Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 06:15:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR054602.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_SRR054602 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR054602.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 06:15:27 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR054602.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,094,079
Mapped reads	8,098,480 / 80.23%
Unmapped reads	1,995,599 / 19.77%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	250 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	1,707,921 / 16.92%
Duplication rate	15.3%
Clipped reads	714,553 / 7.08%

2.2. ACGT Content

Number/percentage of A's	116,757,386 / 30.54%
Number/percentage of C's	71,004,032 / 18.57%
Number/percentage of T's	117,514,884 / 30.74%
Number/percentage of G's	76,949,903 / 20.13%
Number/percentage of N's	58,272 / 0.02%
GC Percentage	38.7%

2.3. Coverage

Mean	0.1235

Standard Deviation	0.8663

2.4. Mapping Quality

Mean Mapping Quality	45.8

2.5. Mismatches and indels

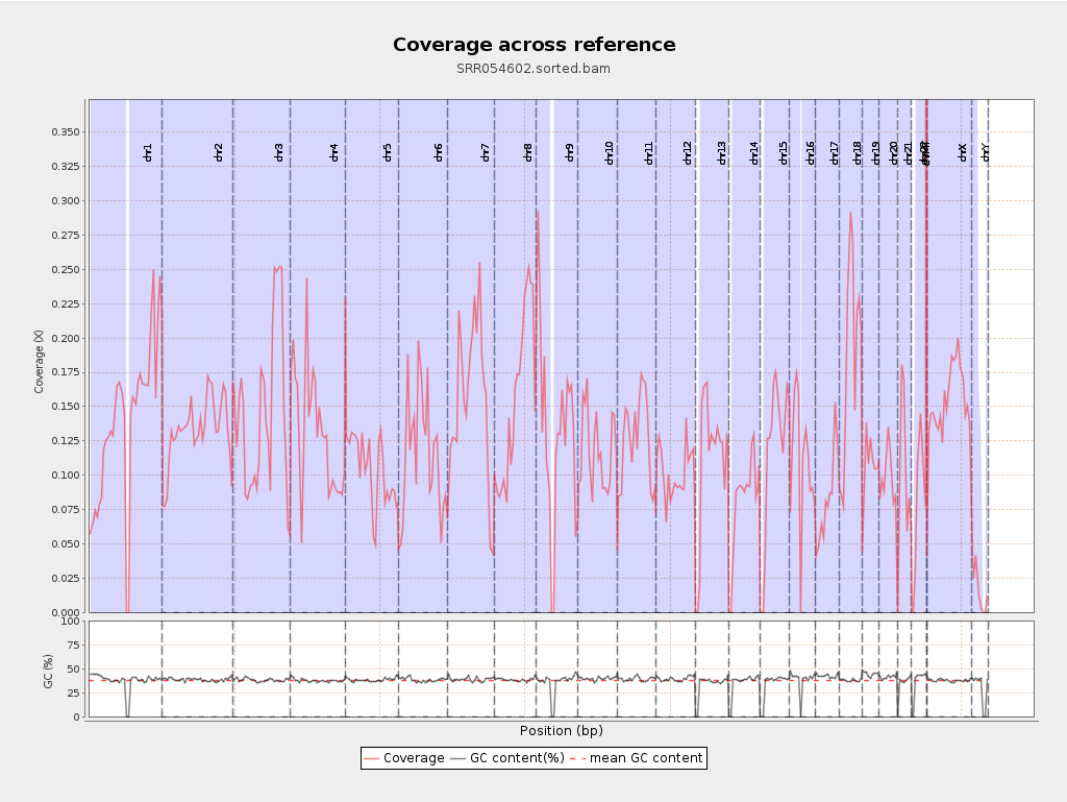
General error rate	0.51%
Mismatches	1,910,358
Insertions	16,876
Mapped reads with at least one insertion	0.21%
Deletions	56,068
Mapped reads with at least one deletion	0.69%
Homopolymer indels	48.7%

2.6. Chromosome stats

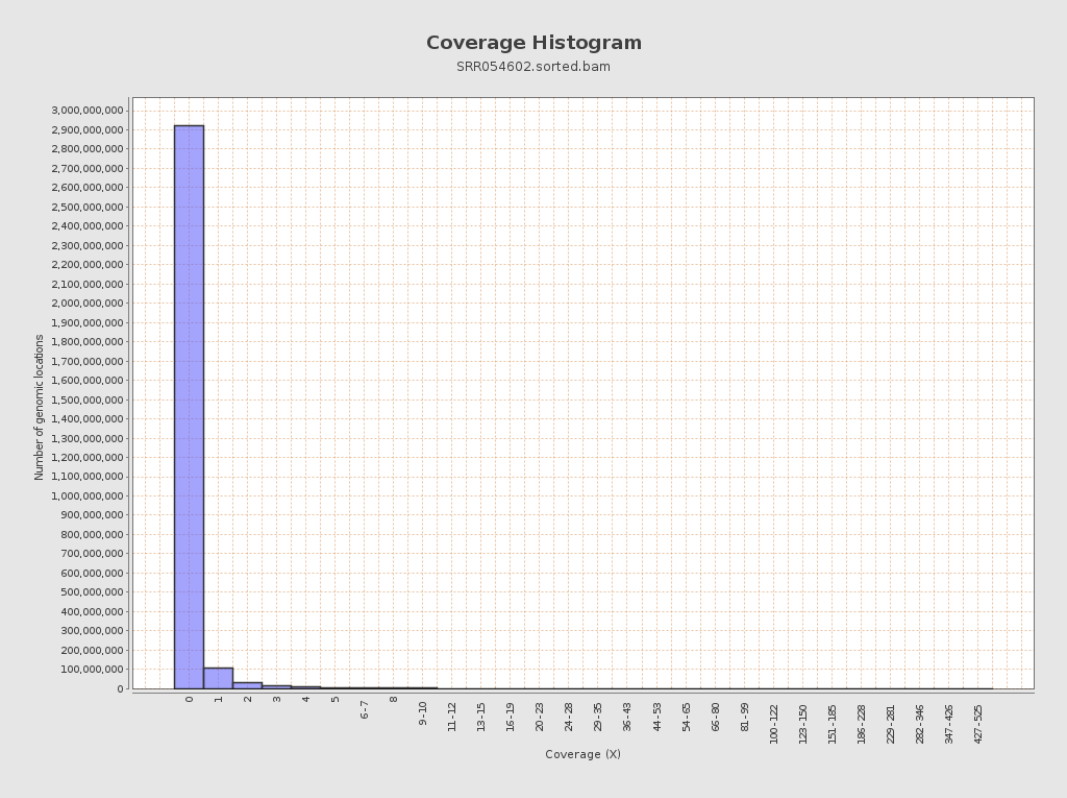
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	34382109	0.1379	0.9618
chr2	243199373	32367181	0.1331	0.9297
chr3	198022430	28763857	0.1453	0.906
chr4	191154276	24924272	0.1304	0.887
chr5	180915260	18944418	0.1047	0.7022
chr6	171115067	19279980	0.1127	0.8042
chr7	159138663	24922133	0.1566	1.0426

chr8	146364022	22879510	0.1563	1.006
chr9	141213431	18678710	0.1323	0.9352
chr10	135534747	16162250	0.1192	0.8343
chr11	135006516	16946195	0.1255	0.8836
chr12	133851895	13599766	0.1016	0.7003
chr13	115169878	12659244	0.1099	0.7418
chr14	107349540	8642519	0.0805	0.6862
chr15	102531392	11945141	0.1165	0.7648
chr16	90354753	10036391	0.1111	0.821
chr17	81195210	6813637	0.0839	0.6084
chr18	78077248	14471623	0.1854	1.2094
chr19	59128983	6448102	0.1091	0.8315
chr20	63025520	6130894	0.0973	0.7267
chr21	48129895	4859416	0.101	0.8317
chr22	51304566	3945138	0.0769	0.5797
chrMT	16571	48274	2.9132	5.758
chrX	155270560	23569168	0.1518	0.9681
chrY	59373566	947354	0.016	0.3523

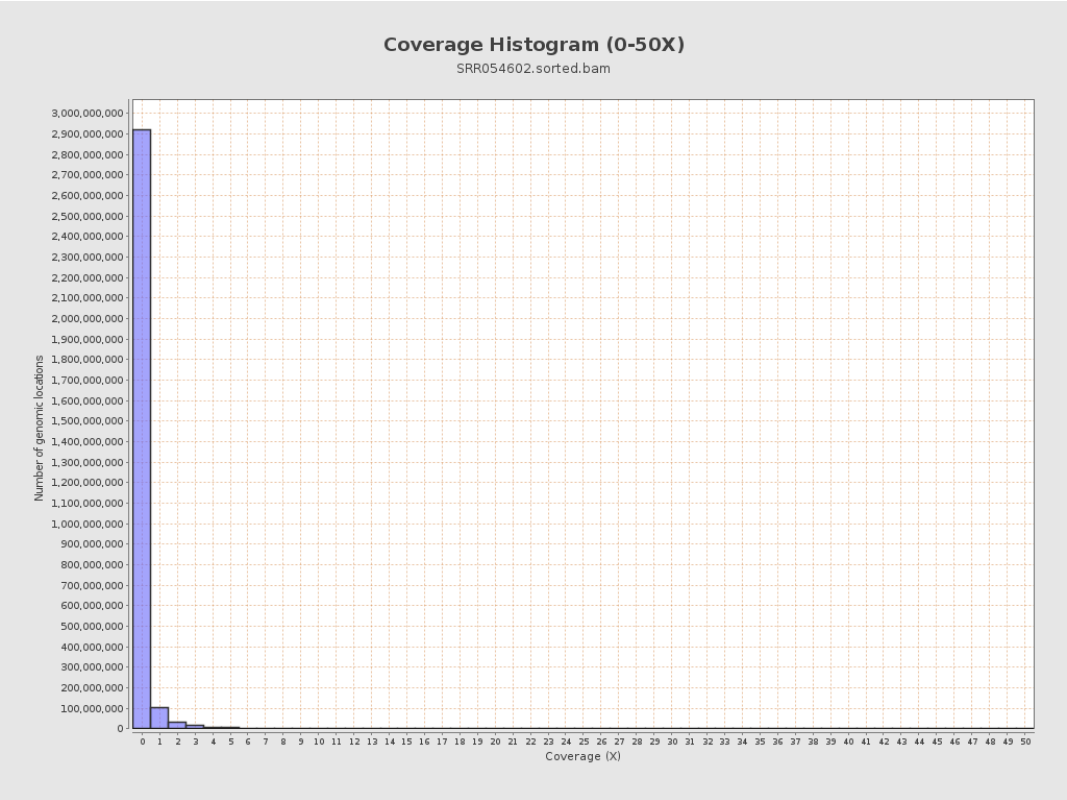
3. Results : Coverage across reference



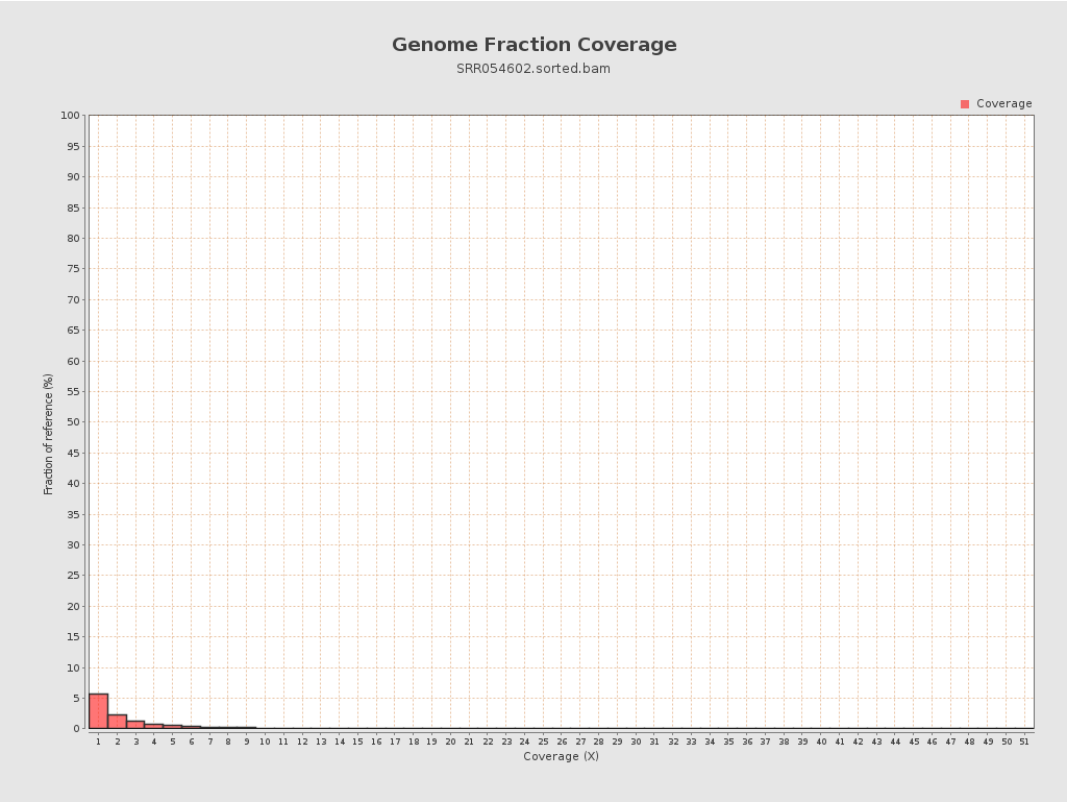
4. Results : Coverage Histogram



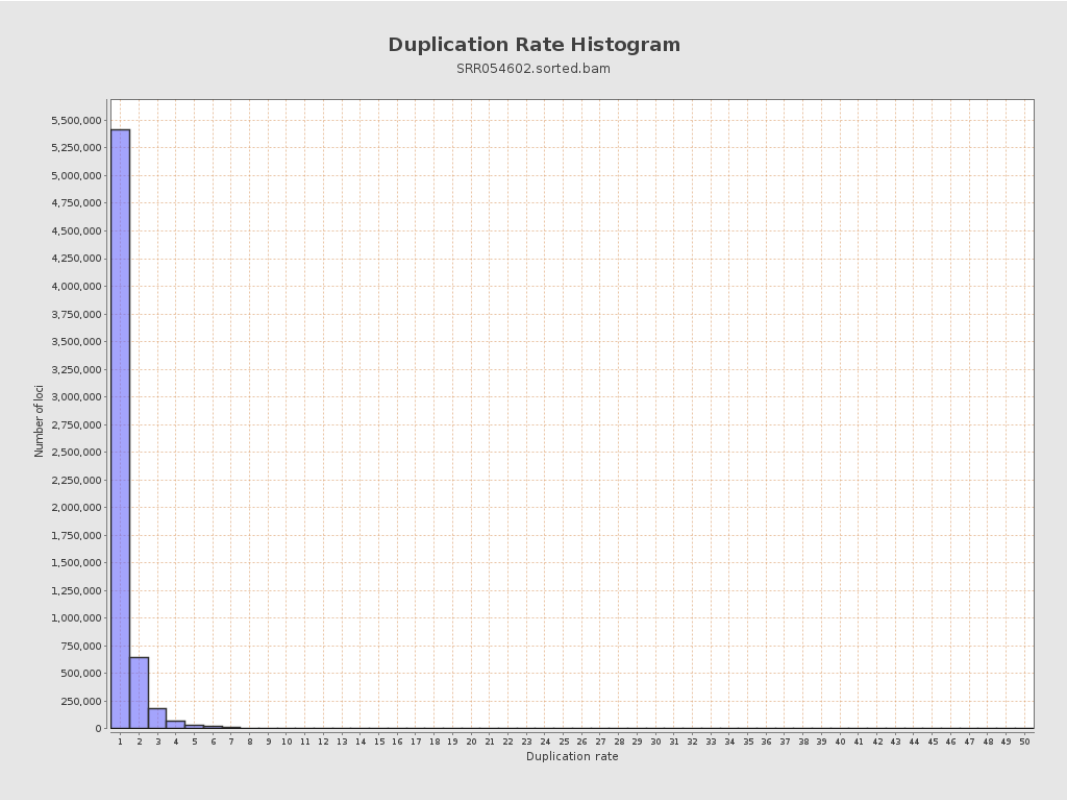
5. Results : Coverage Histogram (0-50X)



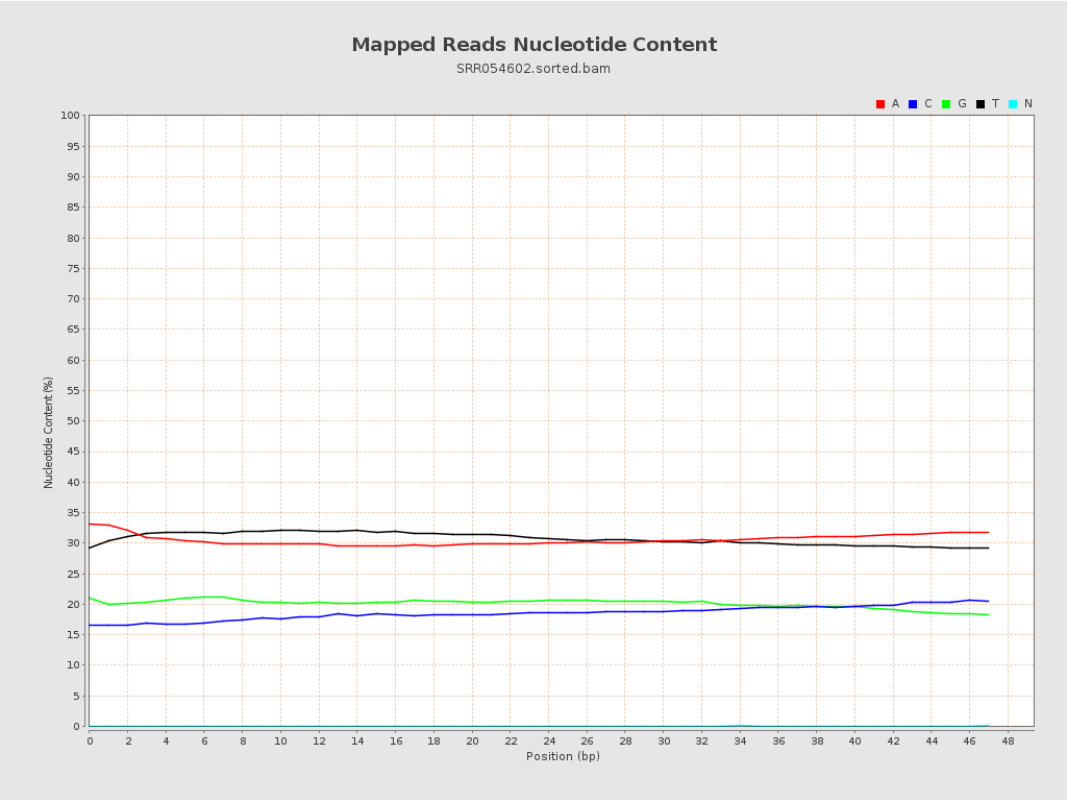
6. Results : Genome Fraction Coverage



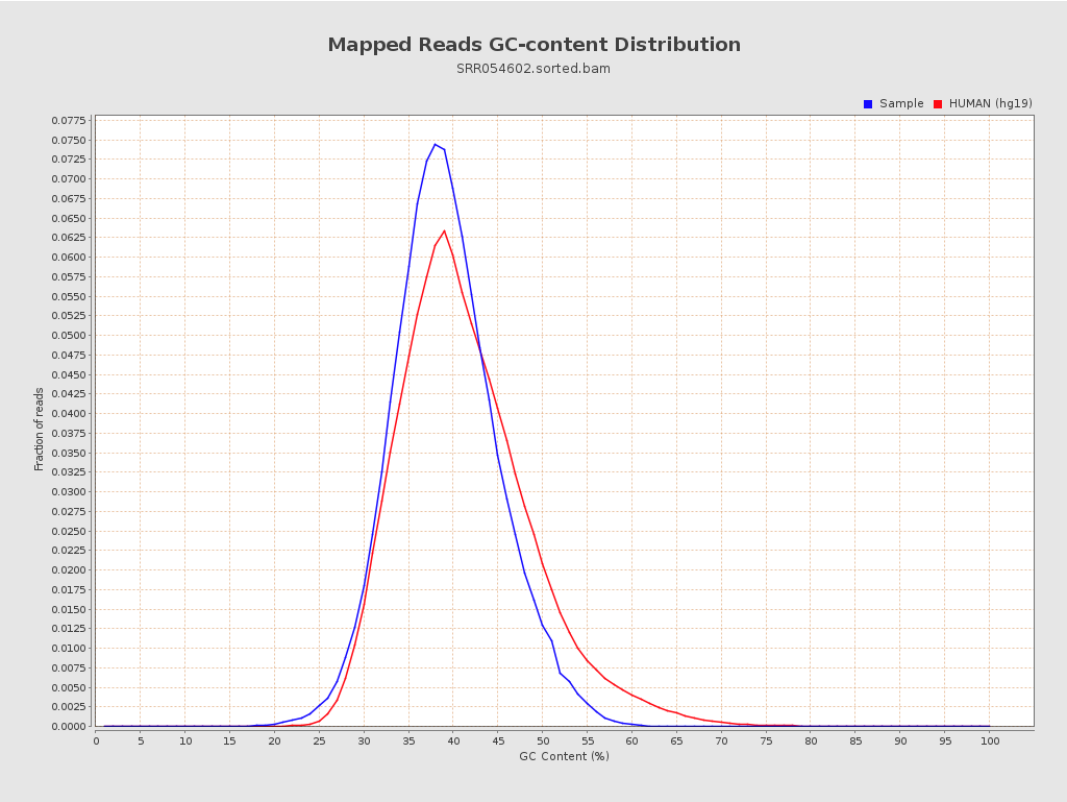
7. Results : Duplication Rate Histogram



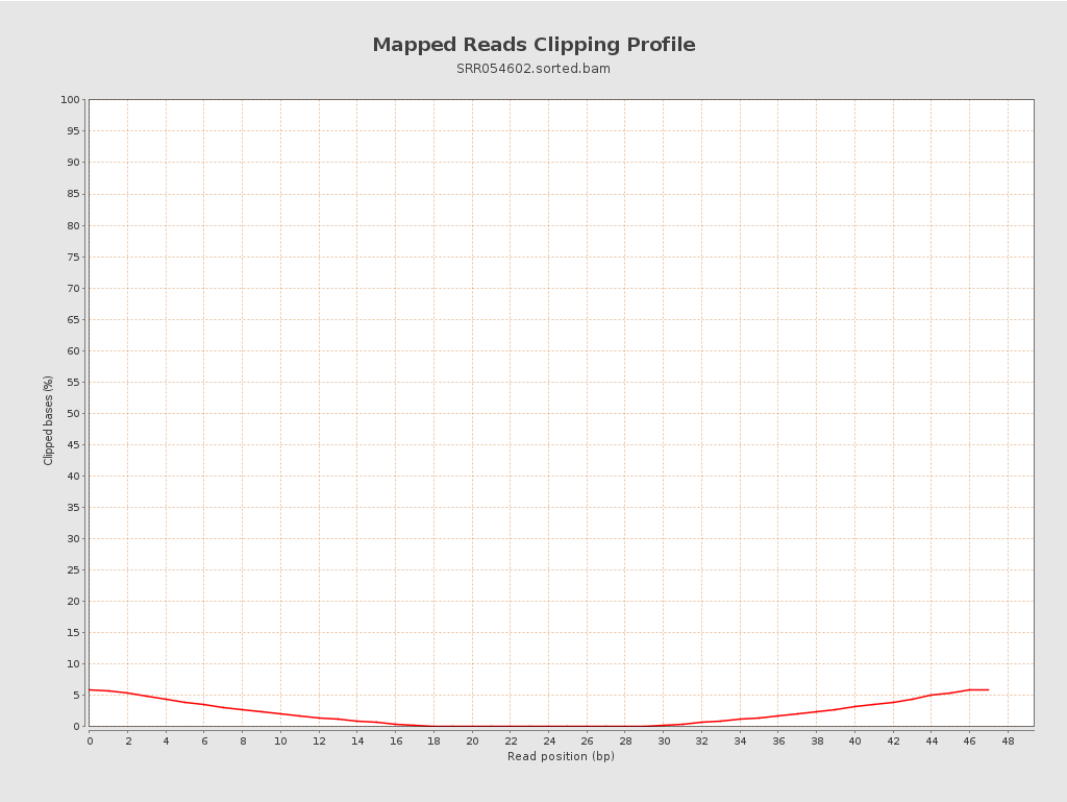
8. Results : Mapped Reads Nucleotide Content



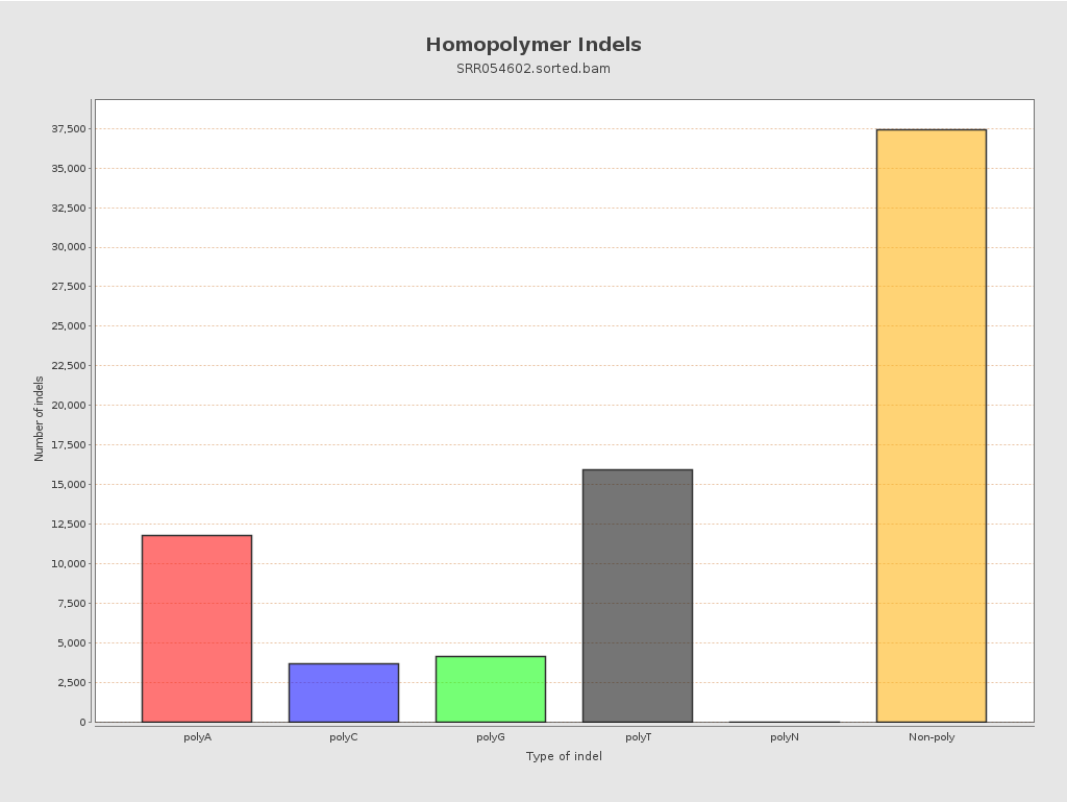
9. Results : Mapped Reads GC-content Distribution



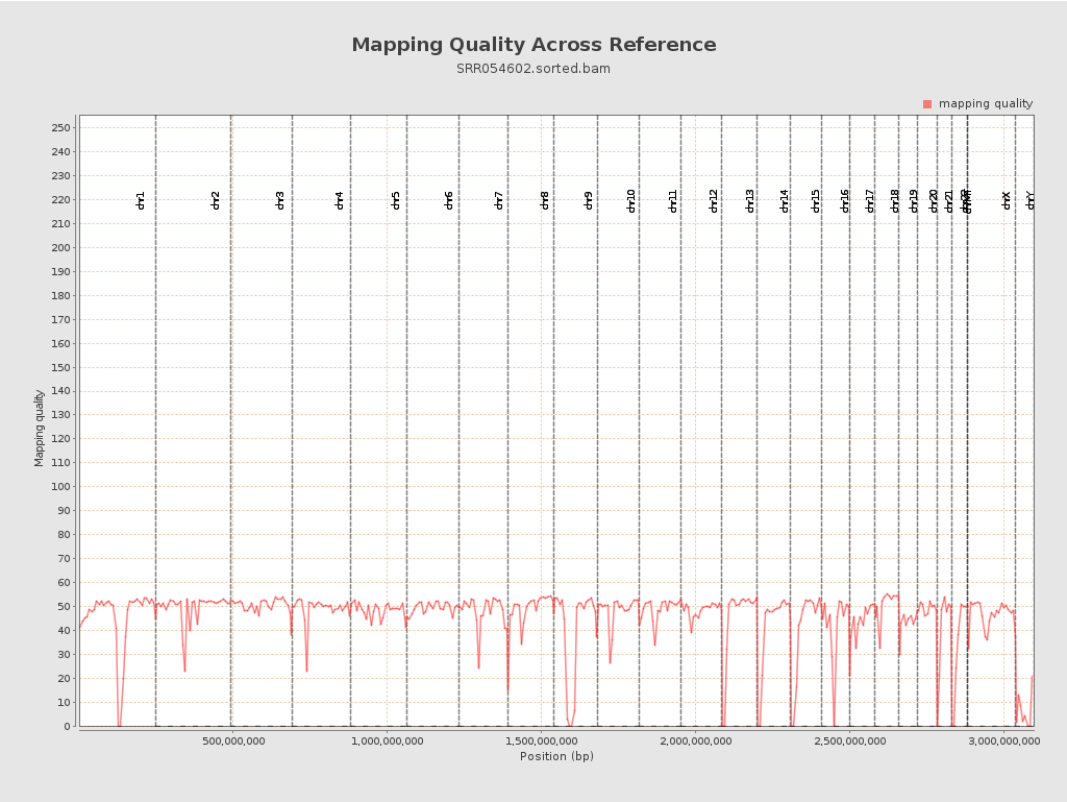
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram