Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 05:05:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004156.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_SRR6004156 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004156.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 05:05:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004156.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,195,746
Mapped reads	1,961,354 / 89.33%
Unmapped reads	234,392 / 10.67%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,220 / 0.92%
Read min/max/mean length	30 / 76 / 76.32
Duplicated reads (estimated)	80,368 / 3.66%
Duplication rate	3.15%
Clipped reads	902,574 / 41.11%

2.2. ACGT Content

Number/percentage of A's	37,448,843 / 28.68%
Number/percentage of C's	23,787,687 / 18.22%
Number/percentage of T's	41,653,800 / 31.9%
Number/percentage of G's	27,671,643 / 21.19%
Number/percentage of N's	9,214 / 0.01%
GC Percentage	39.41%

2.3. Coverage

Mean	0.0422

Standard Deviation	0.3877

2.4. Mapping Quality

Mean Mapping Quality	46.54

2.5. Mismatches and indels

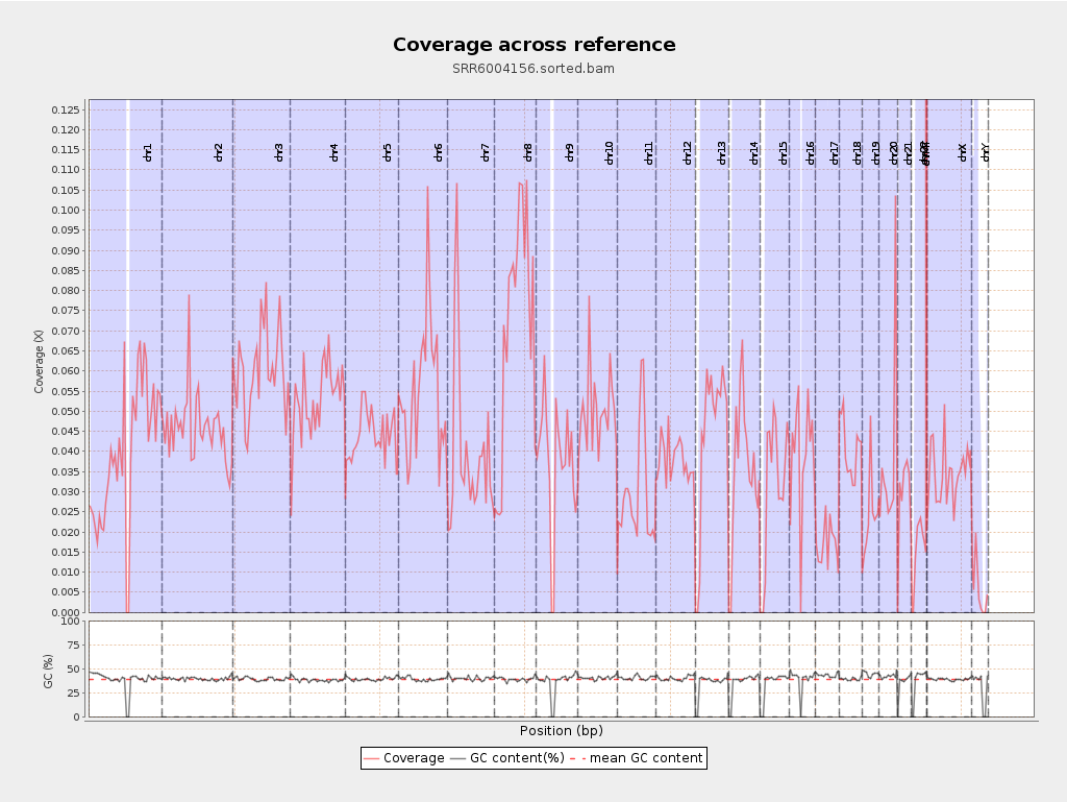
General error rate	0.93%
Mismatches	1,193,907
Insertions	10,501
Mapped reads with at least one insertion	0.53%
Deletions	40,709
Mapped reads with at least one deletion	2.05%
Homopolymer indels	44.94%

2.6. Chromosome stats

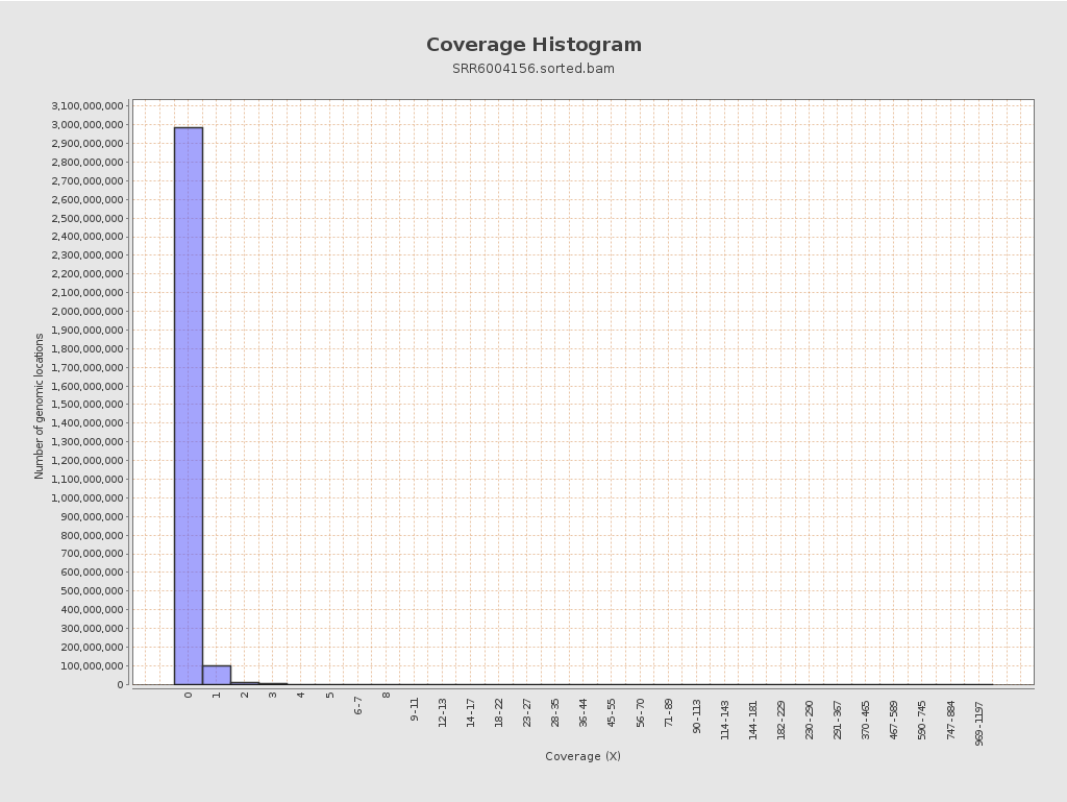
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	9869110	0.0396	0.7069
chr2	243199373	11143231	0.0458	0.3784
chr3	198022430	11930139	0.0602	0.2752
chr4	191154276	10155132	0.0531	0.2847
chr5	180915260	7993875	0.0442	0.2405
chr6	171115067	9464930	0.0553	0.3046
chr7	159138663	6493034	0.0408	0.3139

chr8	146364022	10350752	0.0707	0.7533
chr9	141213431	5305912	0.0376	0.3698
chr10	135534747	6798310	0.0502	0.3994
chr11	135006516	4064234	0.0301	0.2462
chr12	133851895	5048775	0.0377	0.233
chr13	115169878	5075547	0.0441	0.2376
chr14	107349540	3824004	0.0356	0.2327
chr15	102531392	3242253	0.0316	0.1993
chr16	90354753	3550933	0.0393	0.2579
chr17	81195210	1382255	0.017	0.155
chr18	78077248	3174065	0.0407	0.6815
chr19	59128983	1440627	0.0244	0.5145
chr20	63025520	2489715	0.0395	0.2381
chr21	48129895	1388714	0.0289	0.2231
chr22	51304566	764717	0.0149	0.134
chrMT	16571	53572	3.2329	2.8286
chrX	155270560	5322294	0.0343	0.2378
chrY	59373566	313562	0.0053	0.1508

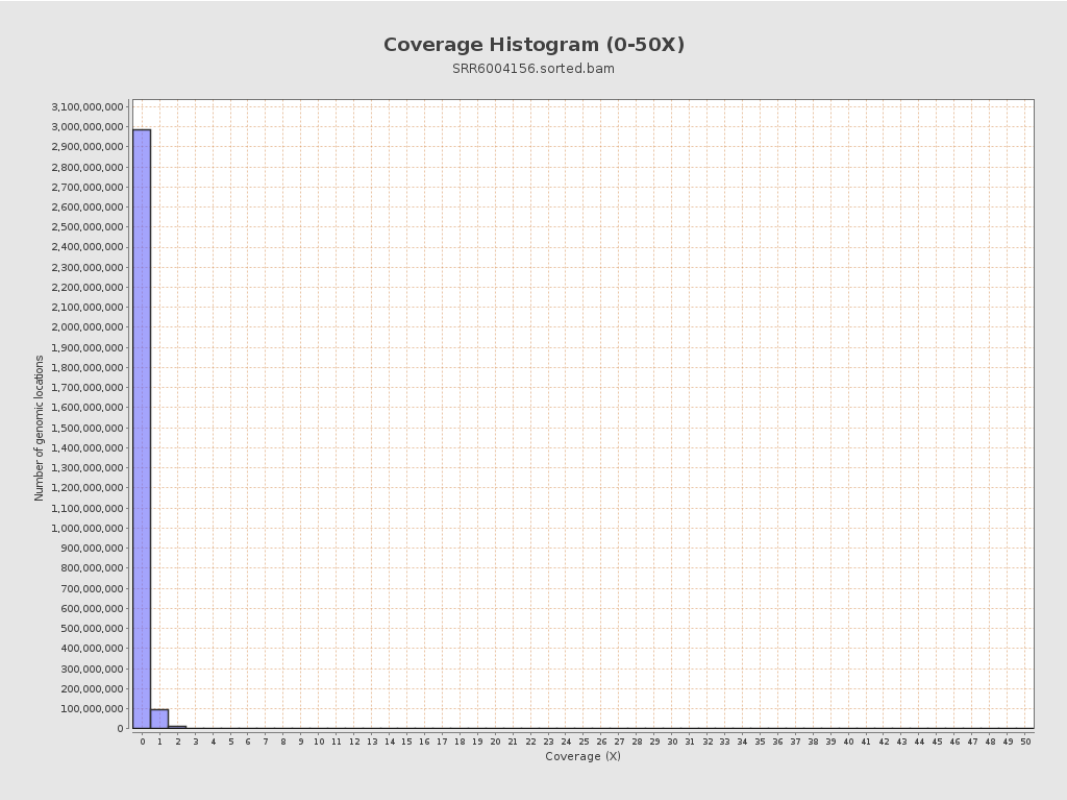
3. Results : Coverage across reference



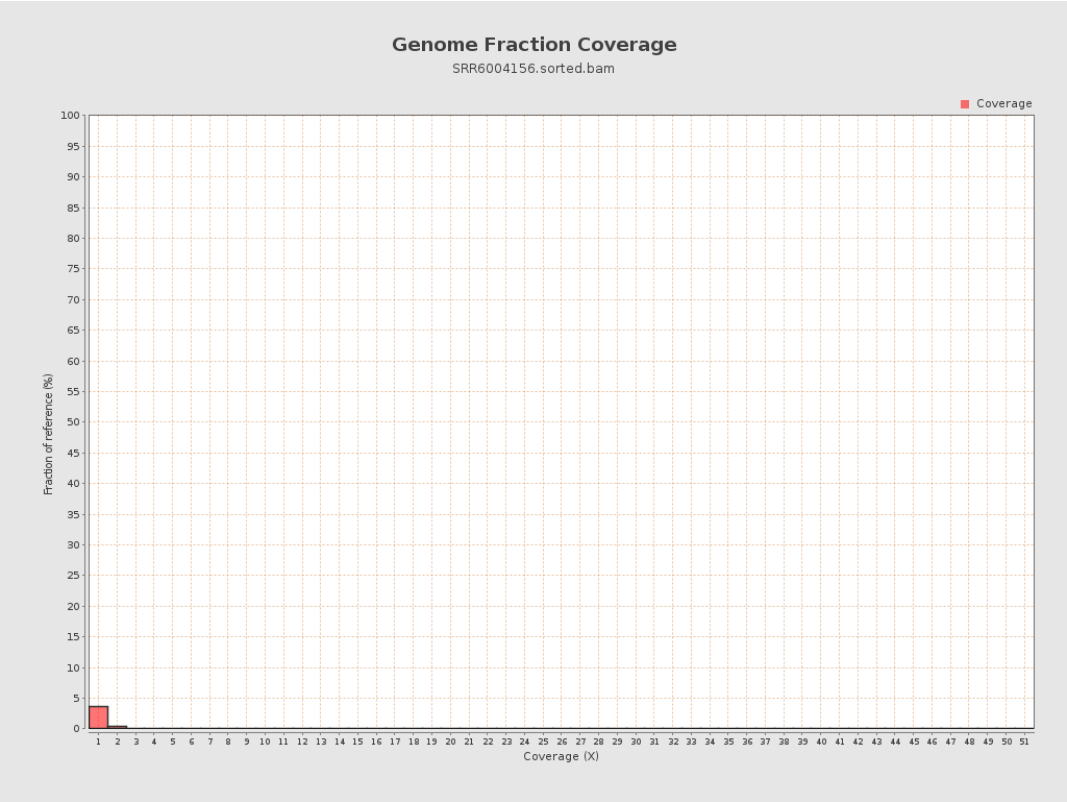
4. Results : Coverage Histogram



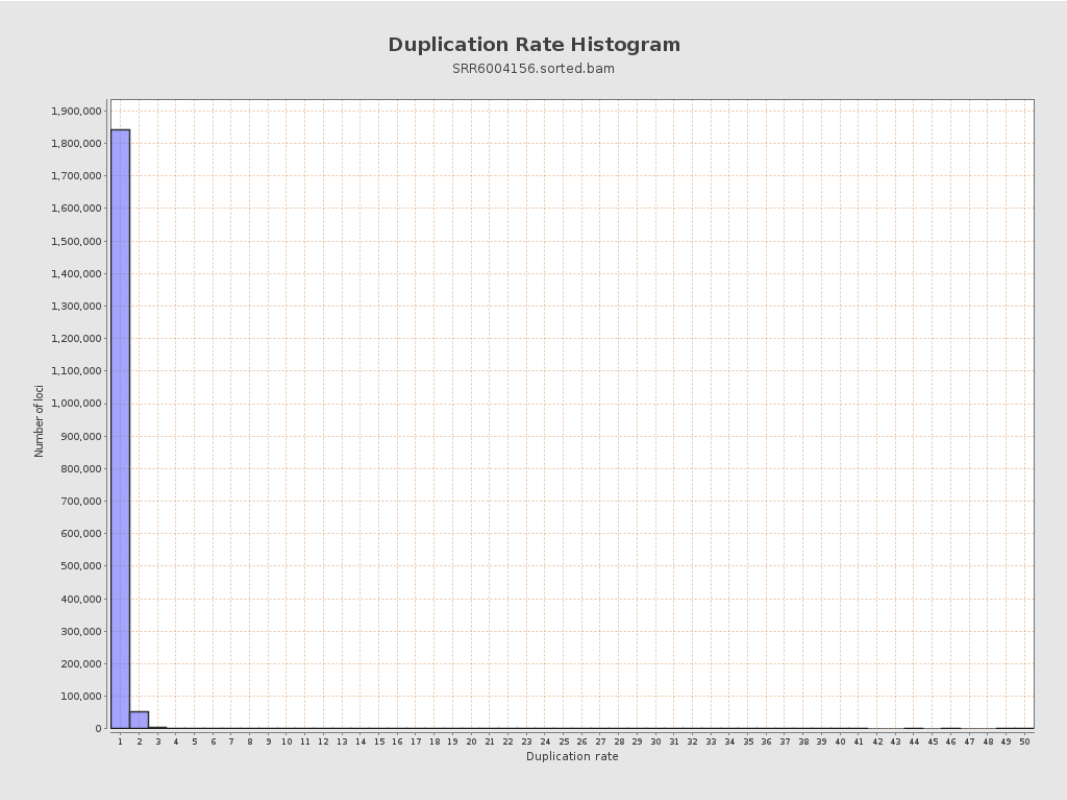
5. Results : Coverage Histogram (0-50X)



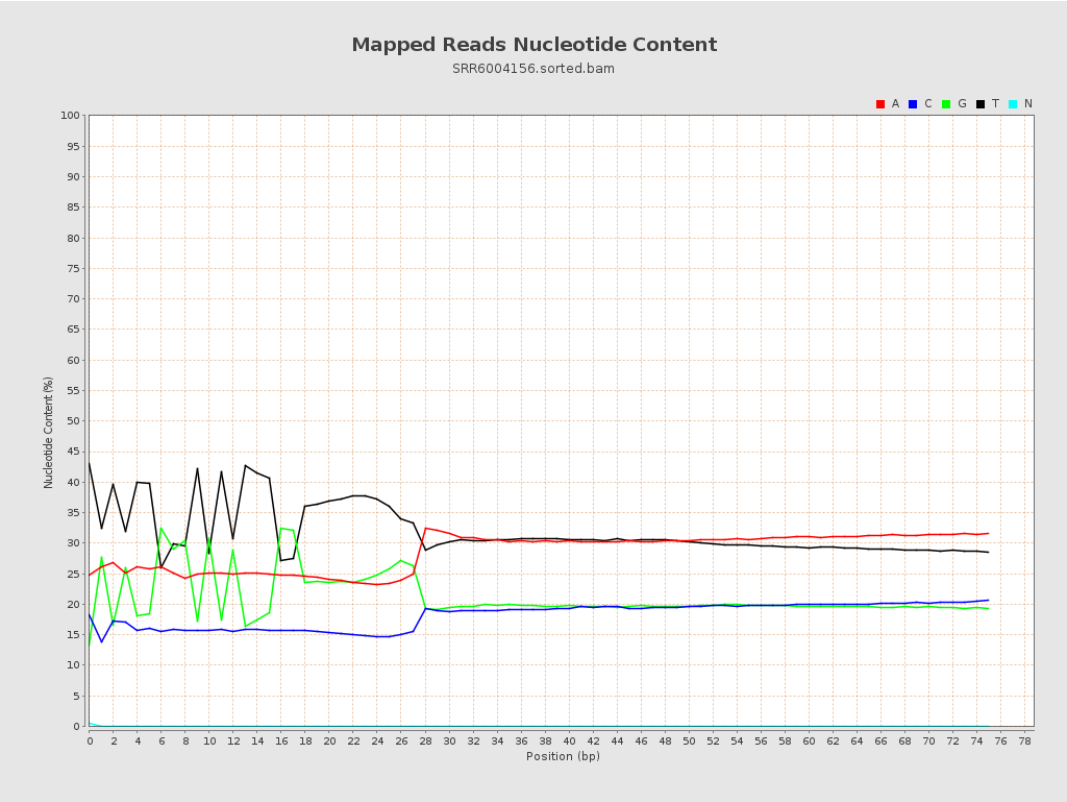
6. Results : Genome Fraction Coverage



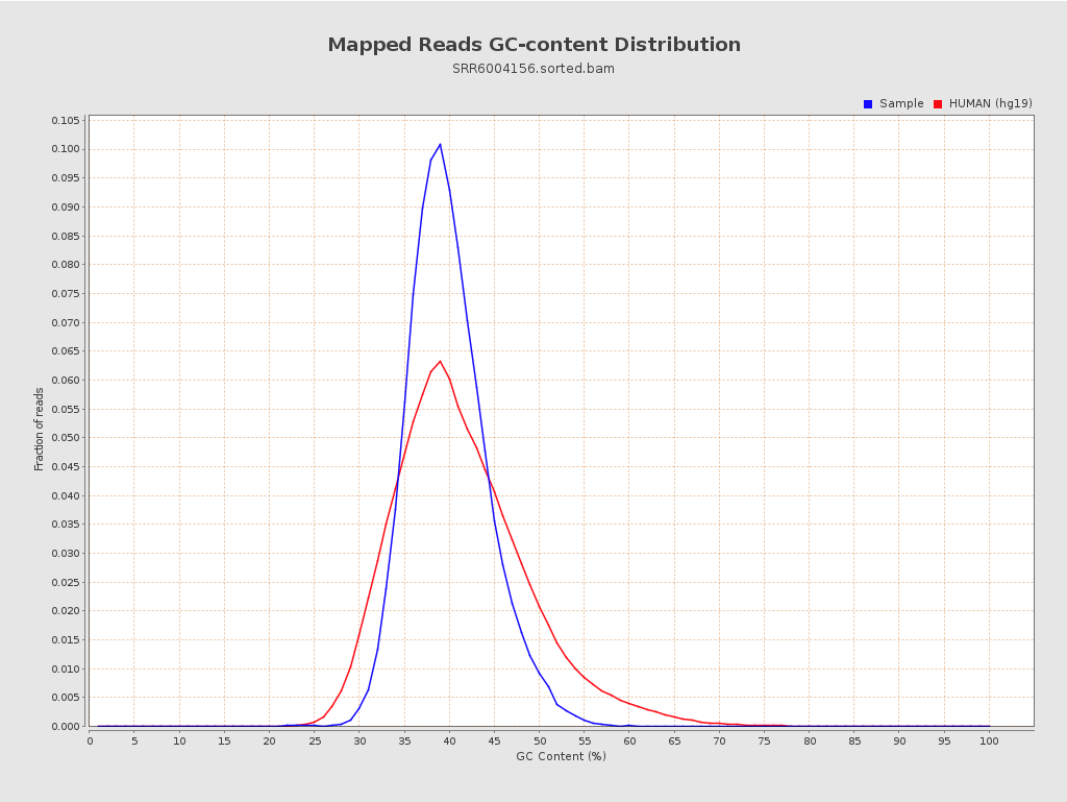
7. Results : Duplication Rate Histogram



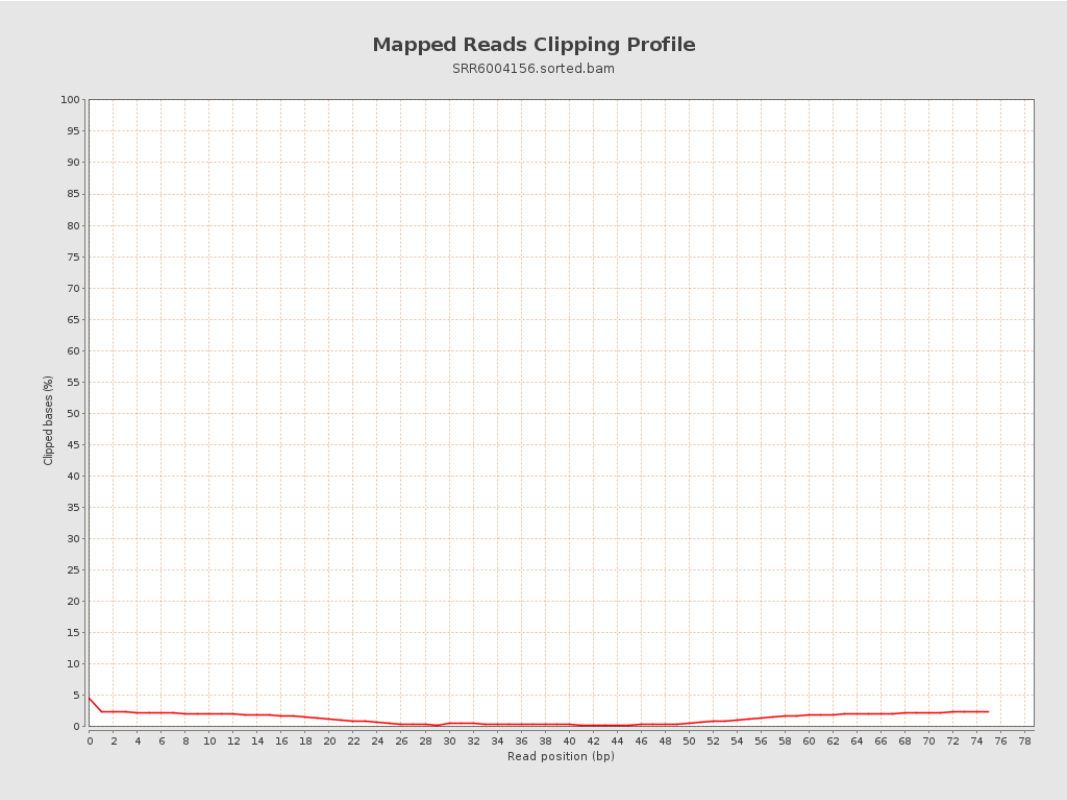
8. Results : Mapped Reads Nucleotide Content



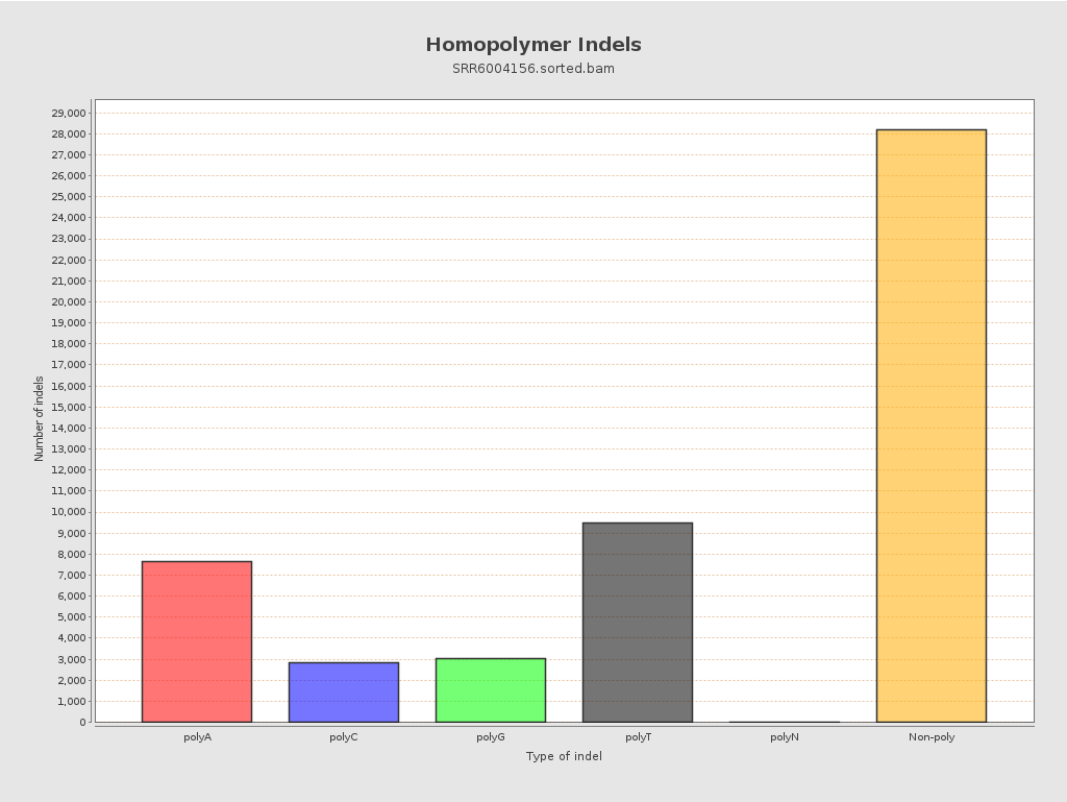
9. Results : Mapped Reads GC-content Distribution



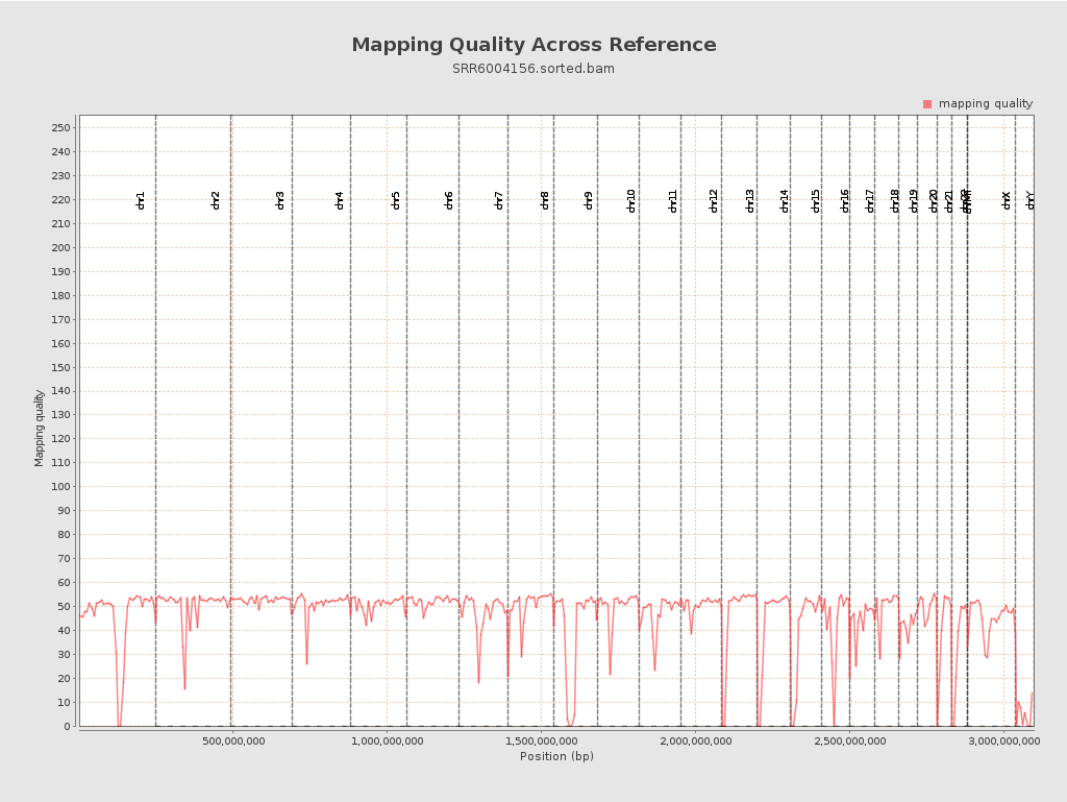
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram