Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/11 08:35:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617668.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_SRR617668 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617668_1.fastq.gz SRR617668_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Oct 11 08:35:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617668.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	30,194,521 / 94.36%
Unmapped reads	1,805,479 / 5.64%
Mapped paired reads	30,194,521 / 94.36%
Mapped reads, first in pair	15,246,186 / 47.64%
Mapped reads, second in pair	14,948,335 / 46.71%
Mapped reads, both in pair	29,506,452 / 92.21%
Mapped reads, singletons	688,069 / 2.15%
Secondary alignments	0
Supplementary alignments	162,669 / 0.51%
Read min/max/mean length	30 / 100 / 100.2
Duplicated reads (estimated)	6,949,362 / 21.72%
Duplication rate	10.75%
Clipped reads	6,523,792 / 20.39%

2.2. ACGT Content

Number/percentage of A's	870,166,852 / 29.78%
Number/percentage of C's	582,001,961 / 19.92%
Number/percentage of T's	869,147,065 / 29.74%
Number/percentage of G's	597,596,957 / 20.45%
Number/percentage of N's	3,307,903 / 0.11%

GC Percentage	40.37%

2.3. Coverage

Mean	0.9445
Standard Deviation	10.5871

2.4. Mapping Quality

Mean Mapping Quality	52.59

2.5. Insert size

Mean	41,868.38
Standard Deviation	1,910,416.43
P25/Median/P75	180 / 224 / 292

2.6. Mismatches and indels

General error rate	1.48%
Mismatches	42,222,607
Insertions	457,375
Mapped reads with at least one insertion	1.49%
Deletions	1,074,258
Mapped reads with at least one deletion	3.48%
Homopolymer indels	47.62%

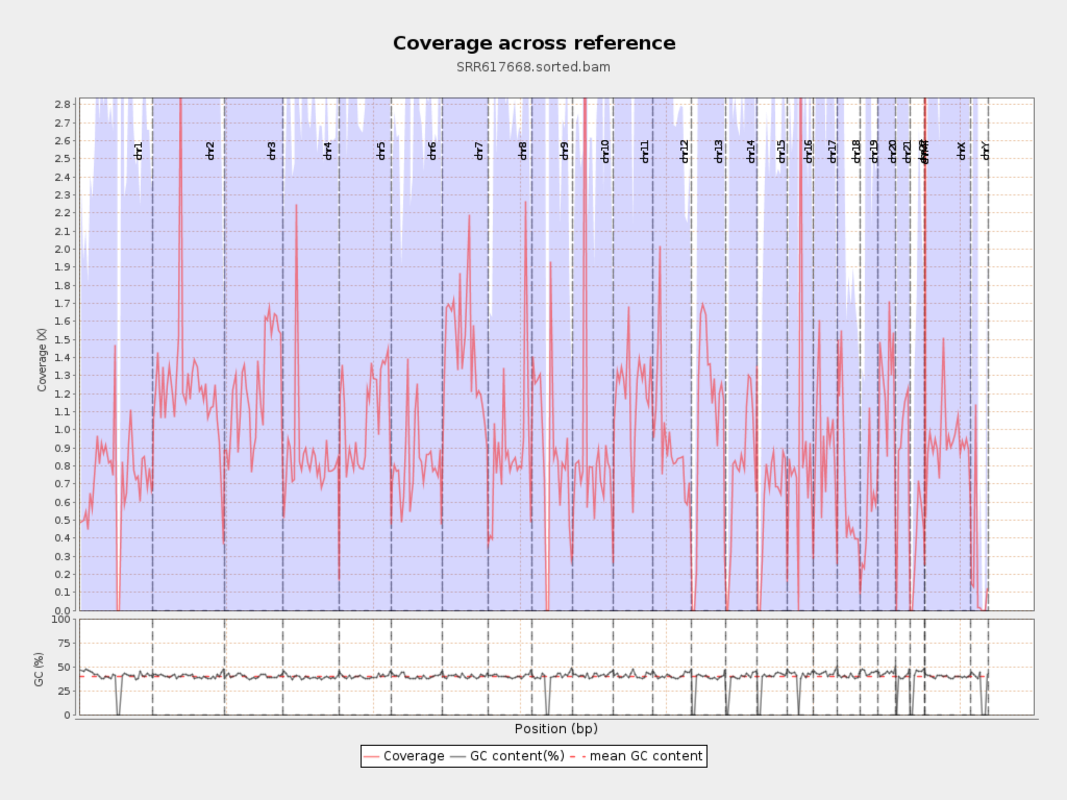
2.7. Chromosome stats

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

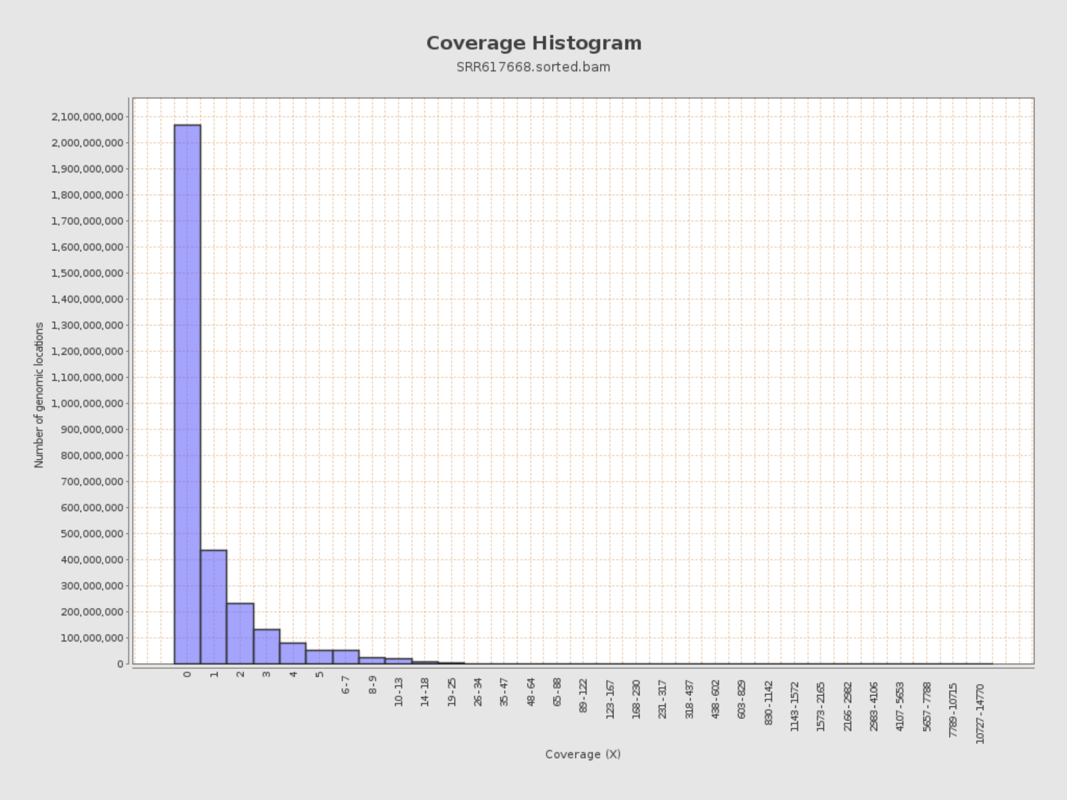
		bases	coverage	deviation
chr1	249250621	179518616	0.7202	10.2675
chr2	243199373	302220473	1.2427	12.1117
chr3	198022430	244601718	1.2352	2.4784
chr4	191154276	163698412	0.8564	8.3251
chr5	180915260	193273407	1.0683	2.3246
chr6	171115067	141726052	0.8282	5.7371
chr7	159138663	228525410	1.436	13.3201
chr8	146364022	129909390	0.8876	4.103
chr9	141213431	120142772	0.8508	20.5148
chr10	135534747	123742055	0.913	21.6074
chr11	135006516	160797566	1.191	11.8538
chr12	133851895	124823098	0.9325	2.1936
chr13	115169878	125739764	1.0918	2.2992
chr14	107349540	83791571	0.7805	2.4724
chr15	102531392	62607998	0.6106	1.6557
chr16	90354753	81073240	0.8973	16.7626
chr17	81195210	71918024	0.8857	12.5234
chr18	78077248	54033483	0.6921	18.1601
chr19	59128983	30995388	0.5242	6.0852
chr20	63025520	79161451	1.256	3.0241
chr21	48129895	42725640	0.8877	4.3626
chr22	51304566	18799587	0.3664	1.2736
chrMT	16571	3078509	185.7769	130.8708
chrX	155270560	145304703	0.9358	4.3215

chrY	59373566	11790448	0.1986	17.3181

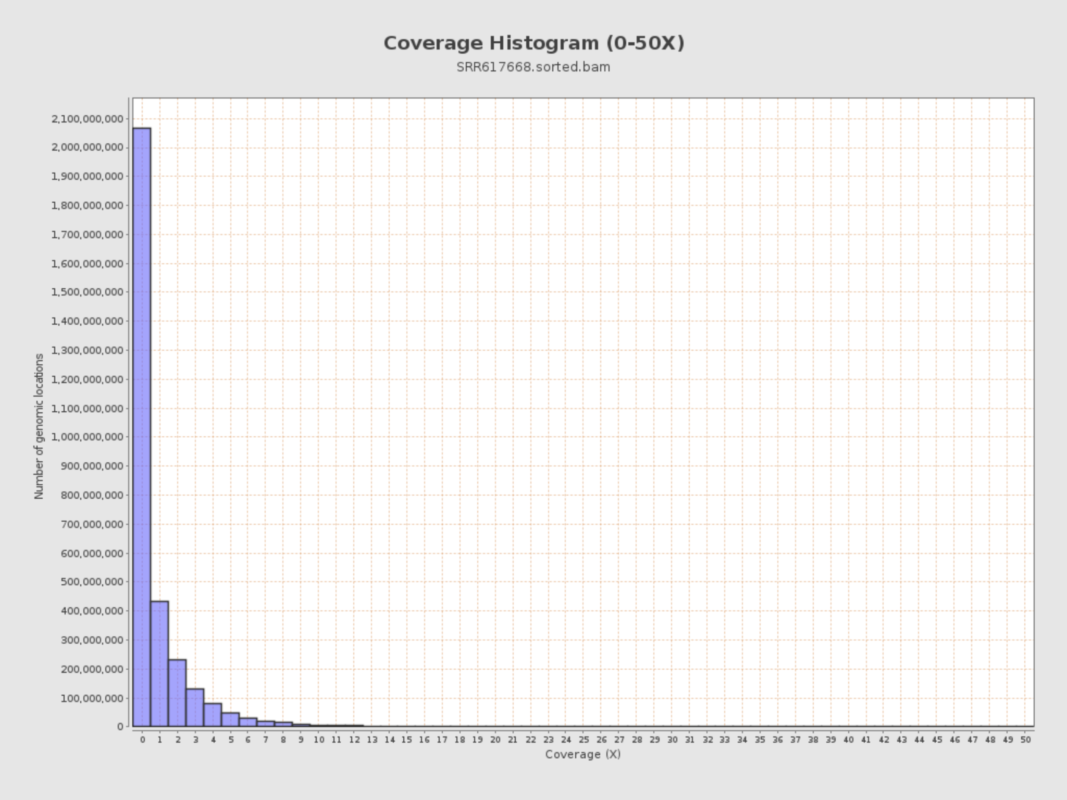
3. Results : Coverage across reference



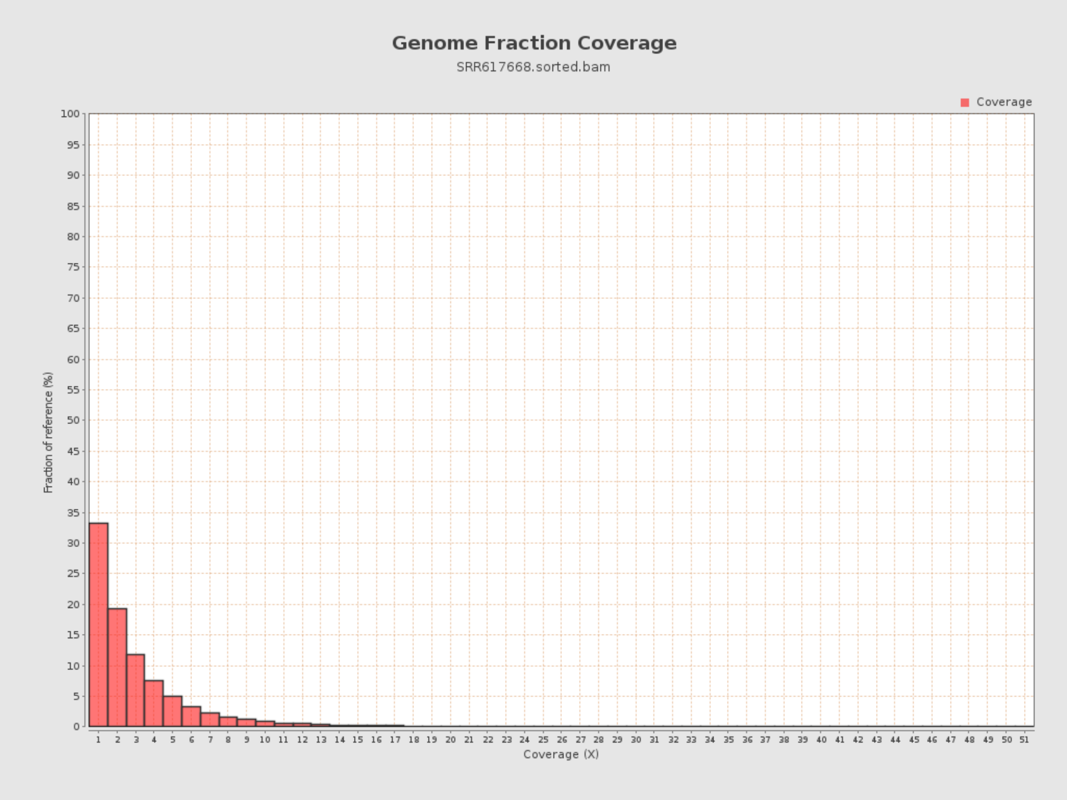
4. Results : Coverage Histogram



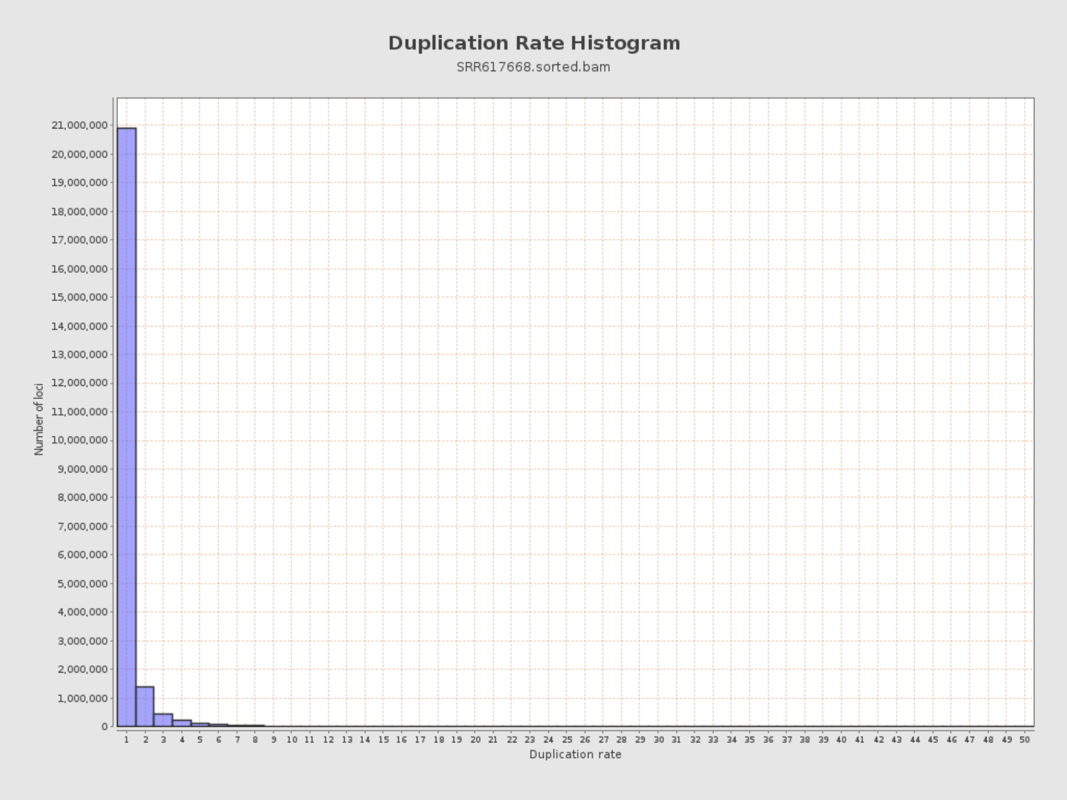
5. Results : Coverage Histogram (0-50X)



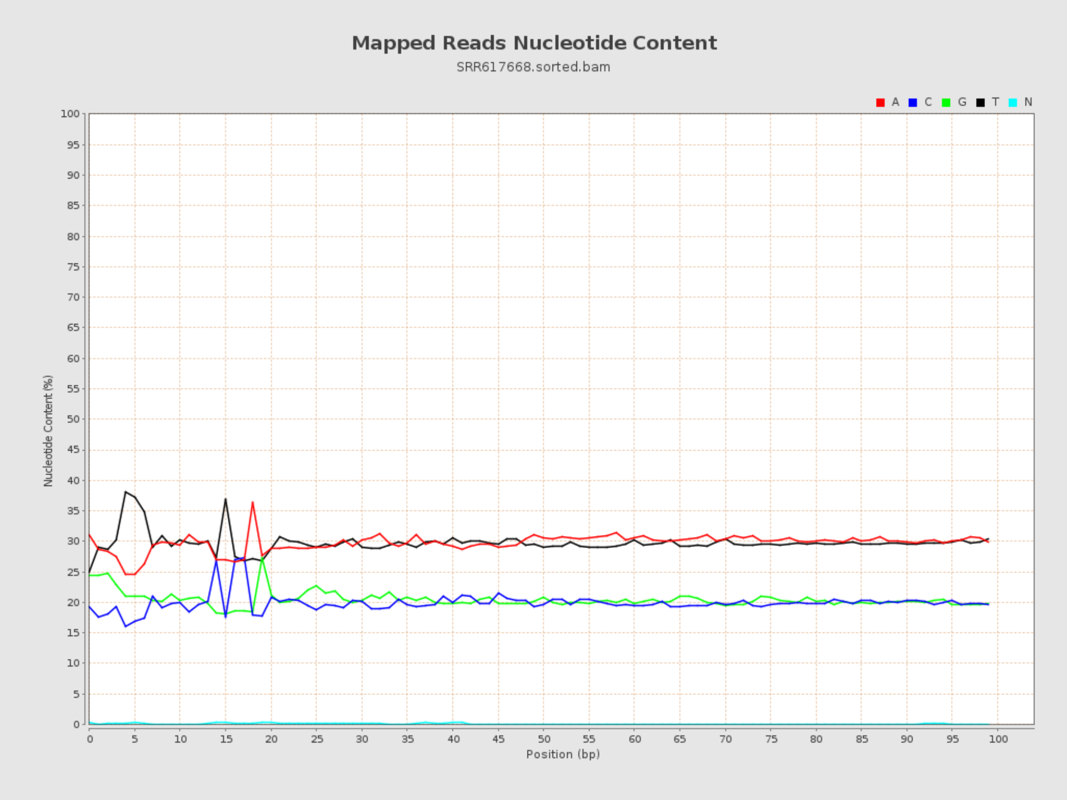
6. Results : Genome Fraction Coverage



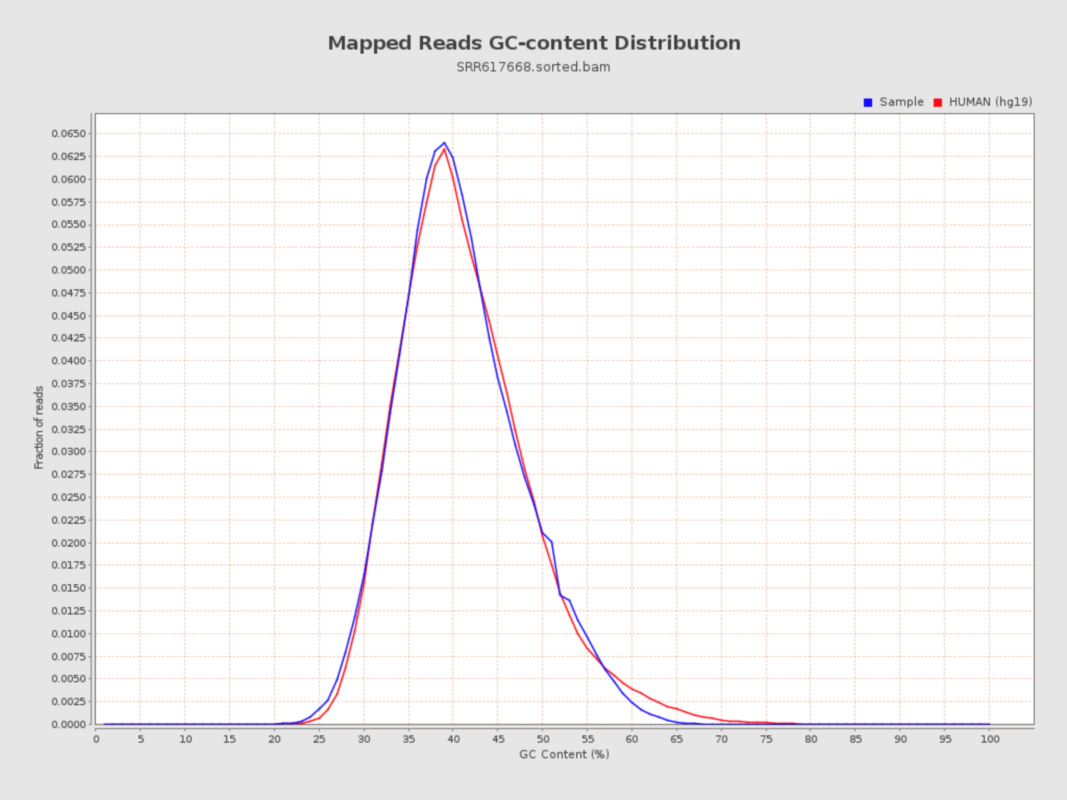
7. Results : Duplication Rate Histogram



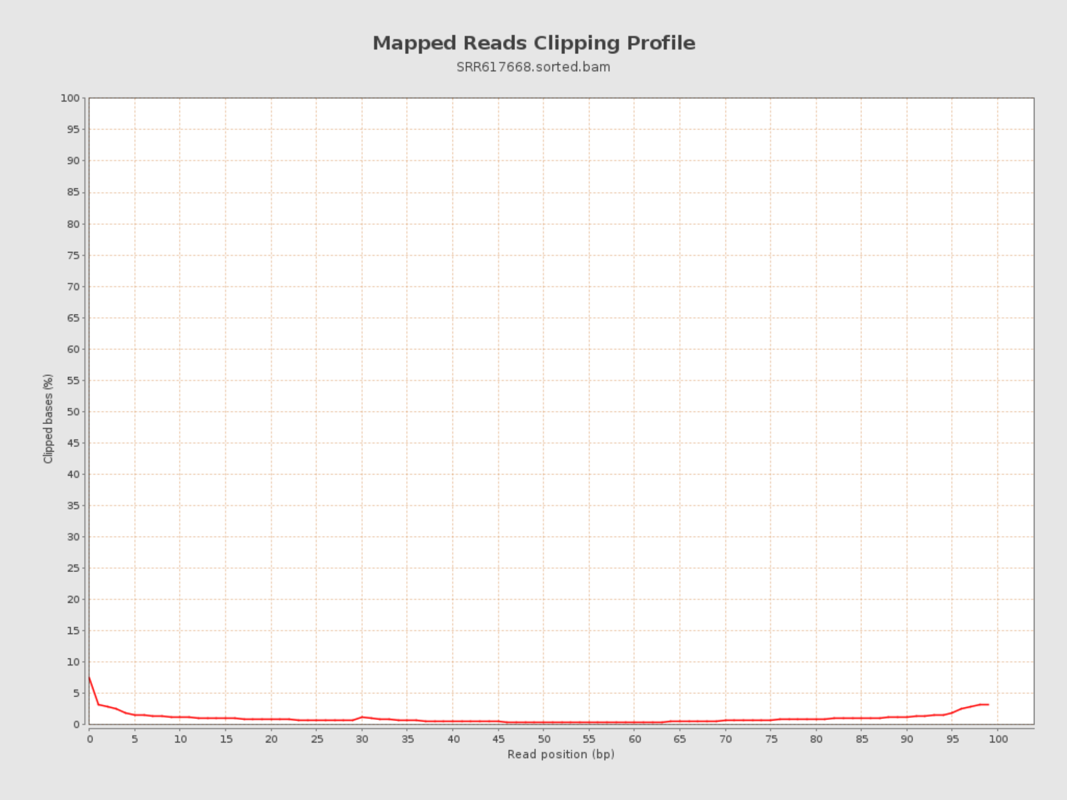
8. Results : Mapped Reads Nucleotide Content



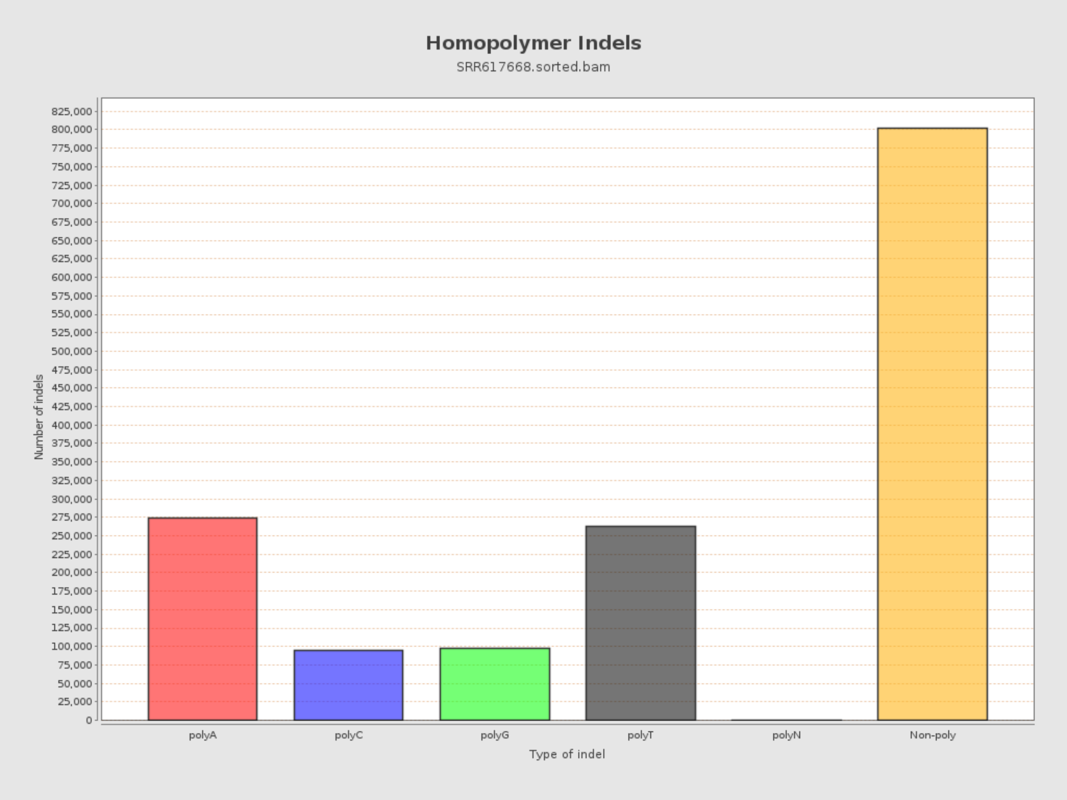
9. Results : Mapped Reads GC-content Distribution



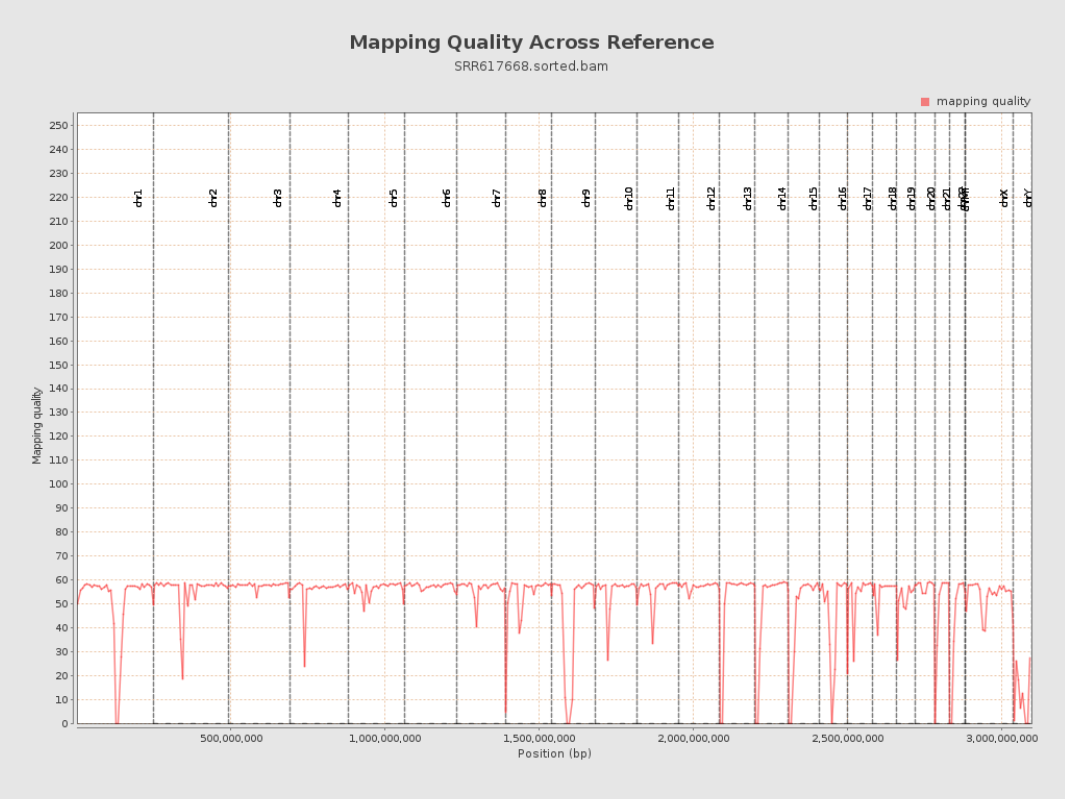
10. Results : Mapped Reads Clipping Profile



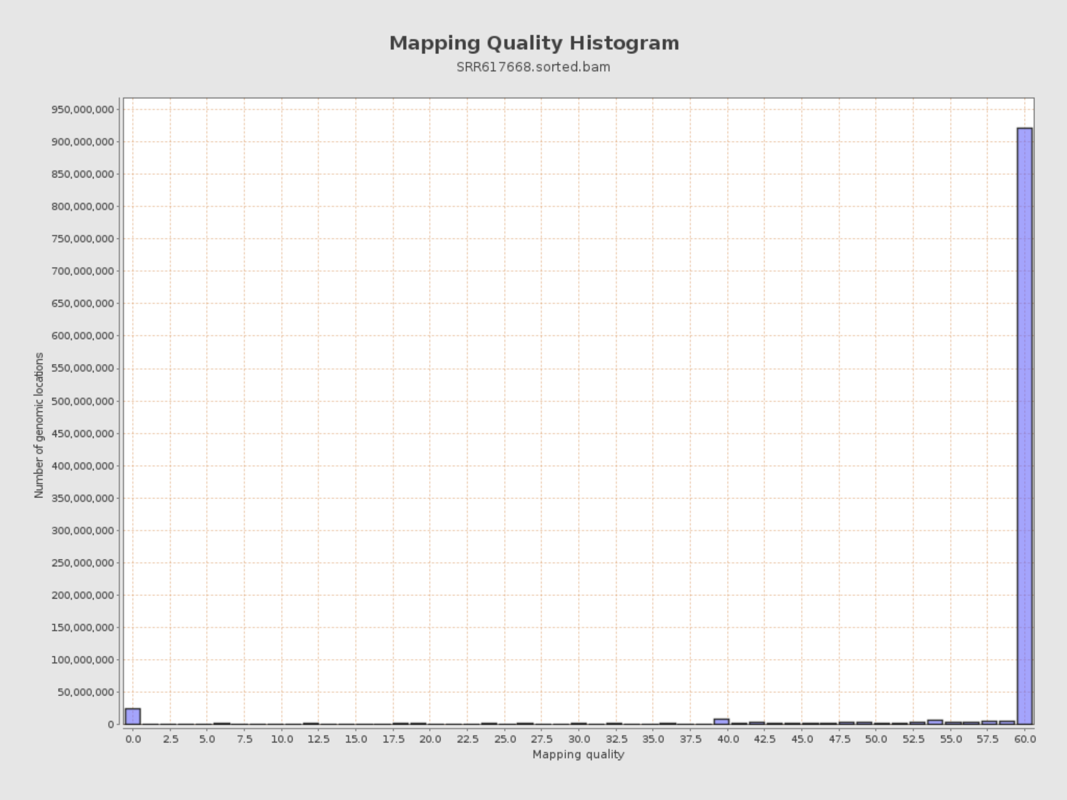
11. Results : Homopolymer Indels



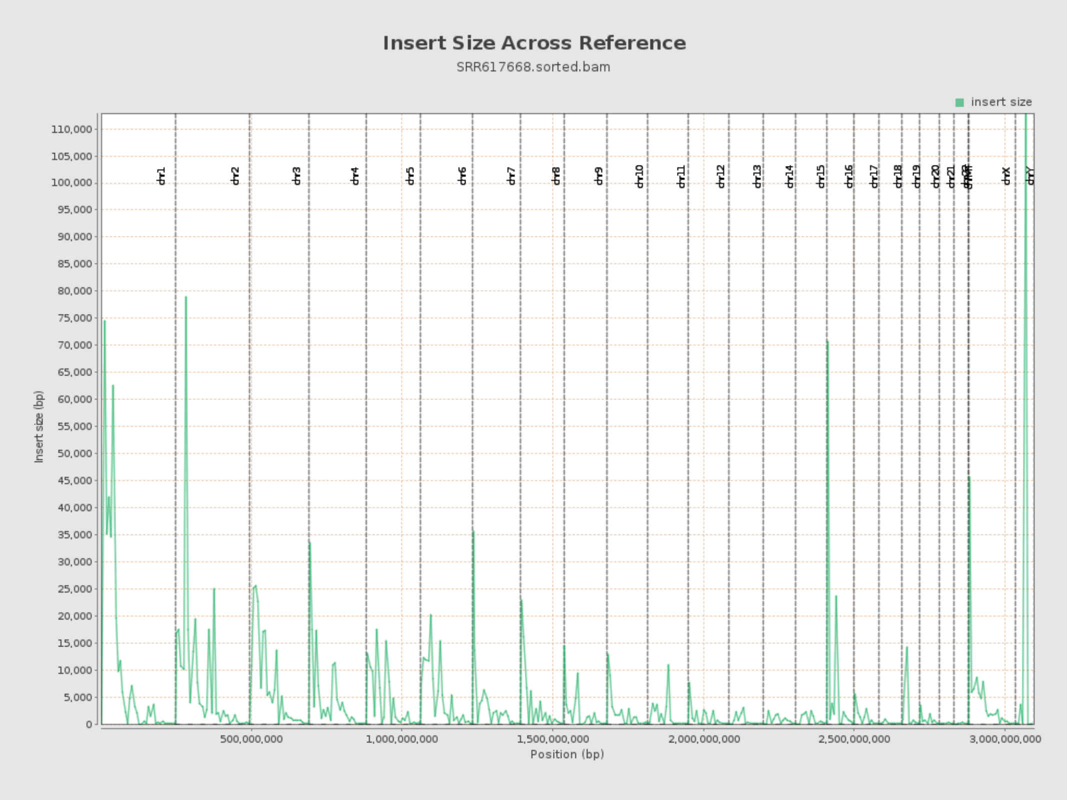
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram