Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/10 21:26:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617654.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_SRR617654 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617654_1.fastq.gz SRR617654_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 10 21:26:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617654.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	30,342,101 / 94.82%
Unmapped reads	1,657,899 / 5.18%
Mapped paired reads	30,342,101 / 94.82%
Mapped reads, first in pair	15,340,241 / 47.94%
Mapped reads, second in pair	15,001,860 / 46.88%
Mapped reads, both in pair	29,643,538 / 92.64%
Mapped reads, singletons	698,563 / 2.18%
Secondary alignments	0
Supplementary alignments	181,446 / 0.57%
Read min/max/mean length	30 / 100 / 100.22
Duplicated reads (estimated)	7,021,379 / 21.94%
Duplication rate	10.81%
Clipped reads	6,664,128 / 20.83%

2.2. ACGT Content

Number/percentage of A's	871,593,709 / 29.75%
Number/percentage of C's	582,809,179 / 19.89%
Number/percentage of T's	870,889,122 / 29.73%
Number/percentage of G's	599,589,319 / 20.47%
Number/percentage of N's	4,663,799 / 0.16%

GC Percentage	40.36%

2.3. Coverage

Mean	0.9469
Standard Deviation	10.528

2.4. Mapping Quality

Mean Mapping Quality	52.54

2.5. Insert size

Mean	47,490.58
Standard Deviation	2,040,155.36
P25/Median/P75	180 / 224 / 292

2.6. Mismatches and indels

General error rate	1.46%
Mismatches	41,876,330
Insertions	461,402
Mapped reads with at least one insertion	1.49%
Deletions	1,080,245
Mapped reads with at least one deletion	3.48%
Homopolymer indels	47.54%

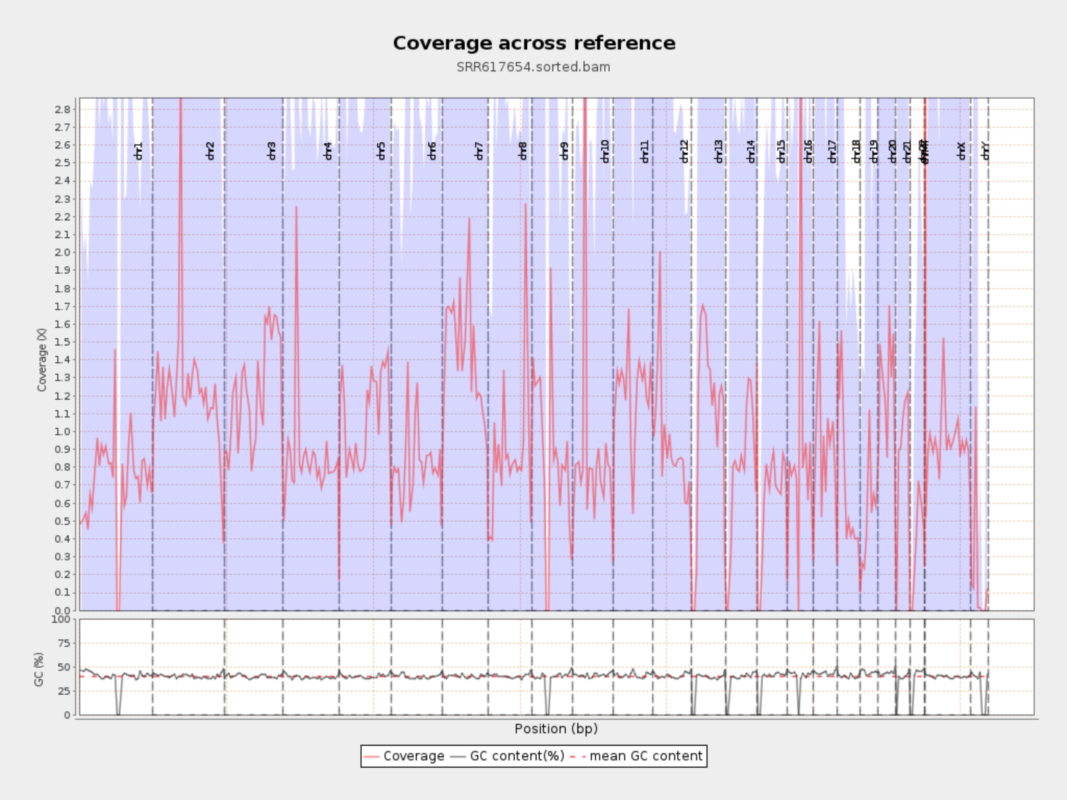
2.7. Chromosome stats

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

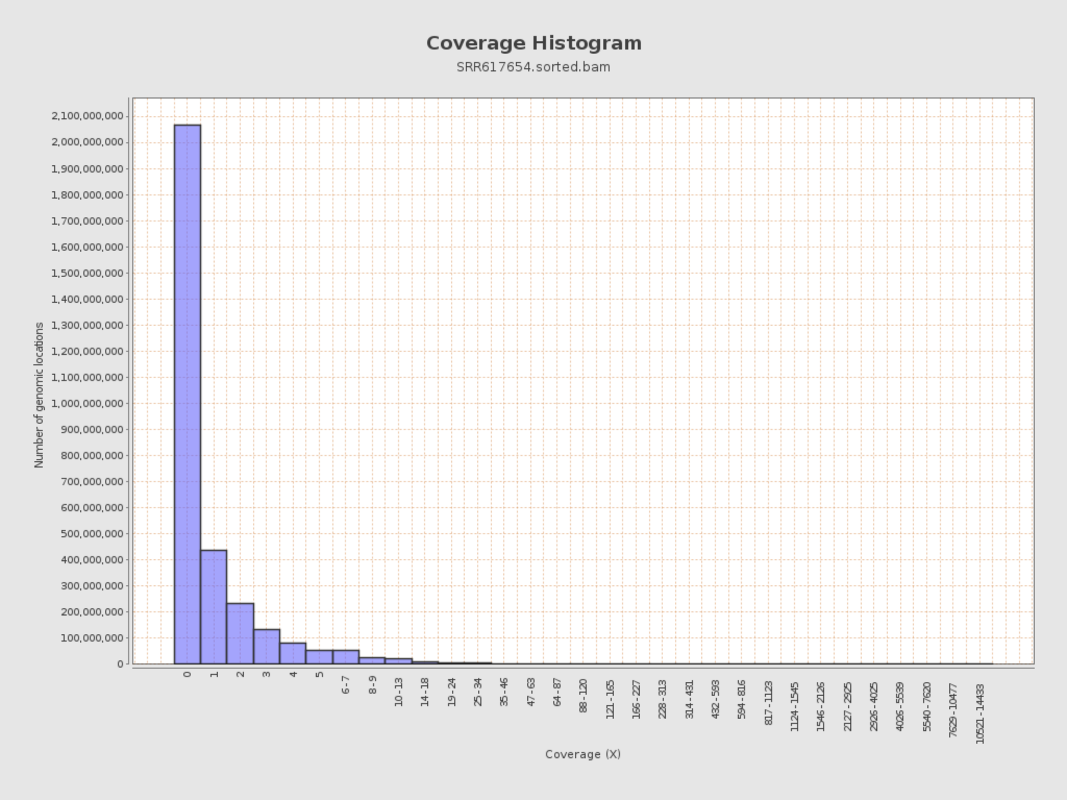
		bases	coverage	deviation
chr1	249250621	179731788	0.7211	10.2171
chr2	243199373	302897584	1.2455	12.0636
chr3	198022430	245661489	1.2406	2.4974
chr4	191154276	163801931	0.8569	8.3212
chr5	180915260	193916920	1.0719	2.3441
chr6	171115067	142145343	0.8307	5.7737
chr7	159138663	228838284	1.438	13.1865
chr8	146364022	130159194	0.8893	4.0821
chr9	141213431	120229039	0.8514	20.1605
chr10	135534747	124320807	0.9173	21.3718
chr11	135006516	161237583	1.1943	12.0715
chr12	133851895	124956502	0.9335	2.2265
chr13	115169878	125883792	1.093	2.3453
chr14	107349540	83980594	0.7823	2.4964
chr15	102531392	62768806	0.6122	1.7701
chr16	90354753	81153331	0.8982	16.5713
chr17	81195210	72561938	0.8937	12.6348
chr18	78077248	54233761	0.6946	18.2966
chr19	59128983	31159651	0.527	6.0779
chr20	63025520	79123813	1.2554	3.0869
chr21	48129895	42857736	0.8905	4.3818
chr22	51304566	18992900	0.3702	1.2804
chrMT	16571	3104360	187.3369	132.5181
chrX	155270560	145886793	0.9396	4.4149

chrY	59373566	11739508	0.1977	17.1063

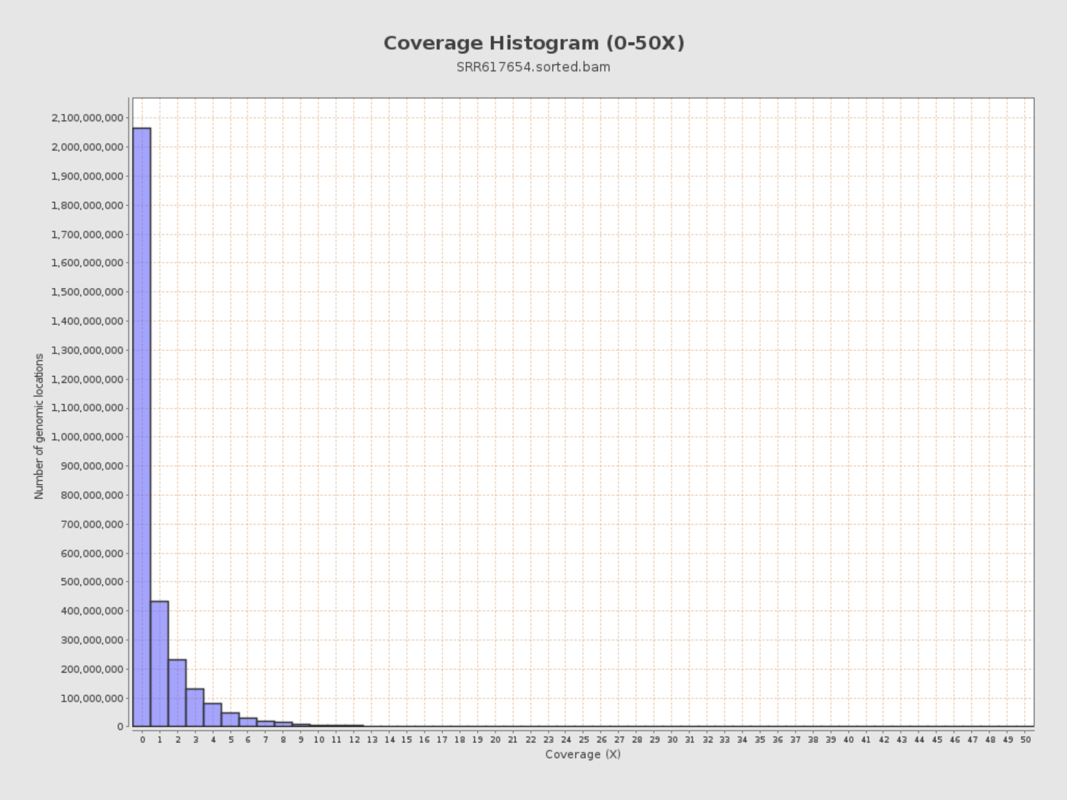
3. Results : Coverage across reference



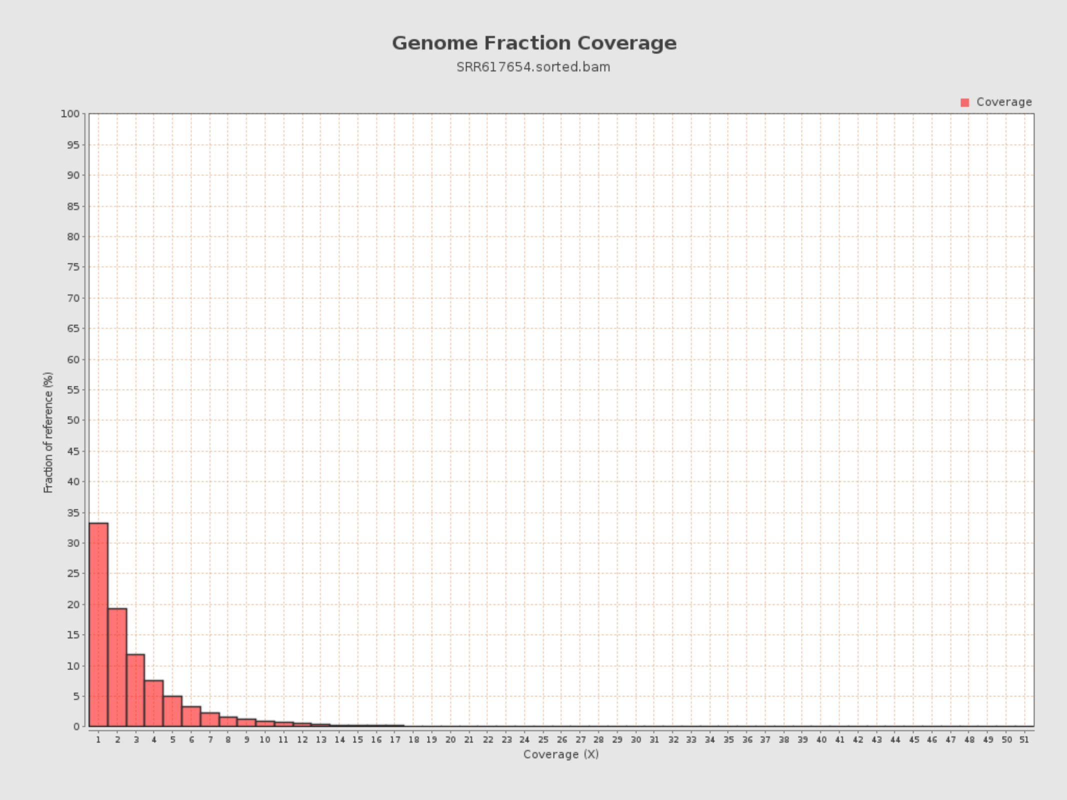
4. Results : Coverage Histogram



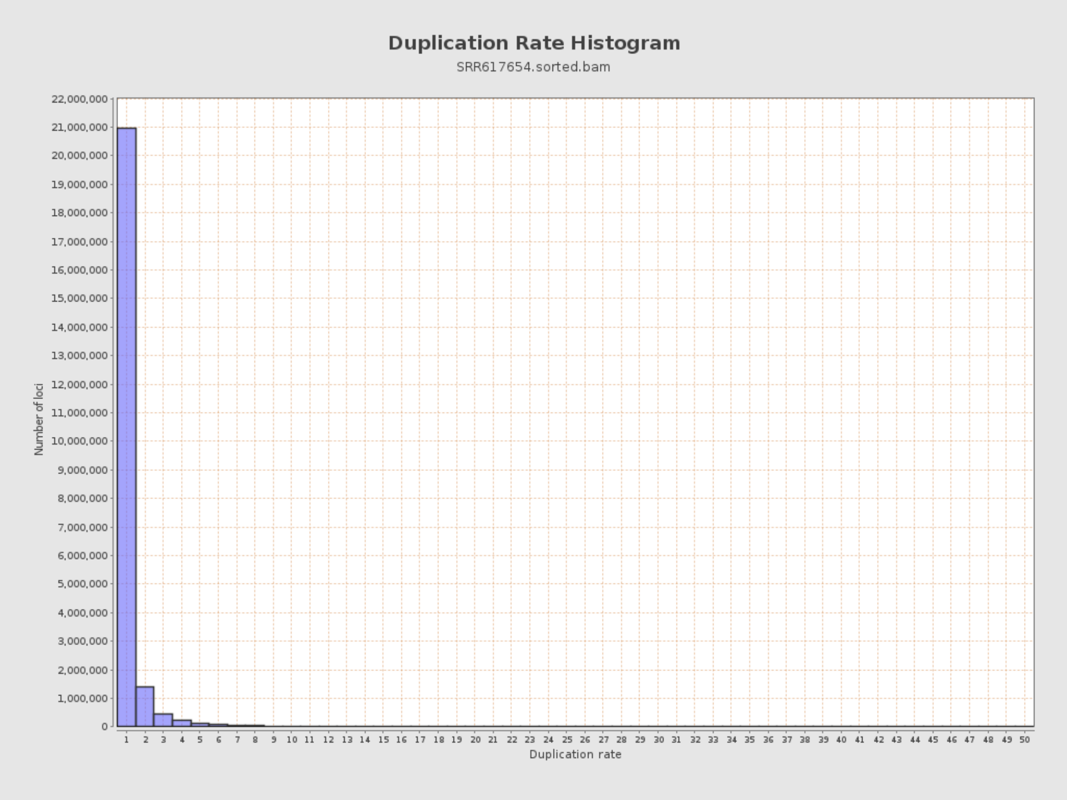
5. Results : Coverage Histogram (0-50X)



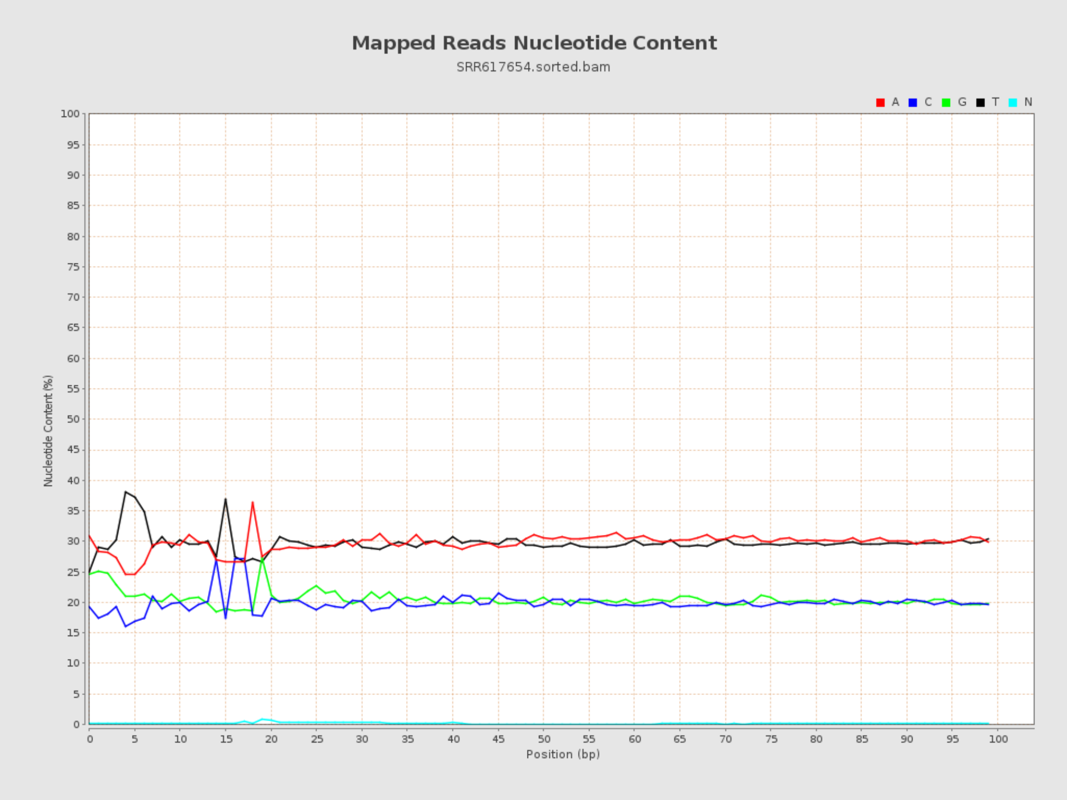
6. Results : Genome Fraction Coverage



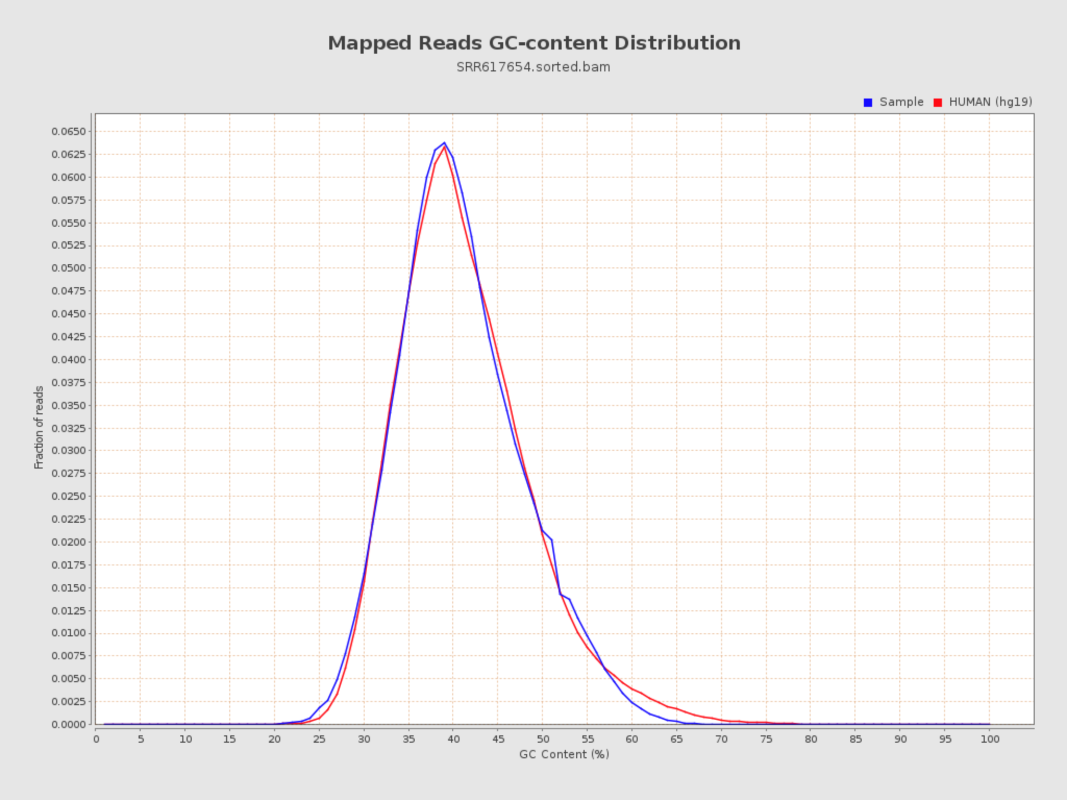
7. Results : Duplication Rate Histogram



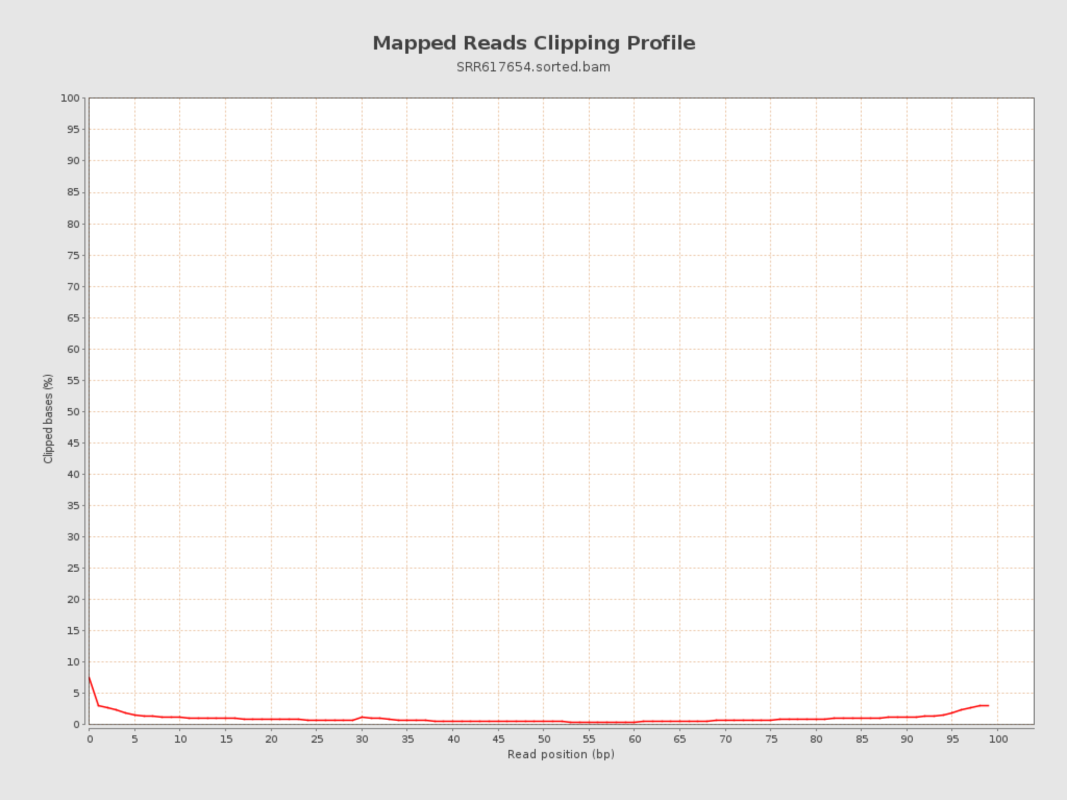
8. Results : Mapped Reads Nucleotide Content



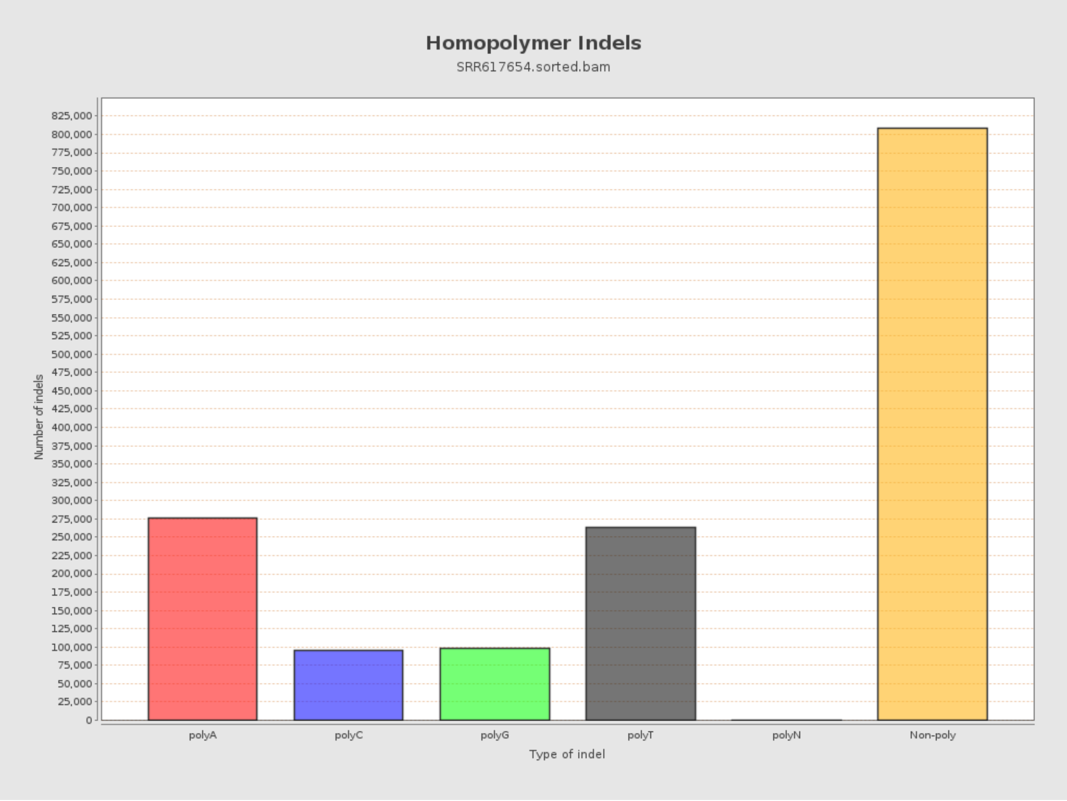
9. Results : Mapped Reads GC-content Distribution



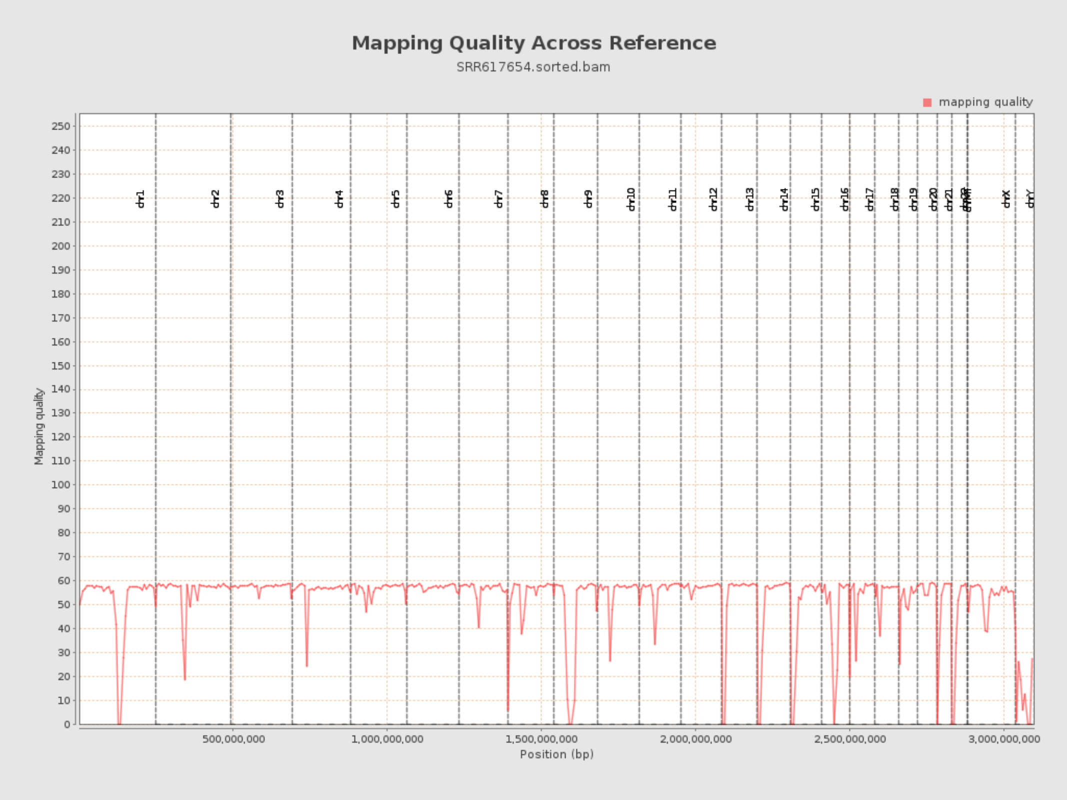
10. Results : Mapped Reads Clipping Profile



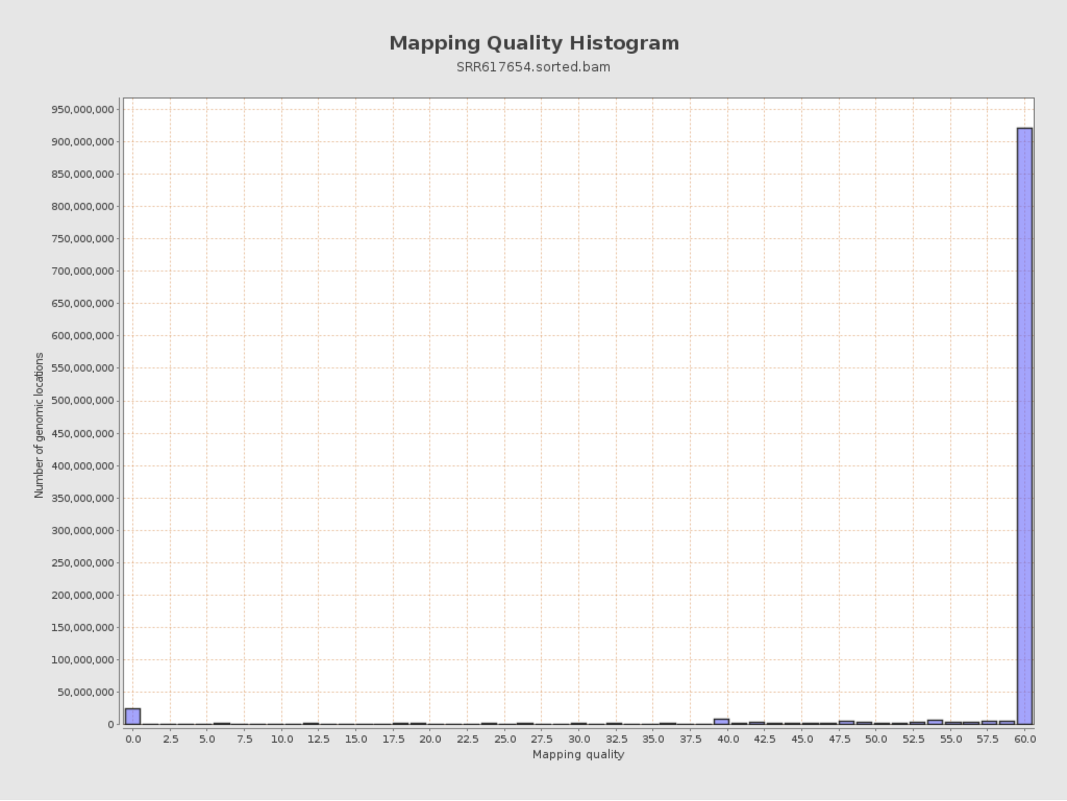
11. Results : Homopolymer Indels



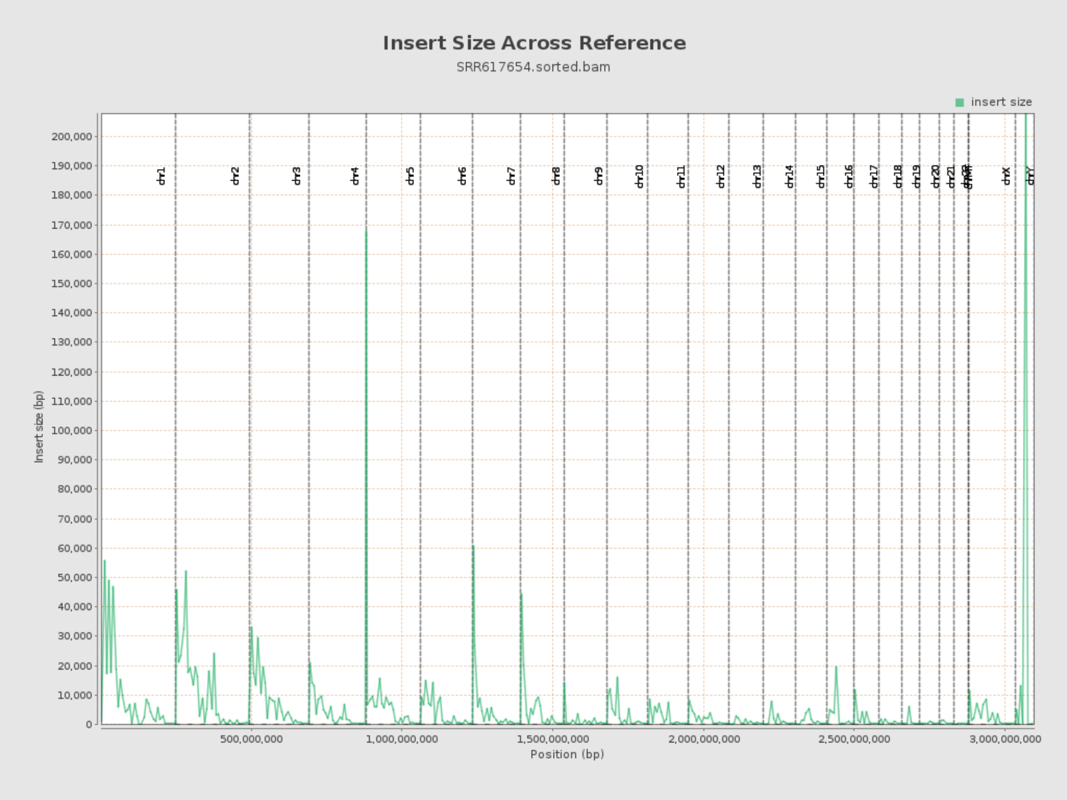
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram