Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 12:50:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR089561.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_SRR089561 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR089561.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 12:50:06 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR089561.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	11,544,476
Mapped reads	9,632,059 / 83.43%
Unmapped reads	1,912,417 / 16.57%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	368 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	3,331,599 / 28.86%
Duplication rate	25.58%
Clipped reads	1,134,394 / 9.83%

2.2. ACGT Content

Number/percentage of A's	145,924,895 / 32.29%
Number/percentage of C's	89,036,285 / 19.7%
Number/percentage of T's	113,741,180 / 25.17%
Number/percentage of G's	103,260,200 / 22.85%
Number/percentage of N's	6,912 / 0%
GC Percentage	42.55%

2.3. Coverage

Mean	0.146

Standard Deviation	1.2544

2.4. Mapping Quality

Mean Mapping Quality	43.49

2.5. Mismatches and indels

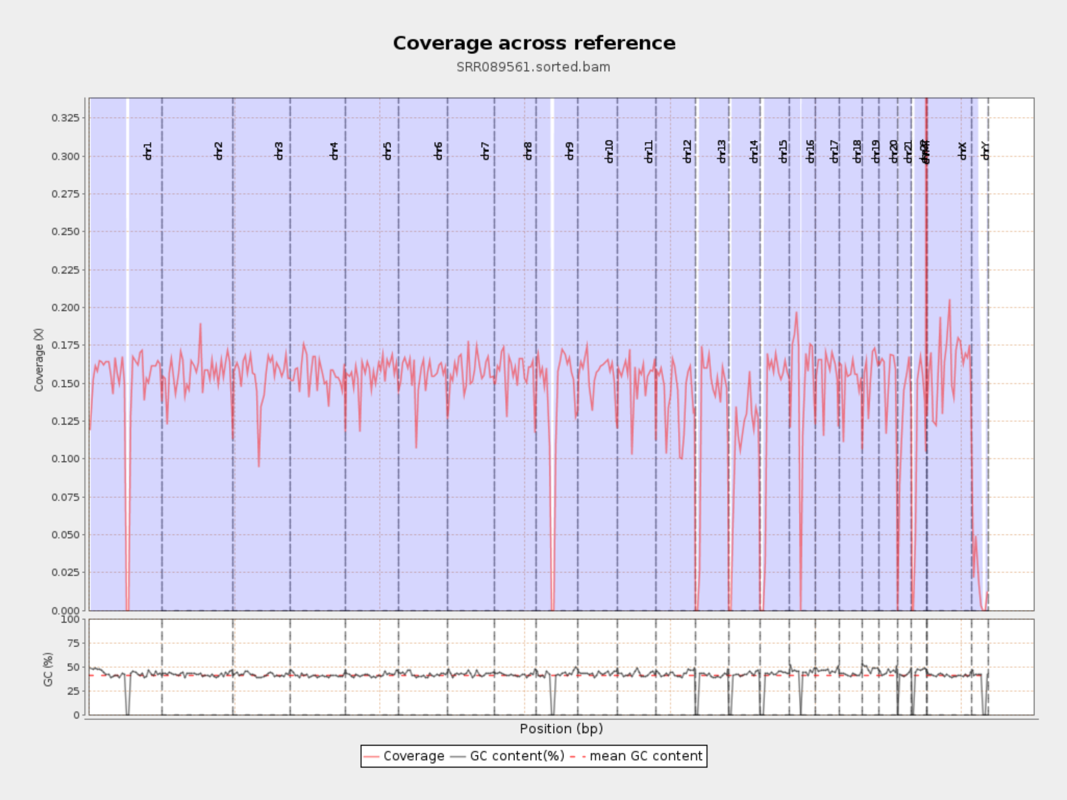
General error rate	0.46%
Mismatches	2,073,035
Insertions	17,964
Mapped reads with at least one insertion	0.19%
Deletions	58,413
Mapped reads with at least one deletion	0.61%
Homopolymer indels	43.89%

2.6. Chromosome stats

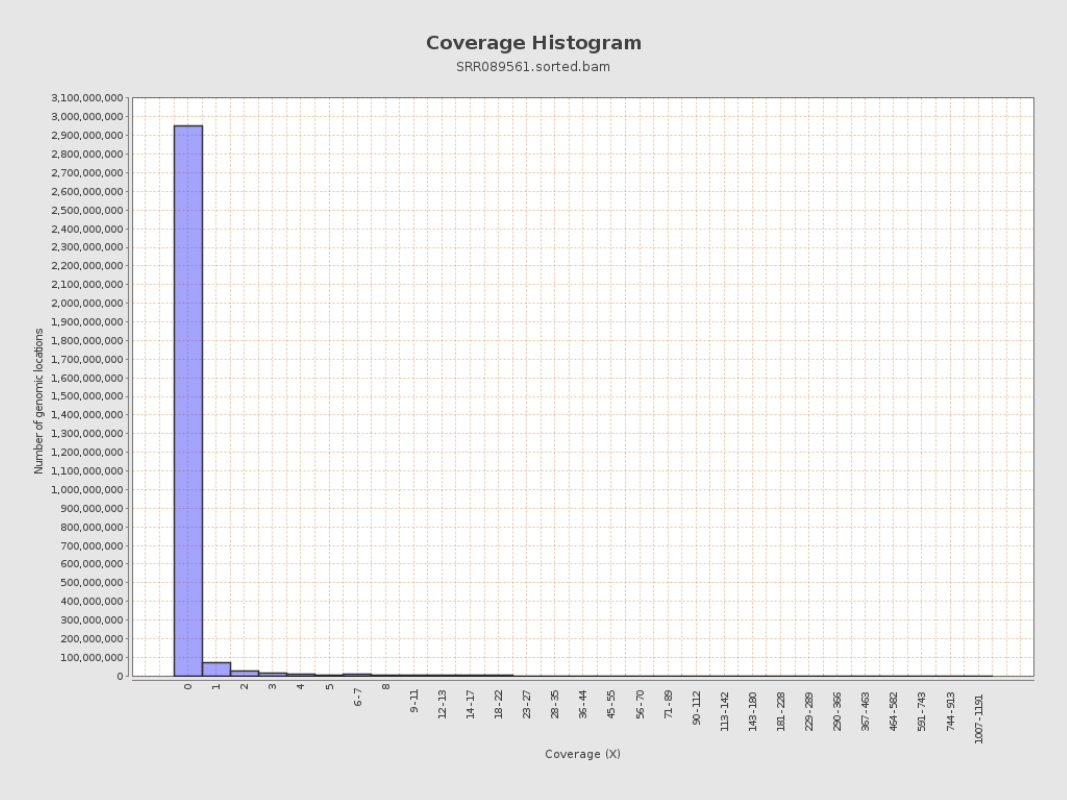
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	36742376	0.1474	1.3512
chr2	243199373	38156965	0.1569	1.3357
chr3	198022430	30660733	0.1548	1.2453
chr4	191154276	29774891	0.1558	1.2728
chr5	180915260	28315586	0.1565	1.2491
chr6	171115067	26533983	0.1551	1.3025
chr7	159138663	25149589	0.158	1.3472

chr8	146364022	22975212	0.157	1.4237
chr9	141213431	19202015	0.136	1.1927
chr10	135534747	21323845	0.1573	1.2892
chr11	135006516	20743196	0.1536	1.2889
chr12	133851895	18796403	0.1404	1.1725
chr13	115169878	14788571	0.1284	1.1502
chr14	107349540	11349896	0.1057	1.1245
chr15	102531392	13149247	0.1282	1.0997
chr16	90354753	13488612	0.1493	1.2336
chr17	81195210	12671897	0.1561	1.2312
chr18	78077248	11902451	0.1524	1.2598
chr19	59128983	9220404	0.1559	1.2793
chr20	63025520	9674390	0.1535	1.225
chr21	48129895	5859182	0.1217	1.1692
chr22	51304566	5320899	0.1037	0.964
chrMT	16571	40260	2.4295	7.069
chrX	155270560	25075458	0.1615	1.2934
chrY	59373566	1142394	0.0192	0.3952

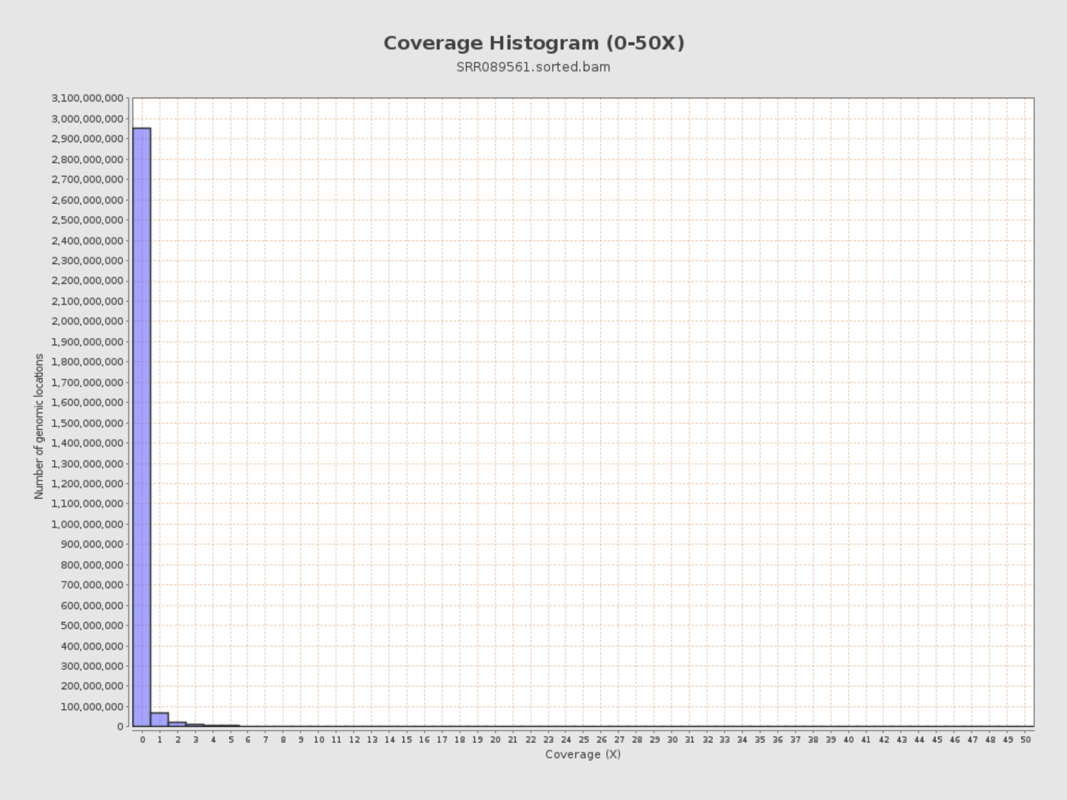
3. Results : Coverage across reference



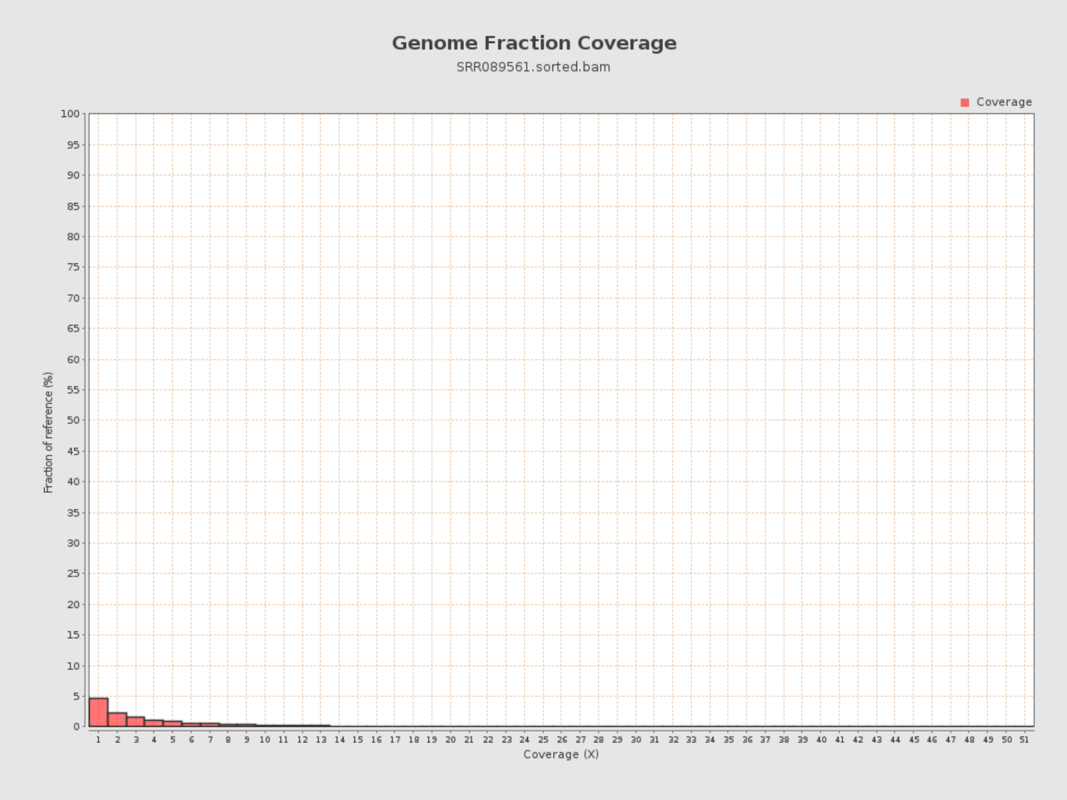
4. Results : Coverage Histogram



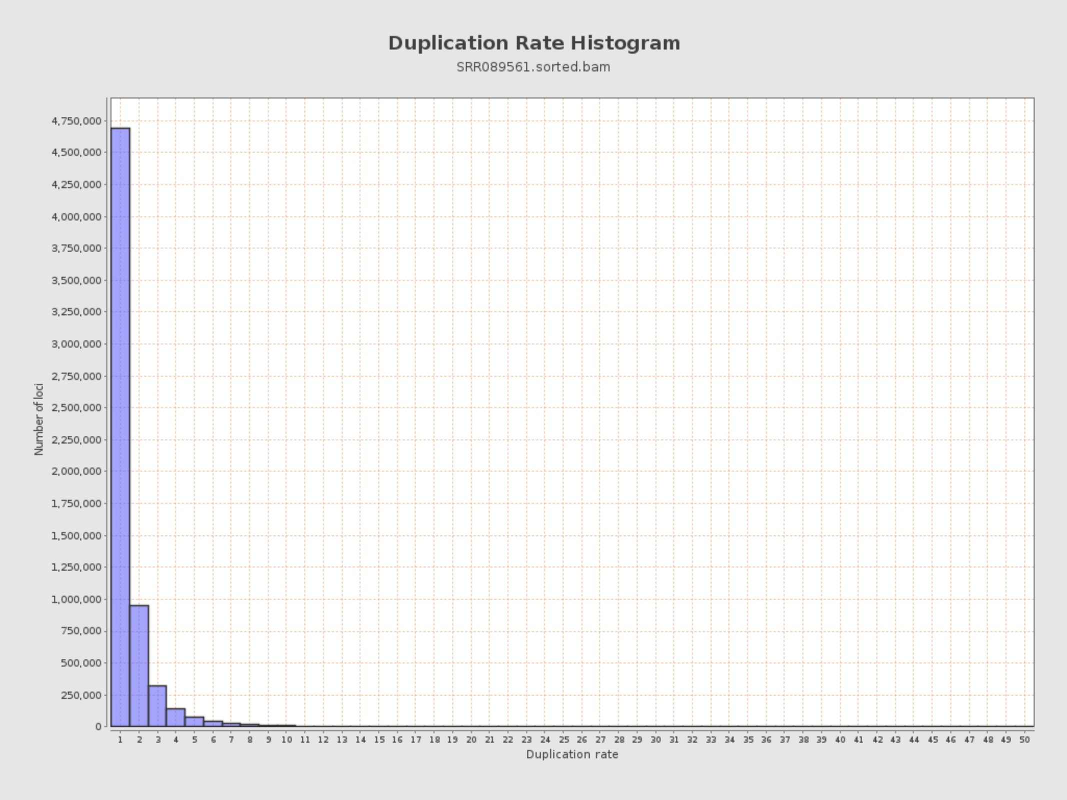
5. Results : Coverage Histogram (0-50X)



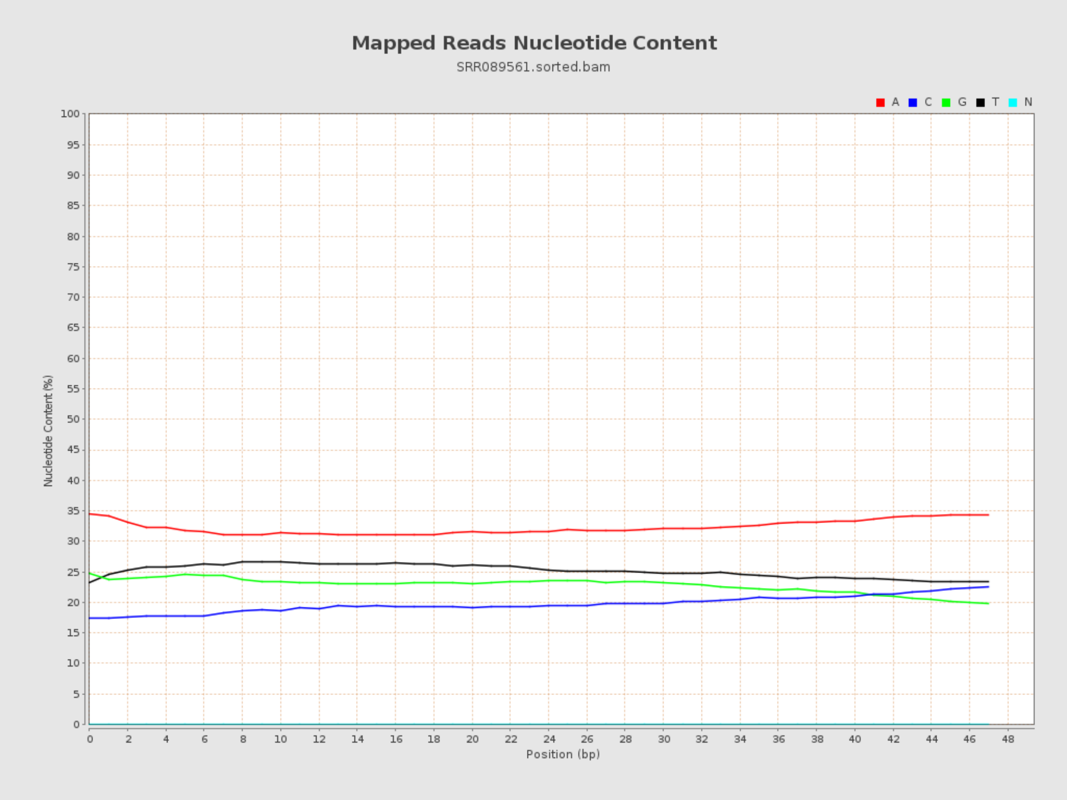
6. Results : Genome Fraction Coverage



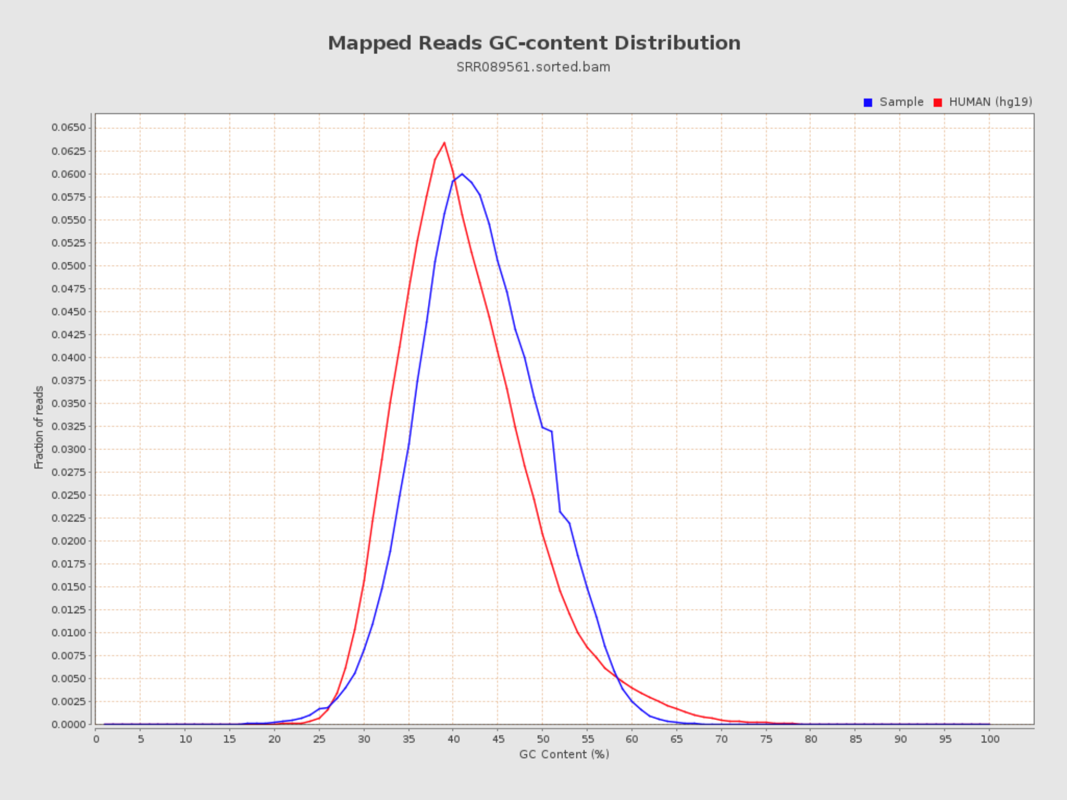
7. Results : Duplication Rate Histogram



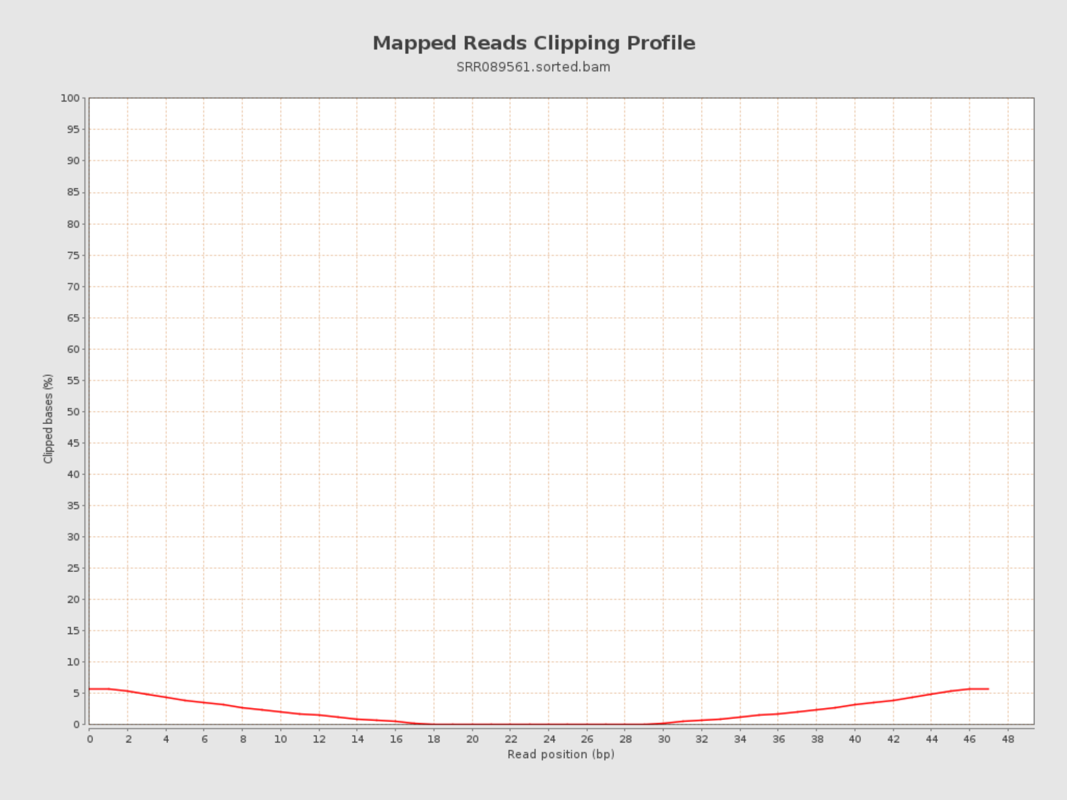
8. Results : Mapped Reads Nucleotide Content



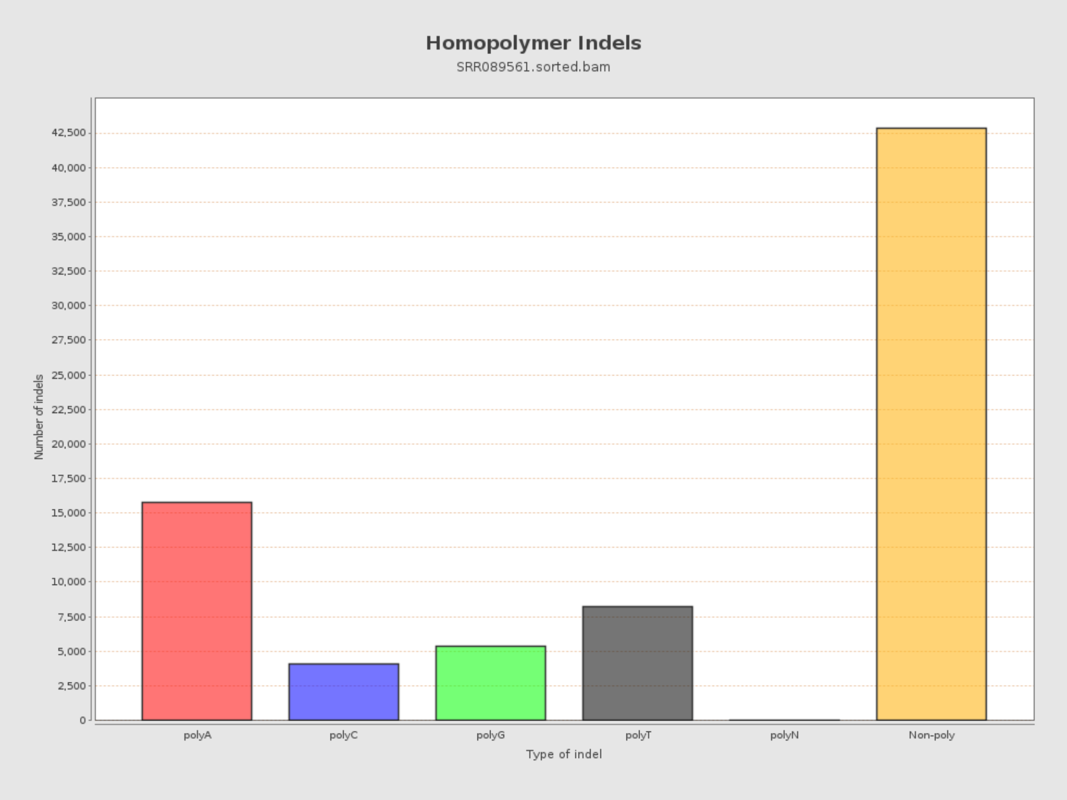
9. Results : Mapped Reads GC-content Distribution



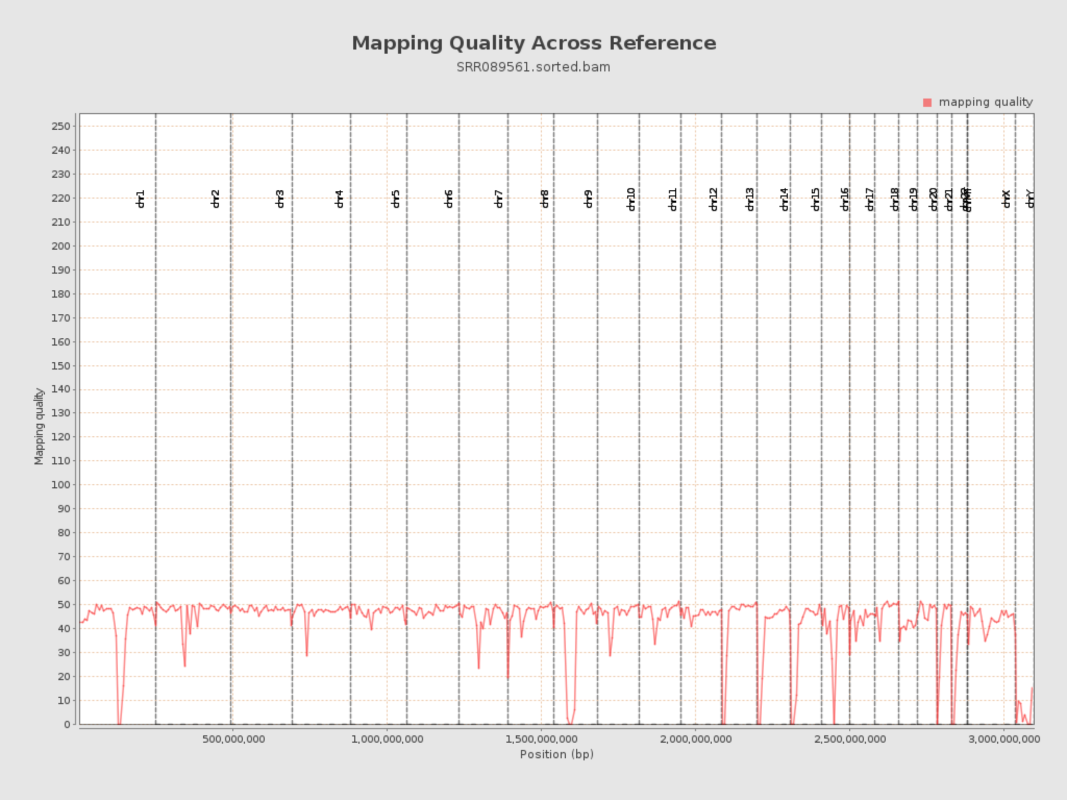
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram