Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/28 20:16:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472643.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_SRR3472643 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472643_1.fastq.gz SRR3472643_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 28 20:16:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472643.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	17,342,350
Mapped reads	17,208,560 / 99.23%
Unmapped reads	133,790 / 0.77%
Mapped paired reads	17,208,560 / 99.23%
Mapped reads, first in pair	8,625,224 / 49.74%
Mapped reads, second in pair	8,583,336 / 49.49%
Mapped reads, both in pair	17,122,564 / 98.73%
Mapped reads, singletons	85,996 / 0.5%
Secondary alignments	0
Supplementary alignments	95,288 / 0.55%
Read min/max/mean length	30 / 101 / 99.78
Duplicated reads (estimated)	12,179,479 / 70.23%
Duplication rate	48.51%
Clipped reads	1,277,955 / 7.37%

2.2. ACGT Content

Number/percentage of A's	454,144,596 / 26.83%
Number/percentage of C's	394,409,085 / 23.3%
Number/percentage of T's	454,420,212 / 26.85%
Number/percentage of G's	389,149,910 / 22.99%
Number/percentage of N's	326,745 / 0.02%

GC Percentage	46.3%

2.3. Coverage

Mean	0.5468
Standard Deviation	26.5198

2.4. Mapping Quality

Mean Mapping Quality	54.93

2.5. Insert size

Mean	19,886.01
Standard Deviation	1,349,900.03
P25/Median/P75	154 / 209 / 280

2.6. Mismatches and indels

General error rate	0.62%
Mismatches	10,329,719
Insertions	113,925
Mapped reads with at least one insertion	0.65%
Deletions	93,141
Mapped reads with at least one deletion	0.53%
Homopolymer indels	46.93%

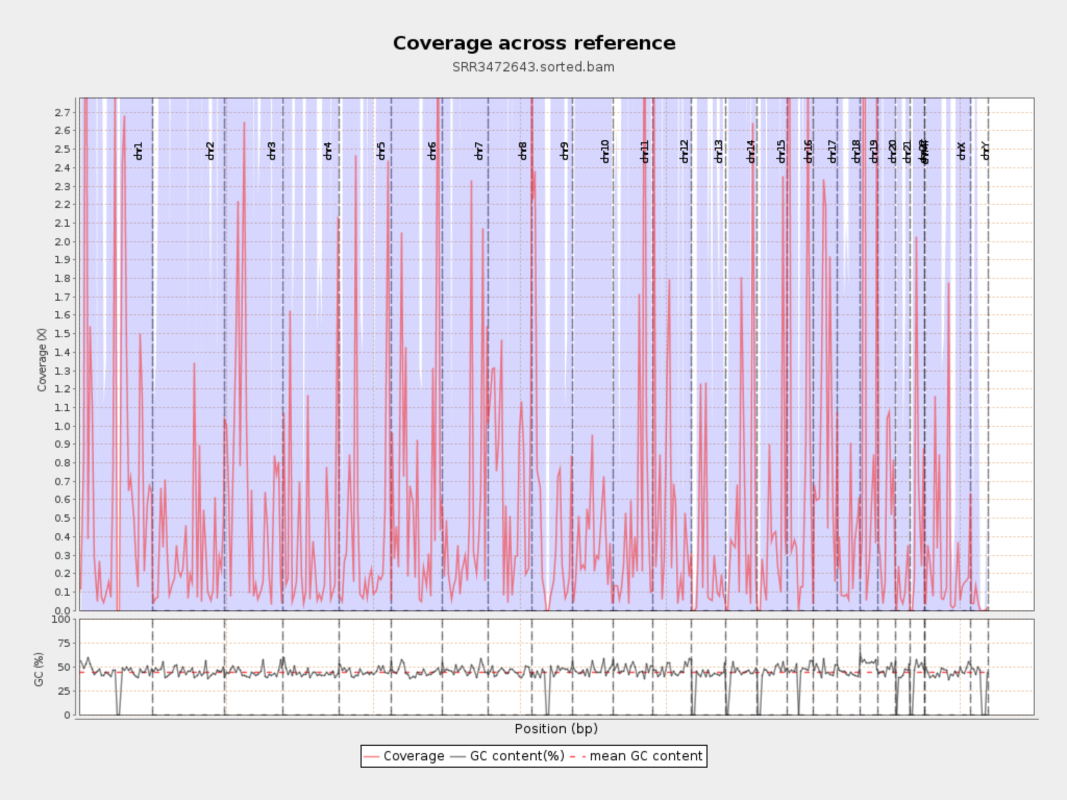
2.7. Chromosome stats

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

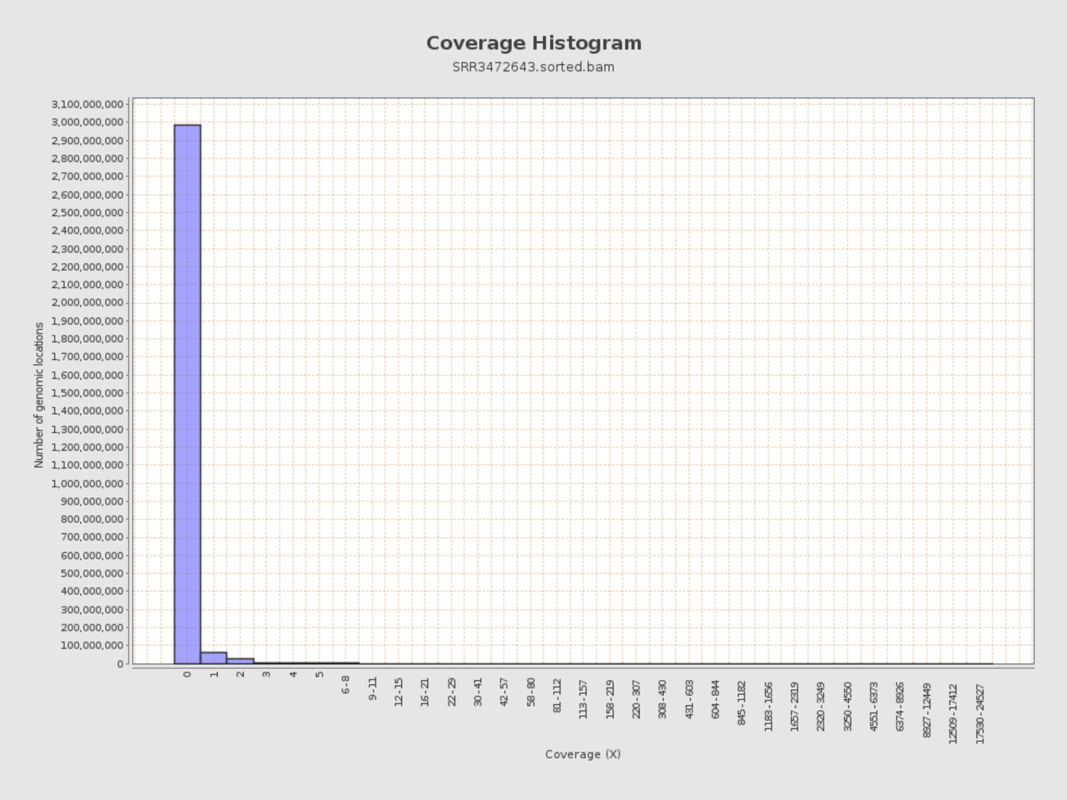
		bases	coverage	deviation
chr1	249250621	208169250	0.8352	36.1184
chr2	243199373	73298178	0.3014	13.4589
chr3	198022430	138527857	0.6996	32.6609
chr4	191154276	75642631	0.3957	23.1367
chr5	180915260	80336667	0.4441	20.736
chr6	171115067	116388928	0.6802	29.9891
chr7	159138663	83291626	0.5234	20.4571
chr8	146364022	102265315	0.6987	31.5462
chr9	141213431	78999027	0.5594	21.5192
chr10	135534747	48447406	0.3575	19.1737
chr11	135006516	77481684	0.5739	40.5006
chr12	133851895	84344894	0.6301	23.841
chr13	115169878	30780832	0.2673	12.2803
chr14	107349540	59265227	0.5521	26.1216
chr15	102531392	44895369	0.4379	19.8447
chr16	90354753	87924847	0.9731	34.4072
chr17	81195210	87376049	1.0761	37.2534
chr18	78077248	24243247	0.3105	13.9686
chr19	59128983	68592937	1.1601	51.3835
chr20	63025520	32785467	0.5202	20.0809
chr21	48129895	6719773	0.1396	7.4789
chr22	51304566	31236415	0.6088	24.3385
chrMT	16571	2224	0.1342	0.4267
chrX	155270560	49656667	0.3198	19.1501

chrY	59373566	2006761	0.0338	1.5254

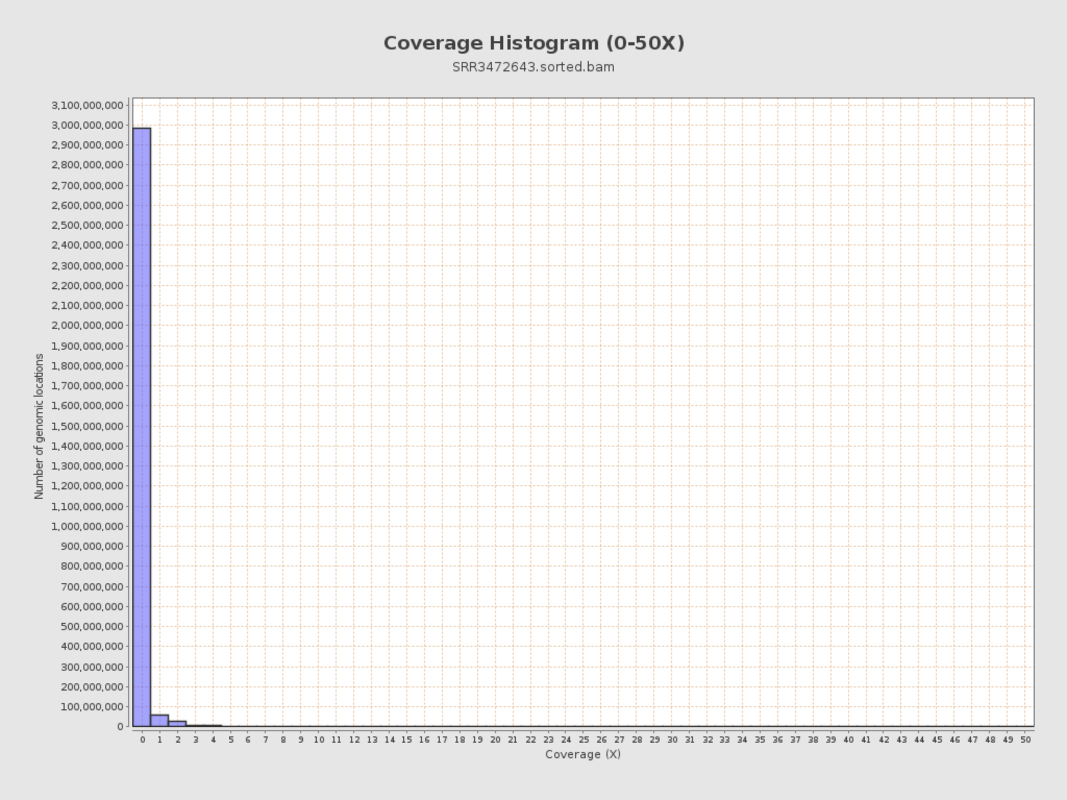
3. Results : Coverage across reference



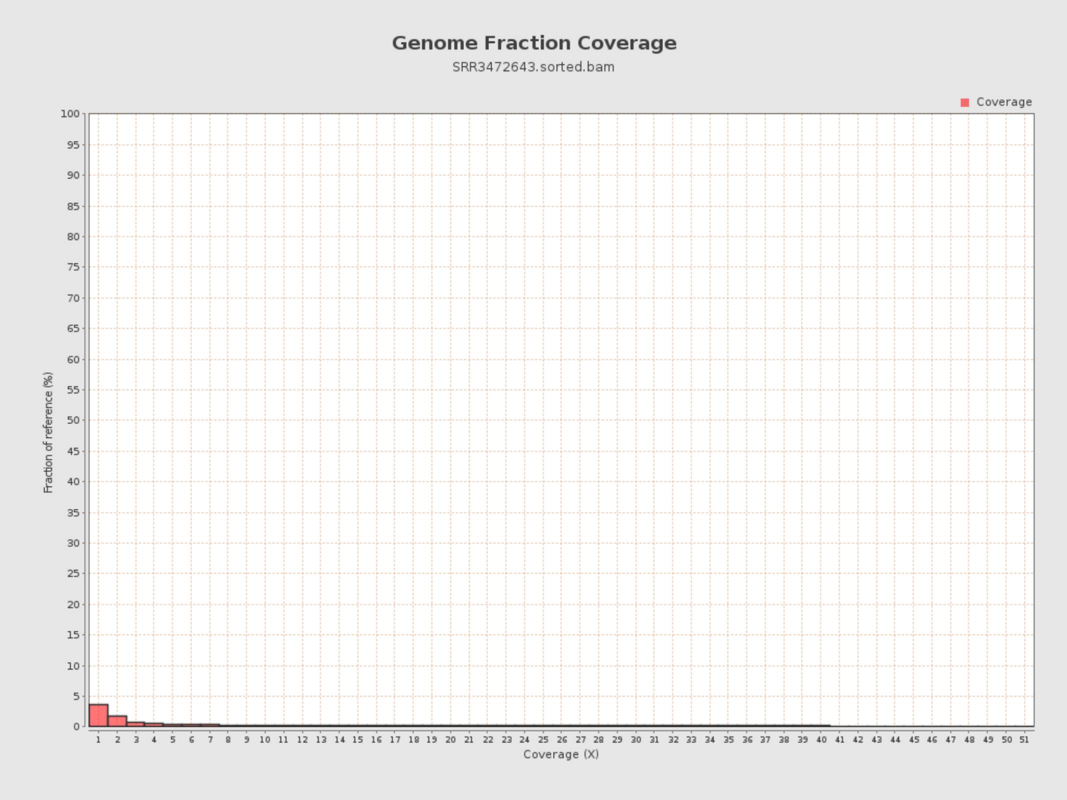
4. Results : Coverage Histogram



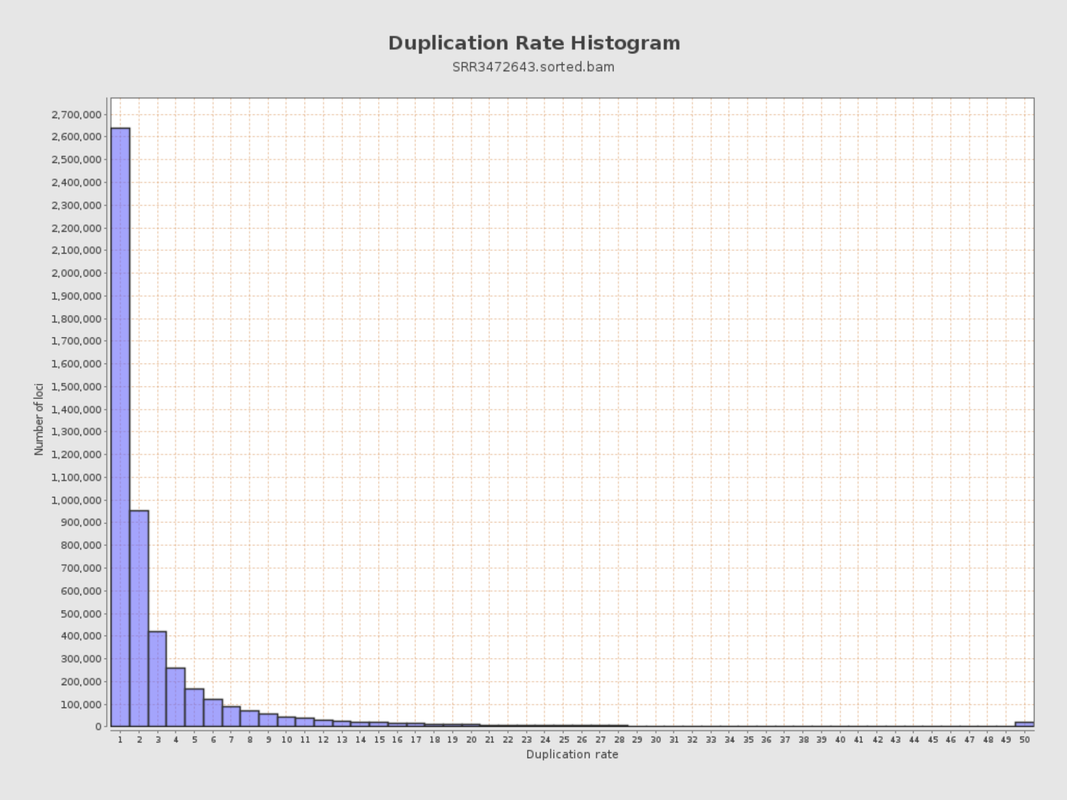
5. Results : Coverage Histogram (0-50X)



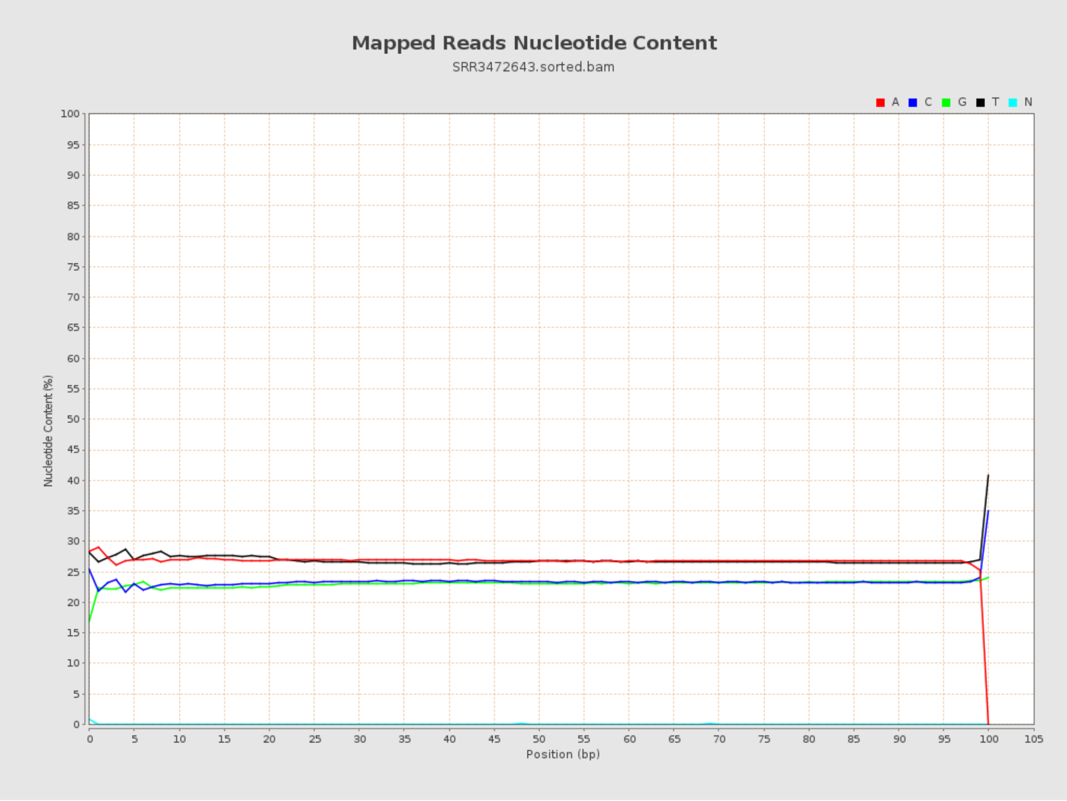
6. Results : Genome Fraction Coverage



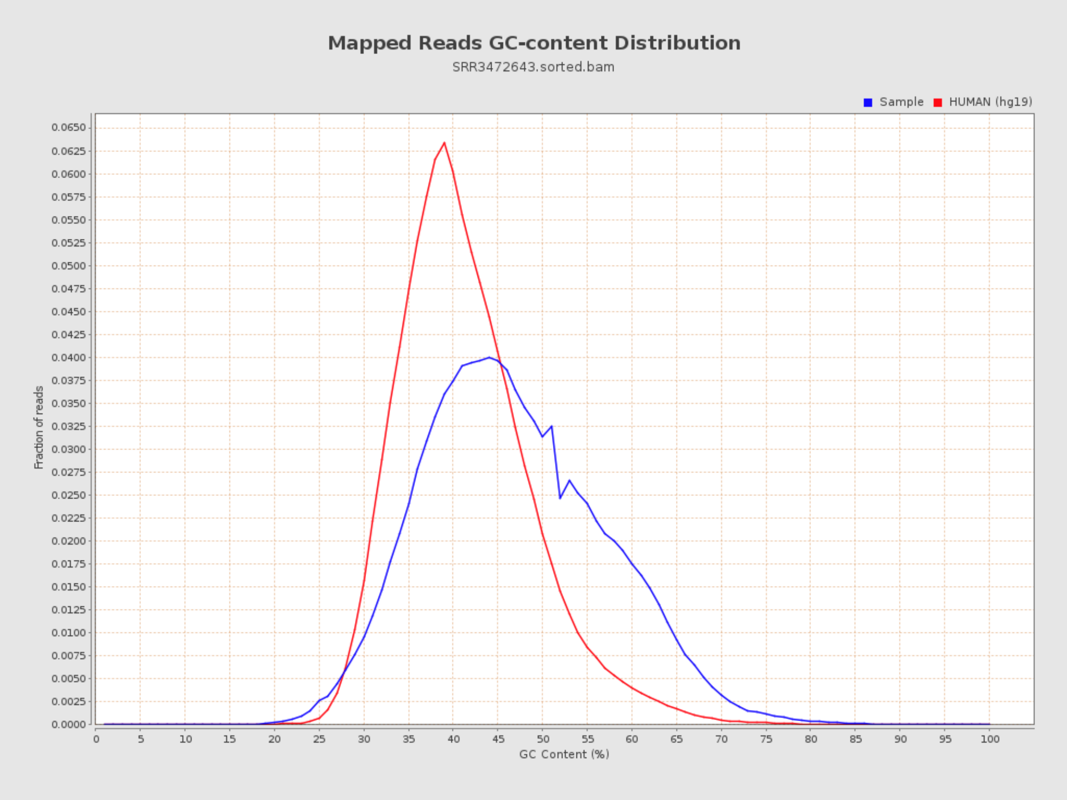
7. Results : Duplication Rate Histogram



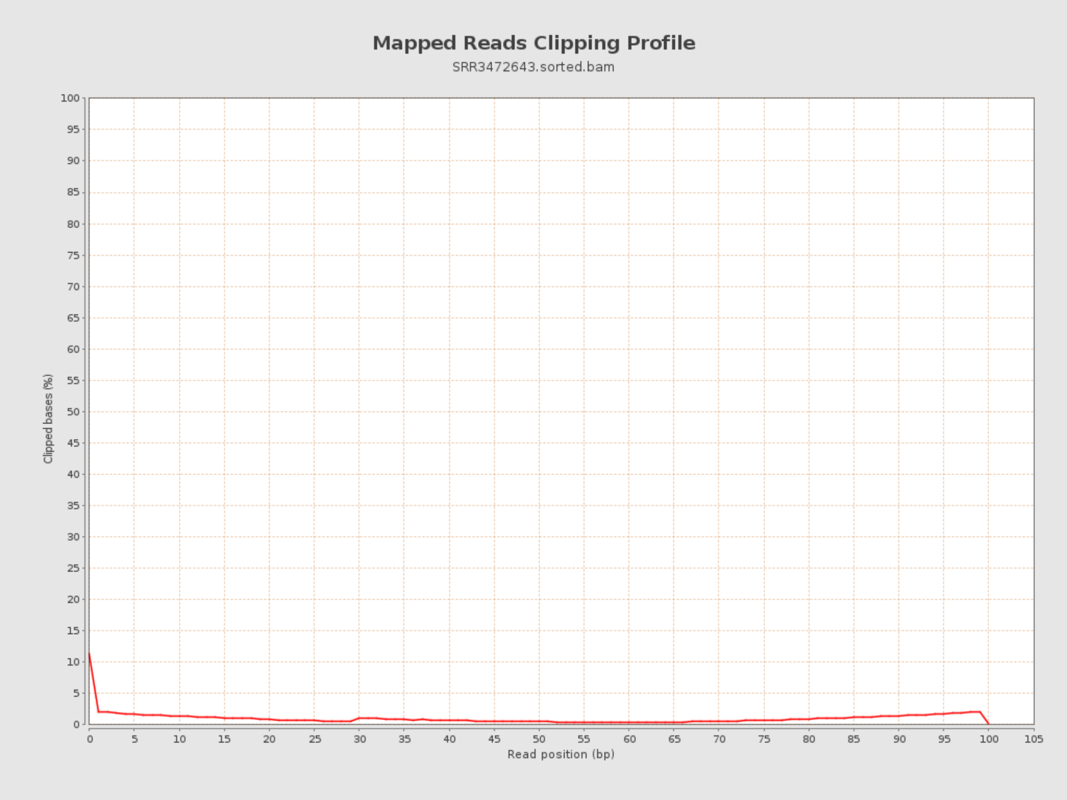
8. Results : Mapped Reads Nucleotide Content



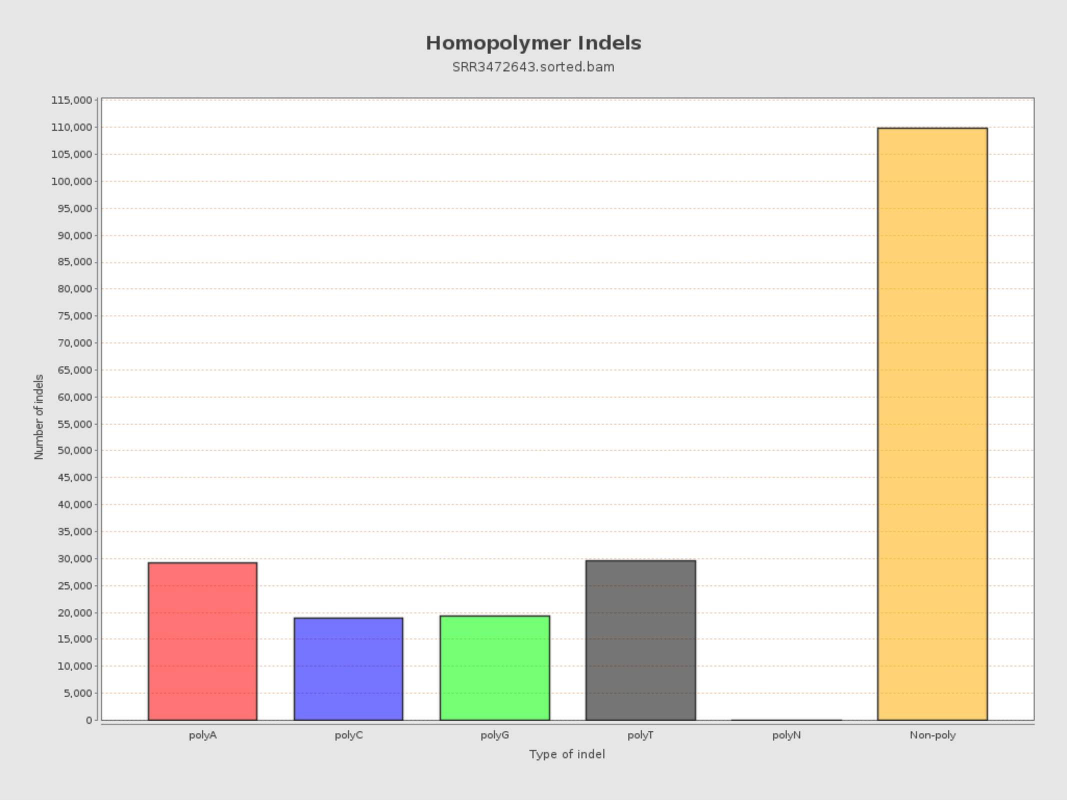
9. Results : Mapped Reads GC-content Distribution



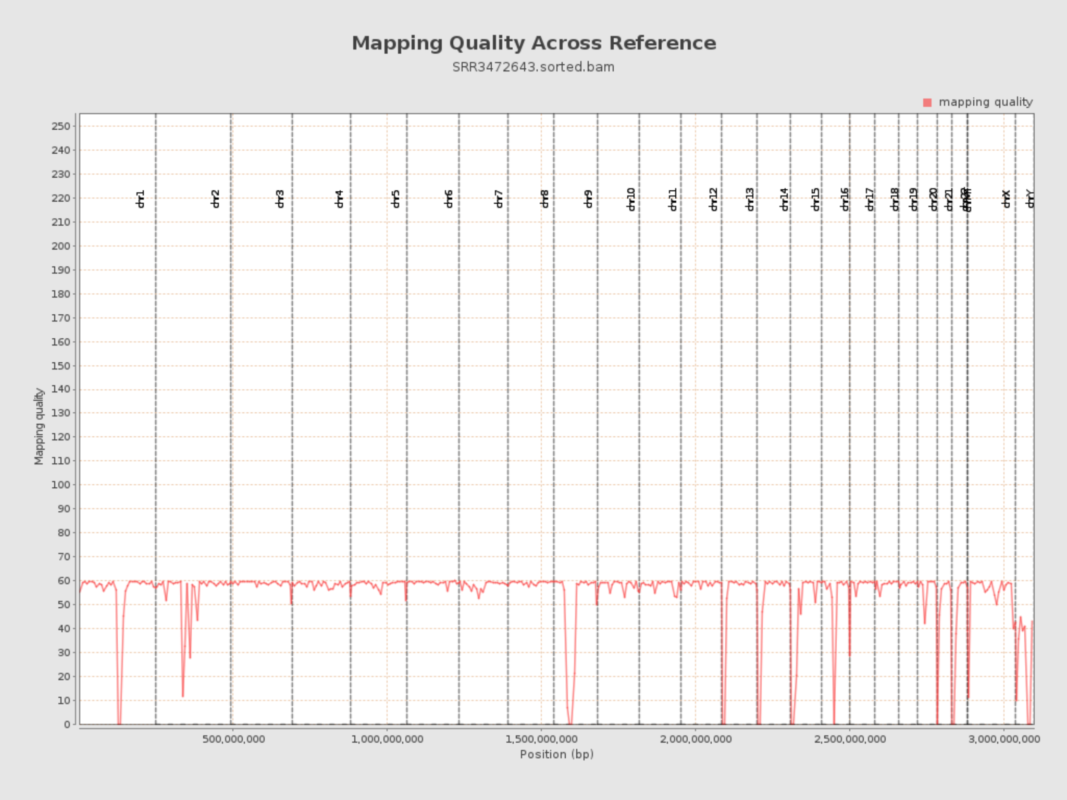
10. Results : Mapped Reads Clipping Profile



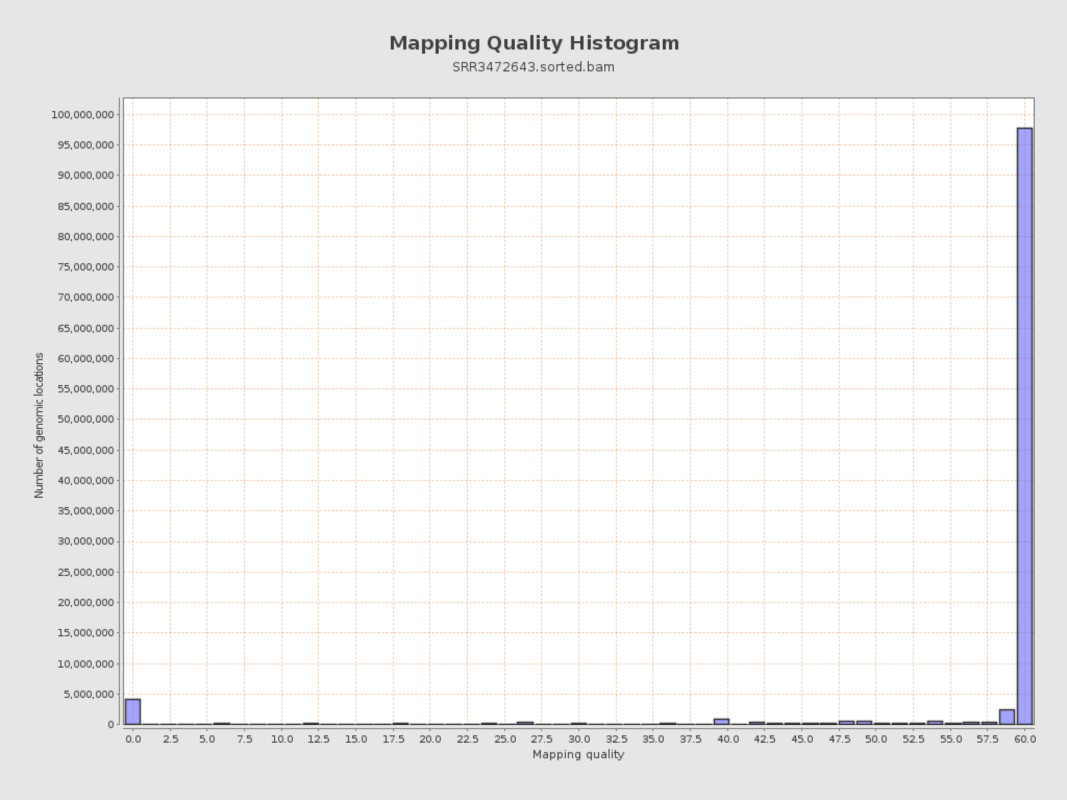
11. Results : Homopolymer Indels



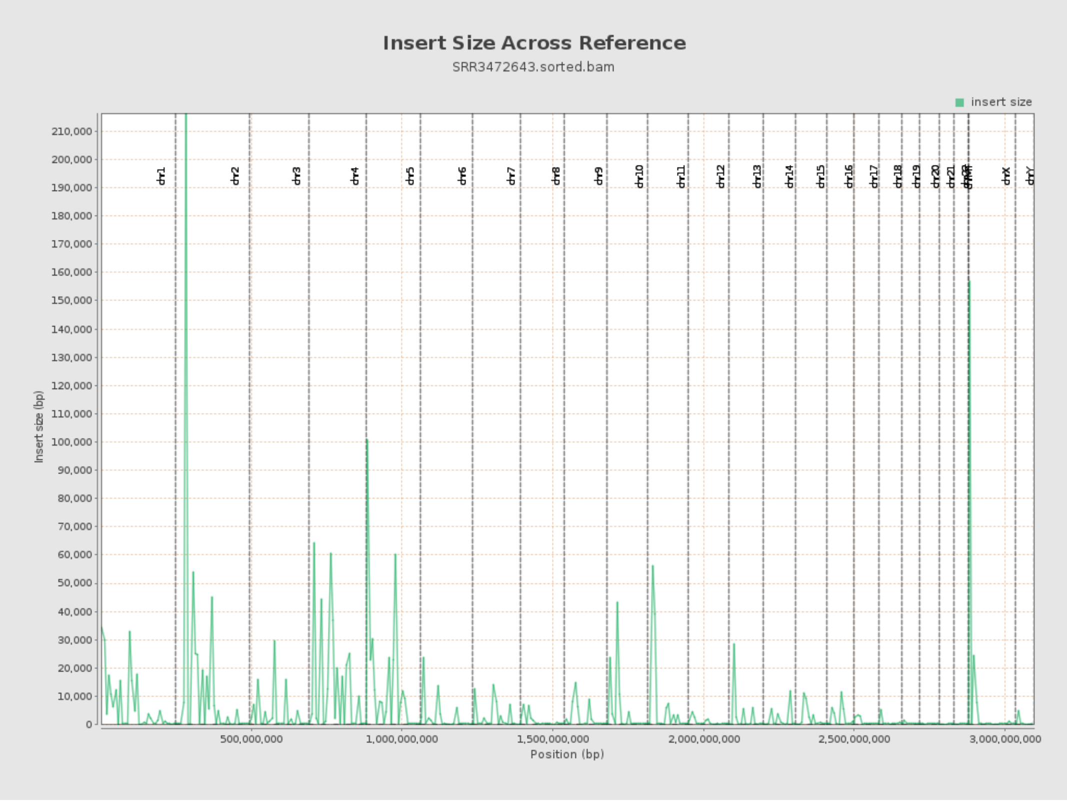
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram