Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/11 04:55:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617663.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_SRR617663 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617663_1.fastq.gz SRR617663_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Oct 11 04:55:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617663.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	30,126,935 / 94.15%
Unmapped reads	1,873,065 / 5.85%
Mapped paired reads	30,126,935 / 94.15%
Mapped reads, first in pair	15,110,465 / 47.22%
Mapped reads, second in pair	15,016,470 / 46.93%
Mapped reads, both in pair	29,492,024 / 92.16%
Mapped reads, singletons	634,911 / 1.98%
Secondary alignments	0
Supplementary alignments	140,153 / 0.44%
Read min/max/mean length	30 / 100 / 100.18
Duplicated reads (estimated)	6,894,127 / 21.54%
Duplication rate	10.7%
Clipped reads	6,408,668 / 20.03%

2.2. ACGT Content

Number/percentage of A's	870,399,693 / 29.79%
Number/percentage of C's	582,934,976 / 19.95%
Number/percentage of T's	868,501,329 / 29.72%
Number/percentage of G's	598,419,880 / 20.48%
Number/percentage of N's	2,000,773 / 0.07%

GC Percentage	40.43%

2.3. Coverage

Mean	0.9445
Standard Deviation	10.5738

2.4. Mapping Quality

Mean Mapping Quality	52.64

2.5. Insert size

Mean	32,497.1
Standard Deviation	1,662,878.03
P25/Median/P75	179 / 223 / 291

2.6. Mismatches and indels

General error rate	1.52%
Mismatches	43,503,507
Insertions	454,201
Mapped reads with at least one insertion	1.48%
Deletions	1,070,232
Mapped reads with at least one deletion	3.48%
Homopolymer indels	47.61%

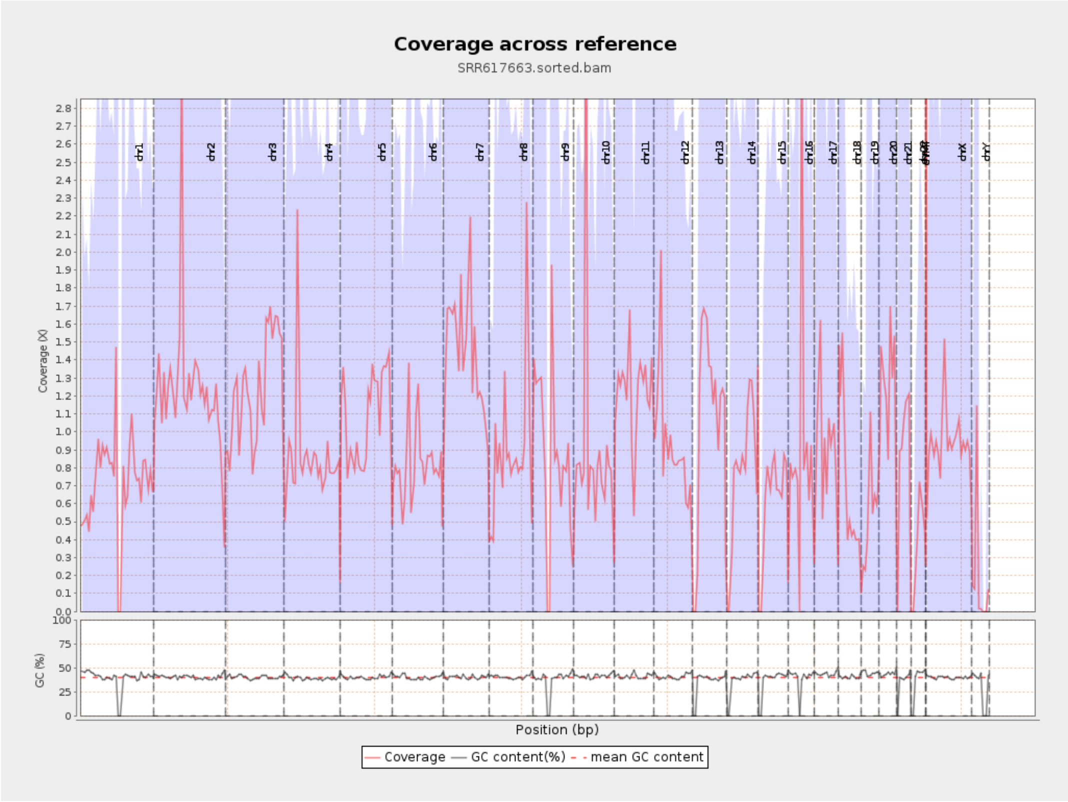
2.7. Chromosome stats

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

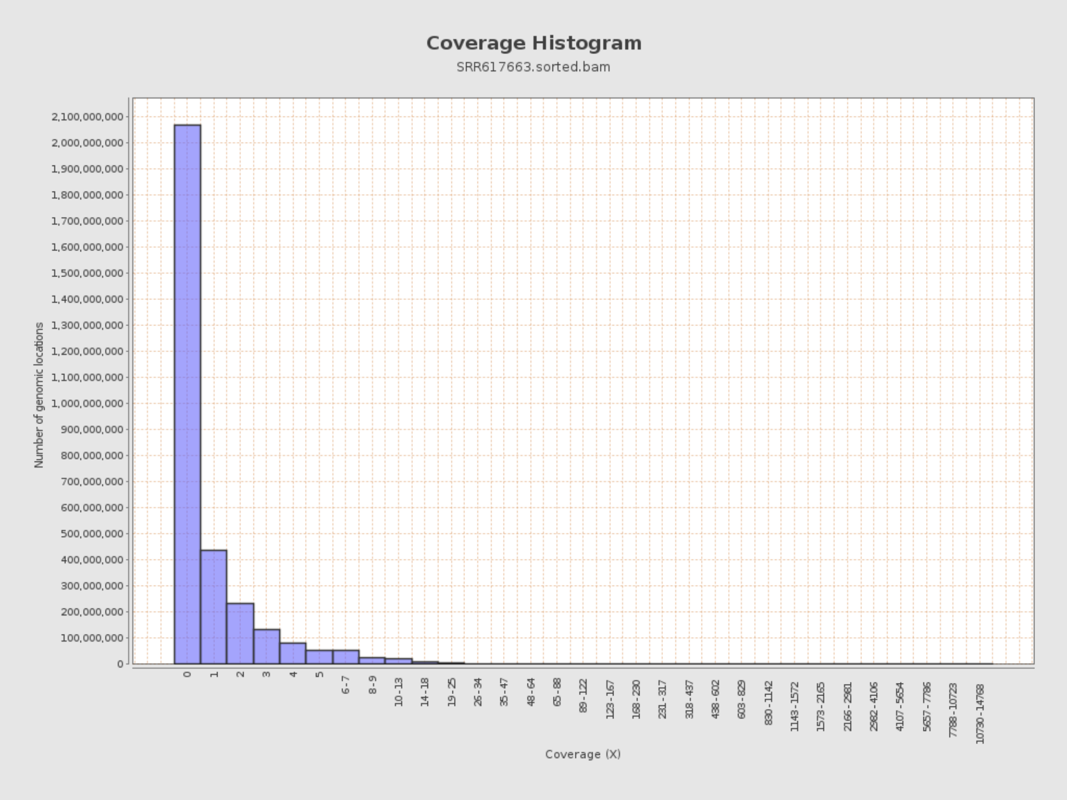
		bases	coverage	deviation
chr1	249250621	179060064	0.7184	10.2551
chr2	243199373	301901553	1.2414	12.0468
chr3	198022430	244765112	1.236	2.4612
chr4	191154276	163621829	0.856	8.3072
chr5	180915260	193704714	1.0707	2.3114
chr6	171115067	142039622	0.8301	5.6905
chr7	159138663	228611736	1.4366	13.3828
chr8	146364022	130145432	0.8892	4.0811
chr9	141213431	120106562	0.8505	20.4631
chr10	135534747	123764263	0.9132	21.4178
chr11	135006516	160718897	1.1905	11.9133
chr12	133851895	124482084	0.93	2.1497
chr13	115169878	125725973	1.0917	2.2788
chr14	107349540	83851413	0.7811	2.4474
chr15	102531392	62505763	0.6096	1.5699
chr16	90354753	80920738	0.8956	16.7294
chr17	81195210	72134272	0.8884	12.7278
chr18	78077248	53997585	0.6916	18.1554
chr19	59128983	30941258	0.5233	6.0443
chr20	63025520	78940886	1.2525	3.0256
chr21	48129895	42766136	0.8886	4.3723
chr22	51304566	18813147	0.3667	1.2512
chrMT	16571	3111223	187.7511	133.7998
chrX	155270560	145612986	0.9378	4.3326

chrY	59373566	11785489	0.1985	17.5517

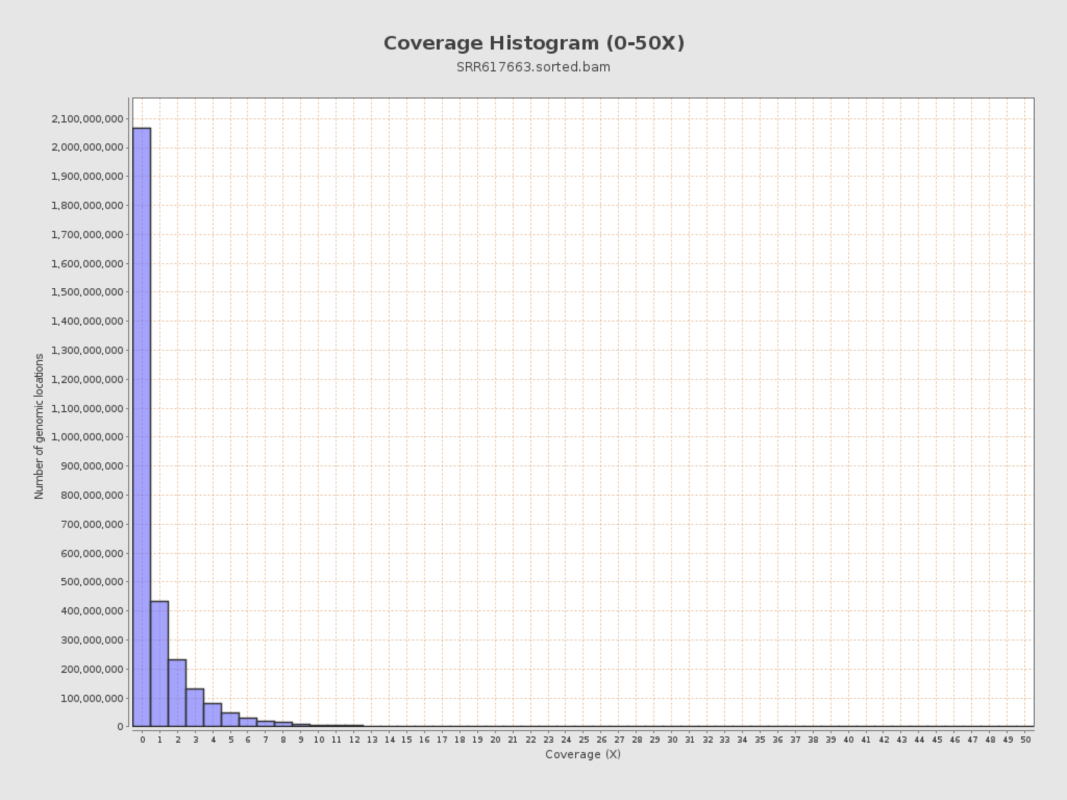
3. Results : Coverage across reference



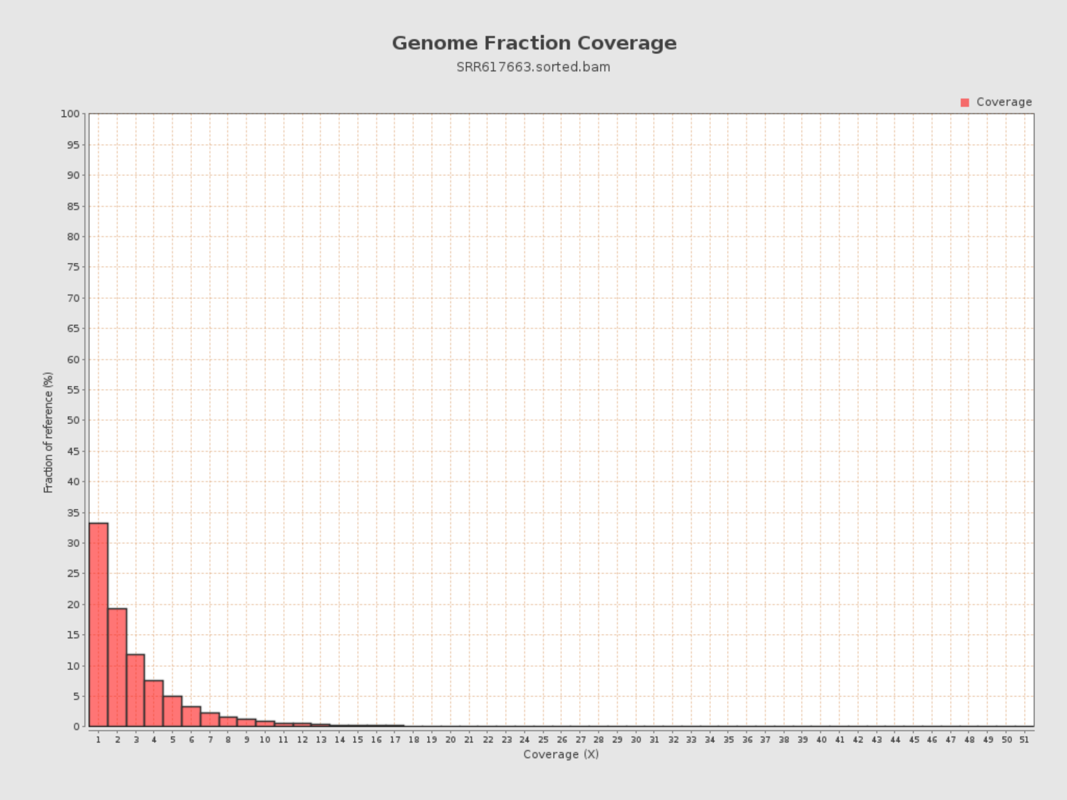
4. Results : Coverage Histogram



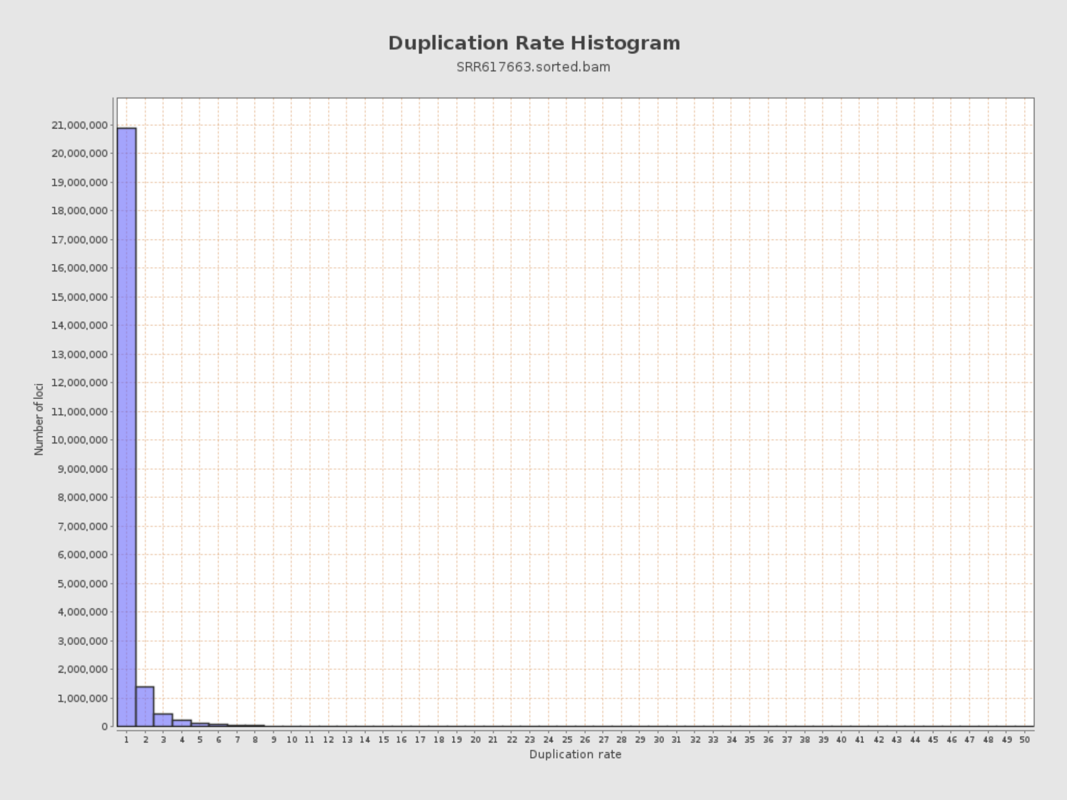
5. Results : Coverage Histogram (0-50X)



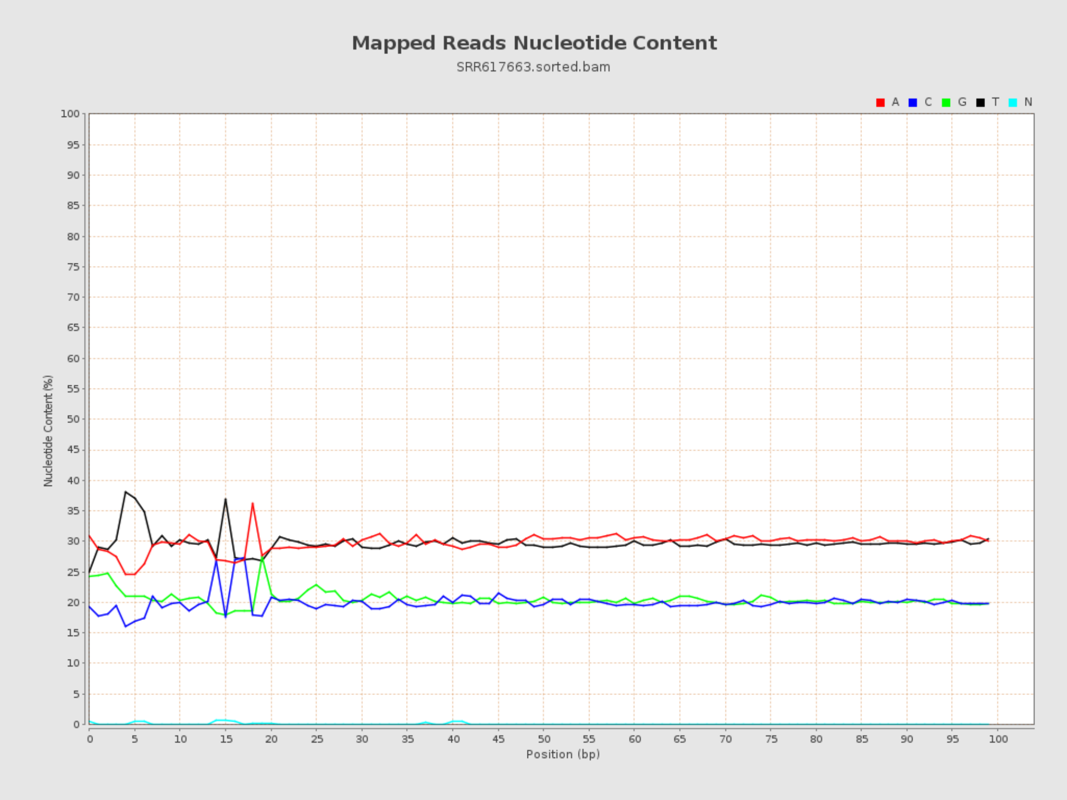
6. Results : Genome Fraction Coverage



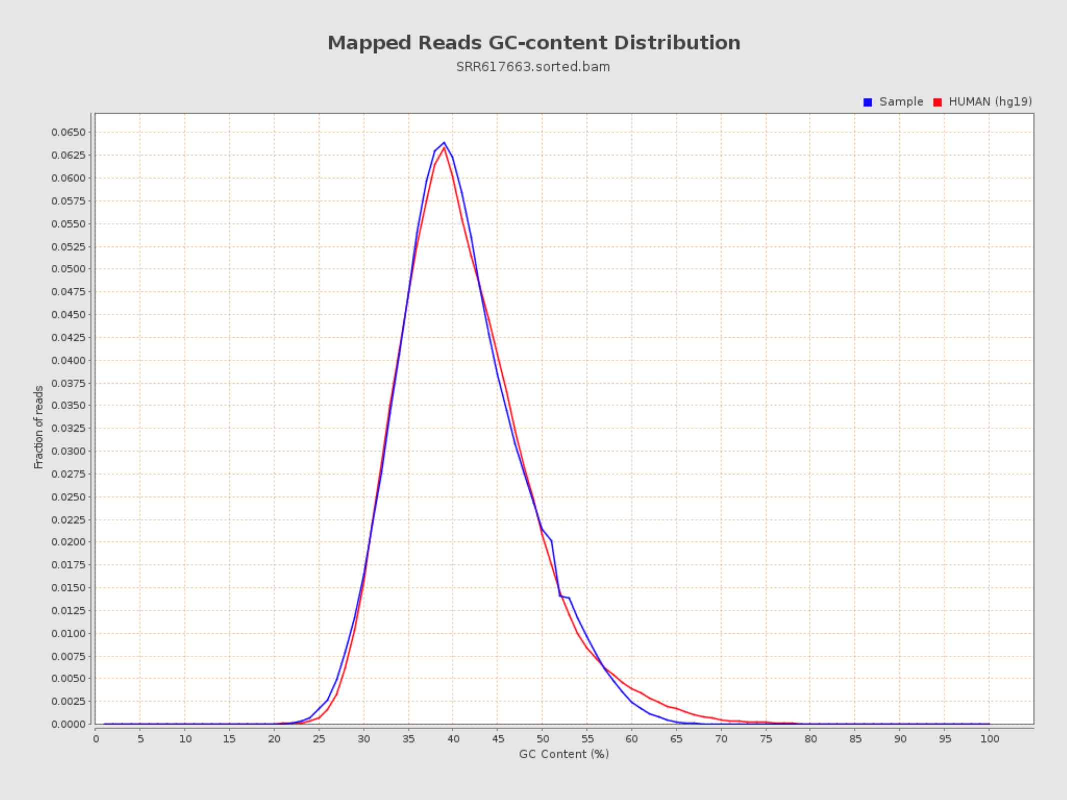
7. Results : Duplication Rate Histogram



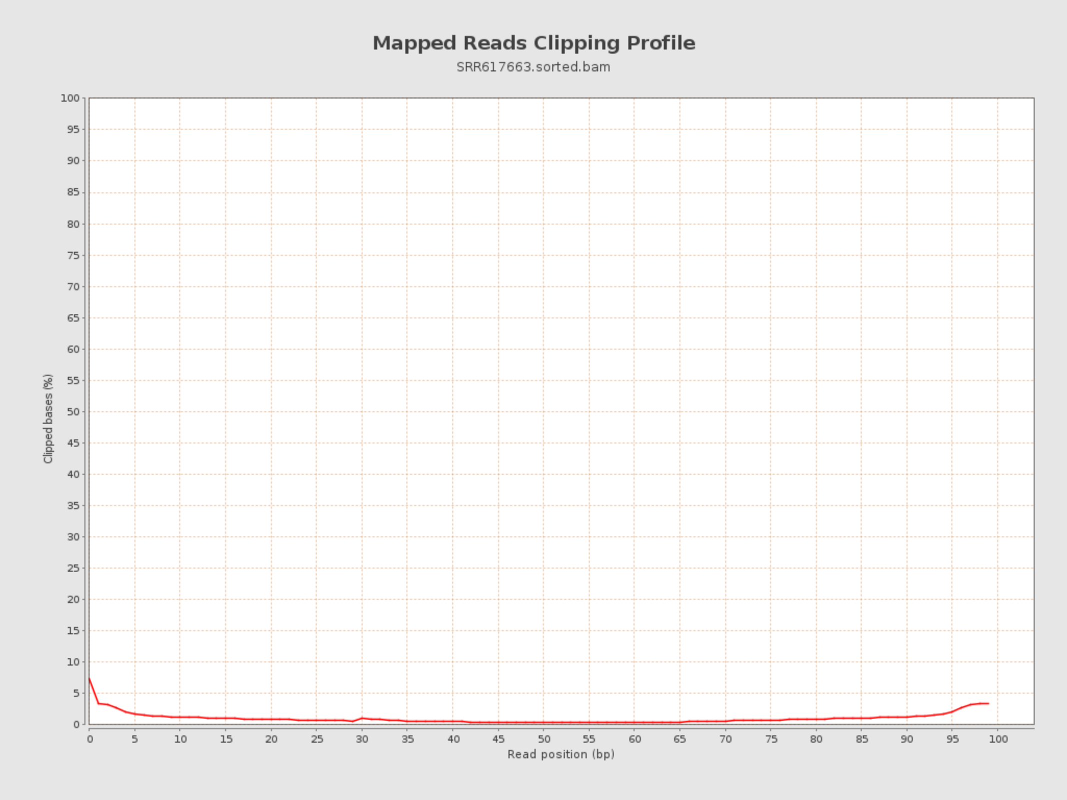
8. Results : Mapped Reads Nucleotide Content



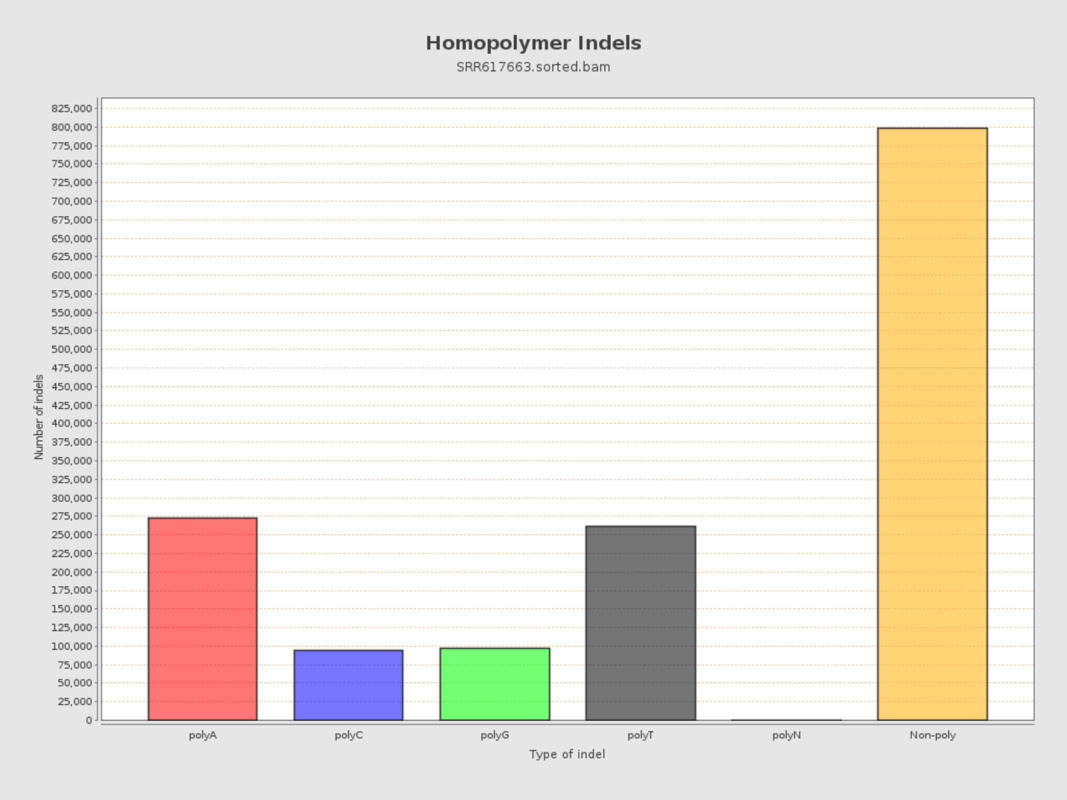
9. Results : Mapped Reads GC-content Distribution



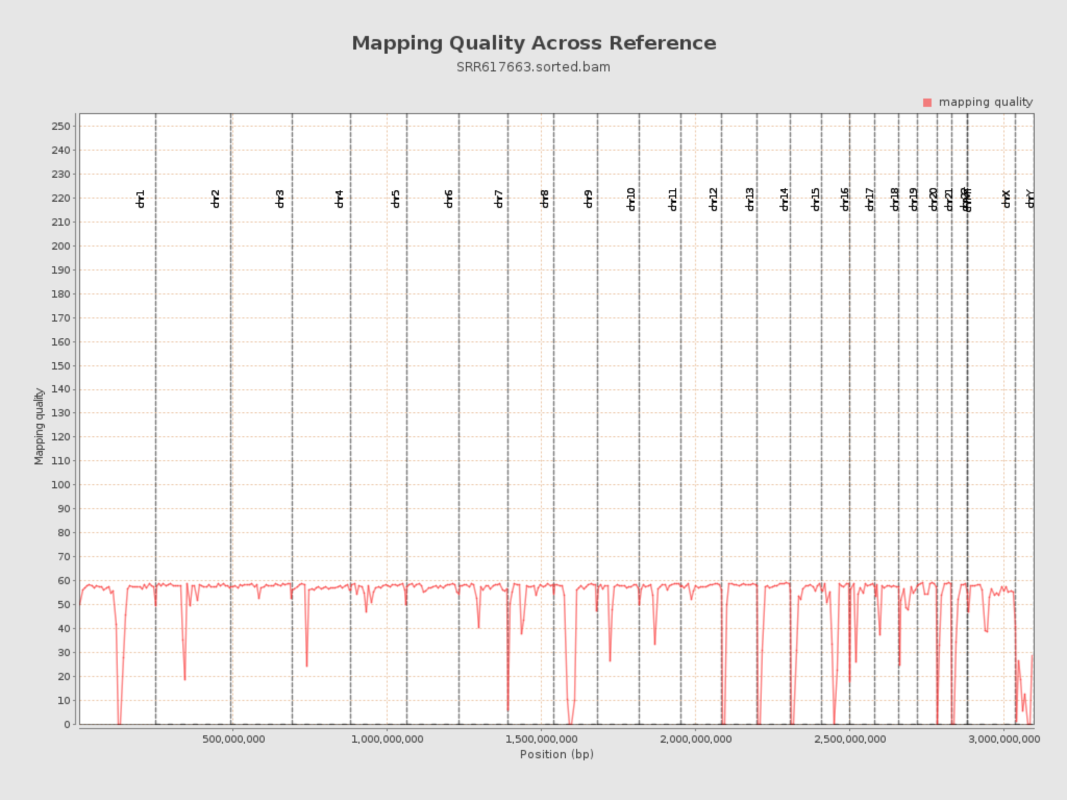
10. Results : Mapped Reads Clipping Profile



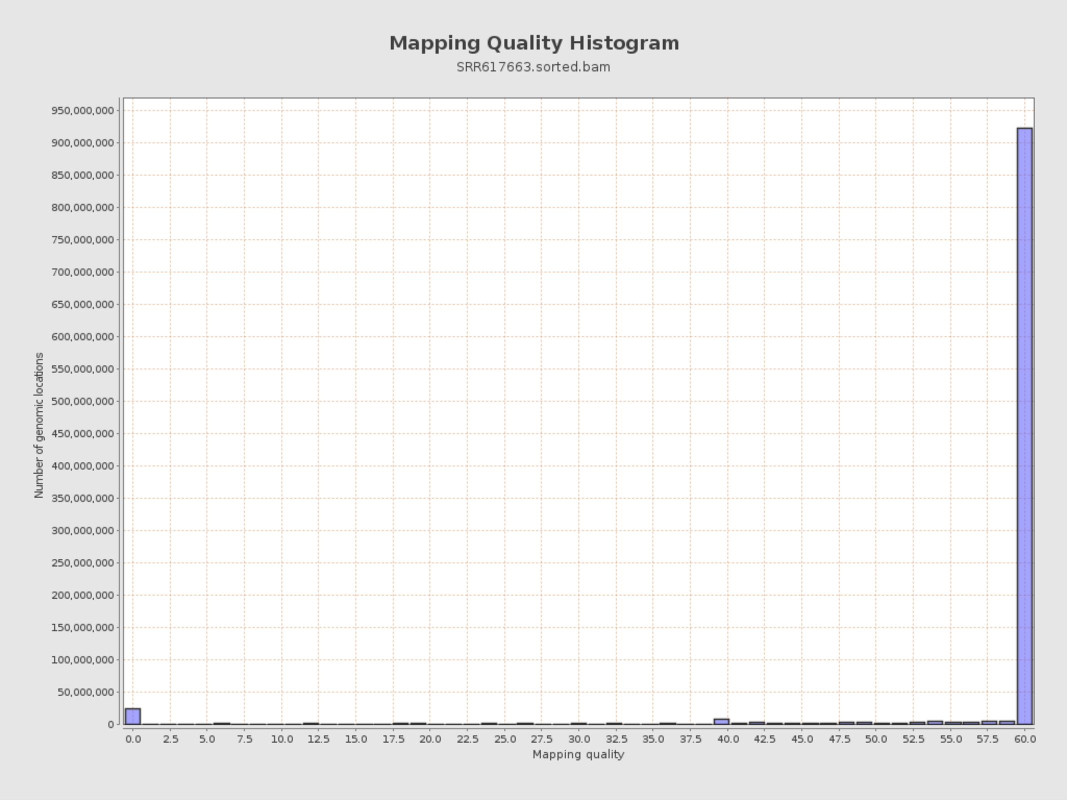
11. Results : Homopolymer Indels



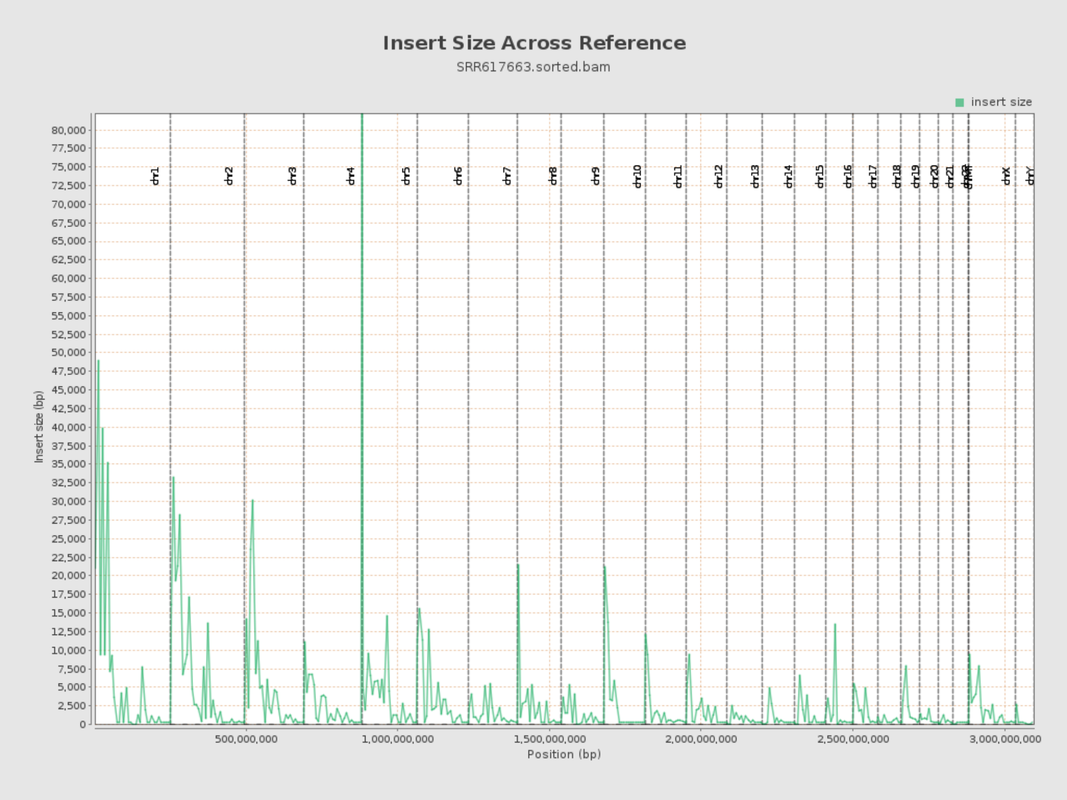
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram