Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/24 04:49:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR927014.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_SRR927014 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR927014_1.fastq.gz SRR927014_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 24 04:48:59 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR927014.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	28,998,104
Mapped reads	27,624,518 / 95.26%
Unmapped reads	1,373,586 / 4.74%
Mapped paired reads	27,624,518 / 95.26%
Mapped reads, first in pair	13,850,049 / 47.76%
Mapped reads, second in pair	13,774,469 / 47.5%
Mapped reads, both in pair	27,338,834 / 94.28%
Mapped reads, singletons	285,684 / 0.99%
Secondary alignments	0
Supplementary alignments	280,697 / 0.97%
Read min/max/mean length	30 / 101 / 101.4
Duplicated reads (estimated)	1,876,894 / 6.47%
Duplication rate	5.31%
Clipped reads	7,090,928 / 24.45%

2.2. ACGT Content

Number/percentage of A's	741,781,251 / 28.44%
Number/percentage of C's	527,728,060 / 20.23%
Number/percentage of T's	749,359,098 / 28.73%
Number/percentage of G's	589,060,643 / 22.58%
Number/percentage of N's	567,694 / 0.02%

GC Percentage	42.81%

2.3. Coverage

Mean	0.8433
Standard Deviation	3.3596

2.4. Mapping Quality

Mean Mapping Quality	53.47

2.5. Insert size

Mean	104,190.96
Standard Deviation	3,179,847.74
P25/Median/P75	149 / 193 / 258

2.6. Mismatches and indels

General error rate	0.95%
Mismatches	23,950,895
Insertions	412,452
Mapped reads with at least one insertion	1.47%
Deletions	1,380,020
Mapped reads with at least one deletion	4.87%
Homopolymer indels	52.89%

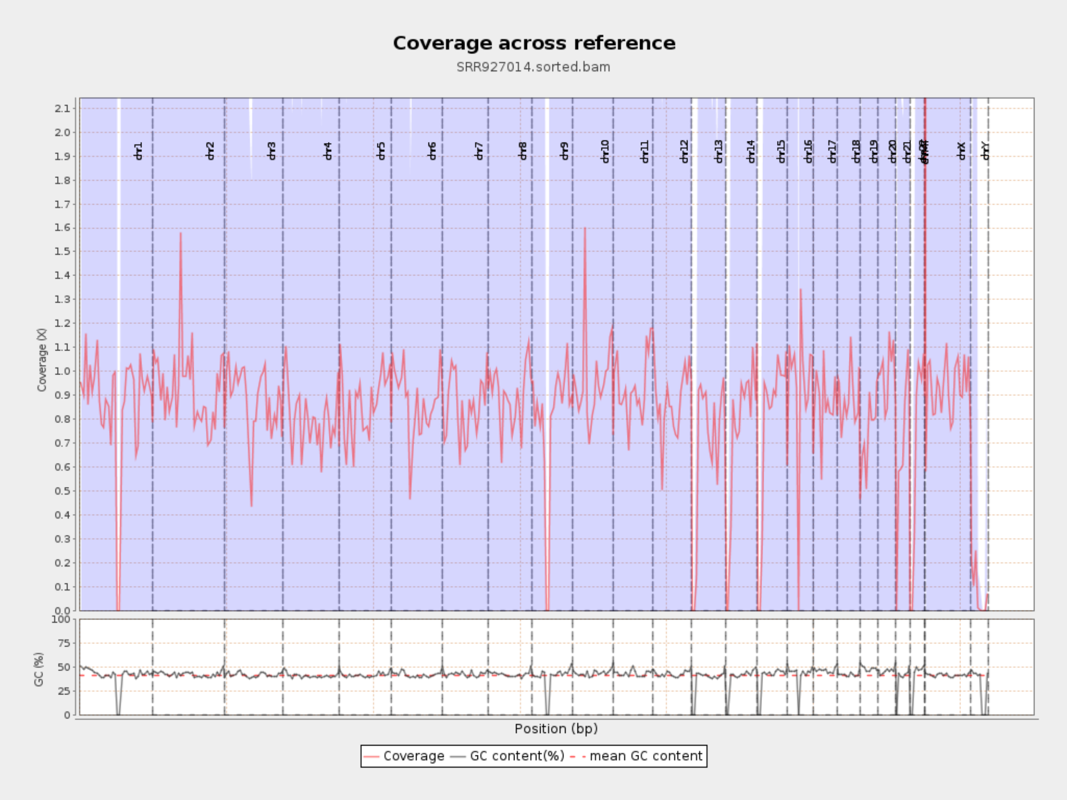
2.7. Chromosome stats

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

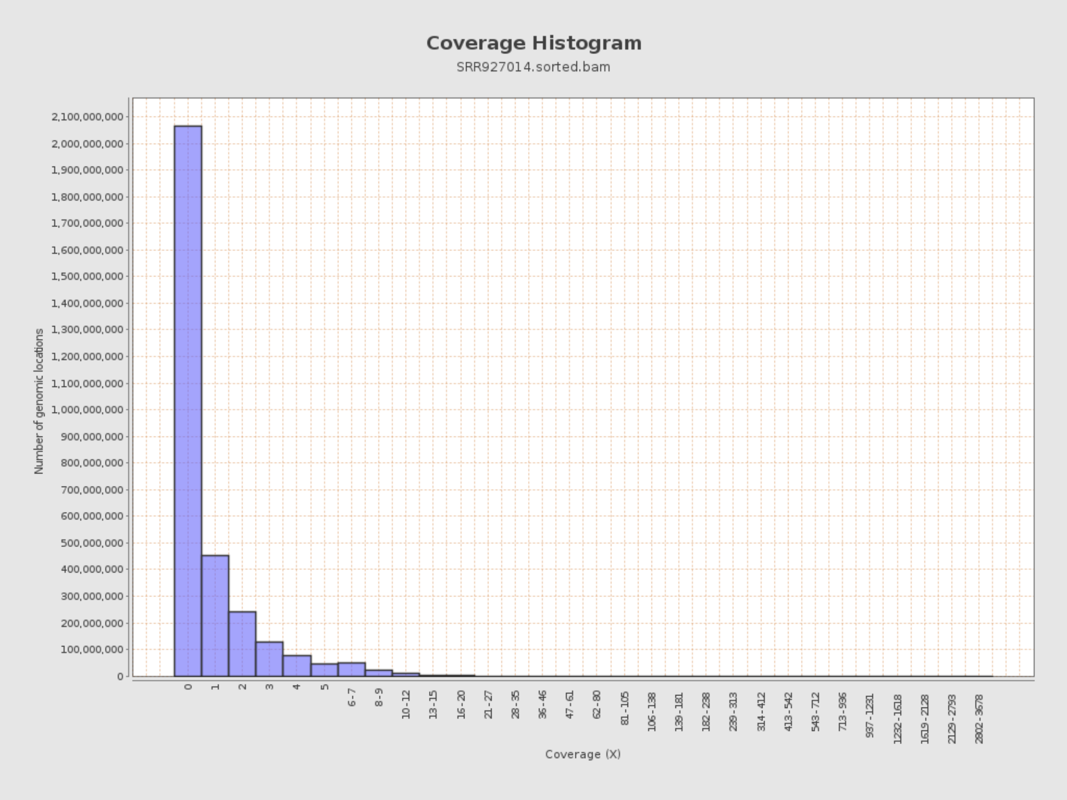
		bases	coverage	deviation
chr1	249250621	214730793	0.8615	4.2629
chr2	243199373	226945257	0.9332	5.1873
chr3	198022430	174436844	0.8809	1.7965
chr4	191154276	153403718	0.8025	2.2986
chr5	180915260	157196565	0.8689	1.7514
chr6	171115067	149573468	0.8741	1.9973
chr7	159138663	136036264	0.8548	2.4765
chr8	146364022	131483180	0.8983	1.9905
chr9	141213431	111256442	0.7879	3.8277
chr10	135534747	131120420	0.9674	7.884
chr11	135006516	125644651	0.9307	3.6047
chr12	133851895	116811060	0.8727	1.7879
chr13	115169878	78272425	0.6796	1.5386
chr14	107349540	78555320	0.7318	1.6745
chr15	102531392	78227035	0.763	1.717
chr16	90354753	83575876	0.925	4.5776
chr17	81195210	70459903	0.8678	2.1798
chr18	78077248	69842487	0.8945	4.2711
chr19	59128983	43327589	0.7328	2.574
chr20	63025520	62731539	0.9953	2.0742
chr21	48129895	33643920	0.699	2.5556
chr22	51304566	34889975	0.6801	1.7344
chrMT	16571	311785	18.8151	14.7404
chrX	155270560	143536462	0.9244	2.1284

chrY	59373566	4444888	0.0749	2.1415

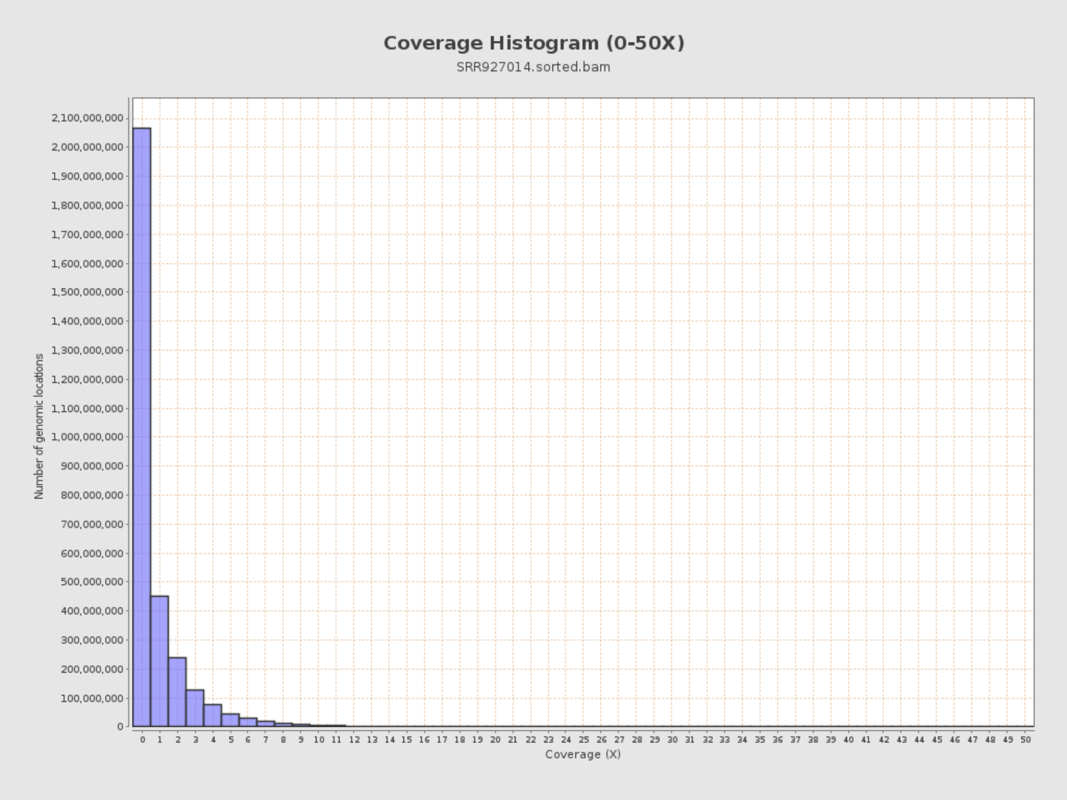
3. Results : Coverage across reference



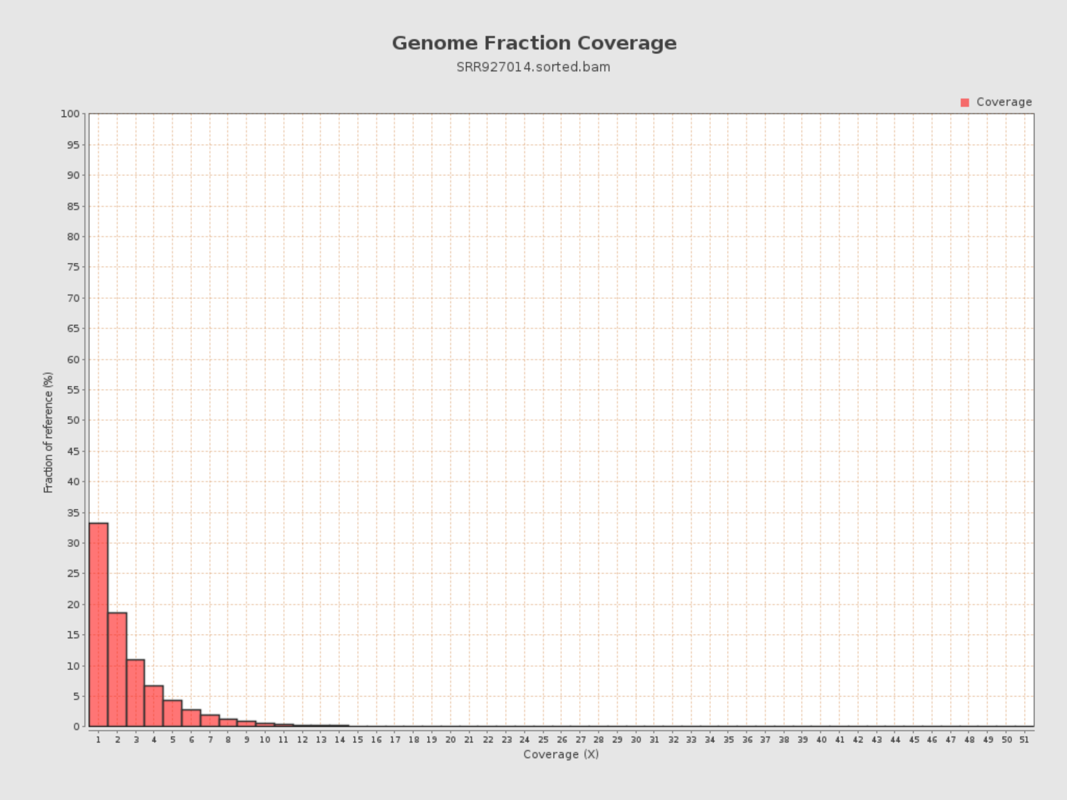
4. Results : Coverage Histogram



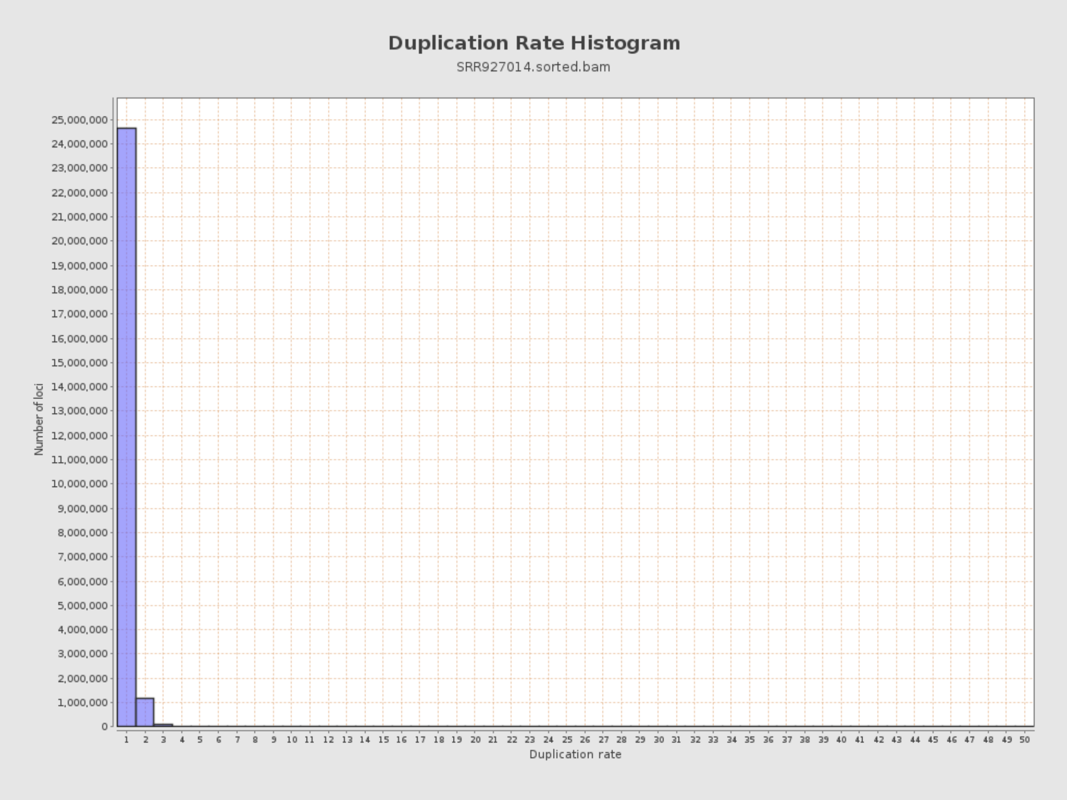
5. Results : Coverage Histogram (0-50X)



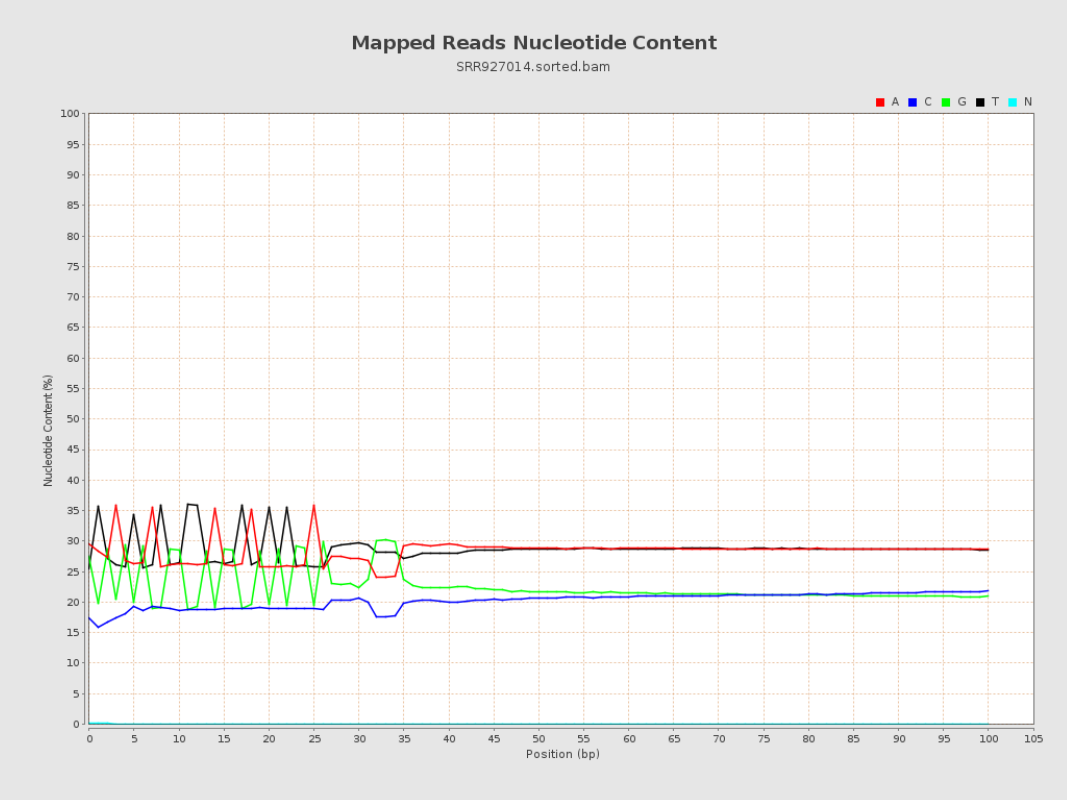
6. Results : Genome Fraction Coverage



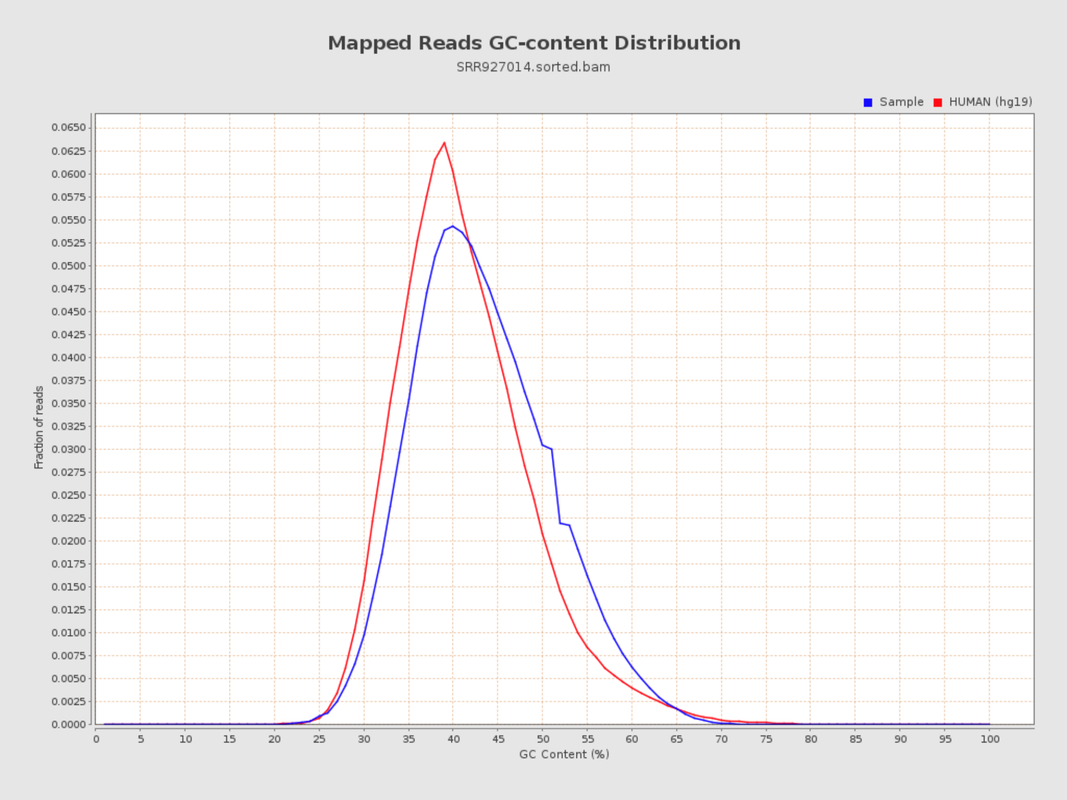
7. Results : Duplication Rate Histogram



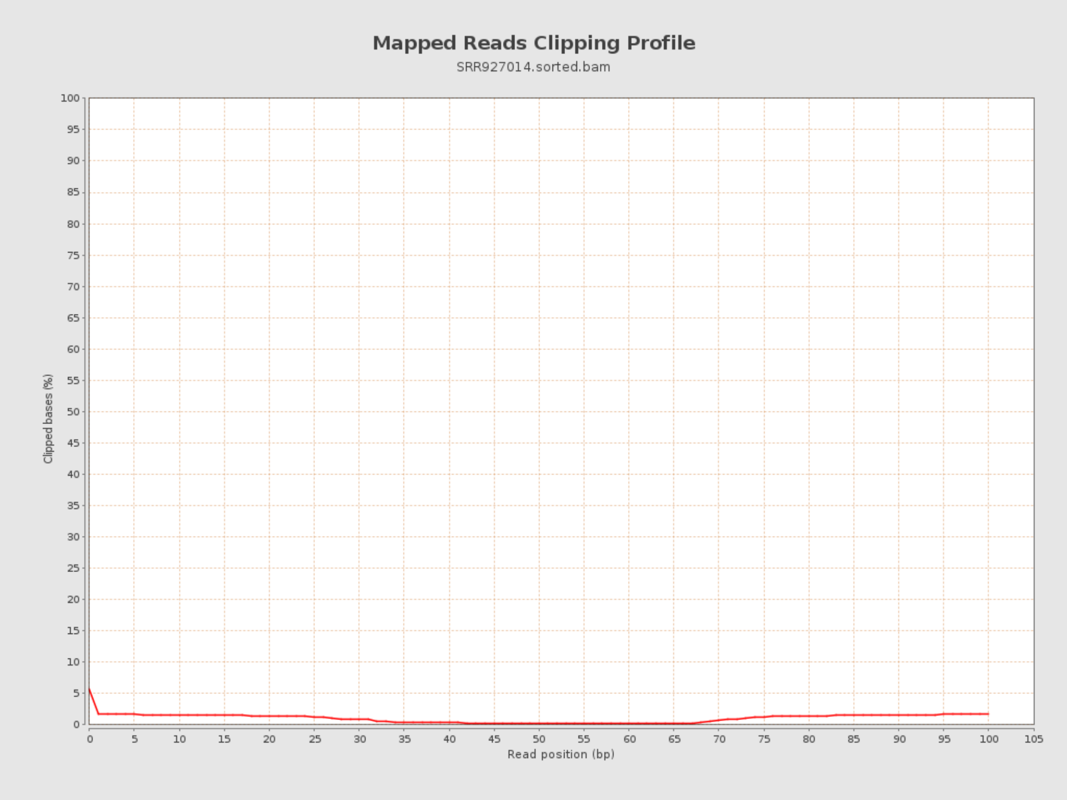
8. Results : Mapped Reads Nucleotide Content



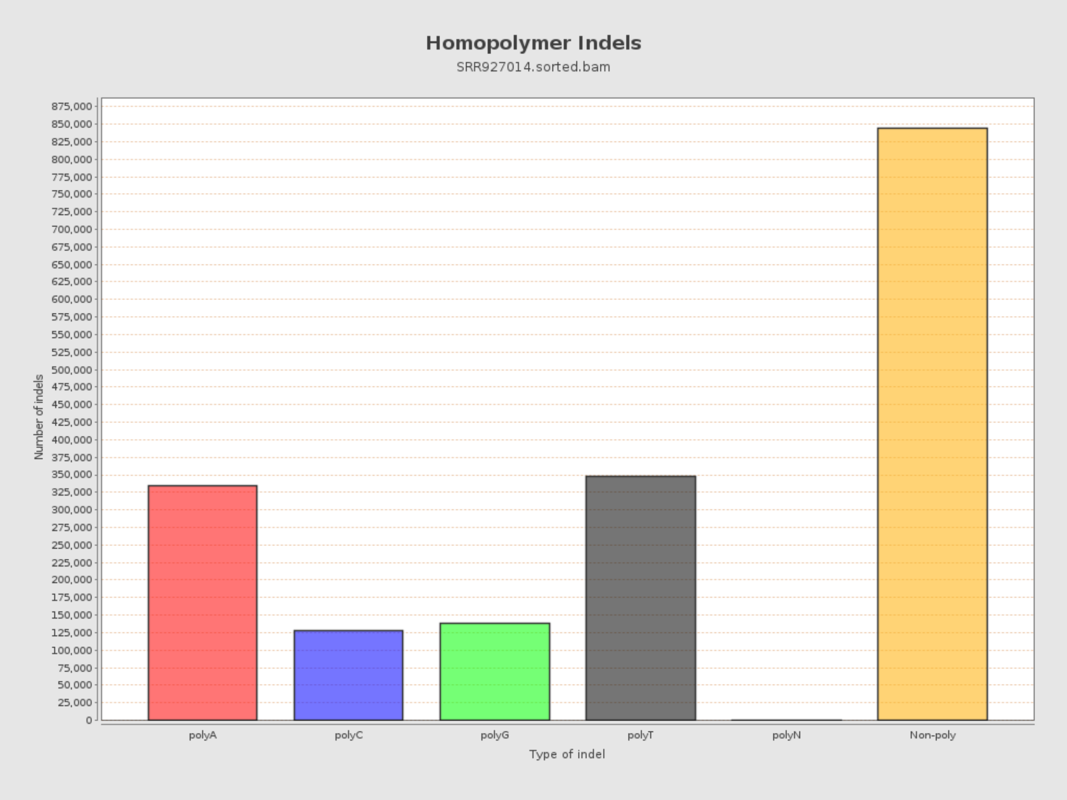
9. Results : Mapped Reads GC-content Distribution



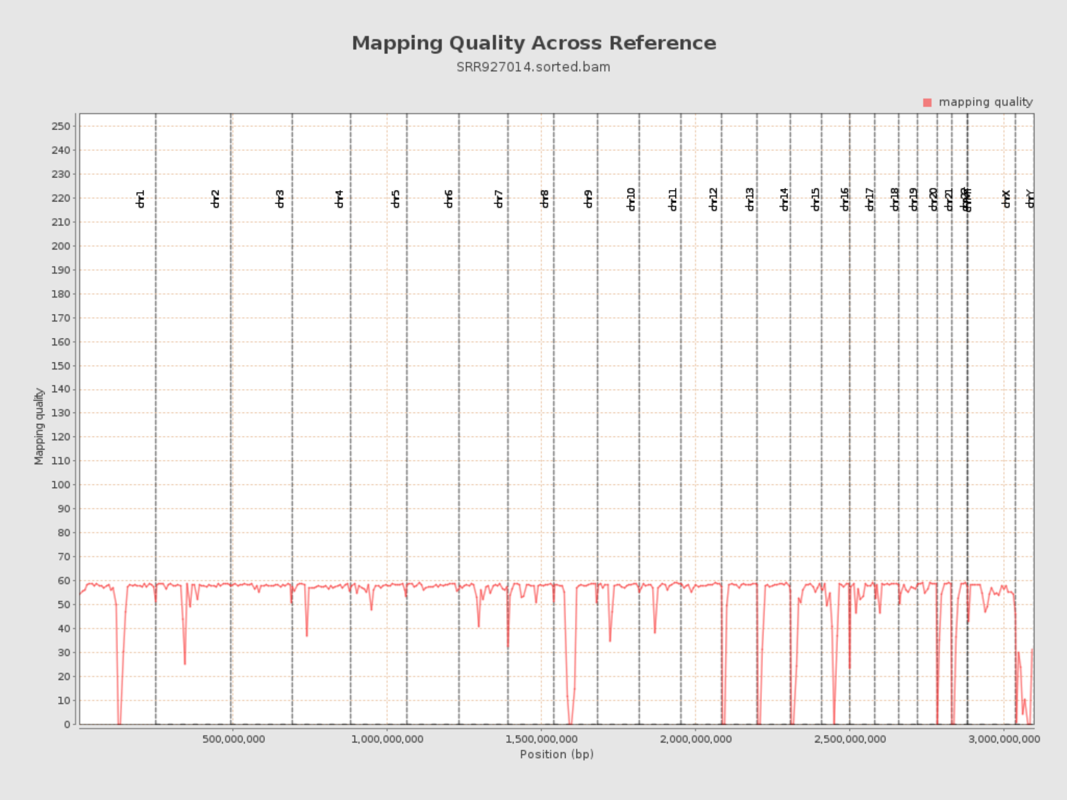
10. Results : Mapped Reads Clipping Profile



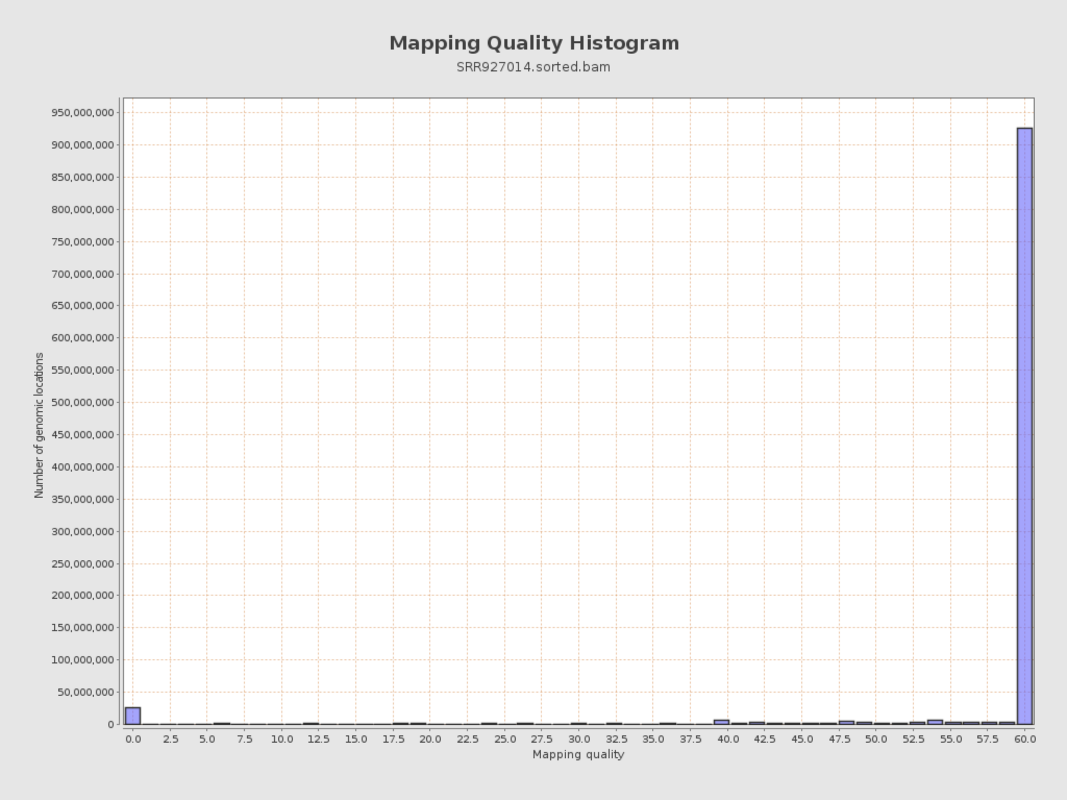
11. Results : Homopolymer Indels



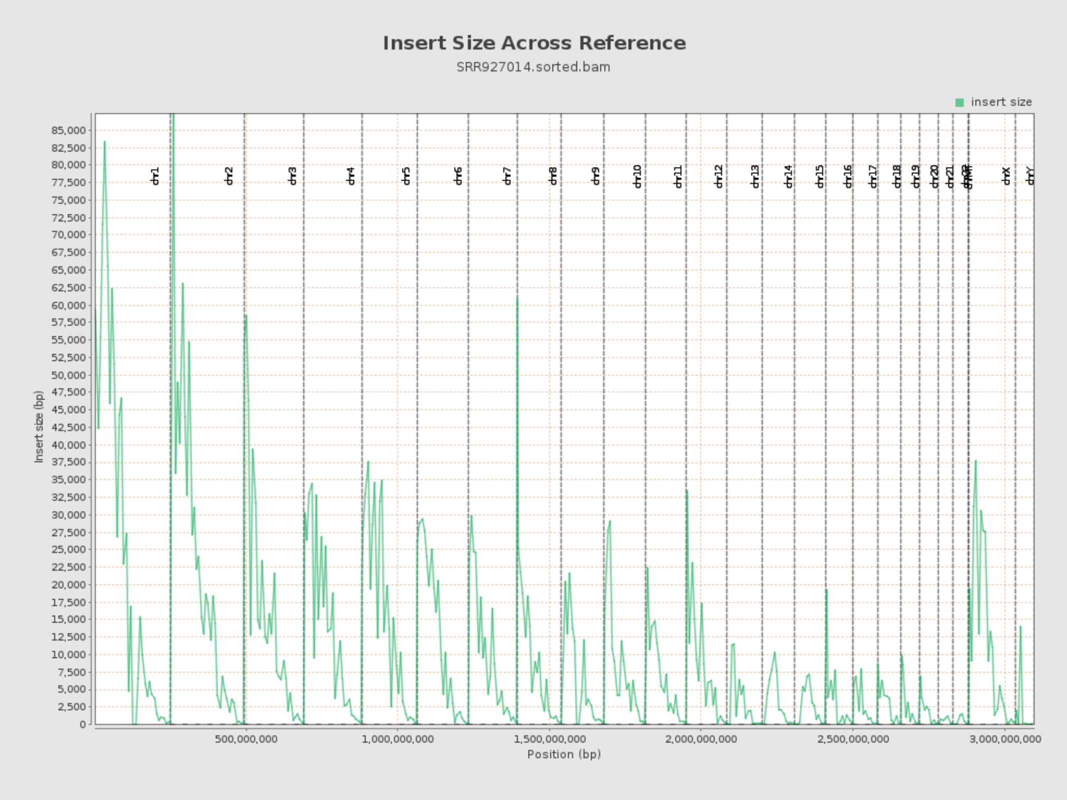
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram