Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 04:49:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004151.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_SRR6004151 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004151.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 04:49:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004151.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,300,187
Mapped reads	3,783,740 / 87.99%
Unmapped reads	516,447 / 12.01%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	26,571 / 0.62%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	221,497 / 5.15%
Duplication rate	4.55%
Clipped reads	1,675,438 / 38.96%

2.2. ACGT Content

Number/percentage of A's	70,596,185 / 27.86%
Number/percentage of C's	45,958,640 / 18.14%
Number/percentage of T's	82,067,197 / 32.38%
Number/percentage of G's	54,773,907 / 21.61%
Number/percentage of N's	27,767 / 0.01%
GC Percentage	39.75%

2.3. Coverage

Mean	0.0819

Standard Deviation	0.7581

2.4. Mapping Quality

Mean Mapping Quality	45.07

2.5. Mismatches and indels

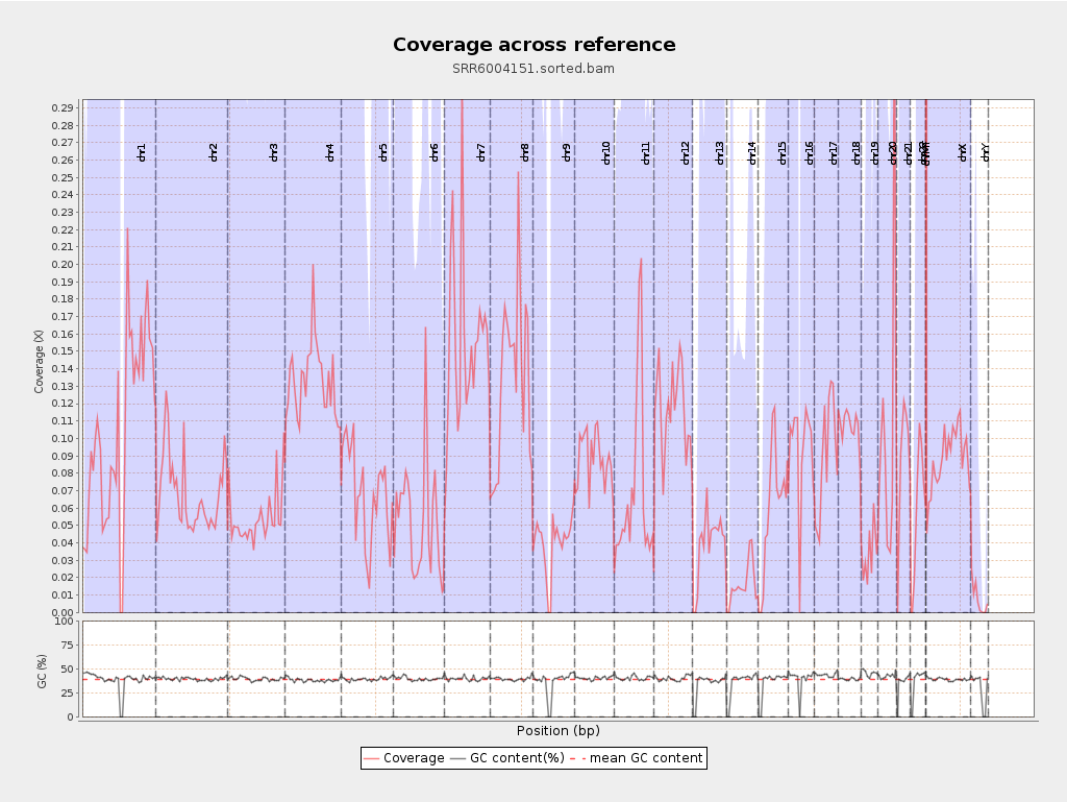
General error rate	0.92%
Mismatches	2,299,400
Insertions	20,698
Mapped reads with at least one insertion	0.54%
Deletions	65,547
Mapped reads with at least one deletion	1.71%
Homopolymer indels	47.71%

2.6. Chromosome stats

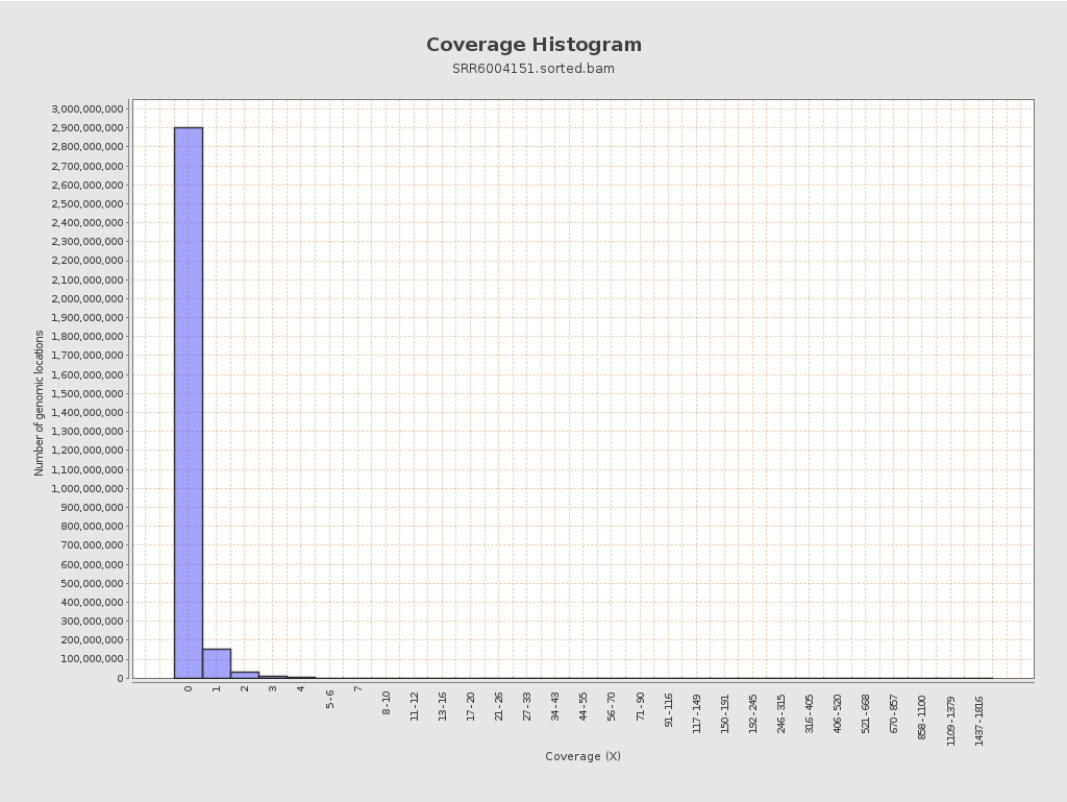
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	25922802	0.104	1.0812
chr2	243199373	16572871	0.0681	0.7428
chr3	198022430	10758424	0.0543	0.2875
chr4	191154276	25573777	0.1338	0.457
chr5	180915260	12258164	0.0678	0.3175
chr6	171115067	8959120	0.0524	0.3577
chr7	159138663	24536604	0.1542	2.2285

chr8	146364022	19409341	0.1326	1.0398
chr9	141213431	5708461	0.0404	0.4395
chr10	135534747	11929766	0.088	0.5341
chr11	135006516	9209626	0.0682	0.4009
chr12	133851895	15715297	0.1174	0.4262
chr13	115169878	4489551	0.039	0.2452
chr14	107349540	1812808	0.0169	0.2179
chr15	102531392	5996875	0.0585	0.3056
chr16	90354753	8290779	0.0918	0.3976
chr17	81195210	7277571	0.0896	0.3988
chr18	78077248	8408393	0.1077	0.8165
chr19	59128983	1979003	0.0335	0.7711
chr20	63025520	7363617	0.1168	0.4653
chr21	48129895	3985266	0.0828	0.3661
chr22	51304566	3030006	0.0591	0.2949
chrMT	16571	225053	13.5811	8.388
chrX	155270560	13679174	0.0881	0.4151
chrY	59373566	439401	0.0074	0.1341

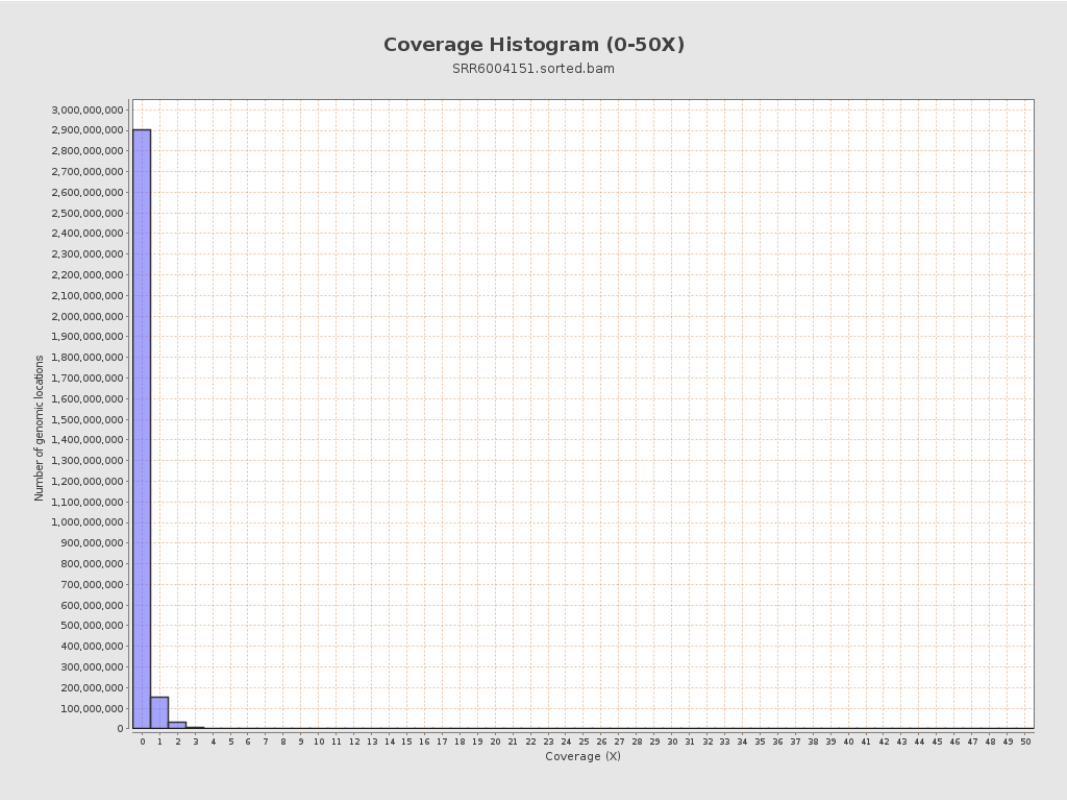
3. Results : Coverage across reference



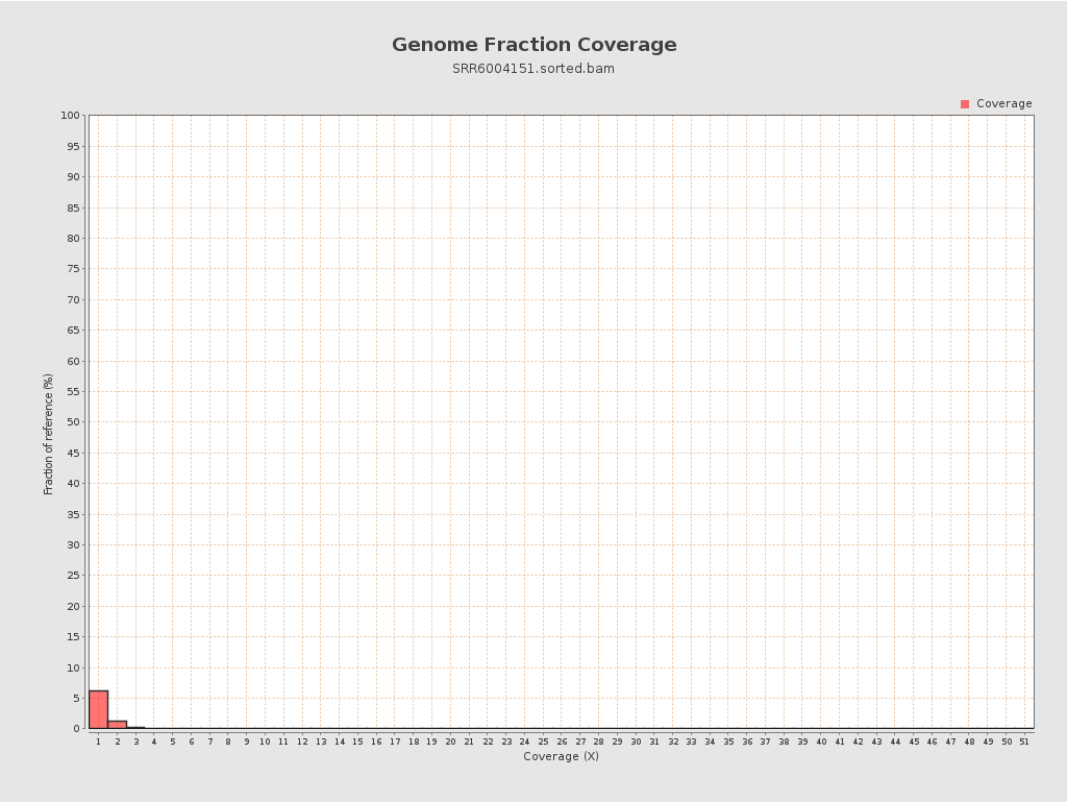
4. Results : Coverage Histogram



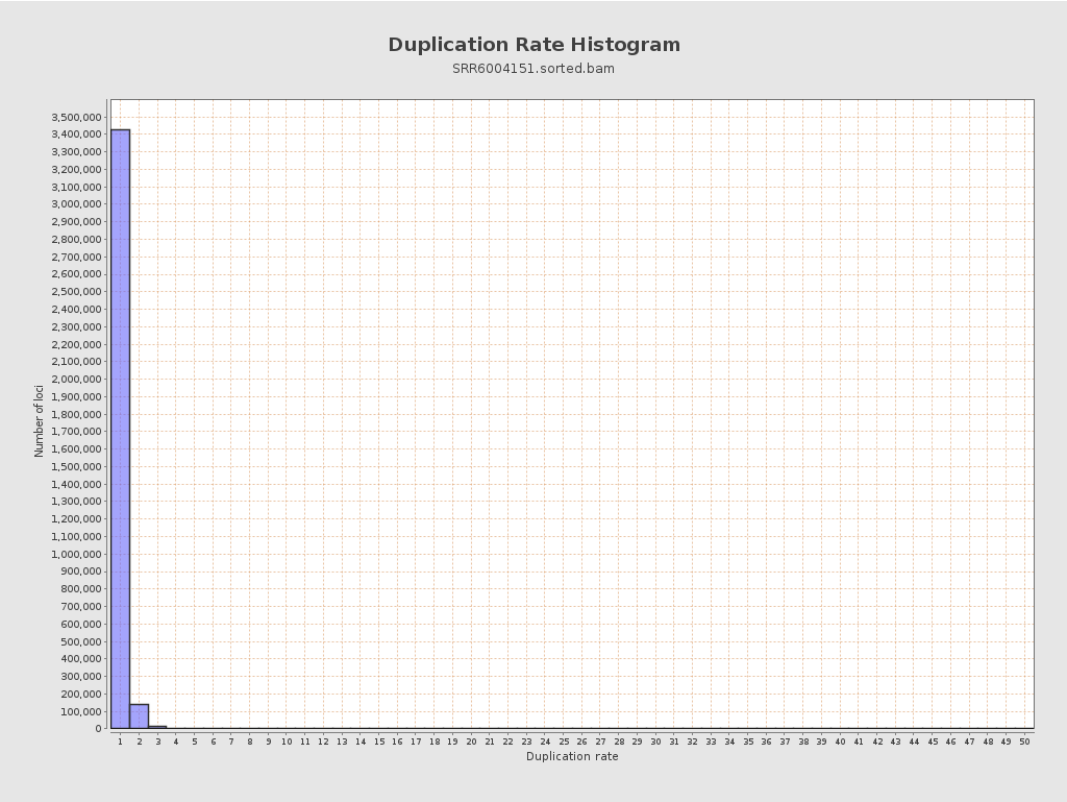
5. Results : Coverage Histogram (0-50X)



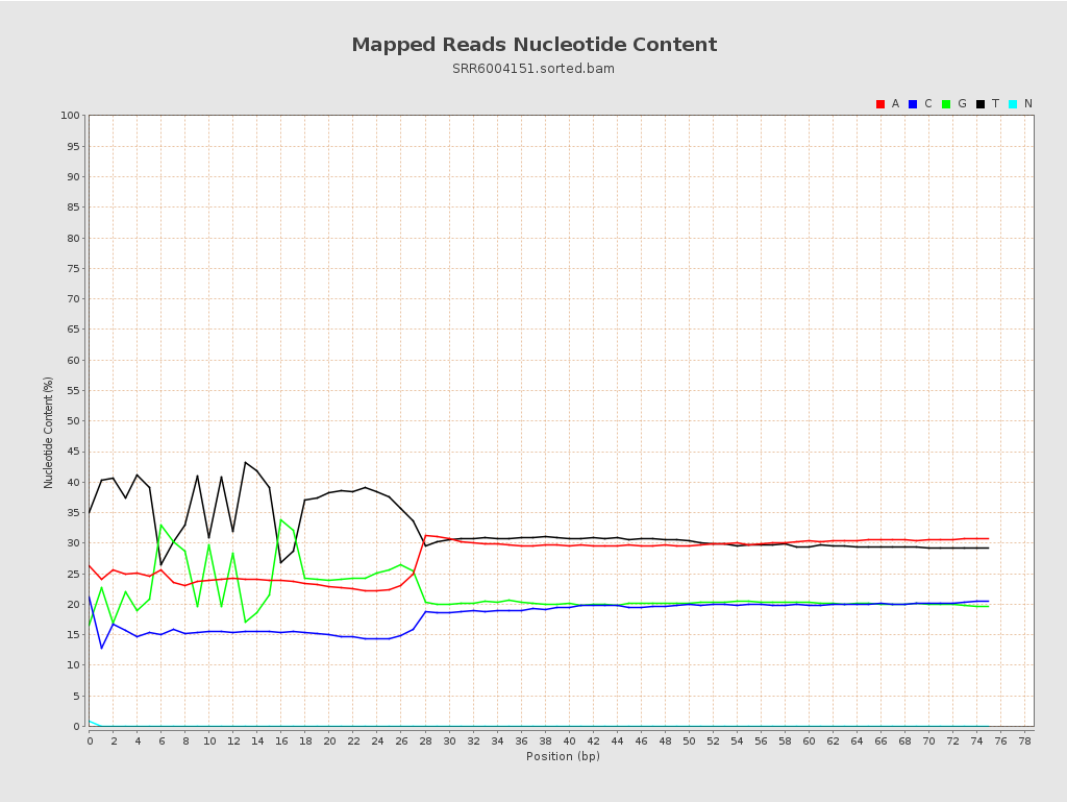
6. Results : Genome Fraction Coverage



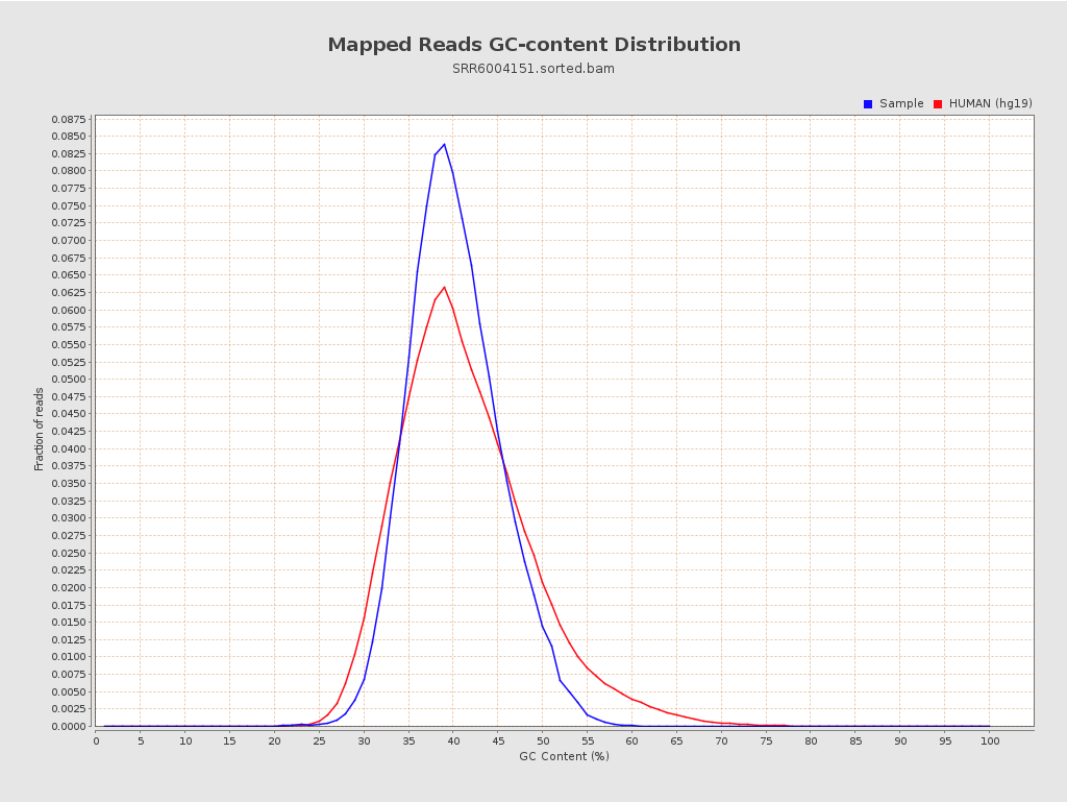
7. Results : Duplication Rate Histogram



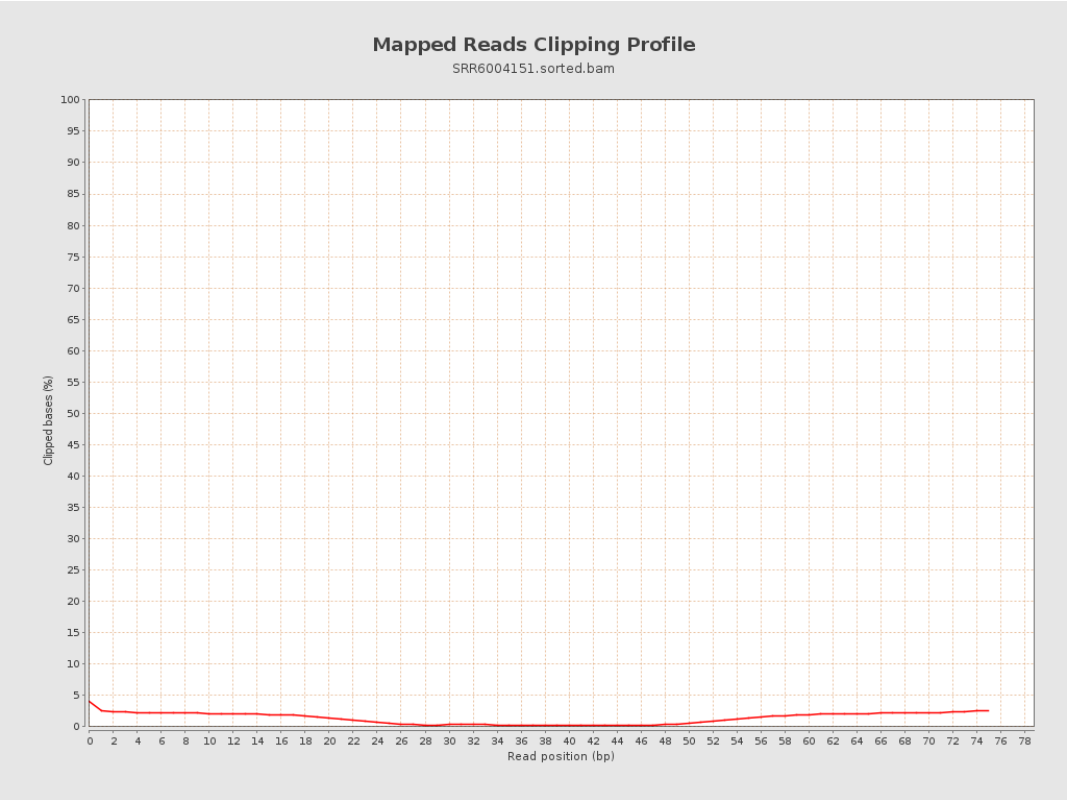
8. Results : Mapped Reads Nucleotide Content



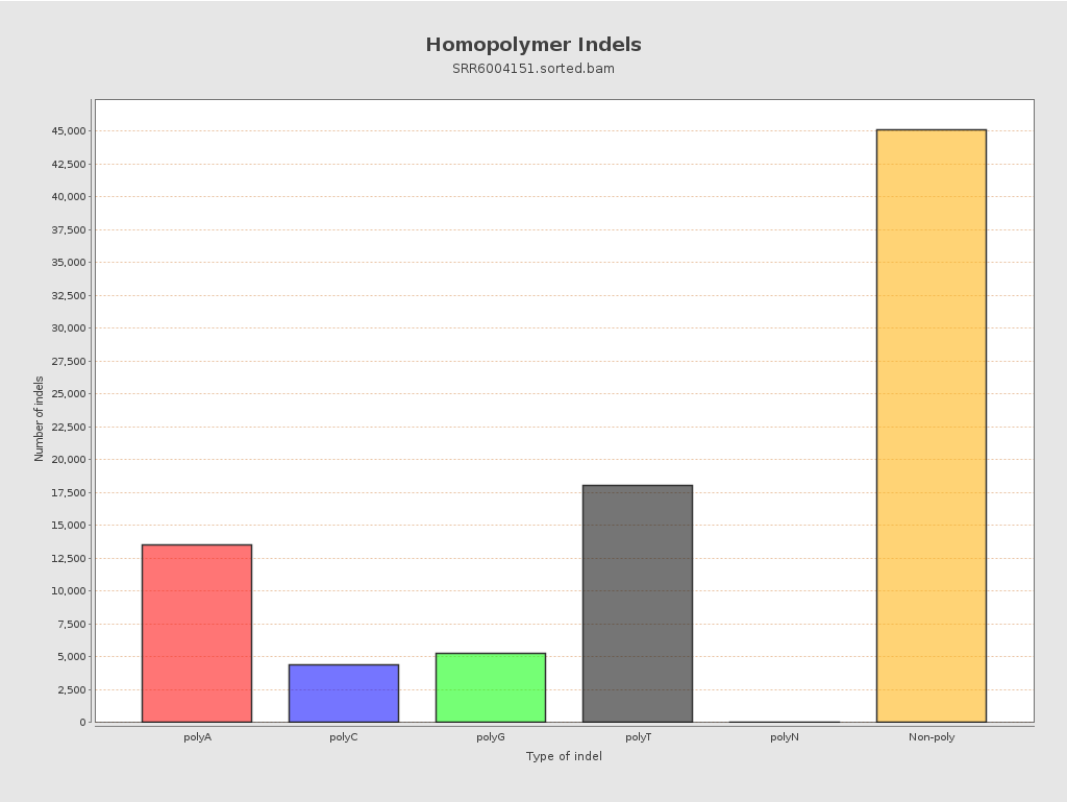
9. Results : Mapped Reads GC-content Distribution



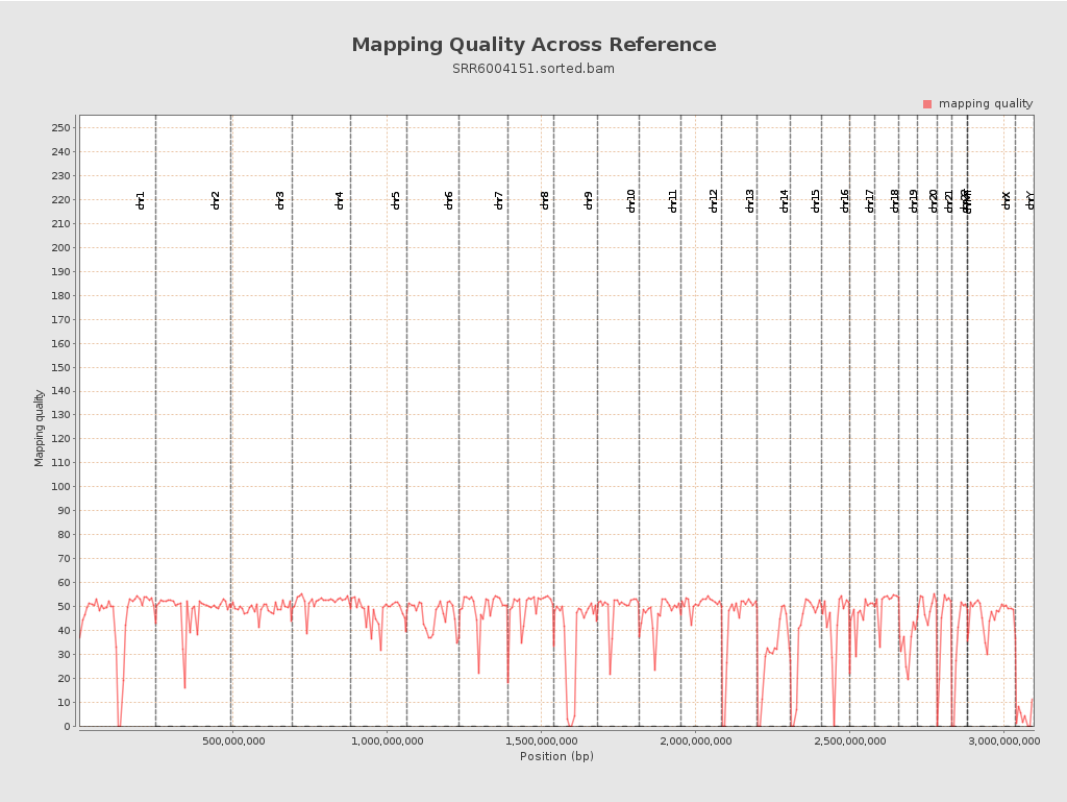
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram