Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 06:36:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124928.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_SRR3124928 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124928_1.fastq.gz SRR3124928_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 06:36:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124928.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,083,784
Mapped reads	5,029,109 / 98.92%
Unmapped reads	54,675 / 1.08%
Mapped paired reads	5,029,109 / 98.92%
Mapped reads, first in pair	2,527,132 / 49.71%
Mapped reads, second in pair	2,501,977 / 49.21%
Mapped reads, both in pair	5,001,360 / 98.38%
Mapped reads, singletons	27,749 / 0.55%
Secondary alignments	0
Supplementary alignments	41,262 / 0.81%
Read min/max/mean length	30 / 151 / 151.39
Duplicated reads (estimated)	823,391 / 16.2%
Duplication rate	12.59%
Clipped reads	2,872,010 / 56.49%

2.2. ACGT Content

Number/percentage of A's	192,454,531 / 28.55%
Number/percentage of C's	133,223,378 / 19.77%
Number/percentage of T's	196,250,054 / 29.12%
Number/percentage of G's	152,104,842 / 22.57%
Number/percentage of N's	189 / 0%

GC Percentage	42.33%

2.3. Coverage

Mean	0.2179
Standard Deviation	2.5594

2.4. Mapping Quality

Mean Mapping Quality	53.87

2.5. Insert size

Mean	36,043.85
Standard Deviation	1,814,619.47
P25/Median/P75	157 / 212 / 292

2.6. Mismatches and indels

General error rate	0.83%
Mismatches	5,294,739
Insertions	101,581
Mapped reads with at least one insertion	1.9%
Deletions	206,321
Mapped reads with at least one deletion	3.95%
Homopolymer indels	48.35%

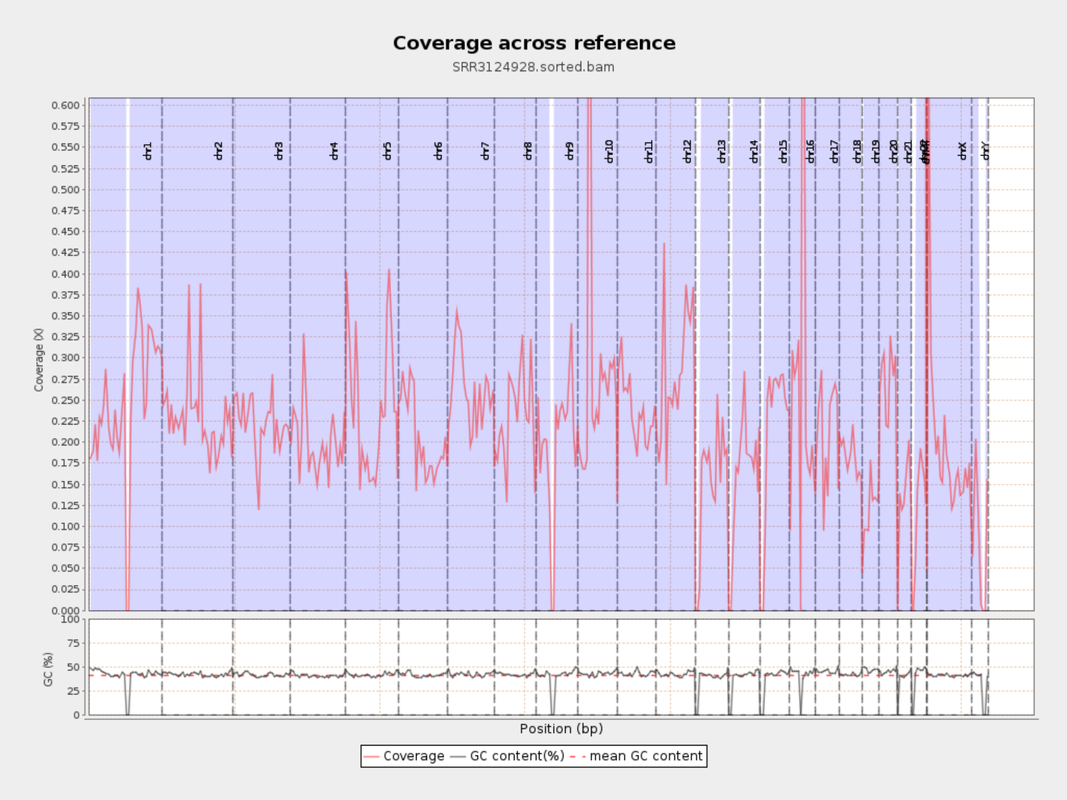
2.7. Chromosome stats

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

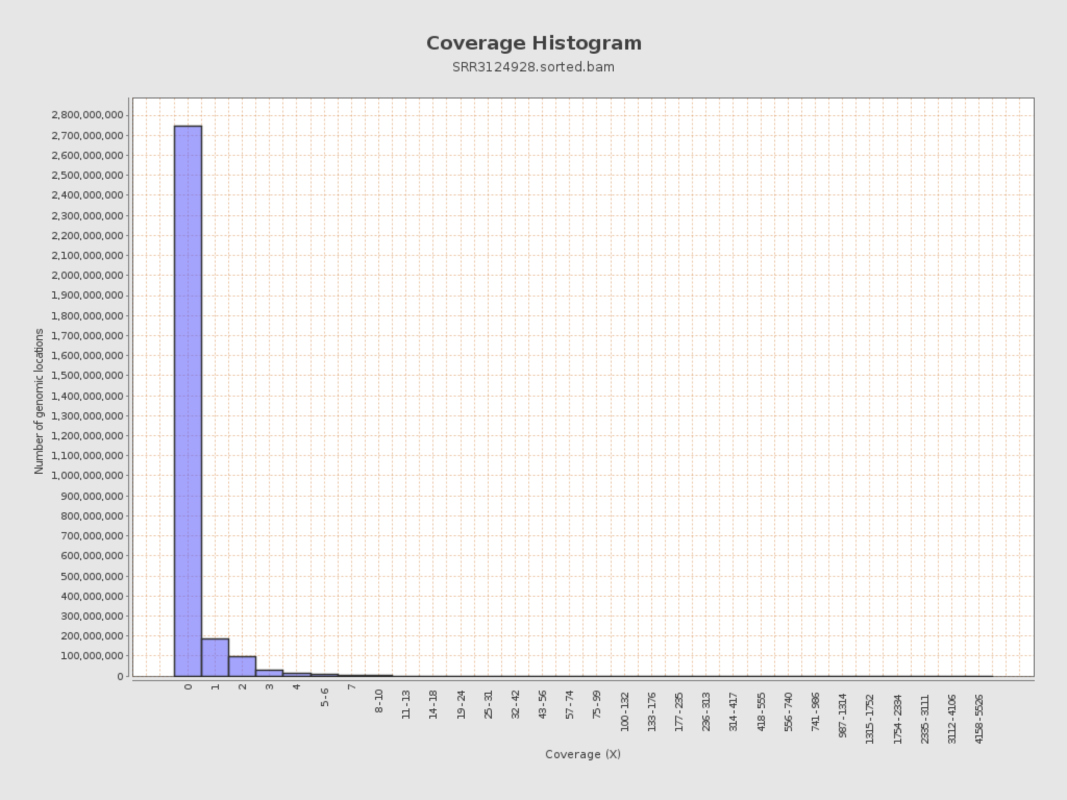
		bases	coverage	deviation
chr1	249250621	61224675	0.2456	1.2408
chr2	243199373	56104724	0.2307	2.1117
chr3	198022430	43660973	0.2205	0.7768
chr4	191154276	38001726	0.1988	1.3895
chr5	180915260	43566045	0.2408	0.819
chr6	171115067	35321538	0.2064	0.8351
chr7	159138663	41917629	0.2634	1.6559
chr8	146364022	34103460	0.233	0.8472
chr9	141213431	28015013	0.1984	1.8754
chr10	135534747	38735813	0.2858	9.2511
chr11	135006516	31937377	0.2366	1.7968
chr12	133851895	37727291	0.2819	0.8898
chr13	115169878	17194520	0.1493	0.6079
chr14	107349540	17061403	0.1589	0.6699
chr15	102531392	21831220	0.2129	0.7599
chr16	90354753	25157773	0.2784	6.3067
chr17	81195210	17139738	0.2111	1.8166
chr18	78077248	14395573	0.1844	2.0247
chr19	59128983	7124537	0.1205	0.8157
chr20	63025520	17021663	0.2701	0.9263
chr21	48129895	6516111	0.1354	0.8664
chr22	51304566	5786936	0.1128	0.6339
chrMT	16571	179022	10.8033	7.4648
chrX	155270560	29970295	0.193	0.9602

chrY	59373566	4758610	0.0801	2.1246

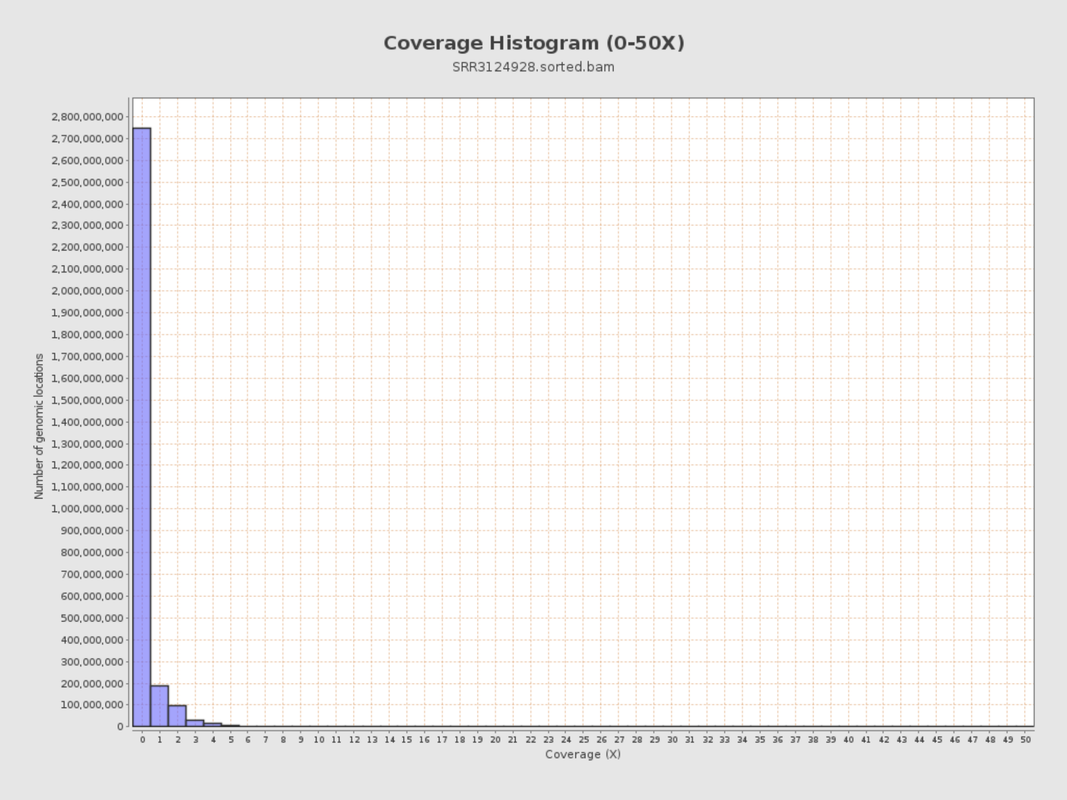
3. Results : Coverage across reference



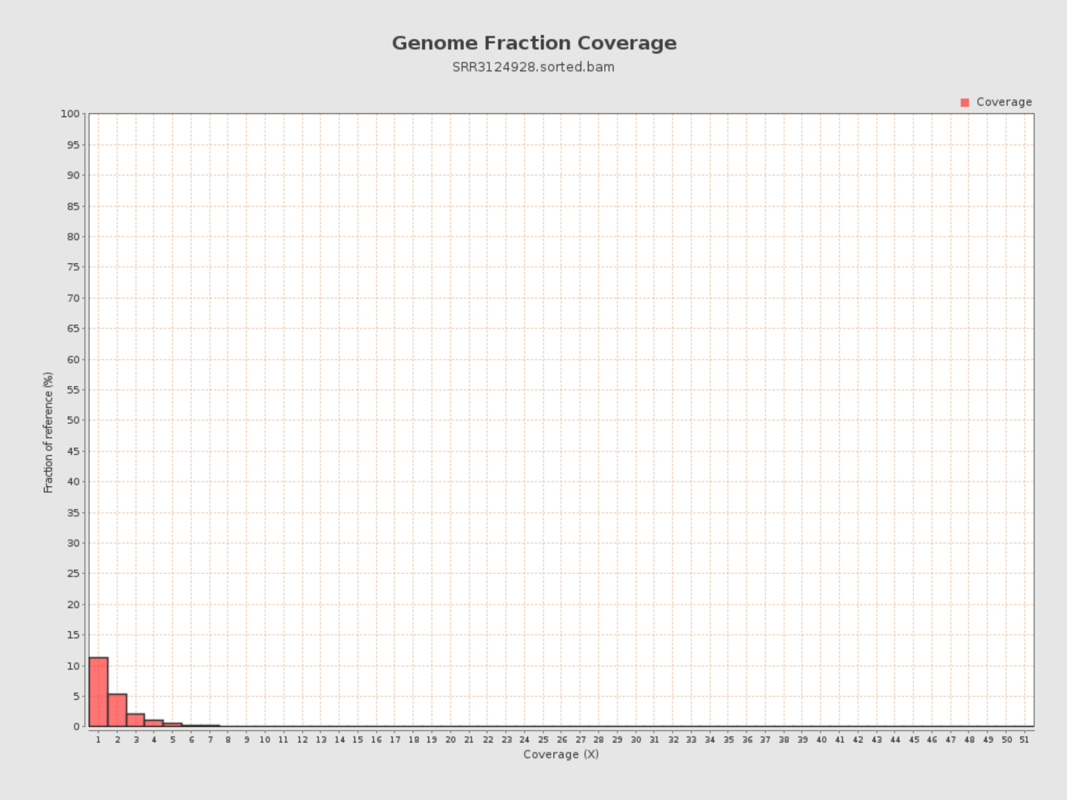
4. Results : Coverage Histogram



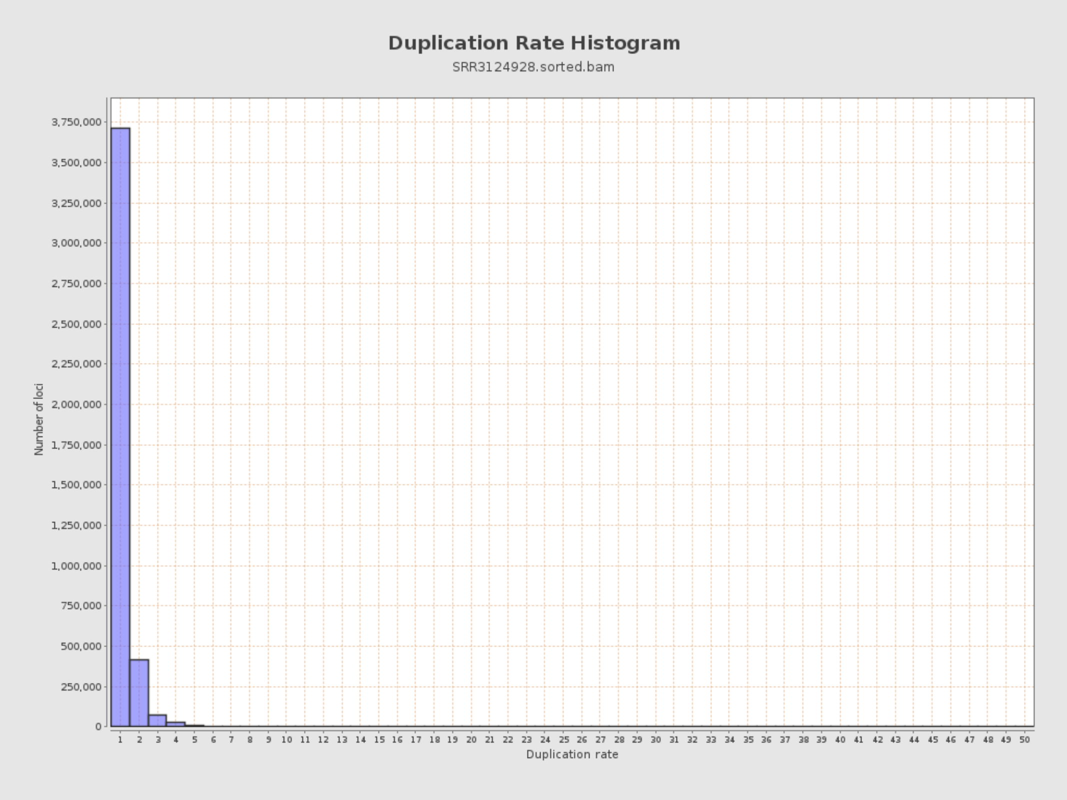
5. Results : Coverage Histogram (0-50X)



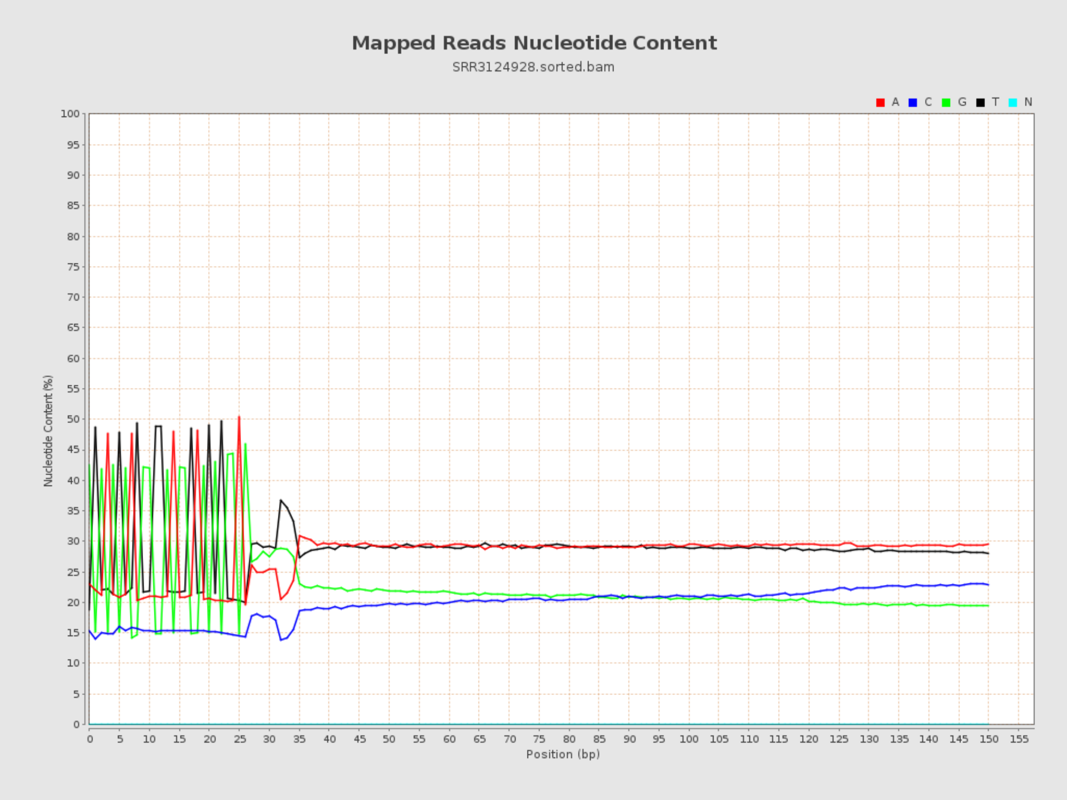
6. Results : Genome Fraction Coverage



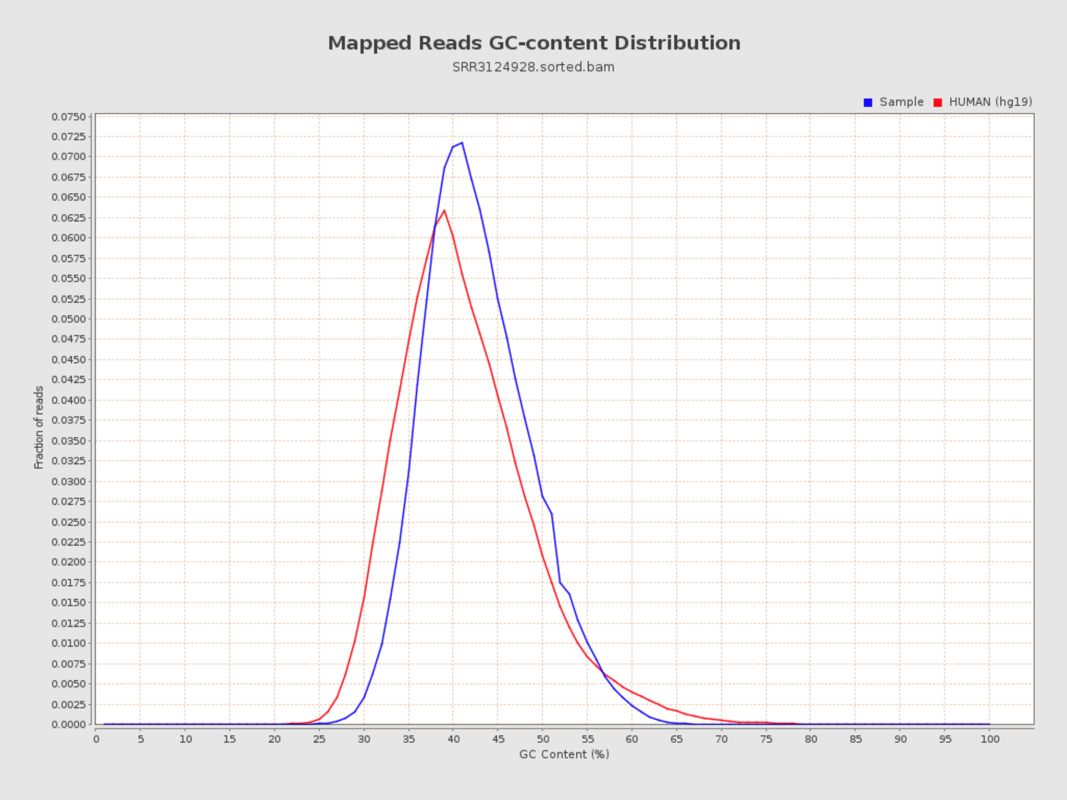
7. Results : Duplication Rate Histogram



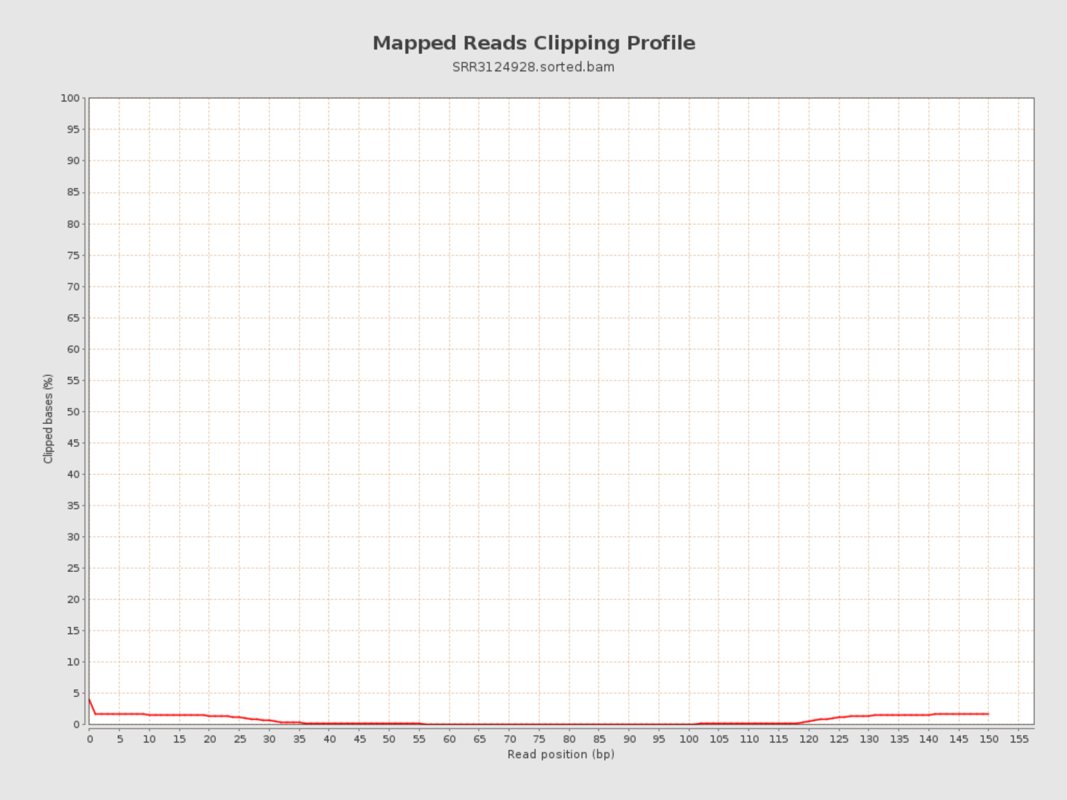
8. Results : Mapped Reads Nucleotide Content



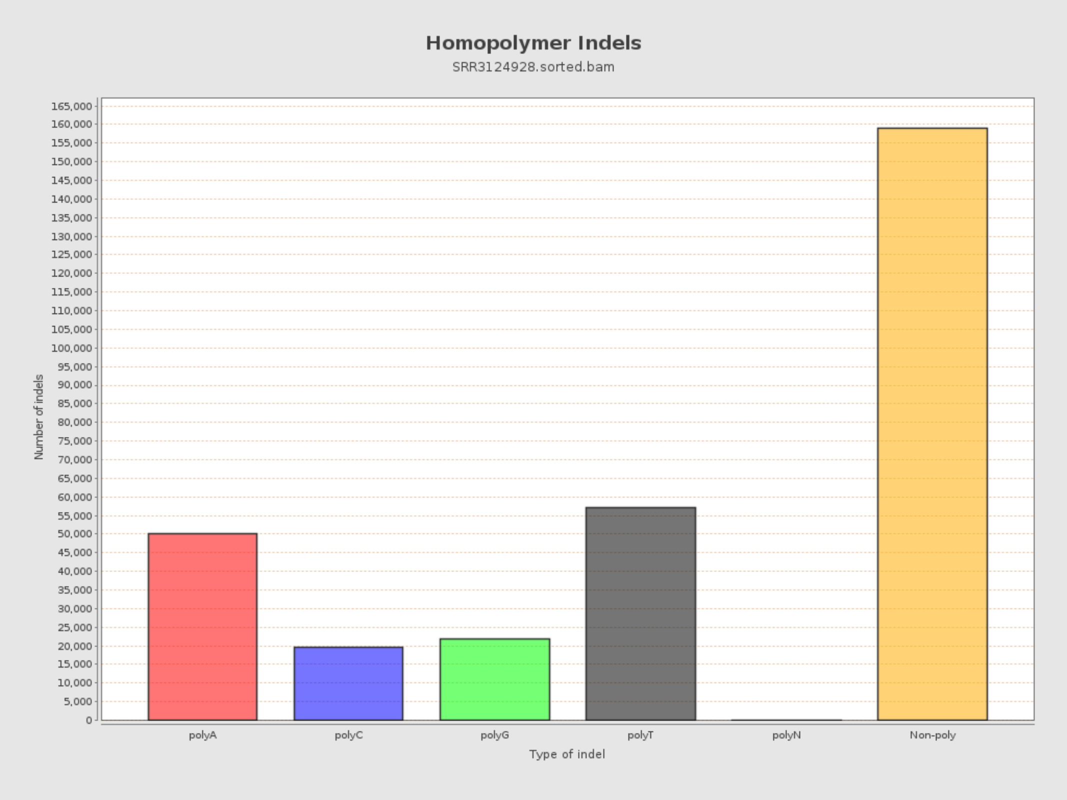
9. Results : Mapped Reads GC-content Distribution



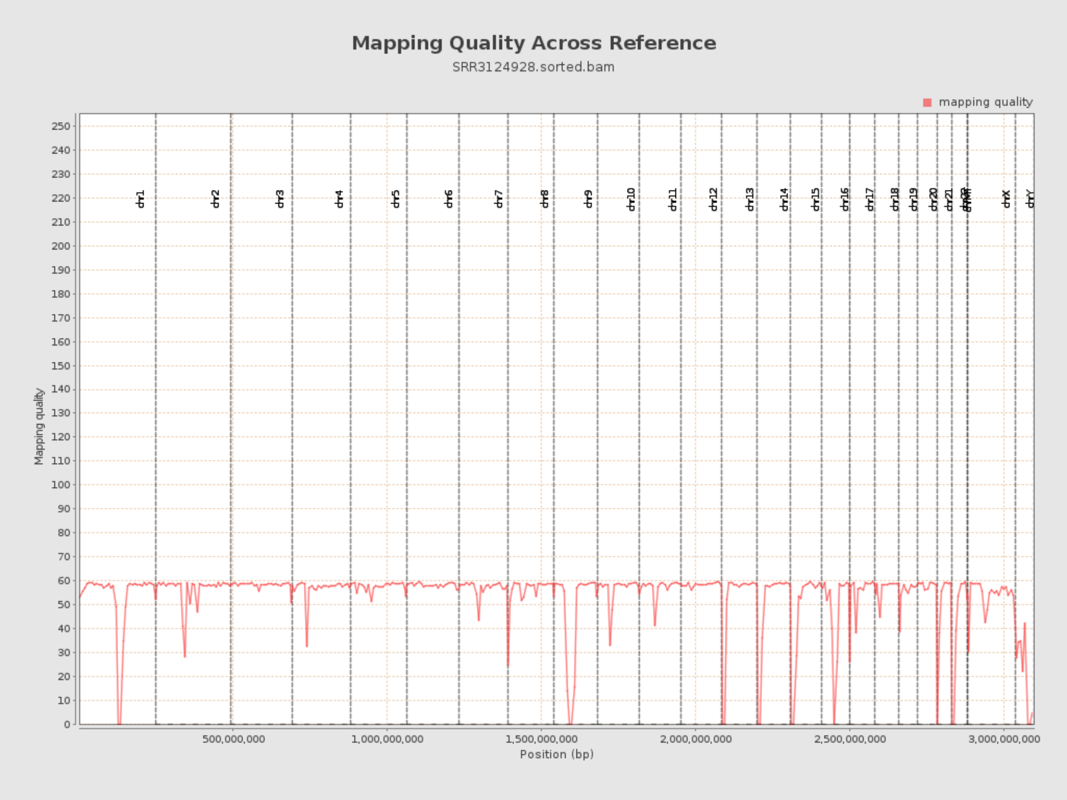
10. Results : Mapped Reads Clipping Profile



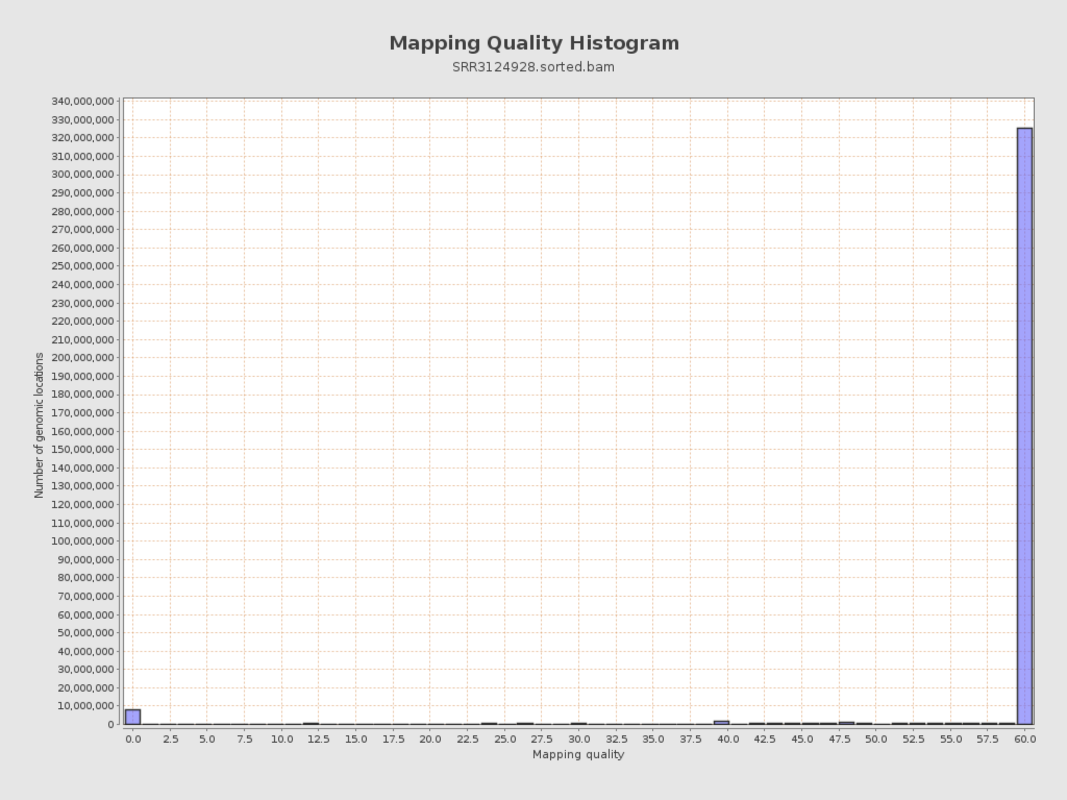
11. Results : Homopolymer Indels



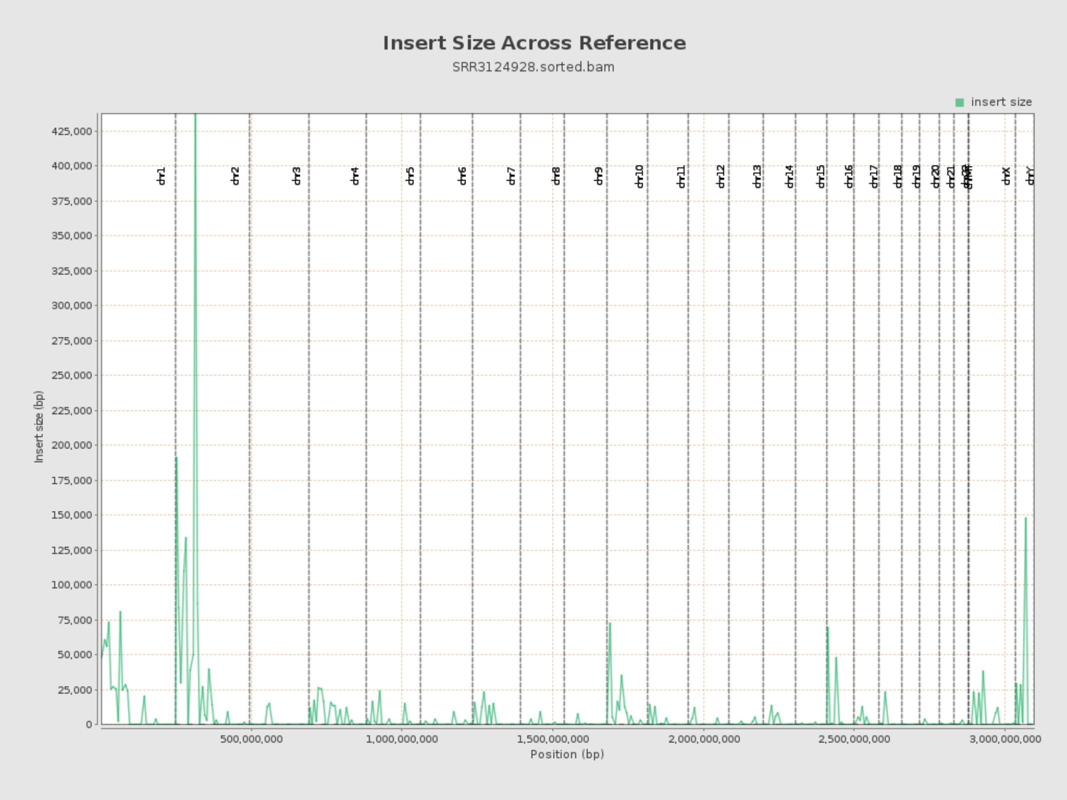
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram