Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 19:06:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6230355.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_SRR6230355 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6230355.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 19:06:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6230355.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,346,834
Mapped reads	1,854,673 / 79.03%
Unmapped reads	492,161 / 20.97%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,643 / 0.33%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	95,962 / 4.09%
Duplication rate	3.64%
Clipped reads	1,143,898 / 48.74%

2.2. ACGT Content

Number/percentage of A's	29,856,243 / 25.64%
Number/percentage of C's	19,567,849 / 16.8%
Number/percentage of T's	39,007,156 / 33.49%
Number/percentage of G's	27,821,348 / 23.89%
Number/percentage of N's	211,470 / 0.18%
GC Percentage	40.69%

2.3. Coverage

Mean	0.0376

Standard Deviation	0.4227

2.4. Mapping Quality

Mean Mapping Quality	43.89

2.5. Mismatches and indels

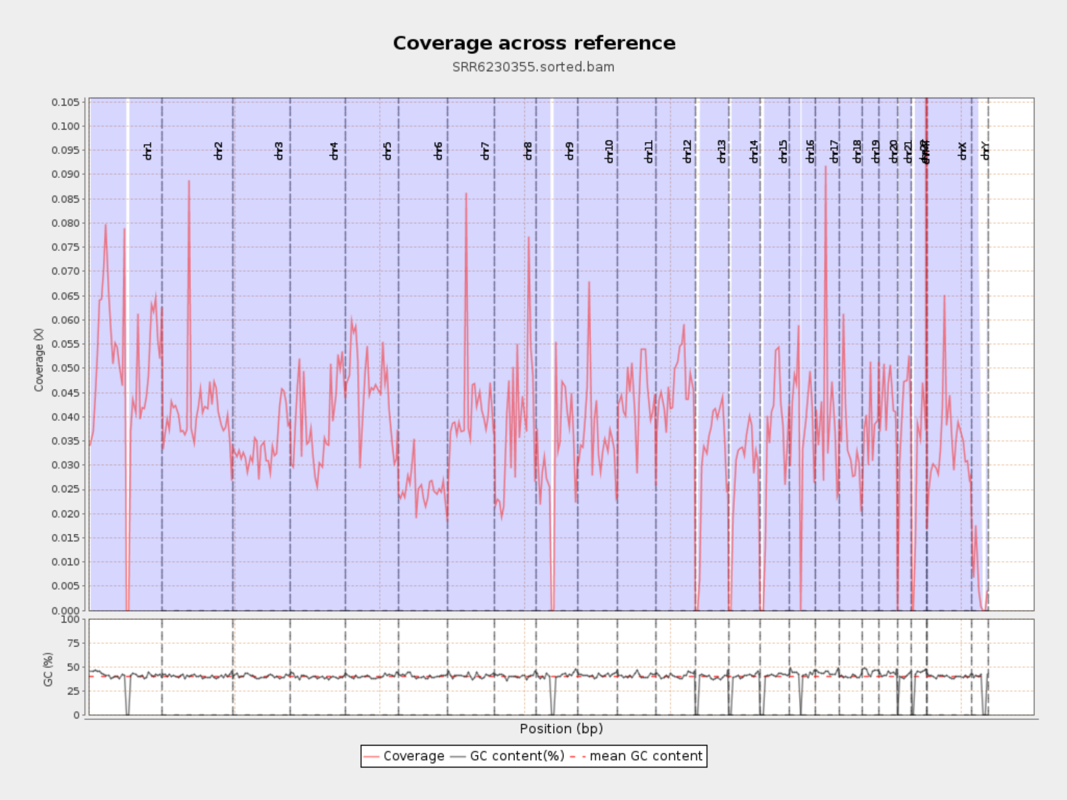
General error rate	0.99%
Mismatches	1,128,833
Insertions	10,923
Mapped reads with at least one insertion	0.58%
Deletions	39,212
Mapped reads with at least one deletion	2.09%
Homopolymer indels	48.48%

2.6. Chromosome stats

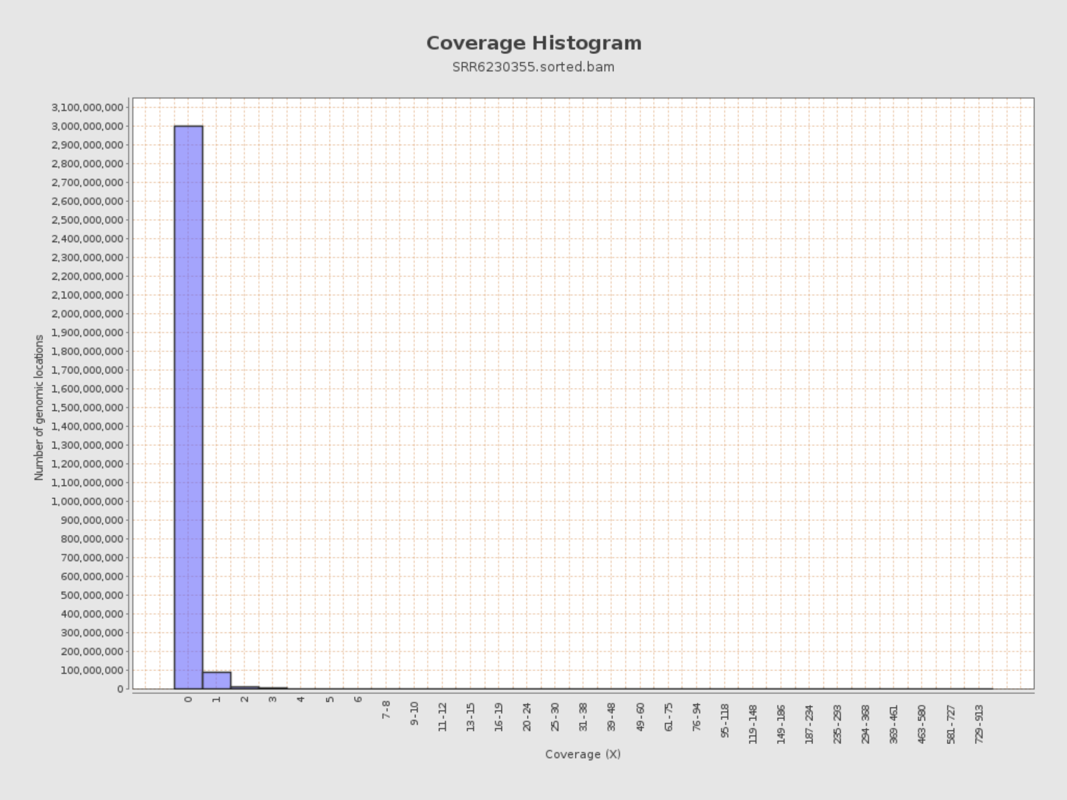
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12493221	0.0501	0.7329
chr2	243199373	10051412	0.0413	0.5034
chr3	198022430	6774590	0.0342	0.2118
chr4	191154276	7434532	0.0389	0.2448
chr5	180915260	8282092	0.0458	0.2462
chr6	171115067	4288805	0.0251	0.2459
chr7	159138663	6666405	0.0419	0.6821

chr8	146364022	5573657	0.0381	0.4847
chr9	141213431	4432028	0.0314	0.485
chr10	135534747	4971978	0.0367	0.3565
chr11	135006516	5964541	0.0442	0.3996
chr12	133851895	6164171	0.0461	0.2531
chr13	115169878	3503173	0.0304	0.1949
chr14	107349540	3034159	0.0283	0.2419
chr15	102531392	3369553	0.0329	0.2082
chr16	90354753	3506174	0.0388	0.2573
chr17	81195210	3316456	0.0408	0.2829
chr18	78077248	2728920	0.035	0.8382
chr19	59128983	2251886	0.0381	0.5828
chr20	63025520	2722301	0.0432	0.2571
chr21	48129895	1867316	0.0388	0.2436
chr22	51304566	1439808	0.0281	0.1885
chrMT	16571	76370	4.6087	4.3547
chrX	155270560	5303840	0.0342	0.2986
chrY	59373566	310180	0.0052	0.1232

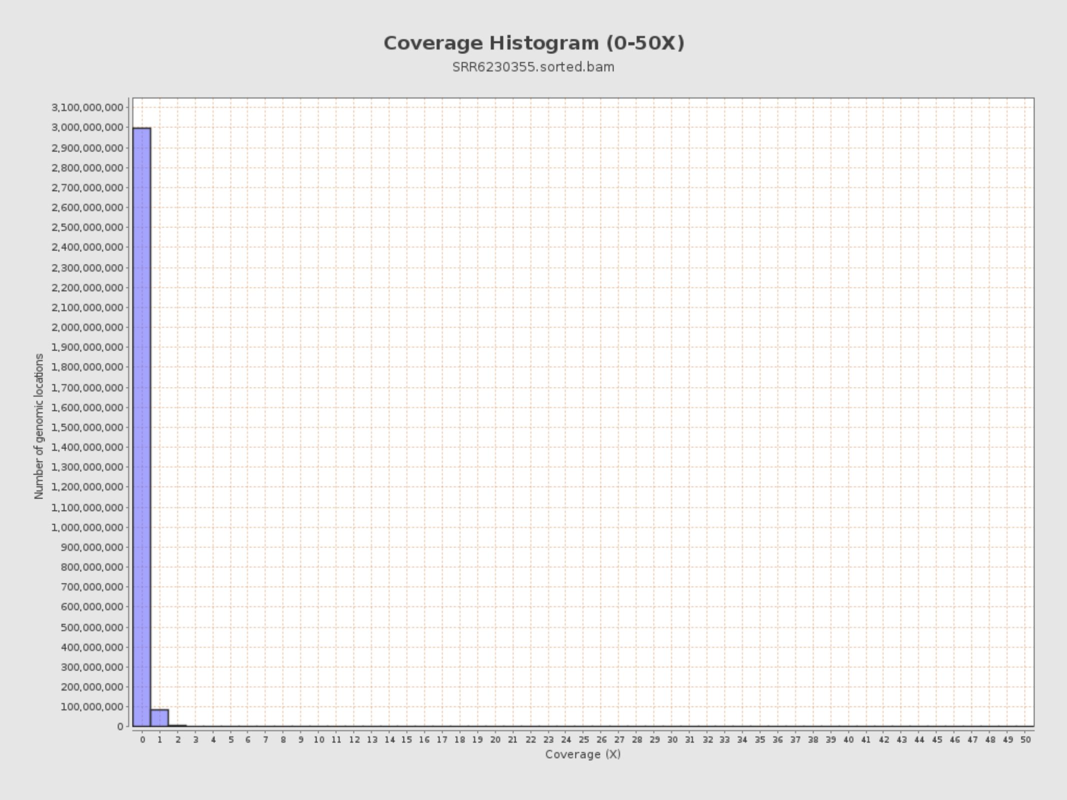
3. Results : Coverage across reference



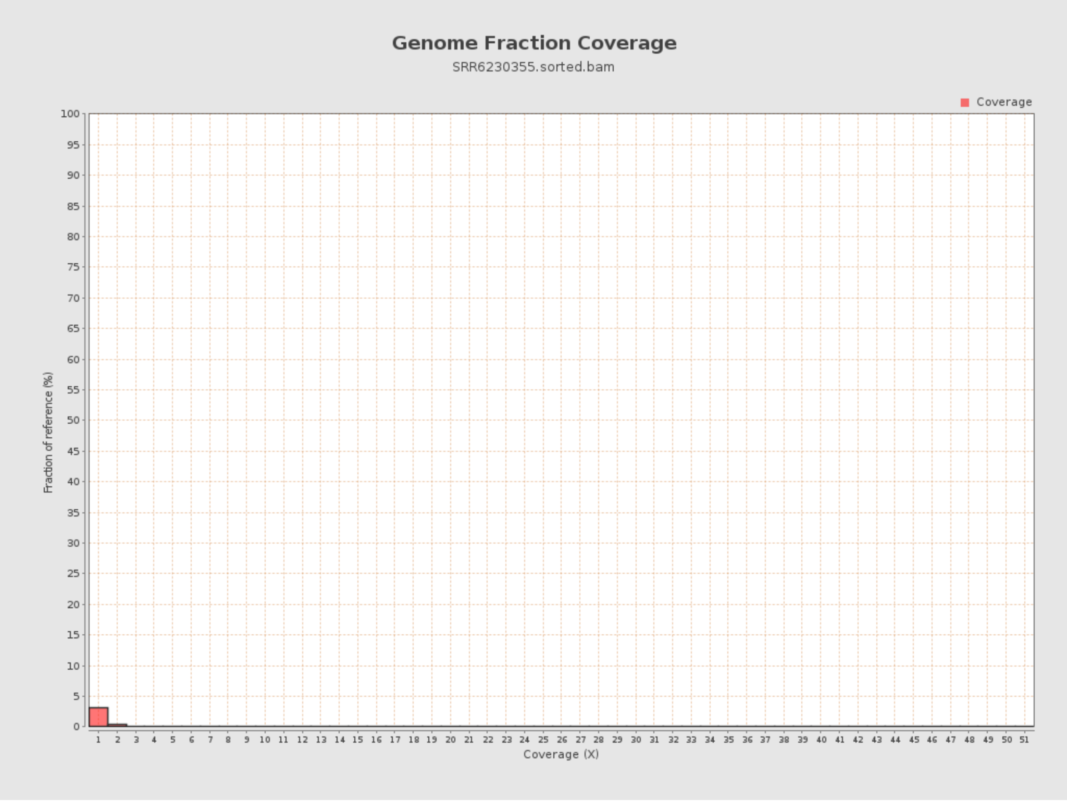
4. Results : Coverage Histogram



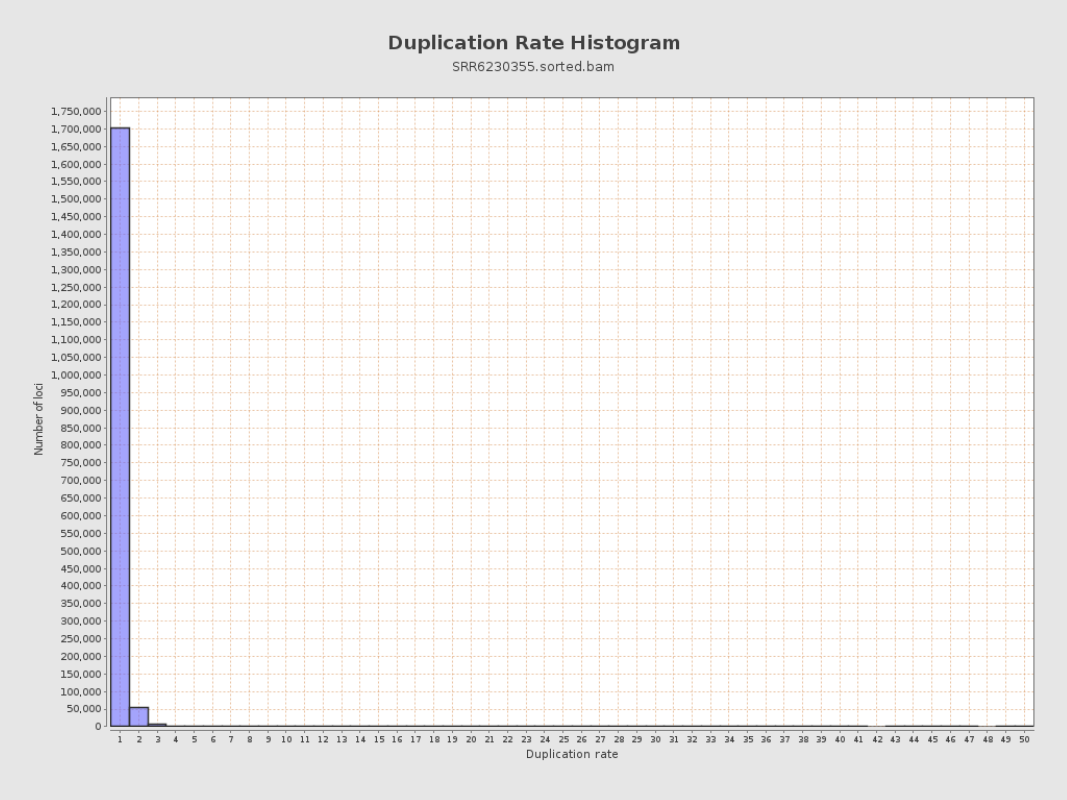
5. Results : Coverage Histogram (0-50X)



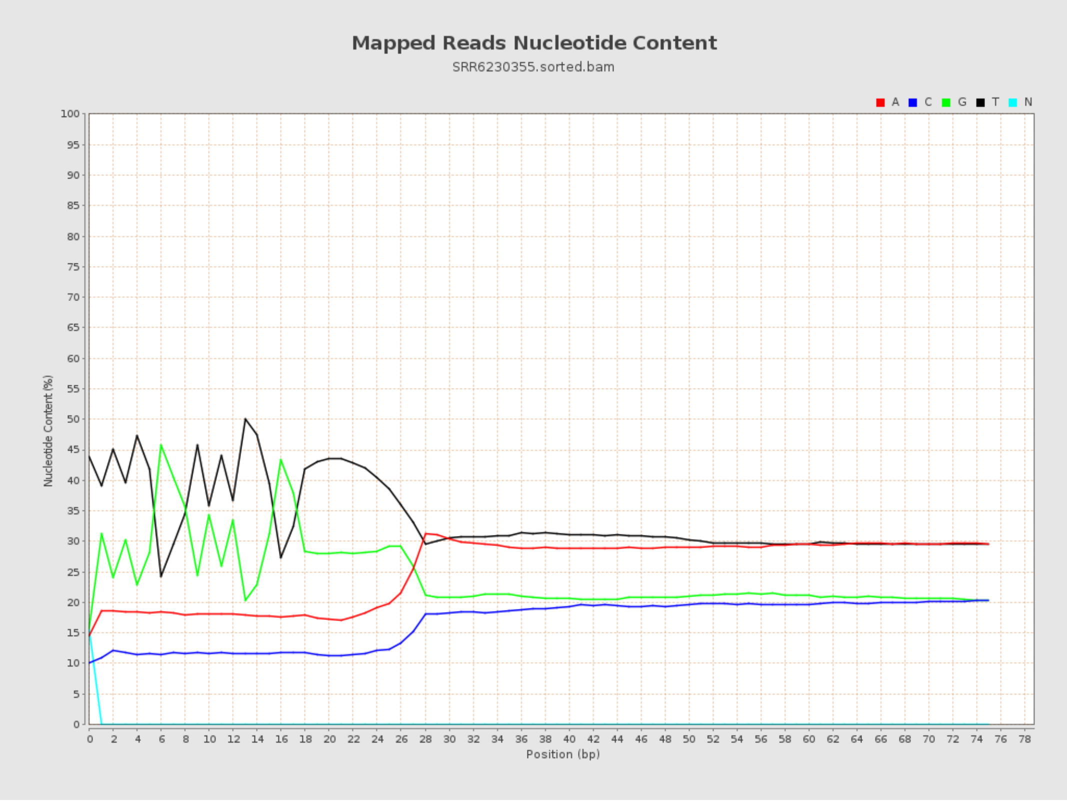
6. Results : Genome Fraction Coverage



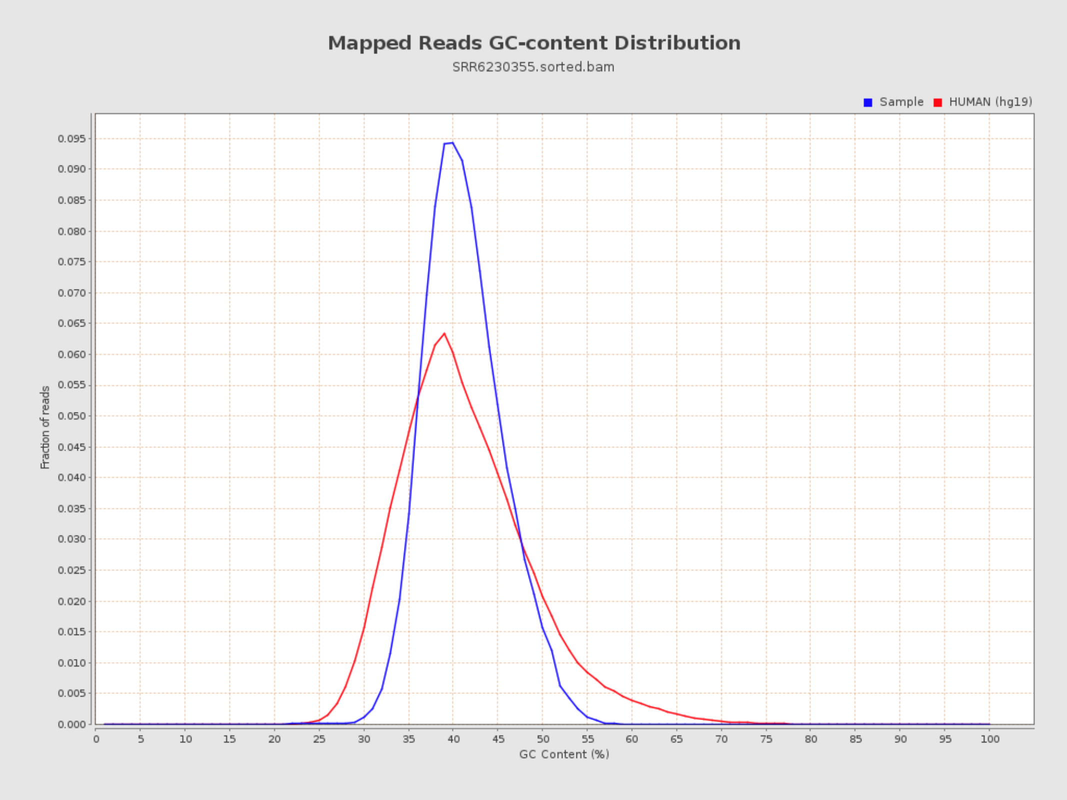
7. Results : Duplication Rate Histogram



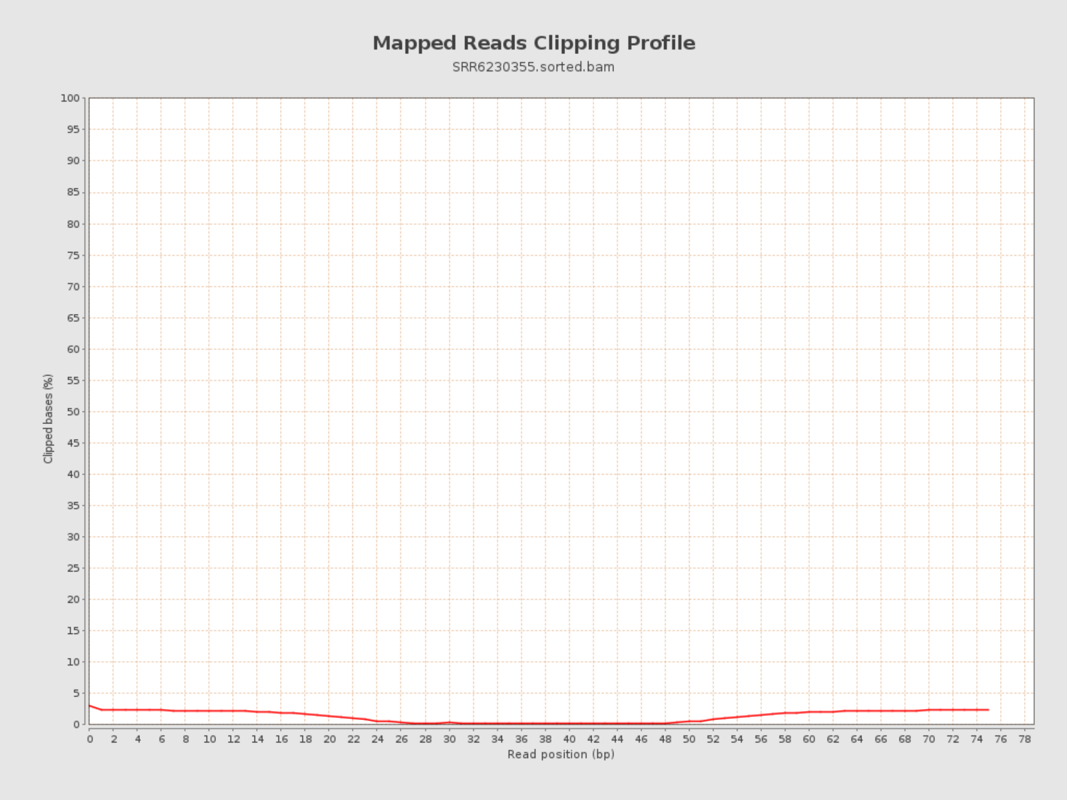
8. Results : Mapped Reads Nucleotide Content



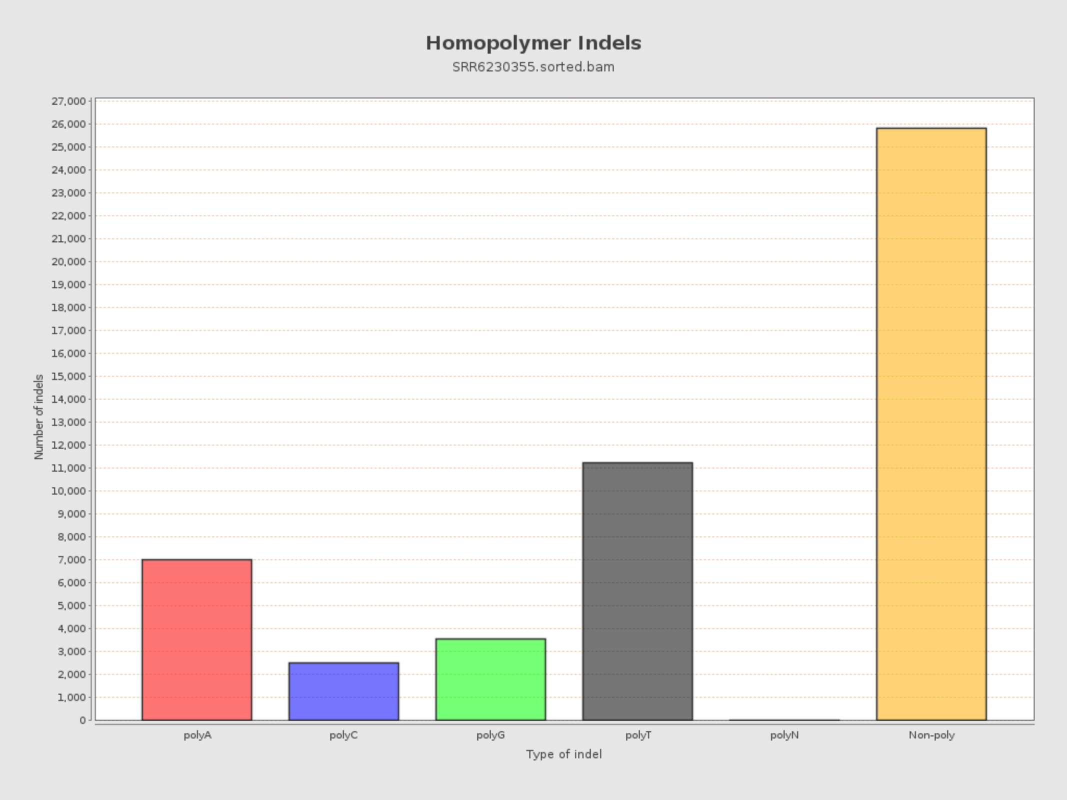
9. Results : Mapped Reads GC-content Distribution



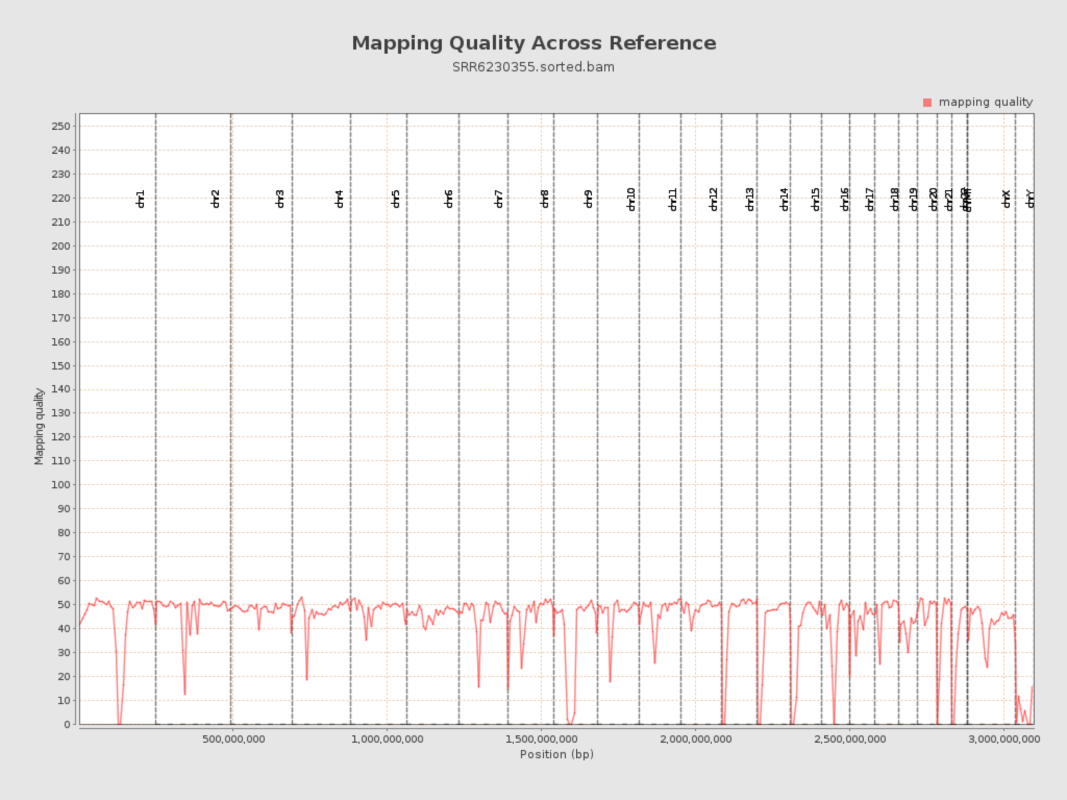
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram