Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/11 04:09:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617662.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_SRR617662 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617662_1.fastq.gz SRR617662_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Oct 11 04:09:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617662.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	30,238,921 / 94.5%
Unmapped reads	1,761,079 / 5.5%
Mapped paired reads	30,238,921 / 94.5%
Mapped reads, first in pair	15,139,367 / 47.31%
Mapped reads, second in pair	15,099,554 / 47.19%
Mapped reads, both in pair	29,643,580 / 92.64%
Mapped reads, singletons	595,341 / 1.86%
Secondary alignments	0
Supplementary alignments	143,054 / 0.45%
Read min/max/mean length	30 / 100 / 100.18
Duplicated reads (estimated)	6,915,058 / 21.61%
Duplication rate	10.66%
Clipped reads	6,358,242 / 19.87%

2.2. ACGT Content

Number/percentage of A's	875,064,921 / 29.81%
Number/percentage of C's	584,802,272 / 19.92%
Number/percentage of T's	872,793,318 / 29.73%
Number/percentage of G's	600,746,060 / 20.47%
Number/percentage of N's	1,965,325 / 0.07%

GC Percentage	40.39%

2.3. Coverage

Mean	0.9488
Standard Deviation	10.727

2.4. Mapping Quality

Mean Mapping Quality	52.65

2.5. Insert size

Mean	32,683.97
Standard Deviation	1,660,676.1
P25/Median/P75	178 / 222 / 287

2.6. Mismatches and indels

General error rate	1.53%
Mismatches	44,064,929
Insertions	455,115
Mapped reads with at least one insertion	1.48%
Deletions	1,076,280
Mapped reads with at least one deletion	3.48%
Homopolymer indels	47.69%

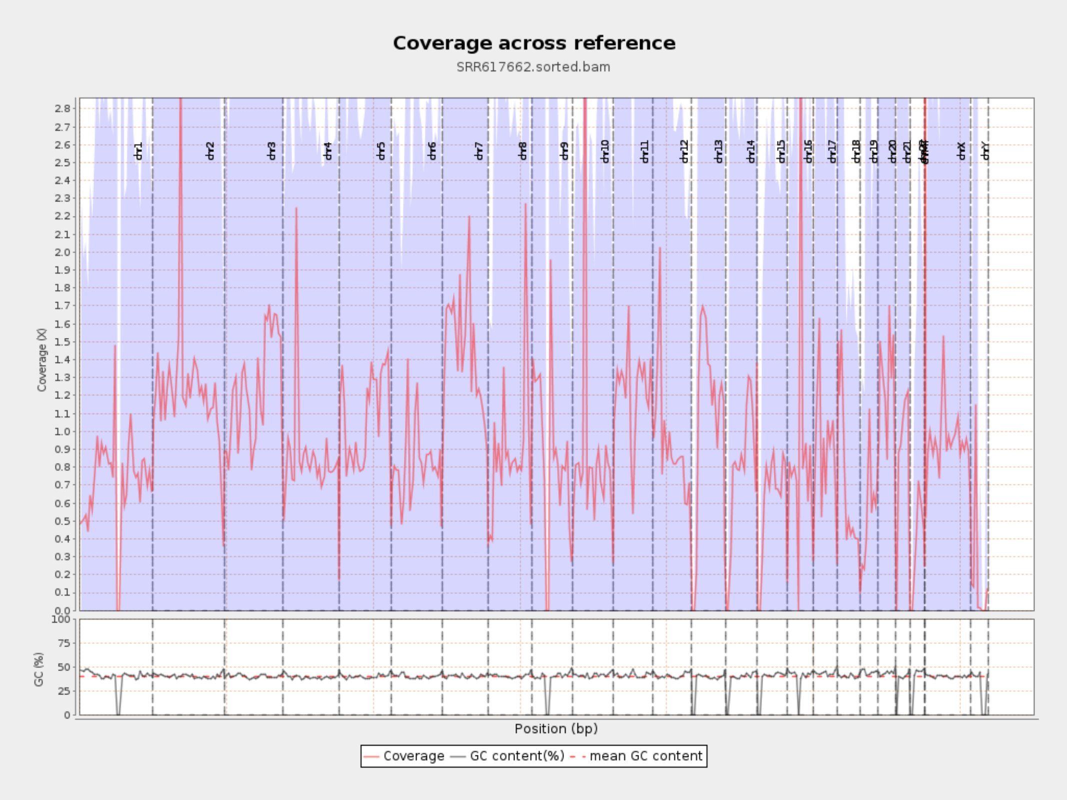
2.7. Chromosome stats

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

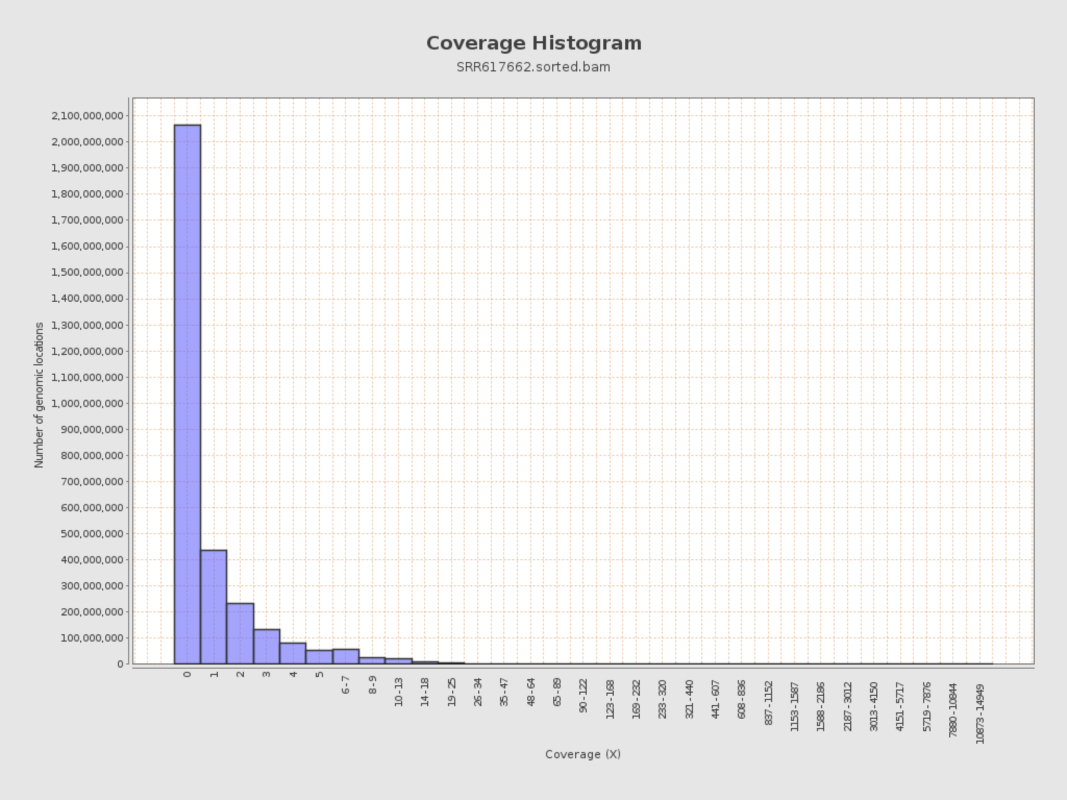
		bases	**coverage**	**deviation**
chr1	249250621	179755160	0.7212	10.5353
chr2	243199373	303153153	1.2465	12.2731
chr3	198022430	246285646	1.2437	2.4825
chr4	191154276	164678956	0.8615	8.3249
chr5	180915260	194387582	1.0745	2.3372
chr6	171115067	142667177	0.8337	5.8519
chr7	159138663	229607229	1.4428	13.3391
chr8	146364022	130581933	0.8922	4.12
chr9	141213431	120791843	0.8554	20.9491
chr10	135534747	124417819	0.918	21.7093
chr11	135006516	161726576	1.1979	12.0936
chr12	133851895	125603702	0.9384	2.1719
chr13	115169878	126114115	1.095	2.2832
chr14	107349540	84093432	0.7834	2.4633
chr15	102531392	62595820	0.6105	1.5719
chr16	90354753	81198209	0.8987	16.9983
chr17	81195210	72259995	0.89	12.8295
chr18	78077248	54302025	0.6955	18.4111
chr19	59128983	31002466	0.5243	6.133
chr20	63025520	79163040	1.256	3.029
chr21	48129895	42819470	0.8897	4.3719
chr22	51304566	18853474	0.3675	1.2638
chrMT	16571	3054479	184.3268	126.7527
chrX	155270560	146200617	0.9416	4.3901

chrY	59373566	11840847	0.1994	17.565

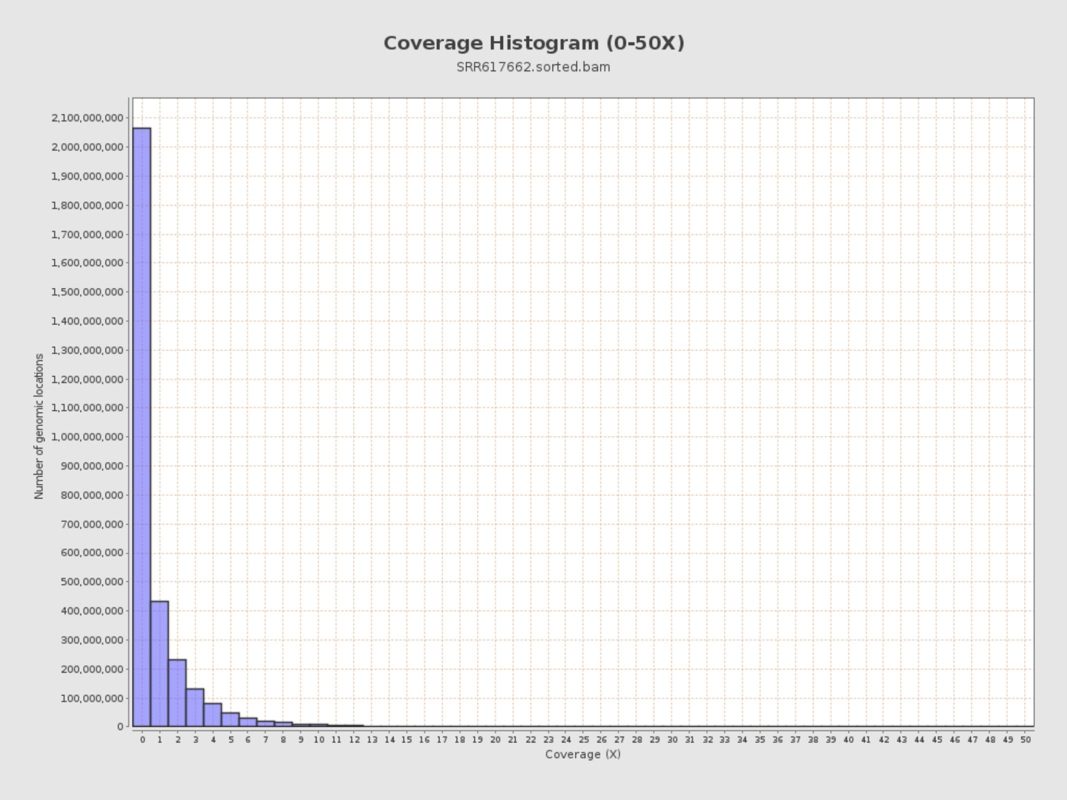
3. Results : Coverage across reference



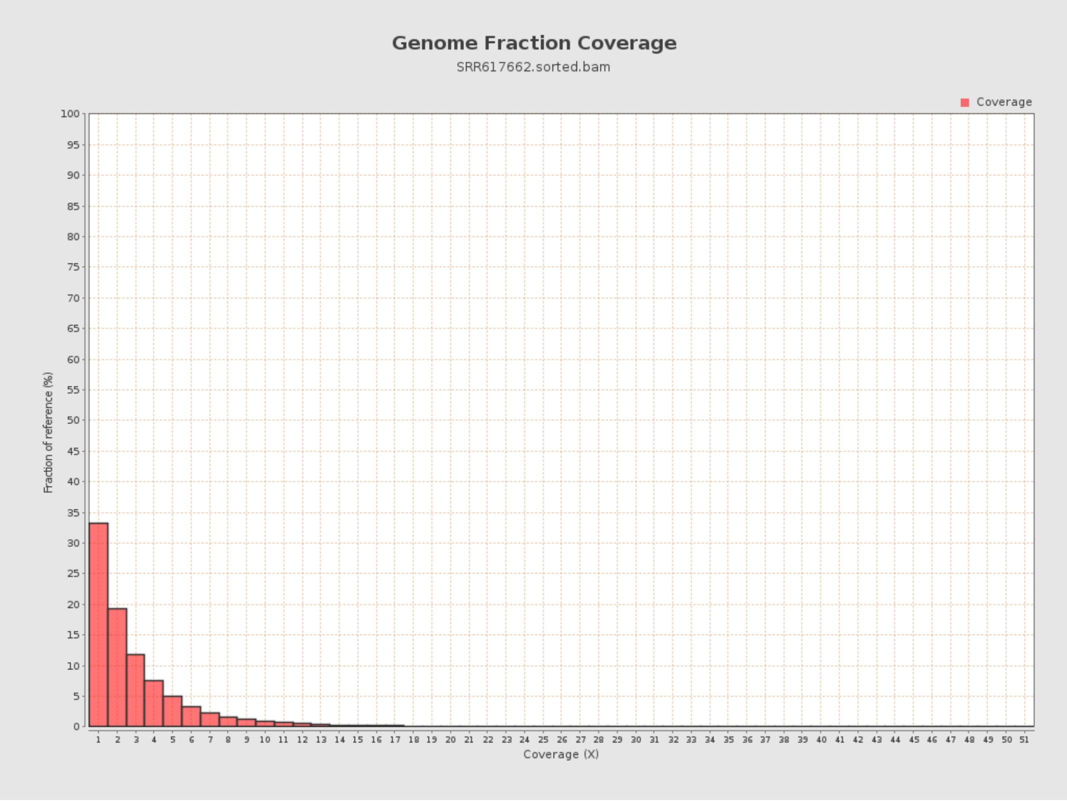
4. Results : Coverage Histogram



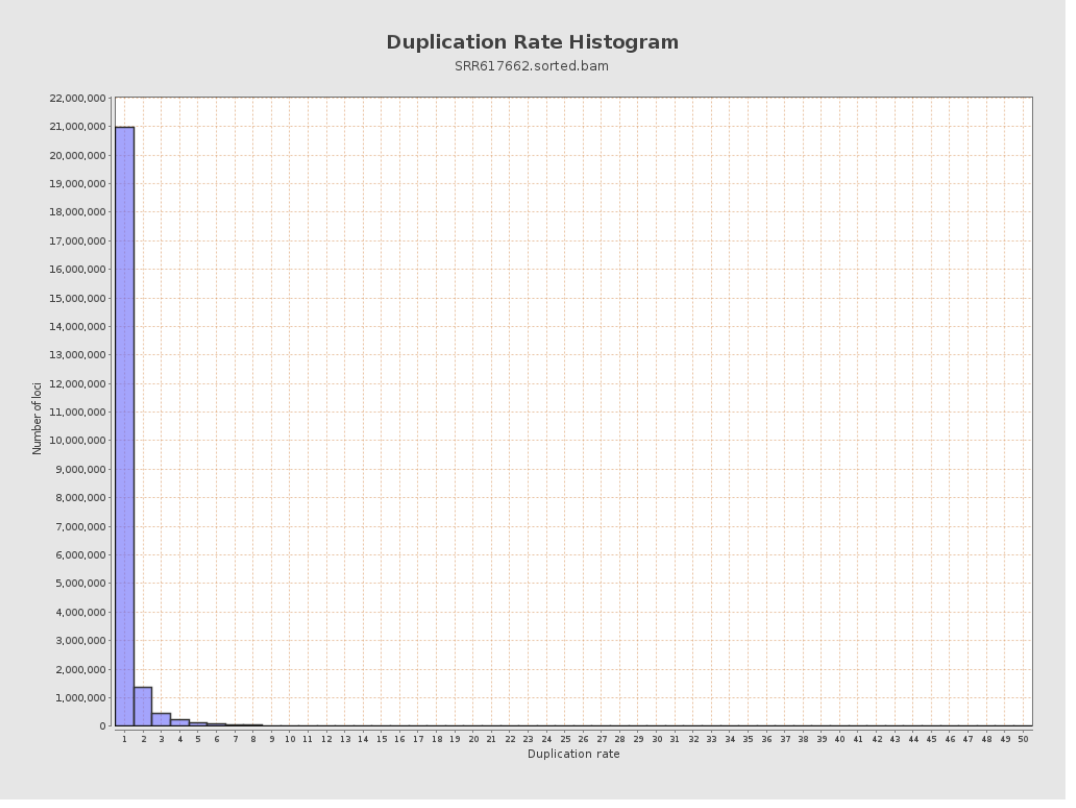
5. Results : Coverage Histogram (0-50X)



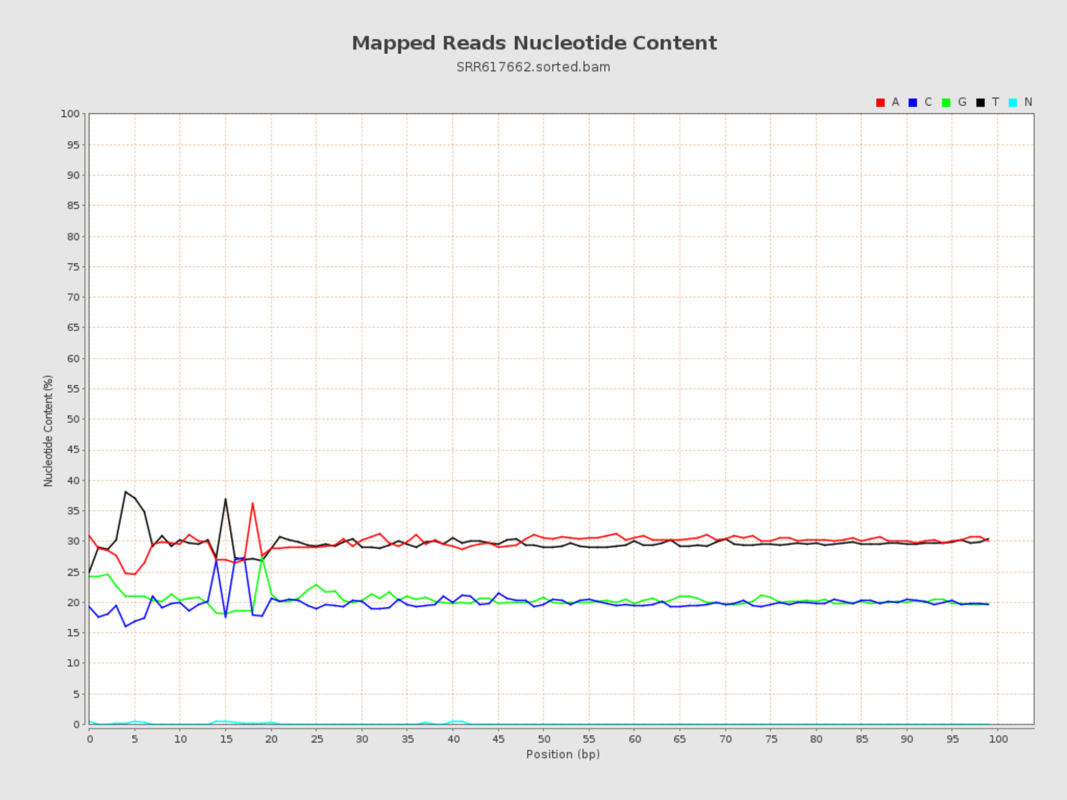
6. Results : Genome Fraction Coverage



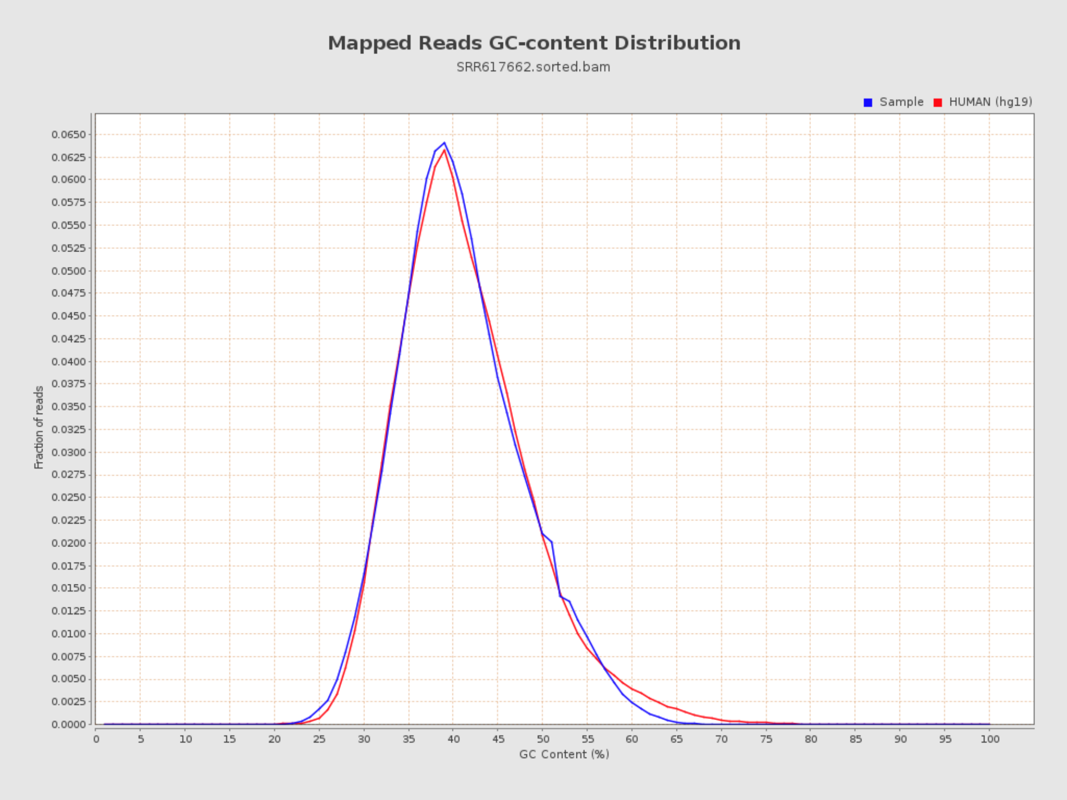
7. Results : Duplication Rate Histogram



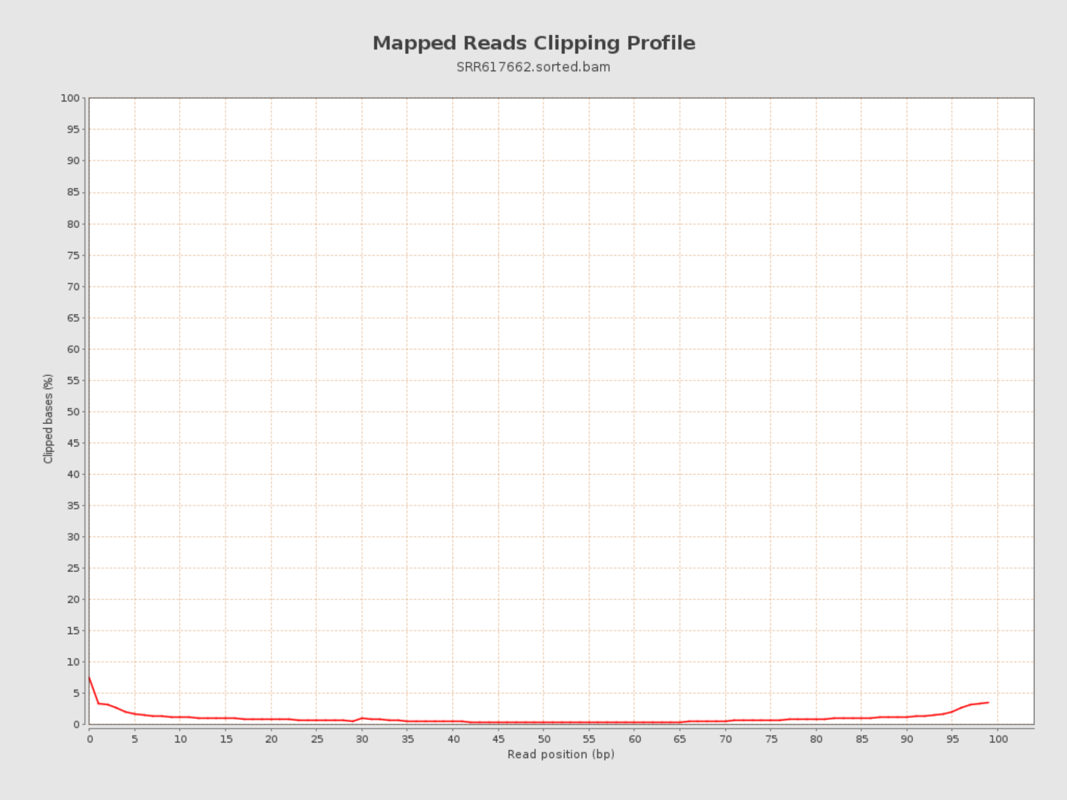
8. Results : Mapped Reads Nucleotide Content



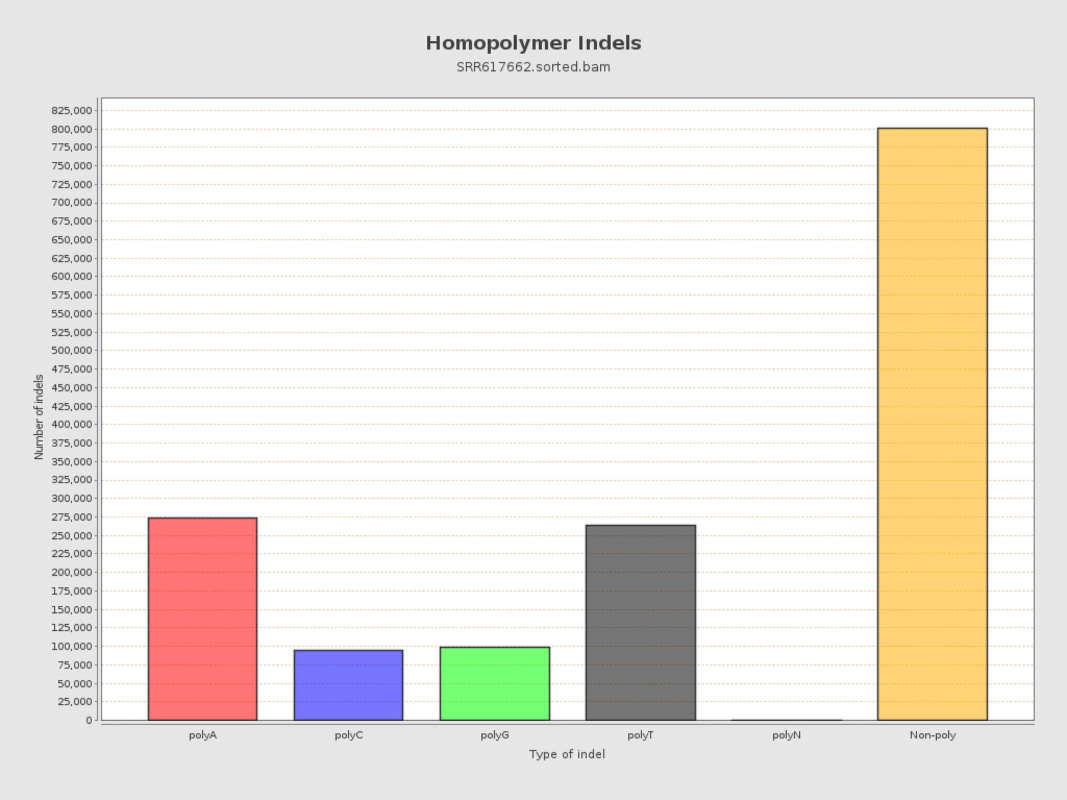
9. Results : Mapped Reads GC-content Distribution



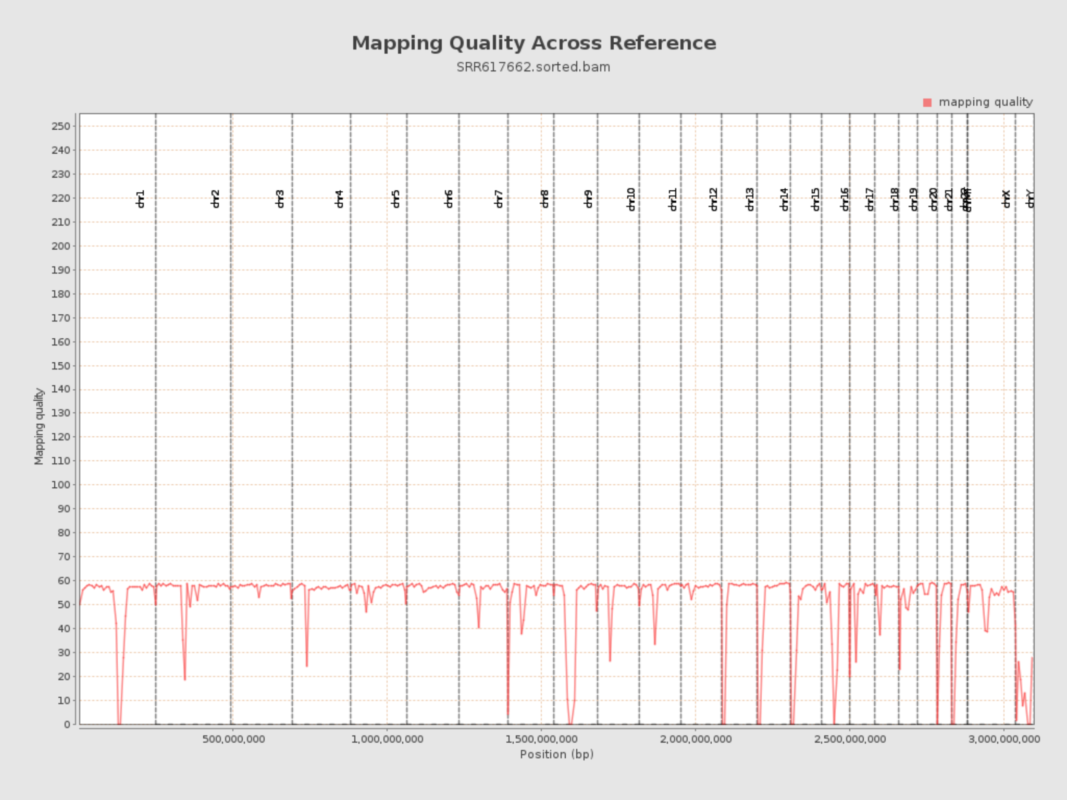
10. Results : Mapped Reads Clipping Profile



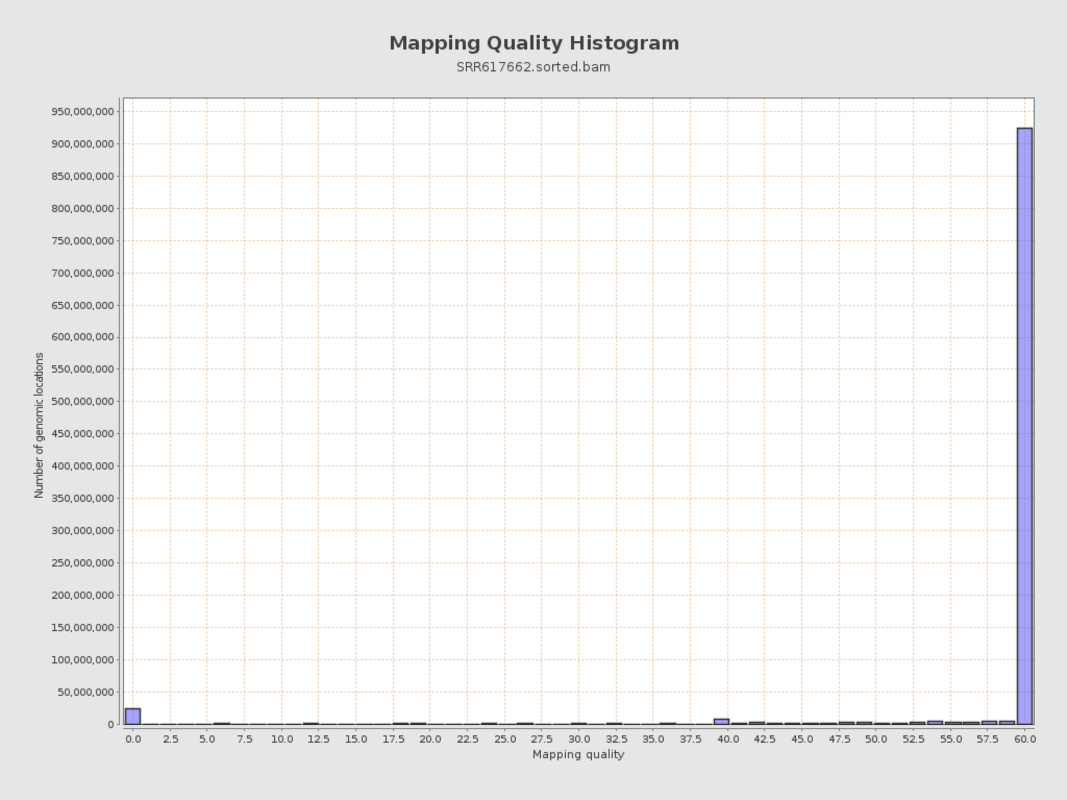
11. Results : Homopolymer Indels



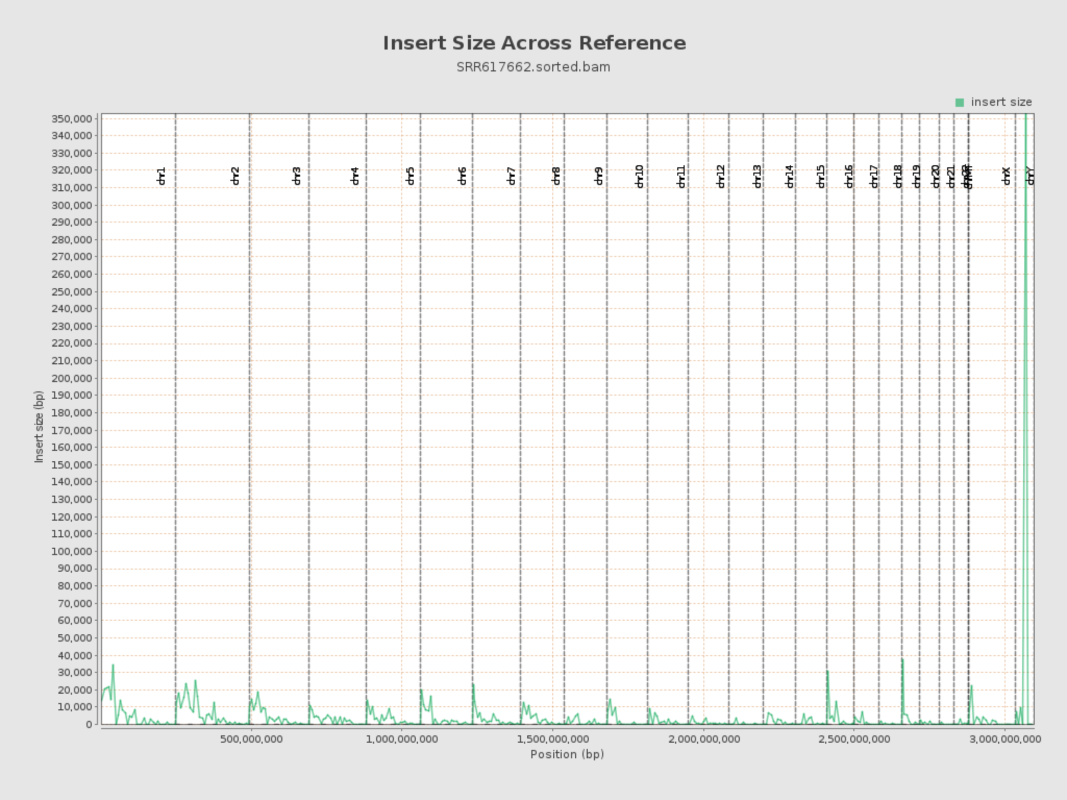
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram