Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/10 19:48:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617652.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_SRR617652 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617652_1.fastq.gz SRR617652_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 10 19:48:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617652.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	30,117,505 / 94.12%
Unmapped reads	1,882,495 / 5.88%
Mapped paired reads	30,117,505 / 94.12%
Mapped reads, first in pair	15,129,692 / 47.28%
Mapped reads, second in pair	14,987,813 / 46.84%
Mapped reads, both in pair	29,497,622 / 92.18%
Mapped reads, singletons	619,883 / 1.94%
Secondary alignments	0
Supplementary alignments	143,278 / 0.45%
Read min/max/mean length	30 / 100 / 100.18
Duplicated reads (estimated)	6,849,160 / 21.4%
Duplication rate	10.59%
Clipped reads	6,337,042 / 19.8%

2.2. ACGT Content

Number/percentage of A's	872,114,601 / 29.84%
Number/percentage of C's	581,489,981 / 19.9%
Number/percentage of T's	869,362,927 / 29.75%
Number/percentage of G's	597,421,580 / 20.44%
Number/percentage of N's	1,861,883 / 0.06%

GC Percentage	40.34%

2.3. Coverage

Mean	0.9445
Standard Deviation	10.6784

2.4. Mapping Quality

Mean Mapping Quality	52.62

2.5. Insert size

Mean	34,294.82
Standard Deviation	1,696,186.66
P25/Median/P75	178 / 221 / 285

2.6. Mismatches and indels

General error rate	1.55%
Mismatches	44,480,315
Insertions	453,178
Mapped reads with at least one insertion	1.48%
Deletions	1,065,640
Mapped reads with at least one deletion	3.46%
Homopolymer indels	47.64%

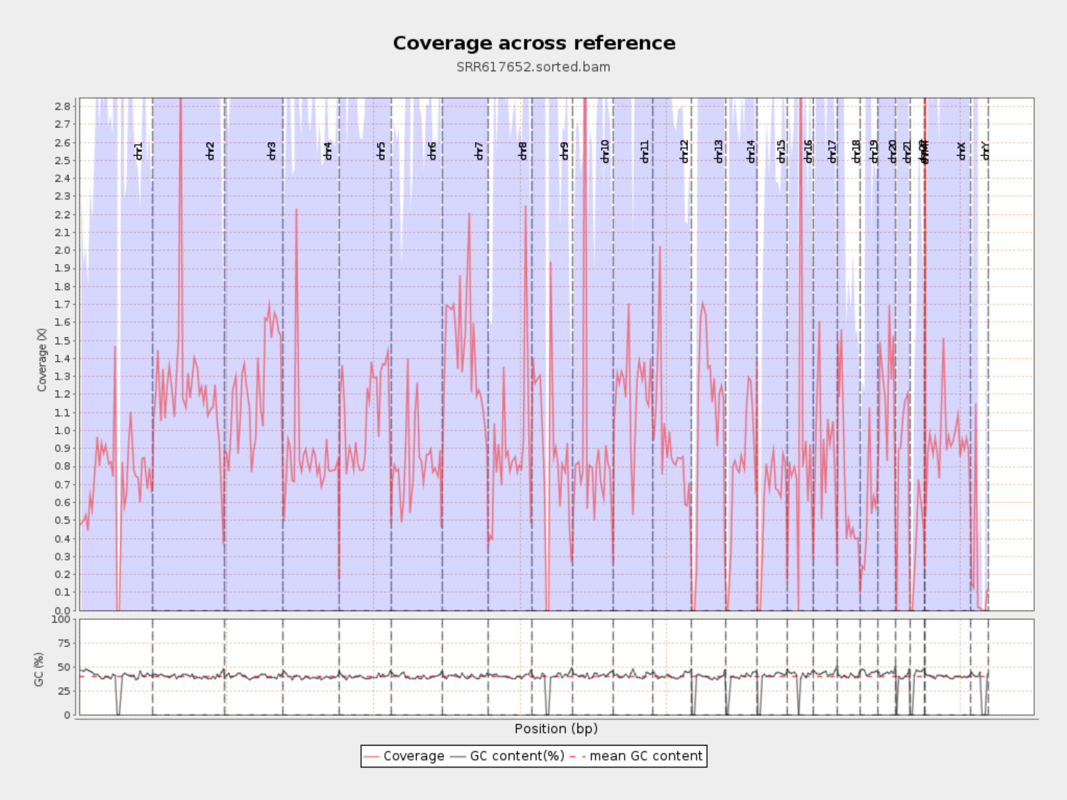
2.7. Chromosome stats

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

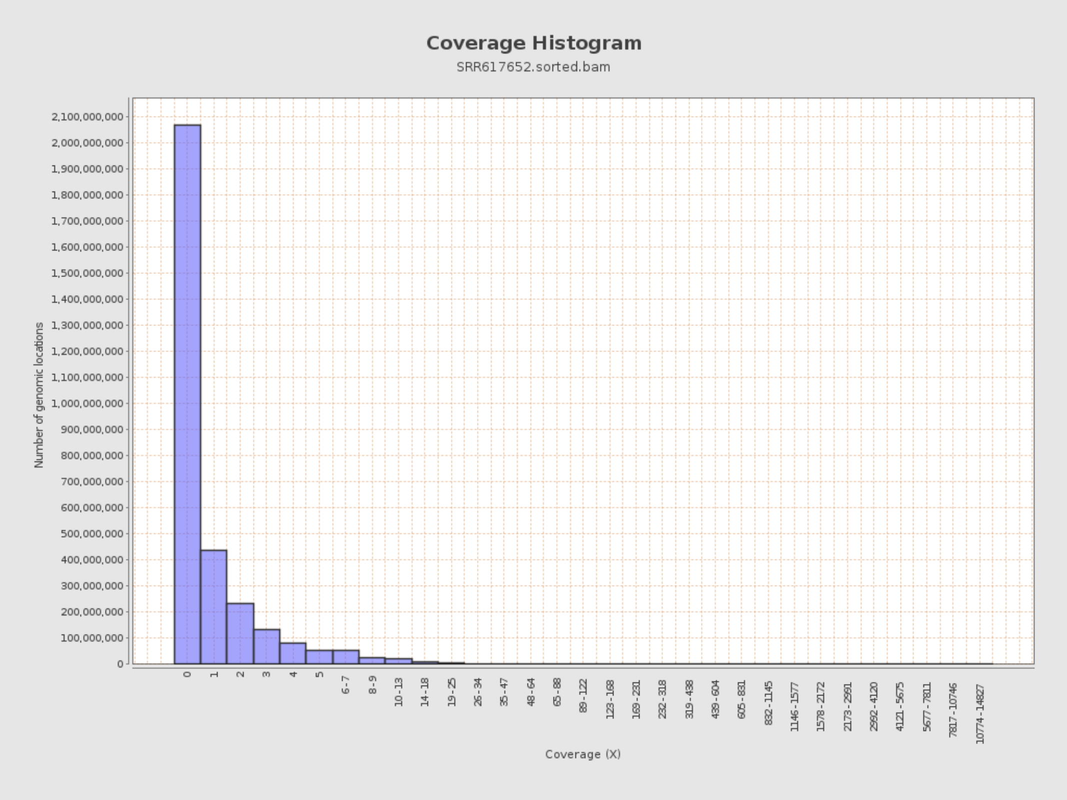
		bases	coverage	deviation
chr1	249250621	179011925	0.7182	10.2839
chr2	243199373	301947057	1.2416	12.1378
chr3	198022430	244909341	1.2368	2.4652
chr4	191154276	164010703	0.858	8.326
chr5	180915260	193840942	1.0714	2.3274
chr6	171115067	142112397	0.8305	5.7877
chr7	159138663	229145438	1.4399	13.3147
chr8	146364022	130240813	0.8898	4.157
chr9	141213431	119909853	0.8491	20.5918
chr10	135534747	124031344	0.9151	21.7858
chr11	135006516	160681029	1.1902	12.2132
chr12	133851895	124684883	0.9315	2.1378
chr13	115169878	125772560	1.0921	2.277
chr14	107349540	83476200	0.7776	2.4469
chr15	102531392	62289772	0.6075	1.5659
chr16	90354753	81309870	0.8999	17.0887
chr17	81195210	71459793	0.8801	12.7645
chr18	78077248	53963909	0.6912	18.488
chr19	59128983	30694195	0.5191	6.2281
chr20	63025520	78472436	1.2451	3.023
chr21	48129895	42651662	0.8862	4.3574
chr22	51304566	18772552	0.3659	1.2607
chrMT	16571	3054753	184.3433	129.7207
chrX	155270560	145798449	0.939	4.3937

chrY	59373566	11766514	0.1982	17.5353

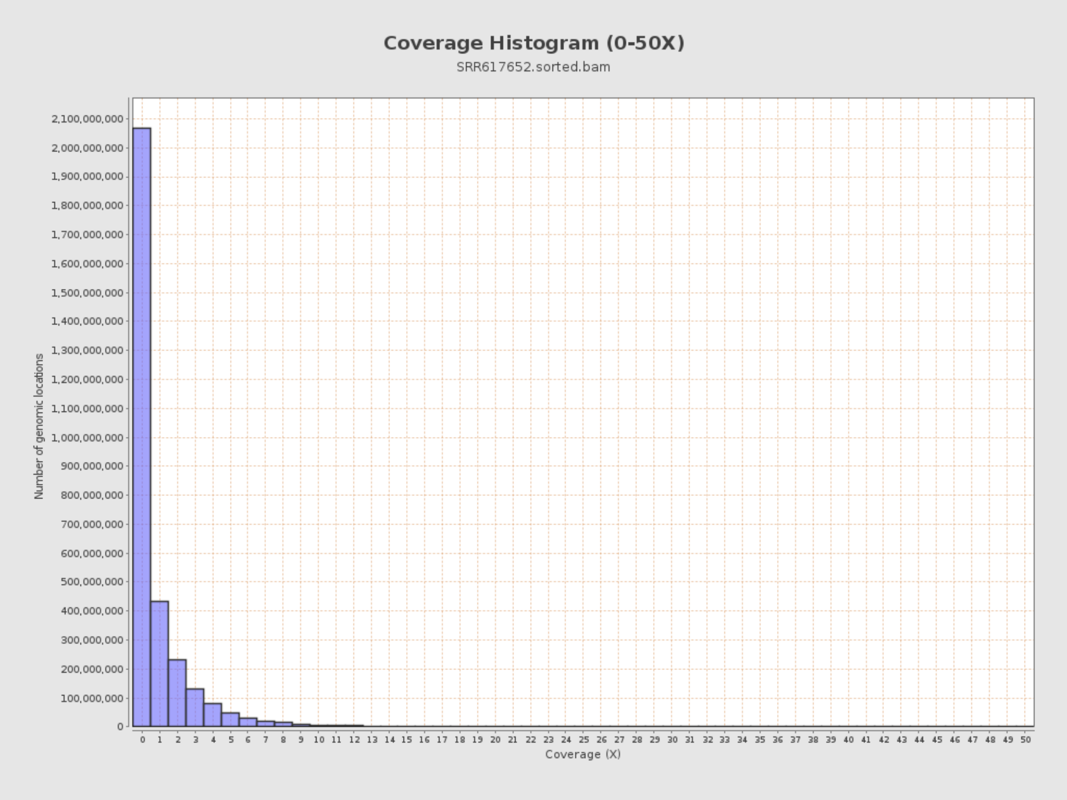
3. Results : Coverage across reference



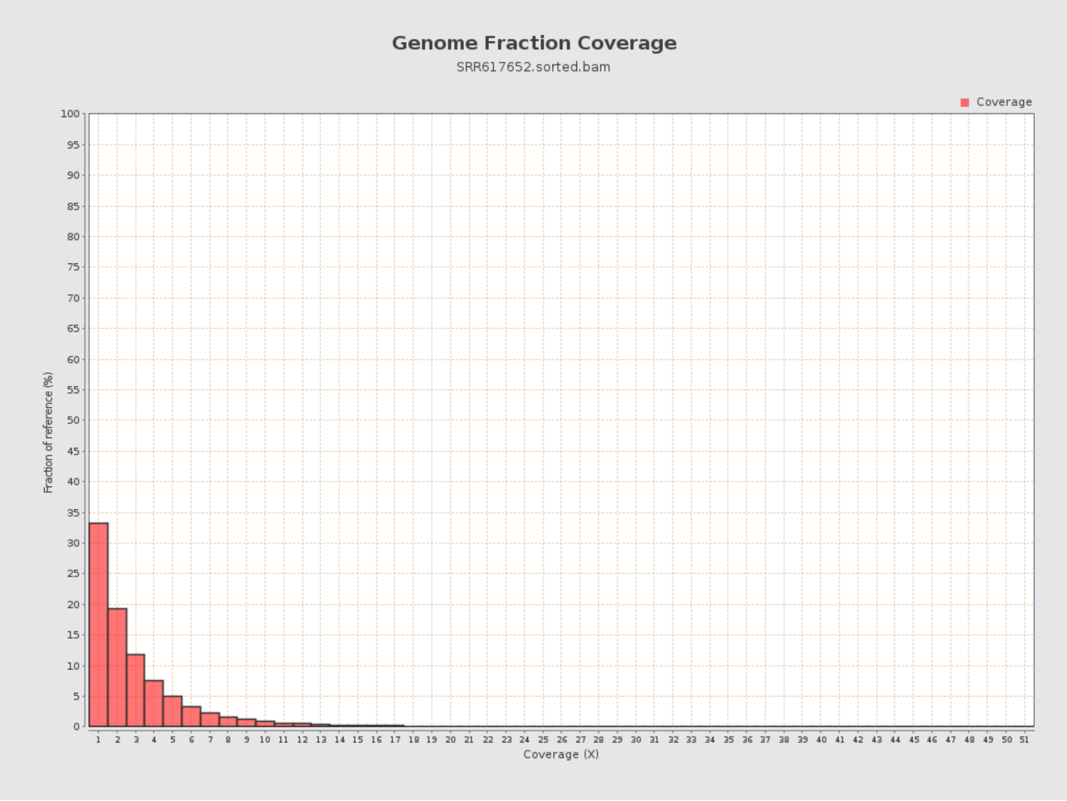
4. Results : Coverage Histogram



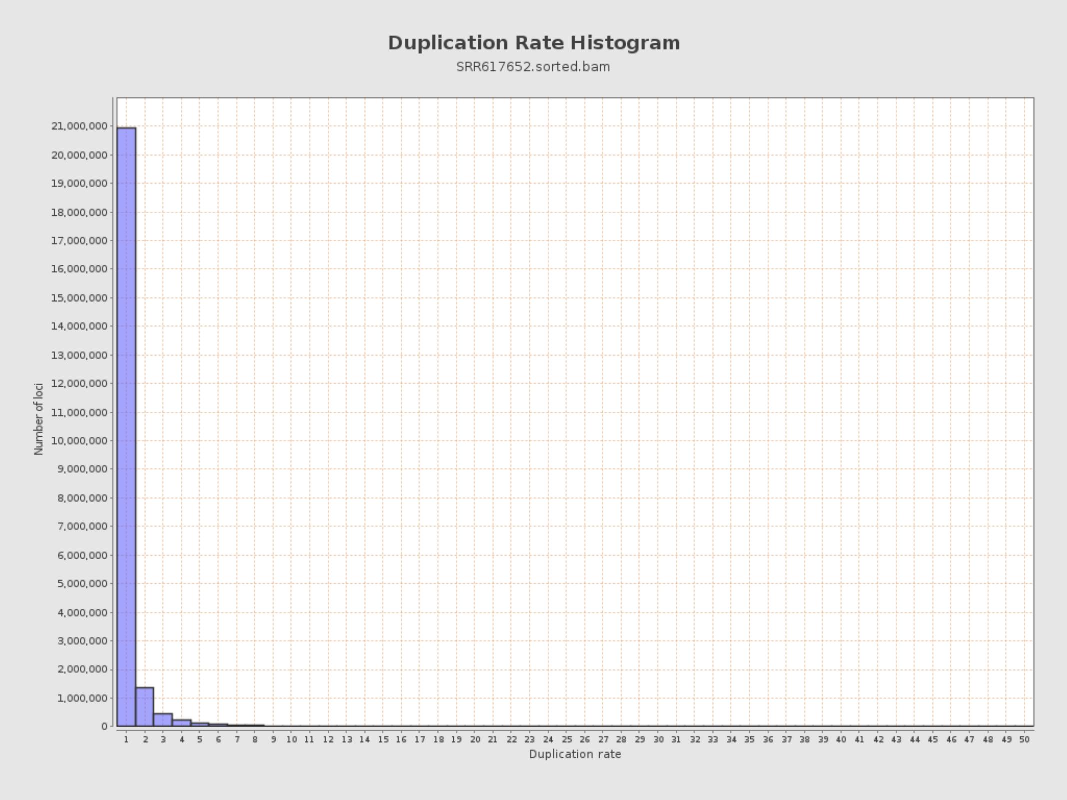
5. Results : Coverage Histogram (0-50X)



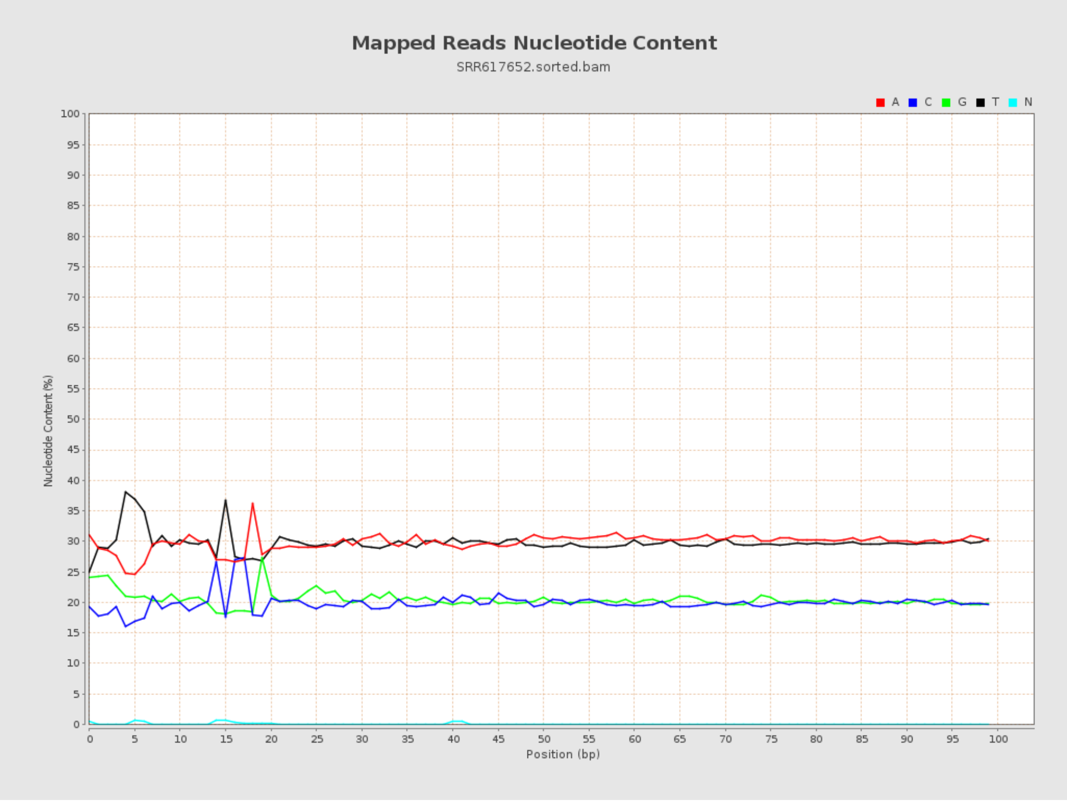
6. Results : Genome Fraction Coverage



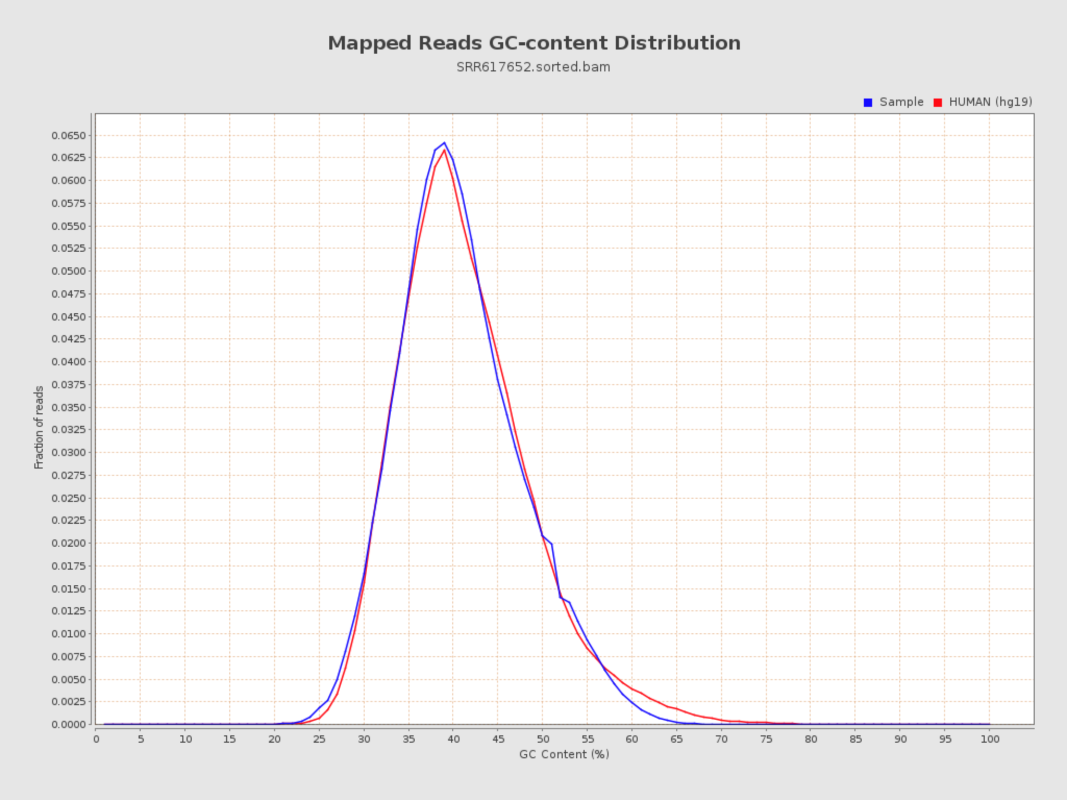
7. Results : Duplication Rate Histogram



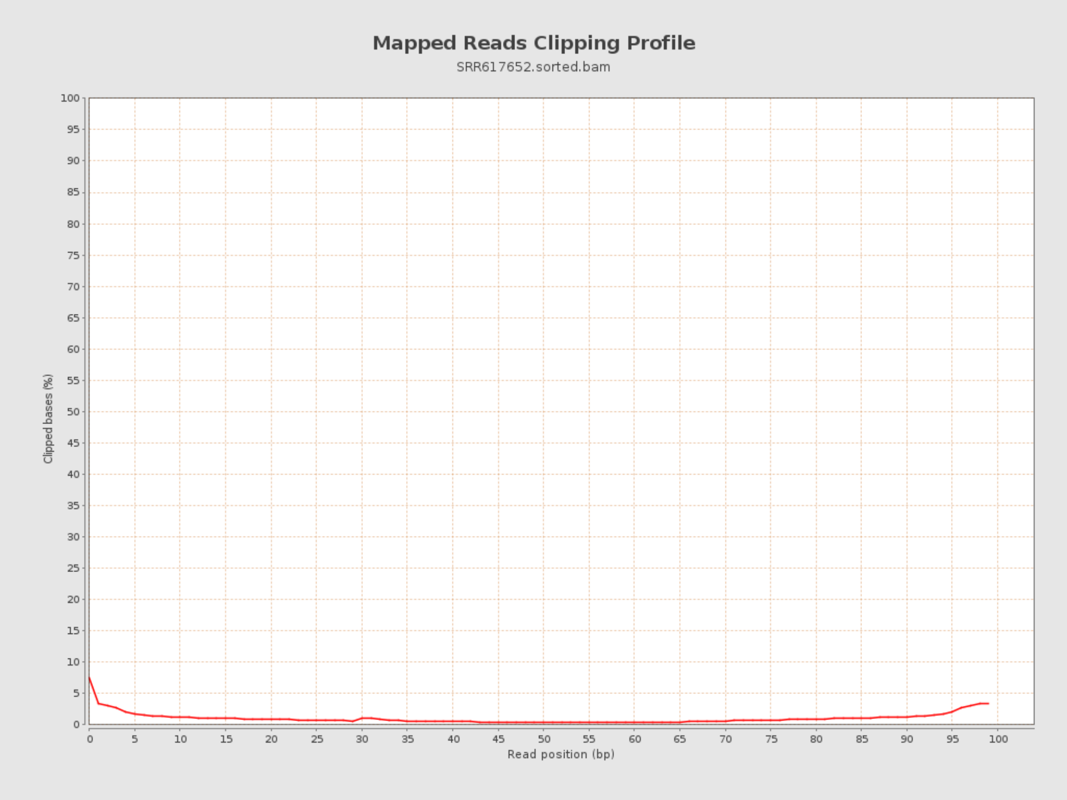
8. Results : Mapped Reads Nucleotide Content



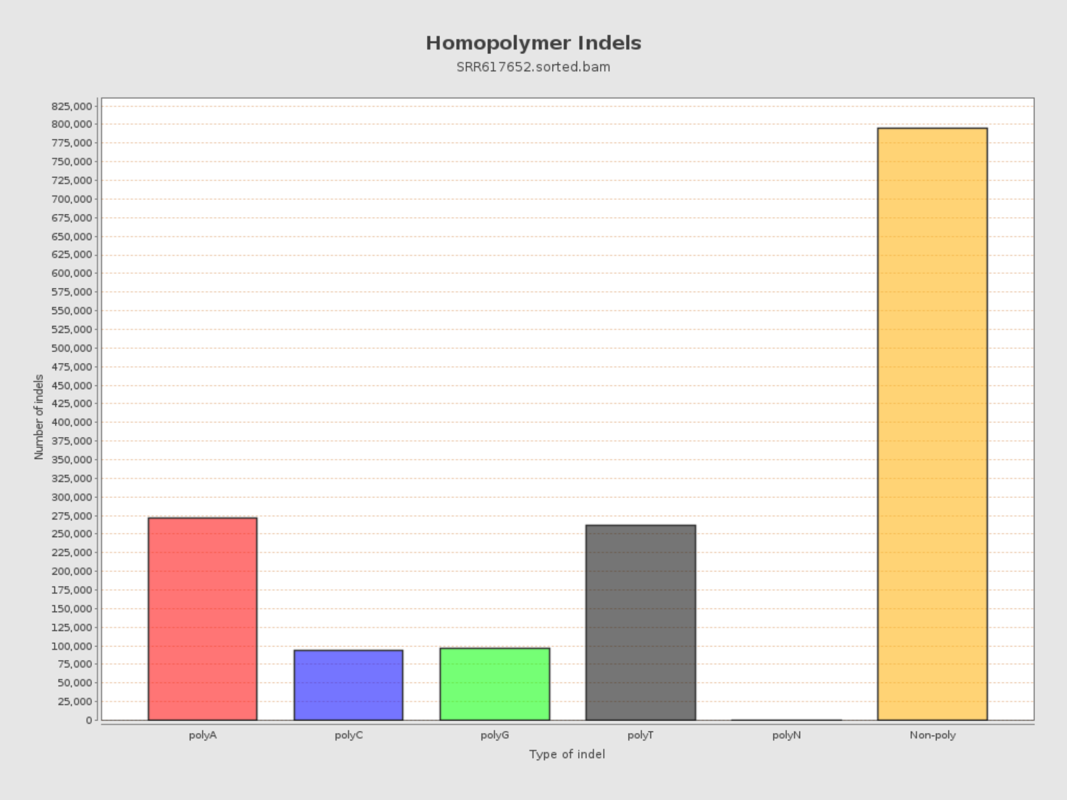
9. Results : Mapped Reads GC-content Distribution



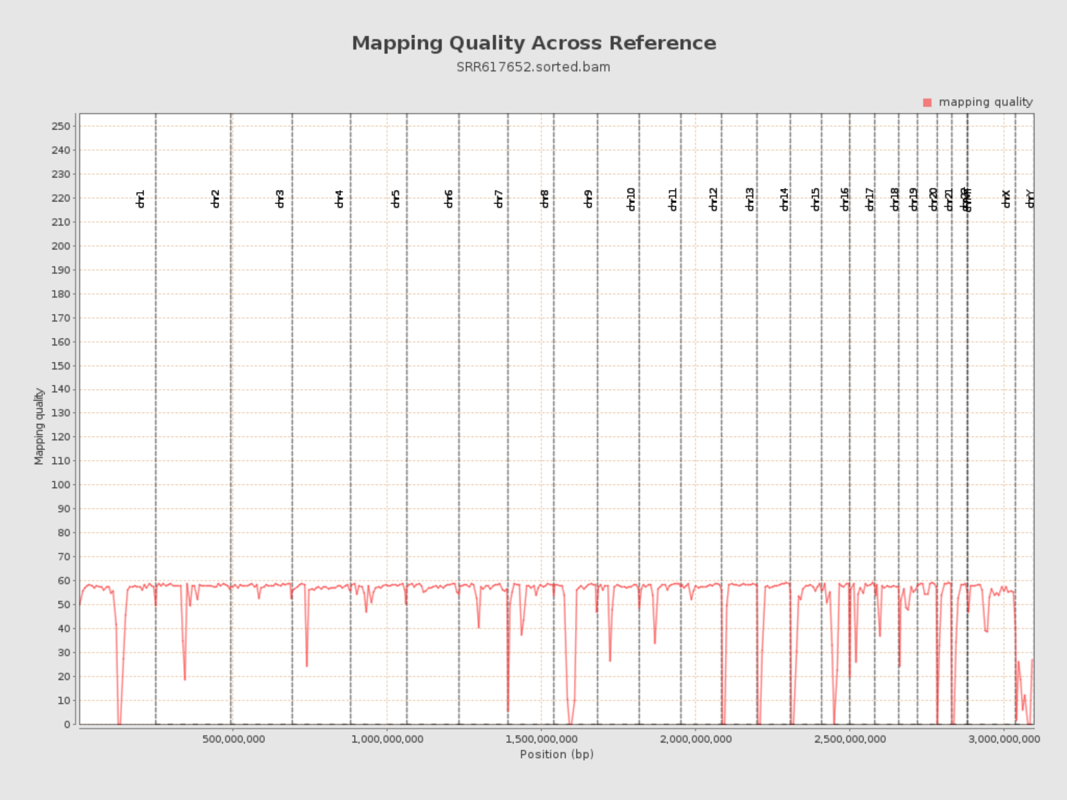
10. Results : Mapped Reads Clipping Profile



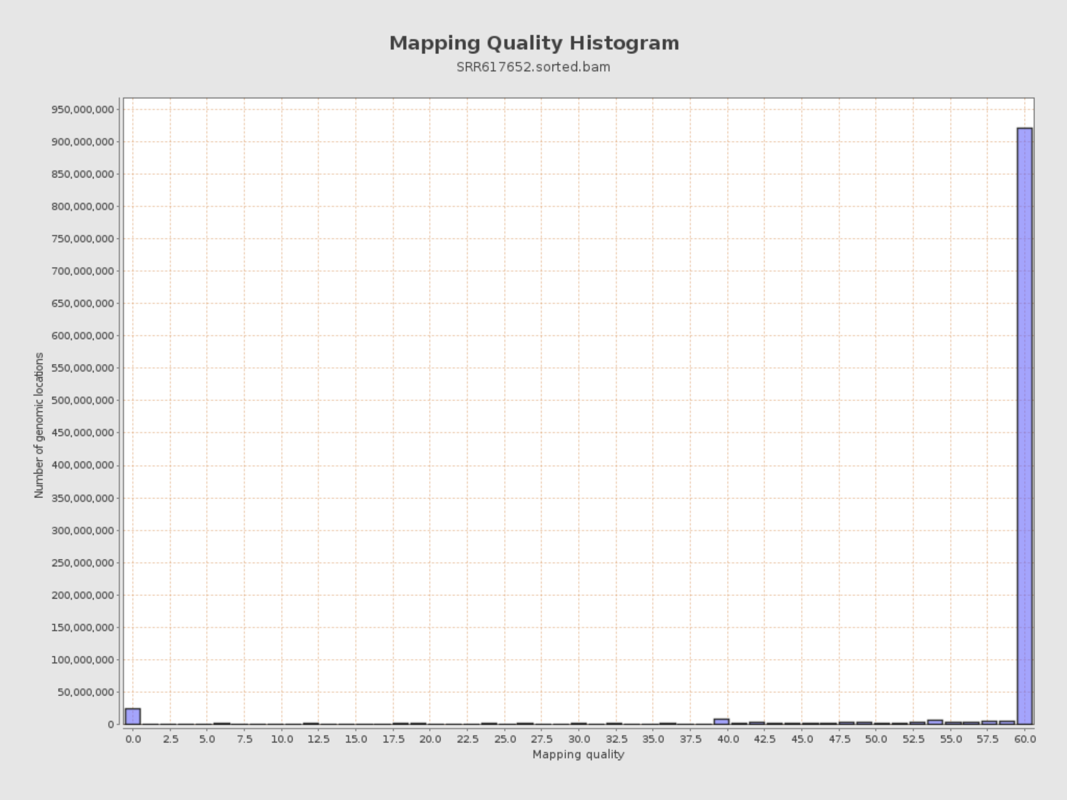
11. Results : Homopolymer Indels



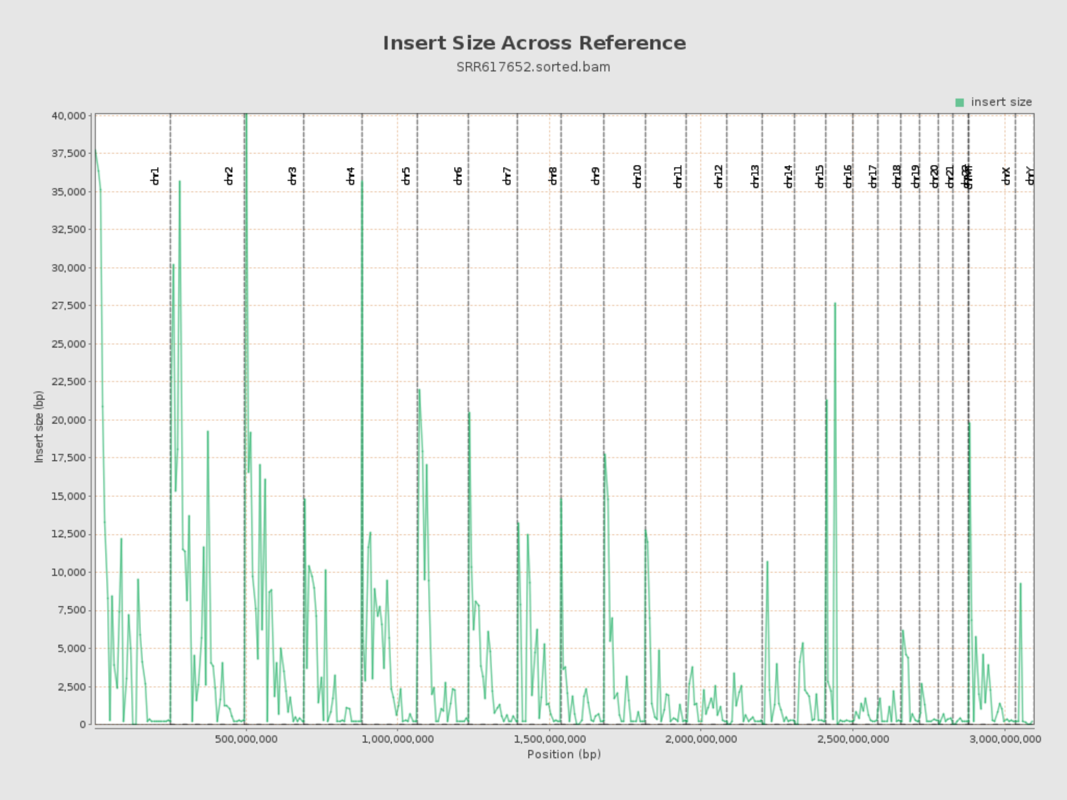
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram