Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/13 22:18:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004043.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_SRR6004043 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004043.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 13 22:18:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004043.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,039,143
Mapped reads	1,898,344 / 93.1%
Unmapped reads	140,799 / 6.9%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,136 / 0.94%
Read min/max/mean length	30 / 76 / 76.33
Duplicated reads (estimated)	80,142 / 3.93%
Duplication rate	3.23%
Clipped reads	842,299 / 41.31%

2.2. ACGT Content

Number/percentage of A's	35,854,954 / 28.24%
Number/percentage of C's	23,411,963 / 18.44%
Number/percentage of T's	40,055,671 / 31.55%
Number/percentage of G's	27,607,137 / 21.75%
Number/percentage of N's	26,586 / 0.02%
GC Percentage	40.19%

2.3. Coverage

Mean	0.041

Standard Deviation	0.3901

2.4. Mapping Quality

Mean Mapping Quality	46.08

2.5. Mismatches and indels

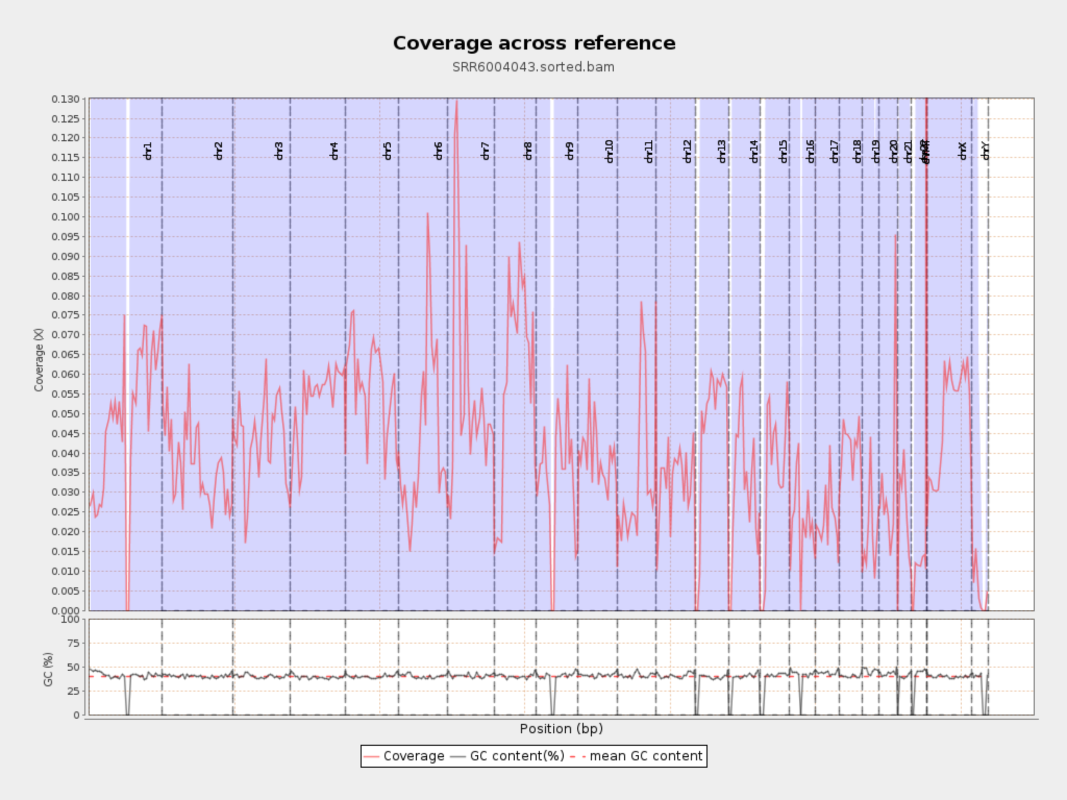
General error rate	0.74%
Mismatches	927,562
Insertions	8,962
Mapped reads with at least one insertion	0.47%
Deletions	29,206
Mapped reads with at least one deletion	1.52%
Homopolymer indels	46.74%

2.6. Chromosome stats

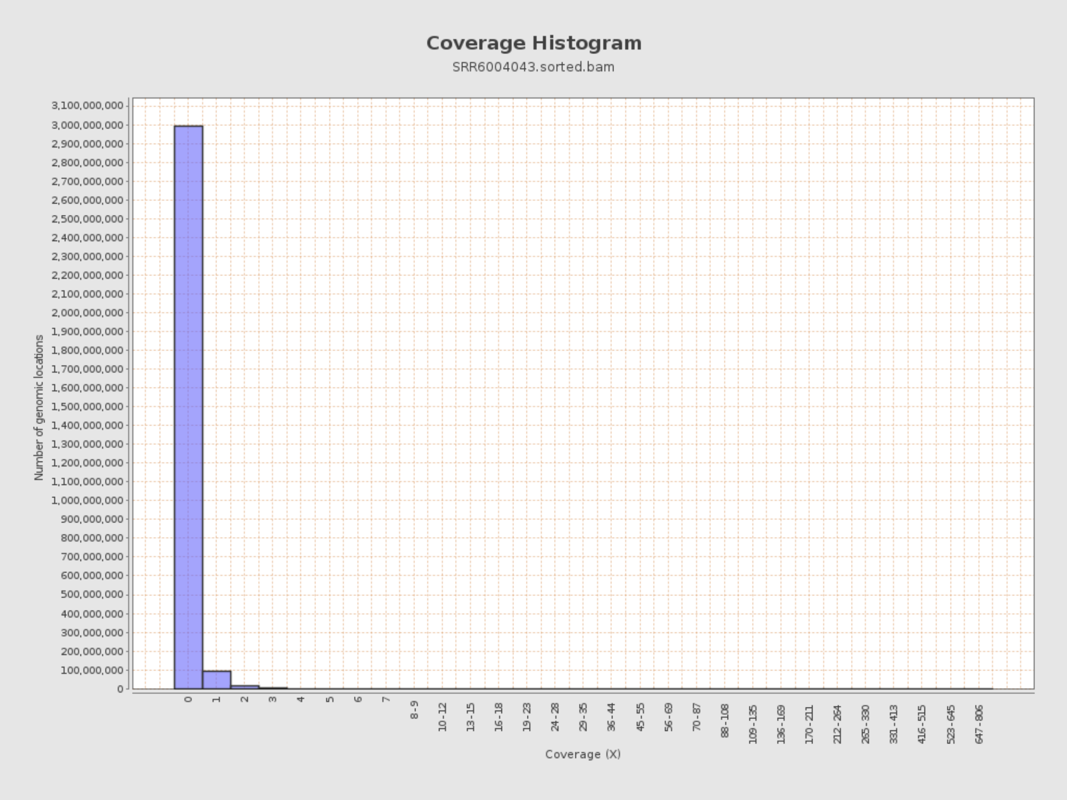
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11927594	0.0479	0.7354
chr2	243199373	8971256	0.0369	0.3716
chr3	198022430	8624650	0.0436	0.24
chr4	191154276	10199461	0.0534	0.2838
chr5	180915260	10400203	0.0575	0.2786
chr6	171115067	7499934	0.0438	0.2679
chr7	159138663	9158546	0.0576	0.6824

chr8	146364022	8731657	0.0597	0.5546
chr9	141213431	4832898	0.0342	0.3305
chr10	135534747	5365494	0.0396	0.3276
chr11	135006516	4574937	0.0339	0.2638
chr12	133851895	4403375	0.0329	0.2164
chr13	115169878	5278254	0.0458	0.2465
chr14	107349540	3342352	0.0311	0.2381
chr15	102531392	3514217	0.0343	0.2196
chr16	90354753	2058343	0.0228	0.2083
chr17	81195210	1905837	0.0235	0.1868
chr18	78077248	3255785	0.0417	0.5986
chr19	59128983	1187716	0.0201	0.4649
chr20	63025520	2212373	0.0351	0.2319
chr21	48129895	1158705	0.0241	0.2061
chr22	51304566	510510	0.01	0.1111
chrMT	16571	11694	0.7057	1.0123
chrX	155270560	7569246	0.0487	0.2783
chrY	59373566	312898	0.0053	0.1152

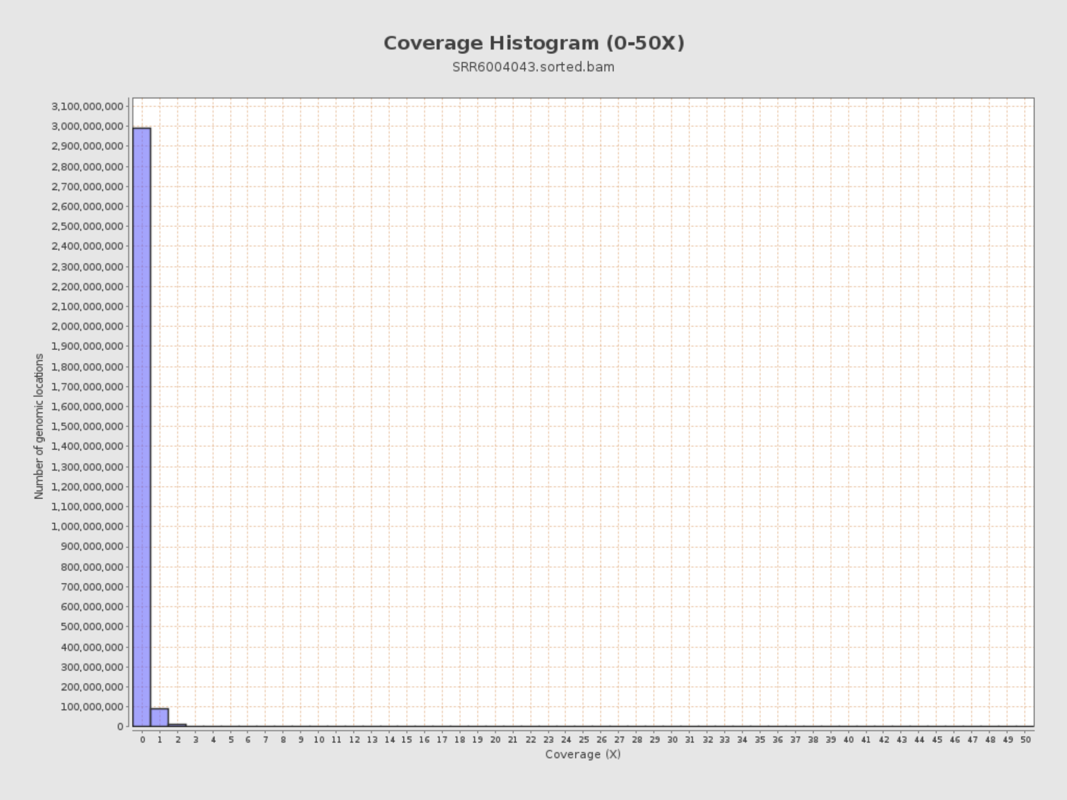
3. Results : Coverage across reference



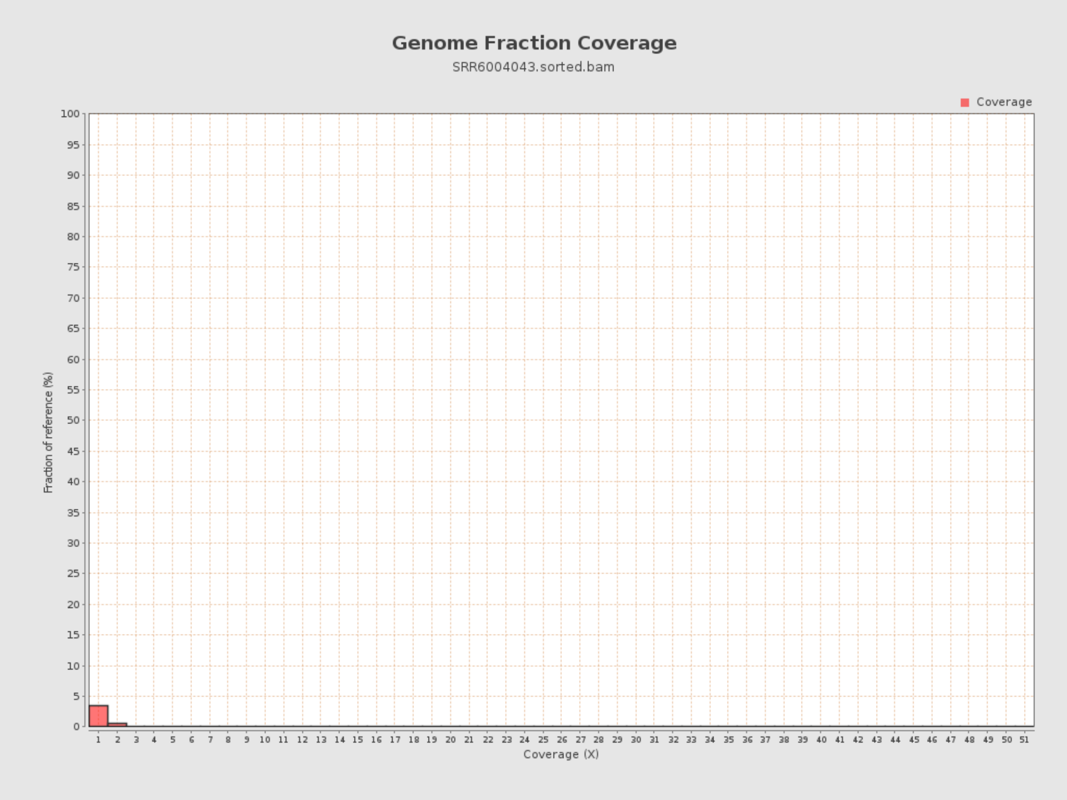
4. Results : Coverage Histogram



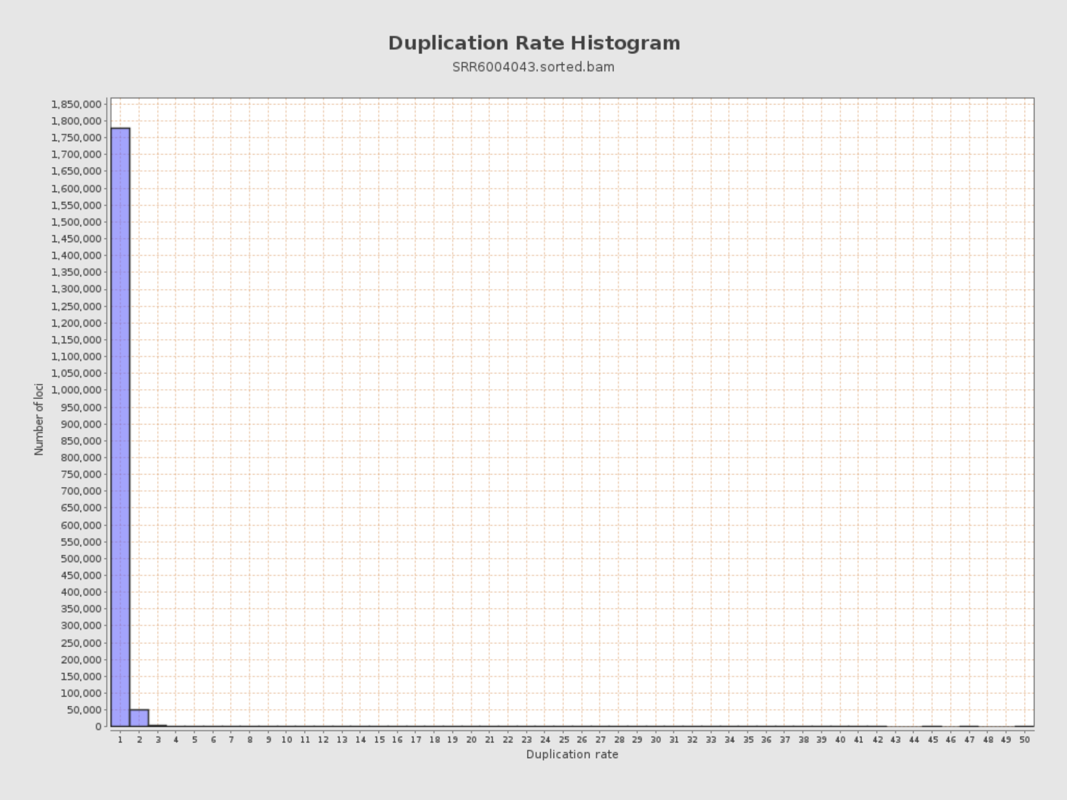
5. Results : Coverage Histogram (0-50X)



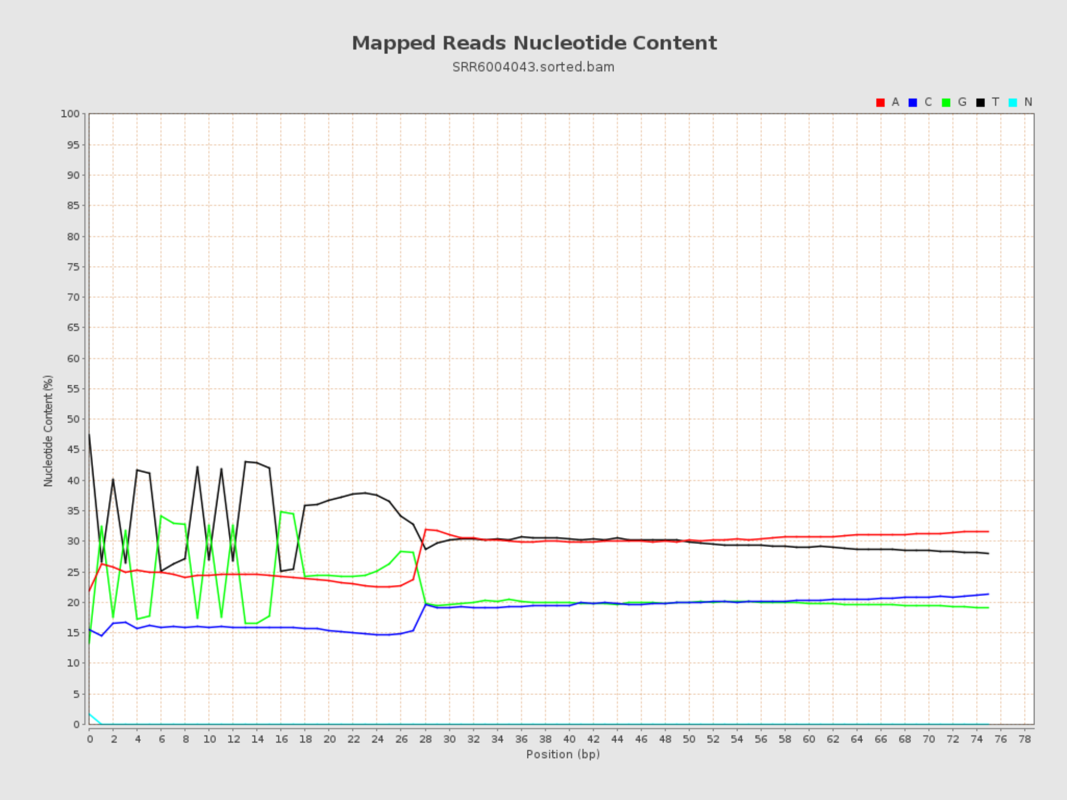
6. Results : Genome Fraction Coverage



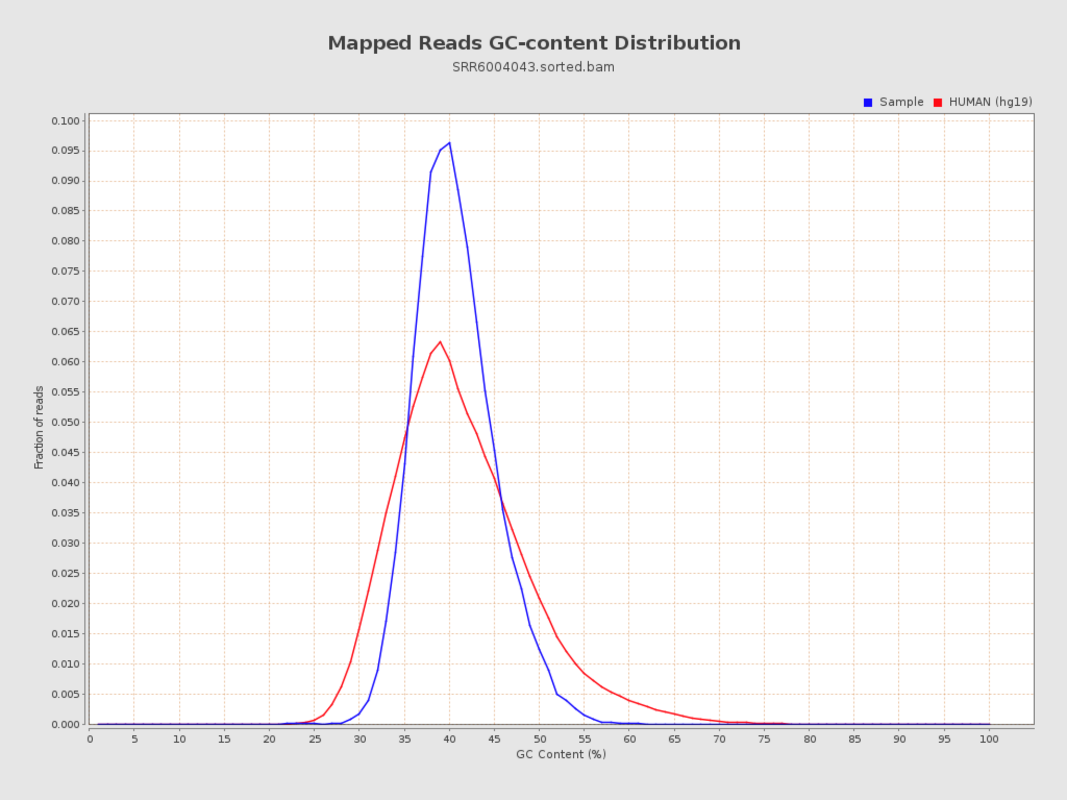
7. Results : Duplication Rate Histogram



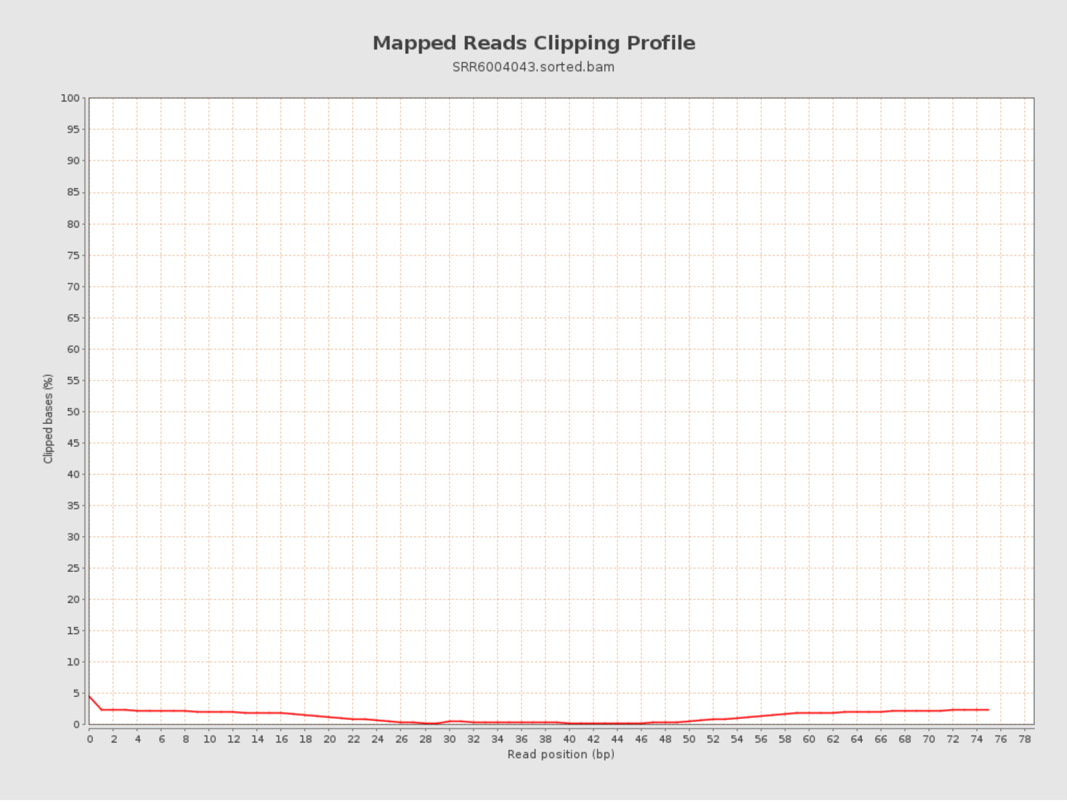
8. Results : Mapped Reads Nucleotide Content



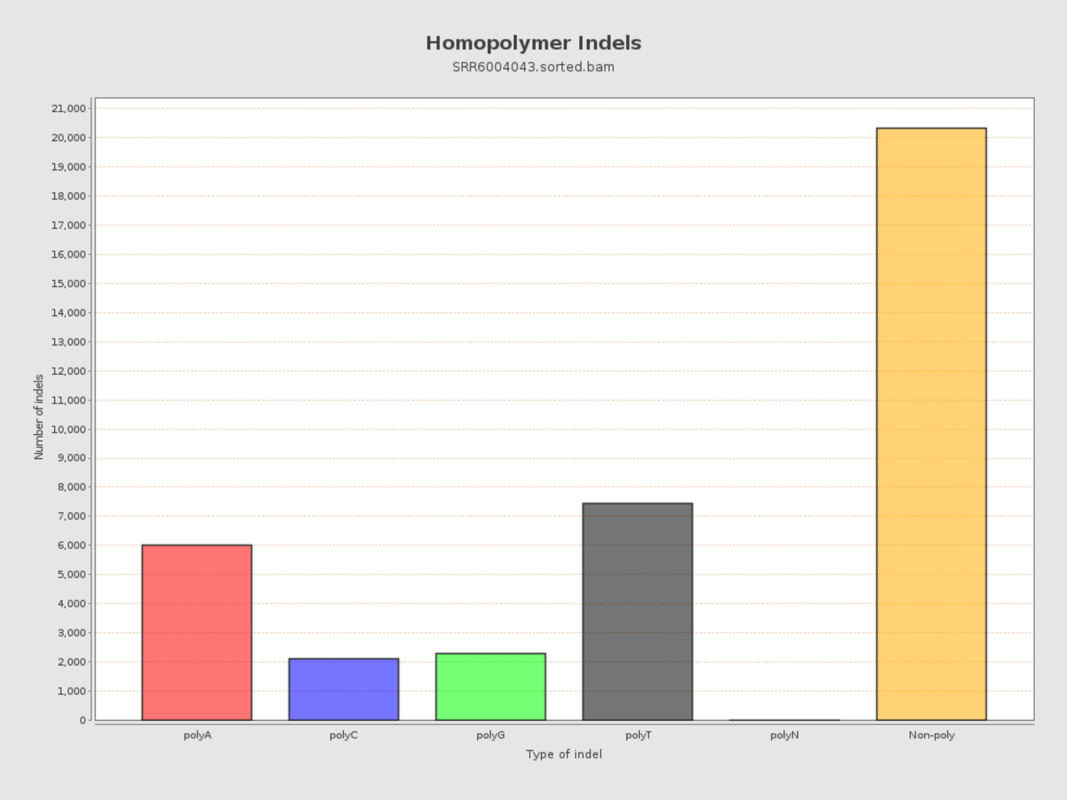
9. Results : Mapped Reads GC-content Distribution



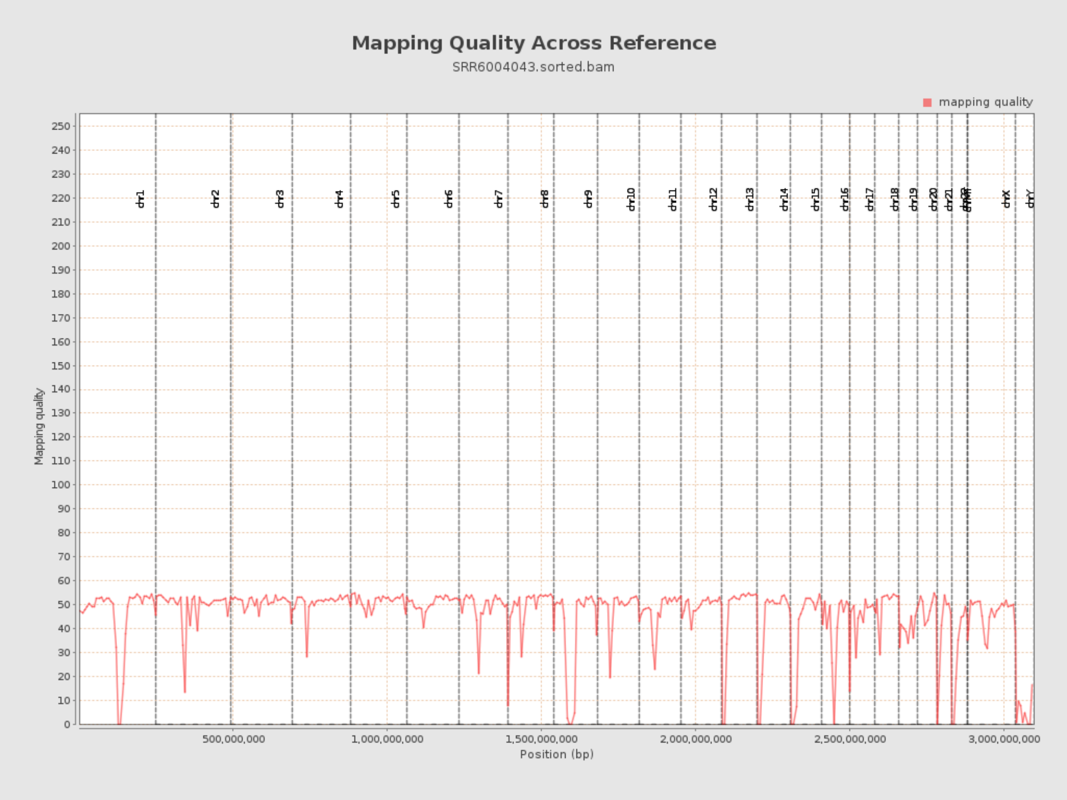
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram