Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/10 01:24:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617501.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_SRR617501 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617501_1.fastq.gz SRR617501_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 10 01:24:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617501.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	30,402,783 / 95.01%
Unmapped reads	1,597,217 / 4.99%
Mapped paired reads	30,402,783 / 95.01%
Mapped reads, first in pair	15,346,854 / 47.96%
Mapped reads, second in pair	15,055,929 / 47.05%
Mapped reads, both in pair	29,786,524 / 93.08%
Mapped reads, singletons	616,259 / 1.93%
Secondary alignments	0
Supplementary alignments	187,344 / 0.59%
Read min/max/mean length	30 / 100 / 100.23
Duplicated reads (estimated)	6,283,178 / 19.63%
Duplication rate	9.97%
Clipped reads	6,183,233 / 19.32%

2.2. ACGT Content

Number/percentage of A's	871,674,438 / 29.53%
Number/percentage of C's	595,590,381 / 20.18%
Number/percentage of T's	871,297,818 / 29.51%
Number/percentage of G's	610,411,809 / 20.68%
Number/percentage of N's	3,110,890 / 0.11%

GC Percentage	40.85%

2.3. Coverage

Mean	0.9542
Standard Deviation	9.6069

2.4. Mapping Quality

Mean Mapping Quality	52.62

2.5. Insert size

Mean	49,989.11
Standard Deviation	2,102,043.24
P25/Median/P75	174 / 220 / 291

2.6. Mismatches and indels

General error rate	1.24%
Mismatches	35,584,534
Insertions	443,698
Mapped reads with at least one insertion	1.43%
Deletions	1,028,793
Mapped reads with at least one deletion	3.31%
Homopolymer indels	47.39%

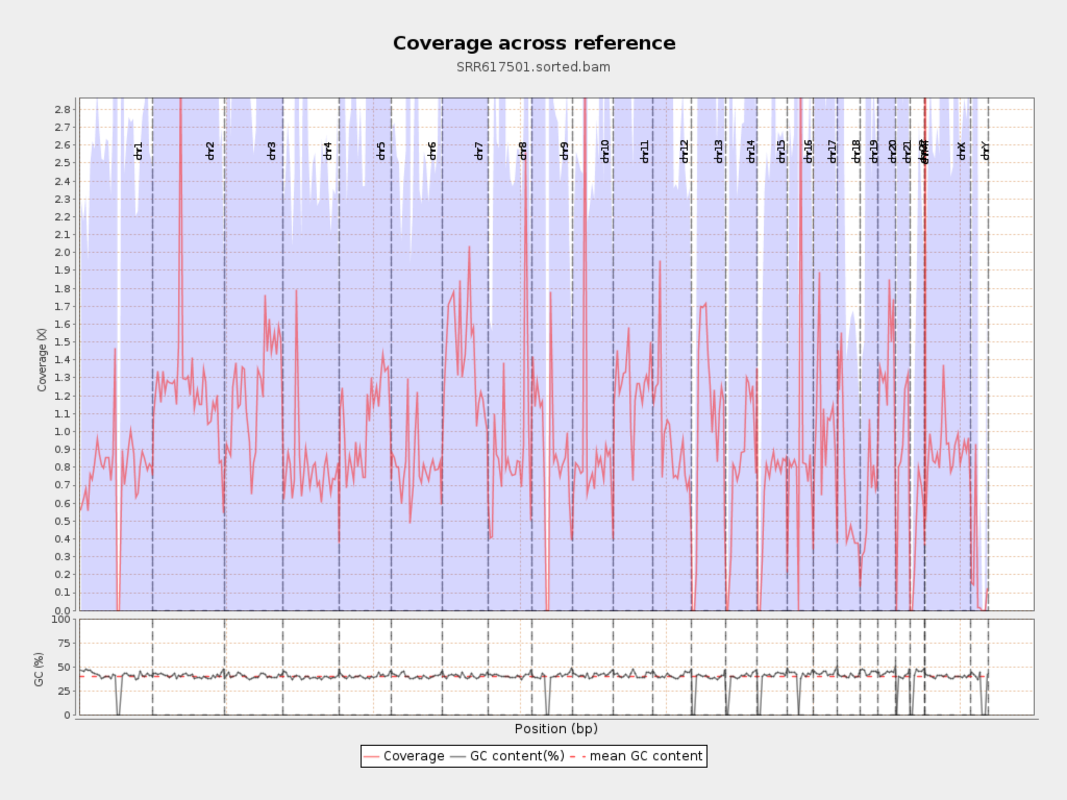
2.7. Chromosome stats

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

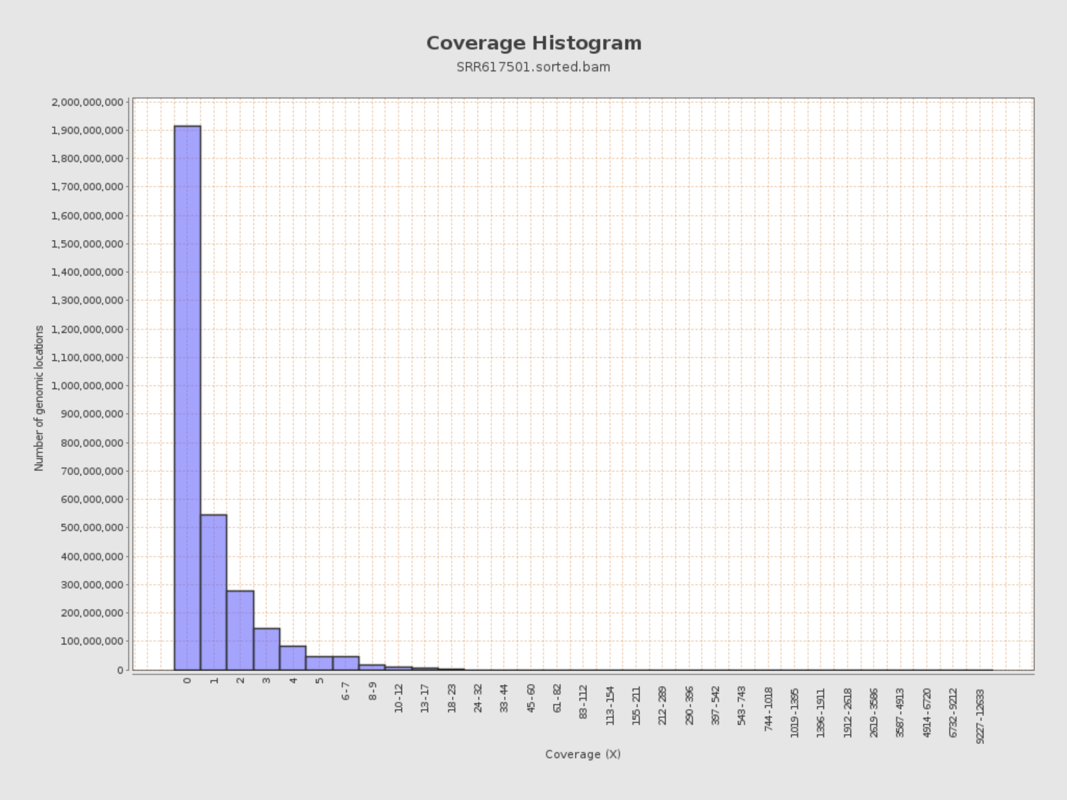
		bases	coverage	deviation
chr1	249250621	189967333	0.7622	9.3606
chr2	243199373	305091620	1.2545	11.3582
chr3	198022430	243876977	1.2316	2.2673
chr4	191154276	152676546	0.7987	6.1485
chr5	180915260	189021490	1.0448	2.0915
chr6	171115067	139284904	0.814	5.3493
chr7	159138663	227866440	1.4319	13.0957
chr8	146364022	131368831	0.8975	3.8355
chr9	141213431	122187568	0.8653	17.9201
chr10	135534747	124969532	0.922	18.535
chr11	135006516	166525474	1.2335	12.5554
chr12	133851895	129009053	0.9638	2.0838
chr13	115169878	125327576	1.0882	2.1923
chr14	107349540	86096766	0.802	2.2525
chr15	102531392	66873100	0.6522	1.6949
chr16	90354753	79728555	0.8824	14.706
chr17	81195210	82581977	1.0171	13.4204
chr18	78077248	53064501	0.6796	16.9832
chr19	59128983	35266882	0.5964	5.8049
chr20	63025520	87132374	1.3825	2.8207
chr21	48129895	42474592	0.8825	3.8091
chr22	51304566	22226143	0.4332	1.267
chrMT	16571	2052882	123.884	93.1977
chrX	155270560	138882569	0.8945	4.1239

chrY	59373566	10285411	0.1732	13.4638

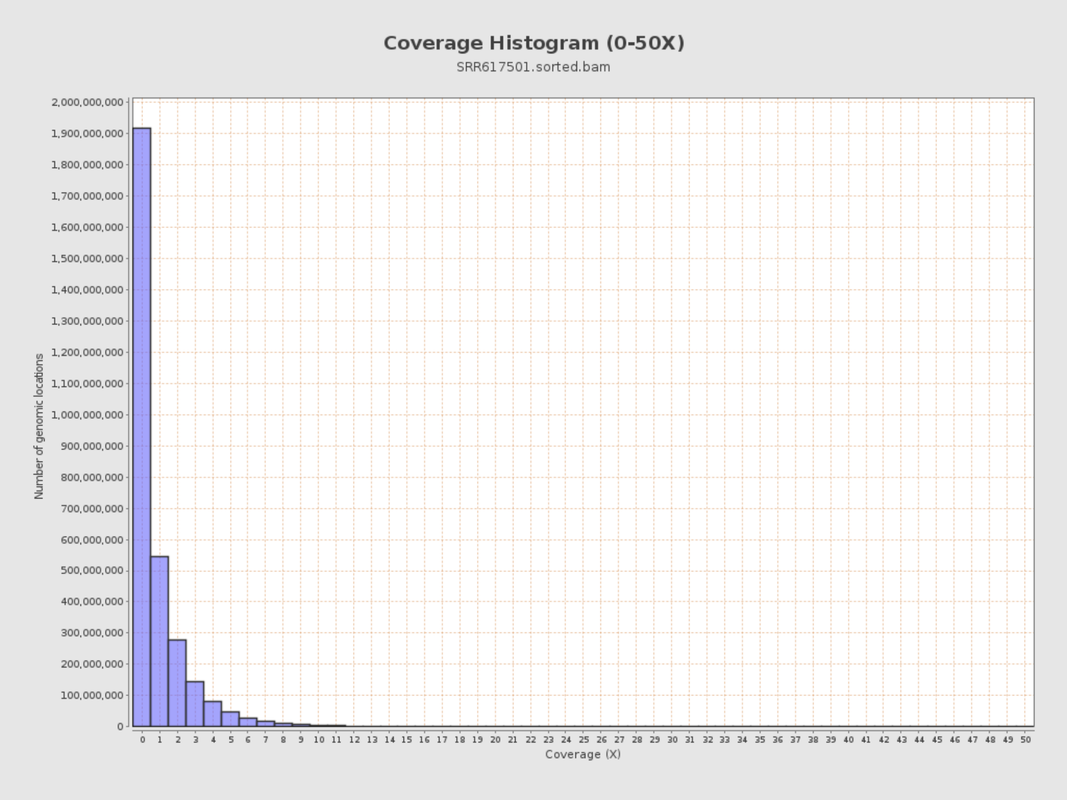
3. Results : Coverage across reference



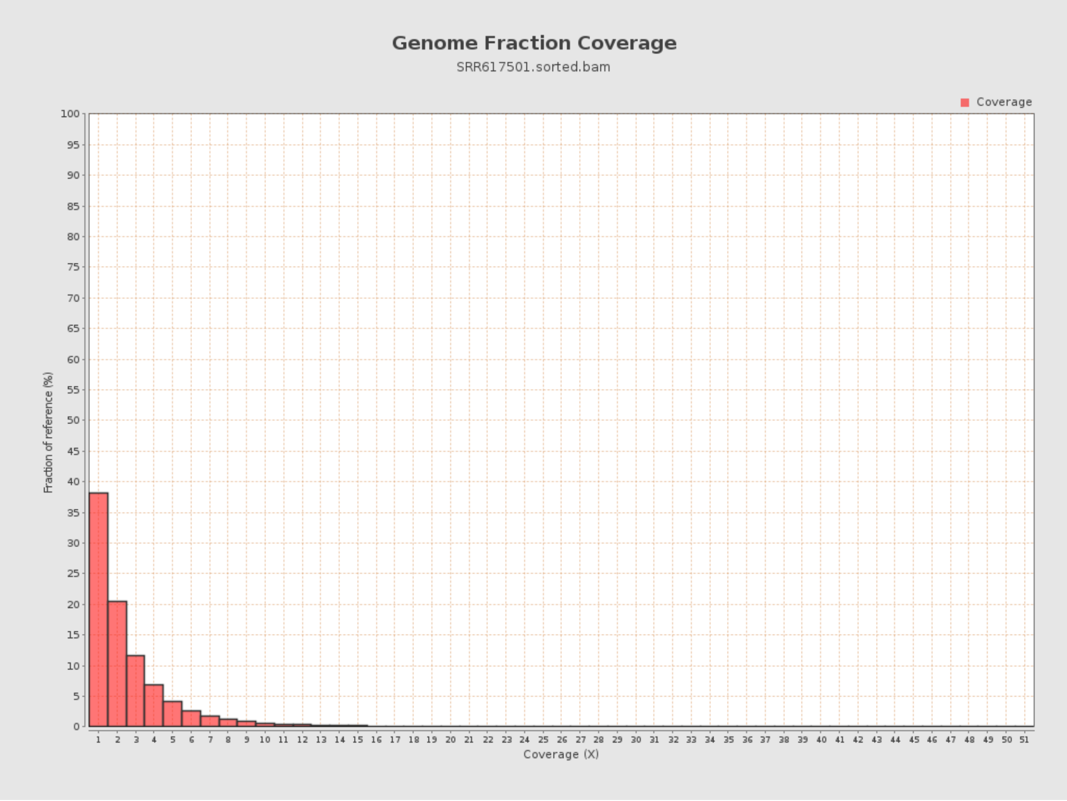
4. Results : Coverage Histogram



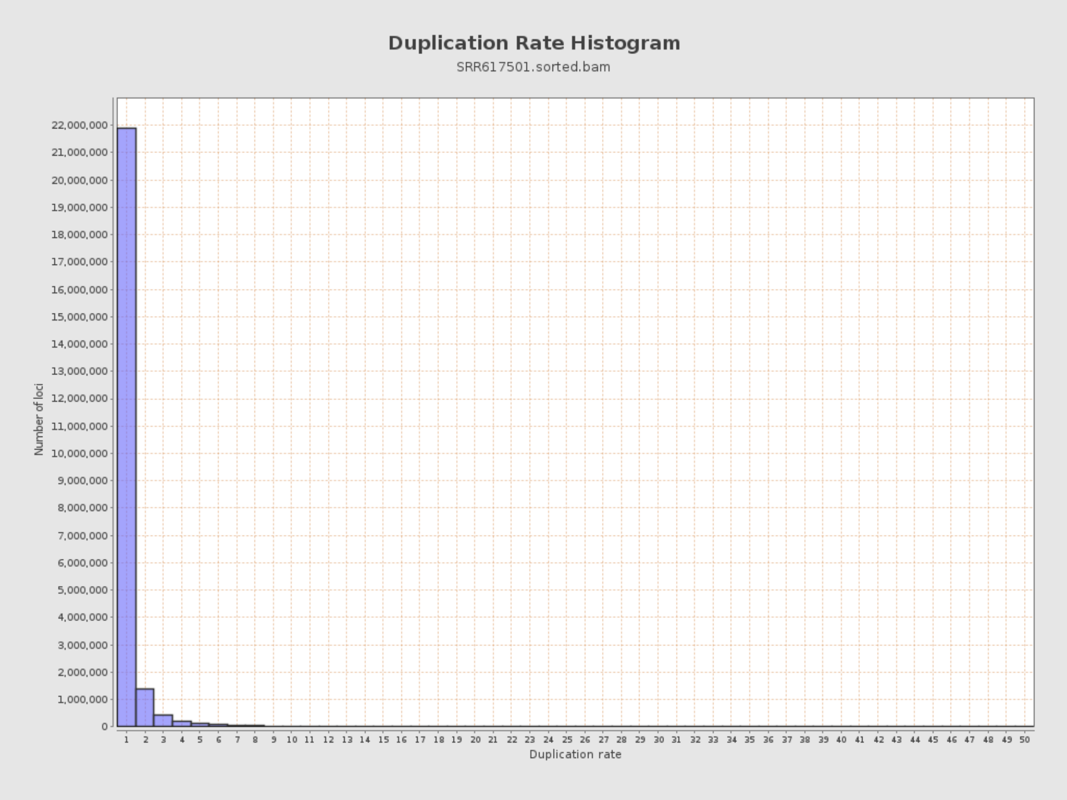
5. Results : Coverage Histogram (0-50X)



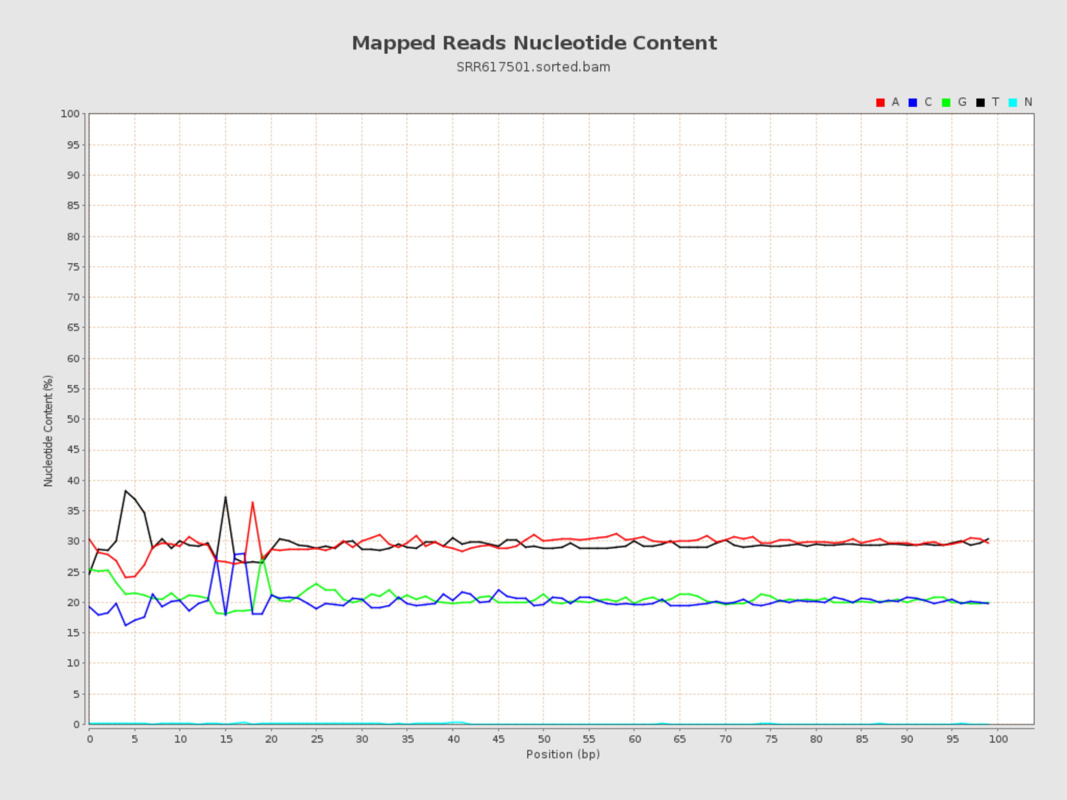
6. Results : Genome Fraction Coverage



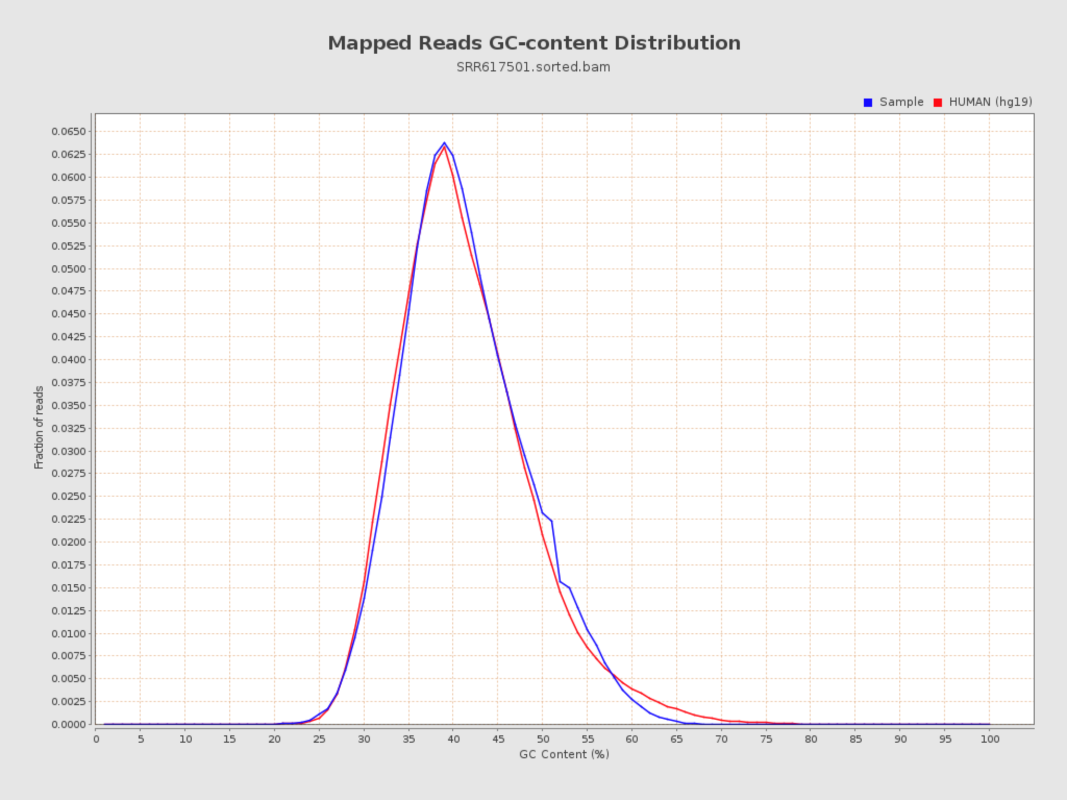
7. Results : Duplication Rate Histogram



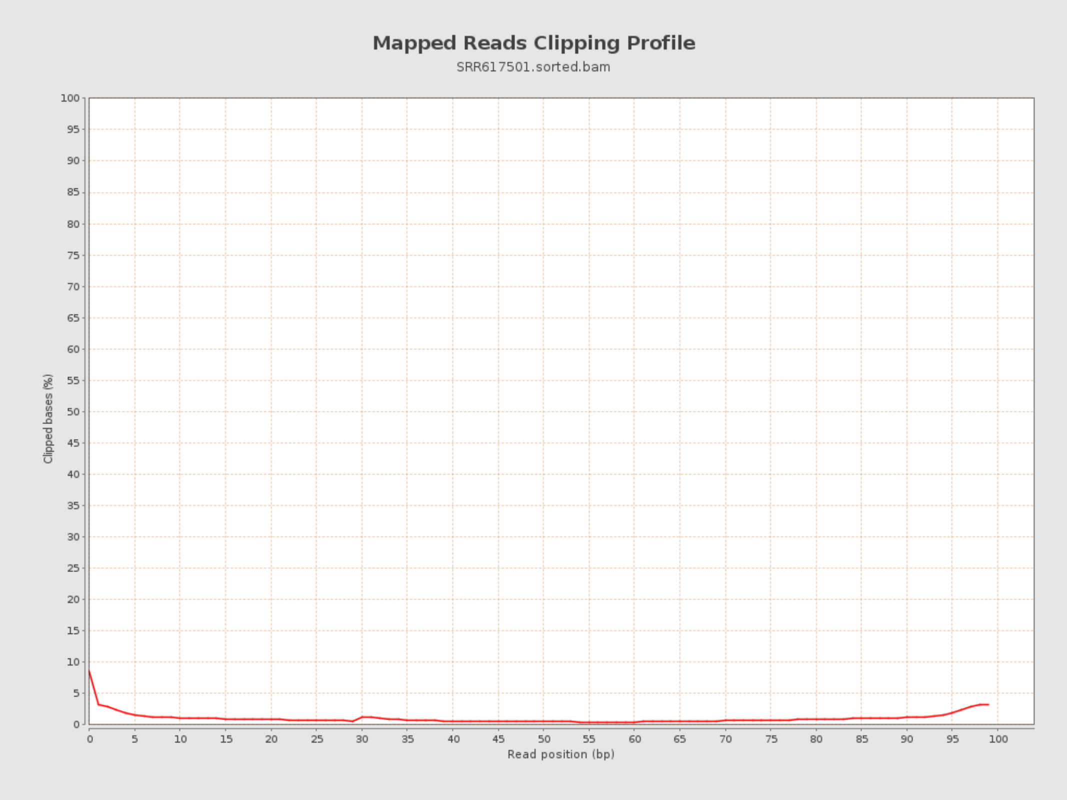
8. Results : Mapped Reads Nucleotide Content



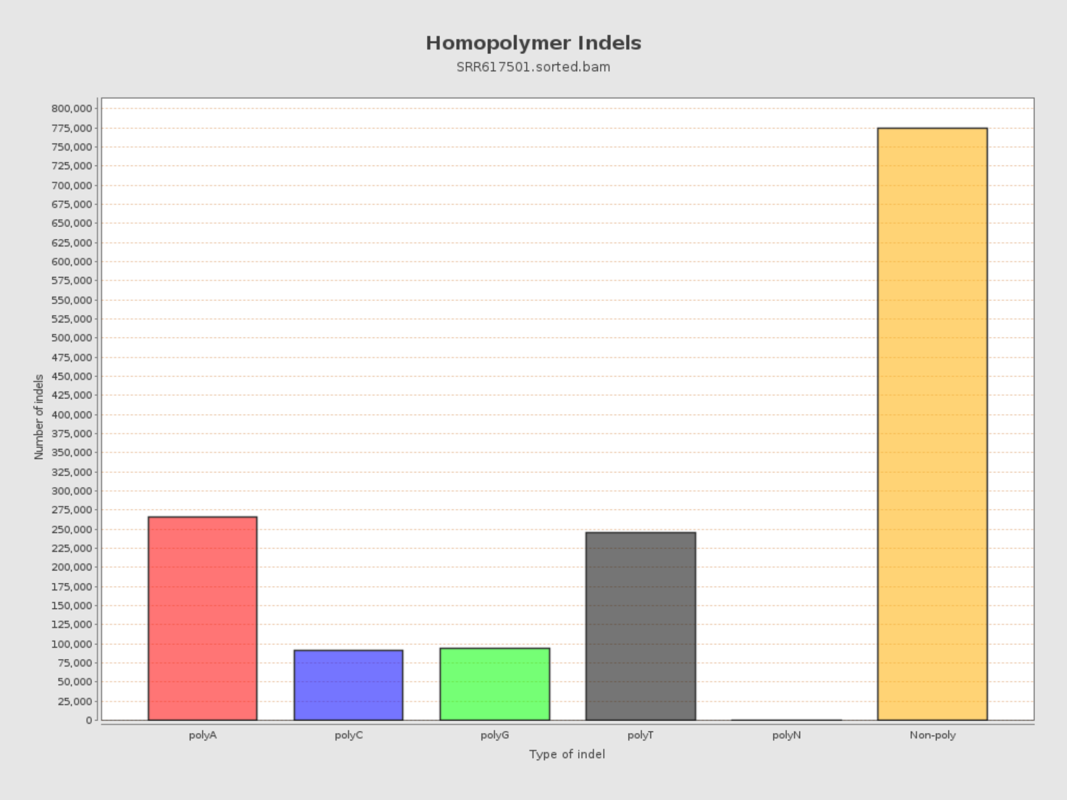
9. Results : Mapped Reads GC-content Distribution



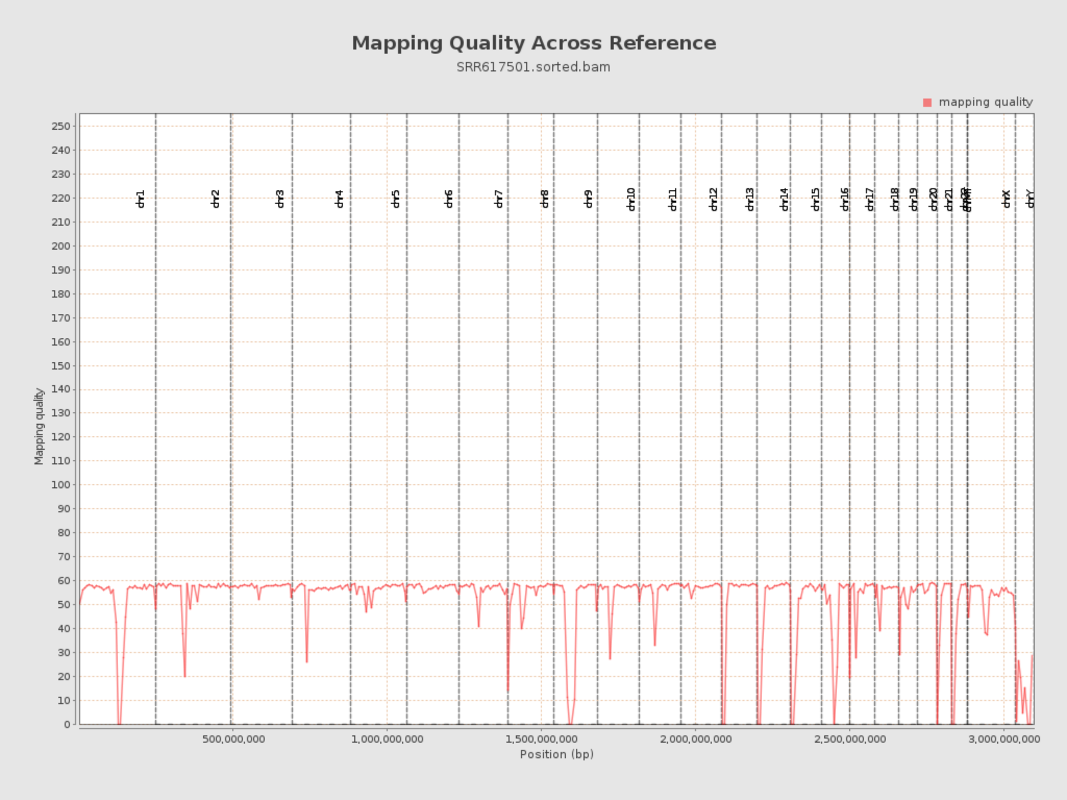
10. Results : Mapped Reads Clipping Profile



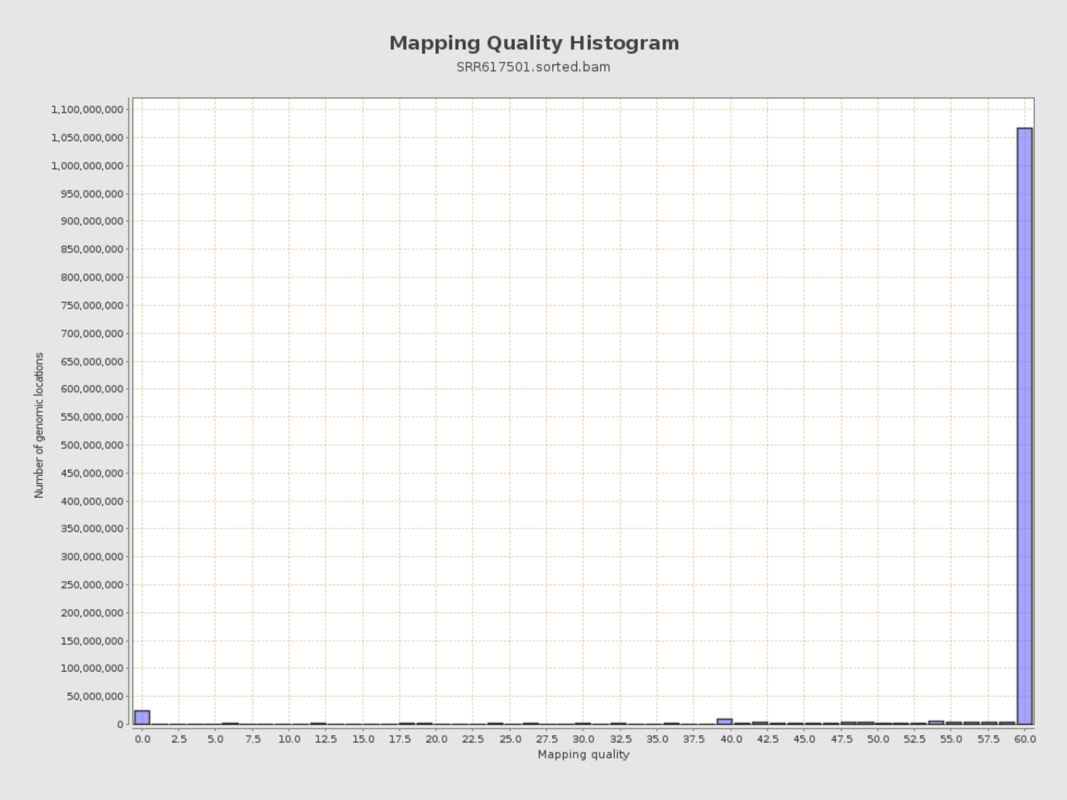
11. Results : Homopolymer Indels



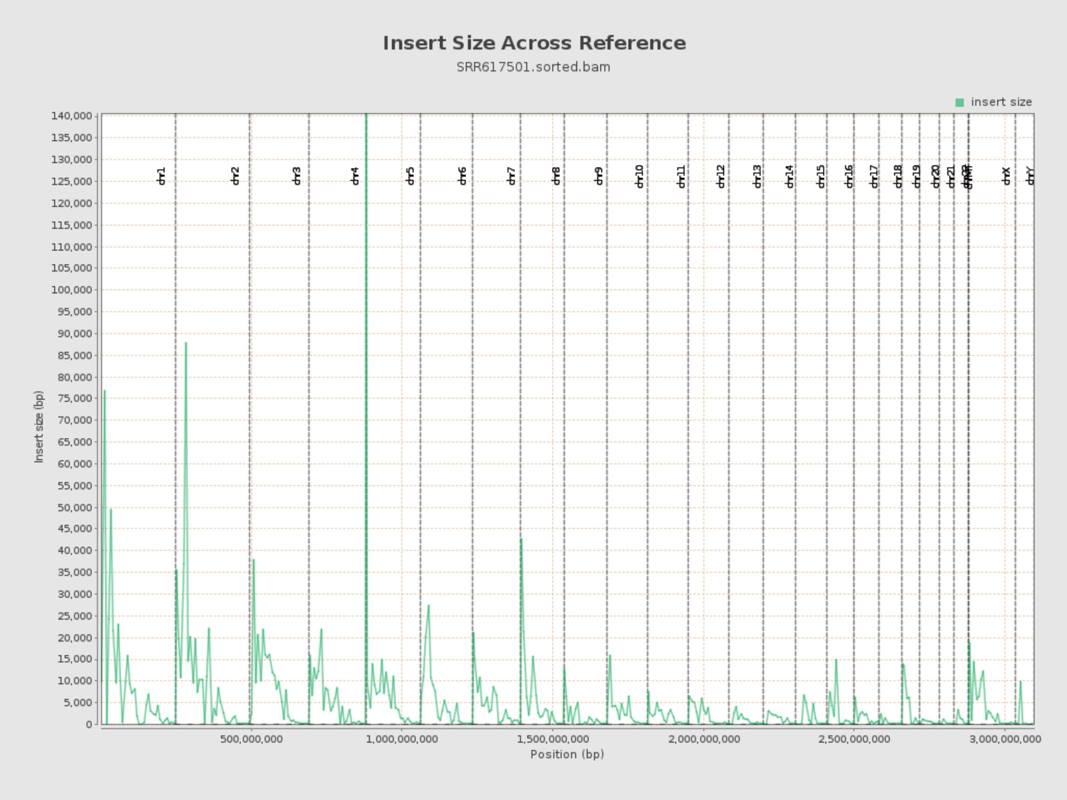
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram