Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 12:21:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234050.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_SRR6234050 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234050.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 12:21:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234050.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,716,902
Mapped reads	4,419,303 / 93.69%
Unmapped reads	297,599 / 6.31%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	23,513 / 0.5%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	448,135 / 9.5%
Duplication rate	8.5%
Clipped reads	2,638,937 / 55.95%

2.2. ACGT Content

Number/percentage of A's	68,111,309 / 24.51%
Number/percentage of C's	50,223,009 / 18.07%
Number/percentage of T's	90,724,633 / 32.65%
Number/percentage of G's	68,804,436 / 24.76%
Number/percentage of N's	25,420 / 0.01%
GC Percentage	42.83%

2.3. Coverage

Mean	0.0898

Standard Deviation	0.9096

2.4. Mapping Quality

Mean Mapping Quality	42.44

2.5. Mismatches and indels

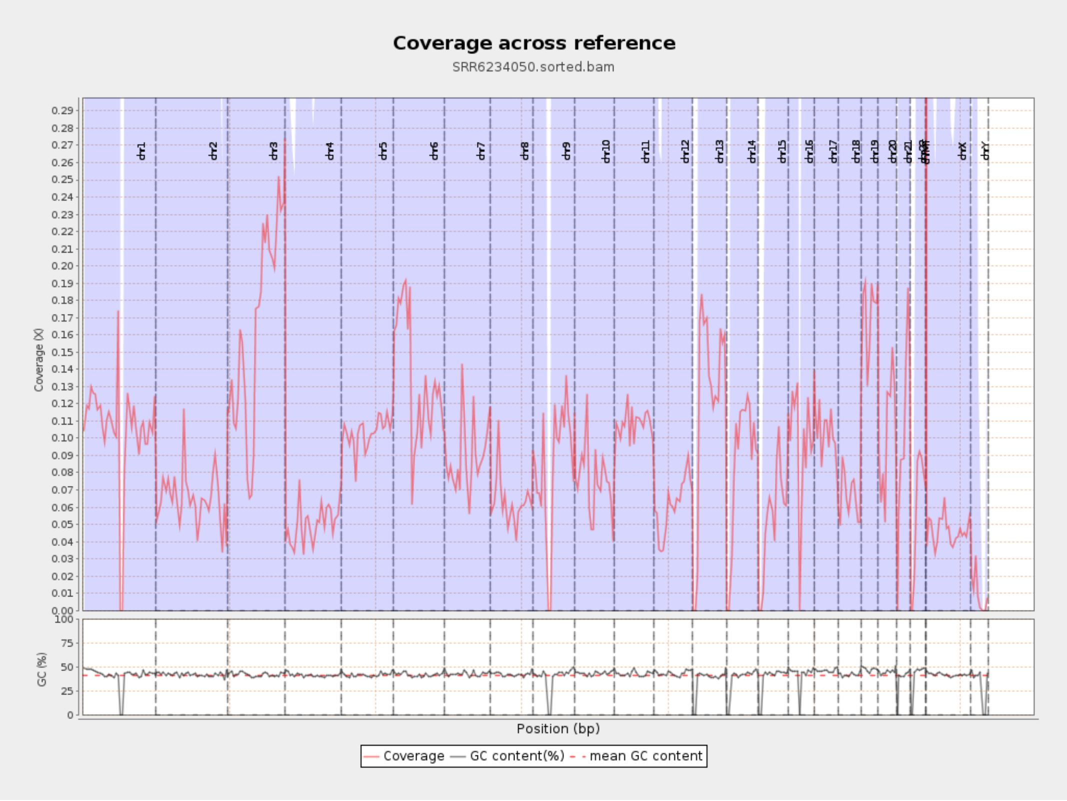
General error rate	0.66%
Mismatches	1,783,655
Insertions	21,113
Mapped reads with at least one insertion	0.47%
Deletions	82,181
Mapped reads with at least one deletion	1.84%
Homopolymer indels	43.71%

2.6. Chromosome stats

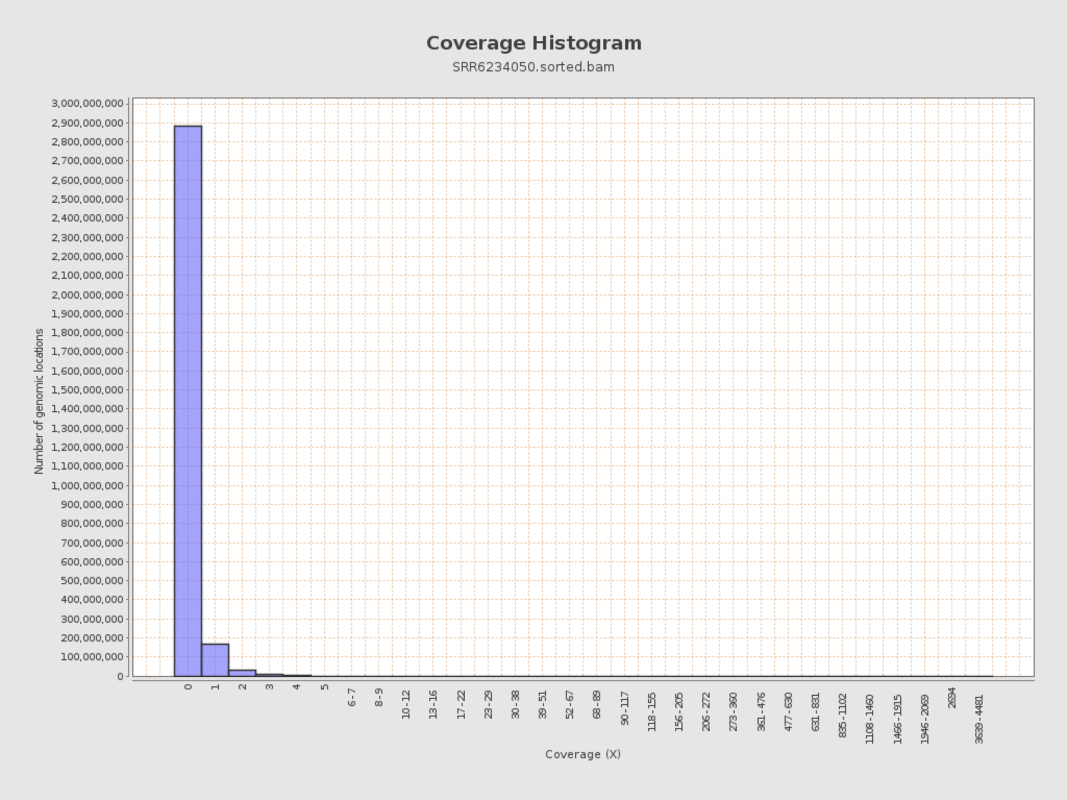
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	26237244	0.1053	1.626
chr2	243199373	15792546	0.0649	1.9789
chr3	198022430	32416102	0.1637	0.5316
chr4	191154276	9599055	0.0502	0.3191
chr5	180915260	18680556	0.1033	0.4132
chr6	171115067	23045638	0.1347	0.8889
chr7	159138663	14363279	0.0903	0.8803

chr8	146364022	9260116	0.0633	0.5051
chr9	141213431	11801007	0.0836	0.4882
chr10	135534747	10208308	0.0753	0.65
chr11	135006516	14577325	0.108	0.6295
chr12	133851895	8227416	0.0615	0.3249
chr13	115169878	14309579	0.1242	0.5647
chr14	107349540	9340916	0.087	0.4007
chr15	102531392	5414431	0.0528	0.3844
chr16	90354753	8657413	0.0958	0.4546
chr17	81195210	8421060	0.1037	0.5
chr18	78077248	5142621	0.0659	1.4129
chr19	59128983	10106570	0.1709	1.0779
chr20	63025520	6497054	0.1031	0.431
chr21	48129895	5051271	0.105	0.4342
chr22	51304566	2983713	0.0582	0.3029
chrMT	16571	128222	7.7377	9.0955
chrX	155270560	7185956	0.0463	0.3609
chrY	59373566	578309	0.0097	0.2846

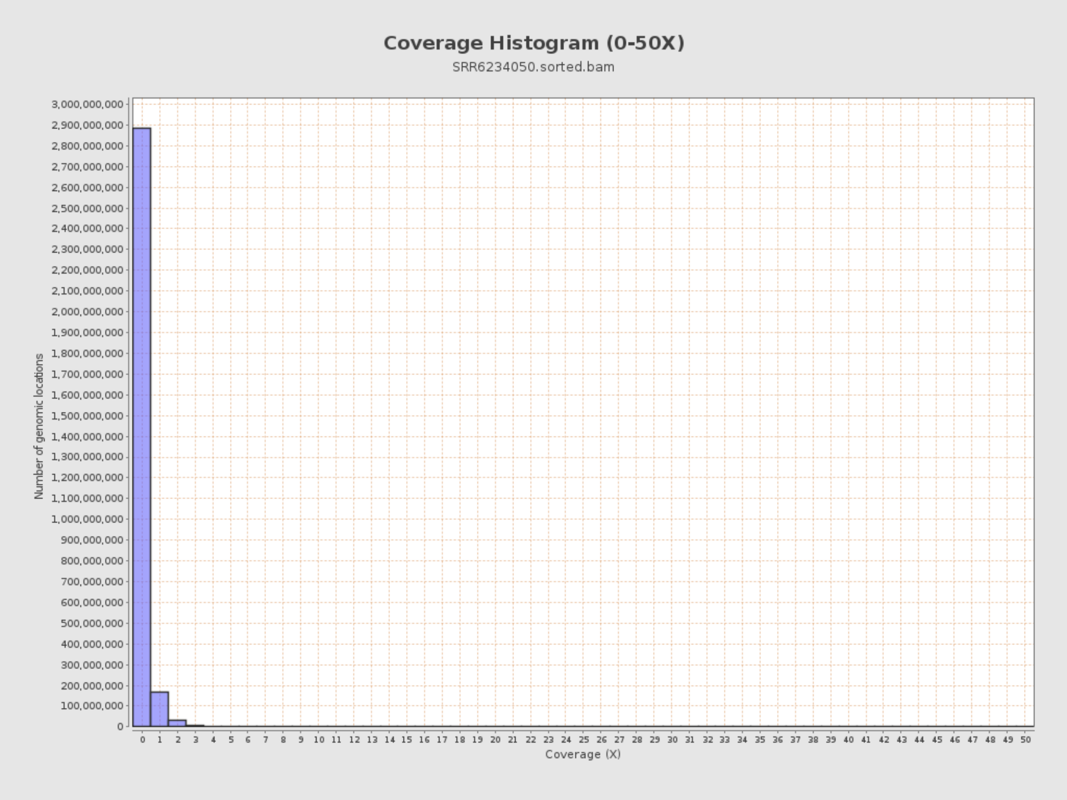
3. Results : Coverage across reference



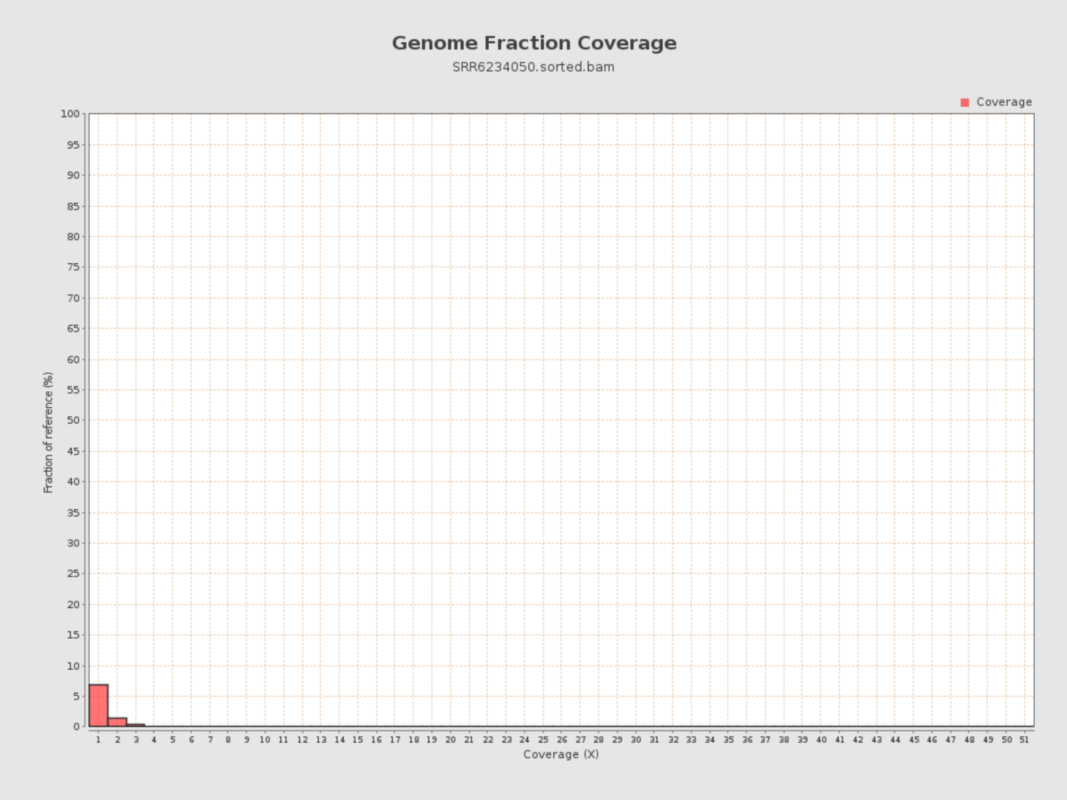
4. Results : Coverage Histogram



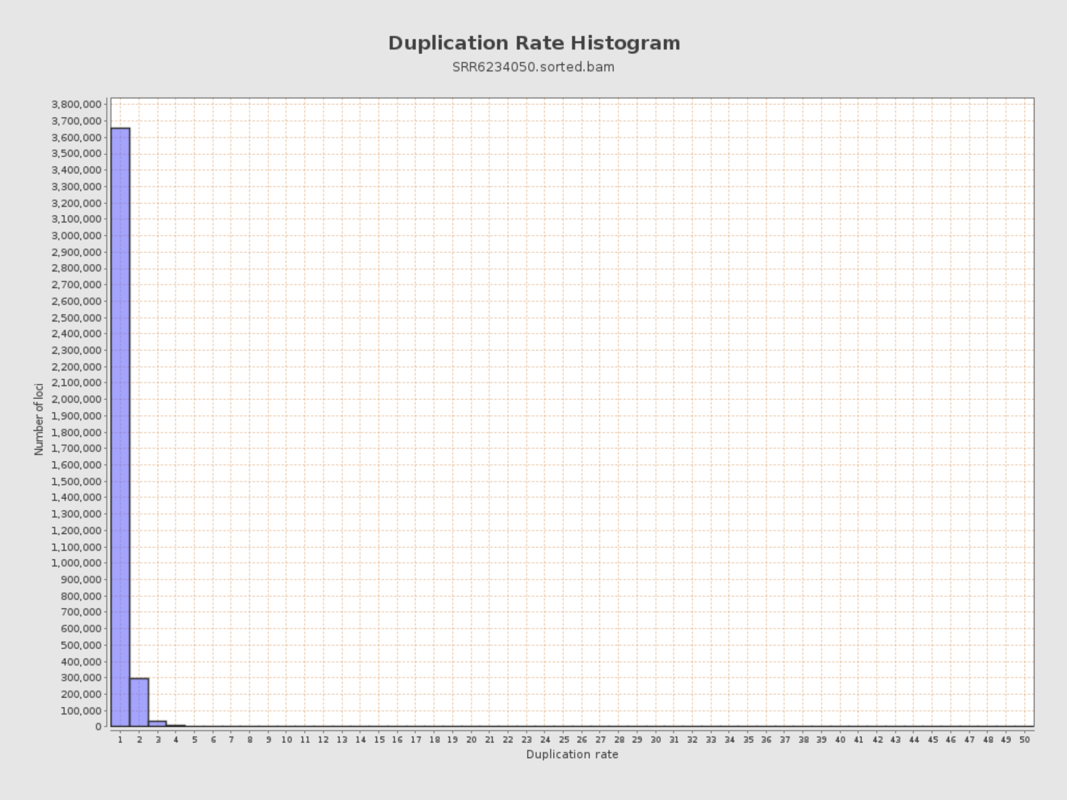
5. Results : Coverage Histogram (0-50X)



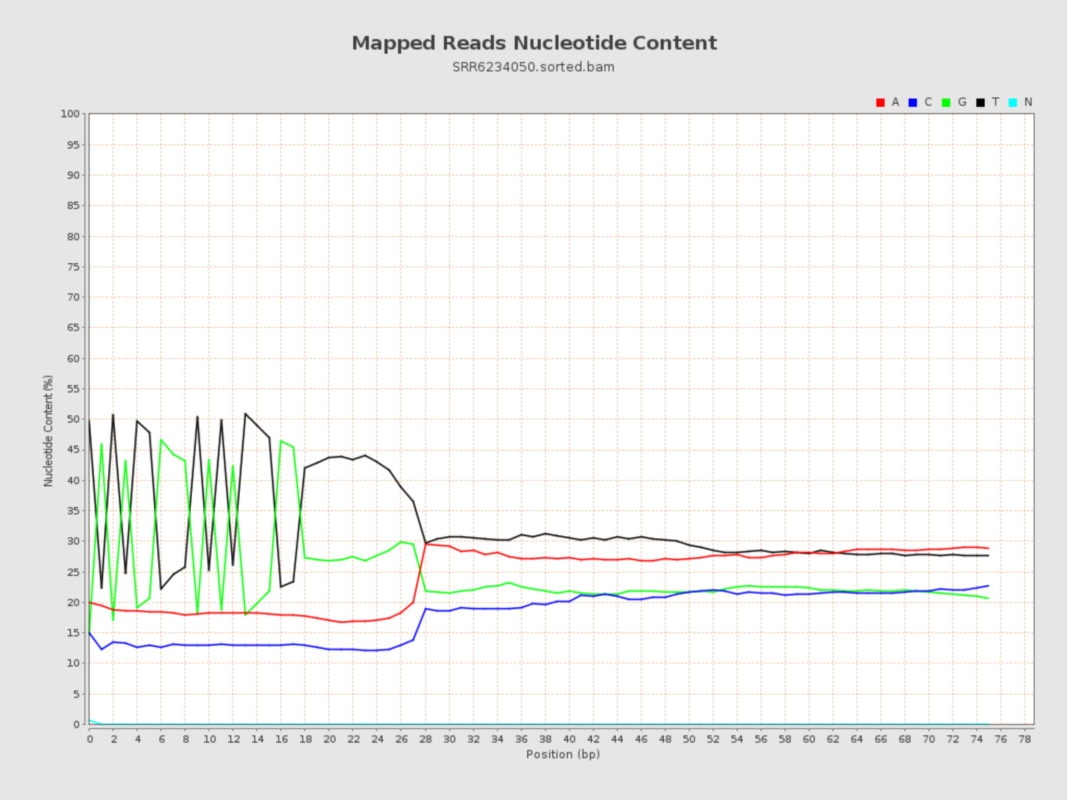
6. Results : Genome Fraction Coverage



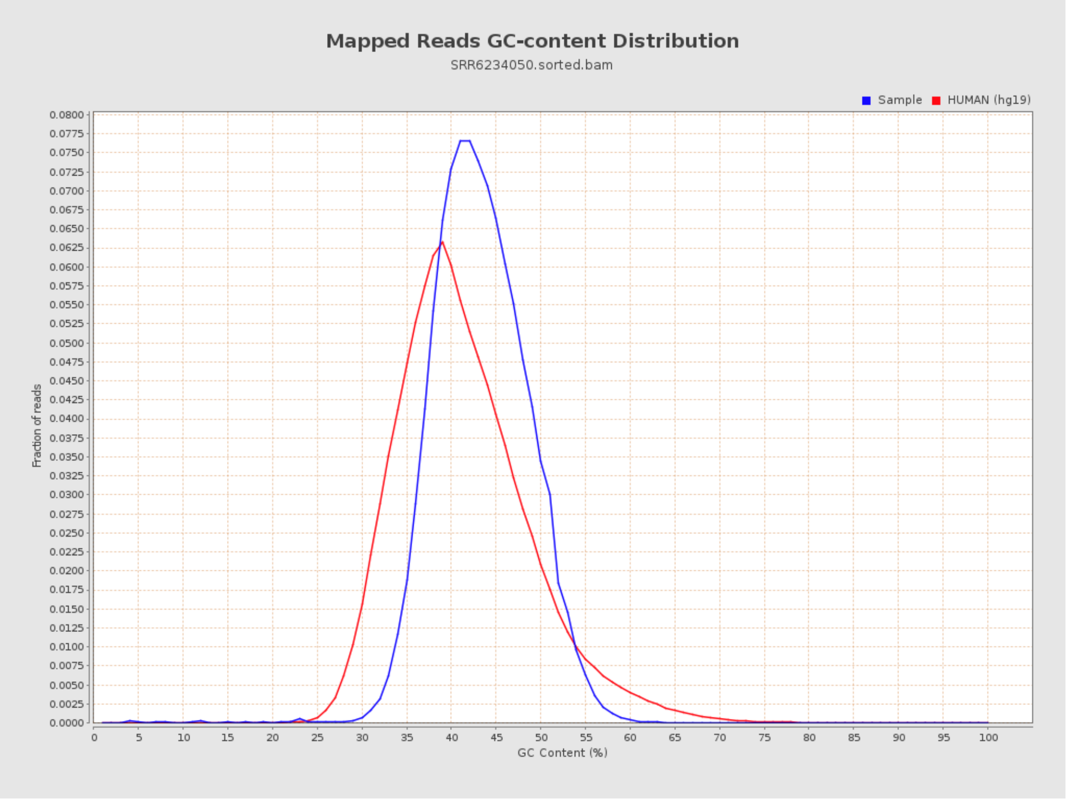
7. Results : Duplication Rate Histogram



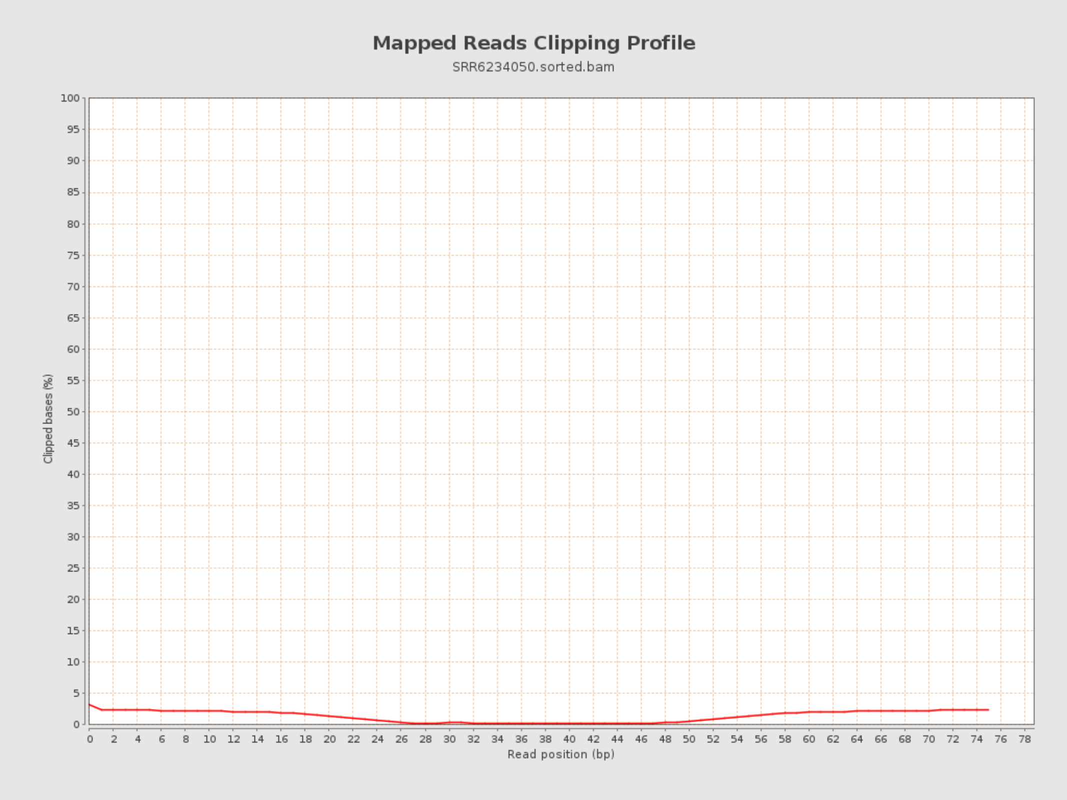
8. Results : Mapped Reads Nucleotide Content



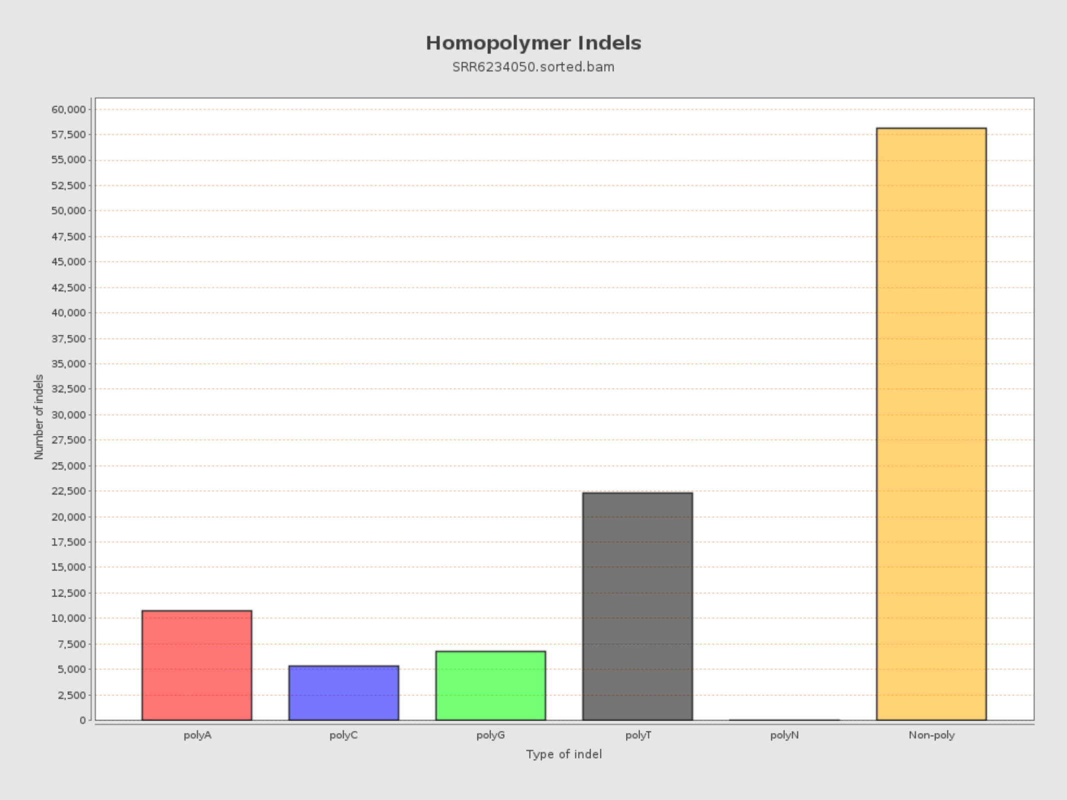
9. Results : Mapped Reads GC-content Distribution



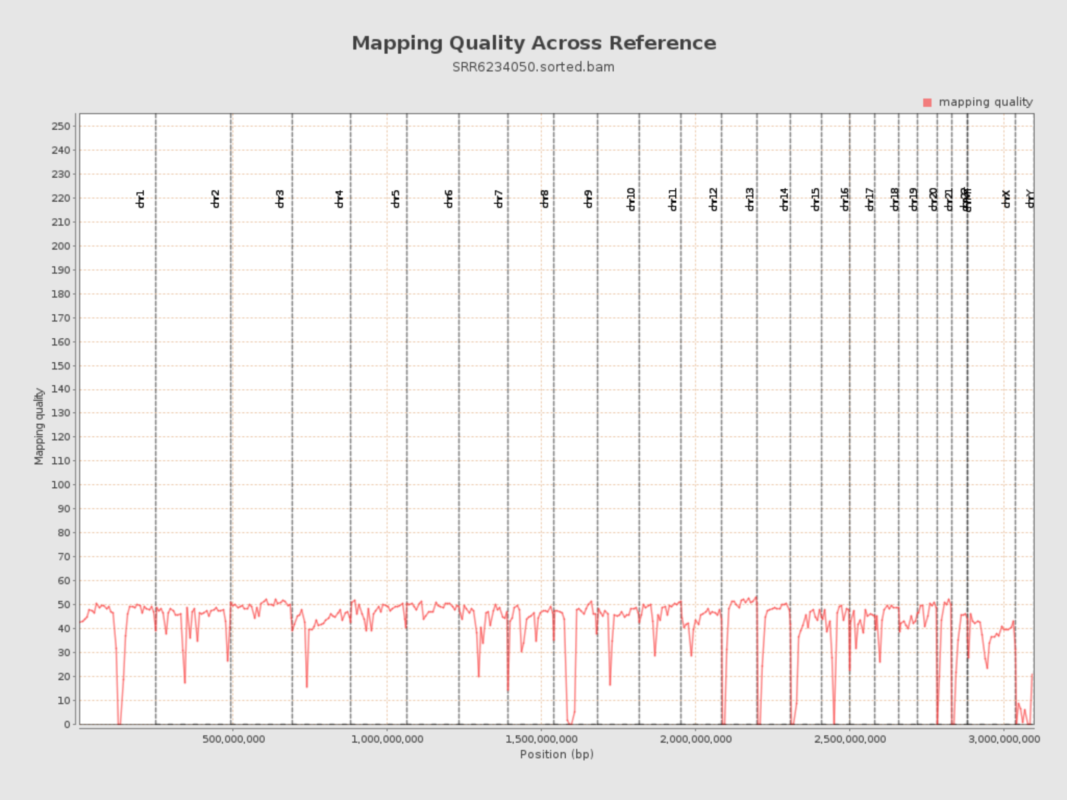
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram