Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/22 09:23:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1264615.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_SRR1264615 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1264615_1.fastq.gz SRR1264615_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Mar 22 09:23:45 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1264615.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,210,368,908
Mapped reads	1,204,965,061 / 99.55%
Unmapped reads	5,403,847 / 0.45%
Mapped paired reads	1,204,965,061 / 99.55%
Mapped reads, first in pair	603,798,982 / 49.89%
Mapped reads, second in pair	601,166,079 / 49.67%
Mapped reads, both in pair	1,201,255,576 / 99.25%
Mapped reads, singletons	3,709,485 / 0.31%
Secondary alignments	0
Supplementary alignments	12,492,325 / 1.03%
Read min/max/mean length	30 / 100 / 100.43
Duplicated reads (estimated)	434,207,487 / 35.87%
Duplication rate	35.65%
Clipped reads	75,199,343 / 6.21%

2.2. ACGT Content

Number/percentage of A's	36,919,191,518 / 30.86%
Number/percentage of C's	22,774,203,692 / 19.04%
Number/percentage of T's	36,793,065,877 / 30.75%
Number/percentage of G's	23,088,869,193 / 19.3%
Number/percentage of N's	63,600,917 / 0.05%

GC Percentage	38.33%

2.3. Coverage

Mean	38.6557
Standard Deviation	37.9184

2.4. Mapping Quality

Mean Mapping Quality	54.42

2.5. Insert size

Mean	128,776.97
Standard Deviation	3,443,563.96
P25/Median/P75	257 / 291 / 328

2.6. Mismatches and indels

General error rate	0.39%
Mismatches	438,670,942
Insertions	12,683,478
Mapped reads with at least one insertion	1.04%
Deletions	12,097,224
Mapped reads with at least one deletion	0.98%
Homopolymer indels	47.09%

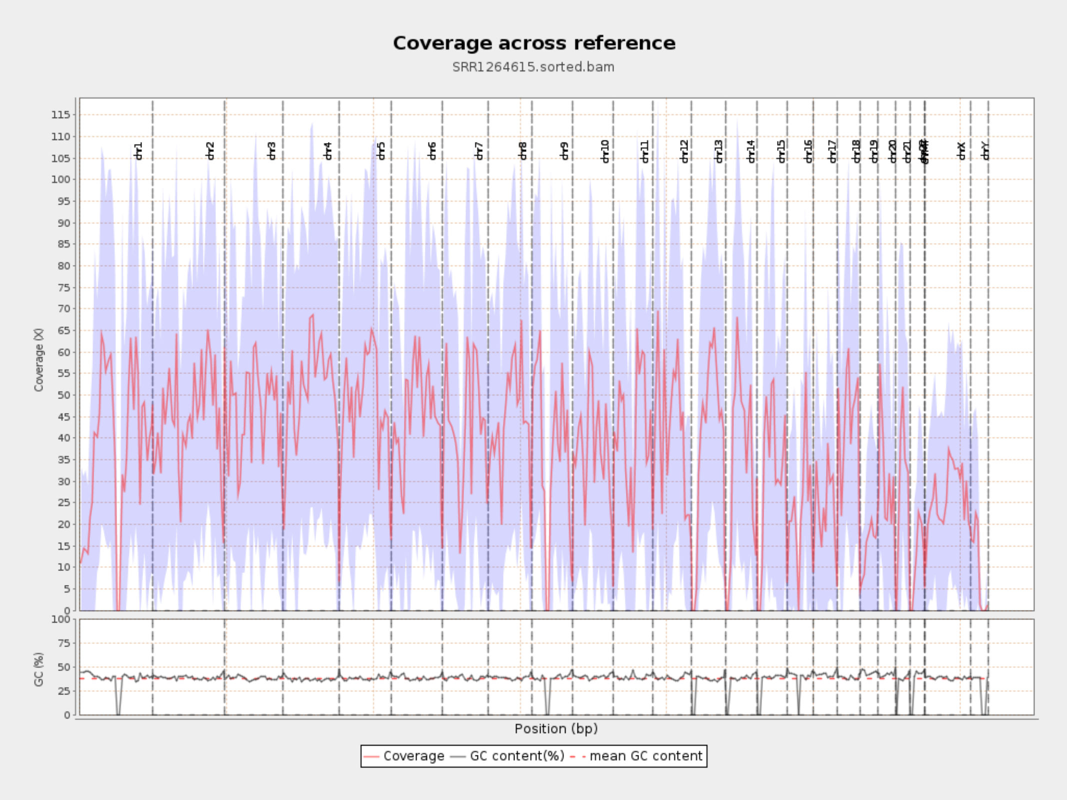
2.7. Chromosome stats

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

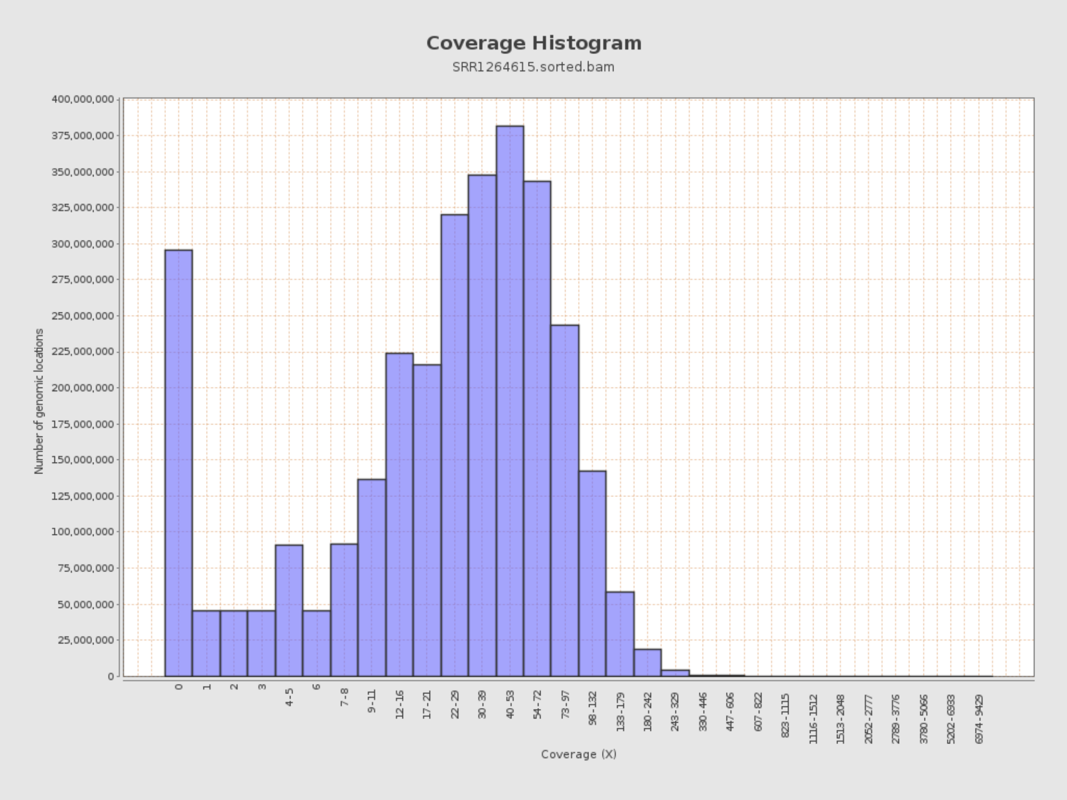
		bases	coverage	deviation
chr1	249250621	9537758370	38.2657	40.182
chr2	243199373	10896124134	44.8033	37.8559
chr3	198022430	9211570848	46.5178	37.8487
chr4	191154276	9915951407	51.8741	39.861
chr5	180915260	8587278070	47.4657	38.4958
chr6	171115067	7915811010	46.2602	38.8956
chr7	159138663	6777459121	42.5884	39.0315
chr8	146364022	6524579858	44.5778	37.4944
chr9	141213431	5097020074	36.0944	39.825
chr10	135534747	5205817269	38.4095	34.6049
chr11	135006516	5599117654	41.4729	39.2781
chr12	133851895	5635748620	42.1044	39.3463
chr13	115169878	4654301192	40.4125	38.4526
chr14	107349540	3843333203	35.802	38.8695
chr15	102531392	3261378588	31.8086	37.9806
chr16	90354753	2053653195	22.7288	28.3545
chr17	81195210	1905746274	23.4712	27.4479
chr18	78077248	3502074827	44.854	36.4675
chr19	59128983	866598571	14.6561	20.5698
chr20	63025520	1898879357	30.1287	35.5293
chr21	48129895	1460837533	30.352	39.9927
chr22	51304566	606835133	11.8281	19.7361
chrMT	16571	323684	19.5332	7.4189
chrX	155270560	4143210599	26.6838	25.5372

chrY	59373566	564895934	9.5143	19.5689

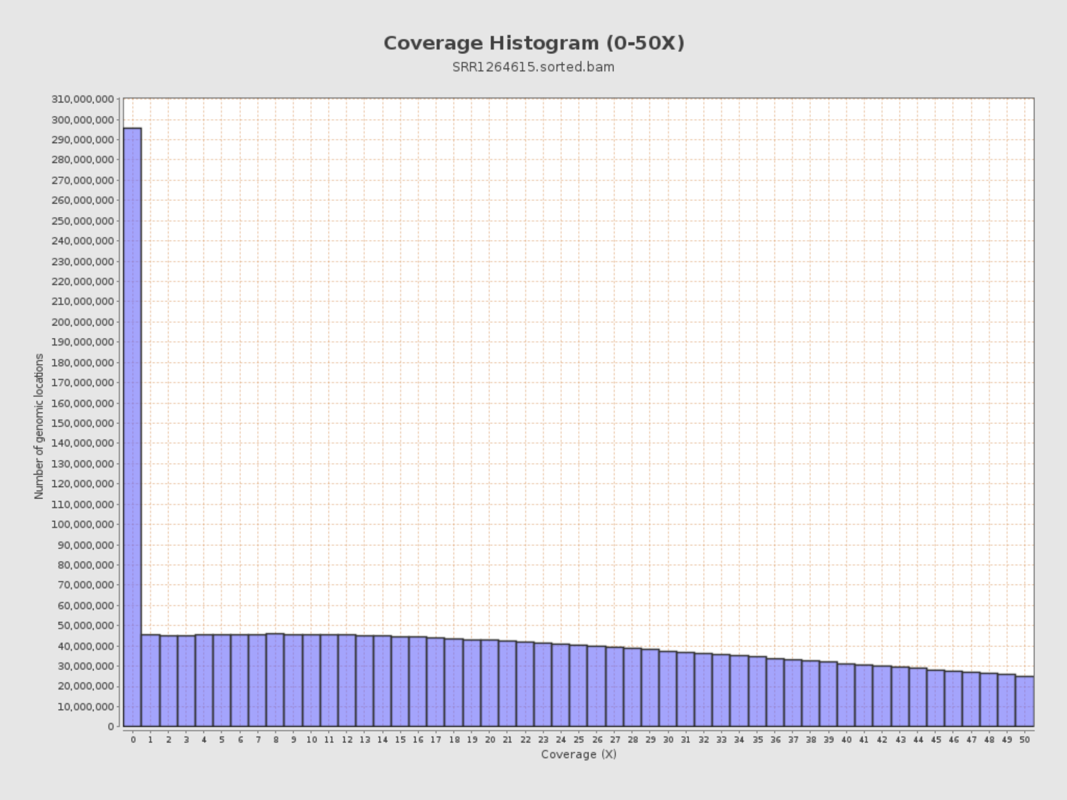
3. Results : Coverage across reference



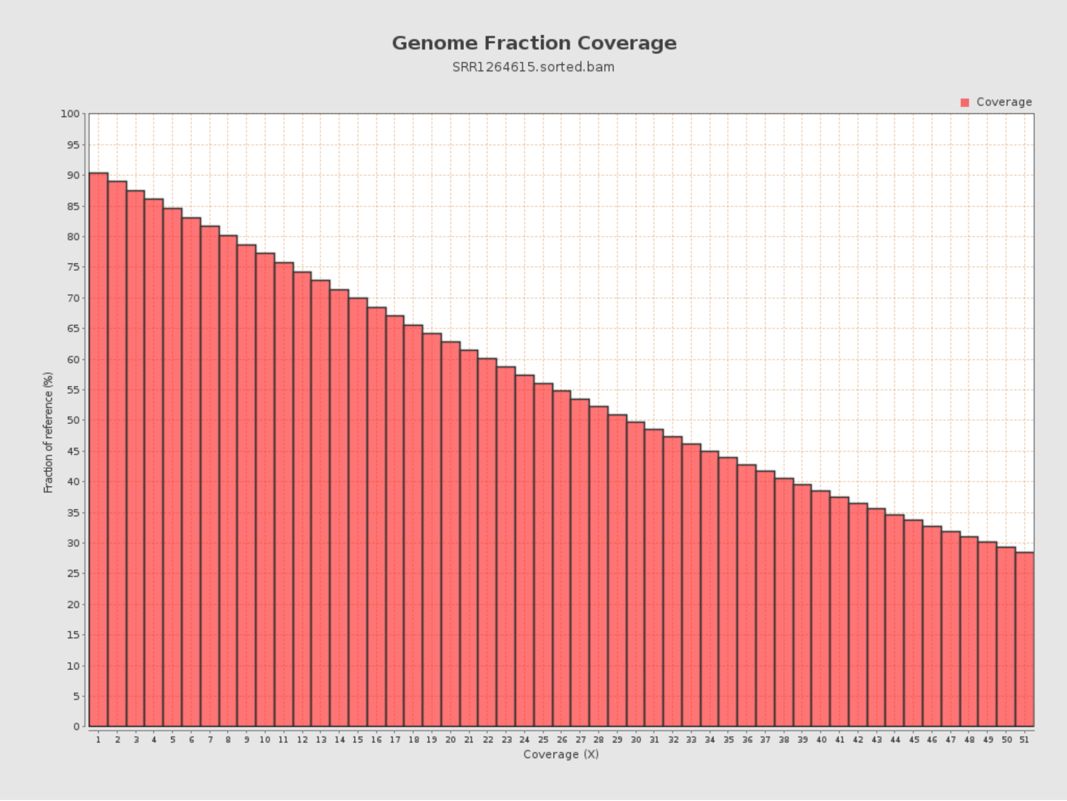
4. Results : Coverage Histogram



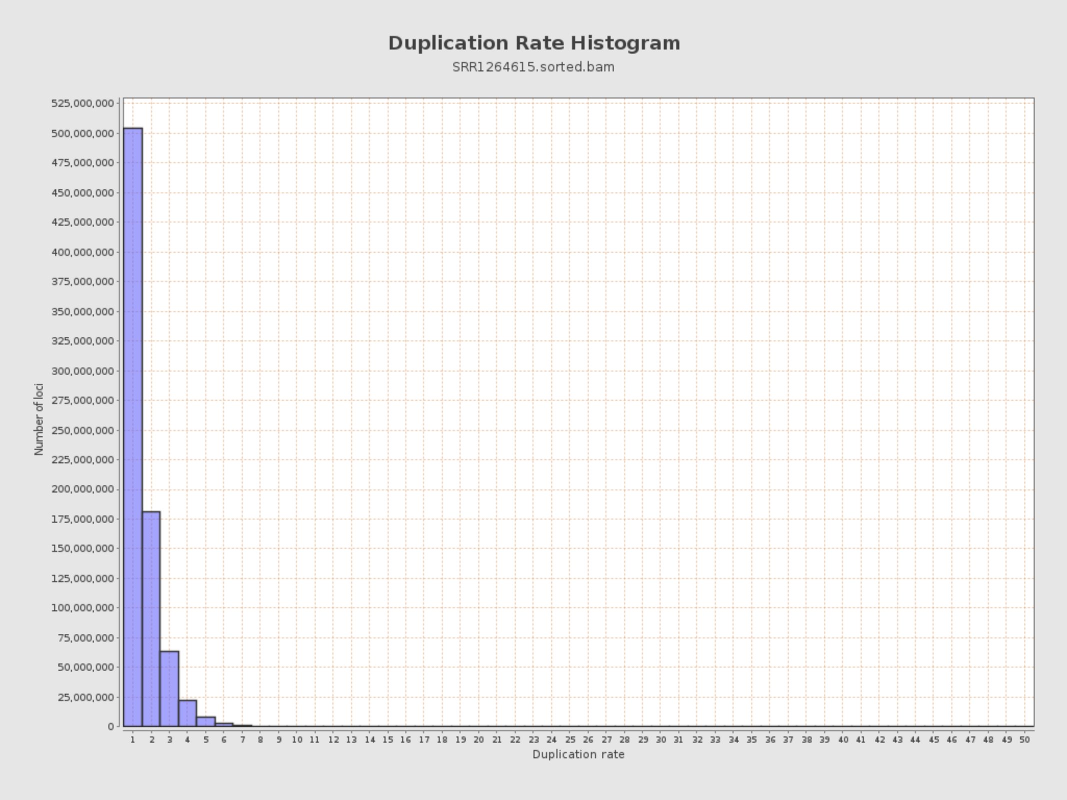
5. Results : Coverage Histogram (0-50X)



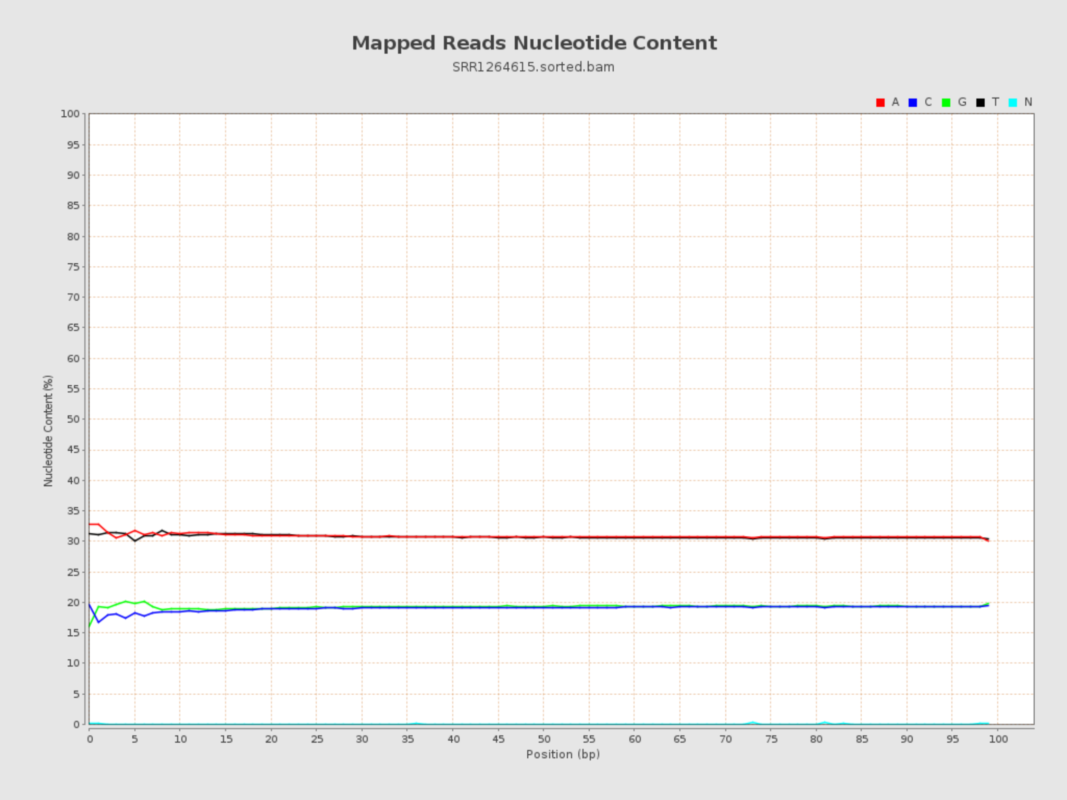
6. Results : Genome Fraction Coverage



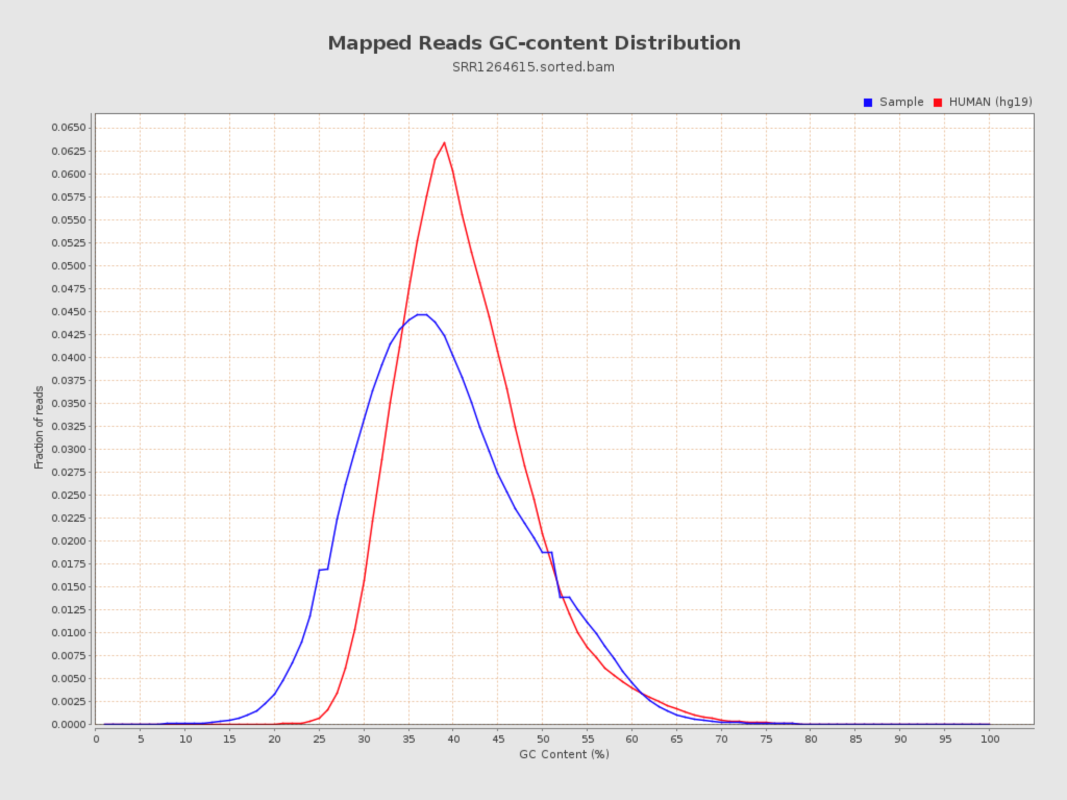
7. Results : Duplication Rate Histogram



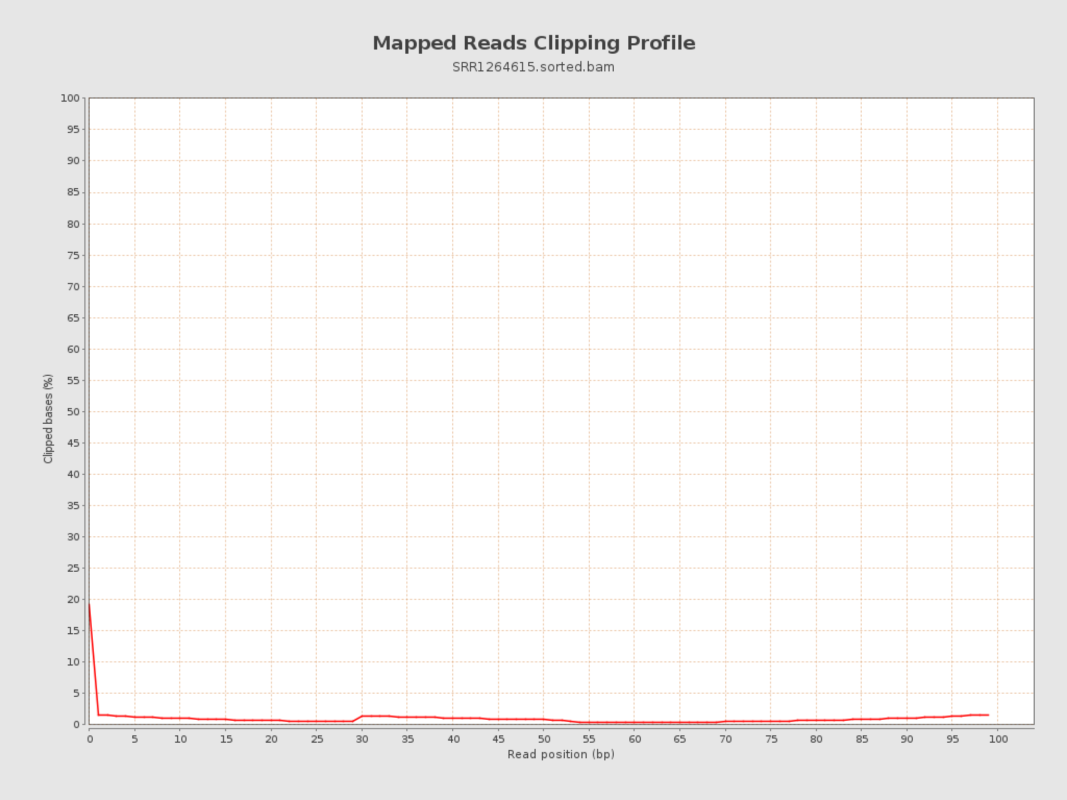
8. Results : Mapped Reads Nucleotide Content



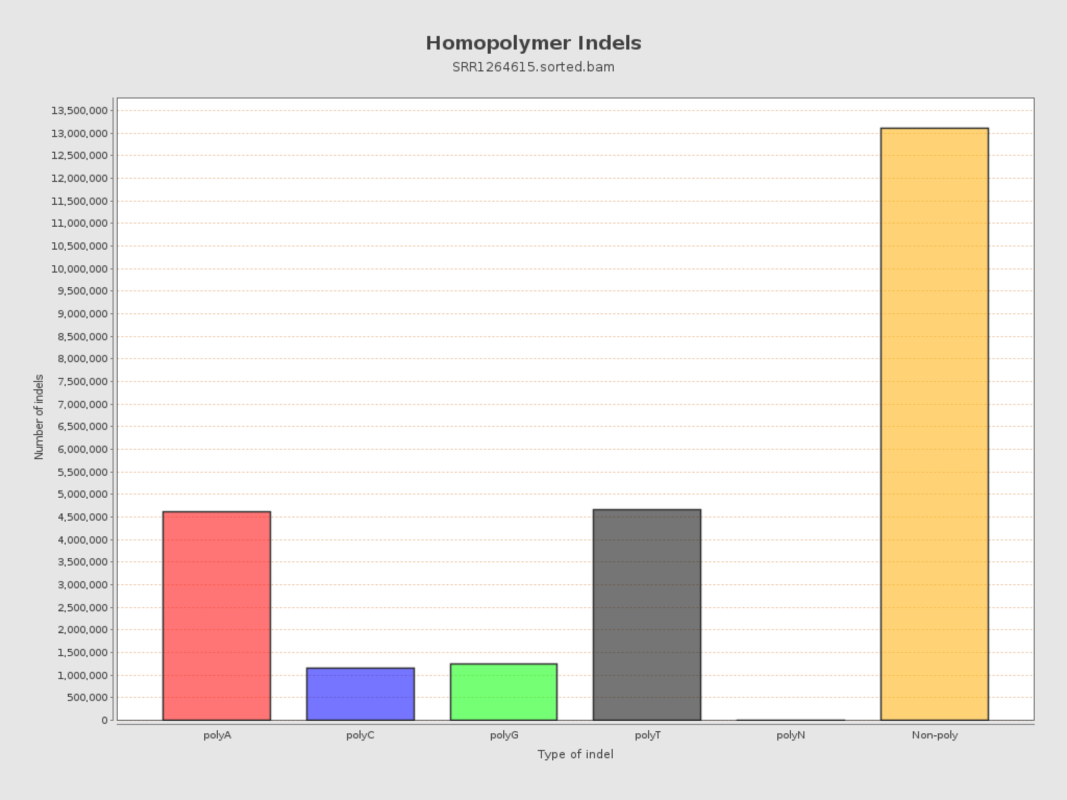
9. Results : Mapped Reads GC-content Distribution



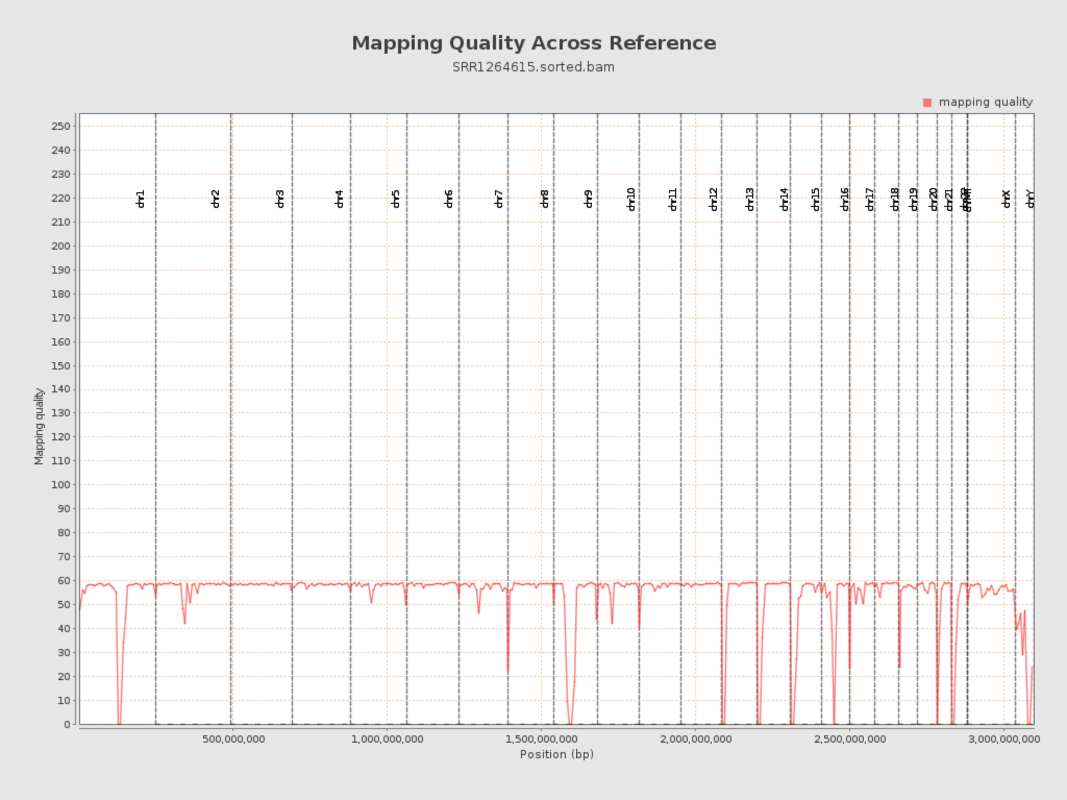
10. Results : Mapped Reads Clipping Profile



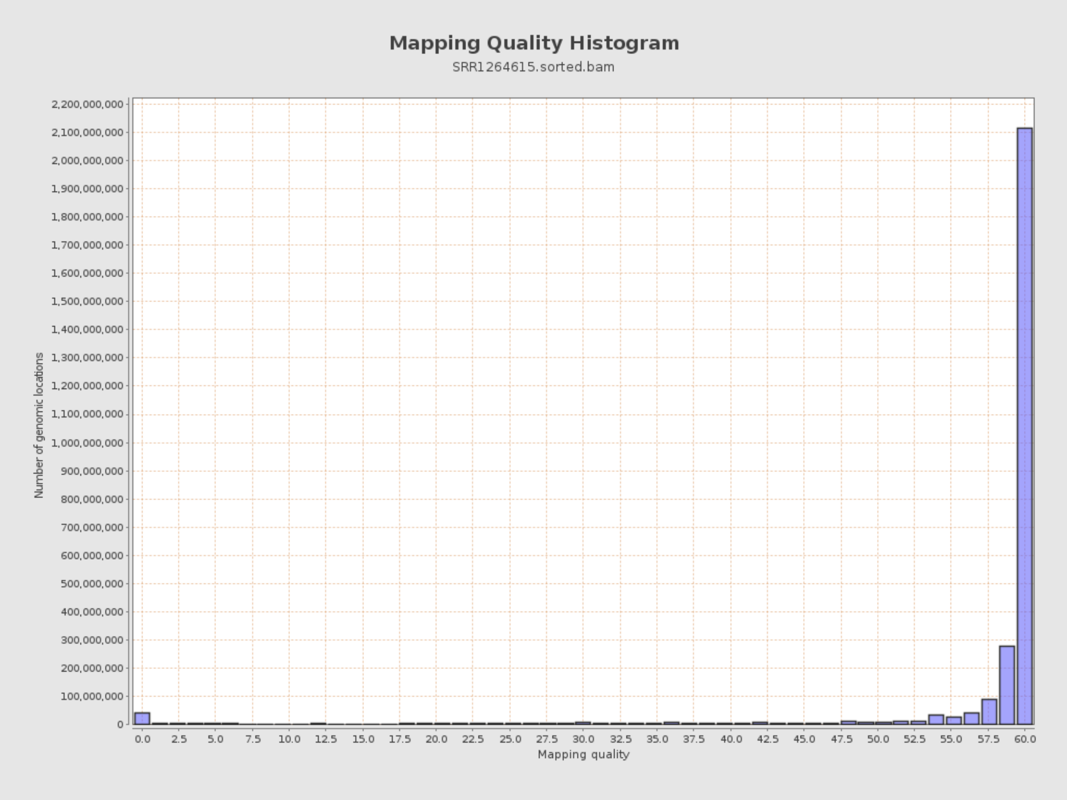
11. Results : Homopolymer Indels



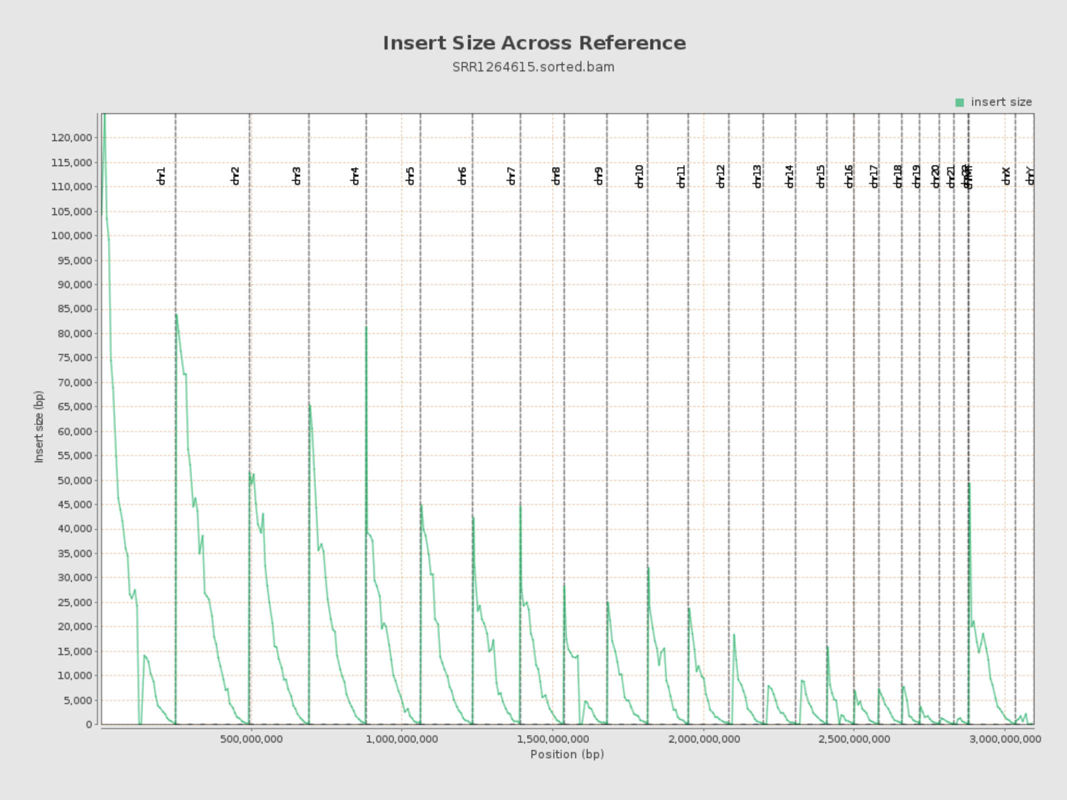
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram