Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/08 15:29:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124852.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_SRR3124852 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124852_1.fastq.gz SRR3124852_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Dec 08 15:29:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124852.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	132,266,496
Mapped reads	128,683,925 / 97.29%
Unmapped reads	3,582,571 / 2.71%
Mapped paired reads	128,683,925 / 97.29%
Mapped reads, first in pair	64,992,370 / 49.14%
Mapped reads, second in pair	63,691,555 / 48.15%
Mapped reads, both in pair	126,876,080 / 95.92%
Mapped reads, singletons	1,807,845 / 1.37%
Secondary alignments	0
Supplementary alignments	1,726,048 / 1.3%
Read min/max/mean length	30 / 150 / 150.63
Duplicated reads (estimated)	48,050,785 / 36.33%
Duplication rate	27.99%
Clipped reads	56,897,061 / 43.02%

2.2. ACGT Content

Number/percentage of A's	4,996,331,629 / 28.55%
Number/percentage of C's	3,489,086,875 / 19.94%
Number/percentage of T's	5,089,583,282 / 29.09%
Number/percentage of G's	3,923,411,167 / 22.42%
Number/percentage of N's	40,002 / 0%

GC Percentage	42.36%

2.3. Coverage

Mean	5.6574
Standard Deviation	53.1799

2.4. Mapping Quality

Mean Mapping Quality	53.85

2.5. Insert size

Mean	50,396.5
Standard Deviation	2,131,597.96
P25/Median/P75	204 / 260 / 326

2.6. Mismatches and indels

General error rate	1.3%
Mismatches	217,166,372
Insertions	3,433,941
Mapped reads with at least one insertion	2.46%
Deletions	7,027,248
Mapped reads with at least one deletion	5.2%
Homopolymer indels	44.6%

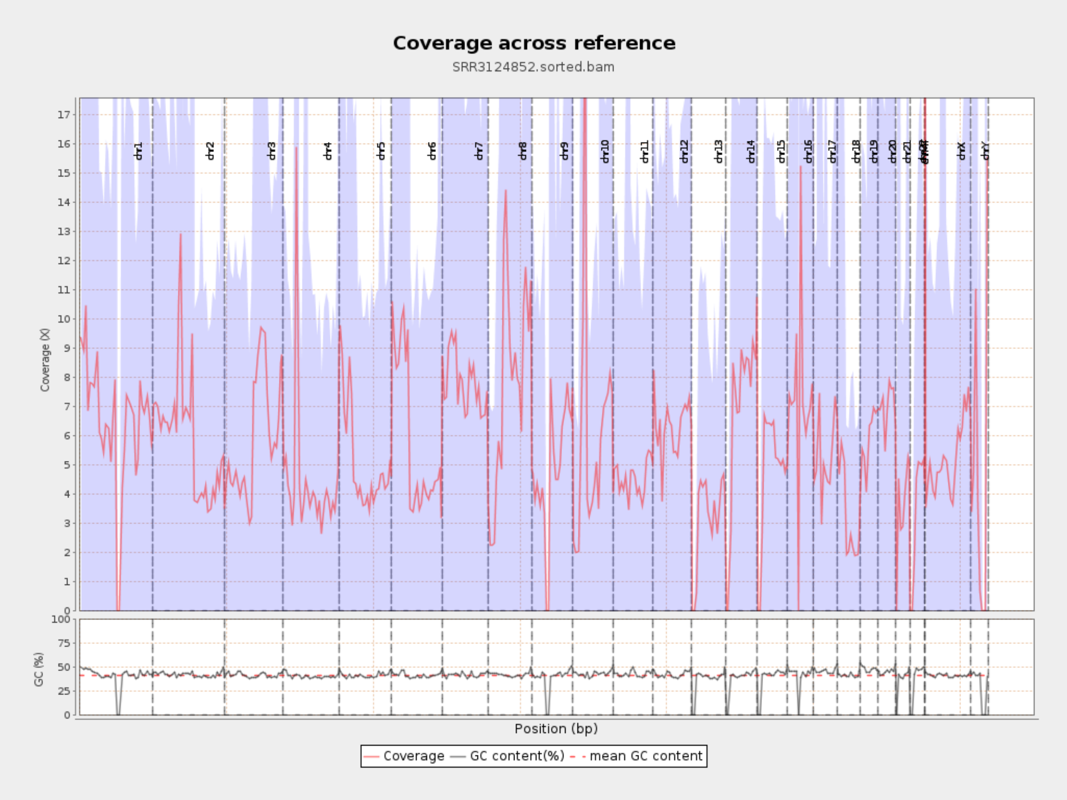
2.7. Chromosome stats

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

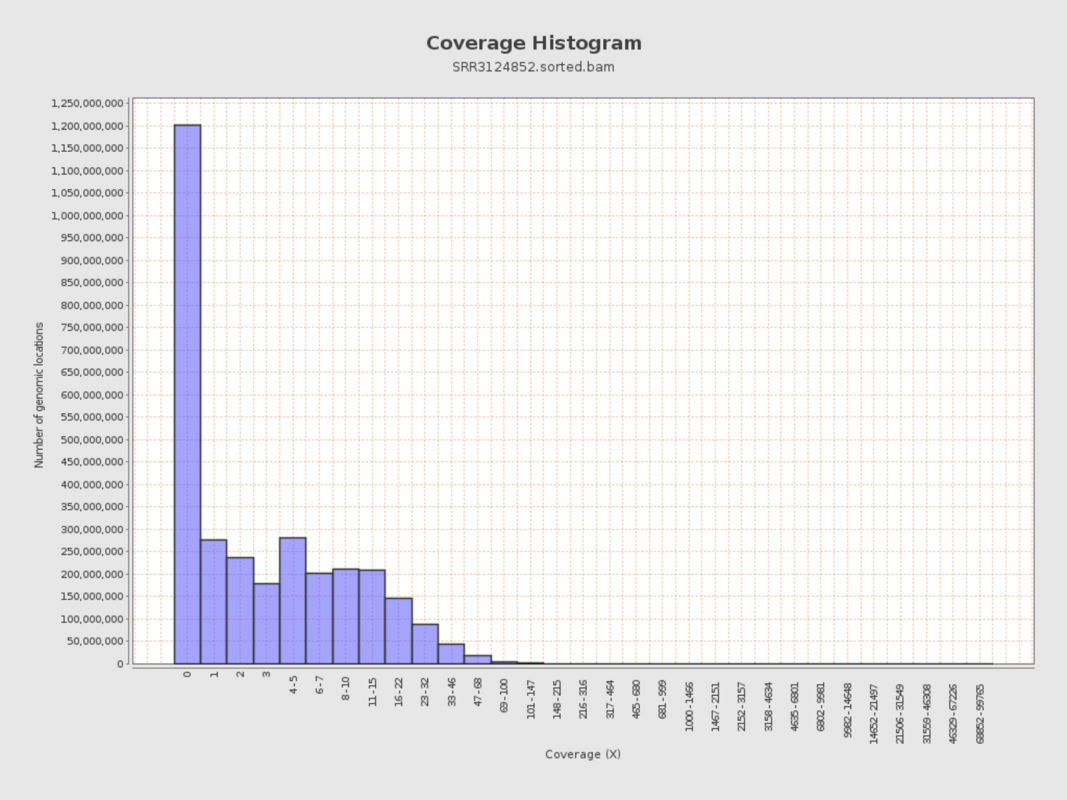
		bases	coverage	deviation
chr1	249250621	1609468209	6.4572	39.6019
chr2	243199373	1448128058	5.9545	66.102
chr3	198022430	1175566504	5.9365	9.793
chr4	191154276	829774263	4.3409	90.1093
chr5	180915260	932779131	5.1559	10.0169
chr6	171115067	1004318502	5.8693	22.5337
chr7	159138663	1242734082	7.8091	43.6668
chr8	146364022	1162065171	7.9396	19.7114
chr9	141213431	676855525	4.7931	69.2637
chr10	135534747	843161545	6.221	133.8445
chr11	135006516	608882918	4.51	15.7944
chr12	133851895	843579912	6.3023	10.2117
chr13	115169878	364209105	3.1624	6.1814
chr14	107349540	726005362	6.763	12.6172
chr15	102531392	481908318	4.7001	8.6042
chr16	90354753	651976008	7.2157	72.8682
chr17	81195210	424961064	5.2338	49.5517
chr18	78077248	247633102	3.1716	53.5989
chr19	59128983	346012747	5.8518	21.9422
chr20	63025520	443596366	7.0384	28.7394
chr21	48129895	175997386	3.6567	40.2306
chr22	51304566	175560625	3.4219	9.0996
chrMT	16571	824670	49.7659	25.9952
chrX	155270560	803315205	5.1736	13.2535

chrY	59373566	294117803	4.9537	128.772

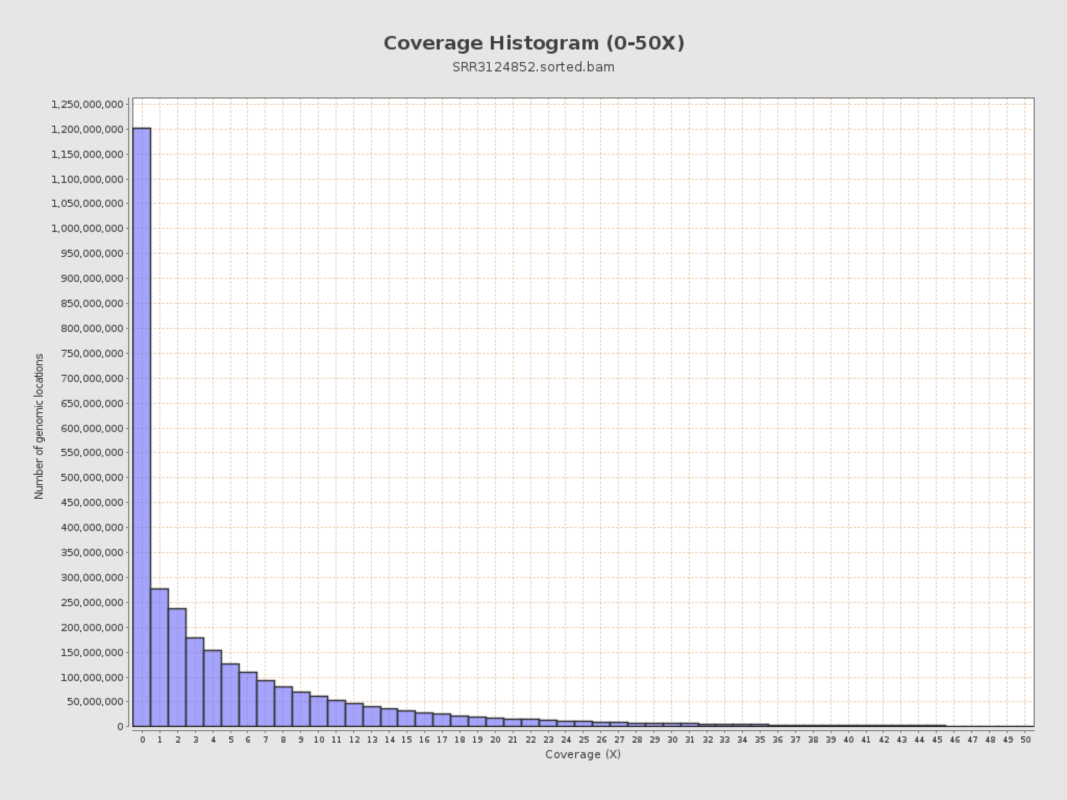
3. Results : Coverage across reference



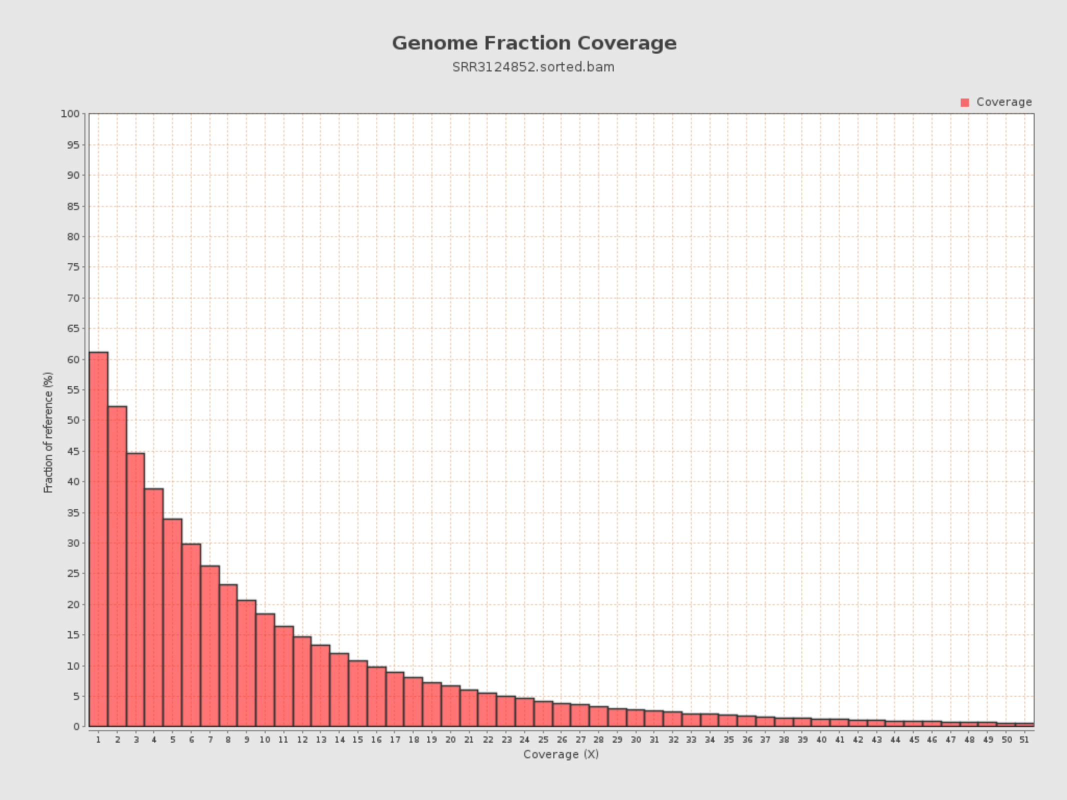
4. Results : Coverage Histogram



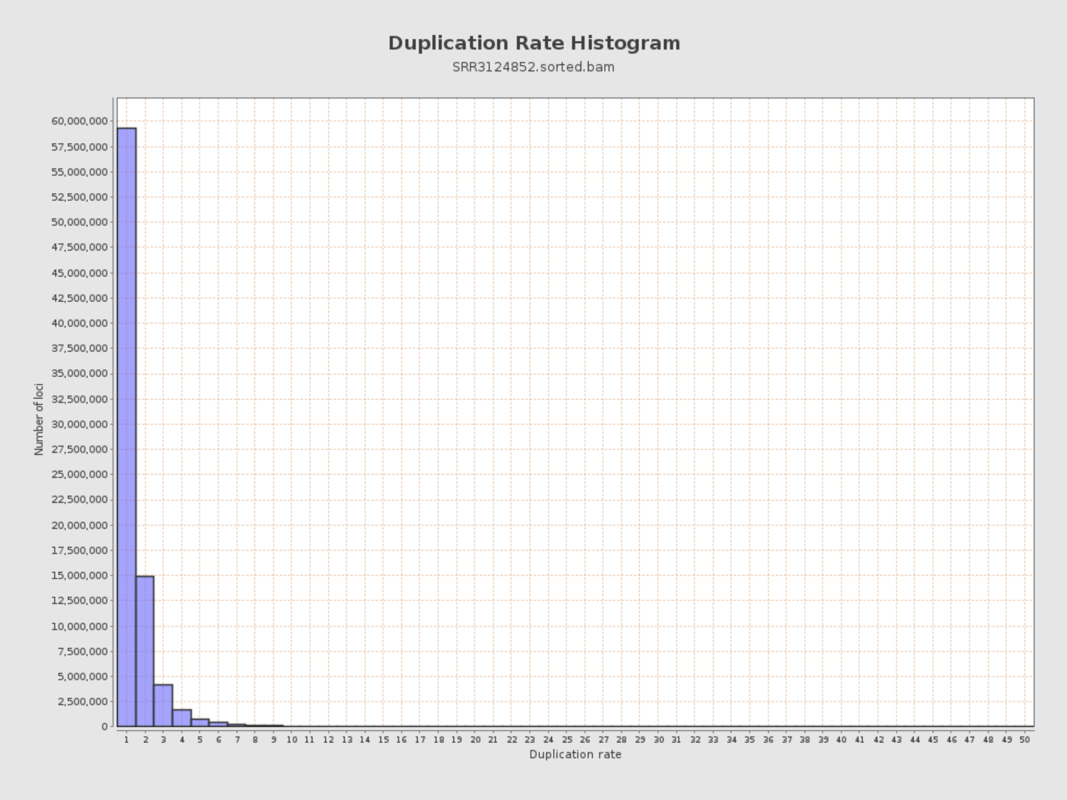
5. Results : Coverage Histogram (0-50X)



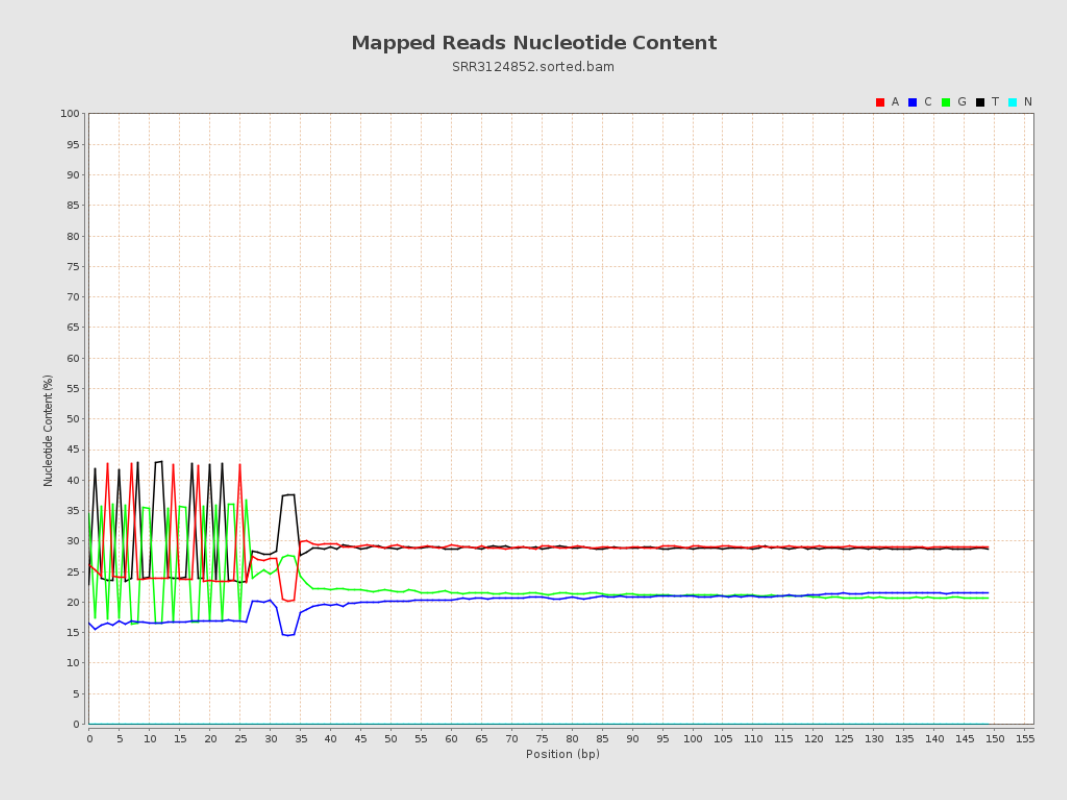
6. Results : Genome Fraction Coverage



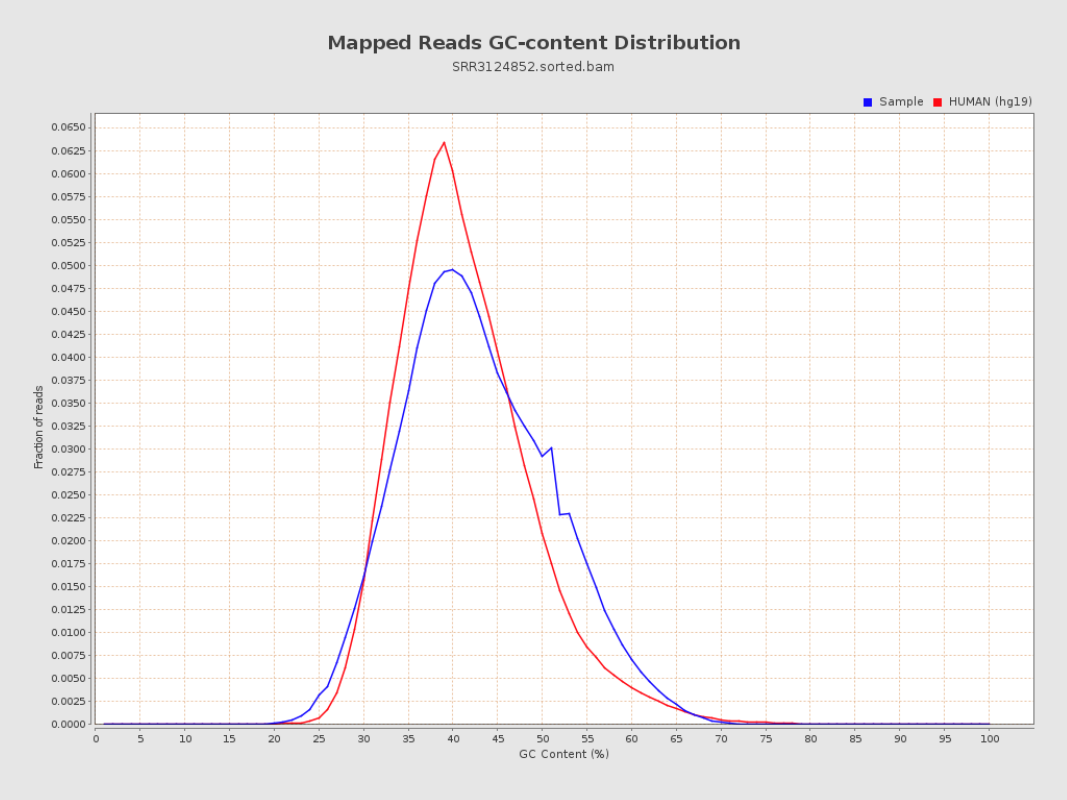
7. Results : Duplication Rate Histogram



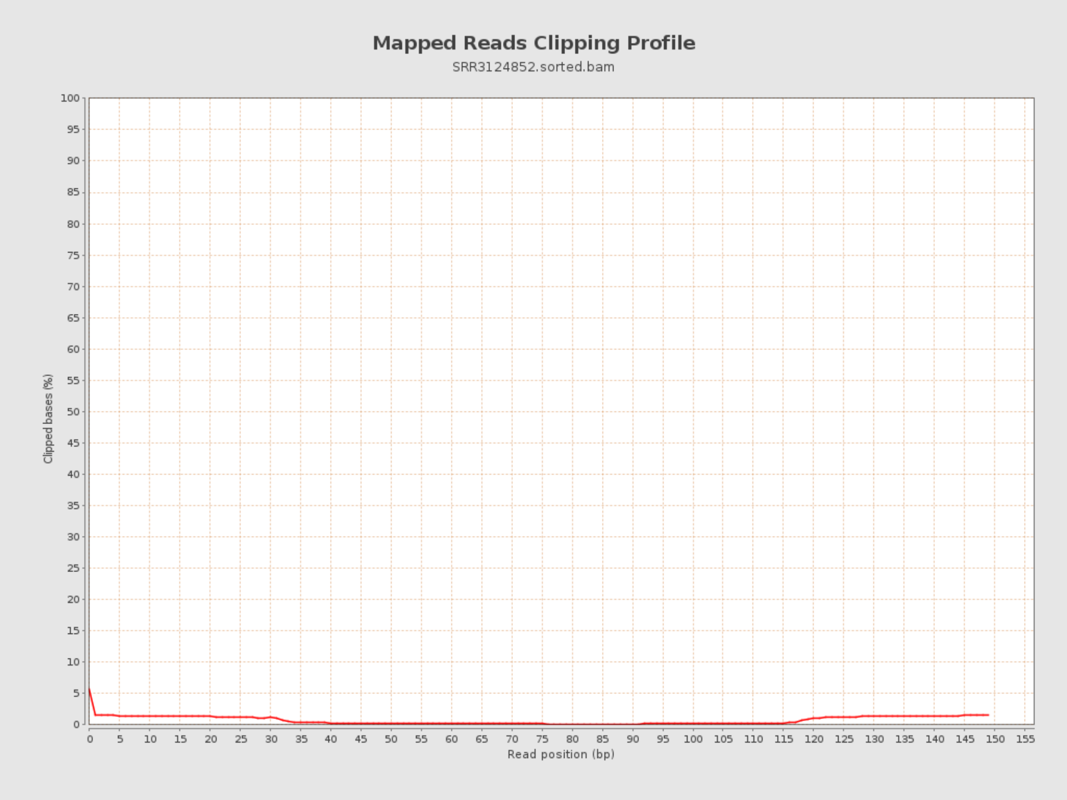
8. Results : Mapped Reads Nucleotide Content



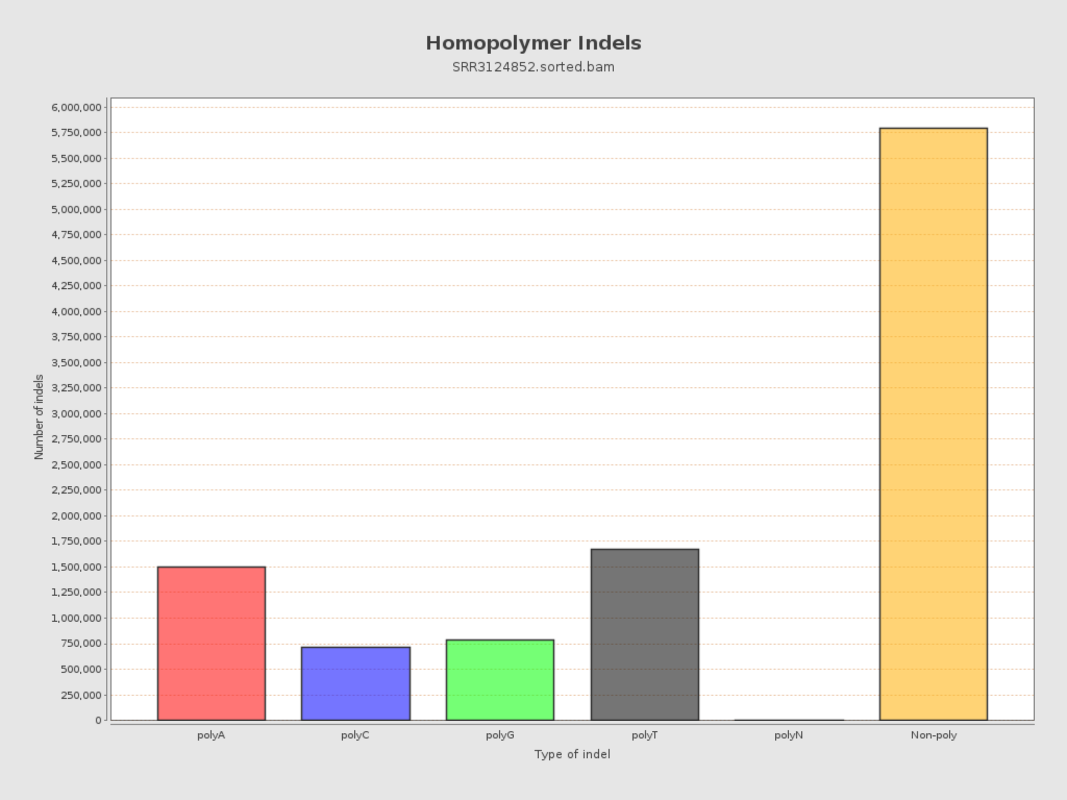
9. Results : Mapped Reads GC-content Distribution



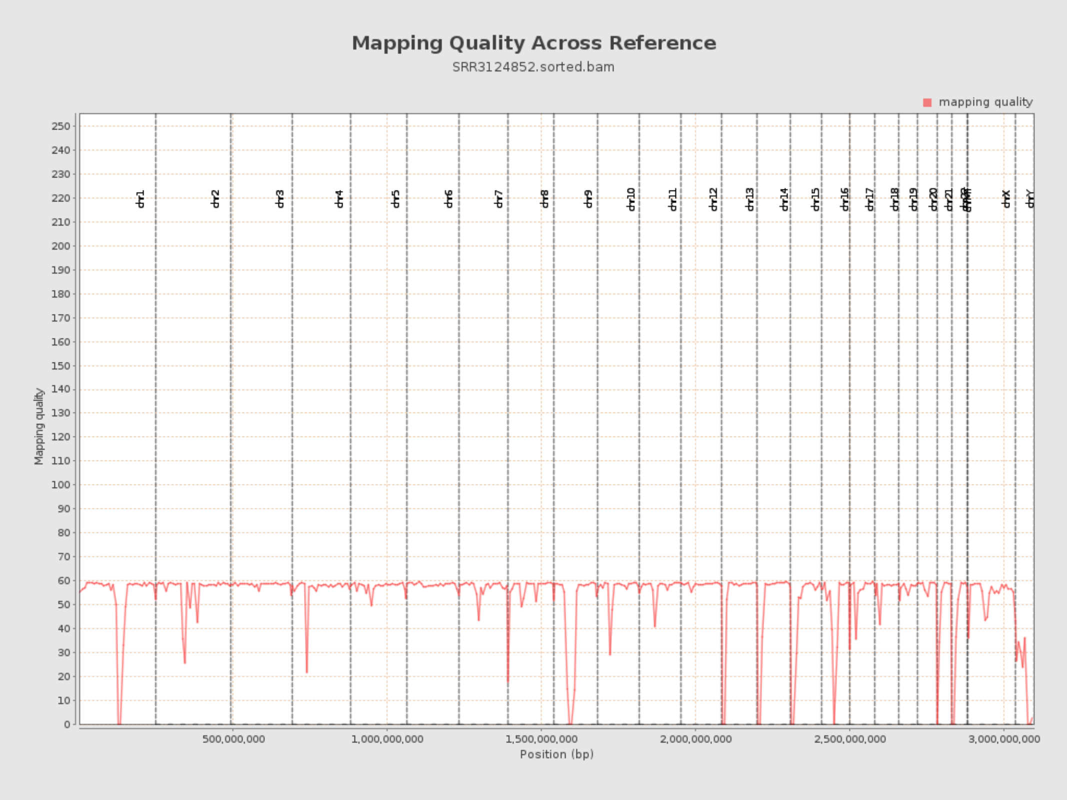
10. Results : Mapped Reads Clipping Profile



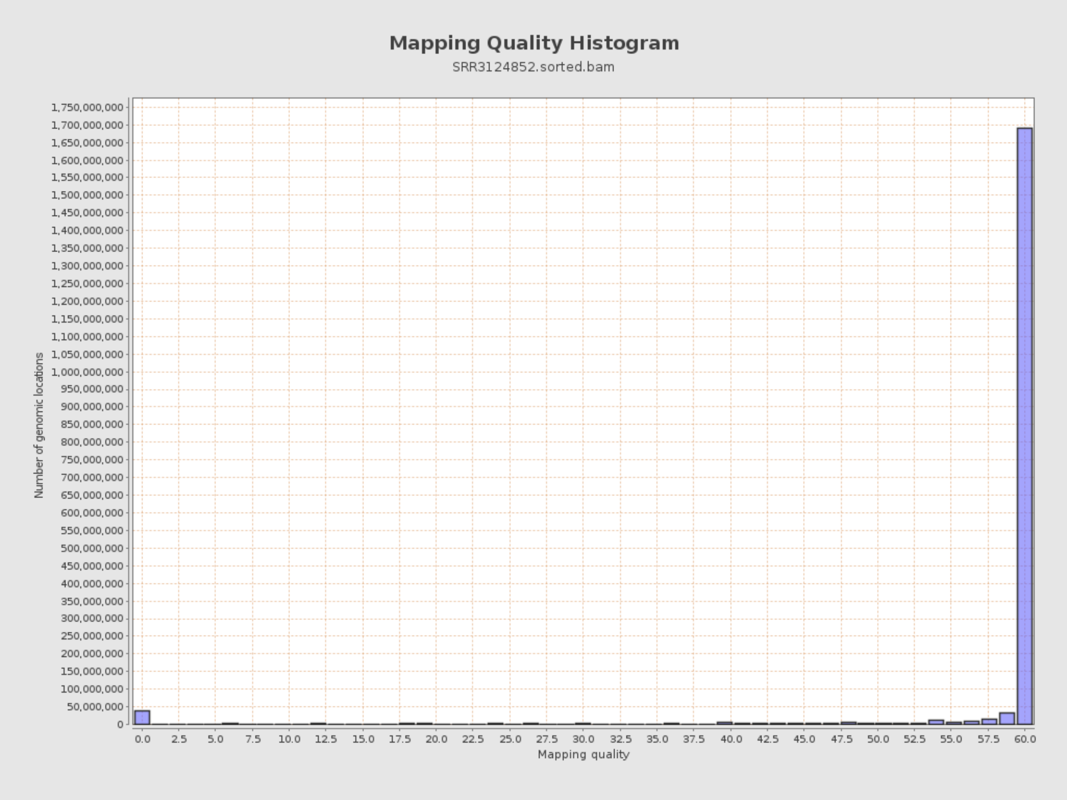
11. Results : Homopolymer Indels



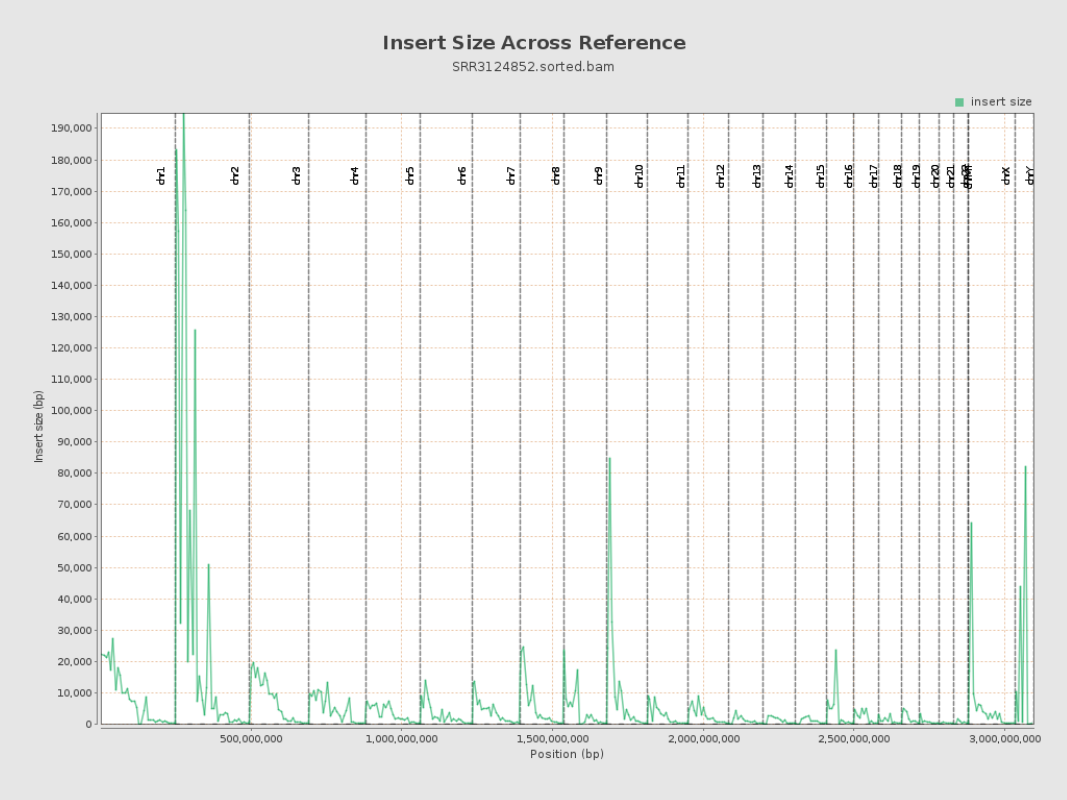
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram