Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/09 10:45:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617484.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_SRR617484 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617484_1.fastq.gz SRR617484_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 09 10:45:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617484.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	29,953,673 / 93.61%
Unmapped reads	2,046,327 / 6.39%
Mapped paired reads	29,953,673 / 93.61%
Mapped reads, first in pair	15,162,231 / 47.38%
Mapped reads, second in pair	14,791,442 / 46.22%
Mapped reads, both in pair	29,270,134 / 91.47%
Mapped reads, singletons	683,539 / 2.14%
Secondary alignments	0
Supplementary alignments	135,880 / 0.42%
Read min/max/mean length	30 / 100 / 100.17
Duplicated reads (estimated)	6,023,158 / 18.82%
Duplication rate	9.75%
Clipped reads	6,177,951 / 19.31%

2.2. ACGT Content

Number/percentage of A's	857,580,288 / 29.52%
Number/percentage of C's	586,381,798 / 20.19%
Number/percentage of T's	855,667,786 / 29.46%
Number/percentage of G's	600,708,540 / 20.68%
Number/percentage of N's	4,586,193 / 0.16%

GC Percentage	40.86%

2.3. Coverage

Mean	0.9389
Standard Deviation	9.4616

2.4. Mapping Quality

Mean Mapping Quality	52.68

2.5. Insert size

Mean	31,694.37
Standard Deviation	1,653,370.04
P25/Median/P75	173 / 218 / 287

2.6. Mismatches and indels

General error rate	1.34%
Mismatches	38,145,513
Insertions	428,615
Mapped reads with at least one insertion	1.4%
Deletions	1,002,095
Mapped reads with at least one deletion	3.28%
Homopolymer indels	47.4%

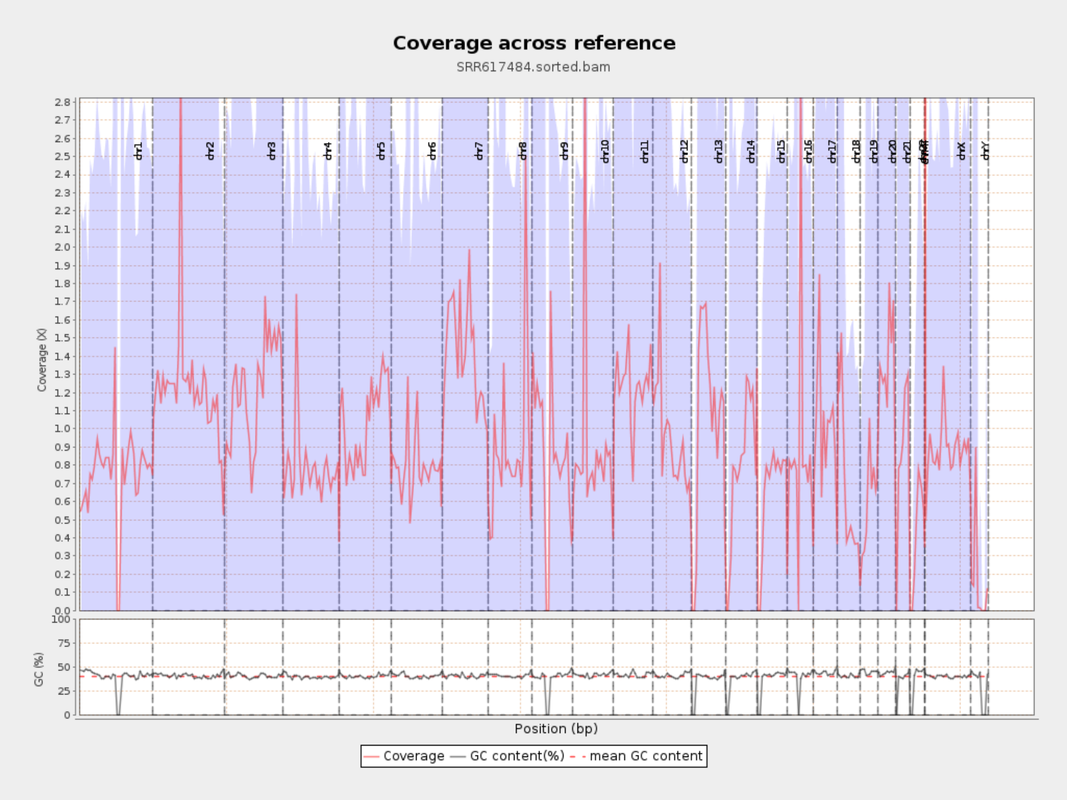
2.7. Chromosome stats

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

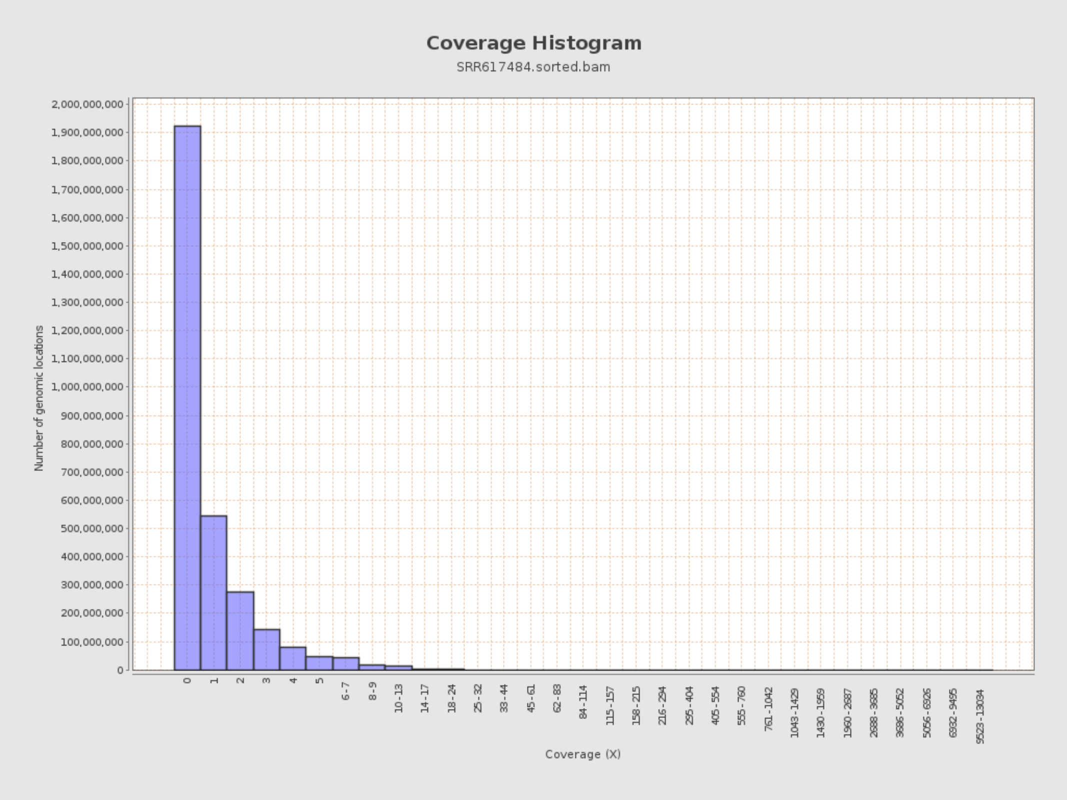
		bases	coverage	deviation
chr1	249250621	187241977	0.7512	9.1858
chr2	243199373	300597459	1.236	11.0536
chr3	198022430	240727937	1.2157	2.2028
chr4	191154276	150420669	0.7869	5.8192
chr5	180915260	186225563	1.0294	2.0308
chr6	171115067	136974408	0.8005	5.3255
chr7	159138663	224384728	1.41	12.9371
chr8	146364022	129178120	0.8826	3.7518
chr9	141213431	120274069	0.8517	18.0551
chr10	135534747	122977019	0.9073	18.3463
chr11	135006516	163901579	1.214	12.2738
chr12	133851895	126693069	0.9465	1.924
chr13	115169878	123630577	1.0735	2.0808
chr14	107349540	84490656	0.7871	2.1535
chr15	102531392	65676818	0.6406	1.4251
chr16	90354753	78292018	0.8665	14.5961
chr17	81195210	80605577	0.9927	13.1188
chr18	78077248	52011229	0.6662	16.5222
chr19	59128983	34600345	0.5852	5.6155
chr20	63025520	85590429	1.358	2.7412
chr21	48129895	41949451	0.8716	3.7271
chr22	51304566	21610549	0.4212	1.22
chrMT	16571	2000235	120.707	88.783
chrX	155270560	136631116	0.88	4.0085

chrY	59373566	9936309	0.1674	13.165

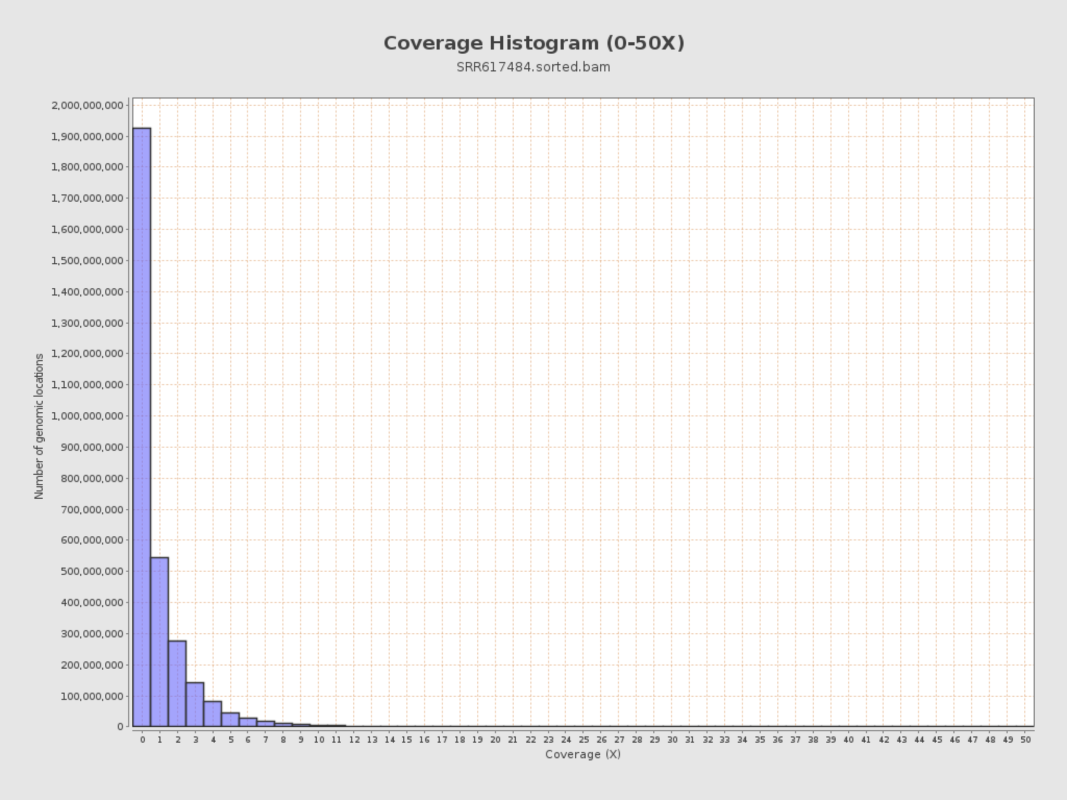
3. Results : Coverage across reference



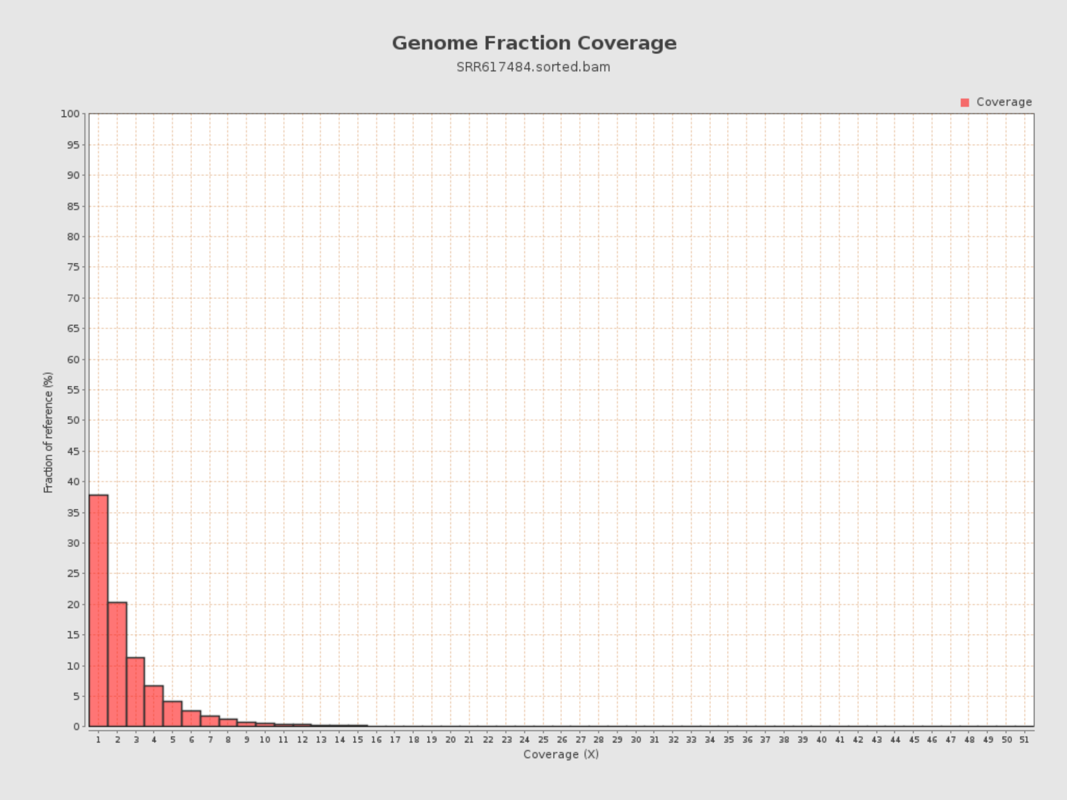
4. Results : Coverage Histogram



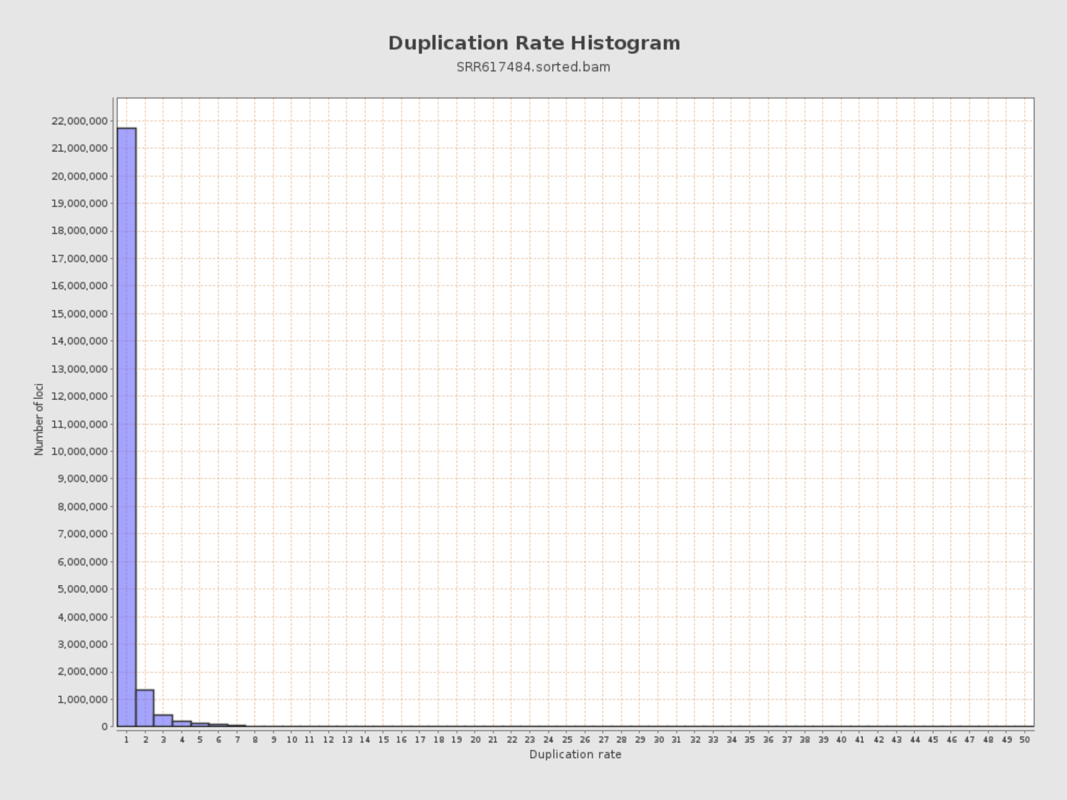
5. Results : Coverage Histogram (0-50X)



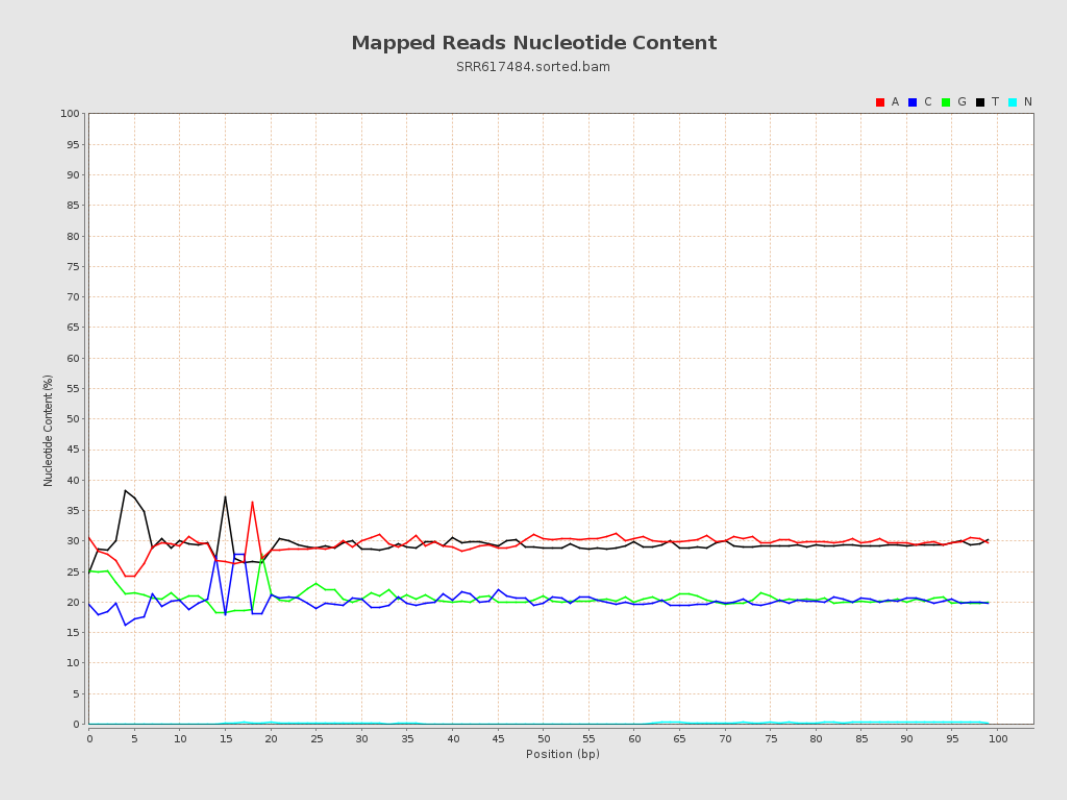
6. Results : Genome Fraction Coverage



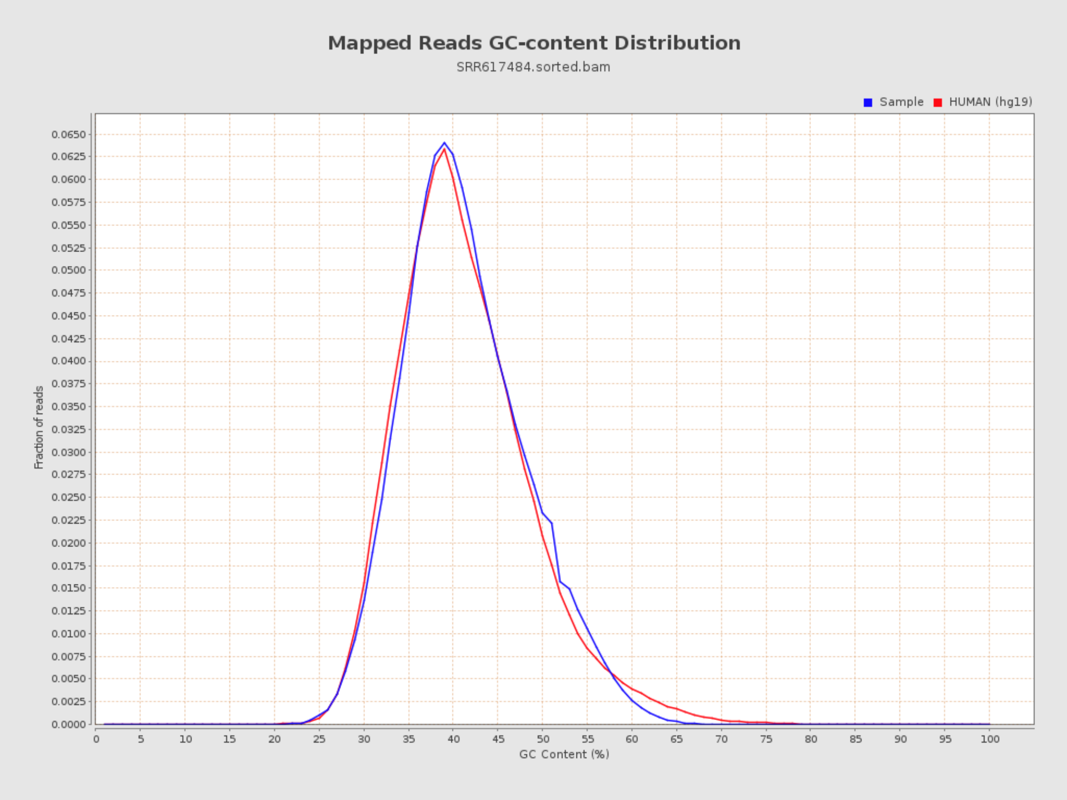
7. Results : Duplication Rate Histogram



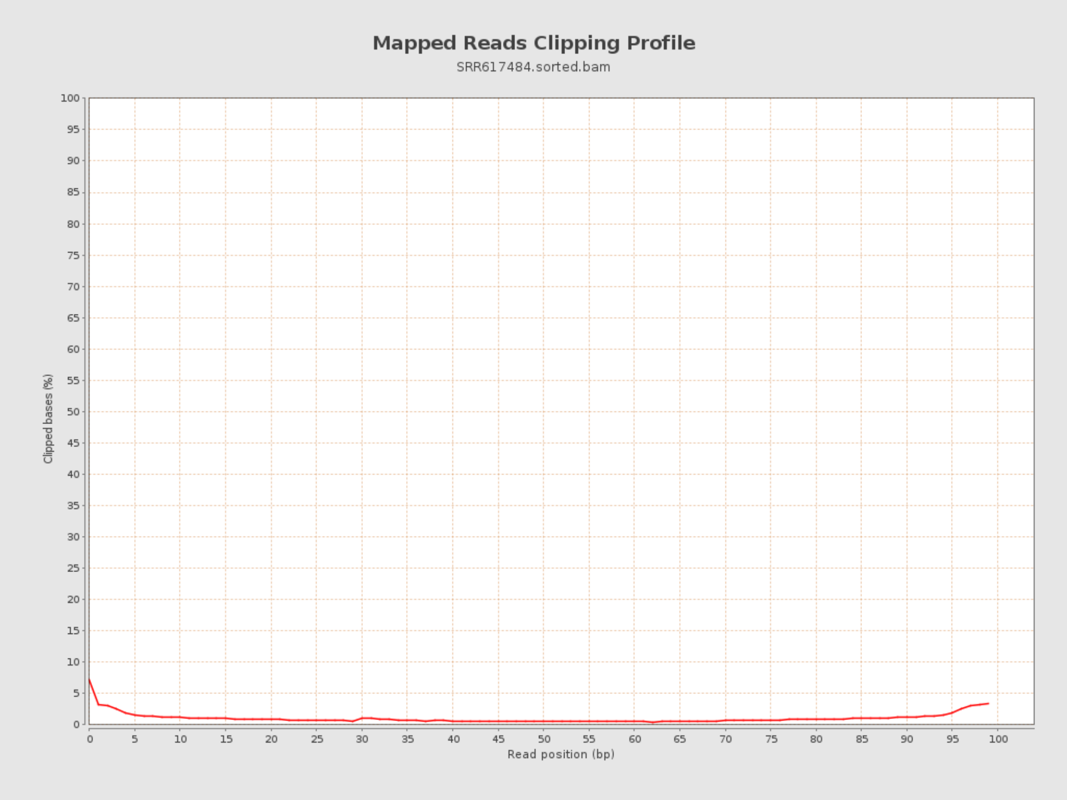
8. Results : Mapped Reads Nucleotide Content



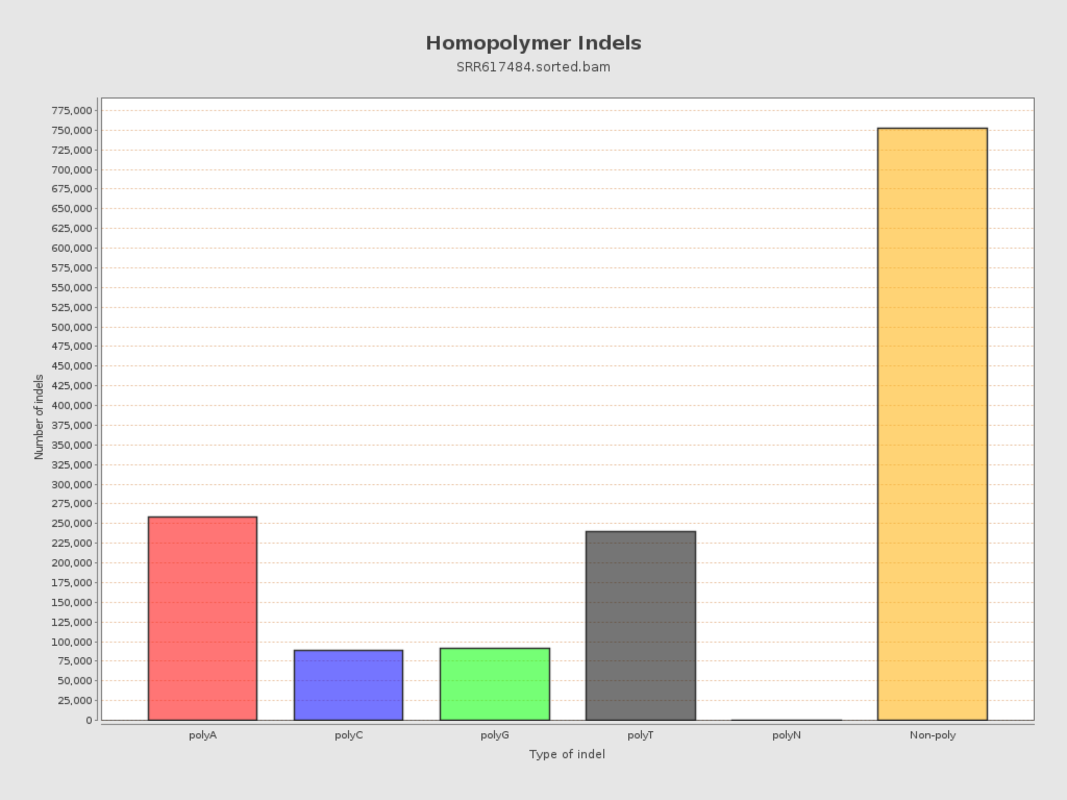
9. Results : Mapped Reads GC-content Distribution



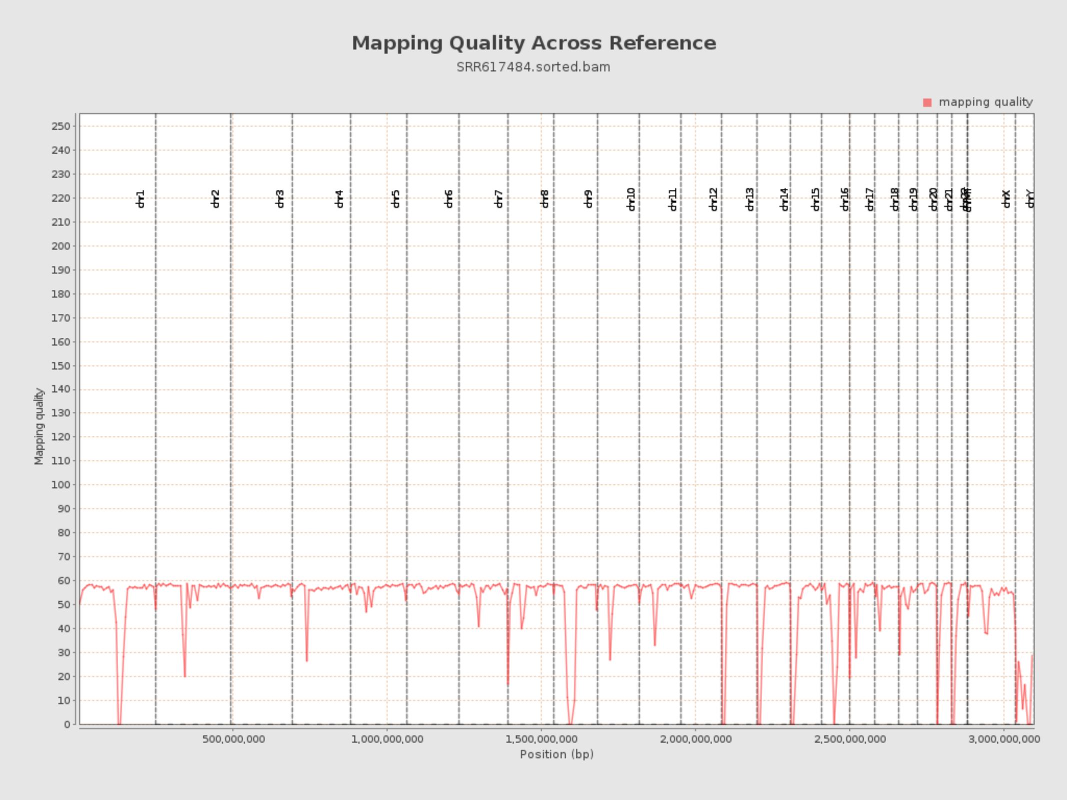
10. Results : Mapped Reads Clipping Profile



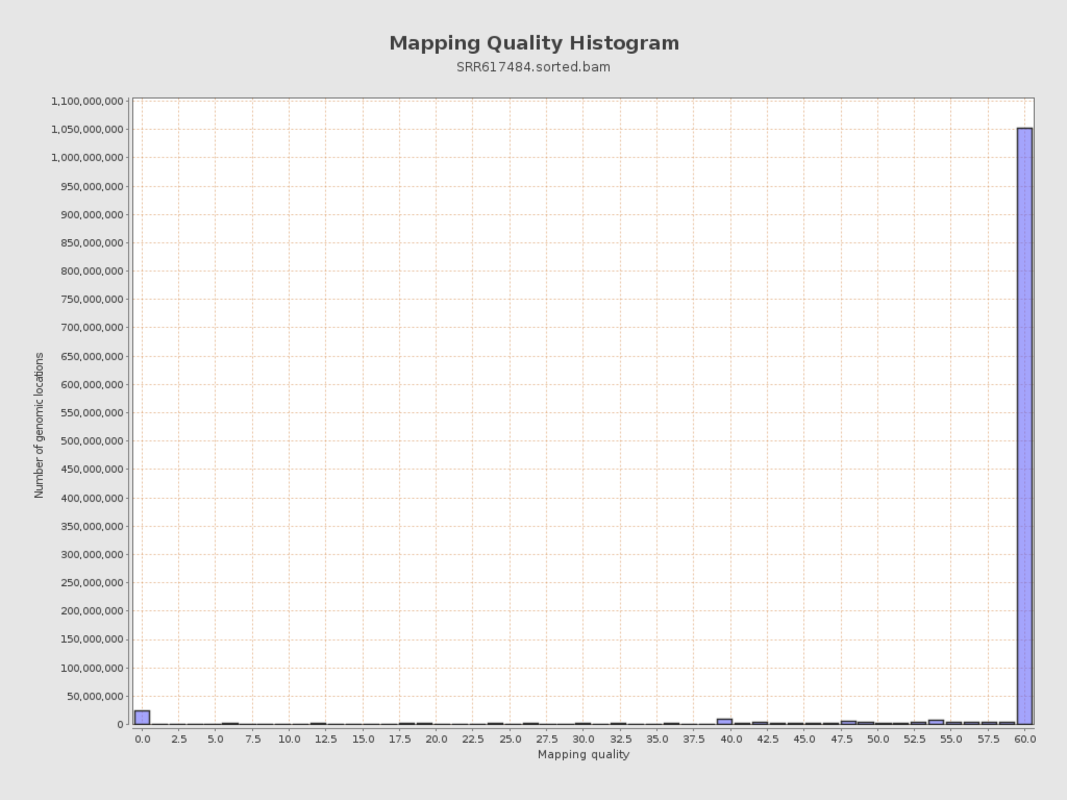
11. Results : Homopolymer Indels



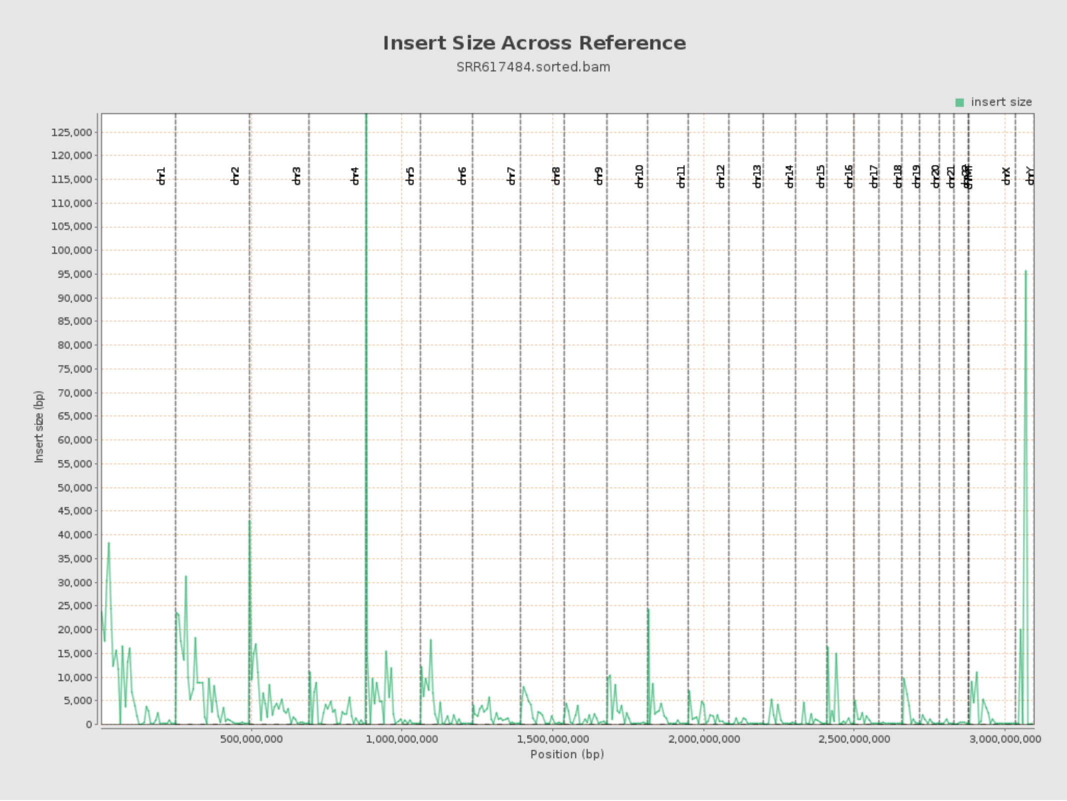
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram