Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 18:19:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013258.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_SRR6013258 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013258.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 18:19:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013258.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,211,855
Mapped reads	1,979,507 / 89.5%
Unmapped reads	232,348 / 10.5%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,180 / 0.6%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	85,832 / 3.88%
Duplication rate	3.15%
Clipped reads	898,119 / 40.6%

2.2. ACGT Content

Number/percentage of A's	36,713,287 / 27.97%
Number/percentage of C's	23,753,517 / 18.1%
Number/percentage of T's	42,014,426 / 32.01%
Number/percentage of G's	28,770,552 / 21.92%
Number/percentage of N's	1,891 / 0%
GC Percentage	40.02%

2.3. Coverage

Mean	0.0424

Standard Deviation	0.4631

2.4. Mapping Quality

Mean Mapping Quality	45.45

2.5. Mismatches and indels

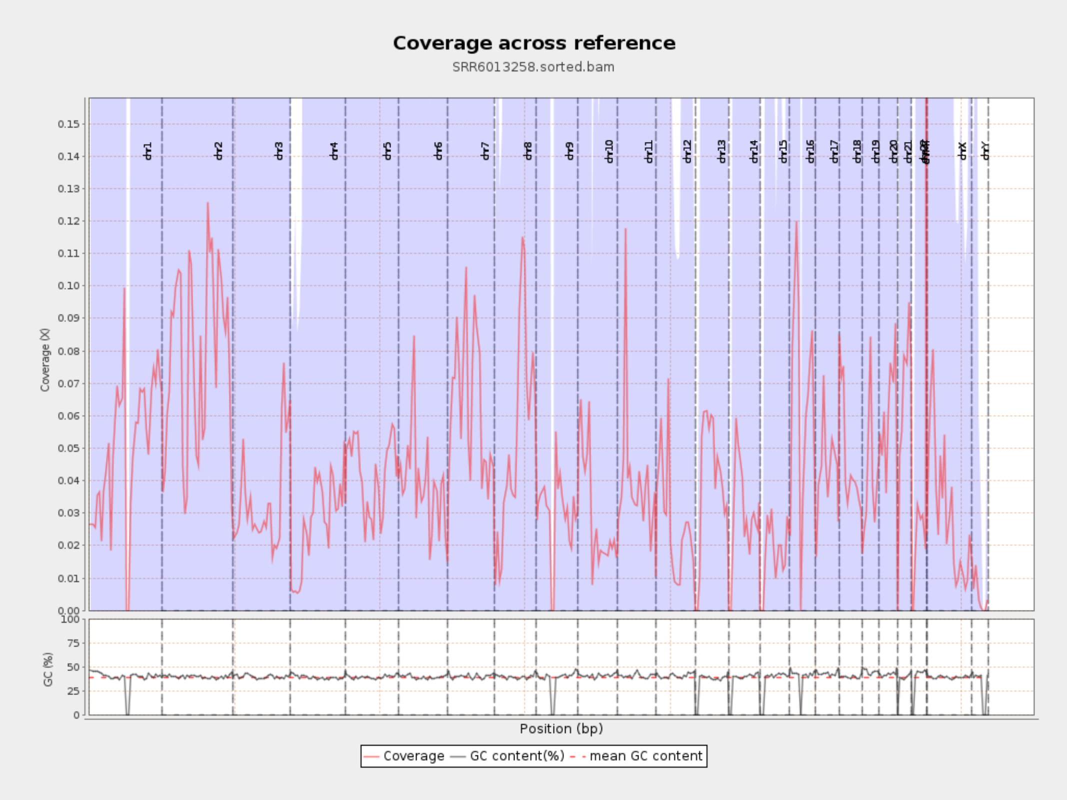
General error rate	0.78%
Mismatches	1,009,607
Insertions	9,206
Mapped reads with at least one insertion	0.46%
Deletions	40,748
Mapped reads with at least one deletion	2.03%
Homopolymer indels	45.49%

2.6. Chromosome stats

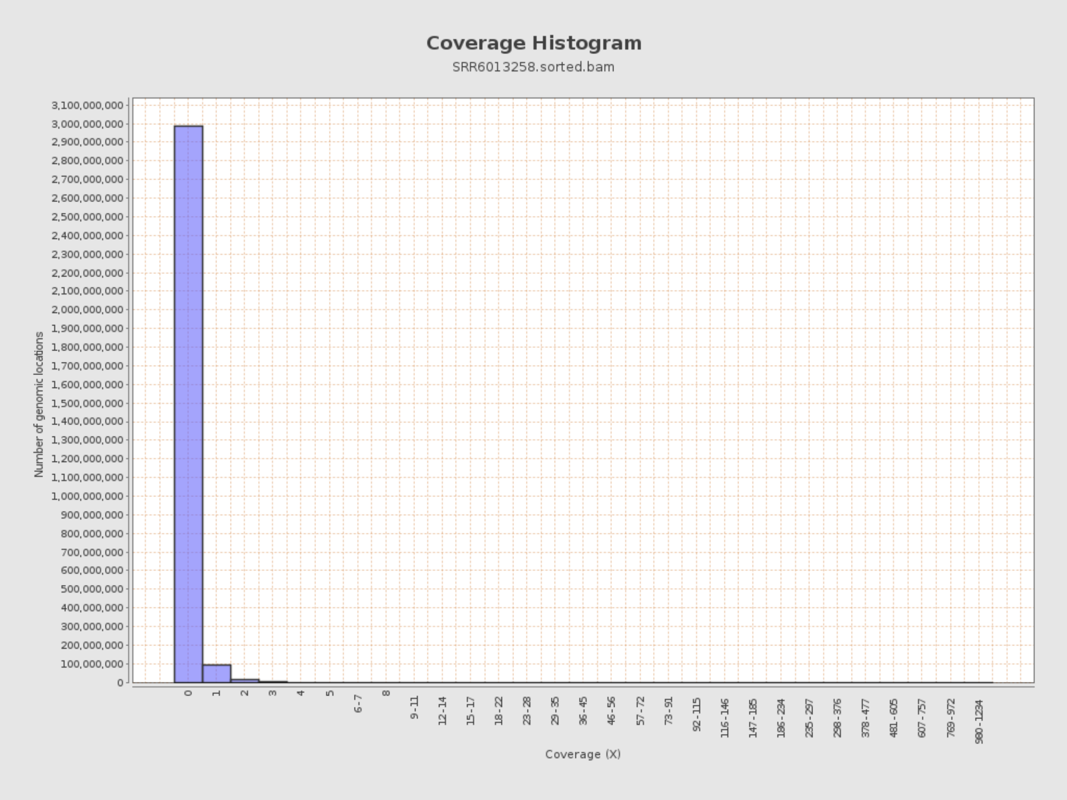
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12439548	0.0499	1.0601
chr2	243199373	19030551	0.0783	0.5763
chr3	198022430	6665127	0.0337	0.2111
chr4	191154276	5169356	0.027	0.1965
chr5	180915260	7594328	0.042	0.2403
chr6	171115067	6779105	0.0396	0.3617
chr7	159138663	10245189	0.0644	0.647

chr8	146364022	7739459	0.0529	0.4177
chr9	141213431	4242264	0.03	0.3752
chr10	135534747	4088802	0.0302	0.3136
chr11	135006516	5367306	0.0398	0.2937
chr12	133851895	3651304	0.0273	0.1961
chr13	115169878	4607184	0.04	0.2283
chr14	107349540	3112985	0.029	0.206
chr15	102531392	1819694	0.0177	0.1579
chr16	90354753	6062890	0.0671	0.3172
chr17	81195210	3541374	0.0436	0.3282
chr18	78077248	3644830	0.0467	0.5898
chr19	59128983	2501236	0.0423	0.7283
chr20	63025520	3882551	0.0616	0.2902
chr21	48129895	3107685	0.0646	0.3058
chr22	51304566	1046059	0.0204	0.1616
chrMT	16571	15020	0.9064	1.1797
chrX	155270560	4693221	0.0302	0.2477
chrY	59373566	276786	0.0047	0.1103

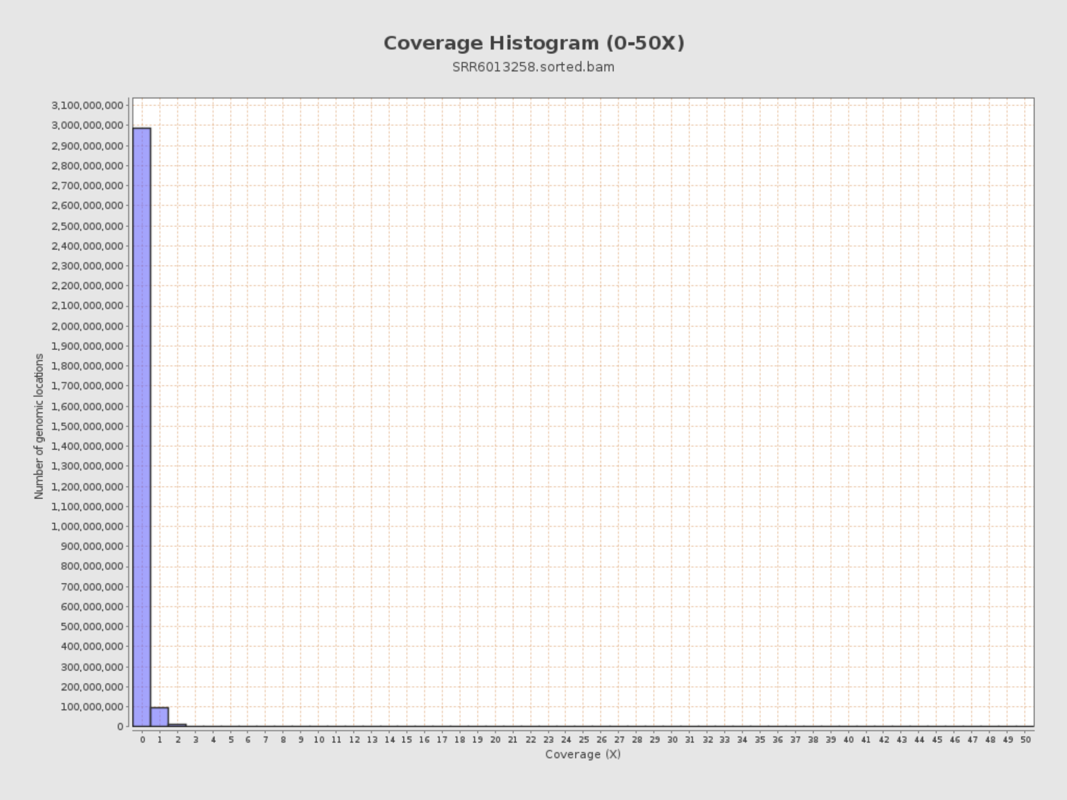
3. Results : Coverage across reference



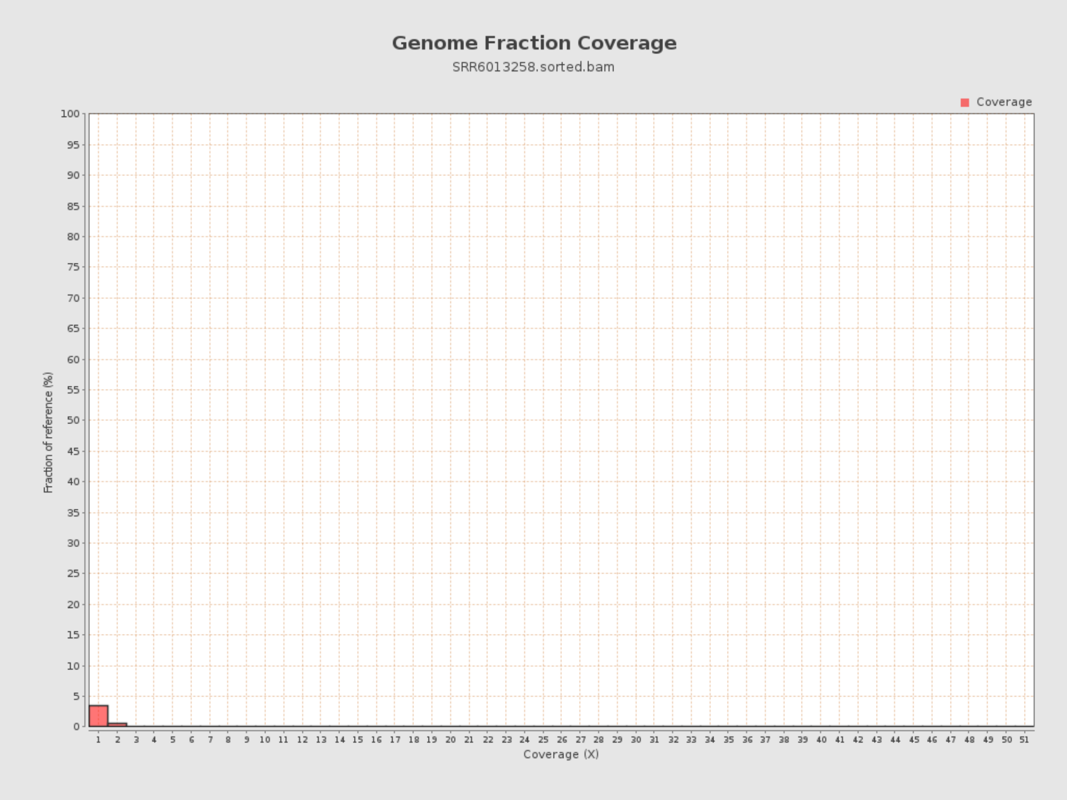
4. Results : Coverage Histogram



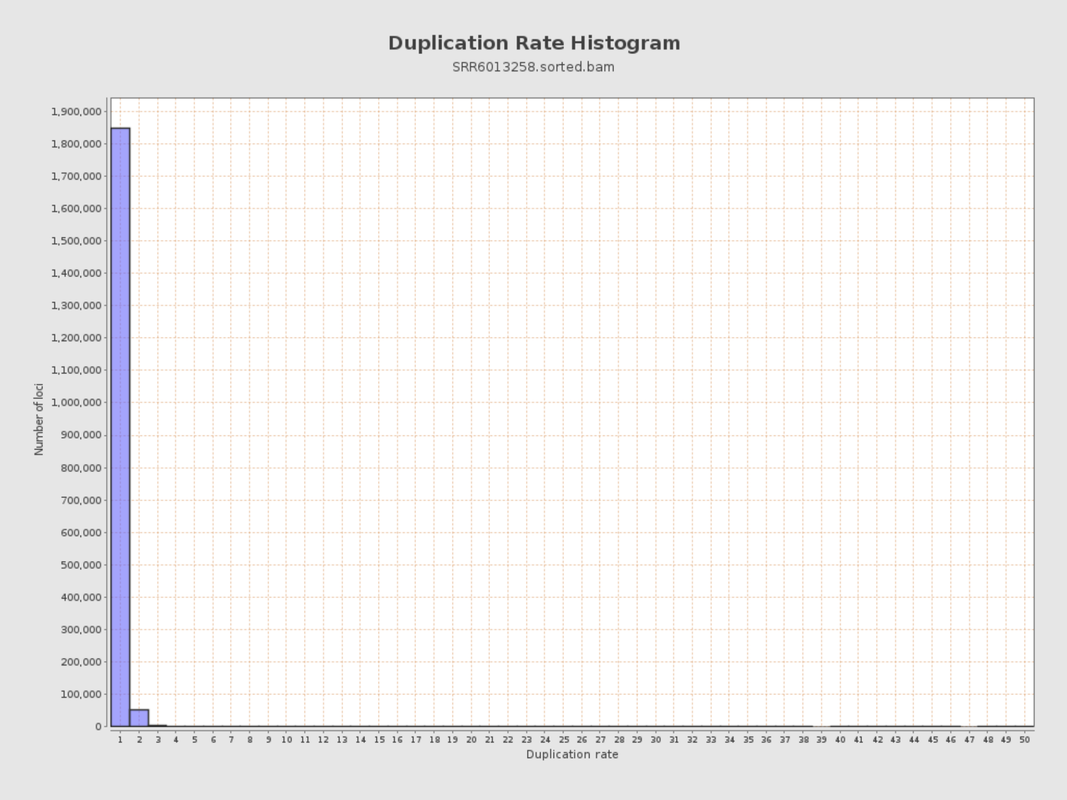
5. Results : Coverage Histogram (0-50X)



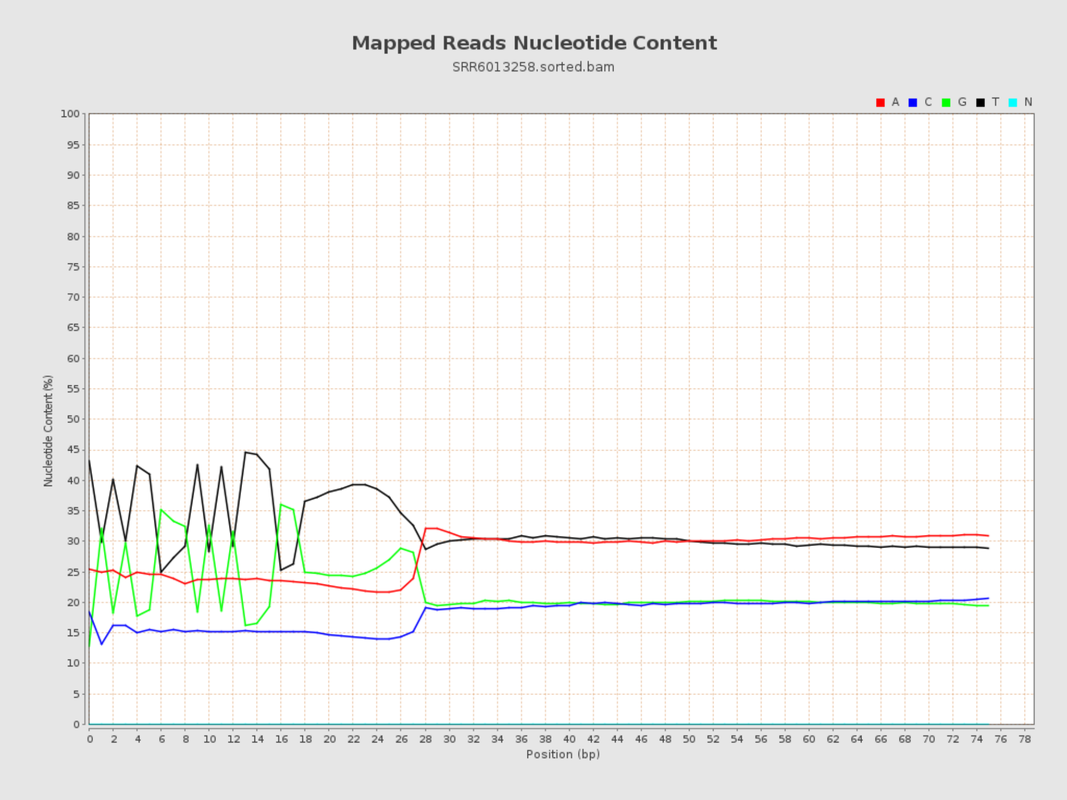
6. Results : Genome Fraction Coverage



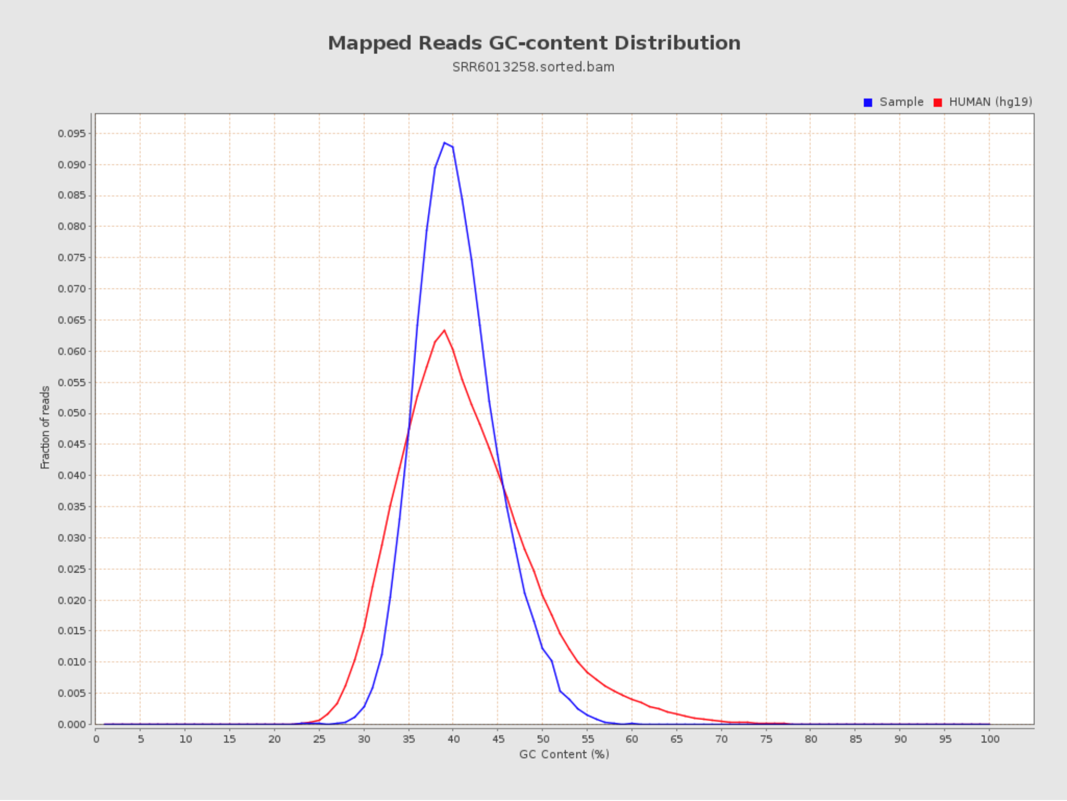
7. Results : Duplication Rate Histogram



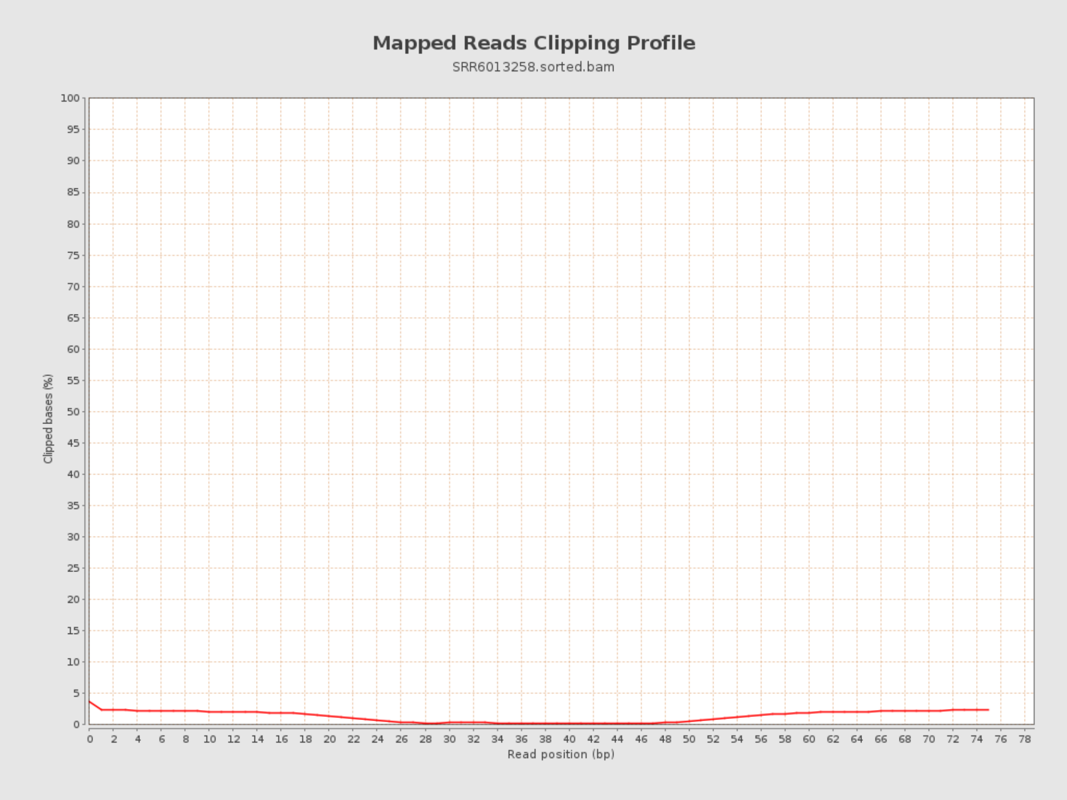
8. Results : Mapped Reads Nucleotide Content



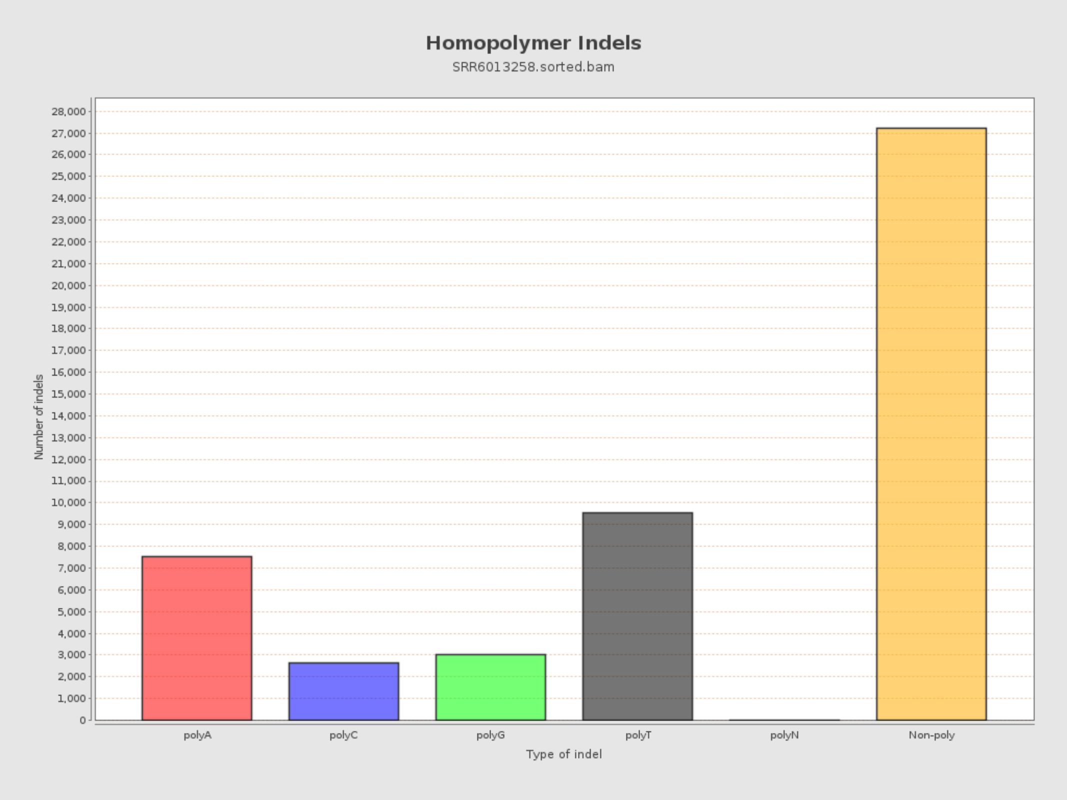
9. Results : Mapped Reads GC-content Distribution



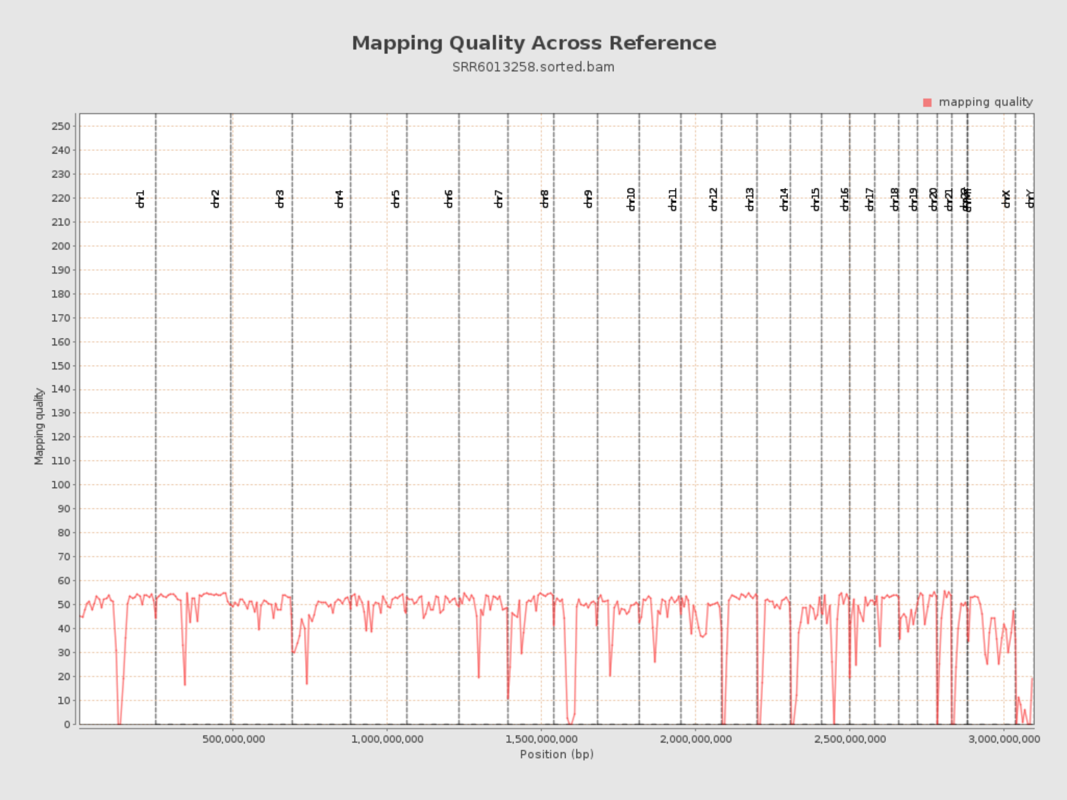
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram