / 39.99%

2.2. ACGT Content

Number/percentage of A's	36,271,308 / 27.08%
Number/percentage of C's	25,835,794 / 19.29%
Number/percentage of T's	41,131,244 / 30.71%
Number/percentage of G's	30,650,263 / 22.89%
Number/percentage of N's	32,298 / 0.02%
GC Percentage	42.18%

2.3. Coverage

Mean	0.0433

Standard Deviation	0.3601

2.4. Mapping Quality

Mean Mapping Quality	45.73

2.5. Mismatches and indels

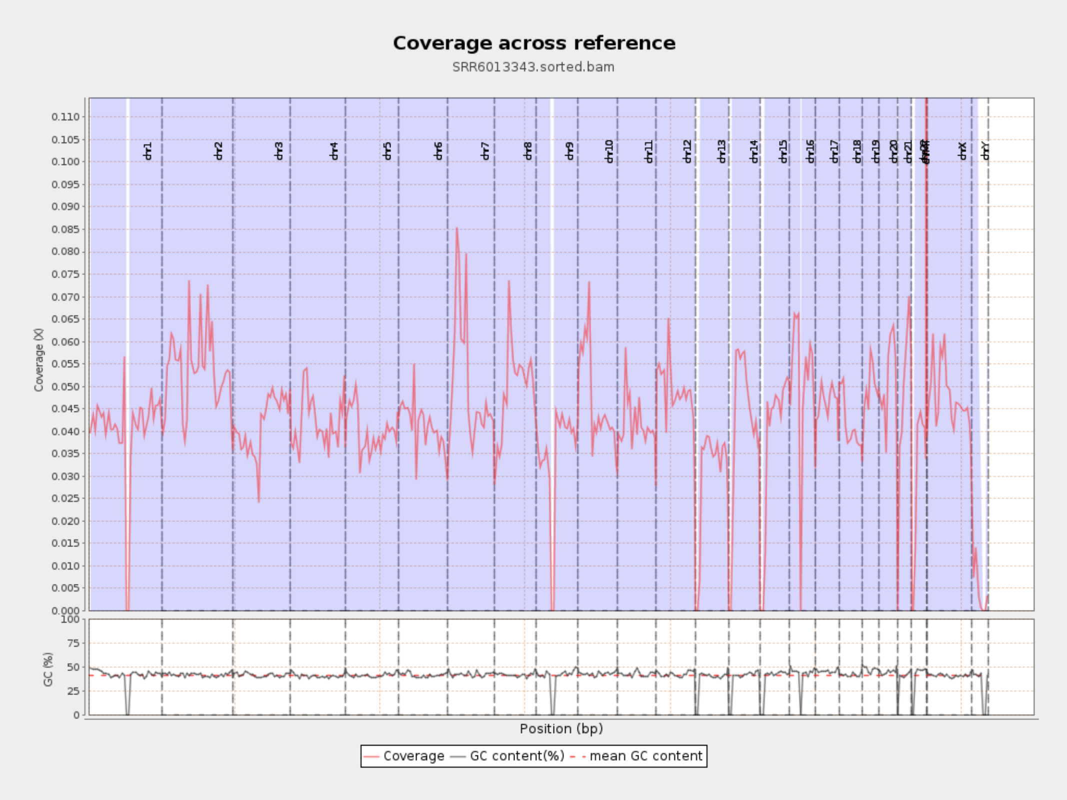
General error rate	0.81%
Mismatches	1,072,500
Insertions	8,980
Mapped reads with at least one insertion	0.44%
Deletions	36,464
Mapped reads with at least one deletion	1.79%
Homopolymer indels	45.28%

2.6. Chromosome stats

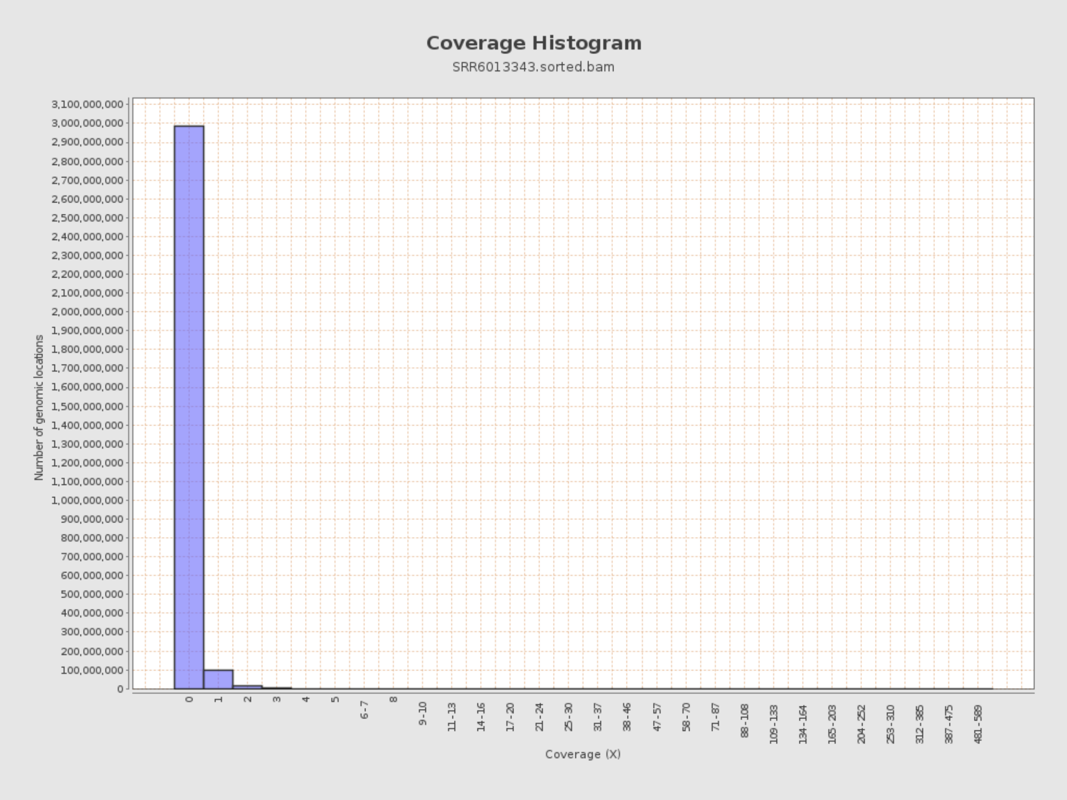
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9994303	0.0401	0.5611
chr2	243199373	13101769	0.0539	0.4356
chr3	198022430	8191676	0.0414	0.2341
chr4	191154276	8027306	0.042	0.2456
chr5	180915260	7216006	0.0399	0.232
chr6	171115067	7047707	0.0412	0.2881
chr7	159138663	8094402	0.0509	0.6079

chr8	146364022	7294013	0.0498	0.3335
chr9	141213431	4830499	0.0342	0.3018
chr10	135534747	6432896	0.0475	0.3766
chr11	135006516	5647333	0.0418	0.2805
chr12	133851895	6630685	0.0495	0.2609
chr13	115169878	3439791	0.0299	0.2011
chr14	107349540	4432654	0.0413	0.2513
chr15	102531392	3873831	0.0378	0.2249
chr16	90354753	4629097	0.0512	0.2987
chr17	81195210	3761383	0.0463	0.2722
chr18	78077248	3256388	0.0417	0.5432
chr19	59128983	2921482	0.0494	0.4657
chr20	63025520	3238093	0.0514	0.2692
chr21	48129895	2291865	0.0476	0.2682
chr22	51304566	1479175	0.0288	0.195
chrMT	16571	421073	25.4102	14.8382
chrX	155270560	7420257	0.0478	0.2748
chrY	59373566	311645	0.0052	0.1244

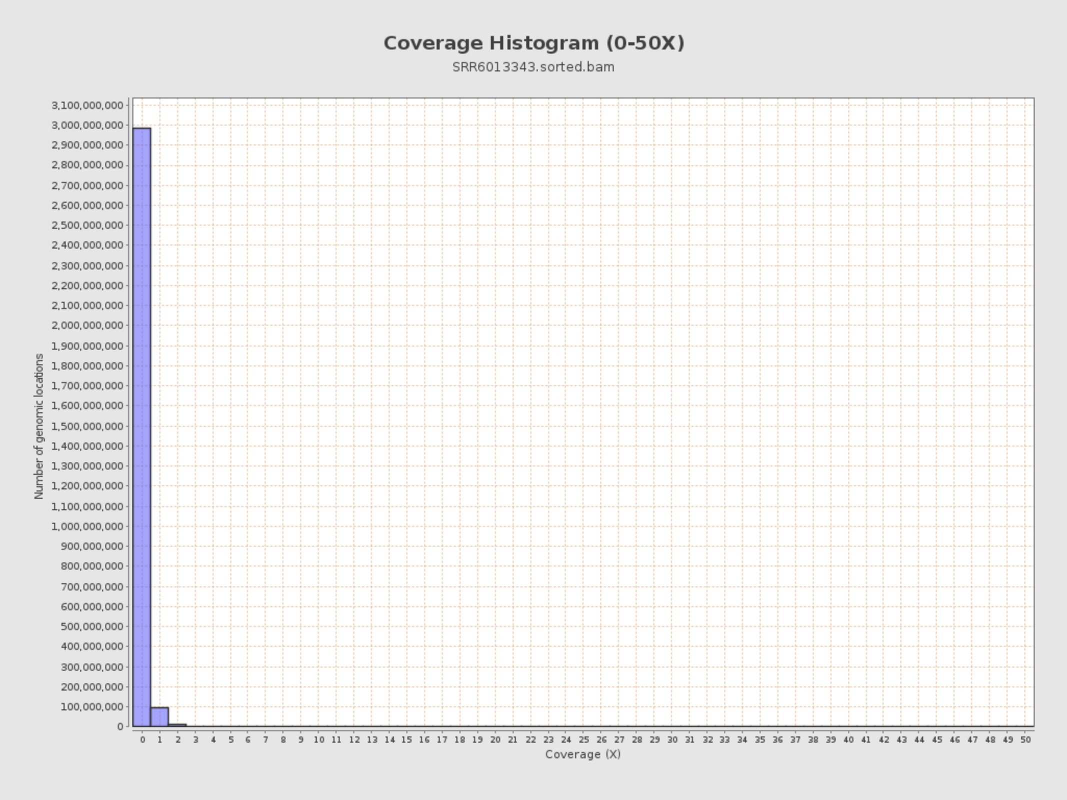
3. Results : Coverage across reference



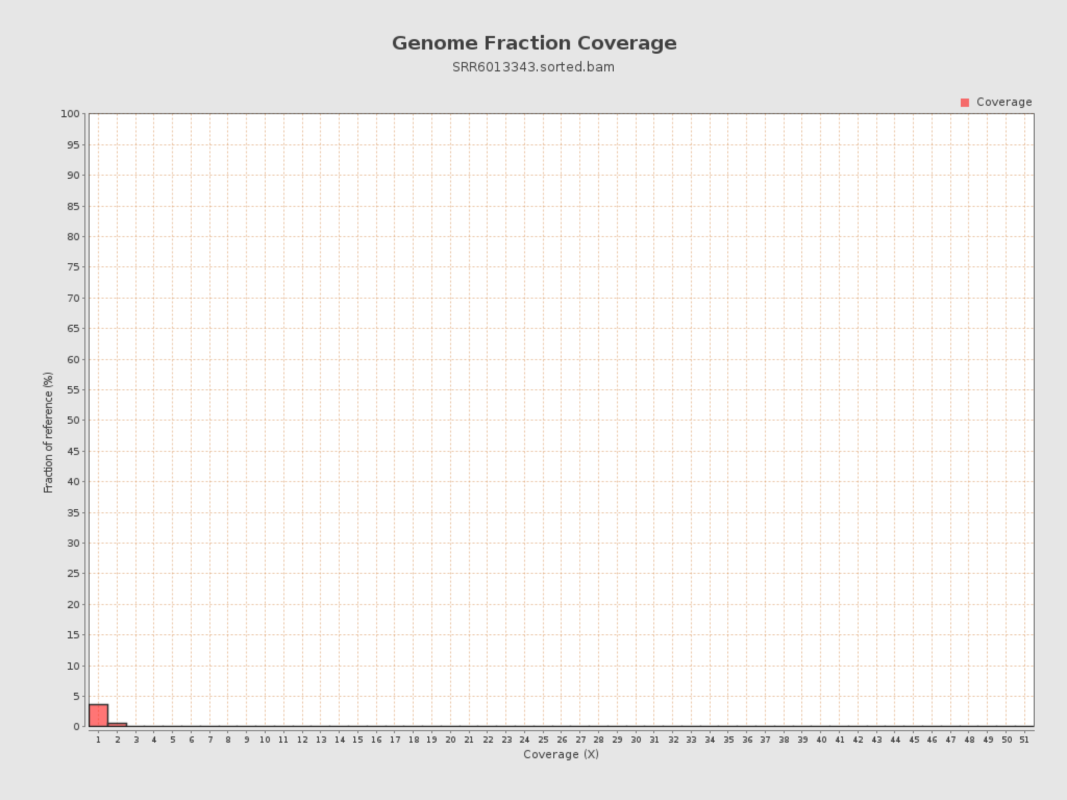
4. Results : Coverage Histogram



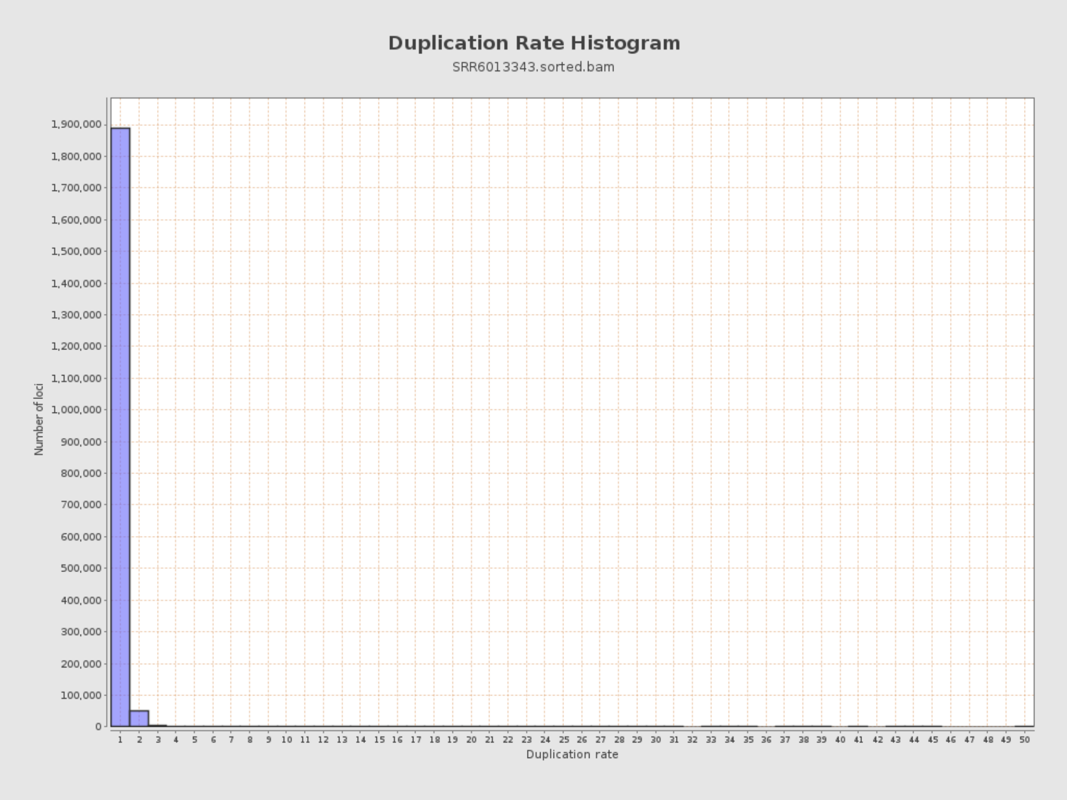
5. Results : Coverage Histogram (0-50X)



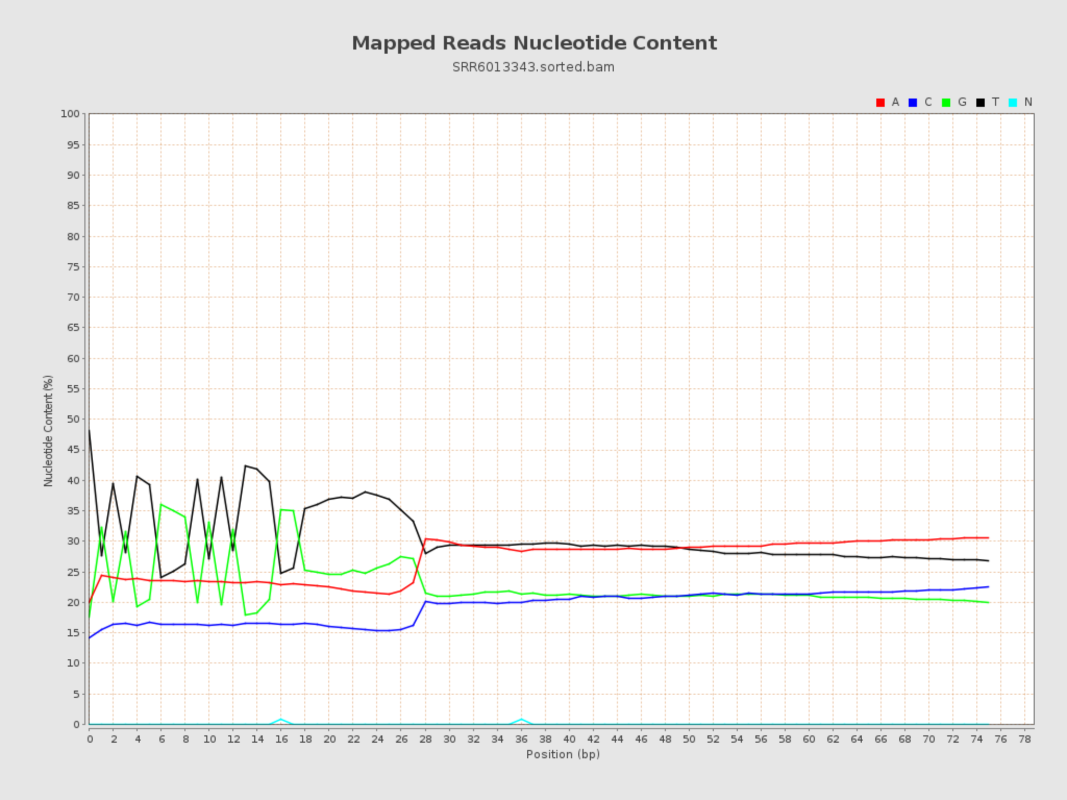
6. Results : Genome Fraction Coverage



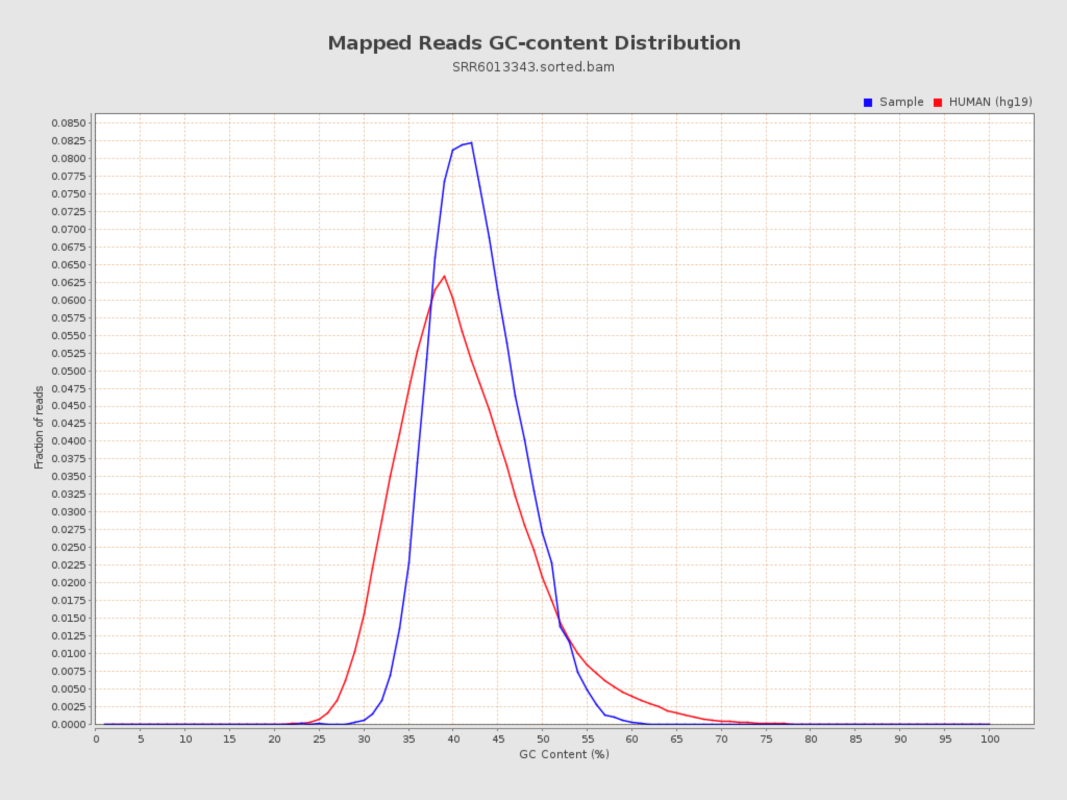
7. Results : Duplication Rate Histogram



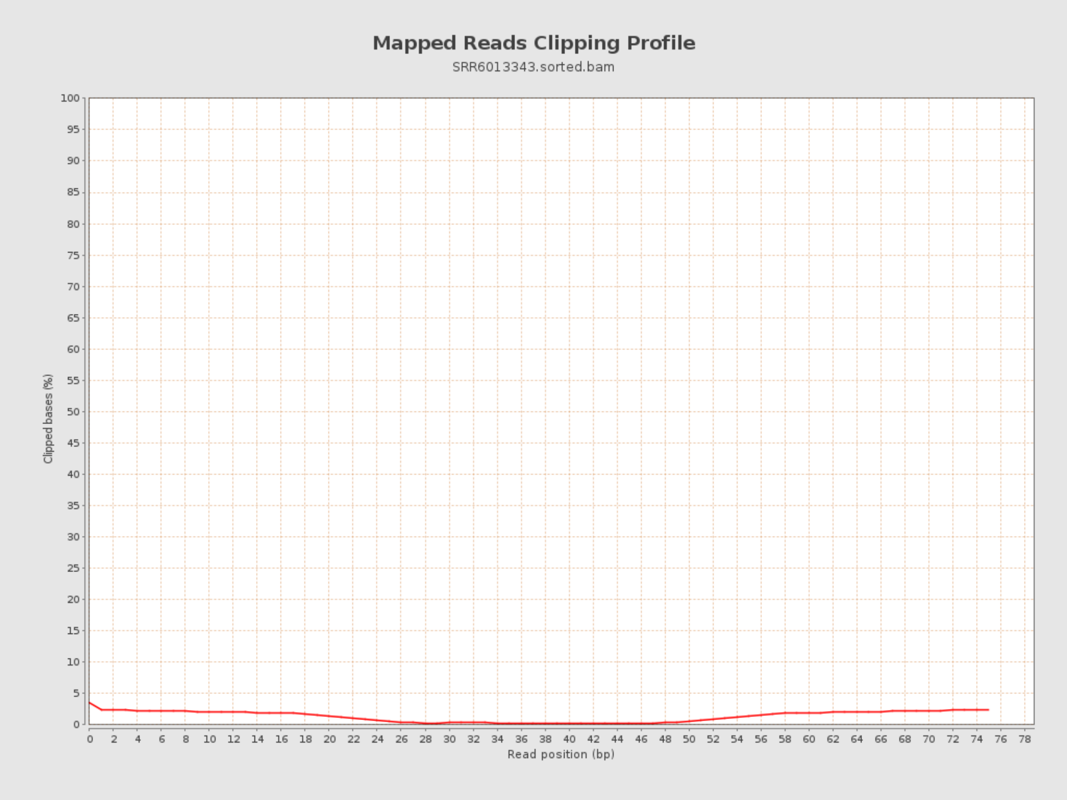
8. Results : Mapped Reads Nucleotide Content



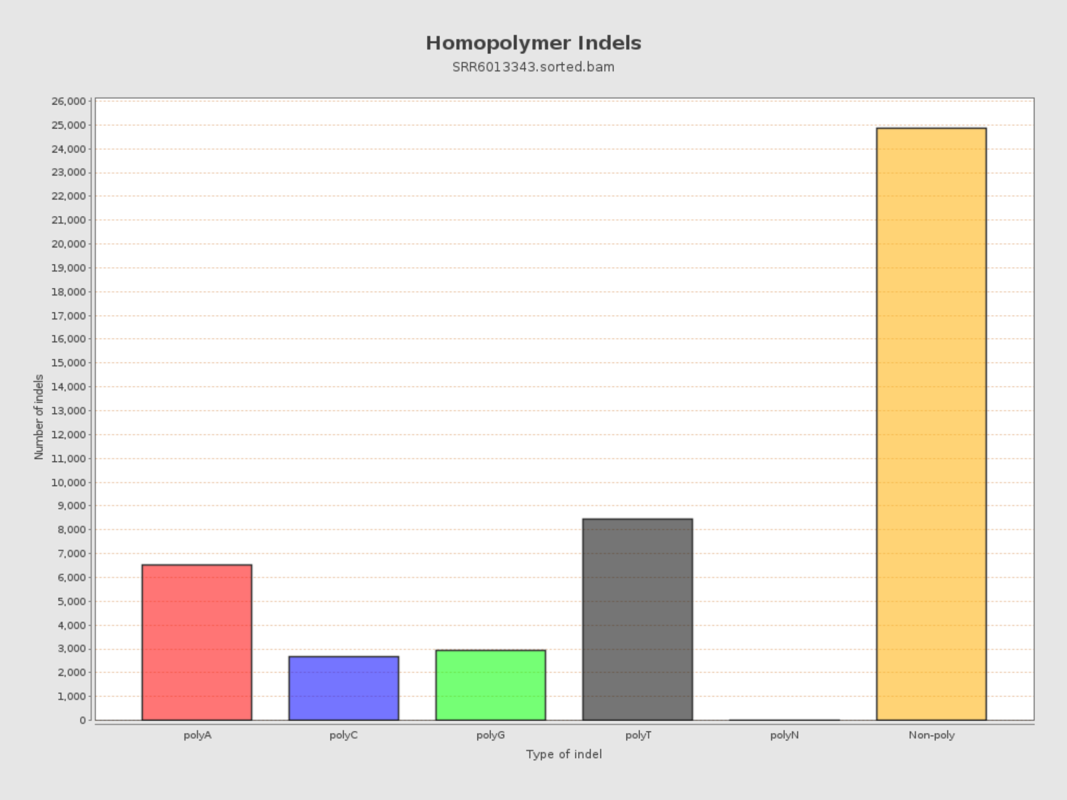
9. Results : Mapped Reads GC-content Distribution



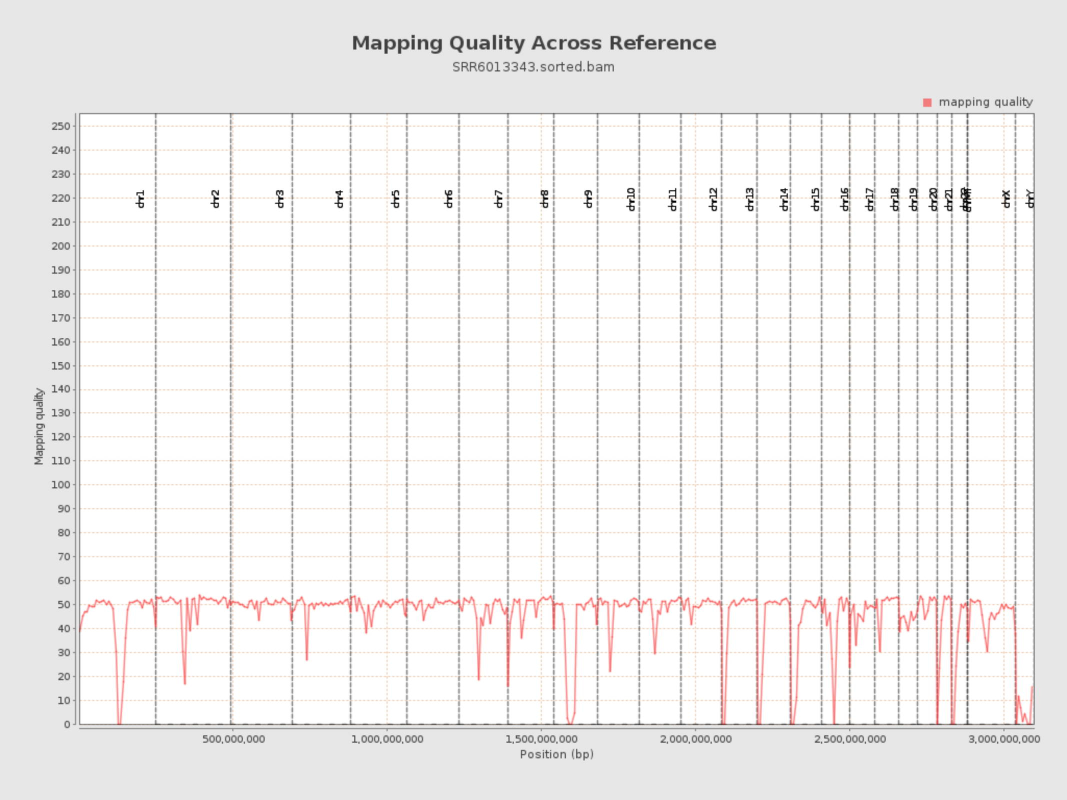
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram