Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 12:12:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR089529.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_SRR089529 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR089529.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 12:12:08 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR089529.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,771,376
Mapped reads	6,612,834 / 75.39%
Unmapped reads	2,158,542 / 24.61%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	266 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	1,913,788 / 21.82%
Duplication rate	21.08%
Clipped reads	995,099 / 11.34%

2.2. ACGT Content

Number/percentage of A's	99,955,958 / 32.42%
Number/percentage of C's	59,856,618 / 19.41%
Number/percentage of T's	77,585,768 / 25.16%
Number/percentage of G's	70,881,740 / 22.99%
Number/percentage of N's	37,770 / 0.01%
GC Percentage	42.4%

2.3. Coverage

Mean	0.0996

Standard Deviation	0.9093

2.4. Mapping Quality

Mean Mapping Quality	41.08

2.5. Mismatches and indels

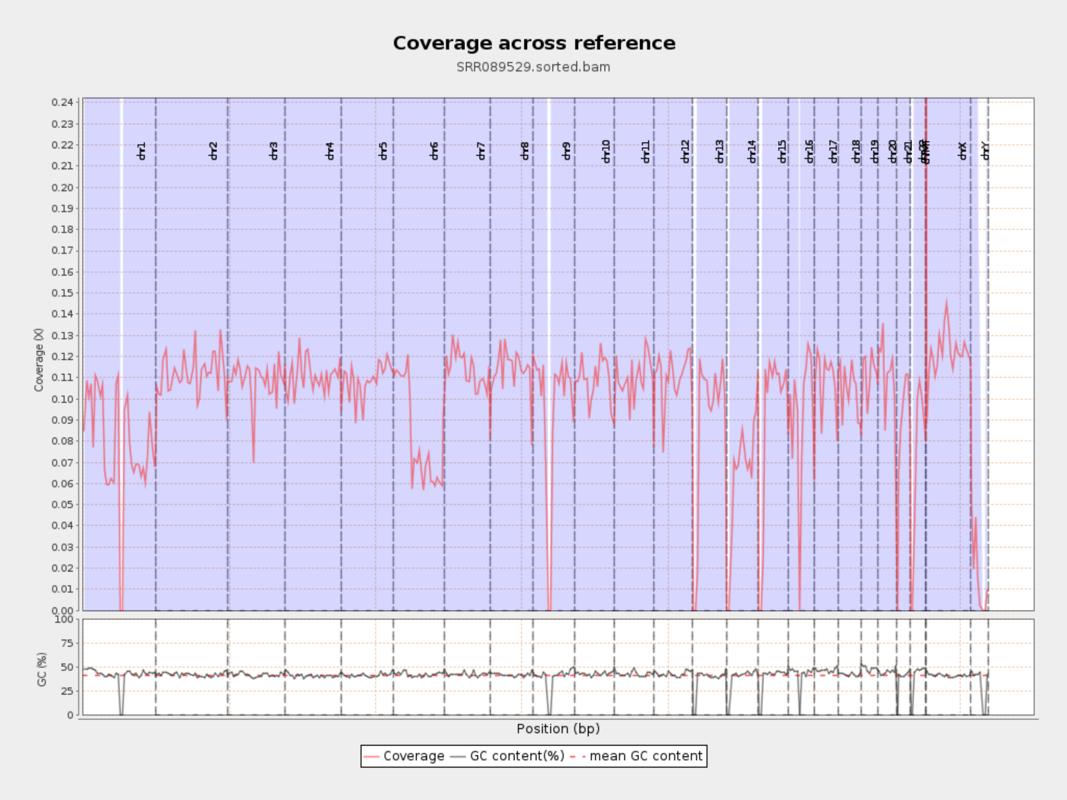
General error rate	0.84%
Mismatches	2,576,858
Insertions	16,998
Mapped reads with at least one insertion	0.26%
Deletions	41,008
Mapped reads with at least one deletion	0.62%
Homopolymer indels	41.76%

2.6. Chromosome stats

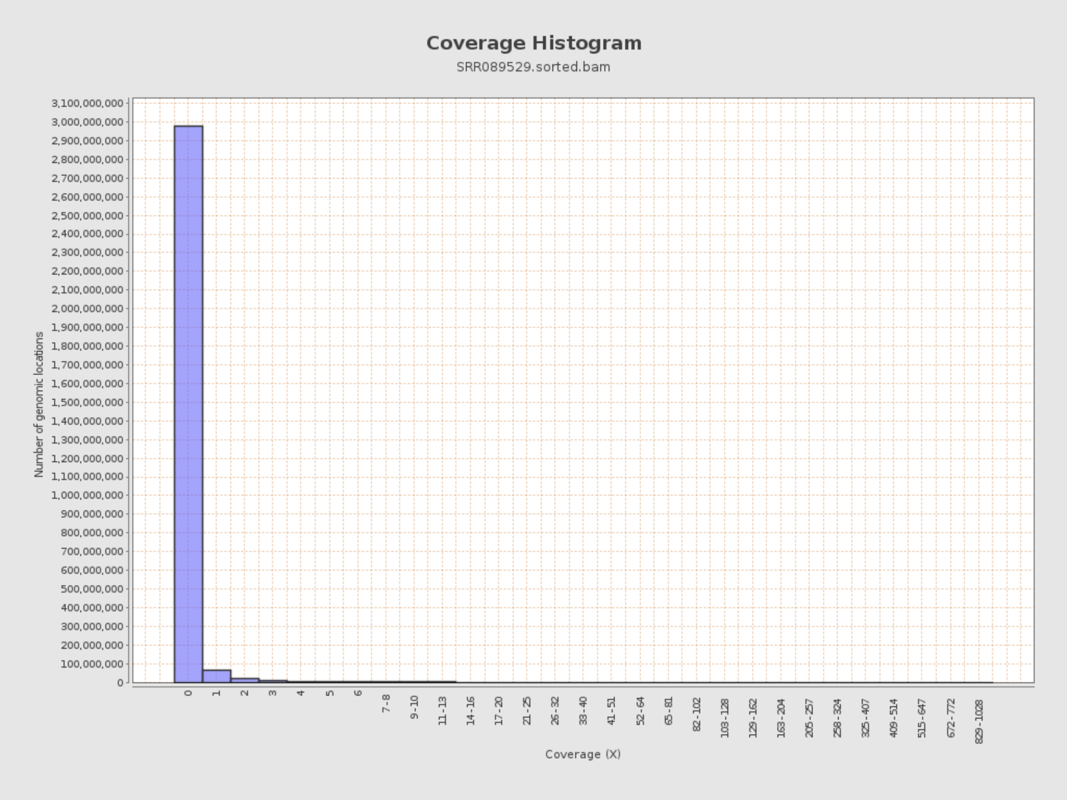
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	19336101	0.0776	0.8659
chr2	243199373	27294790	0.1122	1.0365
chr3	198022430	21556389	0.1089	0.8979
chr4	191154276	21200722	0.1109	0.9406
chr5	180915260	19726888	0.109	0.8927
chr6	171115067	13951232	0.0815	0.8087
chr7	159138663	18121344	0.1139	1.023

chr8	146364022	16650169	0.1138	1.0795
chr9	141213431	13345817	0.0945	0.8488
chr10	135534747	14824632	0.1094	0.9408
chr11	135006516	14845118	0.11	1.0319
chr12	133851895	14924473	0.1115	0.8976
chr13	115169878	10176529	0.0884	0.8151
chr14	107349540	6785495	0.0632	0.7492
chr15	102531392	9101166	0.0888	0.7806
chr16	90354753	8213105	0.0909	0.817
chr17	81195210	8954069	0.1103	0.9035
chr18	78077248	8177515	0.1047	0.9211
chr19	59128983	6572293	0.1112	0.9255
chr20	63025520	7019823	0.1114	0.898
chr21	48129895	4127601	0.0858	0.9218
chr22	51304566	3563711	0.0695	0.6868
chrMT	16571	9763	0.5892	1.665
chrX	155270560	18934307	0.1219	0.9815
chrY	59373566	965651	0.0163	0.3453

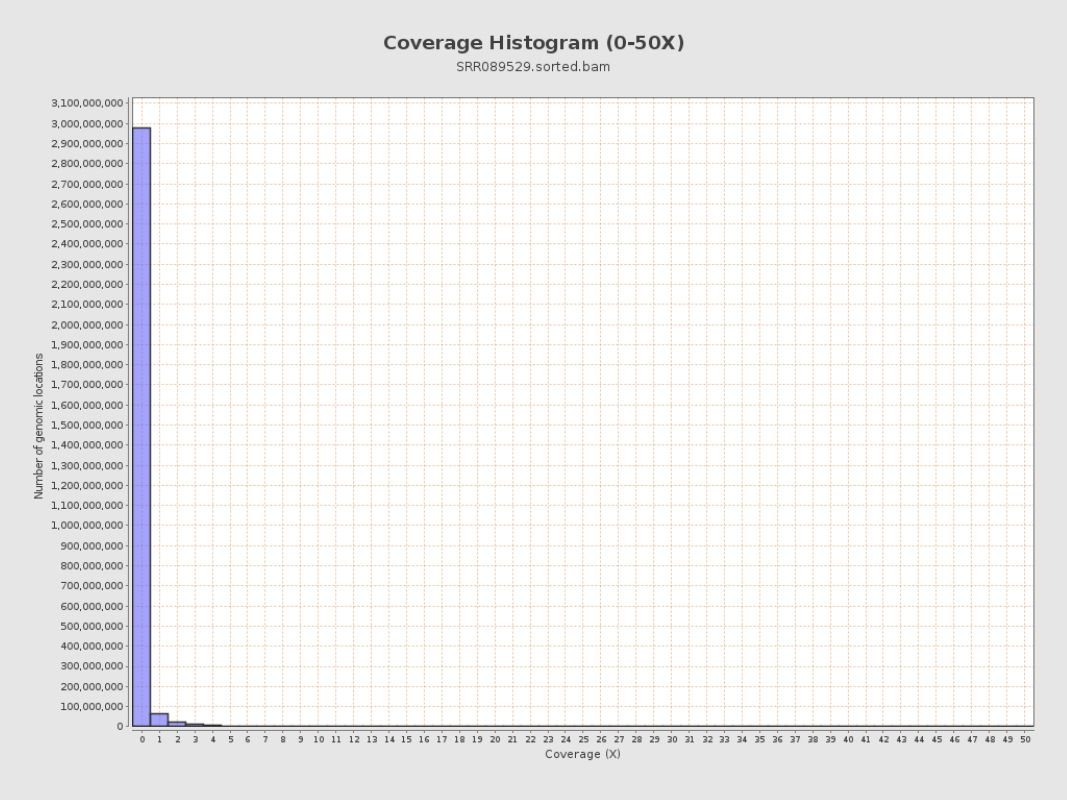
3. Results : Coverage across reference



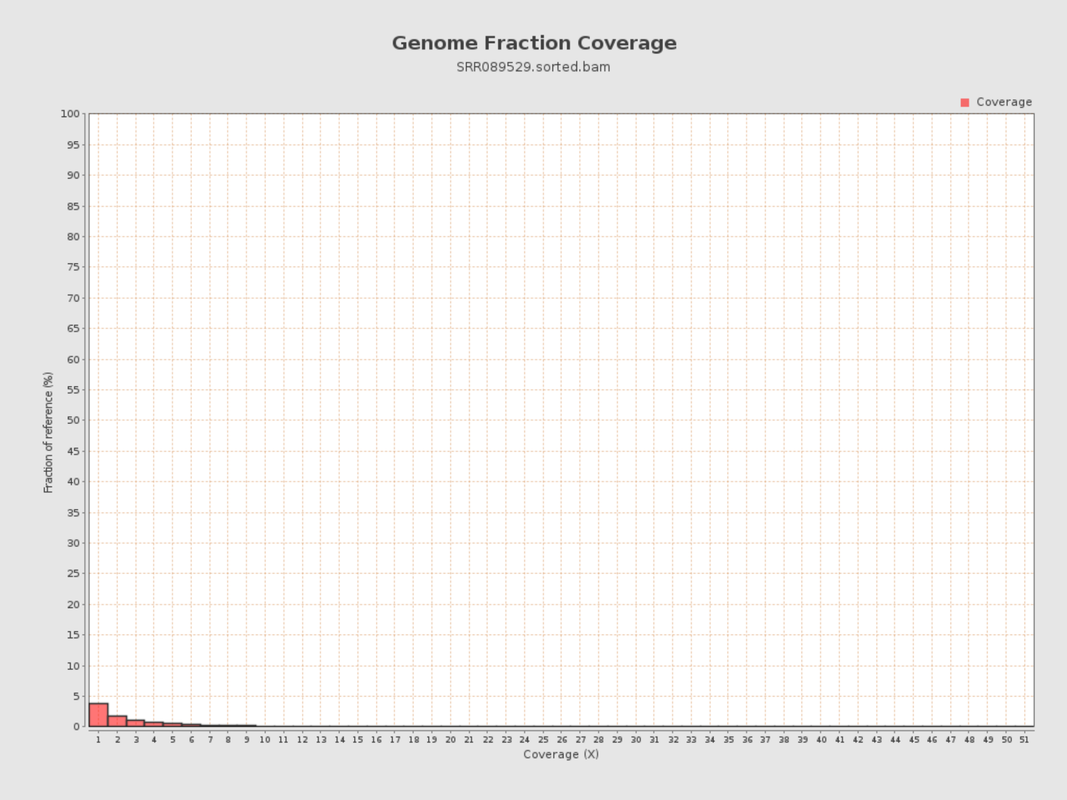
4. Results : Coverage Histogram



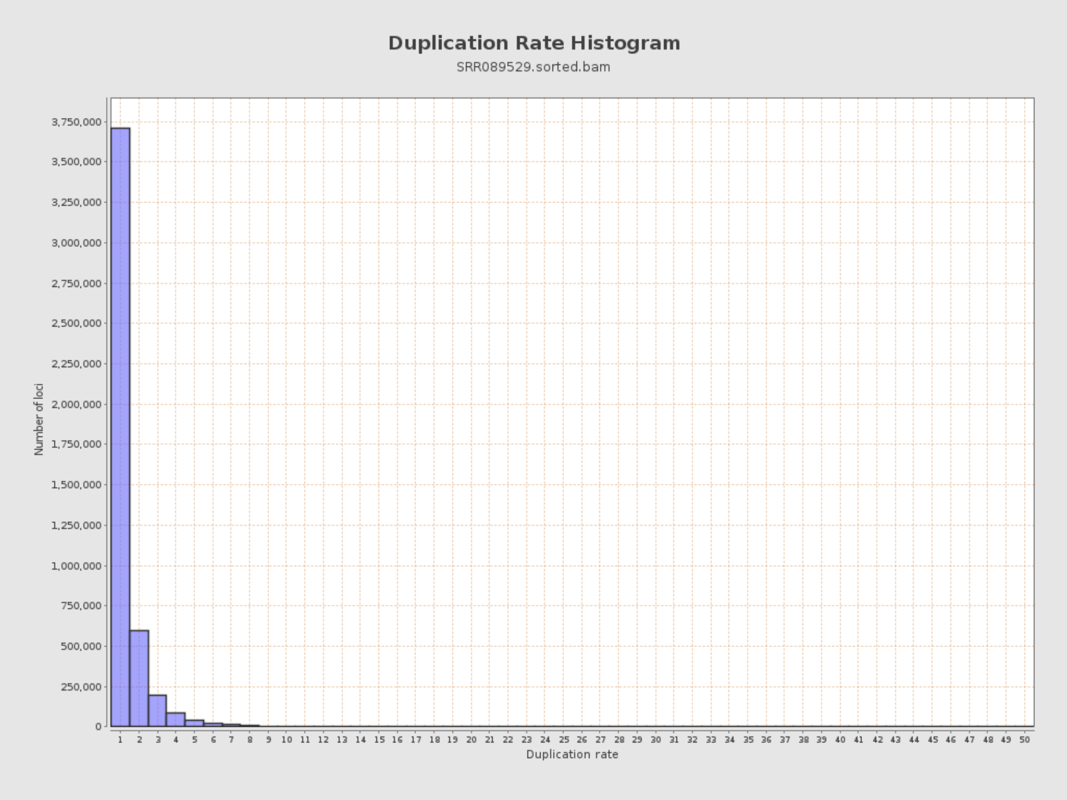
5. Results : Coverage Histogram (0-50X)



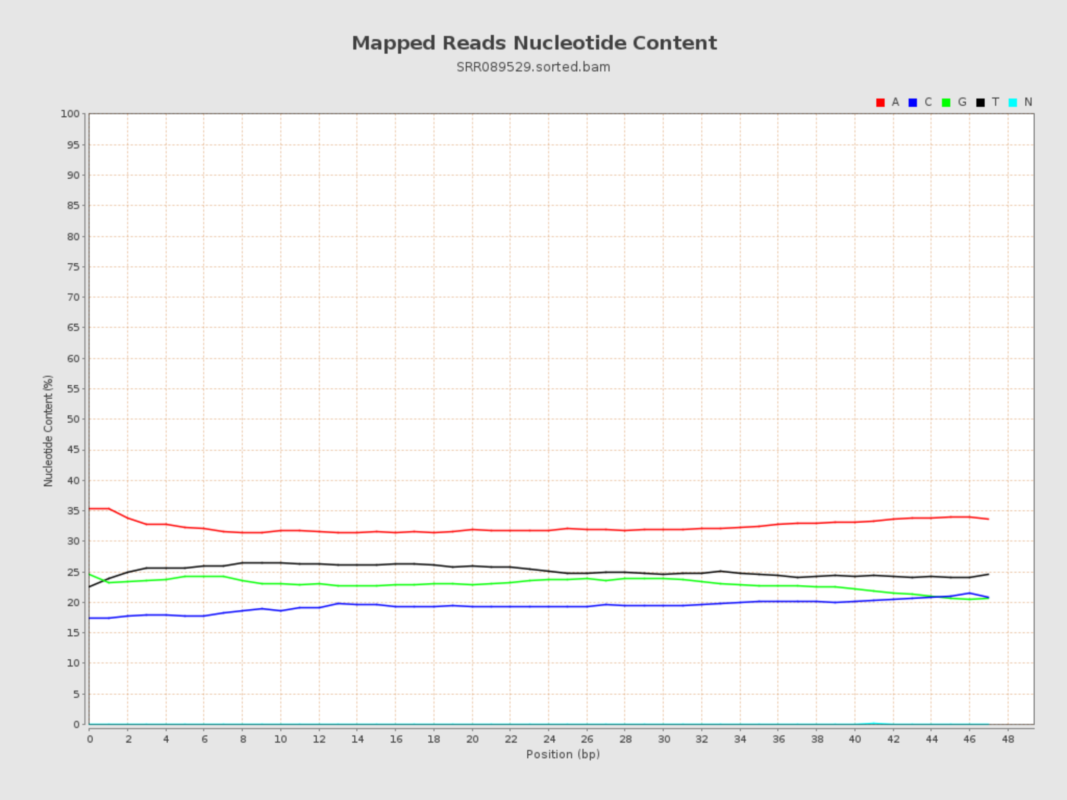
6. Results : Genome Fraction Coverage



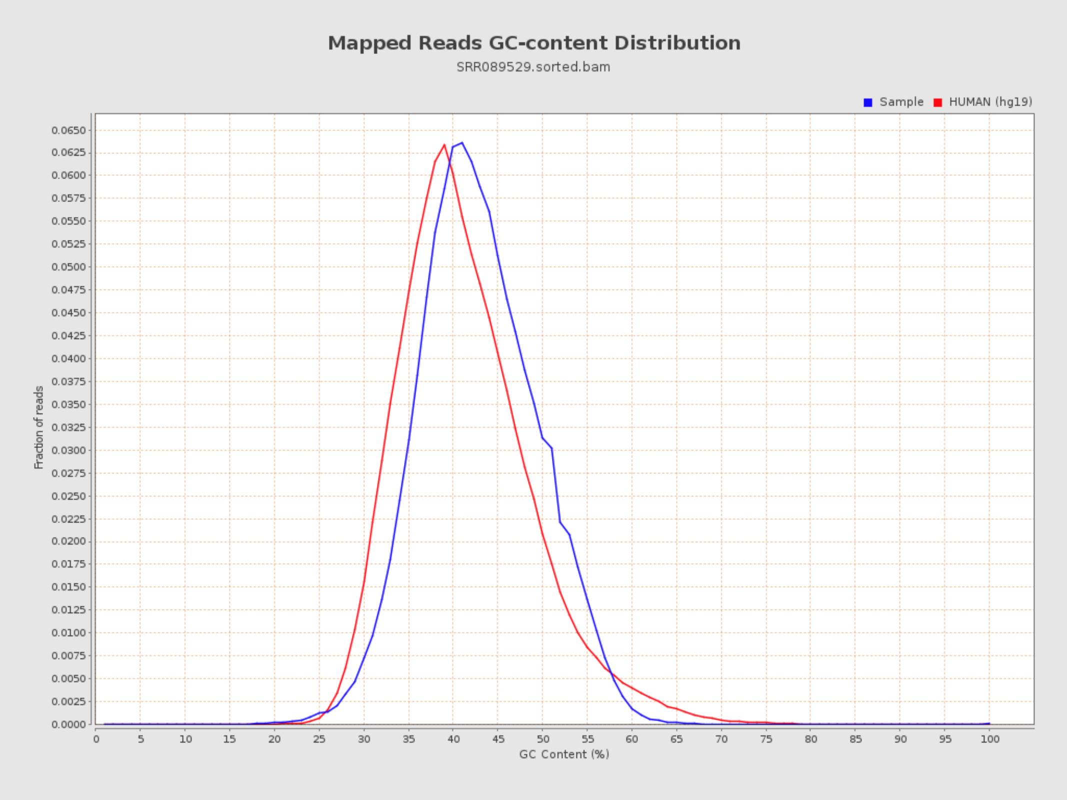
7. Results : Duplication Rate Histogram



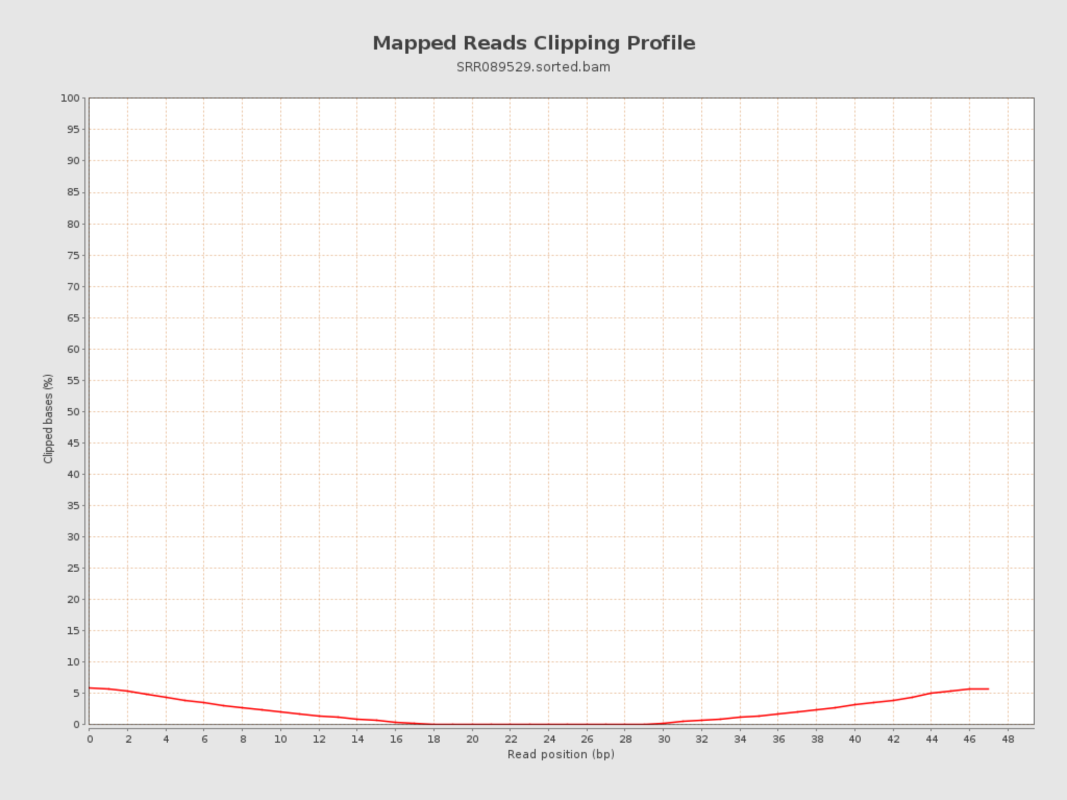
8. Results : Mapped Reads Nucleotide Content



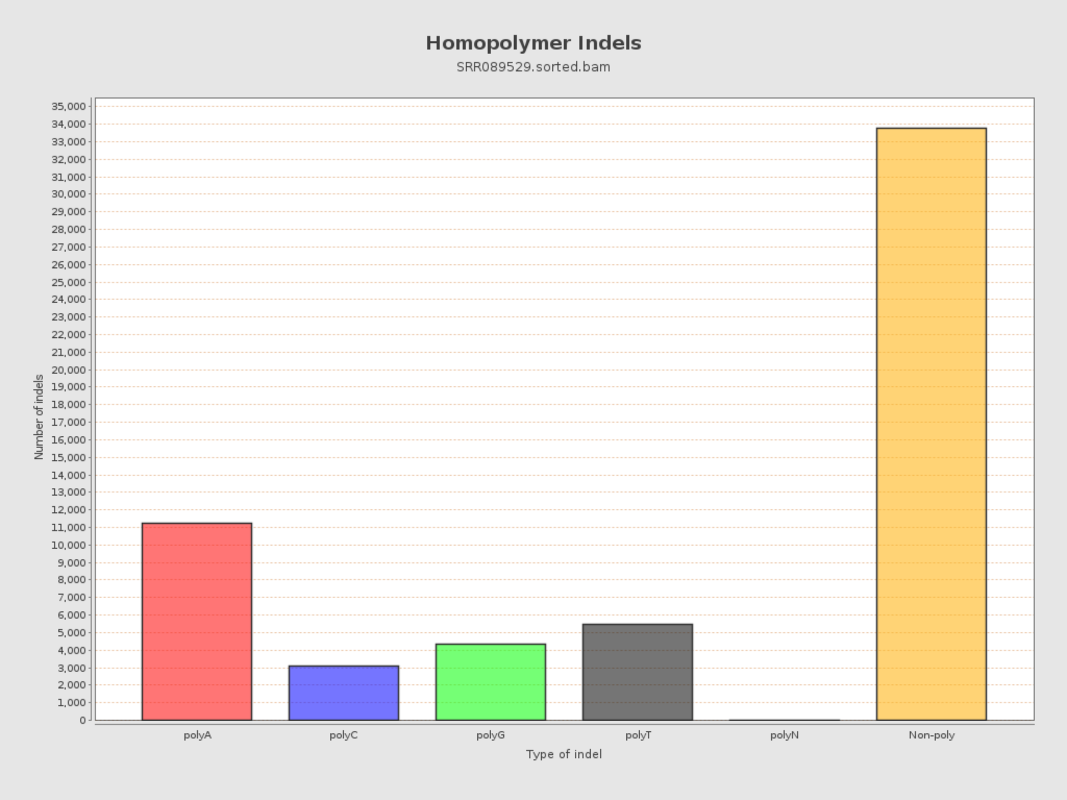
9. Results : Mapped Reads GC-content Distribution



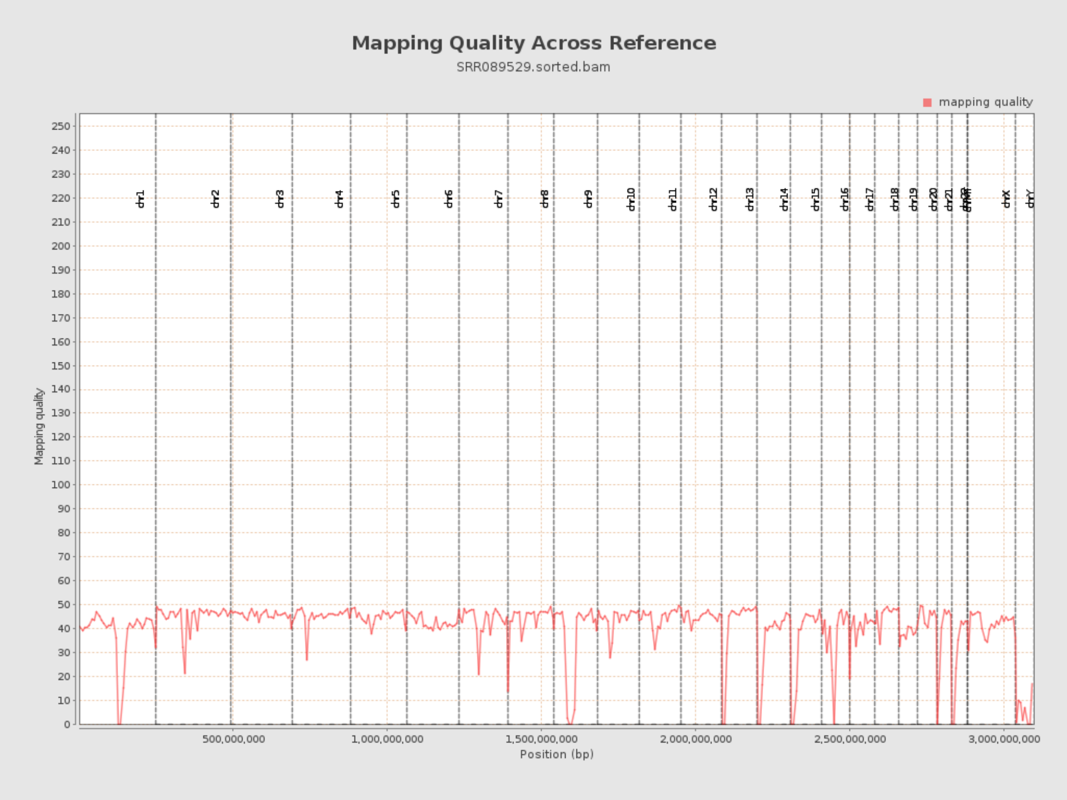
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram