Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/07 06:54:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617362.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_SRR617362 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617362_1.fastq.gz SRR617362_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Oct 07 06:54:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617362.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	30,068,514 / 93.96%
Unmapped reads	1,931,486 / 6.04%
Mapped paired reads	30,068,514 / 93.96%
Mapped reads, first in pair	15,121,612 / 47.26%
Mapped reads, second in pair	14,946,902 / 46.71%
Mapped reads, both in pair	29,490,214 / 92.16%
Mapped reads, singletons	578,300 / 1.81%
Secondary alignments	0
Supplementary alignments	67,268 / 0.21%
Read min/max/mean length	30 / 100 / 100.08
Duplicated reads (estimated)	1,536,301 / 4.8%
Duplication rate	1.48%
Clipped reads	2,551,260 / 7.97%

2.2. ACGT Content

Number/percentage of A's	891,879,852 / 30.25%
Number/percentage of C's	585,798,140 / 19.87%
Number/percentage of T's	879,050,832 / 29.81%
Number/percentage of G's	589,764,049 / 20%
Number/percentage of N's	1,941,339 / 0.07%

GC Percentage	39.87%

2.3. Coverage

Mean	0.9527
Standard Deviation	9.5962

2.4. Mapping Quality

Mean Mapping Quality	53.44

2.5. Insert size

Mean	54,111.35
Standard Deviation	2,220,048.44
P25/Median/P75	172 / 213 / 277

2.6. Mismatches and indels

General error rate	1.23%
Mismatches	35,529,071
Insertions	301,814
Mapped reads with at least one insertion	0.97%
Deletions	362,532
Mapped reads with at least one deletion	1.17%
Homopolymer indels	41.07%

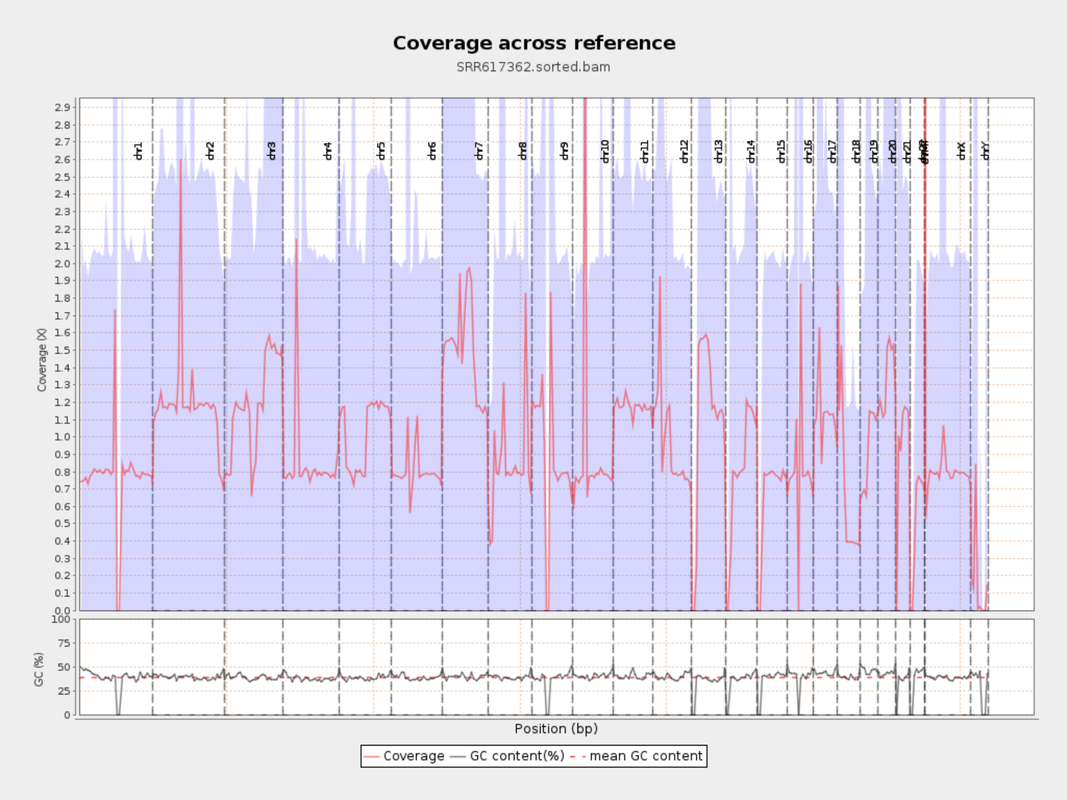
2.7. Chromosome stats

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

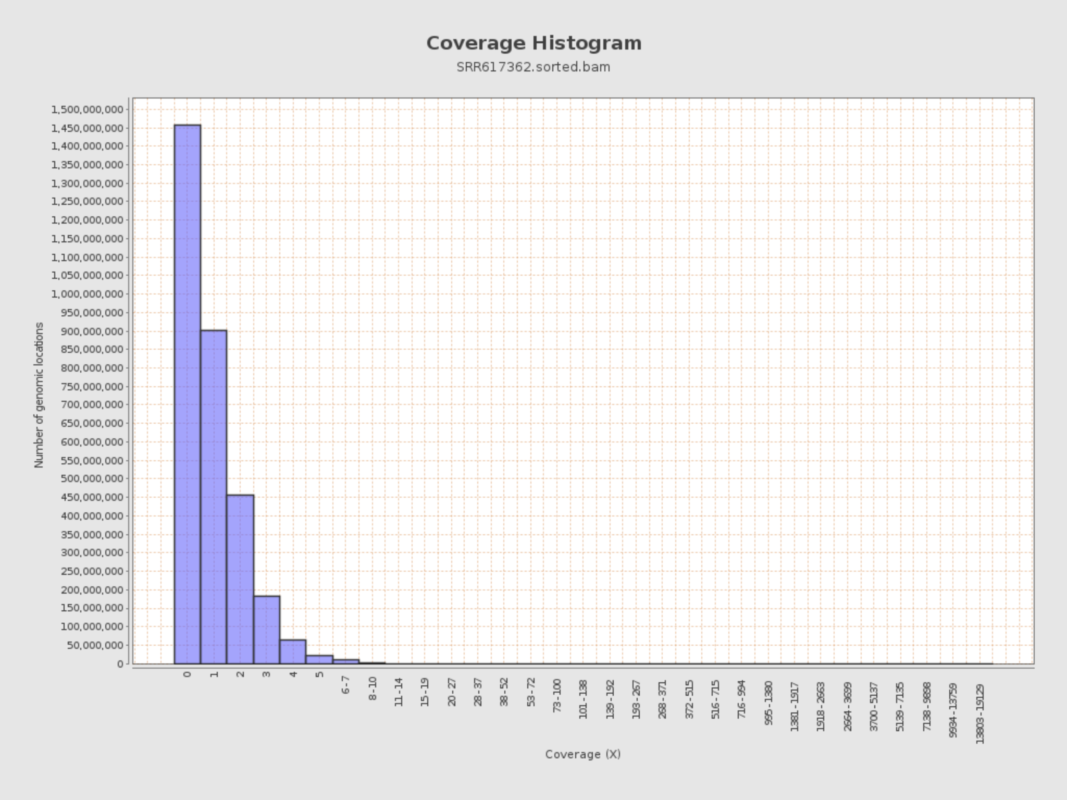
		bases	coverage	deviation
chr1	249250621	192020442	0.7704	19.6041
chr2	243199373	290721399	1.1954	8.6185
chr3	198022430	234544672	1.1844	1.463
chr4	191154276	161535133	0.8451	9.2355
chr5	180915260	185233721	1.0239	1.4328
chr6	171115067	137902356	0.8059	3.6138
chr7	159138663	239528017	1.5052	10.6919
chr8	146364022	124025685	0.8474	7.5103
chr9	141213431	124158403	0.8792	14.35
chr10	135534747	124046764	0.9152	19.7886
chr11	135006516	158177409	1.1716	5.381
chr12	133851895	130144501	0.9723	1.3662
chr13	115169878	128422497	1.1151	1.2878
chr14	107349540	85562030	0.797	1.3638
chr15	102531392	66201683	0.6457	0.9722
chr16	90354753	74182725	0.821	7.81
chr17	81195210	91858112	1.1313	6.94
chr18	78077248	53057965	0.6796	14.9769
chr19	59128983	54970894	0.9297	9.4133
chr20	63025520	84807690	1.3456	2.3927
chr21	48129895	46896127	0.9744	3.1144
chr22	51304566	26418760	0.5149	0.9142
chrMT	16571	2028363	122.4044	20.1791
chrX	155270560	122947582	0.7918	2.9306

chrY	59373566	9915909	0.167	8.0208

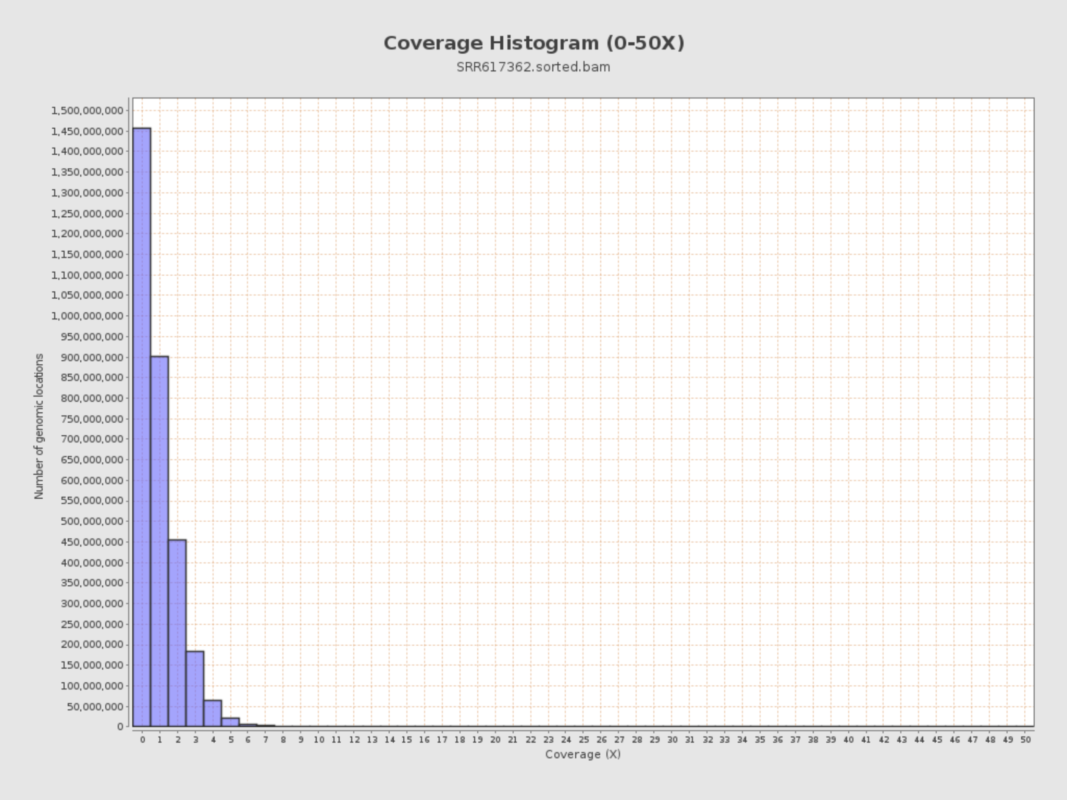
3. Results : Coverage across reference



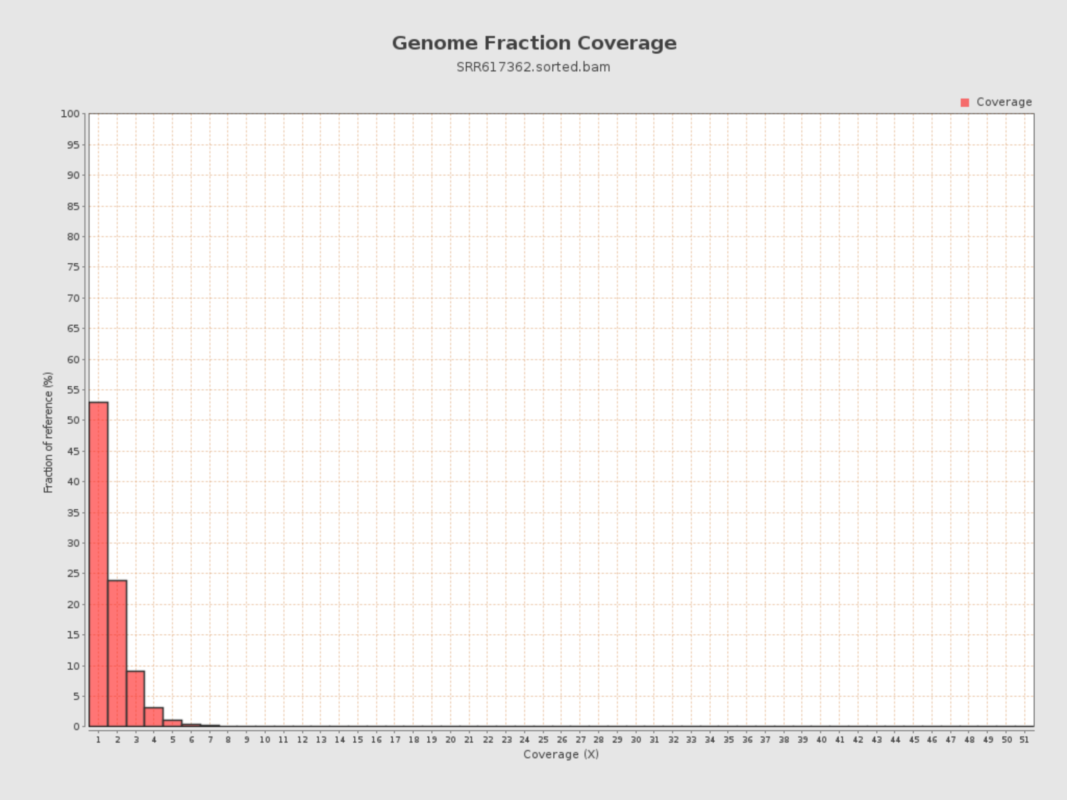
4. Results : Coverage Histogram



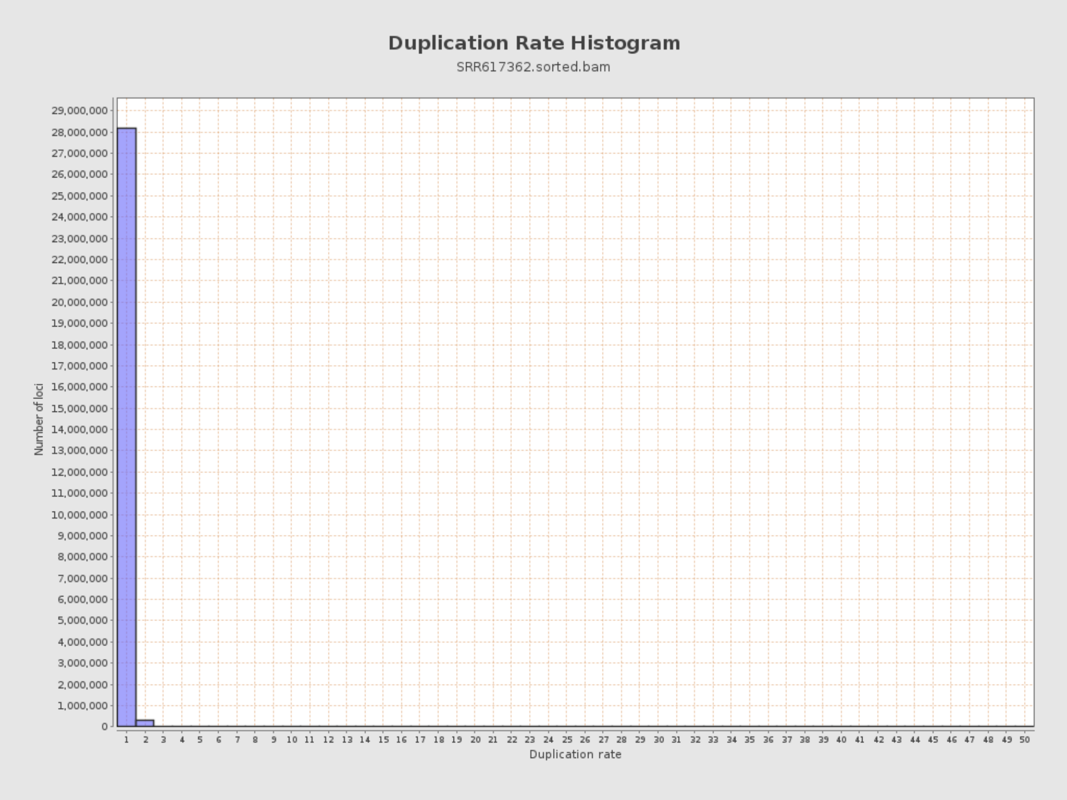
5. Results : Coverage Histogram (0-50X)



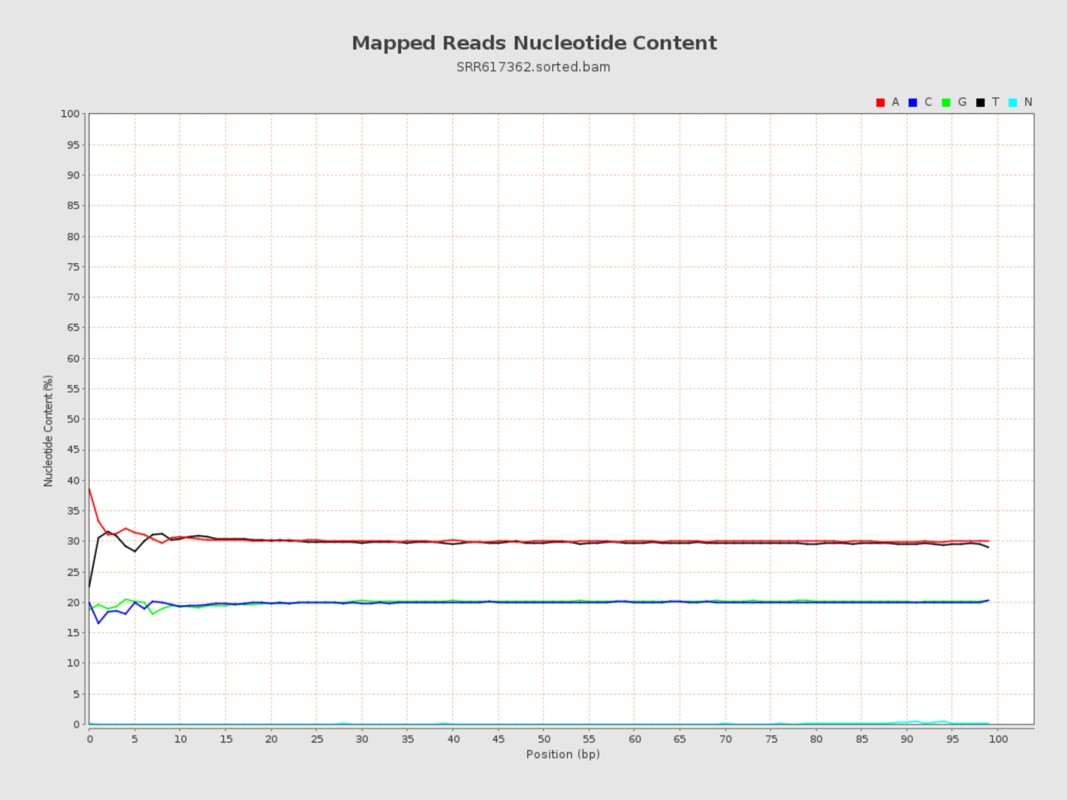
6. Results : Genome Fraction Coverage



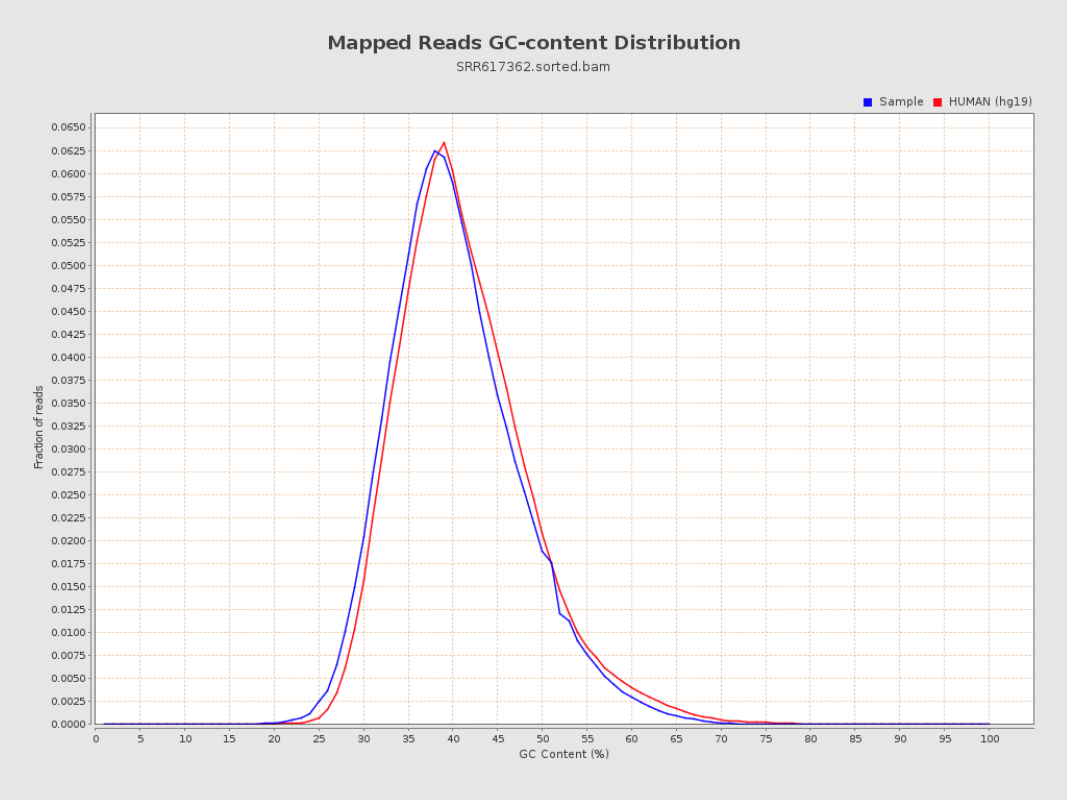
7. Results : Duplication Rate Histogram



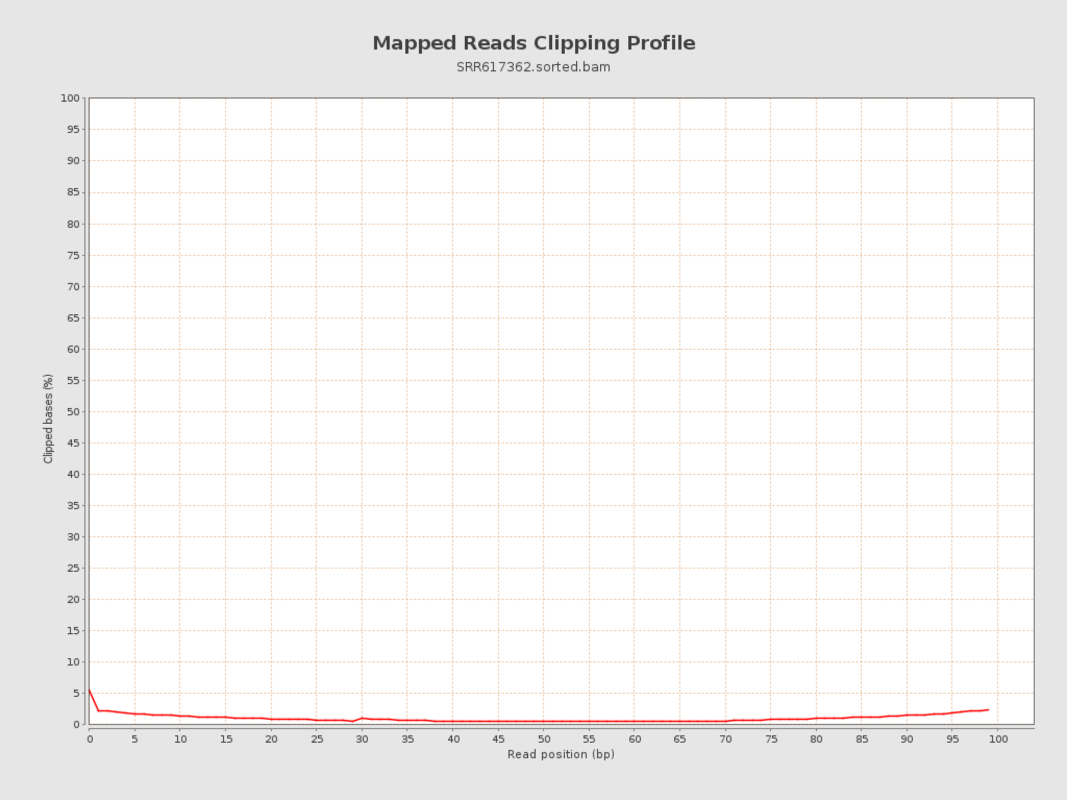
8. Results : Mapped Reads Nucleotide Content



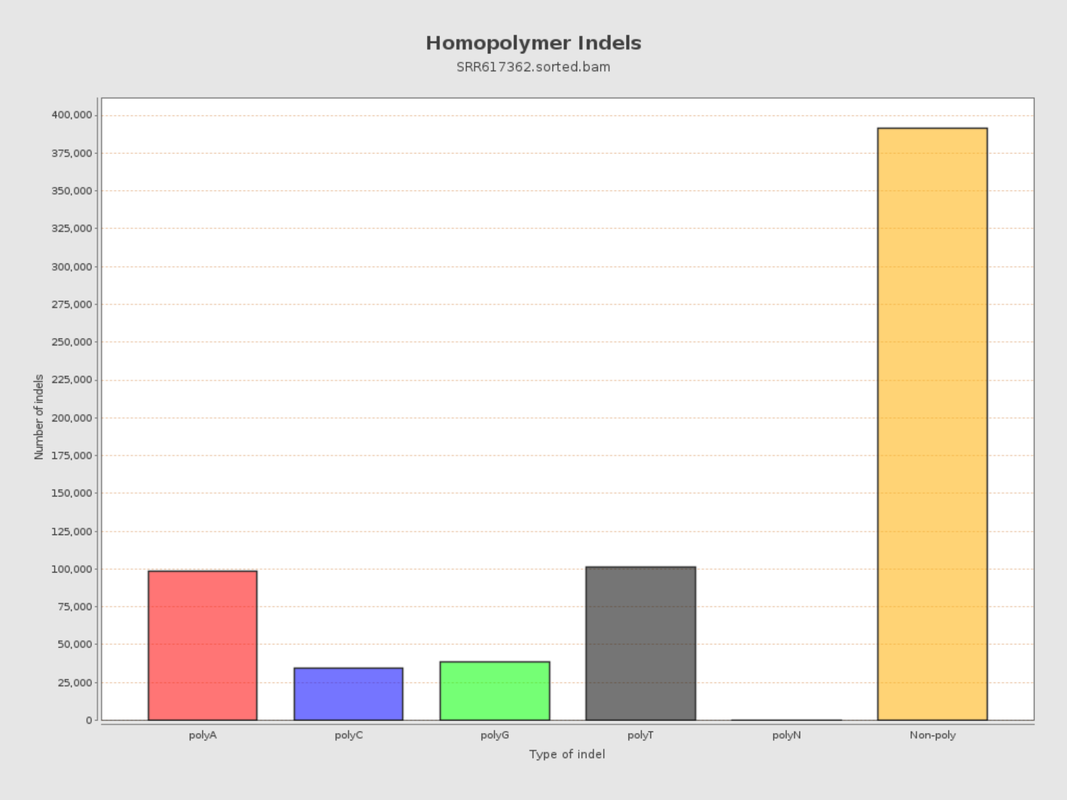
9. Results : Mapped Reads GC-content Distribution



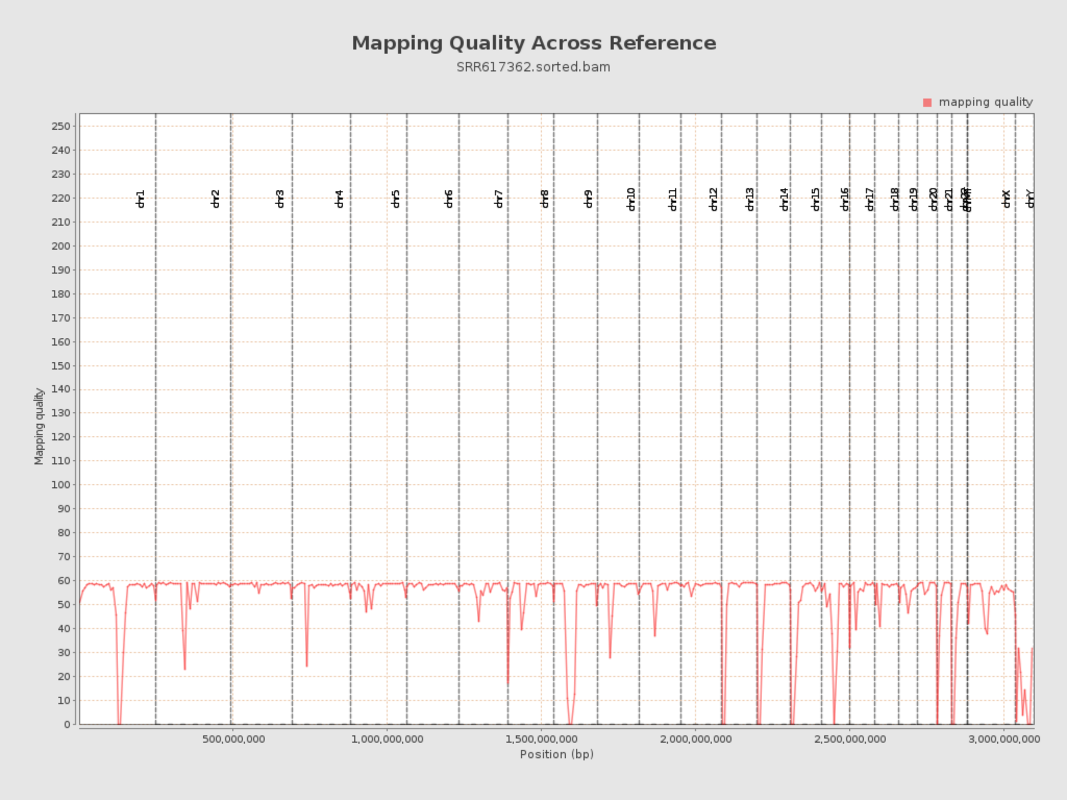
10. Results : Mapped Reads Clipping Profile



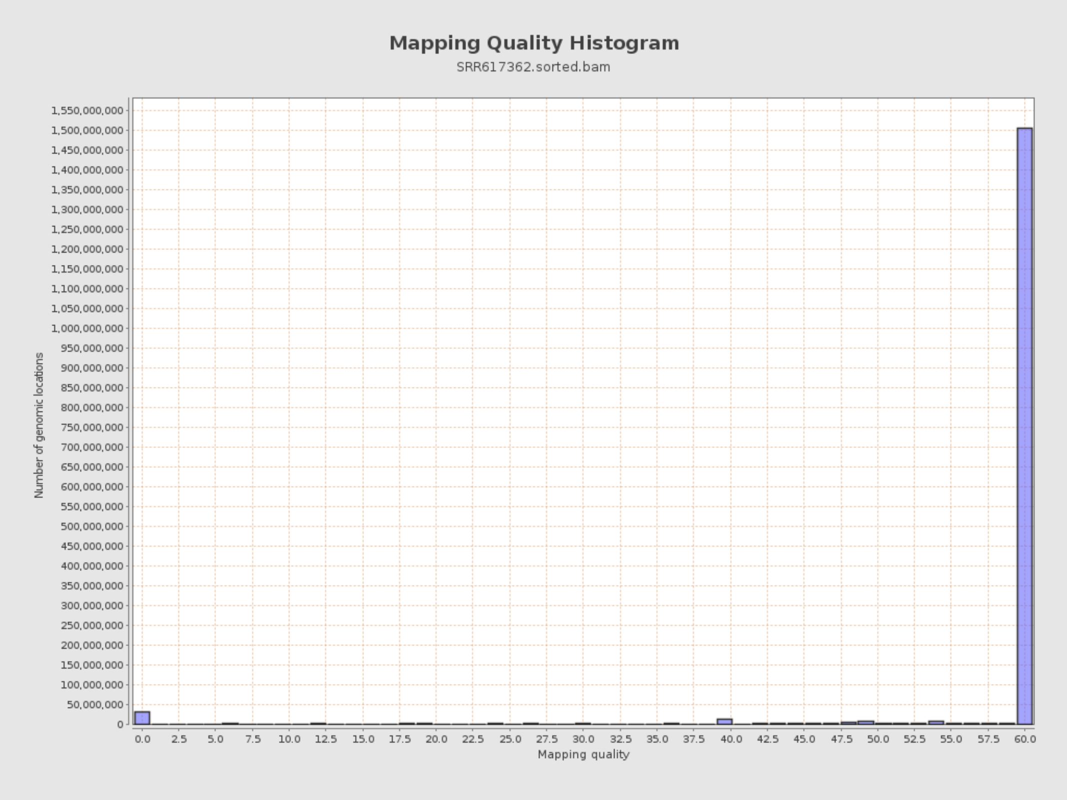
11. Results : Homopolymer Indels



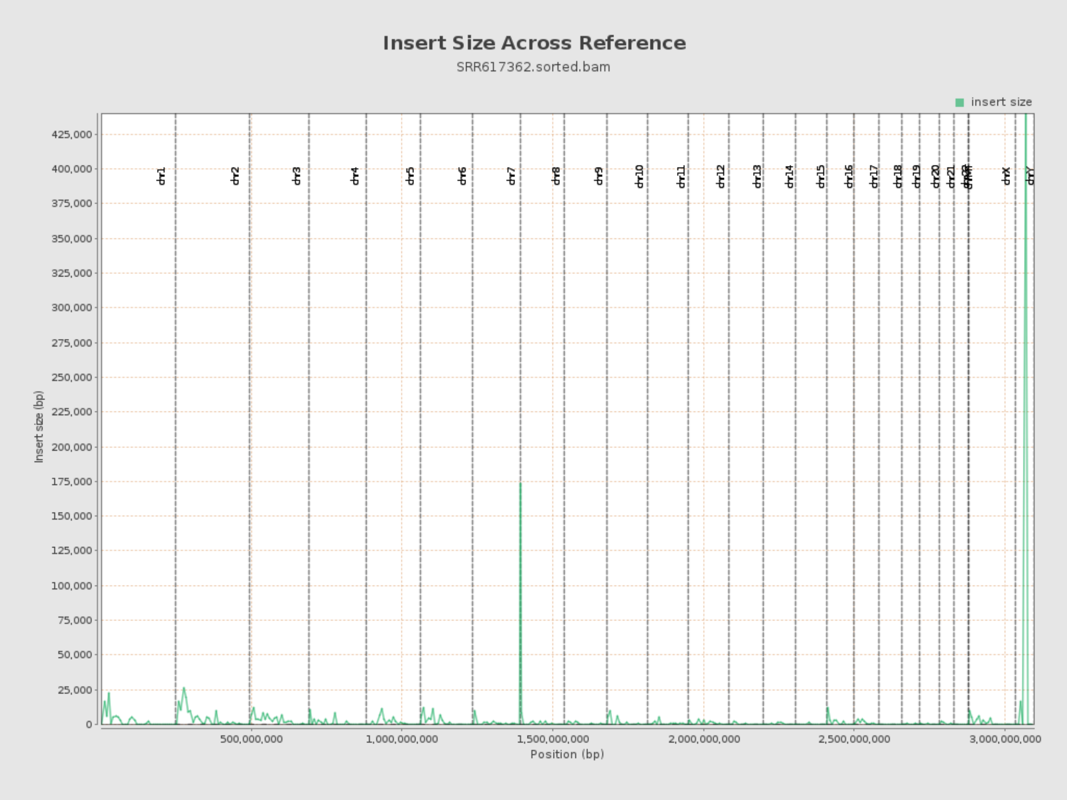
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram