Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/08 21:30:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124854.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_SRR3124854 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124854_1.fastq.gz SRR3124854_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Dec 08 21:30:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124854.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	101,159,220
Mapped reads	99,294,419 / 98.16%
Unmapped reads	1,864,801 / 1.84%
Mapped paired reads	99,294,419 / 98.16%
Mapped reads, first in pair	50,019,016 / 49.45%
Mapped reads, second in pair	49,275,403 / 48.71%
Mapped reads, both in pair	98,386,948 / 97.26%
Mapped reads, singletons	907,471 / 0.9%
Secondary alignments	0
Supplementary alignments	2,569,975 / 2.54%
Read min/max/mean length	30 / 150 / 151.23
Duplicated reads (estimated)	42,622,960 / 42.13%
Duplication rate	23.27%
Clipped reads	57,495,491 / 56.84%

2.2. ACGT Content

Number/percentage of A's	3,744,002,714 / 28.72%
Number/percentage of C's	2,507,840,544 / 19.24%
Number/percentage of T's	3,875,608,988 / 29.73%
Number/percentage of G's	2,908,316,988 / 22.31%
Number/percentage of N's	296,054 / 0%

GC Percentage	41.55%

2.3. Coverage

Mean	4.2145
Standard Deviation	62.1744

2.4. Mapping Quality

Mean Mapping Quality	53.27

2.5. Insert size

Mean	144,104.44
Standard Deviation	3,577,833.37
P25/Median/P75	195 / 265 / 349

2.6. Mismatches and indels

General error rate	1.26%
Mismatches	156,450,359
Insertions	2,658,589
Mapped reads with at least one insertion	2.47%
Deletions	4,823,021
Mapped reads with at least one deletion	4.63%
Homopolymer indels	44.34%

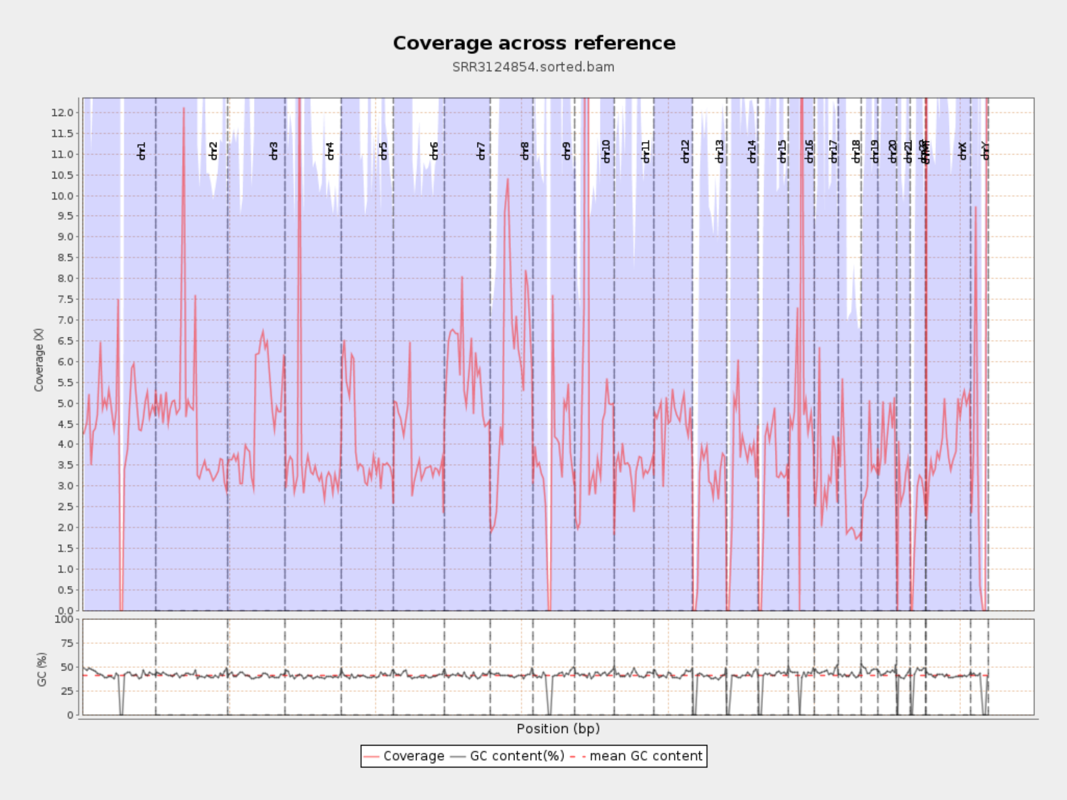
2.7. Chromosome stats

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

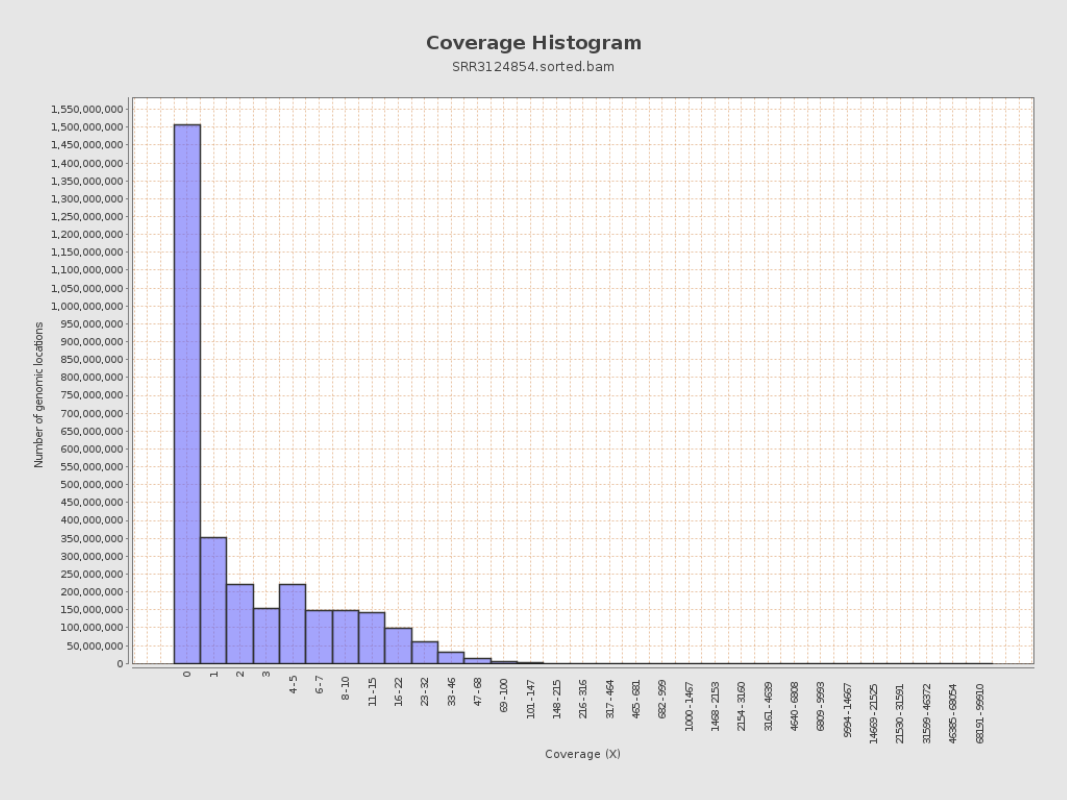
		bases	coverage	deviation
chr1	249250621	1142083951	4.5821	57.2598
chr2	243199373	1128740183	4.6412	64.6152
chr3	198022430	920802200	4.65	10.1674
chr4	191154276	705534832	3.6909	71.7316
chr5	180915260	730641752	4.0386	10.0198
chr6	171115067	665150098	3.8872	22.0552
chr7	159138663	917375341	5.7646	51.6108
chr8	146364022	872914570	5.964	18.8822
chr9	141213431	513793707	3.6384	76.2107
chr10	135534747	724257242	5.3437	197.4742
chr11	135006516	459226628	3.4015	18.794
chr12	133851895	624696580	4.6671	19.3225
chr13	115169878	324689377	2.8192	6.6002
chr14	107349540	379380165	3.5341	10.0467
chr15	102531392	321595208	3.1366	11.3798
chr16	90354753	489002146	5.412	91.5019
chr17	81195210	273598328	3.3696	51.042
chr18	78077248	209805891	2.6872	59.8763
chr19	59128983	196473777	3.3228	29.5609
chr20	63025520	267644071	4.2466	23.4055
chr21	48129895	140498460	2.9192	33.7383
chr22	51304566	110604259	2.1558	8.4769
chrMT	16571	9213067	555.9753	290.2619
chrX	155270560	635796561	4.0948	14.7381

chrY	59373566	283282801	4.7712	122.1024

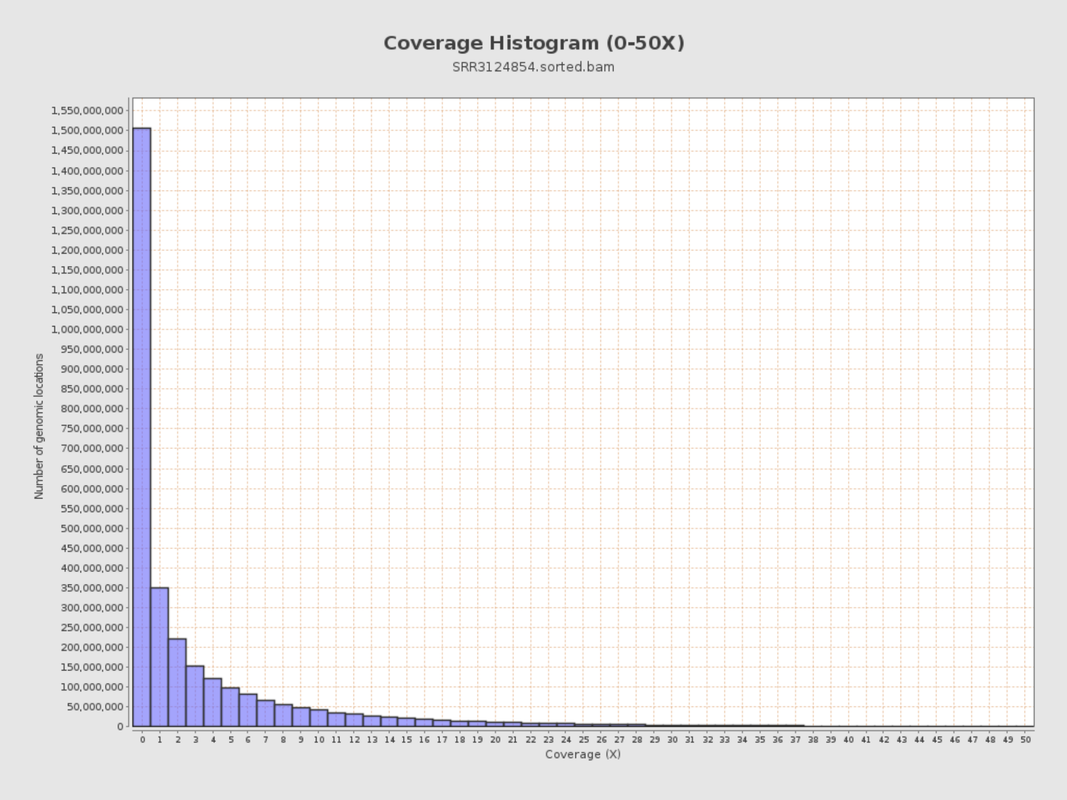
3. Results : Coverage across reference



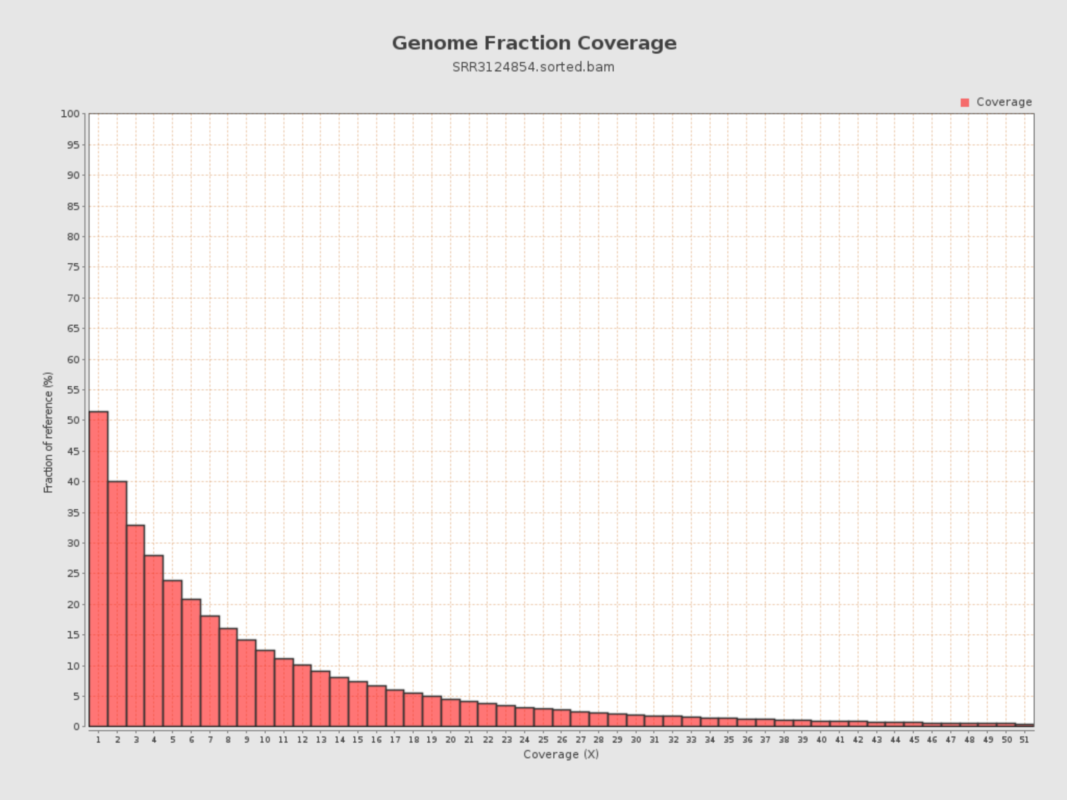
4. Results : Coverage Histogram



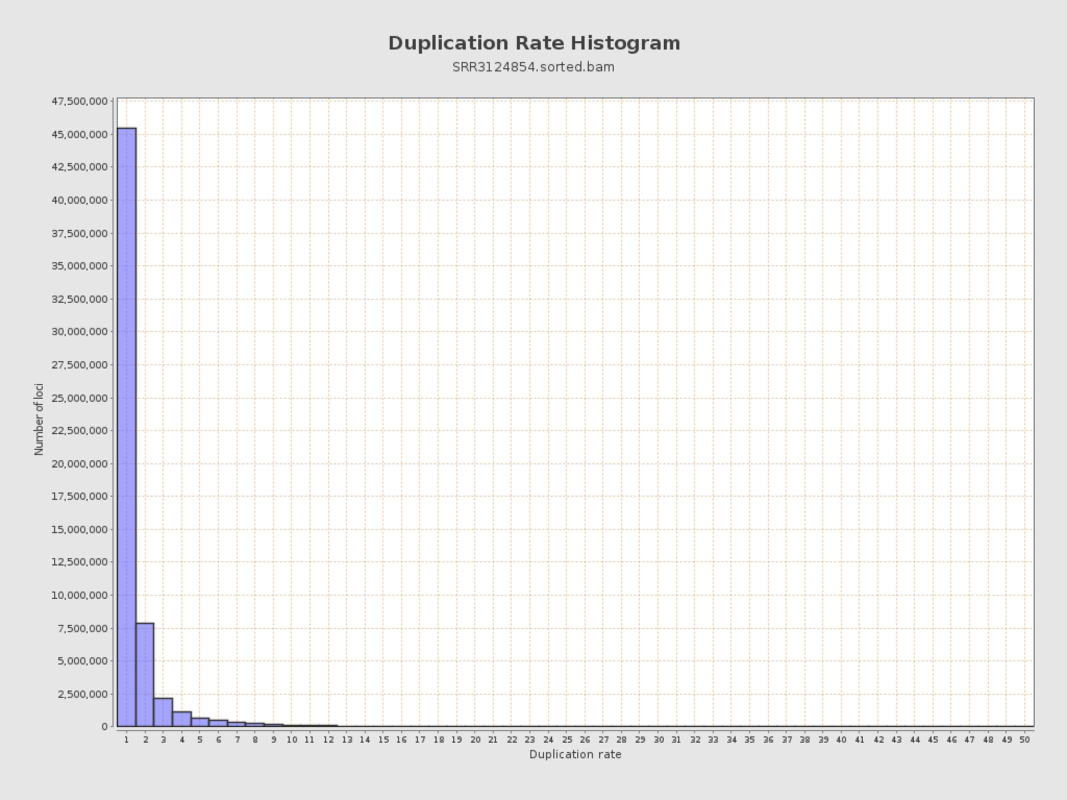
5. Results : Coverage Histogram (0-50X)



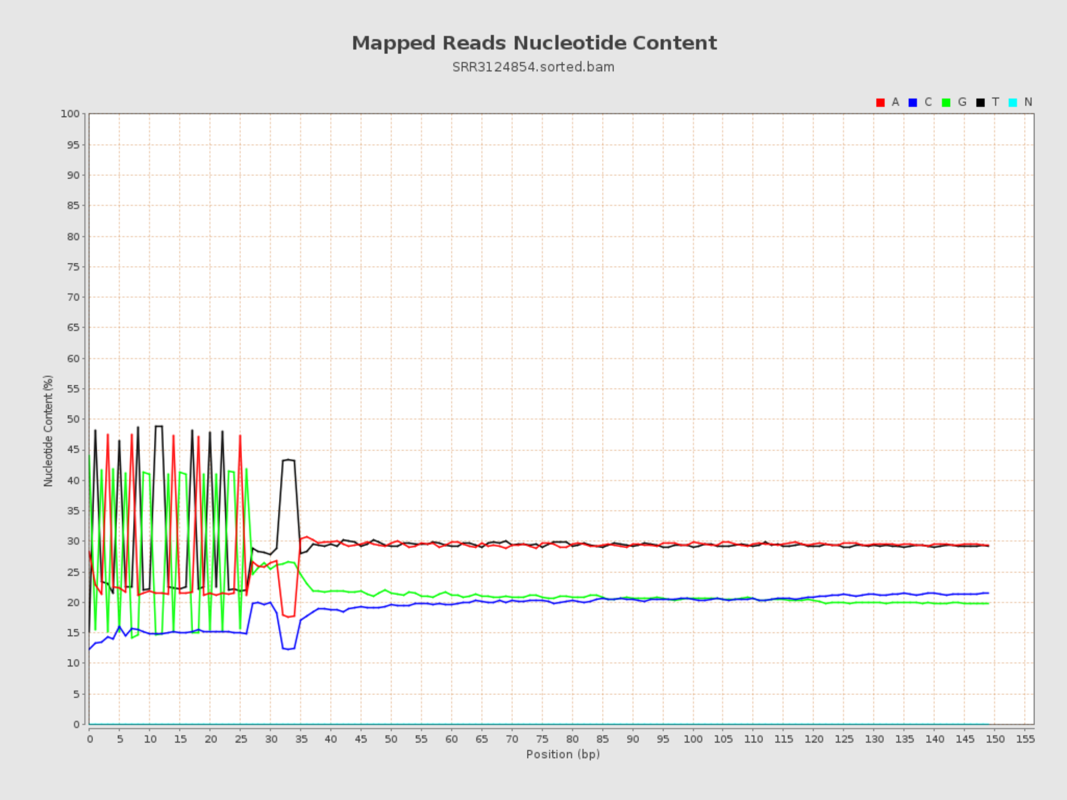
6. Results : Genome Fraction Coverage



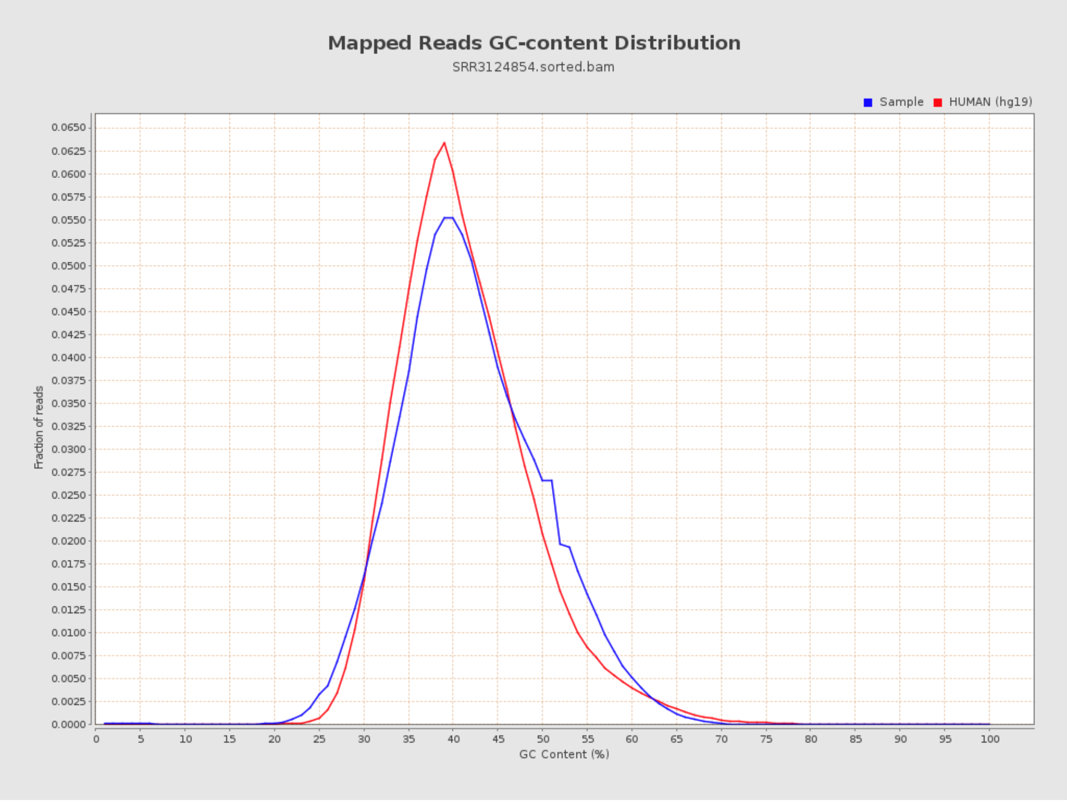
7. Results : Duplication Rate Histogram



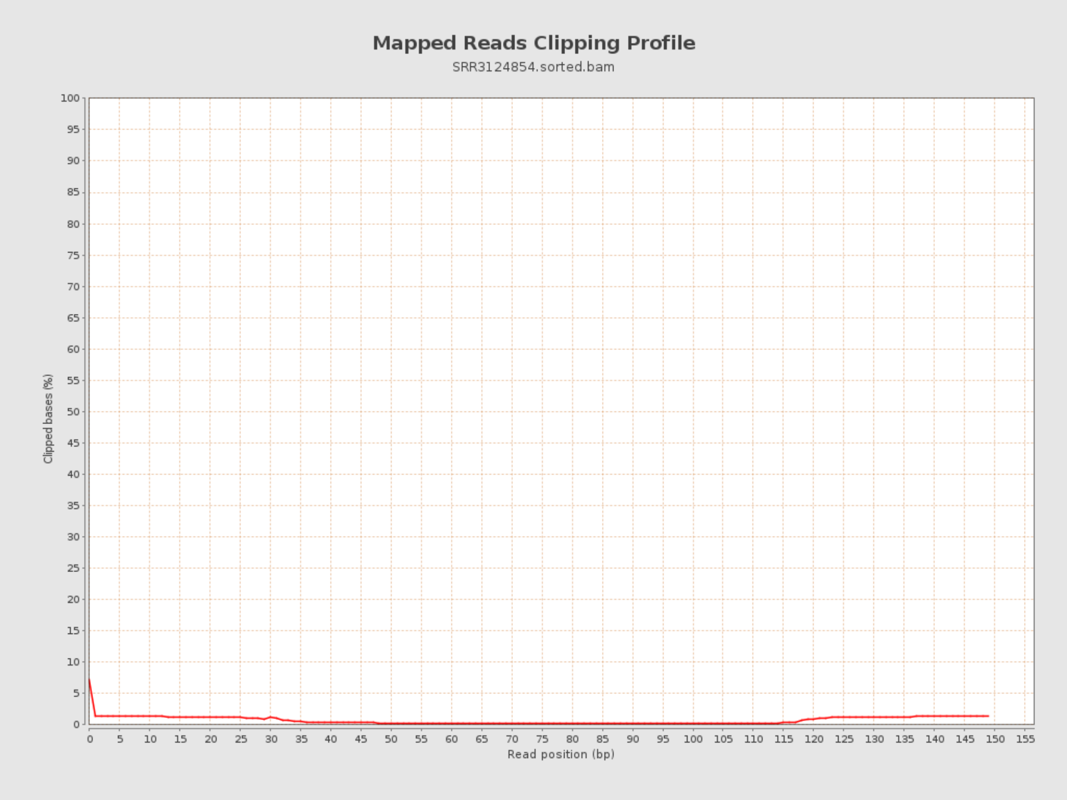
8. Results : Mapped Reads Nucleotide Content



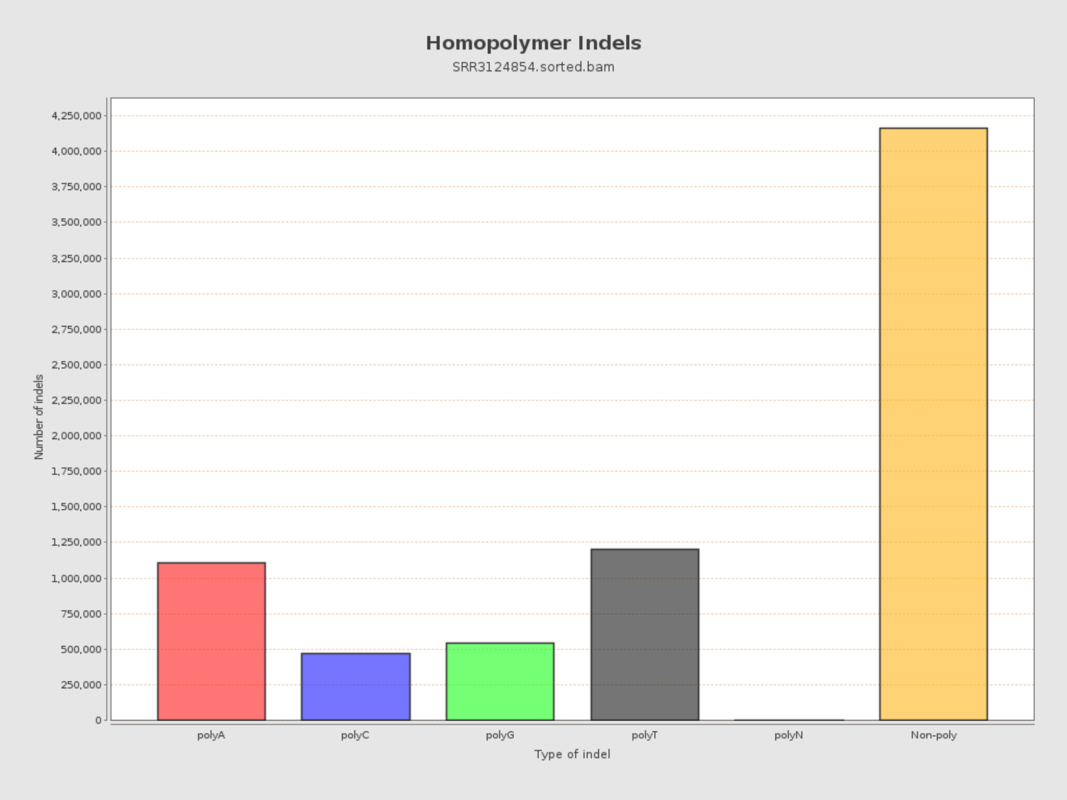
9. Results : Mapped Reads GC-content Distribution



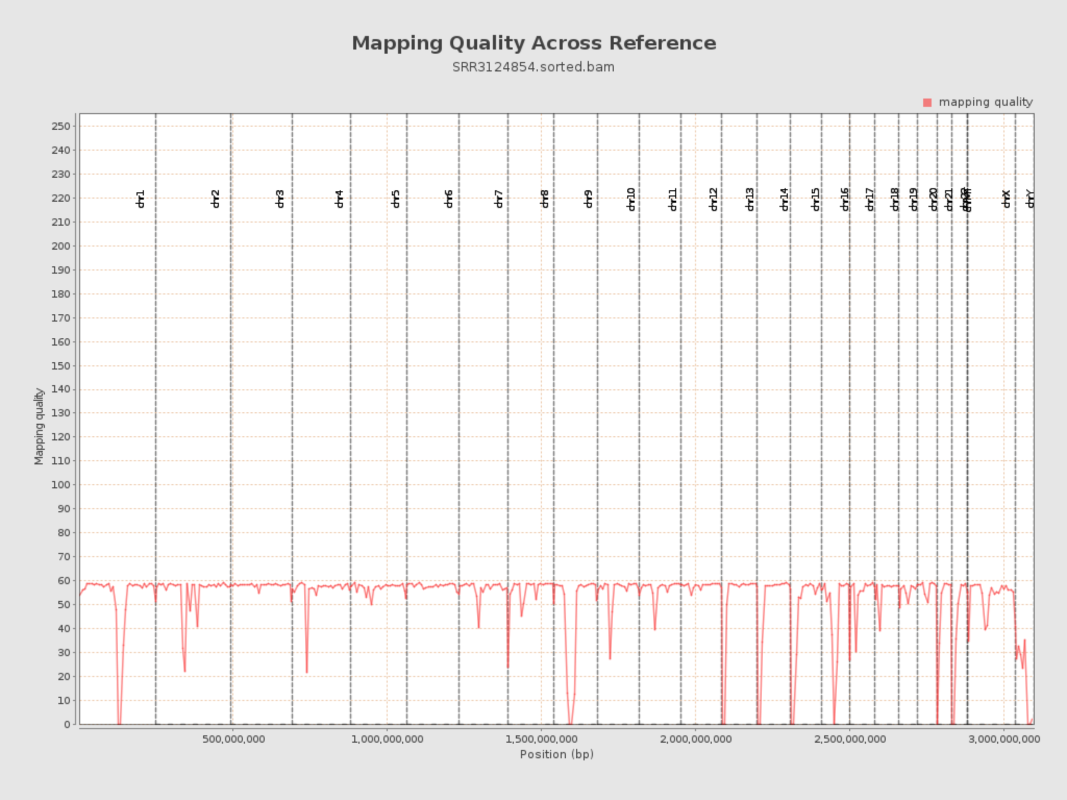
10. Results : Mapped Reads Clipping Profile



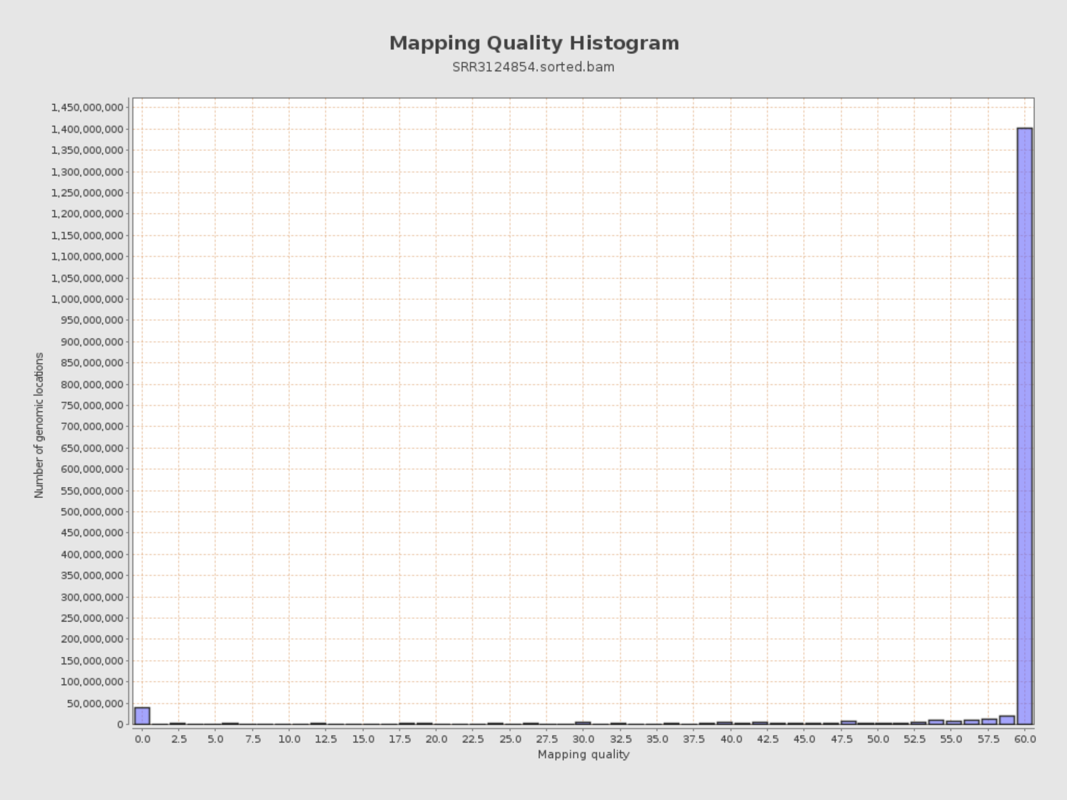
11. Results : Homopolymer Indels



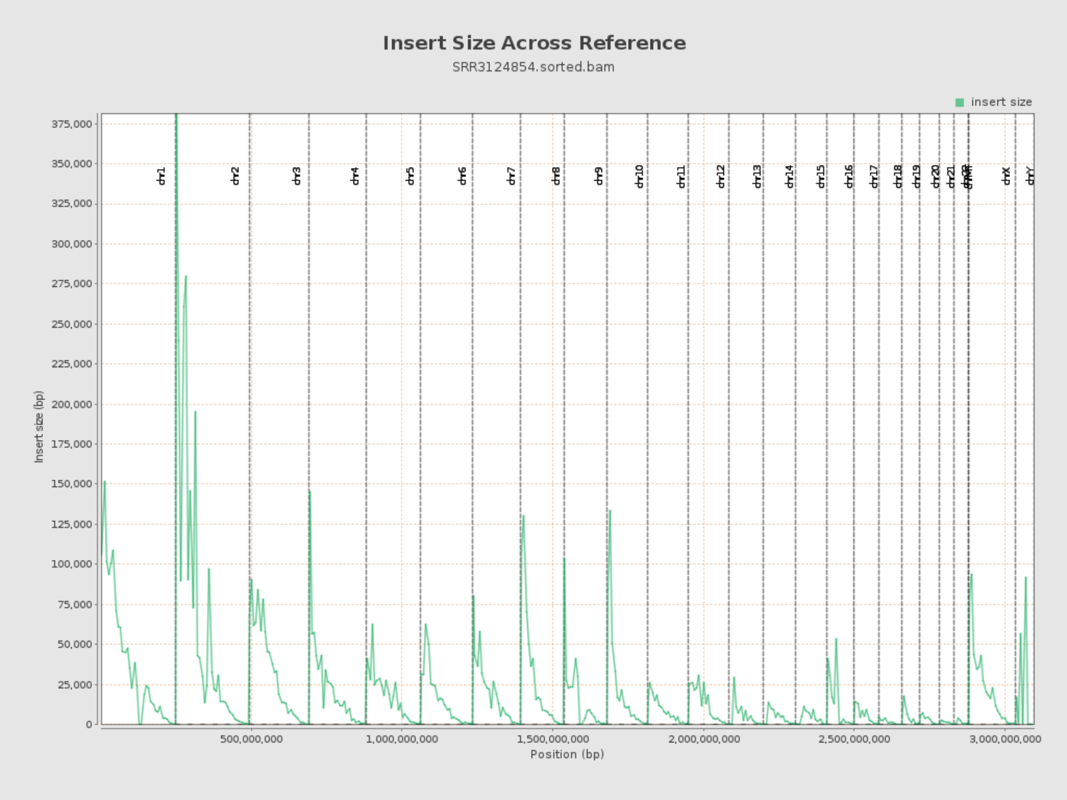
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram