Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 19:09:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR089663.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_SRR089663 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR089663.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 19:09:27 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR089663.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	22,449,905
Mapped reads	17,267,531 / 76.92%
Unmapped reads	5,182,374 / 23.08%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	685 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	1,693,530 / 7.54%
Duplication rate	7.5%
Clipped reads	3,805,784 / 16.95%

2.2. ACGT Content

Number/percentage of A's	258,173,958 / 32.59%
Number/percentage of C's	161,429,852 / 20.38%
Number/percentage of T's	203,059,968 / 25.63%
Number/percentage of G's	169,432,763 / 21.39%
Number/percentage of N's	46,359 / 0.01%
GC Percentage	41.77%

2.3. Coverage

Mean	0.2559

Standard Deviation	1.2968

2.4. Mapping Quality

Mean Mapping Quality	42.28

2.5. Mismatches and indels

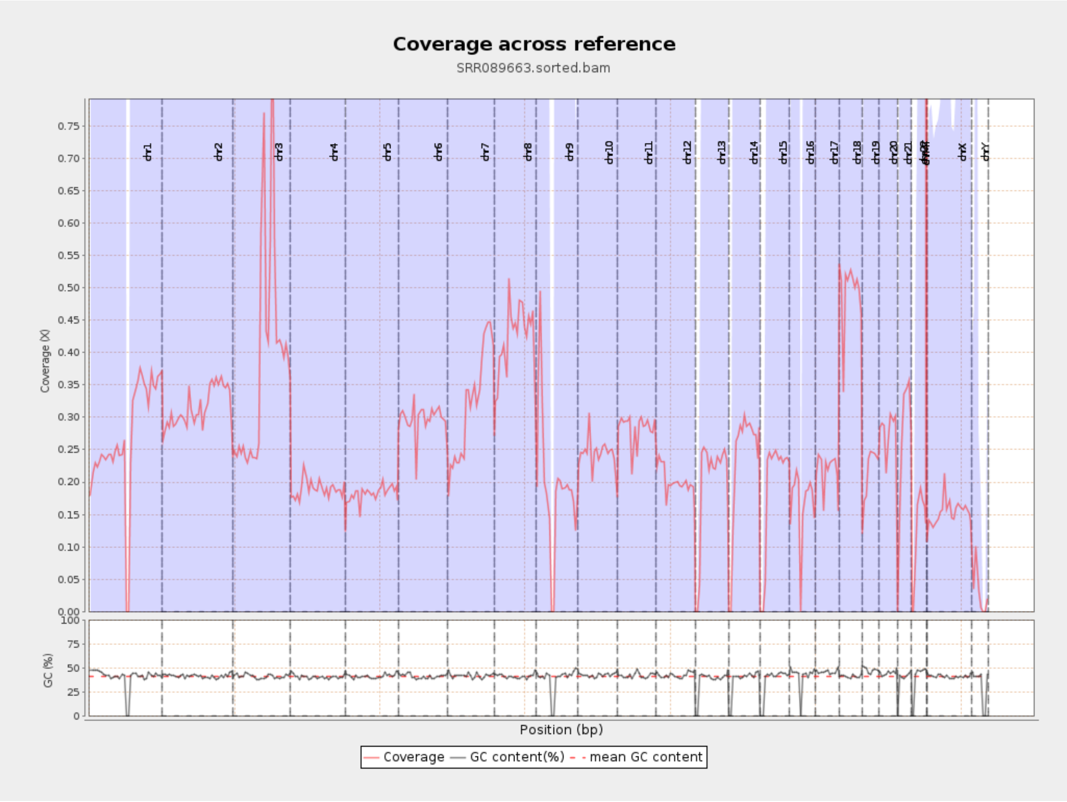
General error rate	0.47%
Mismatches	3,683,547
Insertions	38,739
Mapped reads with at least one insertion	0.22%
Deletions	112,777
Mapped reads with at least one deletion	0.65%
Homopolymer indels	41.97%

2.6. Chromosome stats

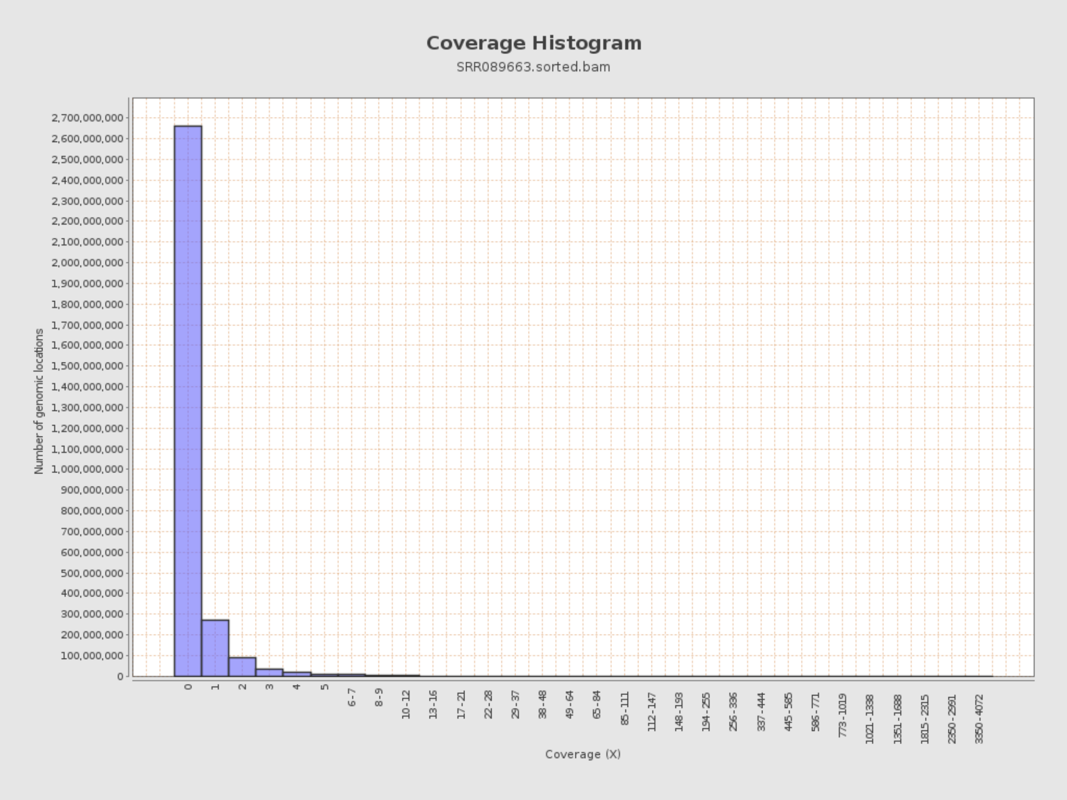
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	66961988	0.2687	1.4842
chr2	243199373	76886794	0.3161	1.8537
chr3	198022430	76175371	0.3847	1.1765
chr4	191154276	36162695	0.1892	0.7767
chr5	180915260	33071614	0.1828	0.7214
chr6	171115067	50828733	0.297	1.1456
chr7	159138663	51303112	0.3224	1.7018

chr8	146364022	61896128	0.4229	2.5625
chr9	141213431	27768038	0.1966	1.1282
chr10	135534747	33186358	0.2449	1.3026
chr11	135006516	37975505	0.2813	1.1927
chr12	133851895	26945616	0.2013	0.7925
chr13	115169878	22613508	0.1963	0.7546
chr14	107349540	24864183	0.2316	0.9161
chr15	102531392	19484094	0.19	0.7394
chr16	90354753	15149898	0.1677	0.7917
chr17	81195210	17624821	0.2171	0.8921
chr18	78077248	38499088	0.4931	1.7798
chr19	59128983	12919177	0.2185	1.3552
chr20	63025520	17315712	0.2747	0.9471
chr21	48129895	12599499	0.2618	1.0437
chr22	51304566	6200467	0.1209	0.5799
chrMT	16571	238078	14.3671	13.8531
chrX	155270560	23802050	0.1533	0.9547
chrY	59373566	1839669	0.031	0.557

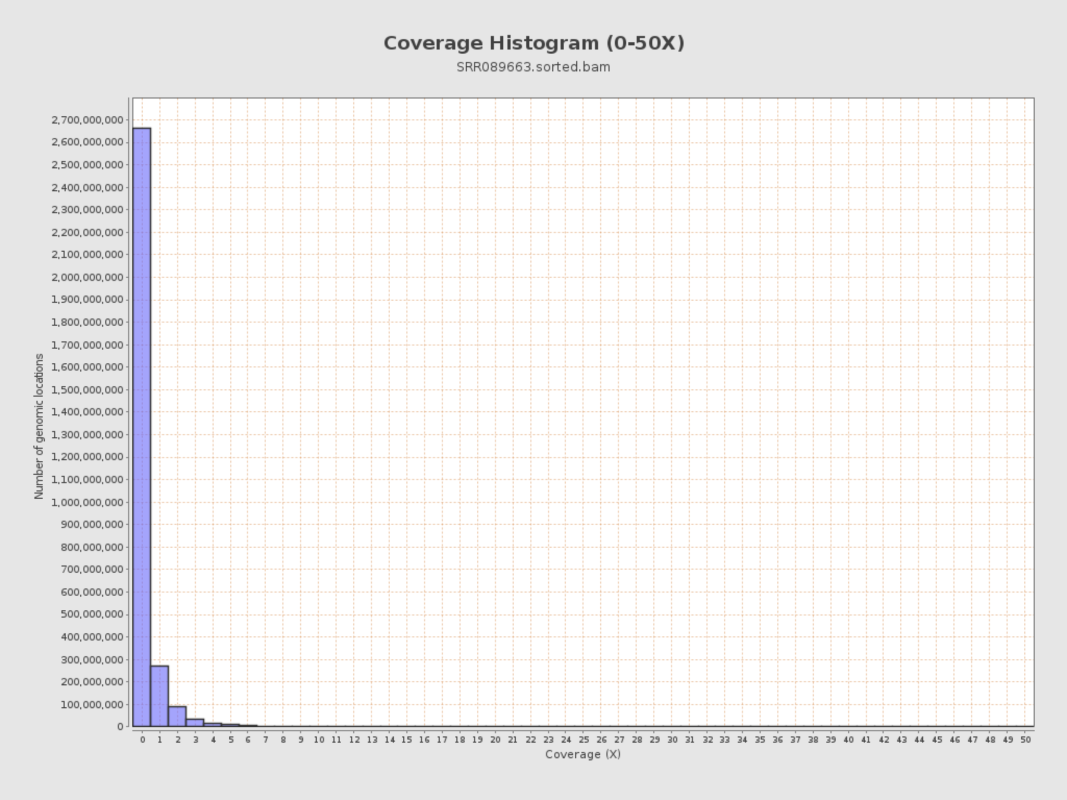
3. Results : Coverage across reference



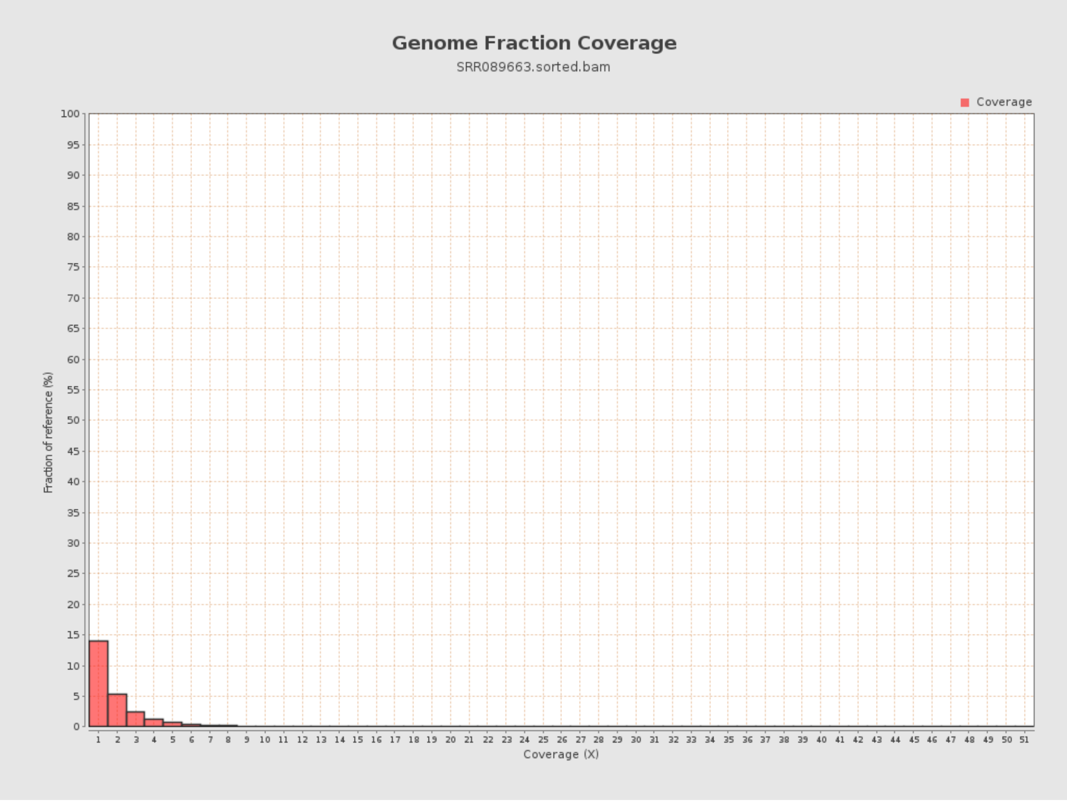
4. Results : Coverage Histogram



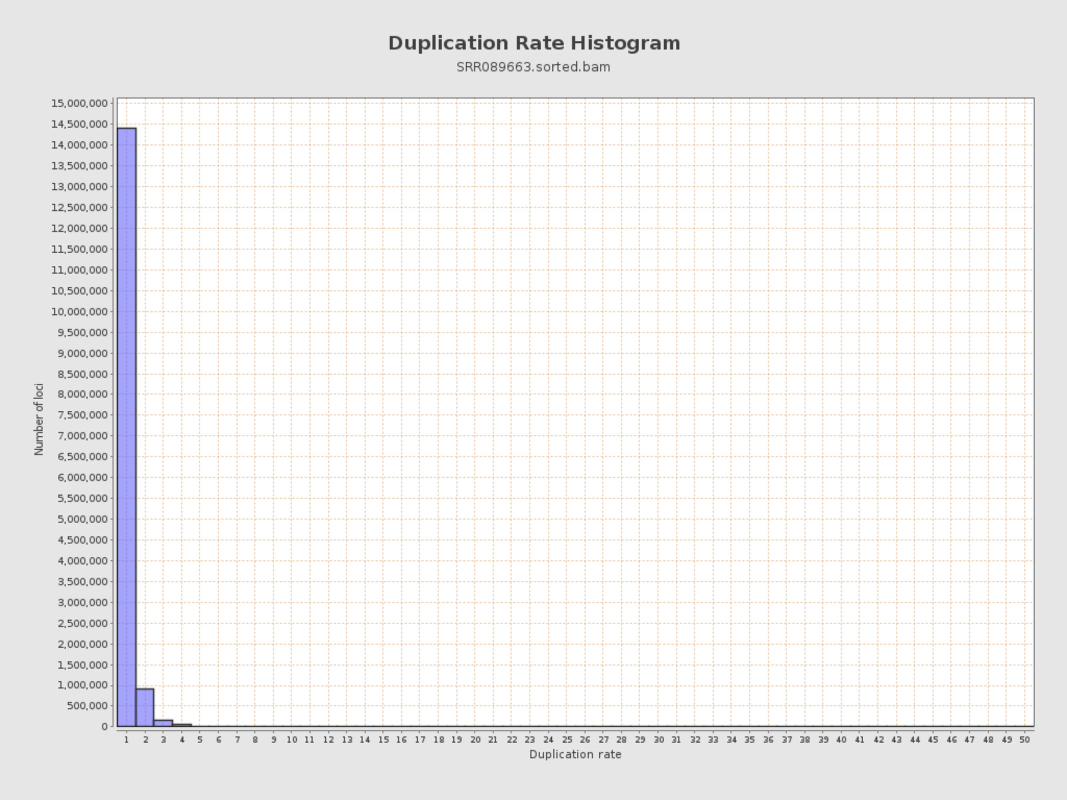
5. Results : Coverage Histogram (0-50X)



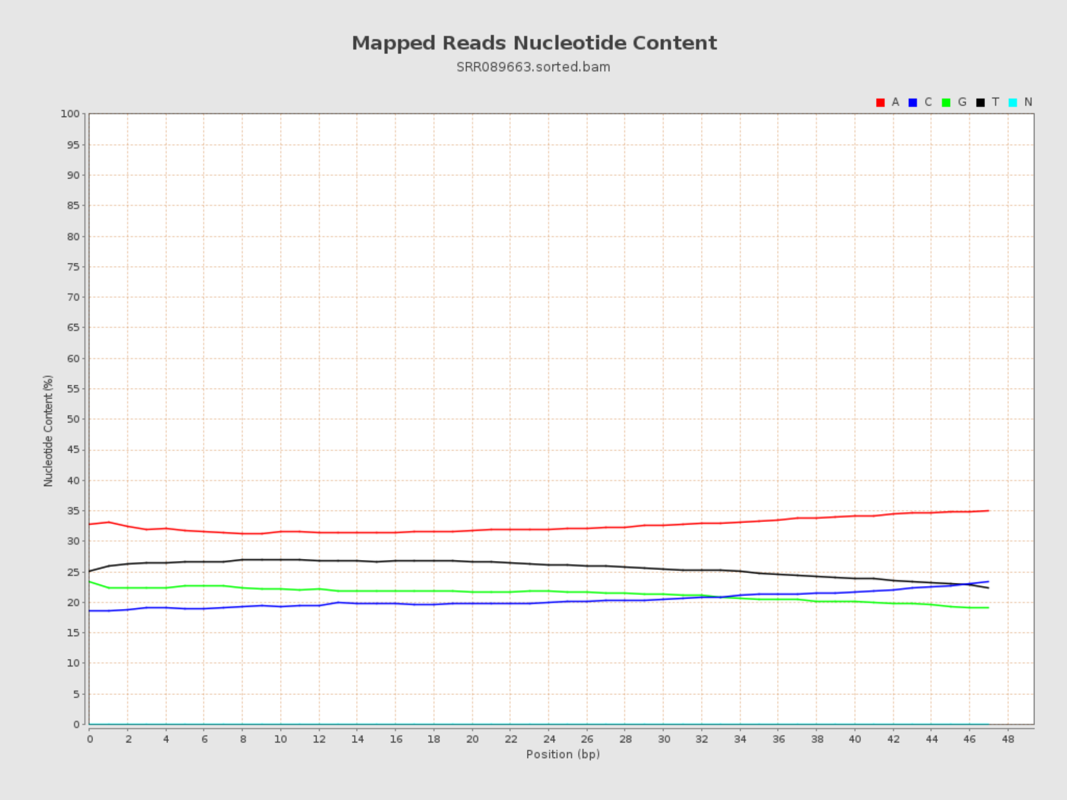
6. Results : Genome Fraction Coverage



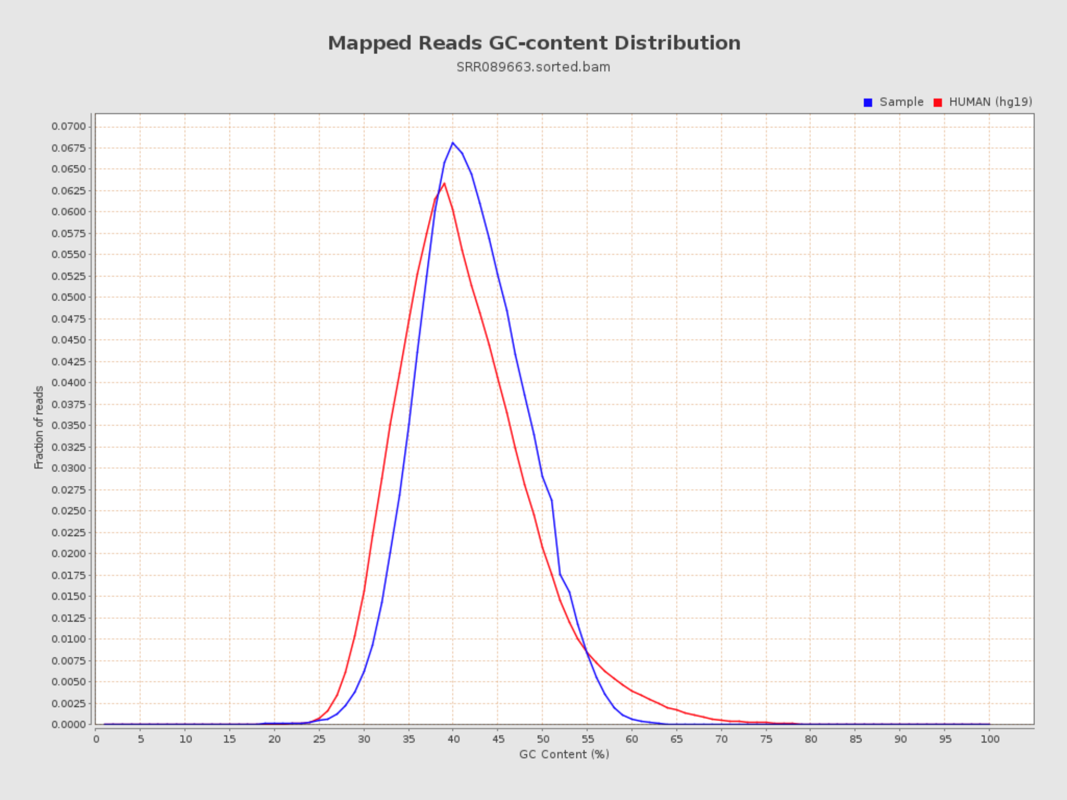
7. Results : Duplication Rate Histogram



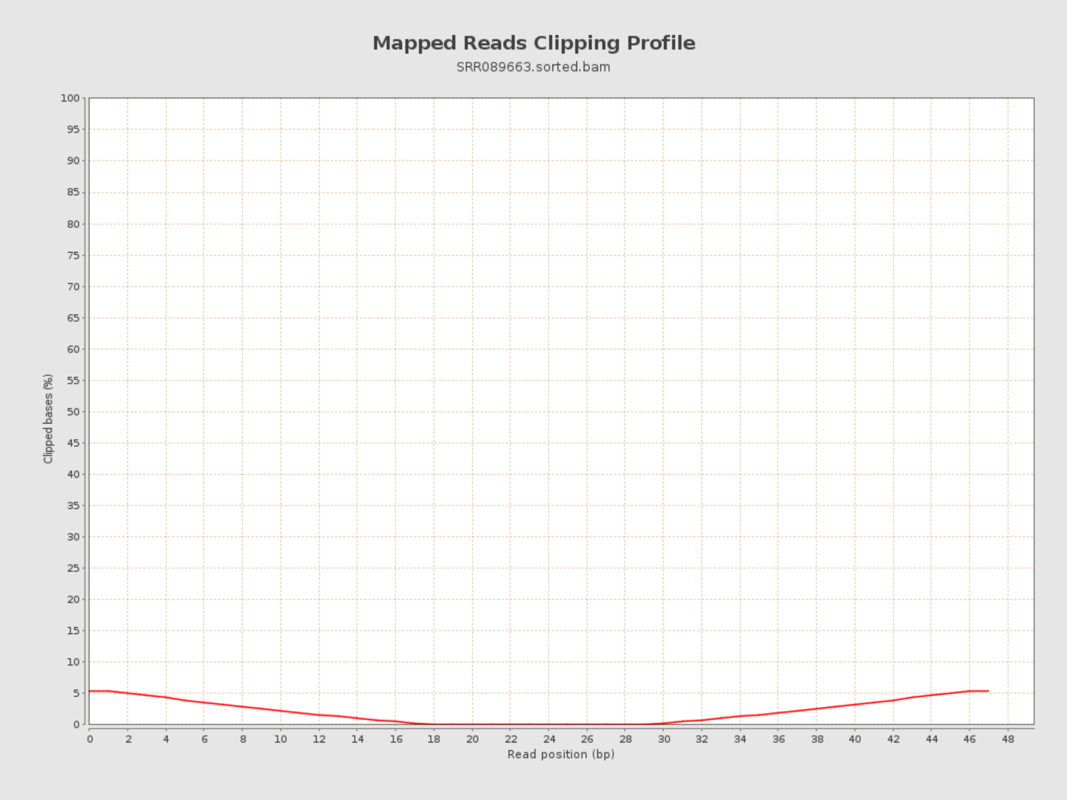
8. Results : Mapped Reads Nucleotide Content



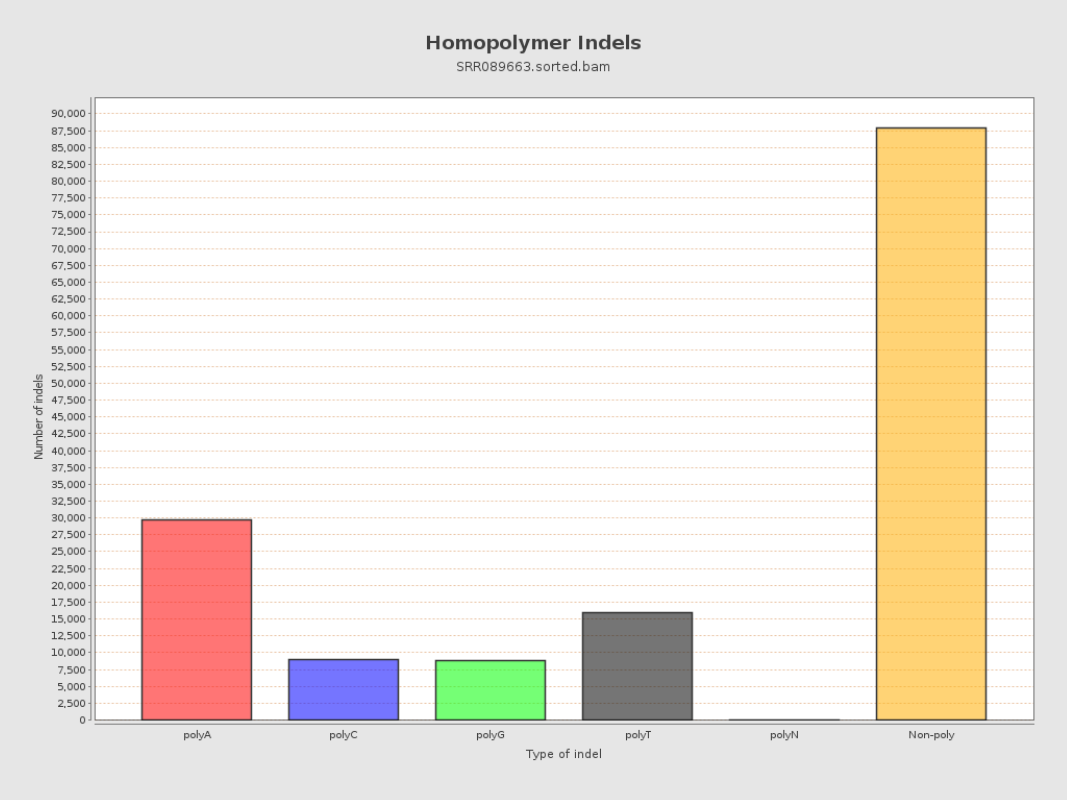
9. Results : Mapped Reads GC-content Distribution



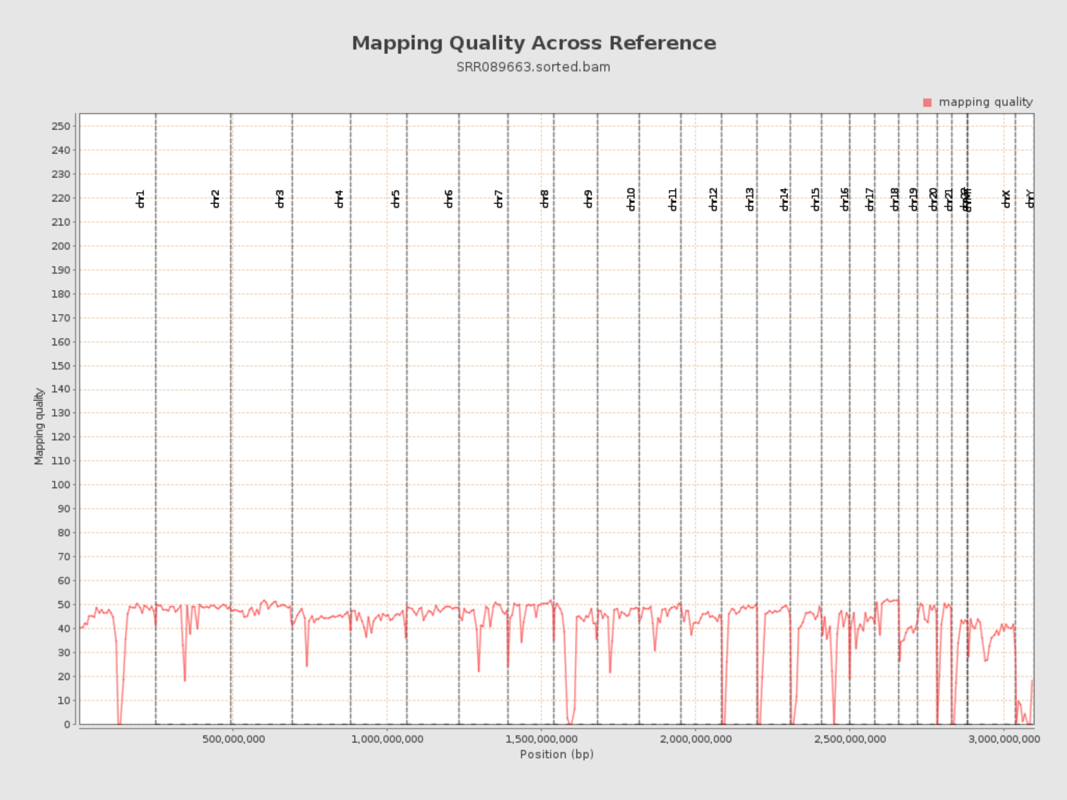
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram