Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 05:02:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004155.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_SRR6004155 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004155.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 05:02:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004155.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,803,582
Mapped reads	1,624,842 / 90.09%
Unmapped reads	178,740 / 9.91%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,590 / 0.81%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	61,540 / 3.41%
Duplication rate	3.11%
Clipped reads	738,863 / 40.97%

2.2. ACGT Content

Number/percentage of A's	30,547,902 / 28.27%
Number/percentage of C's	19,735,512 / 18.27%
Number/percentage of T's	34,437,824 / 31.87%
Number/percentage of G's	23,309,380 / 21.57%
Number/percentage of N's	18,188 / 0.02%
GC Percentage	39.84%

2.3. Coverage

Mean	0.0349

Standard Deviation	0.2796

2.4. Mapping Quality

Mean Mapping Quality	46.25

2.5. Mismatches and indels

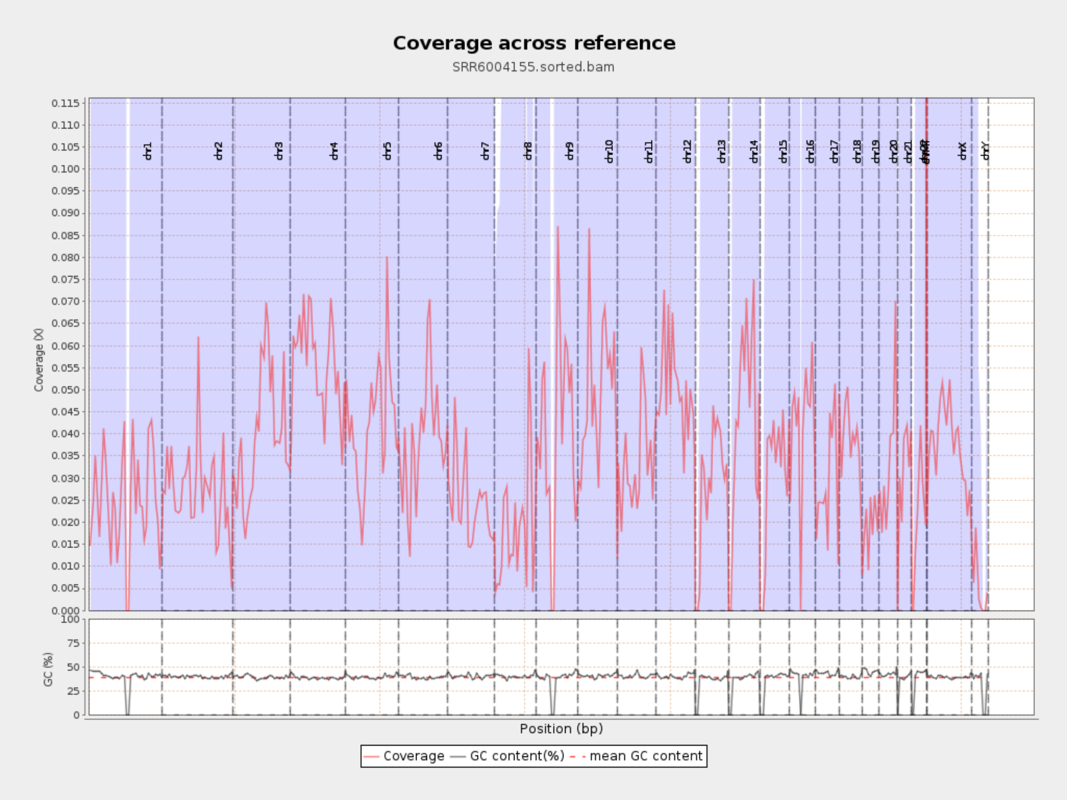
General error rate	0.95%
Mismatches	1,007,453
Insertions	8,453
Mapped reads with at least one insertion	0.52%
Deletions	36,310
Mapped reads with at least one deletion	2.2%
Homopolymer indels	44.34%

2.6. Chromosome stats

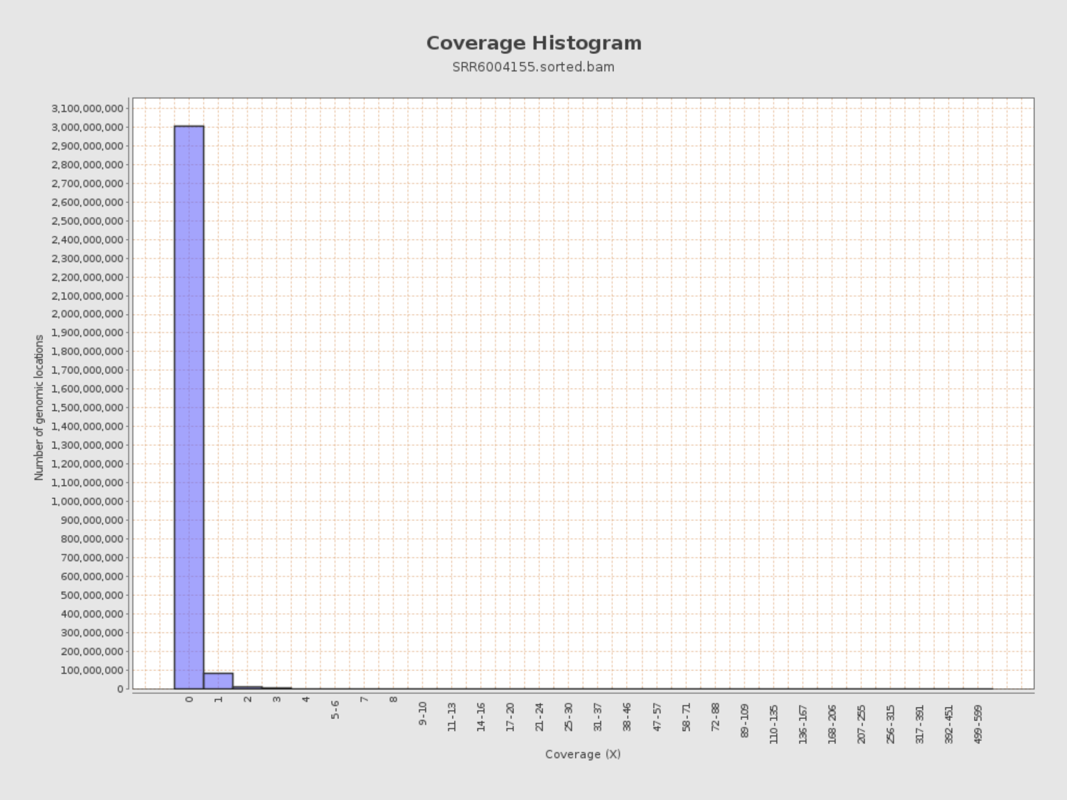
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6151620	0.0247	0.3477
chr2	243199373	6780475	0.0279	0.258
chr3	198022430	7895921	0.0399	0.2249
chr4	191154276	10721429	0.0561	0.2914
chr5	180915260	7664663	0.0424	0.2315
chr6	171115067	6648344	0.0389	0.2435
chr7	159138663	3933263	0.0247	0.2874

chr8	146364022	2638104	0.018	0.3744
chr9	141213431	5799410	0.0411	0.2904
chr10	135534747	6624030	0.0489	0.4251
chr11	135006516	4563688	0.0338	0.2381
chr12	133851895	6716111	0.0502	0.2578
chr13	115169878	3262792	0.0283	0.1886
chr14	107349540	4599038	0.0428	0.24
chr15	102531392	3046603	0.0297	0.1927
chr16	90354753	3806984	0.0421	0.2524
chr17	81195210	2276818	0.028	0.2051
chr18	78077248	3056366	0.0391	0.4889
chr19	59128983	1127237	0.0191	0.2662
chr20	63025520	2162346	0.0343	0.2158
chr21	48129895	1466123	0.0305	0.2223
chr22	51304566	1033077	0.0201	0.158
chrMT	16571	7721	0.4659	0.7447
chrX	155270560	5825292	0.0375	0.2355
chrY	59373566	303301	0.0051	0.1493

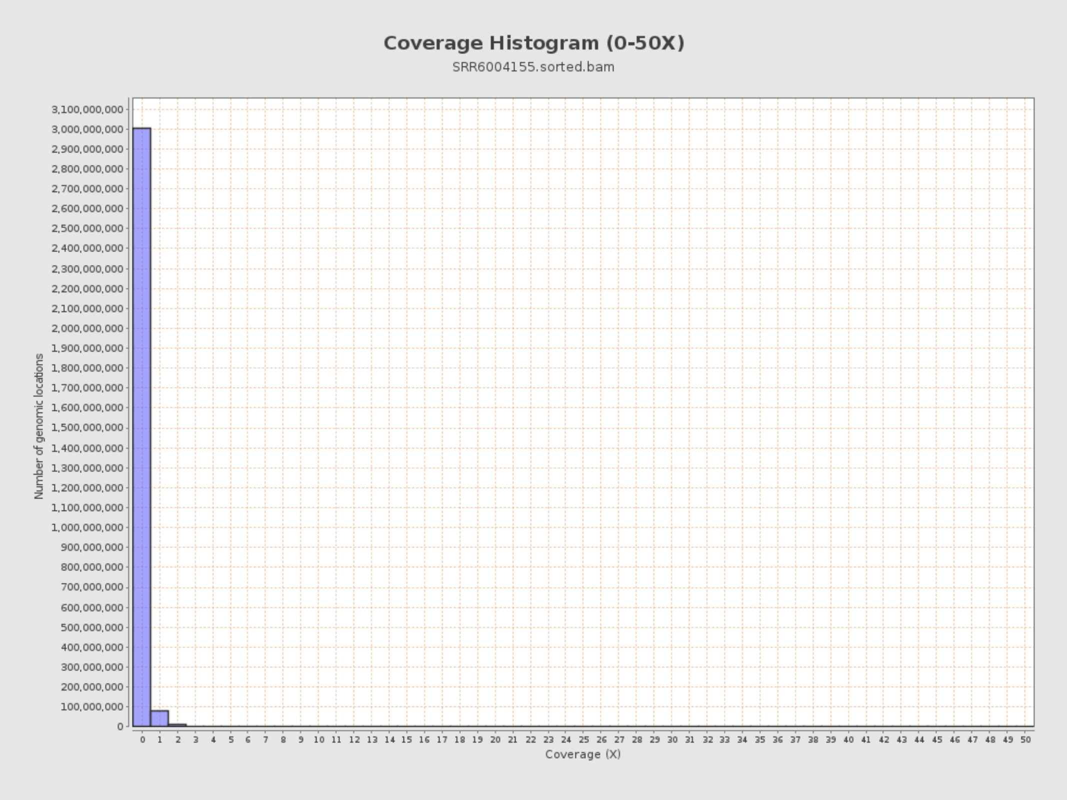
3. Results : Coverage across reference



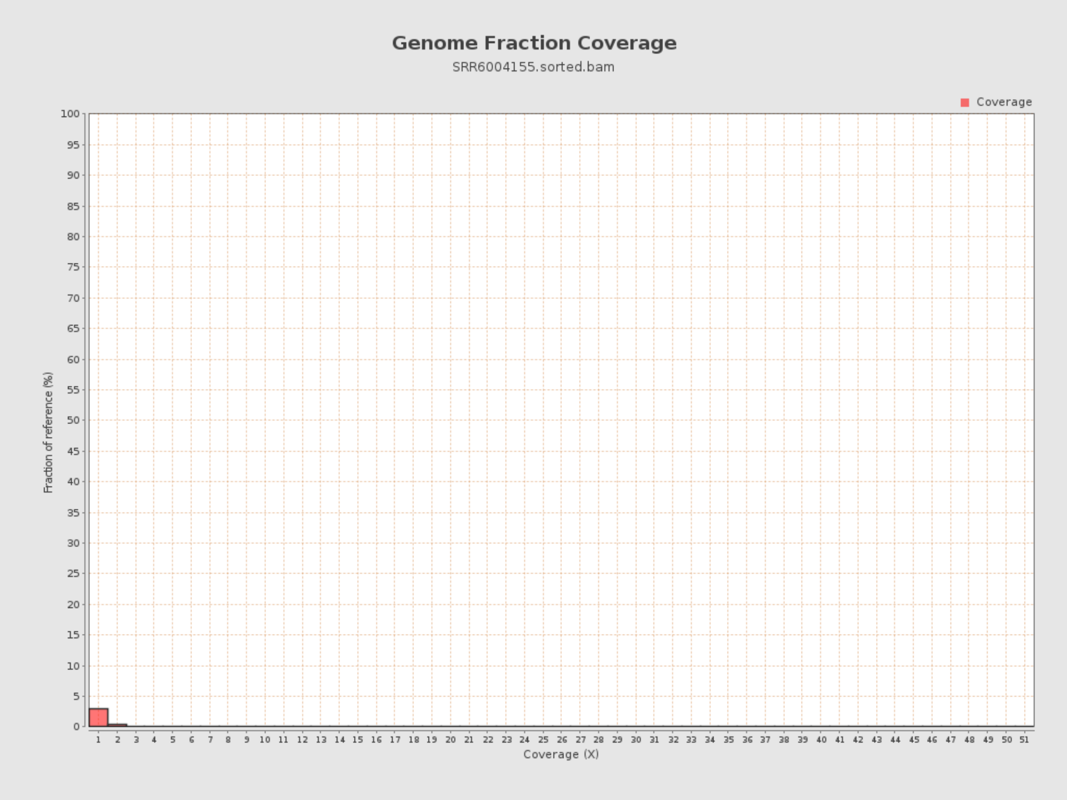
4. Results : Coverage Histogram



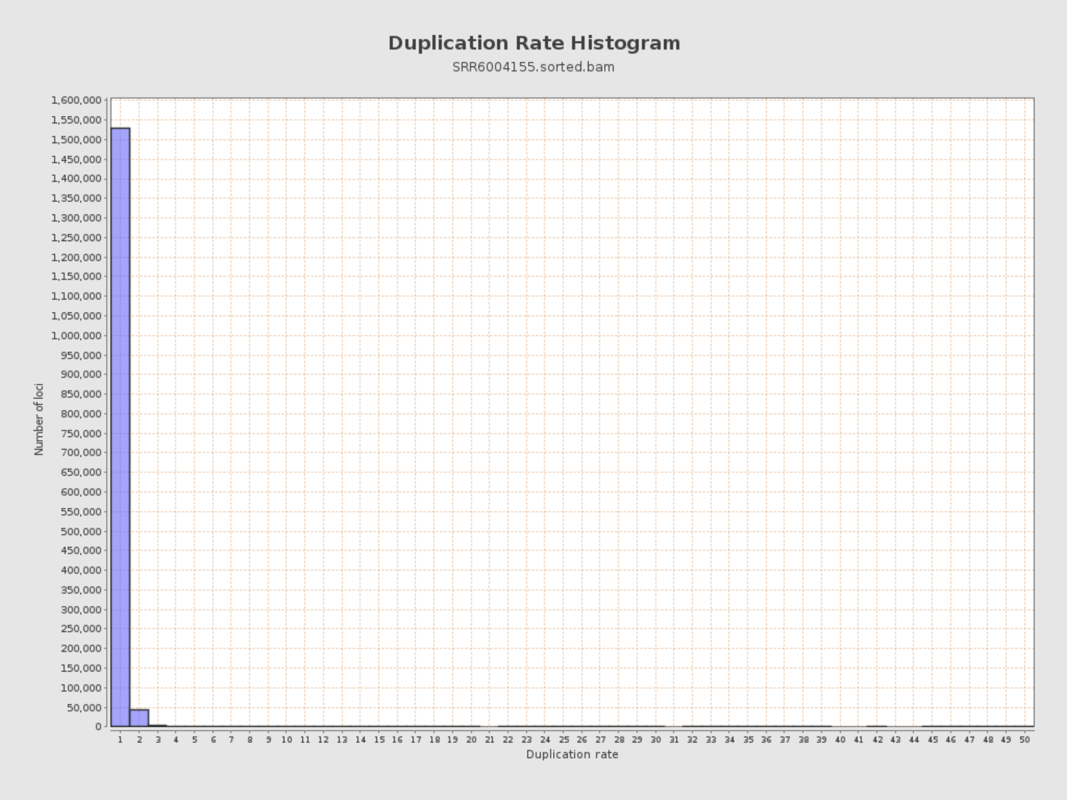
5. Results : Coverage Histogram (0-50X)



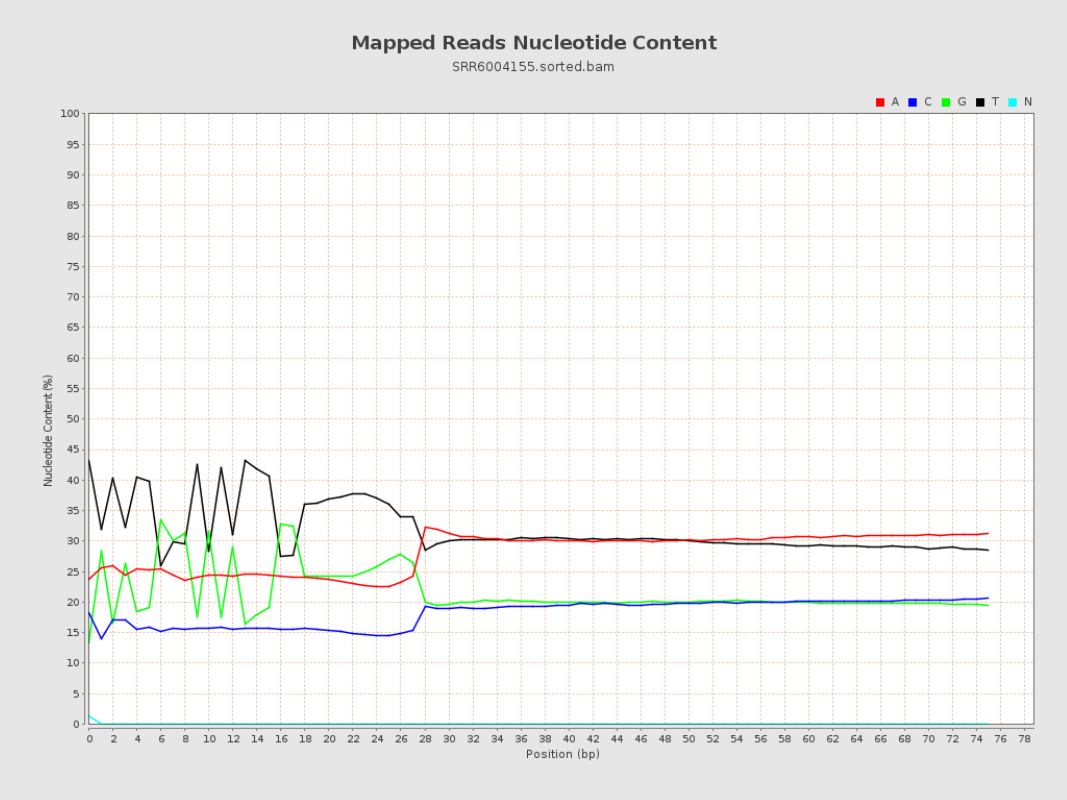
6. Results : Genome Fraction Coverage



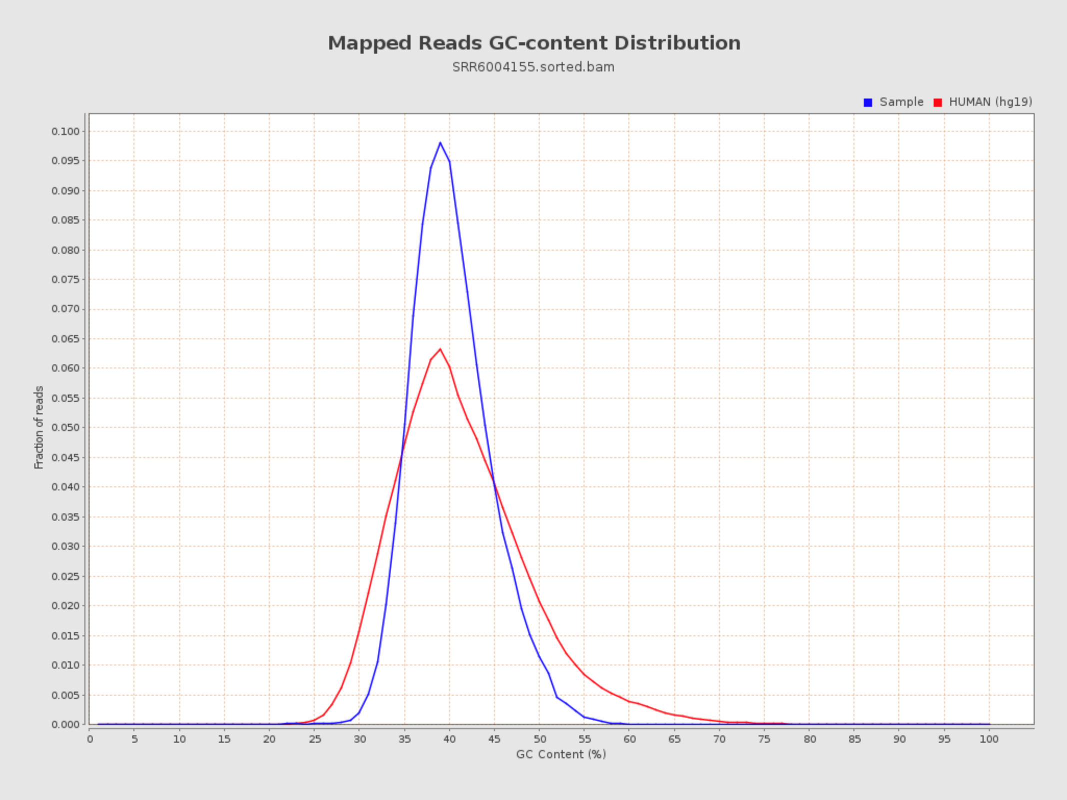
7. Results : Duplication Rate Histogram



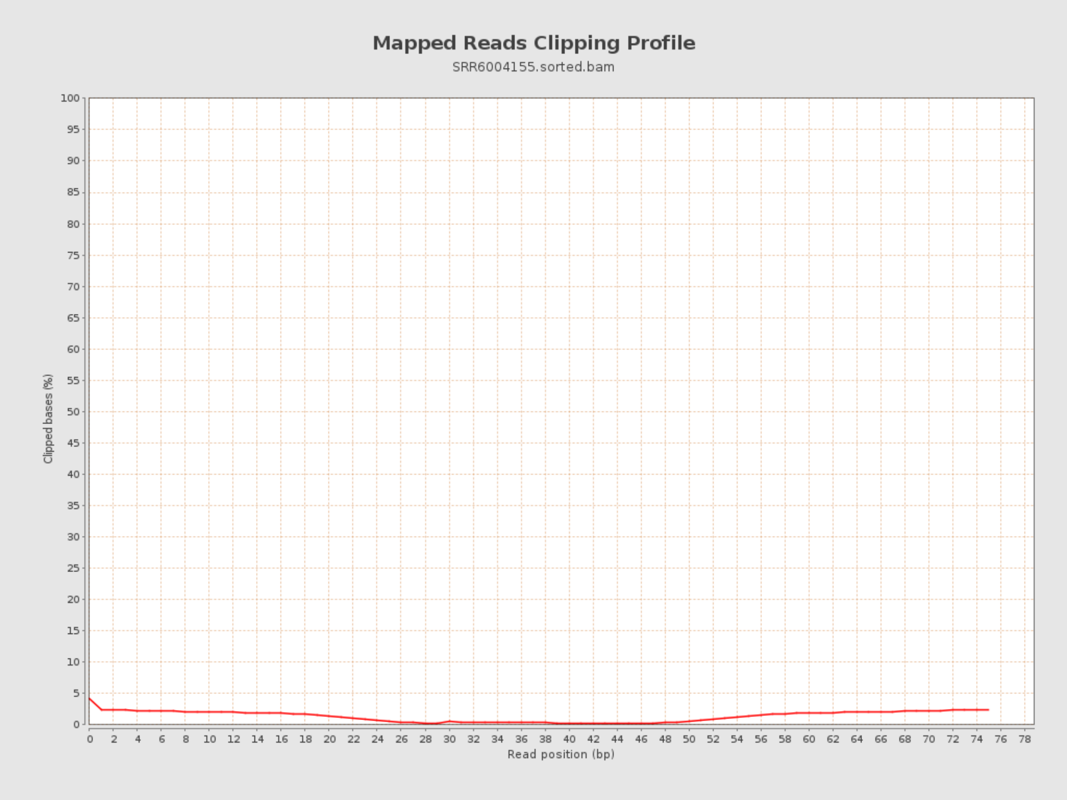
8. Results : Mapped Reads Nucleotide Content



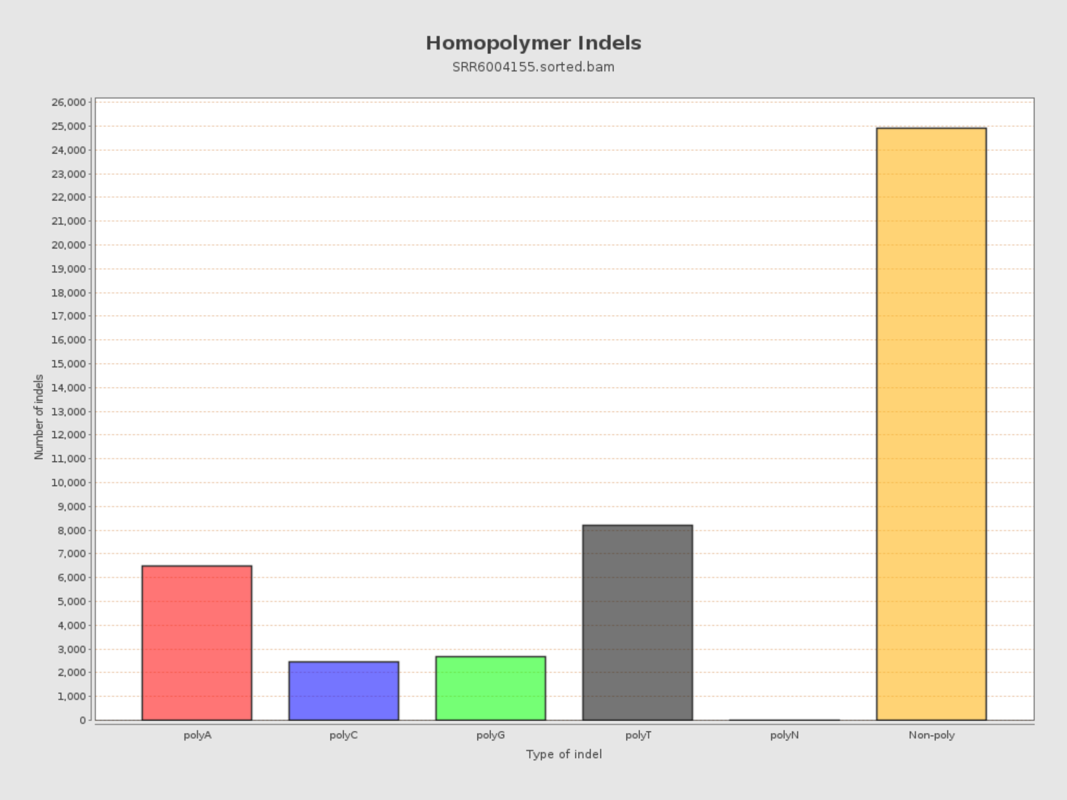
9. Results : Mapped Reads GC-content Distribution



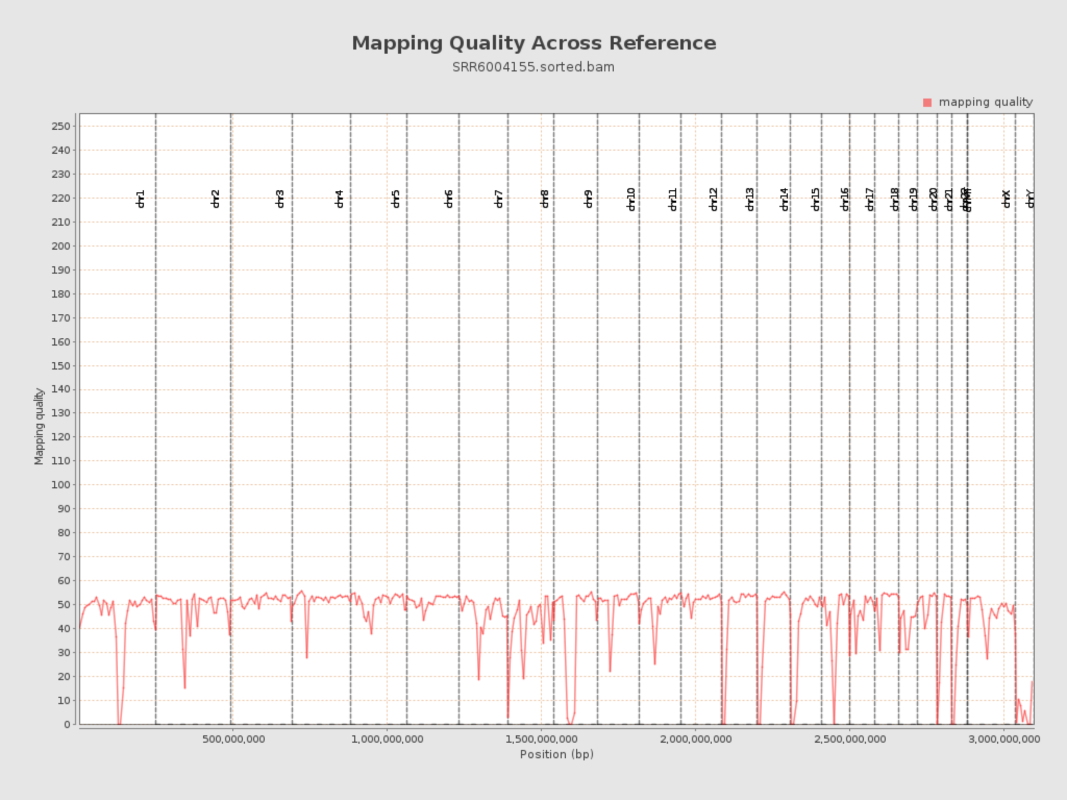
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram