Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/11 12:51:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617674.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_SRR617674 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617674_1.fastq.gz SRR617674_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Oct 11 12:51:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617674.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	30,013,549 / 93.79%
Unmapped reads	1,986,451 / 6.21%
Mapped paired reads	30,013,549 / 93.79%
Mapped reads, first in pair	15,240,917 / 47.63%
Mapped reads, second in pair	14,772,632 / 46.16%
Mapped reads, both in pair	29,166,878 / 91.15%
Mapped reads, singletons	846,671 / 2.65%
Secondary alignments	0
Supplementary alignments	189,309 / 0.59%
Read min/max/mean length	30 / 100 / 100.23
Duplicated reads (estimated)	6,907,274 / 21.59%
Duplication rate	10.74%
Clipped reads	6,663,553 / 20.82%

2.2. ACGT Content

Number/percentage of A's	861,784,737 / 29.8%
Number/percentage of C's	574,750,199 / 19.87%
Number/percentage of T's	860,707,685 / 29.76%
Number/percentage of G's	591,978,472 / 20.47%
Number/percentage of N's	3,047,526 / 0.11%

GC Percentage	40.34%

2.3. Coverage

Mean	0.9349
Standard Deviation	10.4218

2.4. Mapping Quality

Mean Mapping Quality	52.48

2.5. Insert size

Mean	51,866.39
Standard Deviation	2,149,939.74
P25/Median/P75	179 / 223 / 291

2.6. Mismatches and indels

General error rate	1.46%
Mismatches	41,305,299
Insertions	456,141
Mapped reads with at least one insertion	1.49%
Deletions	1,060,454
Mapped reads with at least one deletion	3.46%
Homopolymer indels	47.59%

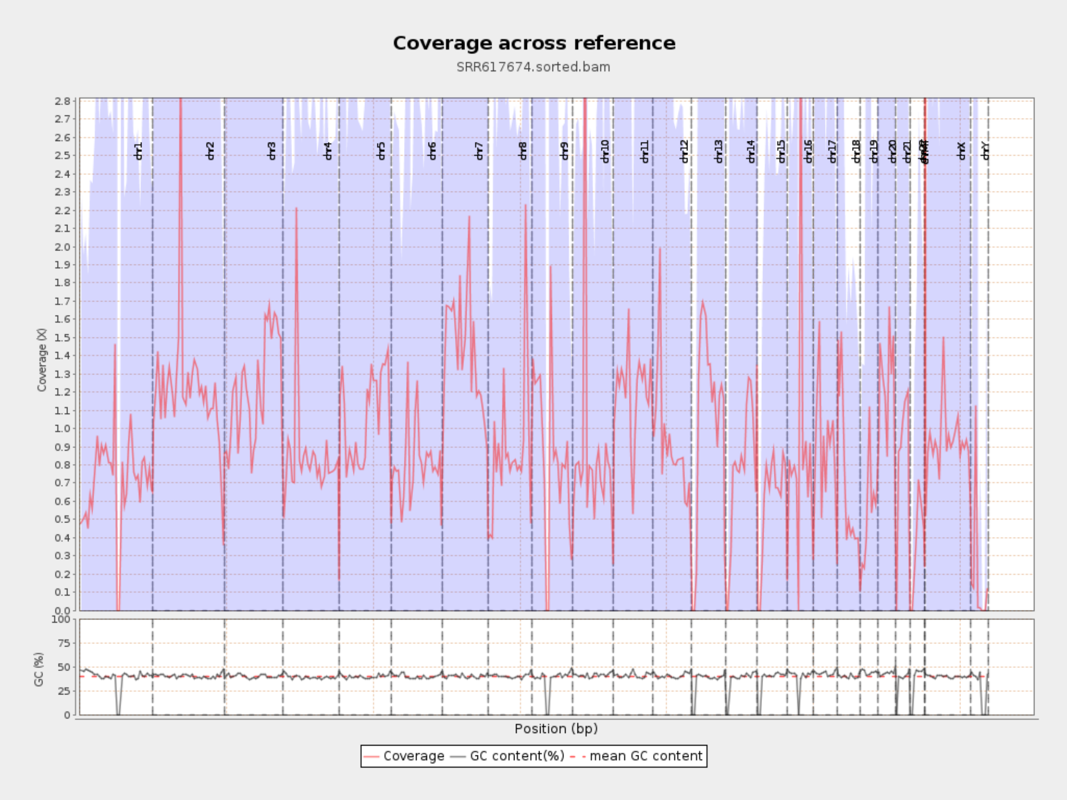
2.7. Chromosome stats

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

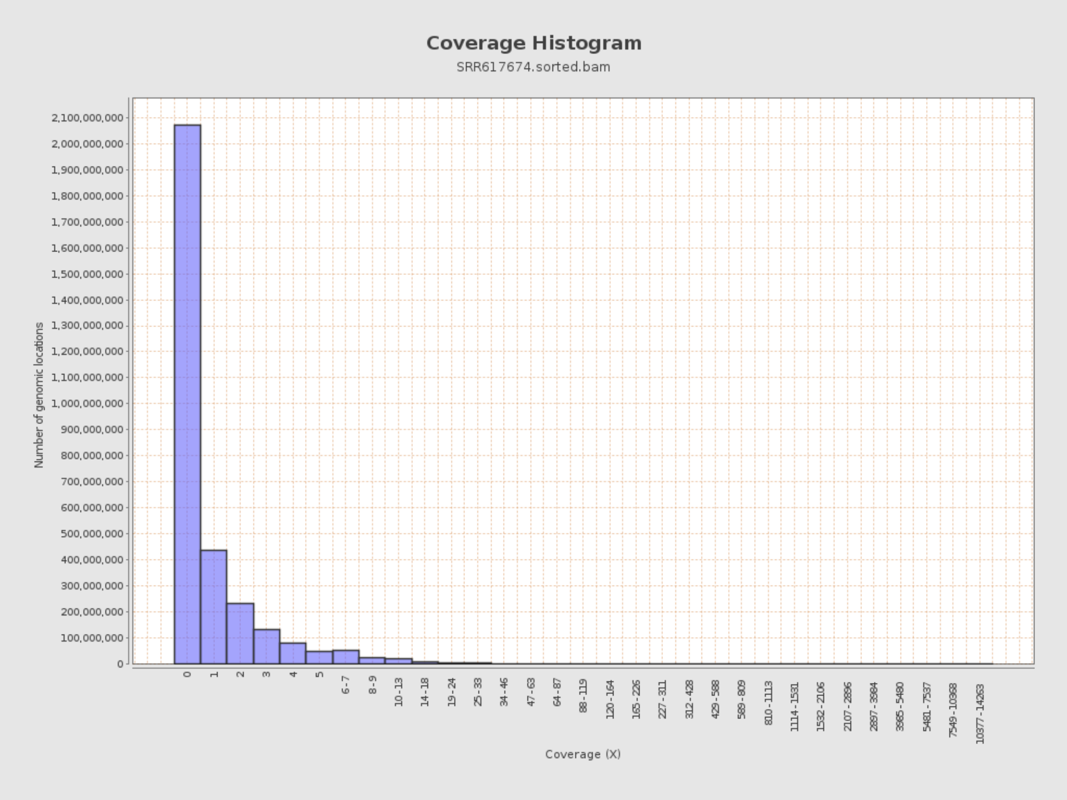
		bases	coverage	deviation
chr1	249250621	177522752	0.7122	10.1709
chr2	243199373	299135179	1.23	11.9835
chr3	198022430	242100035	1.2226	2.4826
chr4	191154276	161710022	0.846	8.2929
chr5	180915260	191166364	1.0567	2.3209
chr6	171115067	140686816	0.8222	5.7339
chr7	159138663	226434498	1.4229	13.1651
chr8	146364022	128653672	0.879	4.0442
chr9	141213431	118811718	0.8414	19.955
chr10	135534747	122646082	0.9049	21.0973
chr11	135006516	158984502	1.1776	11.6893
chr12	133851895	123376908	0.9217	2.2258
chr13	115169878	124564941	1.0816	2.3455
chr14	107349540	82762853	0.771	2.4887
chr15	102531392	61785998	0.6026	1.847
chr16	90354753	80328875	0.889	16.5942
chr17	81195210	71196466	0.8769	12.4269
chr18	78077248	53433470	0.6844	18.0071
chr19	59128983	30890400	0.5224	6.0121
chr20	63025520	78246114	1.2415	3.0308
chr21	48129895	42156490	0.8759	4.3012
chr22	51304566	18695011	0.3644	1.2904
chrMT	16571	3044052	183.6975	130.9852
chrX	155270560	144093264	0.928	4.3595

chrY	59373566	11600297	0.1954	16.8499

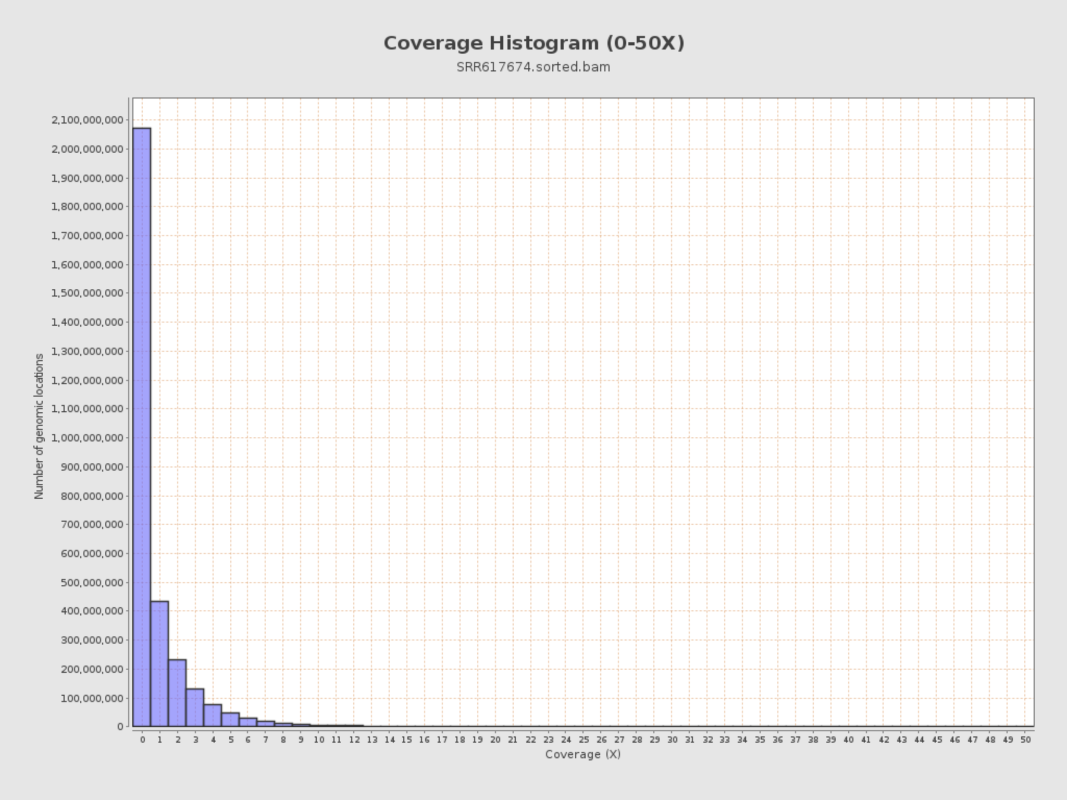
3. Results : Coverage across reference



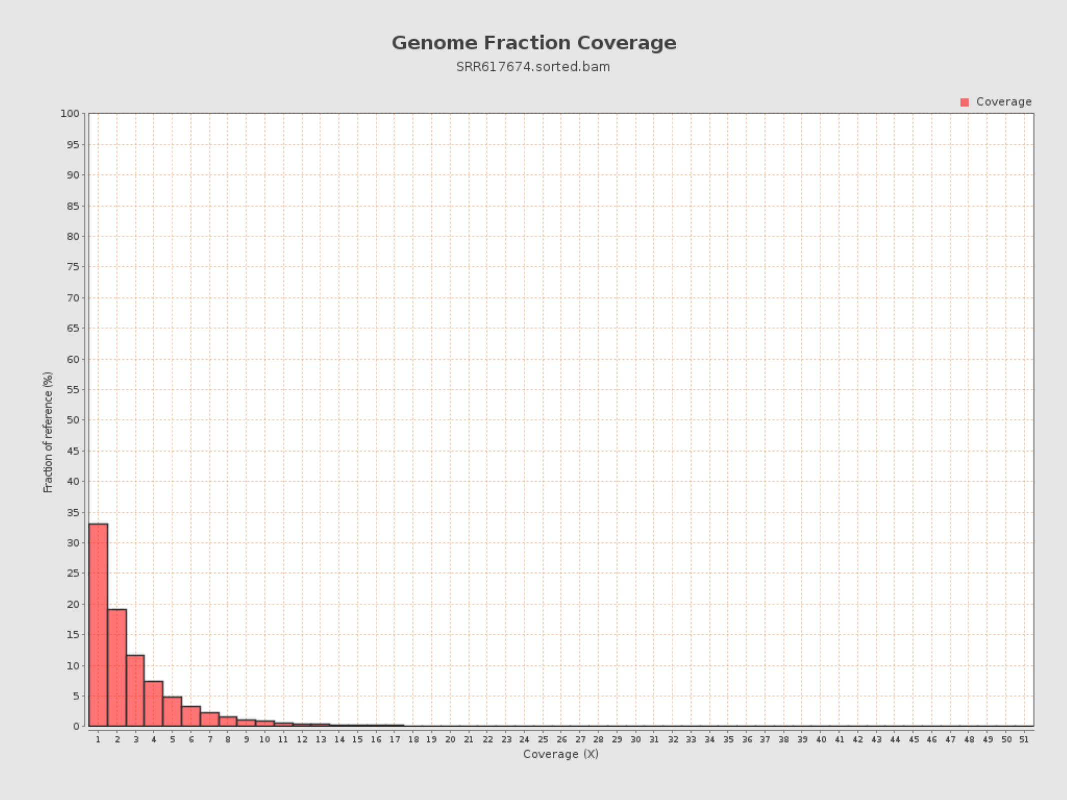
4. Results : Coverage Histogram



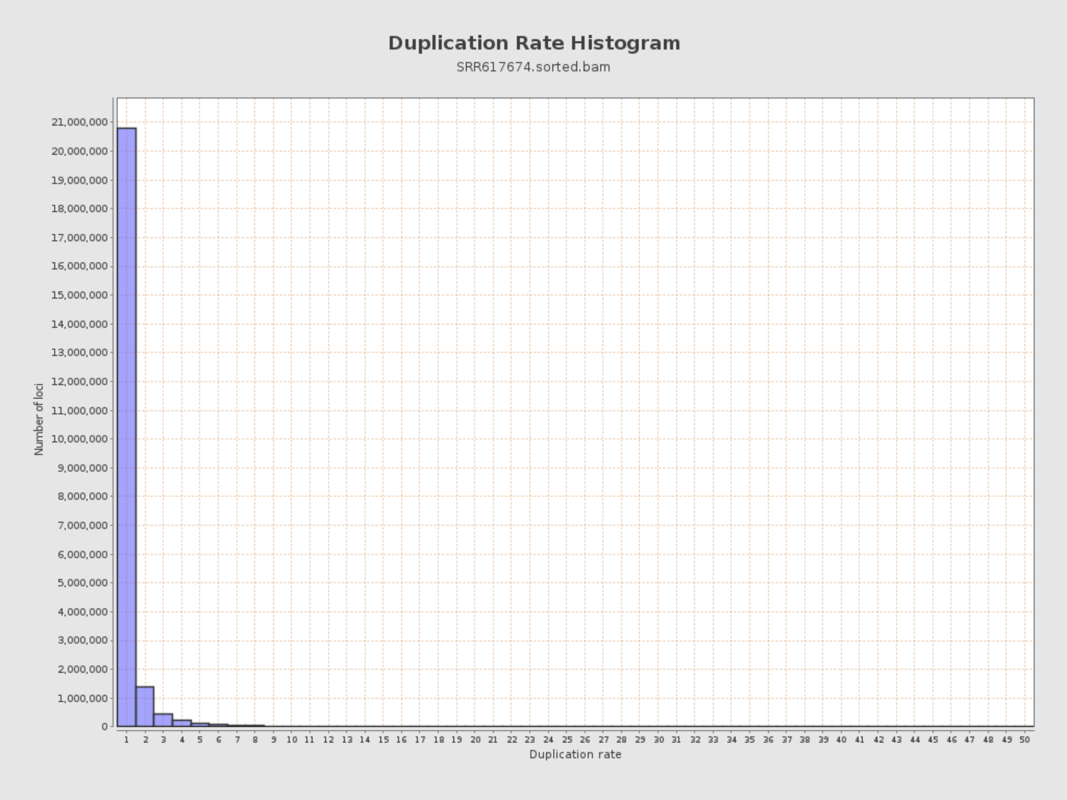
5. Results : Coverage Histogram (0-50X)



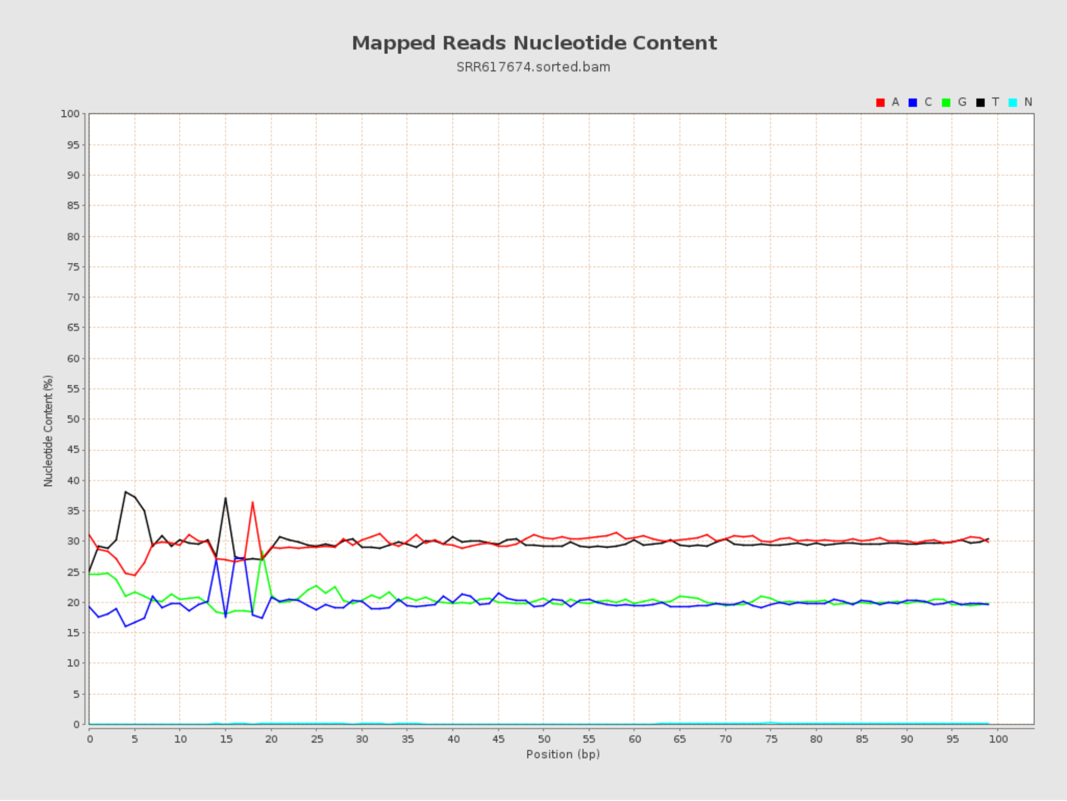
6. Results : Genome Fraction Coverage



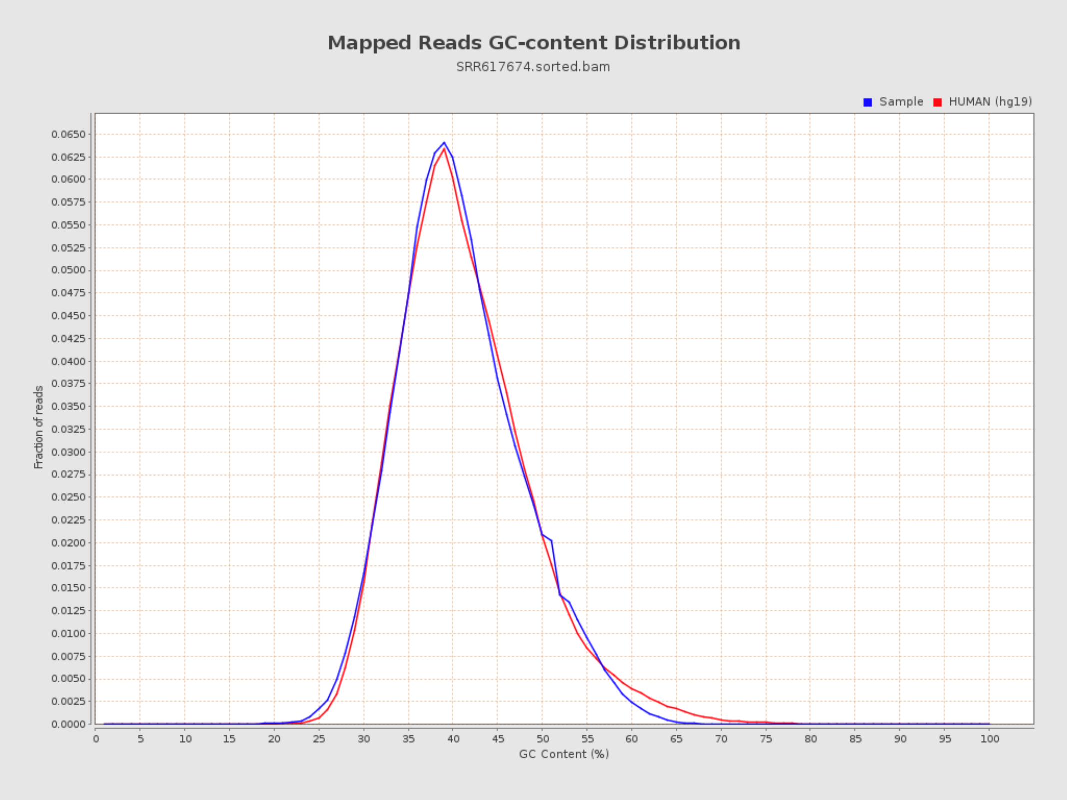
7. Results : Duplication Rate Histogram



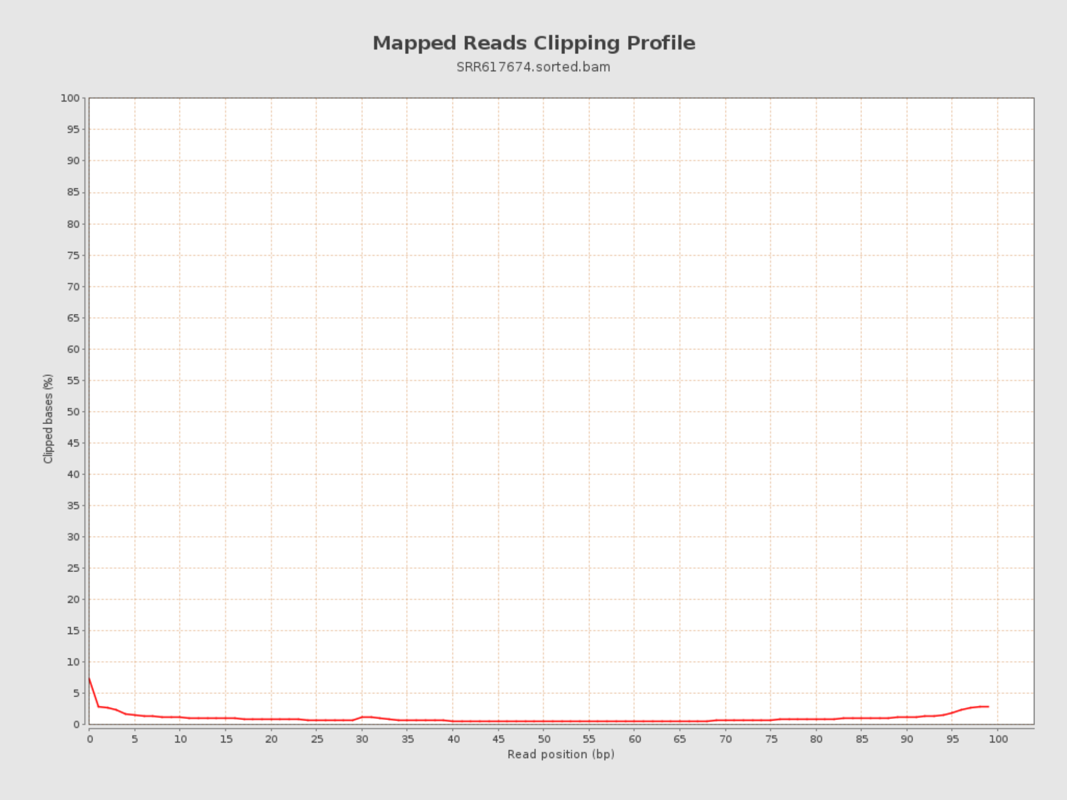
8. Results : Mapped Reads Nucleotide Content



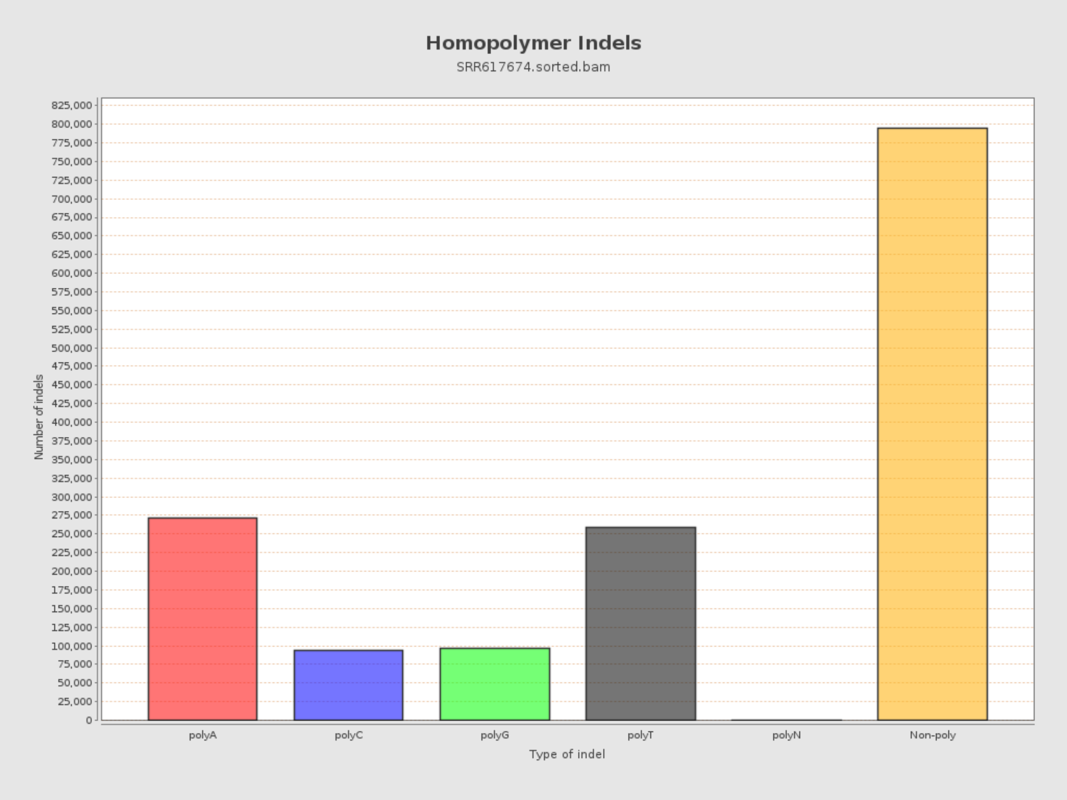
9. Results : Mapped Reads GC-content Distribution



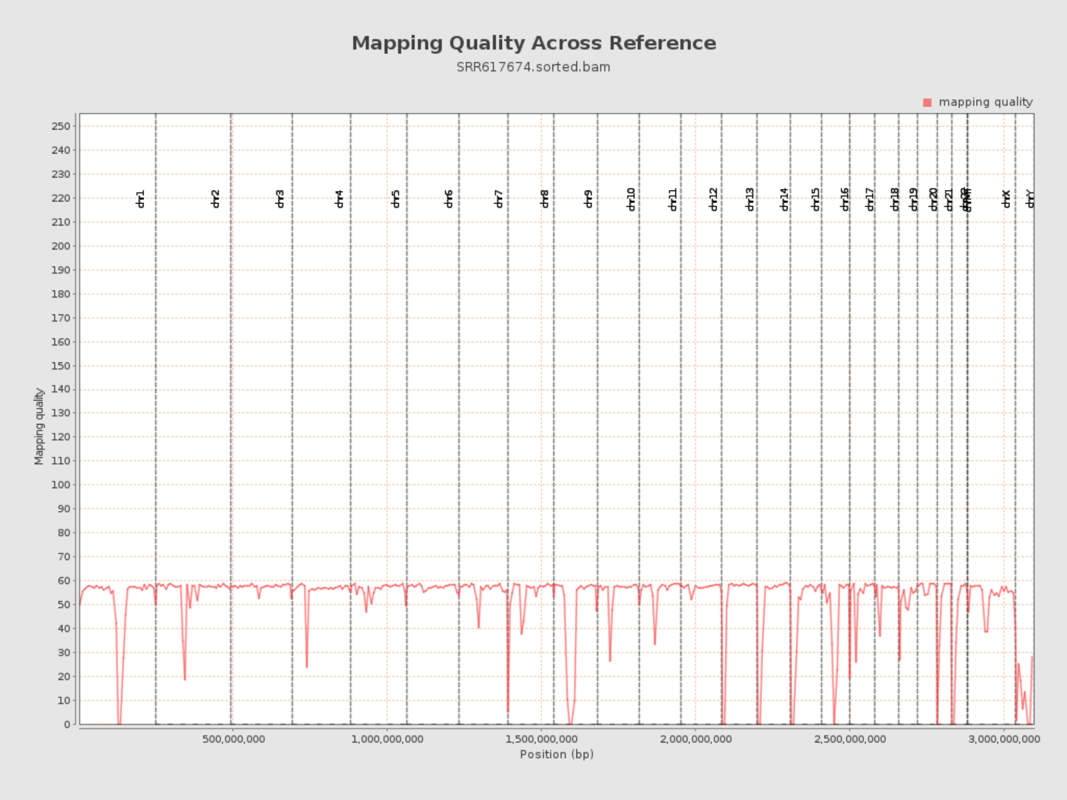
10. Results : Mapped Reads Clipping Profile



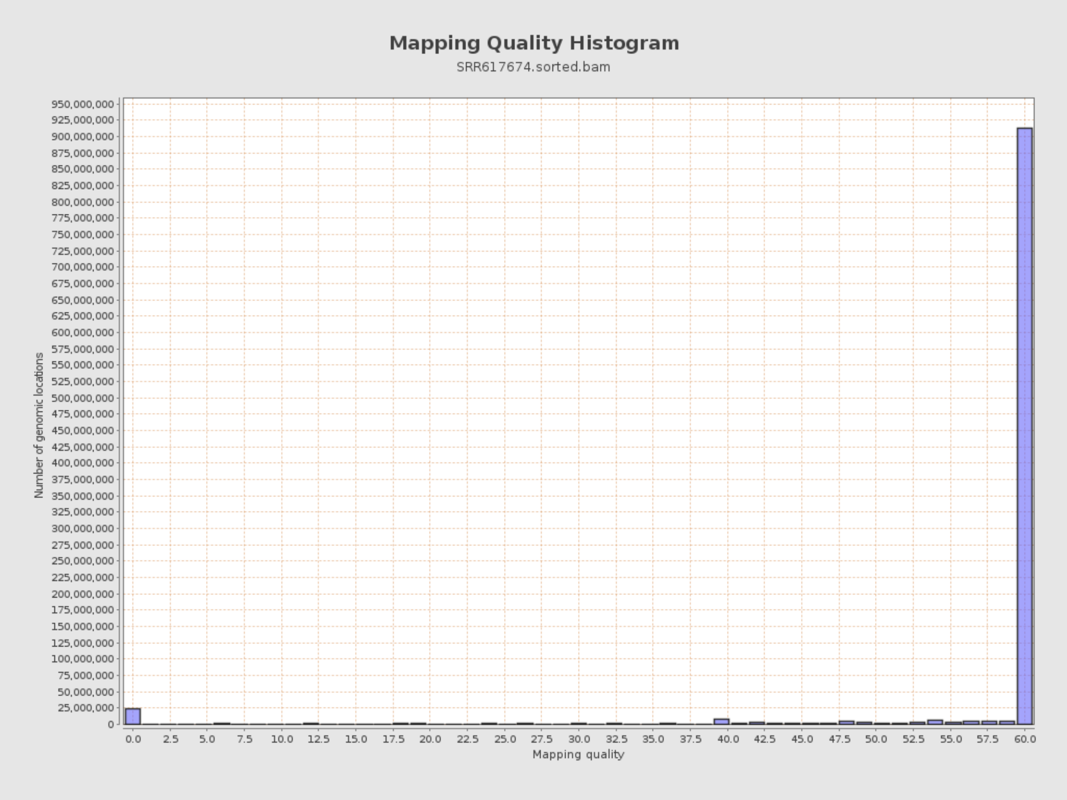
11. Results : Homopolymer Indels



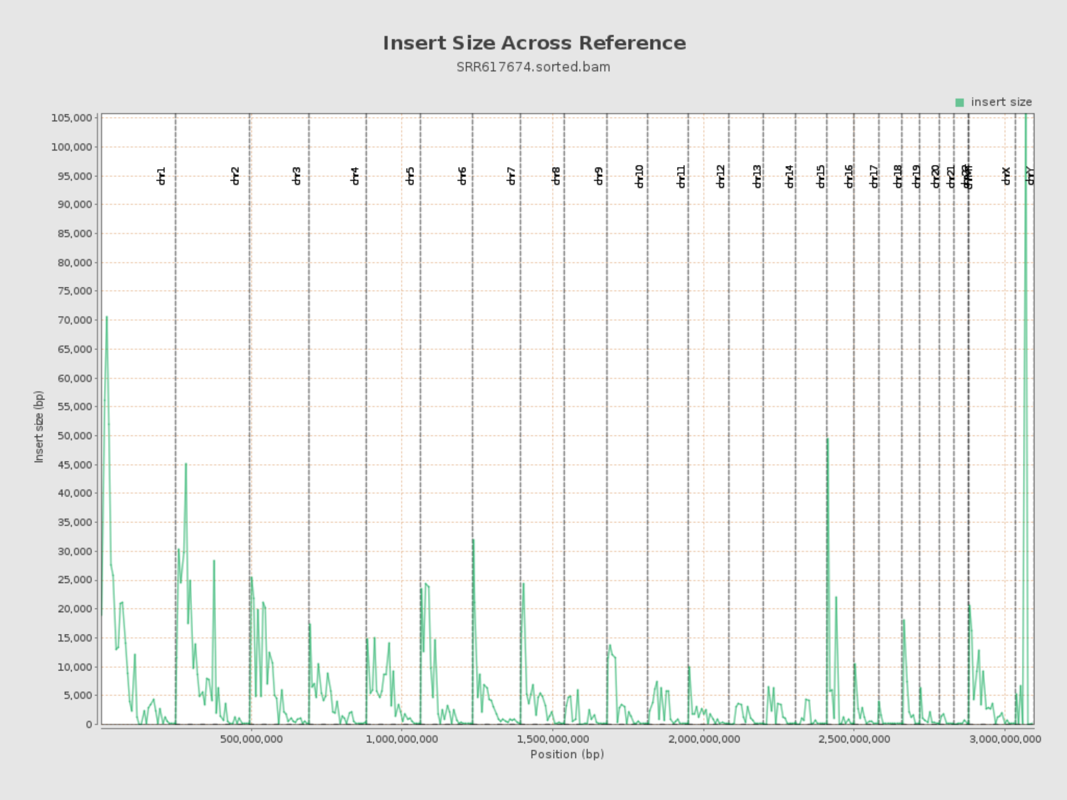
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram