Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/08 06:44:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124849.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_SRR3124849 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124849_1.fastq.gz SRR3124849_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Dec 08 06:44:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124849.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	78,608,894
Mapped reads	75,194,307 / 95.66%
Unmapped reads	3,414,587 / 4.34%
Mapped paired reads	75,194,307 / 95.66%
Mapped reads, first in pair	38,121,508 / 48.5%
Mapped reads, second in pair	37,072,799 / 47.16%
Mapped reads, both in pair	73,909,484 / 94.02%
Mapped reads, singletons	1,284,823 / 1.63%
Secondary alignments	0
Supplementary alignments	1,583,212 / 2.01%
Read min/max/mean length	30 / 150 / 150.96
Duplicated reads (estimated)	32,235,030 / 41.01%
Duplication rate	34.46%
Clipped reads	55,921,472 / 71.14%

2.2. ACGT Content

Number/percentage of A's	2,669,522,937 / 29.21%
Number/percentage of C's	1,807,302,732 / 19.78%
Number/percentage of T's	2,691,631,959 / 29.45%
Number/percentage of G's	1,969,771,420 / 21.55%
Number/percentage of N's	133,977 / 0%

GC Percentage	41.33%

2.3. Coverage

Mean	2.9541
Standard Deviation	37.3372

2.4. Mapping Quality

Mean Mapping Quality	53.2

2.5. Insert size

Mean	80,594.06
Standard Deviation	2,696,717.03
P25/Median/P75	115 / 157 / 216

2.6. Mismatches and indels

General error rate	1.18%
Mismatches	103,543,204
Insertions	1,612,646
Mapped reads with at least one insertion	2%
Deletions	3,026,570
Mapped reads with at least one deletion	3.86%
Homopolymer indels	43.51%

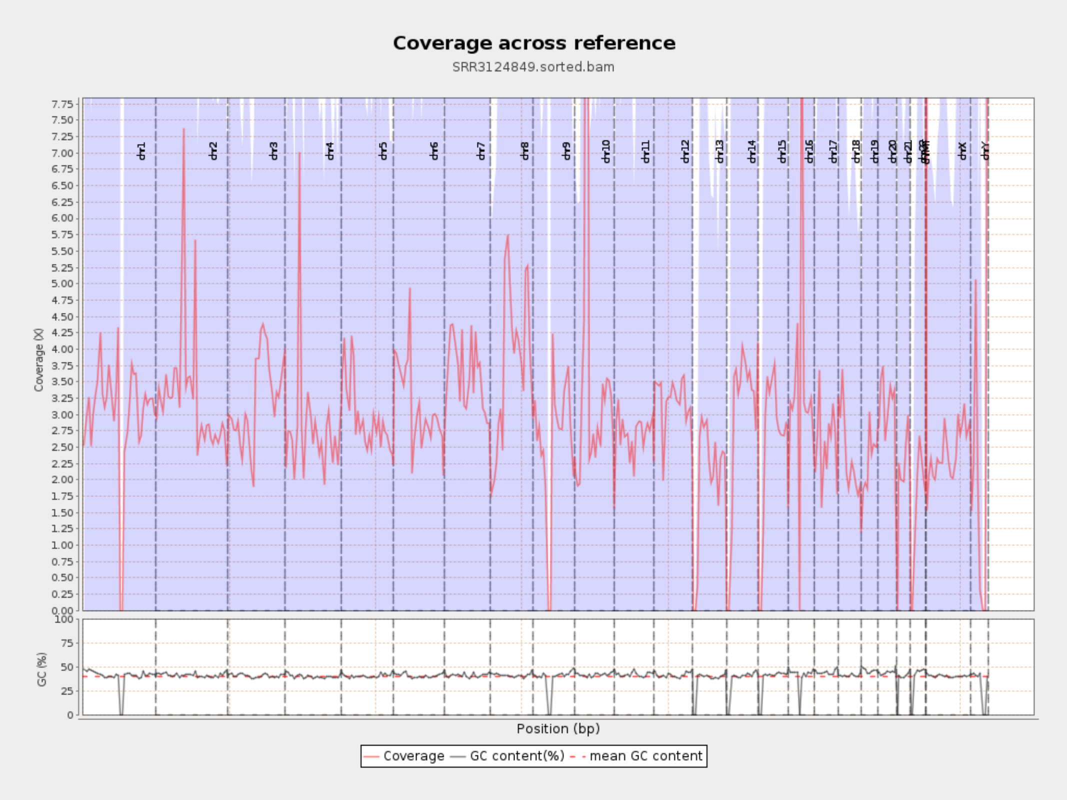
2.7. Chromosome stats

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

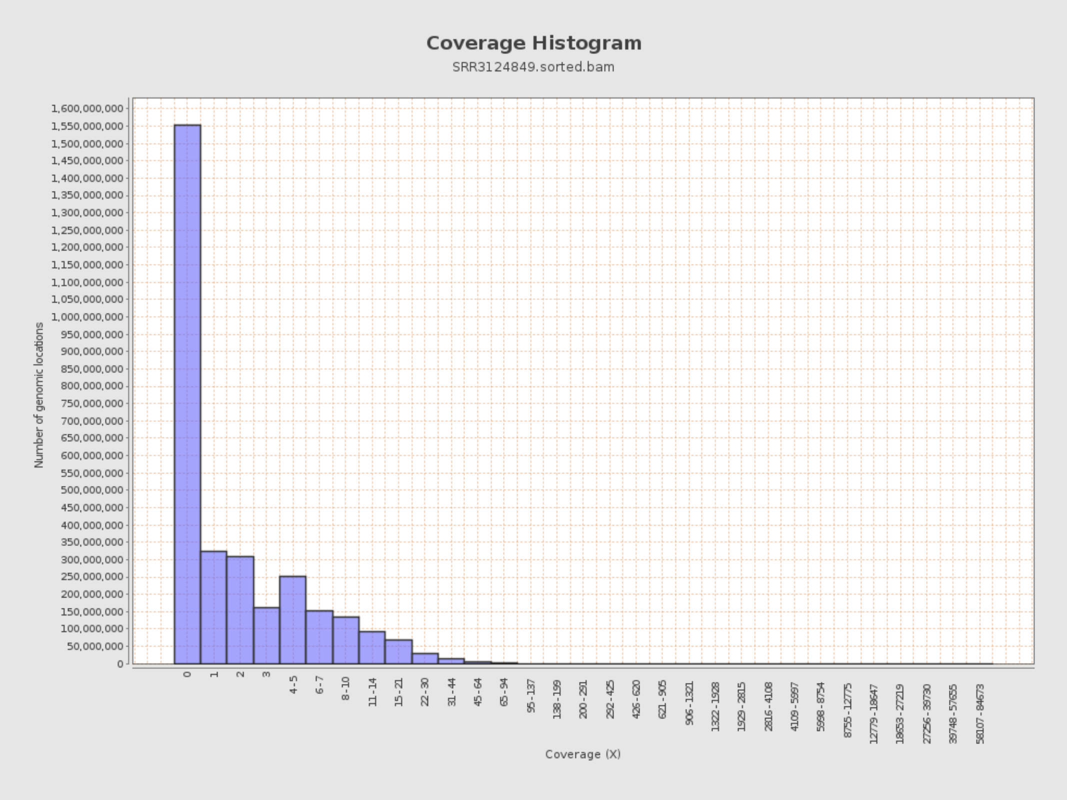
		bases	coverage	deviation
chr1	249250621	751396767	3.0146	26.4302
chr2	243199373	806778079	3.3174	44.7517
chr3	198022430	635421206	3.2088	7.4527
chr4	191154276	532894974	2.7878	28.6518
chr5	180915260	535658755	2.9608	6.674
chr6	171115067	540387988	3.158	14.1471
chr7	159138663	571270164	3.5898	25.7083
chr8	146364022	556550759	3.8025	11.2131
chr9	141213431	367352579	2.6014	37.149
chr10	135534747	493787239	3.6433	131.1854
chr11	135006516	364581753	2.7005	13.9073
chr12	133851895	430886872	3.2191	6.2924
chr13	115169878	230926832	2.0051	4.4668
chr14	107349540	312243128	2.9087	7.3616
chr15	102531392	258747848	2.5236	5.9361
chr16	90354753	316643210	3.5044	58.441
chr17	81195210	210006671	2.5864	25.4948
chr18	78077248	188256461	2.4112	36.7235
chr19	59128983	134179973	2.2693	15.7365
chr20	63025520	198447489	3.1487	11.511
chr21	48129895	101400339	2.1068	16.3284
chr22	51304566	80781752	1.5746	6.1
chrMT	16571	2258948	136.3194	74.9687
chrX	155270560	377415456	2.4307	8.5481

chrY	59373566	146662428	2.4702	62.6769

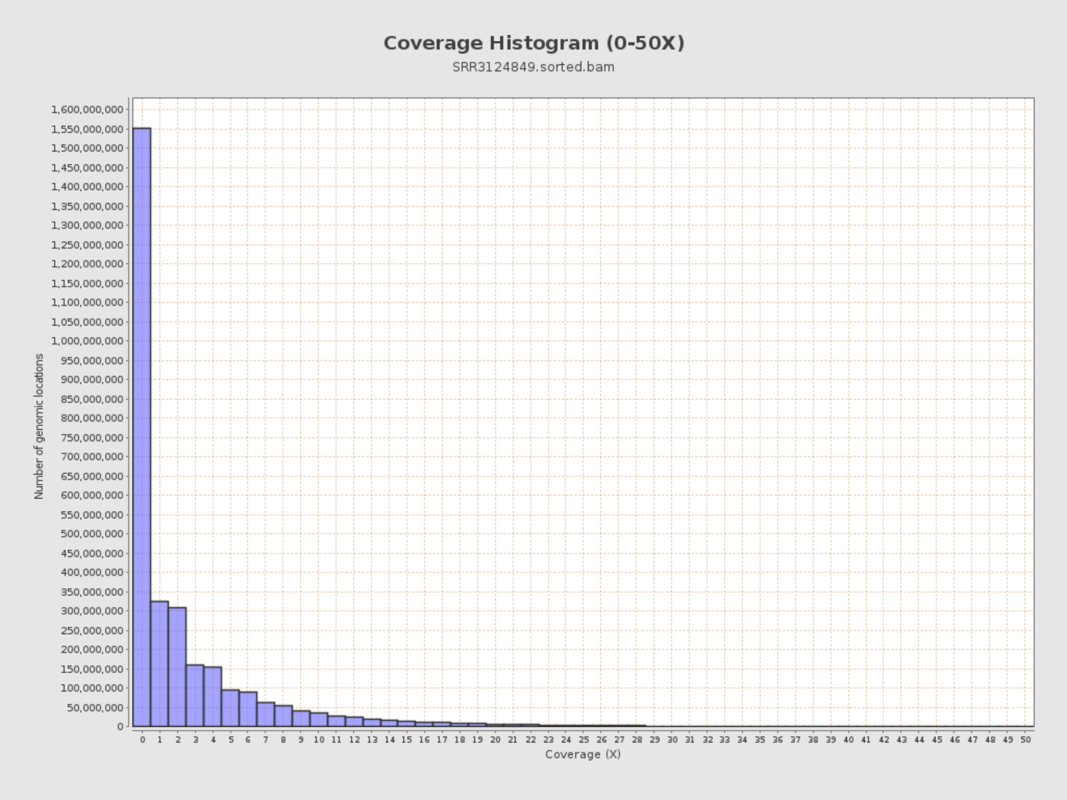
3. Results : Coverage across reference



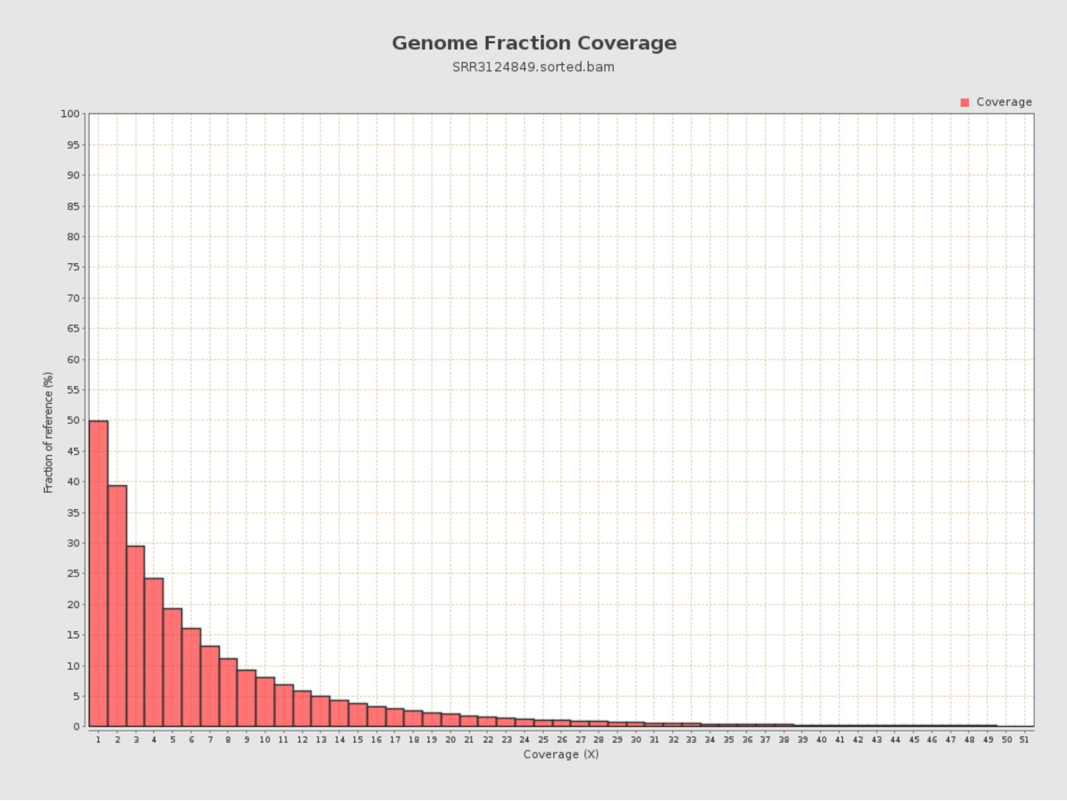
4. Results : Coverage Histogram



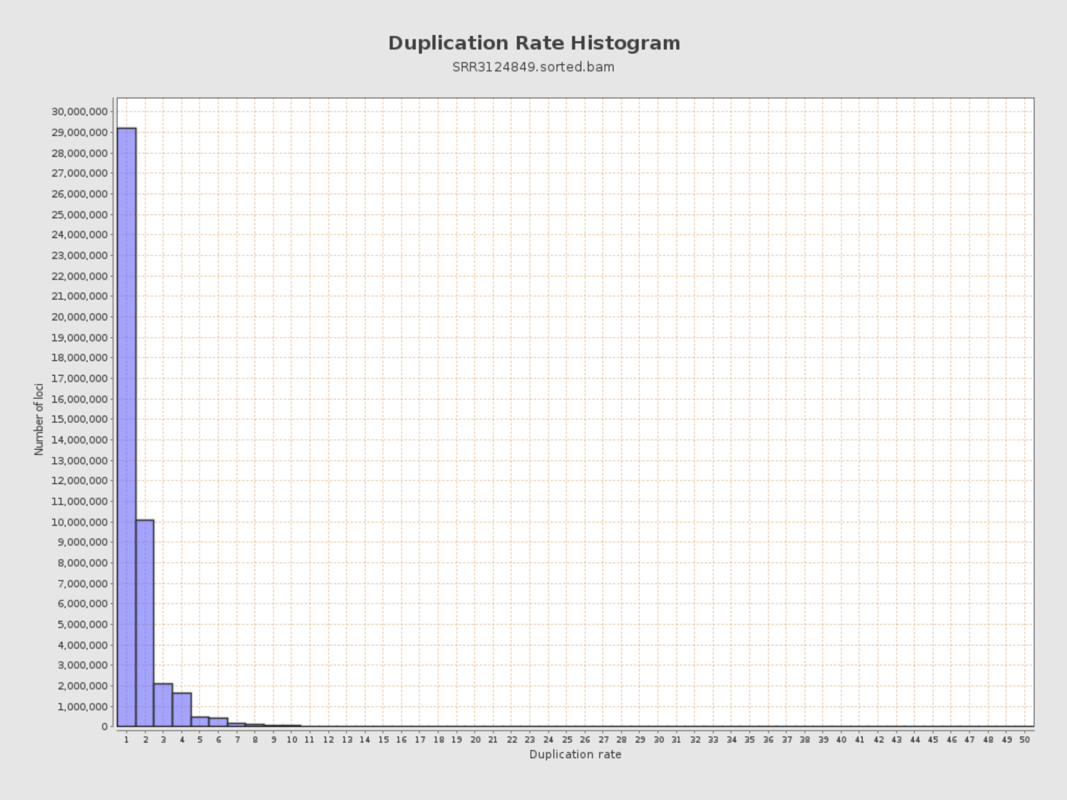
5. Results : Coverage Histogram (0-50X)



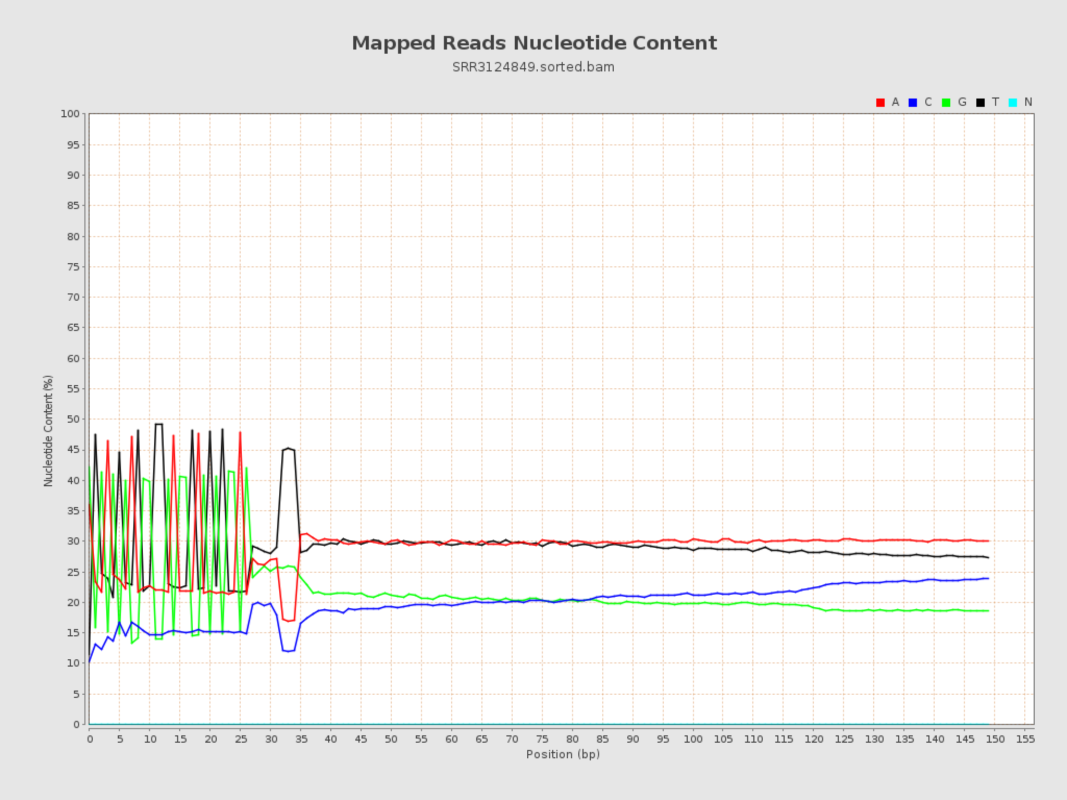
6. Results : Genome Fraction Coverage



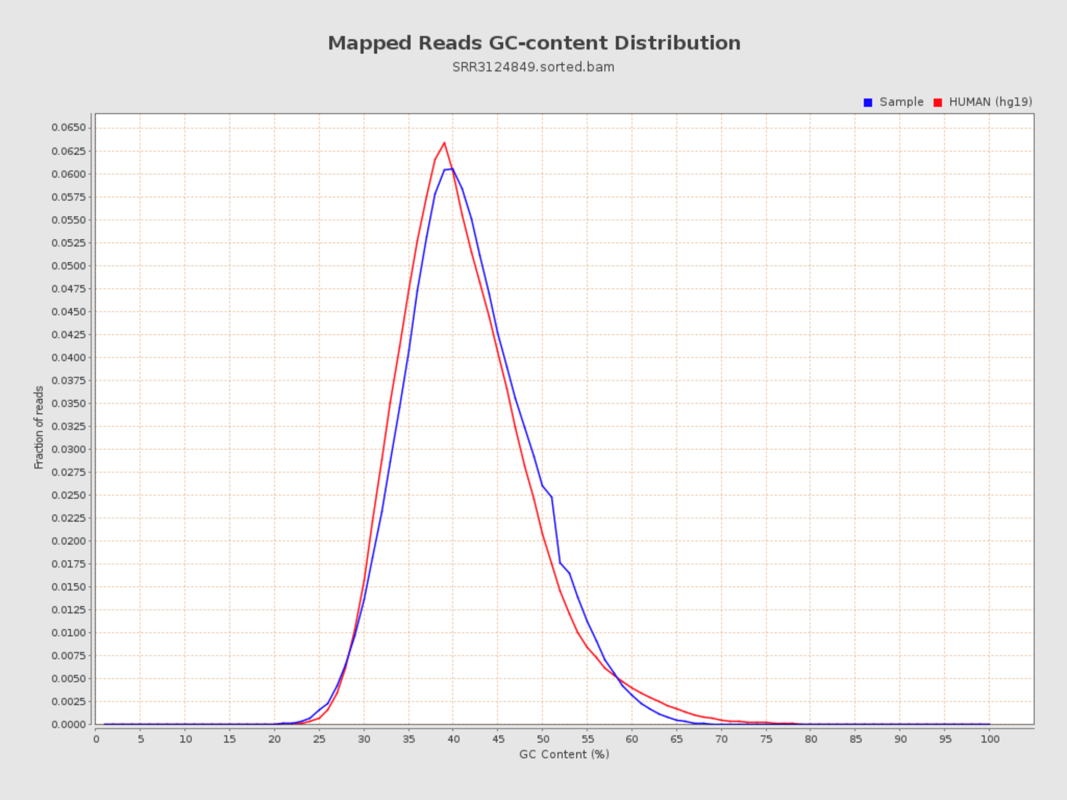
7. Results : Duplication Rate Histogram



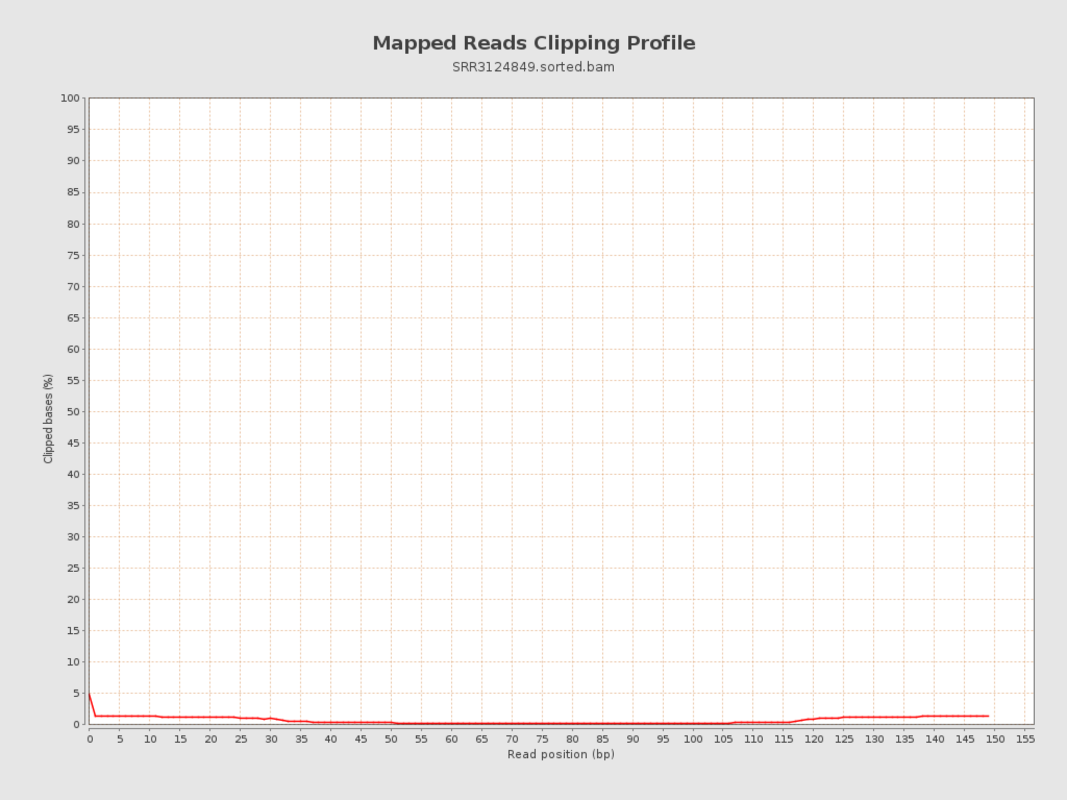
8. Results : Mapped Reads Nucleotide Content



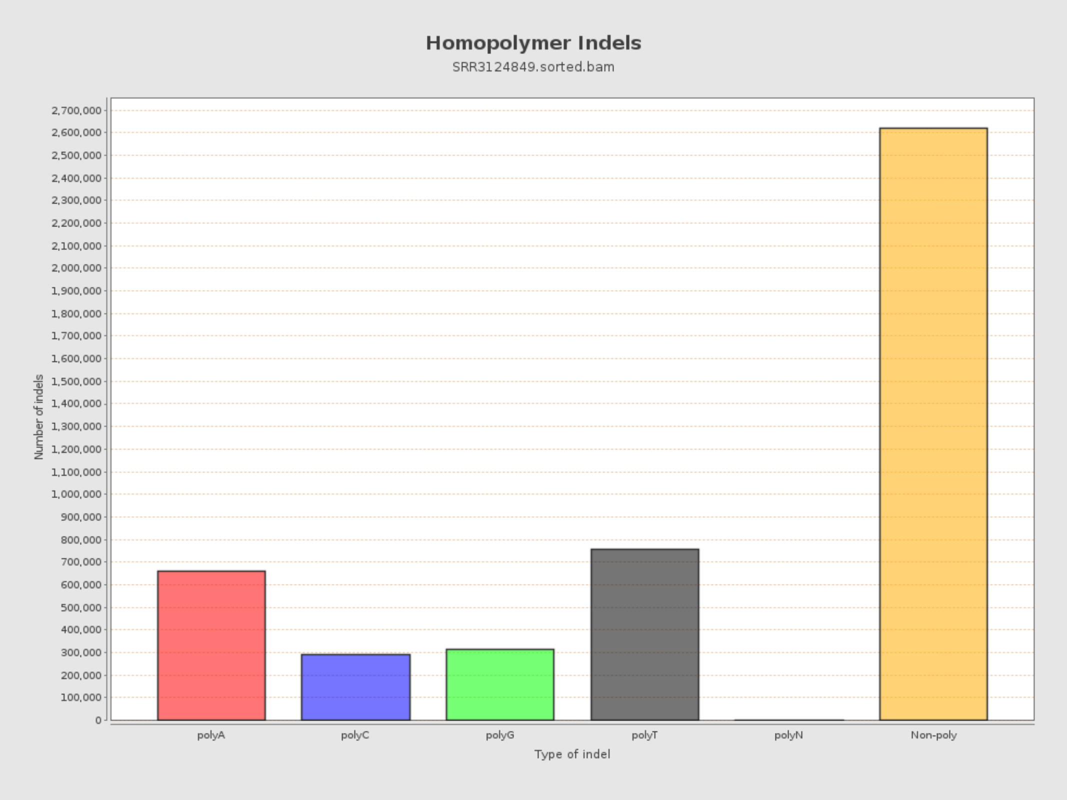
9. Results : Mapped Reads GC-content Distribution



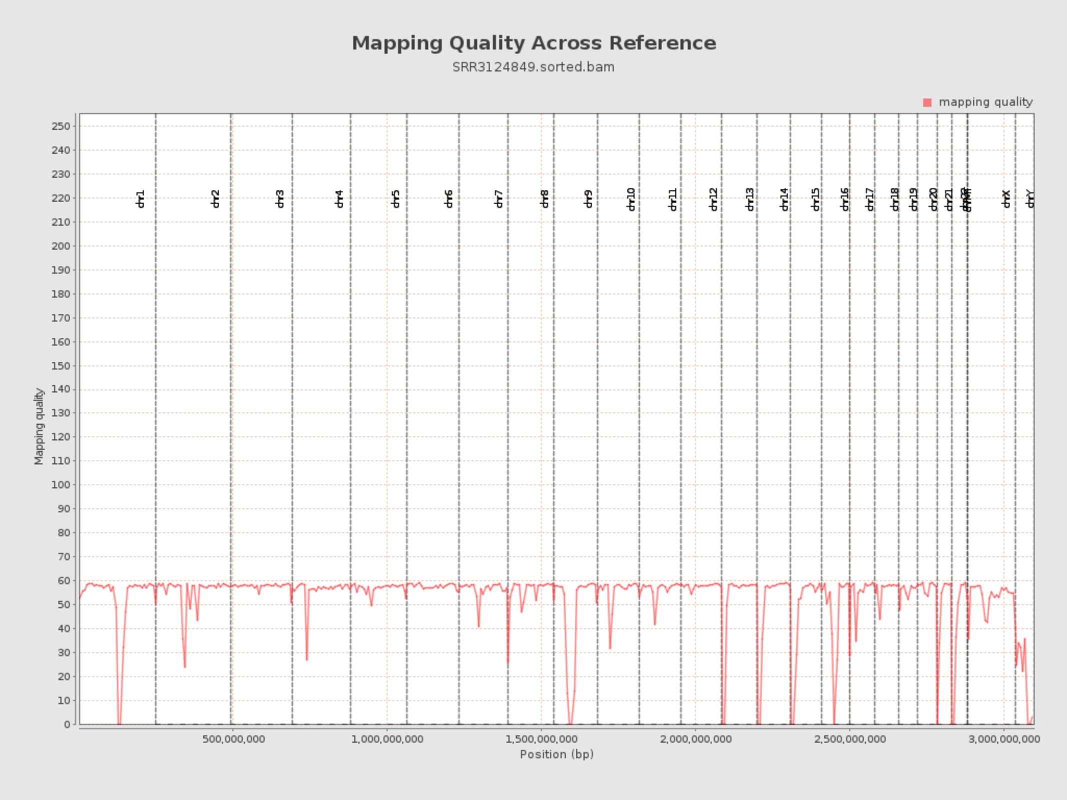
10. Results : Mapped Reads Clipping Profile



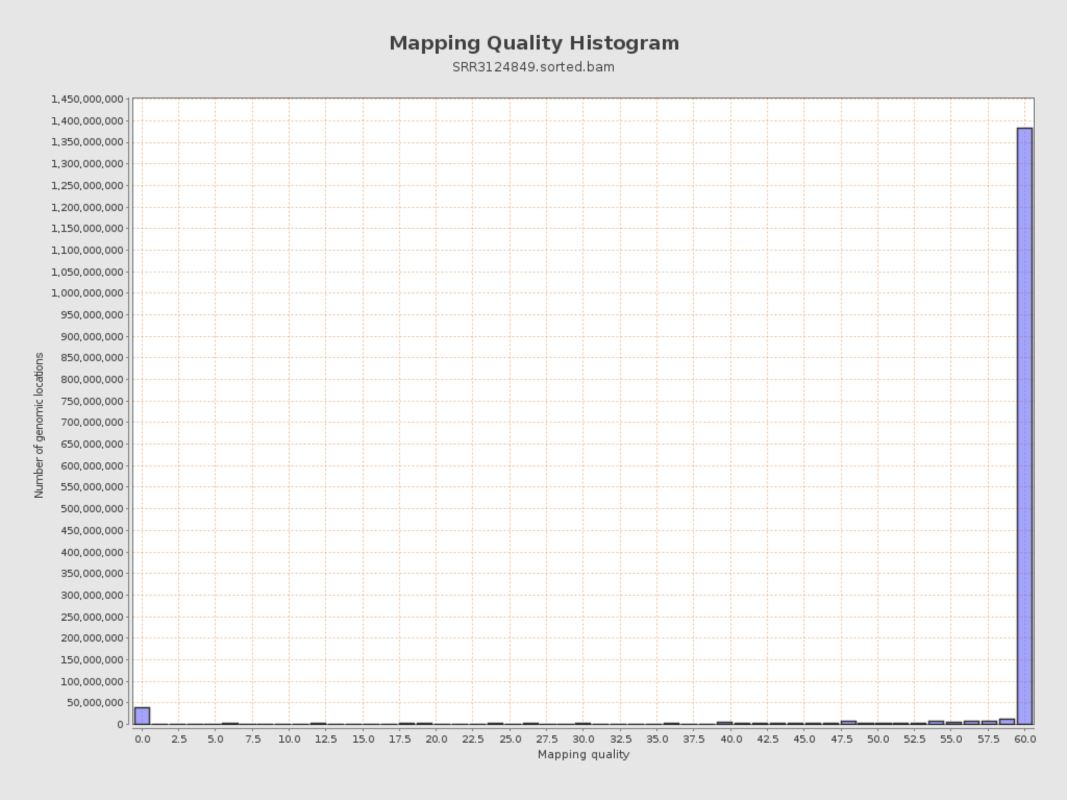
11. Results : Homopolymer Indels



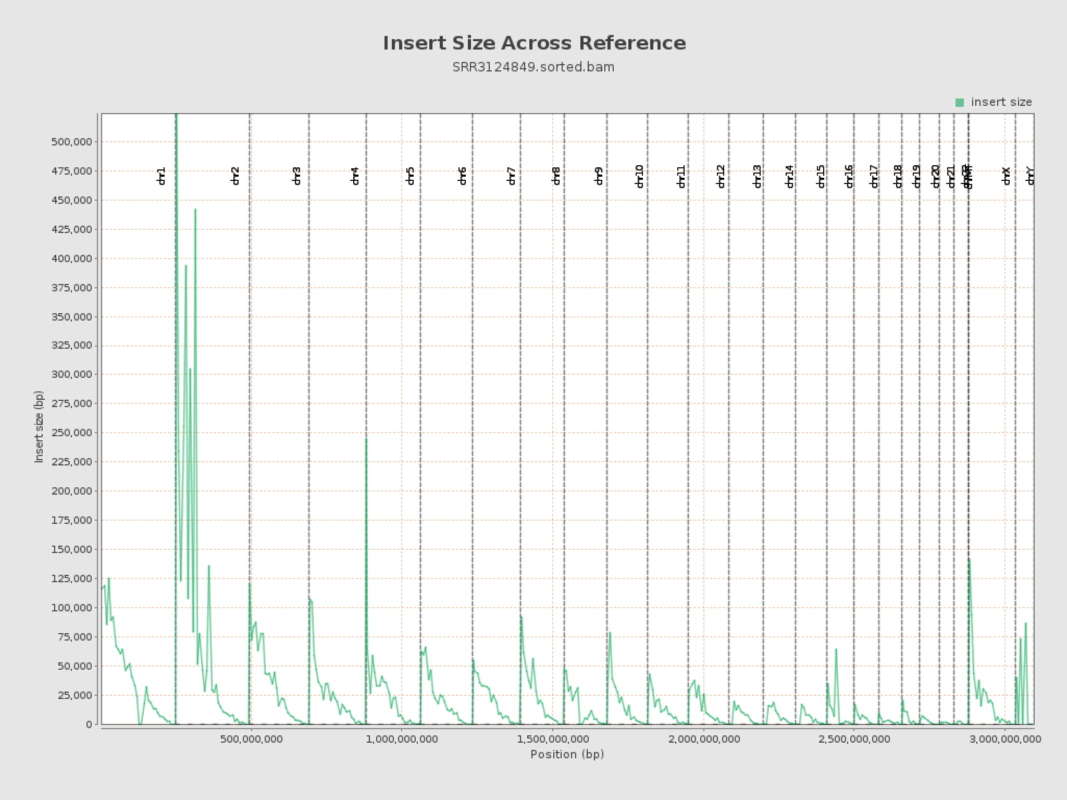
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram