Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 18:58:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472516.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_SRR3472516 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472516_1.fastq.gz SRR3472516_2.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 18:58:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472516.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	15,984,494
Mapped reads	15,793,244 / 98.8%
Unmapped reads	191,250 / 1.2%
Mapped paired reads	15,793,244 / 98.8%
Mapped reads, first in pair	7,921,475 / 49.56%
Mapped reads, second in pair	7,871,769 / 49.25%
Mapped reads, both in pair	15,696,920 / 98.2%
Mapped reads, singletons	96,324 / 0.6%
Secondary alignments	0
Supplementary alignments	69,497 / 0.43%
Read min/max/mean length	30 / 100 / 100.18
Duplicated reads (estimated)	10,091,138 / 63.13%
Duplication rate	44.81%
Clipped reads	1,485,324 / 9.29%

2.2. ACGT Content

Number/percentage of A's	428,929,418 / 27.66%
Number/percentage of C's	348,865,962 / 22.5%
Number/percentage of T's	425,323,138 / 27.43%
Number/percentage of G's	347,221,094 / 22.39%
Number/percentage of N's	239,889 / 0.02%

GC Percentage	44.89%

2.3. Coverage

Mean	0.5009
Standard Deviation	20.6699

2.4. Mapping Quality

Mean Mapping Quality	54.93

2.5. Insert size

Mean	28,792.83
Standard Deviation	1,674,134.46
P25/Median/P75	164 / 231 / 314

2.6. Mismatches and indels

General error rate	0.61%
Mismatches	9,338,803
Insertions	78,938
Mapped reads with at least one insertion	0.49%
Deletions	74,827
Mapped reads with at least one deletion	0.47%
Homopolymer indels	46%

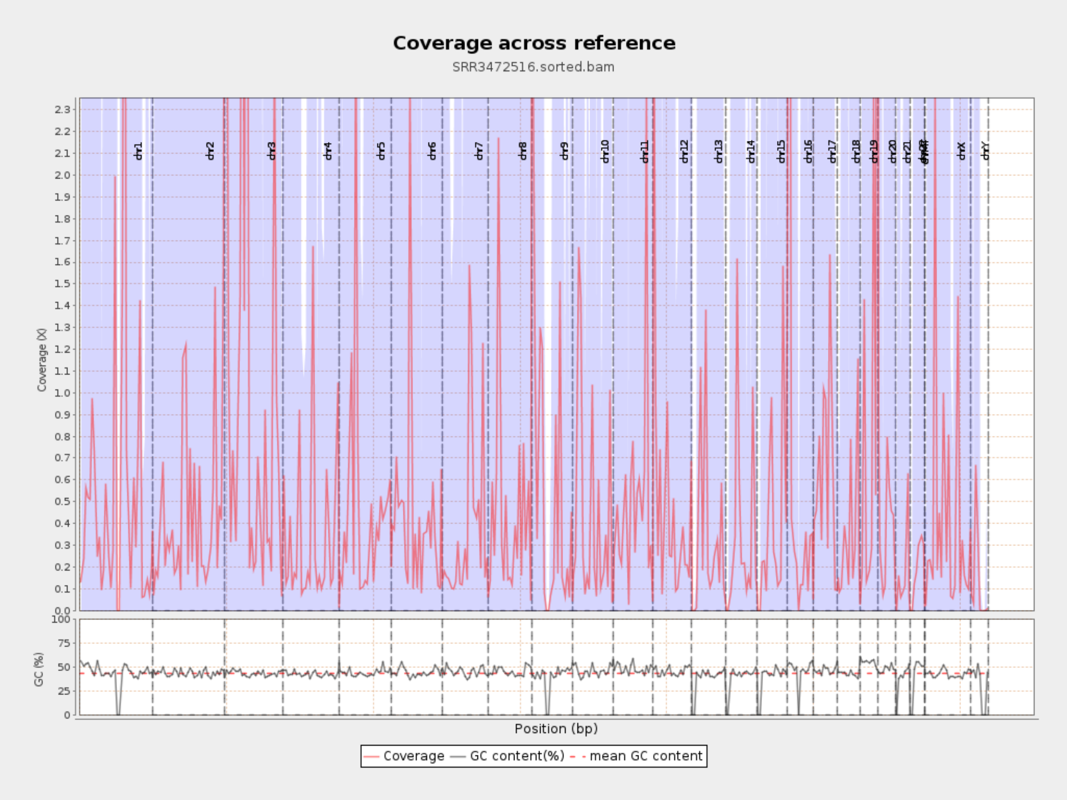
2.7. Chromosome stats

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

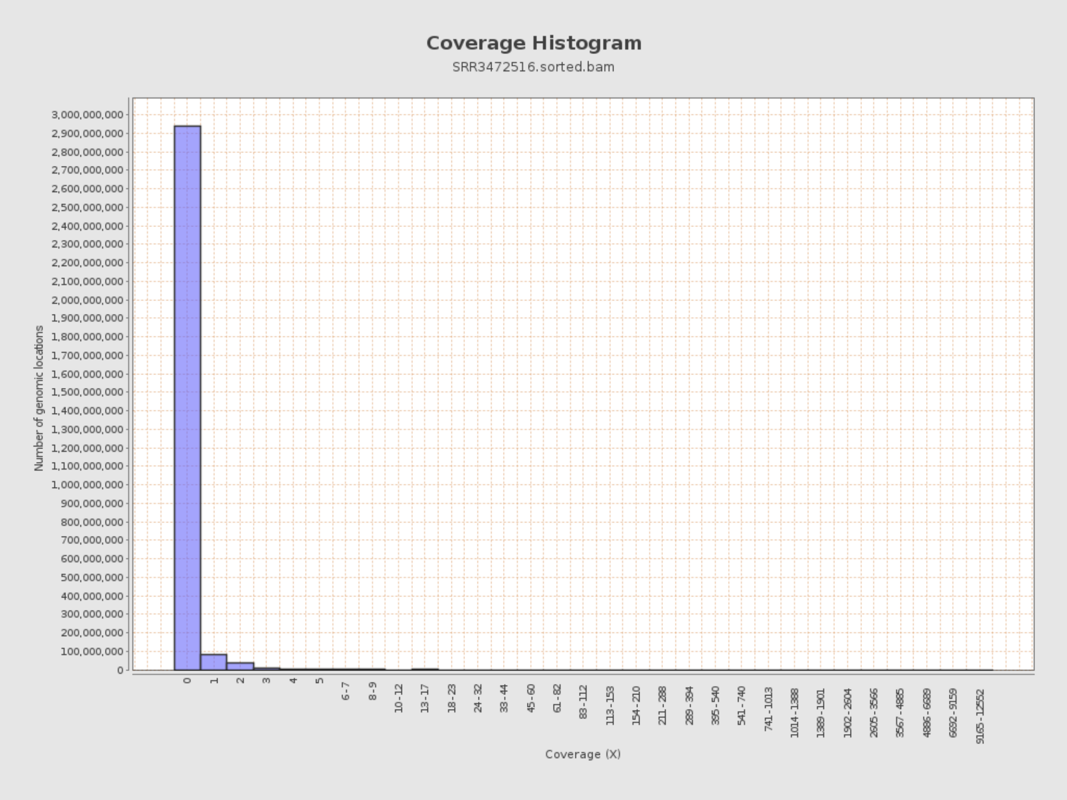
		bases	coverage	deviation
chr1	249250621	143666005	0.5764	30.0229
chr2	243199373	105590172	0.4342	21.3416
chr3	198022430	231631481	1.1697	27.3036
chr4	191154276	64307643	0.3364	13.891
chr5	180915260	86421646	0.4777	14.4011
chr6	171115067	73766091	0.4311	14.0276
chr7	159138663	61751783	0.388	13.1911
chr8	146364022	65014109	0.4442	15.2808
chr9	141213431	84326448	0.5972	20.8262
chr10	135534747	60117129	0.4436	24.2368
chr11	135006516	70265089	0.5205	23.2069
chr12	133851895	67352059	0.5032	20.3361
chr13	115169878	39490942	0.3429	14.1925
chr14	107349540	37244124	0.3469	12.4088
chr15	102531392	41536718	0.4051	16.076
chr16	90354753	68704359	0.7604	40.9787
chr17	81195210	51583721	0.6353	15.1509
chr18	78077248	27455107	0.3516	10.3347
chr19	59128983	53146108	0.8988	36.112
chr20	63025520	25459820	0.404	12.2603
chr21	48129895	8462701	0.1758	8.3
chr22	51304566	9679277	0.1887	7.1071
chrMT	16571	1774	0.1071	0.3476
chrX	155270560	65152643	0.4196	19.3045

chrY	59373566	8638501	0.1455	9.408

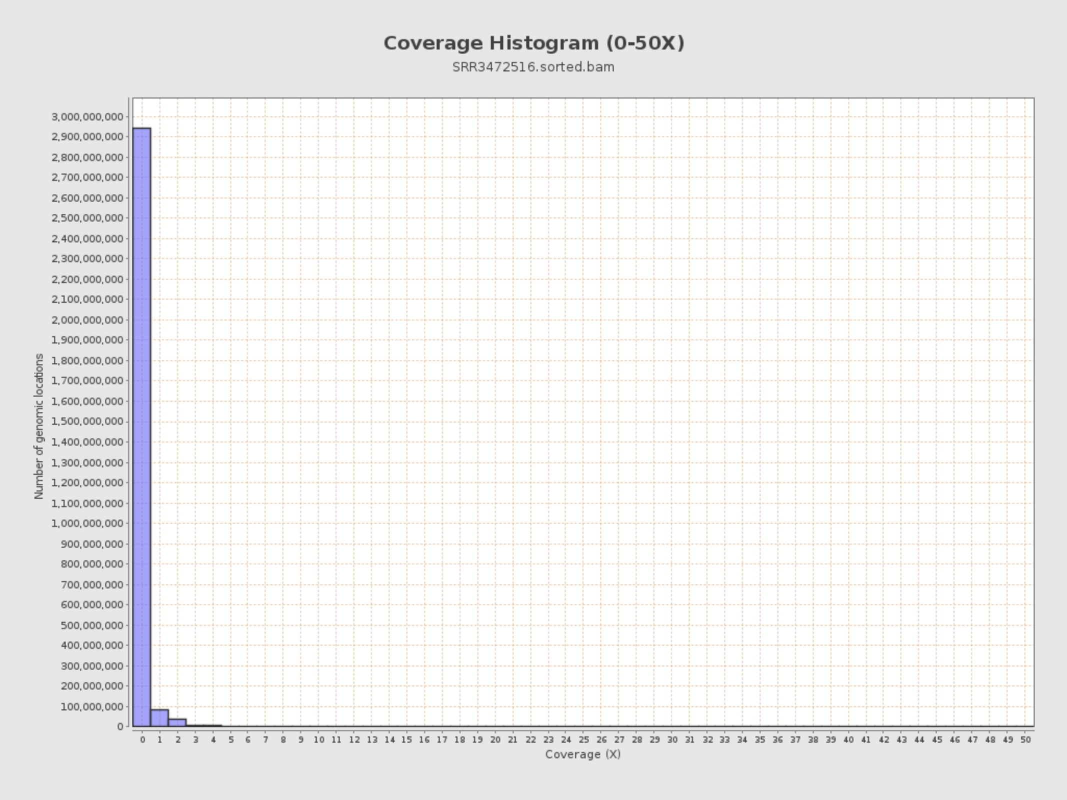
3. Results : Coverage across reference



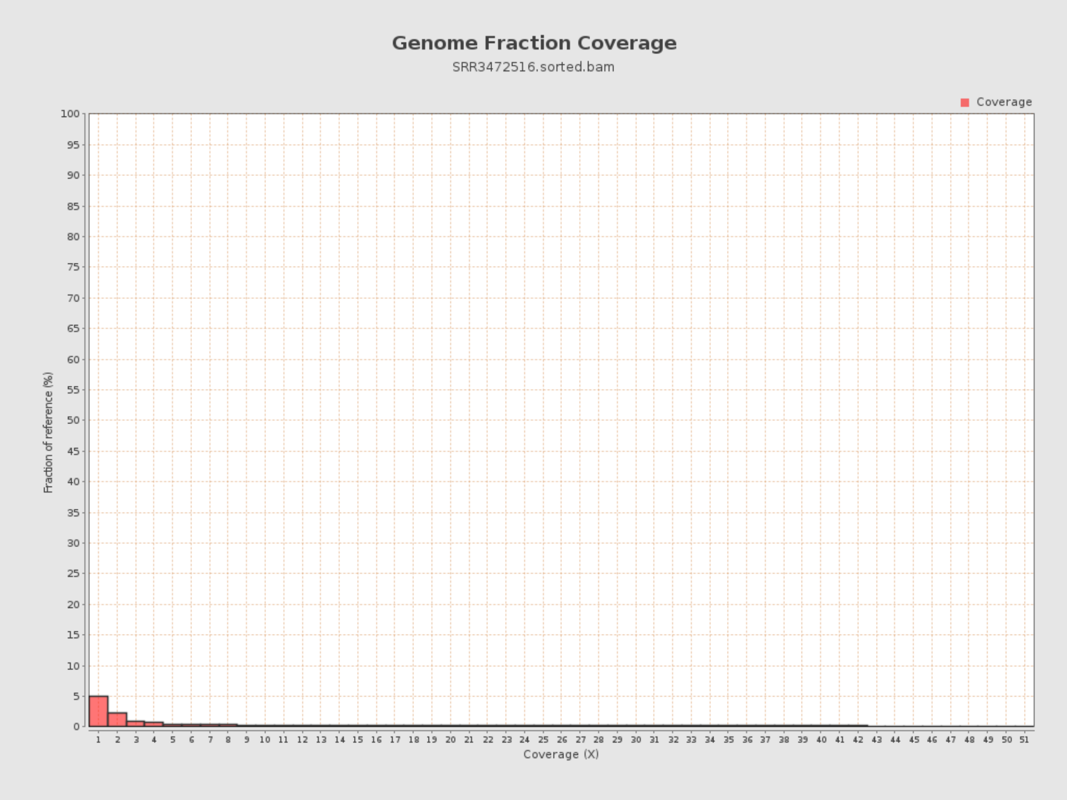
4. Results : Coverage Histogram



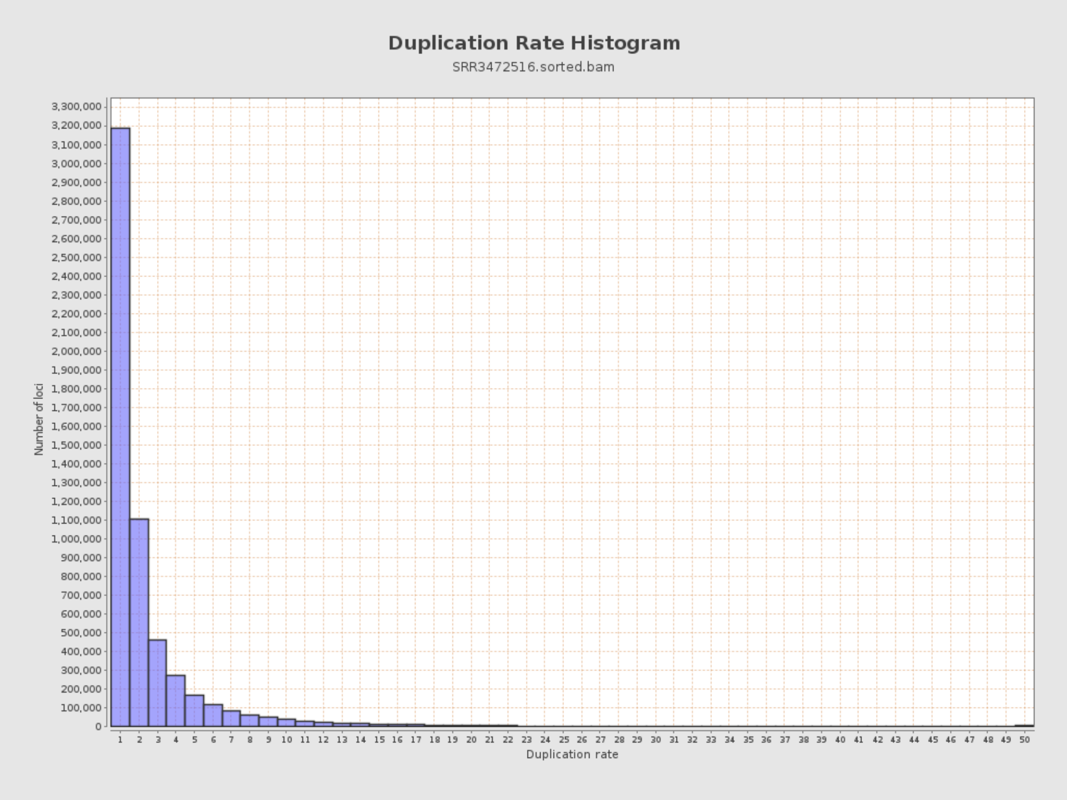
5. Results : Coverage Histogram (0-50X)



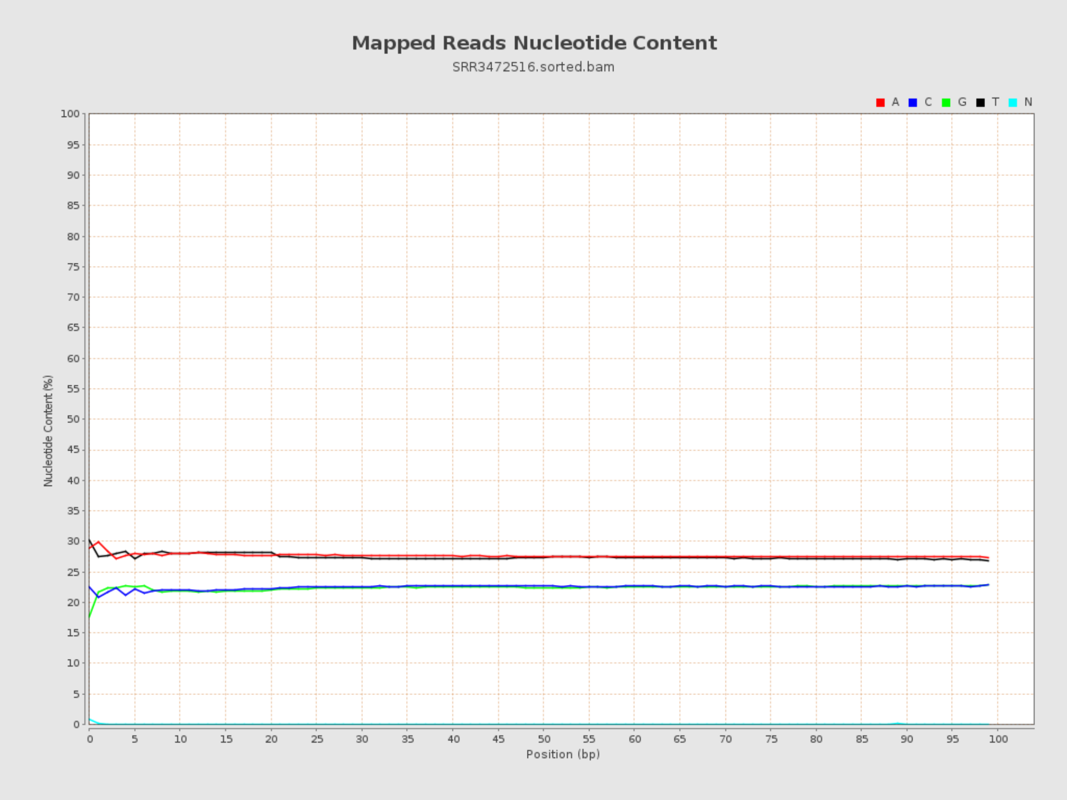
6. Results : Genome Fraction Coverage



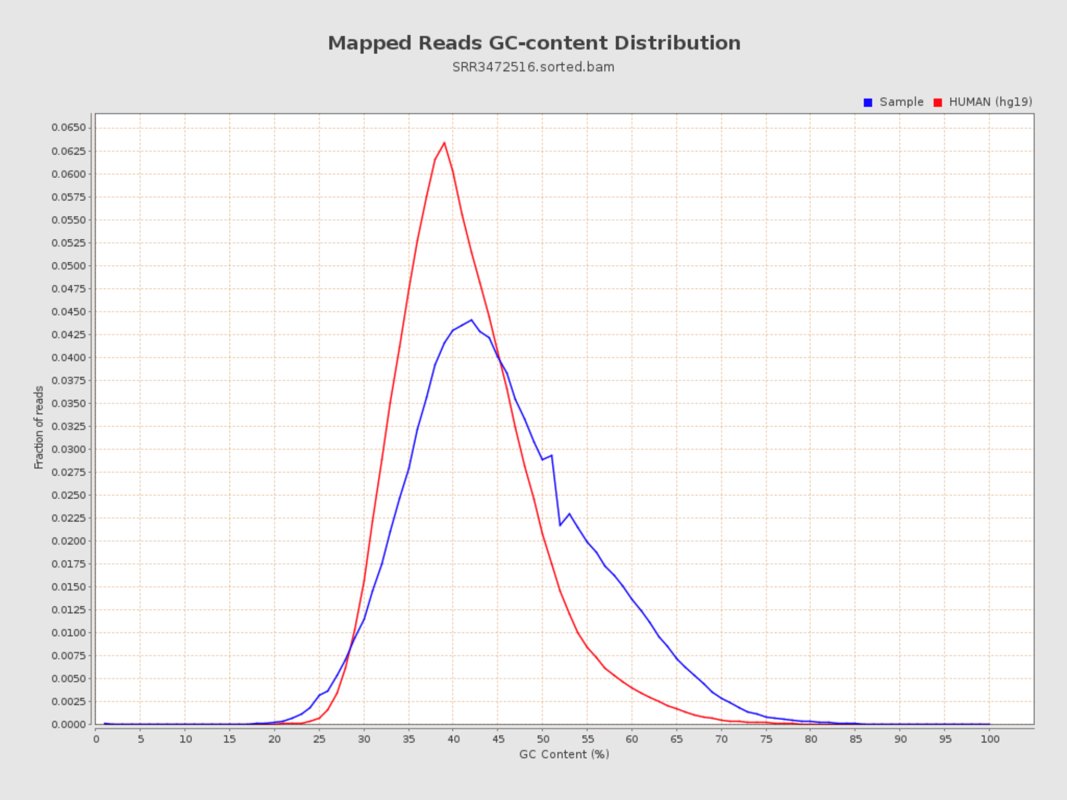
7. Results : Duplication Rate Histogram



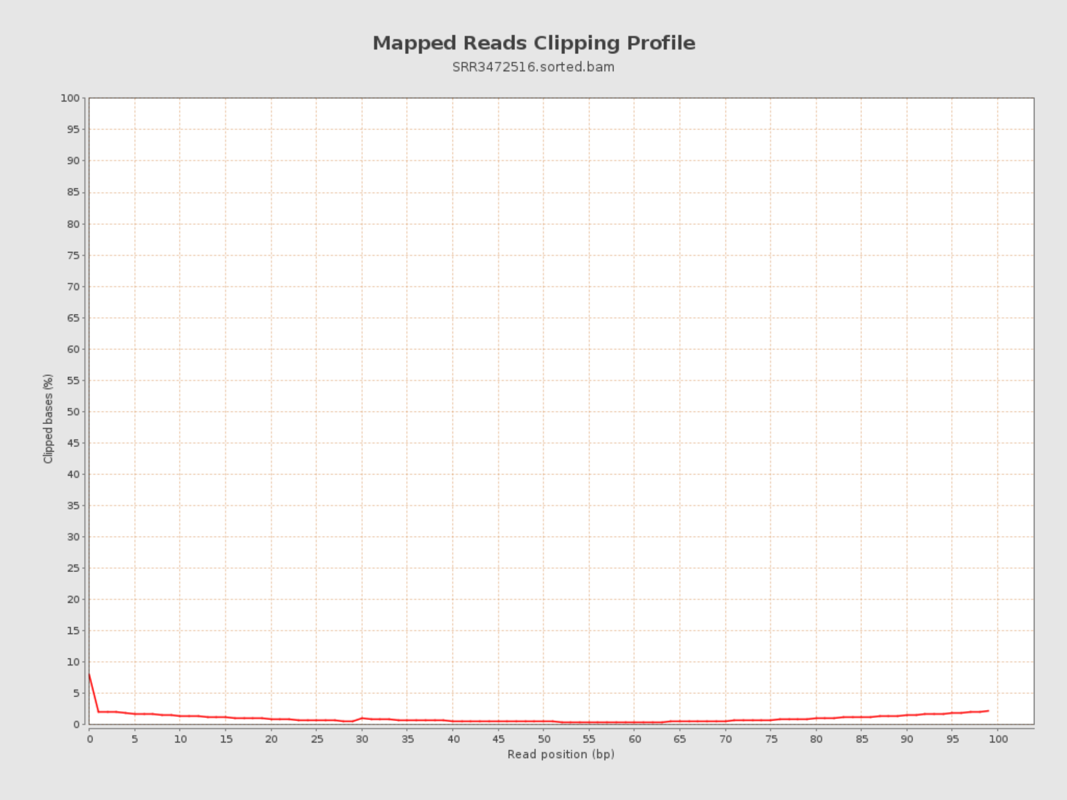
8. Results : Mapped Reads Nucleotide Content



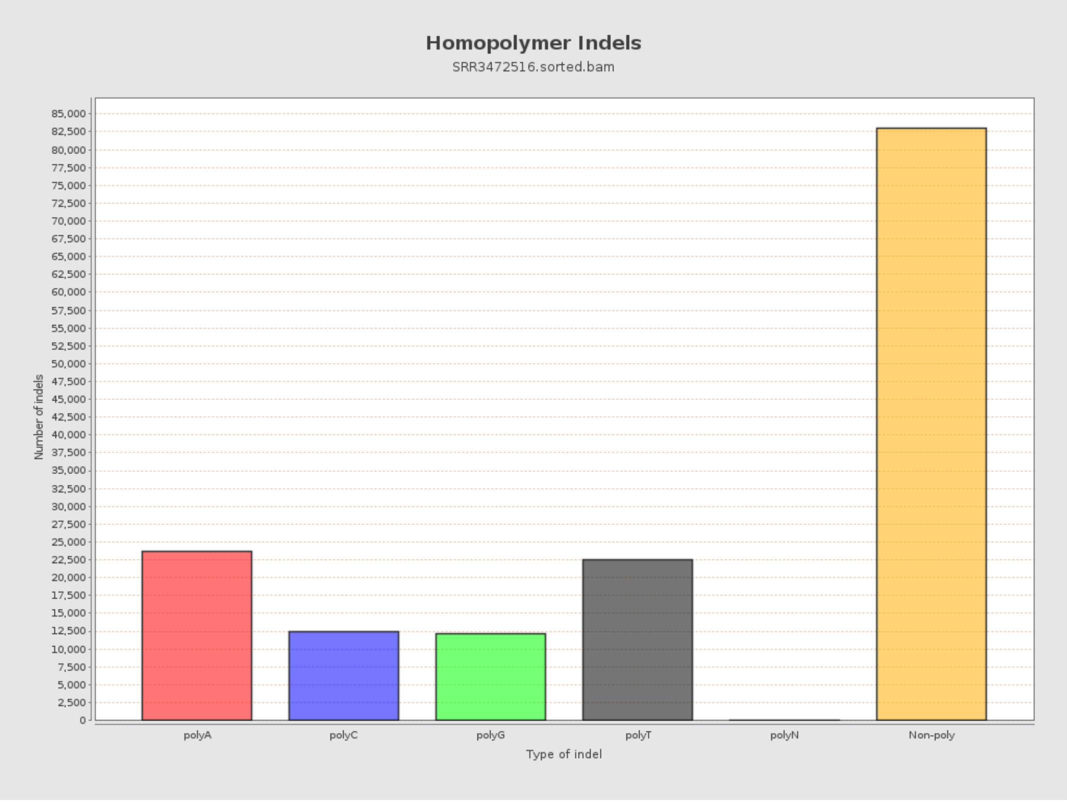
9. Results : Mapped Reads GC-content Distribution



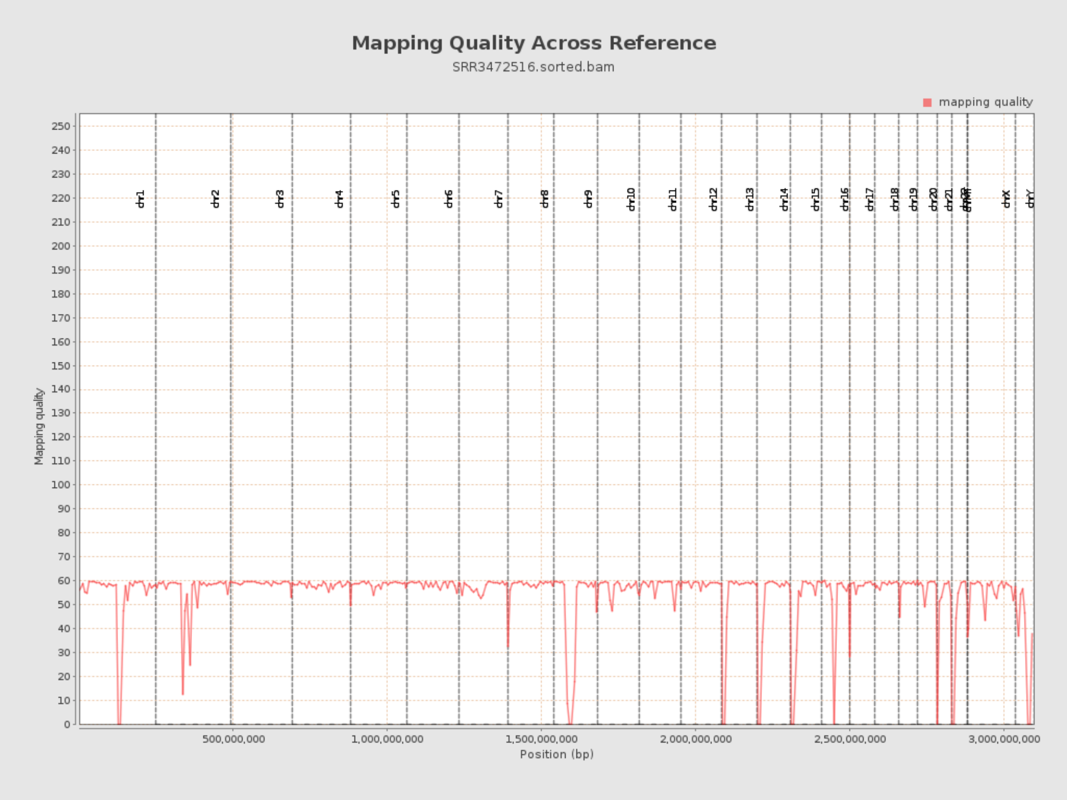
10. Results : Mapped Reads Clipping Profile



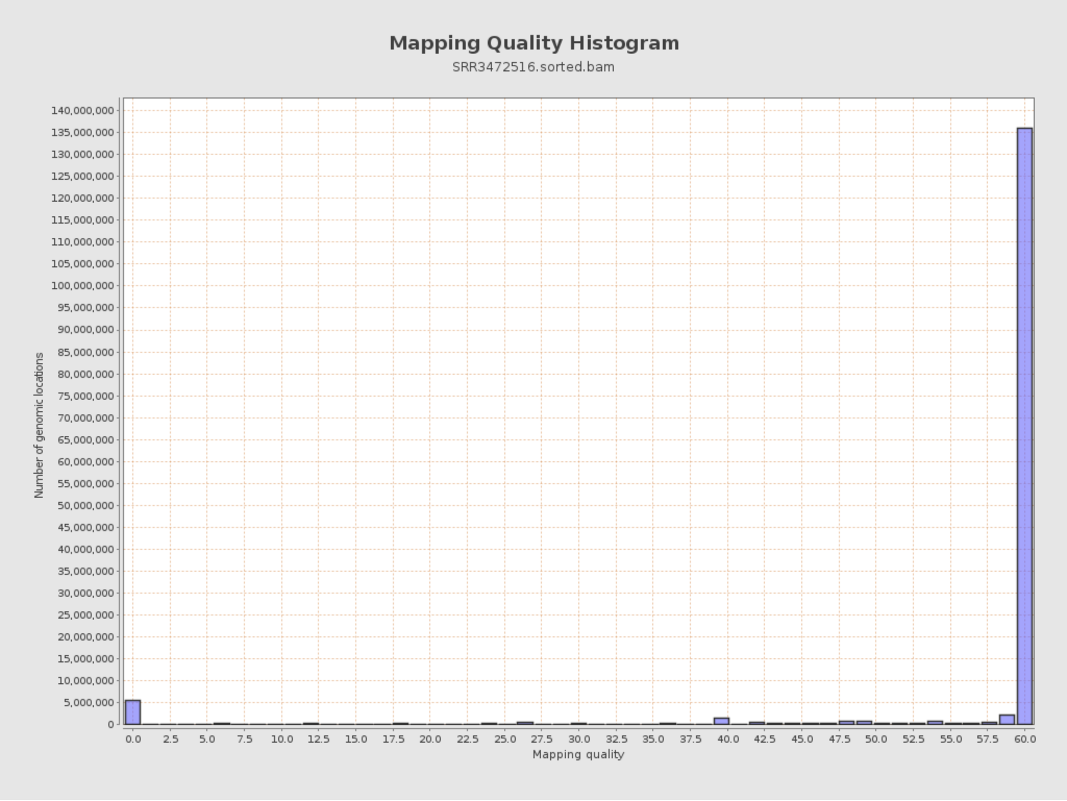
11. Results : Homopolymer Indels



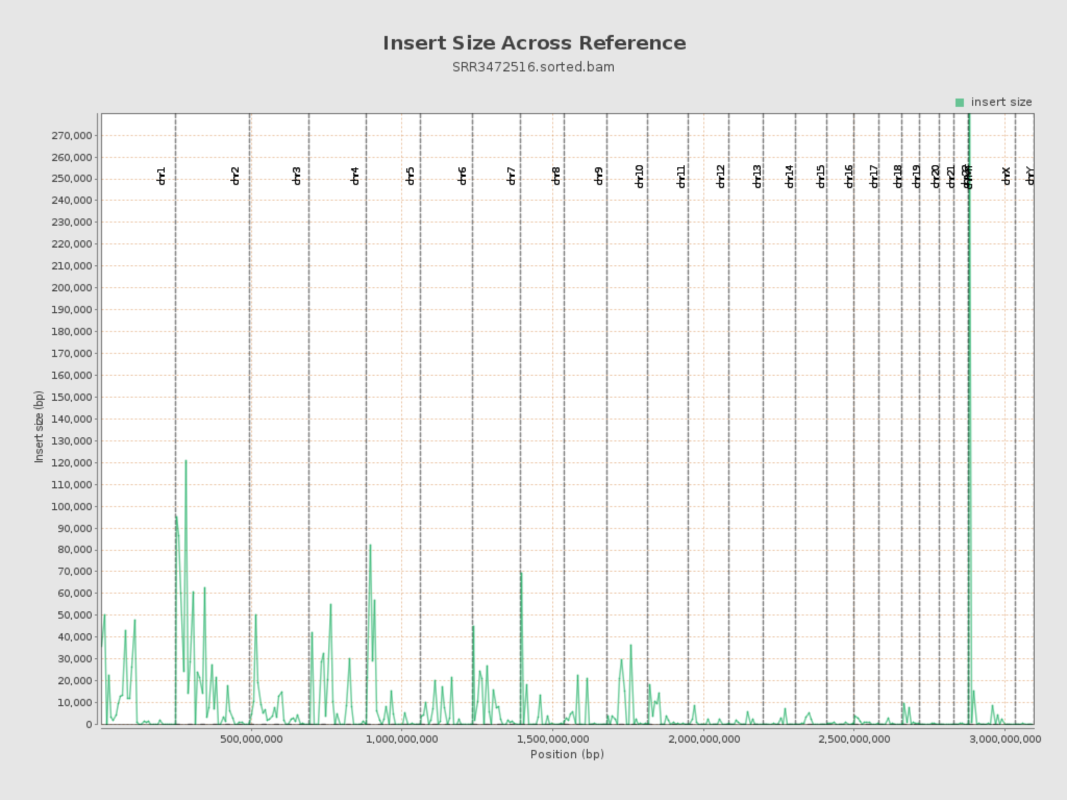
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram