Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/23 21:46:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926997.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_SRR926997 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926997_1.fastq.gz SRR926997_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Apr 23 21:46:00 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926997.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	28,765,196
Mapped reads	28,054,925 / 97.53%
Unmapped reads	710,271 / 2.47%
Mapped paired reads	28,054,925 / 97.53%
Mapped reads, first in pair	14,043,236 / 48.82%
Mapped reads, second in pair	14,011,689 / 48.71%
Mapped reads, both in pair	27,636,240 / 96.08%
Mapped reads, singletons	418,685 / 1.46%
Secondary alignments	0
Supplementary alignments	724,802 / 2.52%
Read min/max/mean length	30 / 101 / 102.05
Duplicated reads (estimated)	3,042,224 / 10.58%
Duplication rate	8.34%
Clipped reads	11,617,494 / 40.39%

2.2. ACGT Content

Number/percentage of A's	741,706,603 / 29.07%
Number/percentage of C's	480,173,756 / 18.82%
Number/percentage of T's	760,025,066 / 29.79%
Number/percentage of G's	569,254,409 / 22.31%
Number/percentage of N's	479,795 / 0.02%

GC Percentage	41.13%

2.3. Coverage

Mean	0.8249
Standard Deviation	3.4992

2.4. Mapping Quality

Mean Mapping Quality	53.09

2.5. Insert size

Mean	244,383.28
Standard Deviation	4,790,914.18
P25/Median/P75	143 / 189 / 257

2.6. Mismatches and indels

General error rate	1%
Mismatches	24,716,678
Insertions	442,029
Mapped reads with at least one insertion	1.55%
Deletions	1,411,783
Mapped reads with at least one deletion	4.9%
Homopolymer indels	52.71%

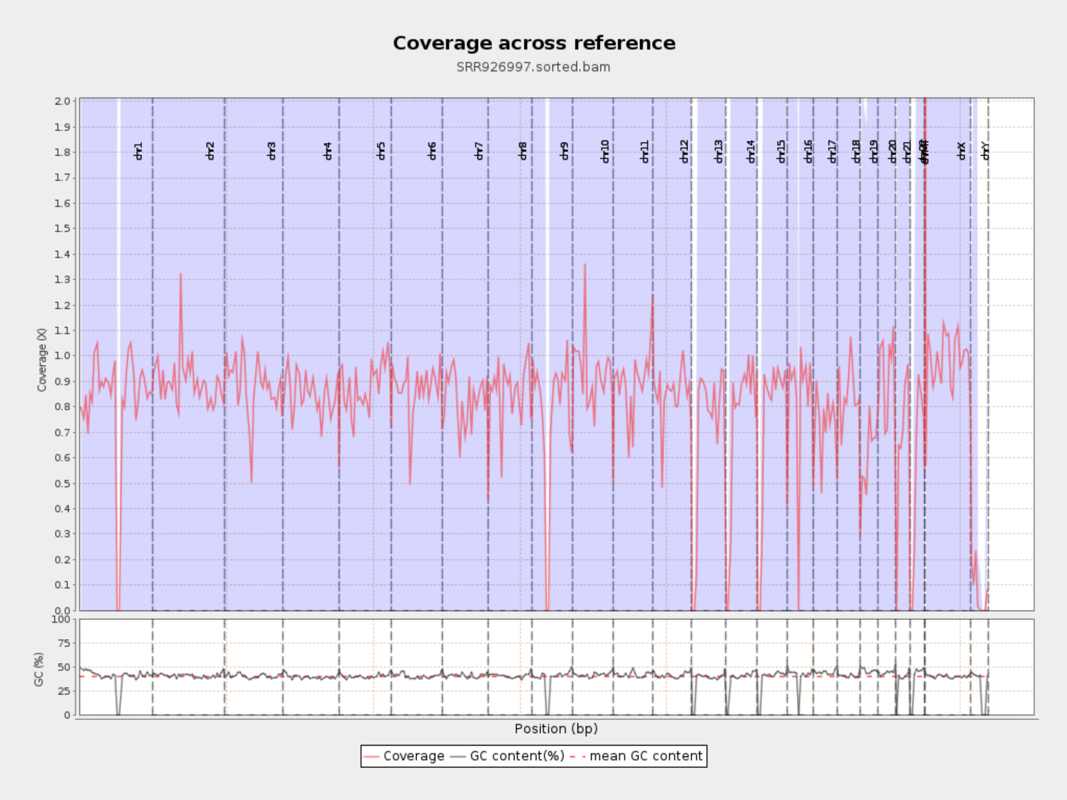
2.7. Chromosome stats

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

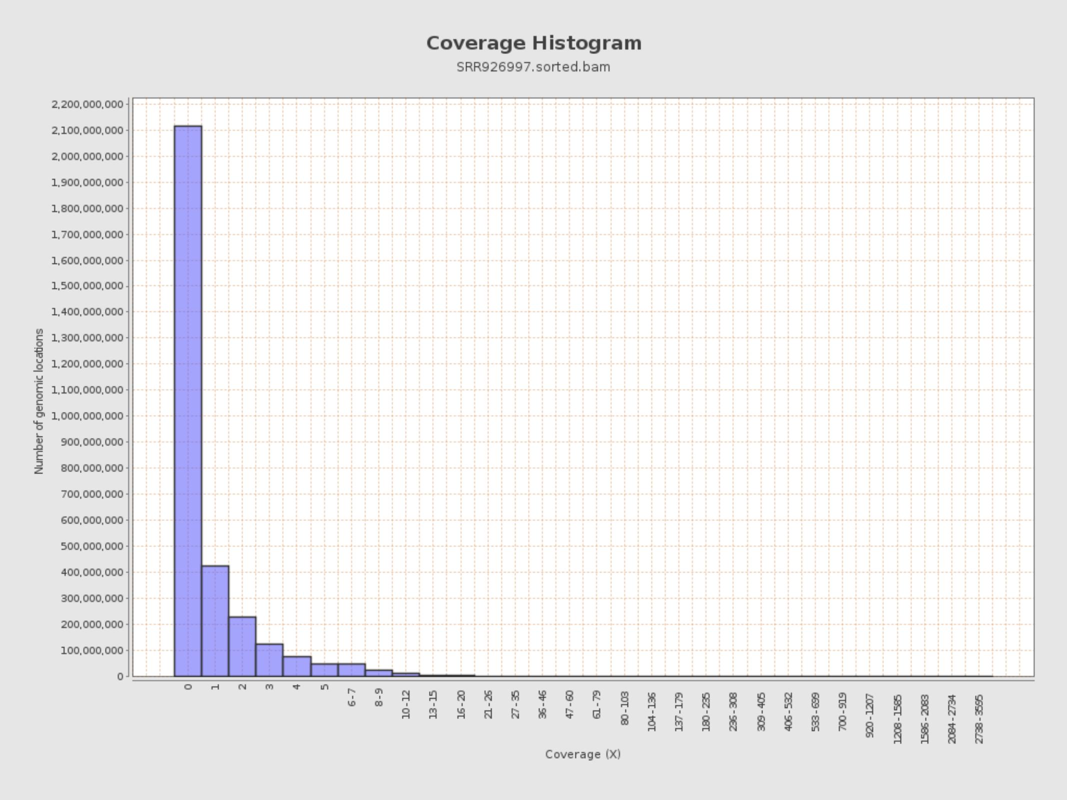
		bases	coverage	deviation
chr1	249250621	206511923	0.8285	3.7007
chr2	243199373	219437547	0.9023	4.3407
chr3	198022430	175102873	0.8843	1.8503
chr4	191154276	162699418	0.8511	2.4742
chr5	180915260	159443587	0.8813	1.8349
chr6	171115067	150185624	0.8777	2.3
chr7	159138663	132161903	0.8305	2.574
chr8	146364022	127340889	0.87	2.0986
chr9	141213431	106020077	0.7508	3.5919
chr10	135534747	127720972	0.9423	6.0811
chr11	135006516	119435327	0.8847	2.7723
chr12	133851895	114107545	0.8525	1.8339
chr13	115169878	80693562	0.7006	1.6393
chr14	107349540	77613602	0.723	1.7274
chr15	102531392	74313915	0.7248	1.738
chr16	90354753	73041931	0.8084	3.5032
chr17	81195210	59050835	0.7273	2.0833
chr18	78077248	67700739	0.8671	3.3988
chr19	59128983	35808627	0.6056	2.3523
chr20	63025520	57861852	0.9181	1.9884
chr21	48129895	33042262	0.6865	2.5815
chr22	51304566	27715720	0.5402	1.5189
chrMT	16571	10385529	626.7292	524.5804
chrX	155270560	151838367	0.9779	2.2676

chrY	59373566	4407517	0.0742	2.2844

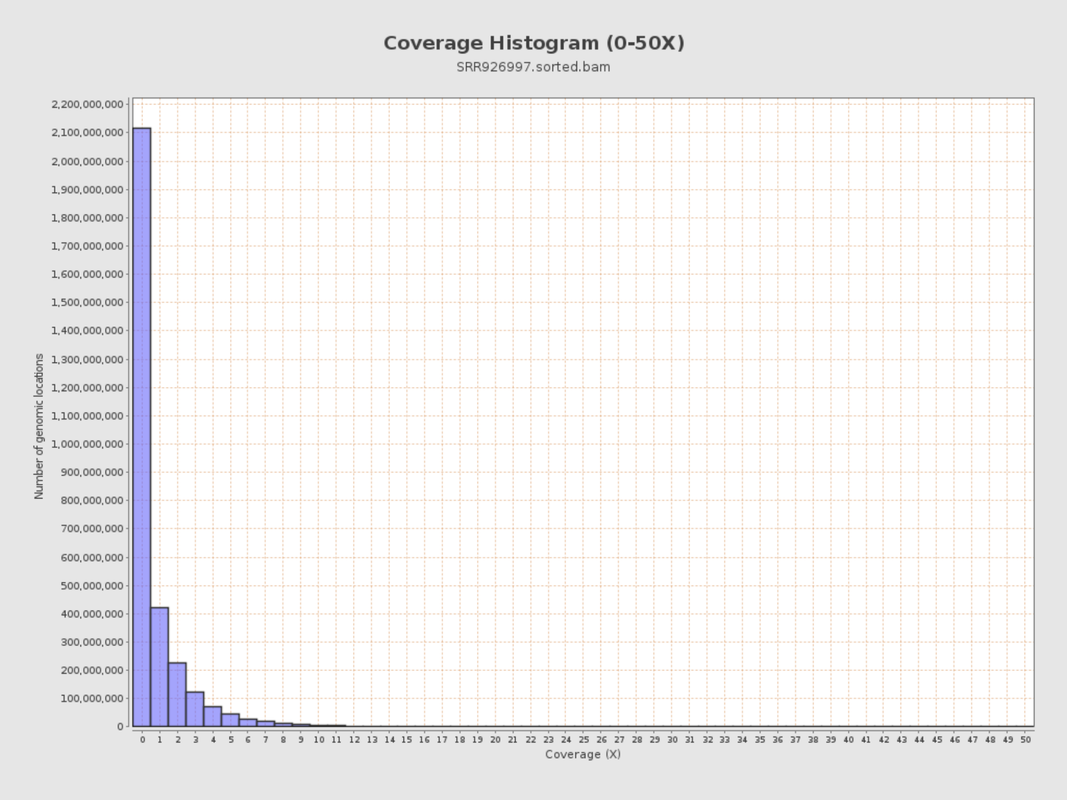
3. Results : Coverage across reference



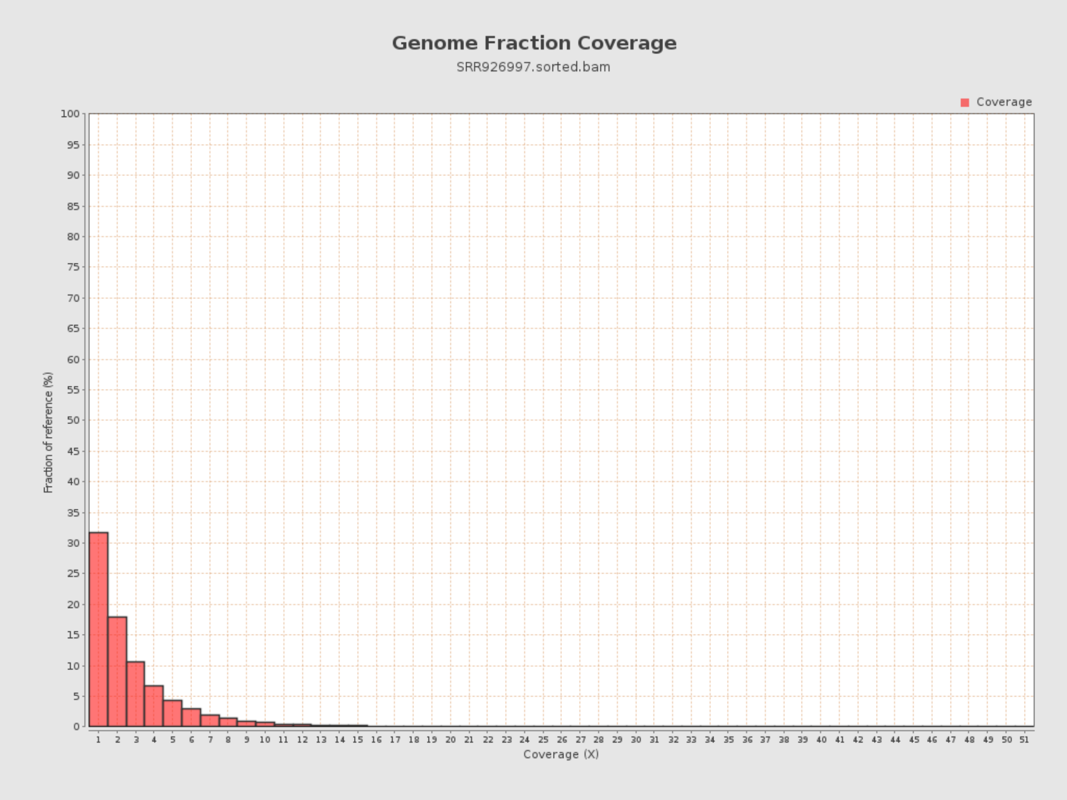
4. Results : Coverage Histogram



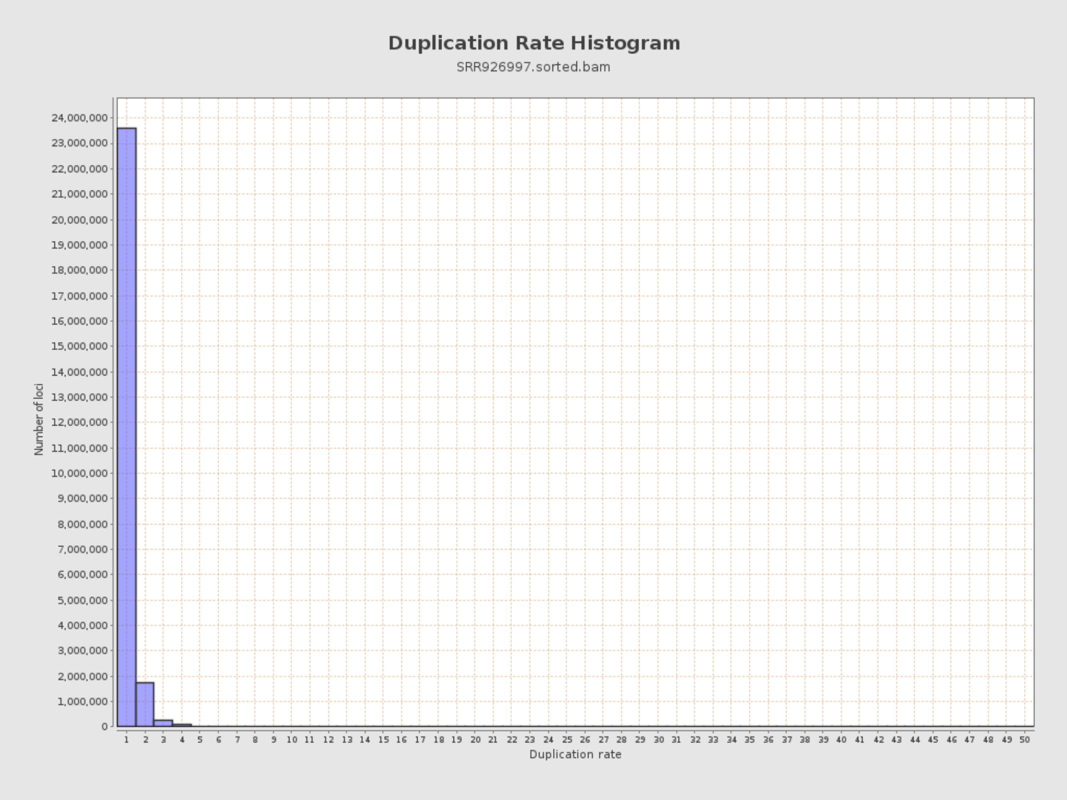
5. Results : Coverage Histogram (0-50X)



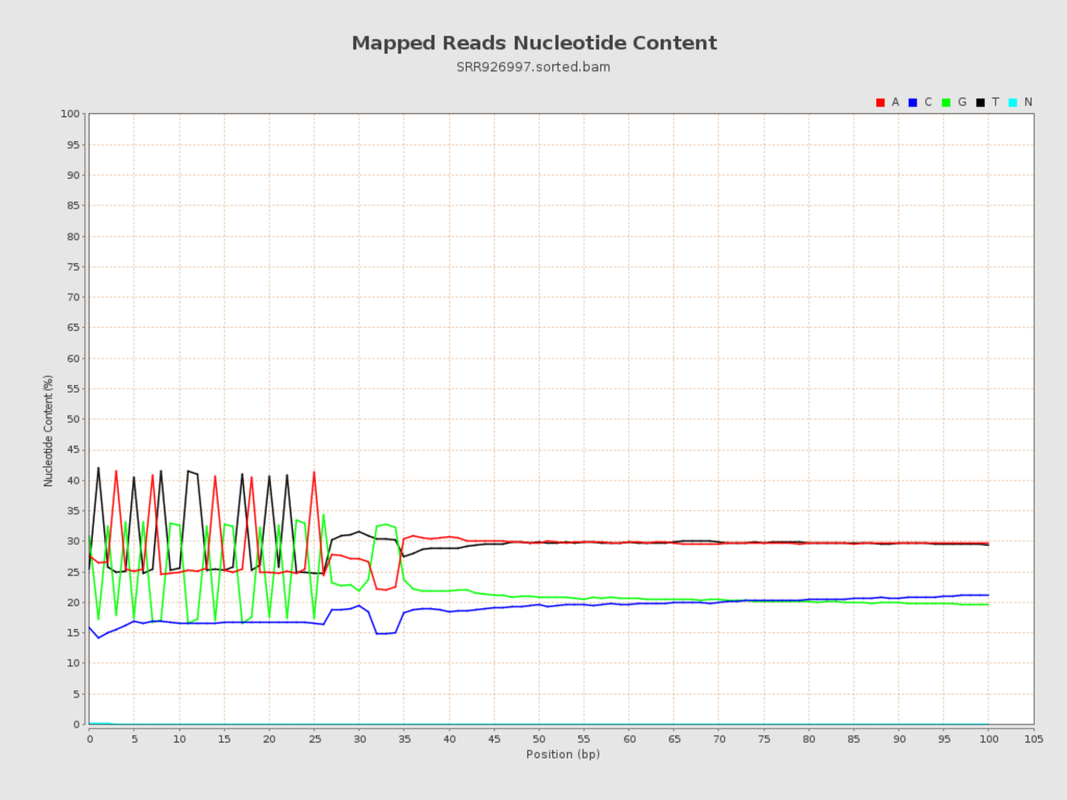
6. Results : Genome Fraction Coverage



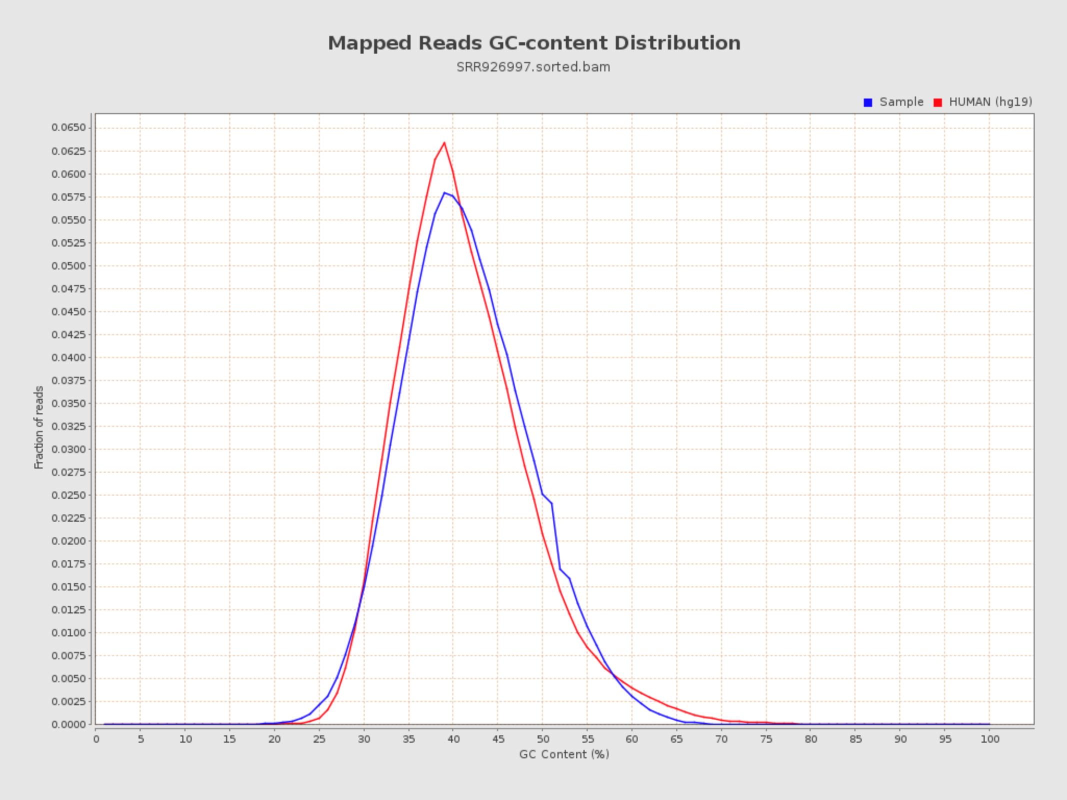
7. Results : Duplication Rate Histogram



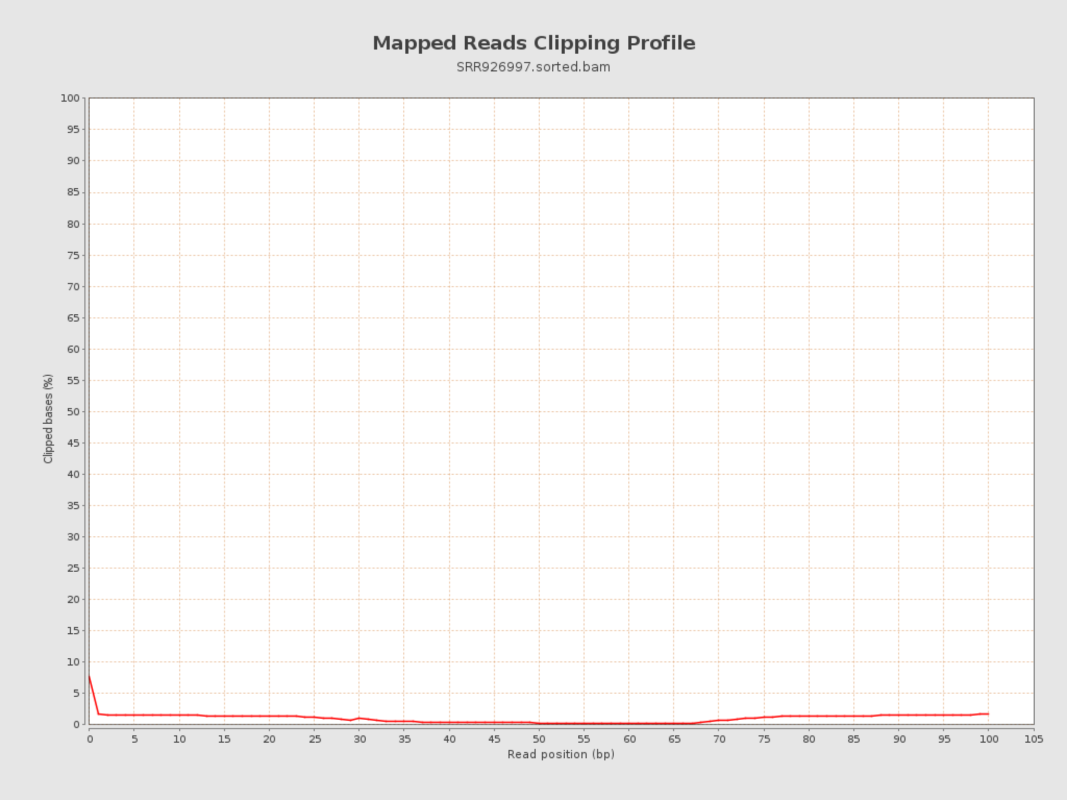
8. Results : Mapped Reads Nucleotide Content



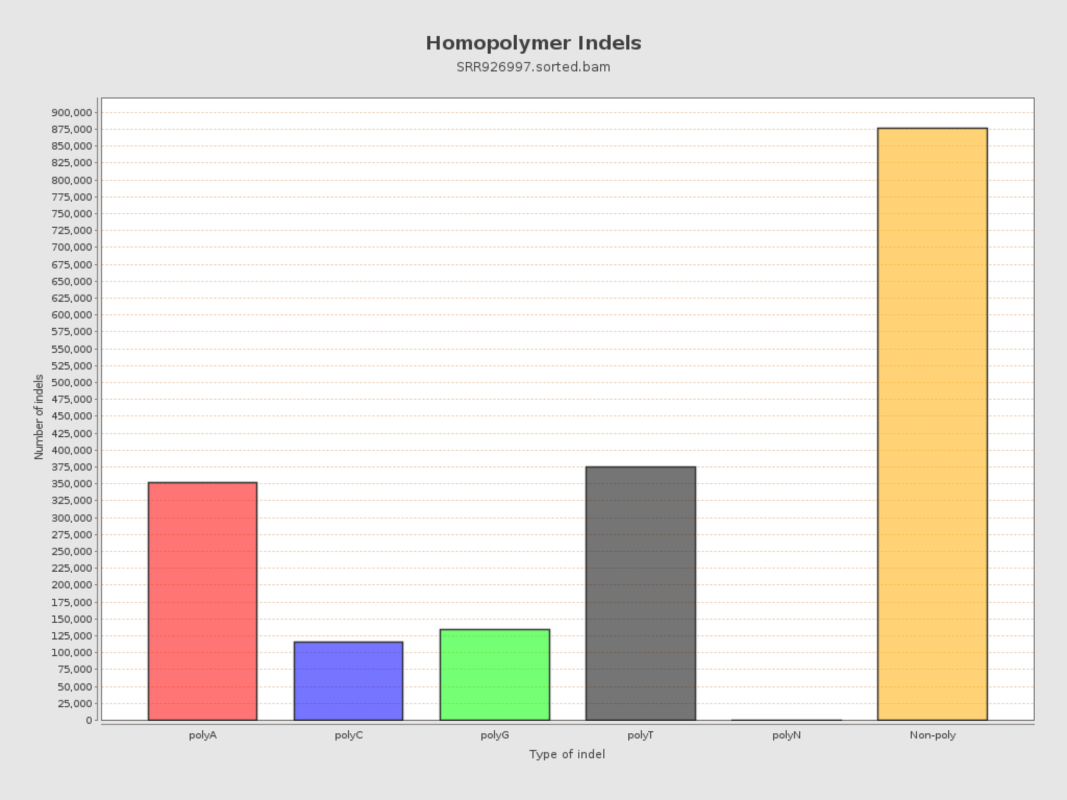
9. Results : Mapped Reads GC-content Distribution



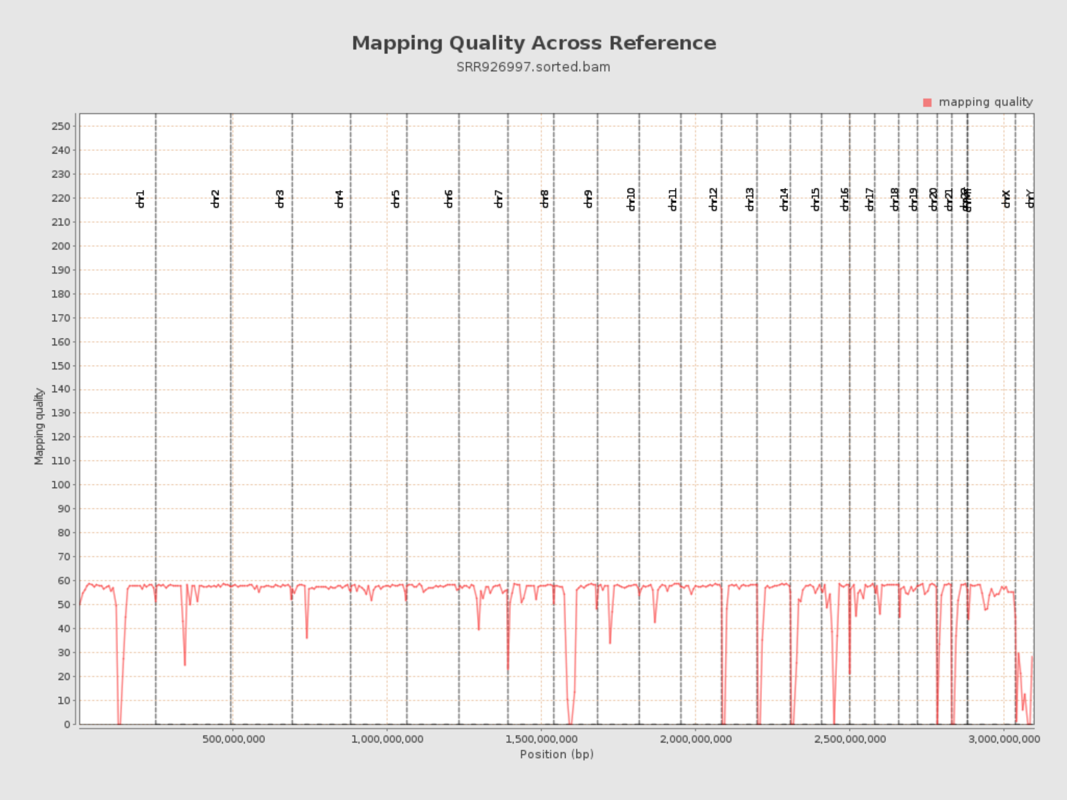
10. Results : Mapped Reads Clipping Profile



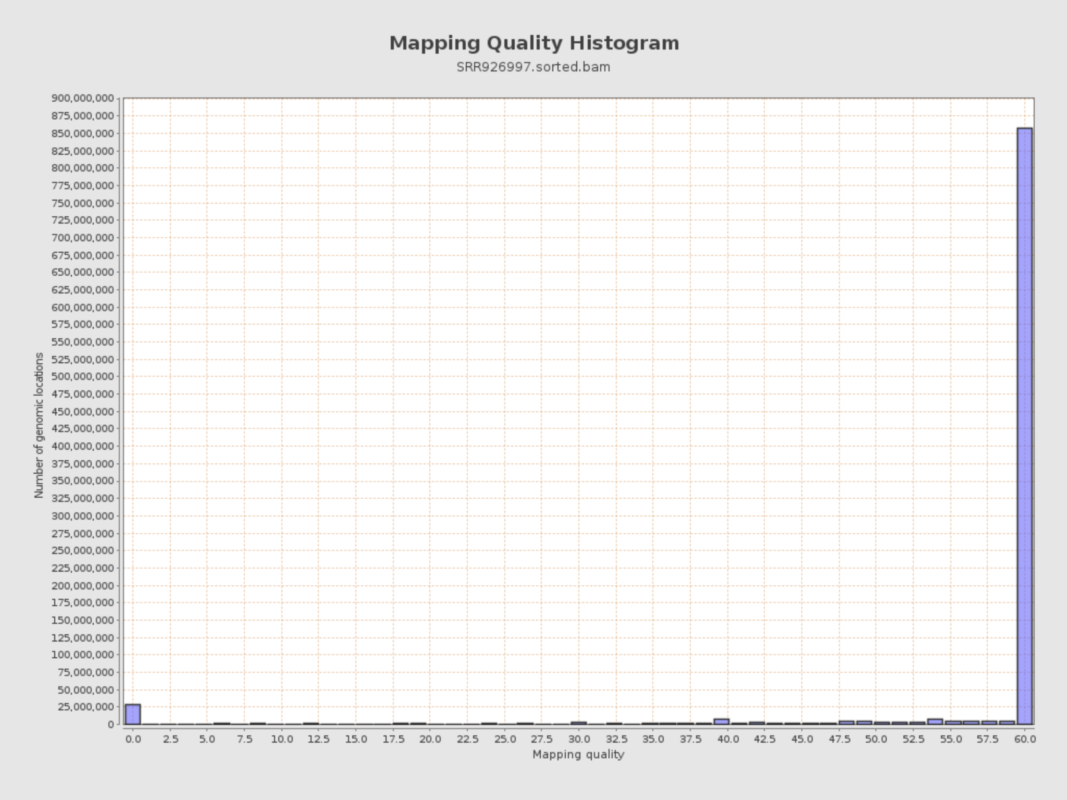
11. Results : Homopolymer Indels



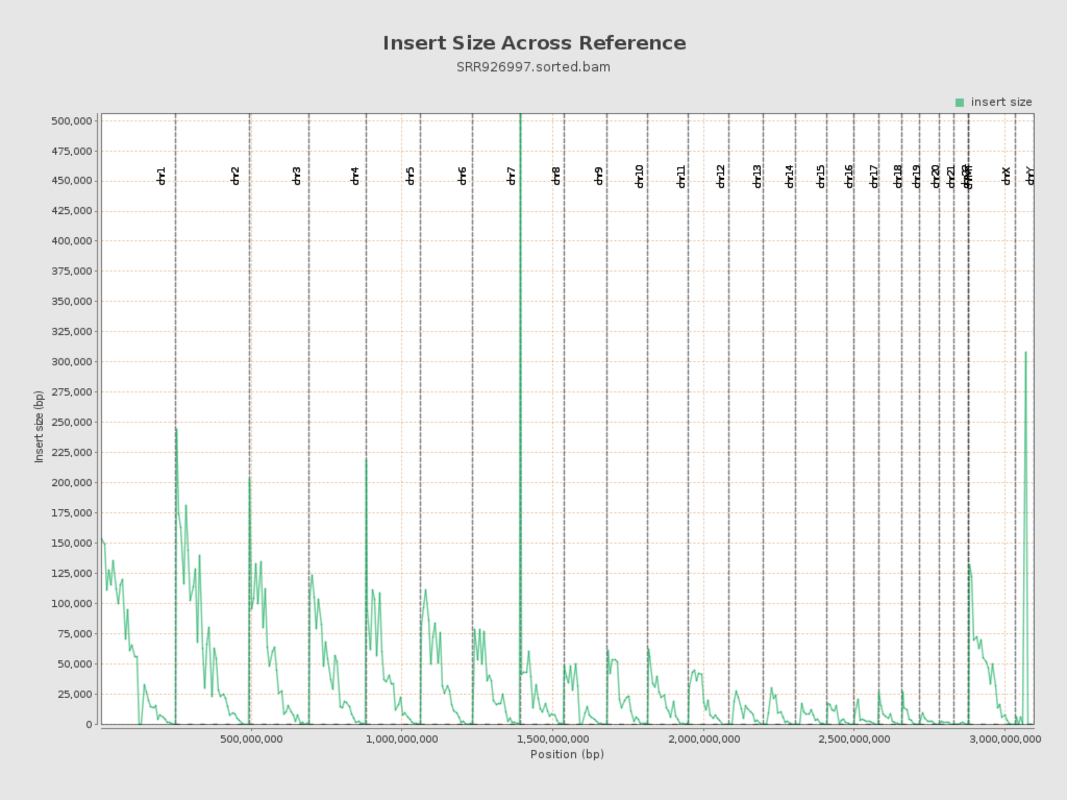
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram