Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 21:08:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013315.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_SRR6013315 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013315.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 21:08:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013315.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,439,583
Mapped reads	2,186,457 / 89.62%
Unmapped reads	253,126 / 10.38%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,314 / 0.63%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	92,836 / 3.81%
Duplication rate	3.4%
Clipped reads	1,071,027 / 43.9%

2.2. ACGT Content

Number/percentage of A's	39,193,369 / 27.33%
Number/percentage of C's	27,384,672 / 19.1%
Number/percentage of T's	44,269,427 / 30.87%
Number/percentage of G's	32,523,908 / 22.68%
Number/percentage of N's	34,938 / 0.02%
GC Percentage	41.78%

2.3. Coverage

Mean	0.0463

Standard Deviation	0.3668

2.4. Mapping Quality

Mean Mapping Quality	45.4

2.5. Mismatches and indels

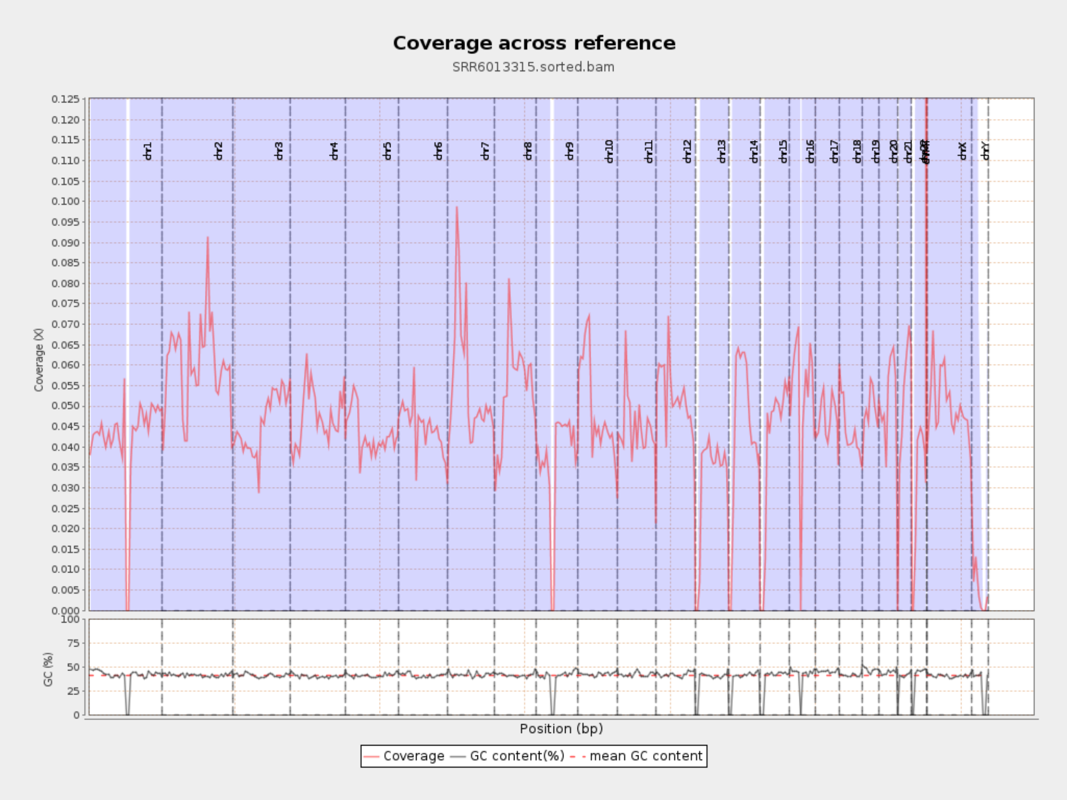
General error rate	0.79%
Mismatches	1,111,101
Insertions	9,579
Mapped reads with at least one insertion	0.43%
Deletions	33,681
Mapped reads with at least one deletion	1.53%
Homopolymer indels	45.66%

2.6. Chromosome stats

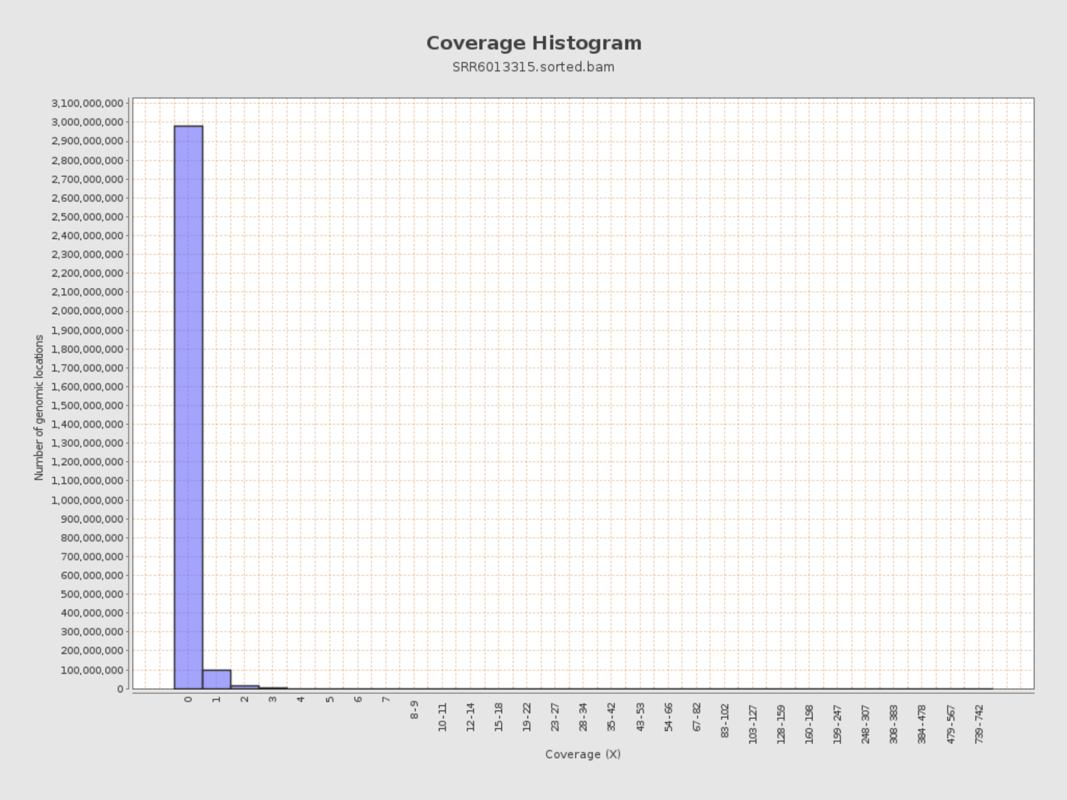
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10506152	0.0422	0.5428
chr2	243199373	14672303	0.0603	0.477
chr3	198022430	9058616	0.0457	0.2504
chr4	191154276	9035357	0.0473	0.2618
chr5	180915260	7803234	0.0431	0.2453
chr6	171115067	7669895	0.0448	0.303
chr7	159138663	8893971	0.0559	0.6111

chr8	146364022	7929799	0.0542	0.397
chr9	141213431	5148925	0.0365	0.3
chr10	135534747	6782036	0.05	0.3917
chr11	135006516	6050018	0.0448	0.283
chr12	133851895	7028345	0.0525	0.2741
chr13	115169878	3617584	0.0314	0.2106
chr14	107349540	4702966	0.0438	0.2582
chr15	102531392	4119868	0.0402	0.2397
chr16	90354753	4752911	0.0526	0.2904
chr17	81195210	3784449	0.0466	0.2799
chr18	78077248	3455792	0.0443	0.5156
chr19	59128983	2909508	0.0492	0.4529
chr20	63025520	3263235	0.0518	0.2727
chr21	48129895	2381870	0.0495	0.2708
chr22	51304566	1483401	0.0289	0.1995
chrMT	16571	346575	20.9145	13.6447
chrX	155270560	7757457	0.05	0.2816
chrY	59373566	310876	0.0052	0.1076

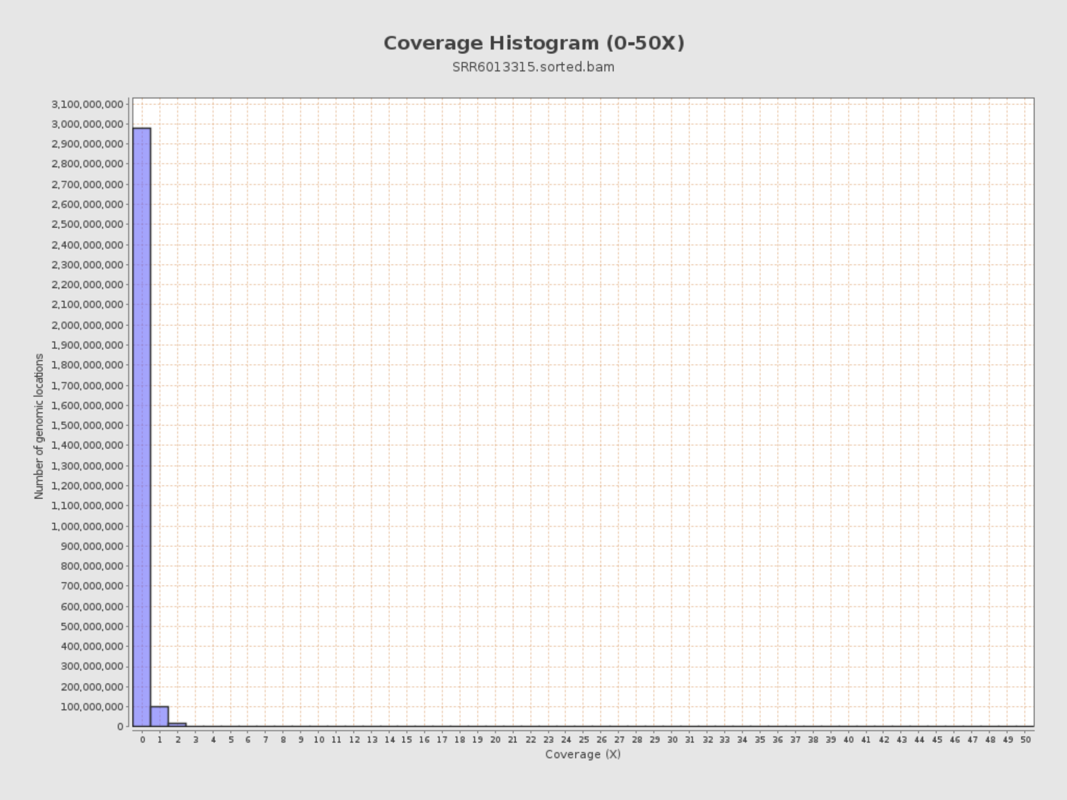
3. Results : Coverage across reference



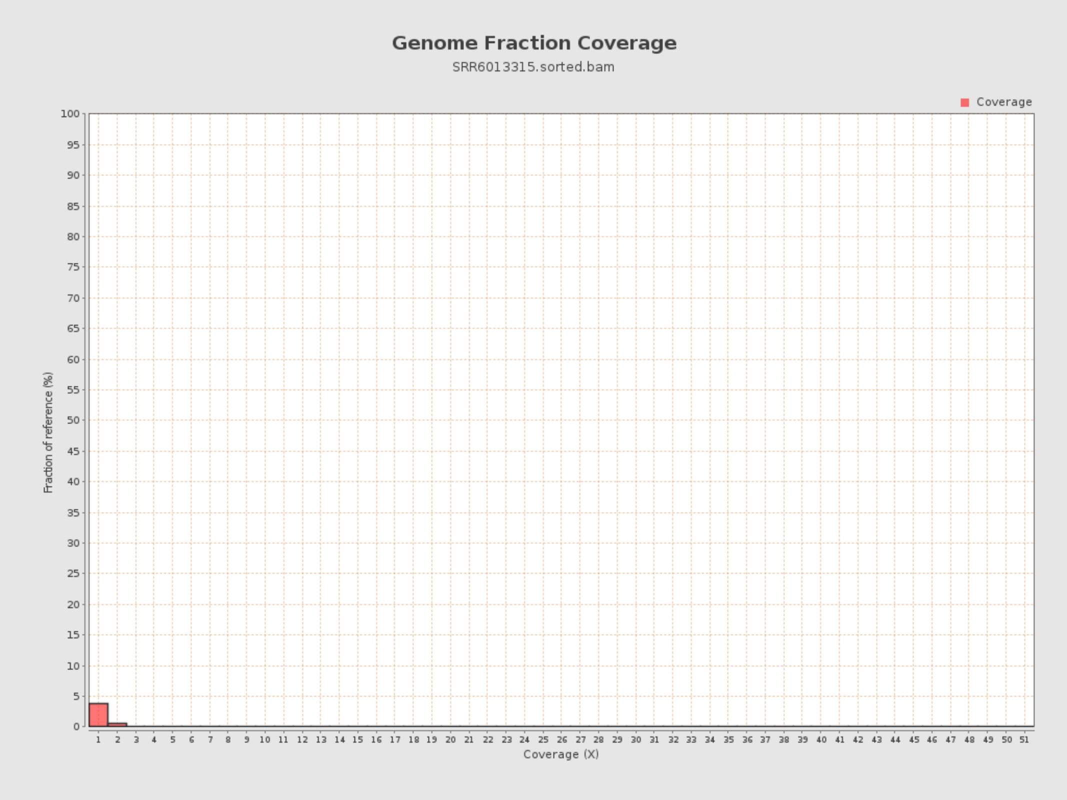
4. Results : Coverage Histogram



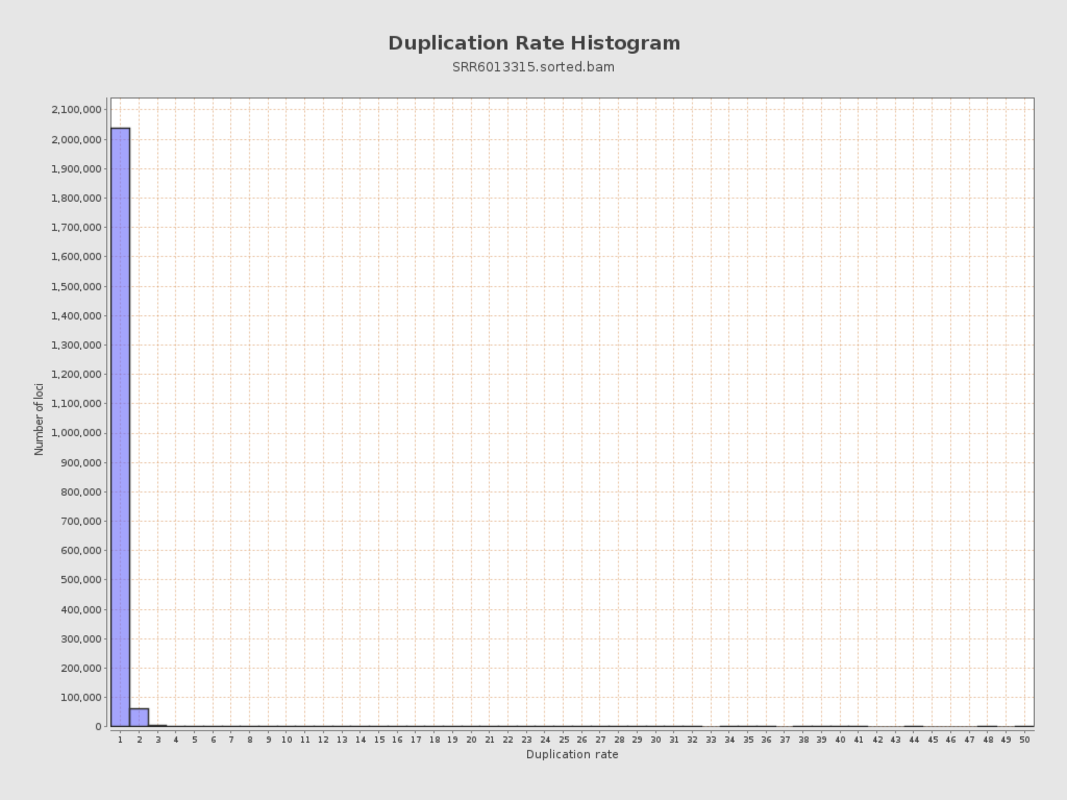
5. Results : Coverage Histogram (0-50X)



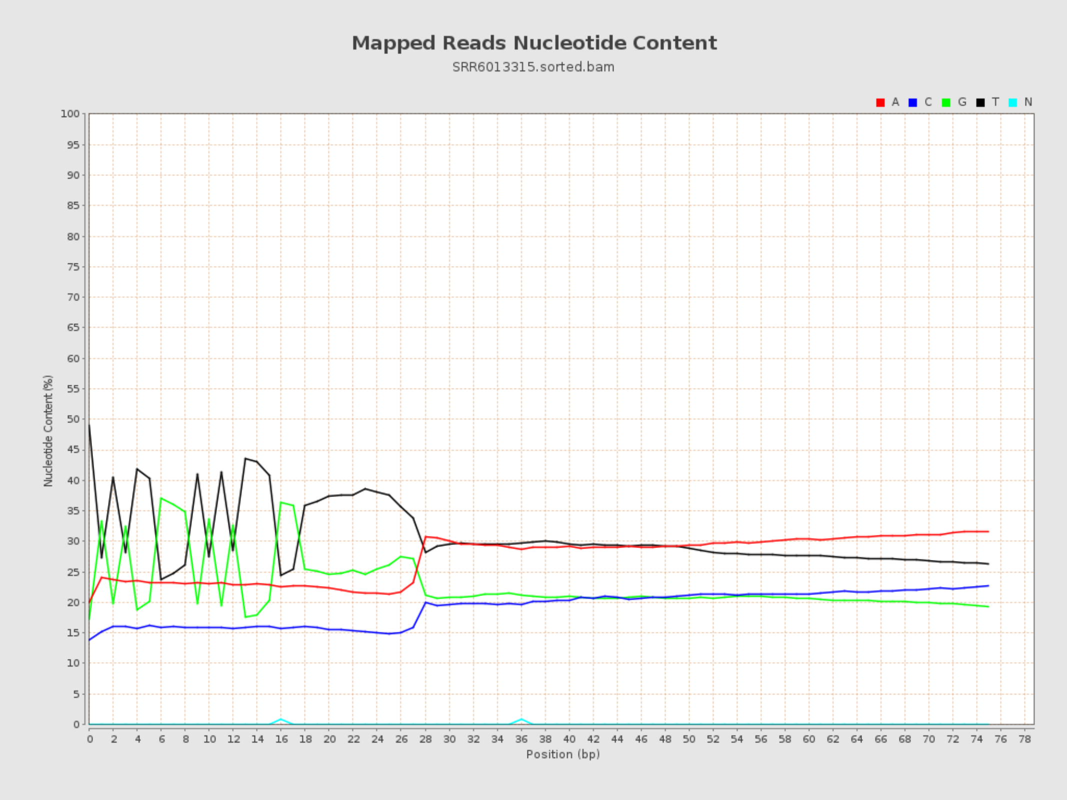
6. Results : Genome Fraction Coverage



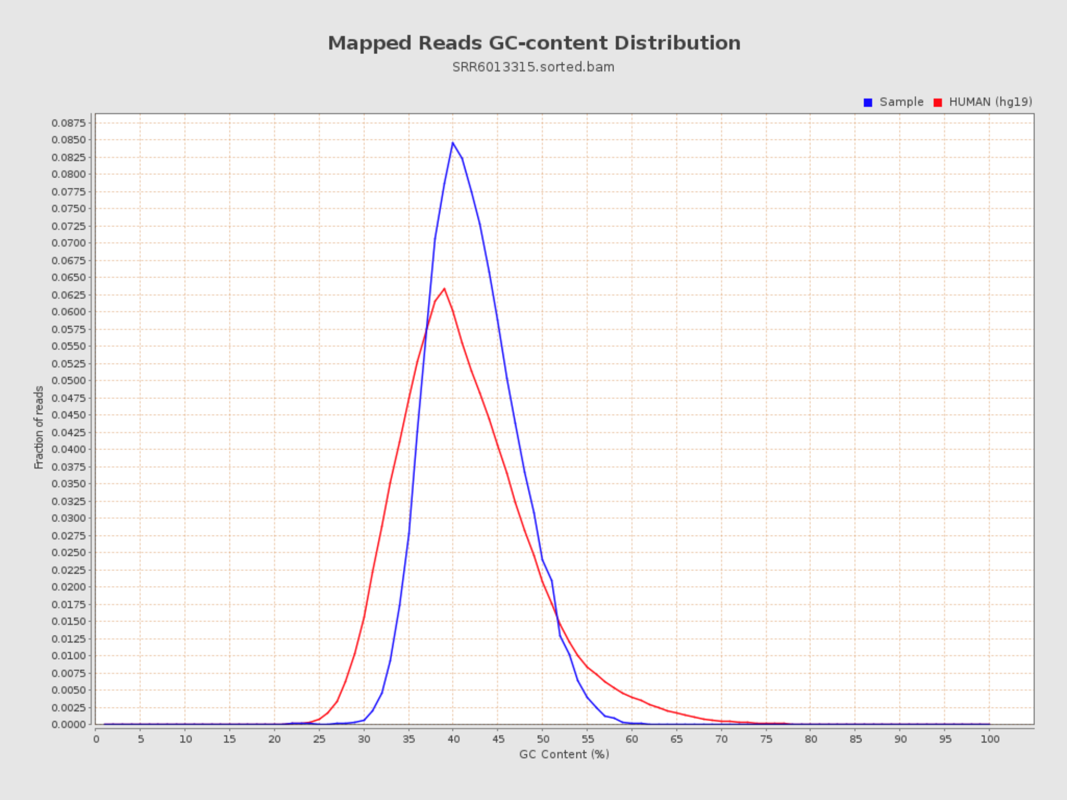
7. Results : Duplication Rate Histogram



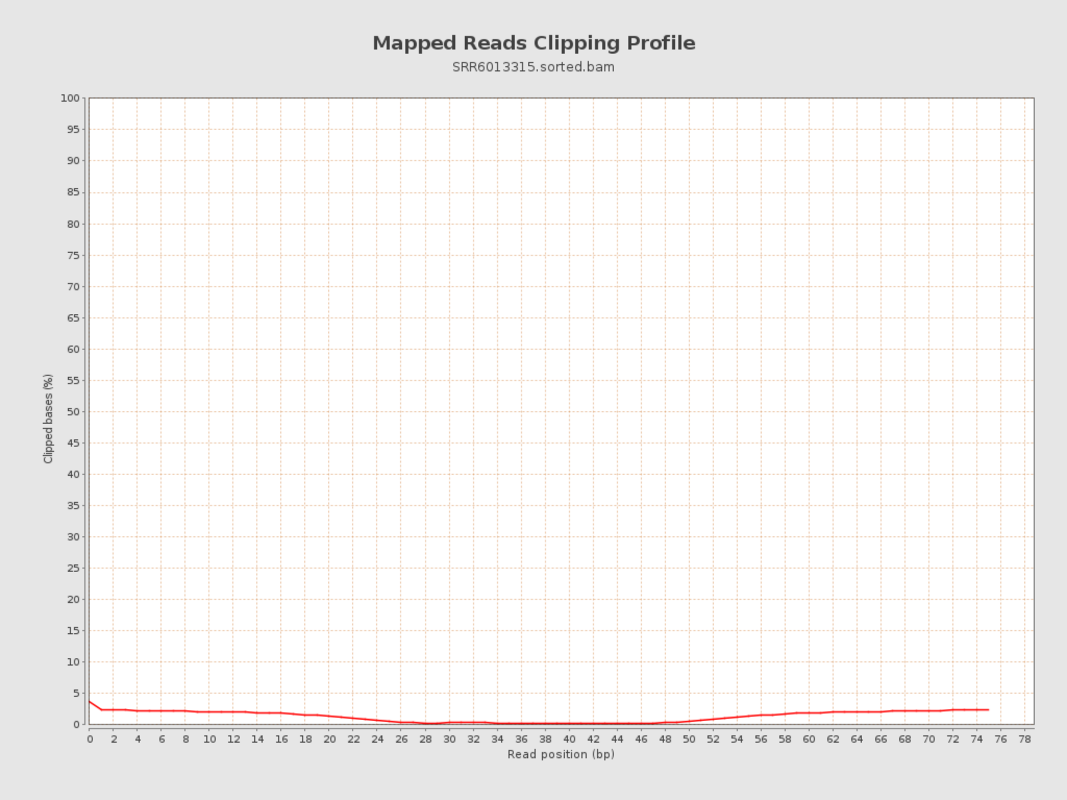
8. Results : Mapped Reads Nucleotide Content



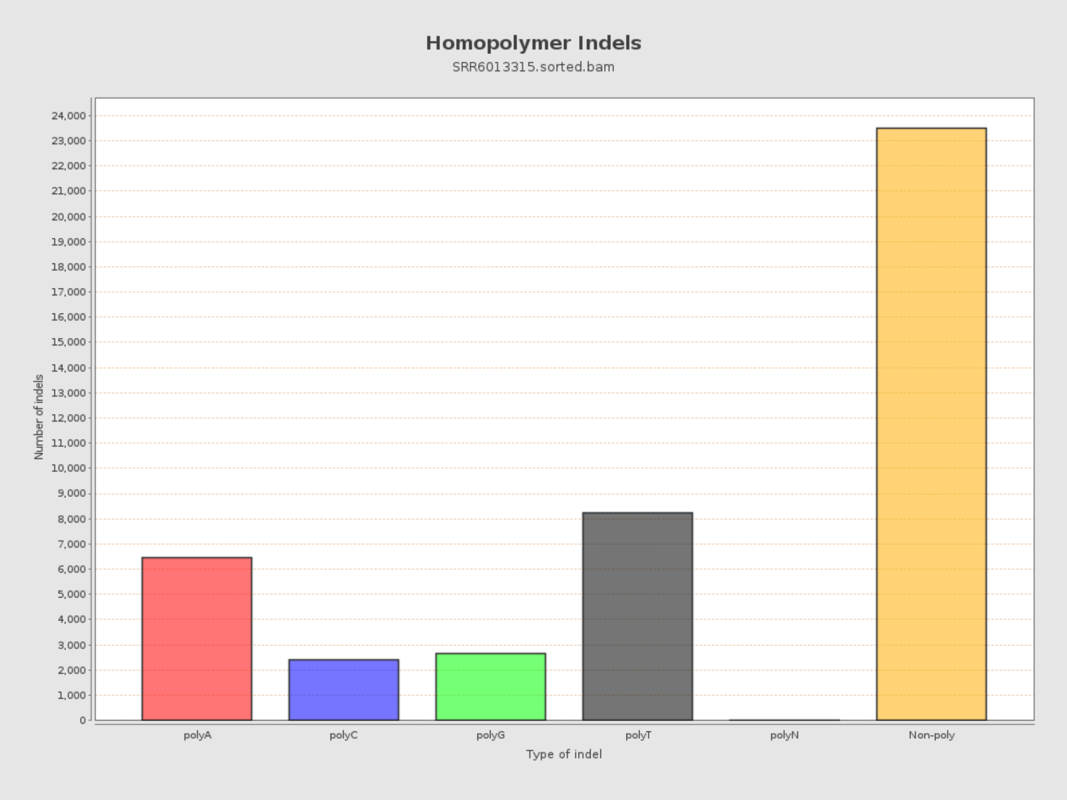
9. Results : Mapped Reads GC-content Distribution



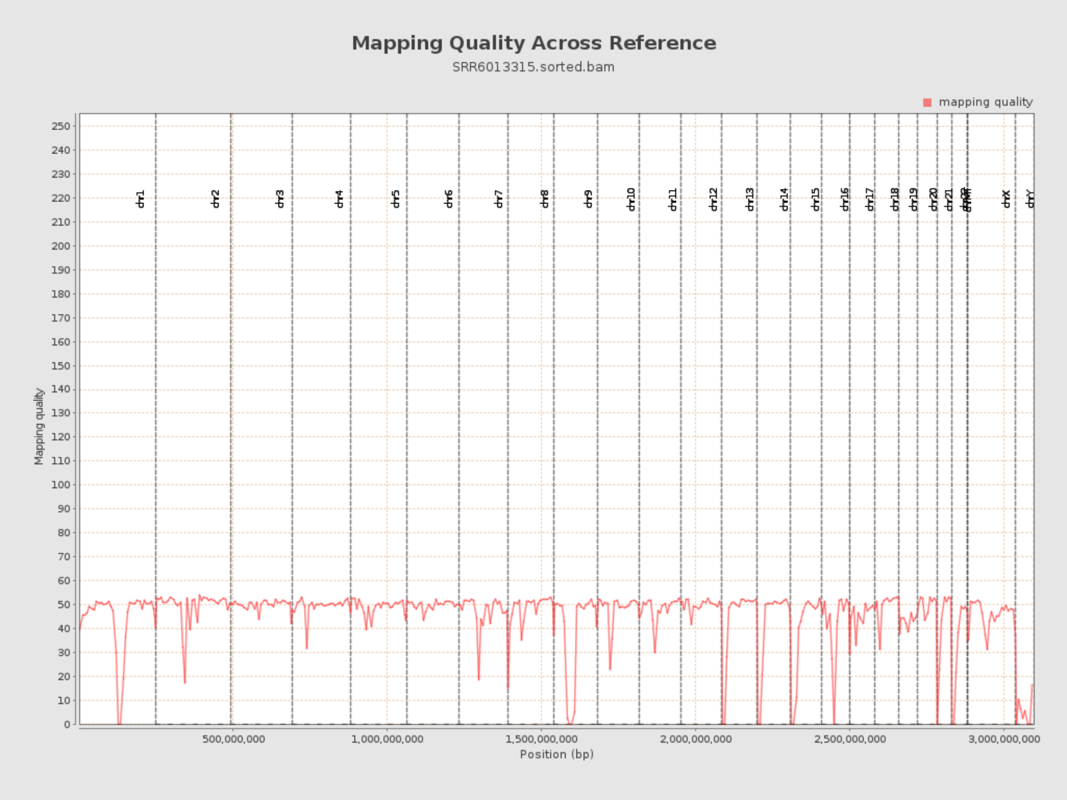
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram