Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 02:21:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004111.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_SRR6004111 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004111.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 02:21:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004111.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,319,960
Mapped reads	3,179,363 / 73.6%
Unmapped reads	1,140,597 / 26.4%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	24,588 / 0.57%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	399,324 / 9.24%
Duplication rate	9.6%
Clipped reads	1,714,354 / 39.68%

2.2. ACGT Content

Number/percentage of A's	56,348,418 / 27.38%
Number/percentage of C's	36,997,217 / 17.98%
Number/percentage of T's	67,239,936 / 32.68%
Number/percentage of G's	45,165,861 / 21.95%
Number/percentage of N's	26,160 / 0.01%
GC Percentage	39.93%

2.3. Coverage

Mean	0.0665

Standard Deviation	0.6029

2.4. Mapping Quality

Mean Mapping Quality	46.08

2.5. Mismatches and indels

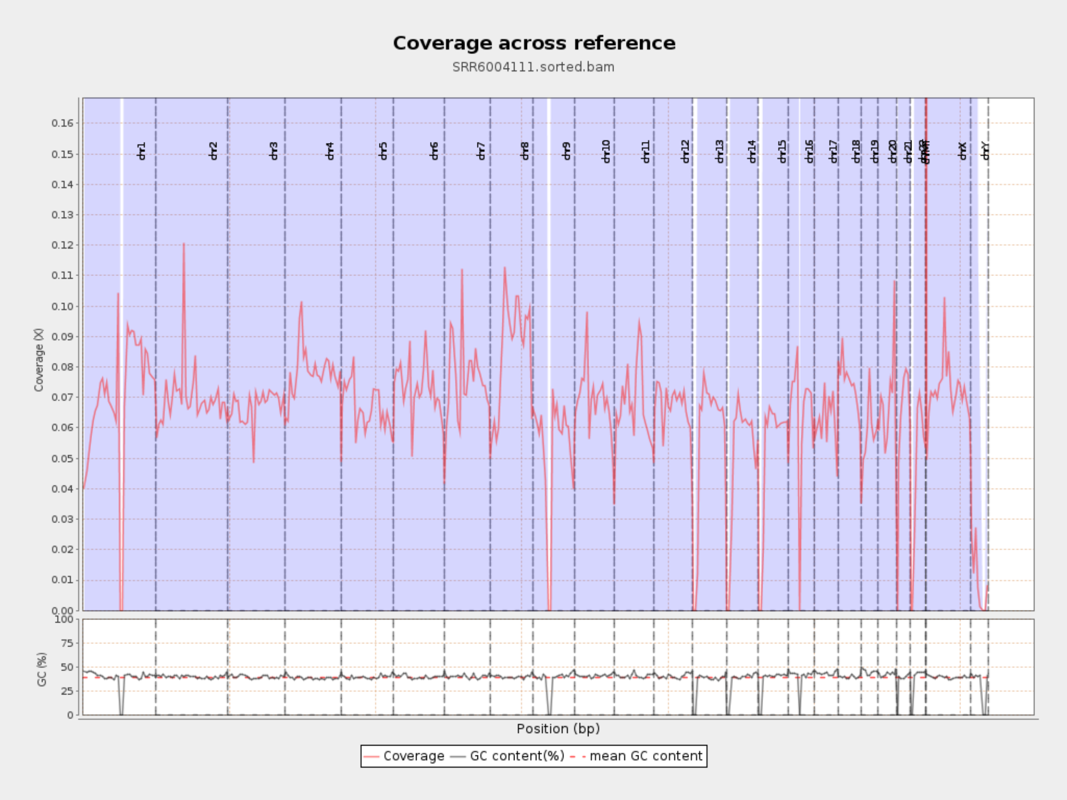
General error rate	1.06%
Mismatches	2,148,451
Insertions	18,051
Mapped reads with at least one insertion	0.56%
Deletions	68,648
Mapped reads with at least one deletion	2.13%
Homopolymer indels	47.55%

2.6. Chromosome stats

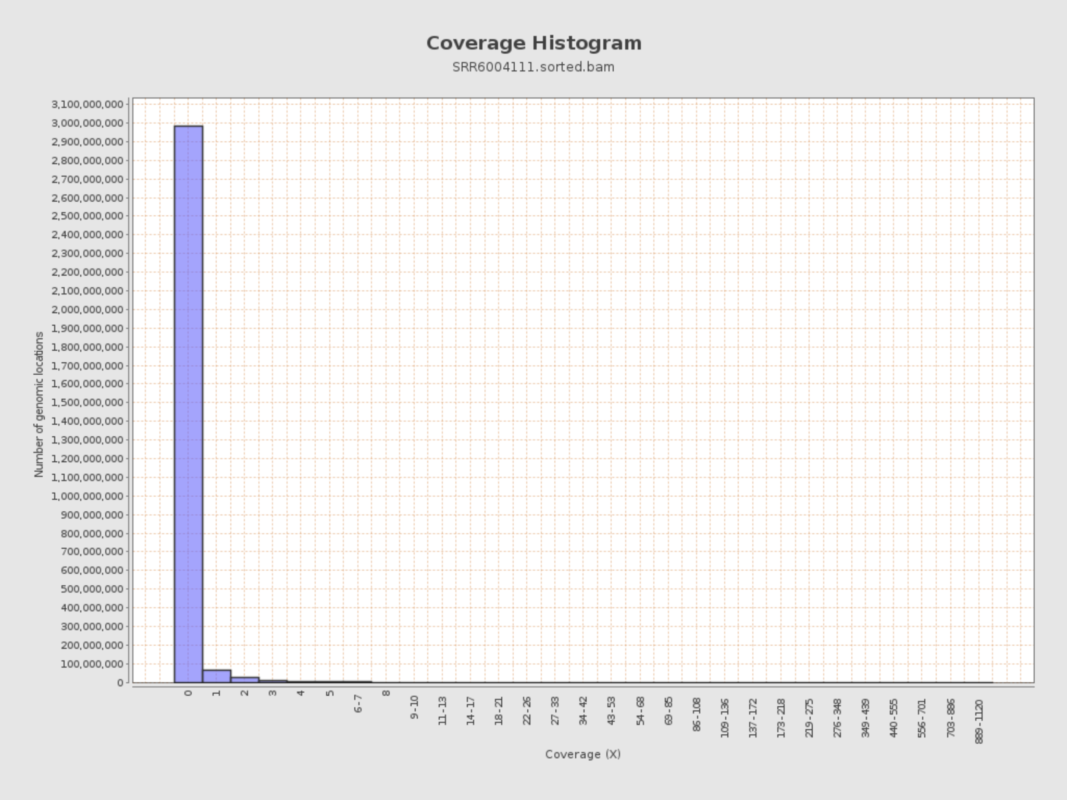
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17346846	0.0696	0.9156
chr2	243199373	17018471	0.07	0.7504
chr3	198022430	13286242	0.0671	0.4346
chr4	191154276	15061312	0.0788	0.489
chr5	180915260	12028236	0.0665	0.4323
chr6	171115067	12533598	0.0732	0.5079
chr7	159138663	12067735	0.0758	0.8394

chr8	146364022	12532707	0.0856	0.7878
chr9	141213431	7450335	0.0528	0.5367
chr10	135534747	9444660	0.0697	0.5607
chr11	135006516	9121026	0.0676	0.579
chr12	133851895	9037114	0.0675	0.4395
chr13	115169878	6513788	0.0566	0.3996
chr14	107349540	5489565	0.0511	0.393
chr15	102531392	5188387	0.0506	0.3765
chr16	90354753	5674784	0.0628	0.4419
chr17	81195210	5084811	0.0626	0.4453
chr18	78077248	5865456	0.0751	1.0271
chr19	59128983	3469861	0.0587	0.6651
chr20	63025520	4401491	0.0698	0.4532
chr21	48129895	2981114	0.0619	0.4352
chr22	51304566	2298858	0.0448	0.3412
chrMT	16571	189186	11.4167	8.3477
chrX	155270560	11239895	0.0724	0.4791
chrY	59373566	564099	0.0095	0.1794

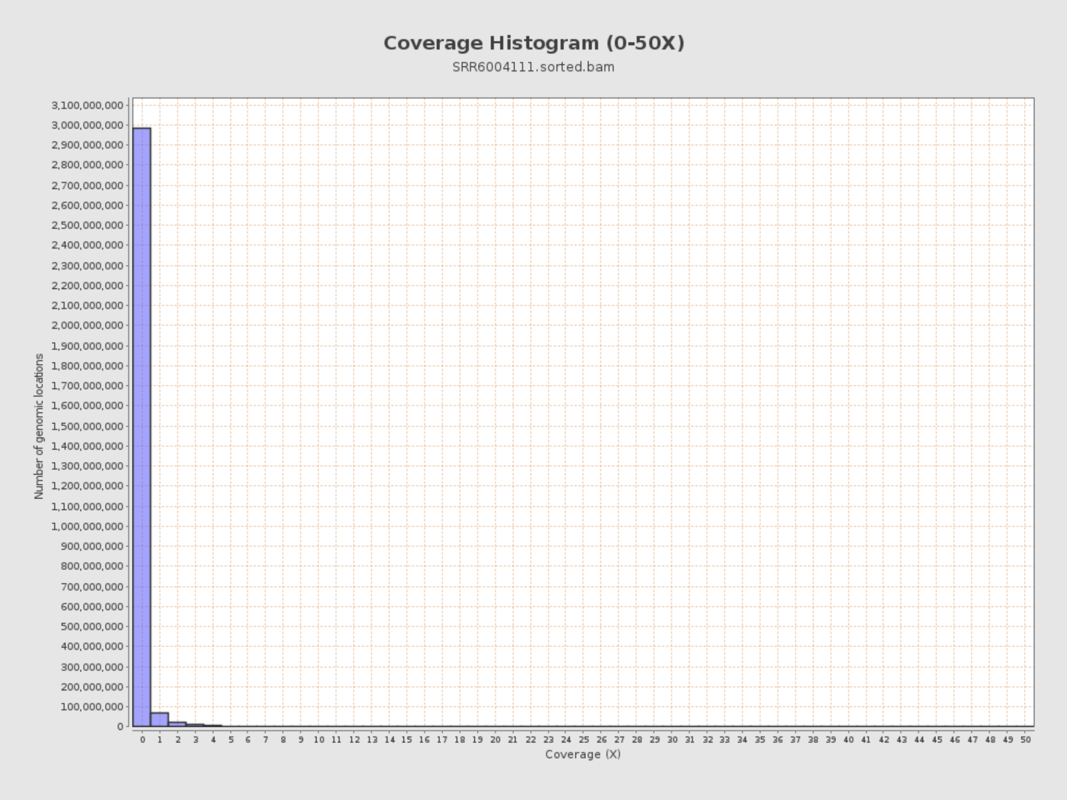
3. Results : Coverage across reference



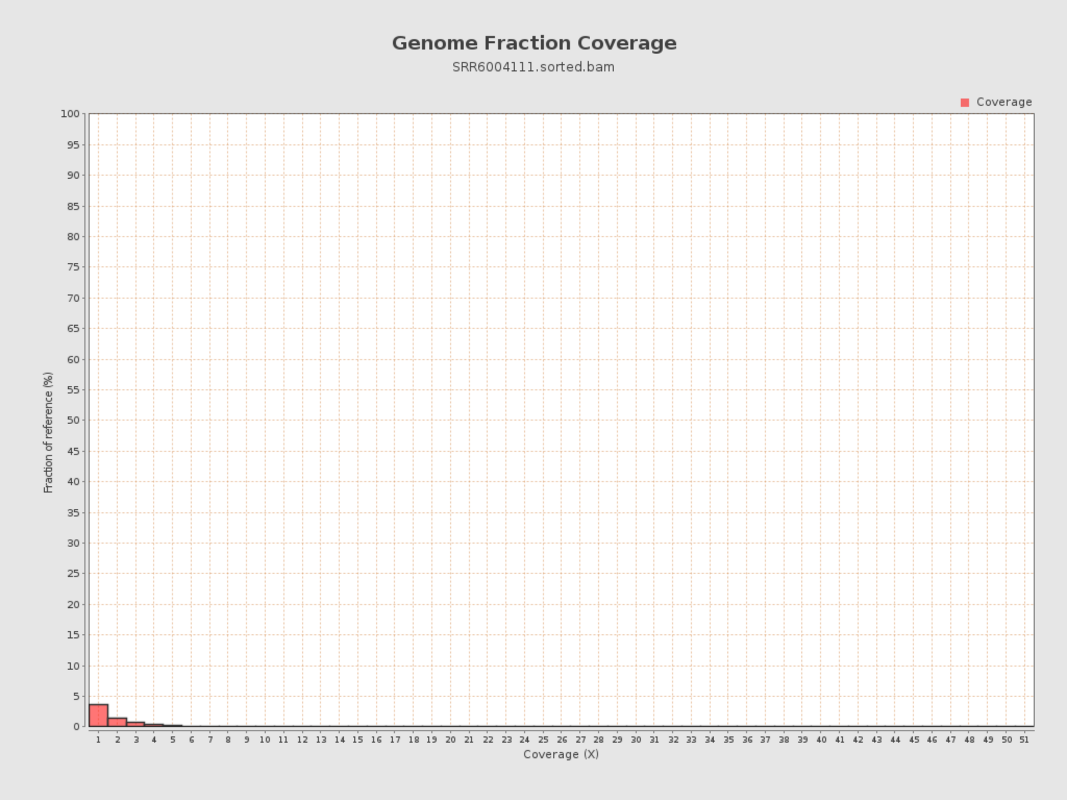
4. Results : Coverage Histogram



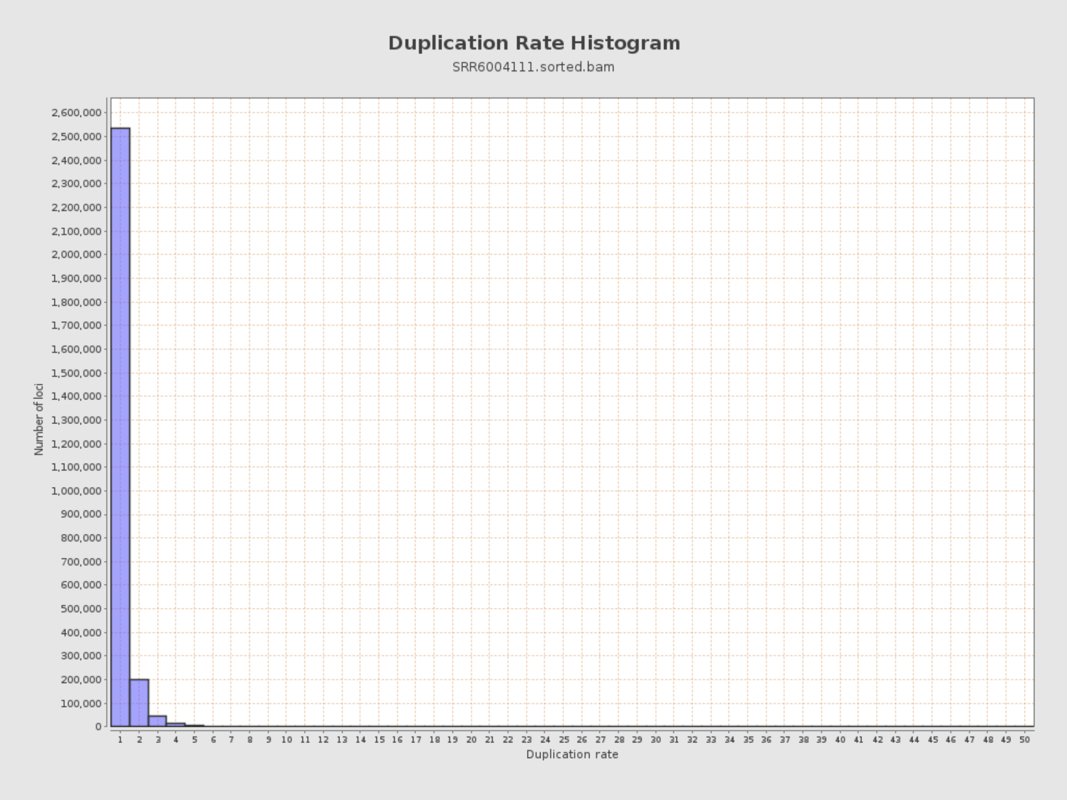
5. Results : Coverage Histogram (0-50X)



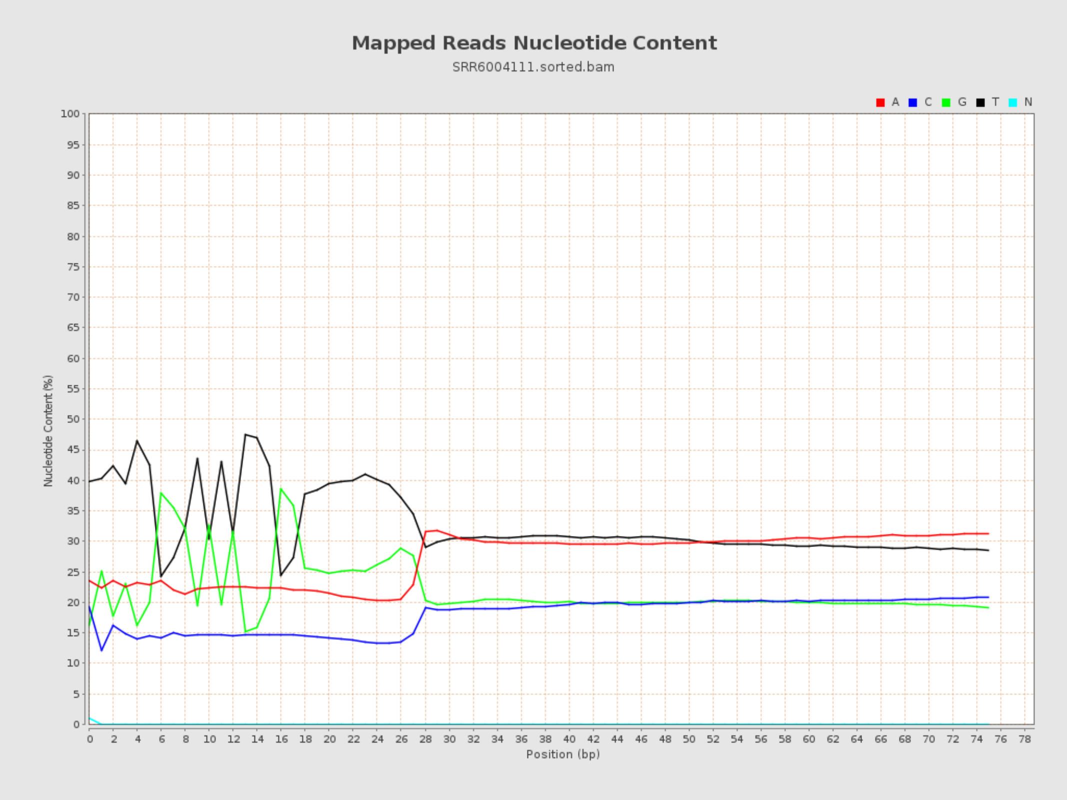
6. Results : Genome Fraction Coverage



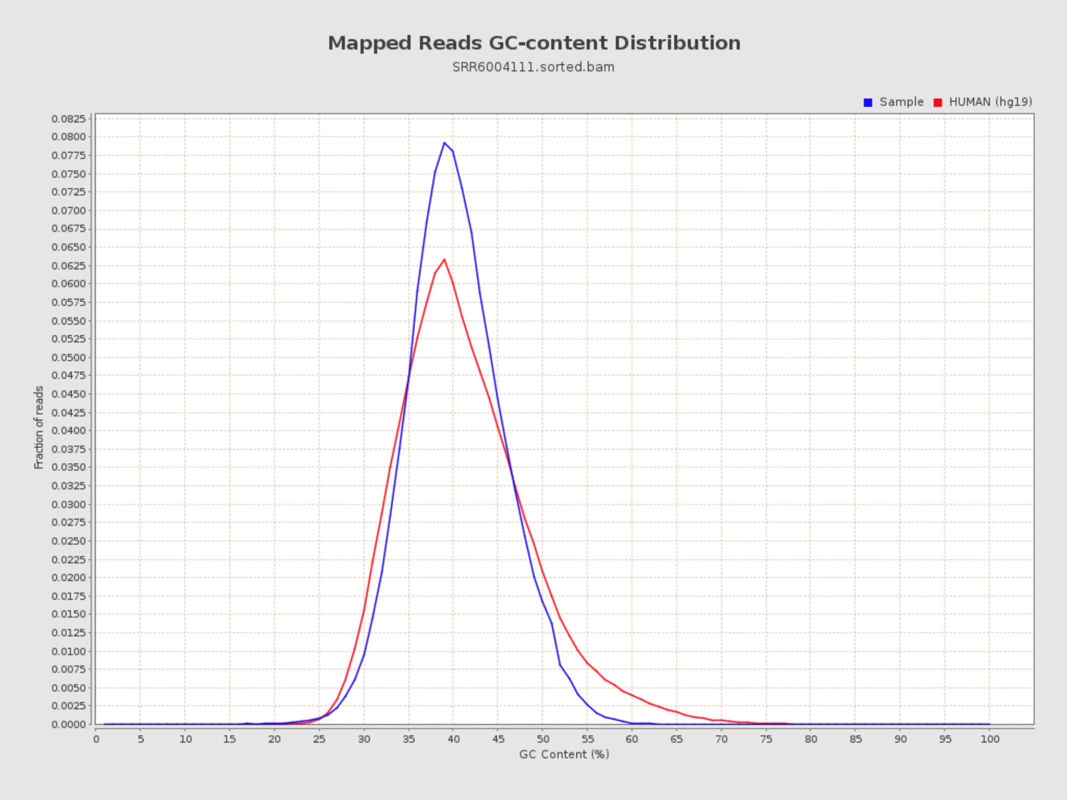
7. Results : Duplication Rate Histogram



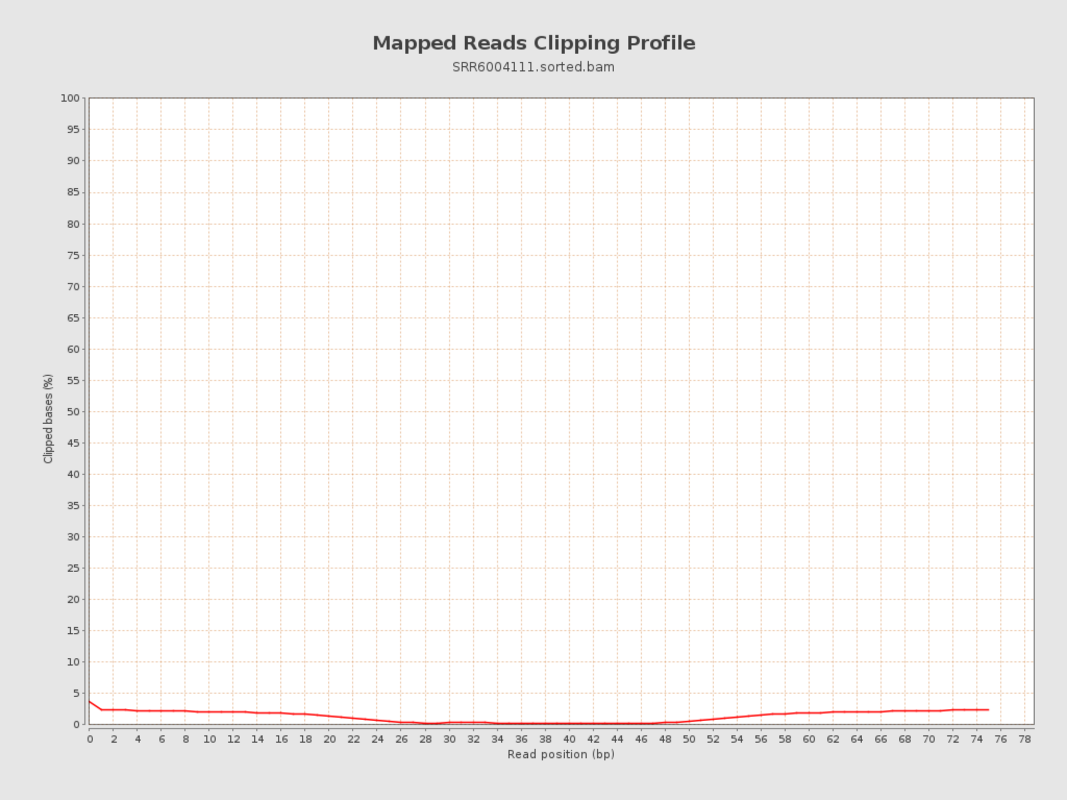
8. Results : Mapped Reads Nucleotide Content



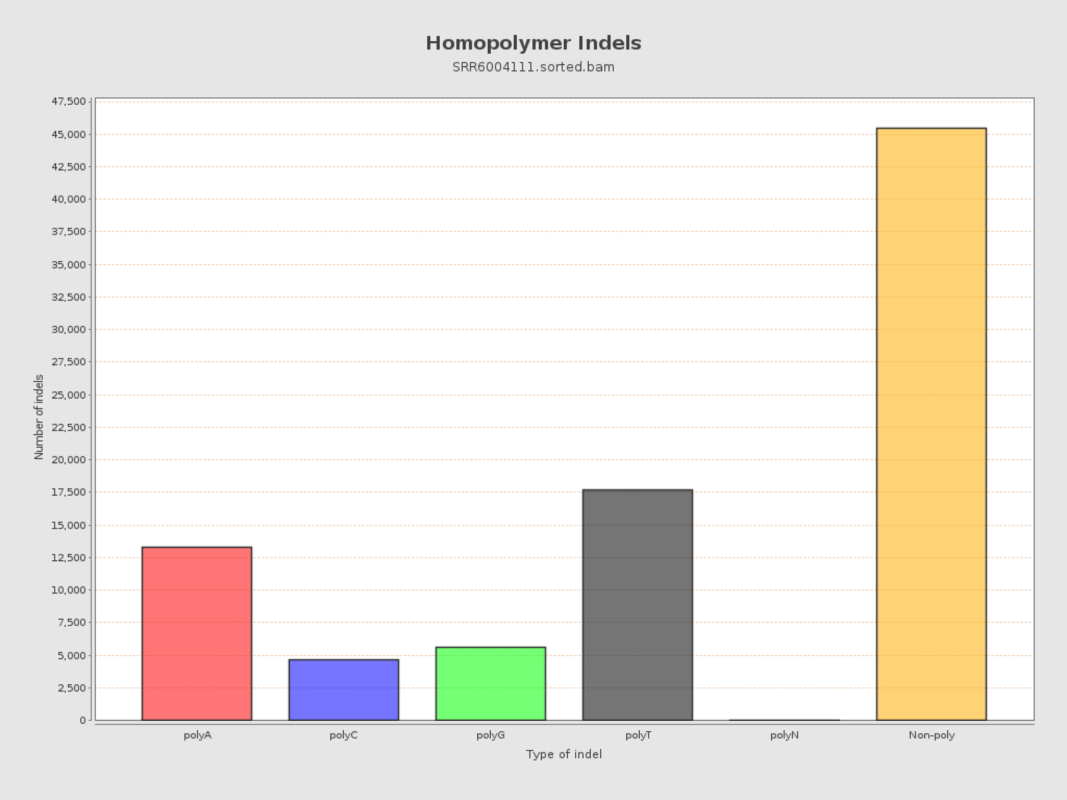
9. Results : Mapped Reads GC-content Distribution



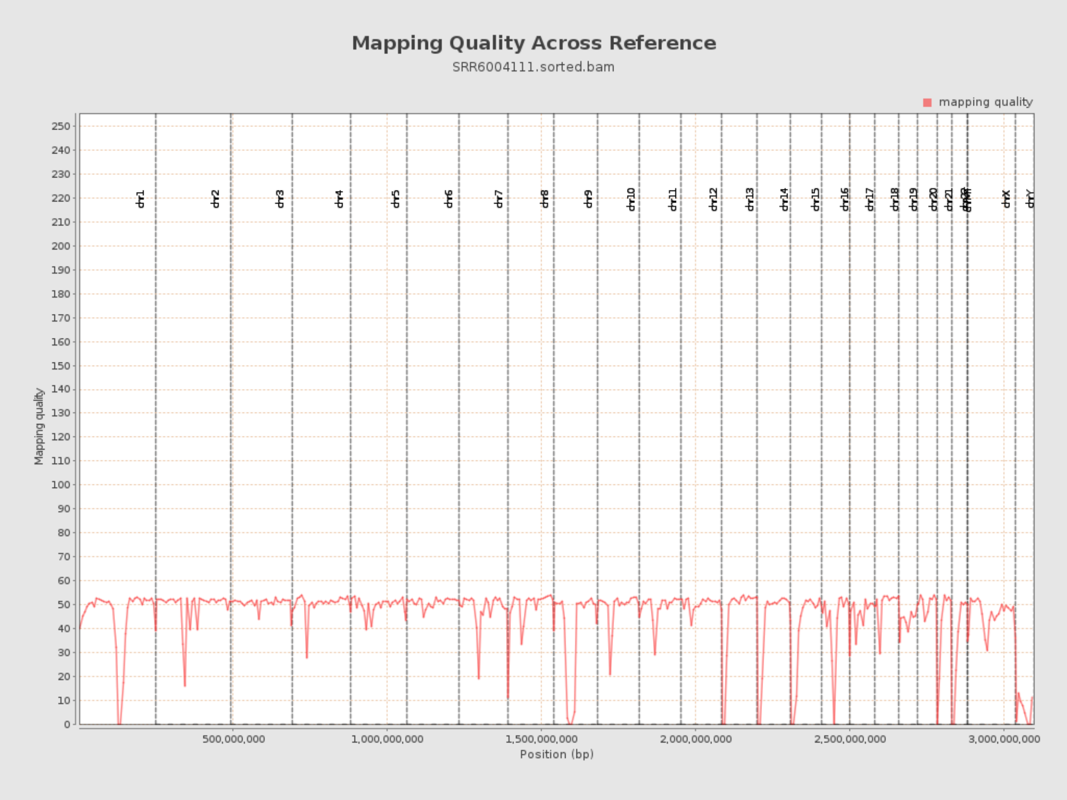
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram