Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/09 02:07:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1264625.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_SRR1264625 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1264625_1.fastq.gz SRR1264625_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Apr 09 02:07:32 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1264625.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,284,690,418
Mapped reads	1,278,712,945 / 99.53%
Unmapped reads	5,977,473 / 0.47%
Mapped paired reads	1,278,712,945 / 99.53%
Mapped reads, first in pair	640,811,740 / 49.88%
Mapped reads, second in pair	637,901,205 / 49.65%
Mapped reads, both in pair	1,274,819,146 / 99.23%
Mapped reads, singletons	3,893,799 / 0.3%
Secondary alignments	0
Supplementary alignments	7,918,335 / 0.62%
Read min/max/mean length	30 / 101 / 101.25
Duplicated reads (estimated)	444,697,130 / 34.62%
Duplication rate	34.28%
Clipped reads	52,030,168 / 4.05%

2.2. ACGT Content

Number/percentage of A's	39,749,580,378 / 30.95%
Number/percentage of C's	24,413,944,381 / 19.01%
Number/percentage of T's	39,648,937,231 / 30.87%
Number/percentage of G's	24,595,485,672 / 19.15%
Number/percentage of N's	11,852,332 / 0.01%

GC Percentage	38.16%

2.3. Coverage

Mean	41.493
Standard Deviation	43.1571

2.4. Mapping Quality

Mean Mapping Quality	54.48

2.5. Insert size

Mean	74,539.45
Standard Deviation	2,635,428.94
P25/Median/P75	289 / 315 / 347

2.6. Mismatches and indels

General error rate	0.37%
Mismatches	445,015,279
Insertions	14,043,440
Mapped reads with at least one insertion	1.08%
Deletions	13,386,085
Mapped reads with at least one deletion	1.03%
Homopolymer indels	48.48%

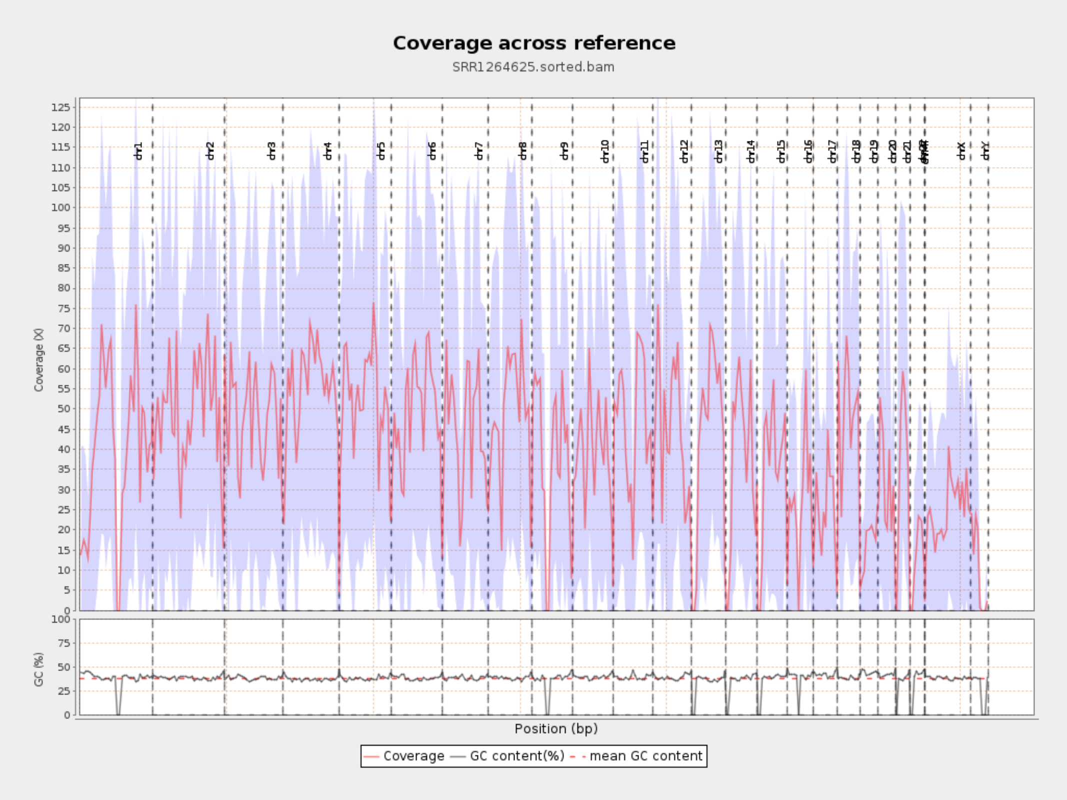
2.7. Chromosome stats

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

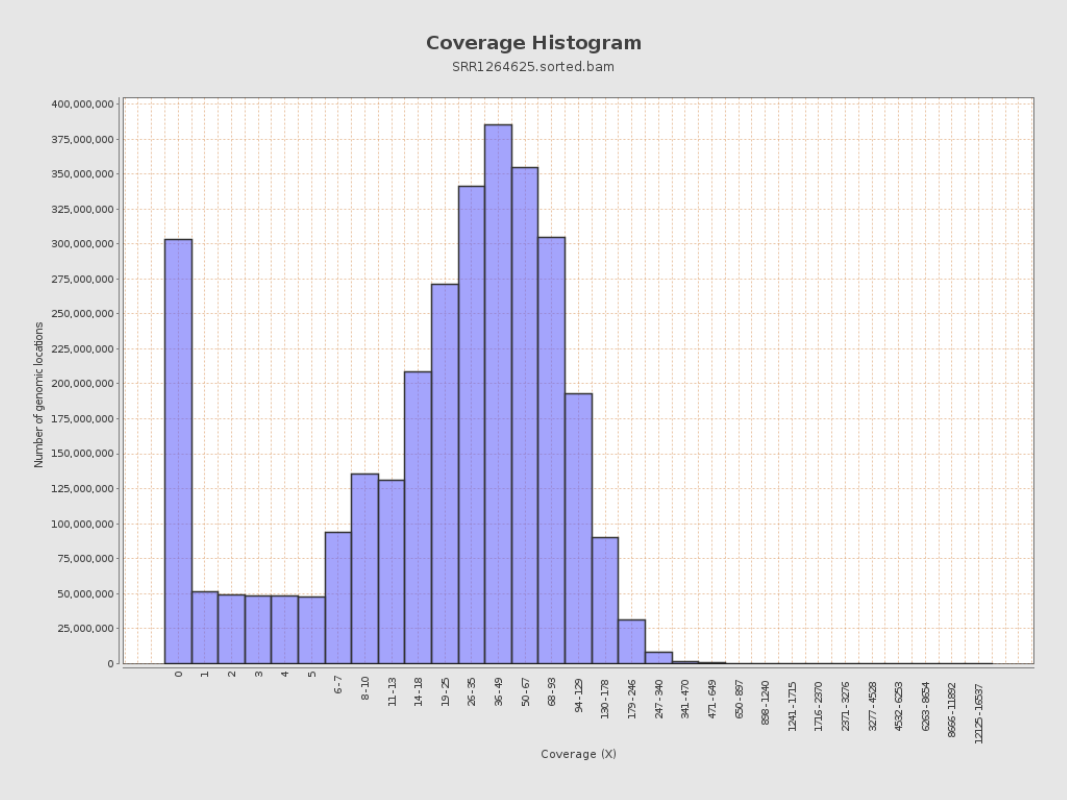
		bases	coverage	deviation
chr1	249250621	10126606670	40.6282	44.5076
chr2	243199373	11946212591	49.1211	44.807
chr3	198022430	9498278663	47.9657	42.7751
chr4	191154276	10693500143	55.9417	45.087
chr5	180915260	9391797593	51.9127	44.4726
chr6	171115067	8590554361	50.2034	44.0315
chr7	159138663	7104574846	44.6439	43.0552
chr8	146364022	7274291465	49.7	43.9361
chr9	141213431	5211086897	36.9022	43.8192
chr10	135534747	5411868928	39.9298	38.3355
chr11	135006516	6322736515	46.8328	46.2569
chr12	133851895	6012113378	44.9162	45.0389
chr13	115169878	5160989953	44.812	44.8697
chr14	107349540	4069653019	37.9103	43.0092
chr15	102531392	3549620997	34.6198	41.4114
chr16	90354753	2359082108	26.1091	32.6191
chr17	81195210	2015136548	24.8184	32.333
chr18	78077248	3856461543	49.3929	43.4454
chr19	59128983	958720186	16.214	24.2402
chr20	63025520	1956211013	31.0384	41.6707
chr21	48129895	1786524119	37.1188	48.3278
chr22	51304566	661633251	12.8962	22.2472
chrMT	16571	38557	2.3268	8.913
chrX	155270560	3896987739	25.098	28.8438

chrY	59373566	594987070	10.0211	22.3452

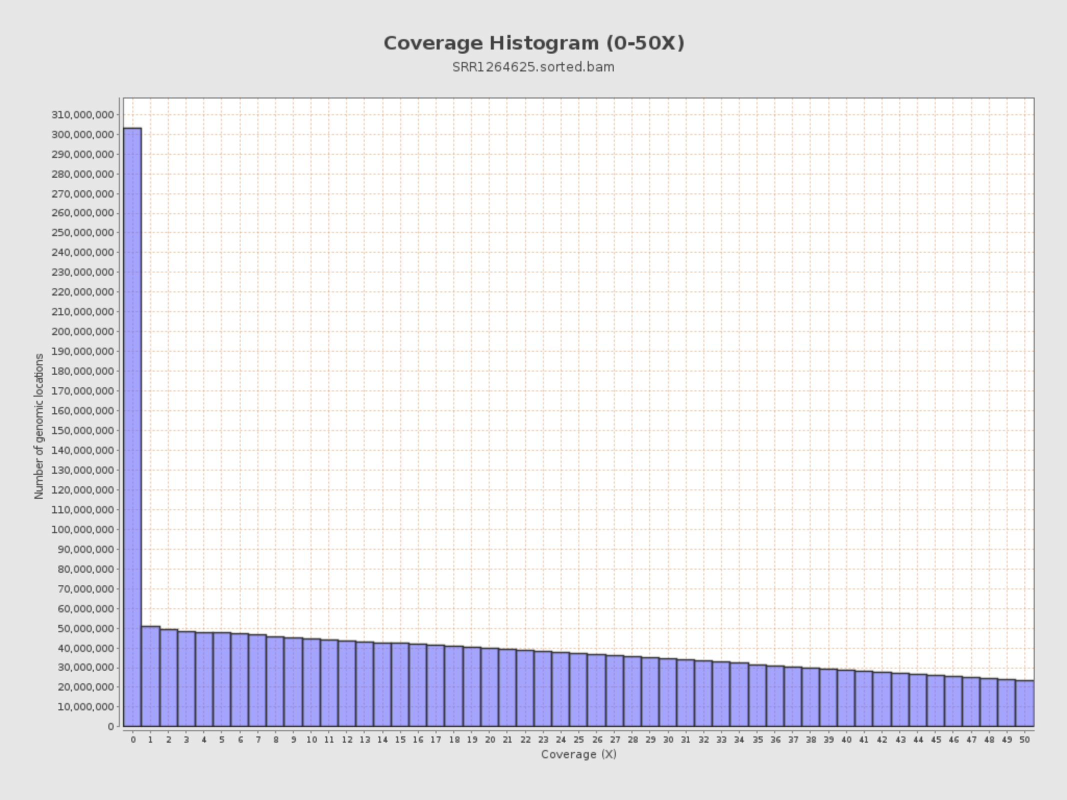
3. Results : Coverage across reference



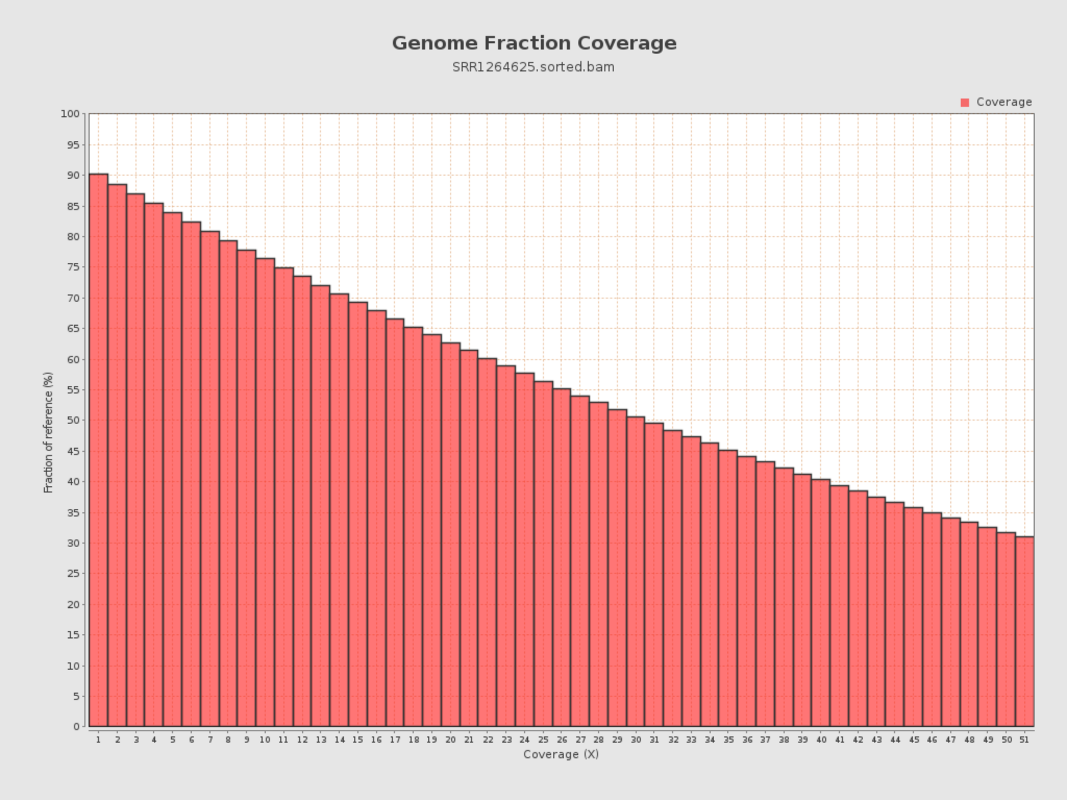
4. Results : Coverage Histogram



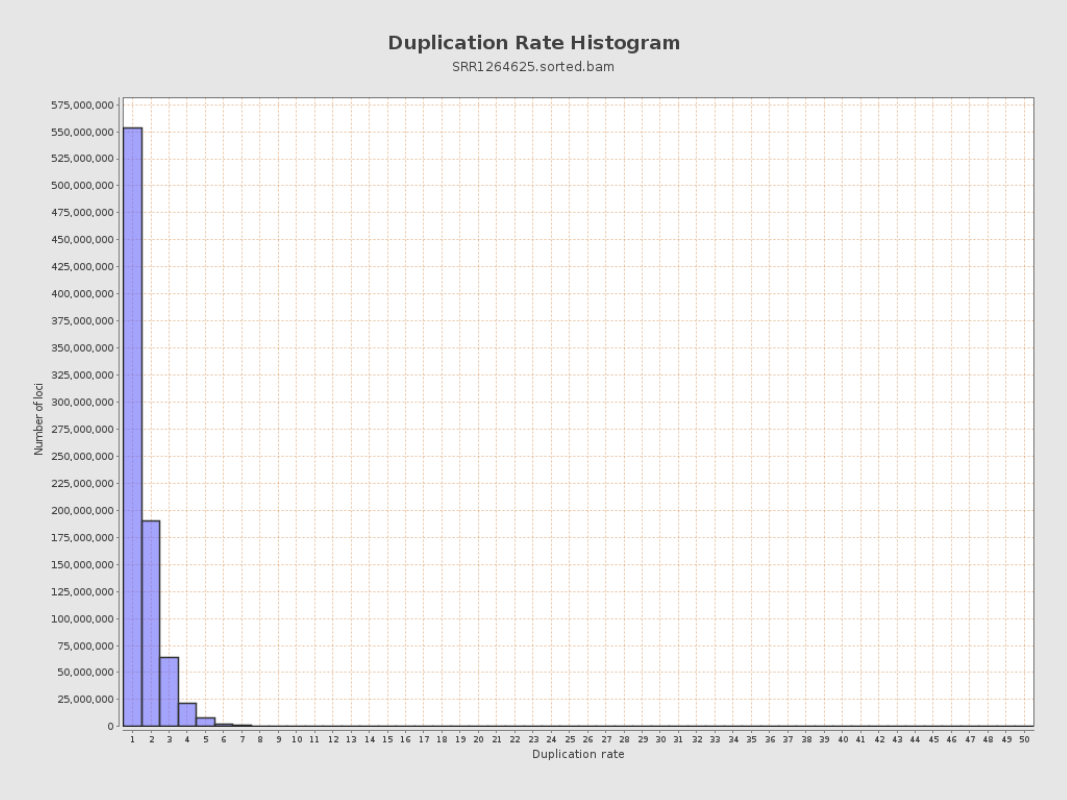
5. Results : Coverage Histogram (0-50X)



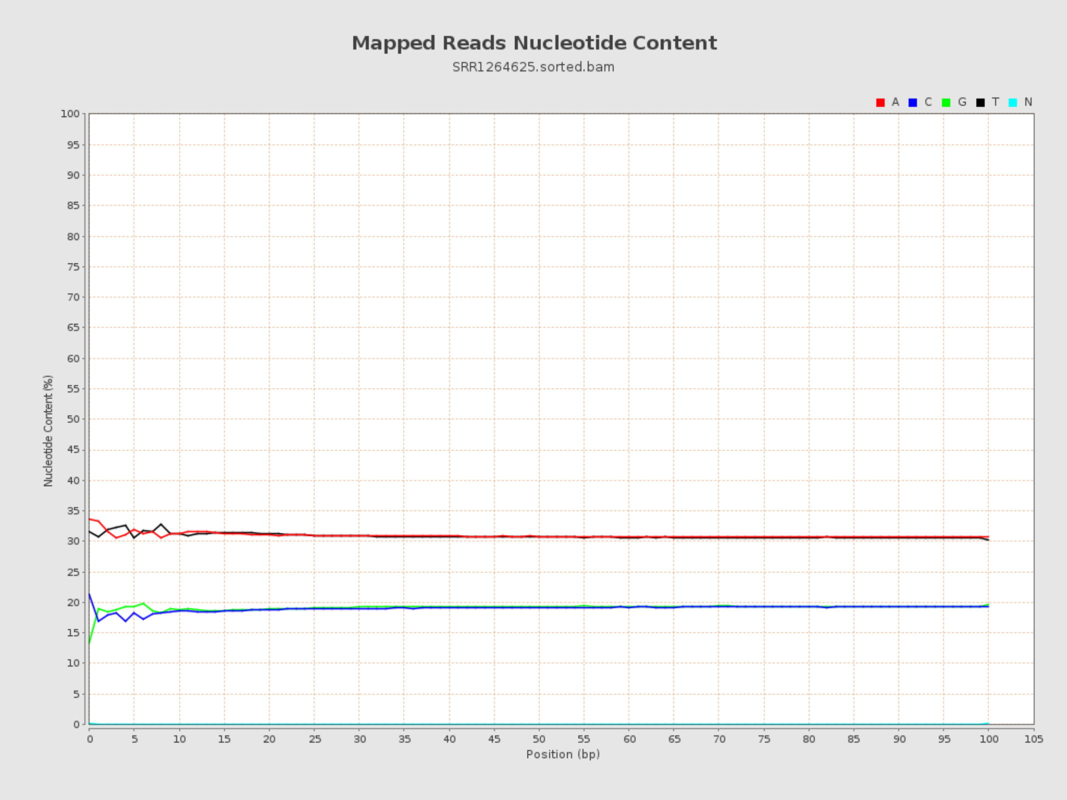
6. Results : Genome Fraction Coverage



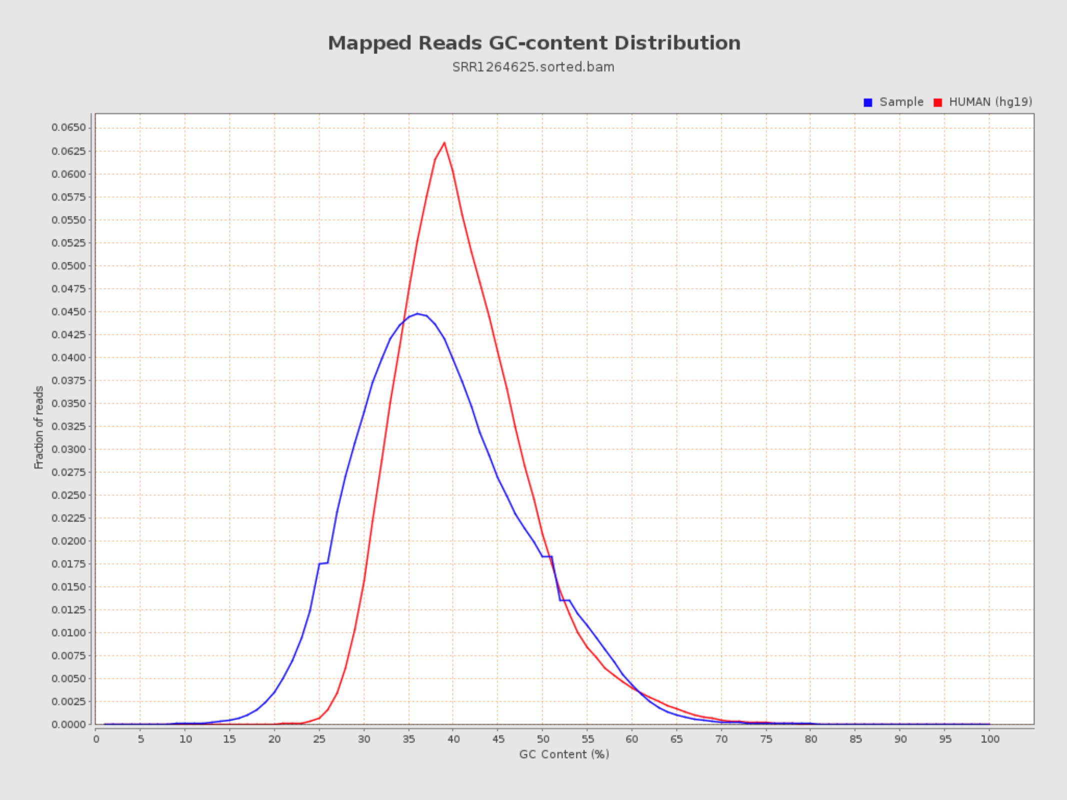
7. Results : Duplication Rate Histogram



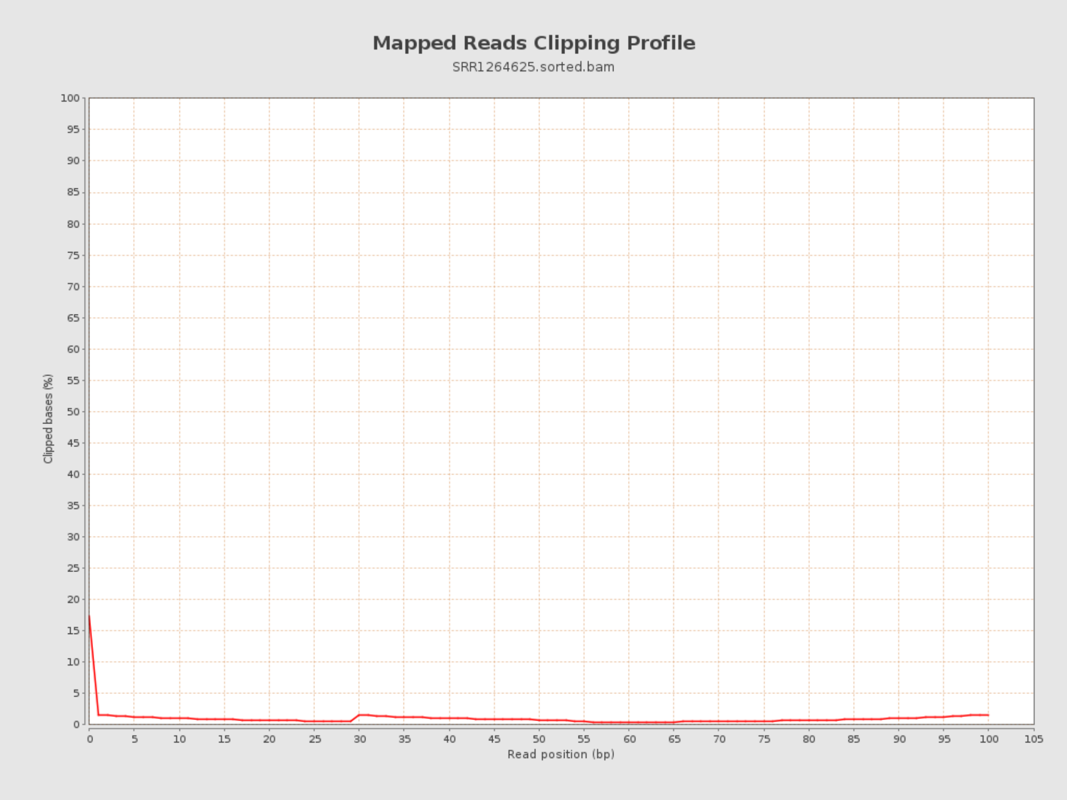
8. Results : Mapped Reads Nucleotide Content



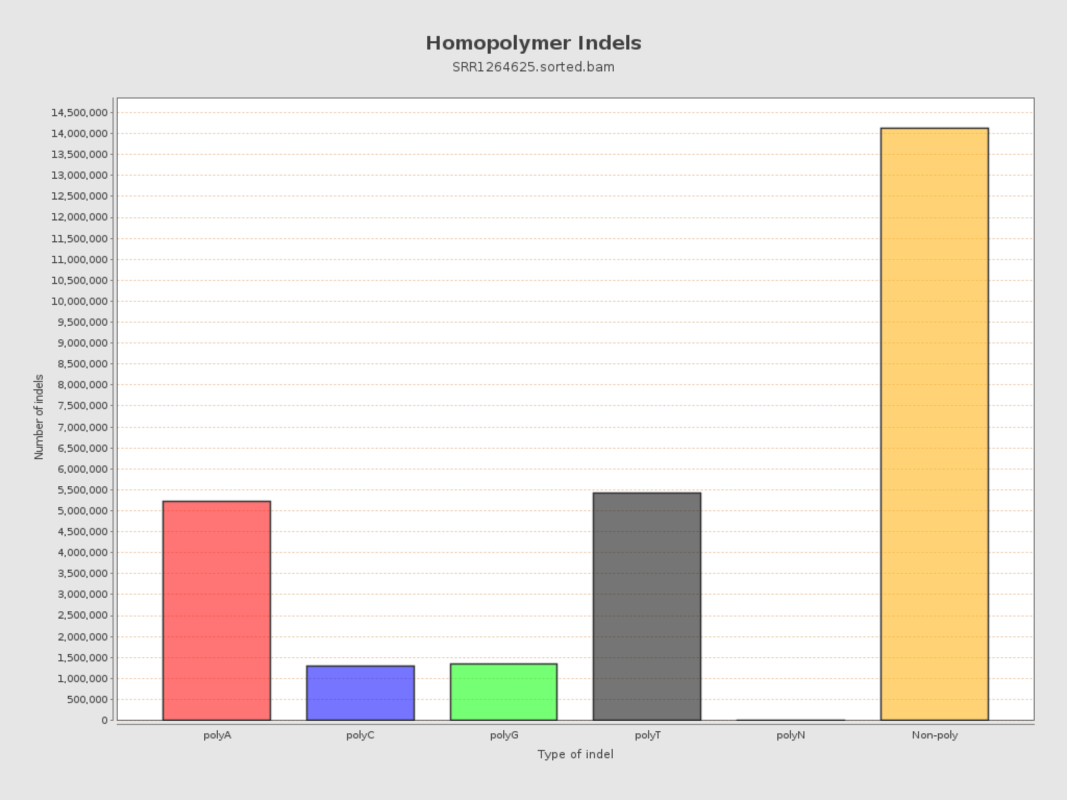
9. Results : Mapped Reads GC-content Distribution



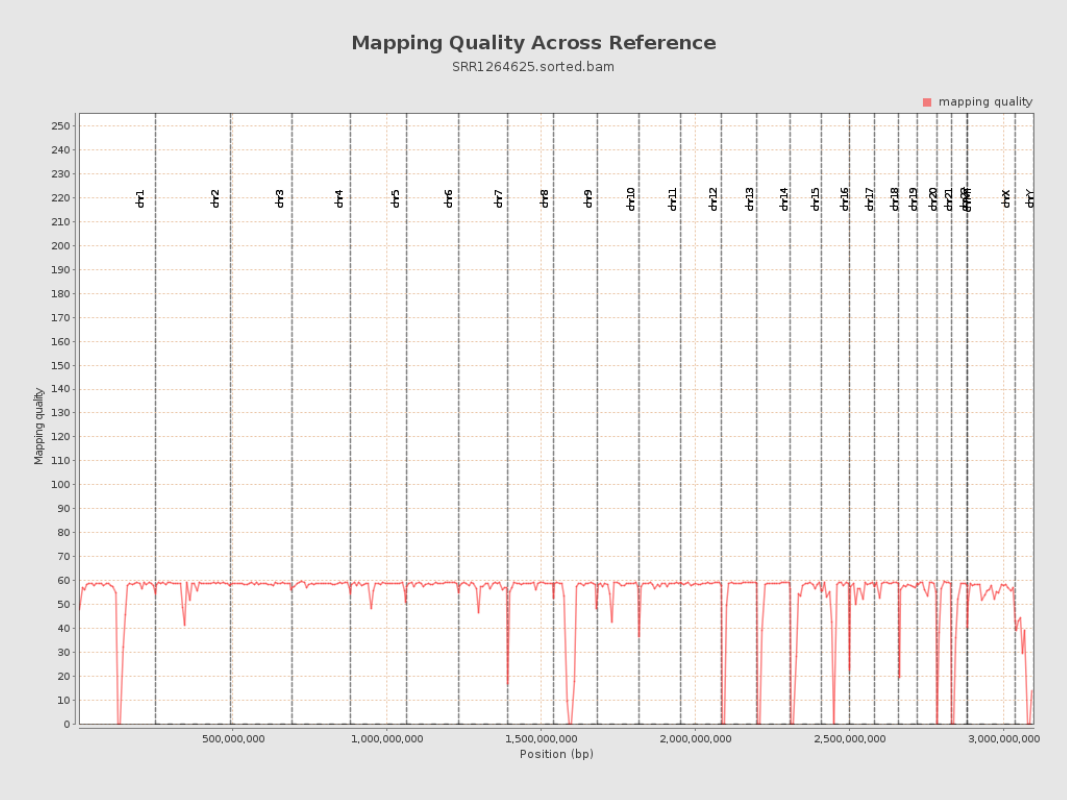
10. Results : Mapped Reads Clipping Profile



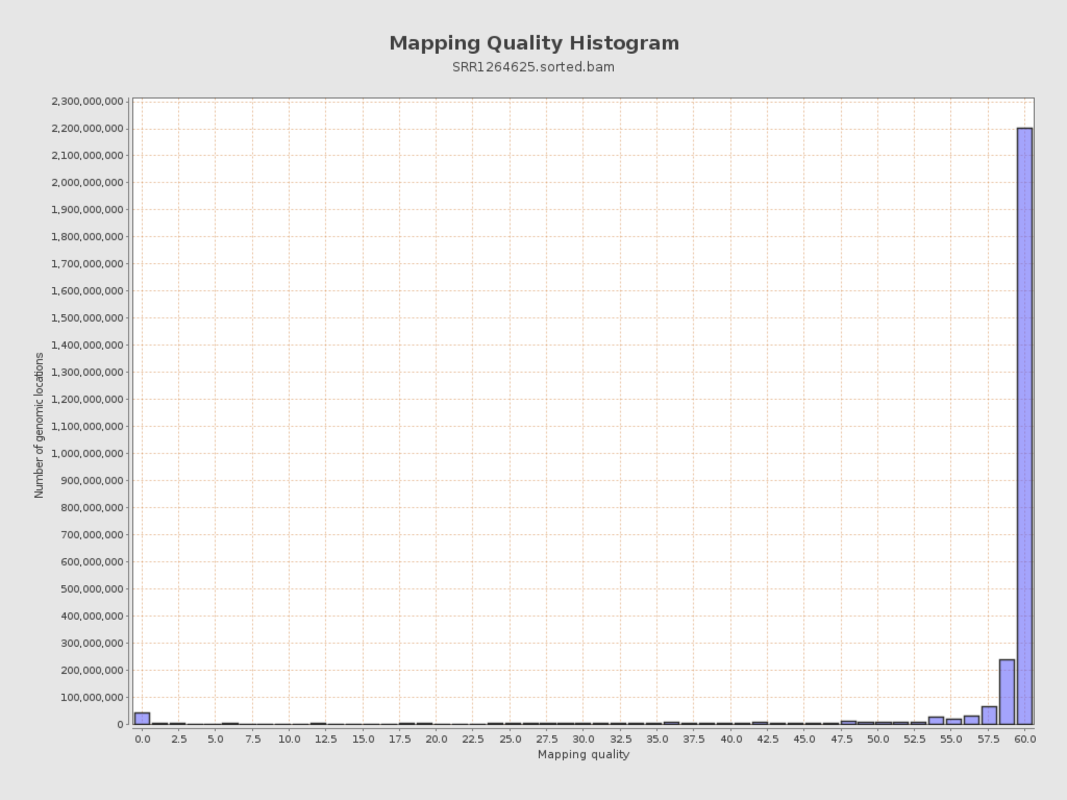
11. Results : Homopolymer Indels



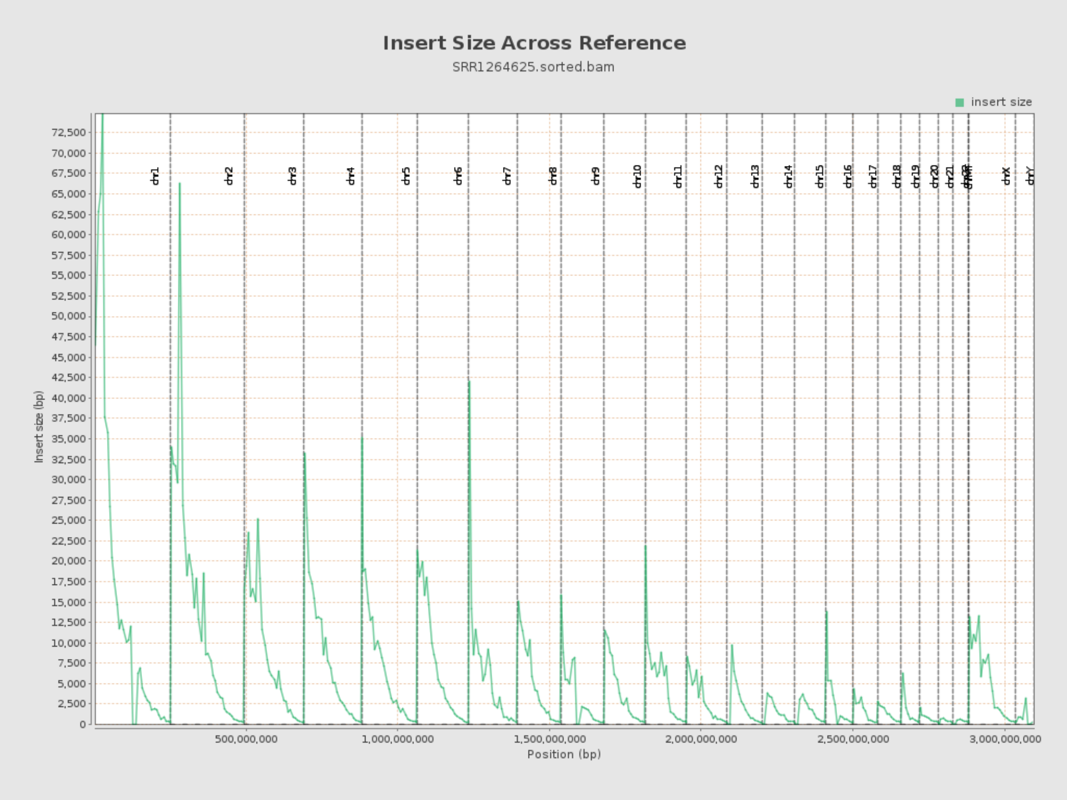
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram