Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/10 03:35:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617504.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_SRR617504 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617504_1.fastq.gz SRR617504_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 10 03:35:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617504.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	30,434,415 / 95.11%
Unmapped reads	1,565,585 / 4.89%
Mapped paired reads	30,434,415 / 95.11%
Mapped reads, first in pair	15,371,636 / 48.04%
Mapped reads, second in pair	15,062,779 / 47.07%
Mapped reads, both in pair	29,830,956 / 93.22%
Mapped reads, singletons	603,459 / 1.89%
Secondary alignments	0
Supplementary alignments	166,687 / 0.52%
Read min/max/mean length	30 / 100 / 100.21
Duplicated reads (estimated)	6,297,039 / 19.68%
Duplication rate	10%
Clipped reads	6,032,178 / 18.85%

2.2. ACGT Content

Number/percentage of A's	872,941,744 / 29.5%
Number/percentage of C's	598,226,551 / 20.21%
Number/percentage of T's	873,232,189 / 29.5%
Number/percentage of G's	612,296,732 / 20.69%
Number/percentage of N's	2,923,696 / 0.1%

GC Percentage	40.9%

2.3. Coverage

Mean	0.9566
Standard Deviation	9.6693

2.4. Mapping Quality

Mean Mapping Quality	52.69

2.5. Insert size

Mean	42,260.88
Standard Deviation	1,933,969.4
P25/Median/P75	175 / 221 / 294

2.6. Mismatches and indels

General error rate	1.14%
Mismatches	32,941,720
Insertions	446,025
Mapped reads with at least one insertion	1.44%
Deletions	1,036,562
Mapped reads with at least one deletion	3.33%
Homopolymer indels	47.4%

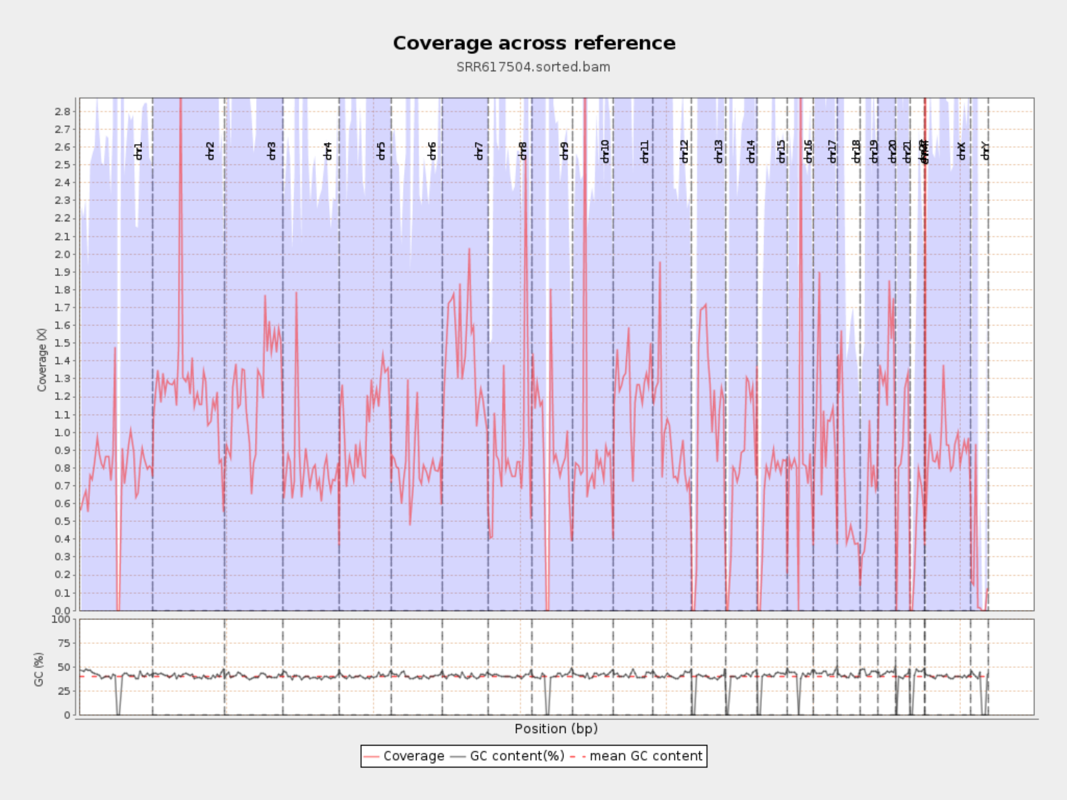
2.7. Chromosome stats

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

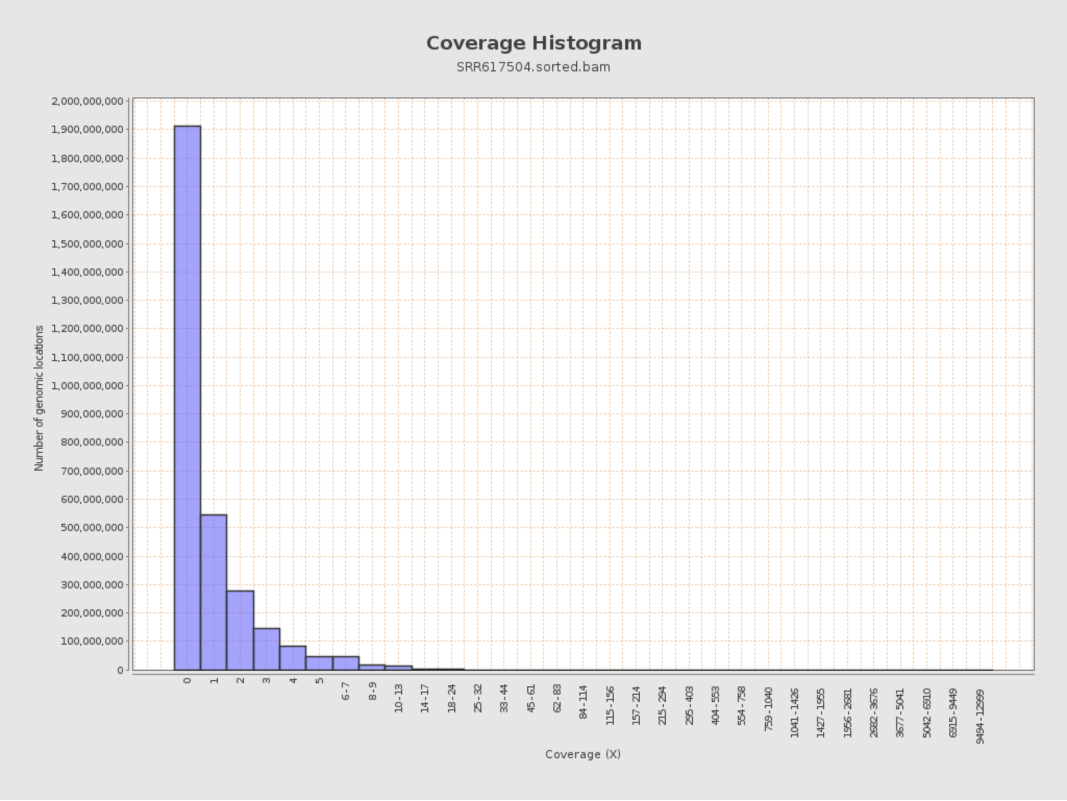
		bases	coverage	deviation
chr1	249250621	191142900	0.7669	9.3787
chr2	243199373	306082513	1.2586	11.4711
chr3	198022430	244426372	1.2343	2.244
chr4	191154276	152828635	0.7995	6.1658
chr5	180915260	189657904	1.0483	2.091
chr6	171115067	139262747	0.8139	5.3174
chr7	159138663	228382665	1.4351	13.0958
chr8	146364022	131473472	0.8983	3.8085
chr9	141213431	122776146	0.8694	18.386
chr10	135534747	125207355	0.9238	18.5513
chr11	135006516	166945288	1.2366	12.5079
chr12	133851895	129148936	0.9649	2.021
chr13	115169878	125703622	1.0915	2.1423
chr14	107349540	86146826	0.8025	2.2365
chr15	102531392	66879131	0.6523	1.548
chr16	90354753	79902720	0.8843	14.6869
chr17	81195210	82631263	1.0177	13.5713
chr18	78077248	53130590	0.6805	17.067
chr19	59128983	35452028	0.5996	5.7752
chr20	63025520	87777974	1.3927	2.7966
chr21	48129895	42661537	0.8864	3.8695
chr22	51304566	22168298	0.4321	1.2577
chrMT	16571	2073548	125.1311	91.7812
chrX	155270560	139227479	0.8967	4.1389

chrY	59373566	10307732	0.1736	13.6928

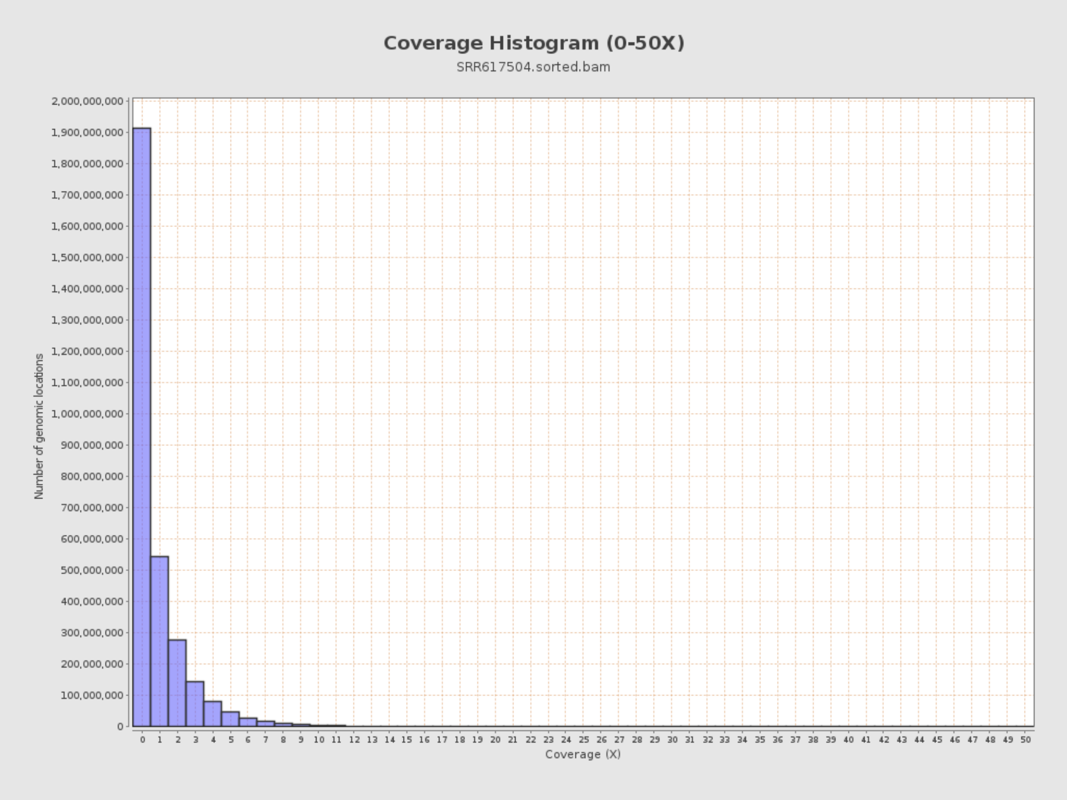
3. Results : Coverage across reference



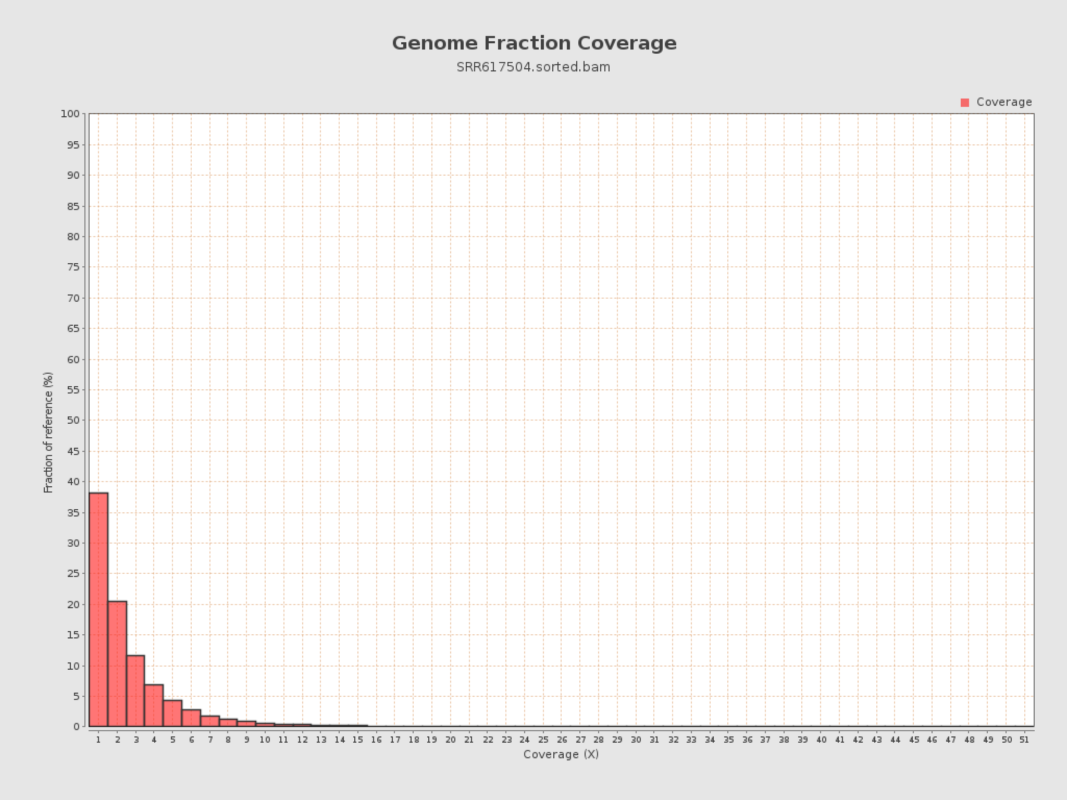
4. Results : Coverage Histogram



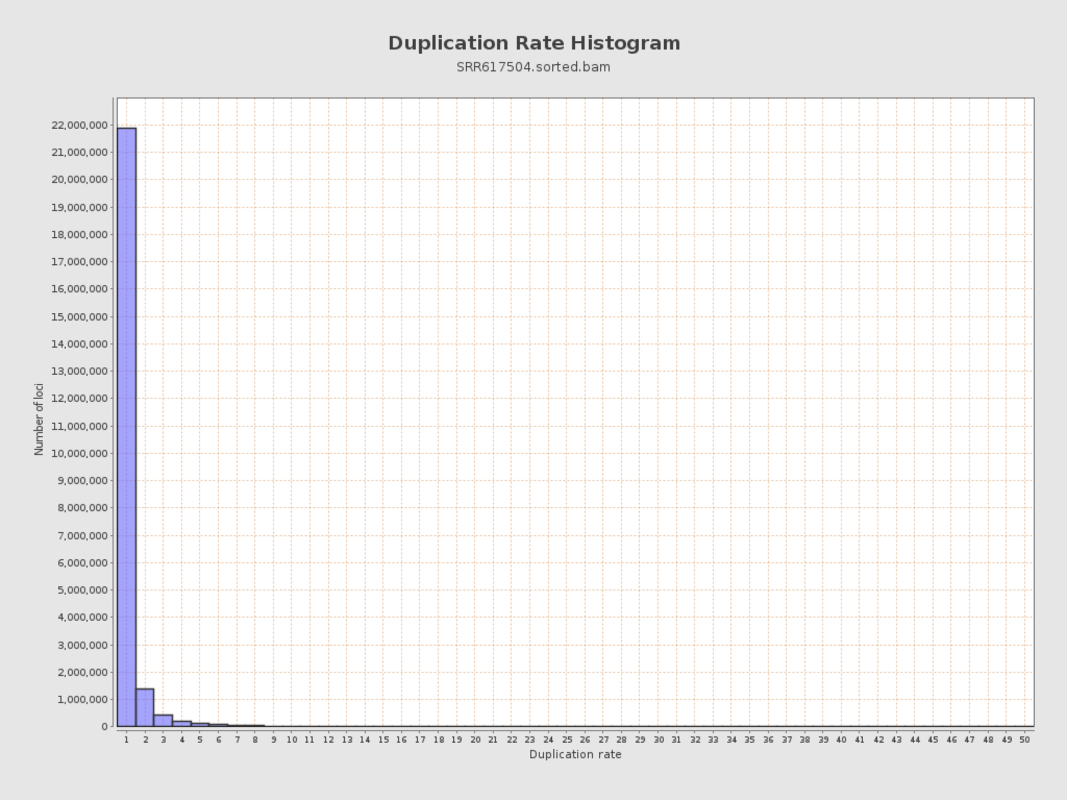
5. Results : Coverage Histogram (0-50X)



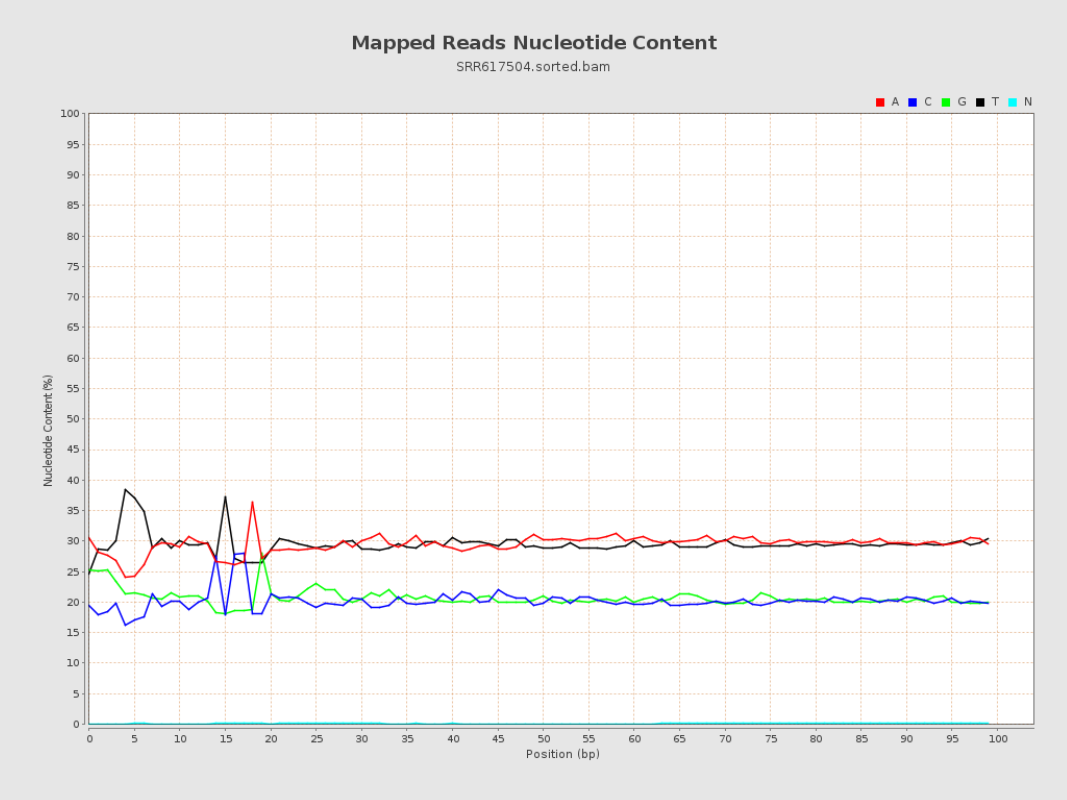
6. Results : Genome Fraction Coverage



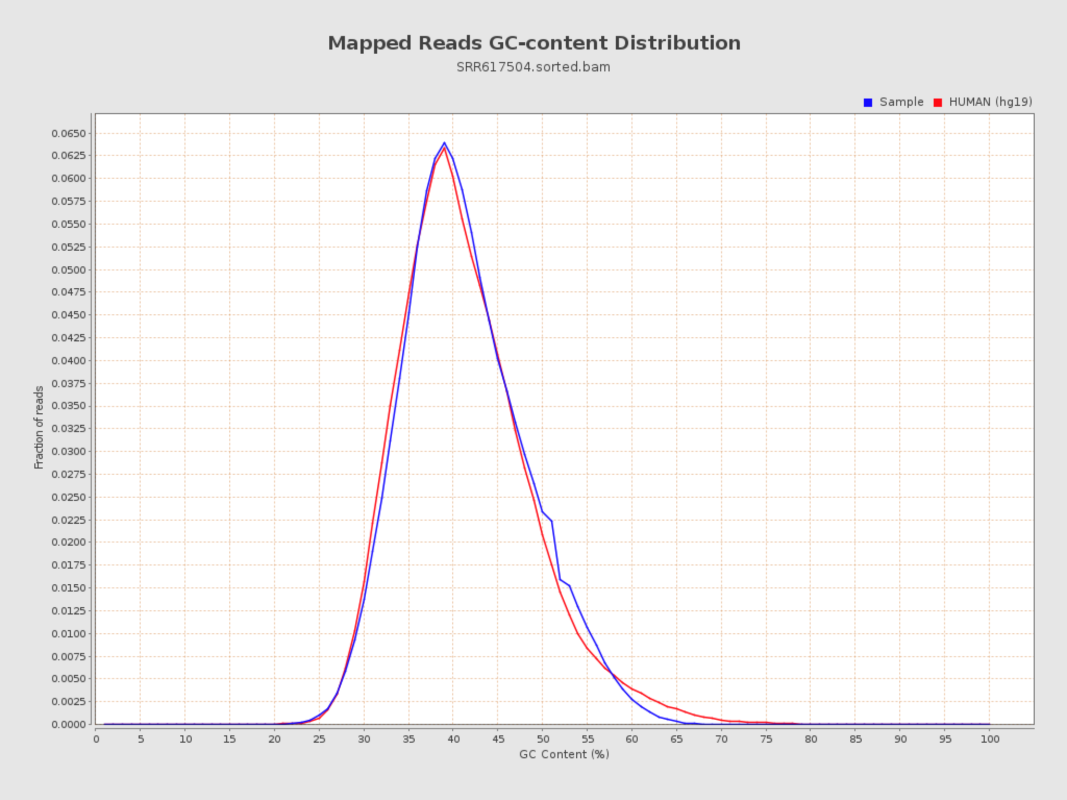
7. Results : Duplication Rate Histogram



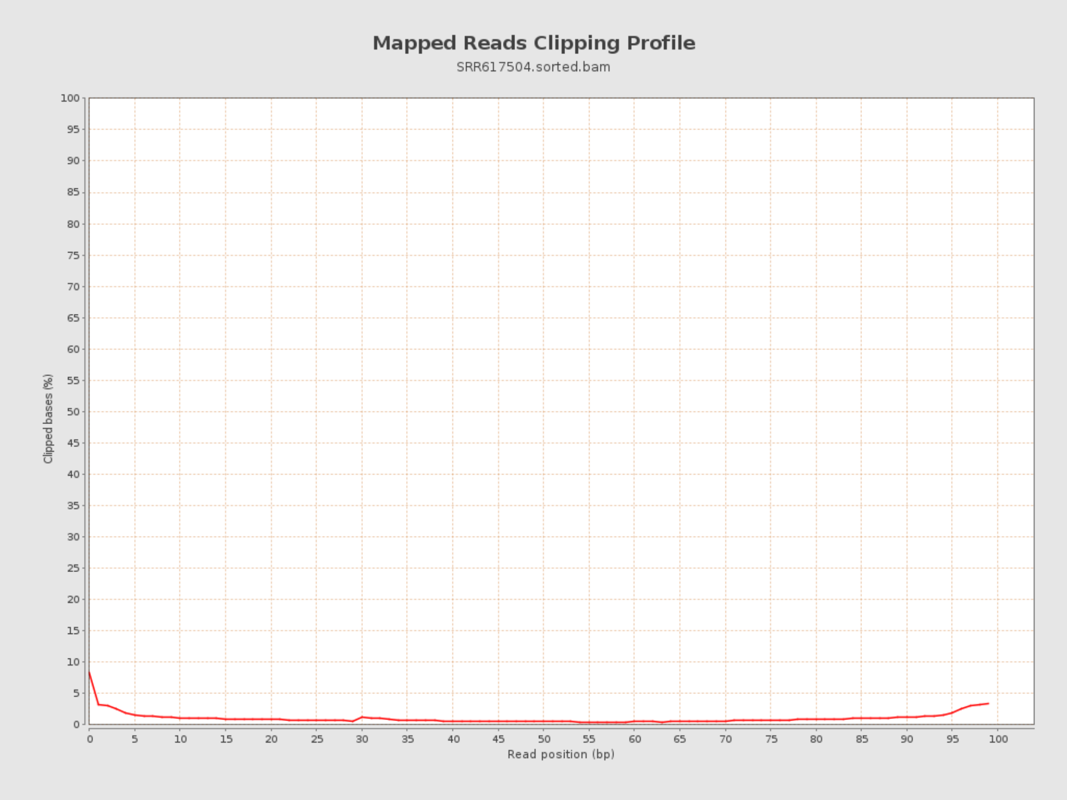
8. Results : Mapped Reads Nucleotide Content



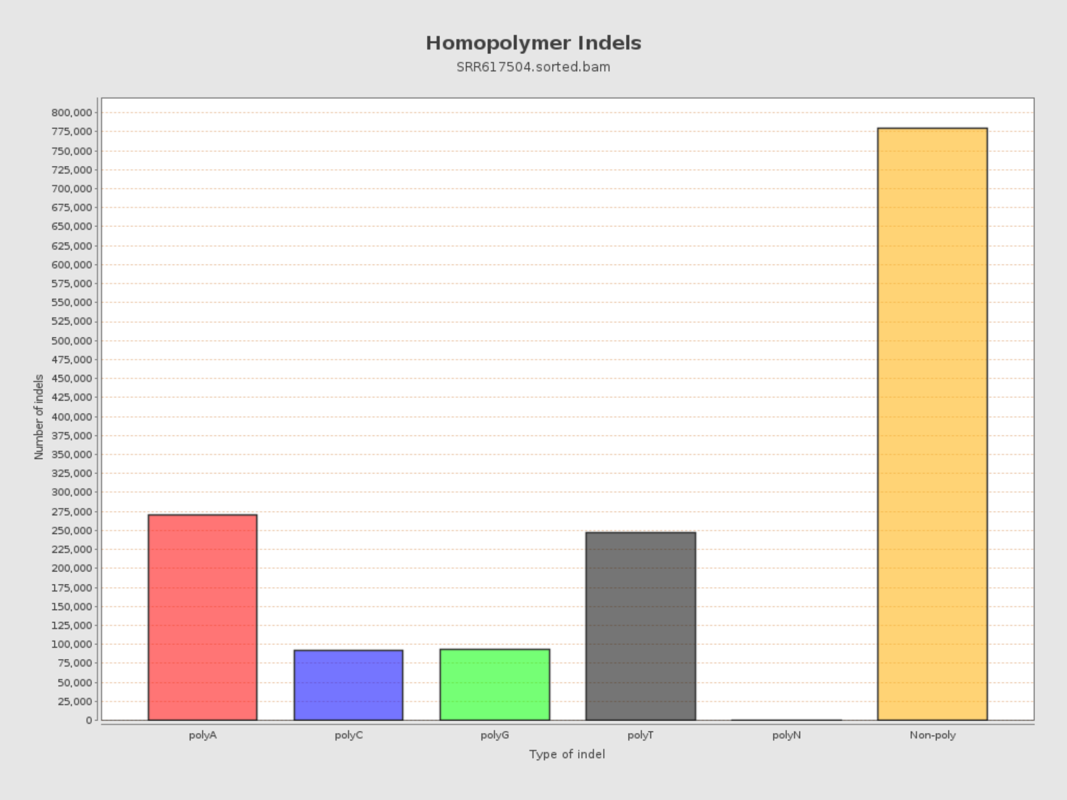
9. Results : Mapped Reads GC-content Distribution



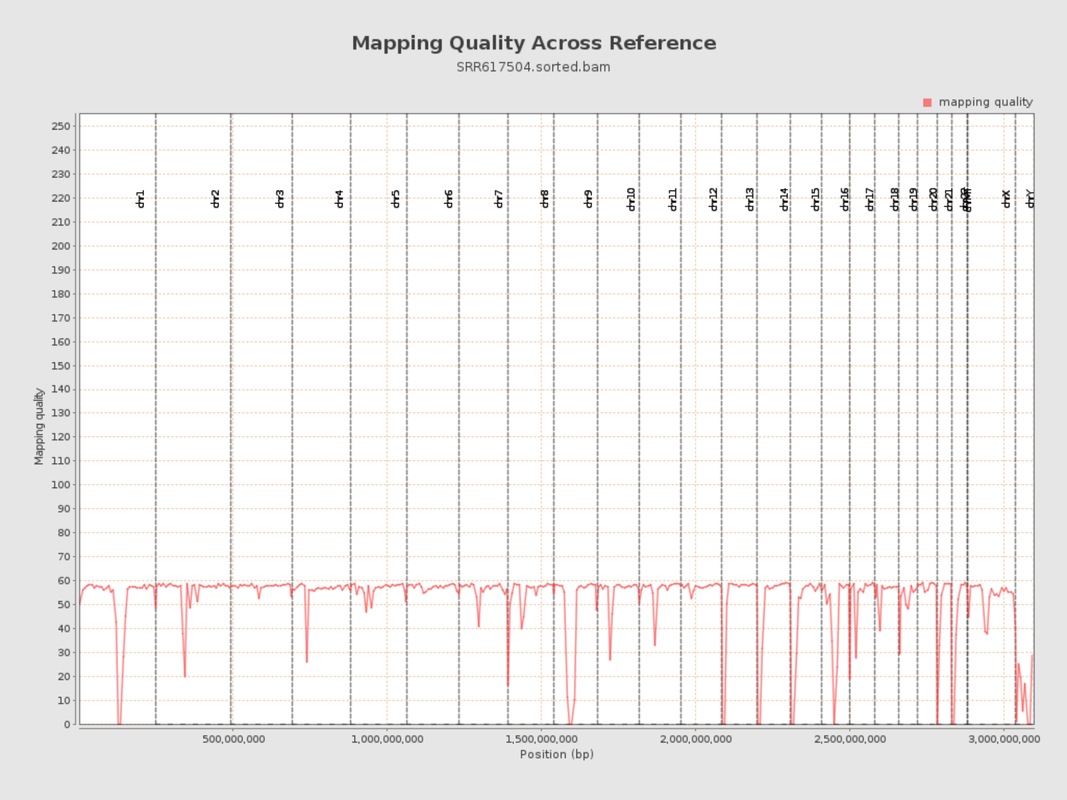
10. Results : Mapped Reads Clipping Profile



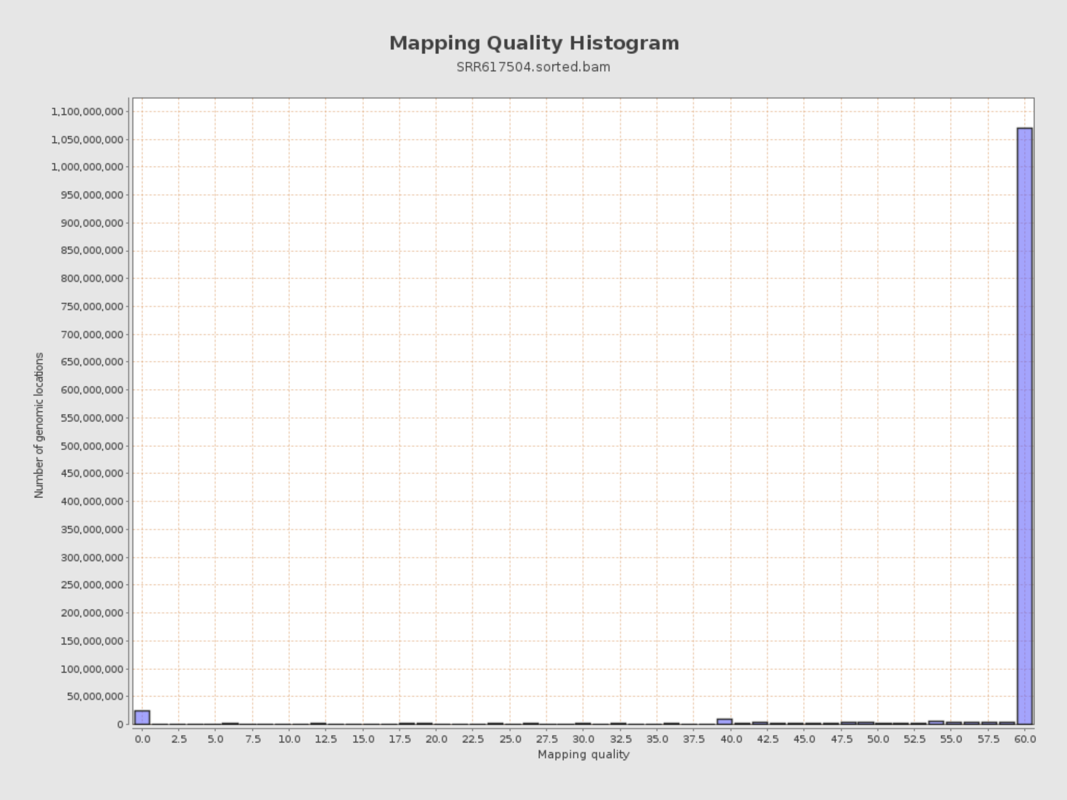
11. Results : Homopolymer Indels



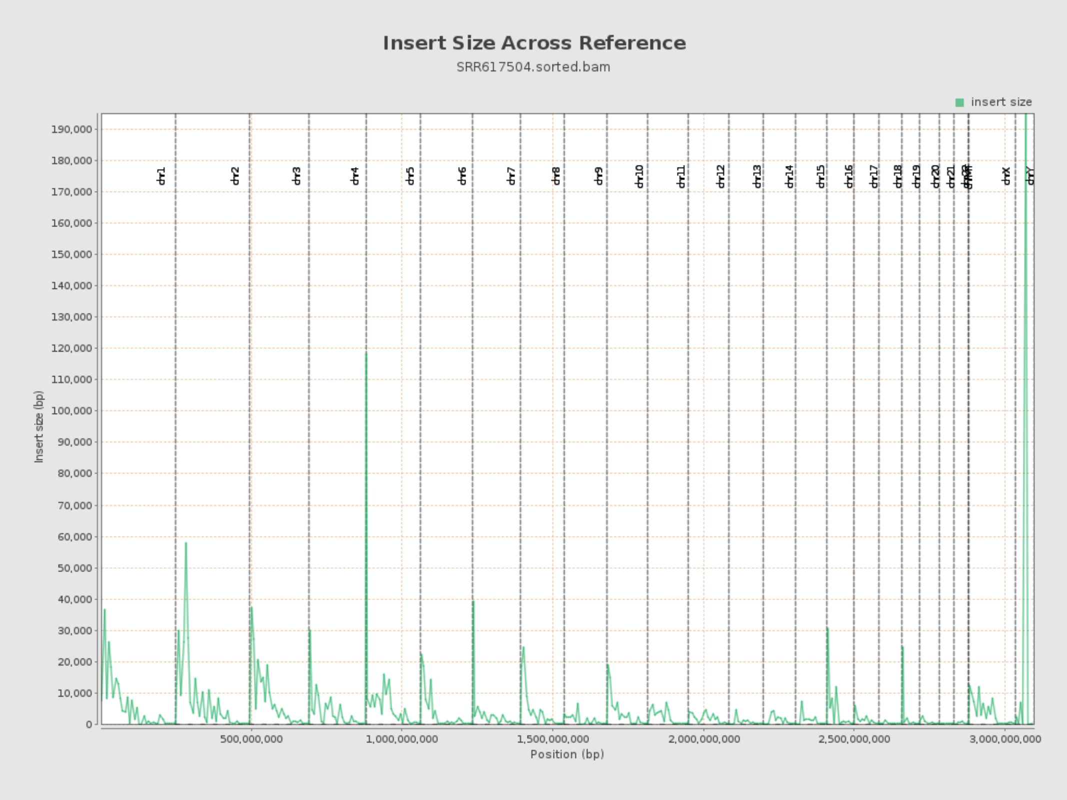
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram