Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/09 13:30:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617487.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_SRR617487 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617487_1.fastq.gz SRR617487_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 09 13:30:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617487.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	30,569,275 / 95.53%
Unmapped reads	1,430,725 / 4.47%
Mapped paired reads	30,569,275 / 95.53%
Mapped reads, first in pair	15,427,302 / 48.21%
Mapped reads, second in pair	15,141,973 / 47.32%
Mapped reads, both in pair	30,033,288 / 93.85%
Mapped reads, singletons	535,987 / 1.67%
Secondary alignments	0
Supplementary alignments	137,514 / 0.43%
Read min/max/mean length	30 / 100 / 100.17
Duplicated reads (estimated)	6,307,837 / 19.71%
Duplication rate	9.97%
Clipped reads	5,836,965 / 18.24%

2.2. ACGT Content

Number/percentage of A's	879,780,462 / 29.48%
Number/percentage of C's	603,548,068 / 20.22%
Number/percentage of T's	879,362,833 / 29.47%
Number/percentage of G's	618,604,027 / 20.73%
Number/percentage of N's	2,878,895 / 0.1%

GC Percentage	40.95%

2.3. Coverage

Mean	0.9646
Standard Deviation	9.7626

2.4. Mapping Quality

Mean Mapping Quality	52.8

2.5. Insert size

Mean	29,068.21
Standard Deviation	1,562,899.25
P25/Median/P75	174 / 220 / 292

2.6. Mismatches and indels

General error rate	1.24%
Mismatches	36,092,553
Insertions	443,983
Mapped reads with at least one insertion	1.42%
Deletions	1,041,549
Mapped reads with at least one deletion	3.34%
Homopolymer indels	47.46%

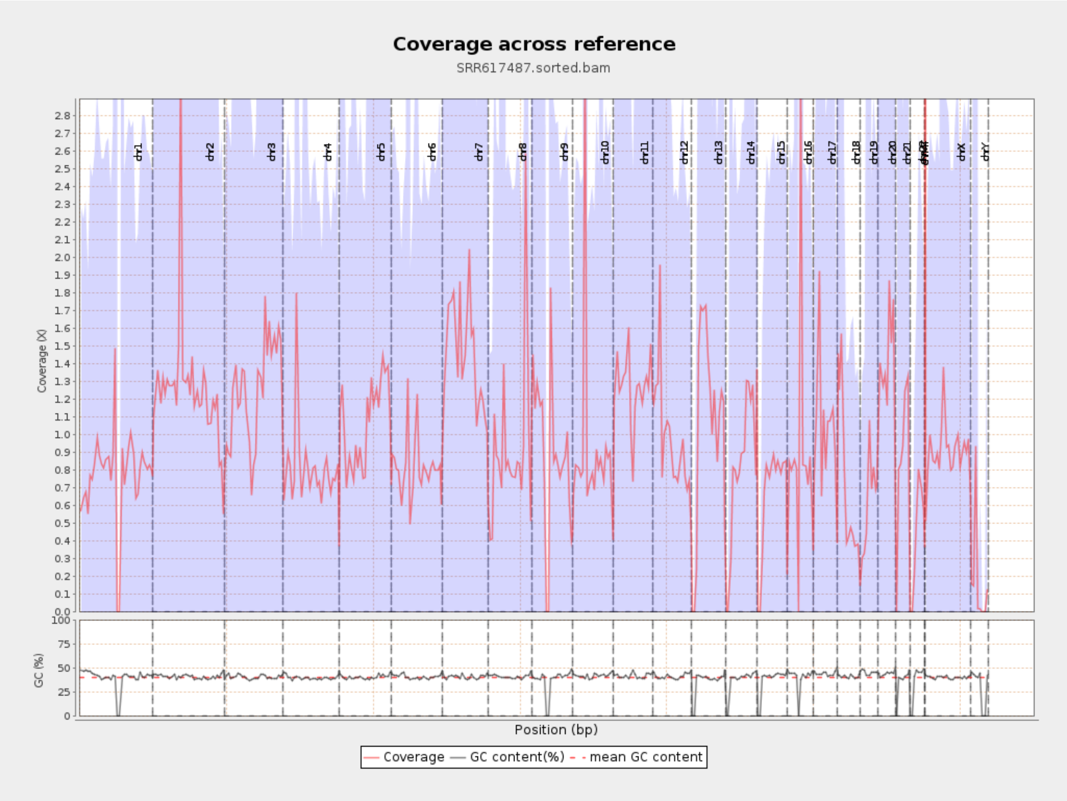
2.7. Chromosome stats

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

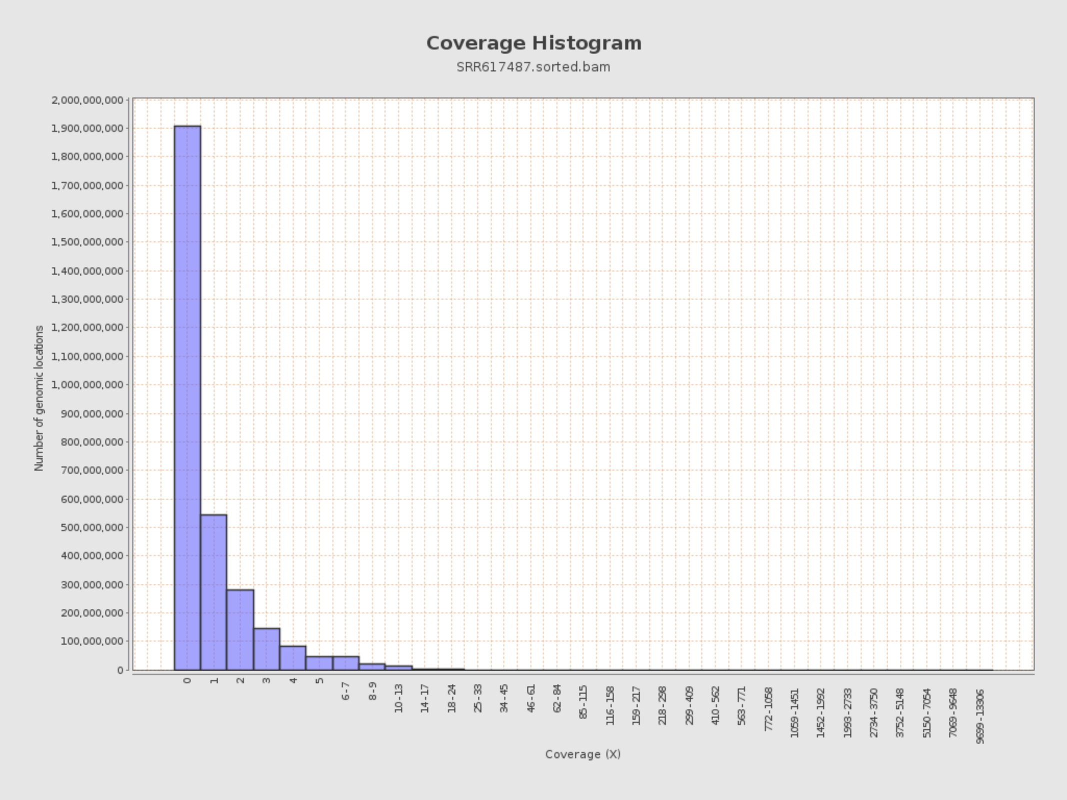
		bases	coverage	deviation
chr1	249250621	192390193	0.7719	9.3753
chr2	243199373	308529640	1.2686	11.4609
chr3	198022430	246323958	1.2439	2.2349
chr4	191154276	154202854	0.8067	6.1828
chr5	180915260	191473088	1.0584	2.092
chr6	171115067	140625524	0.8218	5.4185
chr7	159138663	230388891	1.4477	13.2903
chr8	146364022	132597503	0.9059	3.8983
chr9	141213431	124165686	0.8793	18.7169
chr10	135534747	126393389	0.9326	18.8007
chr11	135006516	168157587	1.2456	12.6628
chr12	133851895	130549929	0.9753	1.9684
chr13	115169878	126654385	1.0997	2.1217
chr14	107349540	86986226	0.8103	2.2133
chr15	102531392	67380410	0.6572	1.4471
chr16	90354753	80332297	0.8891	14.8473
chr17	81195210	83400710	1.0272	13.7183
chr18	78077248	53511180	0.6854	16.9961
chr19	59128983	35581032	0.6018	5.9185
chr20	63025520	88315215	1.4013	2.807
chr21	48129895	42857321	0.8905	3.8239
chr22	51304566	22355492	0.4357	1.2586
chrMT	16571	2096898	126.5402	96.2116
chrX	155270560	140345038	0.9039	4.1921

chrY	59373566	10337716	0.1741	13.9153

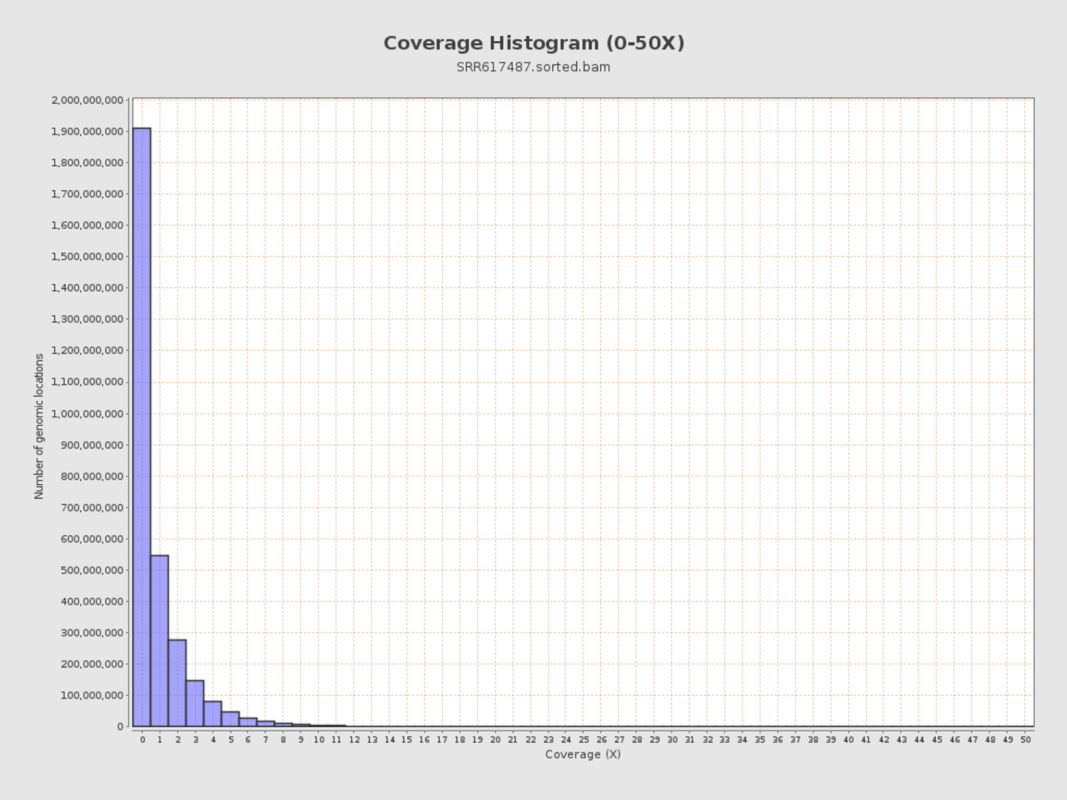
3. Results : Coverage across reference



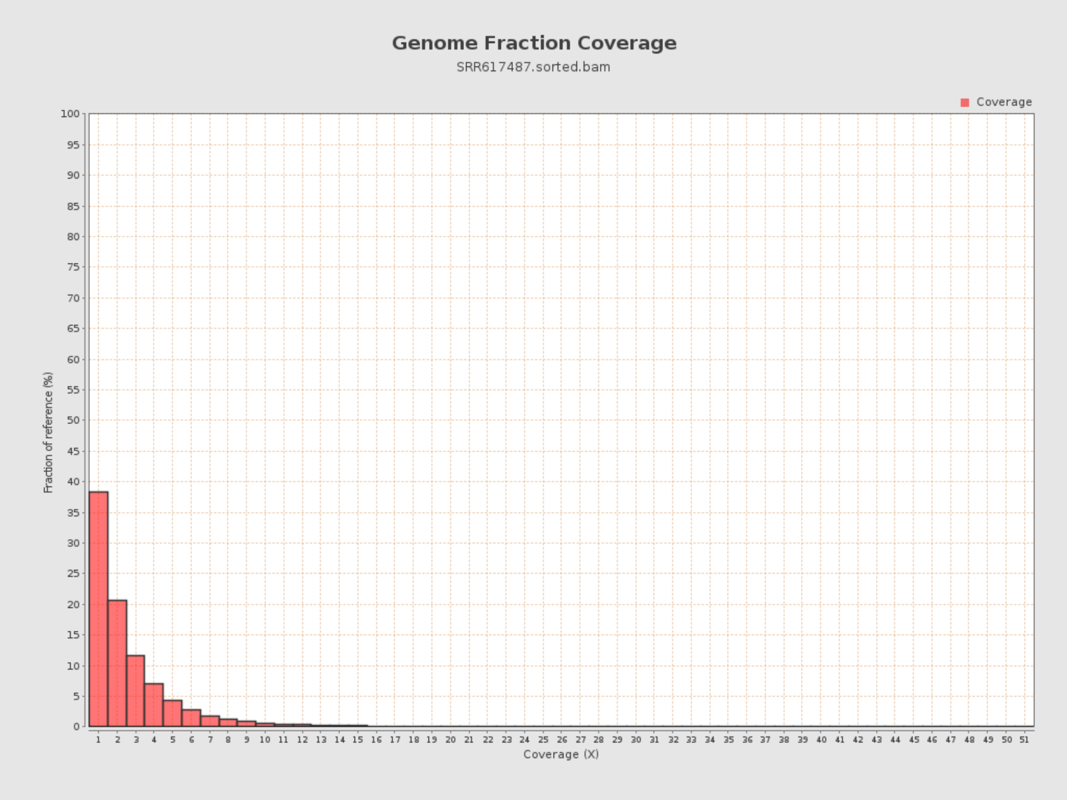
4. Results : Coverage Histogram



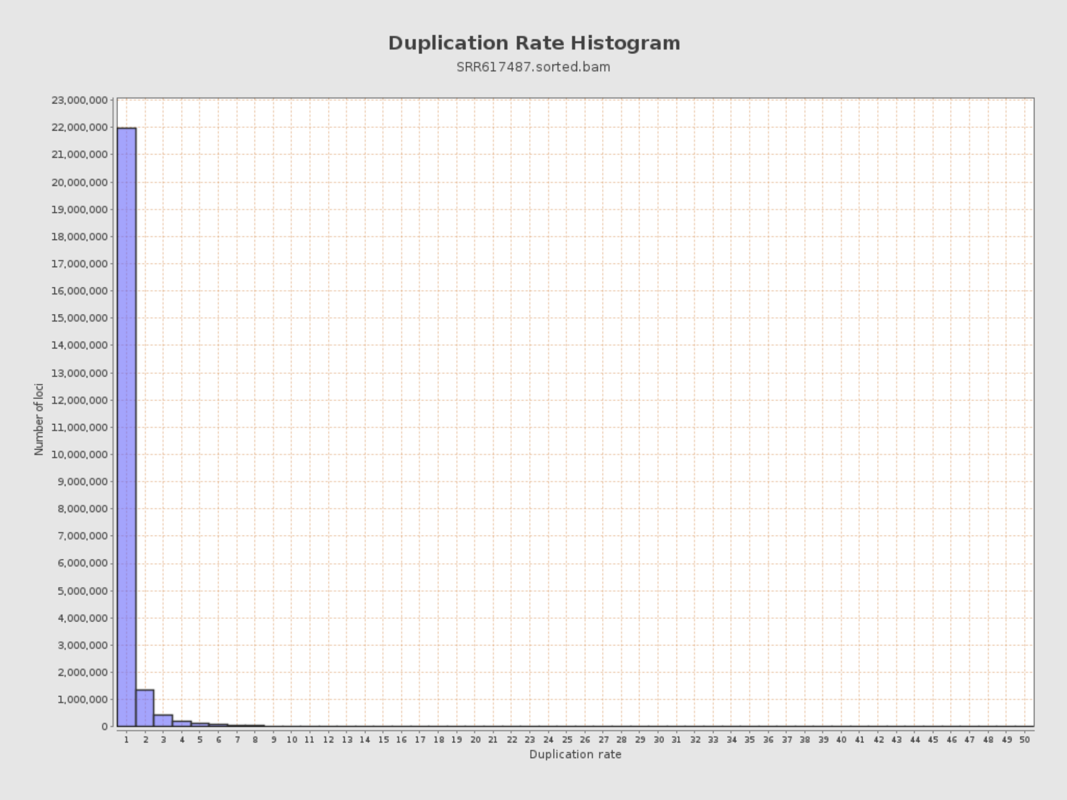
5. Results : Coverage Histogram (0-50X)



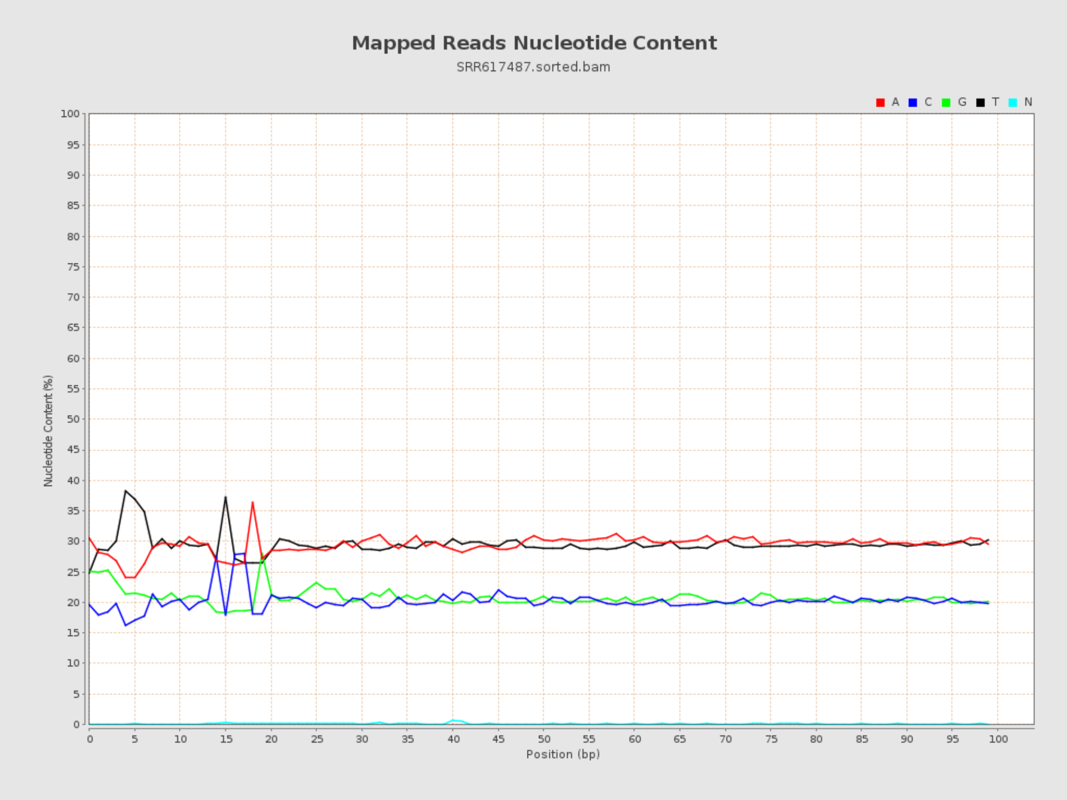
6. Results : Genome Fraction Coverage



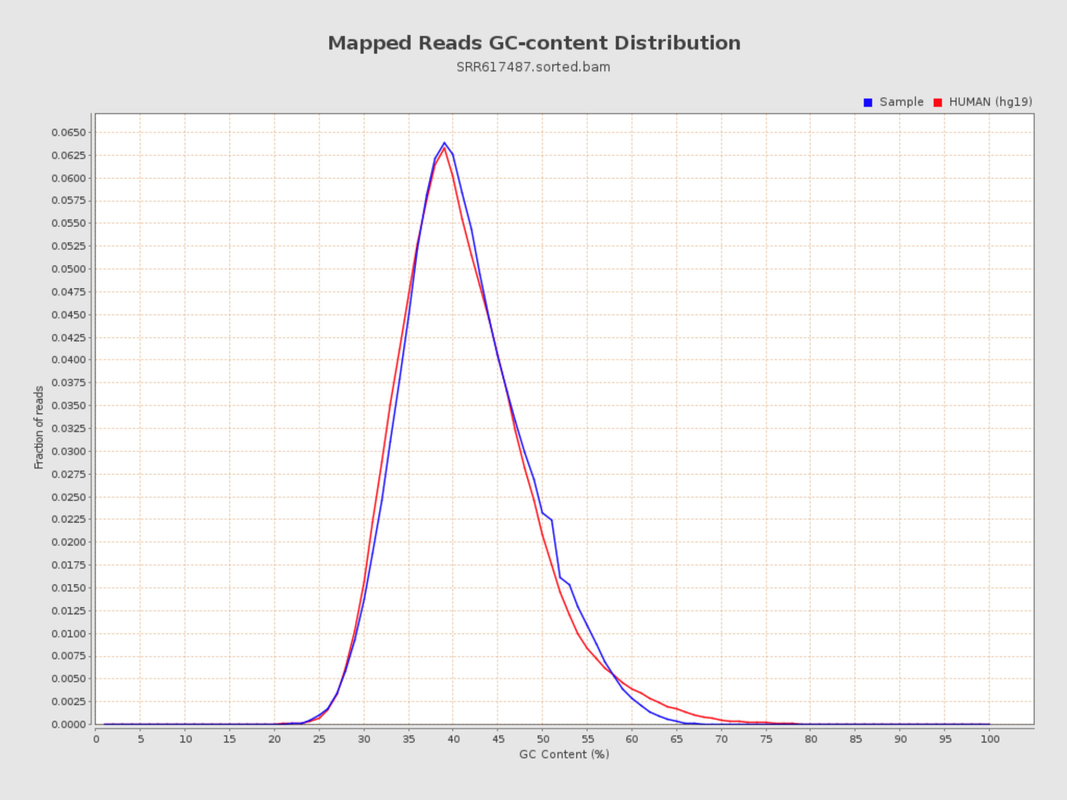
7. Results : Duplication Rate Histogram



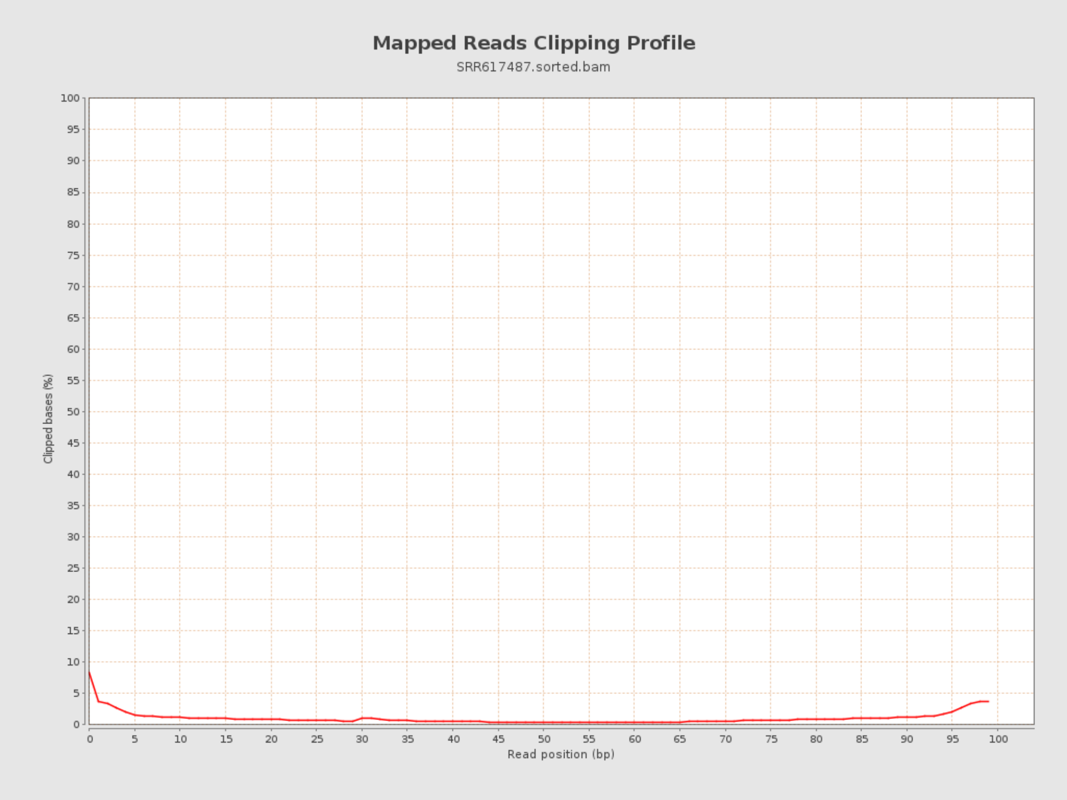
8. Results : Mapped Reads Nucleotide Content



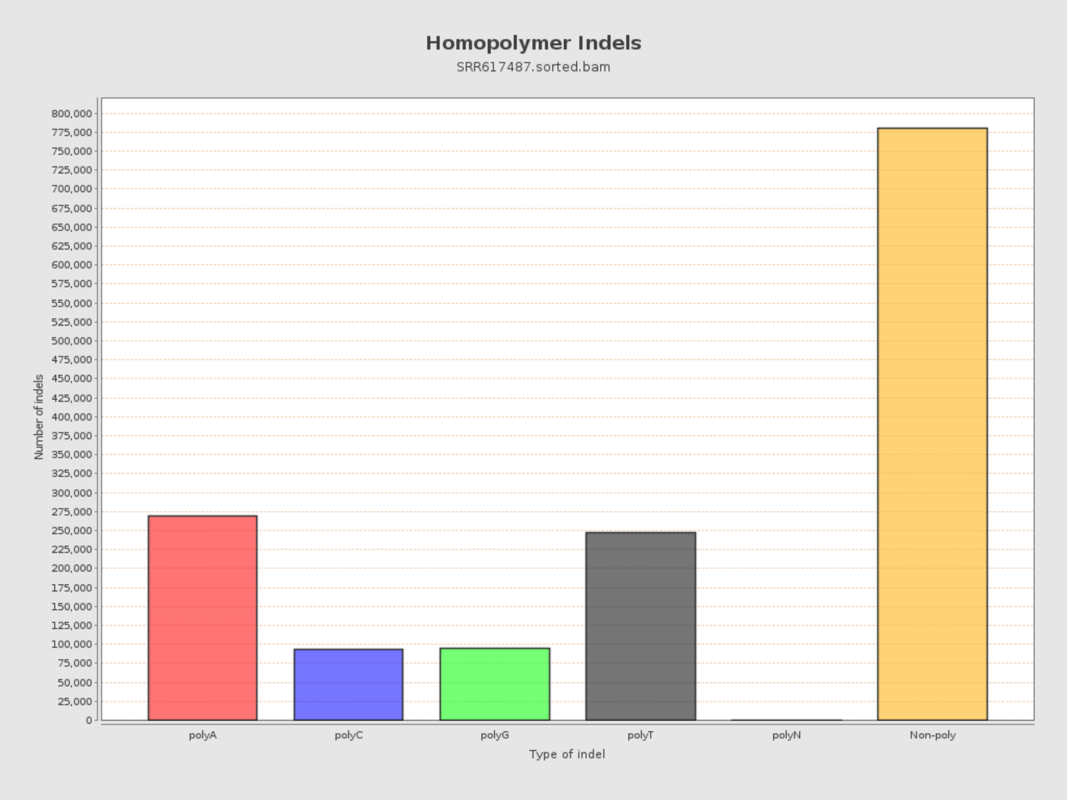
9. Results : Mapped Reads GC-content Distribution



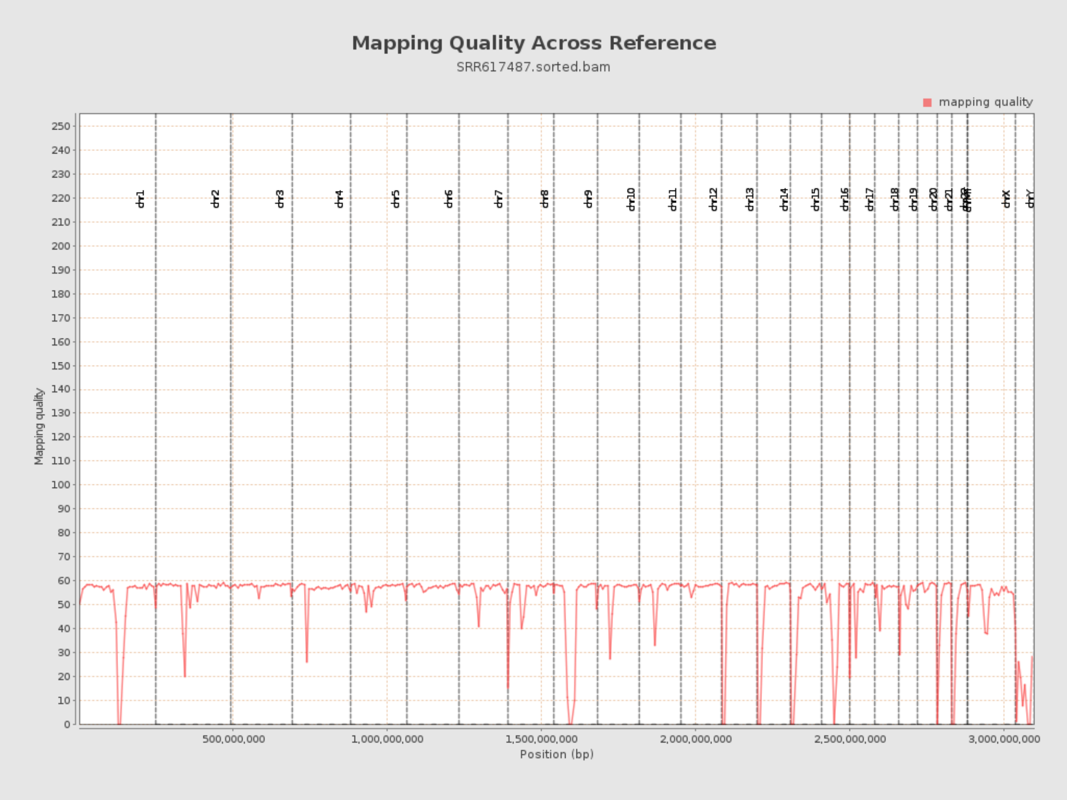
10. Results : Mapped Reads Clipping Profile



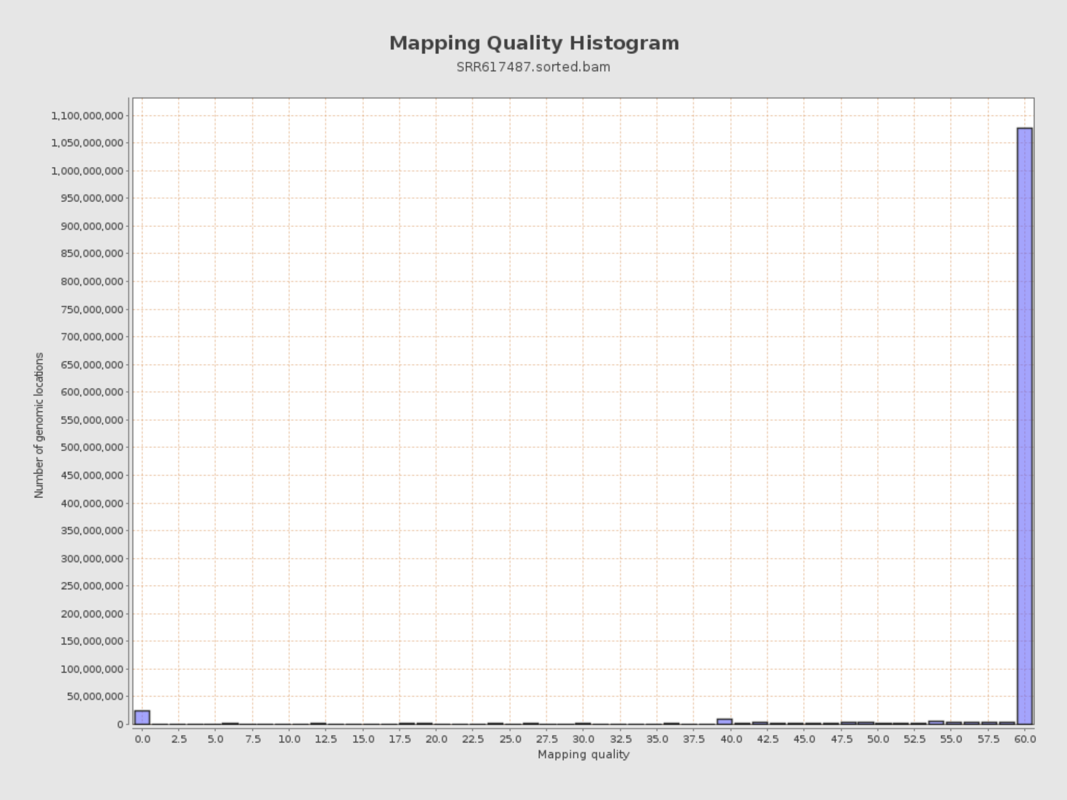
11. Results : Homopolymer Indels



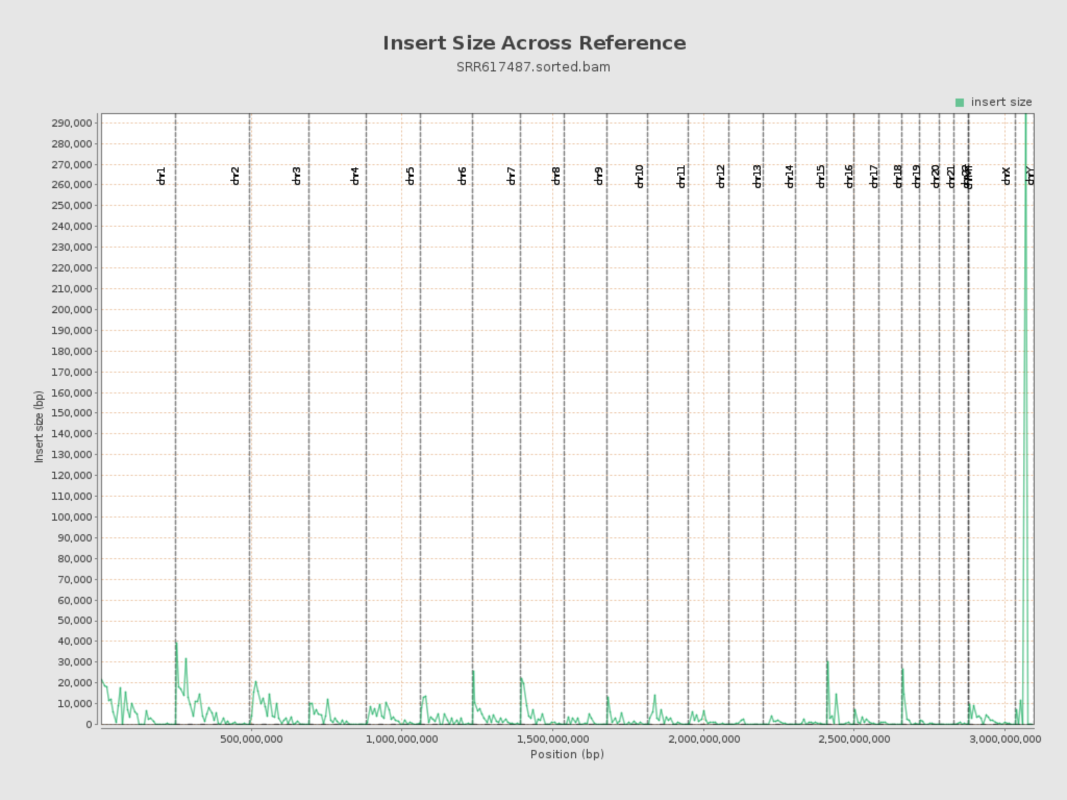
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram