Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 06:25:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124927.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_SRR3124927 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124927_1.fastq.gz SRR3124927_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 06:25:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124927.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,357,310
Mapped reads	2,331,811 / 98.92%
Unmapped reads	25,499 / 1.08%
Mapped paired reads	2,331,811 / 98.92%
Mapped reads, first in pair	1,166,971 / 49.5%
Mapped reads, second in pair	1,164,840 / 49.41%
Mapped reads, both in pair	2,325,620 / 98.66%
Mapped reads, singletons	6,191 / 0.26%
Secondary alignments	0
Supplementary alignments	40,934 / 1.74%
Read min/max/mean length	30 / 151 / 151.81
Duplicated reads (estimated)	390,214 / 16.55%
Duplication rate	15.67%
Clipped reads	1,770,217 / 75.09%

2.2. ACGT Content

Number/percentage of A's	90,509,944 / 29.21%
Number/percentage of C's	62,539,717 / 20.18%
Number/percentage of T's	90,303,097 / 29.14%
Number/percentage of G's	66,515,876 / 21.46%
Number/percentage of N's	26,762 / 0.01%

GC Percentage	41.64%

2.3. Coverage

Mean	0.1002
Standard Deviation	1.2022

2.4. Mapping Quality

Mean Mapping Quality	53.31

2.5. Insert size

Mean	109,323.68
Standard Deviation	3,228,217.97
P25/Median/P75	134 / 167 / 214

2.6. Mismatches and indels

General error rate	1.12%
Mismatches	3,275,081
Insertions	68,090
Mapped reads with at least one insertion	2.7%
Deletions	127,490
Mapped reads with at least one deletion	5.21%
Homopolymer indels	44.34%

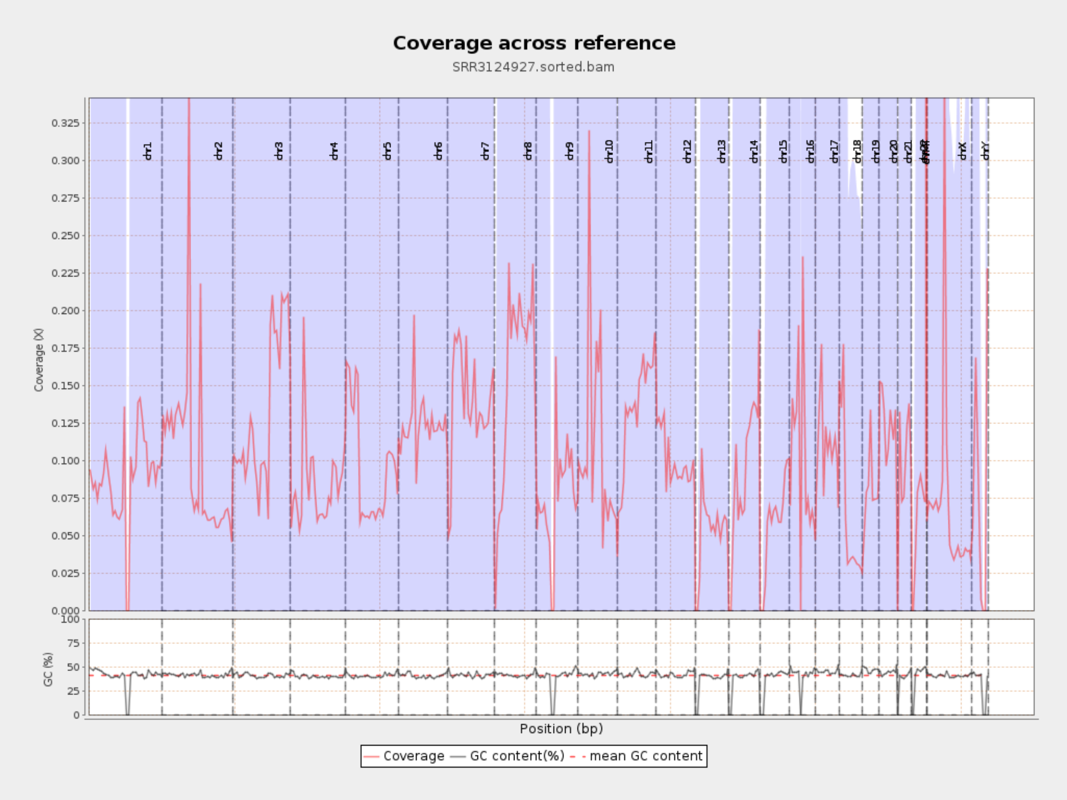
2.7. Chromosome stats

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

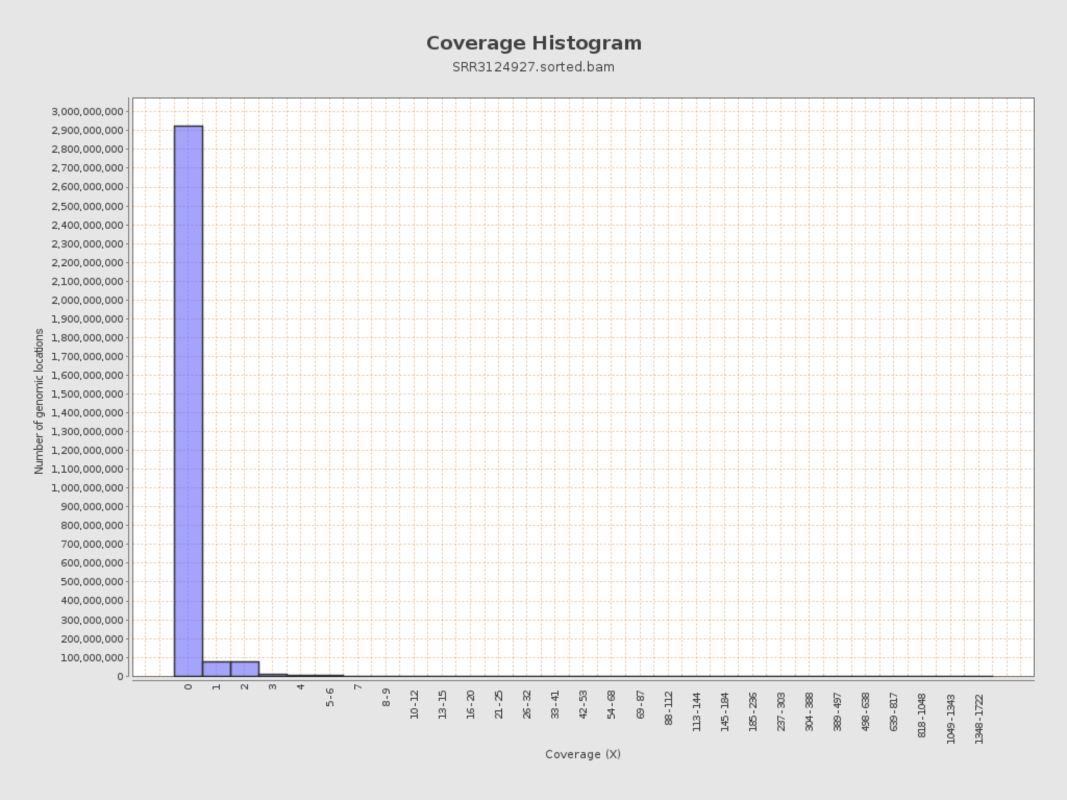
		bases	coverage	deviation
chr1	249250621	21835972	0.0876	1.2573
chr2	243199373	24877718	0.1023	2.2306
chr3	198022430	26172521	0.1322	0.5264
chr4	191154276	15707056	0.0822	0.8294
chr5	180915260	17230228	0.0952	0.4646
chr6	171115067	21223802	0.124	0.9753
chr7	159138663	22366465	0.1405	1.3063
chr8	146364022	22638096	0.1547	0.7474
chr9	141213431	10733177	0.076	1.8343
chr10	135534747	14968054	0.1104	1.966
chr11	135006516	18186167	0.1347	0.8704
chr12	133851895	13364266	0.0998	0.4535
chr13	115169878	6149385	0.0534	0.3274
chr14	107349540	9483578	0.0883	0.4671
chr15	102531392	5892879	0.0575	0.3383
chr16	90354753	9201155	0.1018	1.5768
chr17	81195210	8873313	0.1093	1.1884
chr18	78077248	5093301	0.0652	1.8206
chr19	59128983	4677082	0.0791	0.8317
chr20	63025520	7853634	0.1246	0.5422
chr21	48129895	4660762	0.0968	0.667
chr22	51304566	2913118	0.0568	0.3764
chrMT	16571	394091	23.782	13.3673
chrX	155270560	11020846	0.071	0.5132

chrY	59373566	4645350	0.0782	1.8839

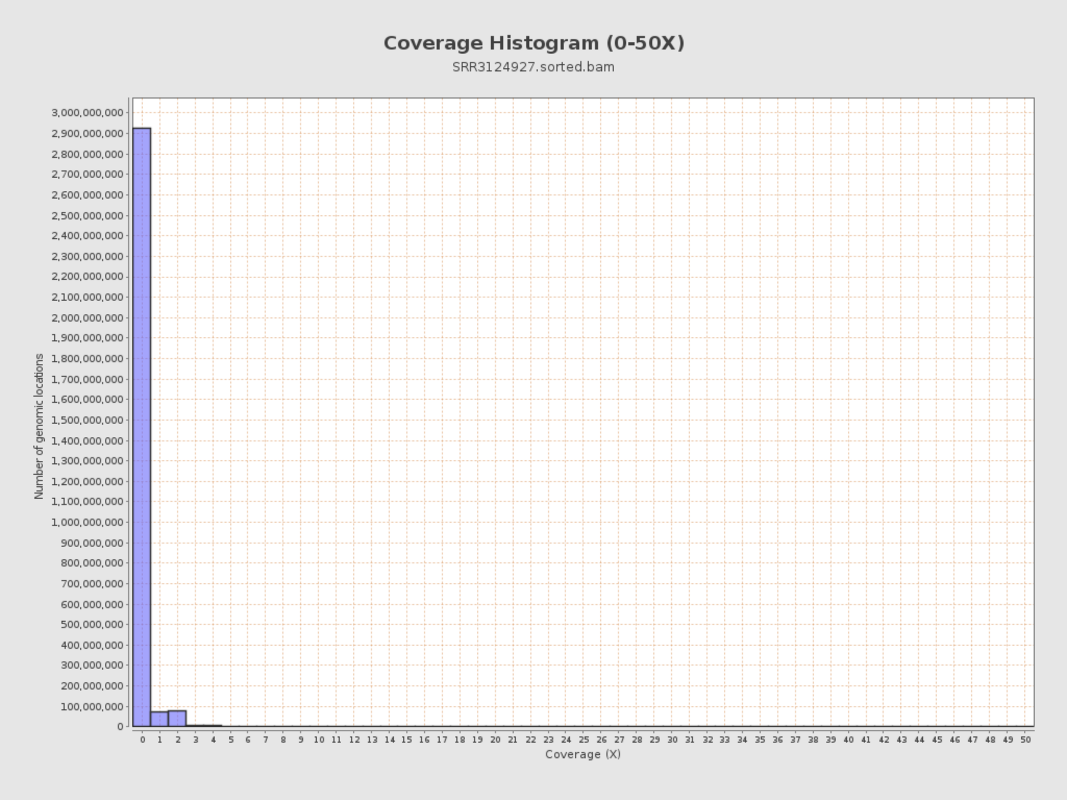
3. Results : Coverage across reference



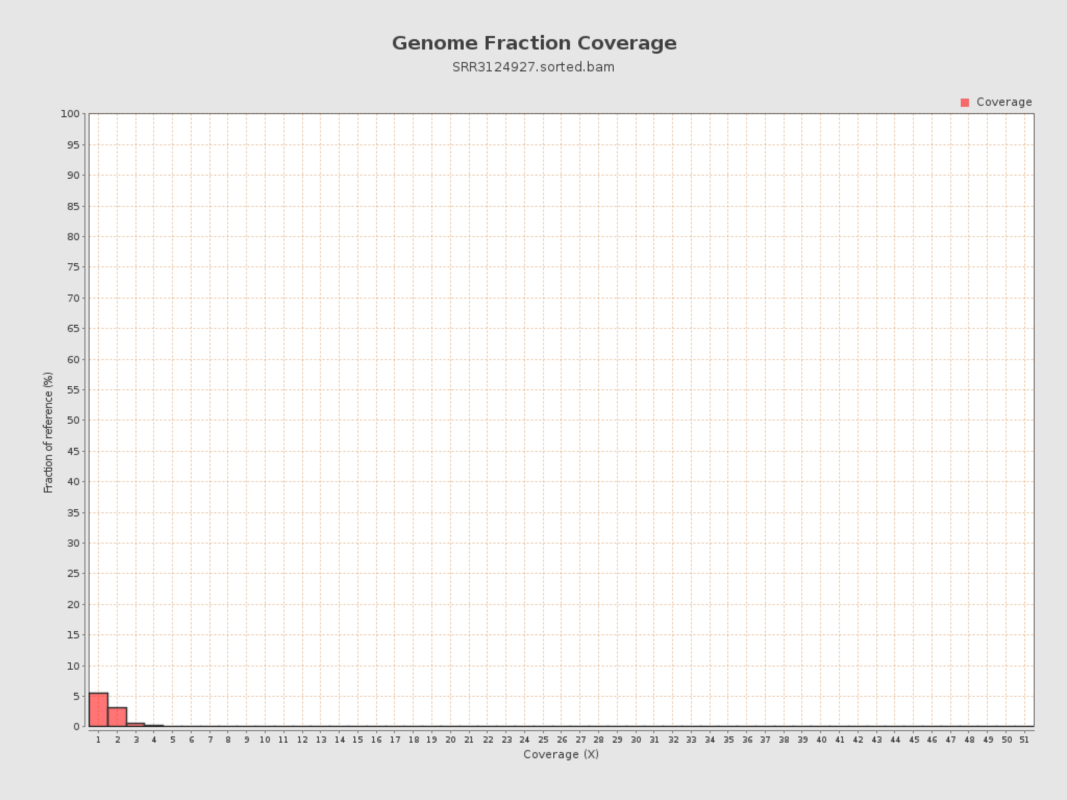
4. Results : Coverage Histogram



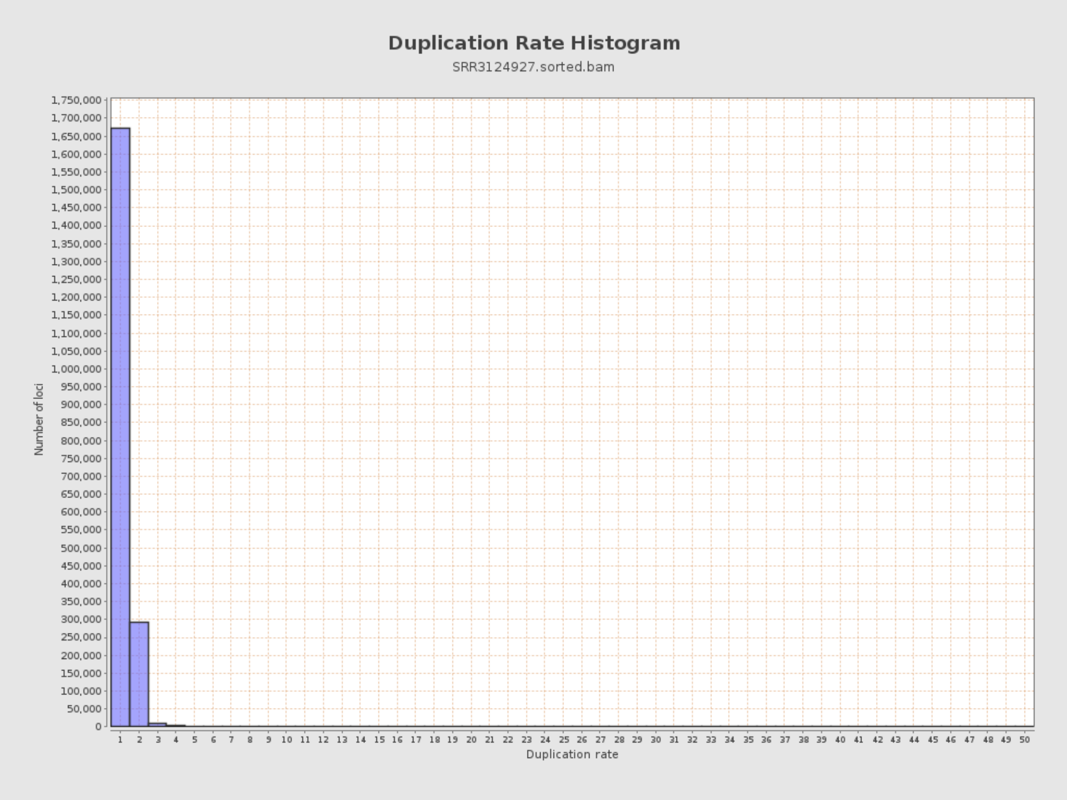
5. Results : Coverage Histogram (0-50X)



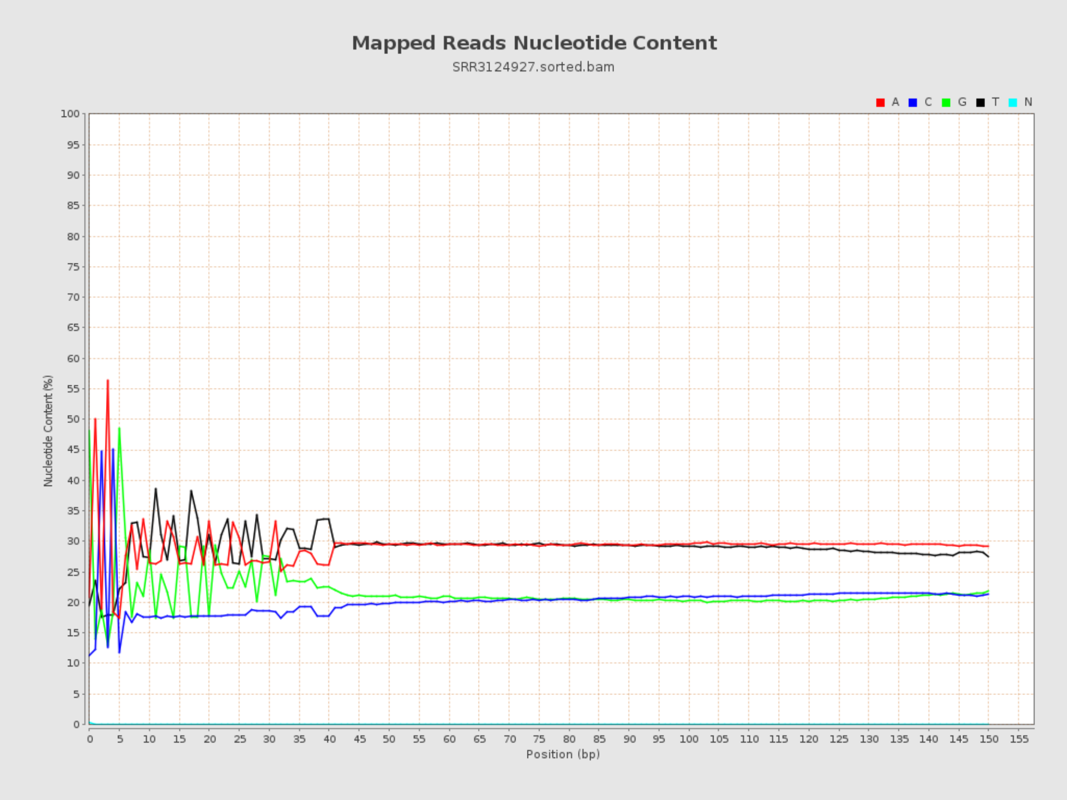
6. Results : Genome Fraction Coverage



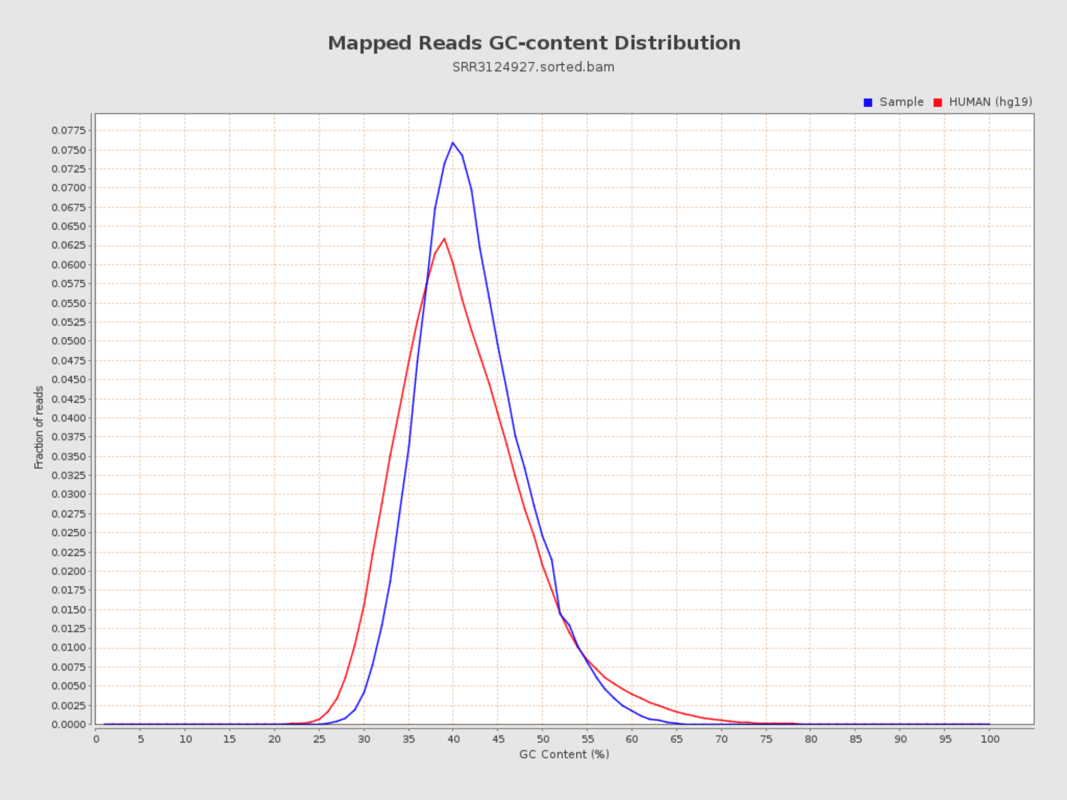
7. Results : Duplication Rate Histogram



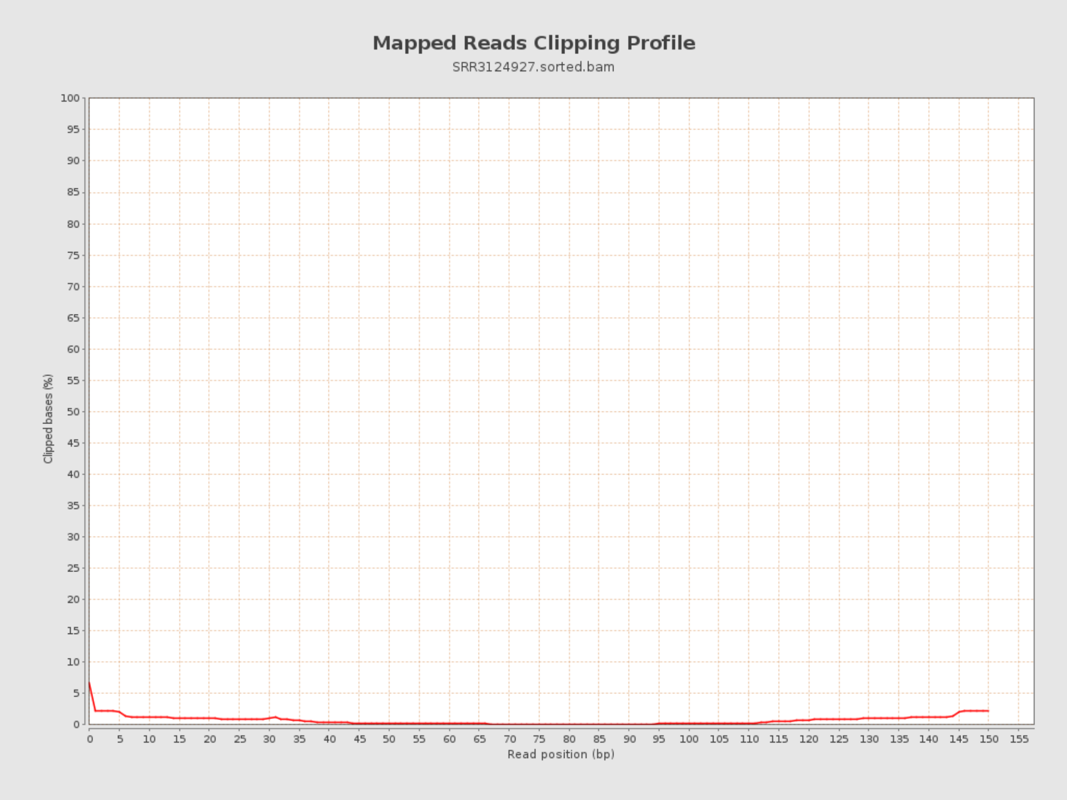
8. Results : Mapped Reads Nucleotide Content



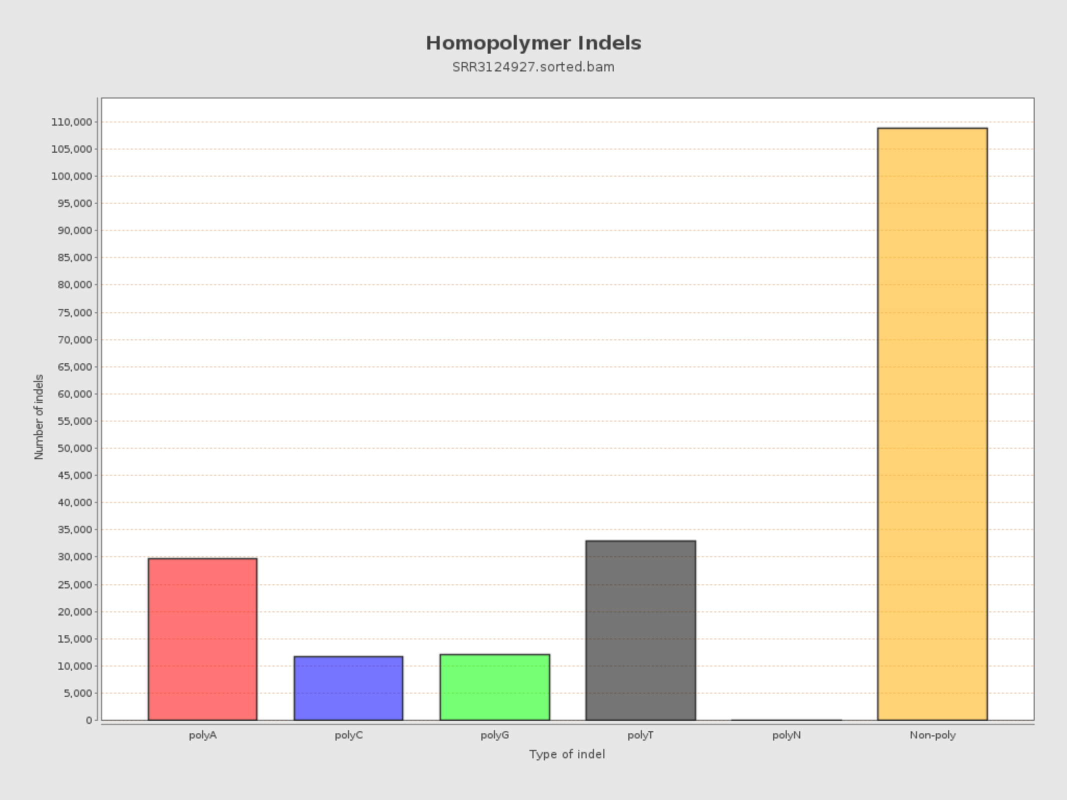
9. Results : Mapped Reads GC-content Distribution



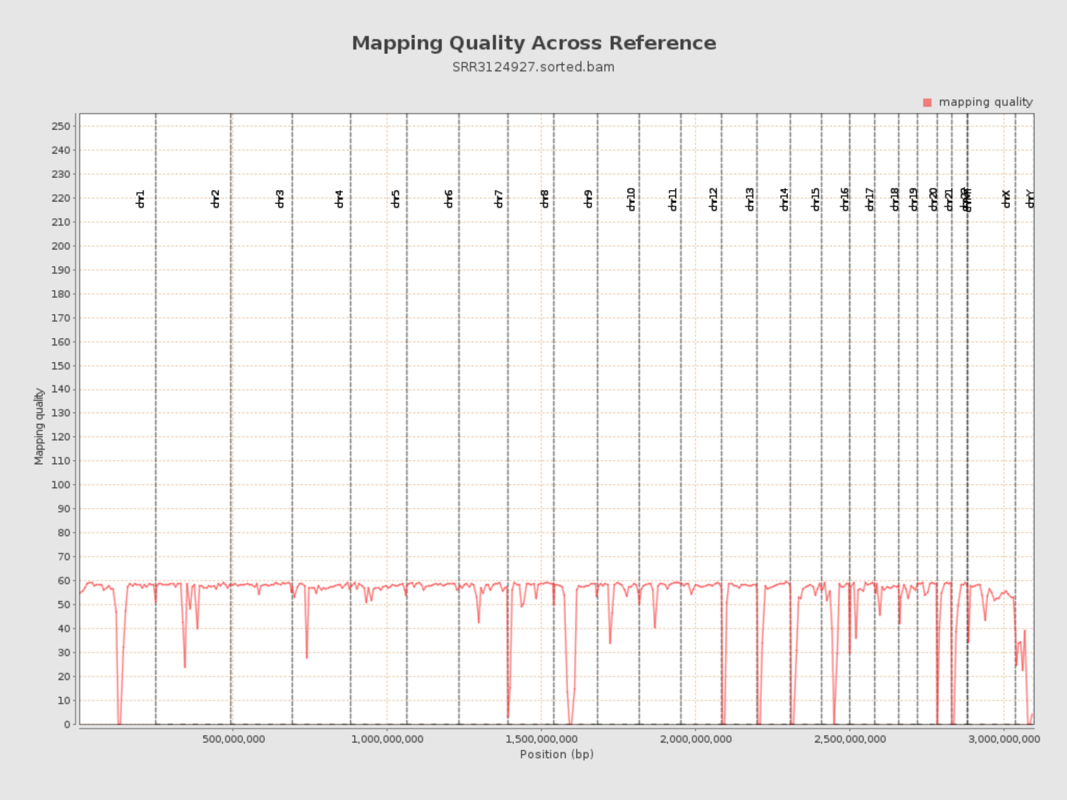
10. Results : Mapped Reads Clipping Profile



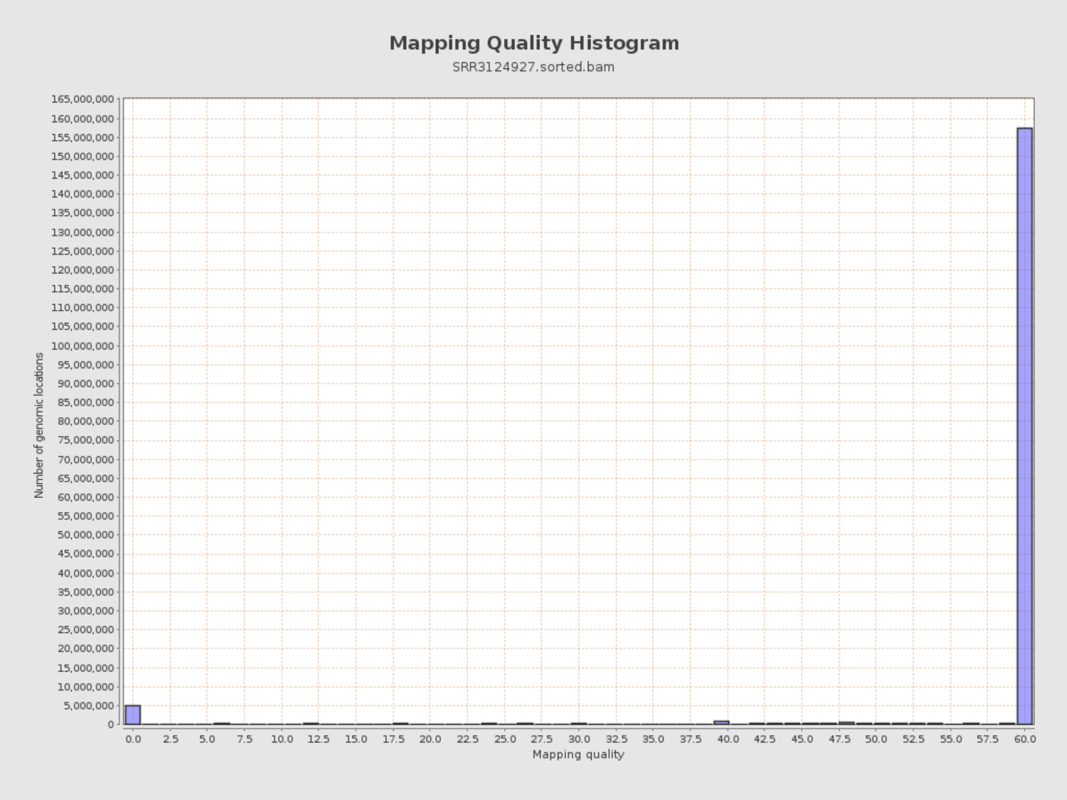
11. Results : Homopolymer Indels



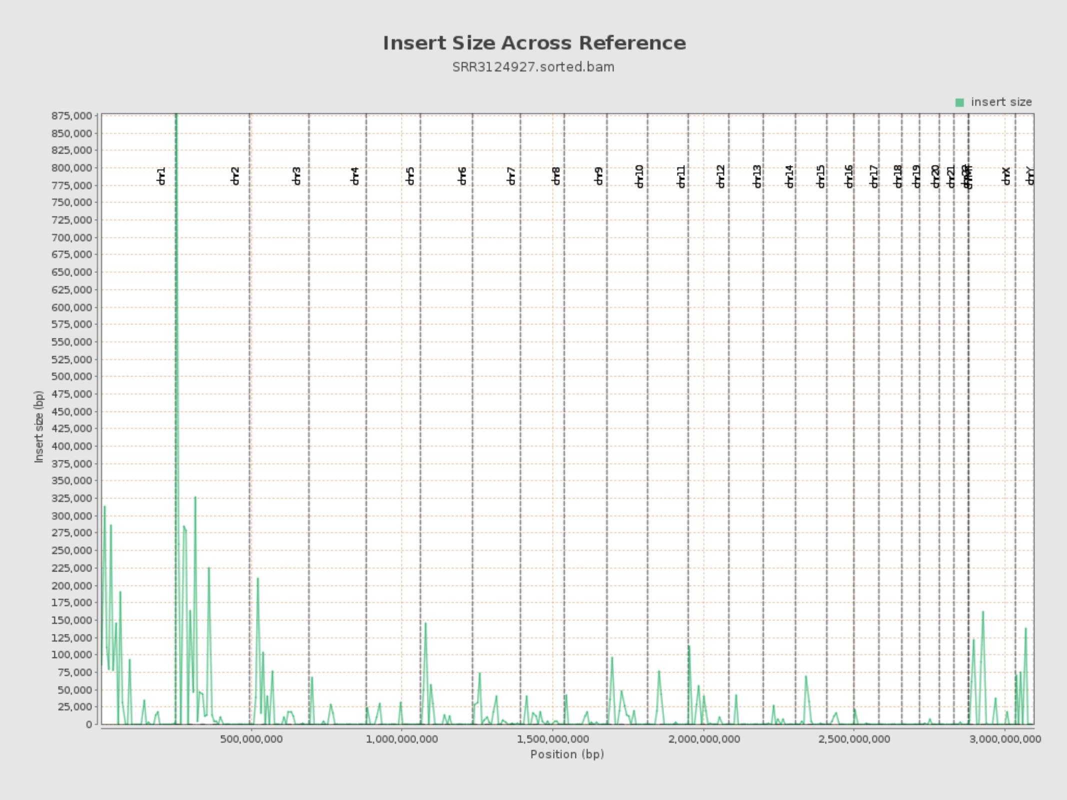
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram