Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/01 03:23:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1264612.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_SRR1264612 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1264612_1.fastq.gz SRR1264612_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 01 03:23:26 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1264612.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,083,764,110
Mapped reads	1,070,976,371 / 98.82%
Unmapped reads	12,787,739 / 1.18%
Mapped paired reads	1,070,976,371 / 98.82%
Mapped reads, first in pair	536,829,196 / 49.53%
Mapped reads, second in pair	534,147,175 / 49.29%
Mapped reads, both in pair	1,064,944,708 / 98.26%
Mapped reads, singletons	6,031,663 / 0.56%
Secondary alignments	0
Supplementary alignments	7,903,273 / 0.73%
Read min/max/mean length	30 / 100 / 100.3
Duplicated reads (estimated)	292,120,525 / 26.95%
Duplication rate	22.39%
Clipped reads	73,479,098 / 6.78%

2.2. ACGT Content

Number/percentage of A's	31,590,389,998 / 29.85%
Number/percentage of C's	21,254,522,018 / 20.09%
Number/percentage of T's	31,610,495,151 / 29.87%
Number/percentage of G's	21,309,866,004 / 20.14%
Number/percentage of N's	52,189,126 / 0.05%

GC Percentage	40.22%

2.3. Coverage

Mean	34.1926
Standard Deviation	434.5009

2.4. Mapping Quality

Mean Mapping Quality	53.61

2.5. Insert size

Mean	123,965.39
Standard Deviation	3,394,659.62
P25/Median/P75	276 / 311 / 352

2.6. Mismatches and indels

General error rate	0.6%
Mismatches	612,077,885
Insertions	10,560,544
Mapped reads with at least one insertion	0.96%
Deletions	13,772,177
Mapped reads with at least one deletion	1.25%
Homopolymer indels	42.81%

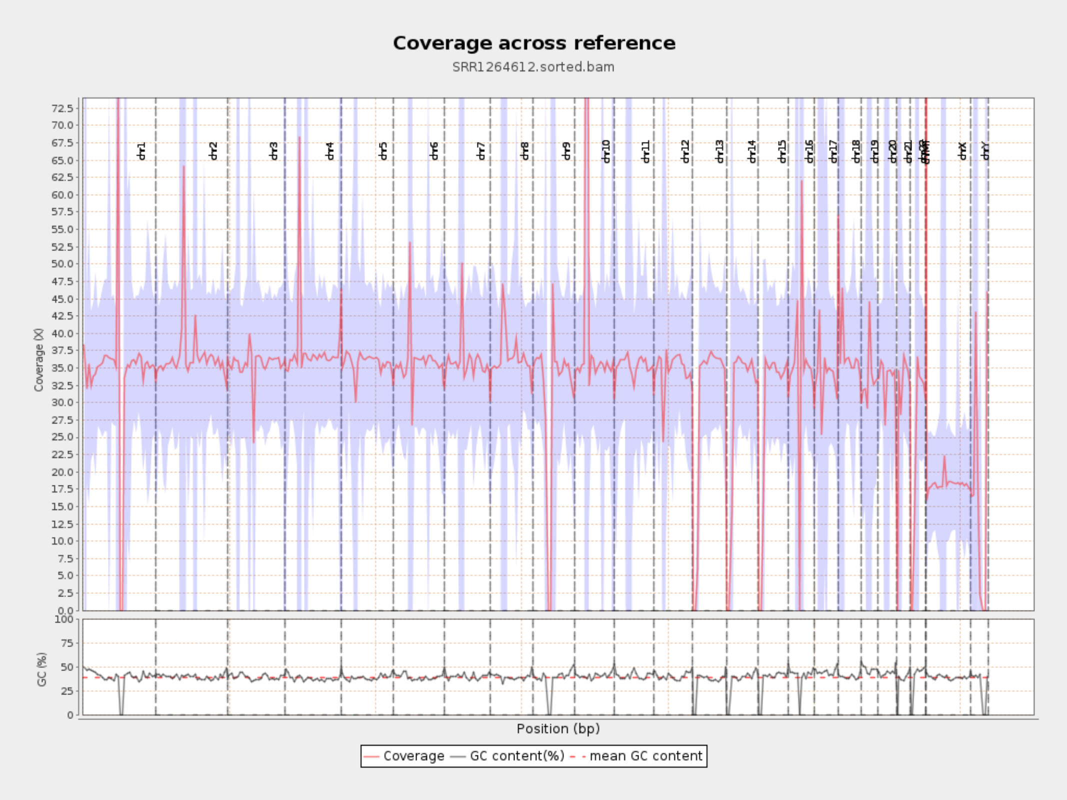
2.7. Chromosome stats

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

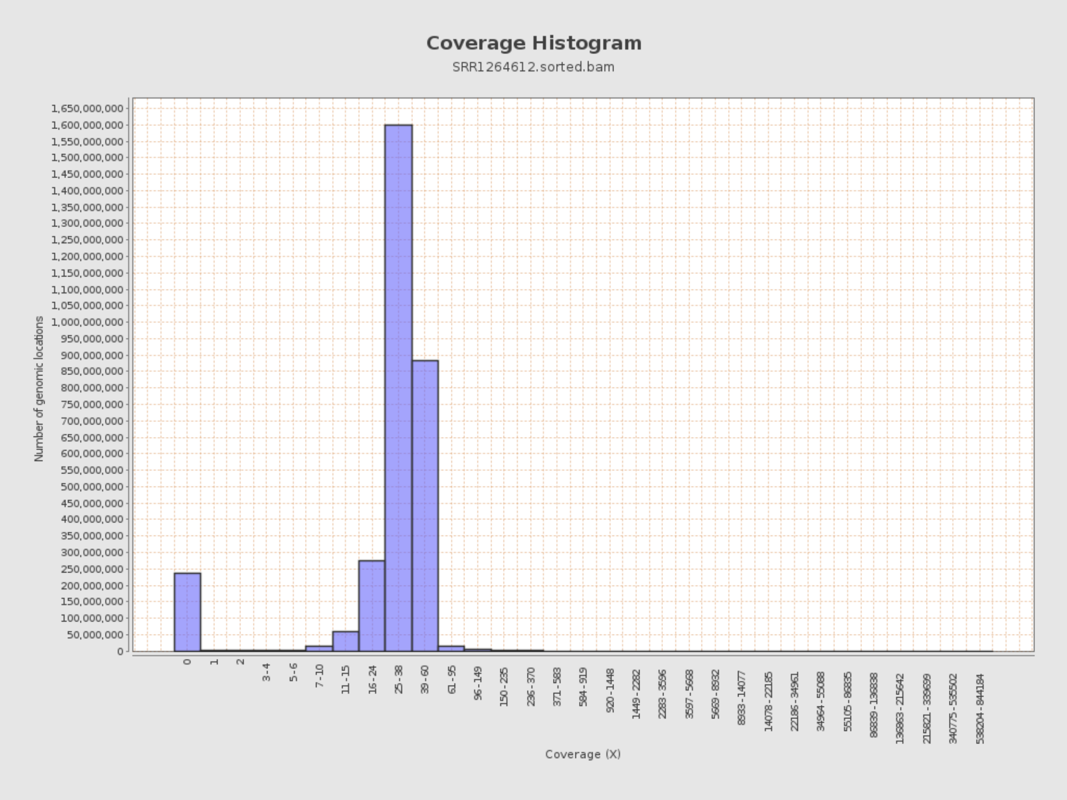
		bases	coverage	deviation
chr1	249250621	8581313460	34.4285	856.852
chr2	243199373	8993437544	36.9797	192.3771
chr3	198022430	7040435503	35.5537	32.5324
chr4	191154276	7220822223	37.7748	256.0378
chr5	180915260	6459077631	35.7022	29.2878
chr6	171115067	6173019453	36.0753	193.8568
chr7	159138663	5743917592	36.0938	298.213
chr8	146364022	5381169614	36.7657	591.353
chr9	141213431	4447258757	31.4932	280.4879
chr10	135534747	5521471007	40.7384	711.9065
chr11	135006516	4770328055	35.3341	141.4983
chr12	133851895	4656347372	34.7873	21.0976
chr13	115169878	3457183602	30.0181	17.1025
chr14	107349540	3156642464	29.4053	24.8745
chr15	102531392	2931752274	28.5937	18.235
chr16	90354753	3139175803	34.7428	220.7411
chr17	81195210	2773988103	34.1644	122.2545
chr18	78077248	2947610741	37.7525	434.9716
chr19	59128983	1995892132	33.7549	364.6827
chr20	63025520	2112276585	33.5146	48.9078
chr21	48129895	1472779786	30.6001	98.3314
chr22	51304566	1208762624	23.5605	102.8008
chrMT	16571	1763361275	106,412.4842	14,405.0308
chrX	155270560	2836598989	18.2687	56.9447

chrY	59373566	1065184407	17.9404	264.3204

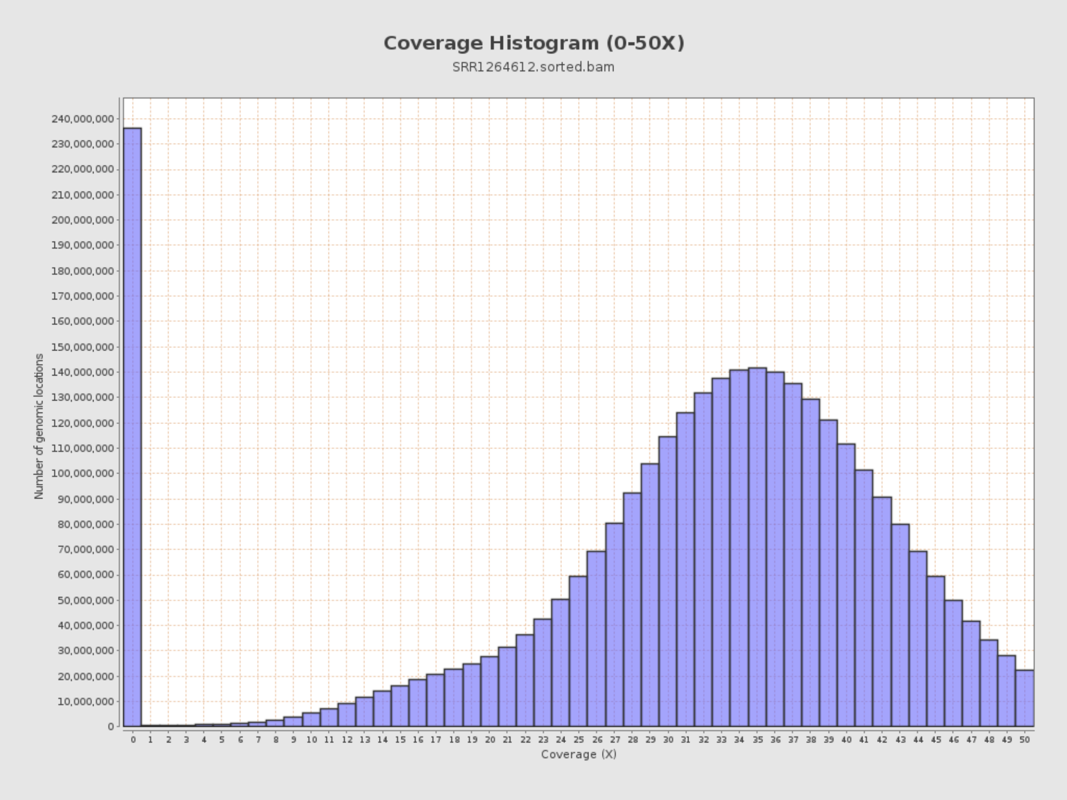
3. Results : Coverage across reference



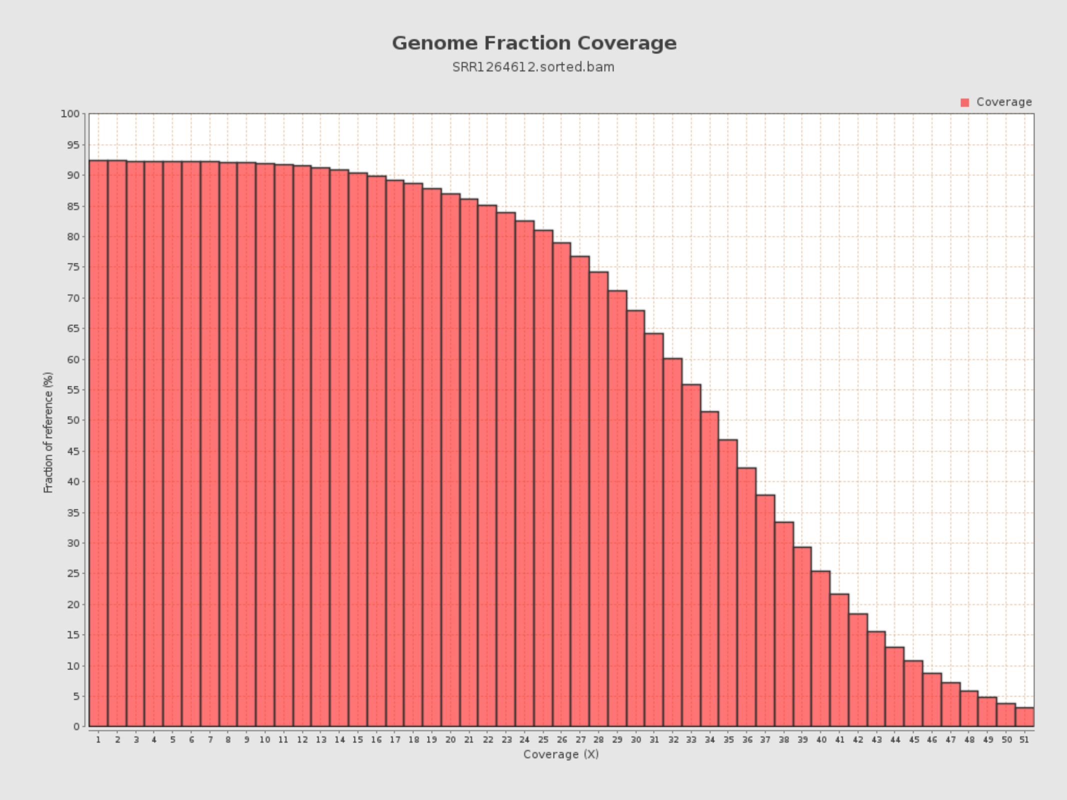
4. Results : Coverage Histogram



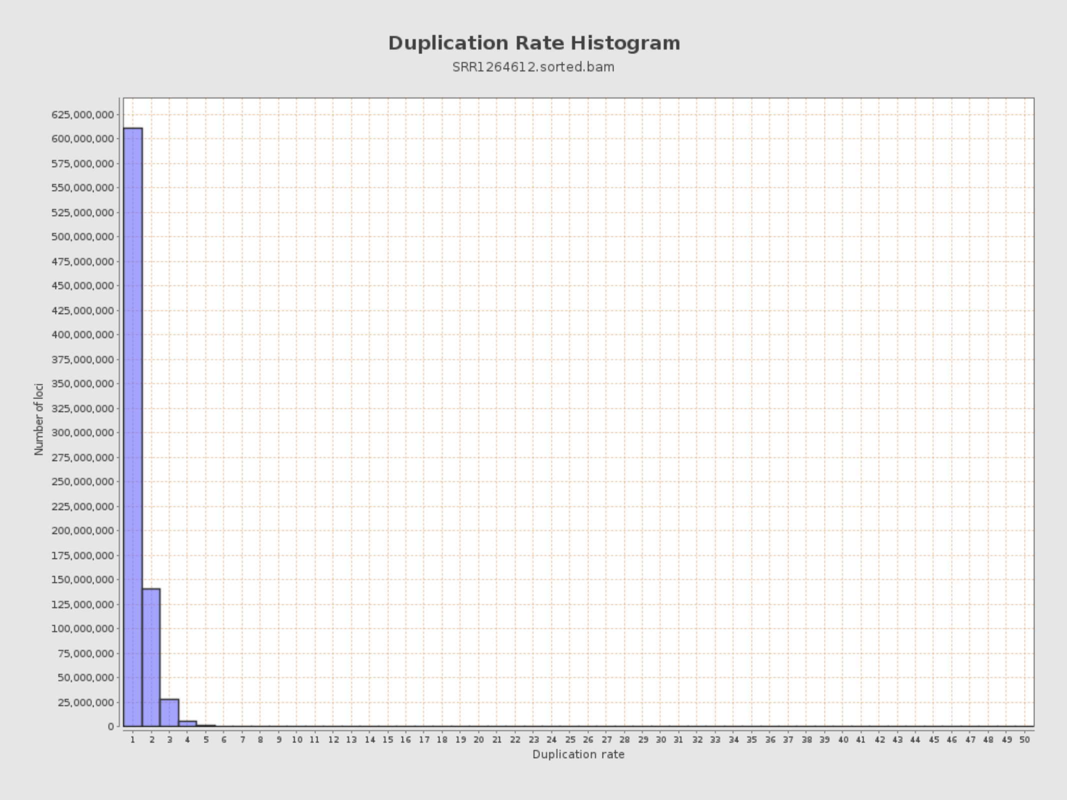
5. Results : Coverage Histogram (0-50X)



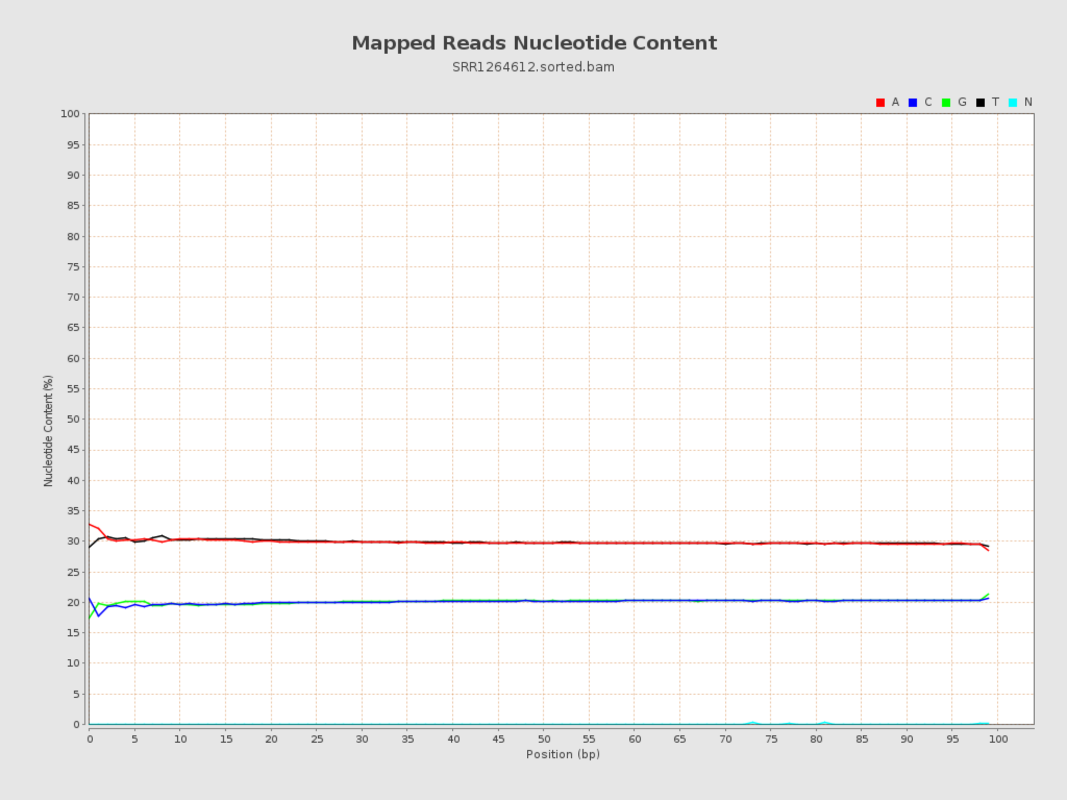
6. Results : Genome Fraction Coverage



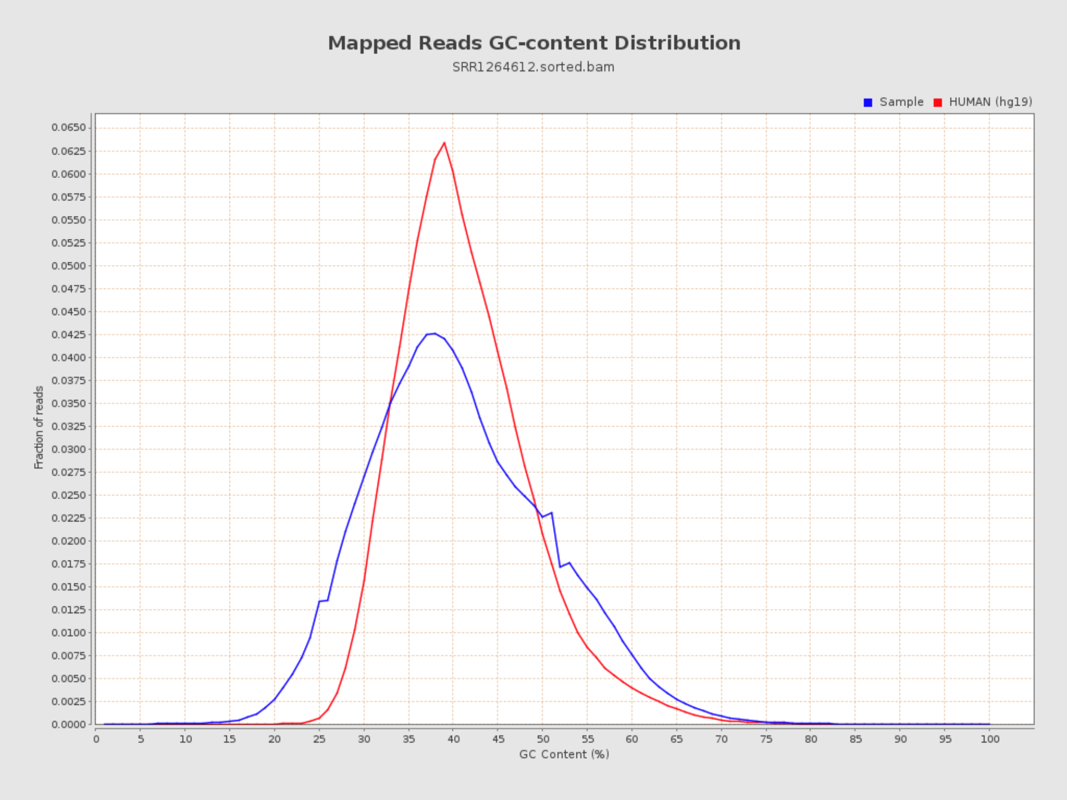
7. Results : Duplication Rate Histogram



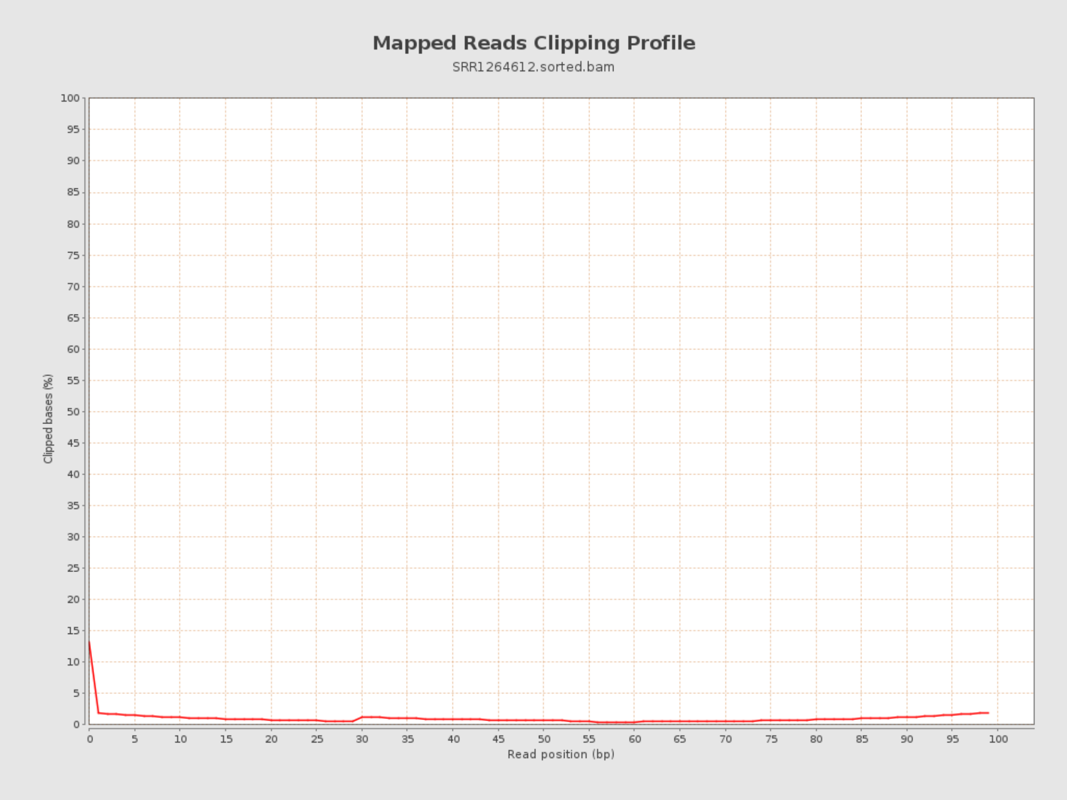
8. Results : Mapped Reads Nucleotide Content



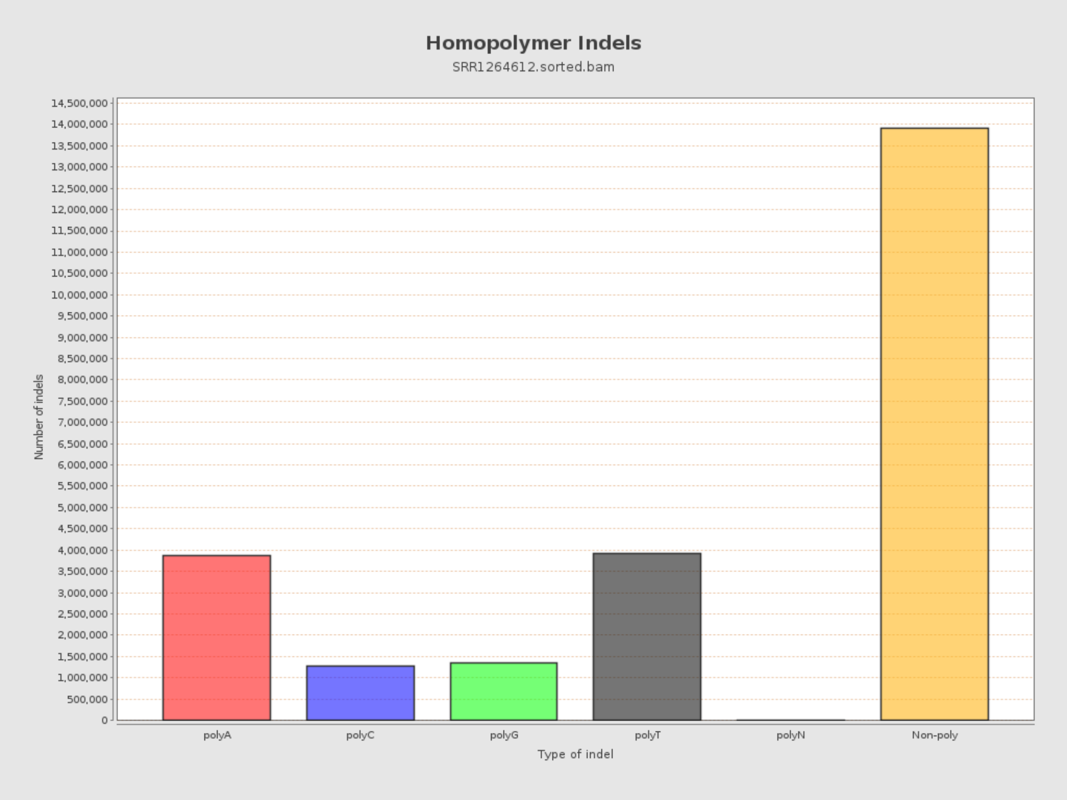
9. Results : Mapped Reads GC-content Distribution



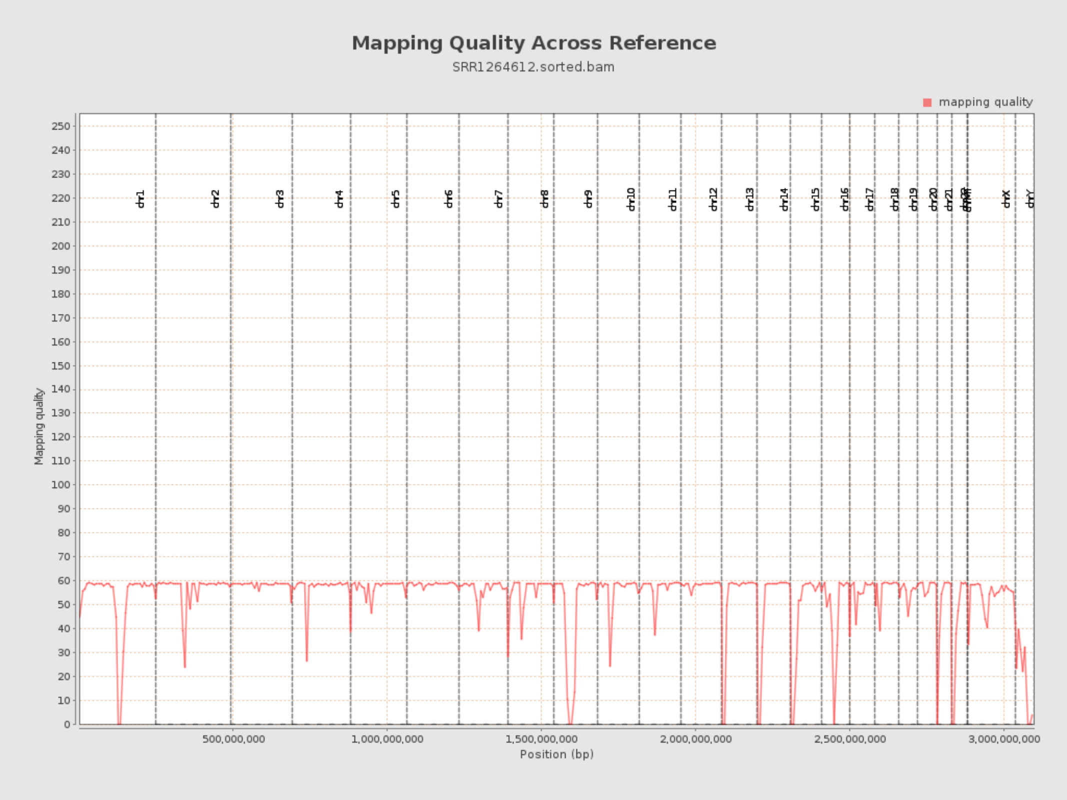
10. Results : Mapped Reads Clipping Profile



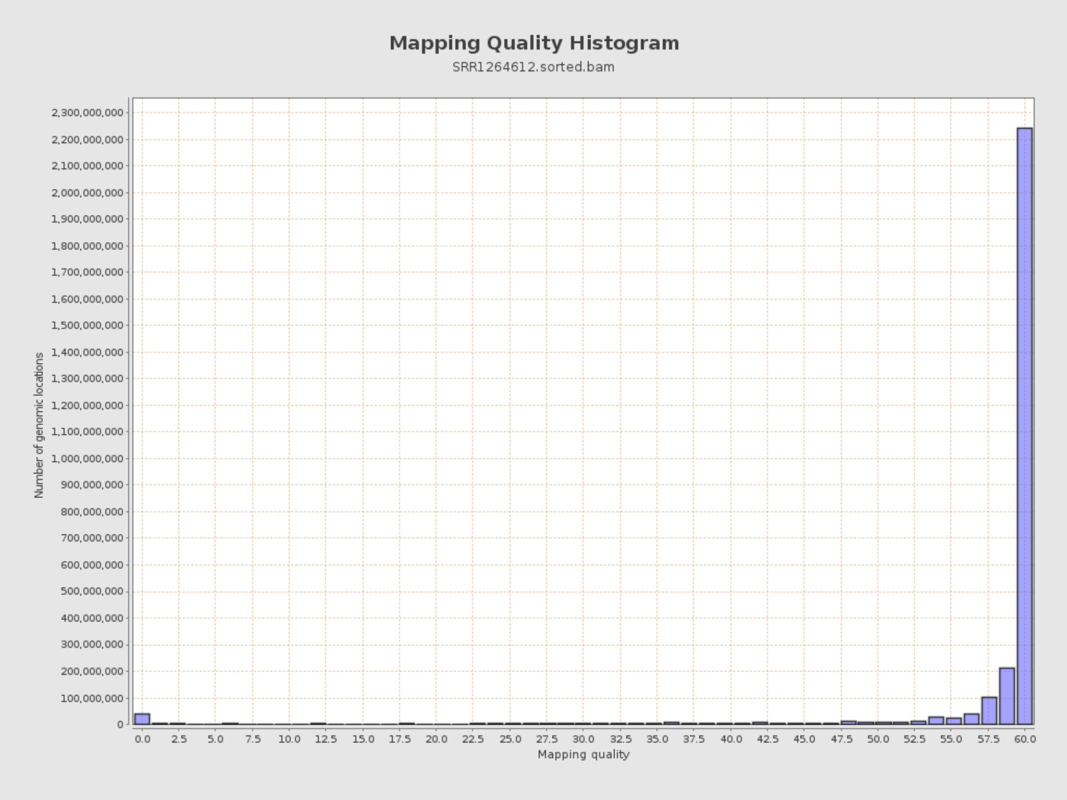
11. Results : Homopolymer Indels



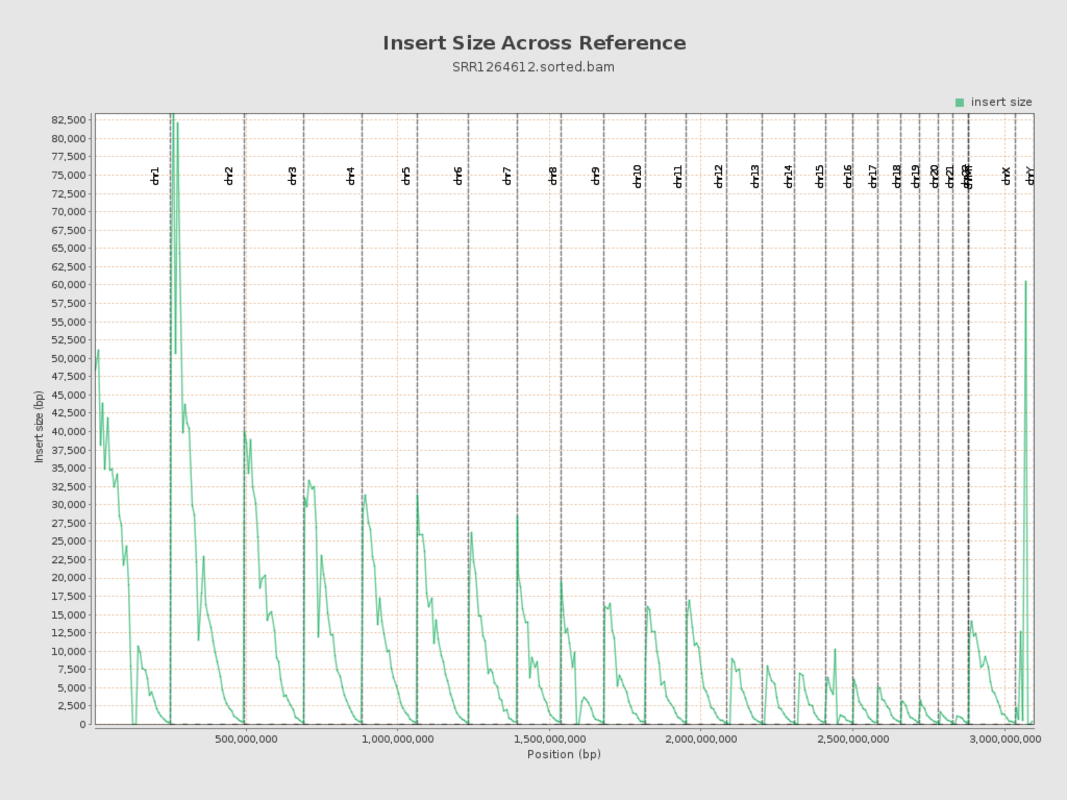
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram