Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/05 02:31:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124824.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_SRR3124824 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124824_1.fastq.gz SRR3124824_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Dec 05 02:31:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124824.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	24,807,268
Mapped reads	24,462,848 / 98.61%
Unmapped reads	344,420 / 1.39%
Mapped paired reads	24,462,848 / 98.61%
Mapped reads, first in pair	12,252,722 / 49.39%
Mapped reads, second in pair	12,210,126 / 49.22%
Mapped reads, both in pair	24,369,736 / 98.24%
Mapped reads, singletons	93,112 / 0.38%
Secondary alignments	0
Supplementary alignments	217,857 / 0.88%
Read min/max/mean length	30 / 101 / 101.36
Duplicated reads (estimated)	4,677,712 / 18.86%
Duplication rate	12.63%
Clipped reads	13,060,938 / 52.65%

2.2. ACGT Content

Number/percentage of A's	599,759,418 / 28.54%
Number/percentage of C's	387,098,952 / 18.42%
Number/percentage of T's	632,515,473 / 30.1%
Number/percentage of G's	482,312,678 / 22.95%
Number/percentage of N's	18,079 / 0%

GC Percentage	41.37%

2.3. Coverage

Mean	0.6793
Standard Deviation	6.956

2.4. Mapping Quality

Mean Mapping Quality	52.53

2.5. Insert size

Mean	96,428.43
Standard Deviation	2,946,496.35
P25/Median/P75	135 / 185 / 258

2.6. Mismatches and indels

General error rate	0.77%
Mismatches	15,653,427
Insertions	256,870
Mapped reads with at least one insertion	1.03%
Deletions	658,309
Mapped reads with at least one deletion	2.64%
Homopolymer indels	48.4%

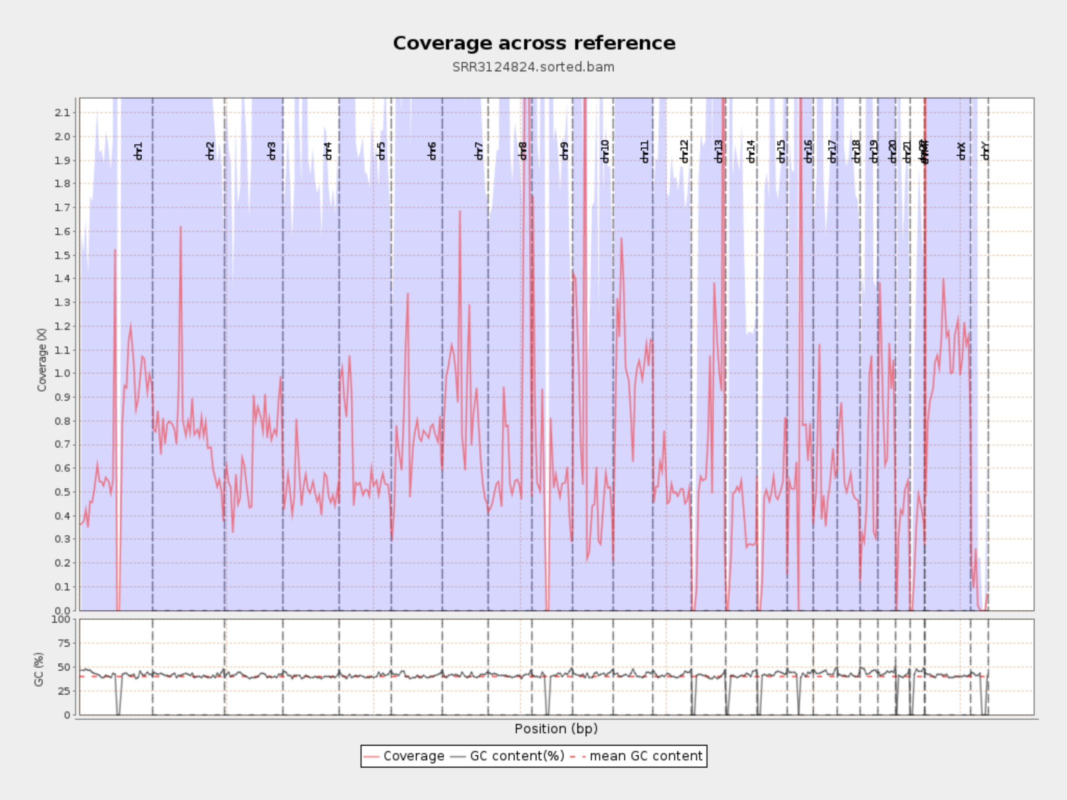
2.7. Chromosome stats

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

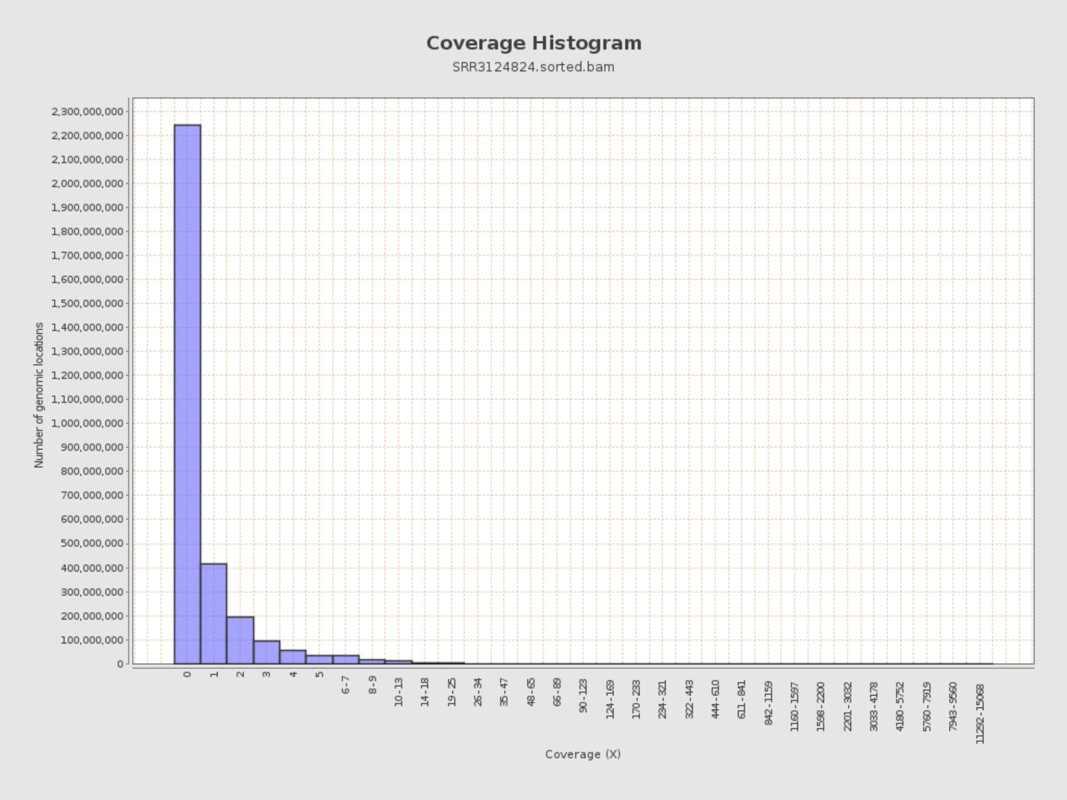
		bases	coverage	deviation
chr1	249250621	176584960	0.7085	8.3733
chr2	243199373	183396852	0.7541	5.9953
chr3	198022430	133418287	0.6738	1.754
chr4	191154276	97569730	0.5104	2.7784
chr5	180915260	113654750	0.6282	1.5598
chr6	171115067	127793095	0.7468	4.796
chr7	159138663	138788934	0.8721	10.4449
chr8	146364022	124579015	0.8512	2.8415
chr9	141213431	80676135	0.5713	6.2197
chr10	135534747	96388004	0.7112	21.0519
chr11	135006516	138724370	1.0275	5.5693
chr12	133851895	69150230	0.5166	1.3556
chr13	115169878	94299898	0.8188	2.5754
chr14	107349540	35892987	0.3344	1.5496
chr15	102531392	44538467	0.4344	1.3993
chr16	90354753	65137784	0.7209	12.3841
chr17	81195210	45086951	0.5553	6.6676
chr18	78077248	45319678	0.5804	7.9296
chr19	59128983	30068770	0.5085	5.1998
chr20	63025520	58727638	0.9318	2.0946
chr21	48129895	18585473	0.3862	1.7868
chr22	51304566	14562397	0.2838	1.0229
chrMT	16571	1302983	78.6303	45.4259
chrX	155270560	164036018	1.0565	3.5828

chrY	59373566	4474210	0.0754	3.358

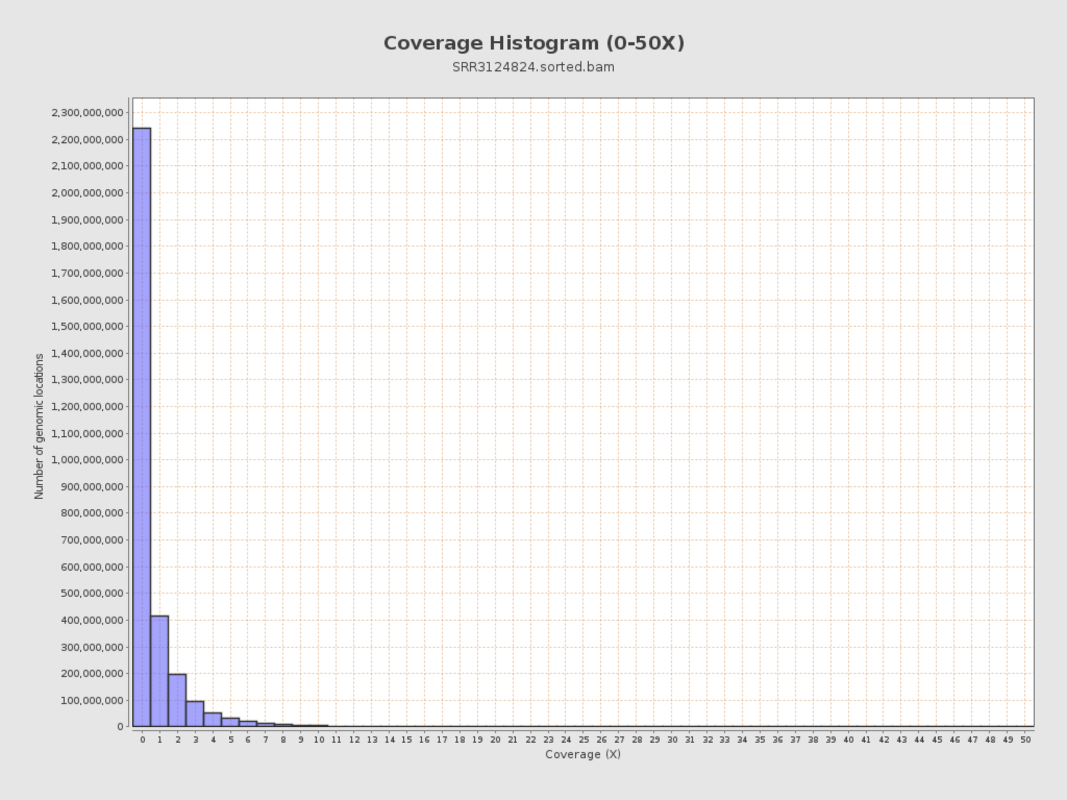
3. Results : Coverage across reference



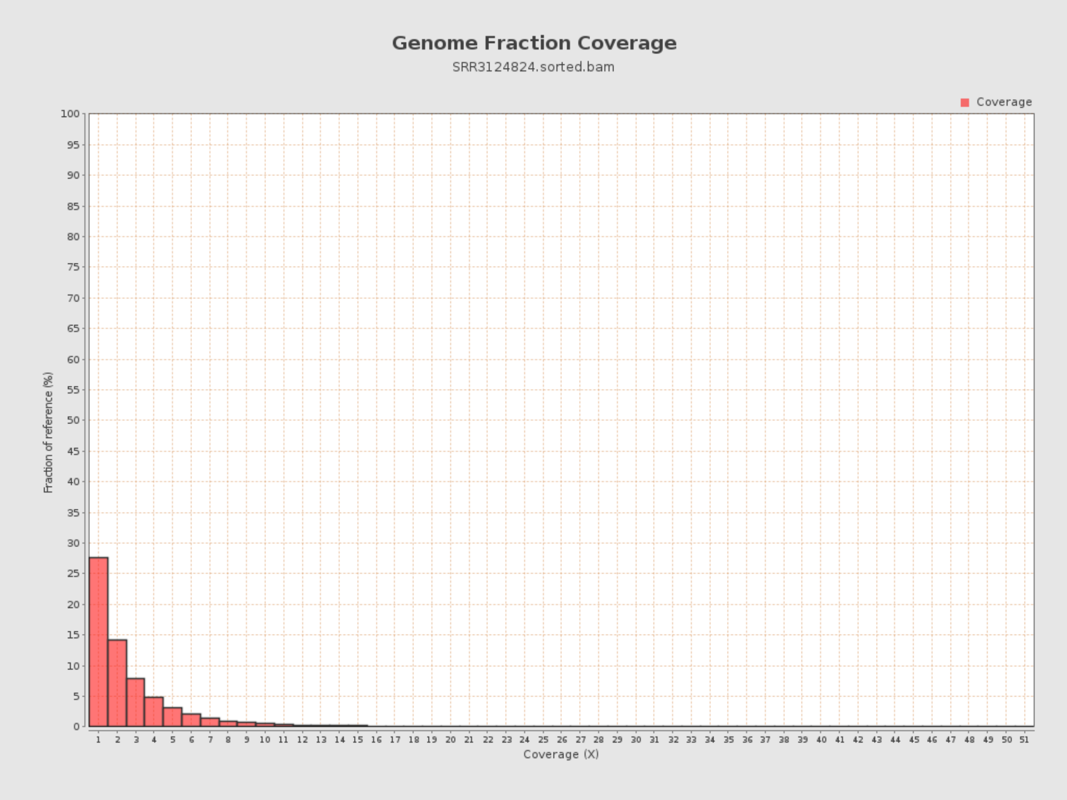
4. Results : Coverage Histogram



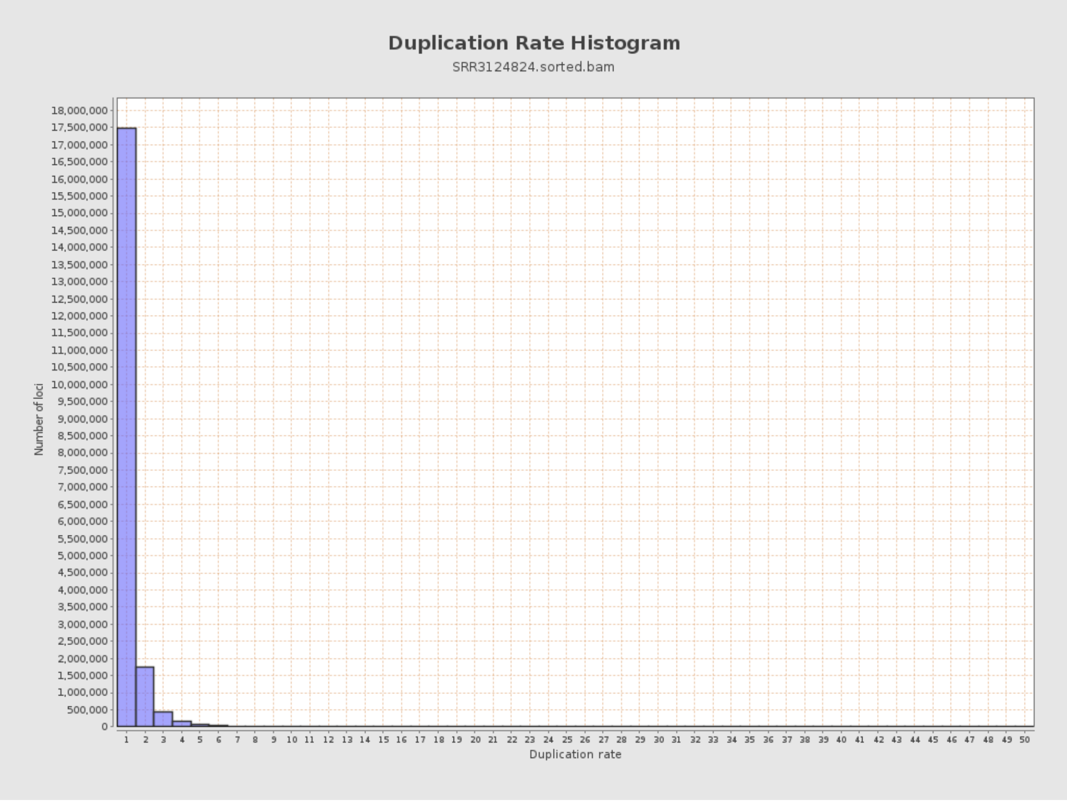
5. Results : Coverage Histogram (0-50X)



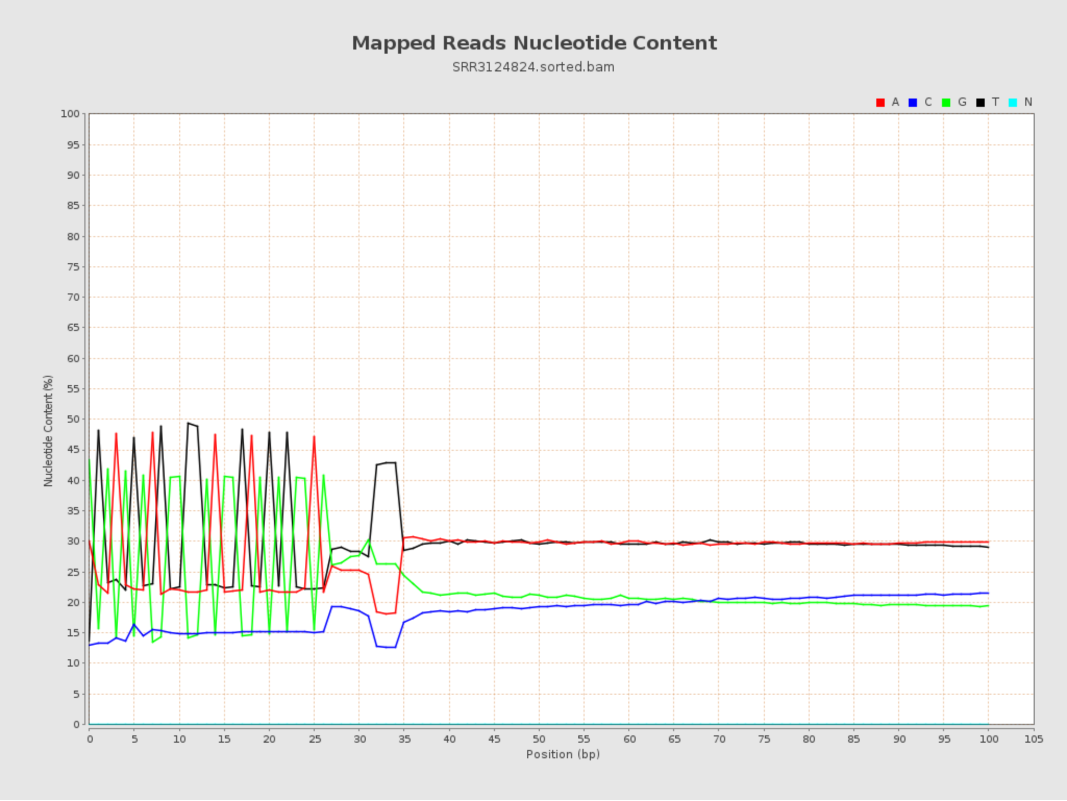
6. Results : Genome Fraction Coverage



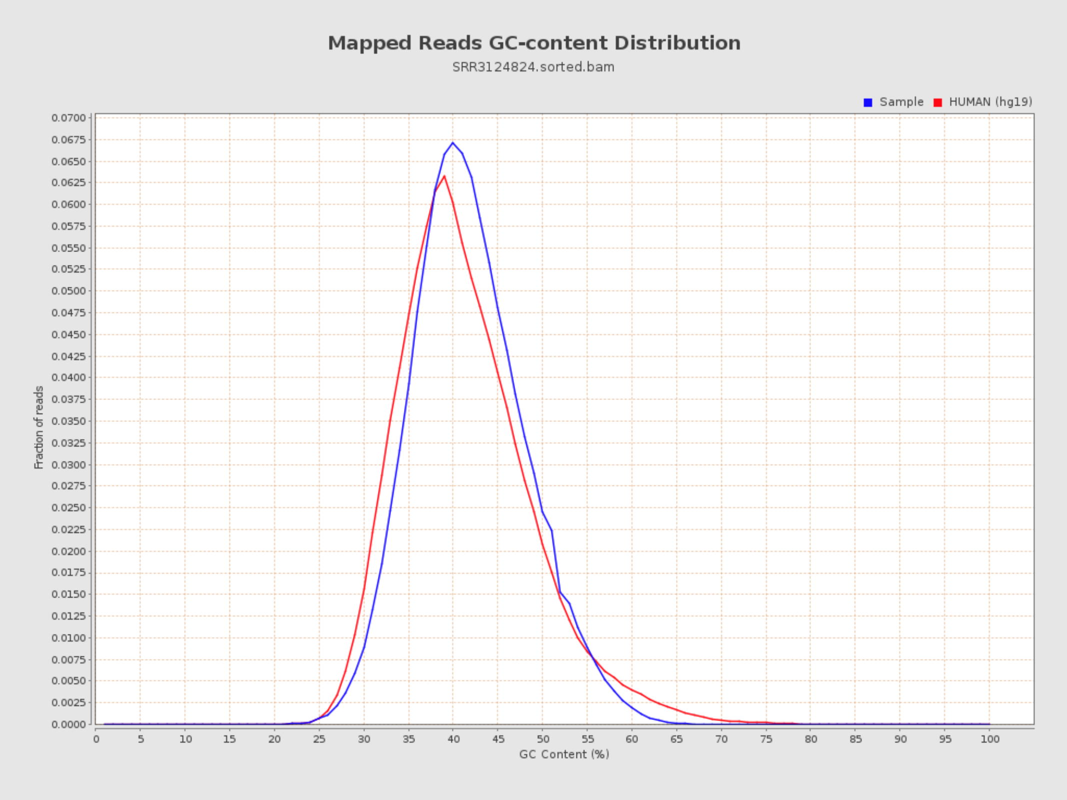
7. Results : Duplication Rate Histogram



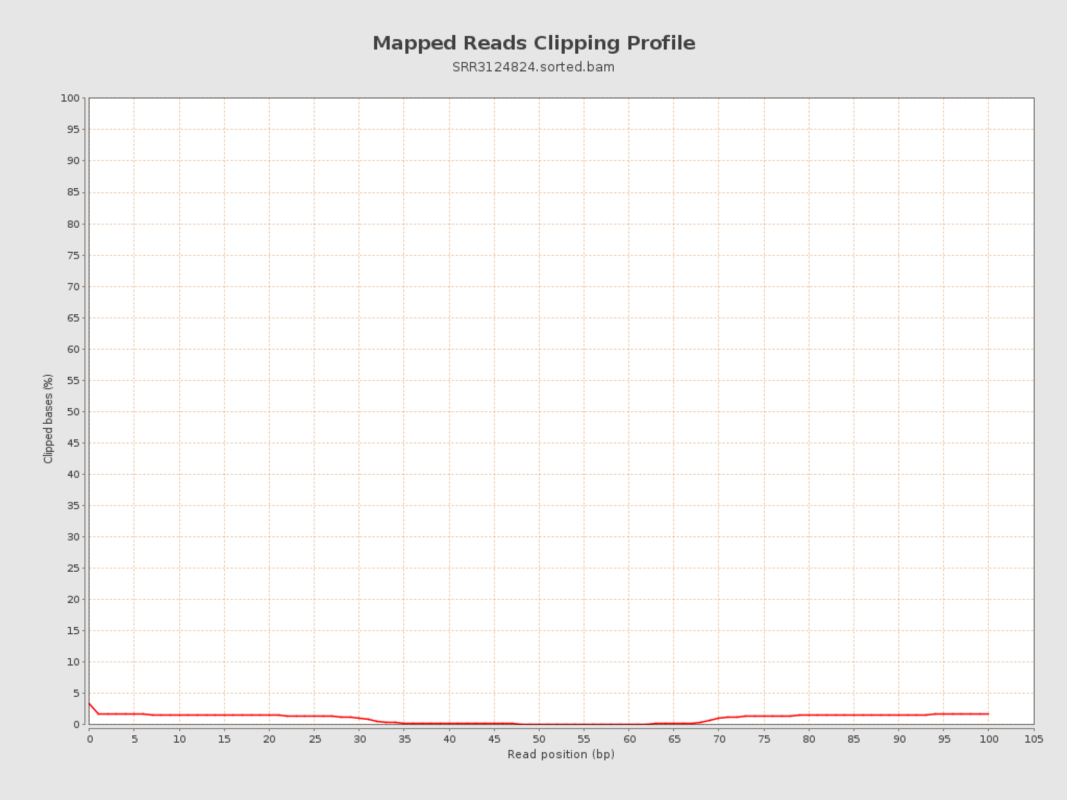
8. Results : Mapped Reads Nucleotide Content



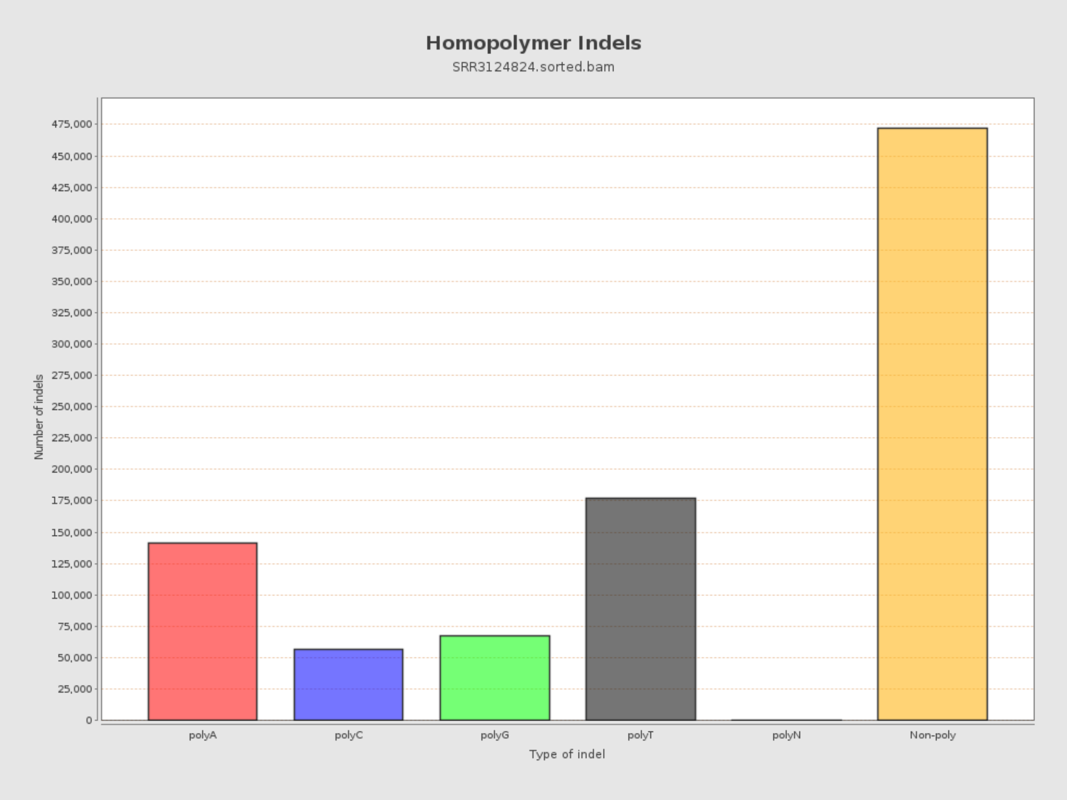
9. Results : Mapped Reads GC-content Distribution



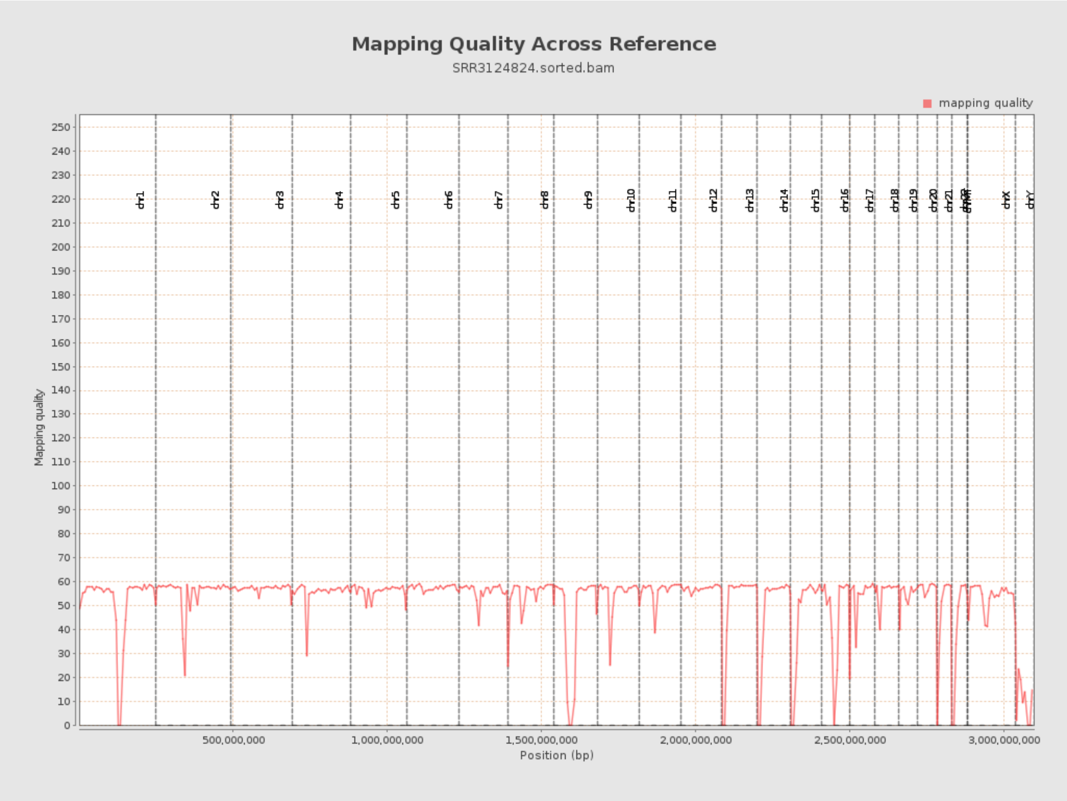
10. Results : Mapped Reads Clipping Profile



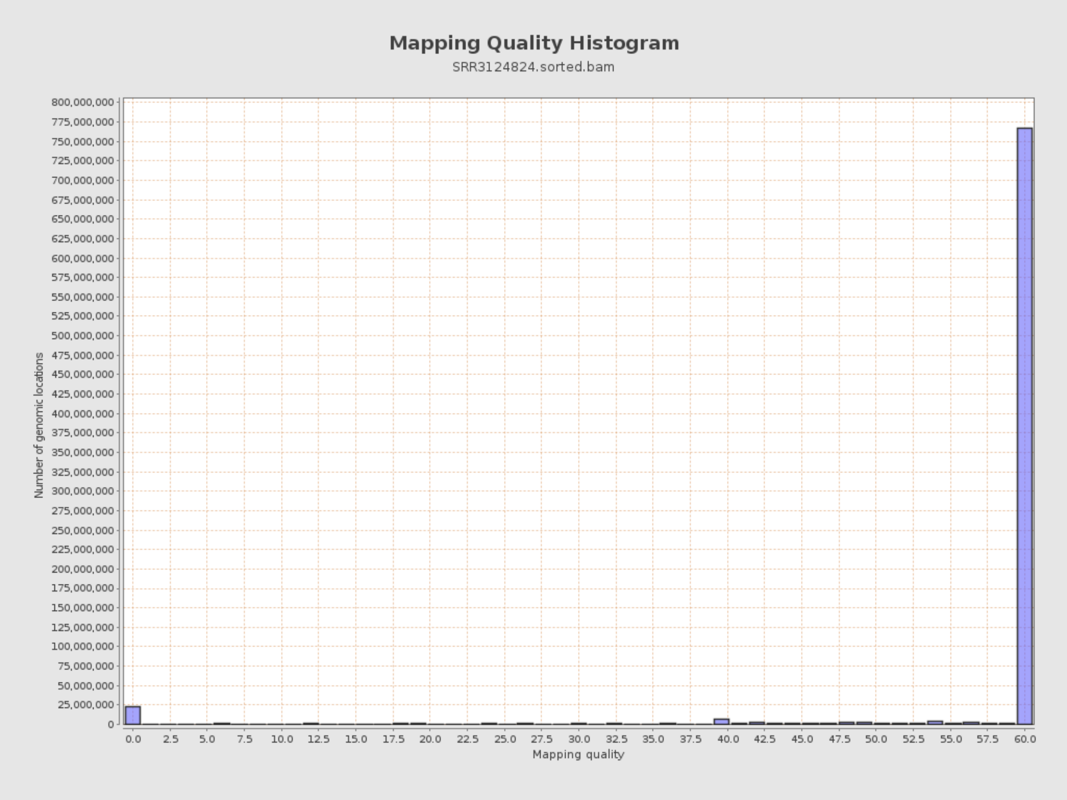
11. Results : Homopolymer Indels



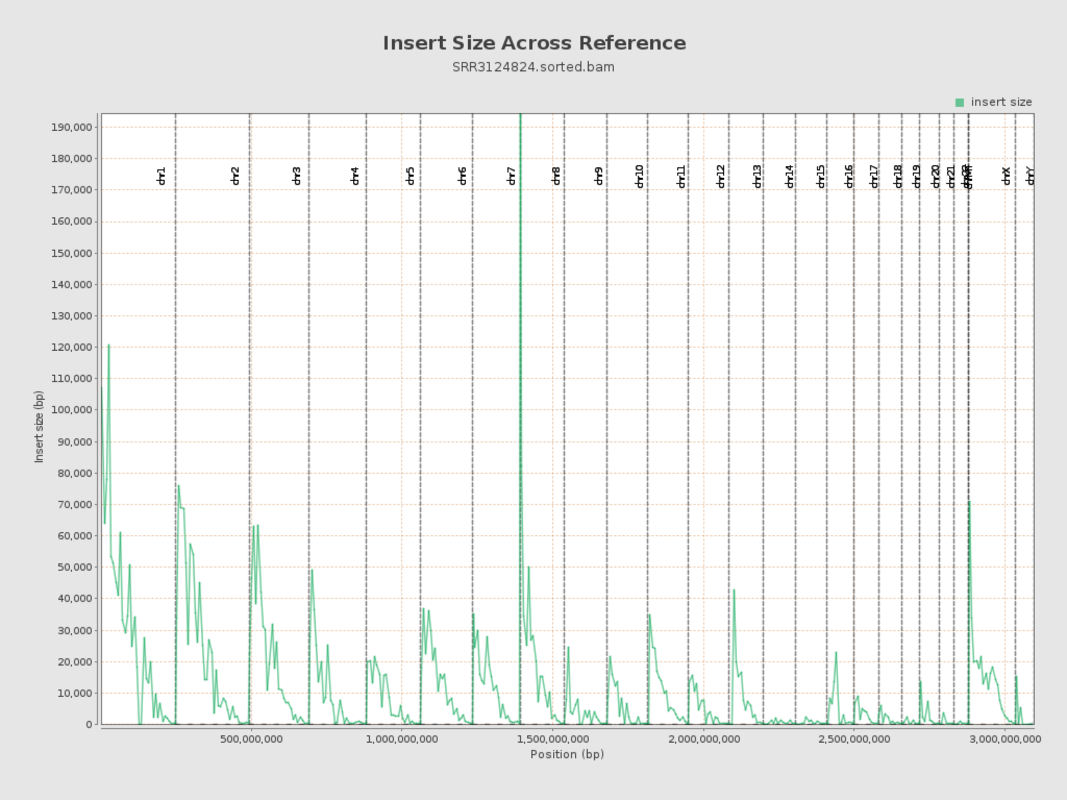
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram