Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 03:42:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124907.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_SRR3124907 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124907_1.fastq.gz SRR3124907_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 03:41:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124907.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,405,348
Mapped reads	2,358,451 / 98.05%
Unmapped reads	46,897 / 1.95%
Mapped paired reads	2,358,451 / 98.05%
Mapped reads, first in pair	1,181,261 / 49.11%
Mapped reads, second in pair	1,177,190 / 48.94%
Mapped reads, both in pair	2,347,604 / 97.6%
Mapped reads, singletons	10,847 / 0.45%
Secondary alignments	0
Supplementary alignments	35,914 / 1.49%
Read min/max/mean length	30 / 151 / 151.72
Duplicated reads (estimated)	388,710 / 16.16%
Duplication rate	15.21%
Clipped reads	1,779,434 / 73.98%

2.2. ACGT Content

Number/percentage of A's	93,475,797 / 29.67%
Number/percentage of C's	62,792,380 / 19.93%
Number/percentage of T's	93,339,057 / 29.62%
Number/percentage of G's	65,441,348 / 20.77%
Number/percentage of N's	30,627 / 0.01%

GC Percentage	40.7%

2.3. Coverage

Mean	0.1019
Standard Deviation	1.4319

2.4. Mapping Quality

Mean Mapping Quality	53.52

2.5. Insert size

Mean	68,119.5
Standard Deviation	2,461,136.91
P25/Median/P75	135 / 168 / 214

2.6. Mismatches and indels

General error rate	1.21%
Mismatches	3,623,363
Insertions	68,187
Mapped reads with at least one insertion	2.72%
Deletions	116,593
Mapped reads with at least one deletion	4.74%
Homopolymer indels	45.82%

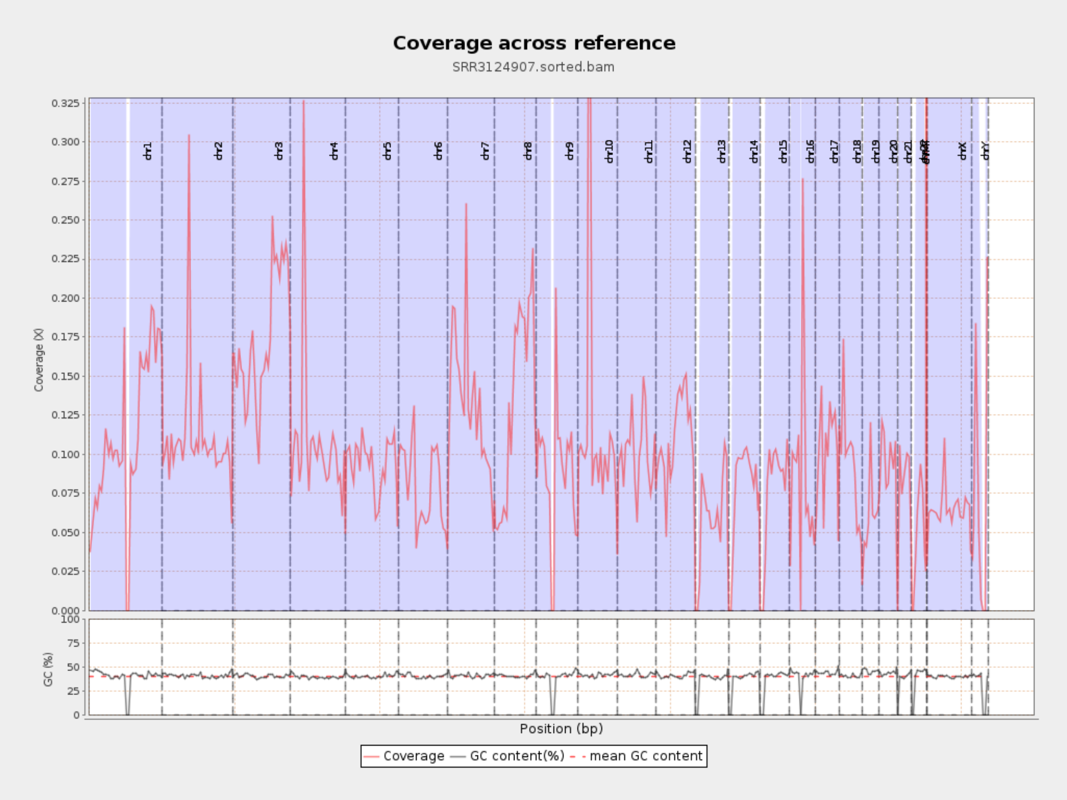
2.7. Chromosome stats

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

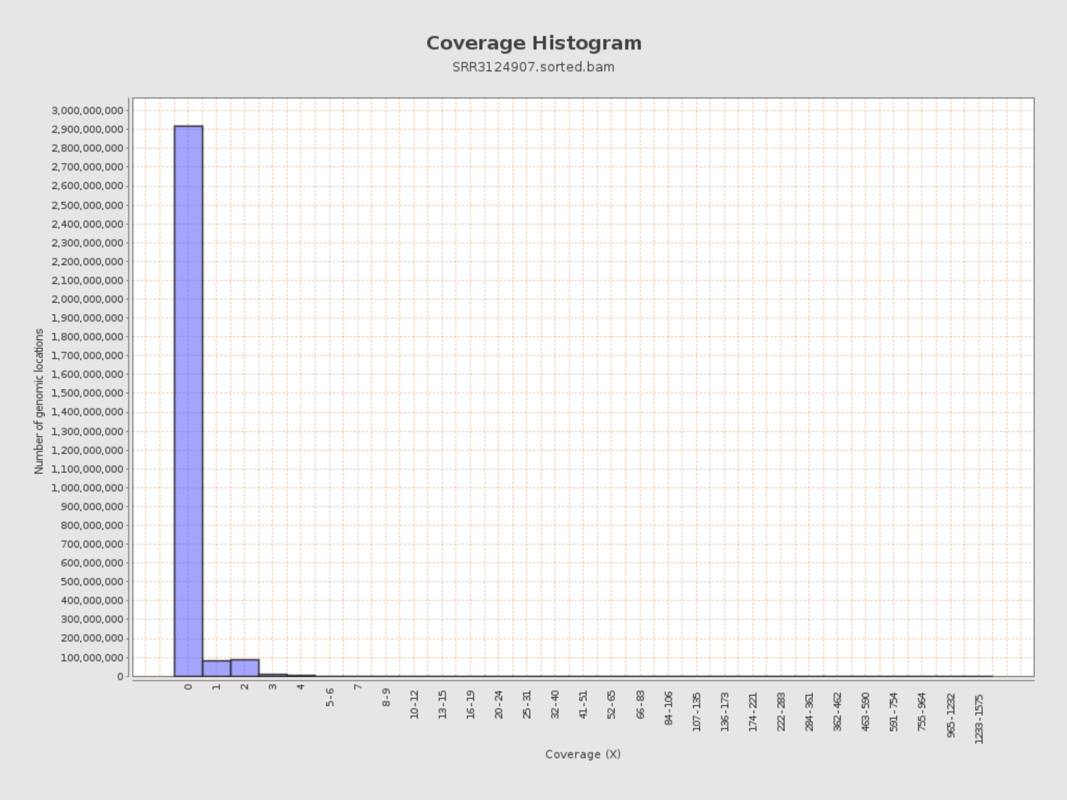
		bases	coverage	deviation
chr1	249250621	27770923	0.1114	1.6747
chr2	243199373	27044102	0.1112	1.4736
chr3	198022430	34533751	0.1744	0.5997
chr4	191154276	20188773	0.1056	1.3542
chr5	180915260	16975257	0.0938	0.4295
chr6	171115067	13652141	0.0798	0.7156
chr7	159138663	21358709	0.1342	2.494
chr8	146364022	19759315	0.135	0.6218
chr9	141213431	12766617	0.0904	2.3013
chr10	135534747	16364369	0.1207	3.2797
chr11	135006516	13611013	0.1008	1.044
chr12	133851895	14766009	0.1103	0.4627
chr13	115169878	6815849	0.0592	0.3328
chr14	107349540	8184488	0.0762	0.4059
chr15	102531392	7750385	0.0756	0.38
chr16	90354753	7587737	0.084	1.4925
chr17	81195210	8263383	0.1018	1.1636
chr18	78077248	7449583	0.0954	2.0972
chr19	59128983	3637900	0.0615	0.9208
chr20	63025520	6020045	0.0955	0.6013
chr21	48129895	3821466	0.0794	0.7674
chr22	51304566	2375669	0.0463	0.3091
chrMT	16571	278214	16.7892	9.8887
chrX	155270560	10146961	0.0654	0.5028

chrY	59373566	4201762	0.0708	2.2308

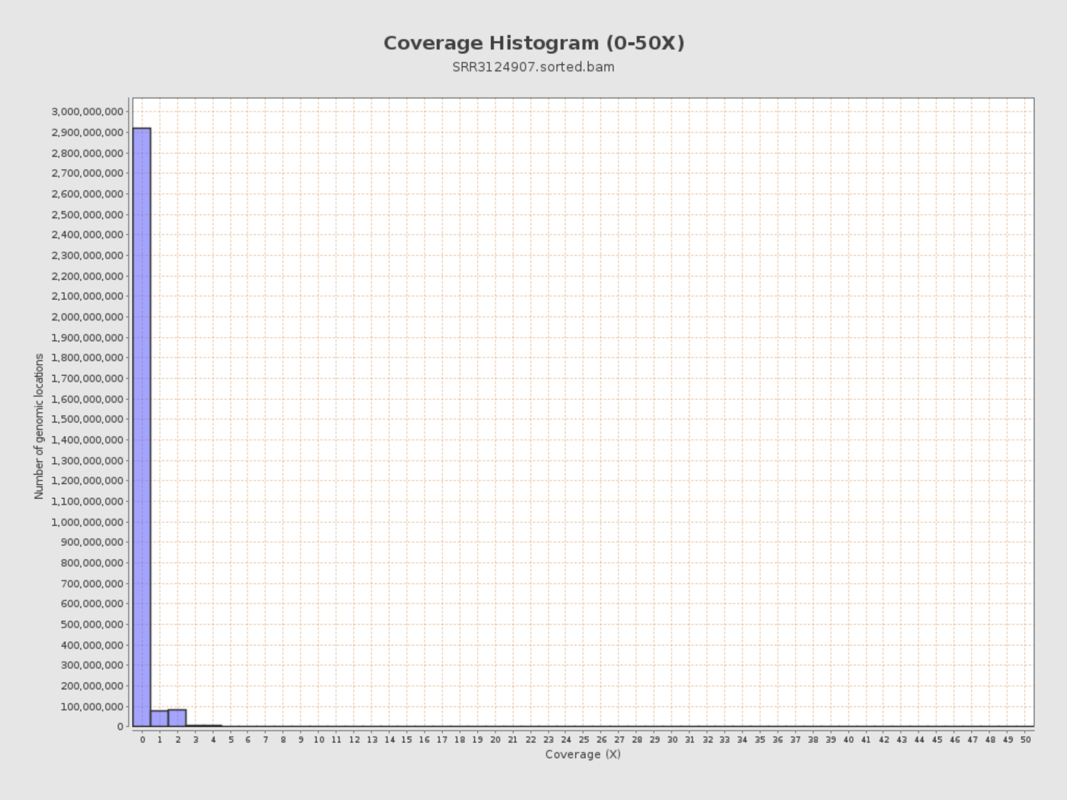
3. Results : Coverage across reference



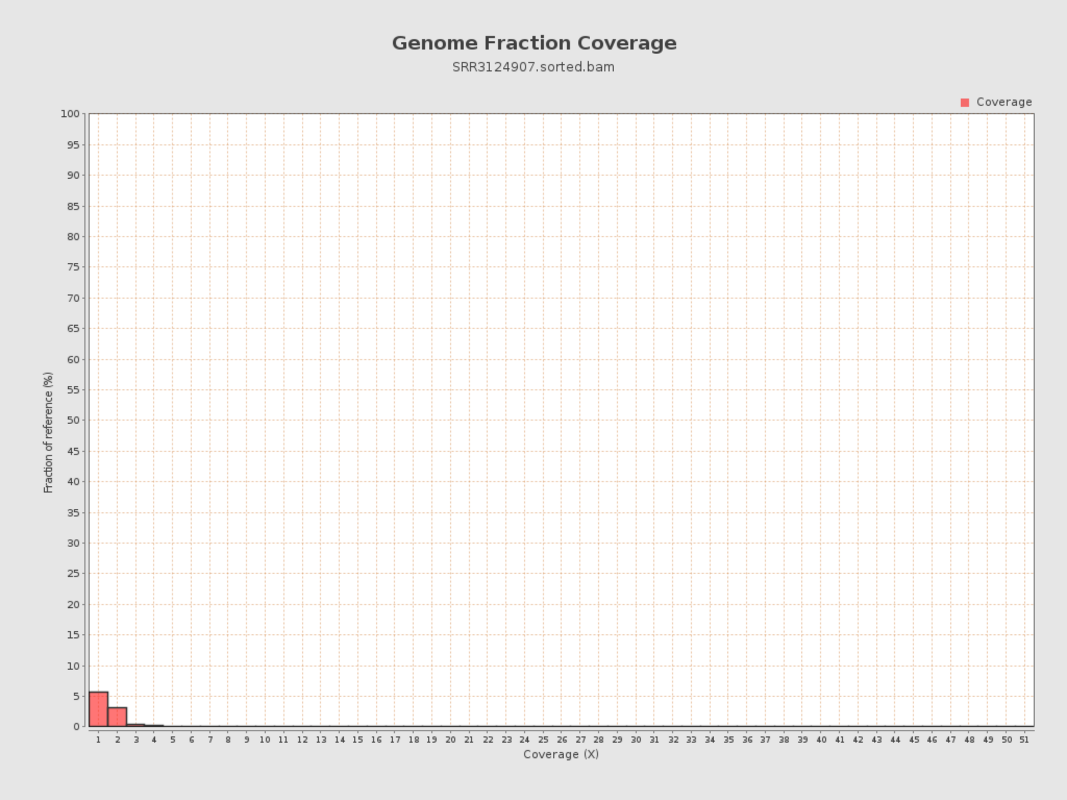
4. Results : Coverage Histogram



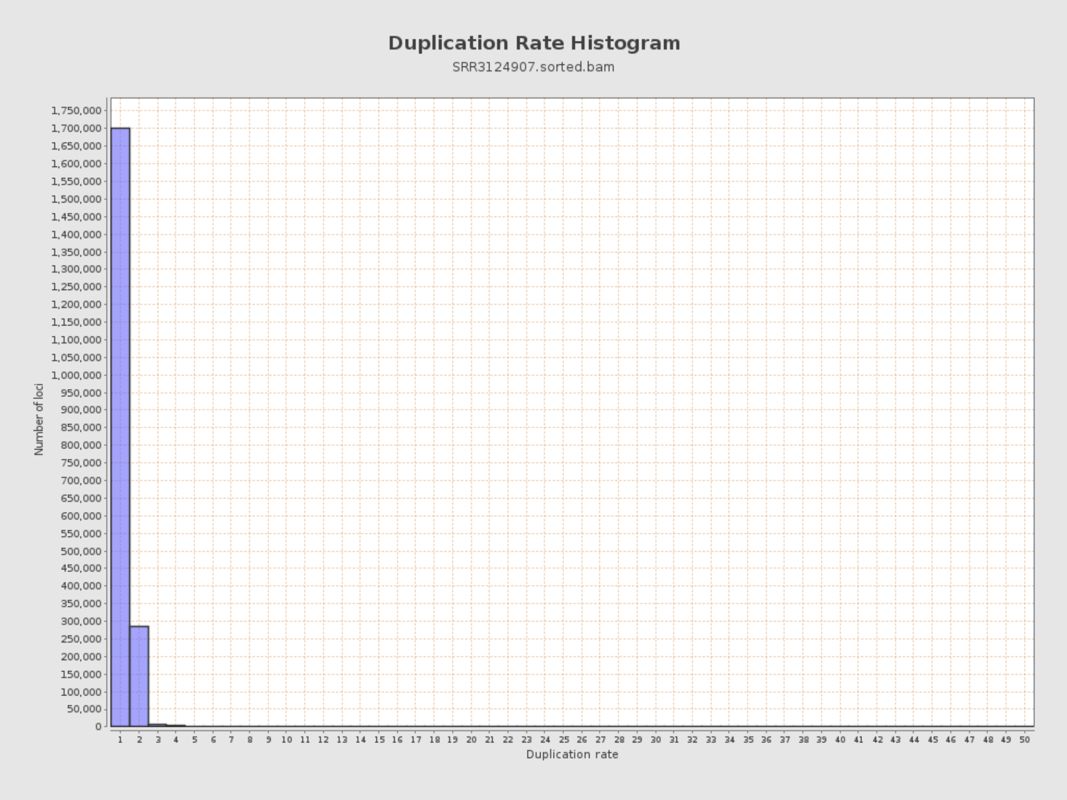
5. Results : Coverage Histogram (0-50X)



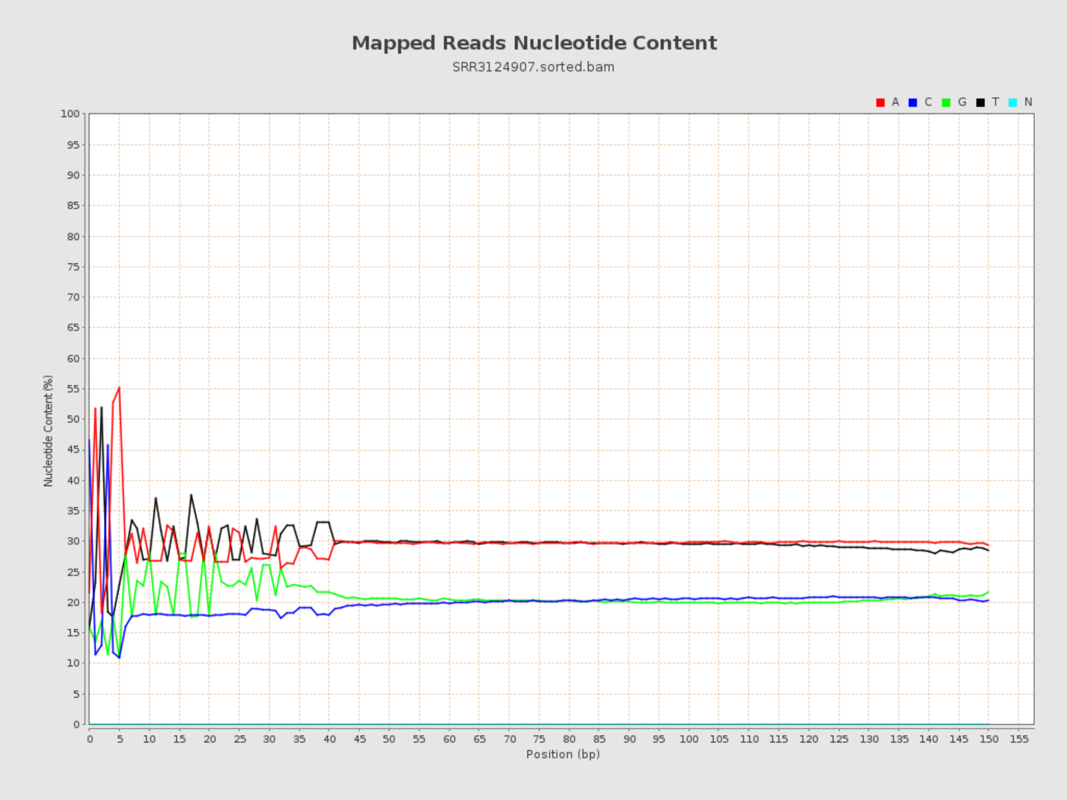
6. Results : Genome Fraction Coverage



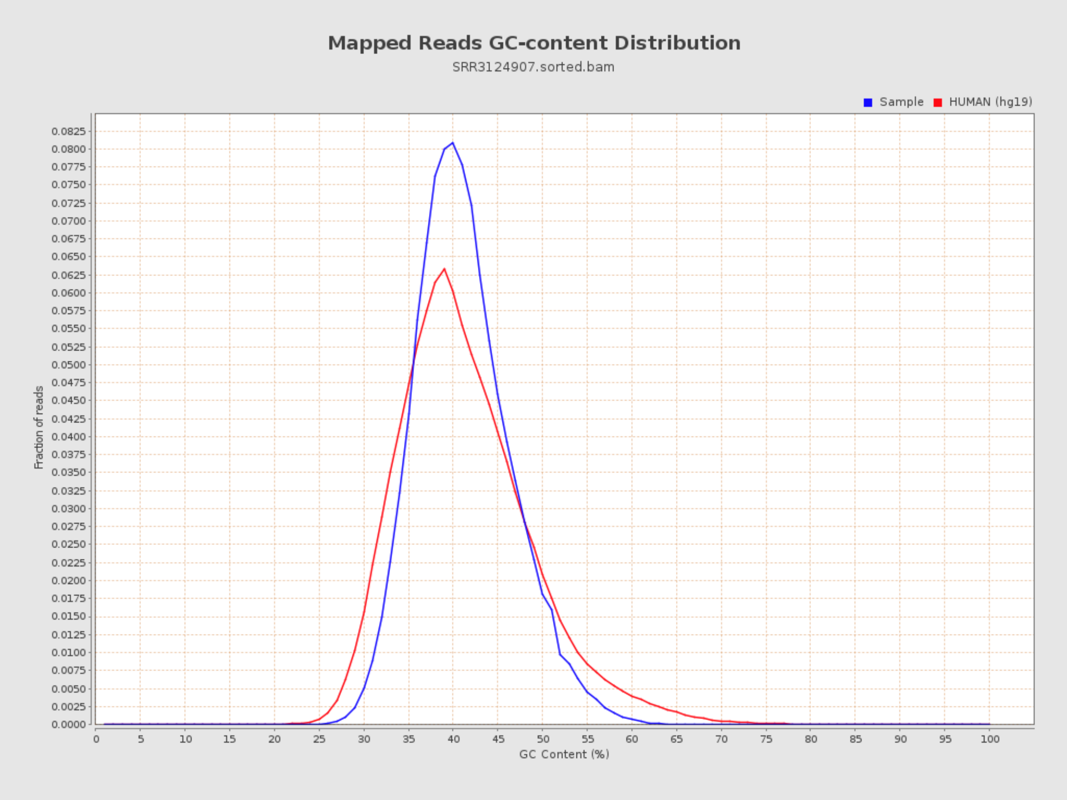
7. Results : Duplication Rate Histogram



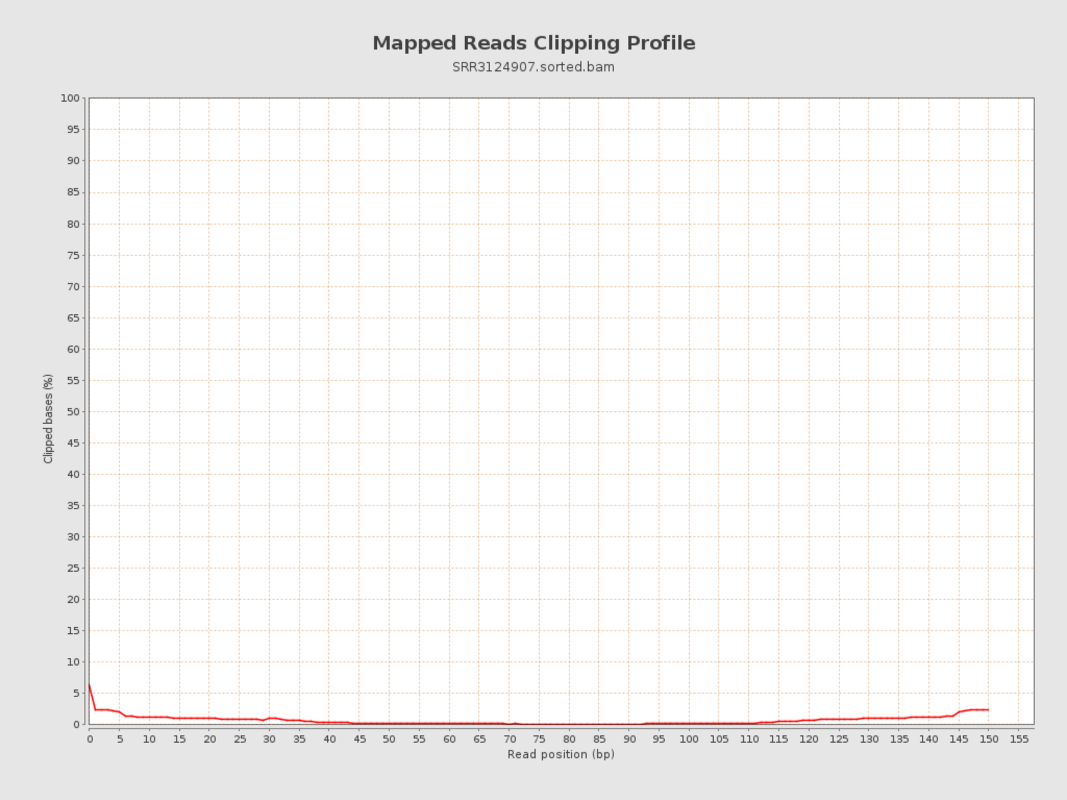
8. Results : Mapped Reads Nucleotide Content



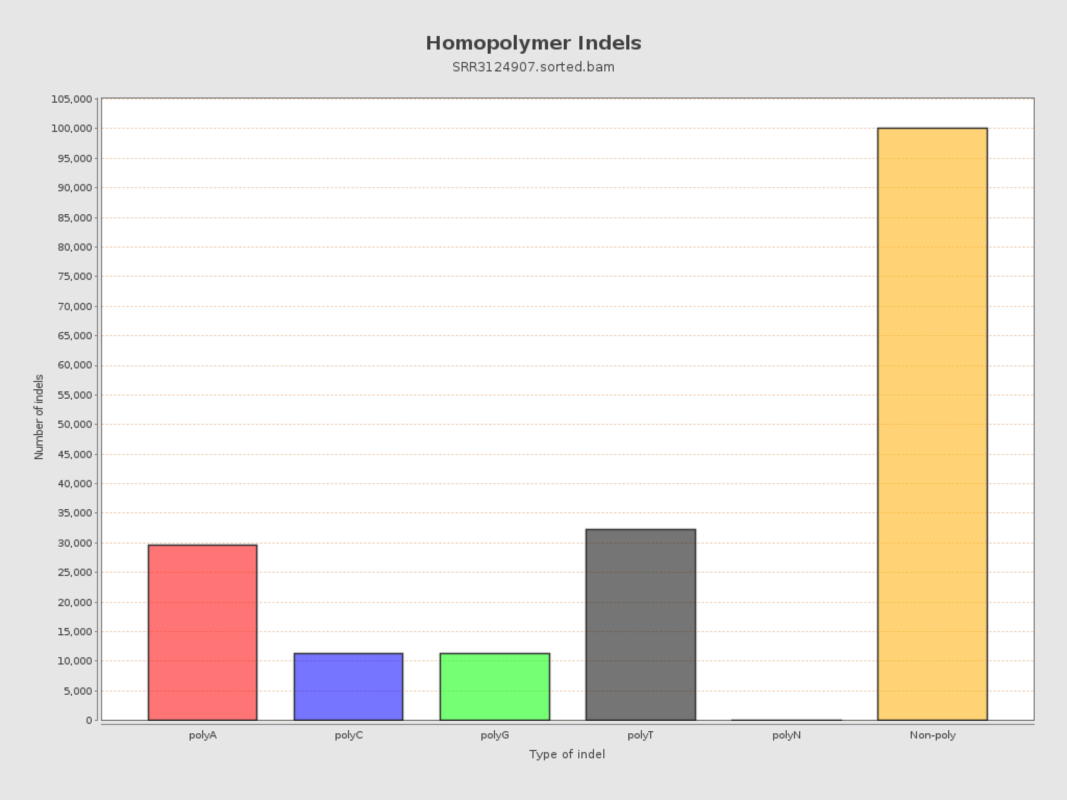
9. Results : Mapped Reads GC-content Distribution



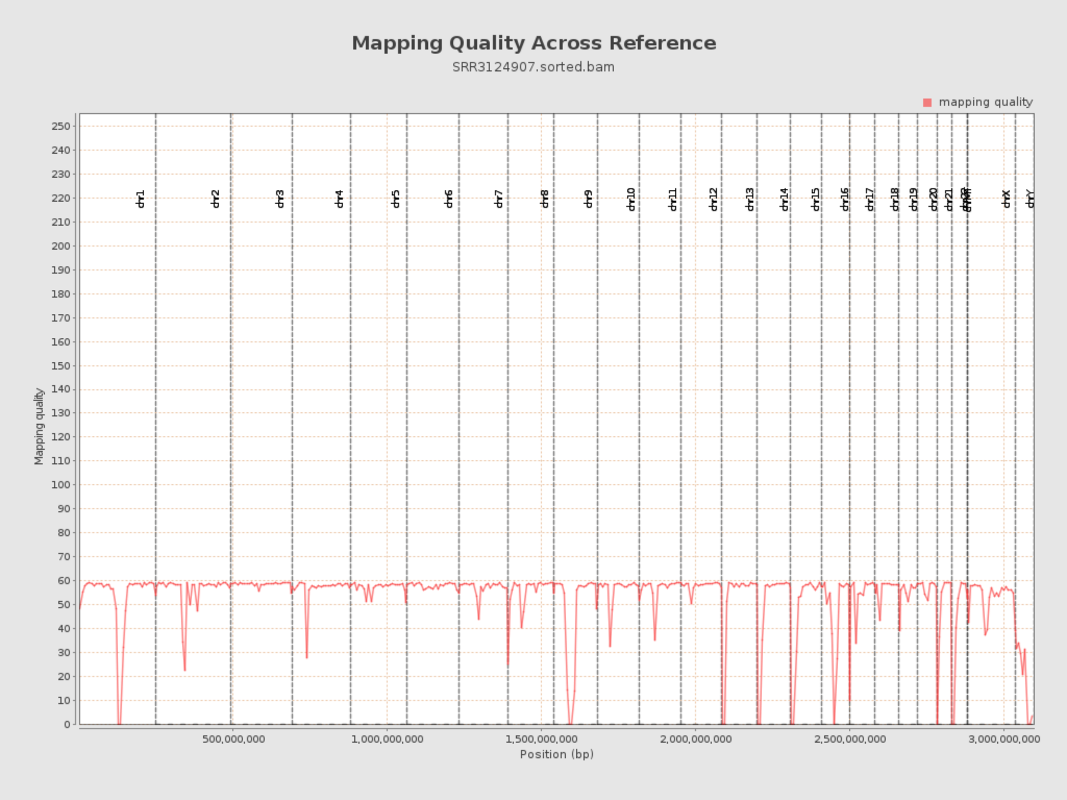
10. Results : Mapped Reads Clipping Profile



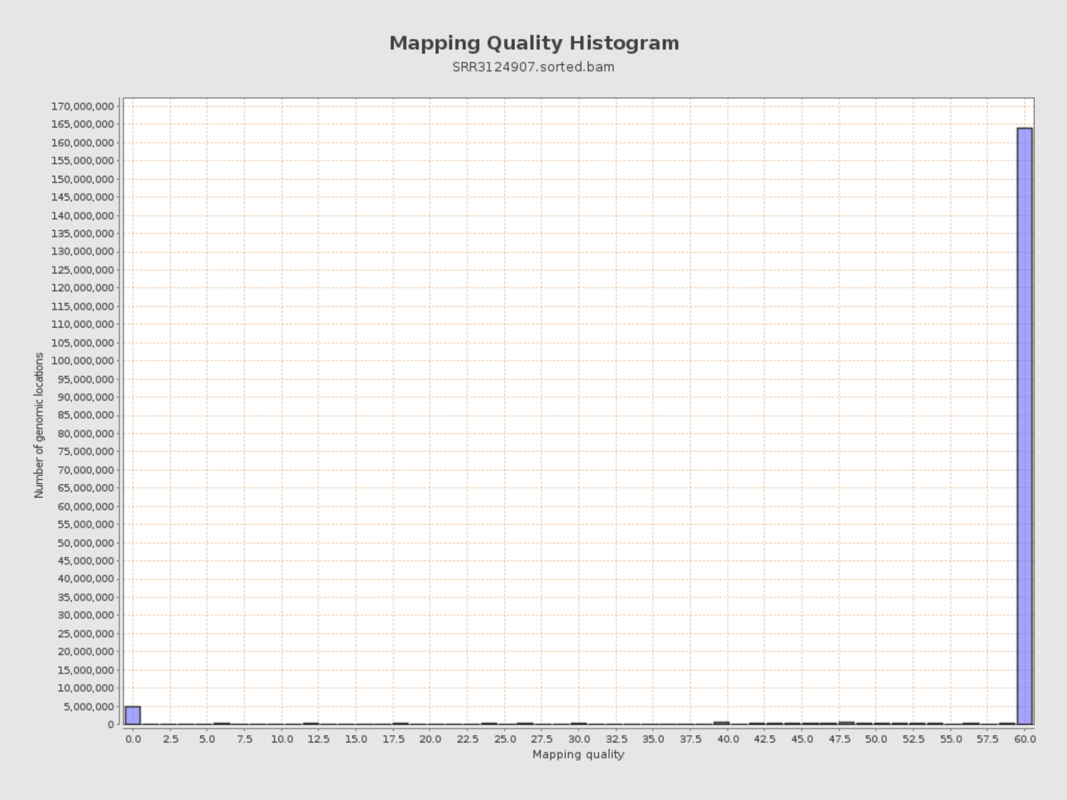
11. Results : Homopolymer Indels



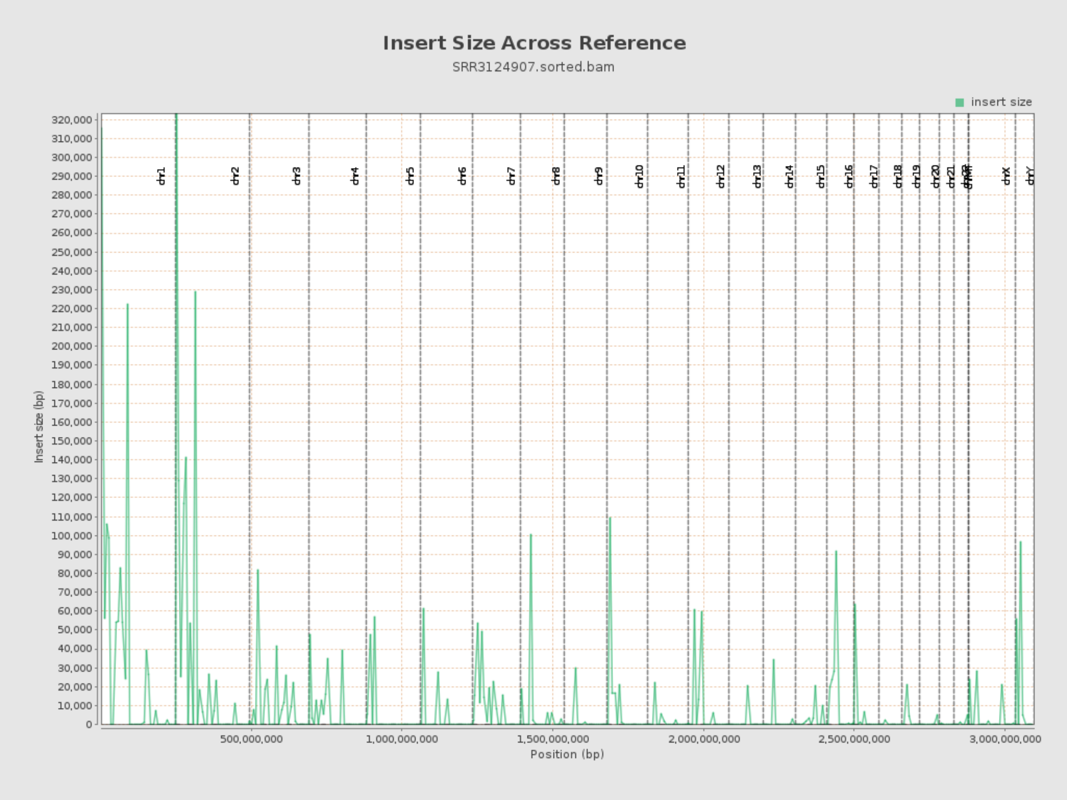
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram