Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/31 04:46:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1264629.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_SRR1264629 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1264629_1.fastq.gz SRR1264629_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Mar 31 04:46:14 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1264629.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,377,589,288
Mapped reads	1,369,699,258 / 99.43%
Unmapped reads	7,890,030 / 0.57%
Mapped paired reads	1,369,699,258 / 99.43%
Mapped reads, first in pair	686,625,899 / 49.84%
Mapped reads, second in pair	683,073,359 / 49.58%
Mapped reads, both in pair	1,364,871,998 / 99.08%
Mapped reads, singletons	4,827,260 / 0.35%
Secondary alignments	0
Supplementary alignments	9,717,583 / 0.71%
Read min/max/mean length	30 / 101 / 101.29
Duplicated reads (estimated)	570,371,279 / 41.4%
Duplication rate	41.51%
Clipped reads	64,523,259 / 4.68%

2.2. ACGT Content

Number/percentage of A's	42,558,316,055 / 30.97%
Number/percentage of C's	26,126,222,806 / 19.01%
Number/percentage of T's	42,304,350,603 / 30.79%
Number/percentage of G's	26,381,959,299 / 19.2%
Number/percentage of N's	38,025,119 / 0.03%

GC Percentage	38.21%

2.3. Coverage

Mean	44.3973
Standard Deviation	45.4889

2.4. Mapping Quality

Mean Mapping Quality	54.45

2.5. Insert size

Mean	89,988.83
Standard Deviation	2,886,188.53
P25/Median/P75	277 / 300 / 328

2.6. Mismatches and indels

General error rate	0.4%
Mismatches	525,198,015
Insertions	15,160,086
Mapped reads with at least one insertion	1.09%
Deletions	14,158,626
Mapped reads with at least one deletion	1.01%
Homopolymer indels	48.57%

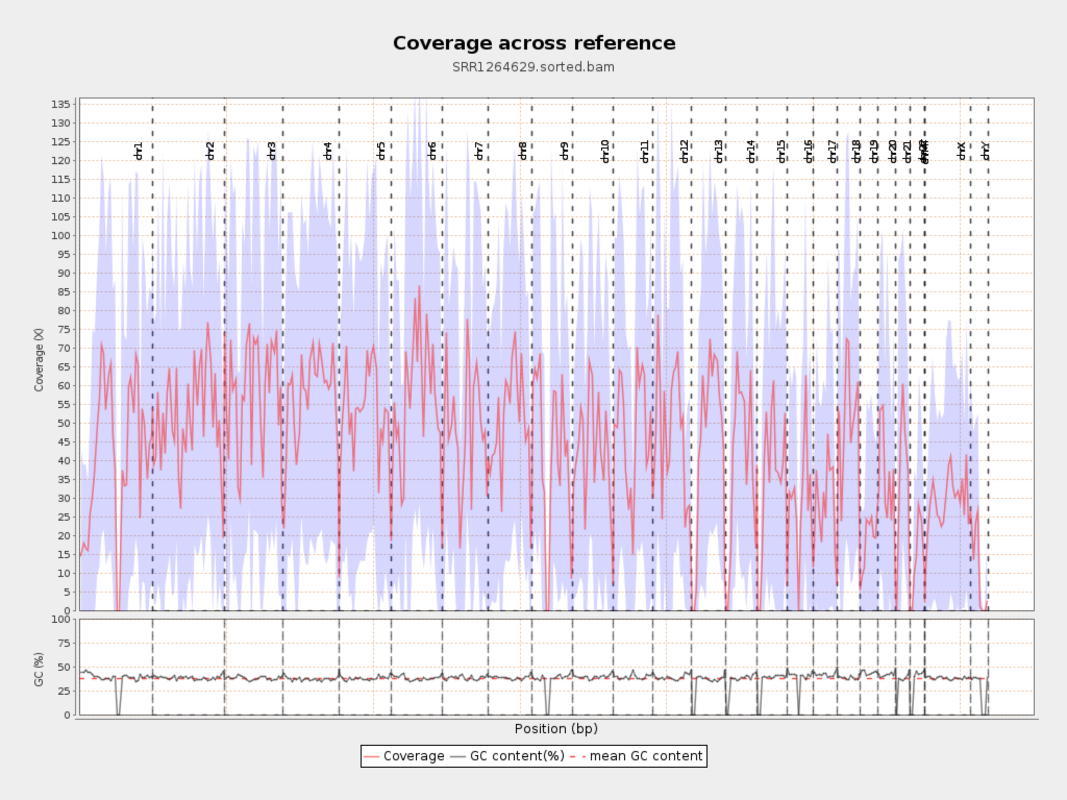
2.7. Chromosome stats

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

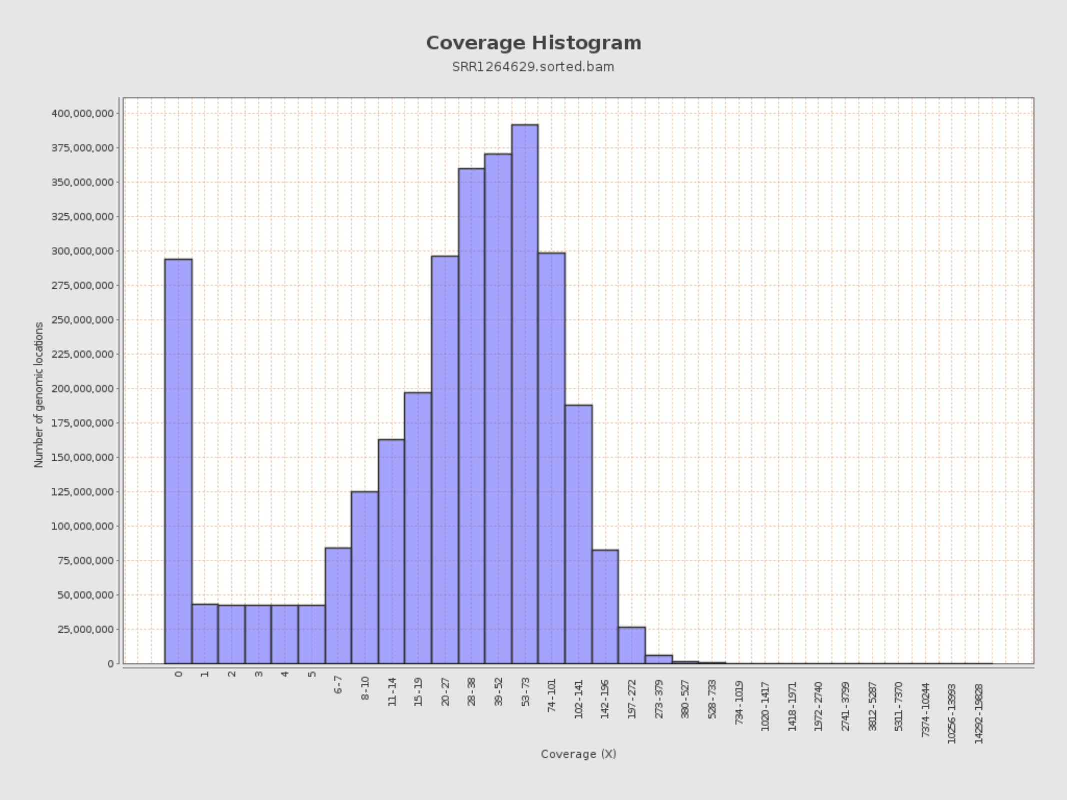
		bases	coverage	deviation
chr1	249250621	10423511352	41.8194	45.9012
chr2	243199373	12500967332	51.4021	46.5062
chr3	198022430	11573013066	58.4429	49.1082
chr4	191154276	11037132180	57.7394	46.4599
chr5	180915260	9486749083	52.4375	44.7744
chr6	171115067	9912727214	57.9302	50.2507
chr7	159138663	7715116776	48.4805	46.6612
chr8	146364022	7445266760	50.8681	43.7055
chr9	141213431	5679854251	40.2218	47.4172
chr10	135534747	5873007181	43.3321	41.2034
chr11	135006516	6421110353	47.5615	46.3763
chr12	133851895	6319209544	47.2105	47.8548
chr13	115169878	5325599301	46.2413	45.8672
chr14	107349540	4278557472	39.8563	43.4812
chr15	102531392	3644243963	35.5427	43.5011
chr16	90354753	2511876848	27.8002	35.1218
chr17	81195210	2278718877	28.0647	34.9207
chr18	78077248	4045645407	51.8159	45.0896
chr19	59128983	1090587617	18.4442	26.8504
chr20	63025520	2208360161	35.0391	43.7883
chr21	48129895	1752642593	36.4148	46.9656
chr22	51304566	719346152	14.0211	24.8414
chrMT	16571	33767	2.0377	5.1486
chrX	155270560	4557082282	29.3493	31.1938

chrY	59373566	640037310	10.7798	24.3893

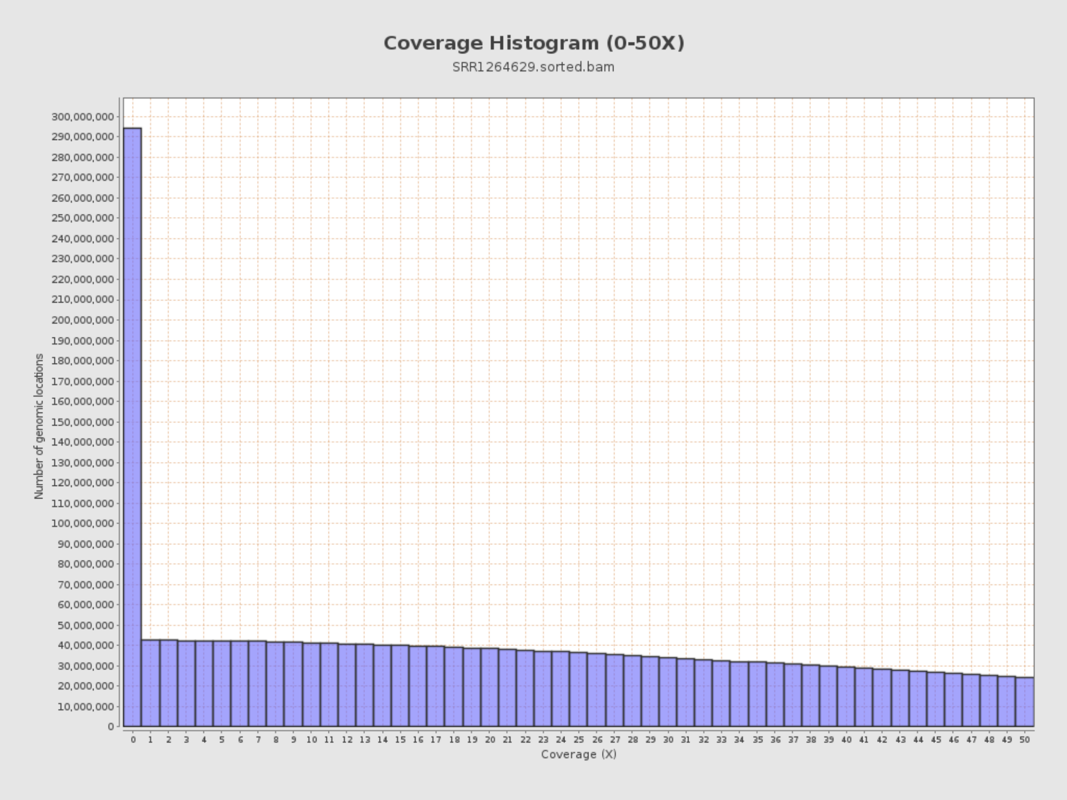
3. Results : Coverage across reference



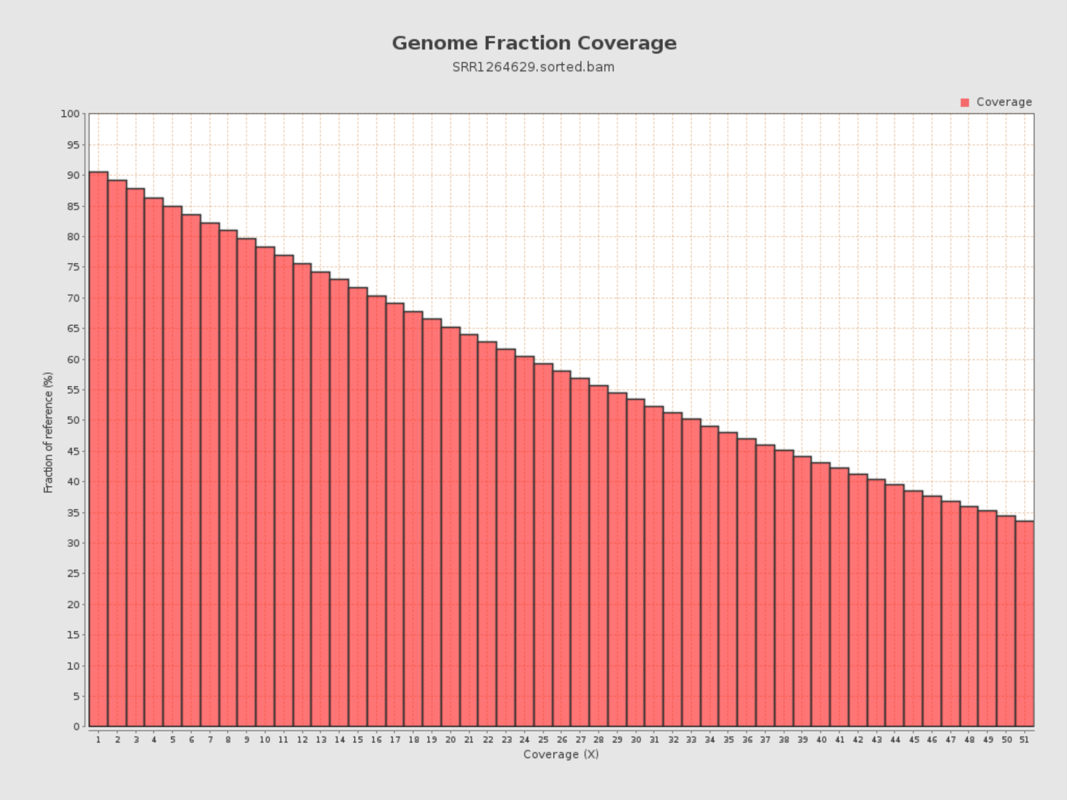
4. Results : Coverage Histogram



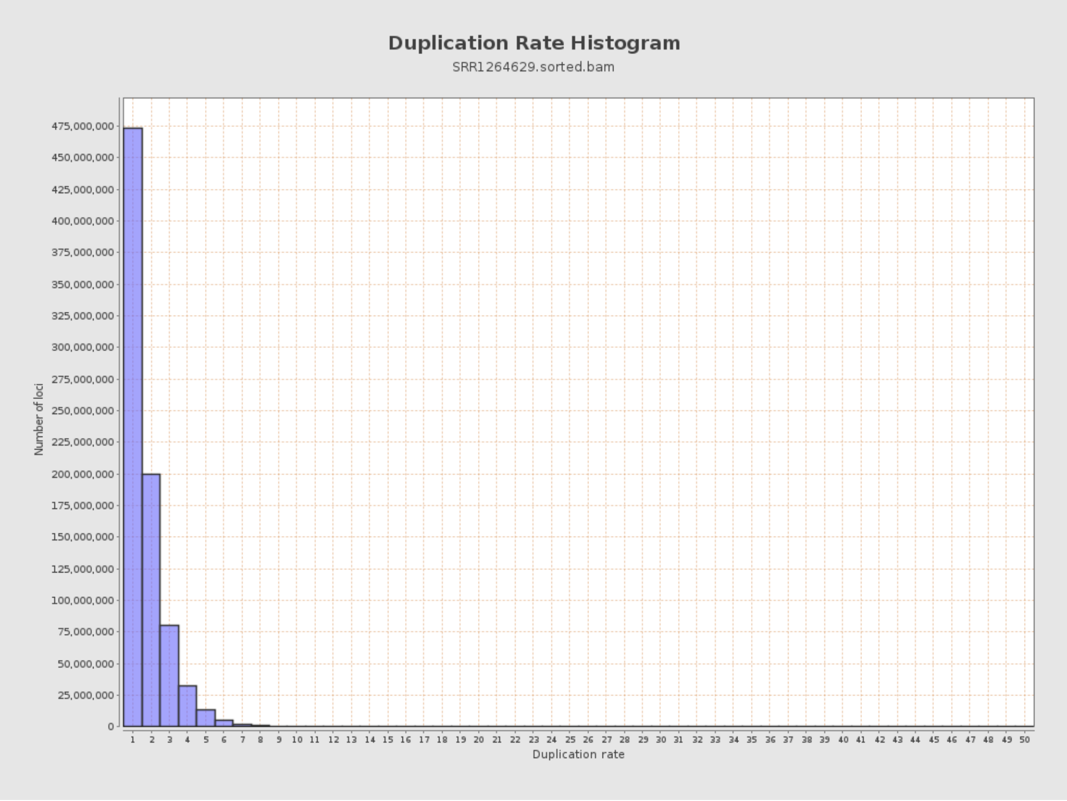
5. Results : Coverage Histogram (0-50X)



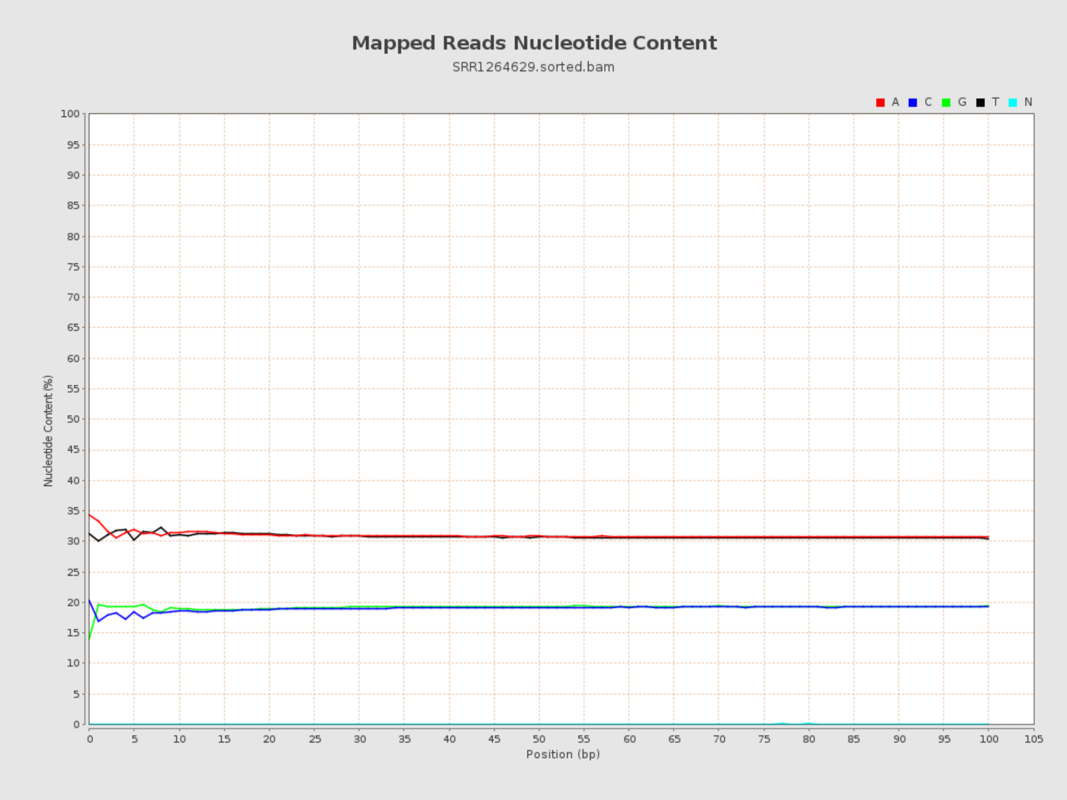
6. Results : Genome Fraction Coverage



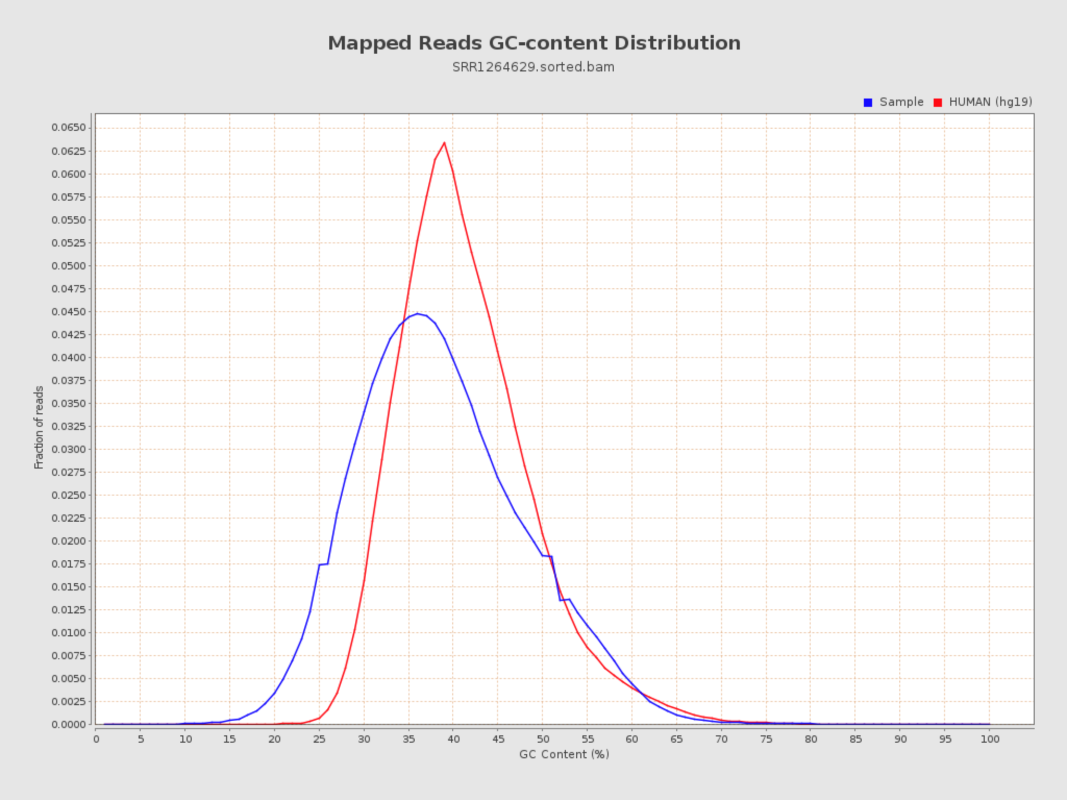
7. Results : Duplication Rate Histogram



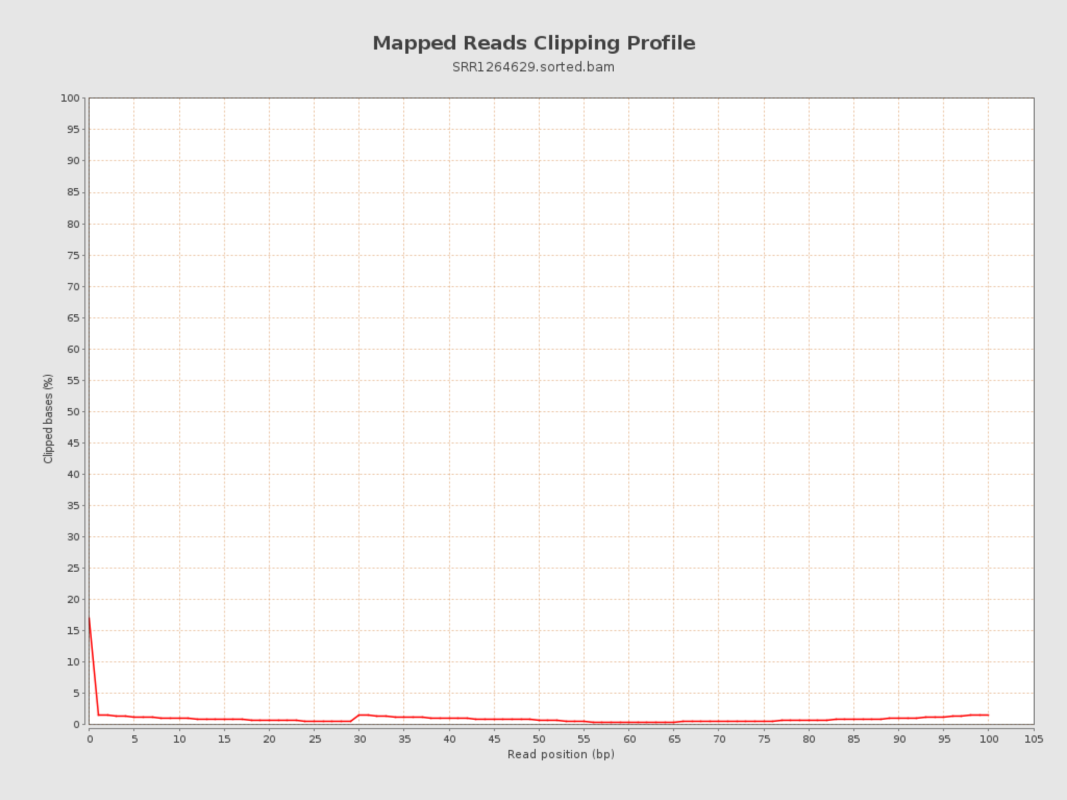
8. Results : Mapped Reads Nucleotide Content



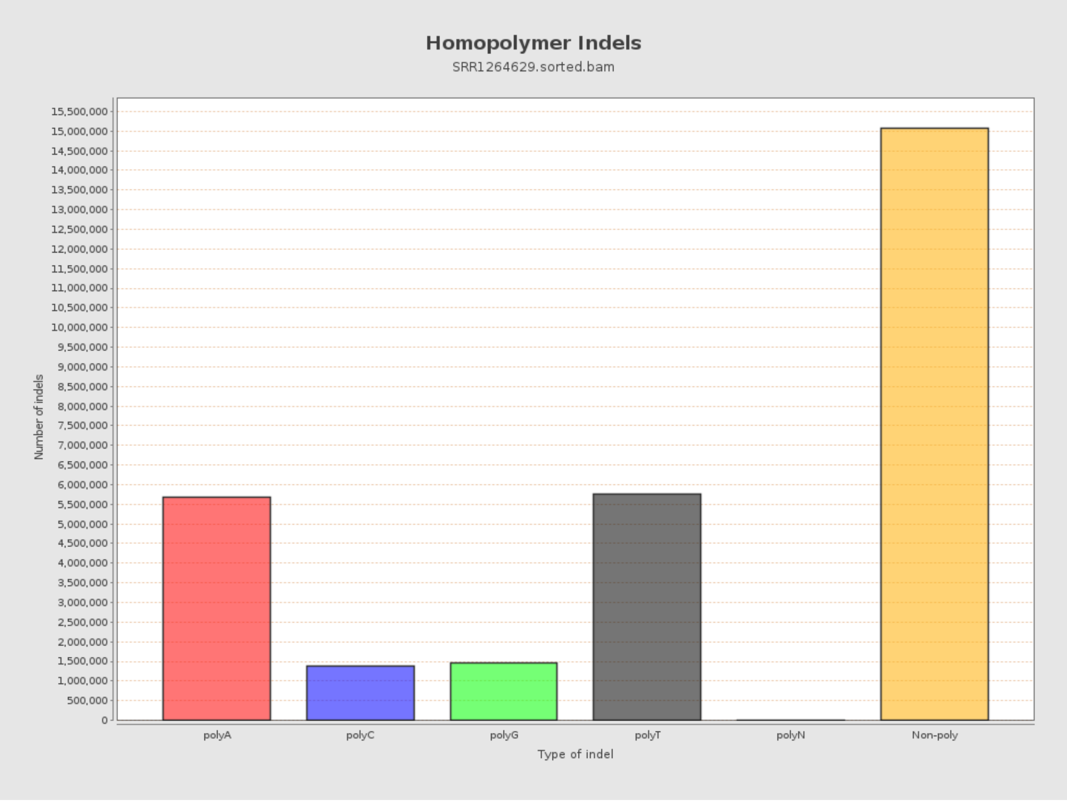
9. Results : Mapped Reads GC-content Distribution



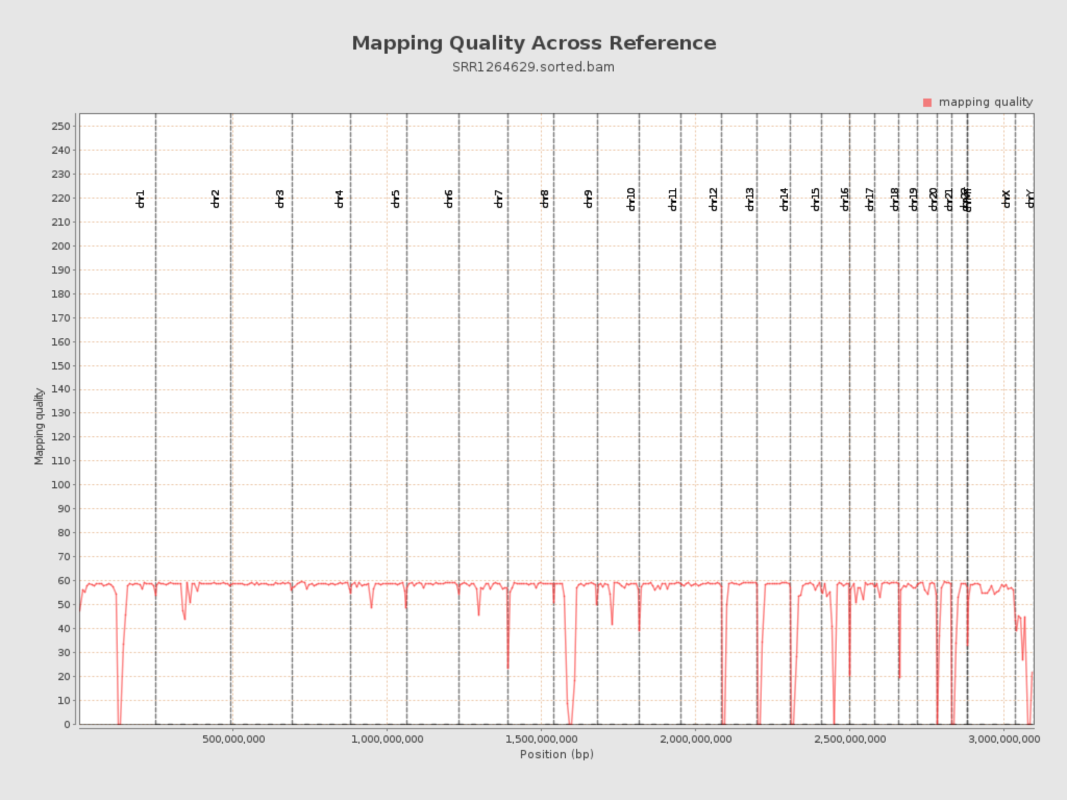
10. Results : Mapped Reads Clipping Profile



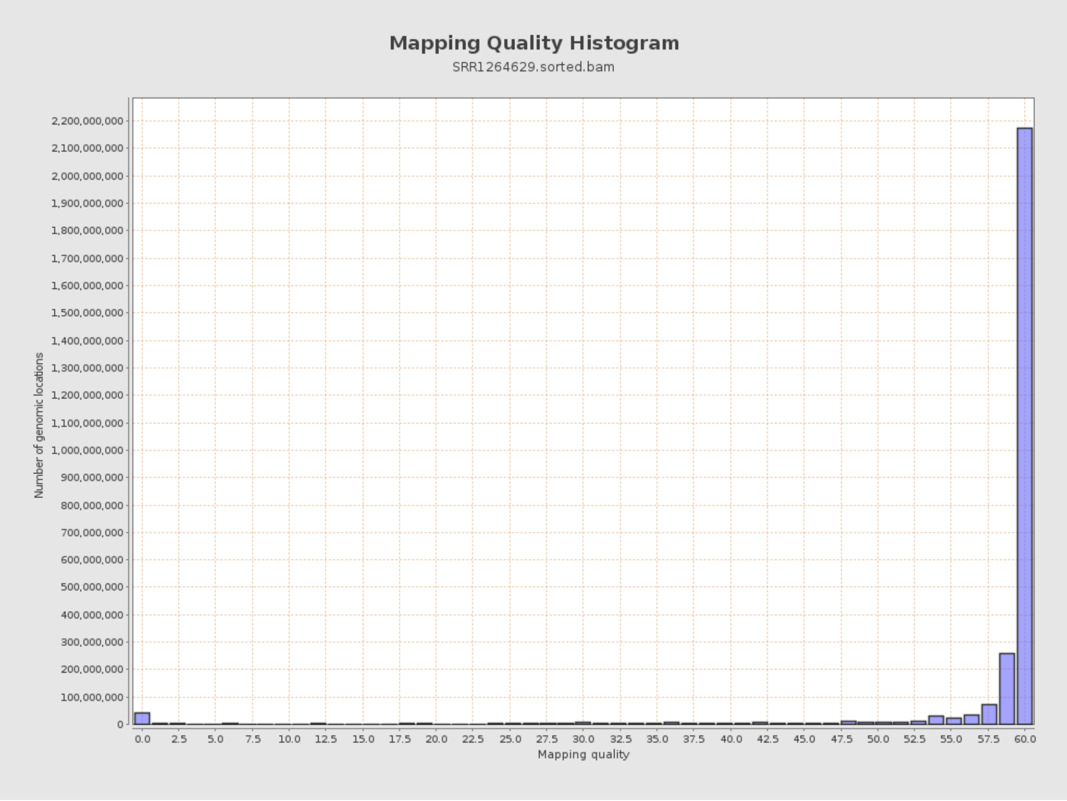
11. Results : Homopolymer Indels



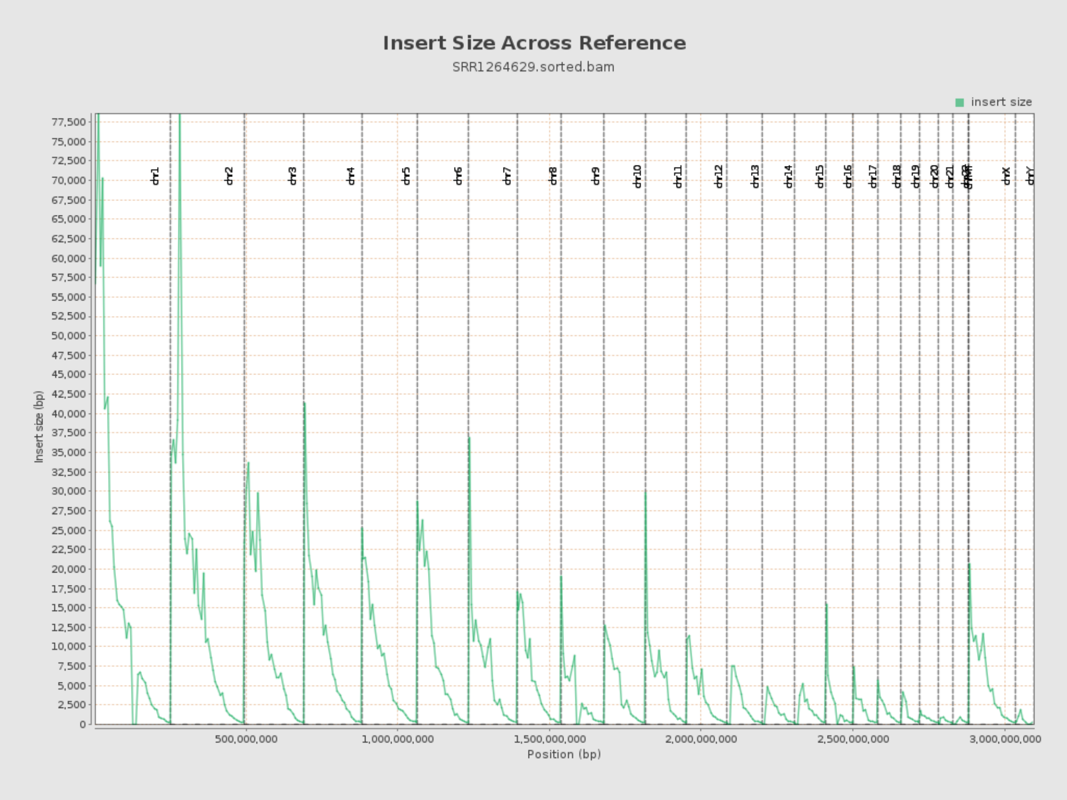
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram