Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 17:26:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013237.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_SRR6013237 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013237.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 17:26:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013237.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,827,707
Mapped reads	1,651,121 / 90.34%
Unmapped reads	176,586 / 9.66%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,939 / 0.49%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	66,608 / 3.64%
Duplication rate	2.66%
Clipped reads	701,319 / 38.37%

2.2. ACGT Content

Number/percentage of A's	31,253,052 / 28.18%
Number/percentage of C's	20,283,341 / 18.29%
Number/percentage of T's	35,104,361 / 31.66%
Number/percentage of G's	24,225,344 / 21.85%
Number/percentage of N's	24,524 / 0.02%
GC Percentage	40.14%

2.3. Coverage

Mean	0.0358

Standard Deviation	0.4366

2.4. Mapping Quality

Mean Mapping Quality	44.98

2.5. Mismatches and indels

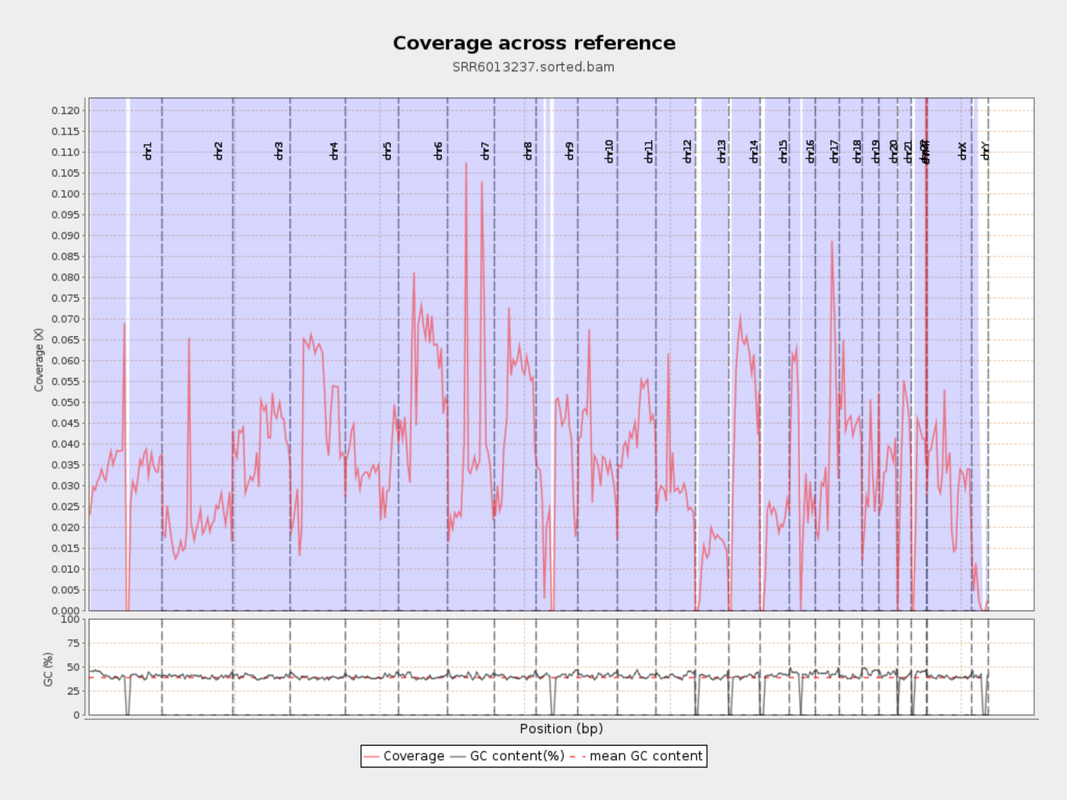
General error rate	0.84%
Mismatches	912,113
Insertions	8,662
Mapped reads with at least one insertion	0.52%
Deletions	27,742
Mapped reads with at least one deletion	1.66%
Homopolymer indels	45.99%

2.6. Chromosome stats

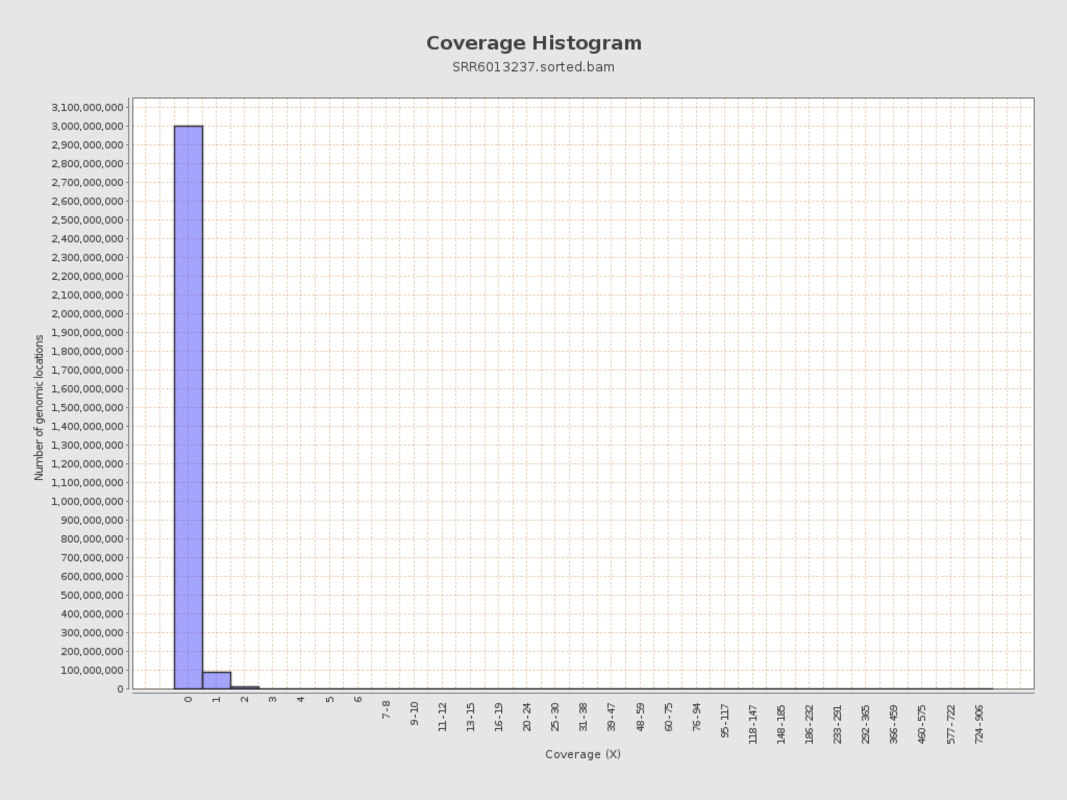
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8149799	0.0327	0.7005
chr2	243199373	5256180	0.0216	0.4711
chr3	198022430	8127819	0.041	0.221
chr4	191154276	8862129	0.0464	0.2503
chr5	180915260	6251142	0.0346	0.2046
chr6	171115067	9802429	0.0573	0.3691
chr7	159138663	6296164	0.0396	0.9952

chr8	146364022	7259983	0.0496	0.4931
chr9	141213431	4412482	0.0312	0.3797
chr10	135534747	5204433	0.0384	0.3939
chr11	135006516	5948415	0.0441	0.3124
chr12	133851895	4000893	0.0299	0.1961
chr13	115169878	1515052	0.0132	0.1244
chr14	107349540	5395092	0.0503	0.2781
chr15	102531392	1914039	0.0187	0.1486
chr16	90354753	3174184	0.0351	0.2465
chr17	81195210	3174010	0.0391	0.2288
chr18	78077248	3686042	0.0472	0.8157
chr19	59128983	1789013	0.0303	0.5437
chr20	63025520	2119614	0.0336	0.2087
chr21	48129895	1830133	0.038	0.2287
chr22	51304566	1527129	0.0298	0.1886
chrMT	16571	28309	1.7083	1.7268
chrX	155270560	4998552	0.0322	0.2318
chrY	59373566	215518	0.0036	0.1163

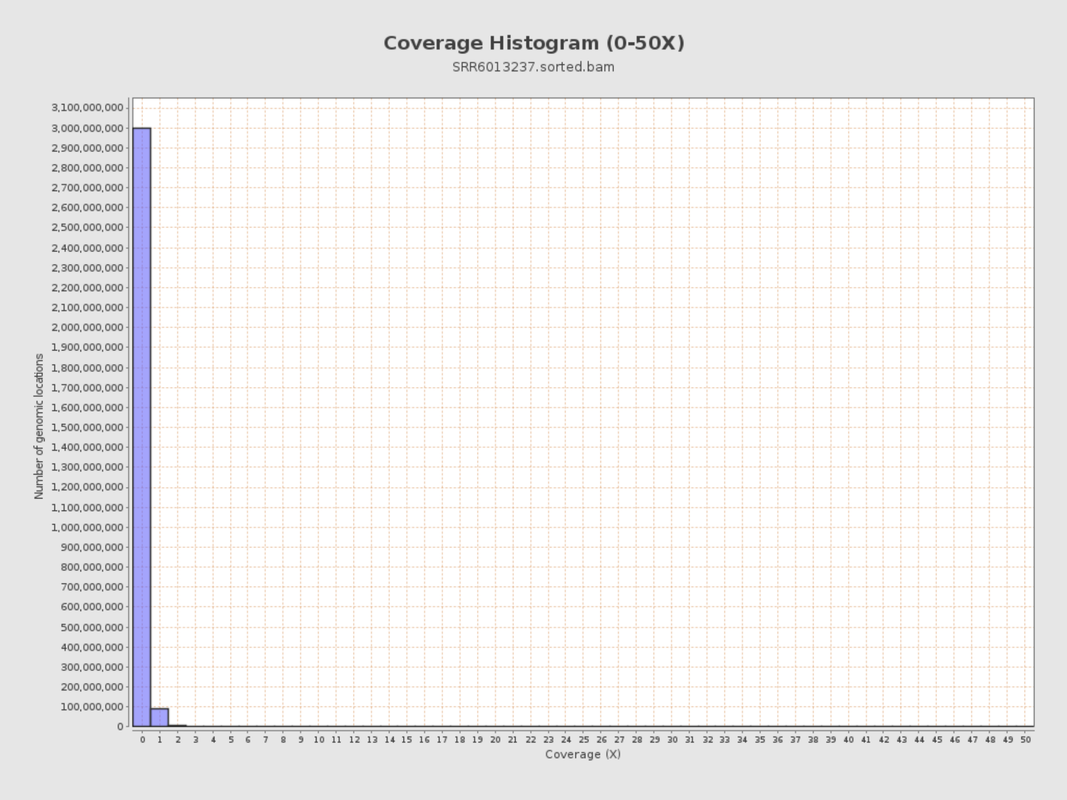
3. Results : Coverage across reference



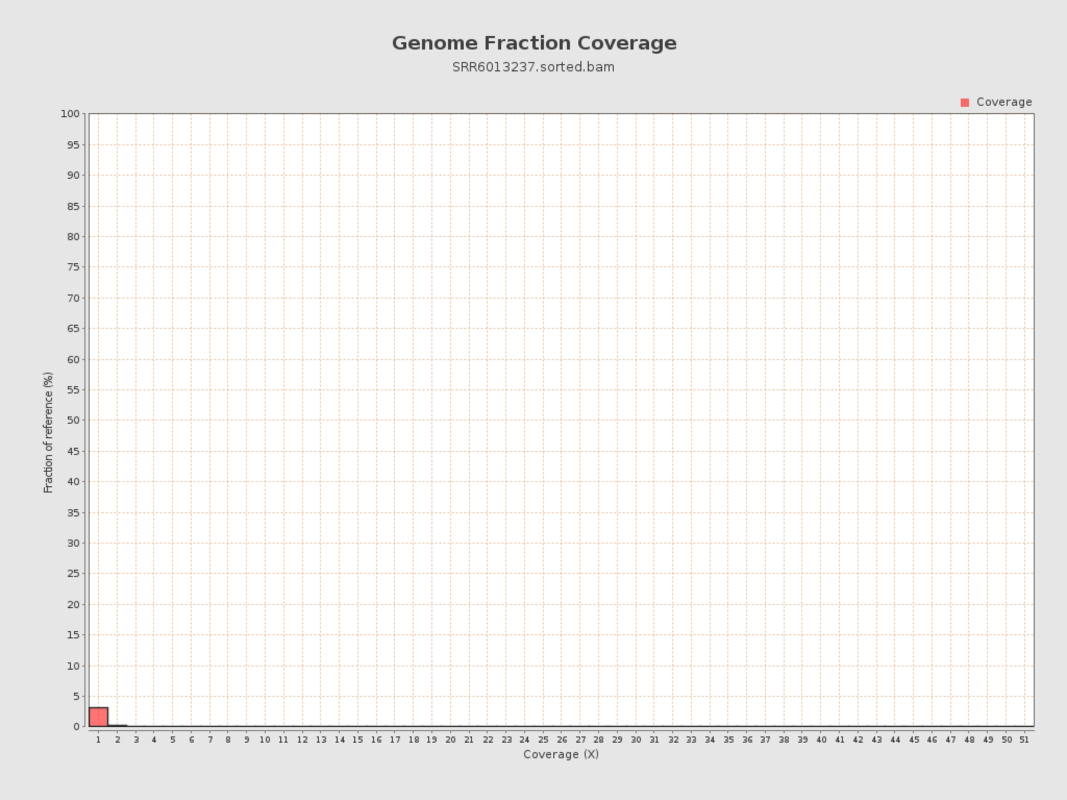
4. Results : Coverage Histogram



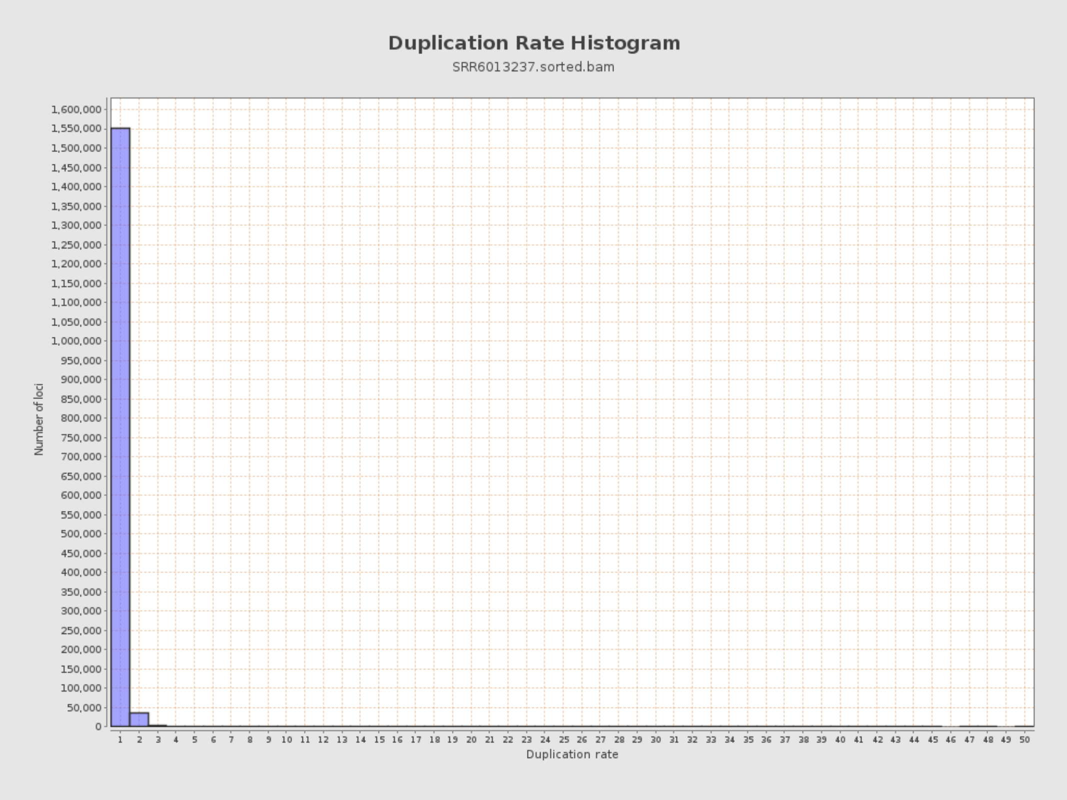
5. Results : Coverage Histogram (0-50X)



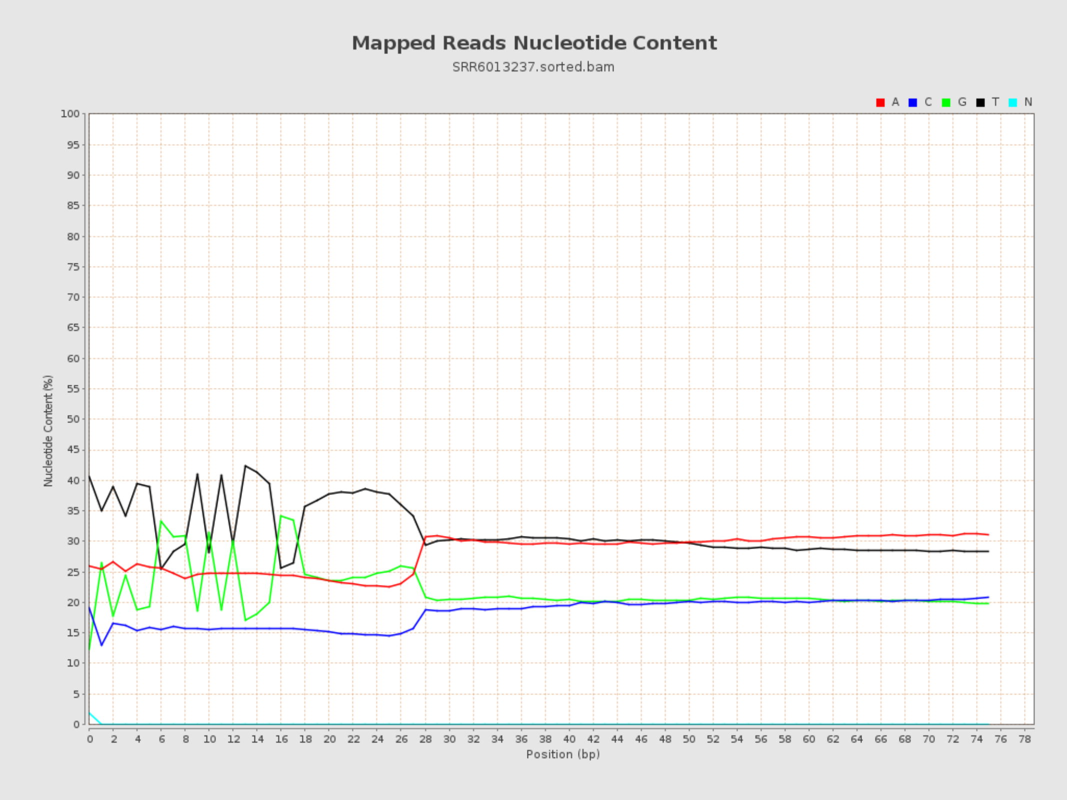
6. Results : Genome Fraction Coverage



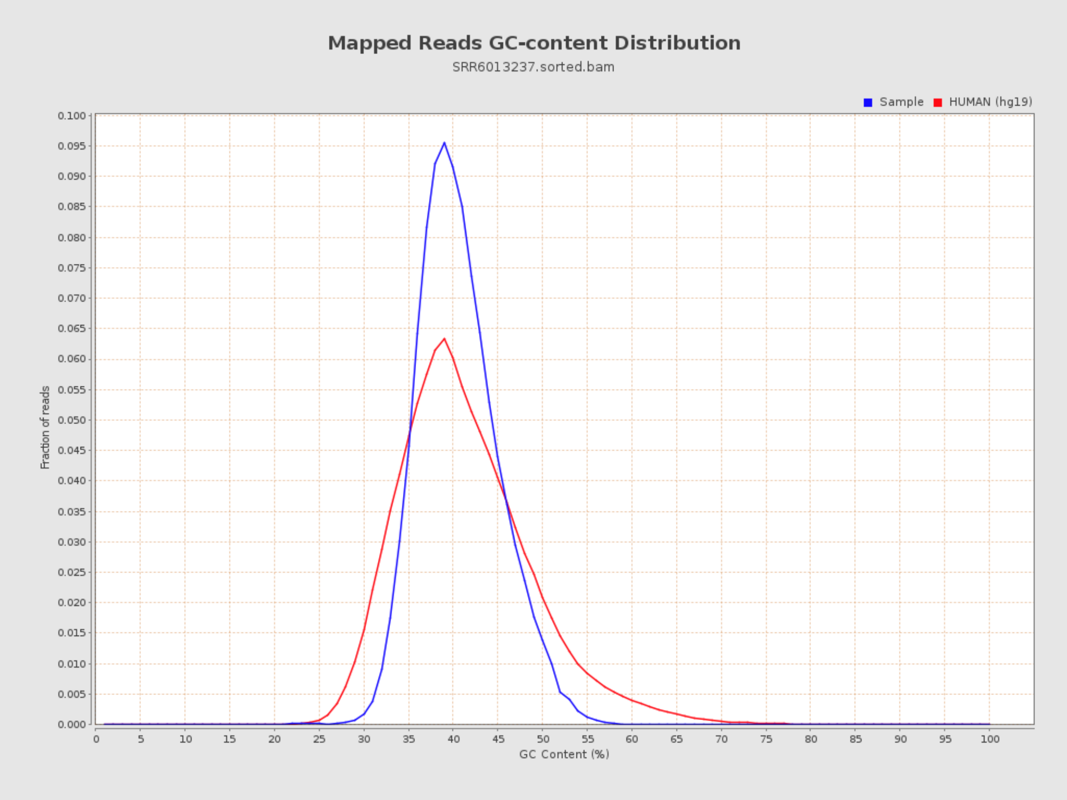
7. Results : Duplication Rate Histogram



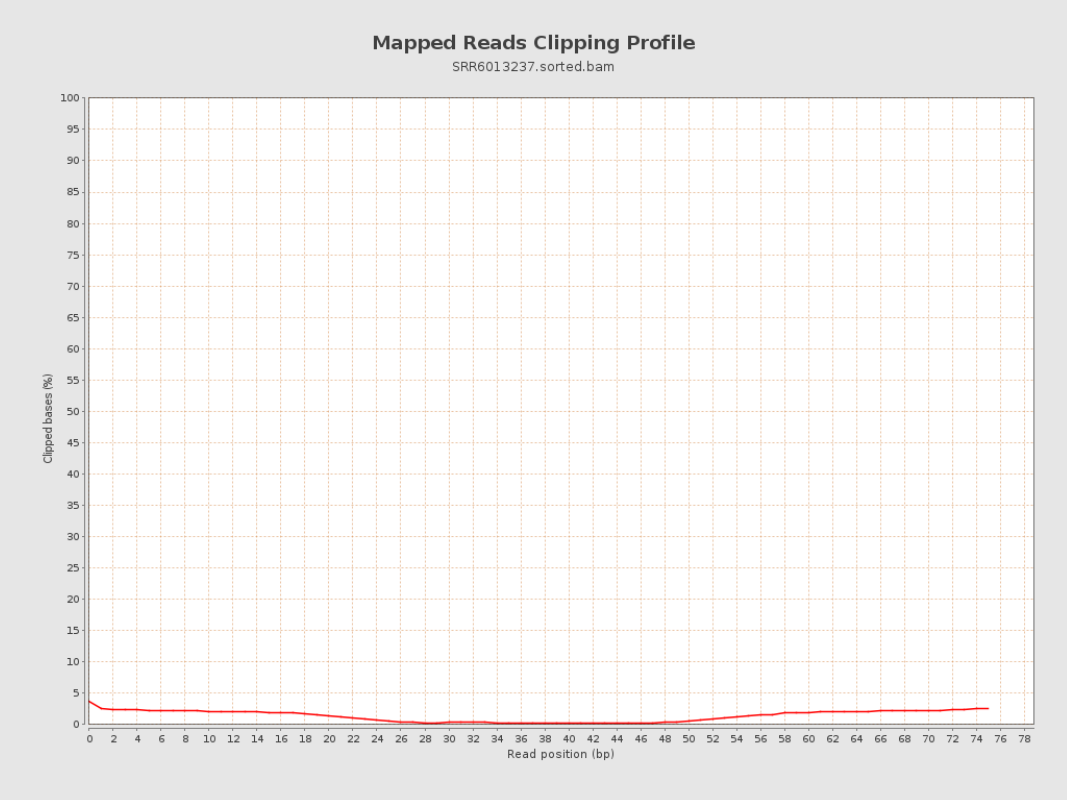
8. Results : Mapped Reads Nucleotide Content



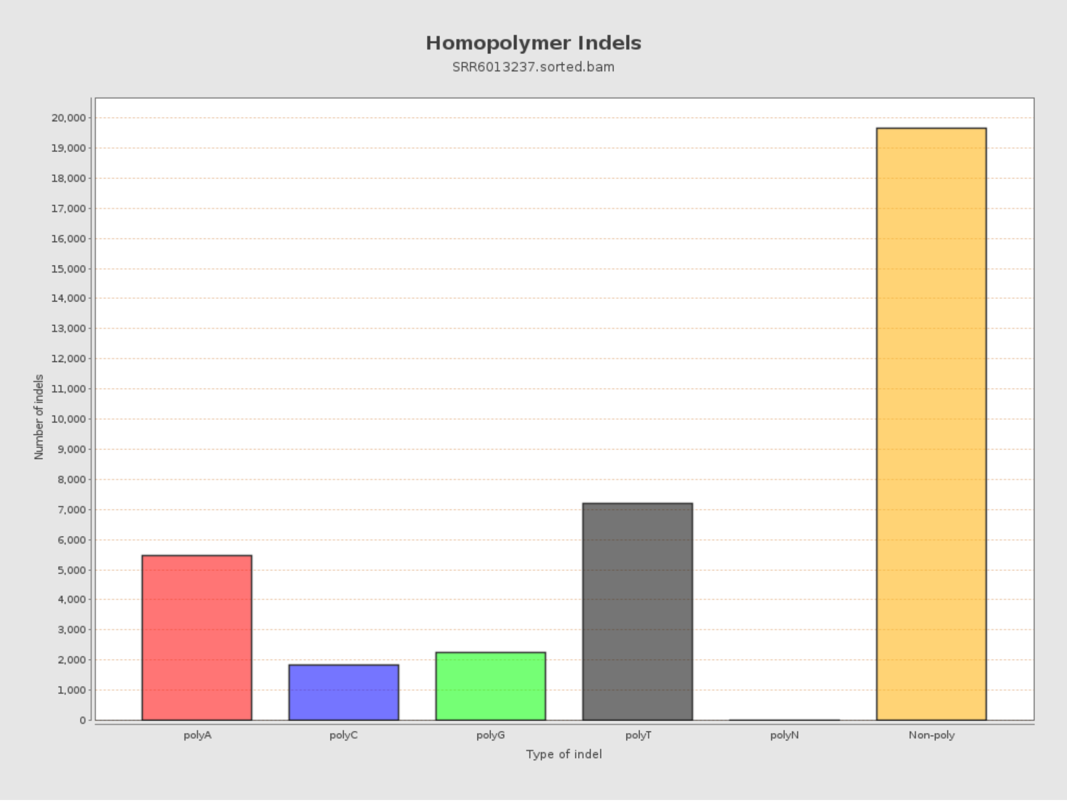
9. Results : Mapped Reads GC-content Distribution



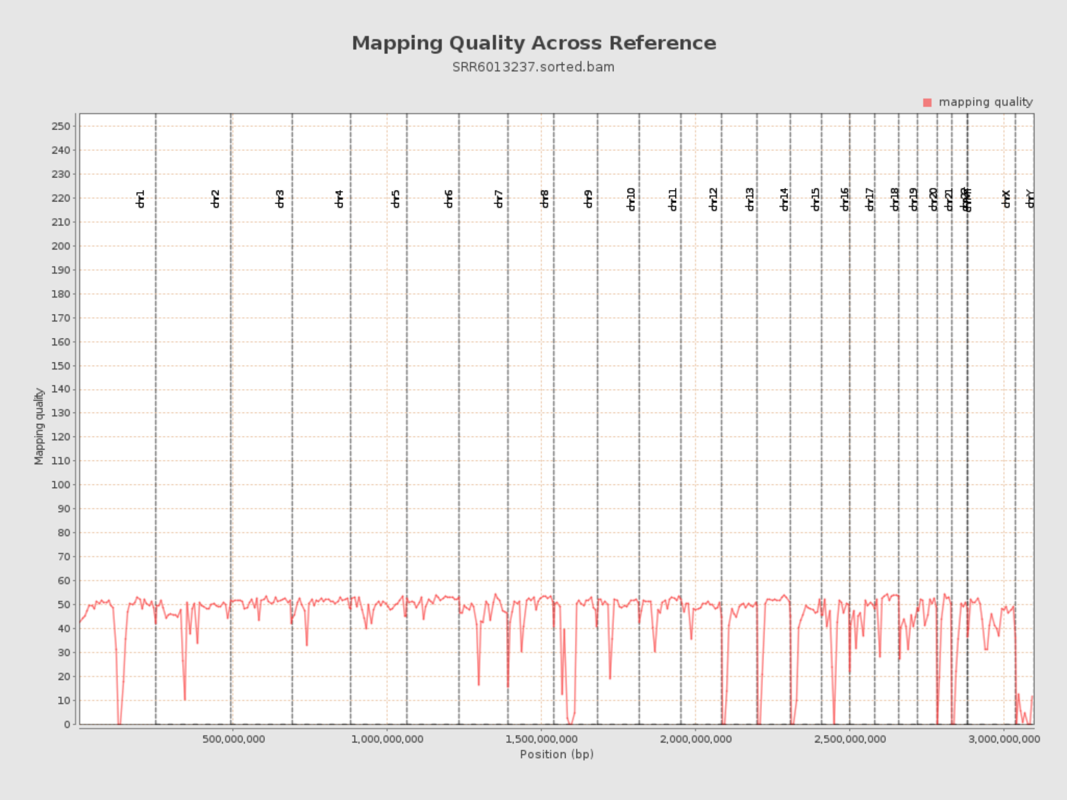
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram