Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/21 11:20:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1264613.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_SRR1264613 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1264613_1.fastq.gz SRR1264613_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Mar 21 11:20:53 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1264613.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,138,187,484
Mapped reads	1,125,040,896 / 98.84%
Unmapped reads	13,146,588 / 1.16%
Mapped paired reads	1,125,040,896 / 98.84%
Mapped reads, first in pair	563,749,337 / 49.53%
Mapped reads, second in pair	561,291,559 / 49.31%
Mapped reads, both in pair	1,119,052,774 / 98.32%
Mapped reads, singletons	5,988,122 / 0.53%
Secondary alignments	0
Supplementary alignments	9,704,839 / 0.85%
Read min/max/mean length	30 / 100 / 100.35
Duplicated reads (estimated)	339,834,217 / 29.86%
Duplication rate	25.01%
Clipped reads	82,033,662 / 7.21%

2.2. ACGT Content

Number/percentage of A's	33,095,889,398 / 29.78%
Number/percentage of C's	22,393,090,466 / 20.15%
Number/percentage of T's	33,150,978,695 / 29.83%
Number/percentage of G's	22,430,084,221 / 20.18%
Number/percentage of N's	59,771,869 / 0.05%

GC Percentage	40.33%

2.3. Coverage

Mean	35.9093
Standard Deviation	511.7754

2.4. Mapping Quality

Mean Mapping Quality	53.55

2.5. Insert size

Mean	135,142.49
Standard Deviation	3,539,910.46
P25/Median/P75	267 / 303 / 342

2.6. Mismatches and indels

General error rate	0.61%
Mismatches	648,854,760
Insertions	11,292,782
Mapped reads with at least one insertion	0.98%
Deletions	14,652,528
Mapped reads with at least one deletion	1.26%
Homopolymer indels	42.78%

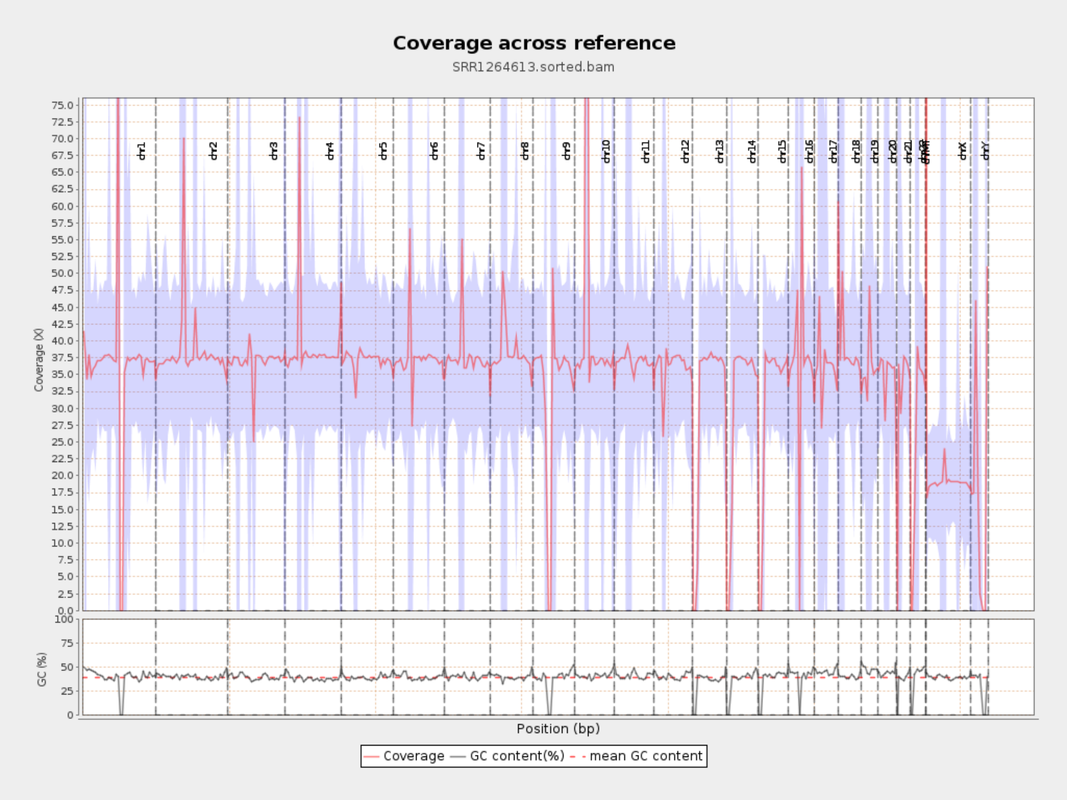
2.7. Chromosome stats

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

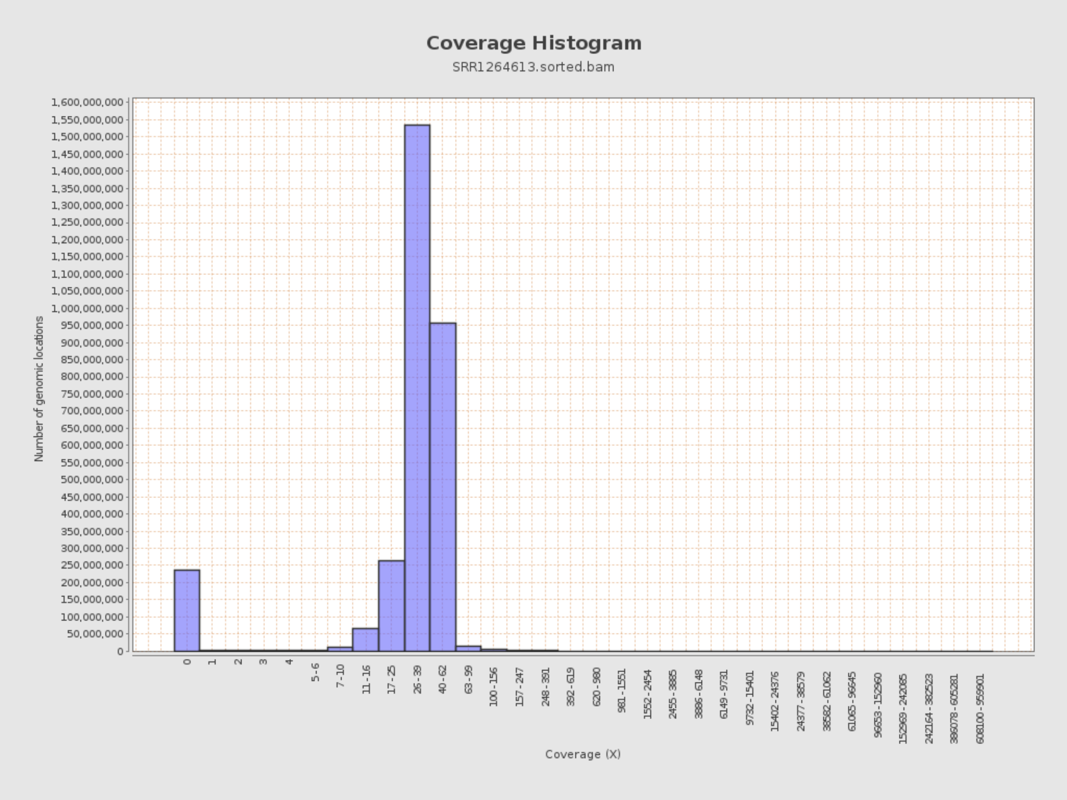
		bases	coverage	deviation
chr1	249250621	9026541162	36.2147	976.276
chr2	243199373	9387207281	38.5988	216.4324
chr3	198022430	7312676270	36.9285	31.5496
chr4	191154276	7490041662	39.1832	278.6404
chr5	180915260	6712526008	37.1031	31.5956
chr6	171115067	6427438604	37.5621	216.7477
chr7	159138663	6010318554	37.7678	342.8555
chr8	146364022	5610576354	38.333	629.7452
chr9	141213431	4655816817	32.9701	322.5776
chr10	135534747	5815980211	42.9114	794.1459
chr11	135006516	4989155882	36.9549	160.3781
chr12	133851895	4861897579	36.323	22.9927
chr13	115169878	3574243933	31.0345	18.0567
chr14	107349540	3295256183	30.6965	26.5522
chr15	102531392	3074719267	29.9881	19.1413
chr16	90354753	3319393123	36.7373	234.8897
chr17	81195210	2949336421	36.324	137.2569
chr18	78077248	3075138258	39.3858	479.1424
chr19	59128983	2149668451	36.3556	414.4843
chr20	63025520	2221895175	35.2539	53.0454
chr21	48129895	1537050145	31.9355	106.5533
chr22	51304566	1286011143	25.0662	109.9682
chrMT	16571	2273176894	137,178.0154	16,592.9205
chrX	155270560	2962555633	19.08	65.1787

chrY	59373566	1145564237	19.2942	292.9051

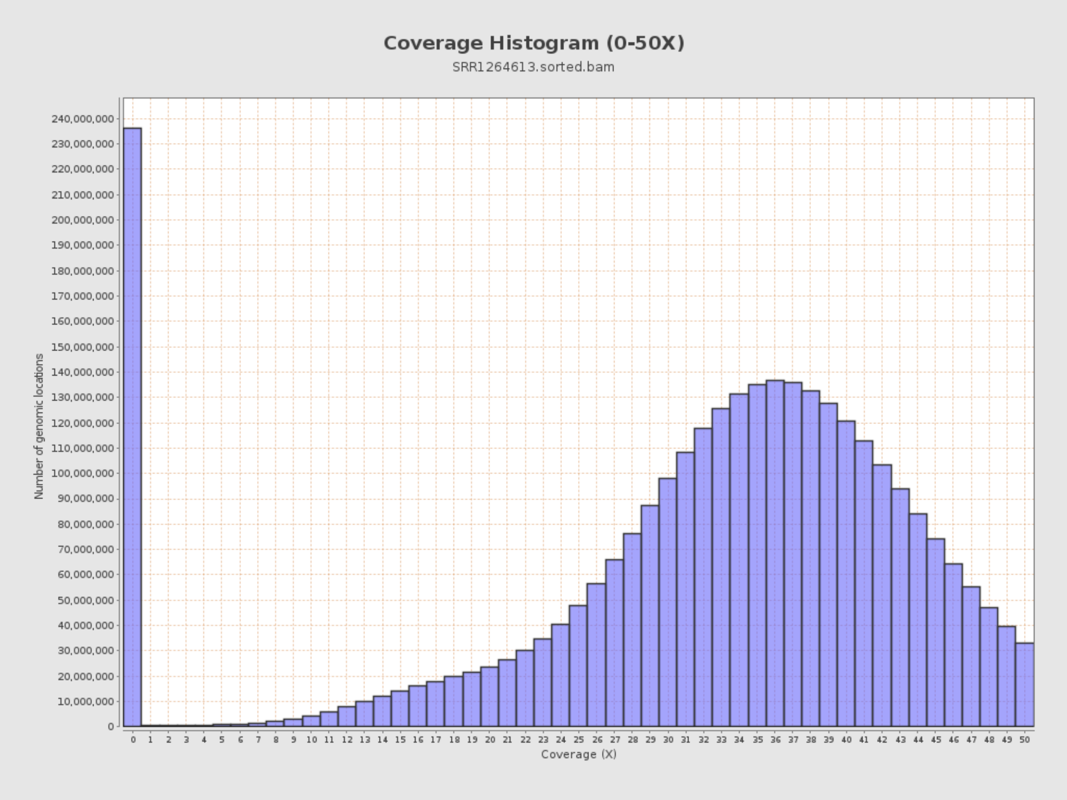
3. Results : Coverage across reference



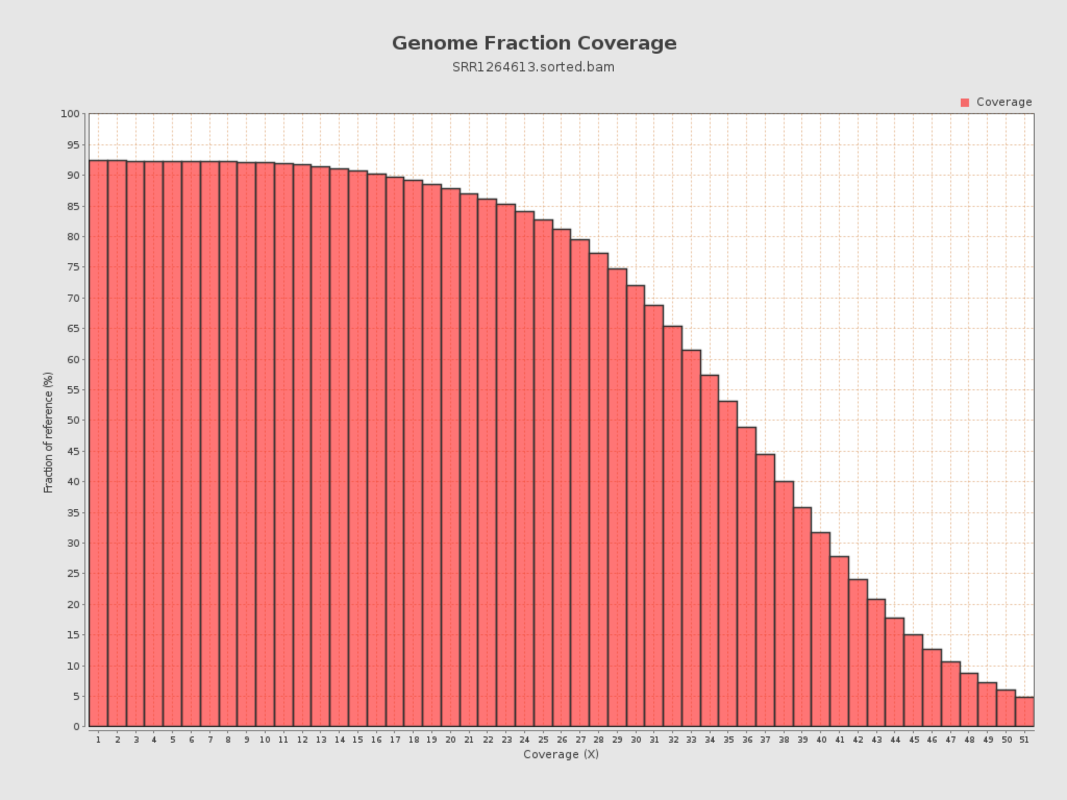
4. Results : Coverage Histogram



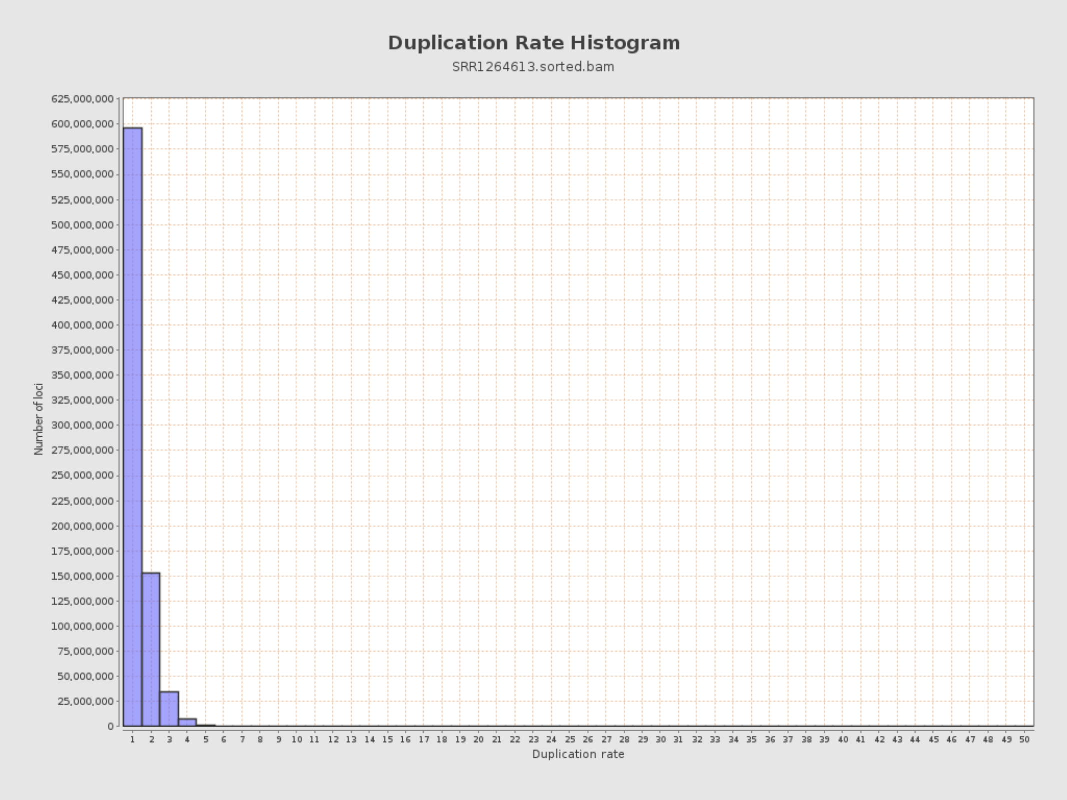
5. Results : Coverage Histogram (0-50X)



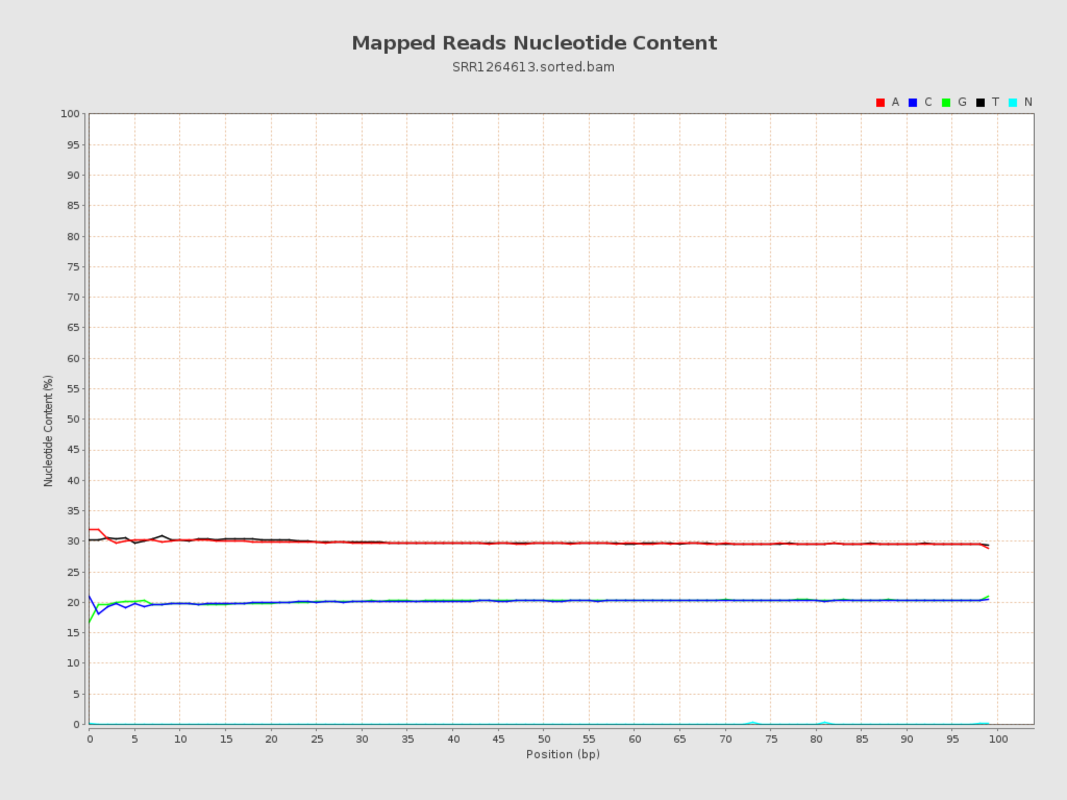
6. Results : Genome Fraction Coverage



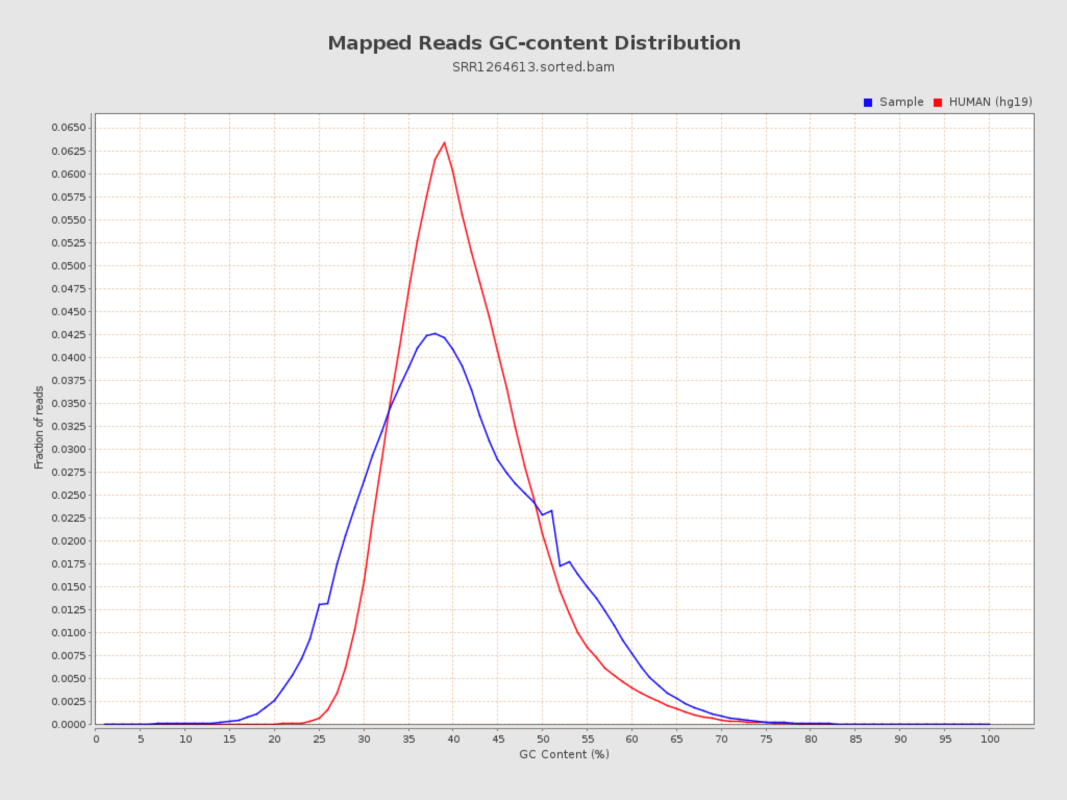
7. Results : Duplication Rate Histogram



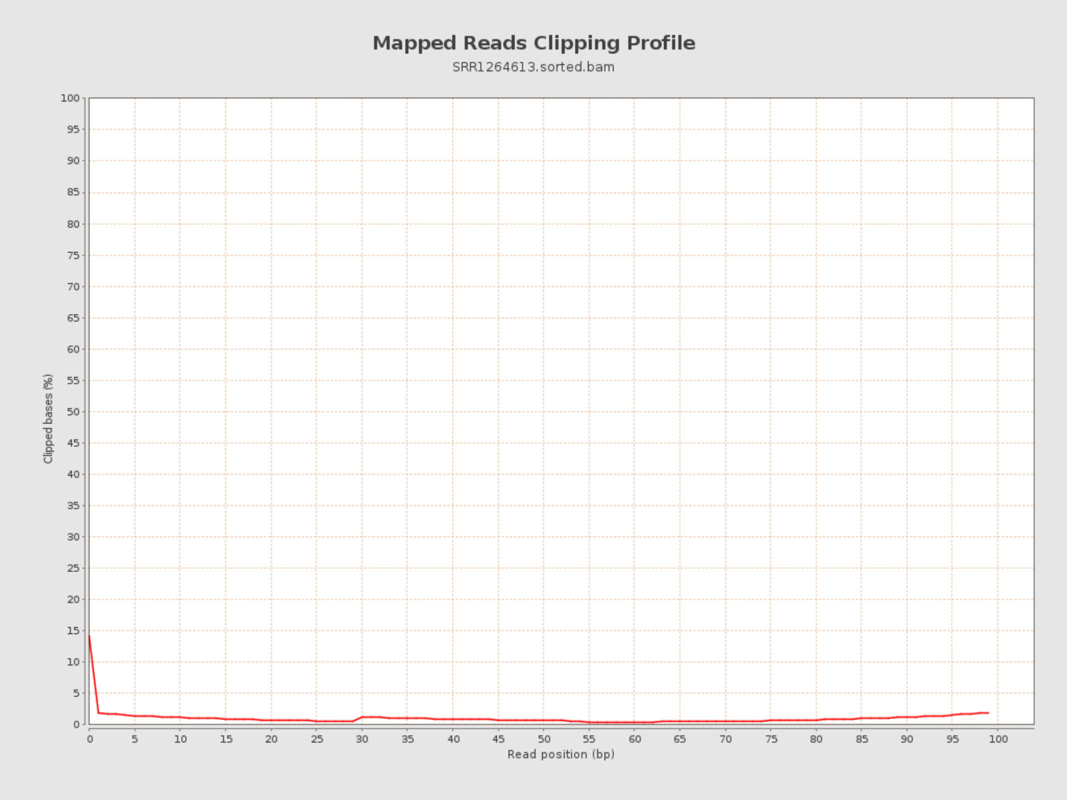
8. Results : Mapped Reads Nucleotide Content



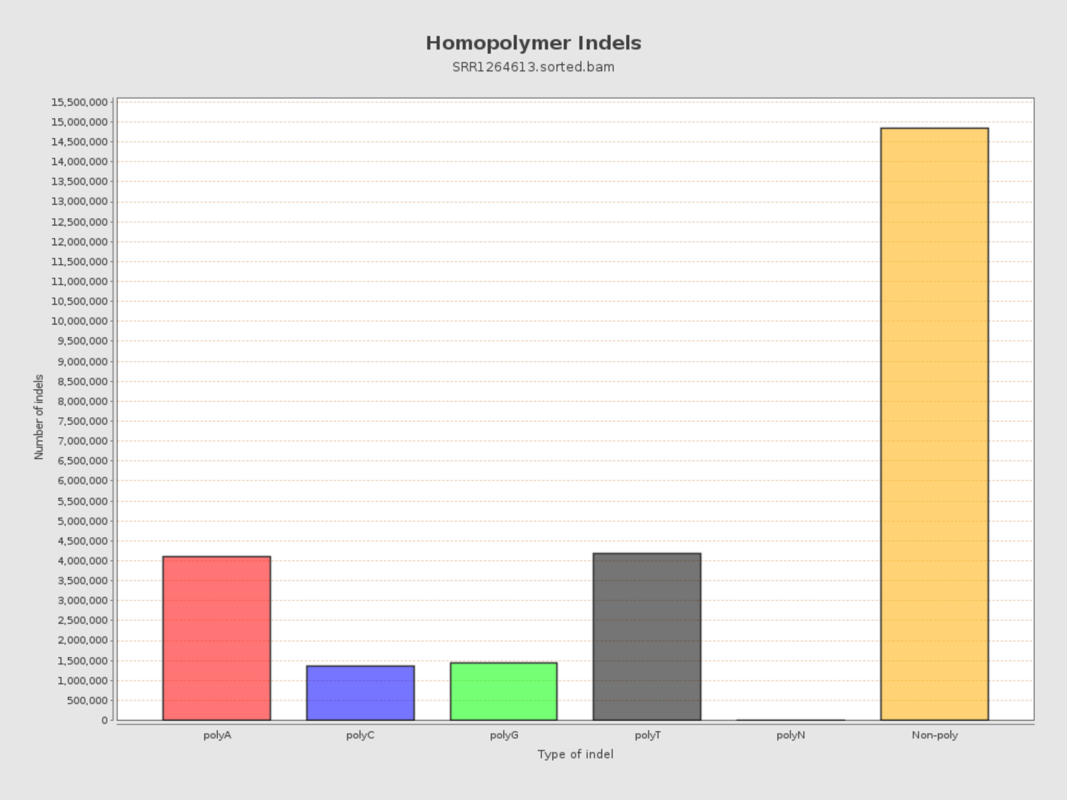
9. Results : Mapped Reads GC-content Distribution



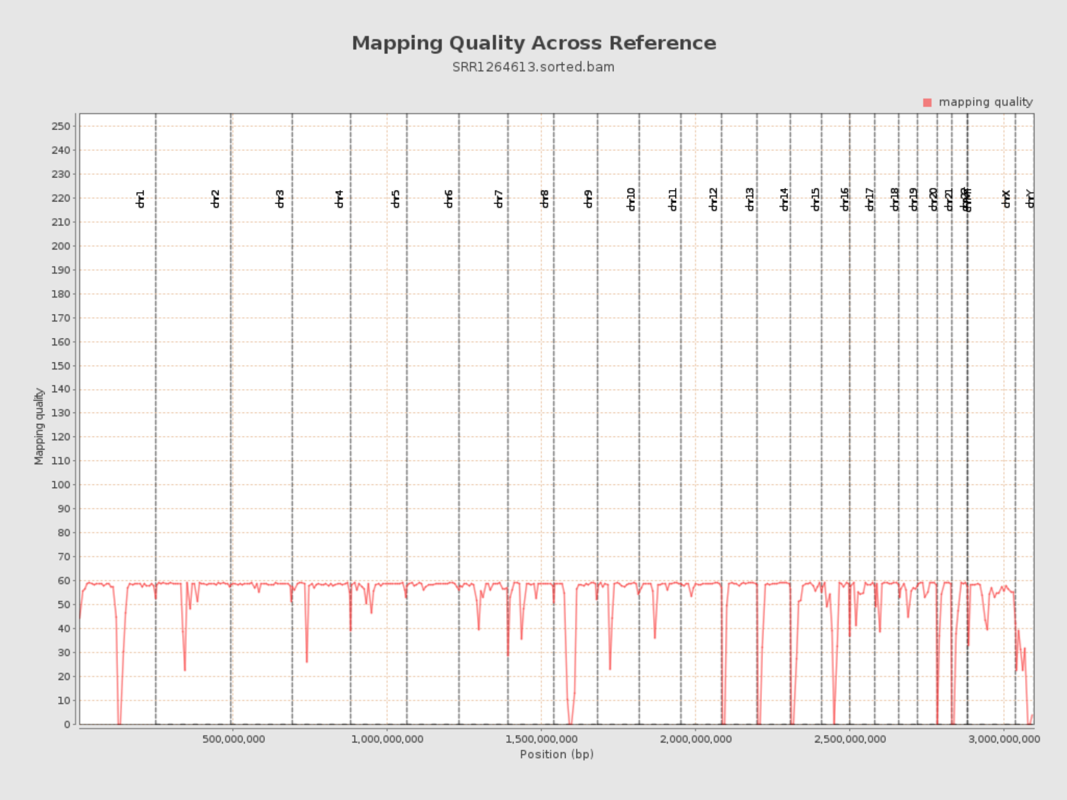
10. Results : Mapped Reads Clipping Profile



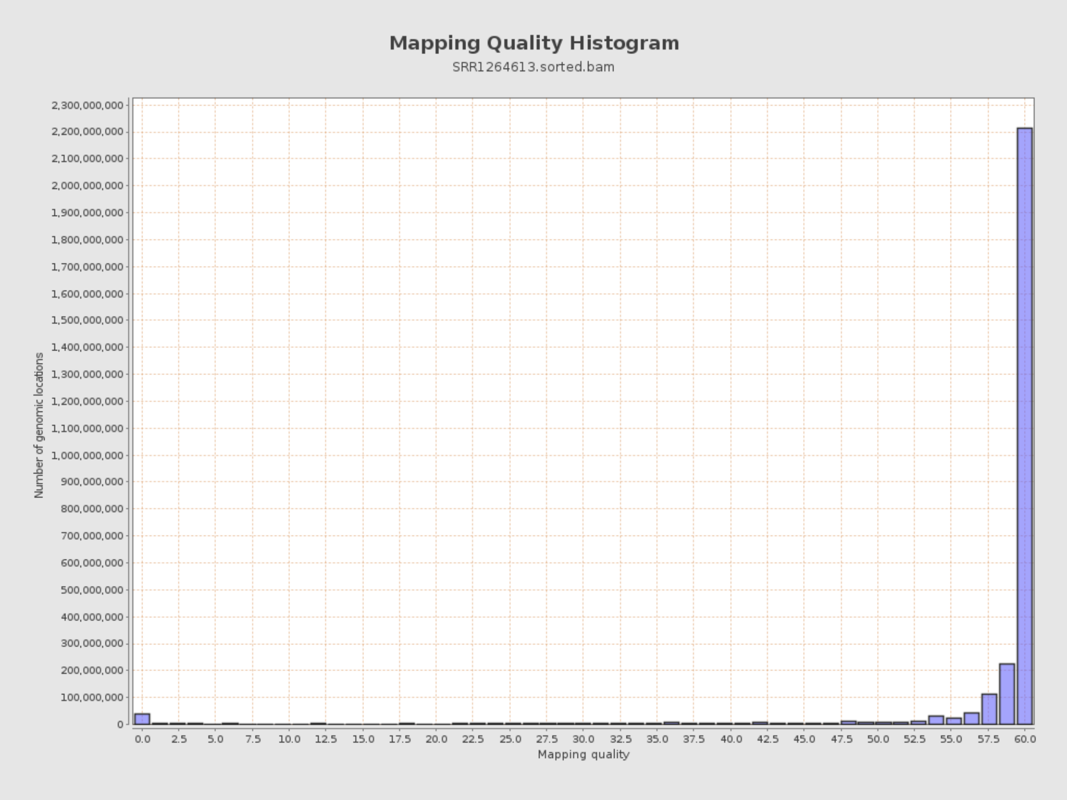
11. Results : Homopolymer Indels



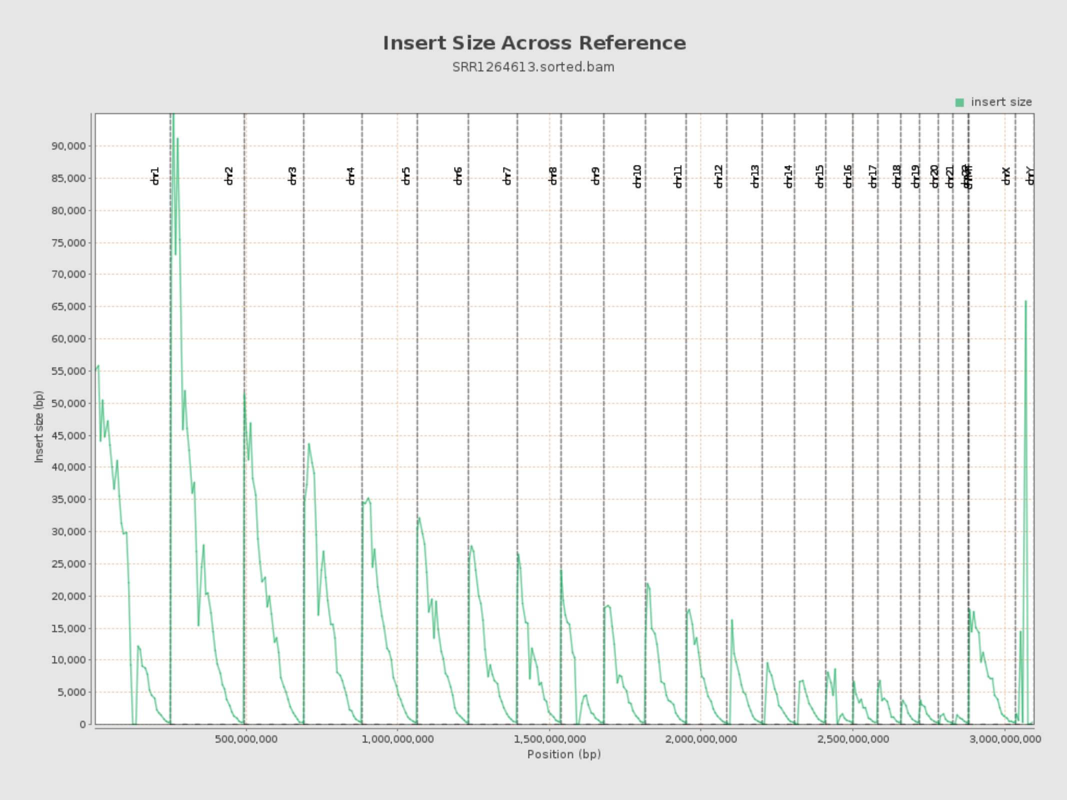
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram