Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/09 07:59:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617422.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_SRR617422 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617422_1.fastq.gz SRR617422_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 09 07:59:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617422.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	30,580,457 / 95.56%
Unmapped reads	1,419,543 / 4.44%
Mapped paired reads	30,580,457 / 95.56%
Mapped reads, first in pair	15,396,536 / 48.11%
Mapped reads, second in pair	15,183,921 / 47.45%
Mapped reads, both in pair	30,110,520 / 94.1%
Mapped reads, singletons	469,937 / 1.47%
Secondary alignments	0
Supplementary alignments	507,121 / 1.58%
Read min/max/mean length	30 / 100 / 100.65
Duplicated reads (estimated)	1,474,469 / 4.61%
Duplication rate	4.3%
Clipped reads	2,960,912 / 9.25%

2.2. ACGT Content

Number/percentage of A's	897,414,879 / 29.75%
Number/percentage of C's	608,409,427 / 20.17%
Number/percentage of T's	890,839,826 / 29.53%
Number/percentage of G's	619,237,862 / 20.53%
Number/percentage of N's	345,421 / 0.01%

GC Percentage	40.7%

2.3. Coverage

Mean	0.9746
Standard Deviation	3.002

2.4. Mapping Quality

Mean Mapping Quality	53.94

2.5. Insert size

Mean	62,060.28
Standard Deviation	2,395,468.74
P25/Median/P75	173 / 214 / 281

2.6. Mismatches and indels

General error rate	0.84%
Mismatches	24,926,334
Insertions	251,774
Mapped reads with at least one insertion	0.81%
Deletions	299,639
Mapped reads with at least one deletion	0.96%
Homopolymer indels	44.9%

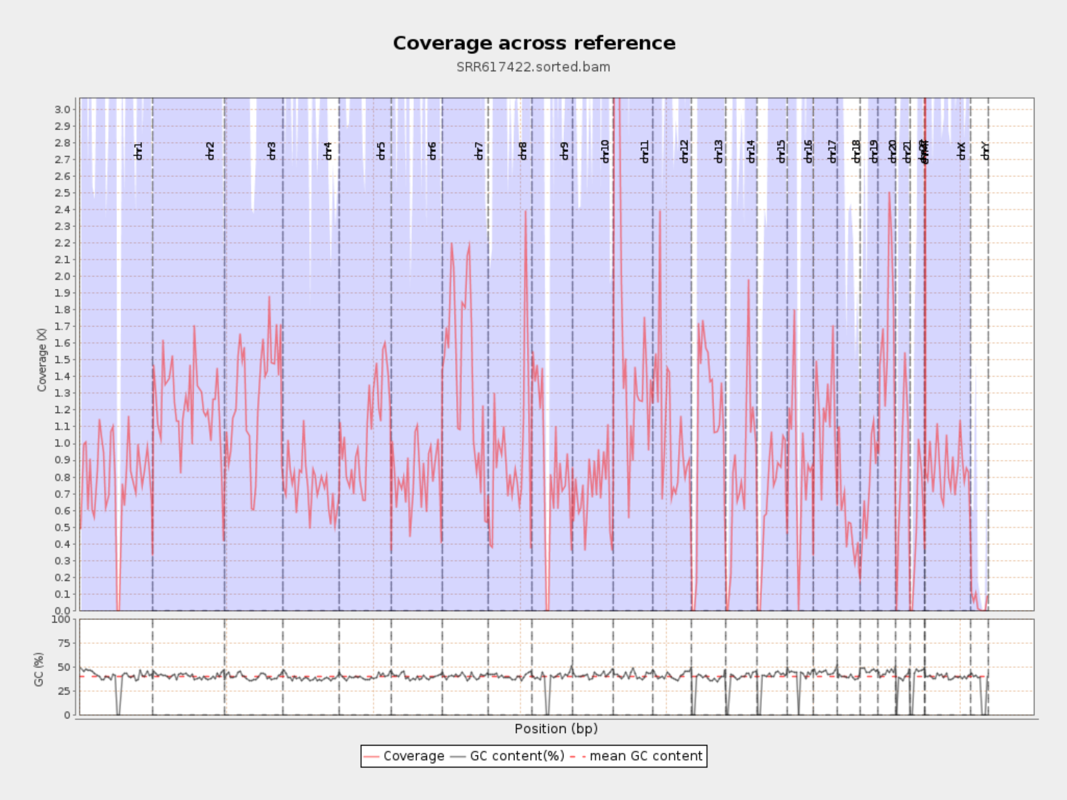
2.7. Chromosome stats

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

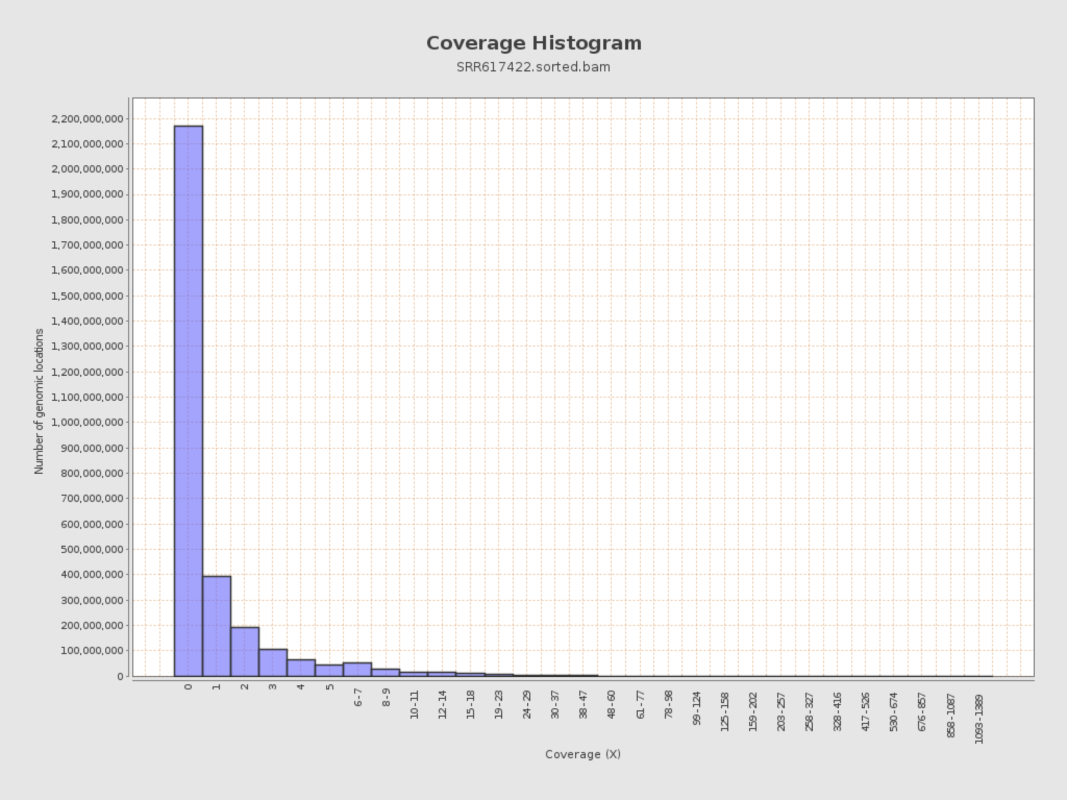
		bases	coverage	deviation
chr1	249250621	194084775	0.7787	2.794
chr2	243199373	300712615	1.2365	3.1912
chr3	198022430	254321117	1.2843	3.4975
chr4	191154276	143781591	0.7522	2.3174
chr5	180915260	192204541	1.0624	2.9092
chr6	171115067	137723809	0.8049	2.658
chr7	159138663	225581797	1.4175	3.3125
chr8	146364022	133277752	0.9106	3.324
chr9	141213431	120546086	0.8536	2.6722
chr10	135534747	97050400	0.7161	2.4957
chr11	135006516	224220108	1.6608	3.9294
chr12	133851895	143773360	1.0741	2.8698
chr13	115169878	130040796	1.1291	2.8177
chr14	107349540	87868998	0.8185	2.9885
chr15	102531392	69492186	0.6778	2.4393
chr16	90354753	76720490	0.8491	3.4216
chr17	81195210	94002505	1.1577	3.8139
chr18	78077248	43113549	0.5522	2.0451
chr19	59128983	43748826	0.7399	2.4032
chr20	63025520	103908942	1.6487	4.9223
chr21	48129895	41357232	0.8593	2.5795
chr22	51304566	24830374	0.484	2.1814
chrMT	16571	200784	12.1166	5.7266
chrX	155270560	131898254	0.8495	2.6318

chrY	59373566	2467997	0.0416	0.6491

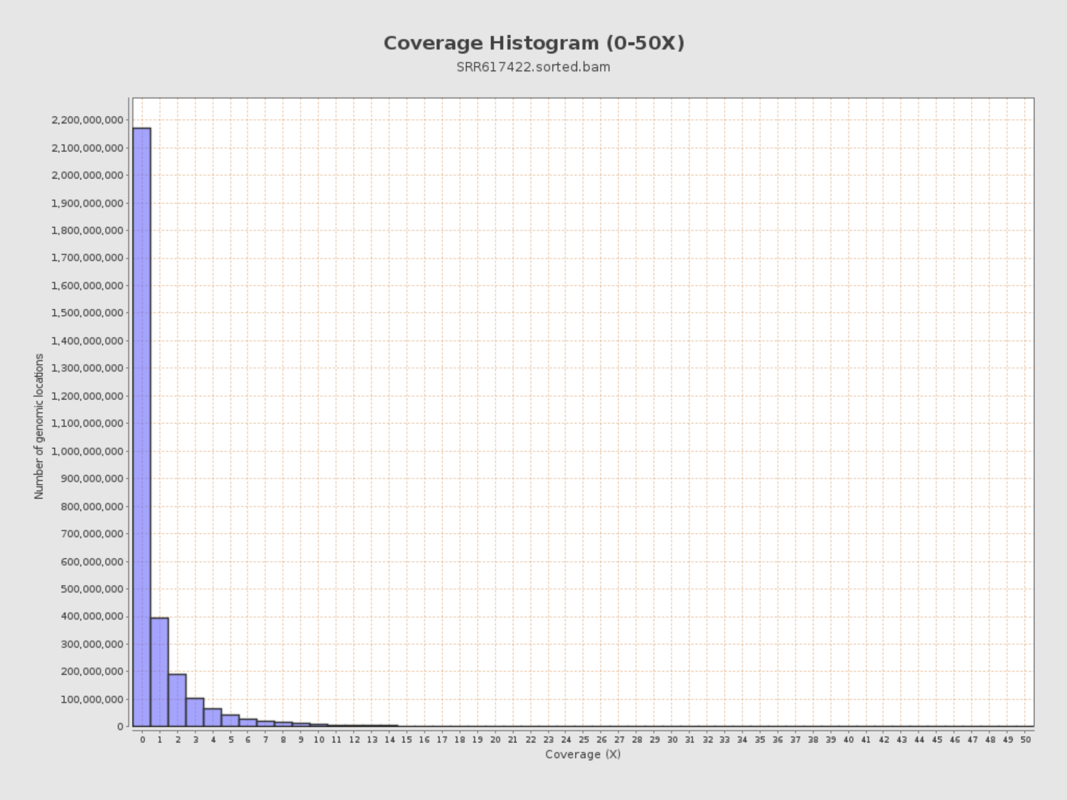
3. Results : Coverage across reference



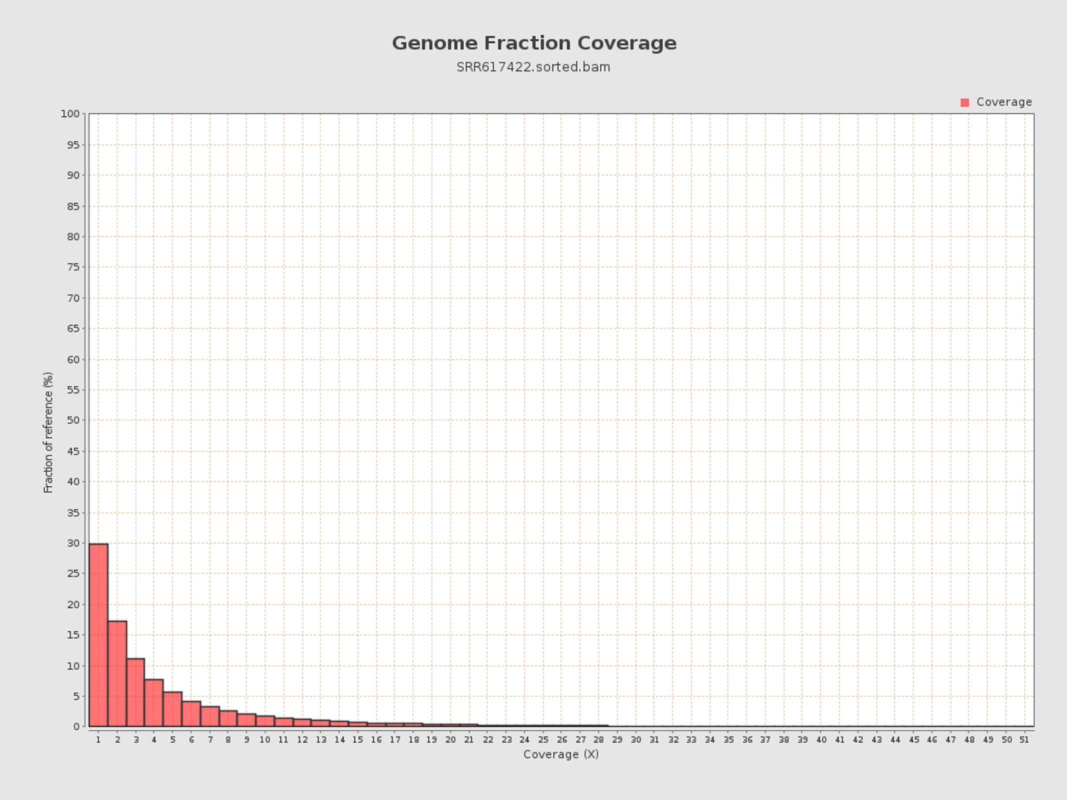
4. Results : Coverage Histogram



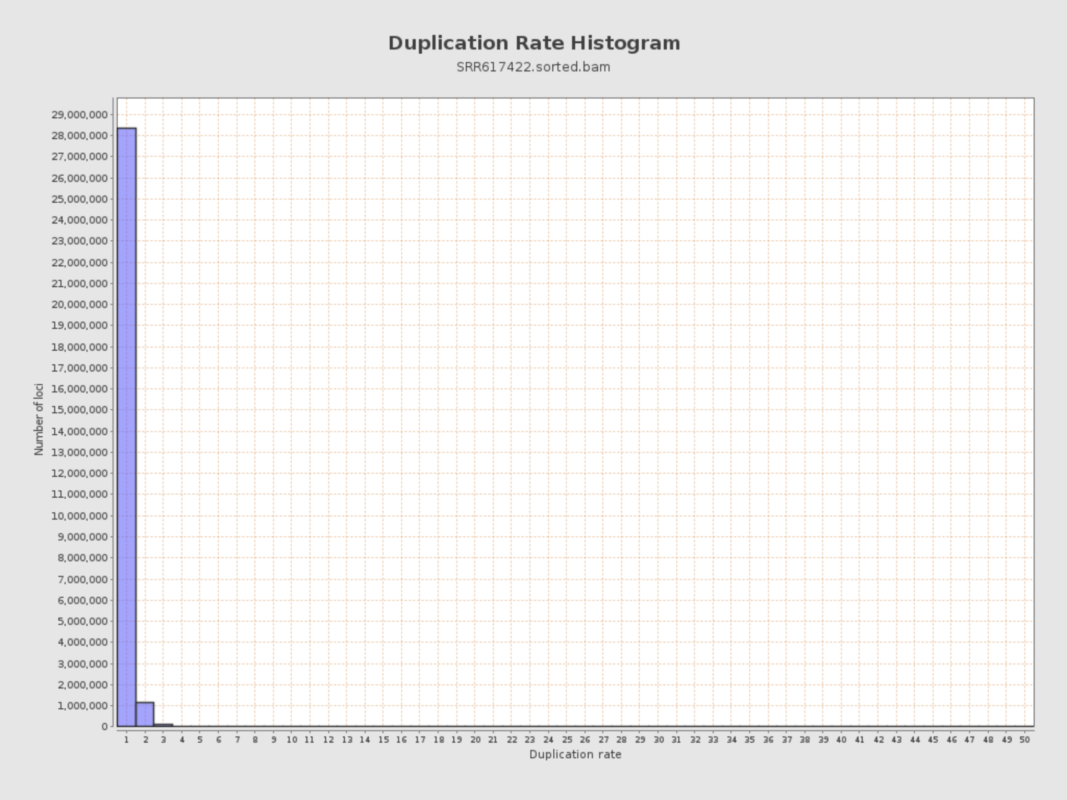
5. Results : Coverage Histogram (0-50X)



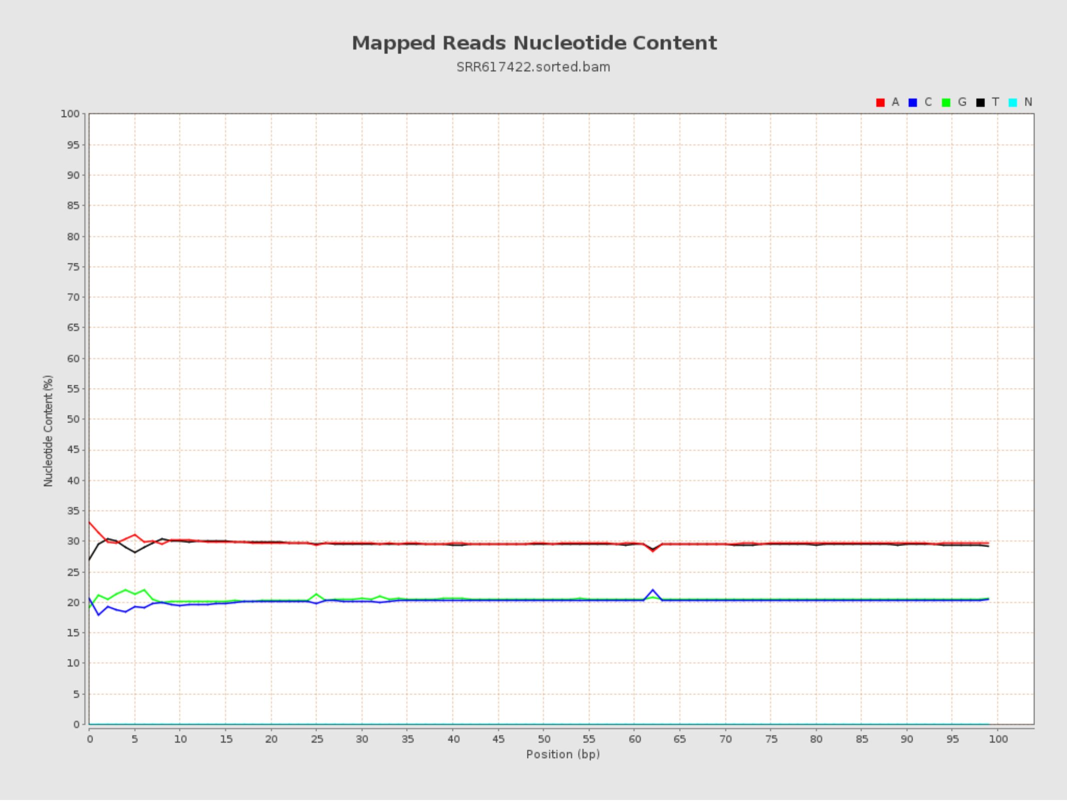
6. Results : Genome Fraction Coverage



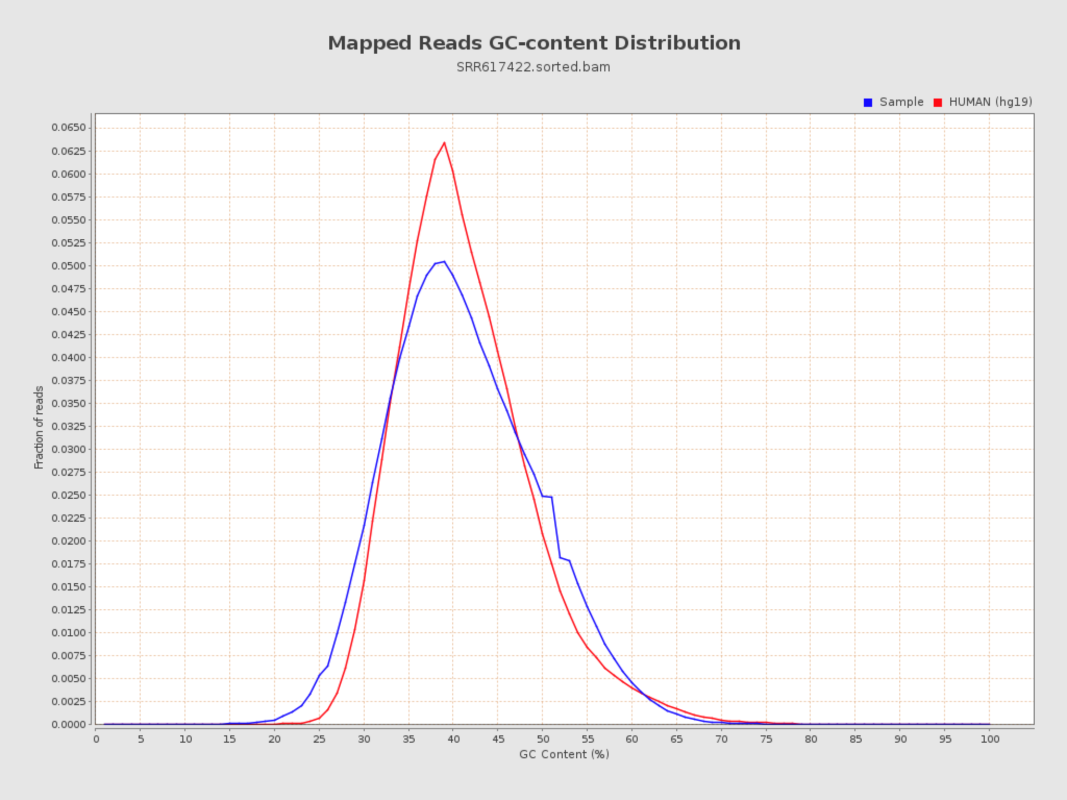
7. Results : Duplication Rate Histogram



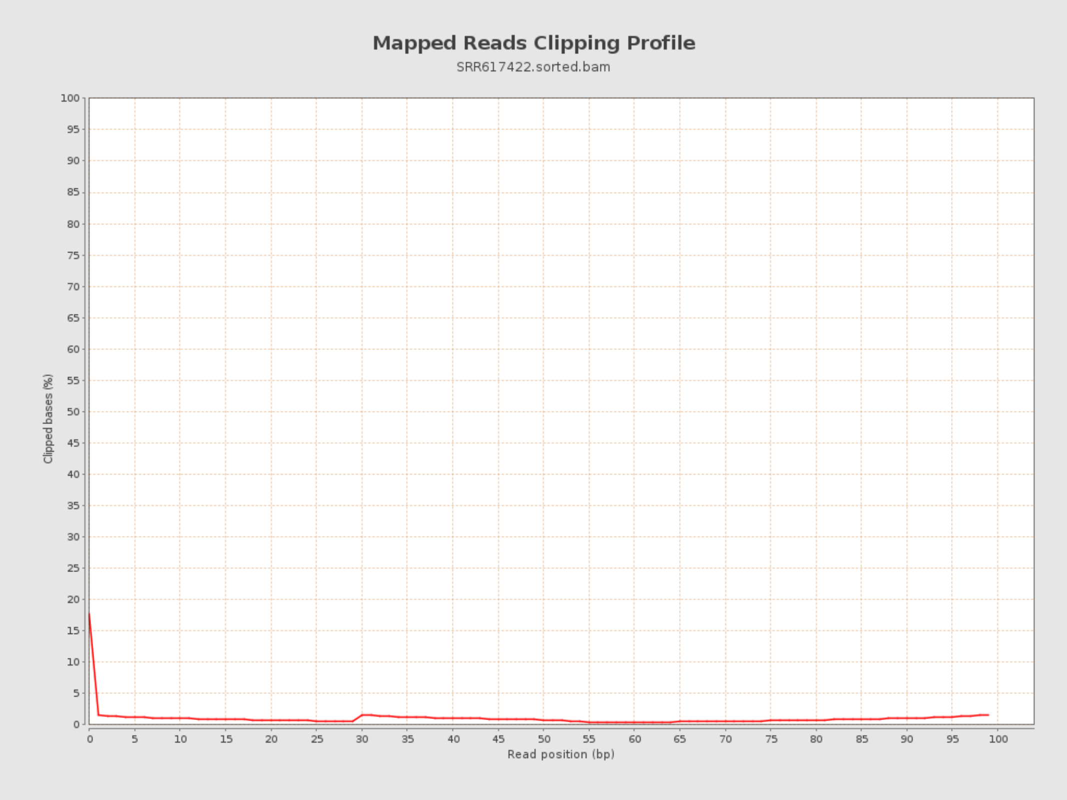
8. Results : Mapped Reads Nucleotide Content



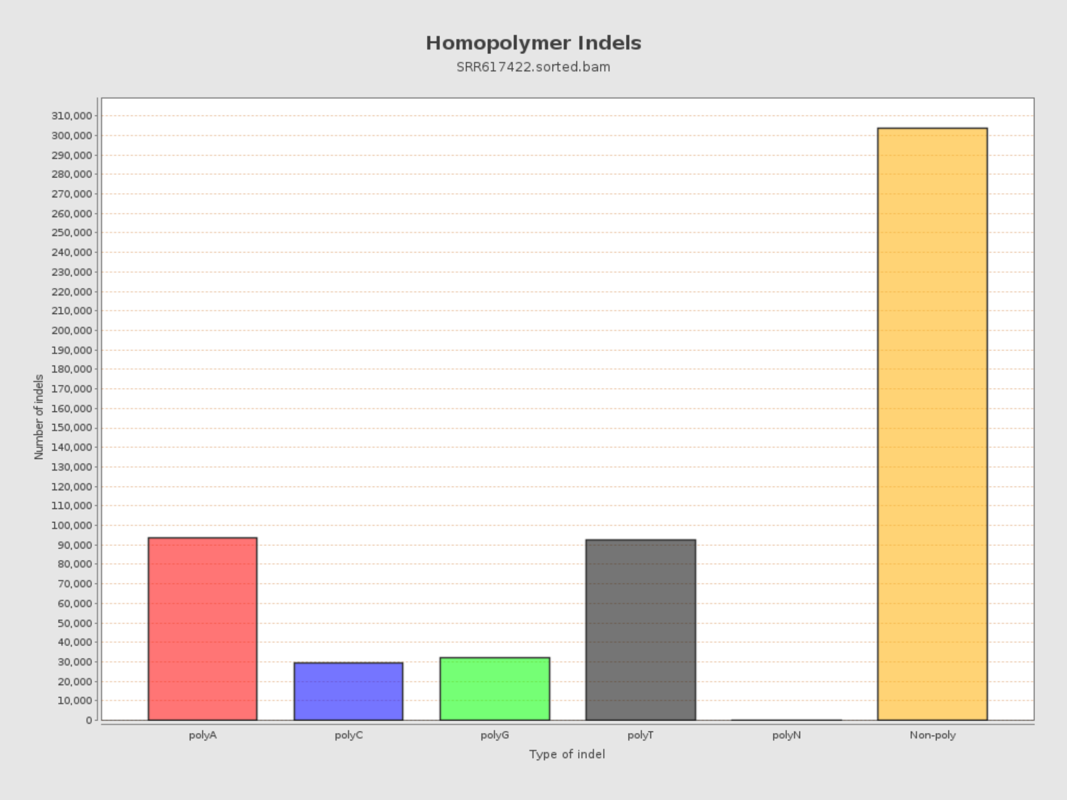
9. Results : Mapped Reads GC-content Distribution



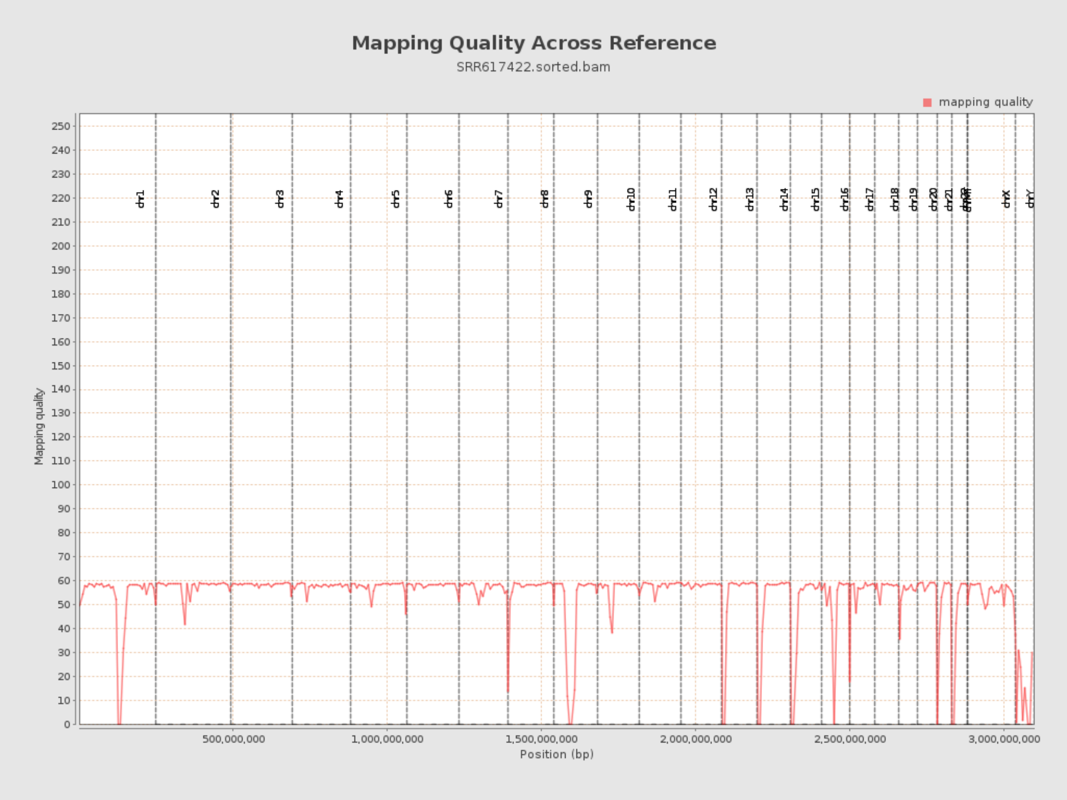
10. Results : Mapped Reads Clipping Profile



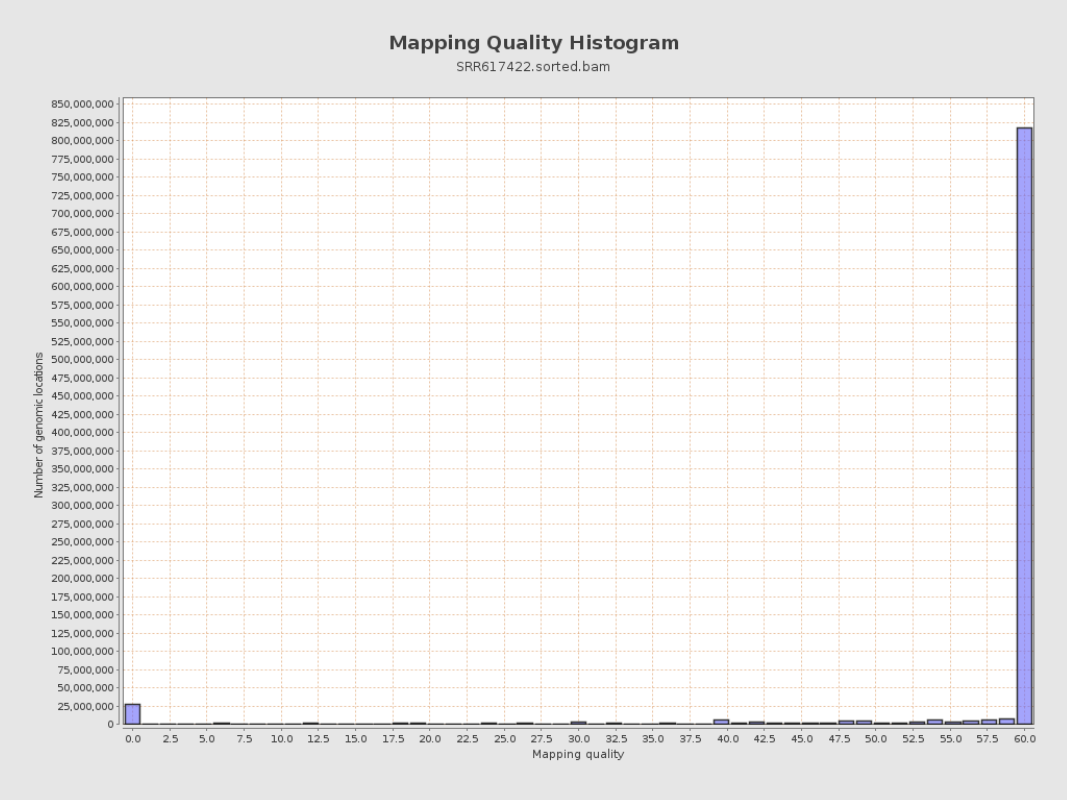
11. Results : Homopolymer Indels



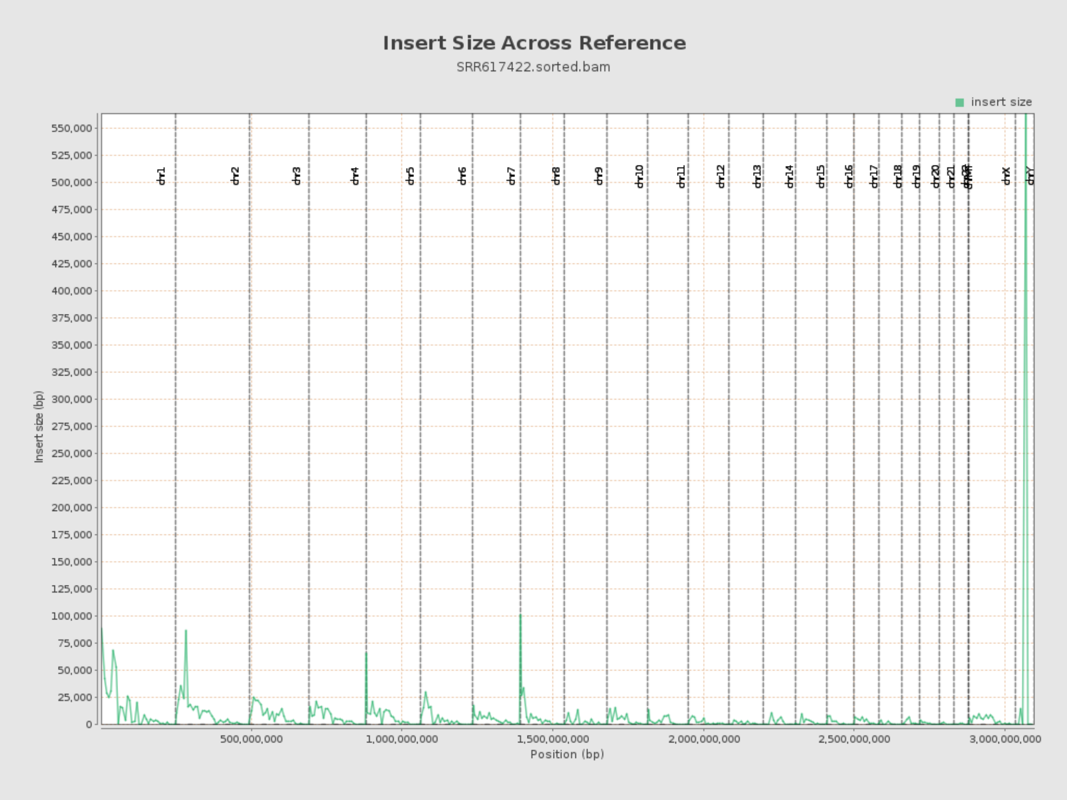
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram