Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/04 21:13:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124815.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_SRR3124815 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124815_1.fastq.gz SRR3124815_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Dec 04 21:13:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124815.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	28,104,362
Mapped reads	27,797,247 / 98.91%
Unmapped reads	307,115 / 1.09%
Mapped paired reads	27,797,247 / 98.91%
Mapped reads, first in pair	13,932,125 / 49.57%
Mapped reads, second in pair	13,865,122 / 49.33%
Mapped reads, both in pair	27,652,186 / 98.39%
Mapped reads, singletons	145,061 / 0.52%
Secondary alignments	0
Supplementary alignments	138,390 / 0.49%
Read min/max/mean length	30 / 101 / 101.19
Duplicated reads (estimated)	6,236,990 / 22.19%
Duplication rate	13.08%
Clipped reads	13,940,162 / 49.6%

2.2. ACGT Content

Number/percentage of A's	685,681,361 / 28.6%
Number/percentage of C's	430,453,051 / 17.96%
Number/percentage of T's	733,382,329 / 30.59%
Number/percentage of G's	547,552,100 / 22.84%
Number/percentage of N's	20,229 / 0%

GC Percentage	40.8%

2.3. Coverage

Mean	0.7747
Standard Deviation	12.1218

2.4. Mapping Quality

Mean Mapping Quality	52.62

2.5. Insert size

Mean	35,350.81
Standard Deviation	1,716,865.34
P25/Median/P75	152 / 202 / 277

2.6. Mismatches and indels

General error rate	0.78%
Mismatches	18,055,662
Insertions	301,428
Mapped reads with at least one insertion	1.06%
Deletions	732,207
Mapped reads with at least one deletion	2.58%
Homopolymer indels	47.21%

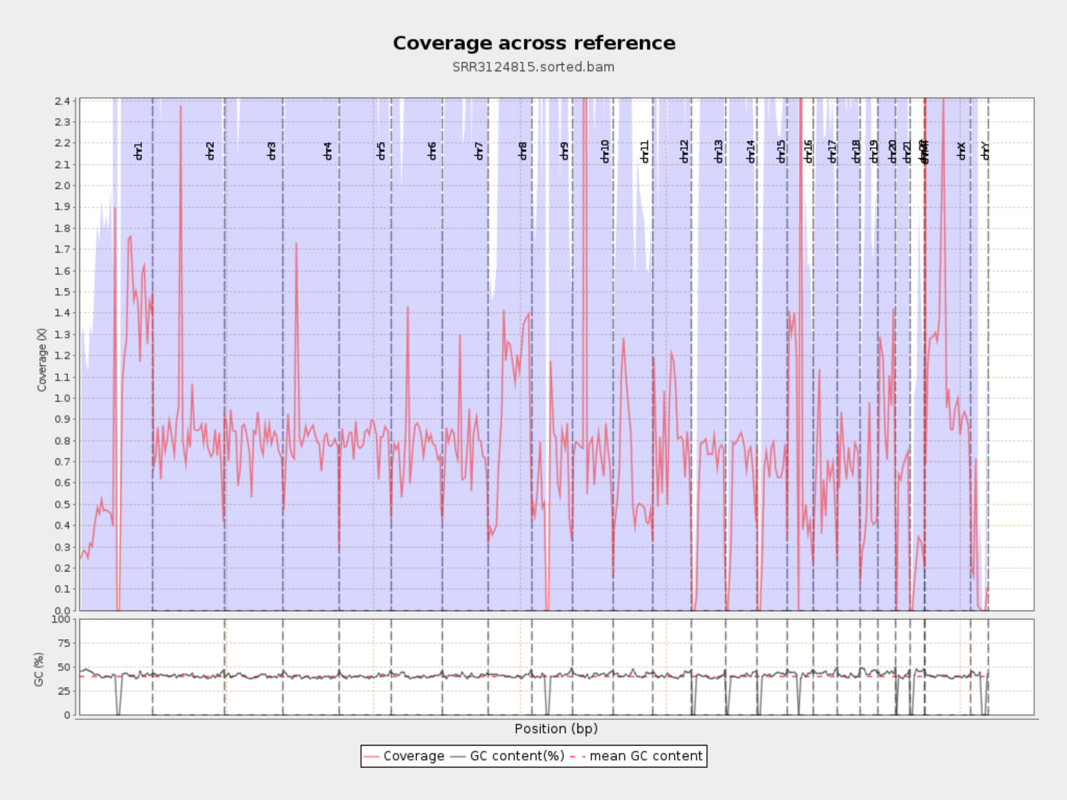
2.7. Chromosome stats

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

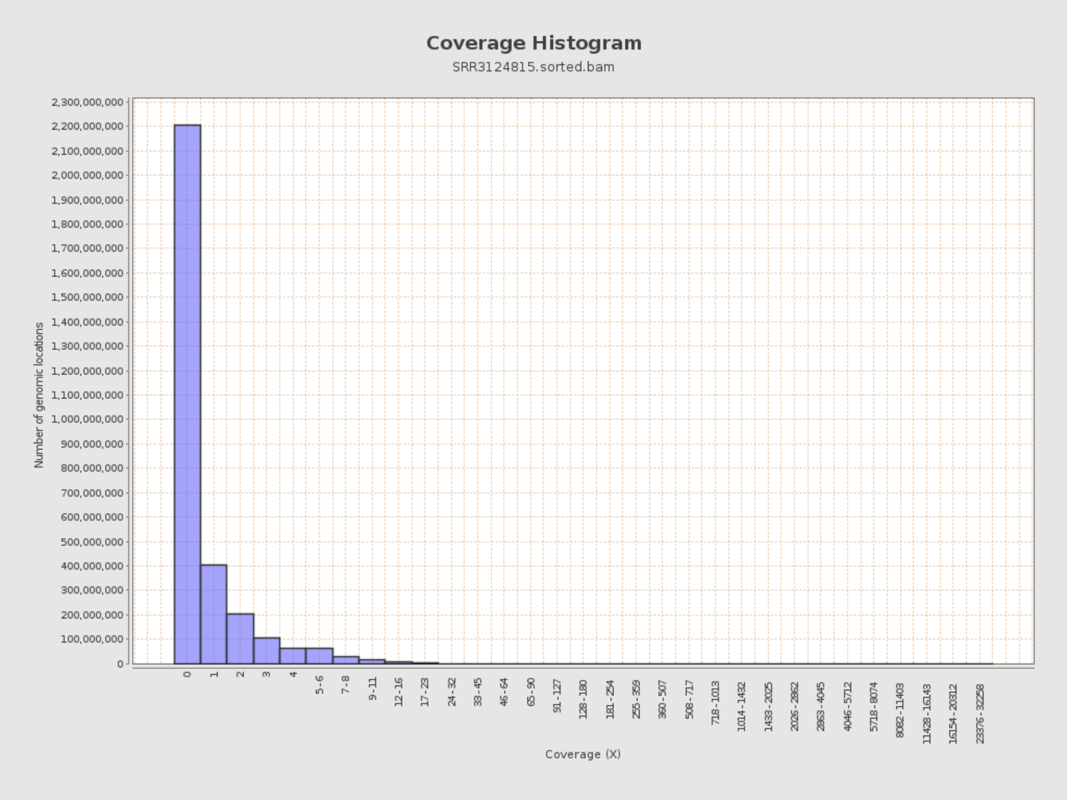
		bases	coverage	deviation
chr1	249250621	216517652	0.8687	12.8616
chr2	243199373	206411684	0.8487	10.7395
chr3	198022430	158047126	0.7981	2.2923
chr4	191154276	157235572	0.8226	5.9598
chr5	180915260	143421564	0.7928	1.8868
chr6	171115067	135297434	0.7907	7.2847
chr7	159138663	122921613	0.7724	10.4368
chr8	146364022	145380503	0.9933	4.0766
chr9	141213431	82052656	0.5811	10.1498
chr10	135534747	137363566	1.0135	44.5359
chr11	135006516	85997571	0.637	4.8591
chr12	133851895	111983354	0.8366	1.9746
chr13	115169878	70104239	0.6087	1.5286
chr14	107349540	65546659	0.6106	2.2523
chr15	102531392	57966514	0.5654	1.5471
chr16	90354753	83038913	0.919	18.0528
chr17	81195210	48791957	0.6009	9.7269
chr18	78077248	55725863	0.7137	9.7153
chr19	59128983	26560325	0.4492	7.1225
chr20	63025520	64406947	1.0219	2.6044
chr21	48129895	27878036	0.5792	3.2296
chr22	51304566	10237252	0.1995	1.0038
chrMT	16571	462437	27.9064	18.6062
chrX	155270560	176024966	1.1337	5.754

chrY	59373566	8962717	0.151	10.3644

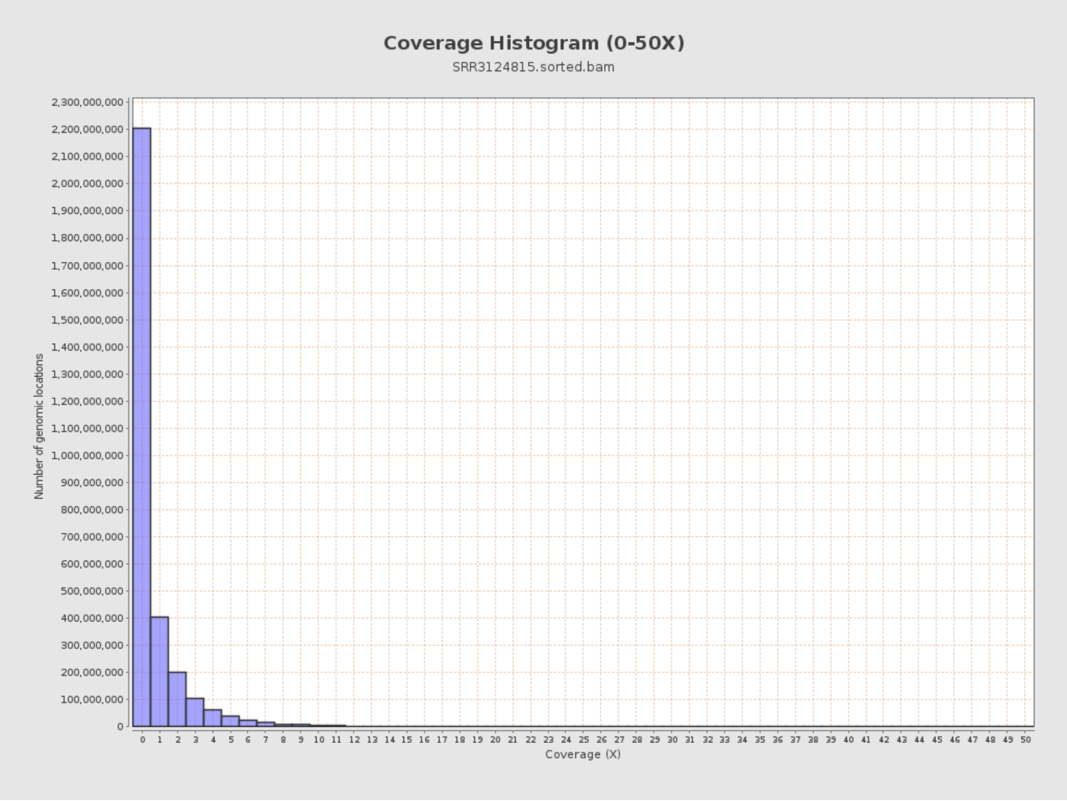
3. Results : Coverage across reference



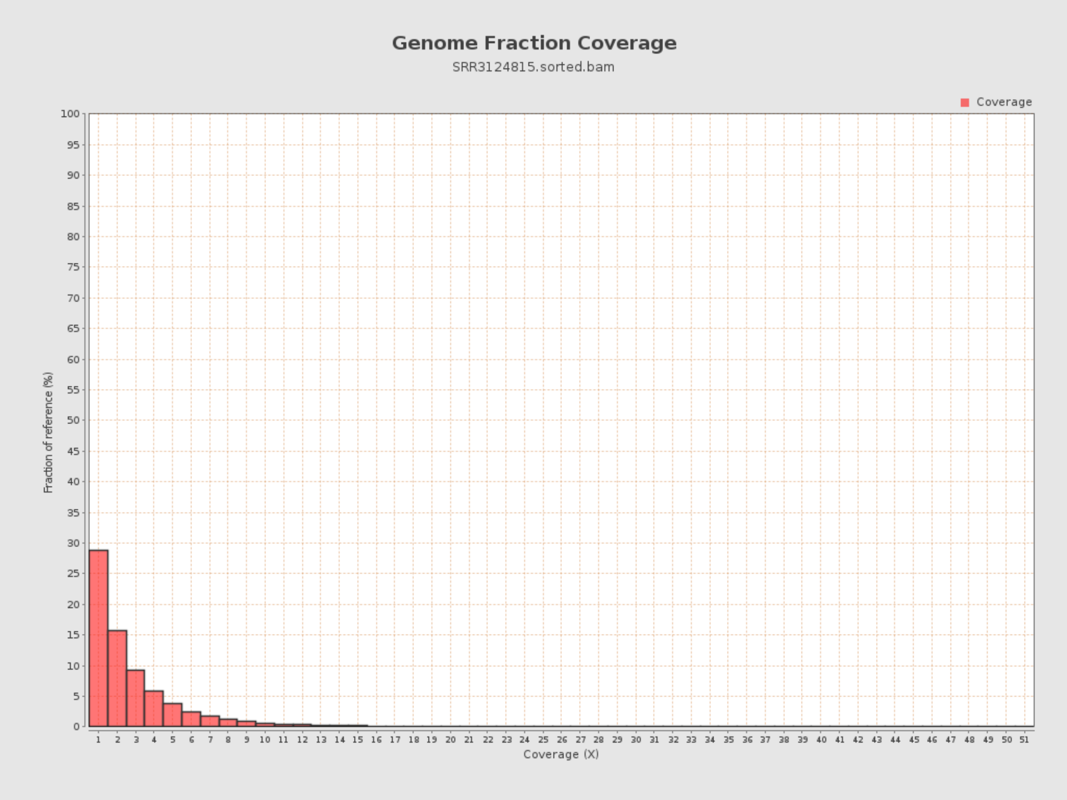
4. Results : Coverage Histogram



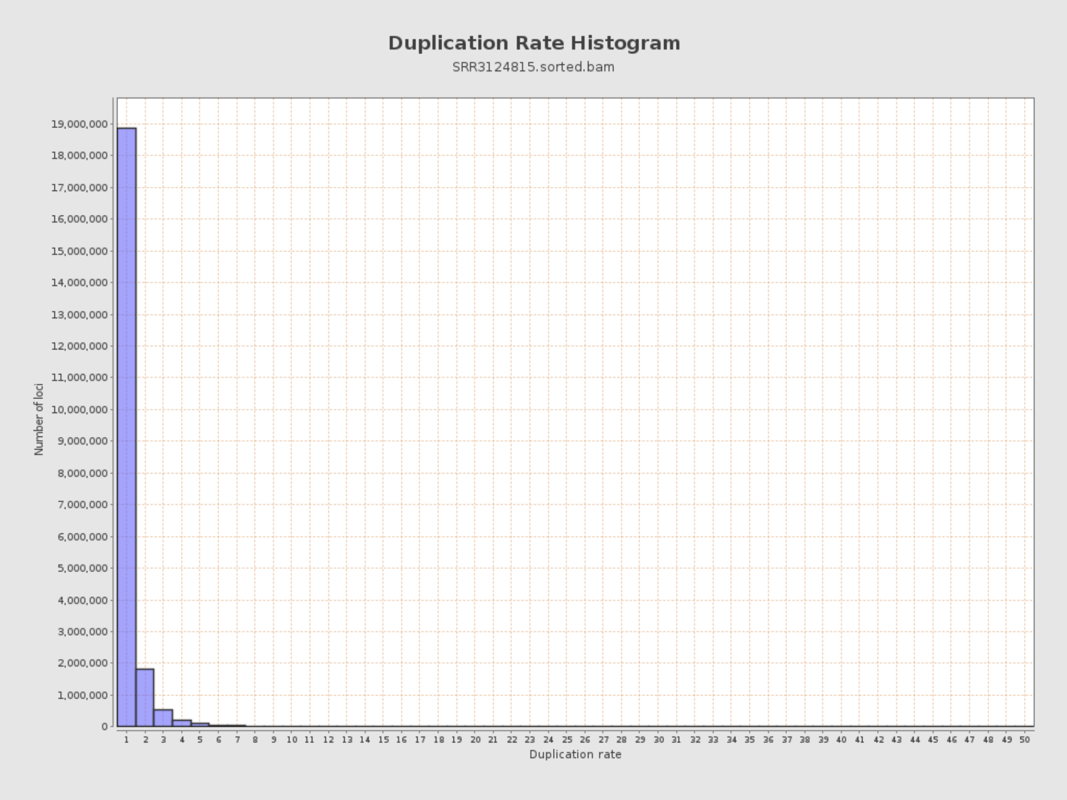
5. Results : Coverage Histogram (0-50X)



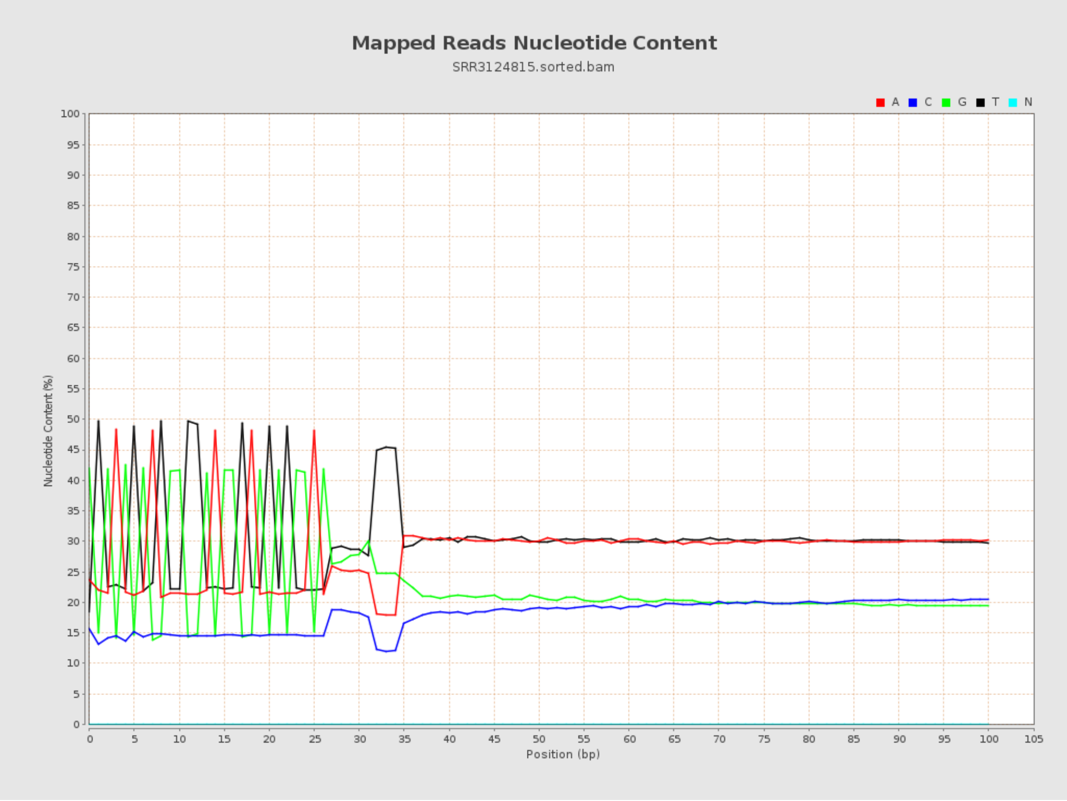
6. Results : Genome Fraction Coverage



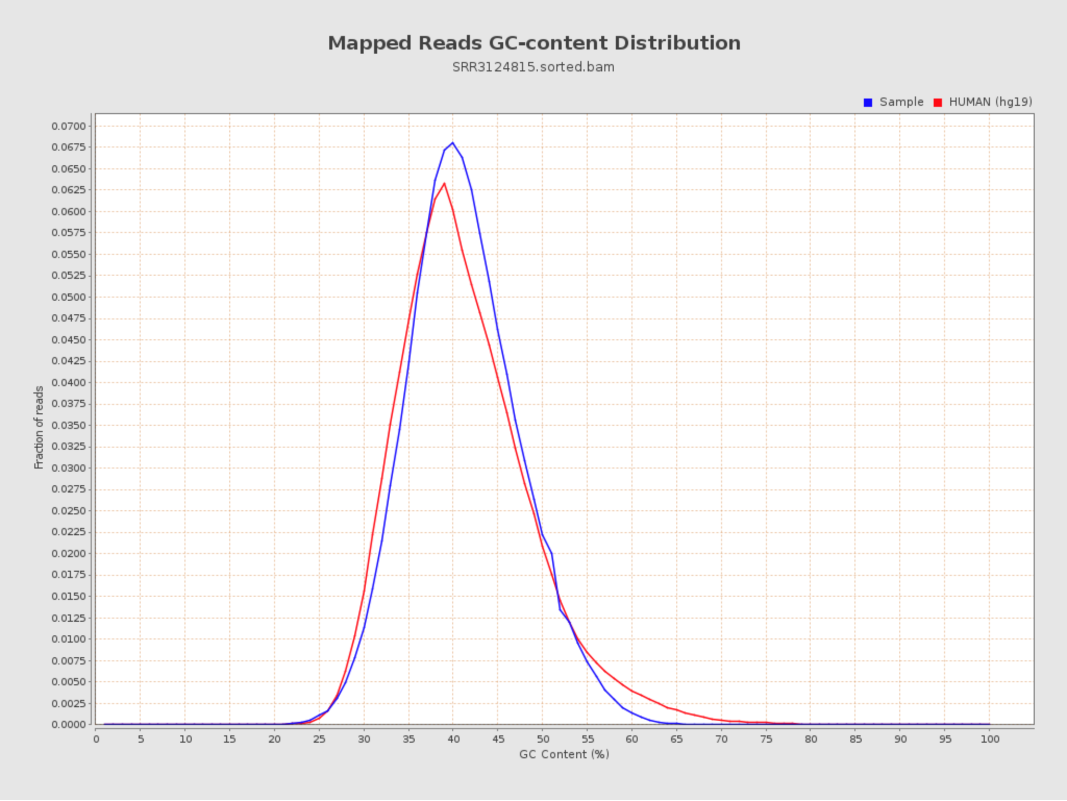
7. Results : Duplication Rate Histogram



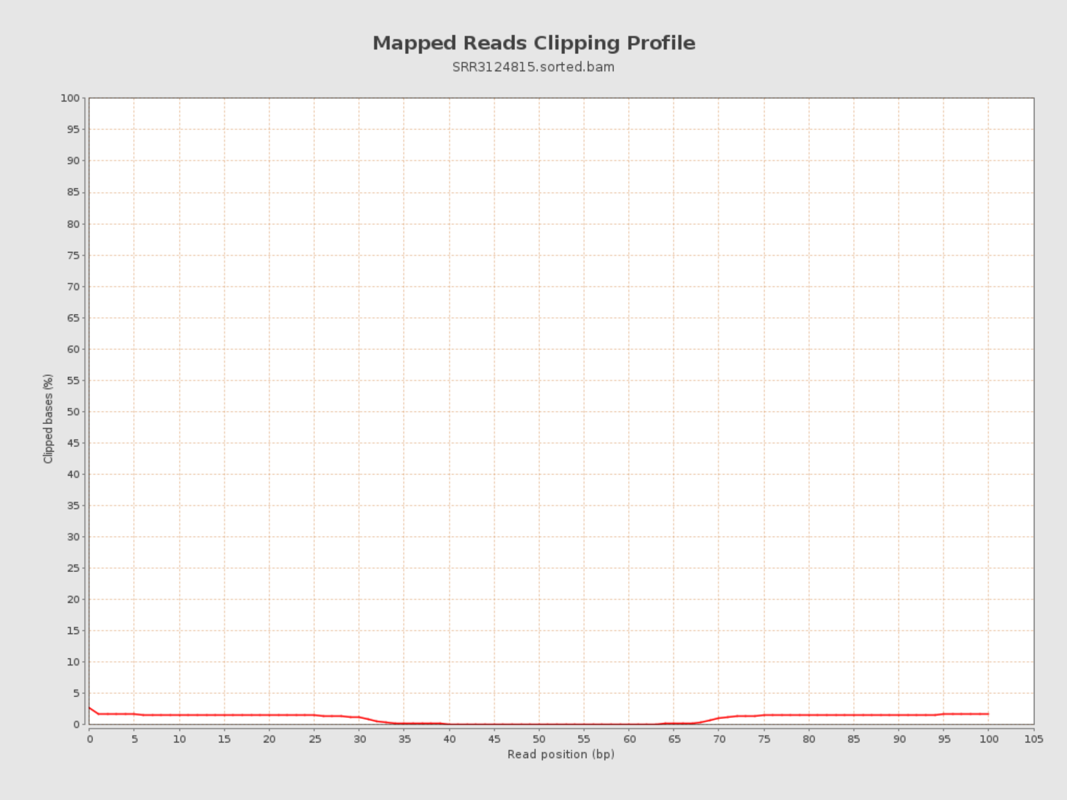
8. Results : Mapped Reads Nucleotide Content



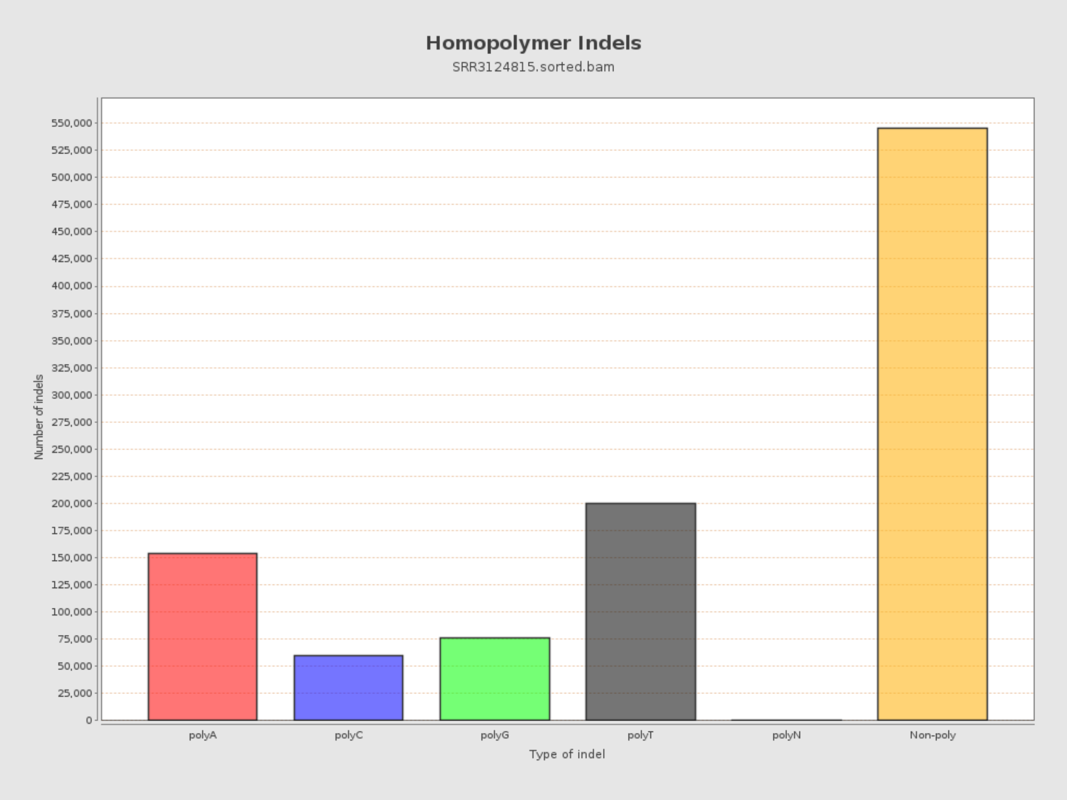
9. Results : Mapped Reads GC-content Distribution



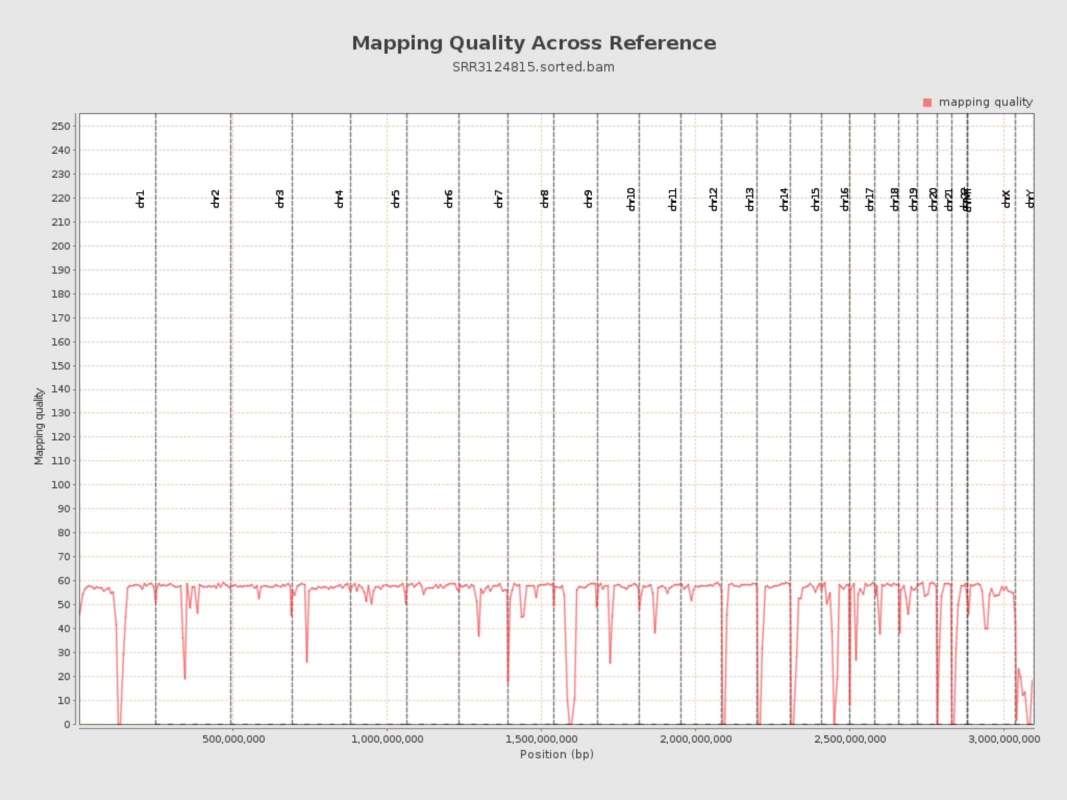
10. Results : Mapped Reads Clipping Profile



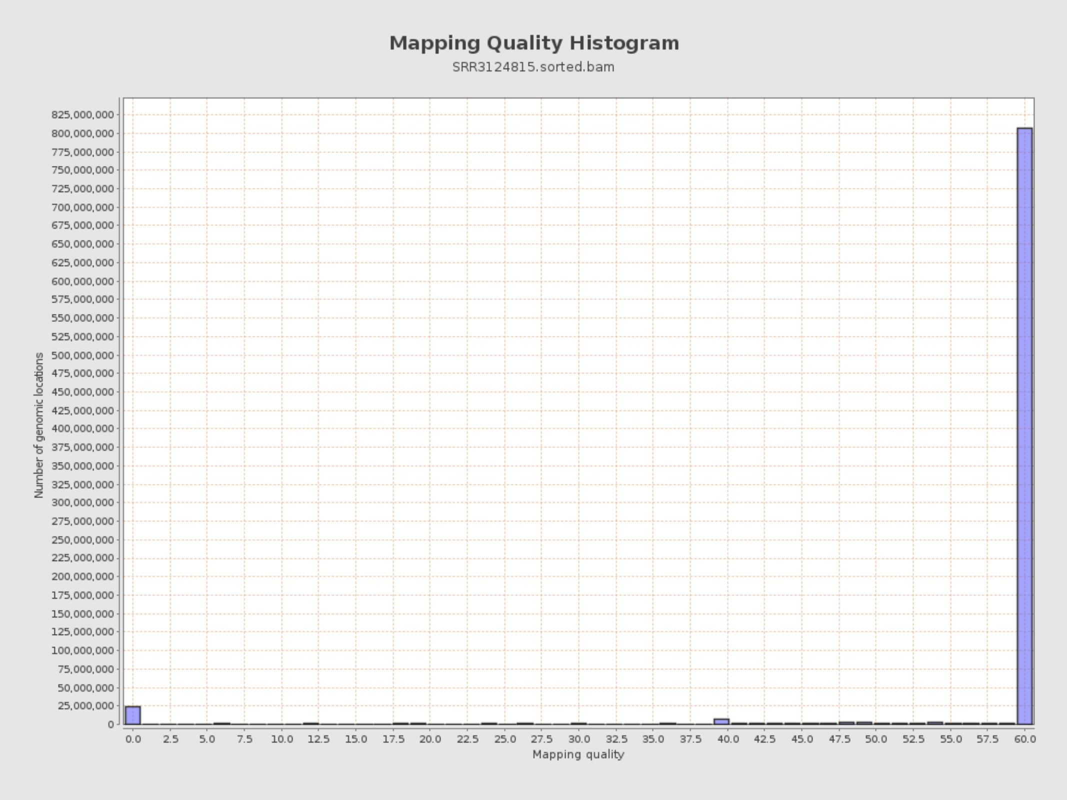
11. Results : Homopolymer Indels



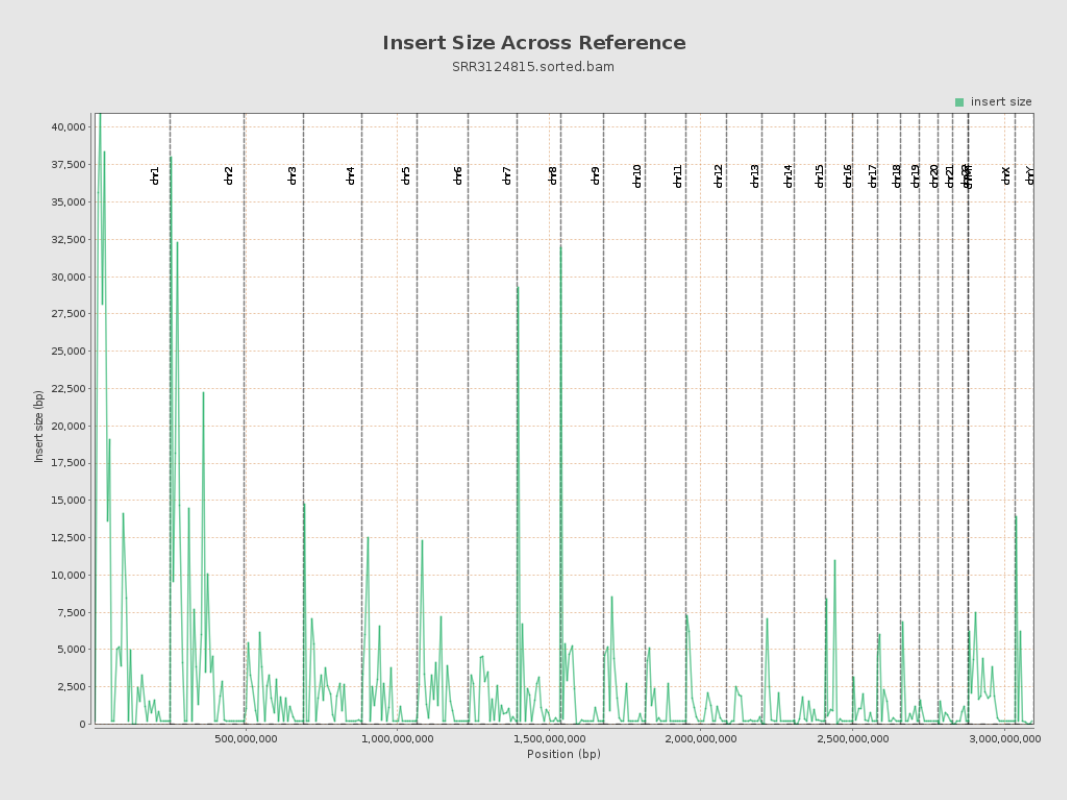
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram