Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 16:58:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013227.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_SRR6013227 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013227.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 16:58:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013227.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,291,513
Mapped reads	1,065,115 / 82.47%
Unmapped reads	226,398 / 17.53%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,285 / 0.87%
Read min/max/mean length	30 / 76 / 76.3
Duplicated reads (estimated)	260,137 / 20.14%
Duplication rate	16.5%
Clipped reads	676,422 / 52.37%

2.2. ACGT Content

Number/percentage of A's	18,089,178 / 27.39%
Number/percentage of C's	11,661,978 / 17.66%
Number/percentage of T's	21,532,797 / 32.6%
Number/percentage of G's	14,751,987 / 22.34%
Number/percentage of N's	7,128 / 0.01%
GC Percentage	40%

2.3. Coverage

Mean	0.0213

Standard Deviation	0.3306

2.4. Mapping Quality

Mean Mapping Quality	43.51

2.5. Mismatches and indels

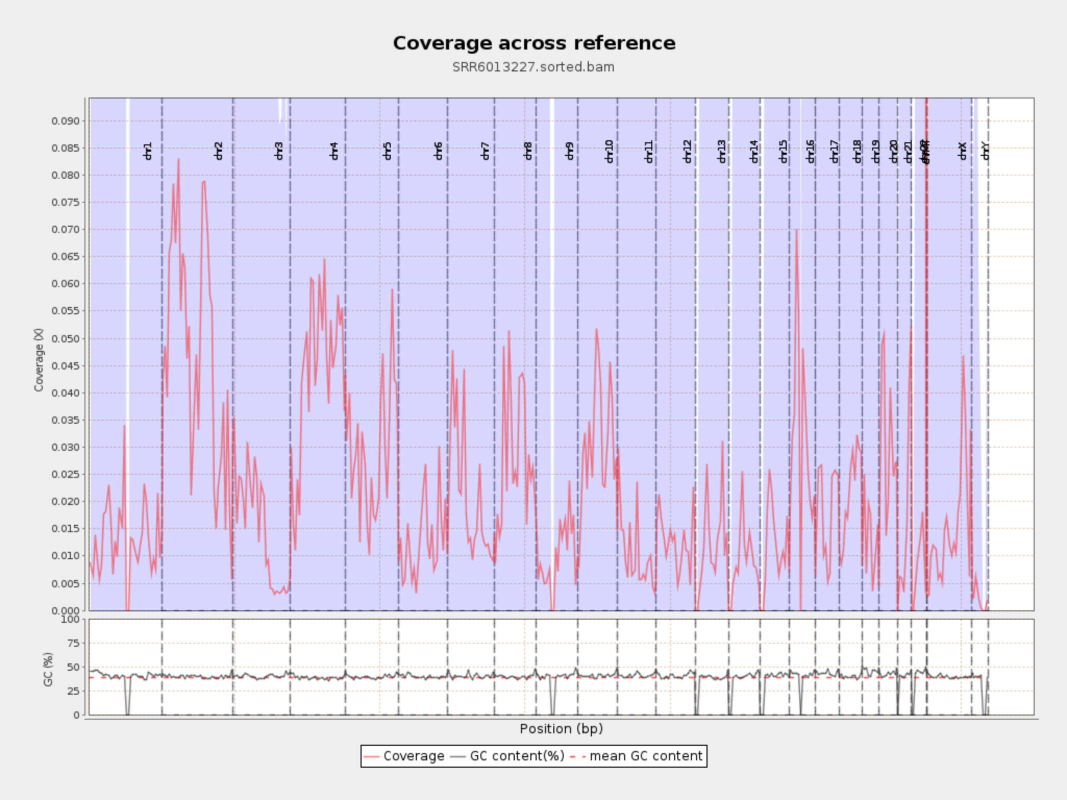
General error rate	0.76%
Mismatches	496,733
Insertions	4,394
Mapped reads with at least one insertion	0.41%
Deletions	18,874
Mapped reads with at least one deletion	1.75%
Homopolymer indels	44.16%

2.6. Chromosome stats

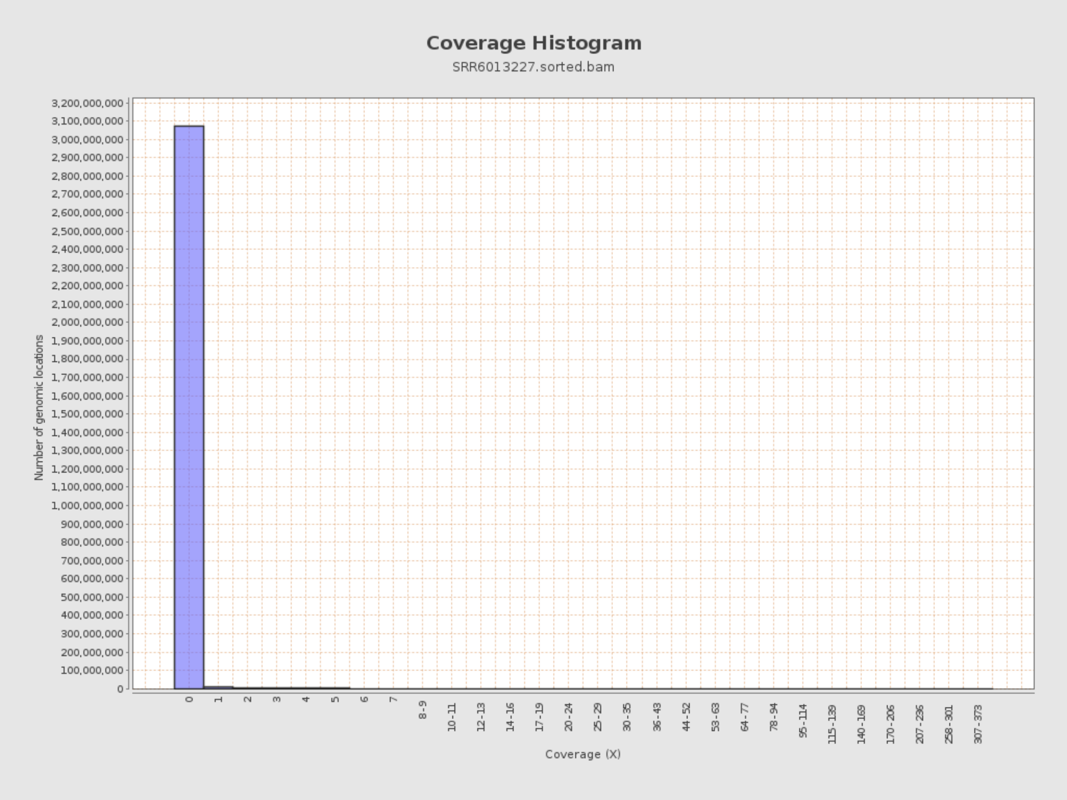
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3186815	0.0128	0.2925
chr2	243199373	11627070	0.0478	0.5089
chr3	198022430	2955553	0.0149	0.2576
chr4	191154276	8401980	0.044	0.4681
chr5	180915260	5304657	0.0293	0.3748
chr6	171115067	2203744	0.0129	0.2453
chr7	159138663	3373508	0.0212	0.3278

chr8	146364022	4102005	0.028	0.4045
chr9	141213431	1381011	0.0098	0.2077
chr10	135534747	4272595	0.0315	0.3991
chr11	135006516	1427386	0.0106	0.2105
chr12	133851895	1724338	0.0129	0.2506
chr13	115169878	1357297	0.0118	0.2292
chr14	107349540	1012324	0.0094	0.2086
chr15	102531392	1211827	0.0118	0.2266
chr16	90354753	2892500	0.032	0.3952
chr17	81195210	1462468	0.018	0.2758
chr18	78077248	1703399	0.0218	0.3492
chr19	59128983	783954	0.0133	0.3745
chr20	63025520	1959215	0.0311	0.3791
chr21	48129895	822047	0.0171	0.2741
chr22	51304566	421235	0.0082	0.1811
chrMT	16571	108191	6.5289	5.4409
chrX	155270560	2266803	0.0146	0.2506
chrY	59373566	113731	0.0019	0.073

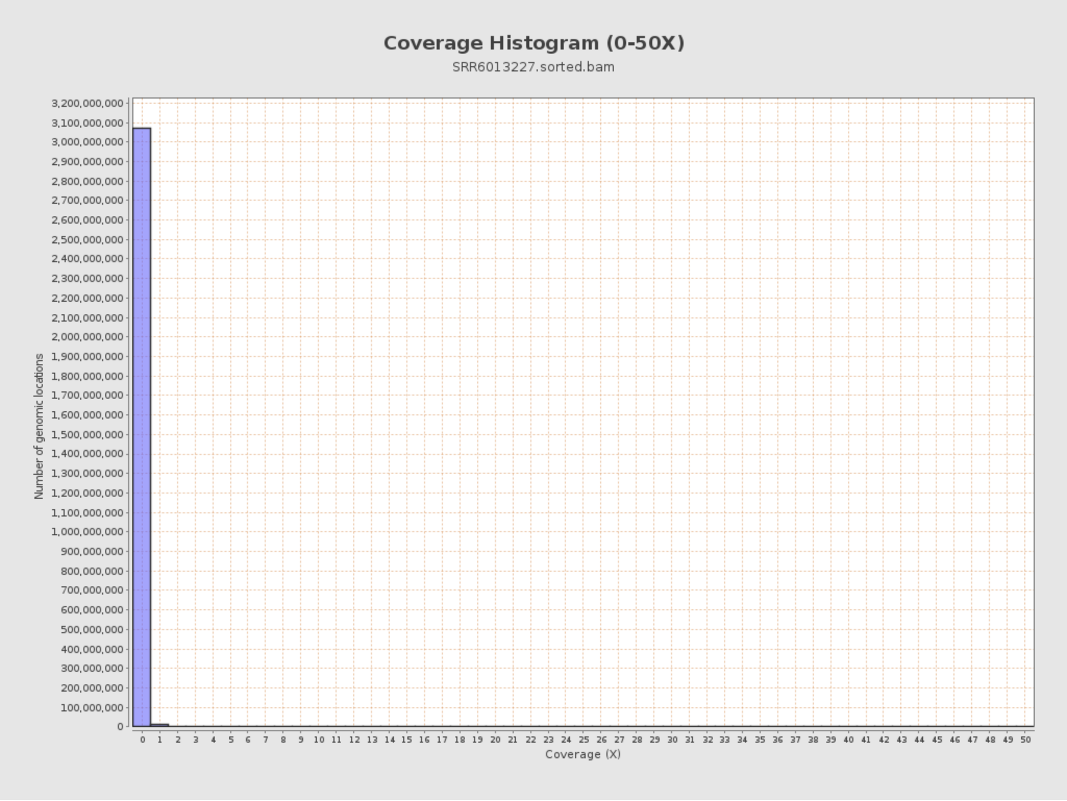
3. Results : Coverage across reference



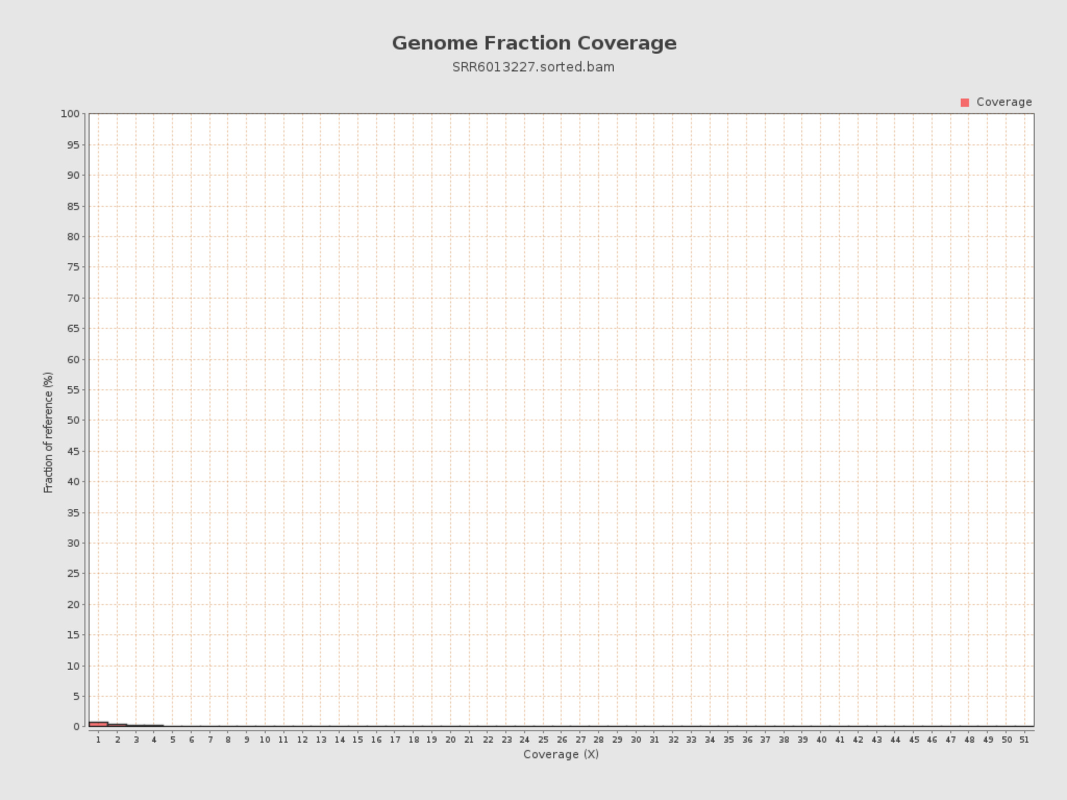
4. Results : Coverage Histogram



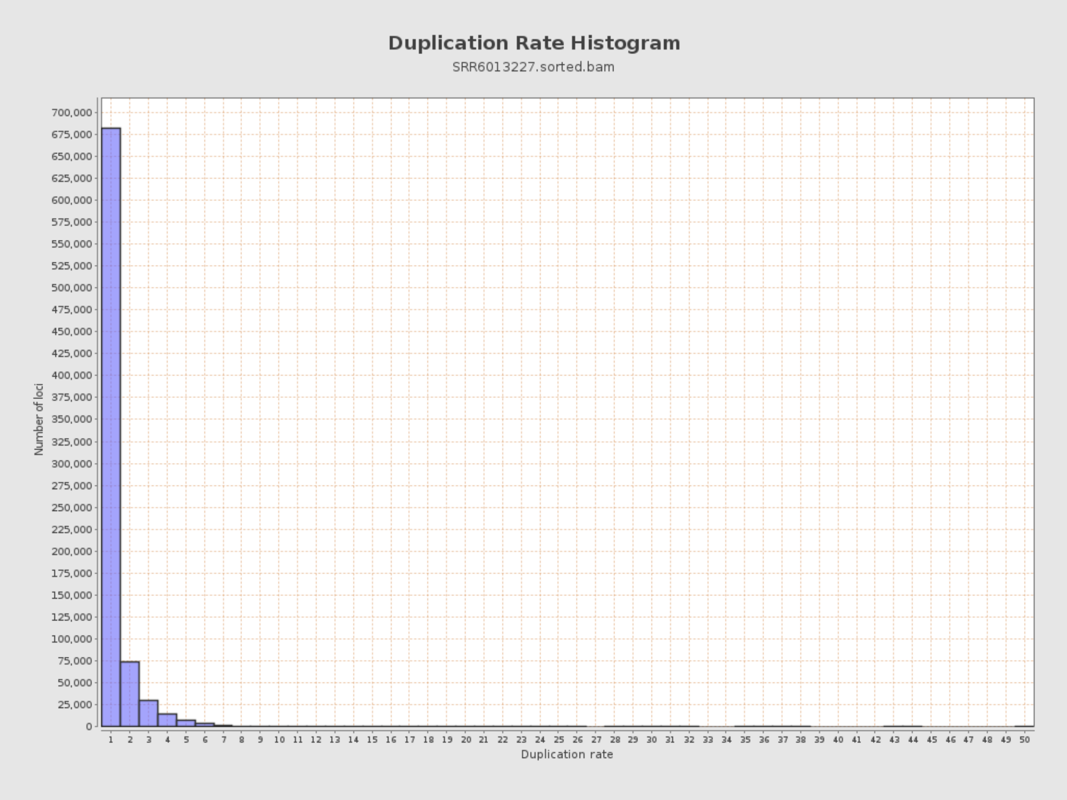
5. Results : Coverage Histogram (0-50X)



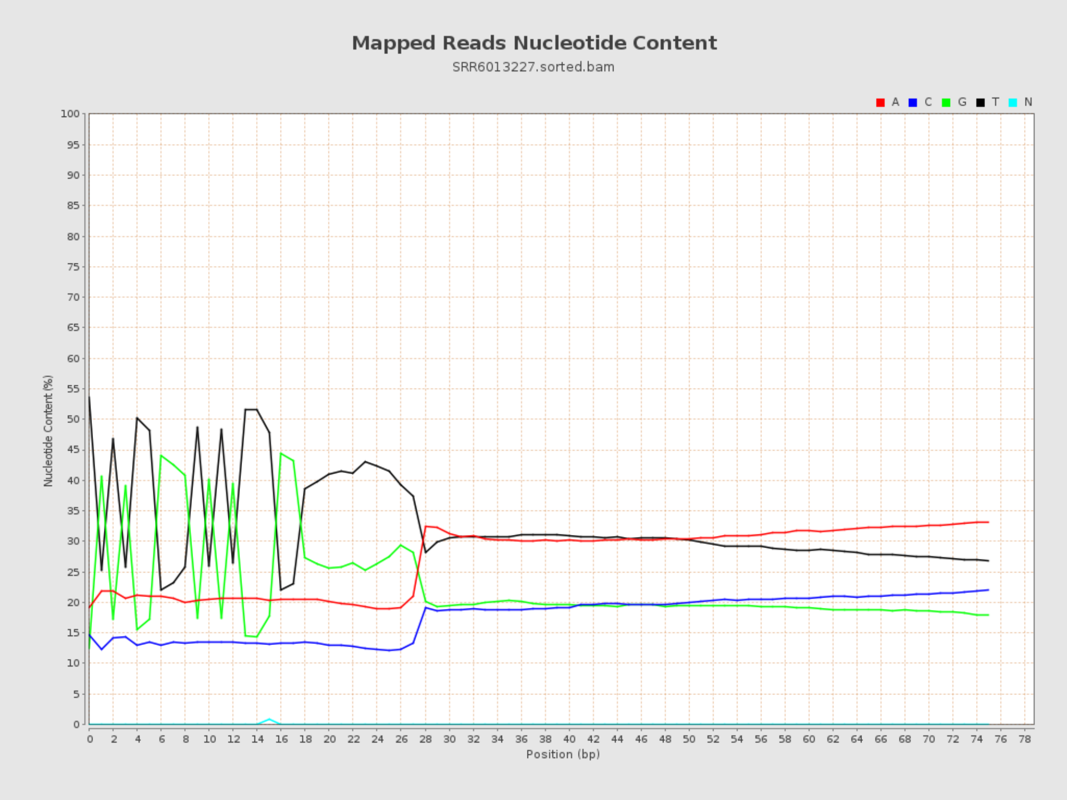
6. Results : Genome Fraction Coverage



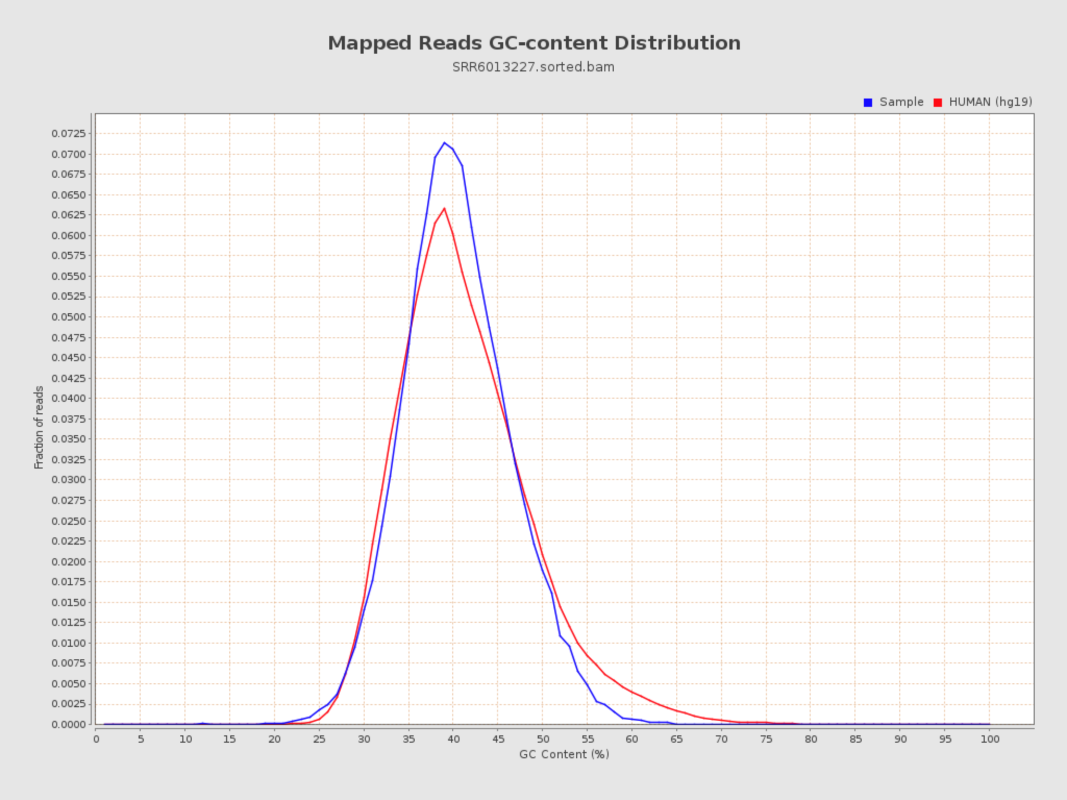
7. Results : Duplication Rate Histogram



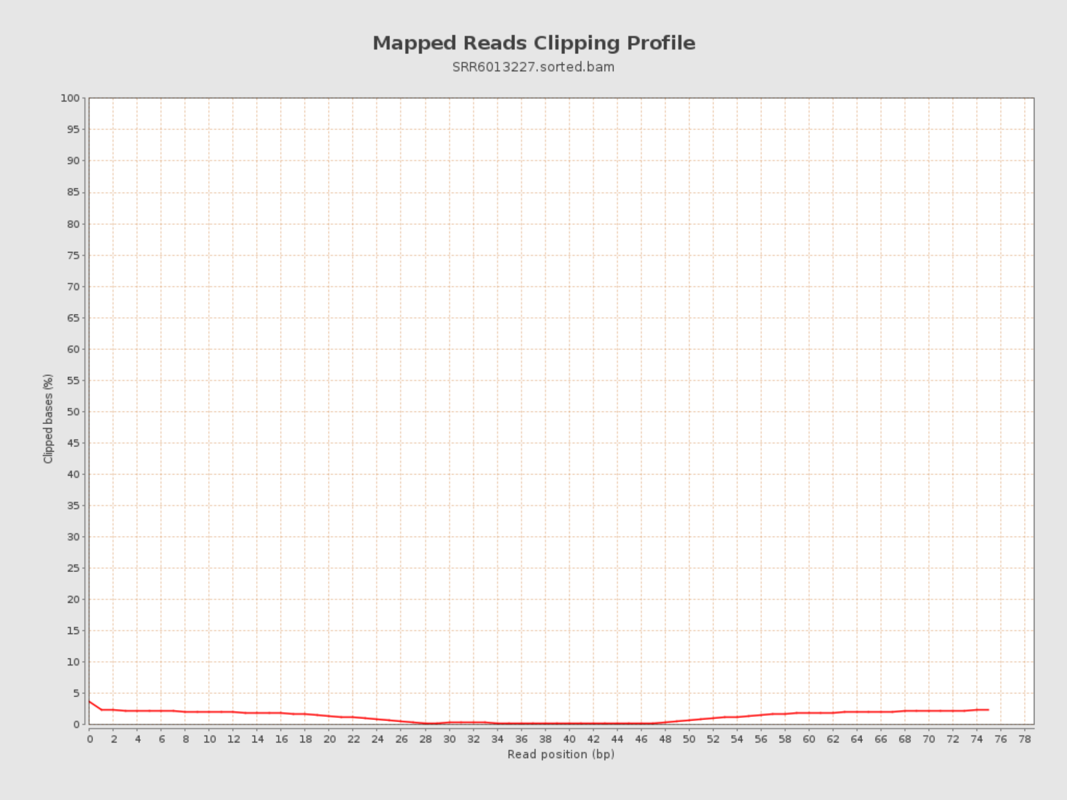
8. Results : Mapped Reads Nucleotide Content



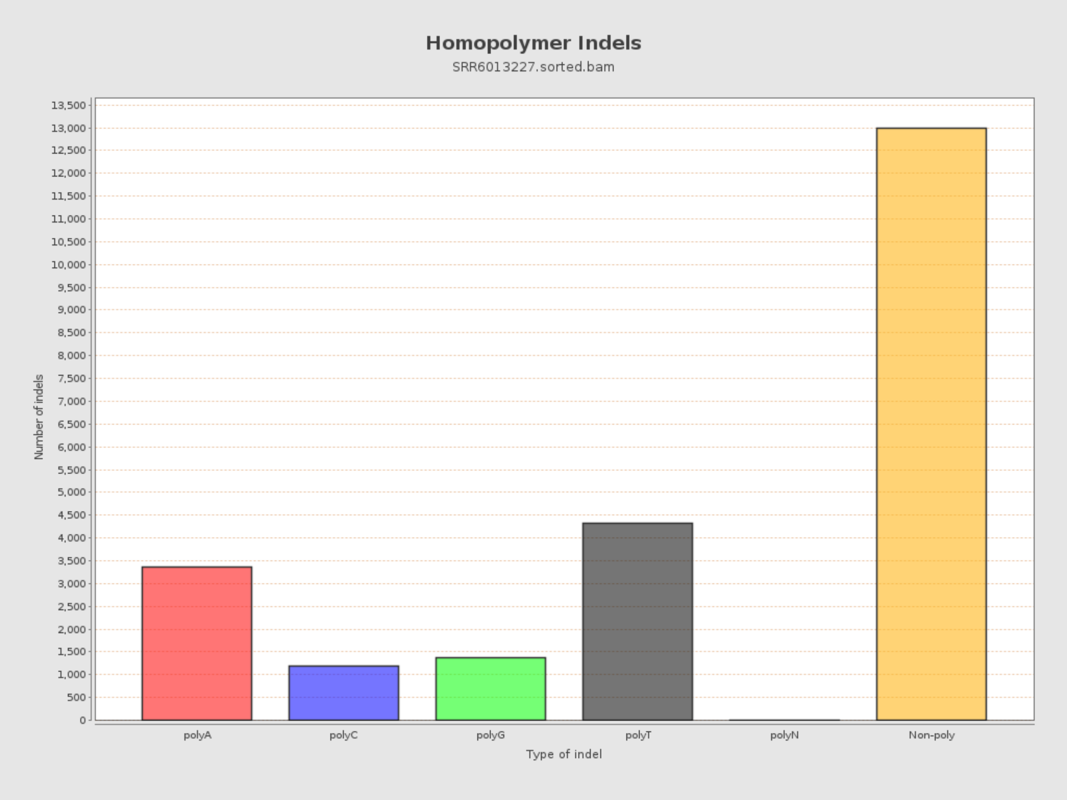
9. Results : Mapped Reads GC-content Distribution



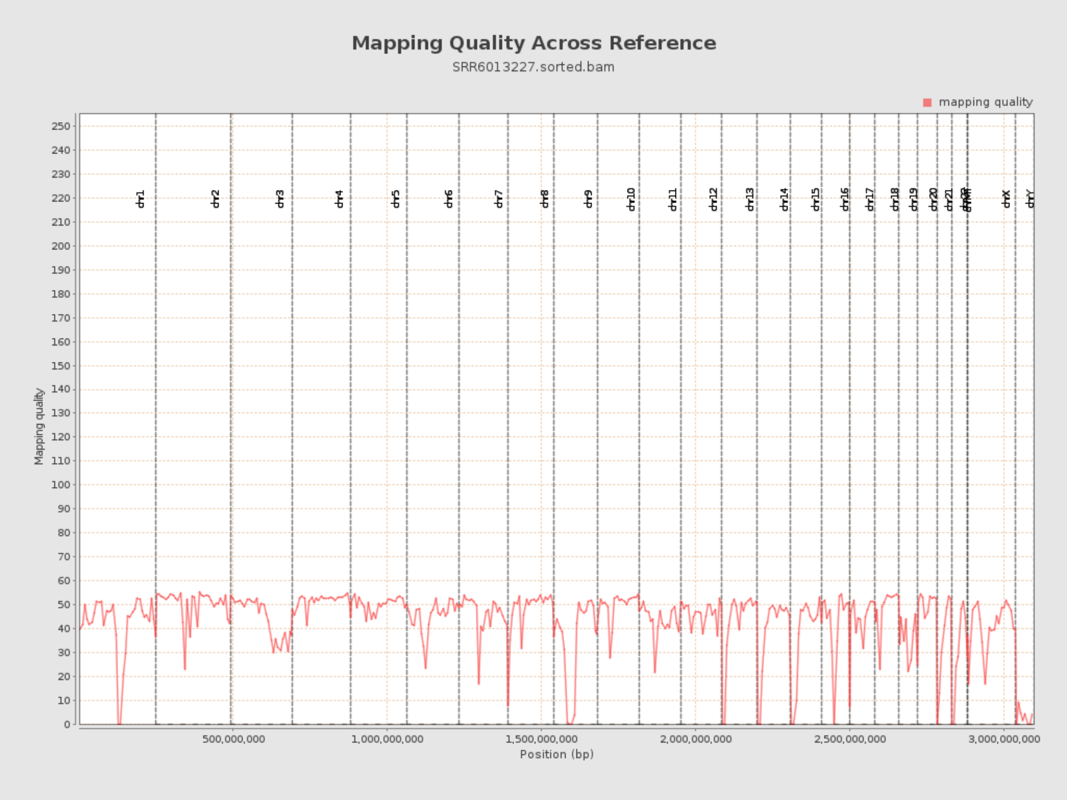
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram