Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 10:59:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234025.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_SRR6234025 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234025.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 10:59:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234025.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,881,146
Mapped reads	512,874 / 17.8%
Unmapped reads	2,368,272 / 82.2%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,927 / 0.17%
Read min/max/mean length	30 / 76 / 76.06
Duplicated reads (estimated)	102,432 / 3.56%
Duplication rate	13.55%
Clipped reads	317,961 / 11.04%

2.2. ACGT Content

Number/percentage of A's	8,154,193 / 26.32%
Number/percentage of C's	5,348,389 / 17.26%
Number/percentage of T's	10,349,629 / 33.41%
Number/percentage of G's	7,118,593 / 22.98%
Number/percentage of N's	8,919 / 0.03%
GC Percentage	40.24%

2.3. Coverage

Mean	0.01

Standard Deviation	0.2394

2.4. Mapping Quality

Mean Mapping Quality	40.53

2.5. Mismatches and indels

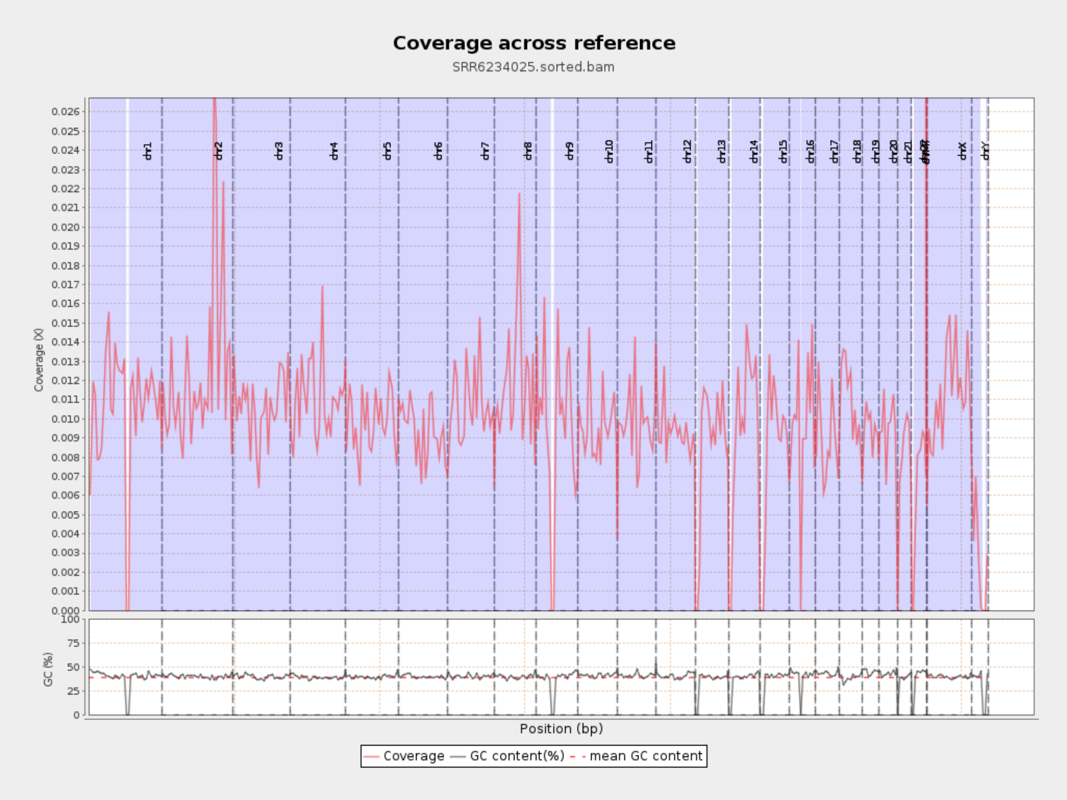
General error rate	0.92%
Mismatches	273,870
Insertions	4,978
Mapped reads with at least one insertion	0.95%
Deletions	8,834
Mapped reads with at least one deletion	1.69%
Homopolymer indels	39.34%

2.6. Chromosome stats

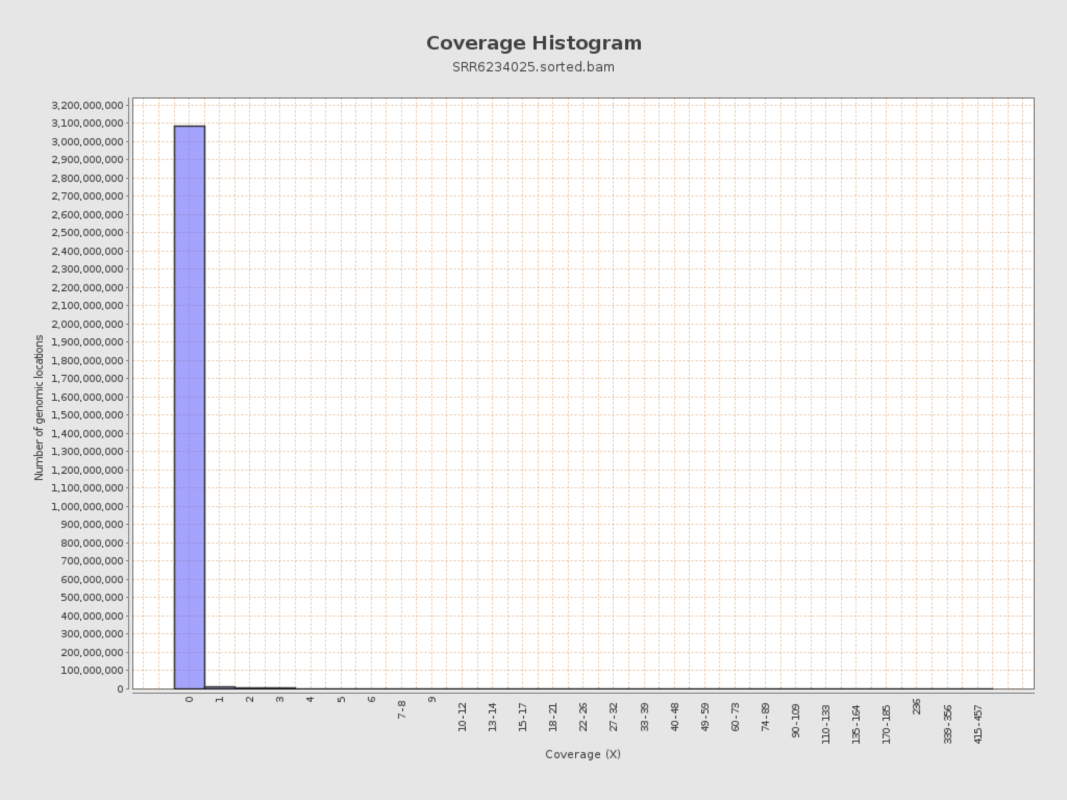
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2625037	0.0105	0.2377
chr2	243199373	3061227	0.0126	0.2997
chr3	198022430	2113876	0.0107	0.2289
chr4	191154276	2106862	0.011	0.2202
chr5	180915260	1760552	0.0097	0.2104
chr6	171115067	1608899	0.0094	0.2126
chr7	159138663	1724621	0.0108	0.2387

chr8	146364022	1743627	0.0119	0.2573
chr9	141213431	1339226	0.0095	0.1945
chr10	135534747	1319894	0.0097	0.2062
chr11	135006516	1306449	0.0097	0.2003
chr12	133851895	1258243	0.0094	0.2097
chr13	115169878	967070	0.0084	0.2451
chr14	107349540	1017084	0.0095	0.2119
chr15	102531392	850135	0.0083	0.1912
chr16	90354753	876328	0.0097	0.2031
chr17	81195210	707394	0.0087	0.1928
chr18	78077248	860324	0.011	0.5921
chr19	59128983	558139	0.0094	0.1947
chr20	63025520	590183	0.0094	0.1956
chr21	48129895	370671	0.0077	0.169
chr22	51304566	317711	0.0062	0.145
chrMT	16571	11335	0.684	1.5766
chrX	155270560	1745456	0.0112	0.222
chrY	59373566	154904	0.0026	0.0955

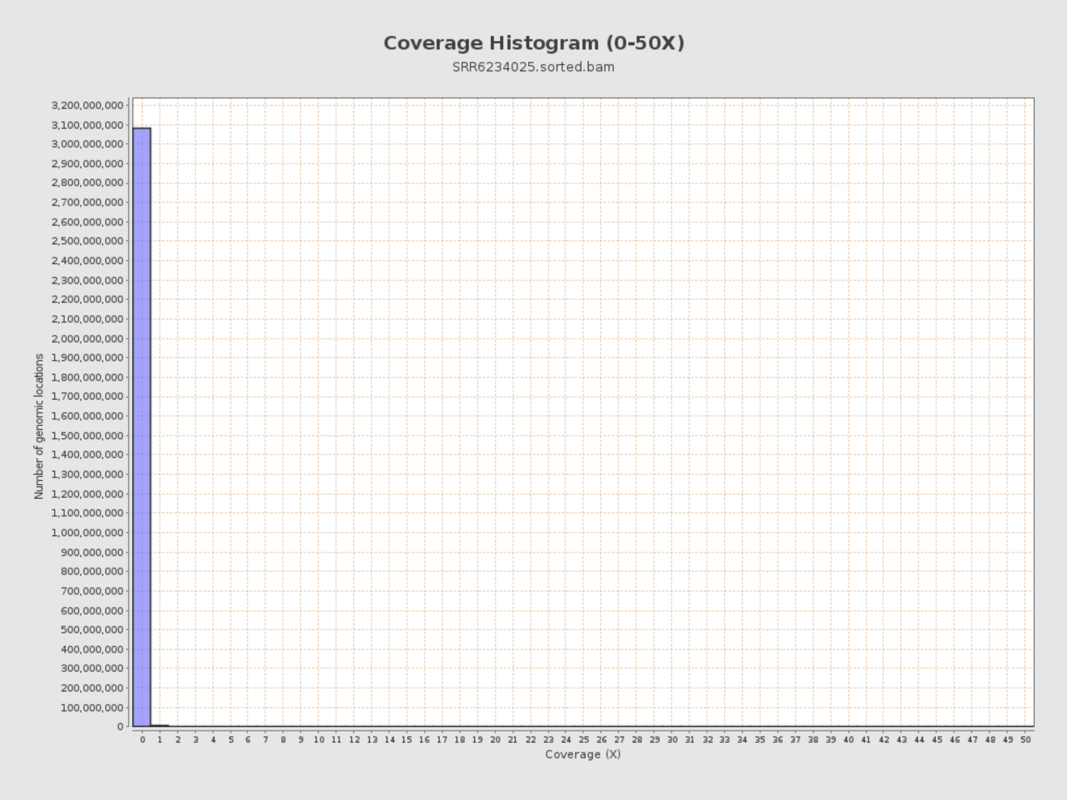
3. Results : Coverage across reference



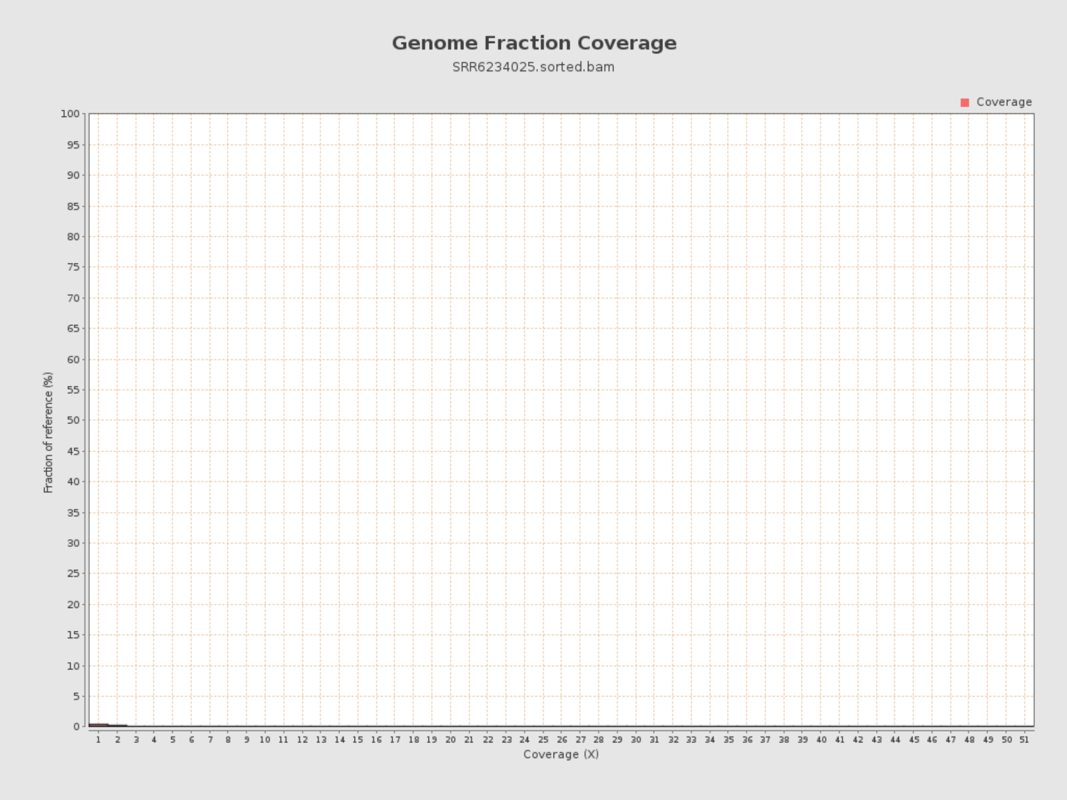
4. Results : Coverage Histogram



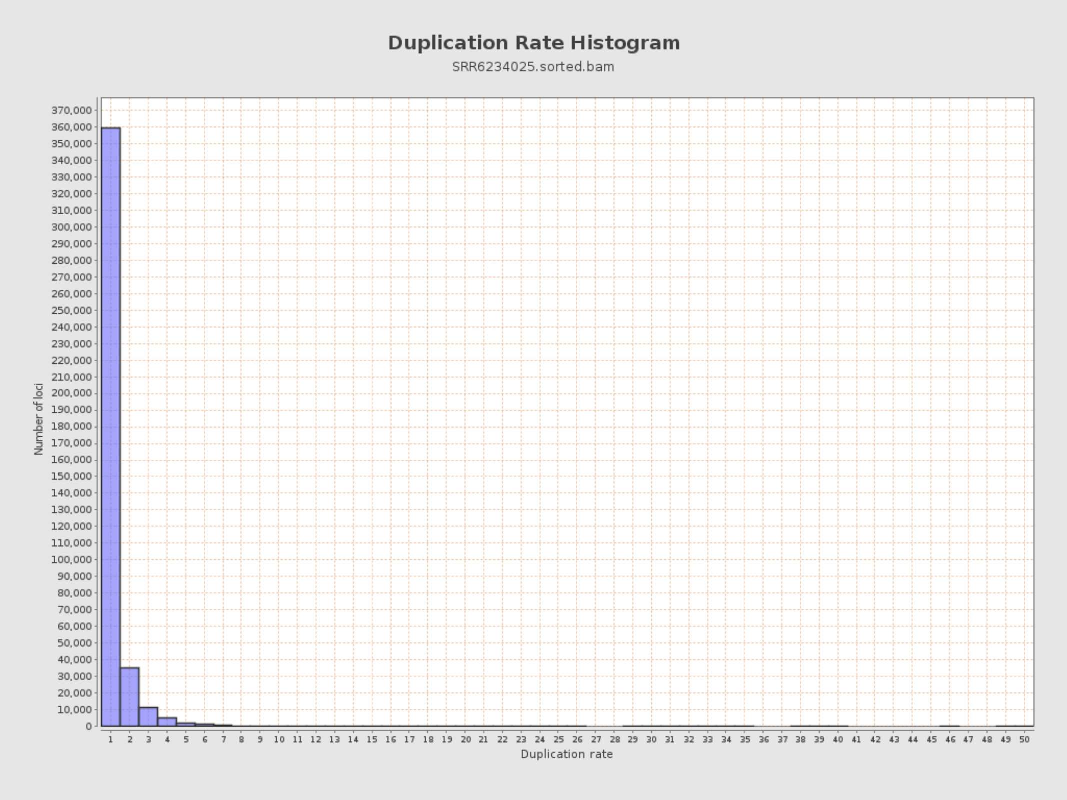
5. Results : Coverage Histogram (0-50X)



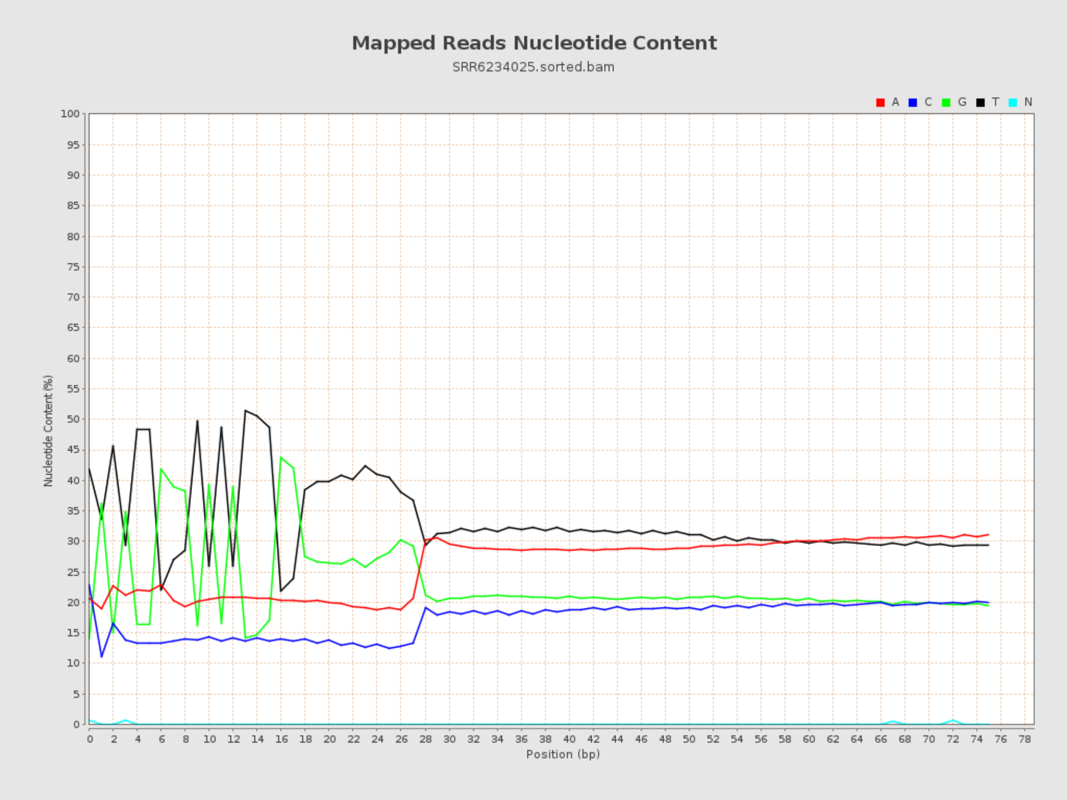
6. Results : Genome Fraction Coverage



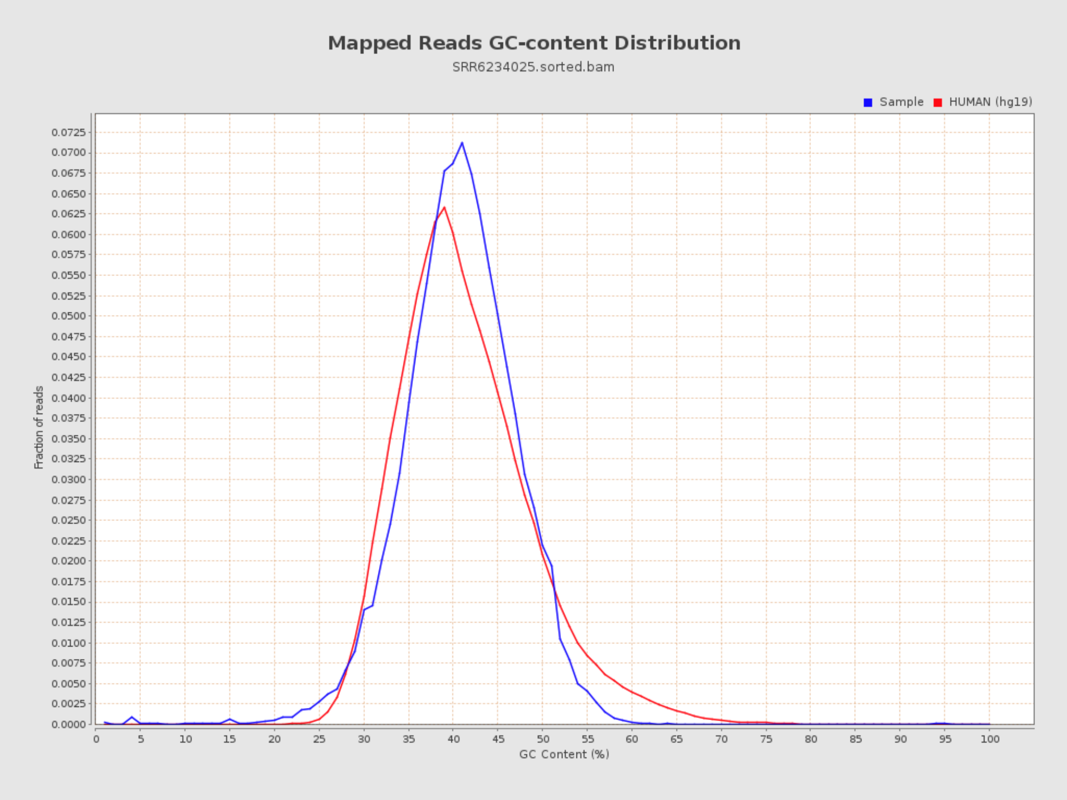
7. Results : Duplication Rate Histogram



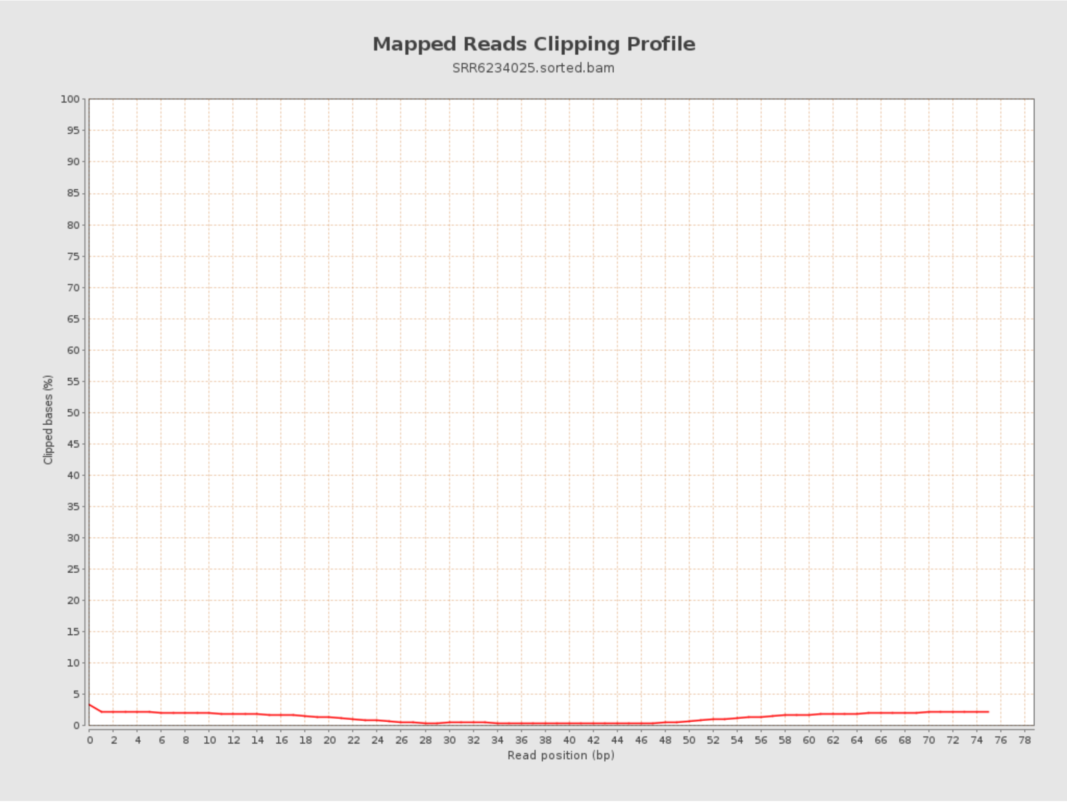
8. Results : Mapped Reads Nucleotide Content



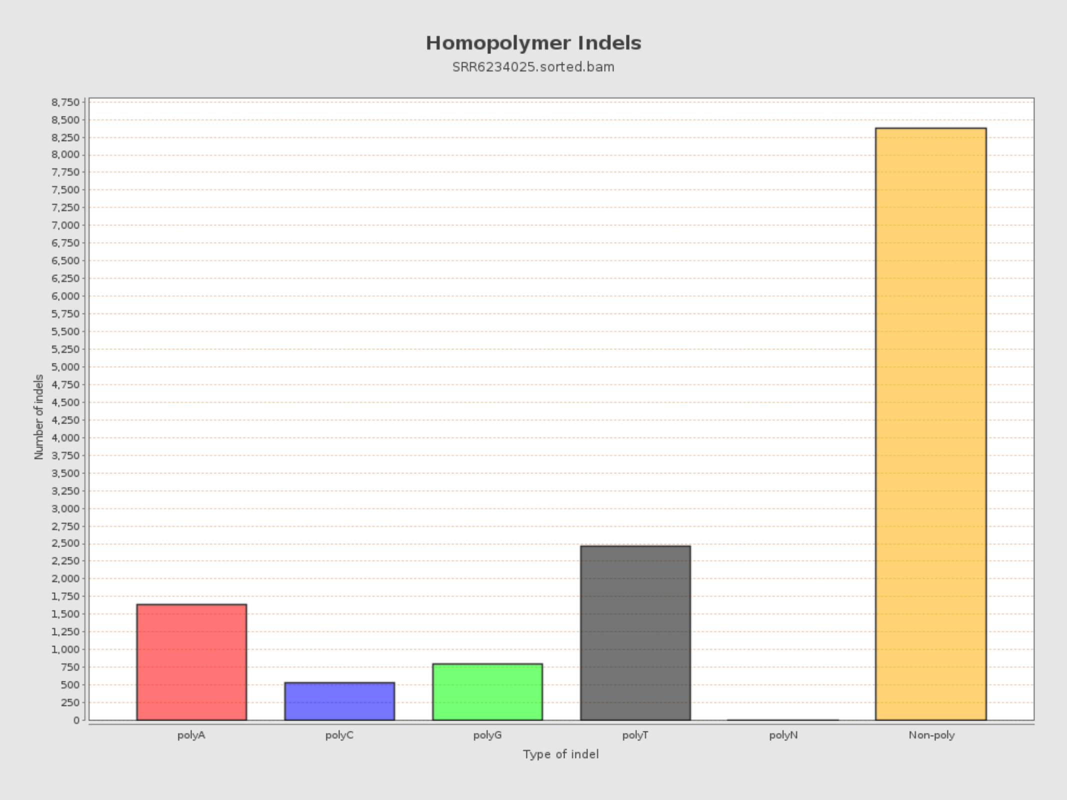
9. Results : Mapped Reads GC-content Distribution



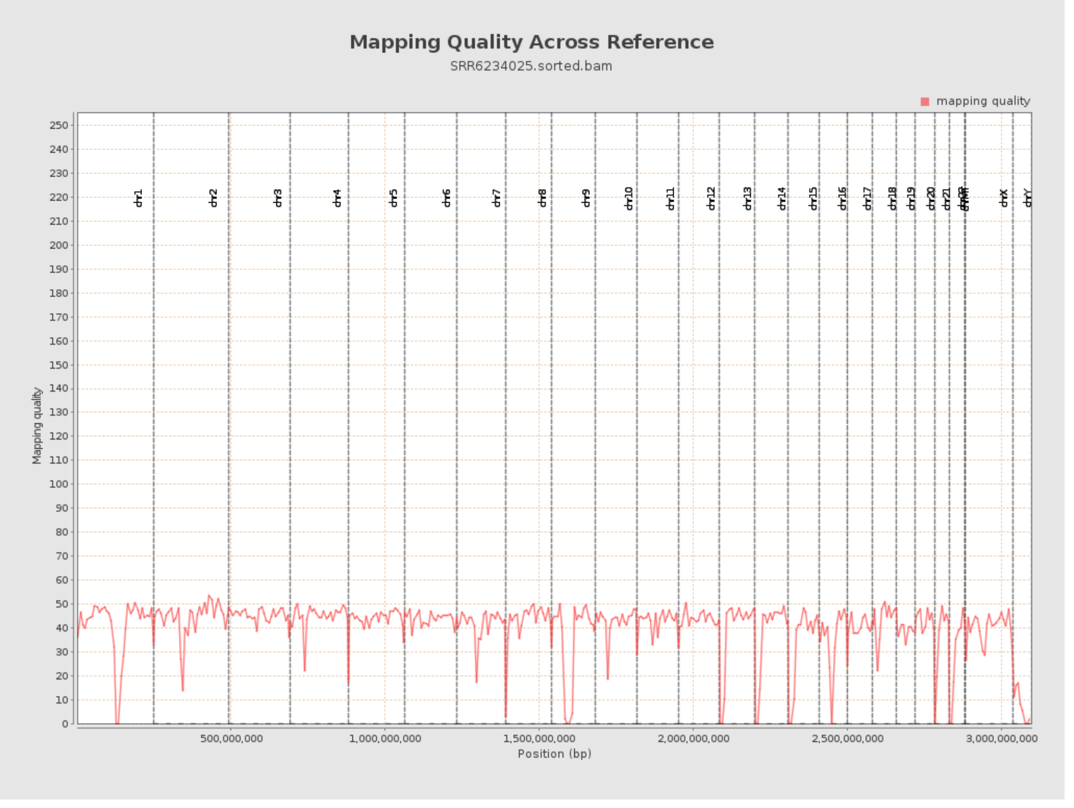
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram