Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/09 06:38:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617420.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_SRR617420 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617420_1.fastq.gz SRR617420_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 09 06:38:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617420.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	30,247,224 / 94.52%
Unmapped reads	1,752,776 / 5.48%
Mapped paired reads	30,247,224 / 94.52%
Mapped reads, first in pair	15,250,878 / 47.66%
Mapped reads, second in pair	14,996,346 / 46.86%
Mapped reads, both in pair	29,702,096 / 92.82%
Mapped reads, singletons	545,128 / 1.7%
Secondary alignments	0
Supplementary alignments	496,808 / 1.55%
Read min/max/mean length	30 / 100 / 100.64
Duplicated reads (estimated)	1,429,708 / 4.47%
Duplication rate	4.23%
Clipped reads	3,150,400 / 9.85%

2.2. ACGT Content

Number/percentage of A's	889,034,652 / 29.85%
Number/percentage of C's	599,001,698 / 20.11%
Number/percentage of T's	880,963,593 / 29.58%
Number/percentage of G's	609,124,760 / 20.45%
Number/percentage of N's	281,030 / 0.01%

GC Percentage	40.56%

2.3. Coverage

Mean	0.9623
Standard Deviation	2.9596

2.4. Mapping Quality

Mean Mapping Quality	53.91

2.5. Insert size

Mean	59,036.93
Standard Deviation	2,317,484.42
P25/Median/P75	171 / 210 / 271

2.6. Mismatches and indels

General error rate	0.86%
Mismatches	25,276,318
Insertions	245,351
Mapped reads with at least one insertion	0.8%
Deletions	293,164
Mapped reads with at least one deletion	0.95%
Homopolymer indels	45.14%

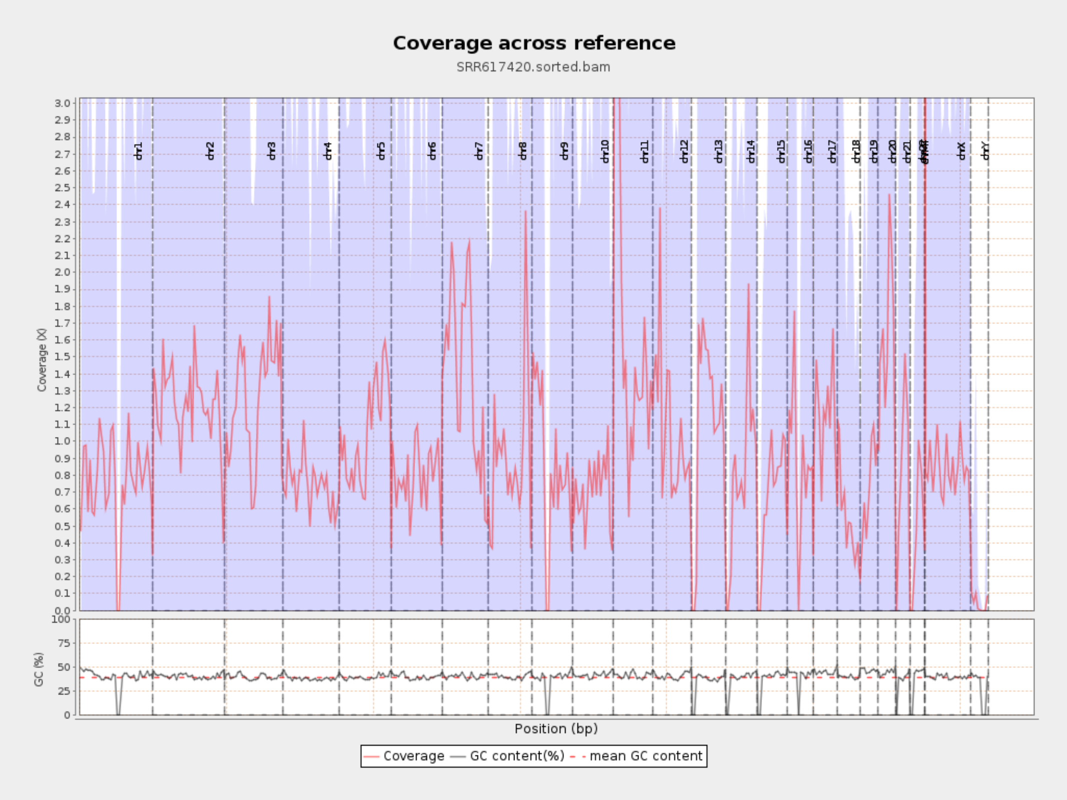
2.7. Chromosome stats

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

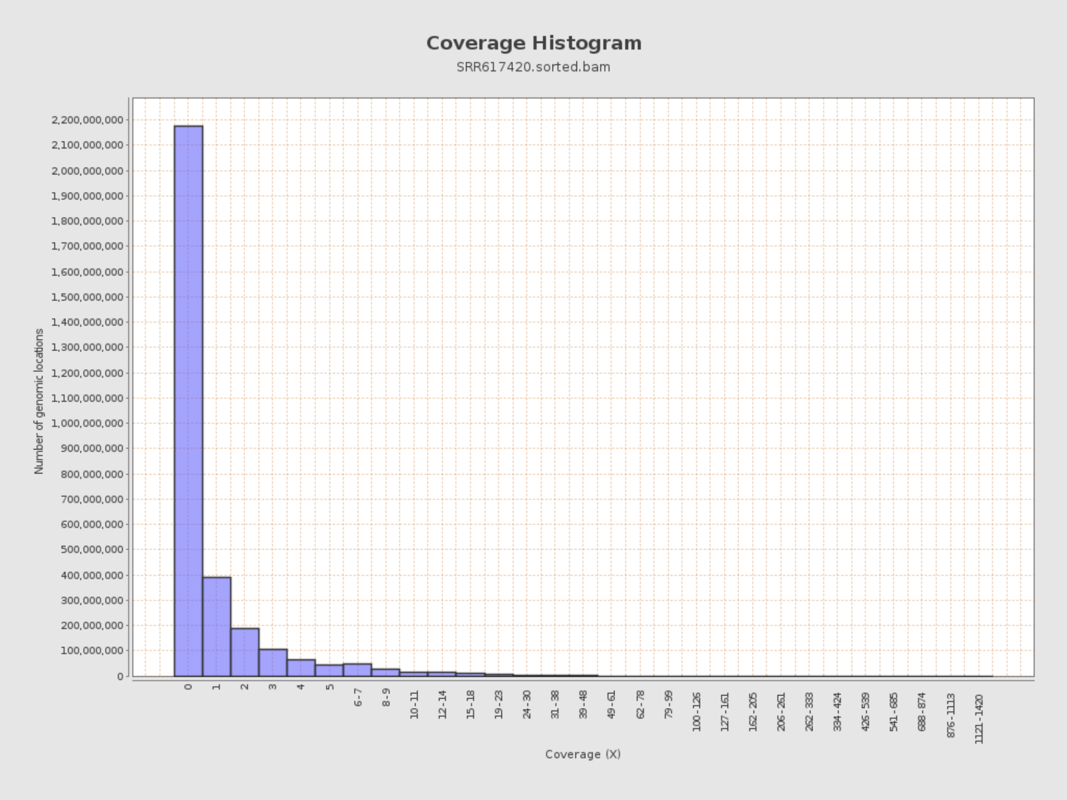
		bases	coverage	deviation
chr1	249250621	191763162	0.7694	2.7853
chr2	243199373	296966010	1.2211	3.1468
chr3	198022430	251508615	1.2701	3.4486
chr4	191154276	142707220	0.7466	2.2939
chr5	180915260	190245800	1.0516	2.8871
chr6	171115067	136196539	0.7959	2.6234
chr7	159138663	222647388	1.3991	3.2631
chr8	146364022	131791332	0.9004	3.2913
chr9	141213431	119172759	0.8439	2.6325
chr10	135534747	95661060	0.7058	2.4381
chr11	135006516	221799270	1.6429	3.8735
chr12	133851895	141953727	1.0605	2.8167
chr13	115169878	129012491	1.1202	2.7865
chr14	107349540	86574531	0.8065	2.9141
chr15	102531392	68405379	0.6672	2.3972
chr16	90354753	75286199	0.8332	3.3499
chr17	81195210	92250849	1.1362	3.7838
chr18	78077248	42553850	0.545	2.0314
chr19	59128983	42667274	0.7216	2.3492
chr20	63025520	101703271	1.6137	4.7973
chr21	48129895	40699808	0.8456	2.5554
chr22	51304566	24175158	0.4712	2.1156
chrMT	16571	183218	11.0565	5.0997
chrX	155270560	130727655	0.8419	2.5929

chrY	59373566	2416433	0.0407	0.6262

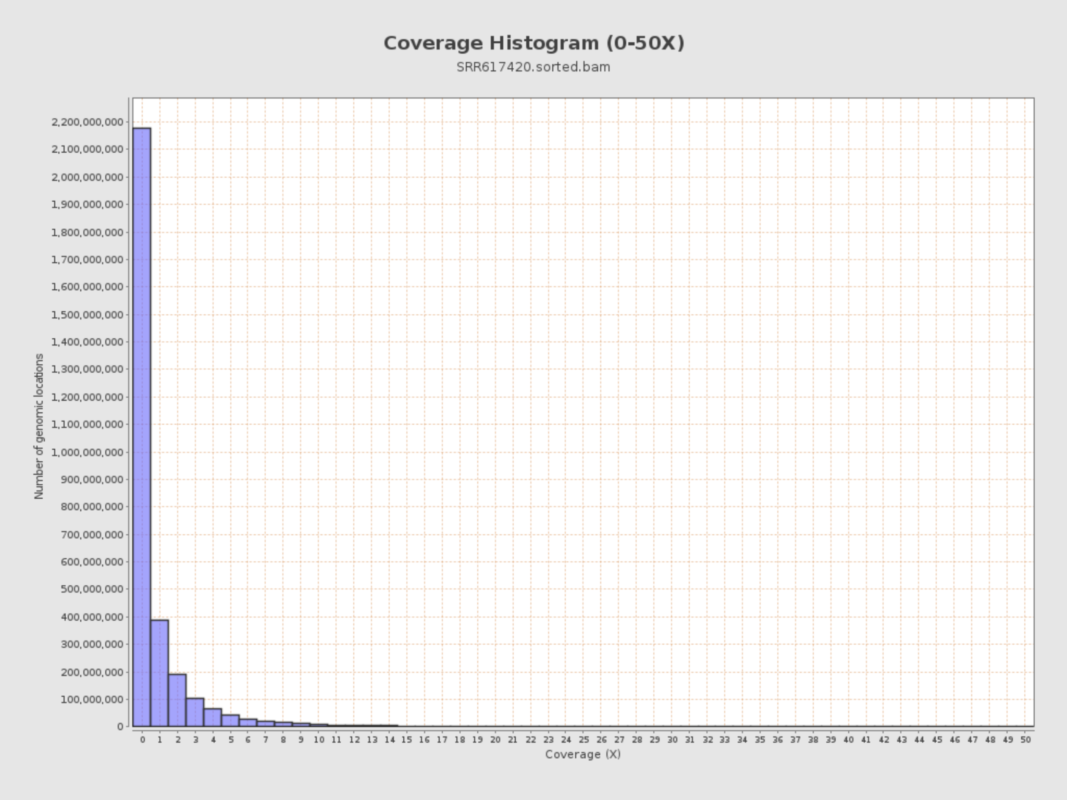
3. Results : Coverage across reference



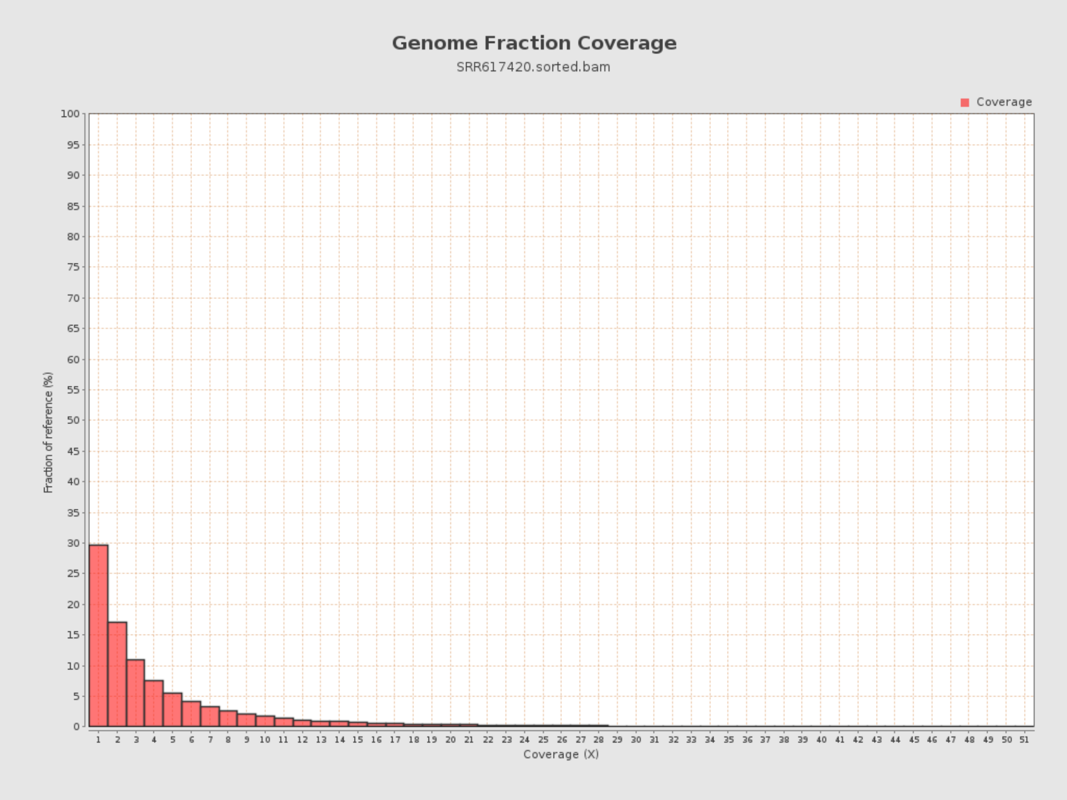
4. Results : Coverage Histogram



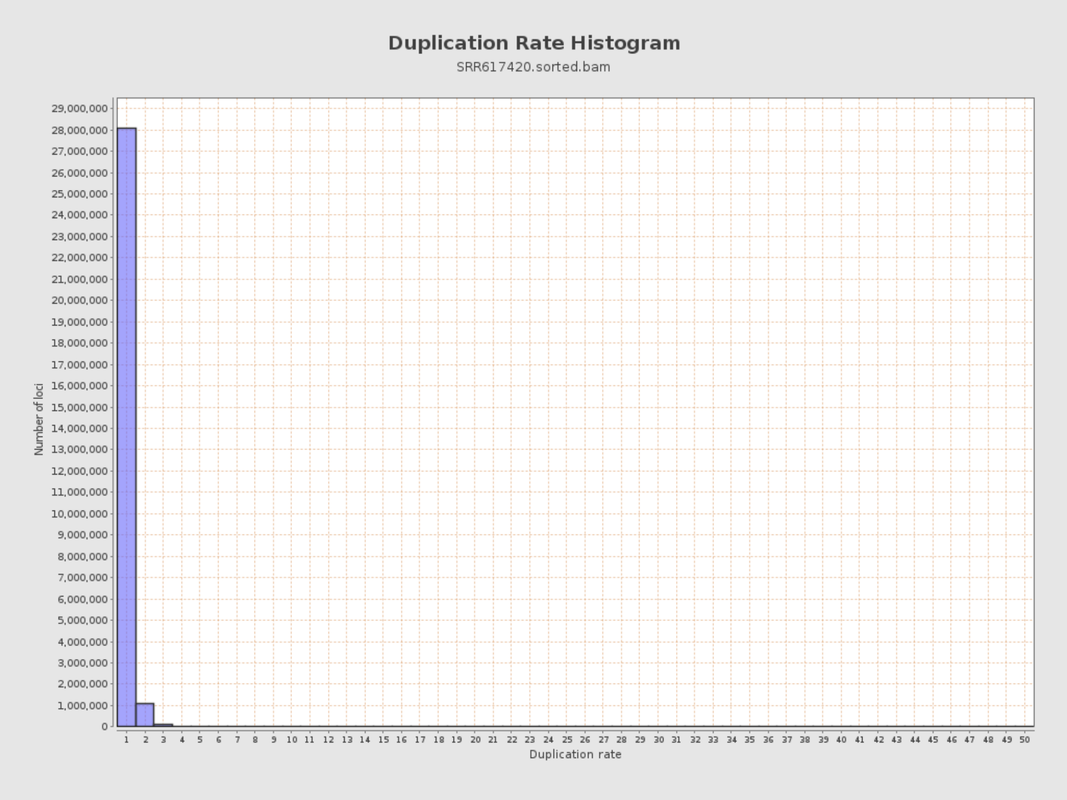
5. Results : Coverage Histogram (0-50X)



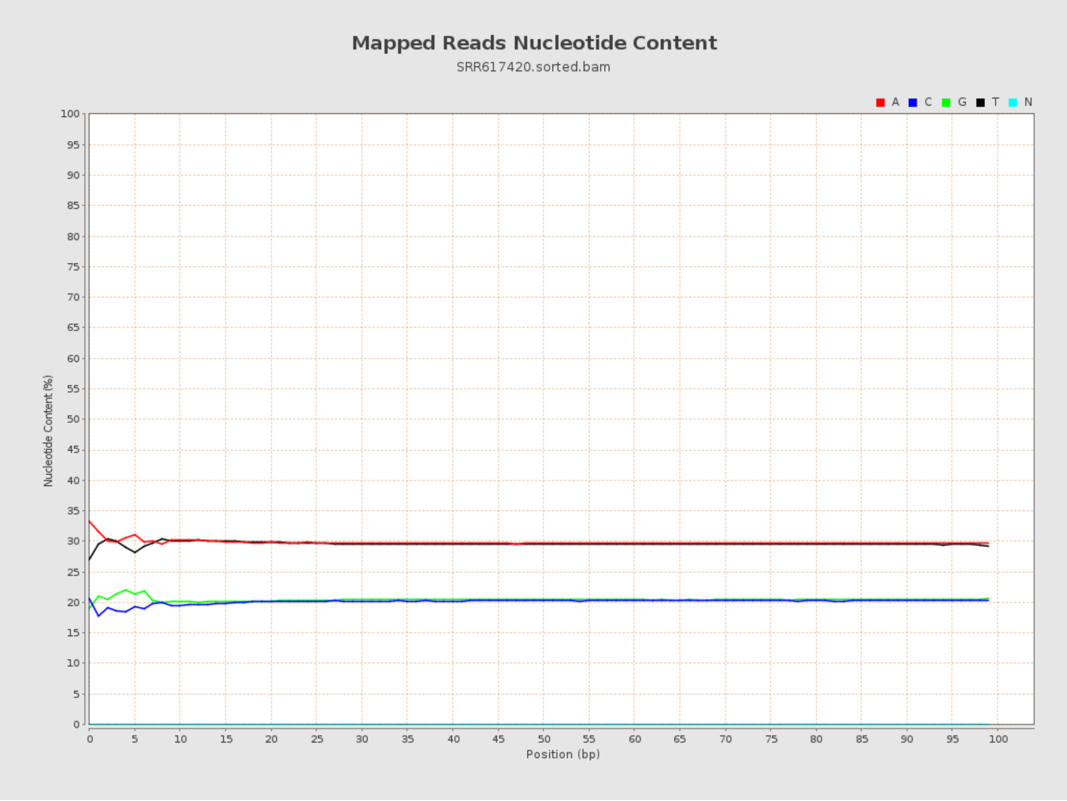
6. Results : Genome Fraction Coverage



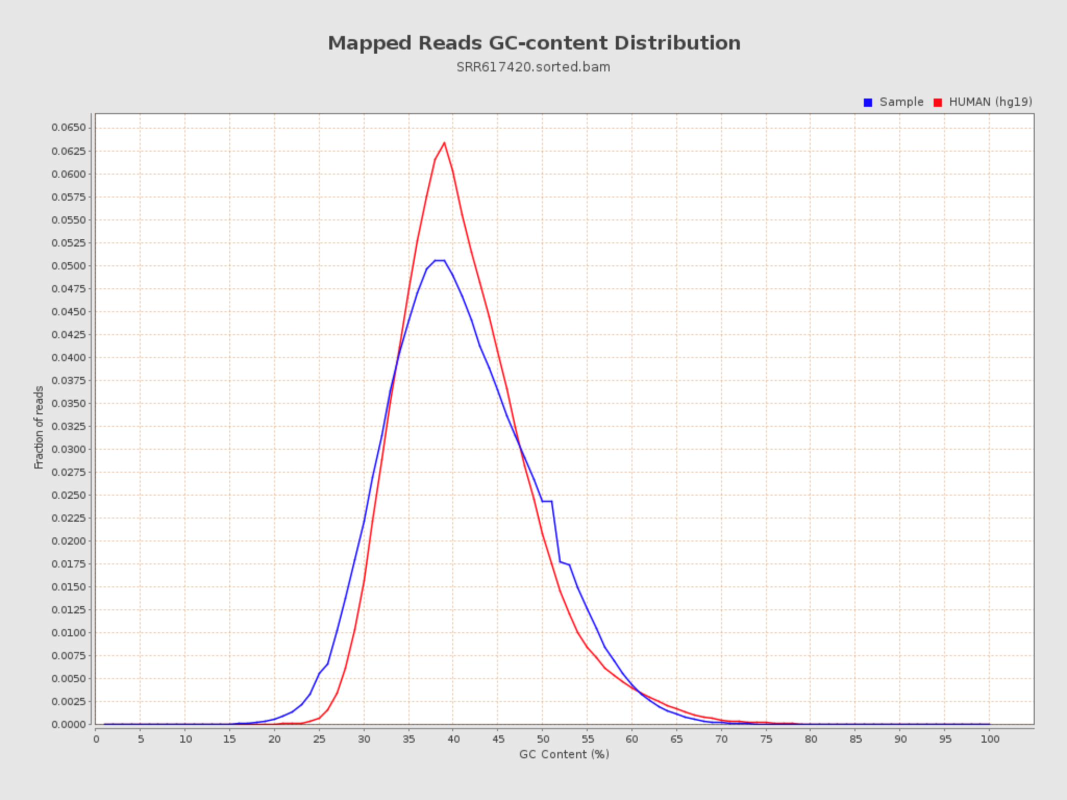
7. Results : Duplication Rate Histogram



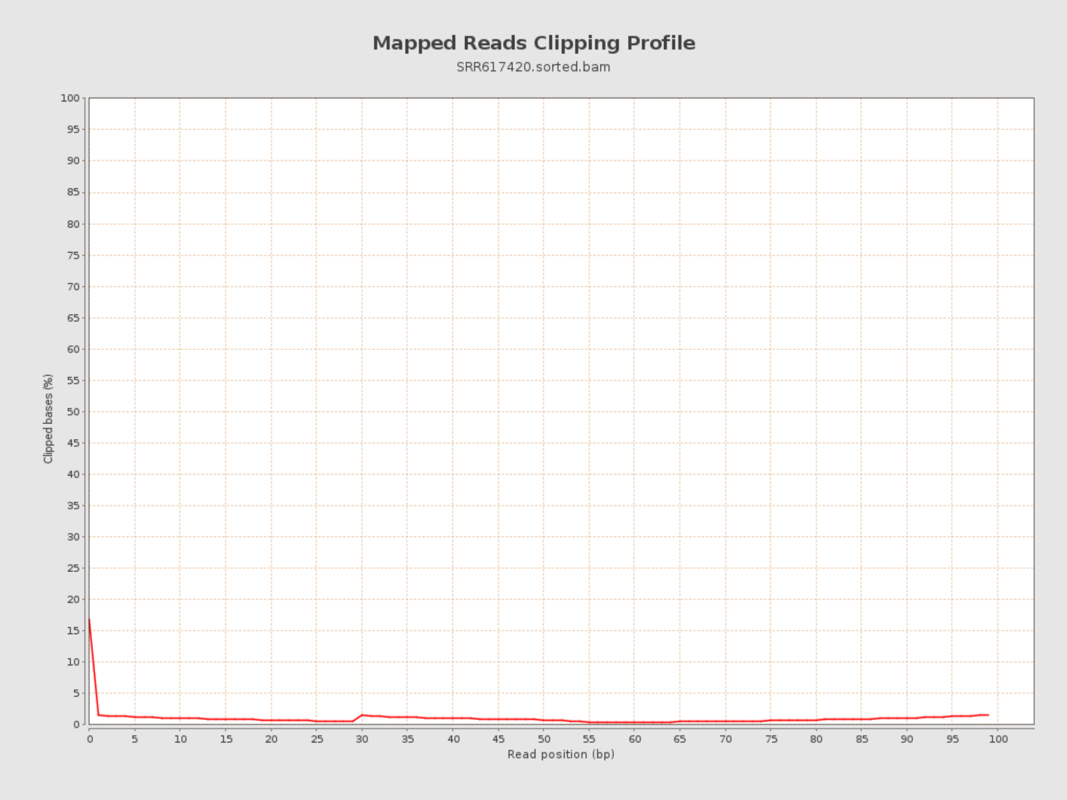
8. Results : Mapped Reads Nucleotide Content



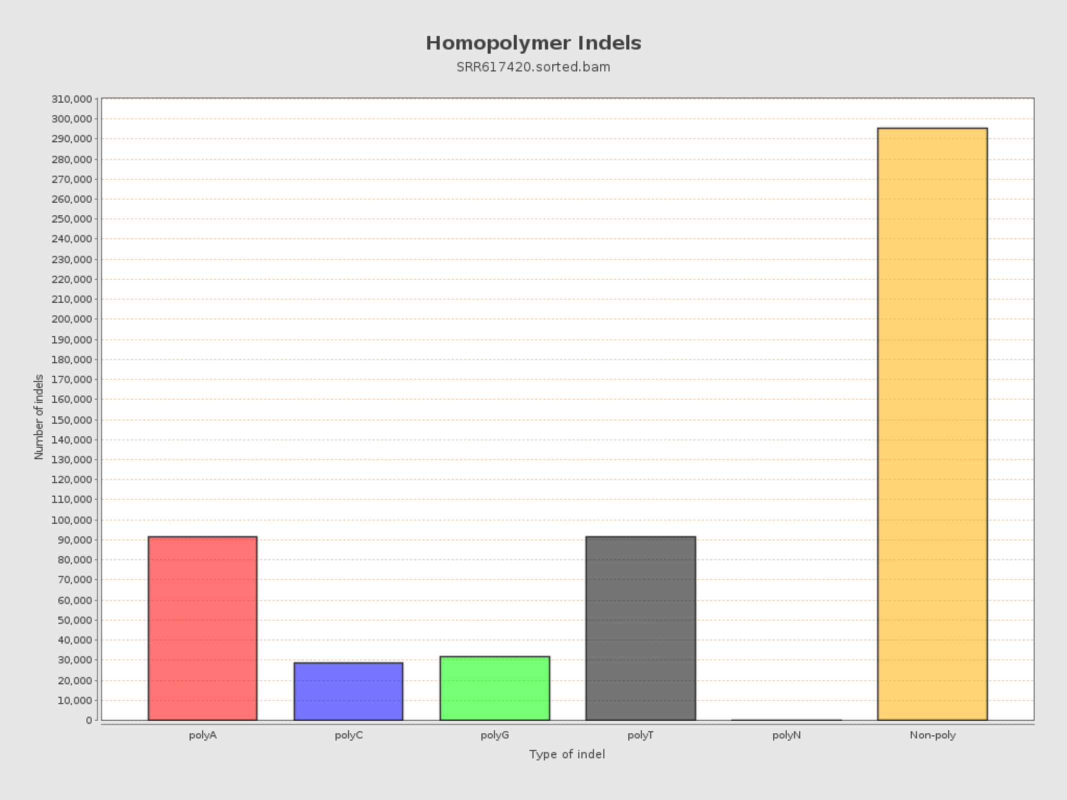
9. Results : Mapped Reads GC-content Distribution



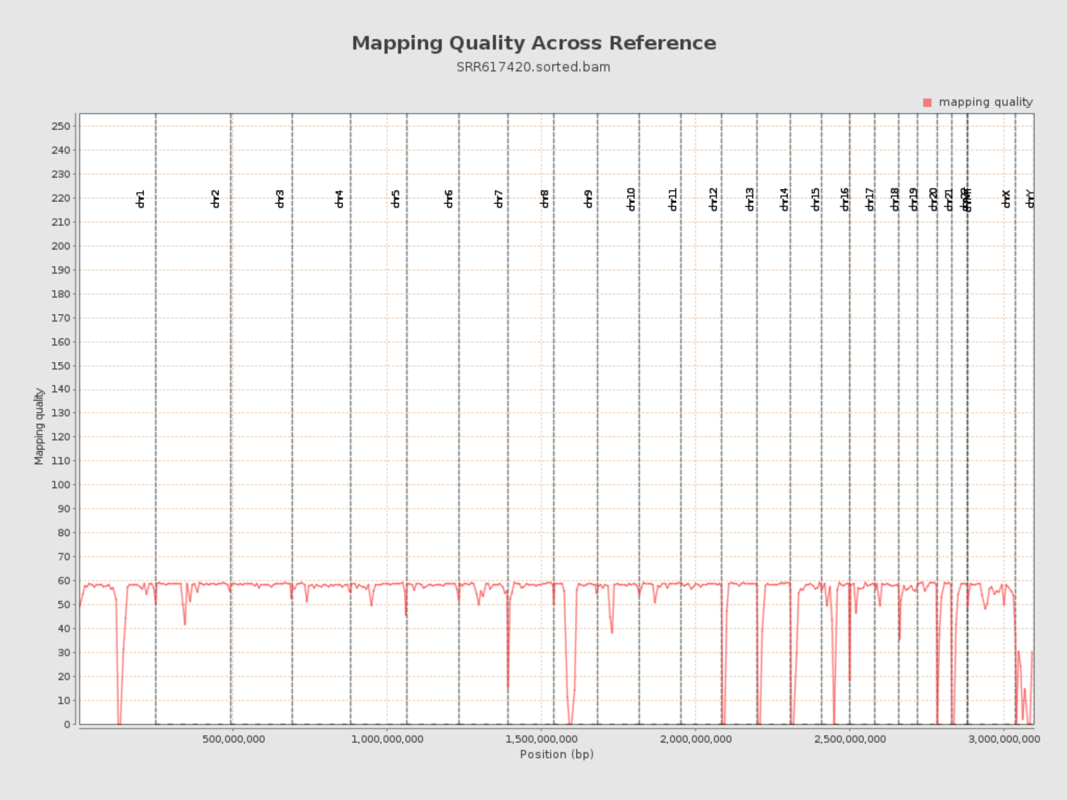
10. Results : Mapped Reads Clipping Profile



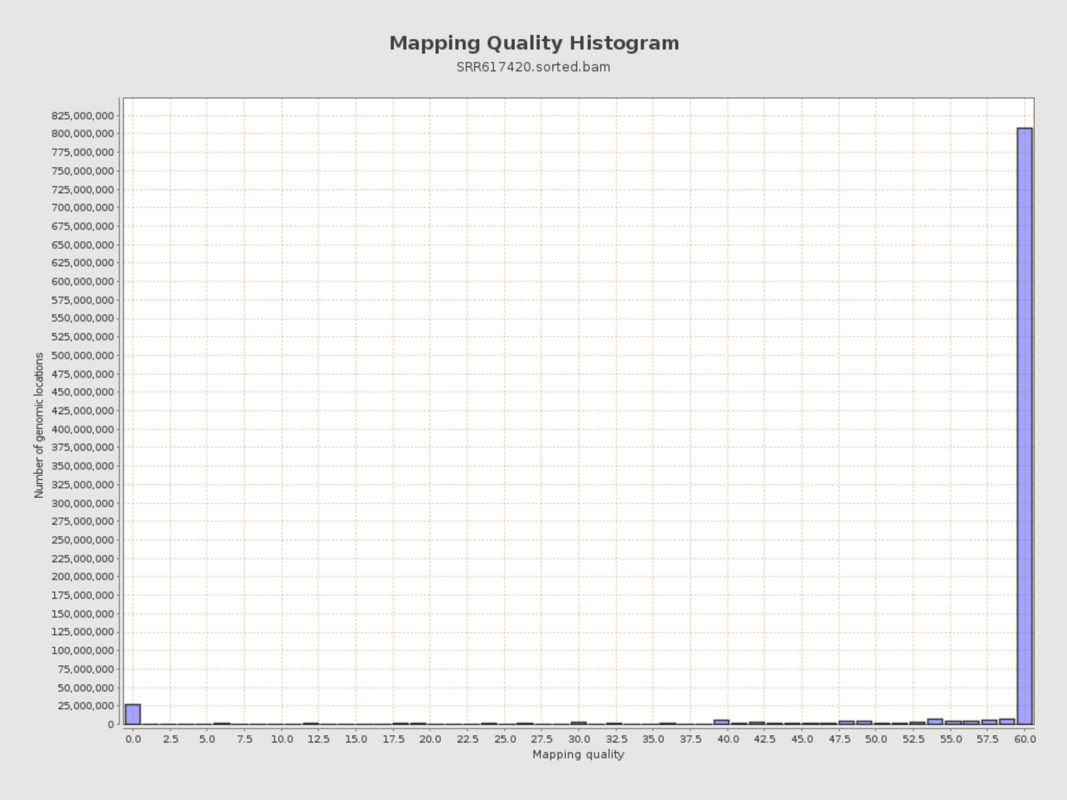
11. Results : Homopolymer Indels



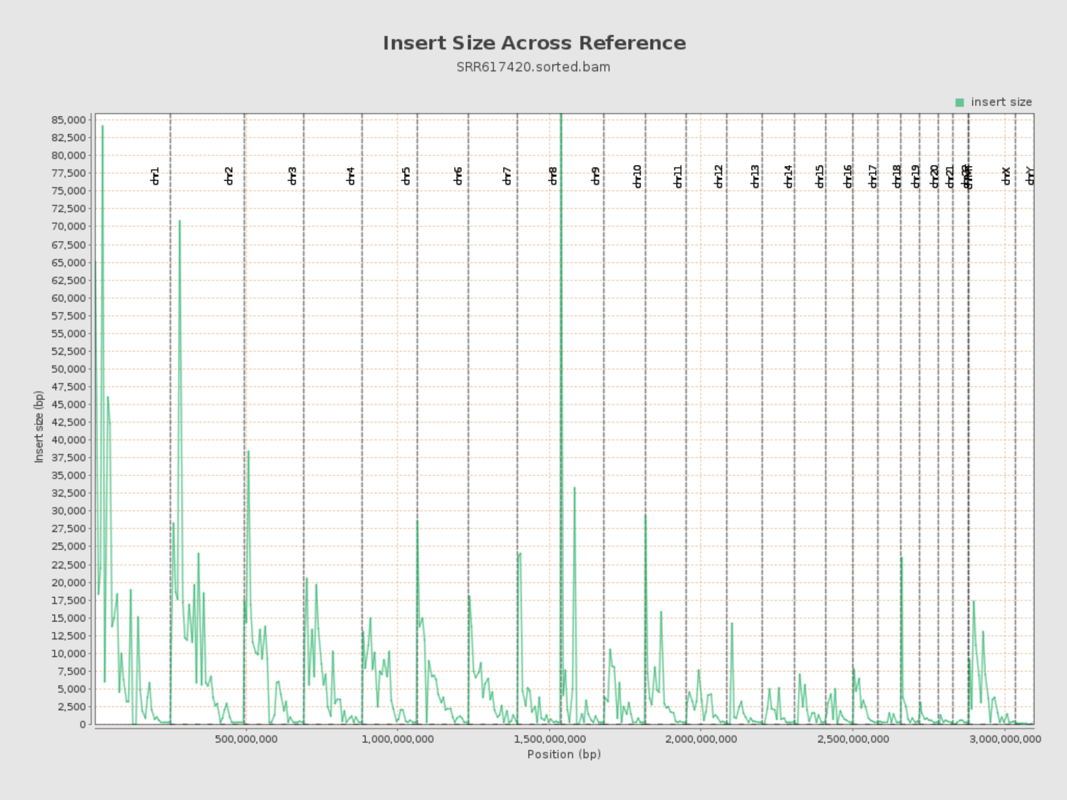
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram