Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/09 04:41:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617417.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_SRR617417 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617417_1.fastq.gz SRR617417_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 09 04:41:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617417.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	30,023,822 / 93.82%
Unmapped reads	1,976,178 / 6.18%
Mapped paired reads	30,023,822 / 93.82%
Mapped reads, first in pair	15,154,886 / 47.36%
Mapped reads, second in pair	14,868,936 / 46.47%
Mapped reads, both in pair	29,450,286 / 92.03%
Mapped reads, singletons	573,536 / 1.79%
Secondary alignments	0
Supplementary alignments	493,588 / 1.54%
Read min/max/mean length	30 / 100 / 100.63
Duplicated reads (estimated)	1,421,997 / 4.44%
Duplication rate	4.22%
Clipped reads	3,195,574 / 9.99%

2.2. ACGT Content

Number/percentage of A's	881,835,552 / 29.84%
Number/percentage of C's	594,090,271 / 20.1%
Number/percentage of T's	873,733,011 / 29.57%
Number/percentage of G's	604,835,513 / 20.47%
Number/percentage of N's	697,738 / 0.02%

GC Percentage	40.57%

2.3. Coverage

Mean	0.9548
Standard Deviation	2.9433

2.4. Mapping Quality

Mean Mapping Quality	53.9

2.5. Insert size

Mean	61,225.43
Standard Deviation	2,367,692.33
P25/Median/P75	171 / 210 / 273

2.6. Mismatches and indels

General error rate	0.89%
Mismatches	25,848,968
Insertions	243,627
Mapped reads with at least one insertion	0.8%
Deletions	290,826
Mapped reads with at least one deletion	0.95%
Homopolymer indels	45.01%

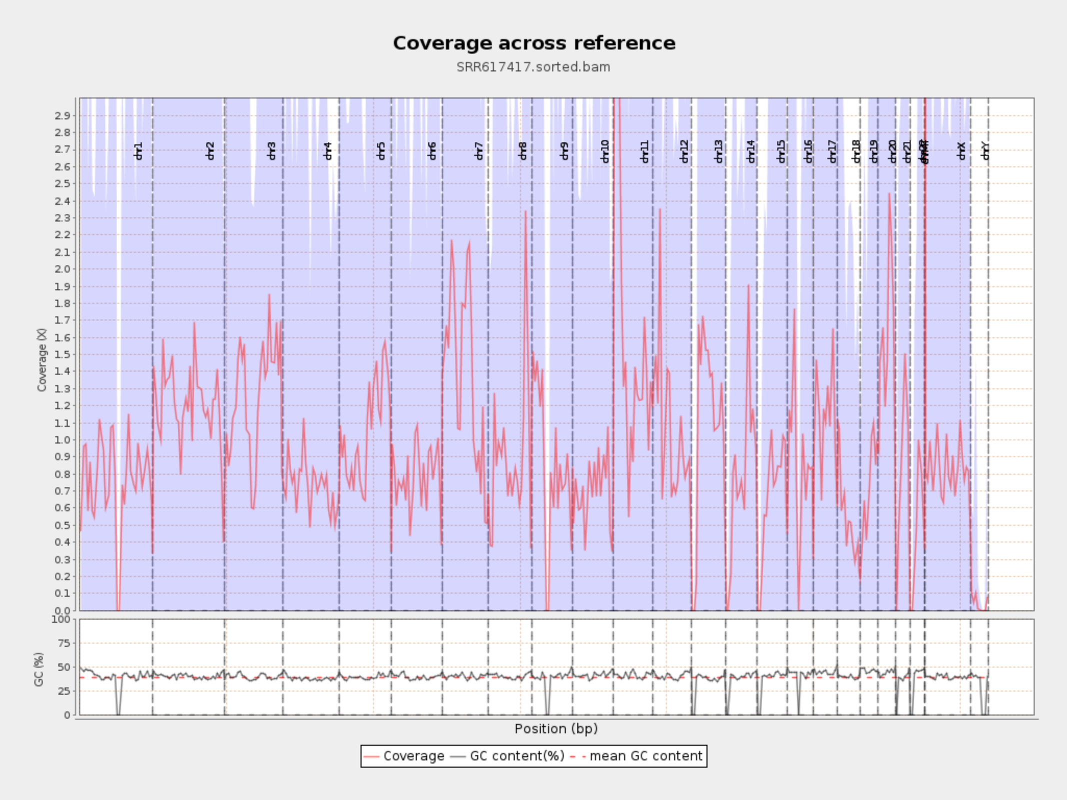
2.7. Chromosome stats

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

		bases	coverage	deviation
chr1	249250621	190350788	0.7637	2.7539
chr2	243199373	295005137	1.213	3.1424
chr3	198022430	249387867	1.2594	3.4218
chr4	191154276	141502322	0.7403	2.2871
chr5	180915260	188981910	1.0446	2.8646
chr6	171115067	135221878	0.7902	2.6051
chr7	159138663	221020093	1.3889	3.2432
chr8	146364022	130840120	0.8939	3.2693
chr9	141213431	118218837	0.8372	2.6248
chr10	135534747	94801333	0.6995	2.426
chr11	135006516	219464946	1.6256	3.843
chr12	133851895	140777282	1.0517	2.8423
chr13	115169878	128041939	1.1118	2.7765
chr14	107349540	85542806	0.7969	2.8954
chr15	102531392	67749380	0.6608	2.3903
chr16	90354753	74807495	0.8279	3.343
chr17	81195210	91566623	1.1277	3.7581
chr18	78077248	42375366	0.5427	2.0194
chr19	59128983	42485196	0.7185	2.3479
chr20	63025520	101235711	1.6063	4.7514
chr21	48129895	40378216	0.8389	2.5199
chr22	51304566	24042571	0.4686	2.1087
chrMT	16571	180687	10.9038	5.3918
chrX	155270560	129483381	0.8339	2.578

chrY	59373566	2388716	0.0402	0.6368

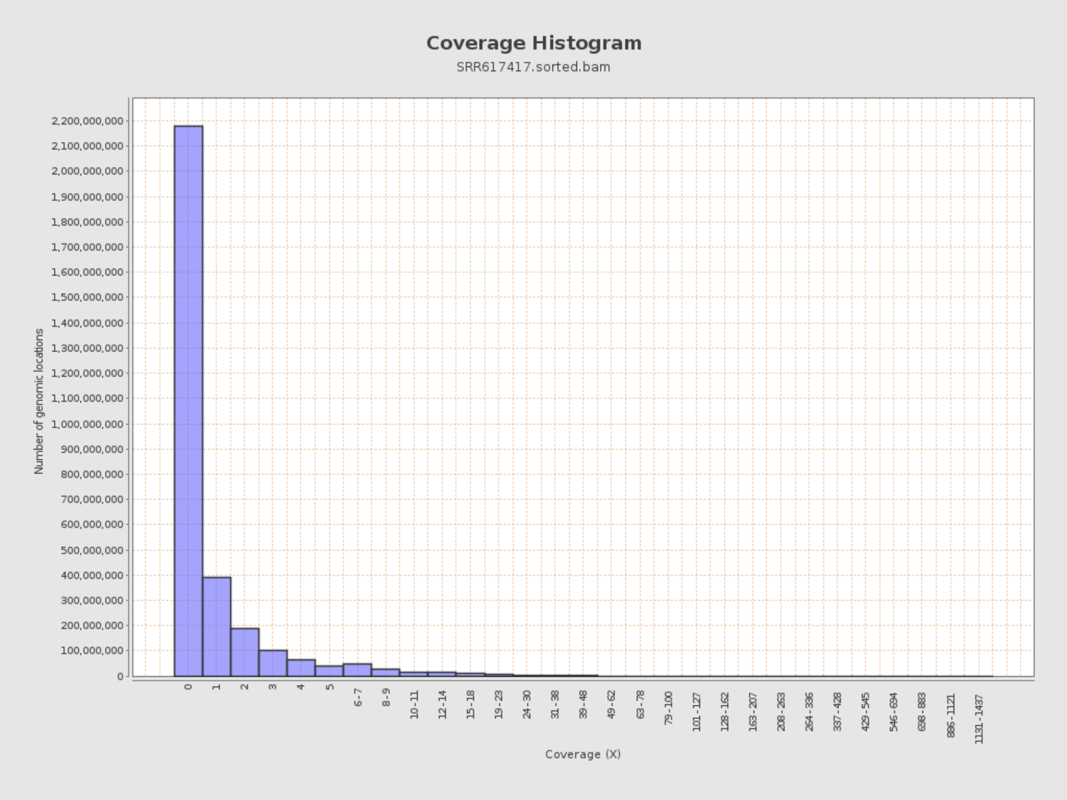
3. Results : Coverage across reference



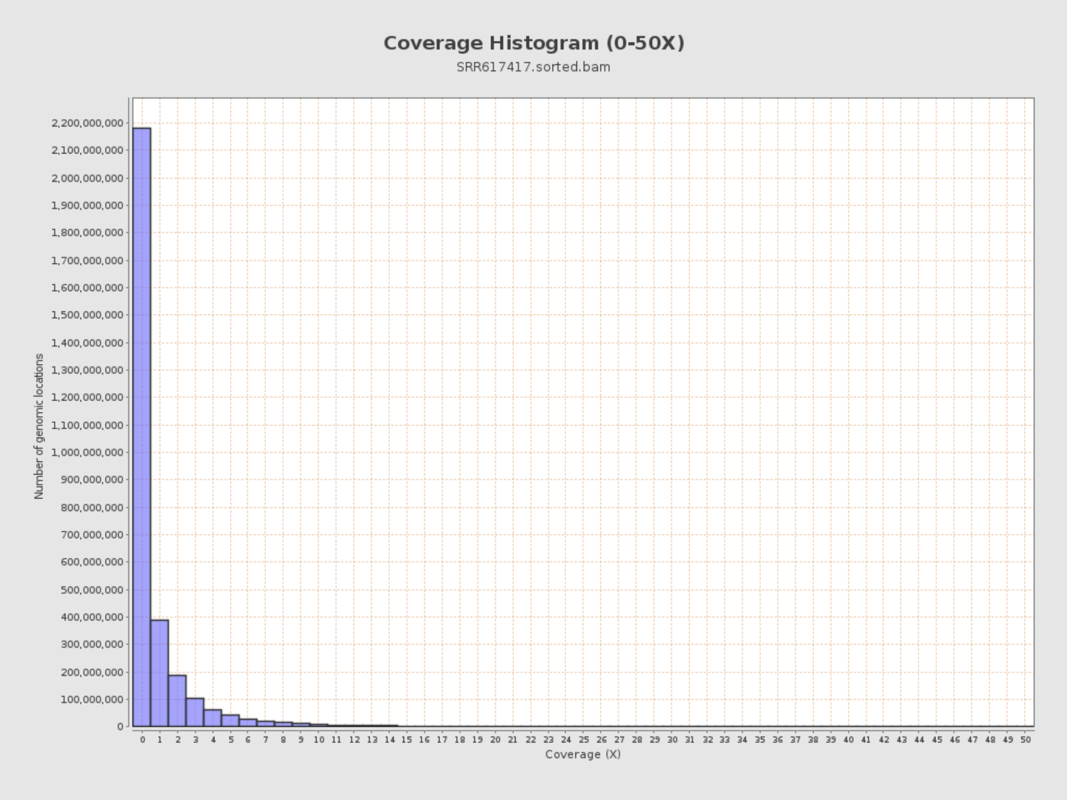
Coverage across reference

SRR617417.sorted.bam

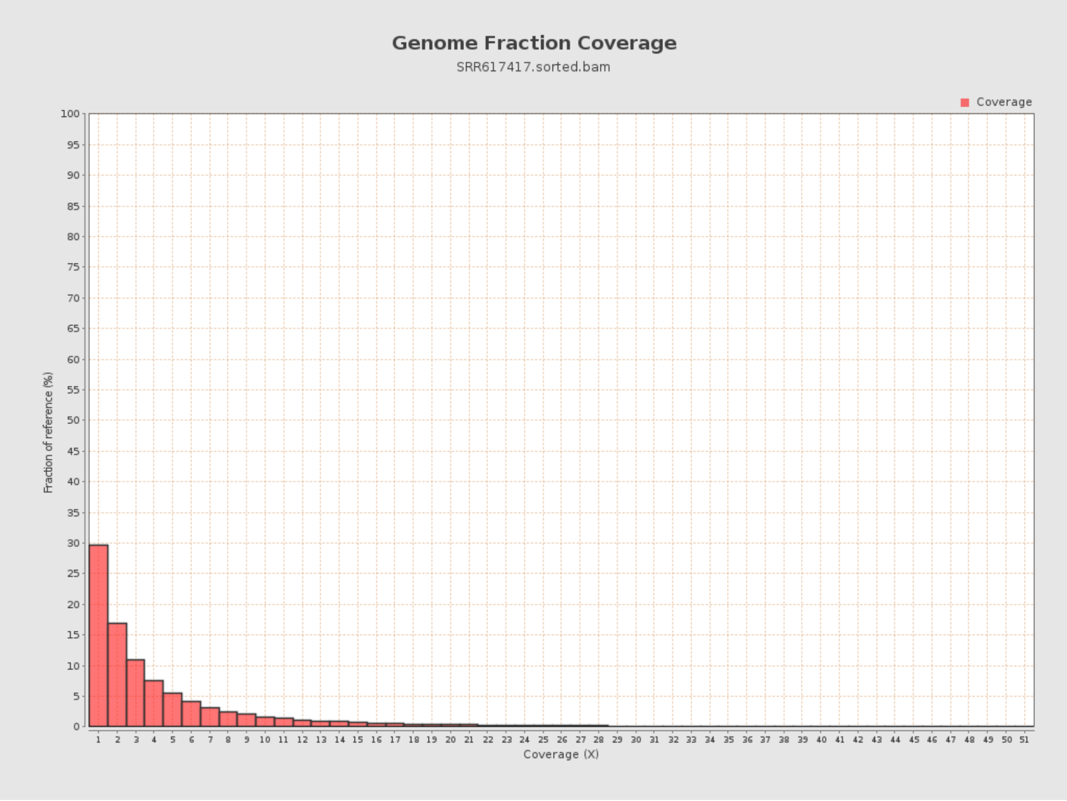
4. Results : Coverage Histogram



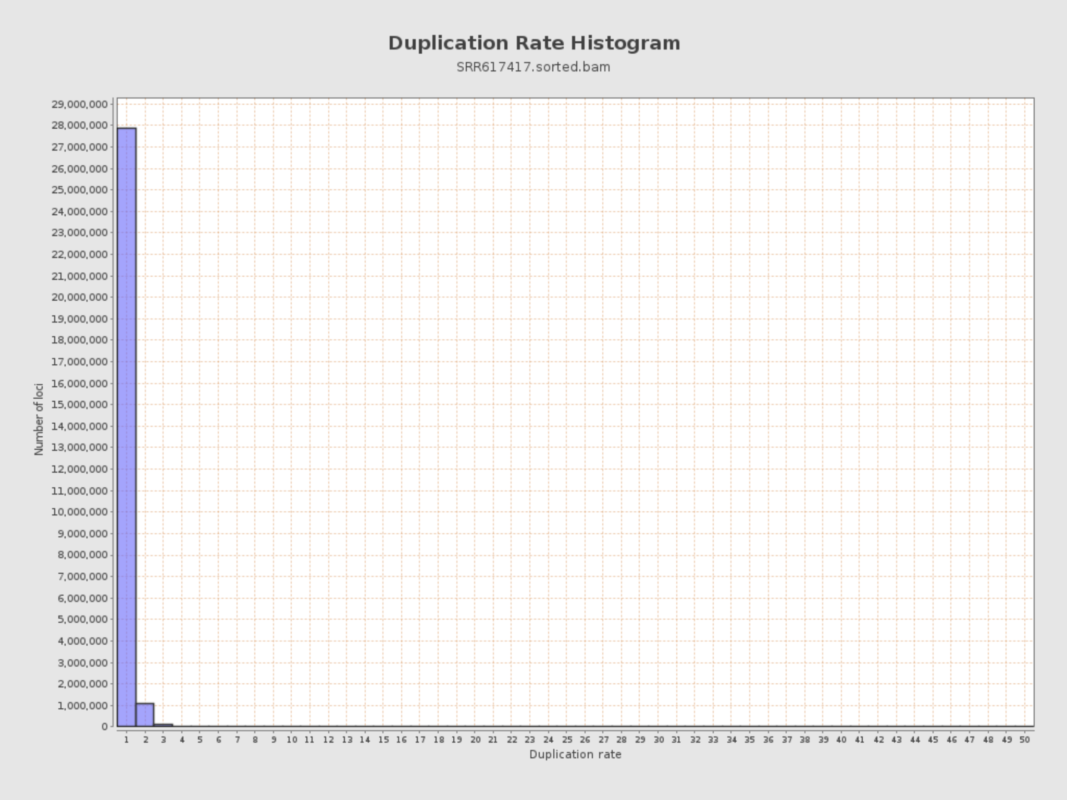
5. Results : Coverage Histogram (0-50X)



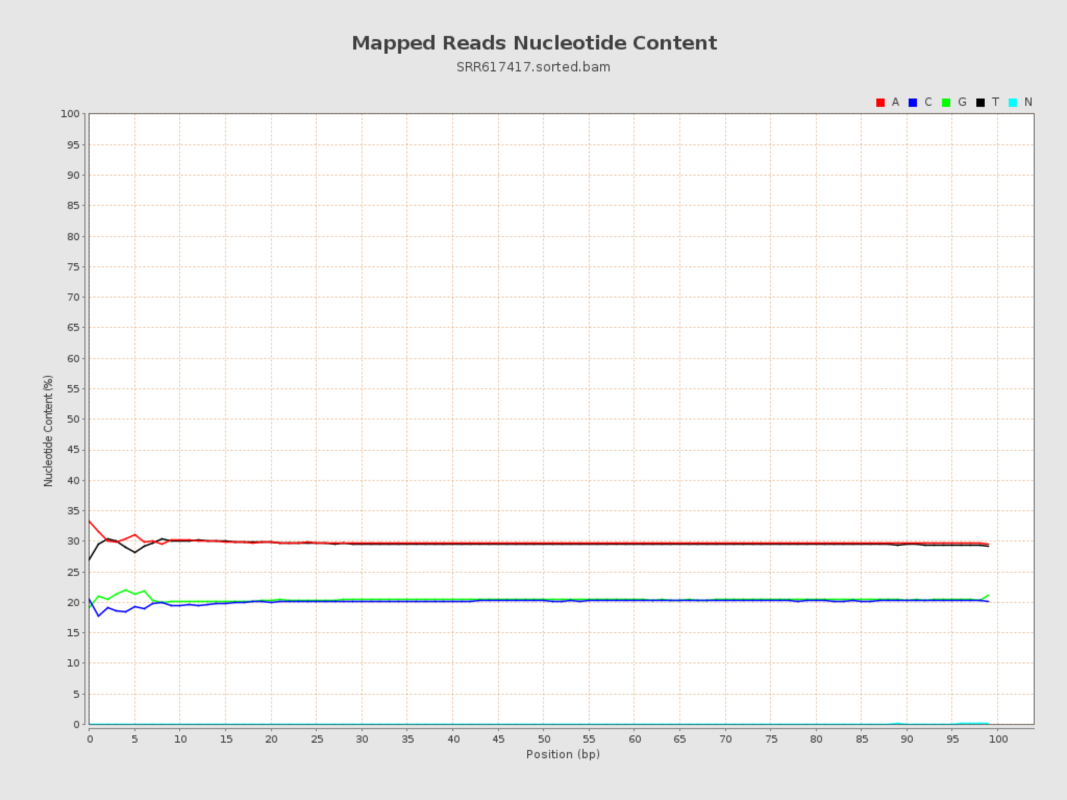
6. Results : Genome Fraction Coverage



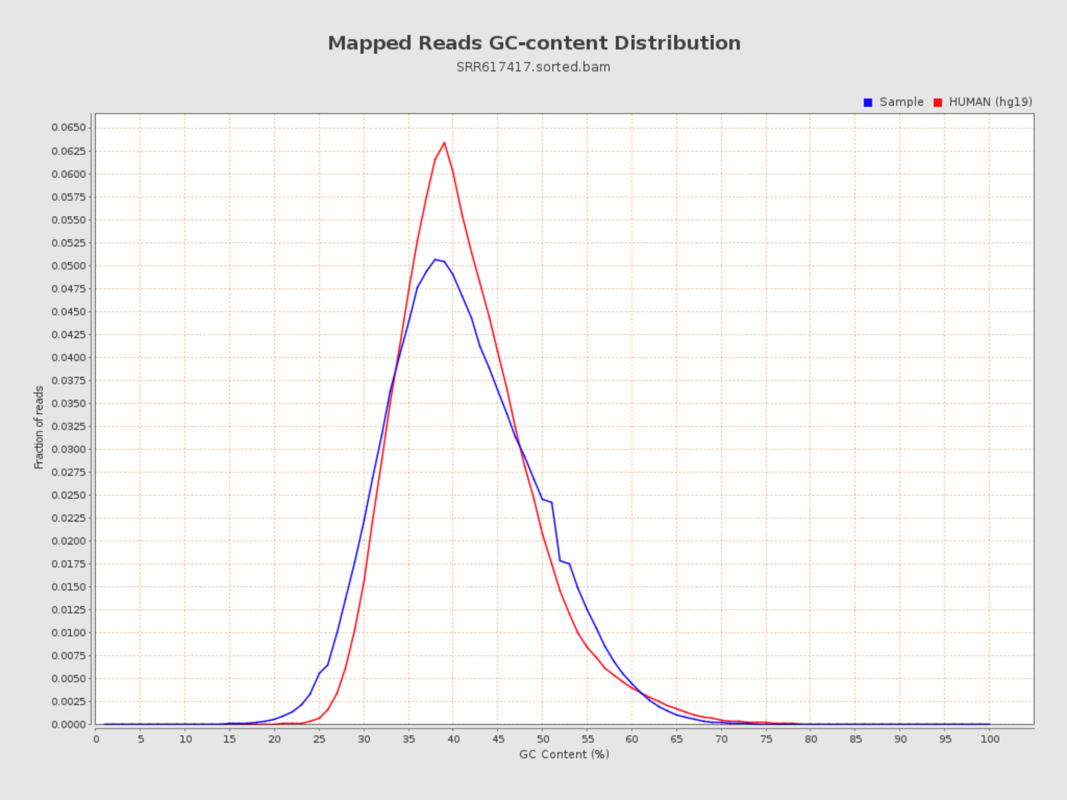
7. Results : Duplication Rate Histogram



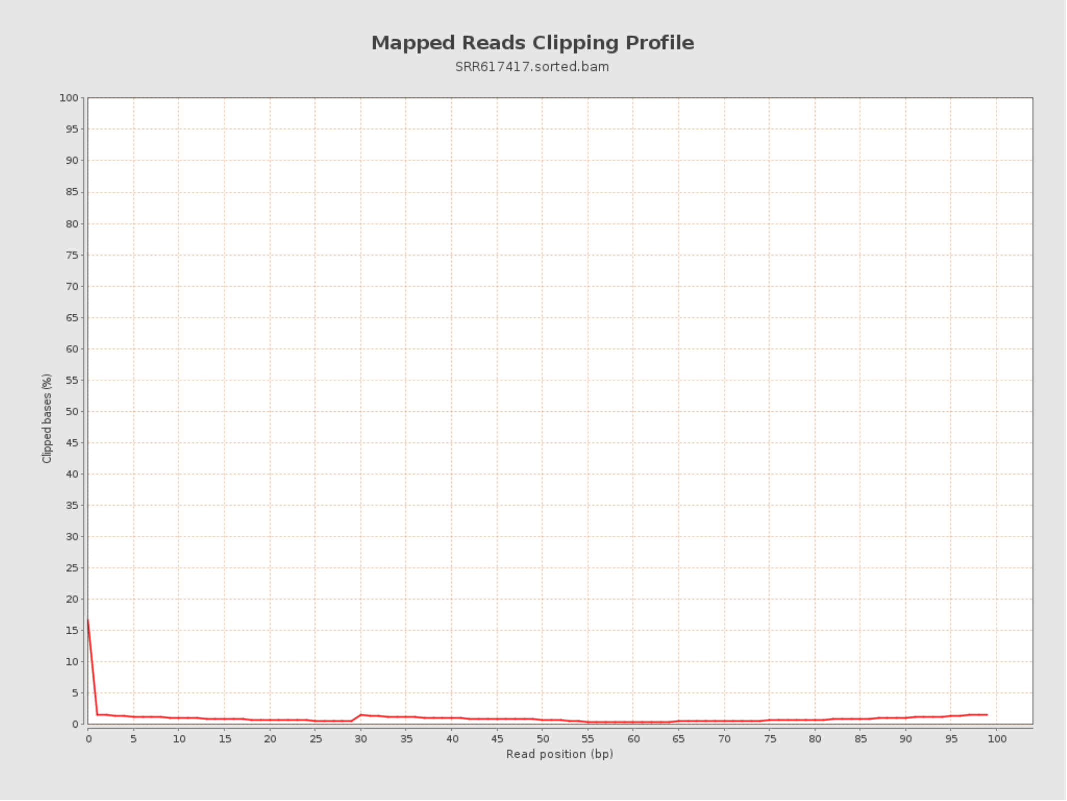
8. Results : Mapped Reads Nucleotide Content



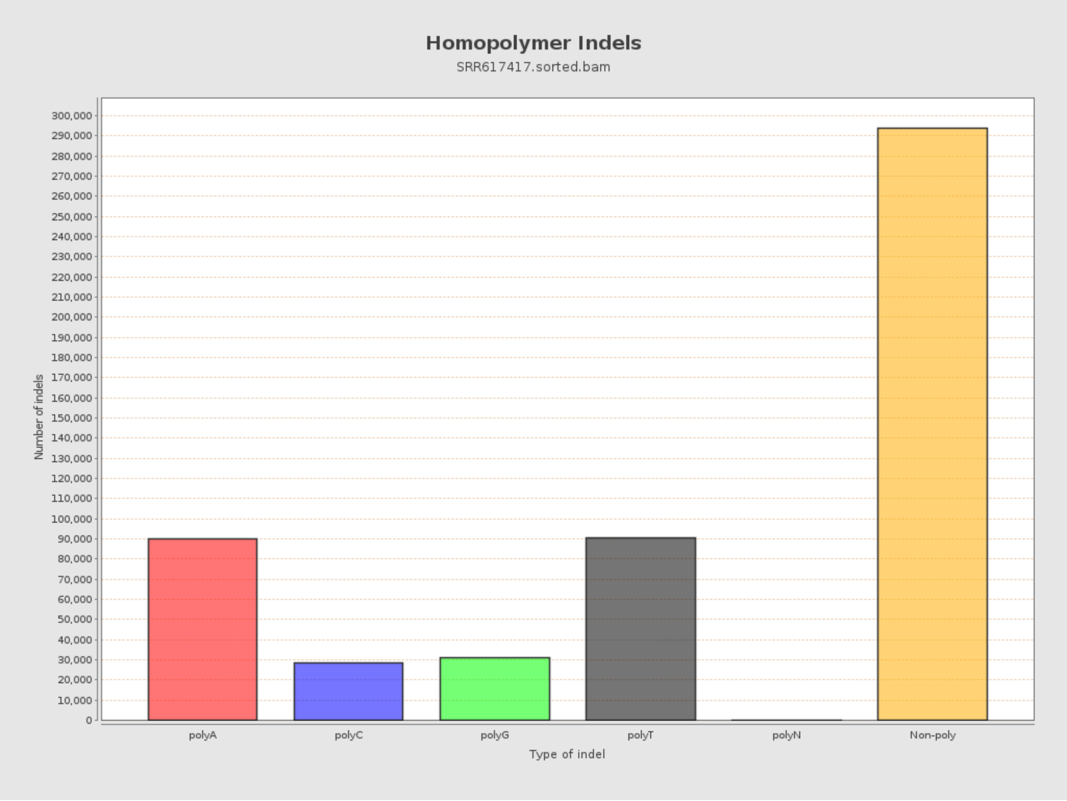
9. Results : Mapped Reads GC-content Distribution



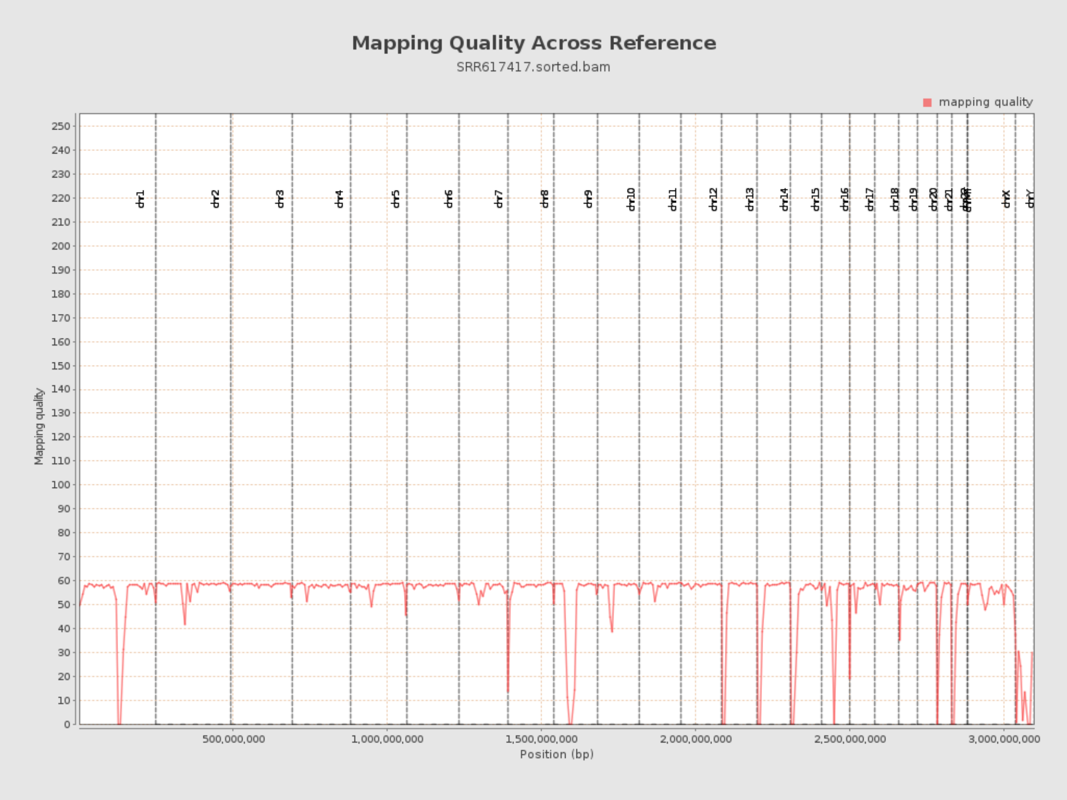
10. Results : Mapped Reads Clipping Profile



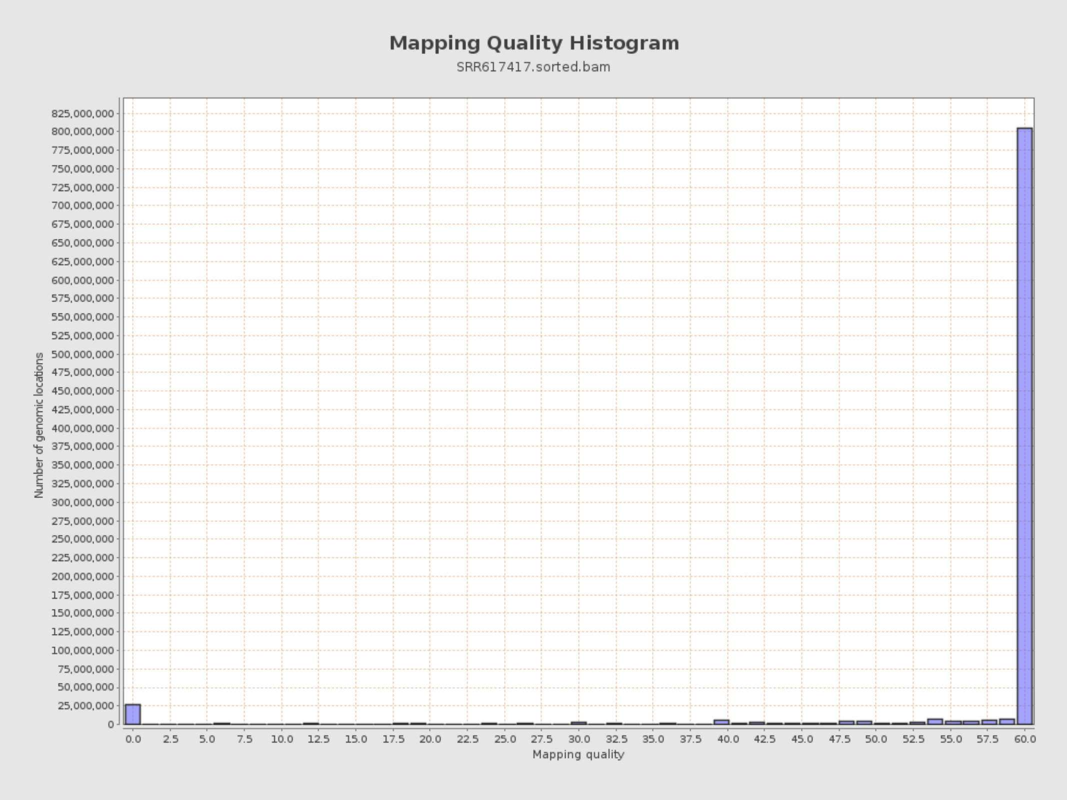
11. Results : Homopolymer Indels



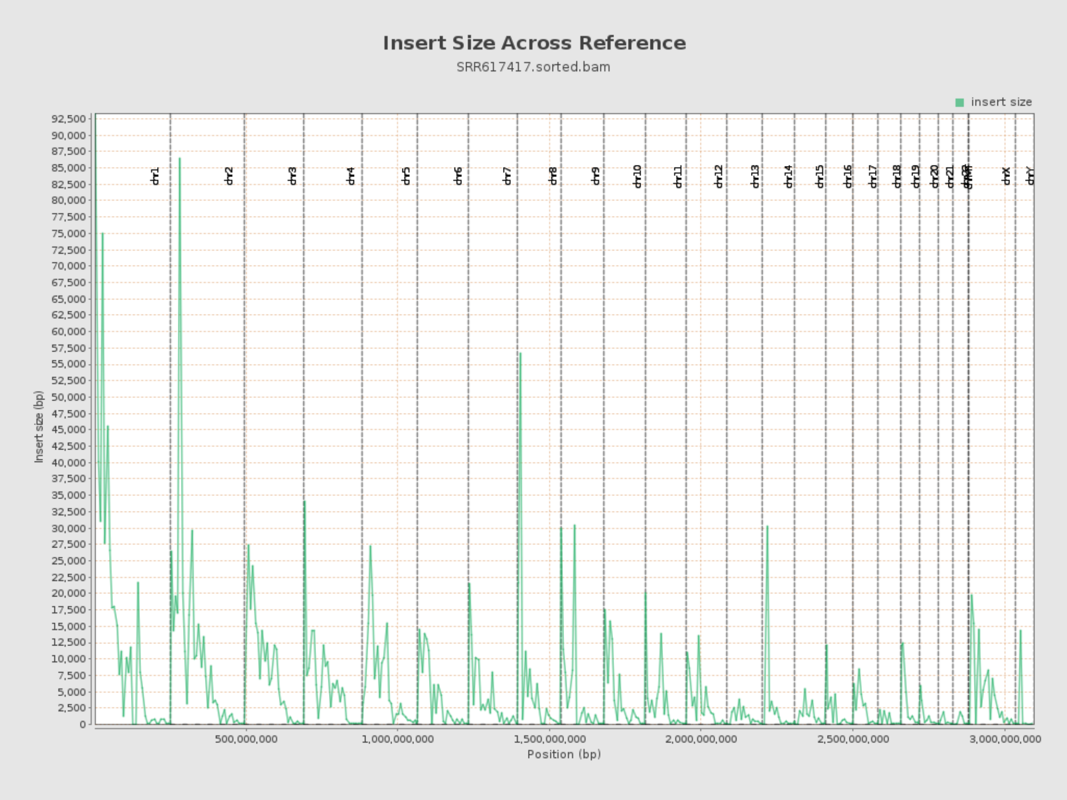
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram