Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/27 16:25:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR504621.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_SRR504621 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR504621_1.fastq.gz SRR504621_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Dec 27 16:25:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR504621.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	543,755,692
Mapped reads	495,326,978 / 91.09%
Unmapped reads	48,428,714 / 8.91%
Mapped paired reads	495,326,978 / 91.09%
Mapped reads, first in pair	246,265,319 / 45.29%
Mapped reads, second in pair	249,061,659 / 45.8%
Mapped reads, both in pair	480,108,240 / 88.29%
Mapped reads, singletons	15,218,738 / 2.8%
Secondary alignments	0
Supplementary alignments	4,752,758 / 0.87%
Read min/max/mean length	30 / 100 / 100.35
Duplicated reads (estimated)	184,751,467 / 33.98%
Duplication rate	27.12%
Clipped reads	85,474,087 / 15.72%

2.2. ACGT Content

Number/percentage of A's	12,642,165,120 / 26.63%
Number/percentage of C's	10,943,565,838 / 23.05%
Number/percentage of T's	12,795,441,442 / 26.95%
Number/percentage of G's	10,937,258,269 / 23.04%
Number/percentage of N's	152,478,739 / 0.32%

GC Percentage	46.09%

2.3. Coverage

Mean	15.3475
Standard Deviation	354.5768

2.4. Mapping Quality

Mean Mapping Quality	52.21

2.5. Insert size

Mean	97,435.36
Standard Deviation	2,926,064.4
P25/Median/P75	278 / 329 / 386

2.6. Mismatches and indels

General error rate	1.83%
Mismatches	813,003,709
Insertions	13,639,503
Mapped reads with at least one insertion	2.56%
Deletions	12,250,219
Mapped reads with at least one deletion	2.31%
Homopolymer indels	34.31%

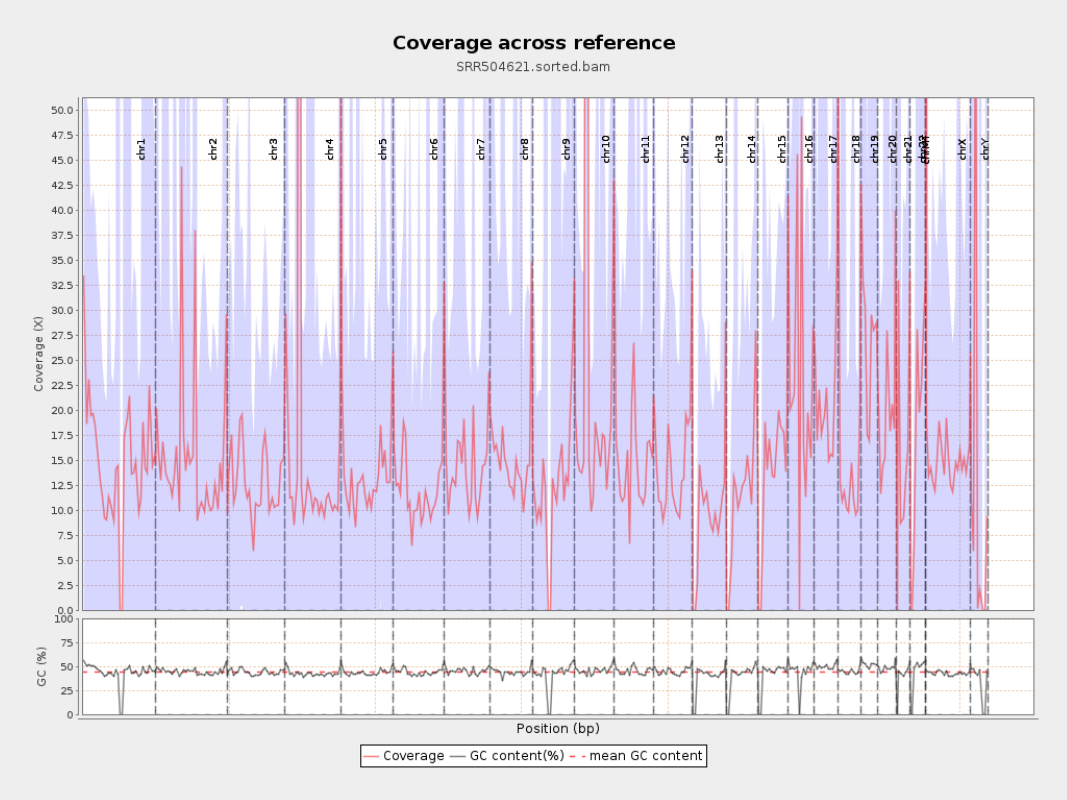
2.7. Chromosome stats

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

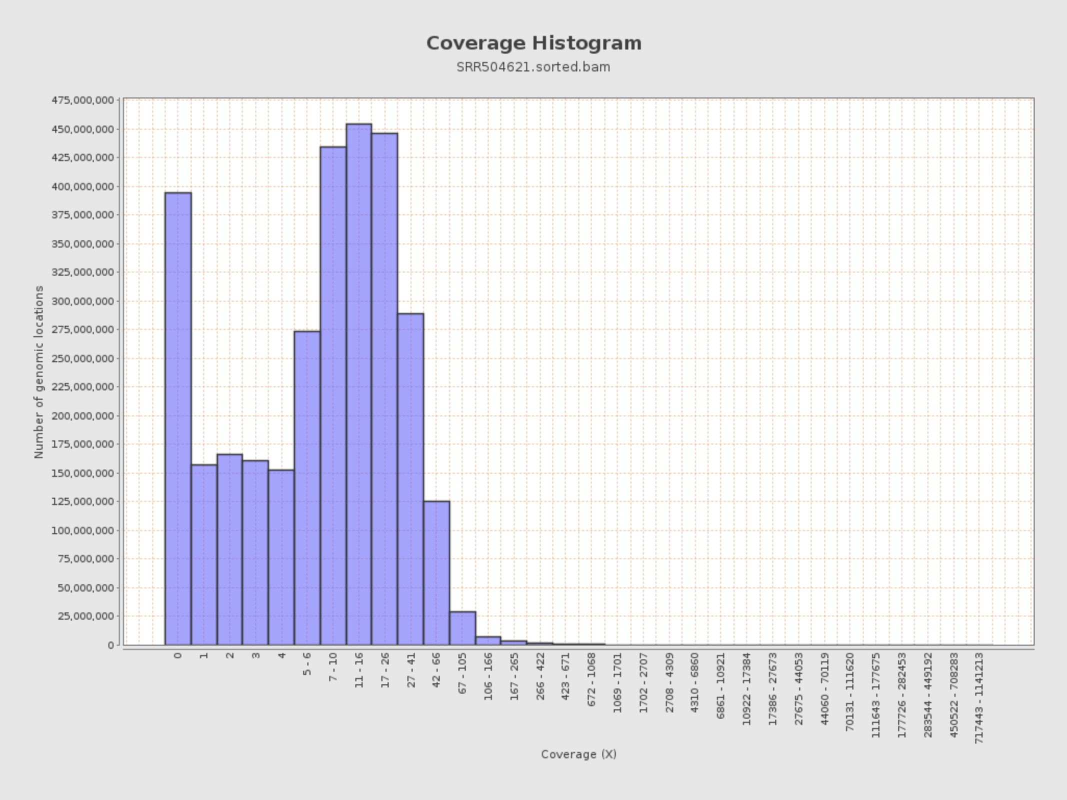
		bases	coverage	deviation
chr1	249250621	3673124673	14.7367	108.9757
chr2	243199373	3732629532	15.348	342.6125
chr3	198022430	2543212281	12.8431	32.7062
chr4	191154276	3560293504	18.6252	994.4688
chr5	180915260	2472372656	13.6659	45.0894
chr6	171115067	2038152473	11.911	44.0115
chr7	159138663	2343158290	14.724	51.5244
chr8	146364022	2231823622	15.2484	261.2769
chr9	141213431	1738888358	12.3139	125.7721
chr10	135534747	3116279643	22.9925	787.1652
chr11	135006516	2044986600	15.1473	42.7423
chr12	133851895	1903154413	14.2184	26.5511
chr13	115169878	1061608456	9.2178	19.9407
chr14	107349540	1271842974	11.8477	41.4974
chr15	102531392	1389013283	13.5472	22.8891
chr16	90354753	2131877435	23.5945	276.4391
chr17	81195210	1634027628	20.1247	102.0209
chr18	78077248	1075219899	13.7712	410.7656
chr19	59128983	1595682503	26.9865	60.0074
chr20	63025520	1218329248	19.3307	242.4234
chr21	48129895	788066134	16.3737	327.5566
chr22	51304566	882210802	17.1956	41.6024
chrMT	16571	17920809	1,081.4561	512.471
chrX	155270560	2326414457	14.983	30.105

chrY	59373566	721019444	12.1438	822.739

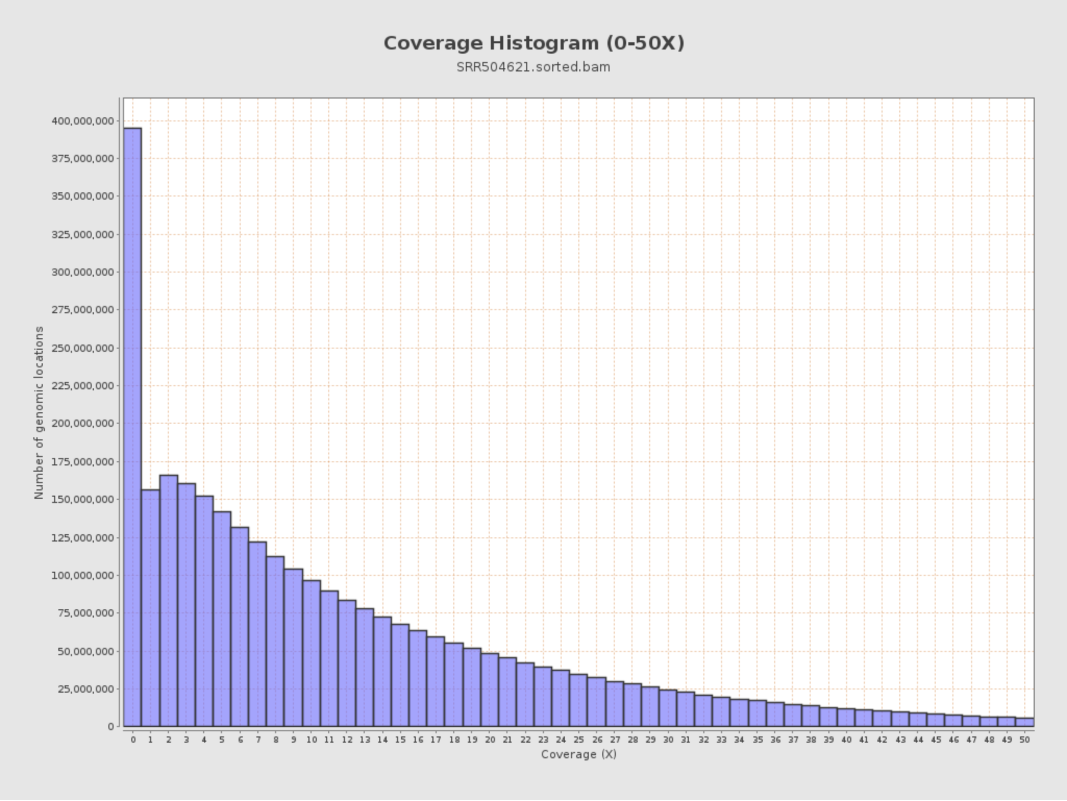
3. Results : Coverage across reference



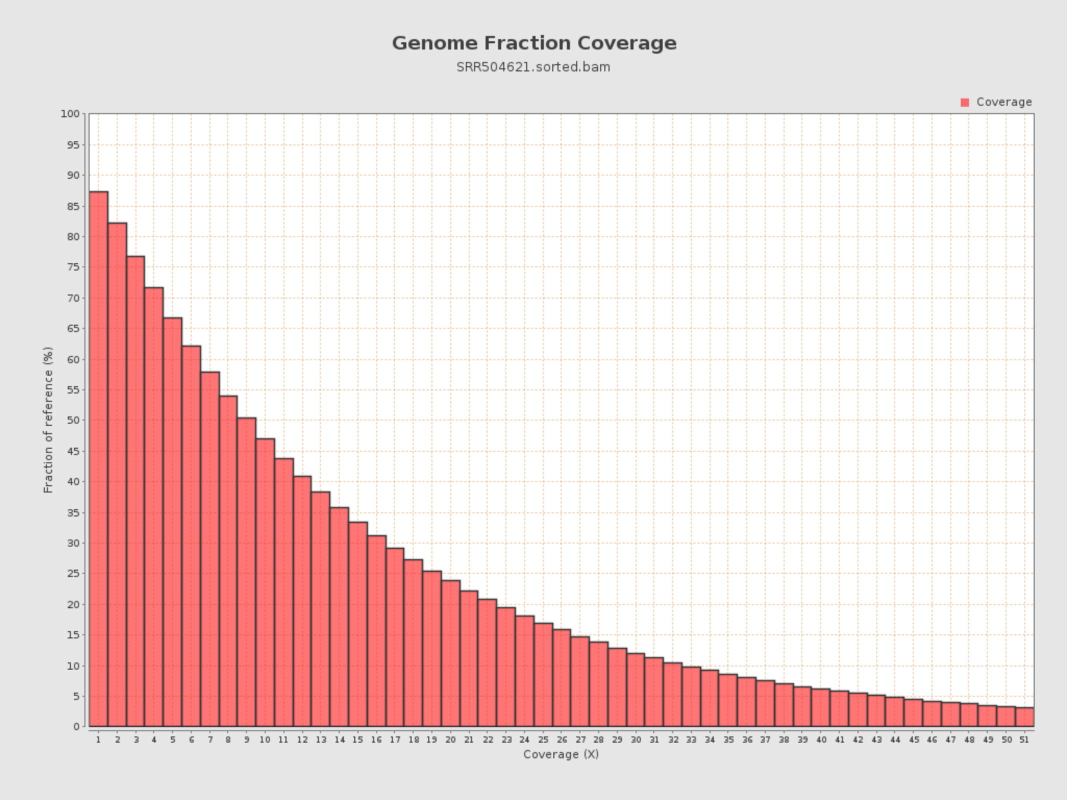
4. Results : Coverage Histogram



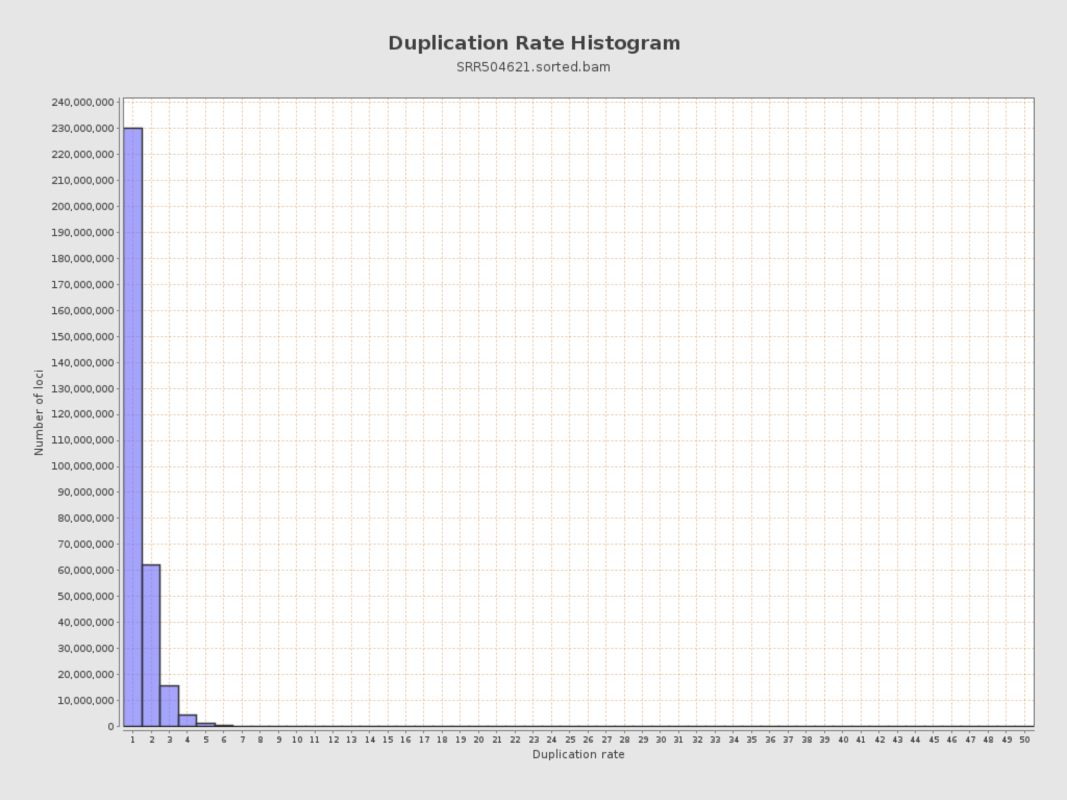
5. Results : Coverage Histogram (0-50X)



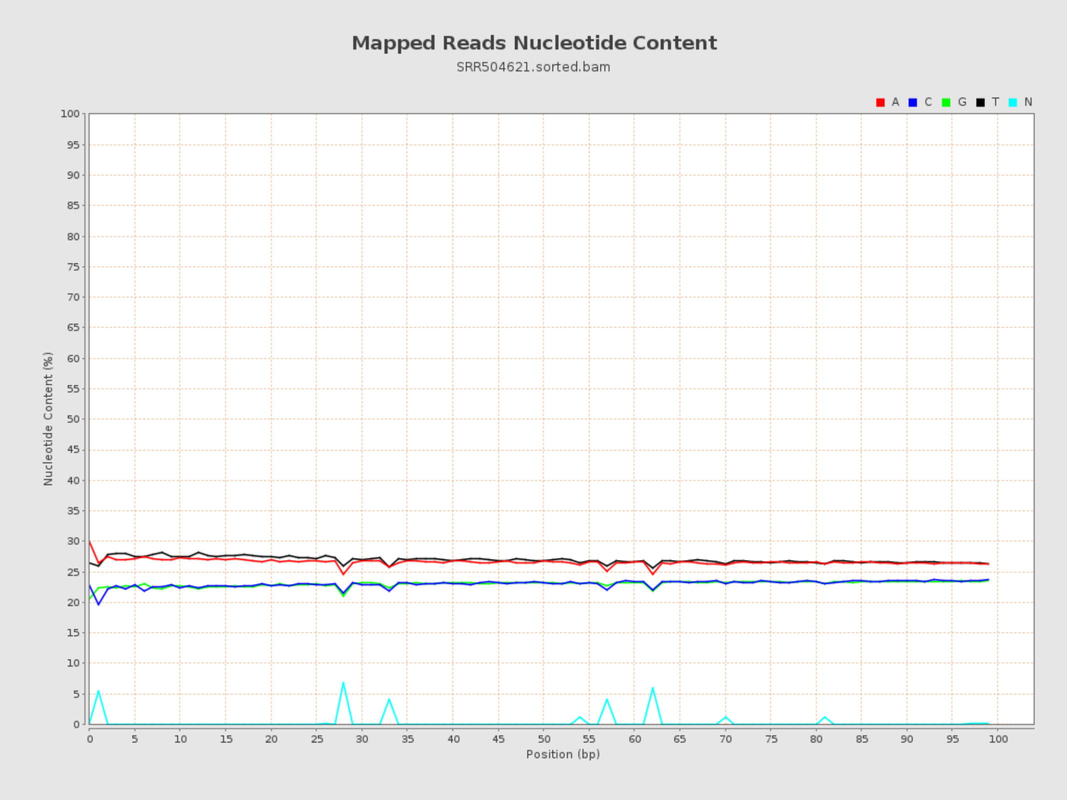
6. Results : Genome Fraction Coverage



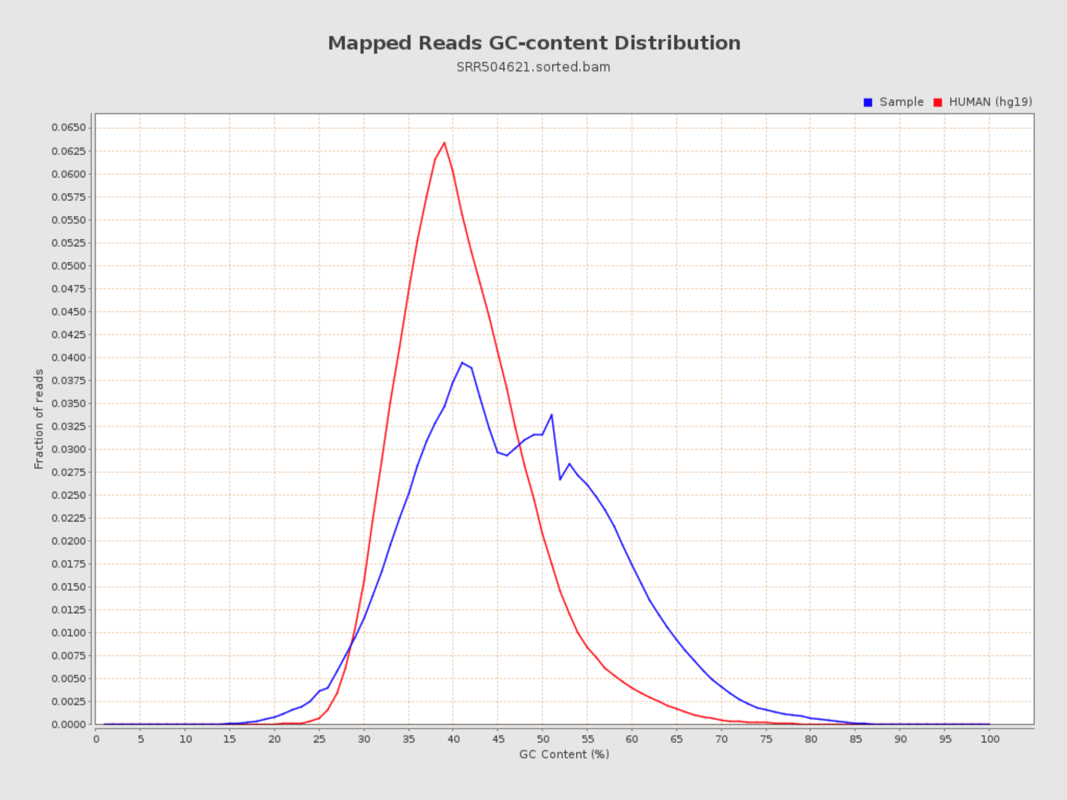
7. Results : Duplication Rate Histogram



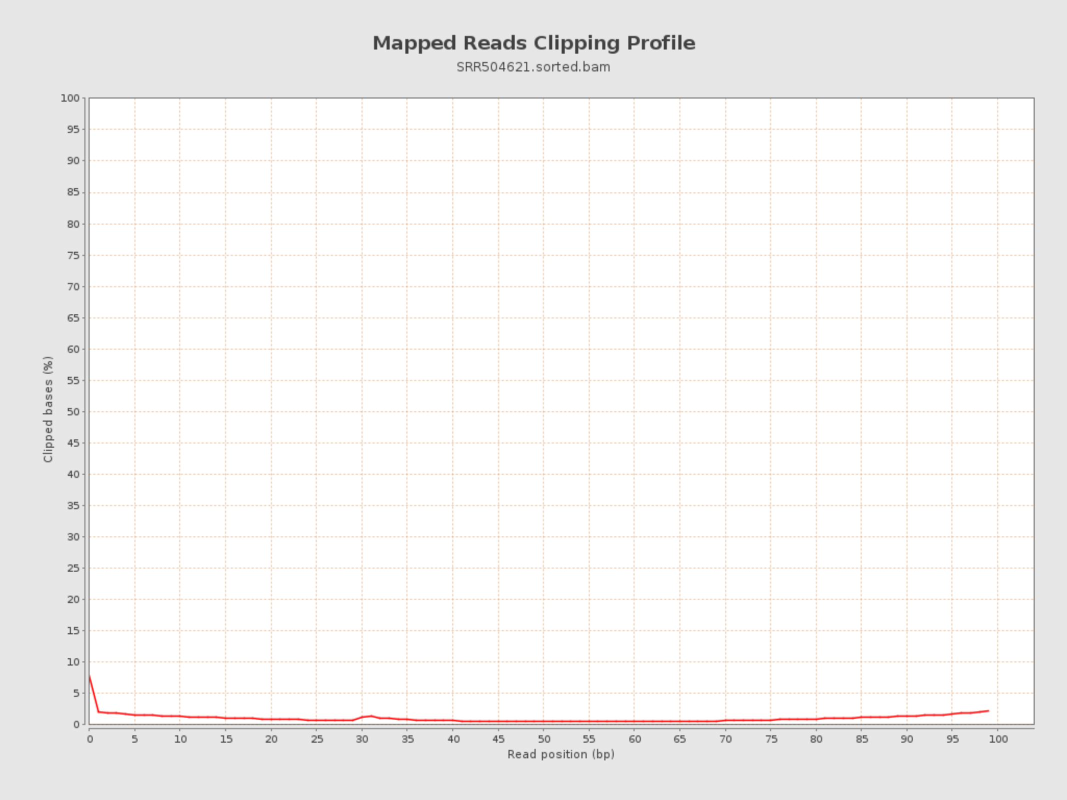
8. Results : Mapped Reads Nucleotide Content



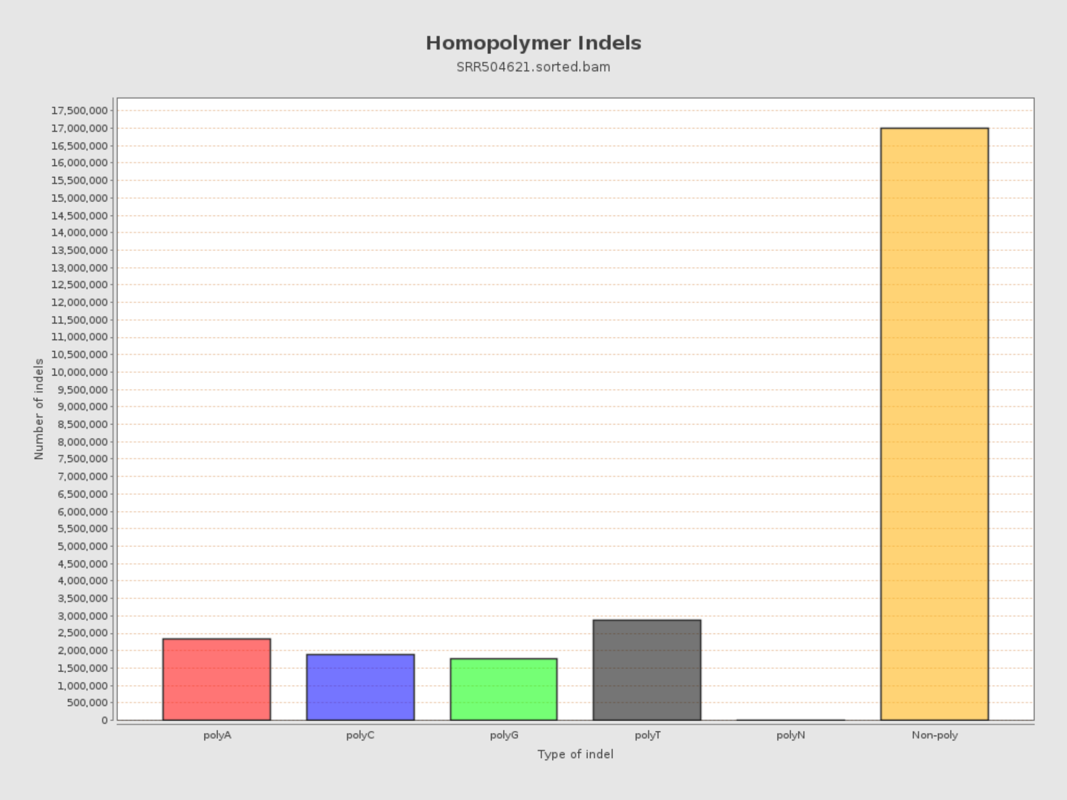
9. Results : Mapped Reads GC-content Distribution



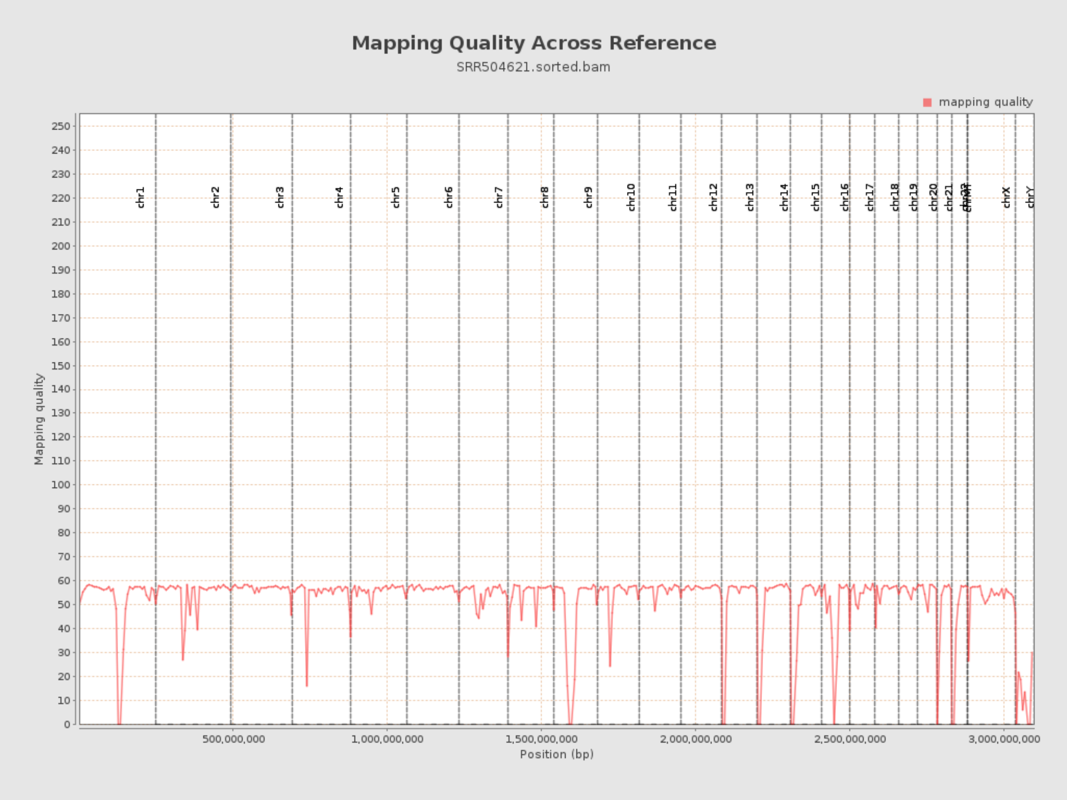
10. Results : Mapped Reads Clipping Profile



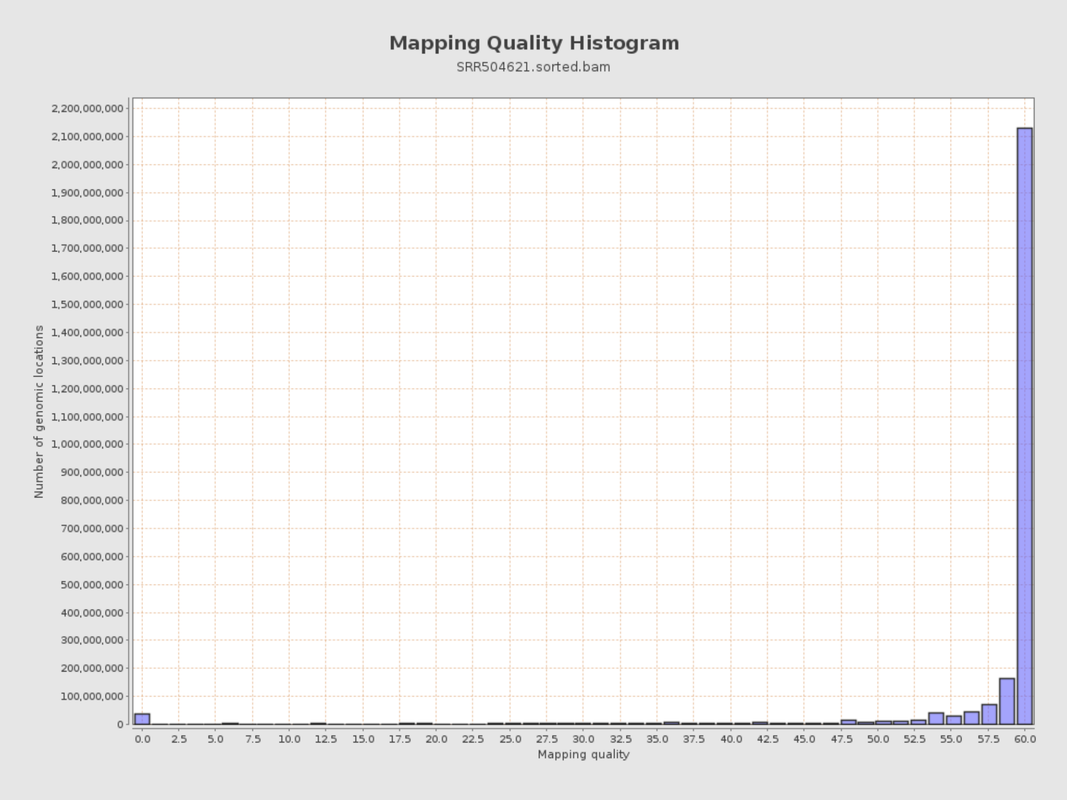
11. Results : Homopolymer Indels



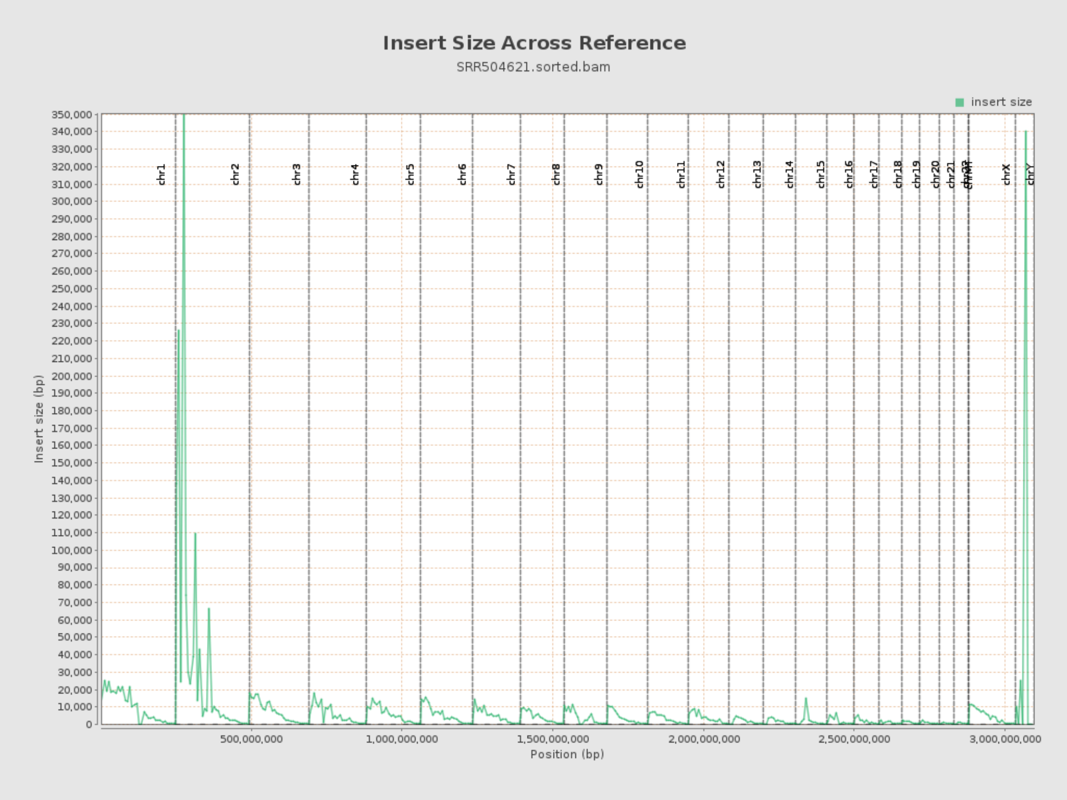
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram