Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/28 11:34:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472615.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_SRR3472615 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472615_1.fastq.gz SRR3472615_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 28 11:34:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472615.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	19,549,616
Mapped reads	19,381,671 / 99.14%
Unmapped reads	167,945 / 0.86%
Mapped paired reads	19,381,671 / 99.14%
Mapped reads, first in pair	9,720,430 / 49.72%
Mapped reads, second in pair	9,661,241 / 49.42%
Mapped reads, both in pair	19,281,874 / 98.63%
Mapped reads, singletons	99,797 / 0.51%
Secondary alignments	0
Supplementary alignments	99,545 / 0.51%
Read min/max/mean length	30 / 101 / 99.52
Duplicated reads (estimated)	13,799,616 / 70.59%
Duplication rate	50.59%
Clipped reads	1,492,577 / 7.63%

2.2. ACGT Content

Number/percentage of A's	498,203,168 / 26.21%
Number/percentage of C's	454,377,656 / 23.91%
Number/percentage of T's	498,842,343 / 26.25%
Number/percentage of G's	448,832,220 / 23.62%
Number/percentage of N's	360,857 / 0.02%

GC Percentage	47.52%

2.3. Coverage

Mean	0.614
Standard Deviation	25.9917

2.4. Mapping Quality

Mean Mapping Quality	54.61

2.5. Insert size

Mean	20,282.56
Standard Deviation	1,438,559.63
P25/Median/P75	144 / 198 / 265

2.6. Mismatches and indels

General error rate	0.58%
Mismatches	10,835,005
Insertions	106,245
Mapped reads with at least one insertion	0.54%
Deletions	93,295
Mapped reads with at least one deletion	0.47%
Homopolymer indels	45.06%

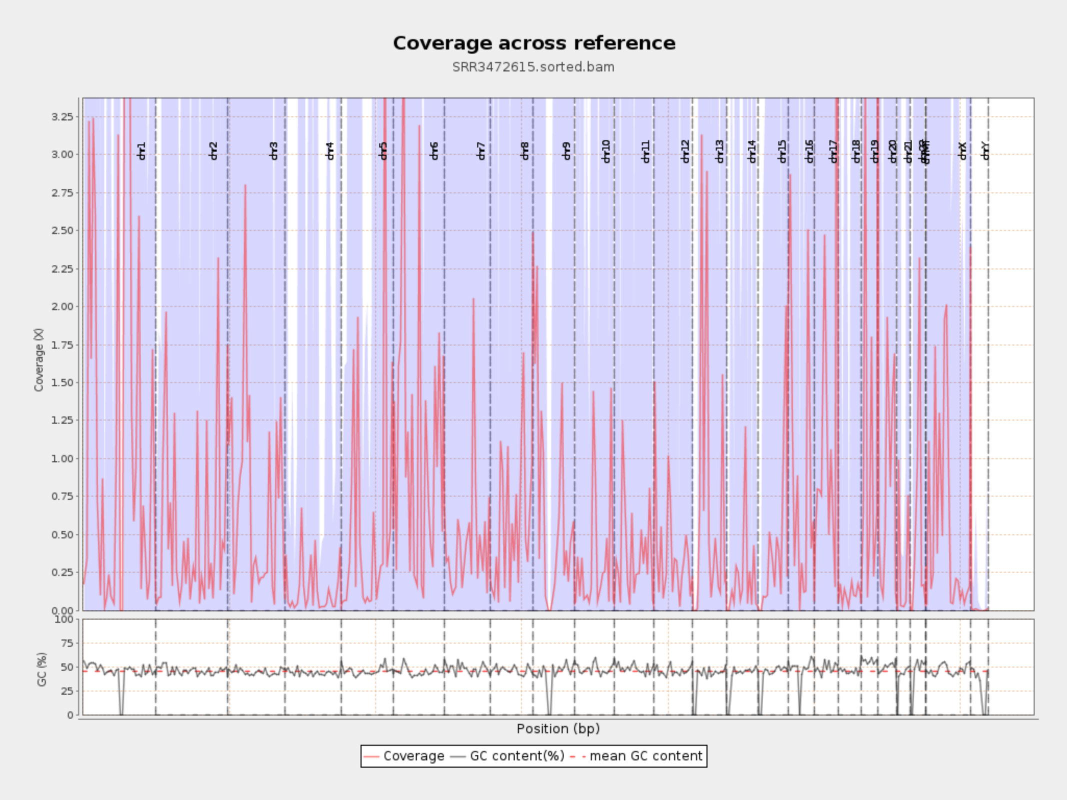
2.7. Chromosome stats

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

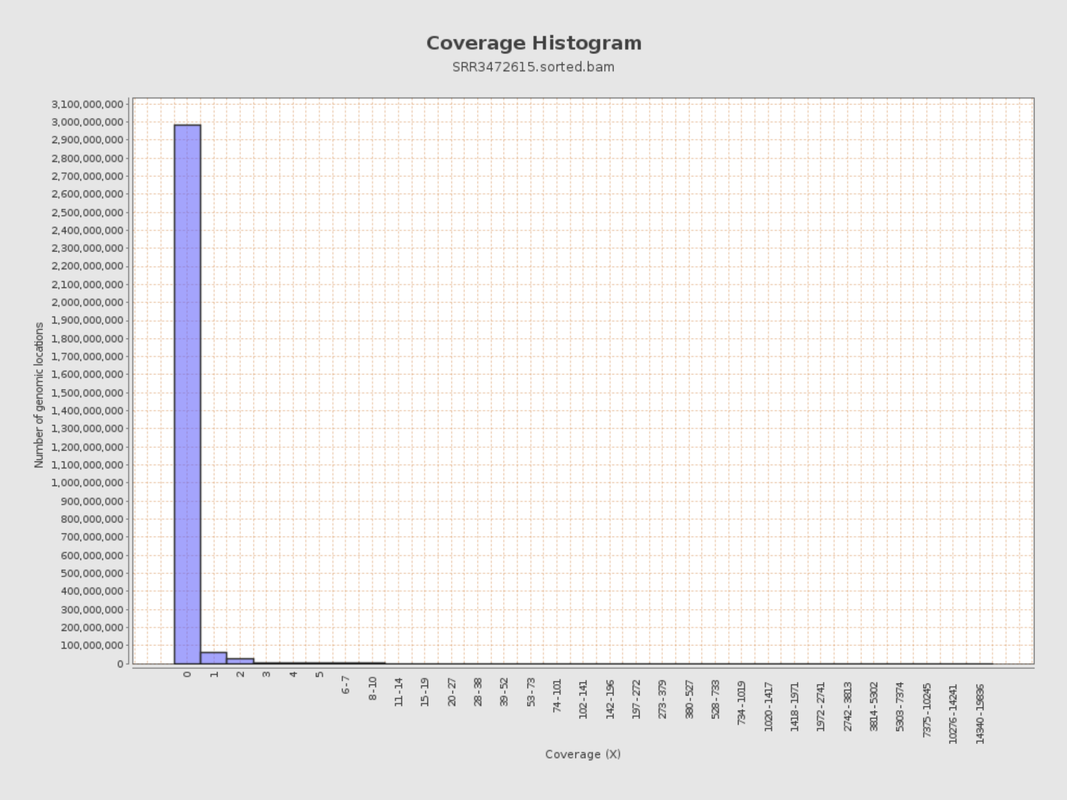
		bases	coverage	deviation
chr1	249250621	302666801	1.2143	40.7235
chr2	243199373	122944344	0.5055	31.6957
chr3	198022430	141509052	0.7146	20.9777
chr4	191154276	27467431	0.1437	7.7946
chr5	180915260	112441086	0.6215	31.951
chr6	171115067	189804853	1.1092	34.0807
chr7	159138663	74285231	0.4668	16.4235
chr8	146364022	84966583	0.5805	20.4537
chr9	141213431	89797118	0.6359	19.1144
chr10	135534747	48970106	0.3613	23.6393
chr11	135006516	50929840	0.3772	22.8839
chr12	133851895	53650940	0.4008	14.6552
chr13	115169878	82769398	0.7187	32.4838
chr14	107349540	23058554	0.2148	9.508
chr15	102531392	43929349	0.4284	18.7418
chr16	90354753	82145353	0.9091	29.9275
chr17	81195210	98524032	1.2134	32.2383
chr18	78077248	8753881	0.1121	3.4106
chr19	59128983	69053322	1.1678	42.3054
chr20	63025520	54314072	0.8618	28.0176
chr21	48129895	14701146	0.3054	19.9276
chr22	51304566	30237636	0.5894	28.906
chrMT	16571	4844	0.2923	0.7138
chrX	155270560	93602829	0.6028	21.1479

chrY	59373566	328778	0.0055	0.4339

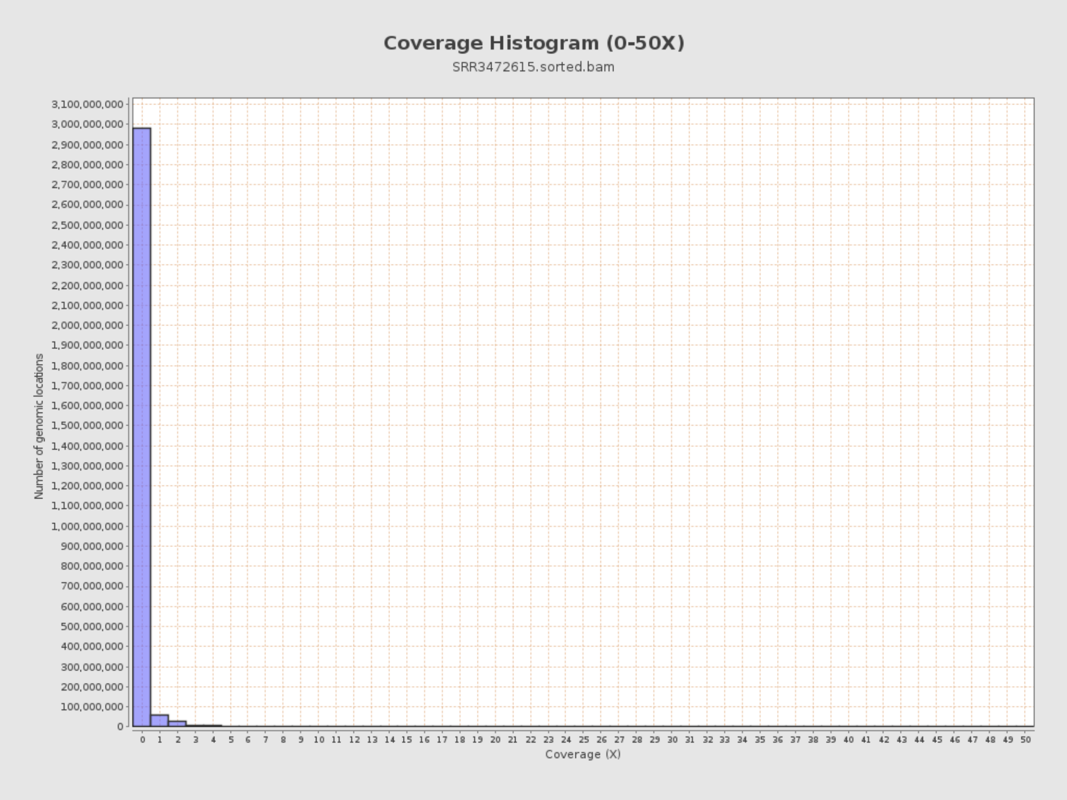
3. Results : Coverage across reference



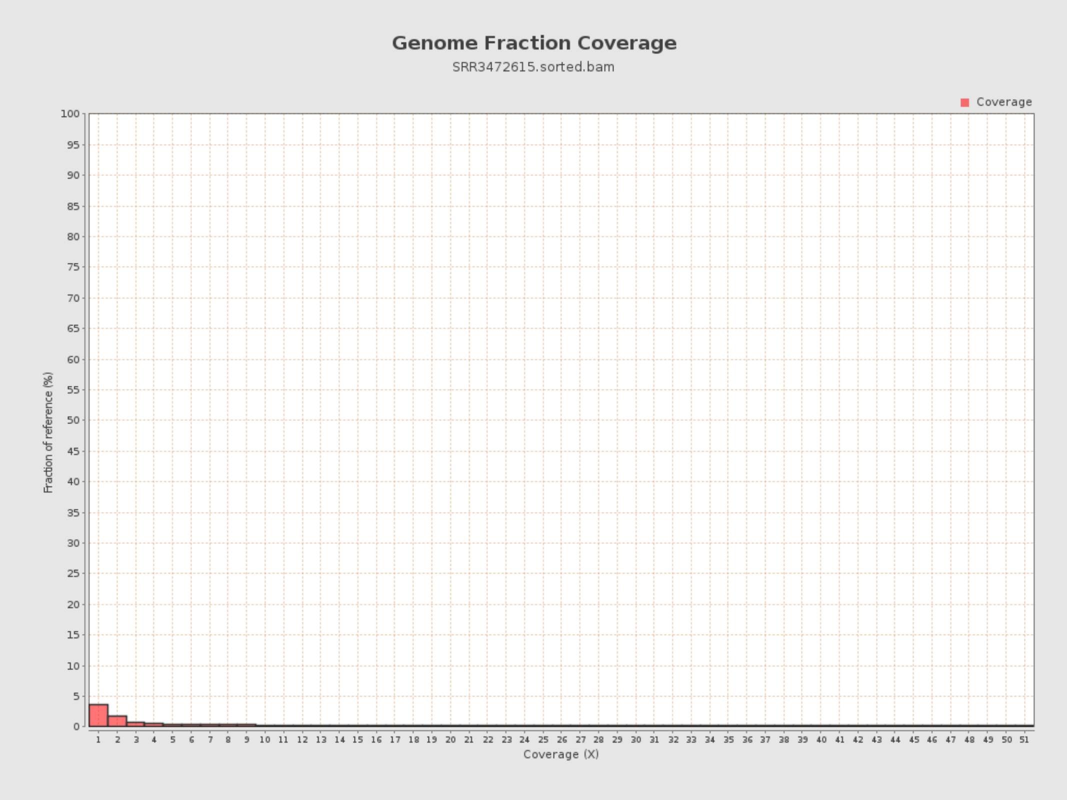
4. Results : Coverage Histogram



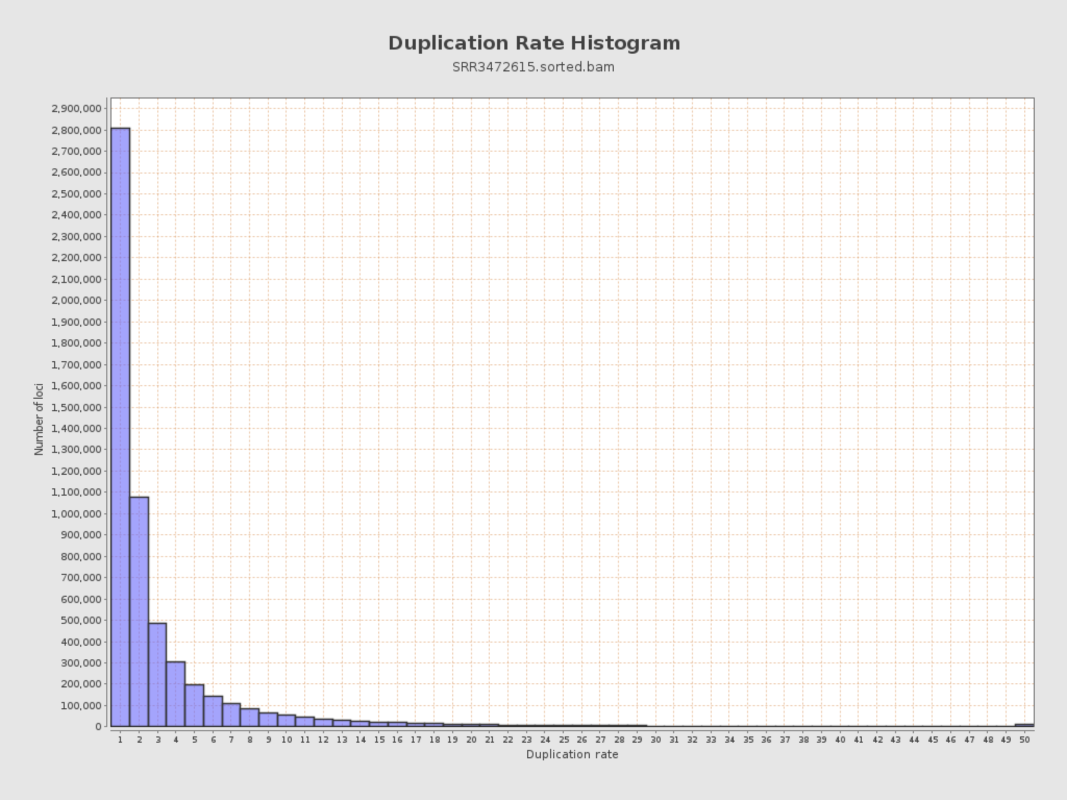
5. Results : Coverage Histogram (0-50X)



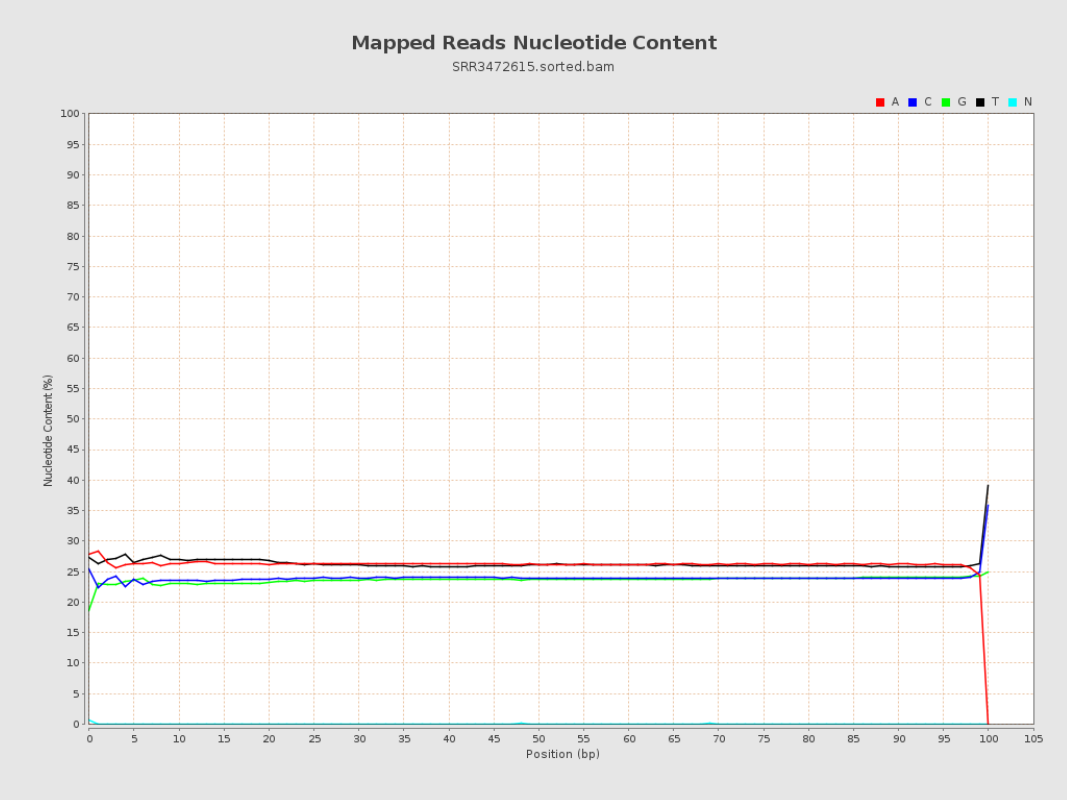
6. Results : Genome Fraction Coverage



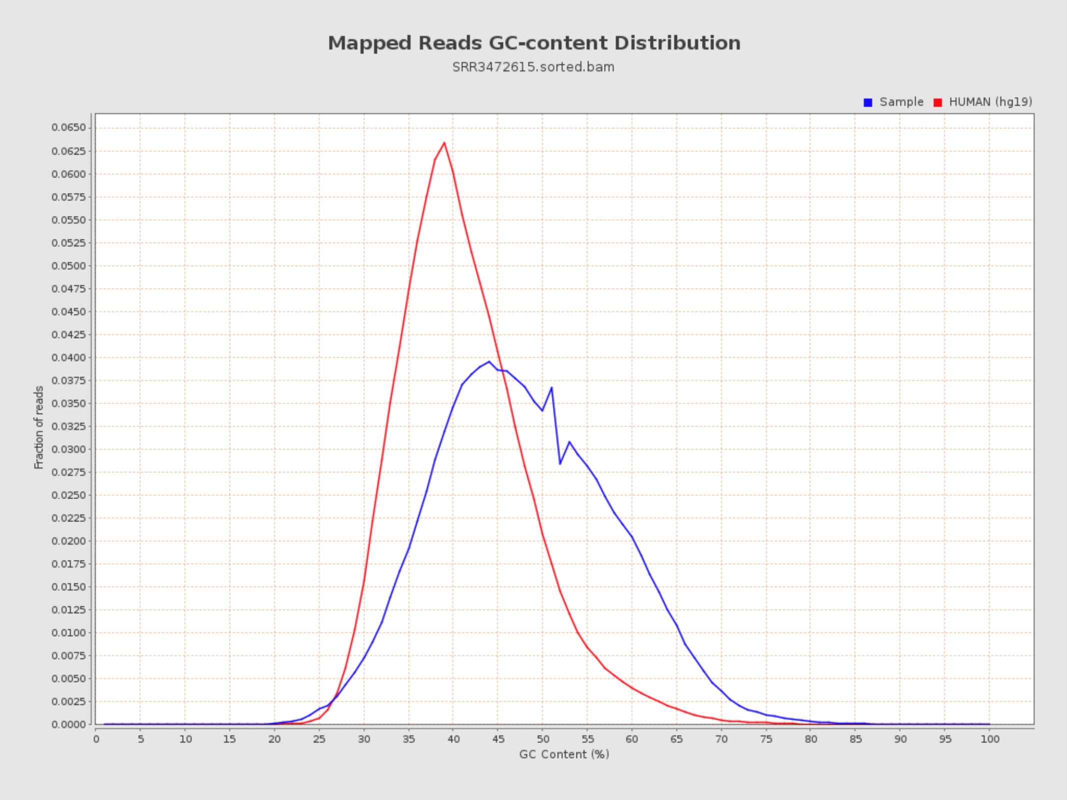
7. Results : Duplication Rate Histogram



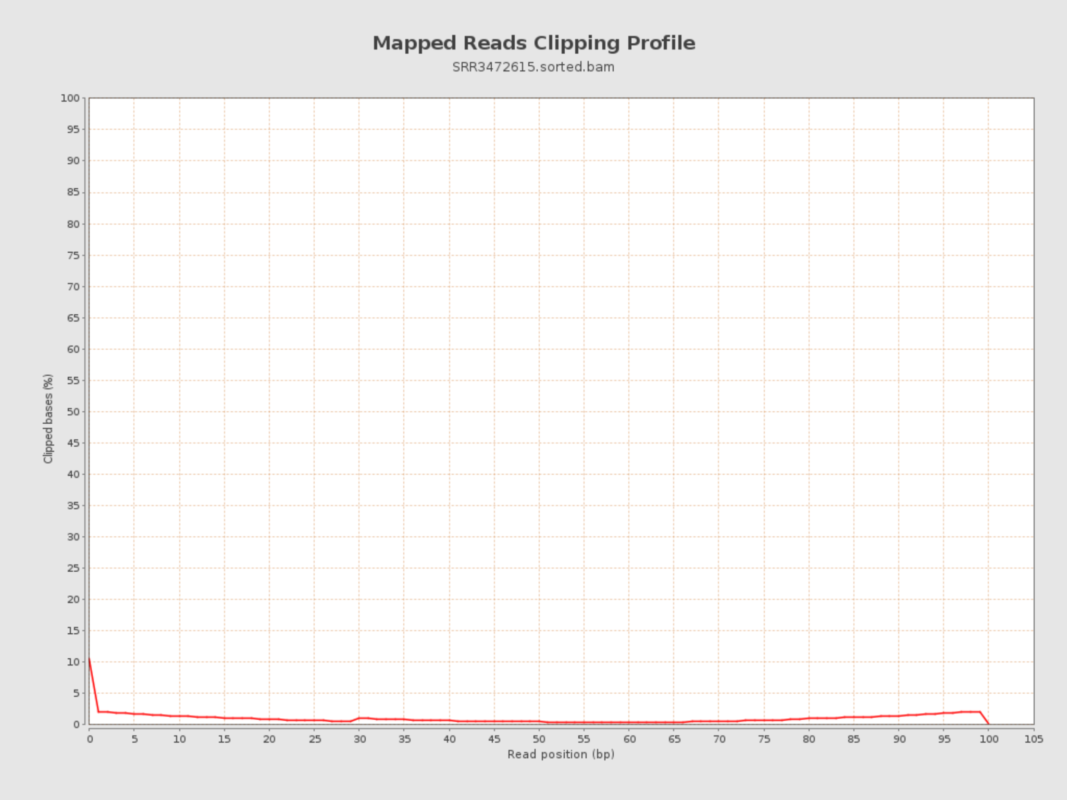
8. Results : Mapped Reads Nucleotide Content



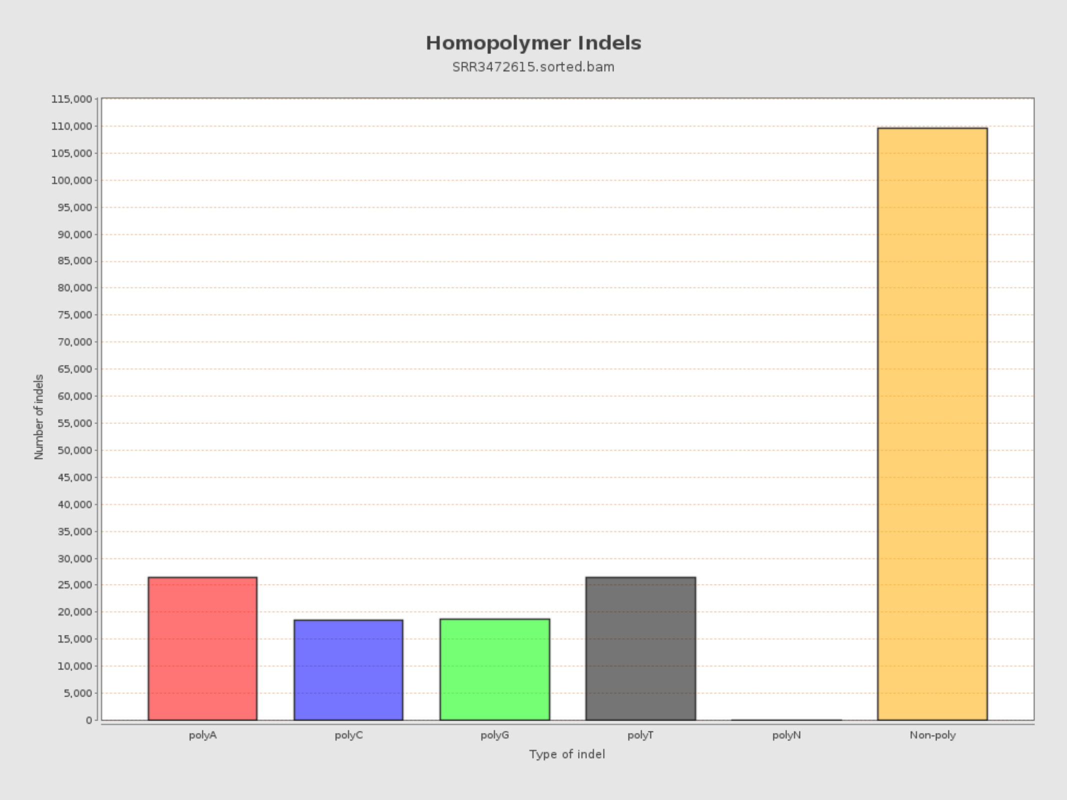
9. Results : Mapped Reads GC-content Distribution



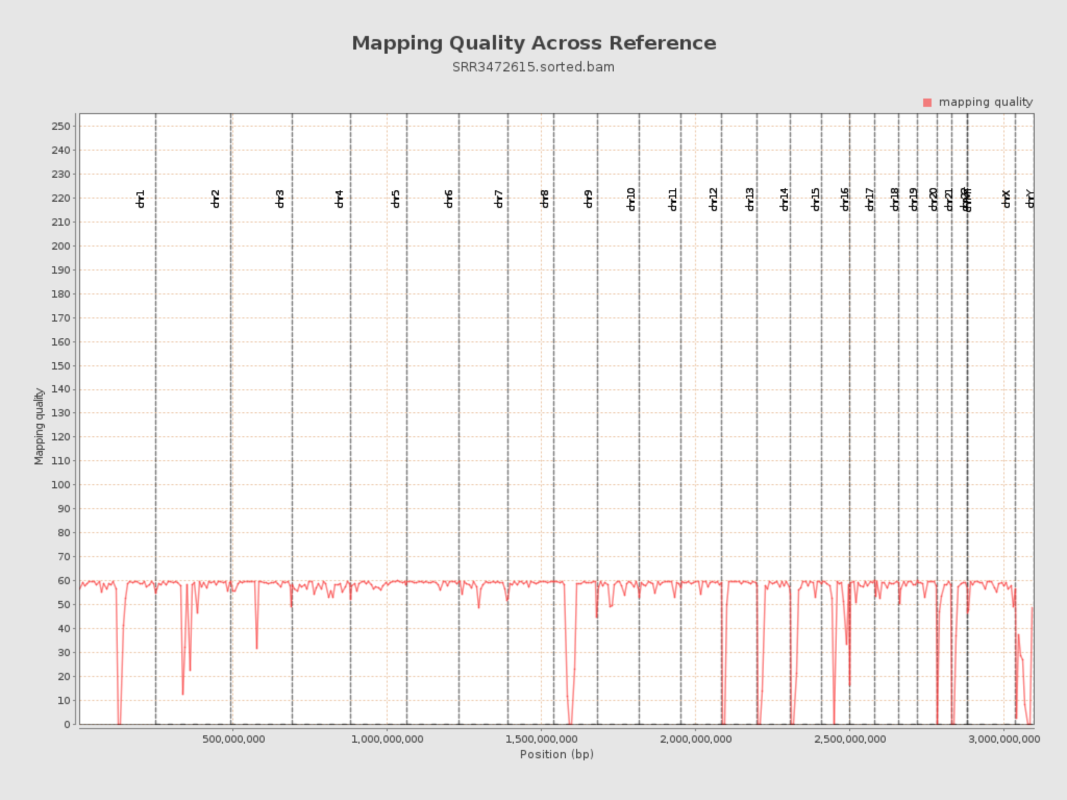
10. Results : Mapped Reads Clipping Profile



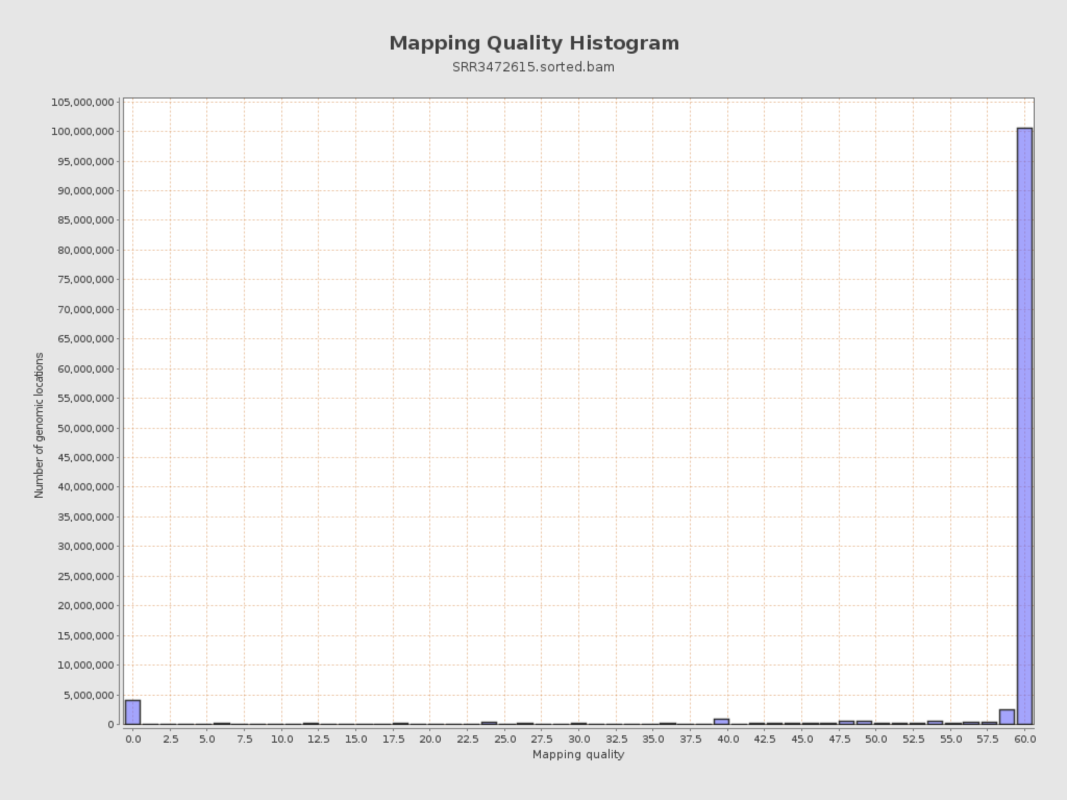
11. Results : Homopolymer Indels



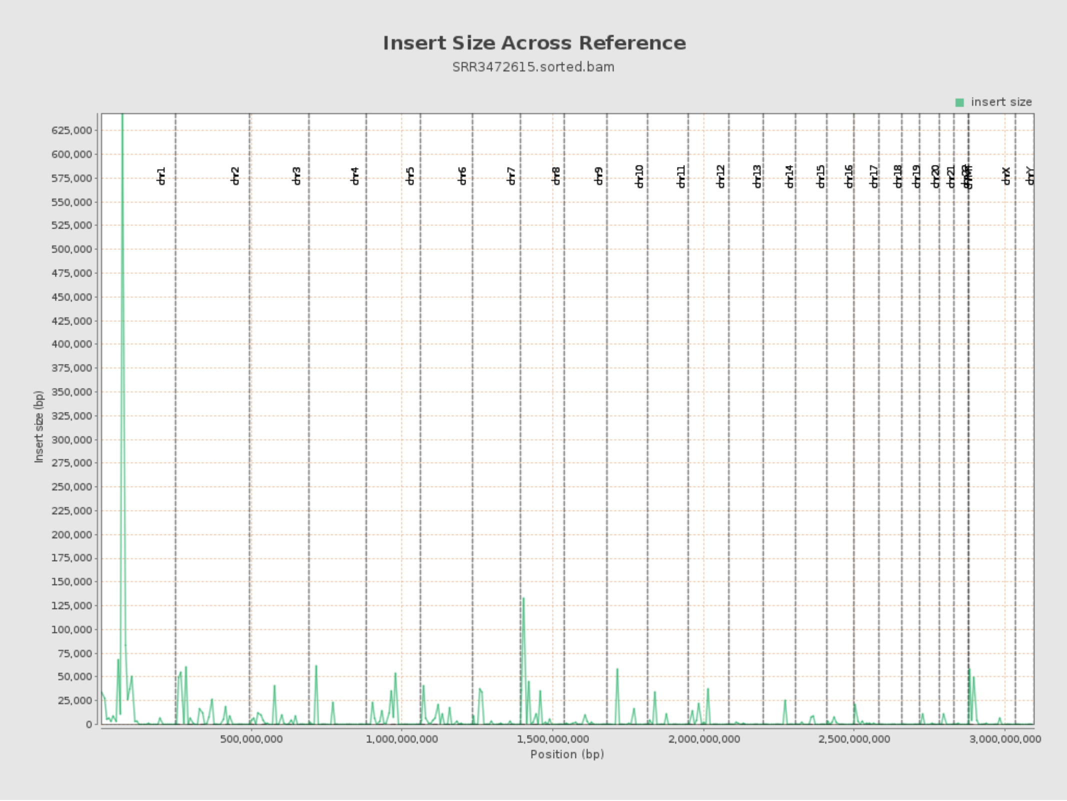
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram