Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 14:54:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR089591.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_SRR089591 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR089591.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 14:54:03 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR089591.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	21,778,295
Mapped reads	15,291,656 / 70.22%
Unmapped reads	6,486,639 / 29.78%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	605 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	2,531,166 / 11.62%
Duplication rate	11.79%
Clipped reads	1,396,509 / 6.41%

2.2. ACGT Content

Number/percentage of A's	212,299,768 / 29.44%
Number/percentage of C's	149,832,297 / 20.78%
Number/percentage of T's	209,136,852 / 29%
Number/percentage of G's	149,890,966 / 20.78%
Number/percentage of N's	13,480 / 0%
GC Percentage	41.56%

2.3. Coverage

Mean	0.233

Standard Deviation	1.2968

2.4. Mapping Quality

Mean Mapping Quality	45.26

2.5. Mismatches and indels

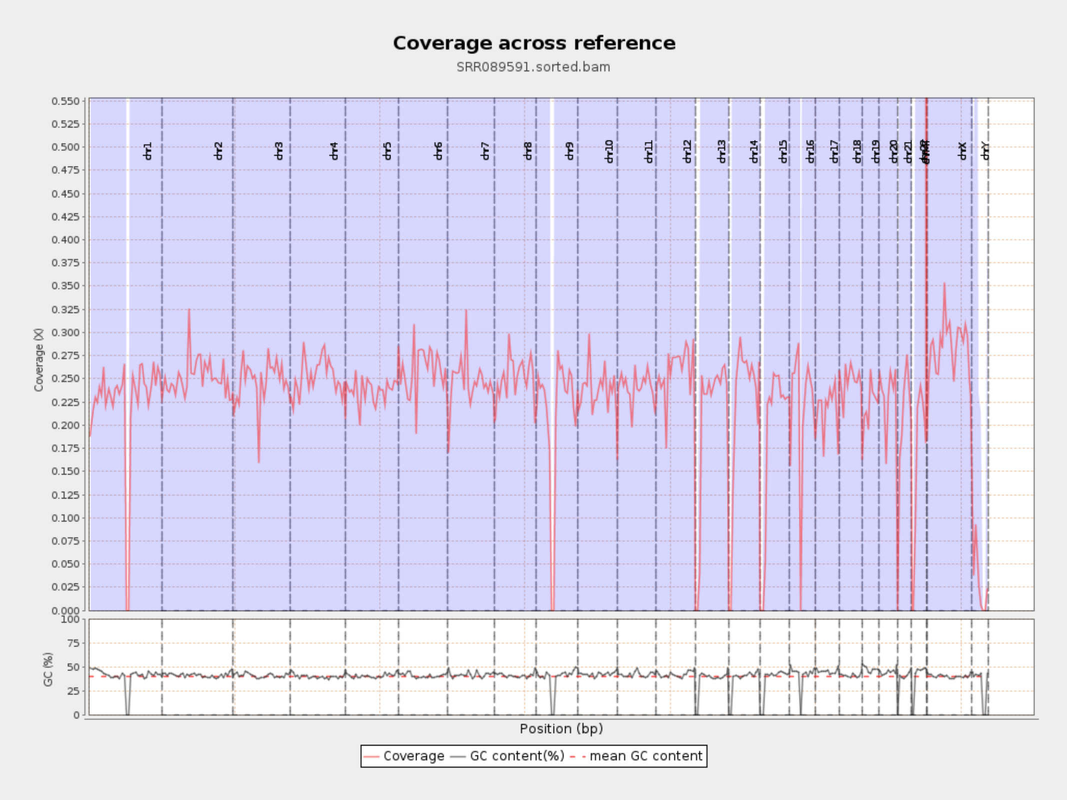
General error rate	0.44%
Mismatches	3,130,089
Insertions	28,037
Mapped reads with at least one insertion	0.18%
Deletions	96,761
Mapped reads with at least one deletion	0.63%
Homopolymer indels	46.41%

2.6. Chromosome stats

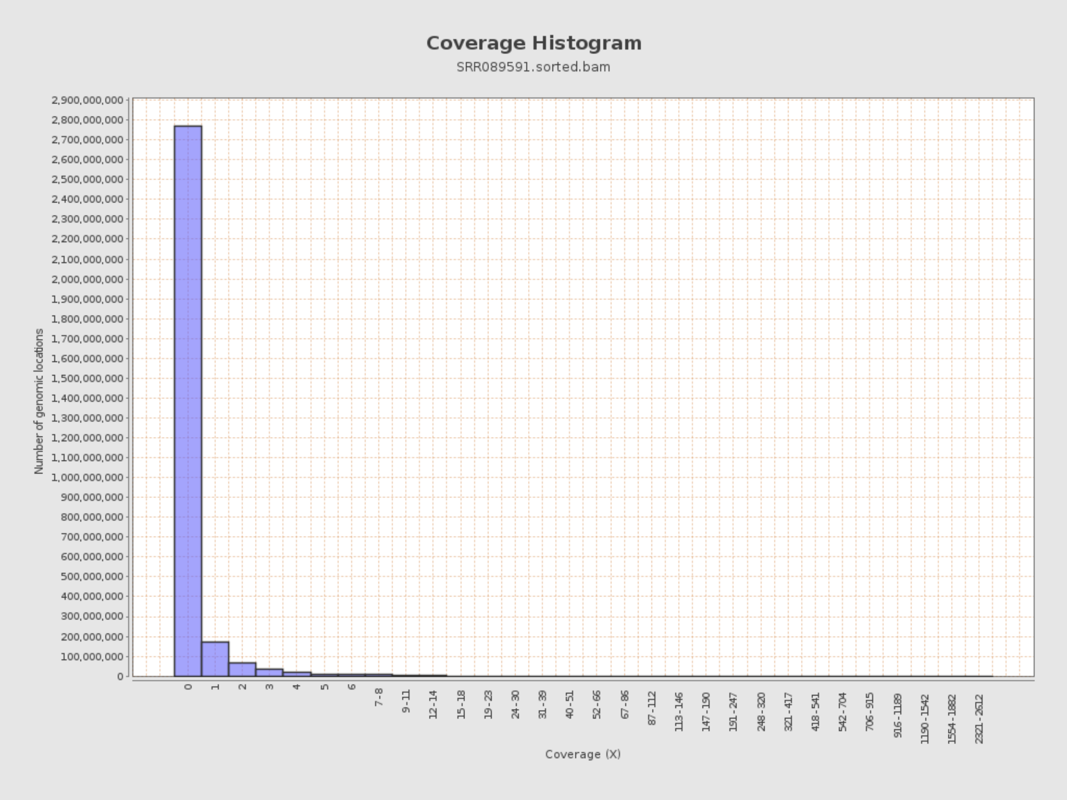
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	55786752	0.2238	1.6943
chr2	243199373	61271094	0.2519	1.6131
chr3	198022430	48974008	0.2473	0.9919
chr4	191154276	48240774	0.2524	1.0387
chr5	180915260	42988271	0.2376	0.9754
chr6	171115067	44447261	0.2598	1.204
chr7	159138663	39391584	0.2475	1.8171

chr8	146364022	36769160	0.2512	1.782
chr9	141213431	29752381	0.2107	1.1629
chr10	135534747	32460155	0.2395	1.2878
chr11	135006516	32269976	0.239	1.2087
chr12	133851895	34640370	0.2588	1.0535
chr13	115169878	23569522	0.2047	0.8985
chr14	107349540	23214094	0.2162	1.0511
chr15	102531392	19330746	0.1885	0.8612
chr16	90354753	20015587	0.2215	1.0126
chr17	81195210	17469495	0.2152	0.9856
chr18	78077248	19355100	0.2479	1.8187
chr19	59128983	13128253	0.222	1.5893
chr20	63025520	14413694	0.2287	1.0048
chr21	48129895	9587595	0.1992	0.9935
chr22	51304566	7958095	0.1551	0.7768
chrMT	16571	497210	30.0048	23.0153
chrX	155270560	43811163	0.2822	1.2262
chrY	59373566	1975541	0.0333	0.4969

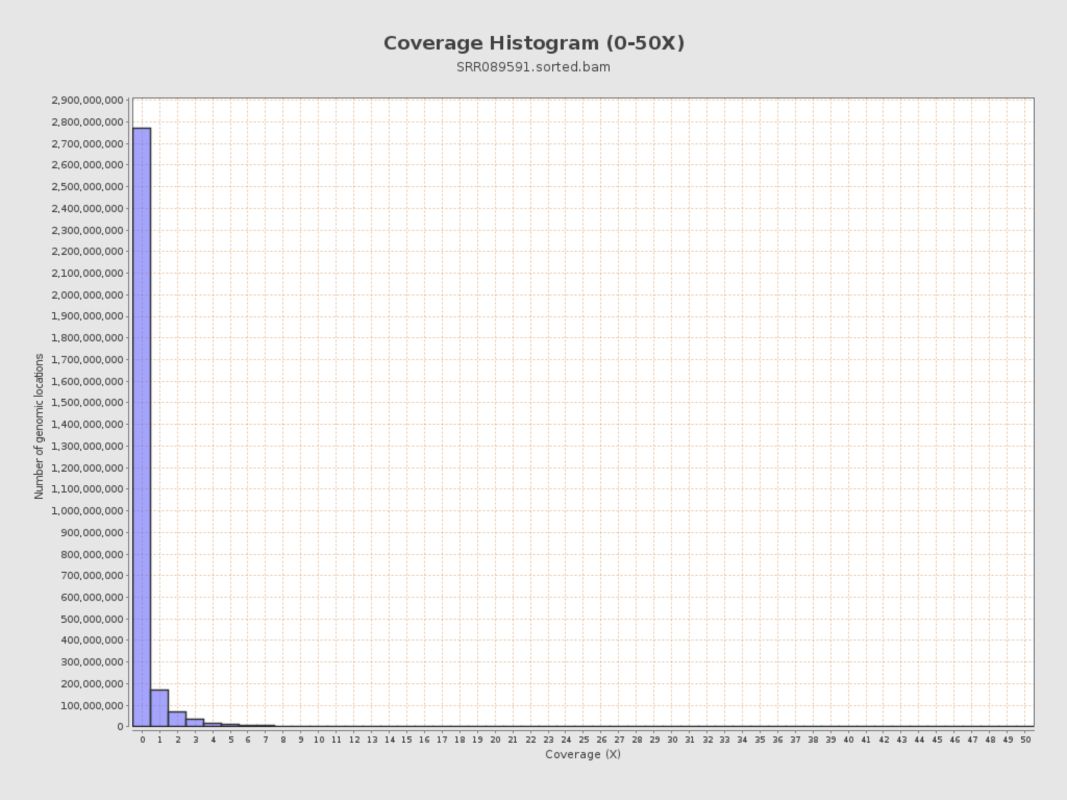
3. Results : Coverage across reference



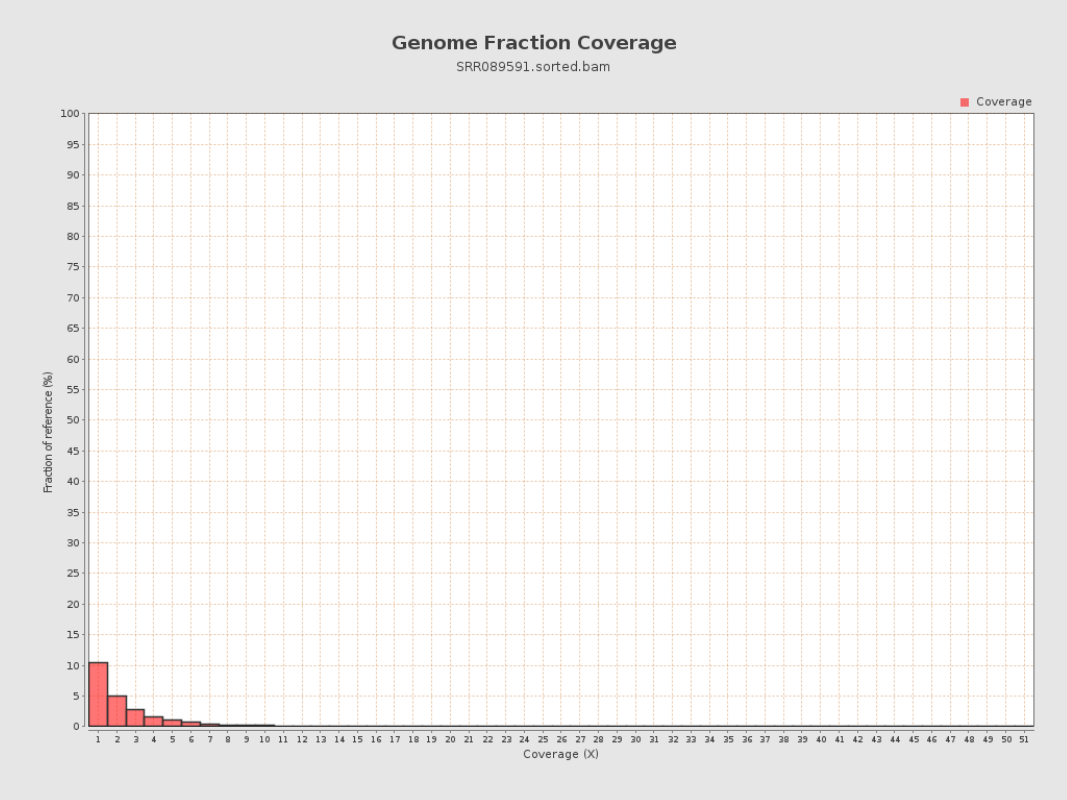
4. Results : Coverage Histogram



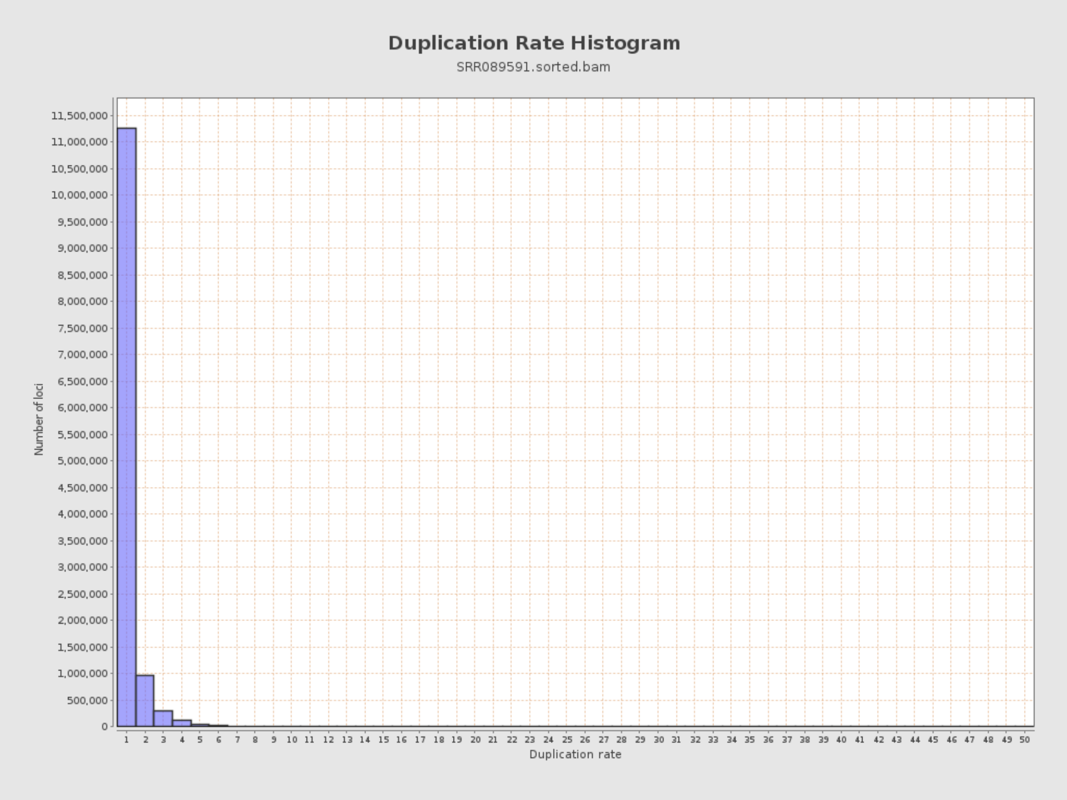
5. Results : Coverage Histogram (0-50X)



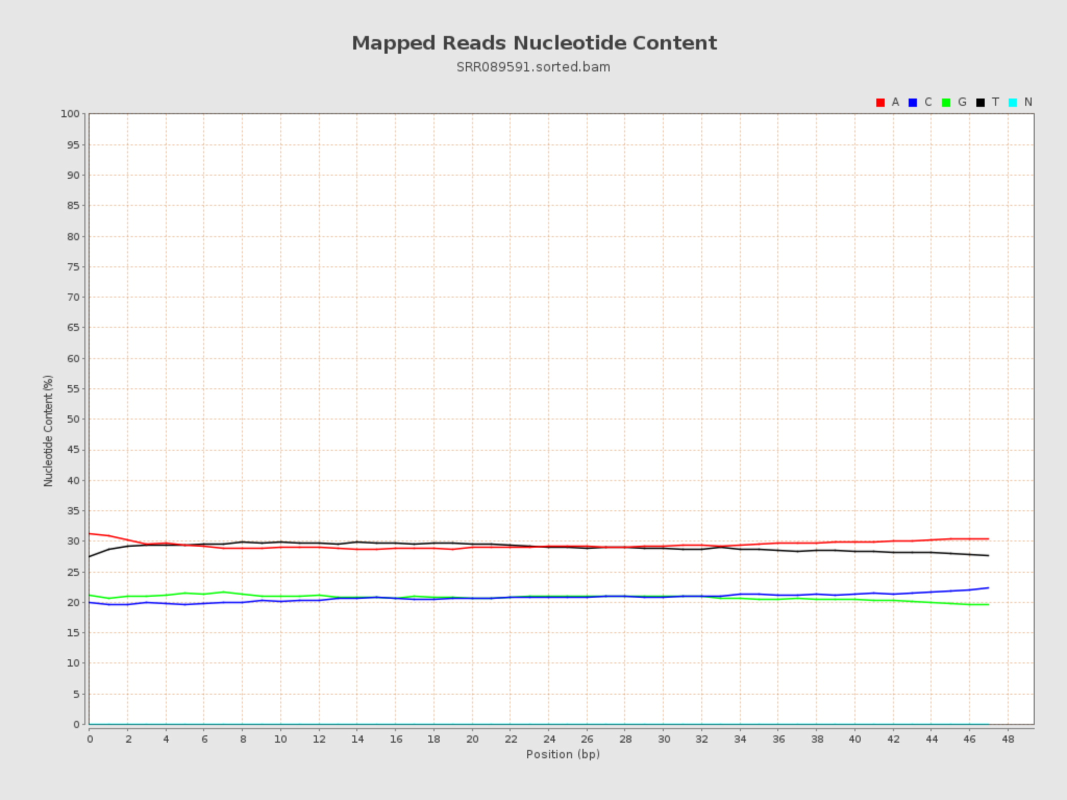
6. Results : Genome Fraction Coverage



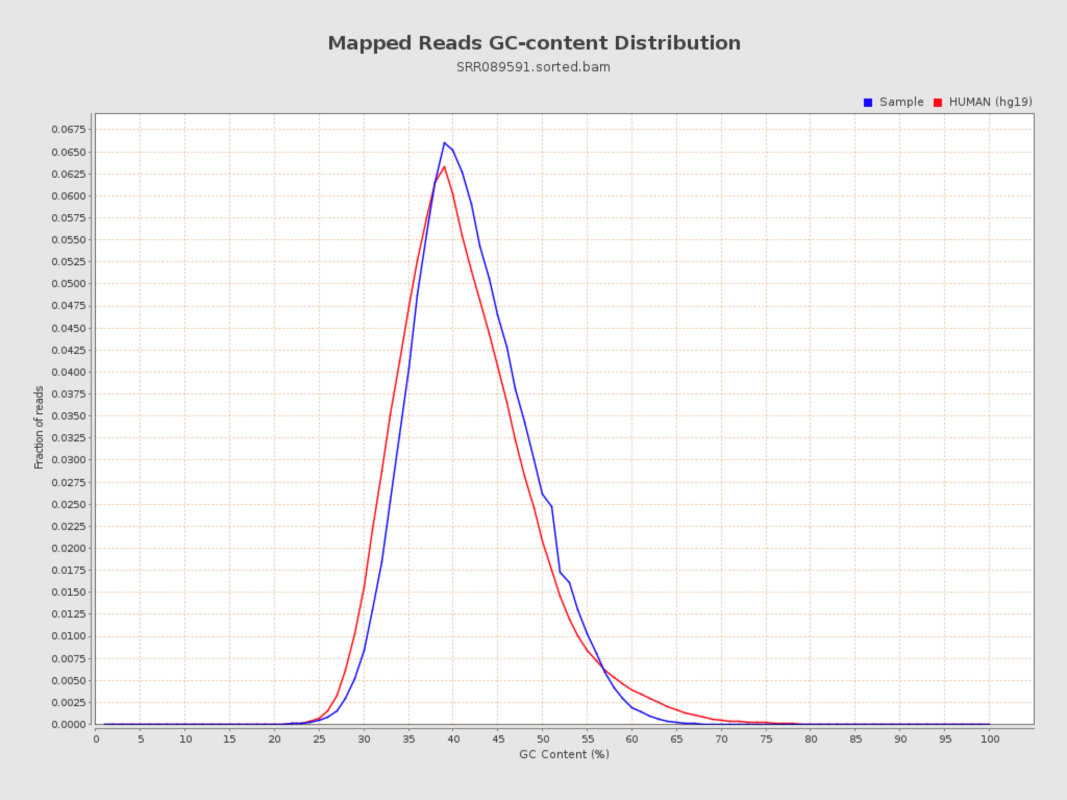
7. Results : Duplication Rate Histogram



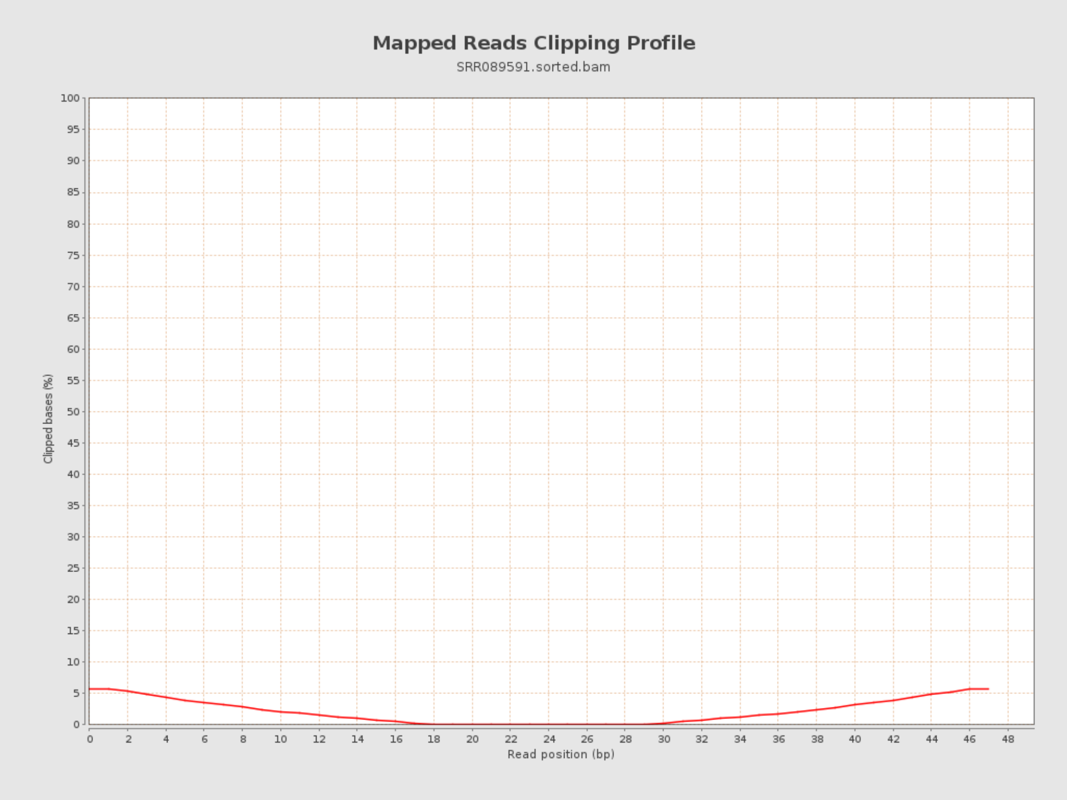
8. Results : Mapped Reads Nucleotide Content



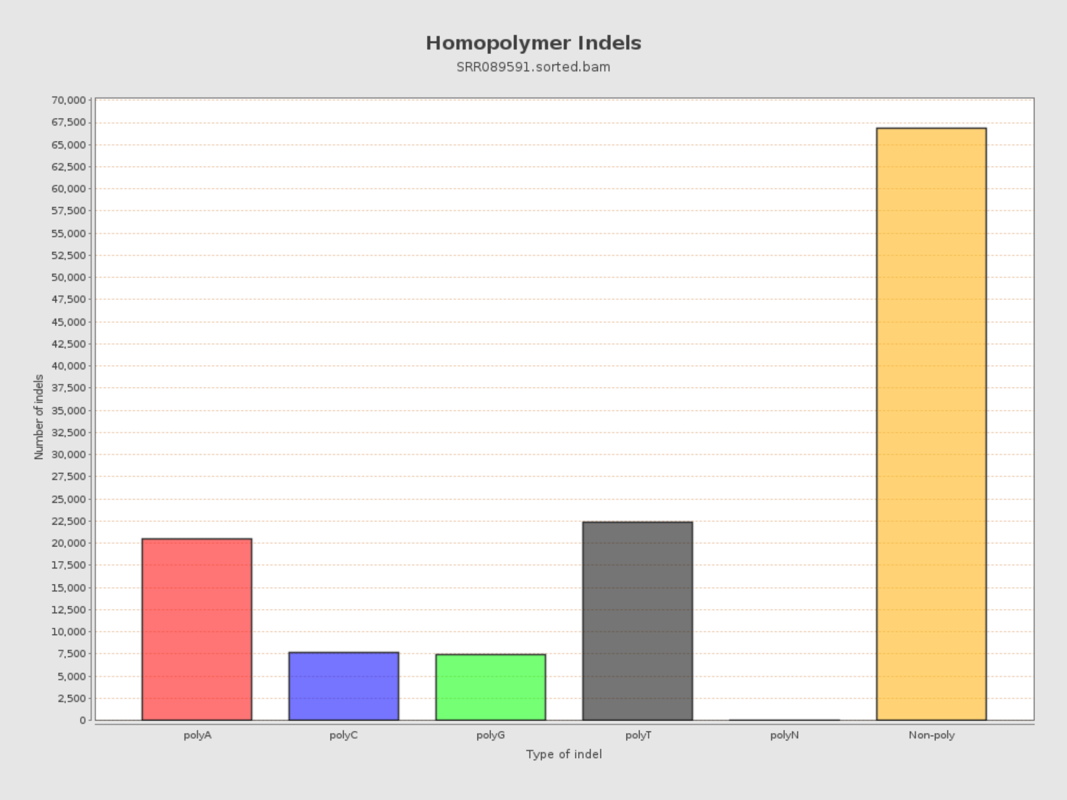
9. Results : Mapped Reads GC-content Distribution



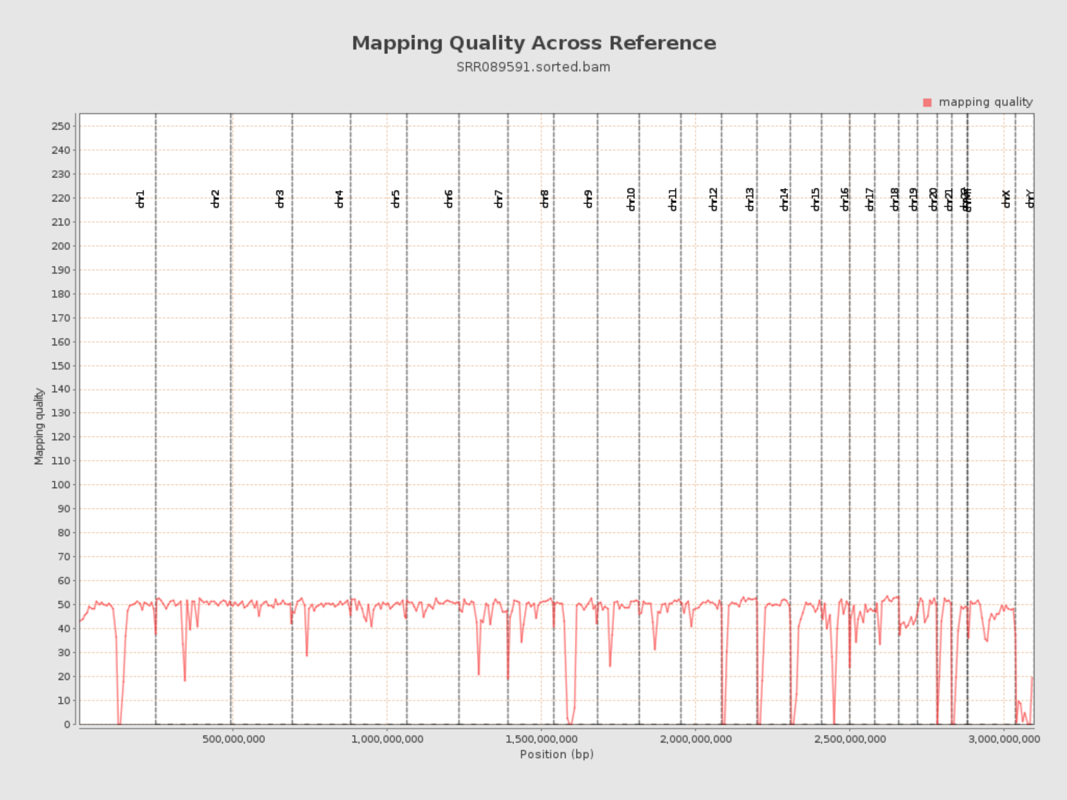
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram