Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/11 02:35:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617660.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_SRR617660 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617660_1.fastq.gz SRR617660_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Oct 11 02:35:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617660.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	27,456,926
Mapped reads	25,361,127 / 92.37%
Unmapped reads	2,095,799 / 7.63%
Mapped paired reads	25,361,127 / 92.37%
Mapped reads, first in pair	12,874,736 / 46.89%
Mapped reads, second in pair	12,486,391 / 45.48%
Mapped reads, both in pair	24,619,904 / 89.67%
Mapped reads, singletons	741,223 / 2.7%
Secondary alignments	0
Supplementary alignments	152,583 / 0.56%
Read min/max/mean length	30 / 100 / 100.22
Duplicated reads (estimated)	5,402,520 / 19.68%
Duplication rate	10.17%
Clipped reads	5,739,377 / 20.9%

2.2. ACGT Content

Number/percentage of A's	729,929,854 / 29.88%
Number/percentage of C's	484,694,724 / 19.84%
Number/percentage of T's	727,781,454 / 29.79%
Number/percentage of G's	498,409,831 / 20.4%
Number/percentage of N's	2,451,633 / 0.1%

GC Percentage	40.24%

2.3. Coverage

Mean	0.7897
Standard Deviation	8.9089

2.4. Mapping Quality

Mean Mapping Quality	52.42

2.5. Insert size

Mean	47,685.48
Standard Deviation	2,040,805.97
P25/Median/P75	177 / 219 / 283

2.6. Mismatches and indels

General error rate	1.56%
Mismatches	37,326,149
Insertions	382,647
Mapped reads with at least one insertion	1.48%
Deletions	890,140
Mapped reads with at least one deletion	3.44%
Homopolymer indels	47.59%

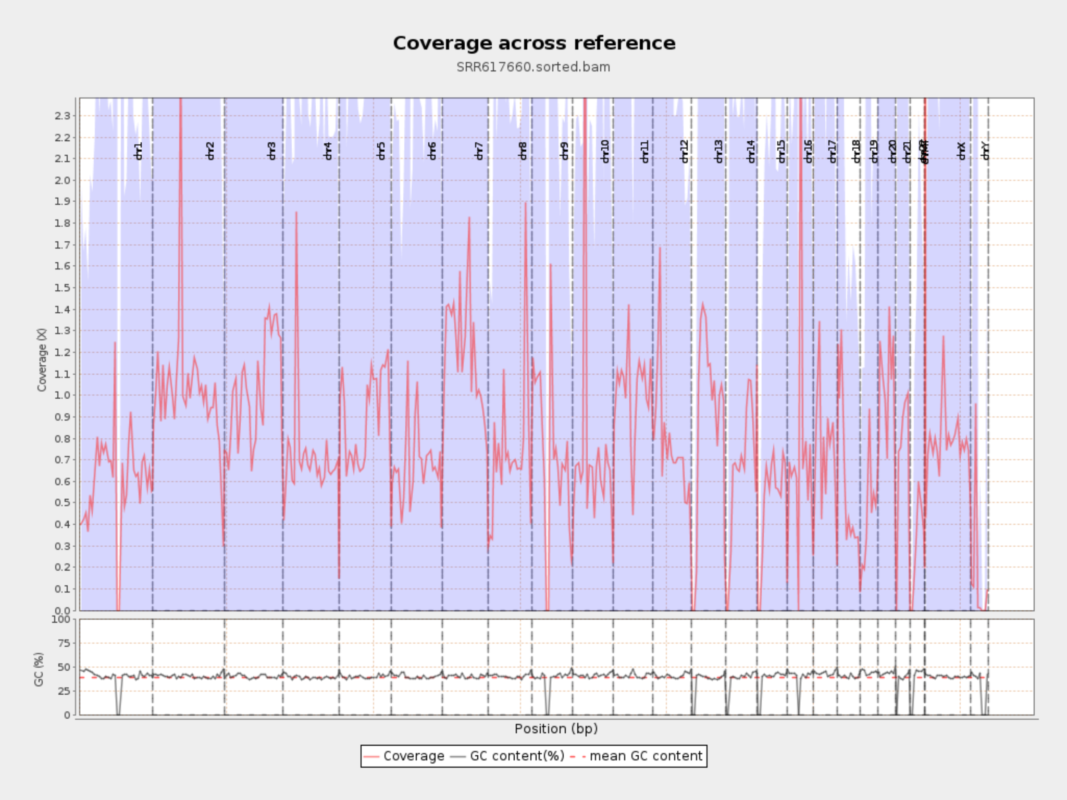
2.7. Chromosome stats

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

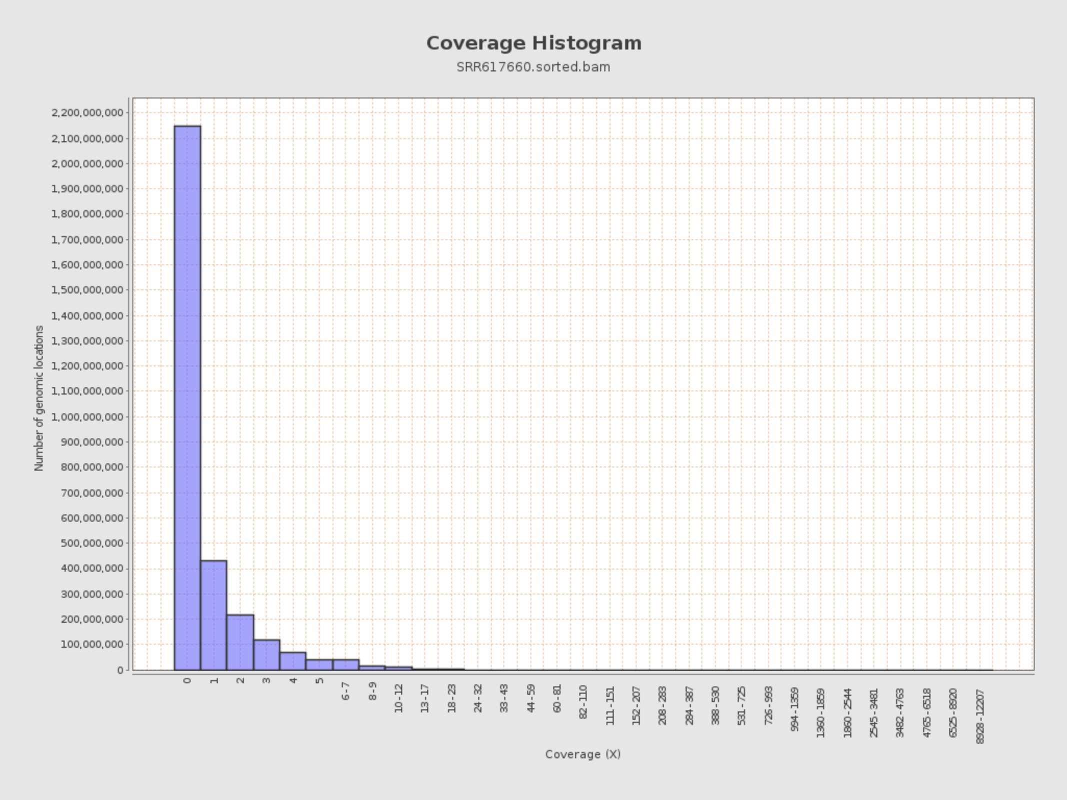
		bases	coverage	deviation
chr1	249250621	150035259	0.6019	8.741
chr2	243199373	252261067	1.0373	10.1885
chr3	198022430	204877283	1.0346	2.1371
chr4	191154276	136772020	0.7155	6.8368
chr5	180915260	161762864	0.8941	2.0022
chr6	171115067	118654292	0.6934	4.8941
chr7	159138663	191275795	1.2019	11.2701
chr8	146364022	108837762	0.7436	3.4743
chr9	141213431	100530107	0.7119	17.0532
chr10	135534747	103941906	0.7669	18.111
chr11	135006516	134330121	0.995	10.1839
chr12	133851895	104584979	0.7813	1.9733
chr13	115169878	105131394	0.9128	2.018
chr14	107349540	69761002	0.6498	2.1172
chr15	102531392	52090837	0.508	1.6132
chr16	90354753	67884778	0.7513	14.2448
chr17	81195210	59781402	0.7363	10.6303
chr18	78077248	45128819	0.578	15.2252
chr19	59128983	25841378	0.437	5.1572
chr20	63025520	65703246	1.0425	2.5703
chr21	48129895	35614316	0.74	3.6798
chr22	51304566	15629975	0.3047	1.1113
chrMT	16571	2572803	155.2594	107.3605
chrX	155270560	121864572	0.7849	3.698

chrY	59373566	9870126	0.1662	14.4197

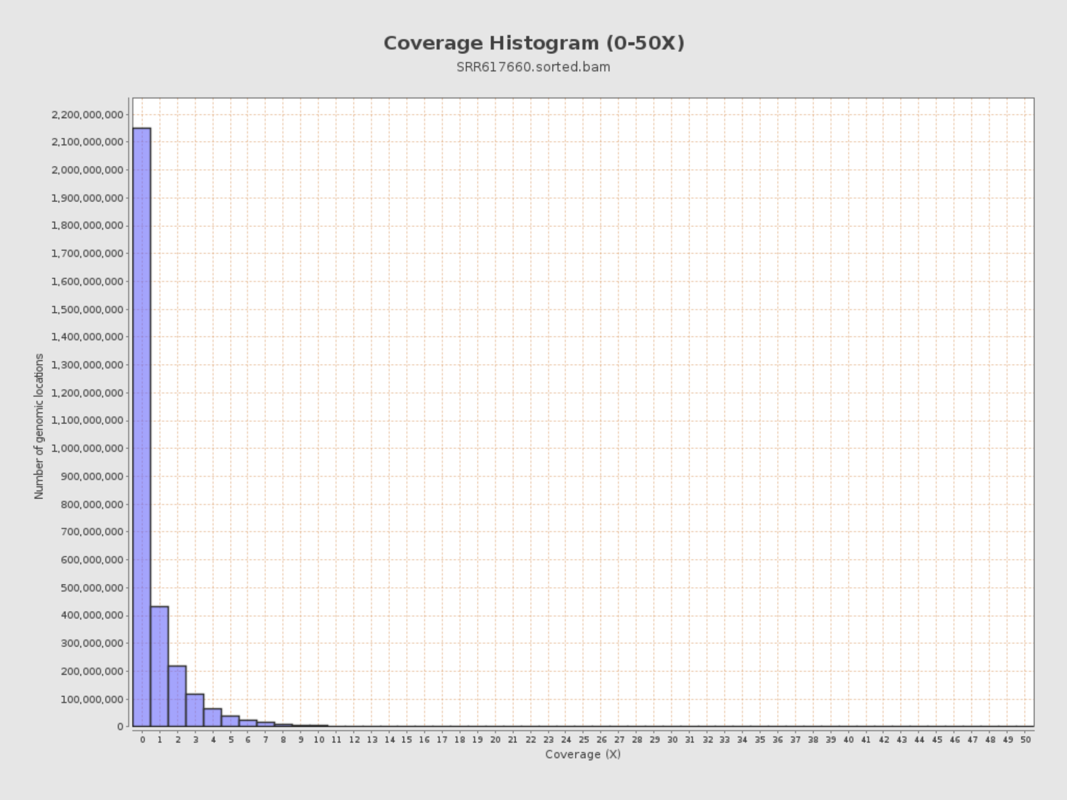
3. Results : Coverage across reference



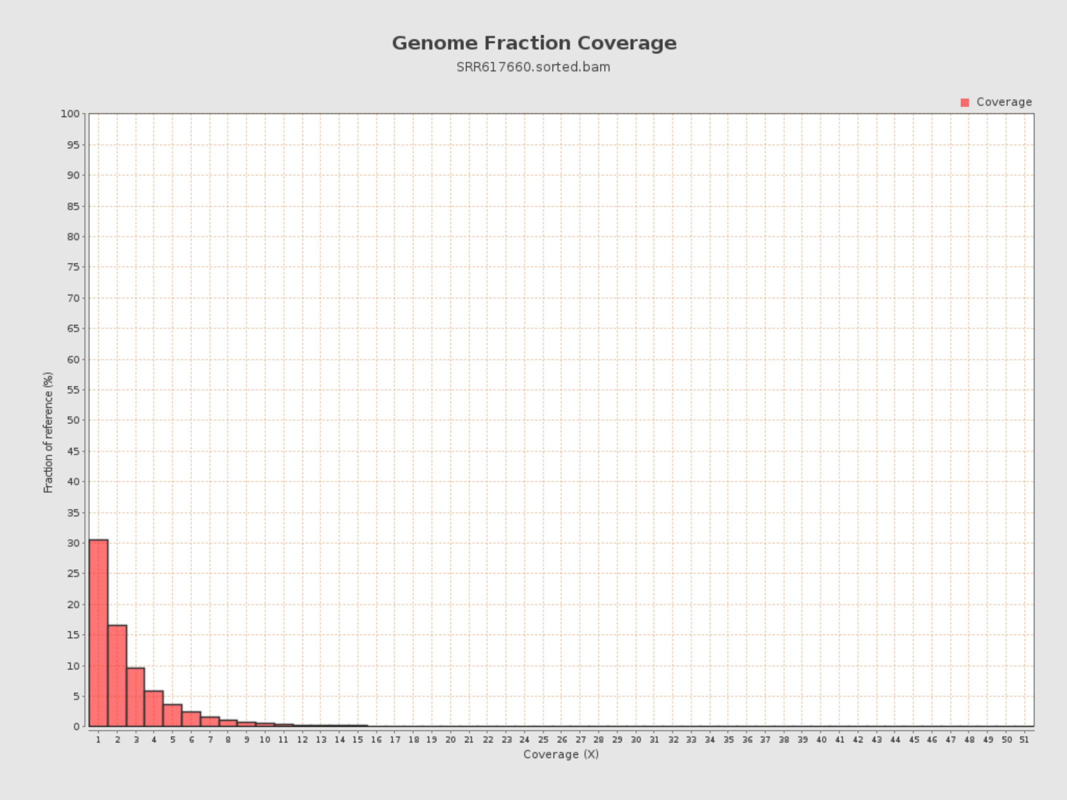
4. Results : Coverage Histogram



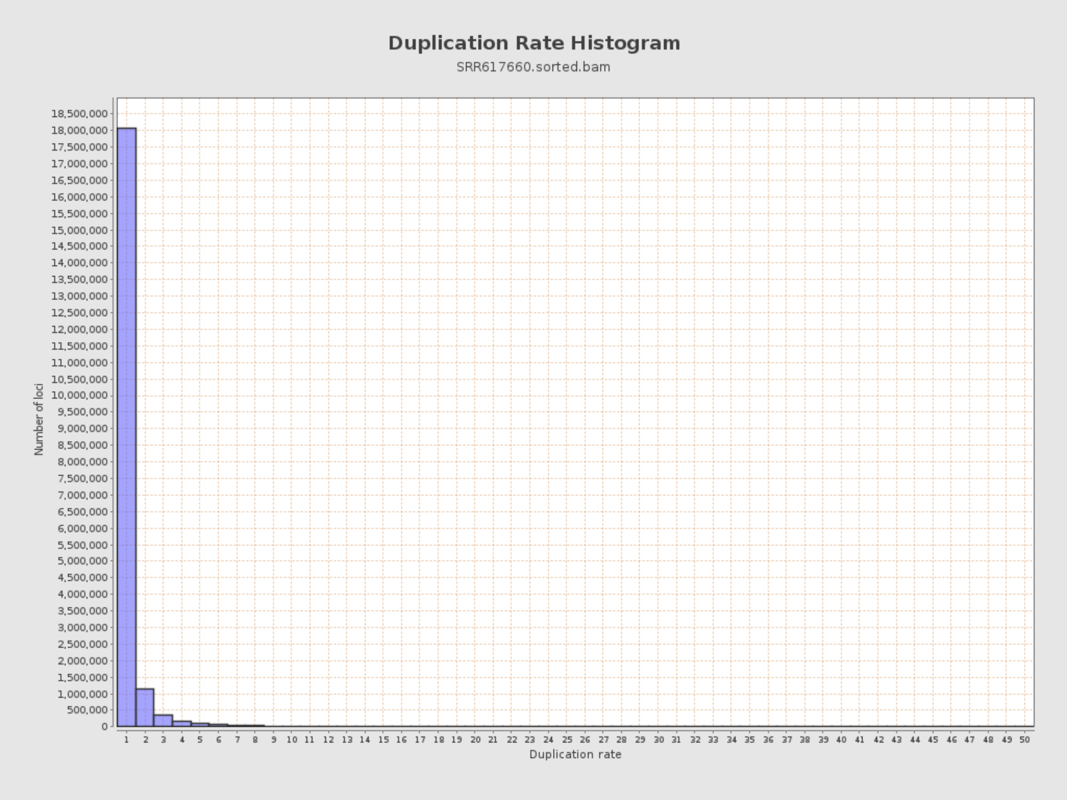
5. Results : Coverage Histogram (0-50X)



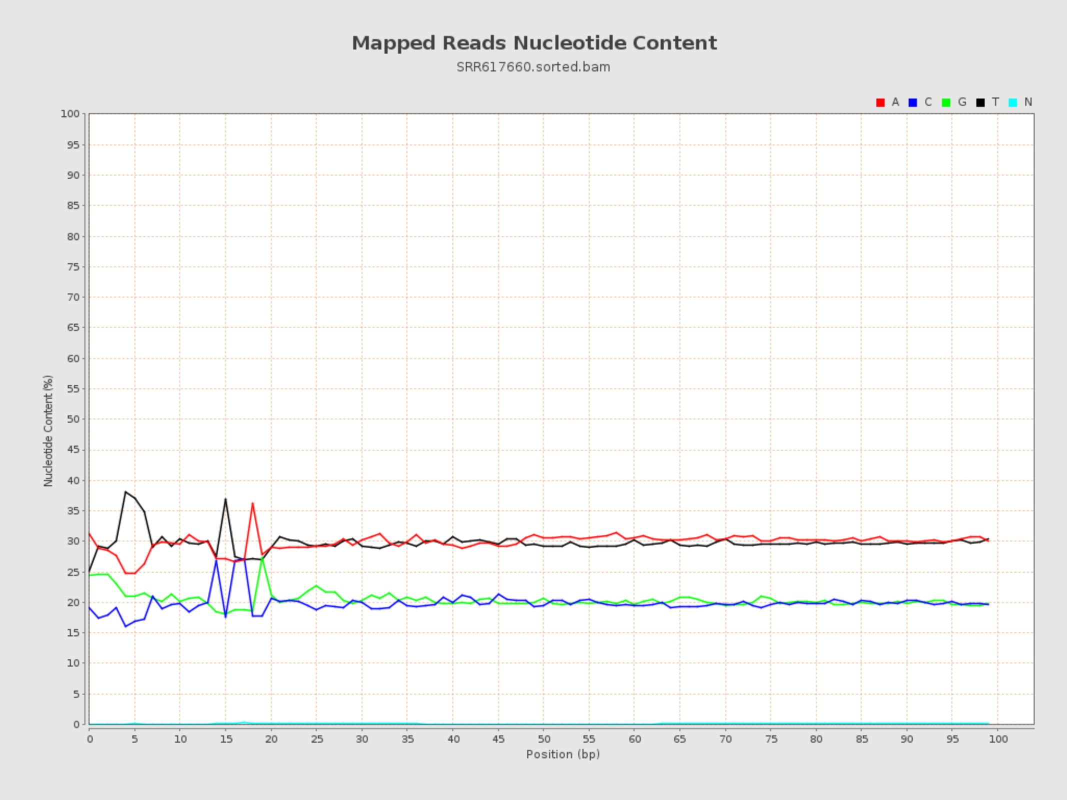
6. Results : Genome Fraction Coverage



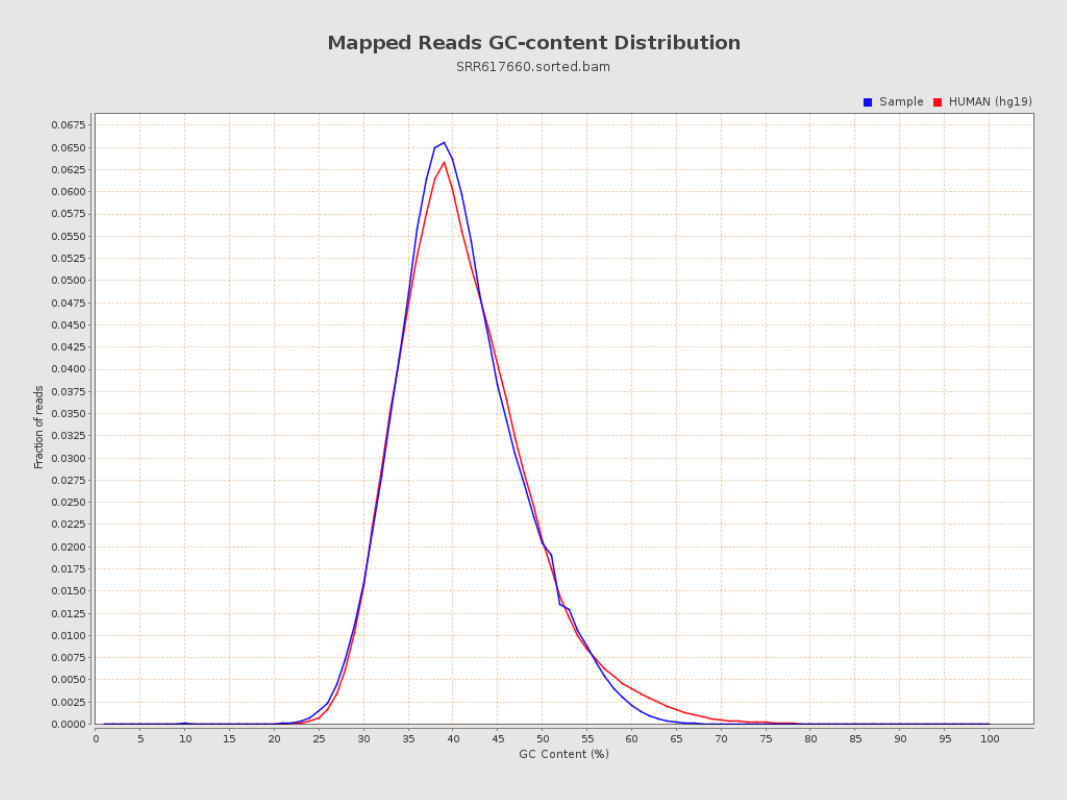
7. Results : Duplication Rate Histogram



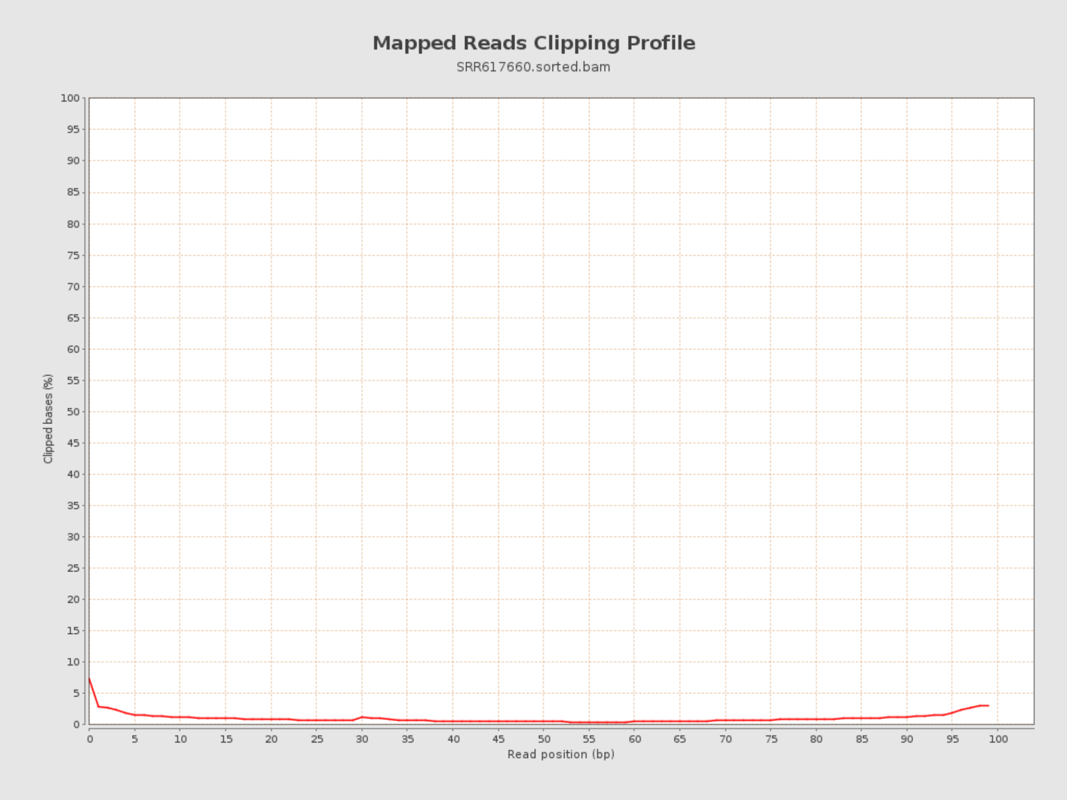
8. Results : Mapped Reads Nucleotide Content



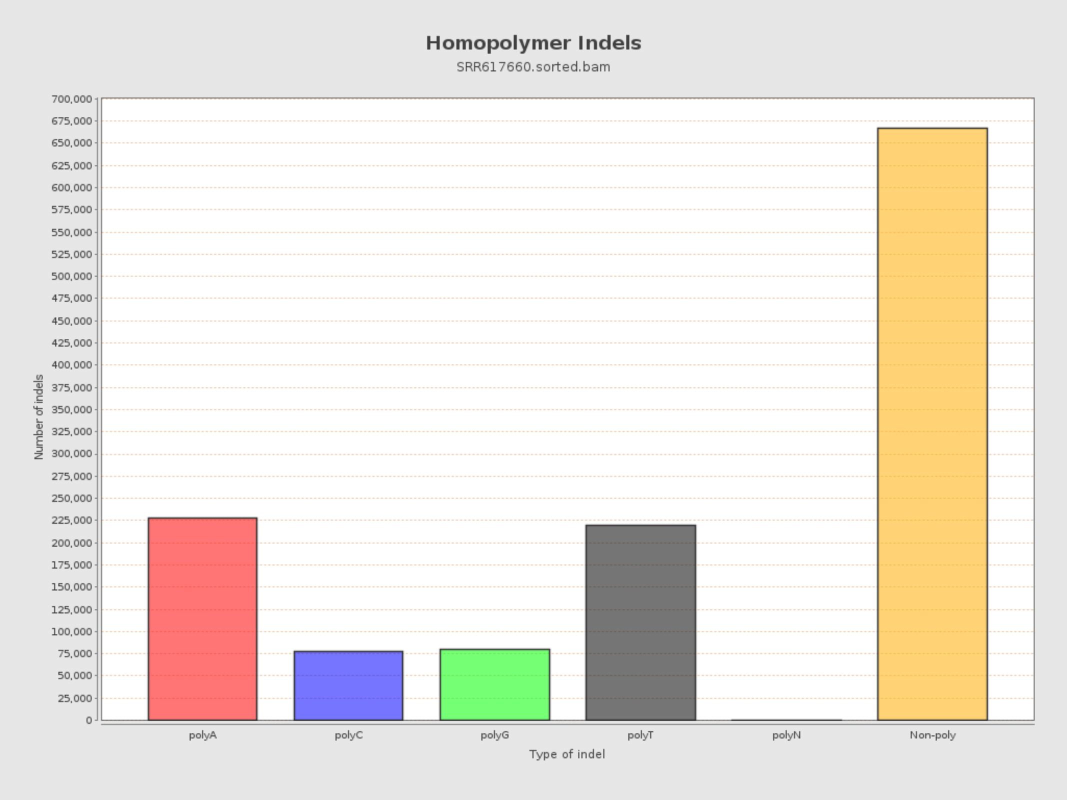
9. Results : Mapped Reads GC-content Distribution



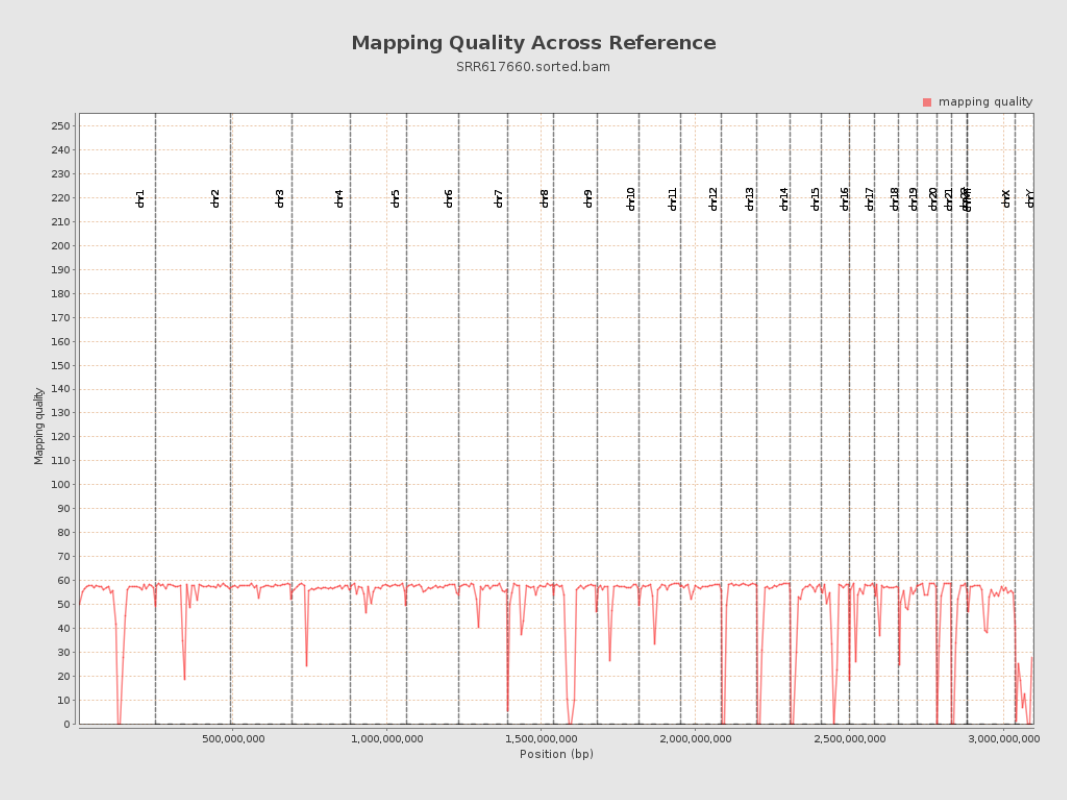
10. Results : Mapped Reads Clipping Profile



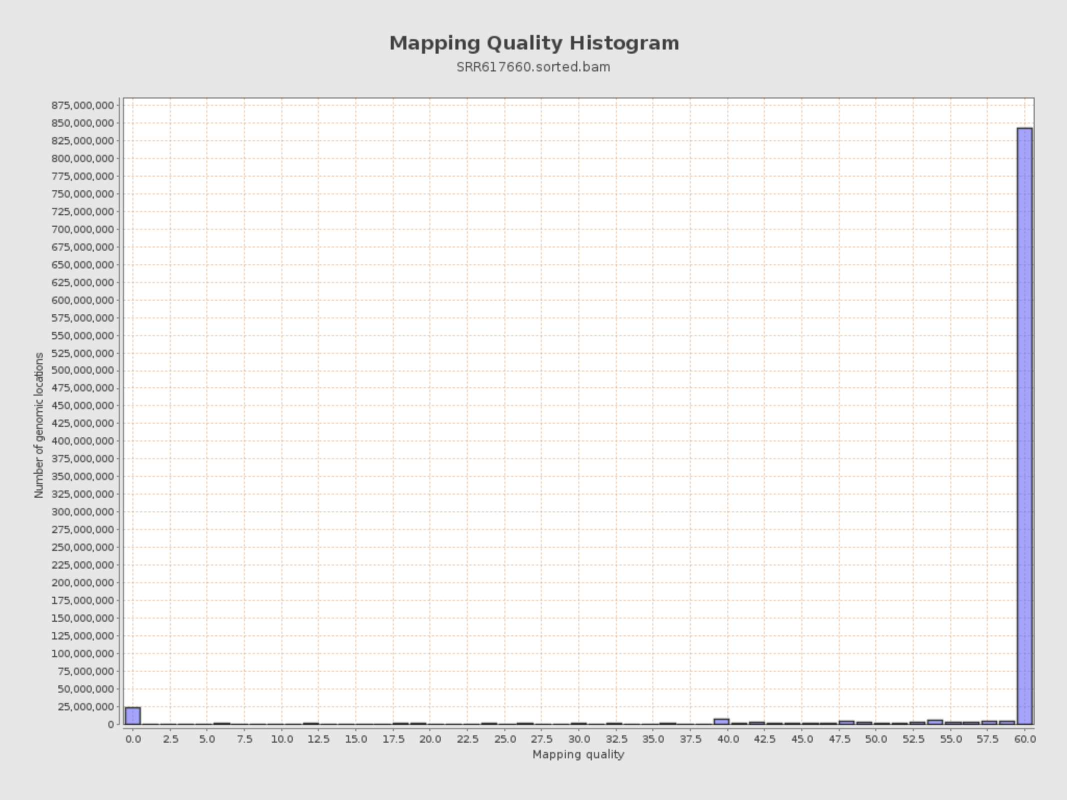
11. Results : Homopolymer Indels



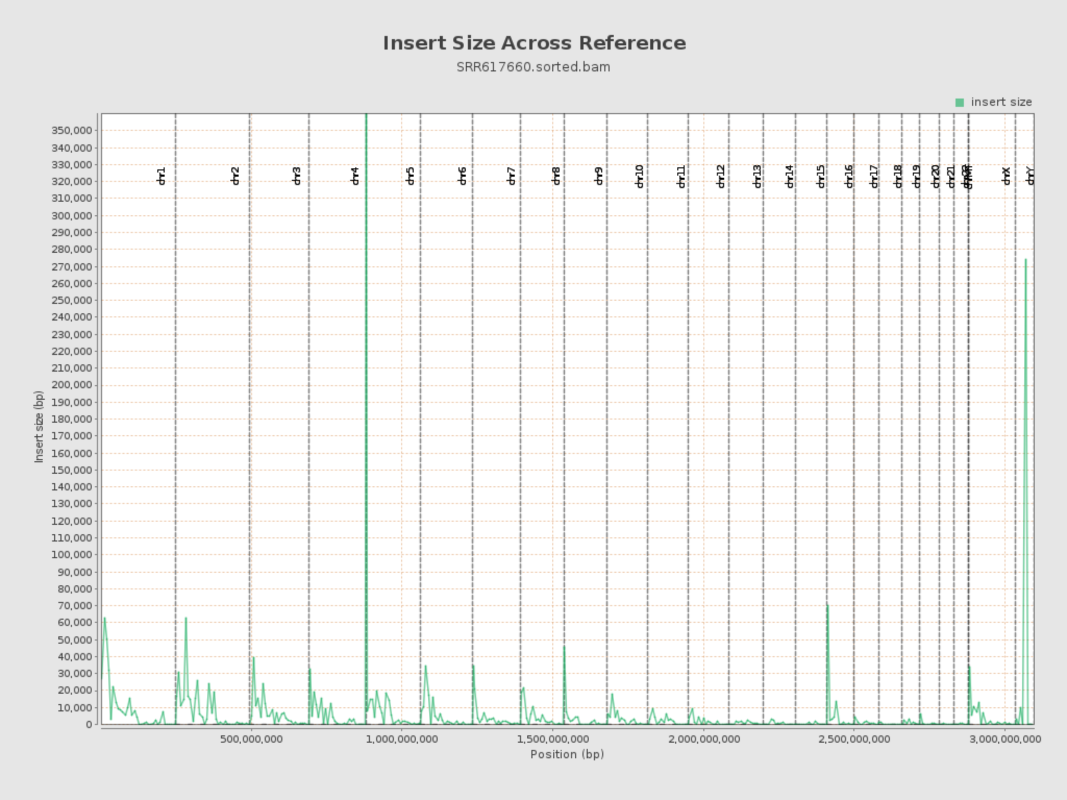
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram