Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/11 06:25:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617665.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_SRR617665 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617665_1.fastq.gz SRR617665_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Oct 11 06:25:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617665.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	30,114,314 / 94.11%
Unmapped reads	1,885,686 / 5.89%
Mapped paired reads	30,114,314 / 94.11%
Mapped reads, first in pair	15,123,769 / 47.26%
Mapped reads, second in pair	14,990,545 / 46.85%
Mapped reads, both in pair	29,476,694 / 92.11%
Mapped reads, singletons	637,620 / 1.99%
Secondary alignments	0
Supplementary alignments	141,383 / 0.44%
Read min/max/mean length	30 / 100 / 100.18
Duplicated reads (estimated)	6,854,828 / 21.42%
Duplication rate	10.6%
Clipped reads	6,366,810 / 19.9%

2.2. ACGT Content

Number/percentage of A's	871,650,444 / 29.83%
Number/percentage of C's	582,213,893 / 19.92%
Number/percentage of T's	869,405,105 / 29.75%
Number/percentage of G's	597,522,752 / 20.45%
Number/percentage of N's	1,740,674 / 0.06%

GC Percentage	40.37%

2.3. Coverage

Mean	0.9446
Standard Deviation	10.6961

2.4. Mapping Quality

Mean Mapping Quality	52.64

2.5. Insert size

Mean	31,517.1
Standard Deviation	1,624,033.11
P25/Median/P75	178 / 220 / 285

2.6. Mismatches and indels

General error rate	1.56%
Mismatches	44,558,615
Insertions	454,000
Mapped reads with at least one insertion	1.48%
Deletions	1,069,044
Mapped reads with at least one deletion	3.48%
Homopolymer indels	47.67%

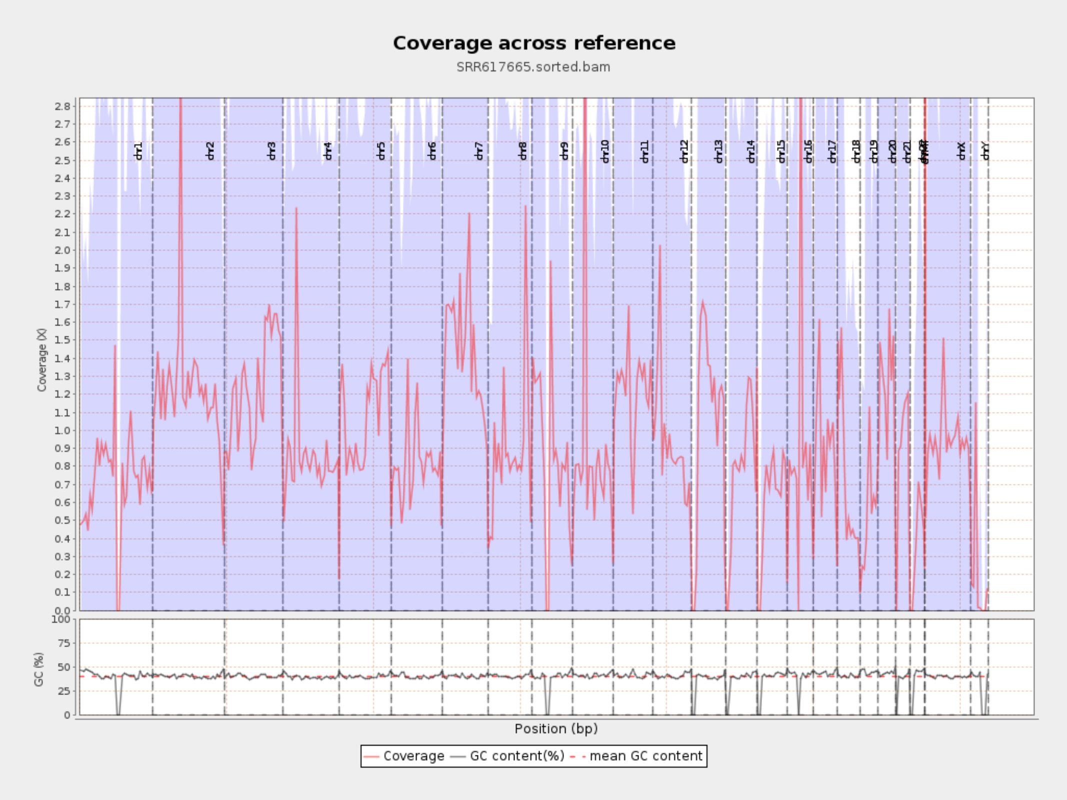
2.7. Chromosome stats

Name	**Length**	**Mapped**	**Mean**	**Standard**

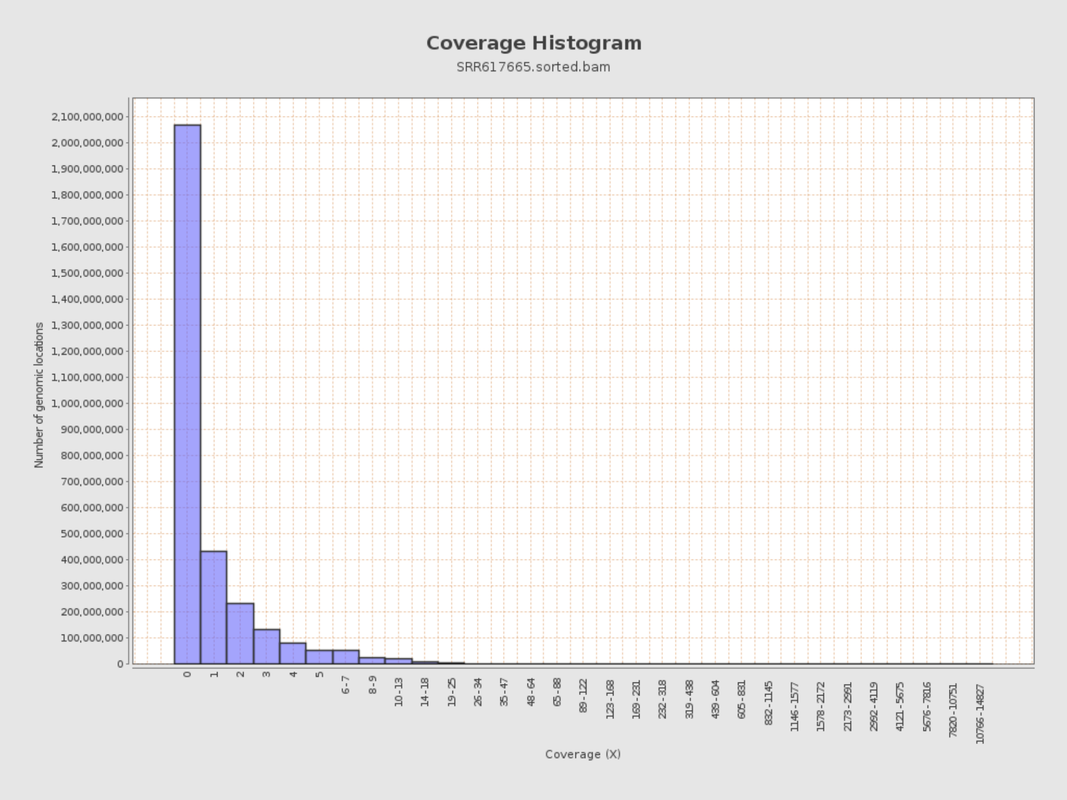
		bases	coverage	deviation
chr1	249250621	179039872	0.7183	10.3284
chr2	243199373	302046649	1.242	12.1681
chr3	198022430	245609880	1.2403	2.4722
chr4	191154276	163773156	0.8568	8.3597
chr5	180915260	193530630	1.0697	2.3191
chr6	171115067	141884234	0.8292	5.8206
chr7	159138663	228773205	1.4376	13.4769
chr8	146364022	129971756	0.888	4.1212
chr9	141213431	120013171	0.8499	20.7022
chr10	135534747	123892166	0.9141	21.8724
chr11	135006516	160858262	1.1915	12.0272
chr12	133851895	124705778	0.9317	2.1711
chr13	115169878	126044132	1.0944	2.2905
chr14	107349540	83682613	0.7795	2.4687
chr15	102531392	62534768	0.6099	1.5803
chr16	90354753	81309408	0.8999	16.9954
chr17	81195210	71705046	0.8831	12.7682
chr18	78077248	53927789	0.6907	18.4296
chr19	59128983	30743321	0.5199	6.0746
chr20	63025520	78477084	1.2452	3.0114
chr21	48129895	42685379	0.8869	4.3969
chr22	51304566	18633383	0.3632	1.2621
chrMT	16571	3084998	186.1685	130.3637
chrX	155270560	145526761	0.9372	4.3278

chrY	59373566	11845392	0.1995	17.5215

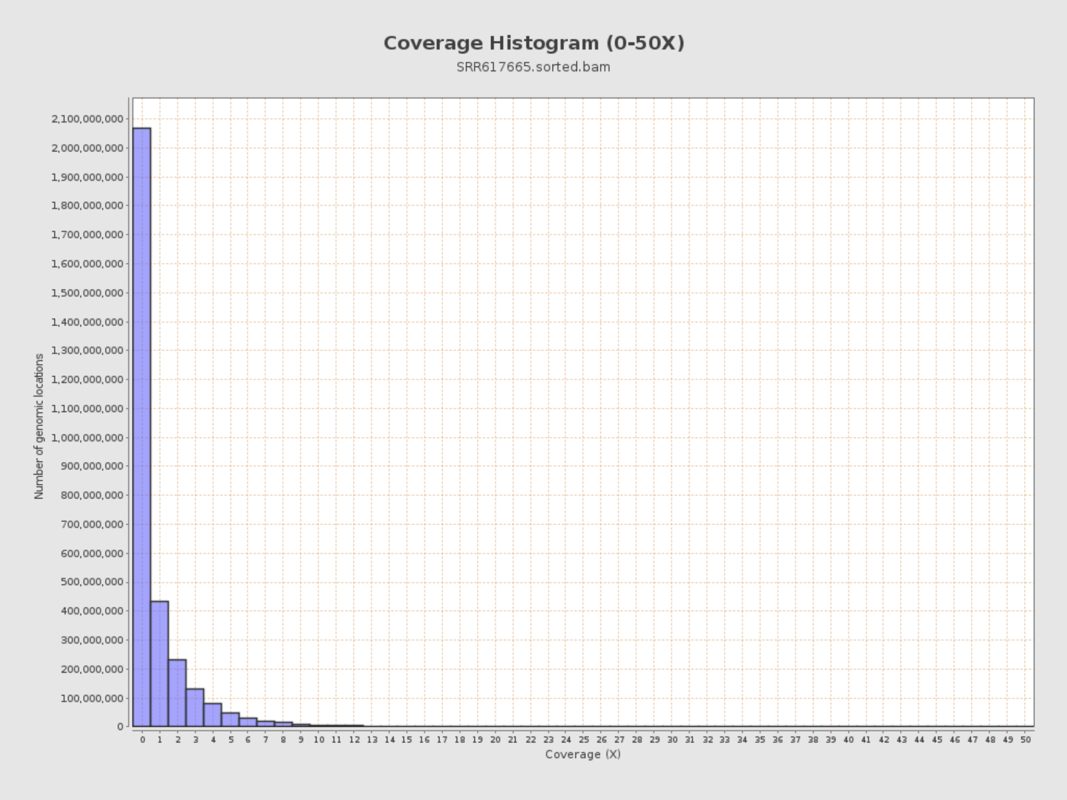
3. Results : Coverage across reference



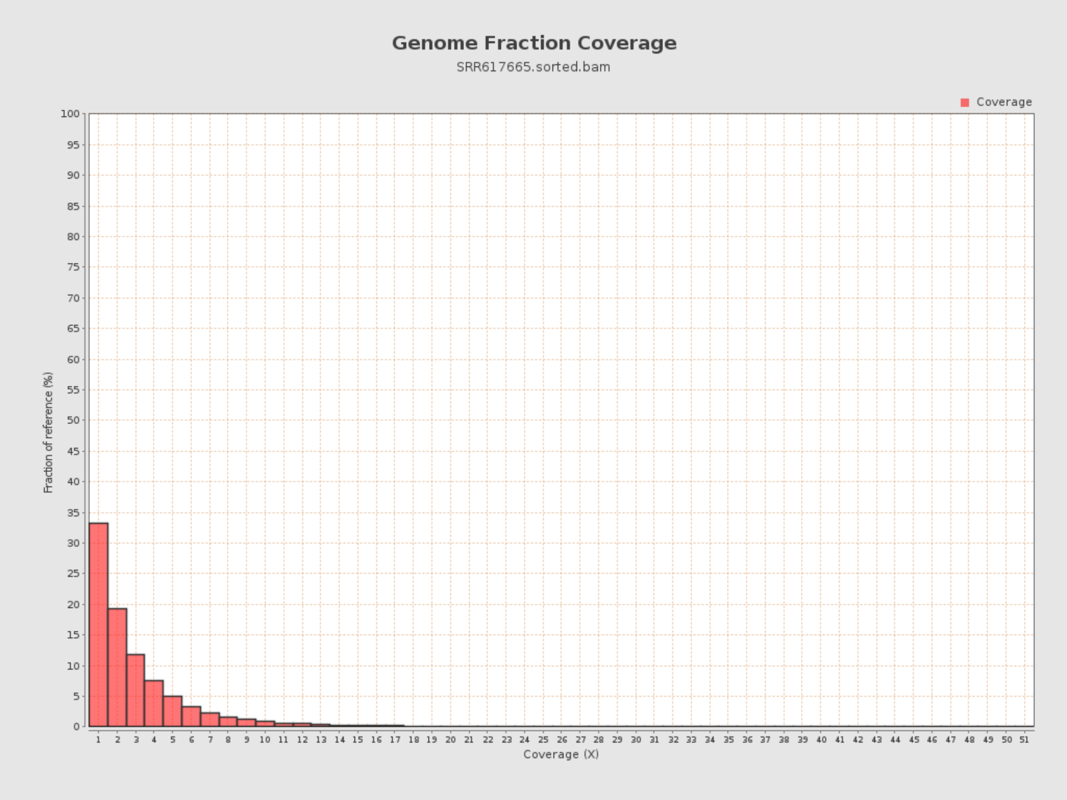
4. Results : Coverage Histogram



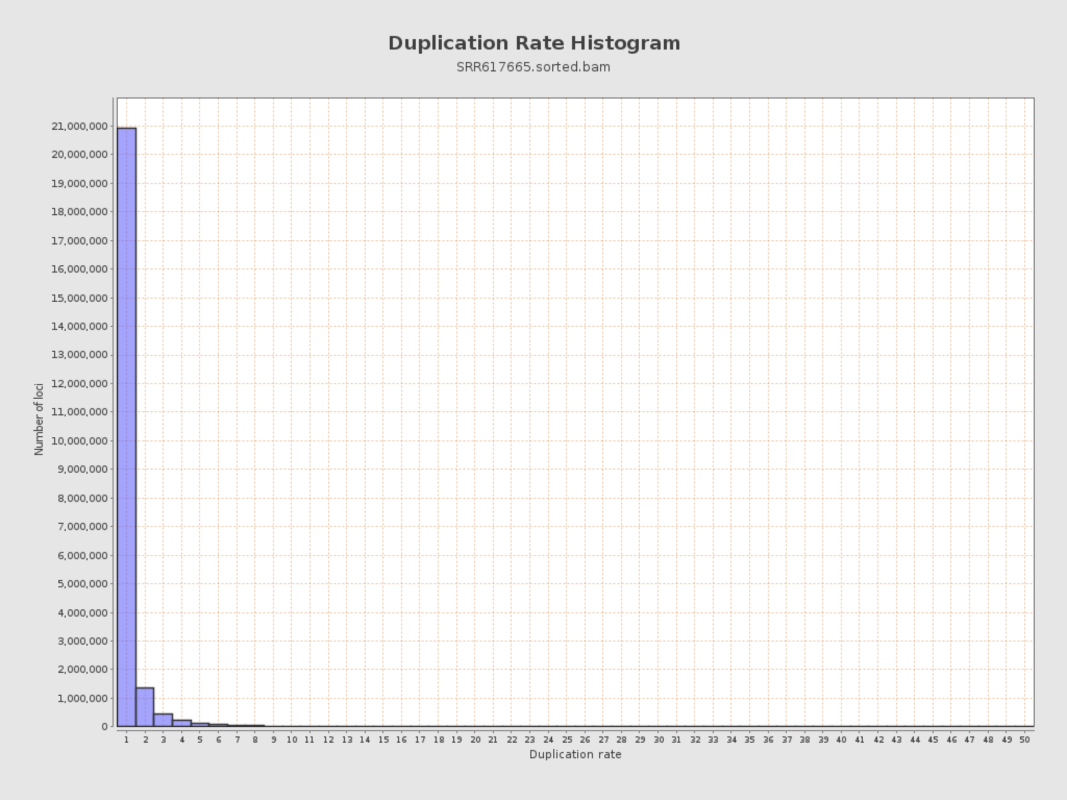
5. Results : Coverage Histogram (0-50X)



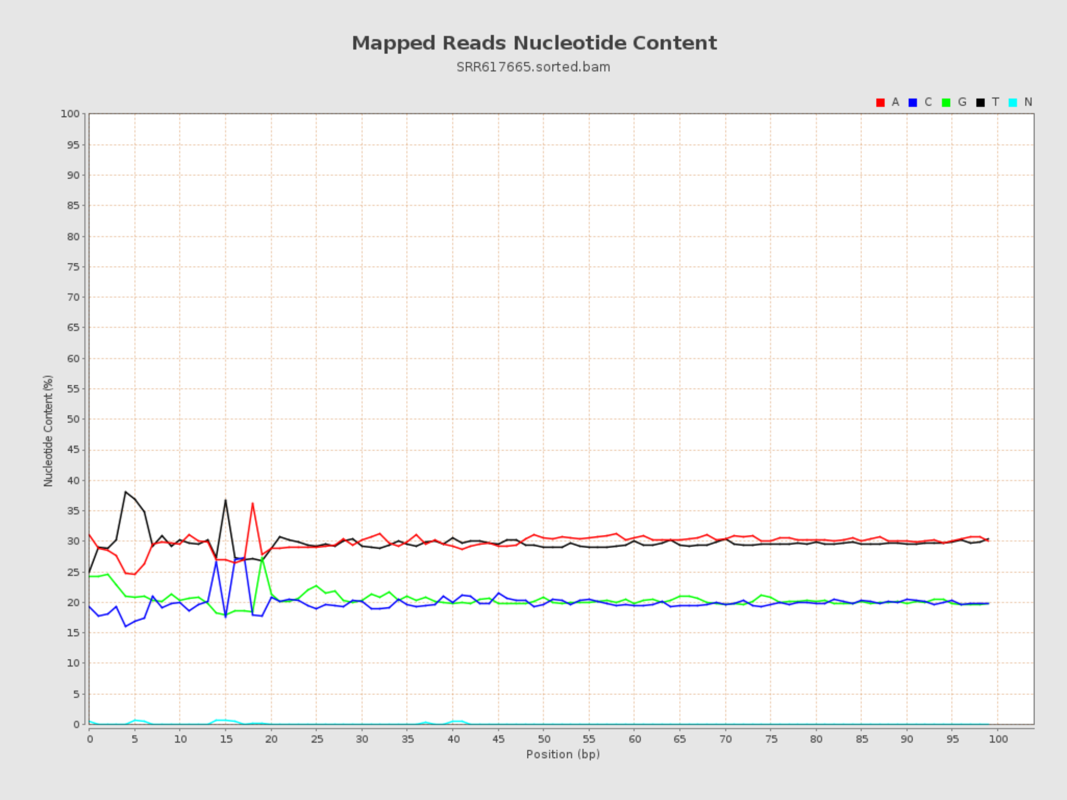
6. Results : Genome Fraction Coverage



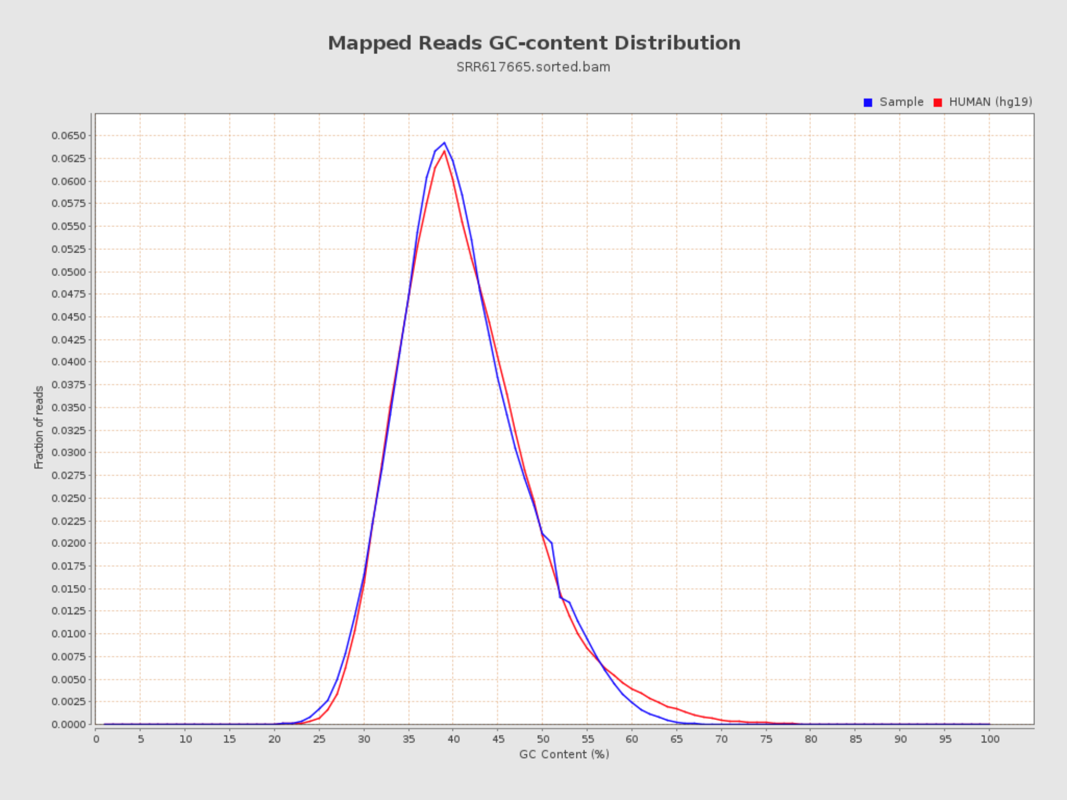
7. Results : Duplication Rate Histogram



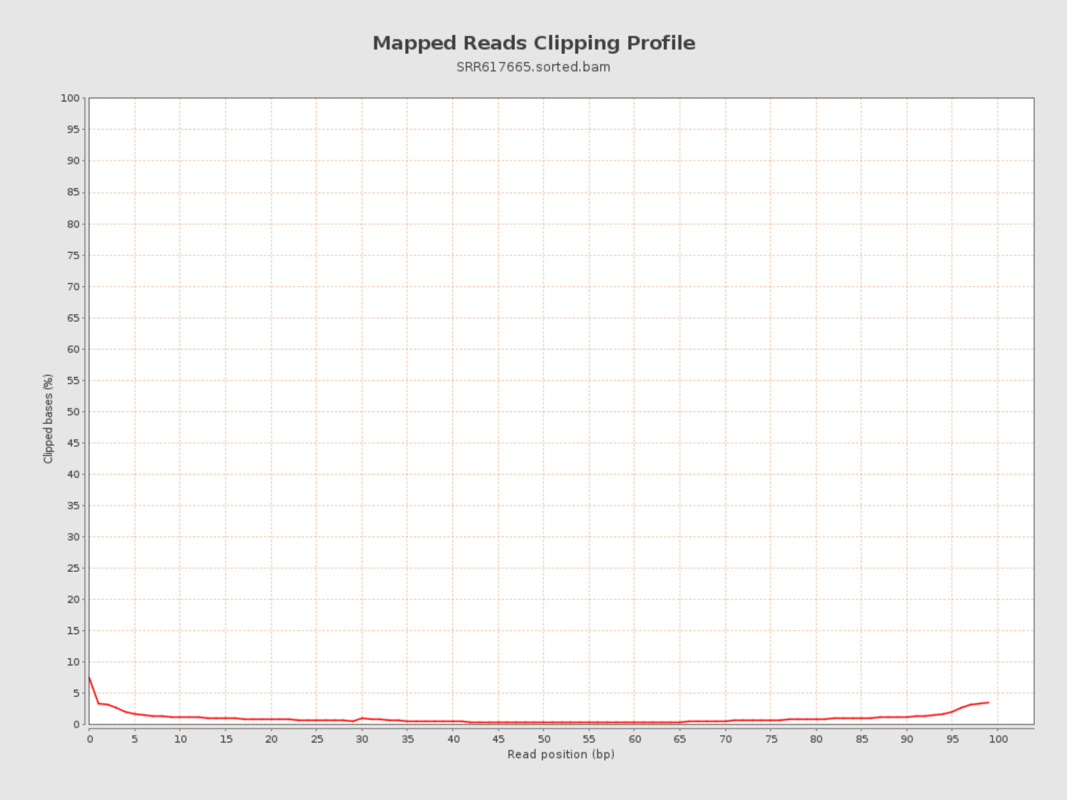
8. Results : Mapped Reads Nucleotide Content



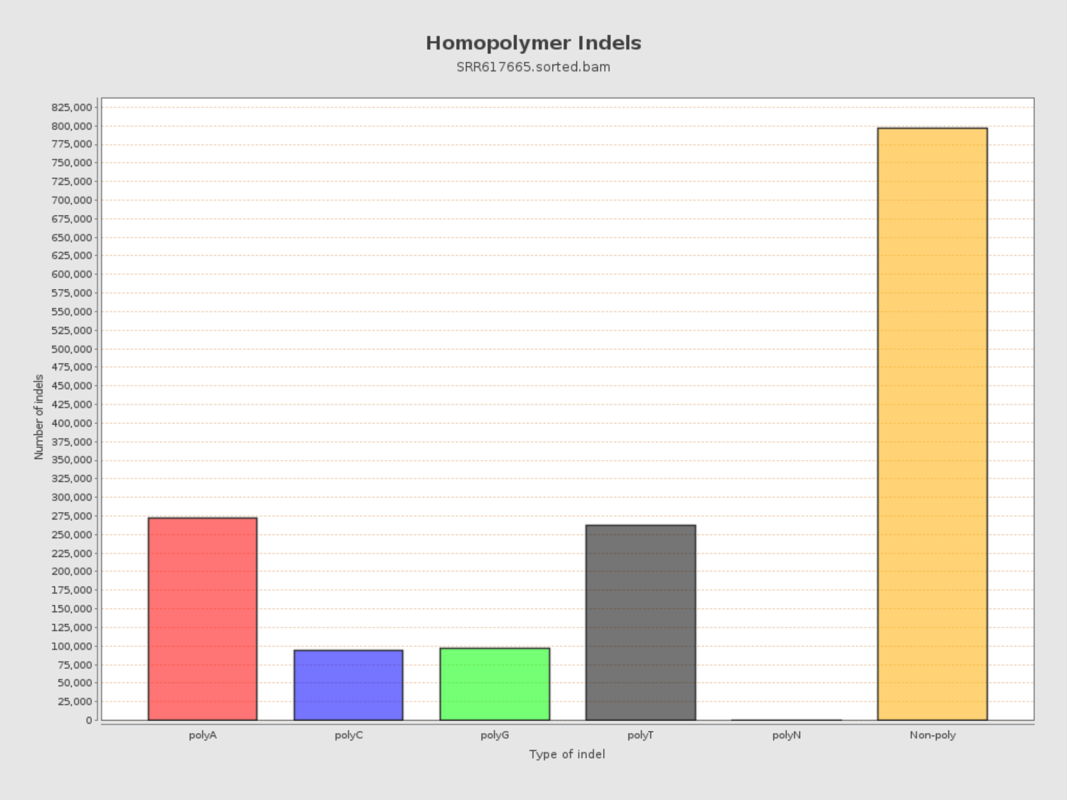
9. Results : Mapped Reads GC-content Distribution



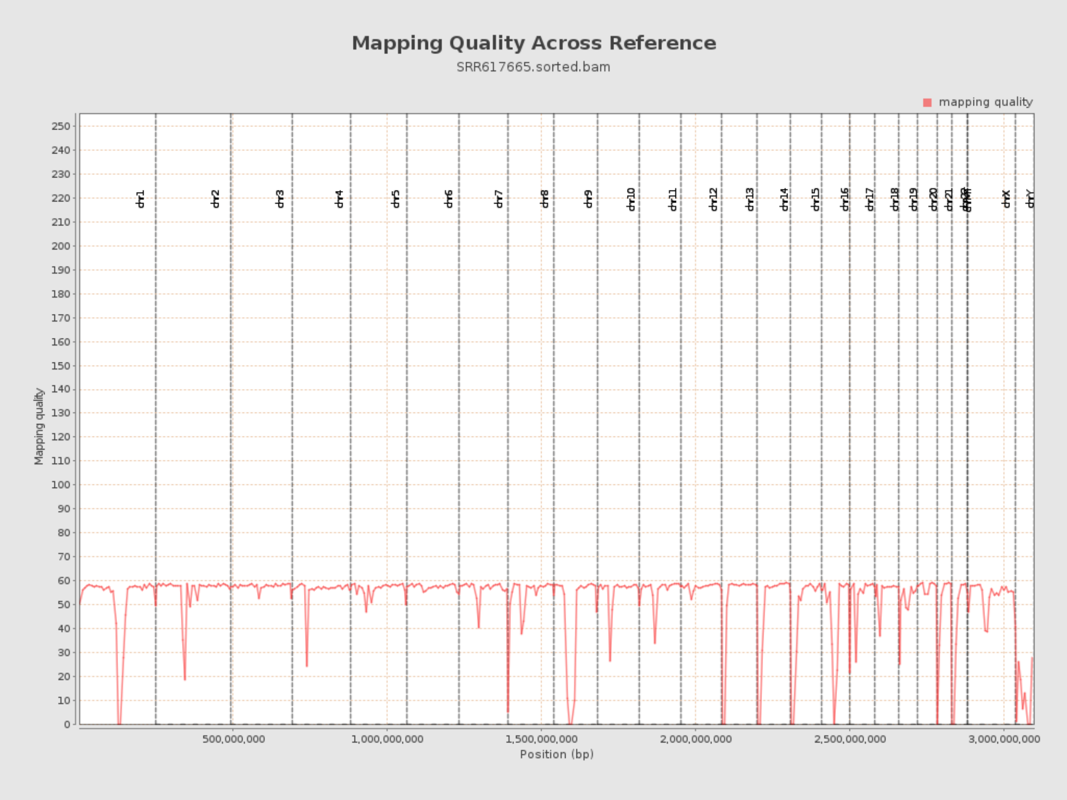
10. Results : Mapped Reads Clipping Profile



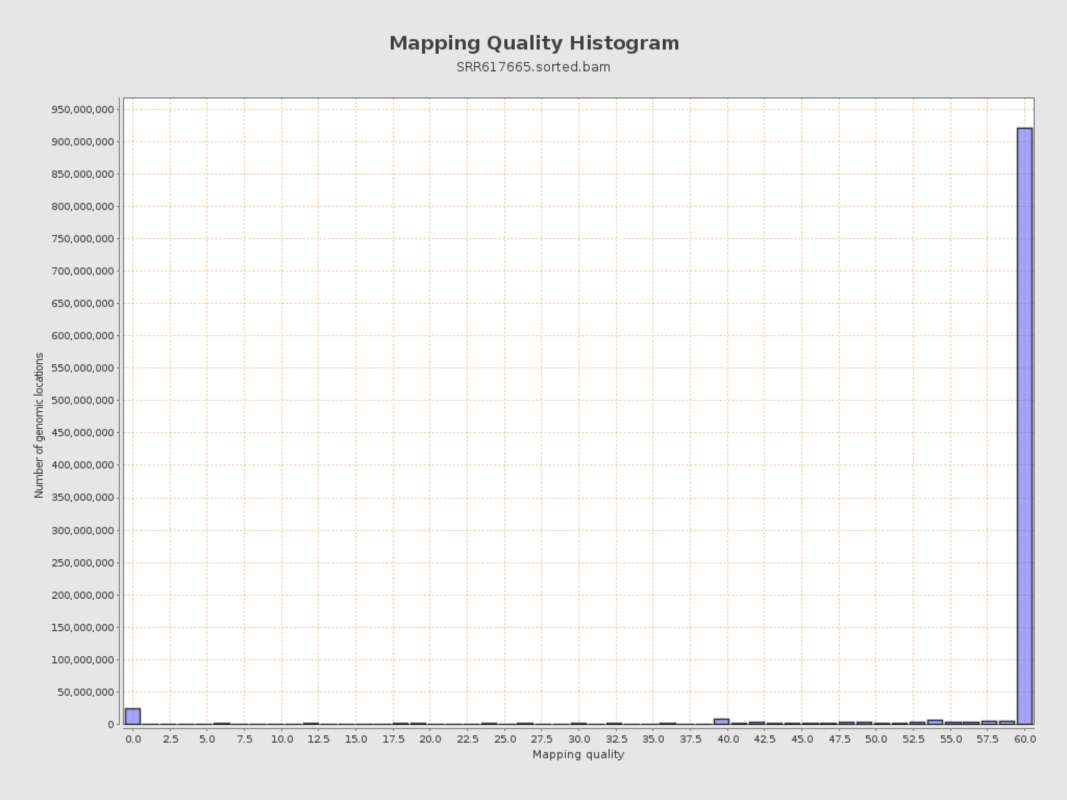
11. Results : Homopolymer Indels



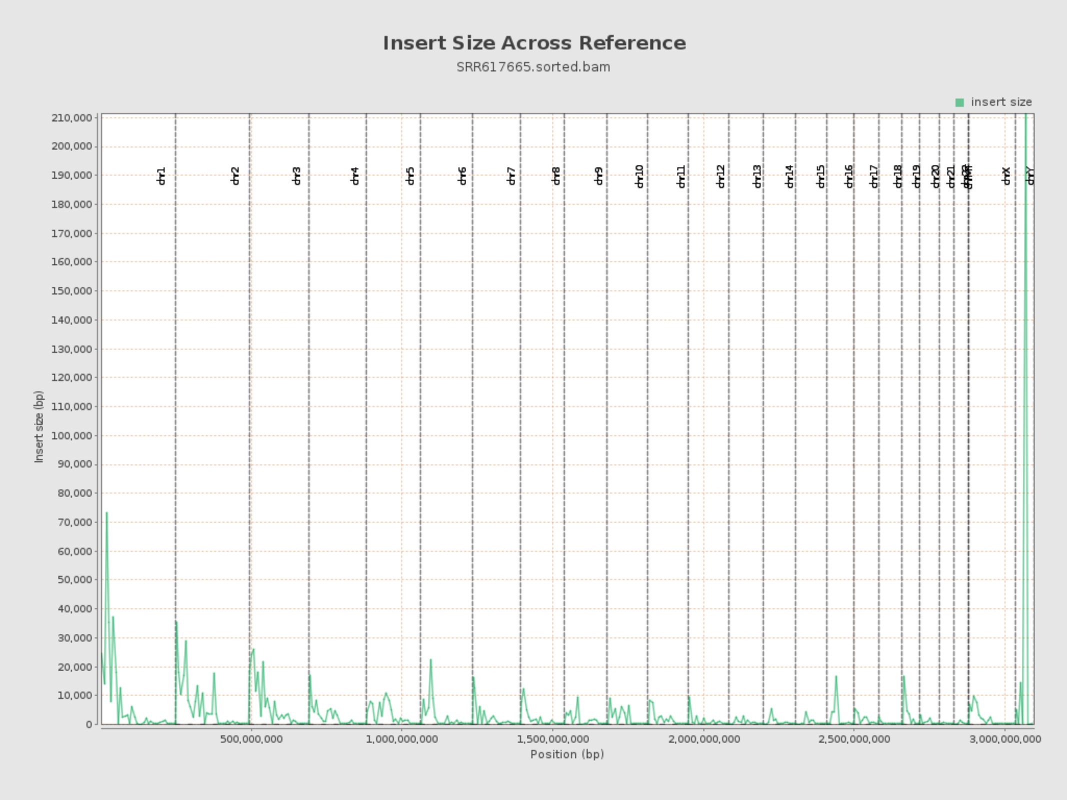
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram