Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/07 21:29:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124845.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_SRR3124845 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124845_1.fastq.gz SRR3124845_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Dec 07 21:29:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124845.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	80,086,784
Mapped reads	76,014,408 / 94.92%
Unmapped reads	4,072,376 / 5.08%
Mapped paired reads	76,014,408 / 94.92%
Mapped reads, first in pair	39,067,471 / 48.78%
Mapped reads, second in pair	36,946,937 / 46.13%
Mapped reads, both in pair	73,455,830 / 91.72%
Mapped reads, singletons	2,558,578 / 3.19%
Secondary alignments	0
Supplementary alignments	2,529,236 / 3.16%
Read min/max/mean length	30 / 150 / 151.48
Duplicated reads (estimated)	30,588,200 / 38.19%
Duplication rate	22.27%
Clipped reads	45,610,171 / 56.95%

2.2. ACGT Content

Number/percentage of A's	2,864,729,035 / 29.01%
Number/percentage of C's	1,887,553,511 / 19.11%
Number/percentage of T's	2,950,807,794 / 29.88%
Number/percentage of G's	2,172,812,031 / 22%
Number/percentage of N's	169,580 / 0%

GC Percentage	41.11%

2.3. Coverage

Mean	3.1935
Standard Deviation	58.6471

2.4. Mapping Quality

Mean Mapping Quality	53.02

2.5. Insert size

Mean	181,143.96
Standard Deviation	4,014,686.76
P25/Median/P75	197 / 255 / 324

2.6. Mismatches and indels

General error rate	1.51%
Mismatches	140,460,526
Insertions	2,477,166
Mapped reads with at least one insertion	2.97%
Deletions	4,309,068
Mapped reads with at least one deletion	5.36%
Homopolymer indels	42.72%

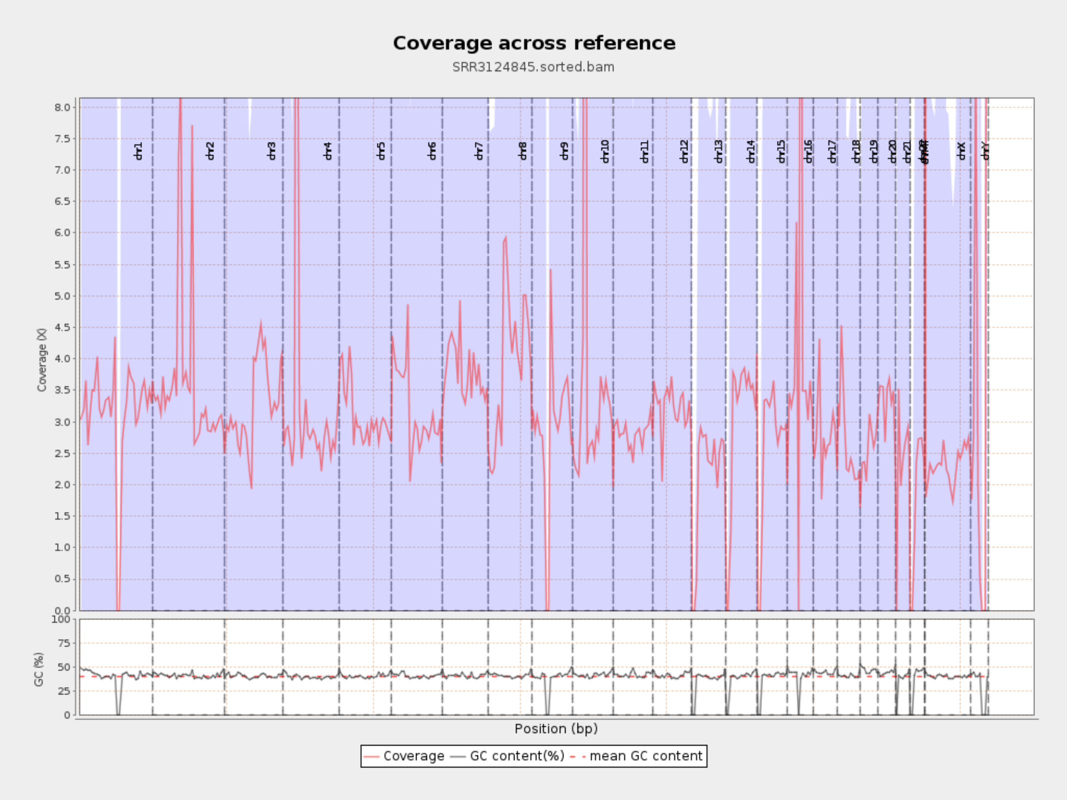
2.7. Chromosome stats

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

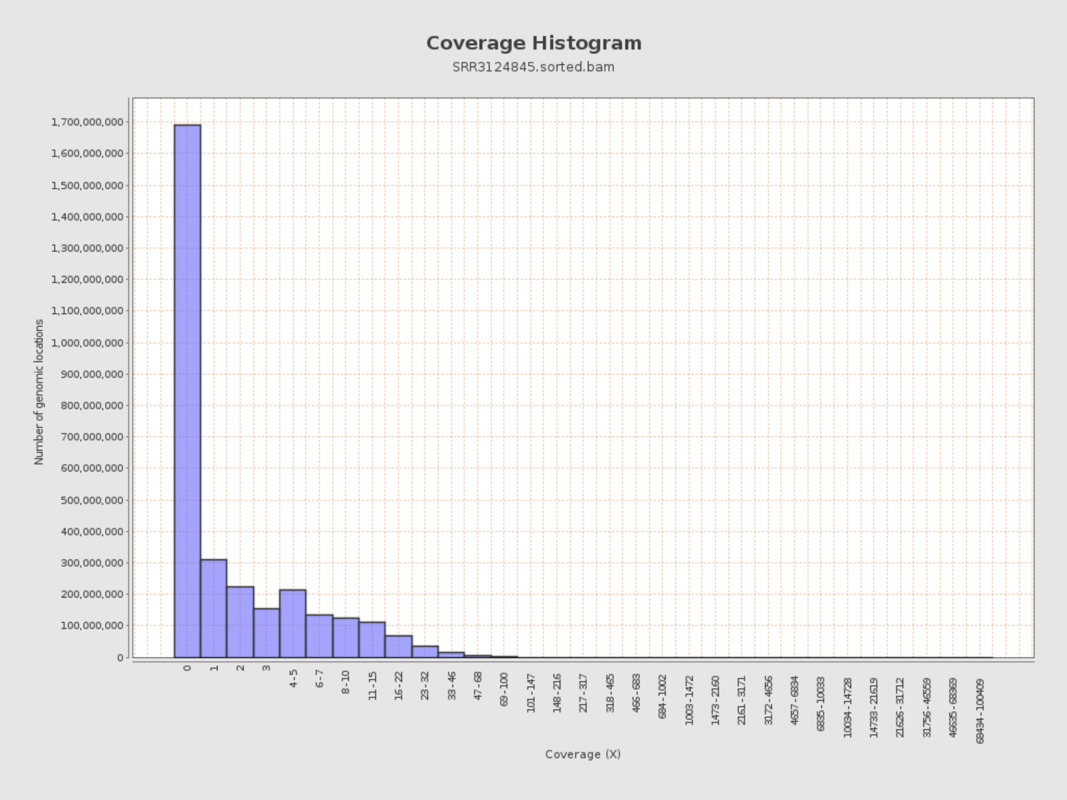
		bases	**coverage**	**deviation**
chr1	249250621	783837770	3.1448	22.9798
chr2	243199373	891251398	3.6647	65.3852
chr3	198022430	648631199	3.2755	8.3
chr4	191154276	625063798	3.2699	81.8652
chr5	180915260	560495319	3.0981	8.4583
chr6	171115067	548905743	3.2078	14.5494
chr7	159138663	604589665	3.7991	24.8737
chr8	146364022	583384858	3.9858	12.1434
chr9	141213431	399547650	2.8294	53.902
chr10	135534747	589390866	4.3486	196.7863
chr11	135006516	377876512	2.799	13.777
chr12	133851895	433203833	3.2364	19.3678
chr13	115169878	246150285	2.1373	5.4218
chr14	107349540	319280192	2.9742	8.773
chr15	102531392	261399446	2.5495	10.1198
chr16	90354753	391768482	4.3359	91.0892
chr17	81195210	223116904	2.7479	31.2813
chr18	78077248	207291094	2.6549	45.8206
chr19	59128983	151069971	2.5549	14.343
chr20	63025520	210772452	3.3442	26.2685
chr21	48129895	116420077	2.4189	38.954
chr22	51304566	91273376	1.779	8.6128
chrMT	16571	4004037	241.6292	113.25
chrX	155270560	356869036	2.2984	9.4249

chrY	59373566	260591182	4.389	136.9645

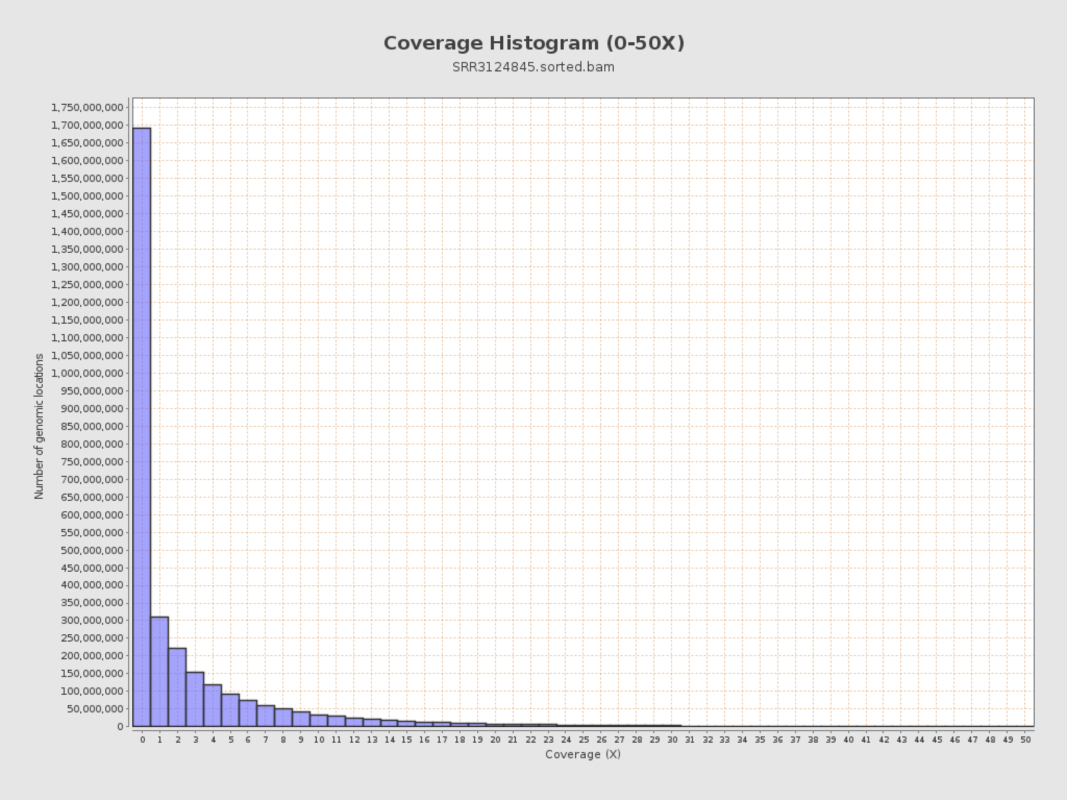
3. Results : Coverage across reference



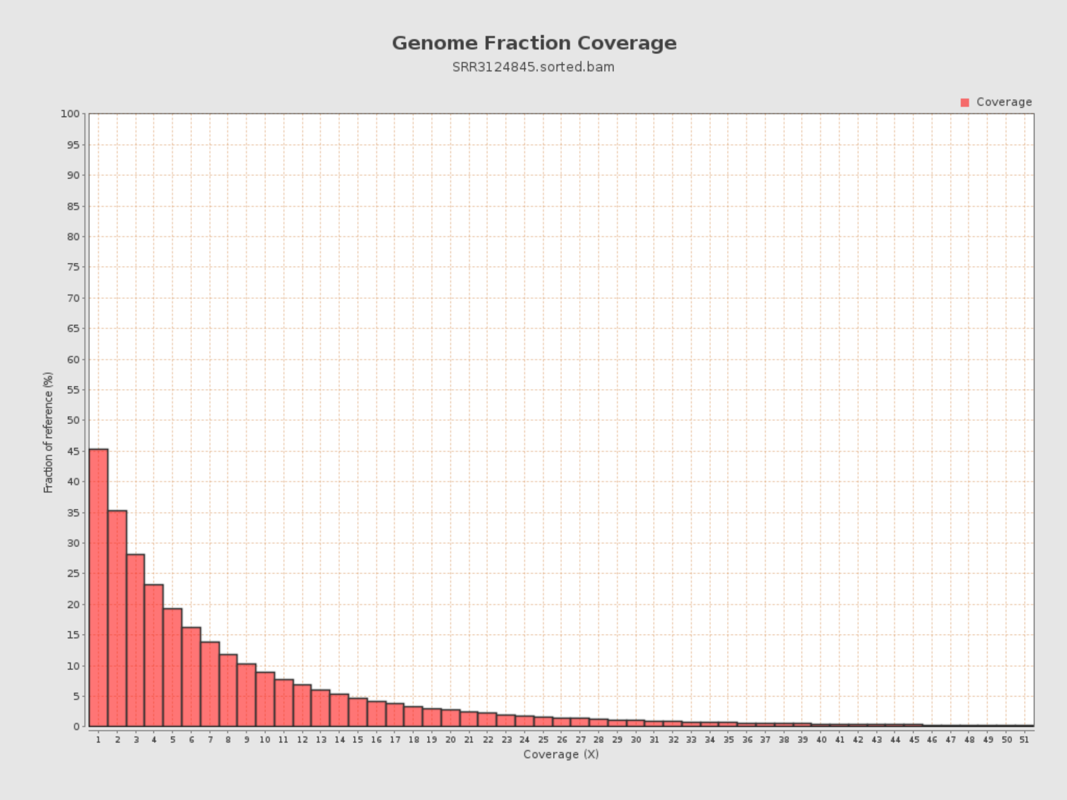
4. Results : Coverage Histogram



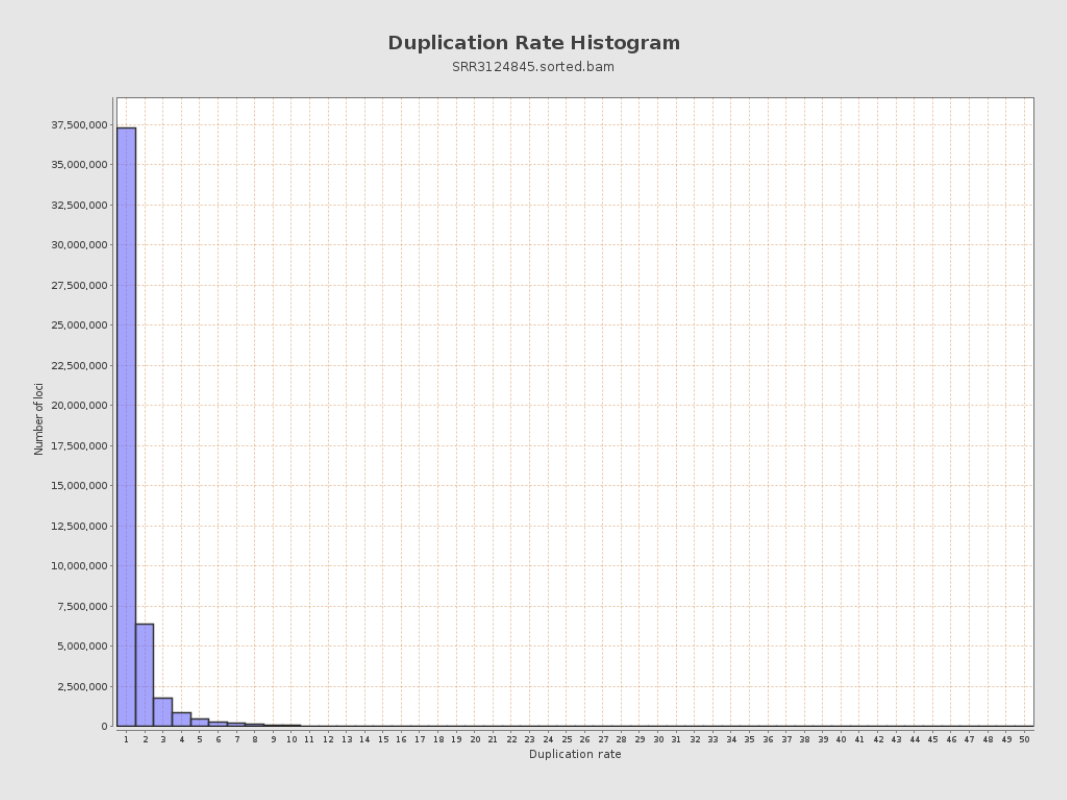
5. Results : Coverage Histogram (0-50X)



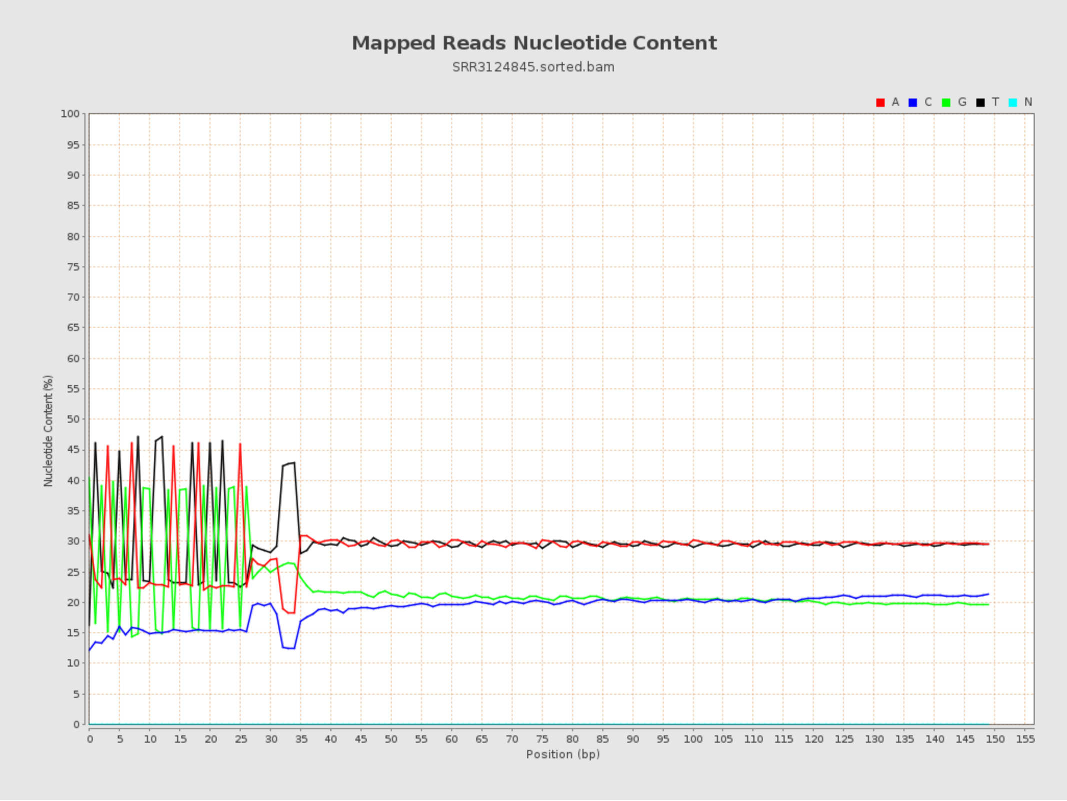
6. Results : Genome Fraction Coverage



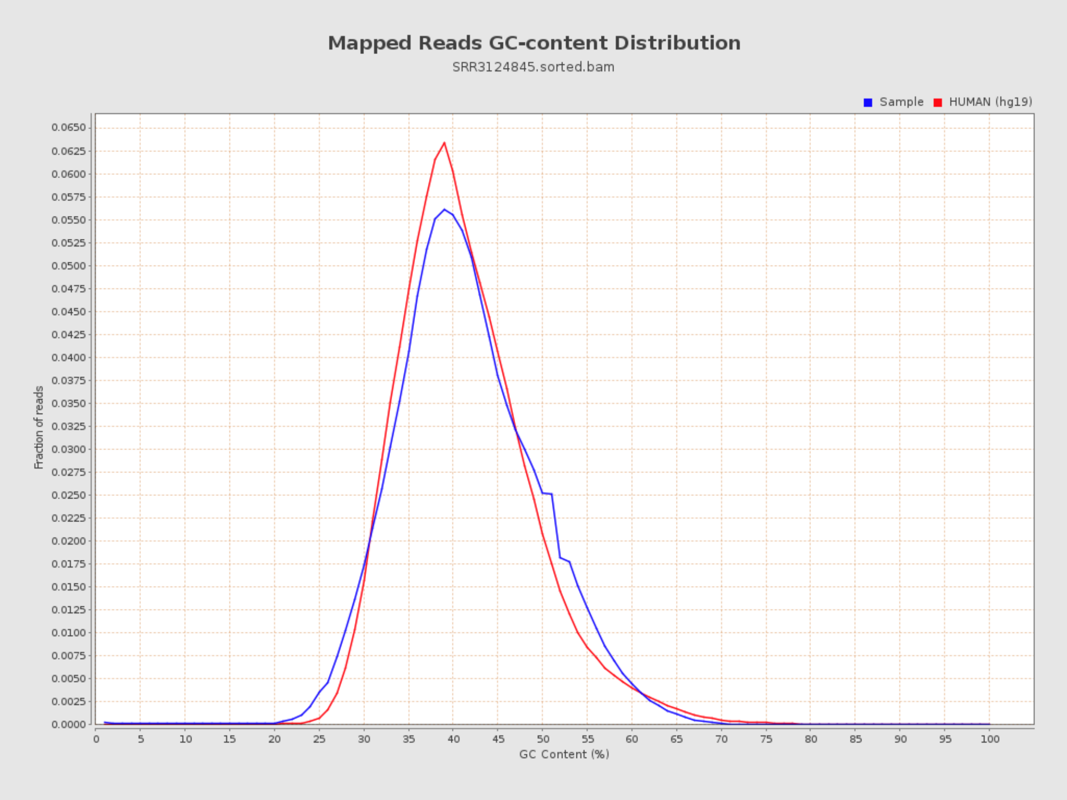
7. Results : Duplication Rate Histogram



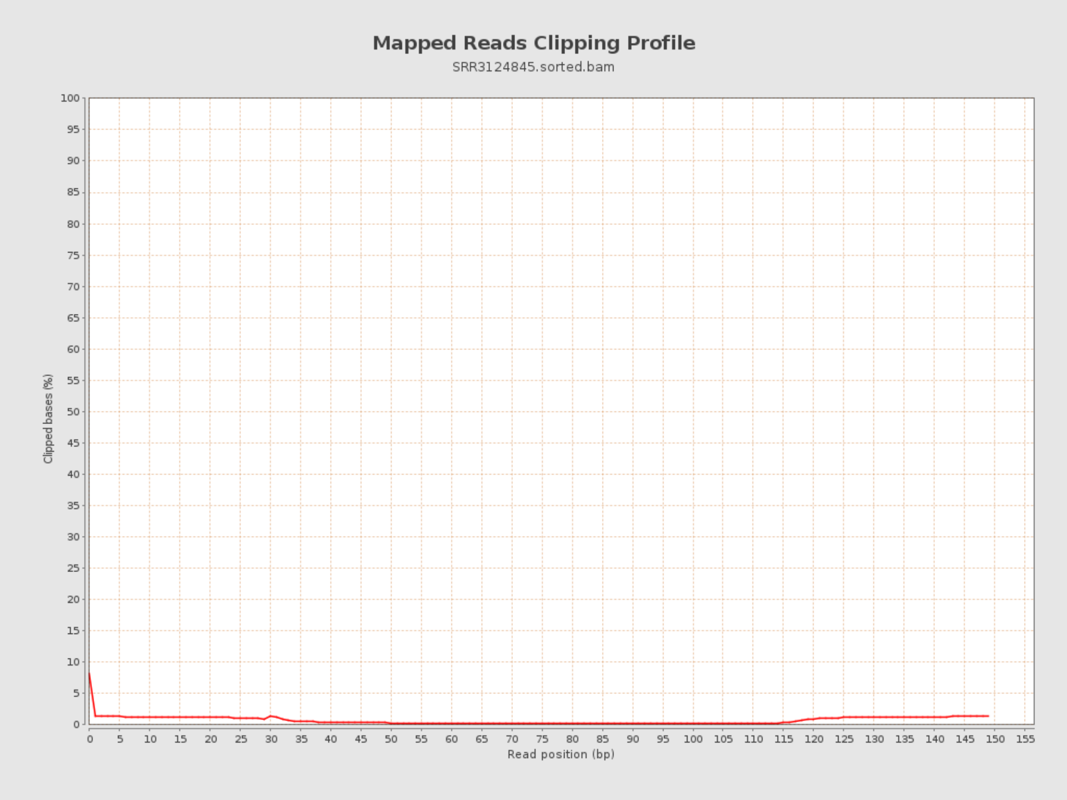
8. Results : Mapped Reads Nucleotide Content



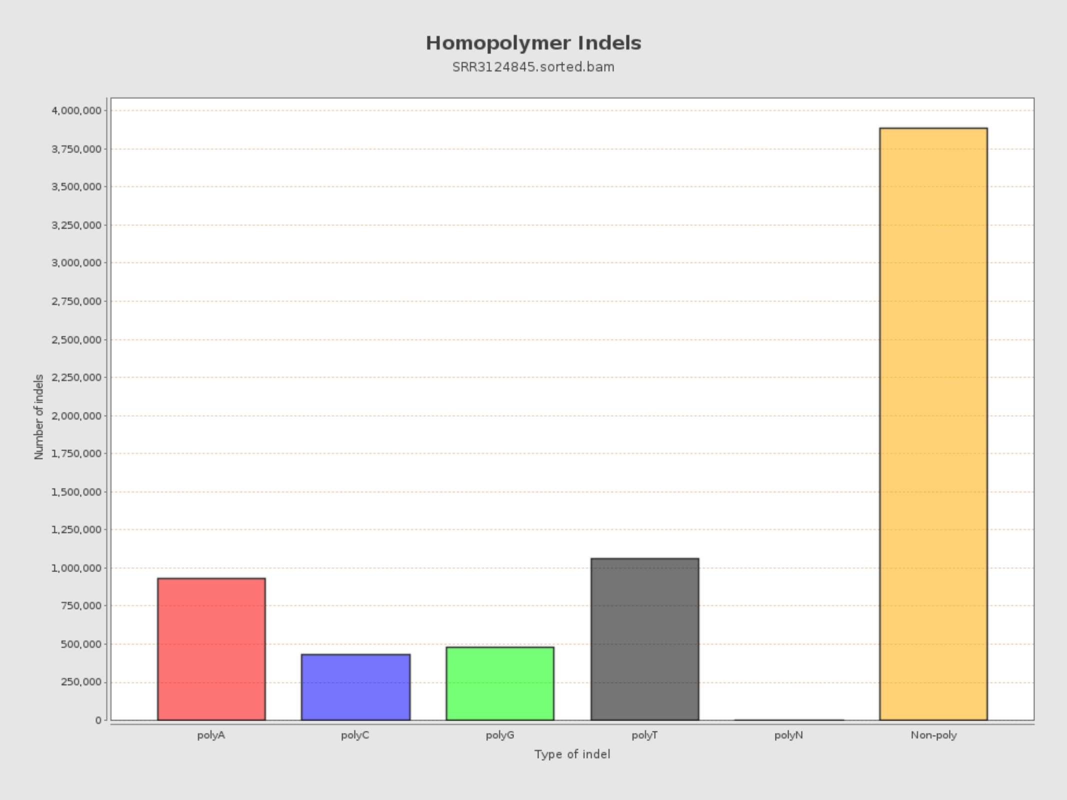
9. Results : Mapped Reads GC-content Distribution



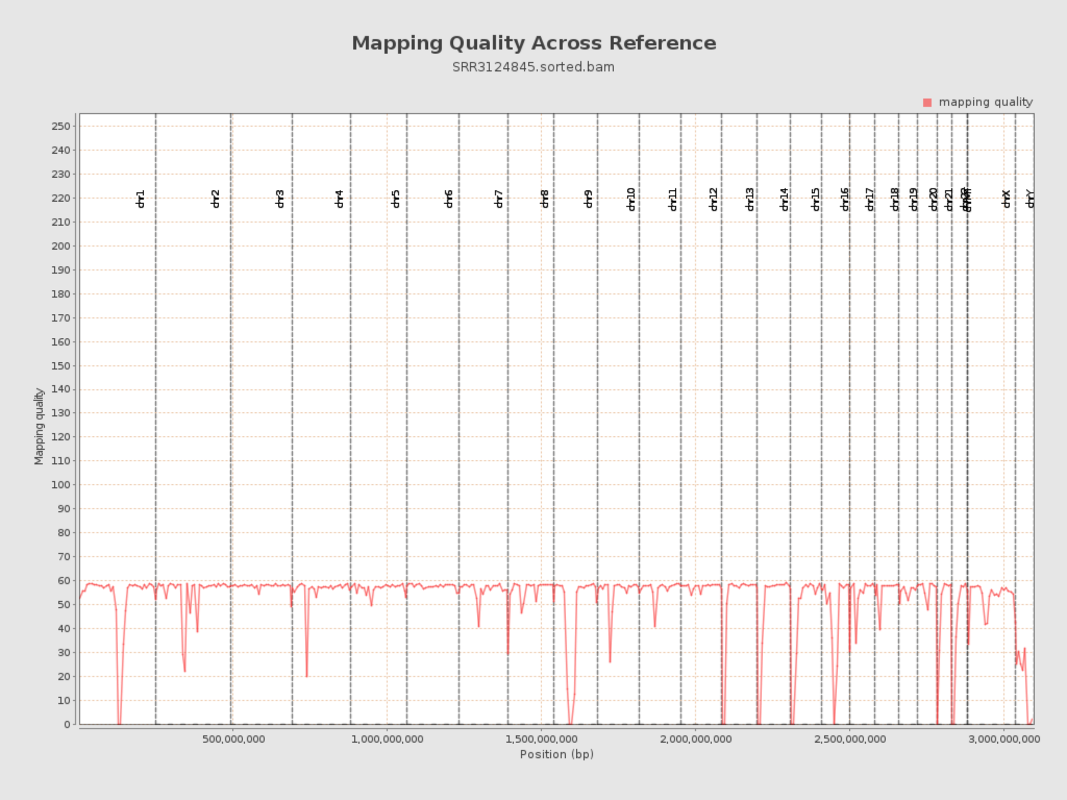
10. Results : Mapped Reads Clipping Profile



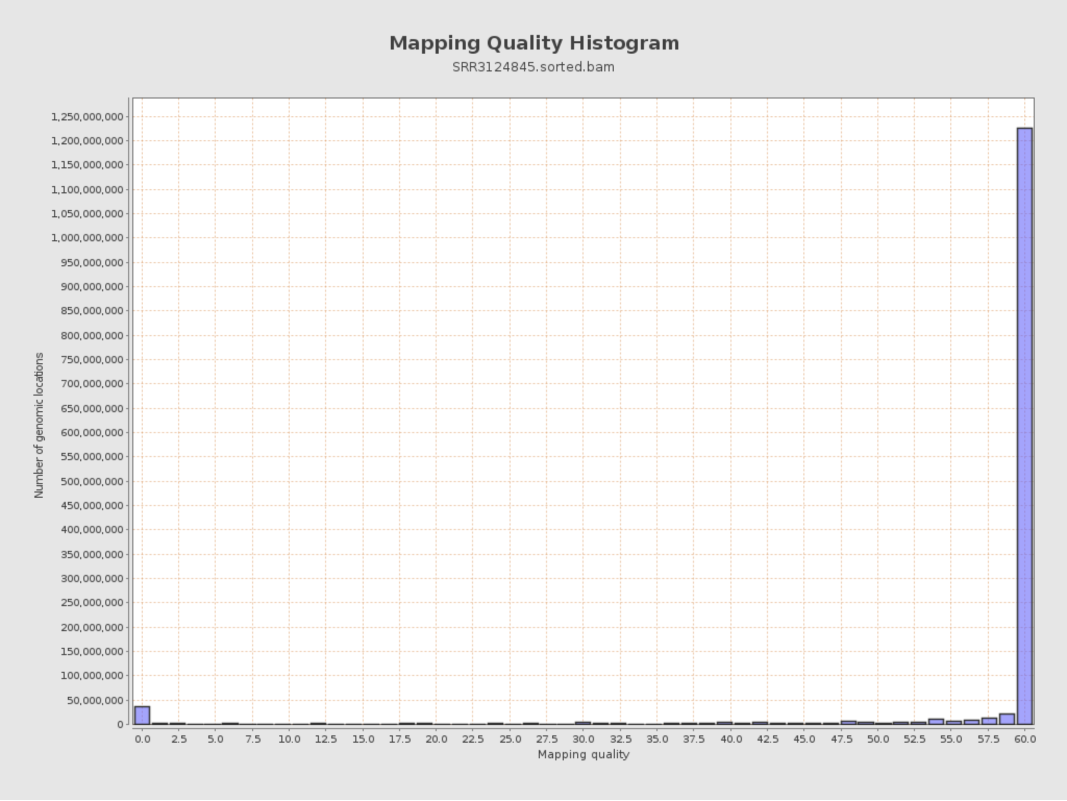
11. Results : Homopolymer Indels



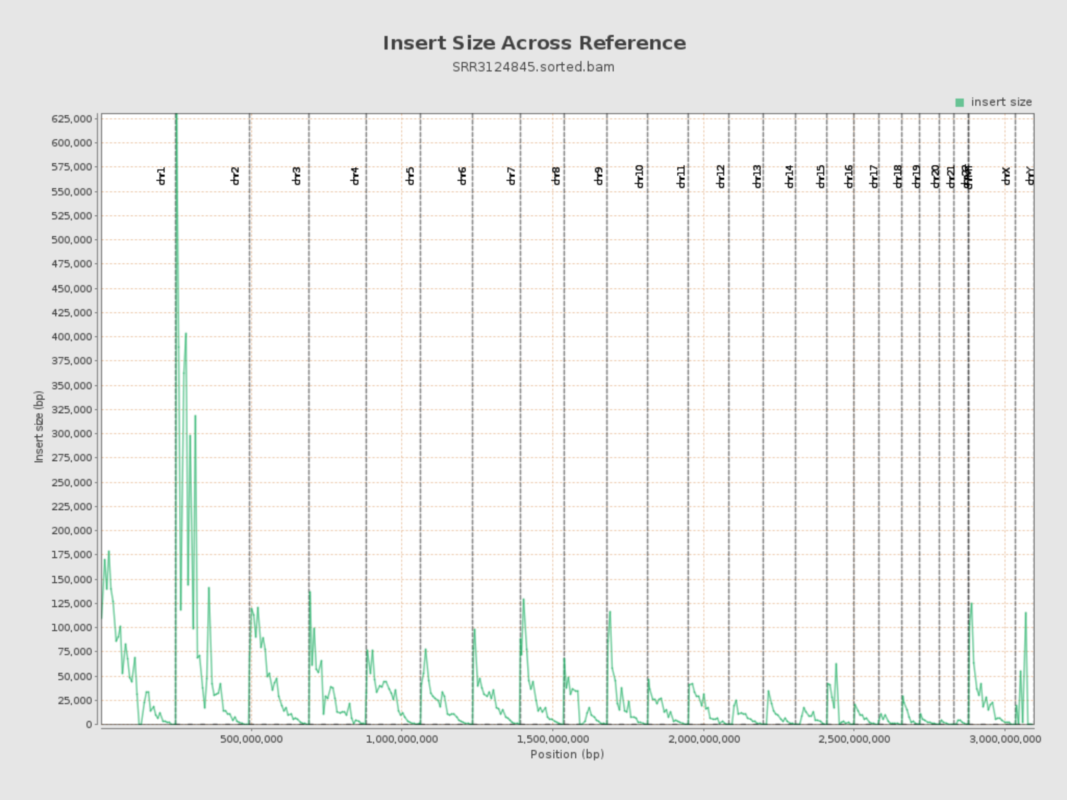
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram