Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/23 14:09:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926981.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_SRR926981 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926981_1.fastq.gz SRR926981_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Apr 23 14:09:18 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926981.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	26,733,388
Mapped reads	26,127,359 / 97.73%
Unmapped reads	606,029 / 2.27%
Mapped paired reads	26,127,359 / 97.73%
Mapped reads, first in pair	13,168,583 / 49.26%
Mapped reads, second in pair	12,958,776 / 48.47%
Mapped reads, both in pair	25,726,022 / 96.23%
Mapped reads, singletons	401,337 / 1.5%
Secondary alignments	0
Supplementary alignments	763,103 / 2.85%
Read min/max/mean length	30 / 101 / 102.19
Duplicated reads (estimated)	2,568,748 / 9.61%
Duplication rate	7.7%
Clipped reads	11,210,034 / 41.93%

2.2. ACGT Content

Number/percentage of A's	678,346,870 / 28.6%
Number/percentage of C's	460,715,186 / 19.43%
Number/percentage of T's	692,382,116 / 29.19%
Number/percentage of G's	540,032,923 / 22.77%
Number/percentage of N's	181,151 / 0.01%

GC Percentage	42.2%

2.3. Coverage

Mean	0.7667
Standard Deviation	2.9722

2.4. Mapping Quality

Mean Mapping Quality	52.61

2.5. Insert size

Mean	335,783.08
Standard Deviation	5,713,338.53
P25/Median/P75	128 / 166 / 223

2.6. Mismatches and indels

General error rate	0.98%
Mismatches	22,396,950
Insertions	420,945
Mapped reads with at least one insertion	1.58%
Deletions	1,258,199
Mapped reads with at least one deletion	4.69%
Homopolymer indels	51.74%

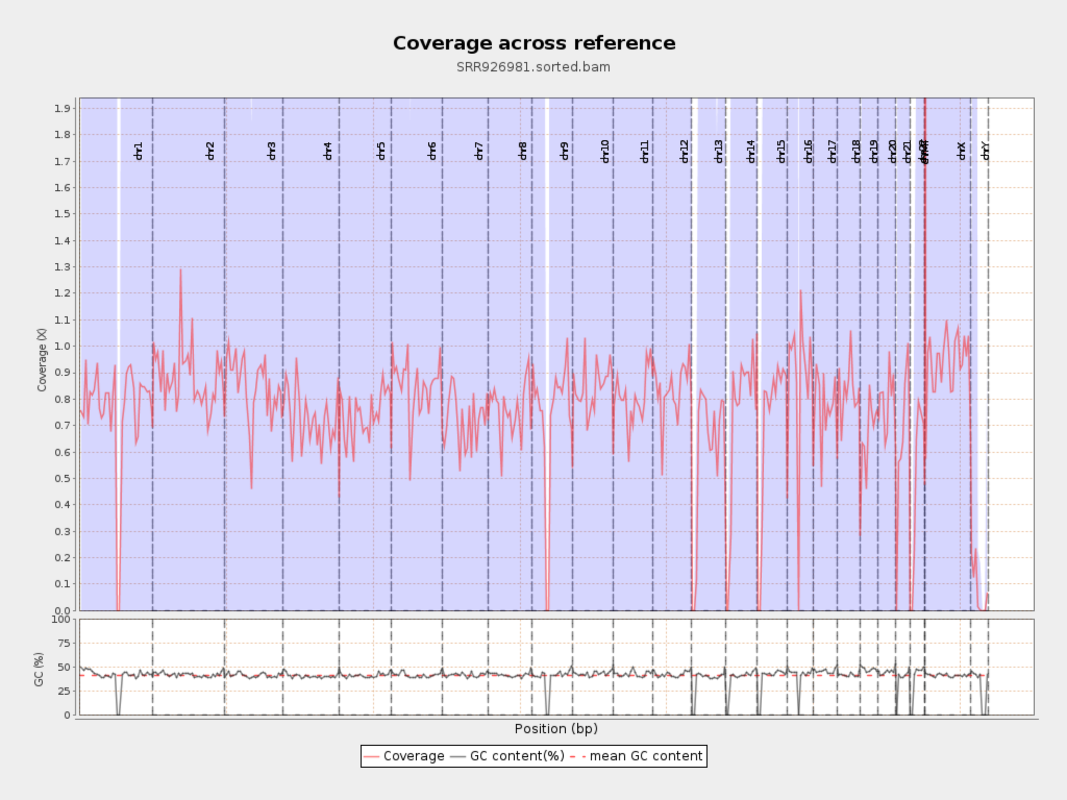
2.7. Chromosome stats

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

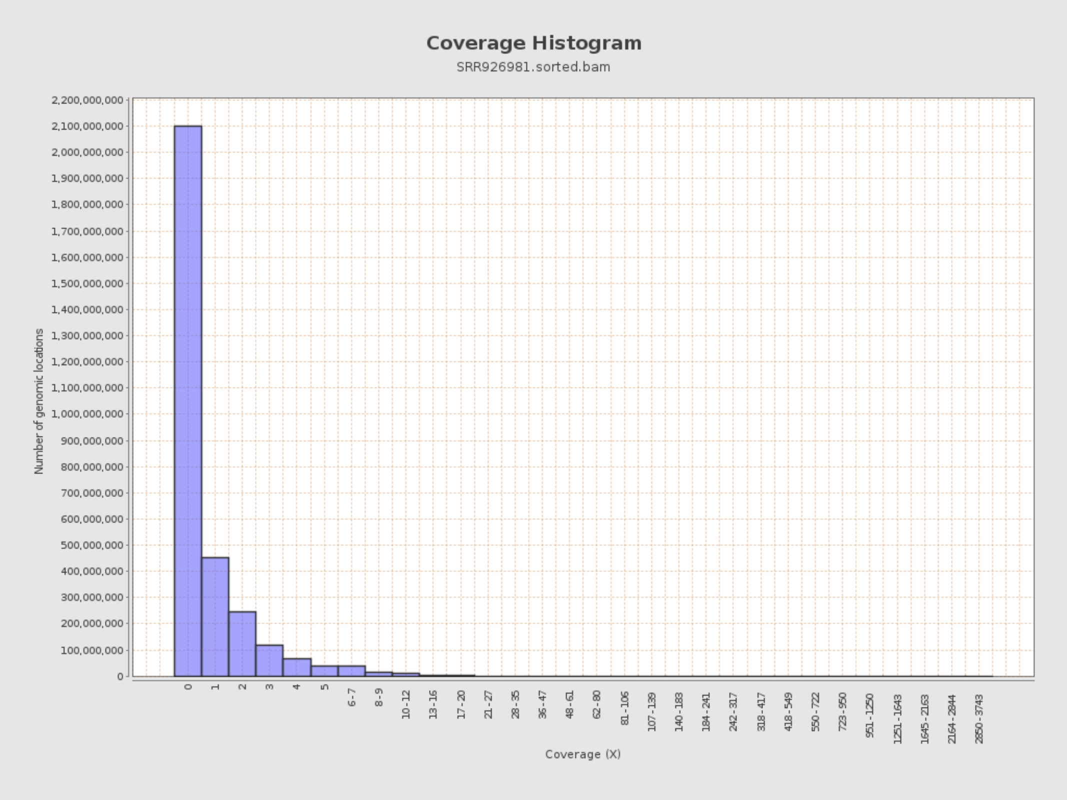
		bases	coverage	deviation
chr1	249250621	188697714	0.7571	3.5714
chr2	243199373	215119197	0.8845	5.2263
chr3	198022430	167576245	0.8462	1.7125
chr4	191154276	138865846	0.7265	2.5954
chr5	180915260	134105103	0.7413	1.5681
chr6	171115067	145933383	0.8528	2.6567
chr7	159138663	114460089	0.7192	2.5834
chr8	146364022	111351519	0.7608	1.9211
chr9	141213431	102124810	0.7232	3.4123
chr10	135534747	115302922	0.8507	3.7451
chr11	135006516	108294718	0.8021	3.659
chr12	133851895	112257616	0.8387	2.1853
chr13	115169878	69146136	0.6004	1.5342
chr14	107349540	76783235	0.7153	1.7068
chr15	102531392	71175797	0.6942	1.6845
chr16	90354753	77831546	0.8614	4.378
chr17	81195210	62033677	0.764	2.9036
chr18	78077248	65863099	0.8436	3.5833
chr19	59128983	39319474	0.665	2.2204
chr20	63025520	49678607	0.7882	1.7767
chr21	48129895	32015379	0.6652	2.4846
chr22	51304566	24993140	0.4872	1.4091
chrMT	16571	406290	24.5181	23.8306
chrX	155270560	145618303	0.9378	2.2446

chrY	59373566	4557309	0.0768	2.5115

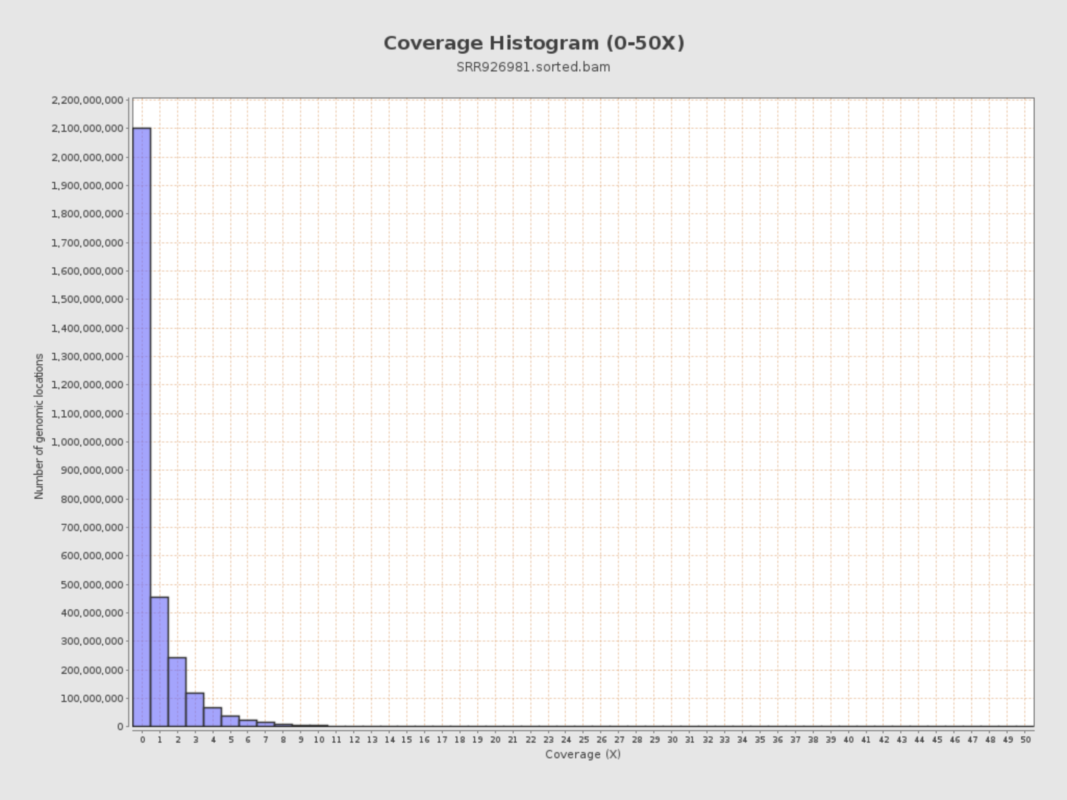
3. Results : Coverage across reference



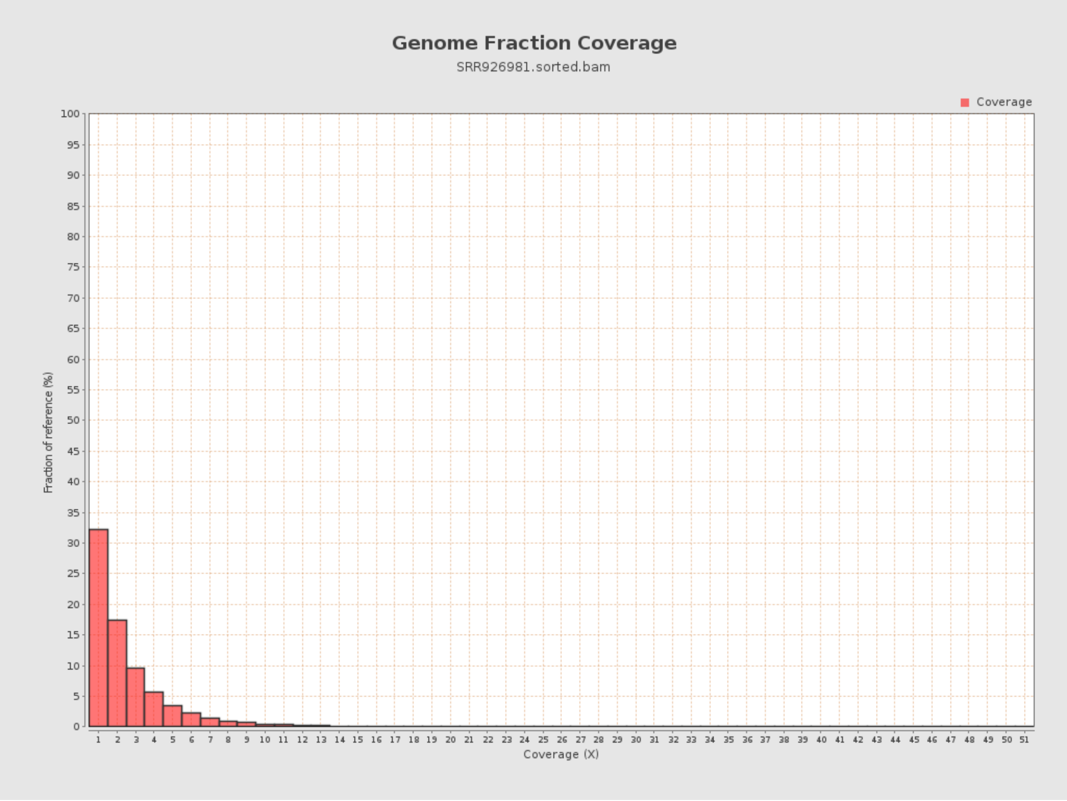
4. Results : Coverage Histogram



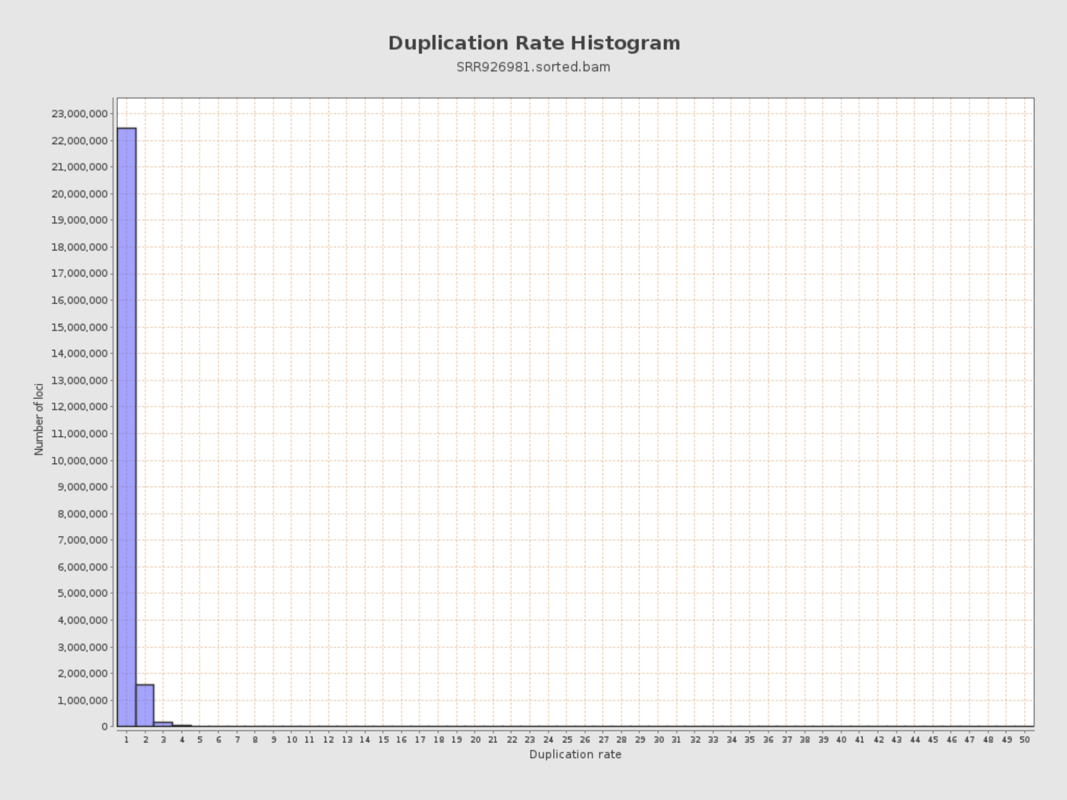
5. Results : Coverage Histogram (0-50X)



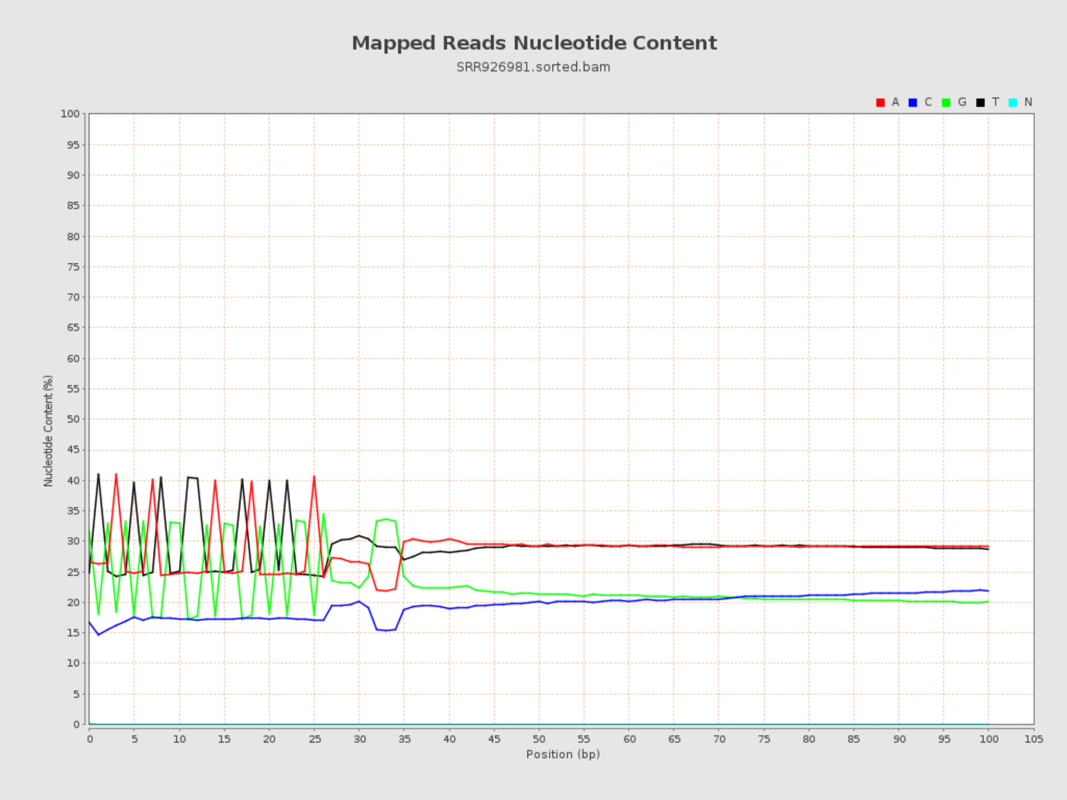
6. Results : Genome Fraction Coverage



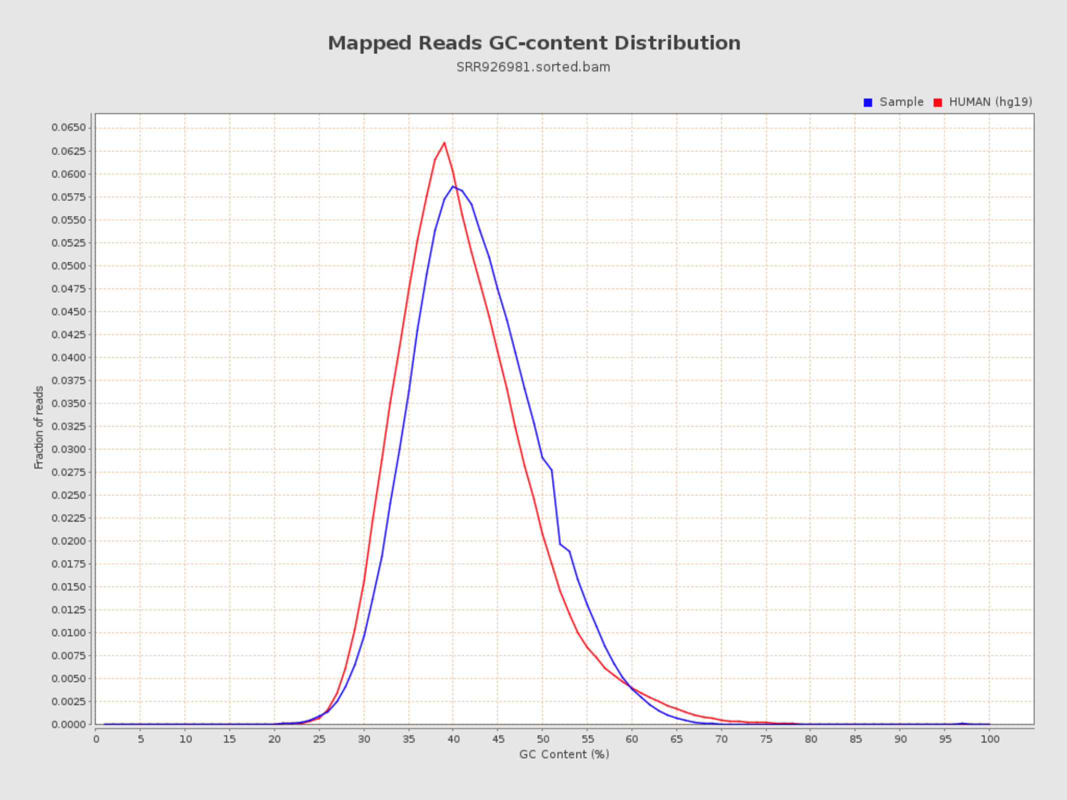
7. Results : Duplication Rate Histogram



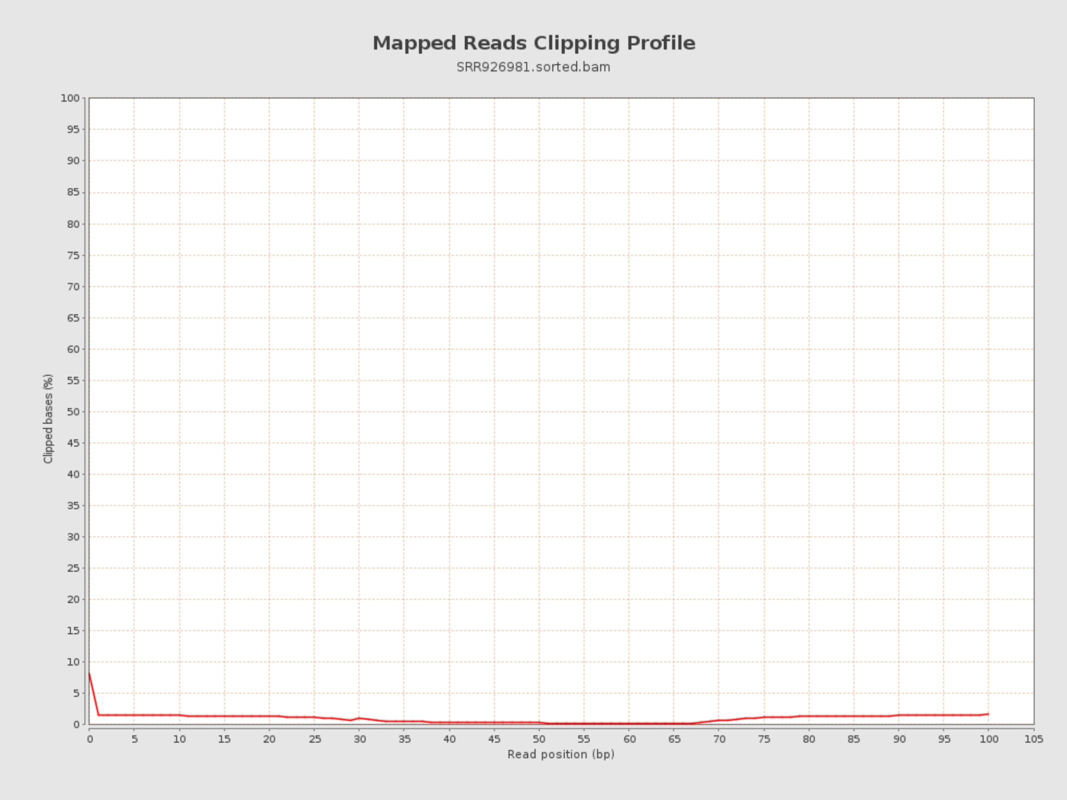
8. Results : Mapped Reads Nucleotide Content



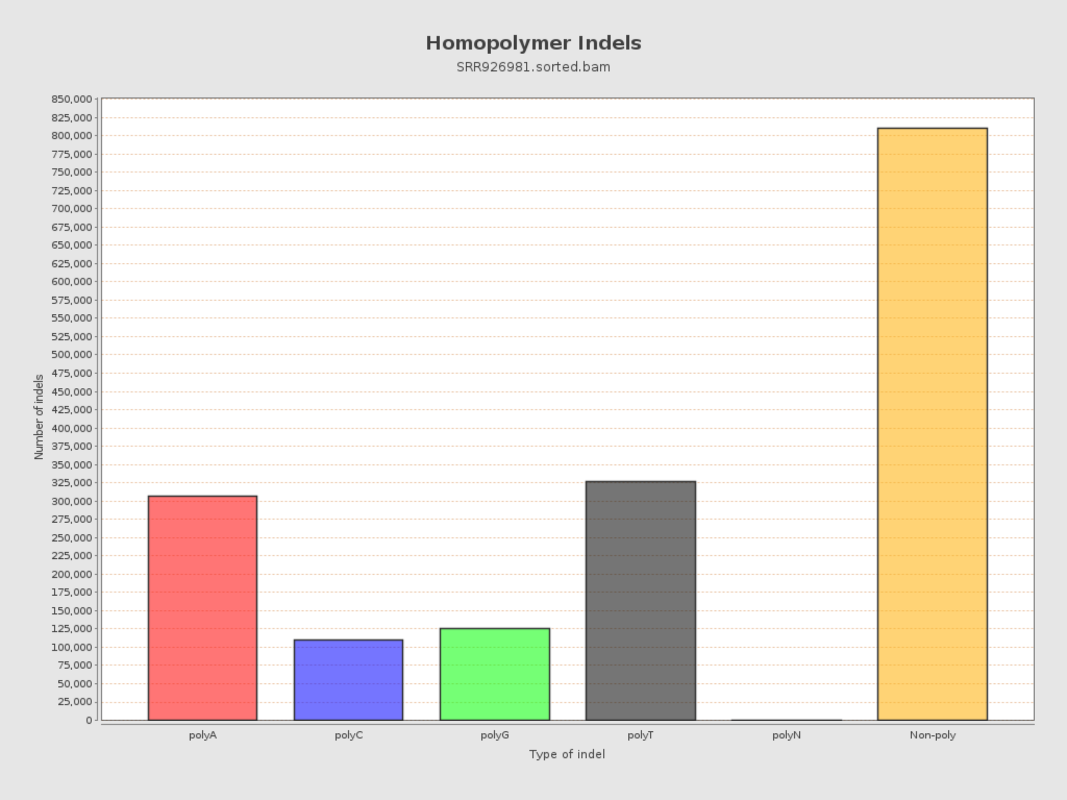
9. Results : Mapped Reads GC-content Distribution



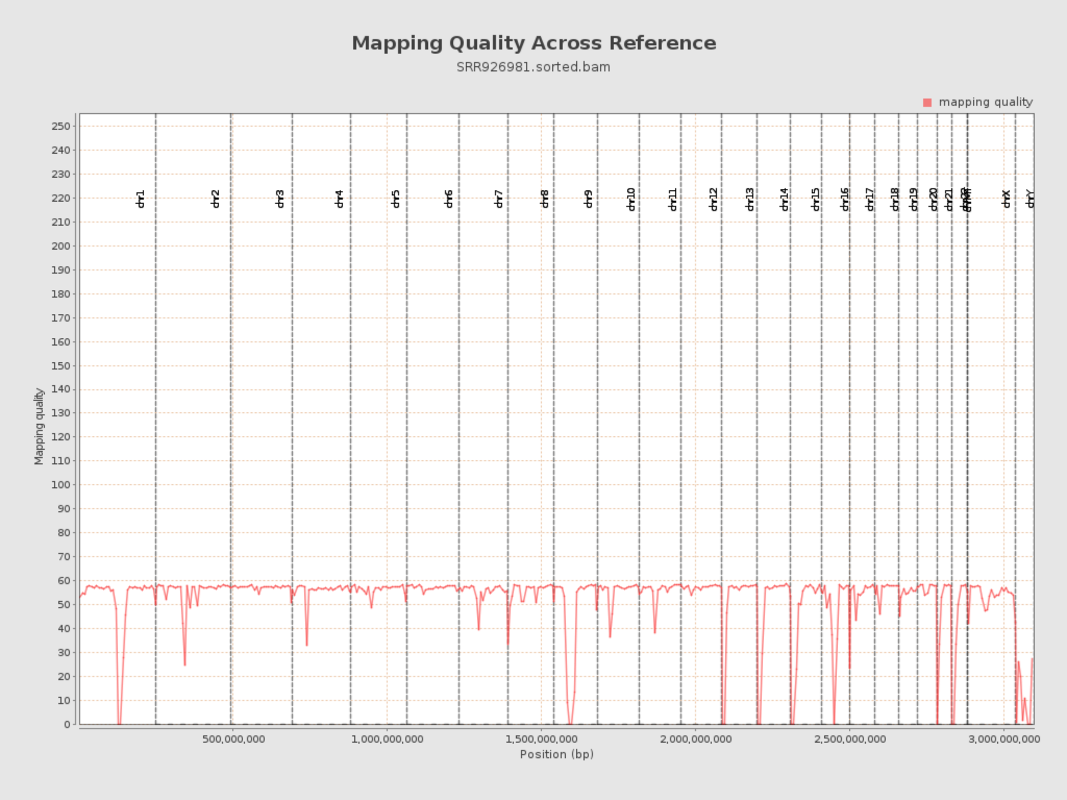
10. Results : Mapped Reads Clipping Profile



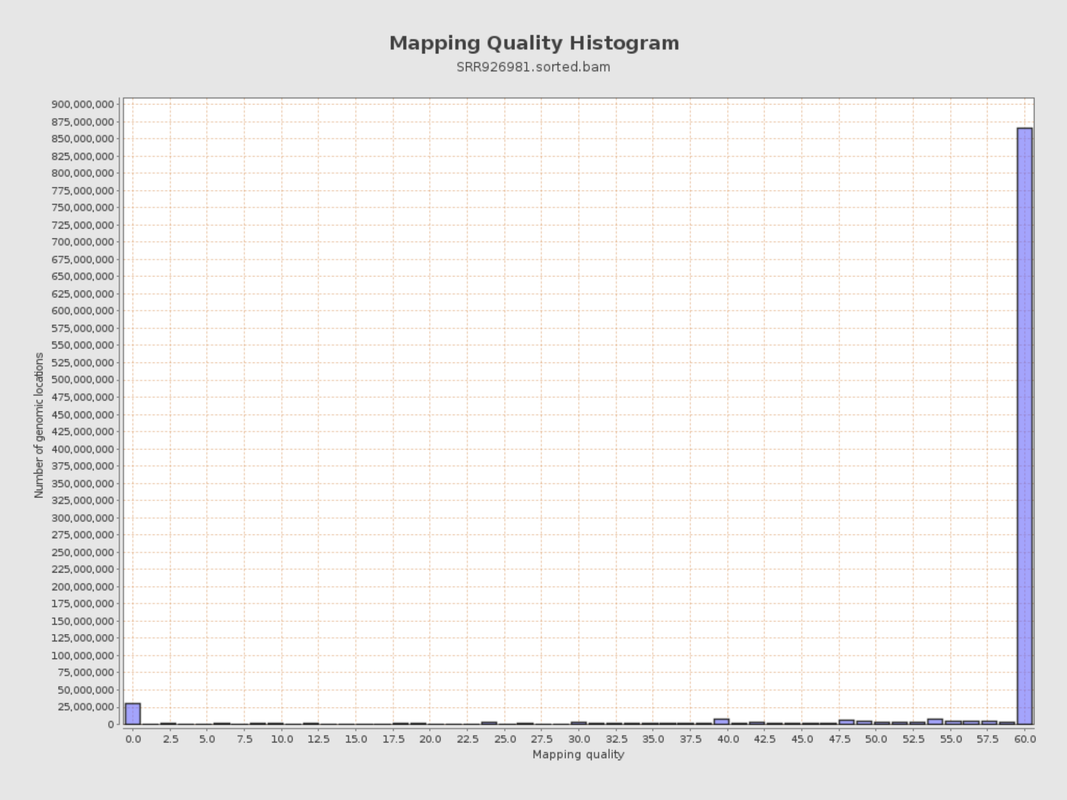
11. Results : Homopolymer Indels



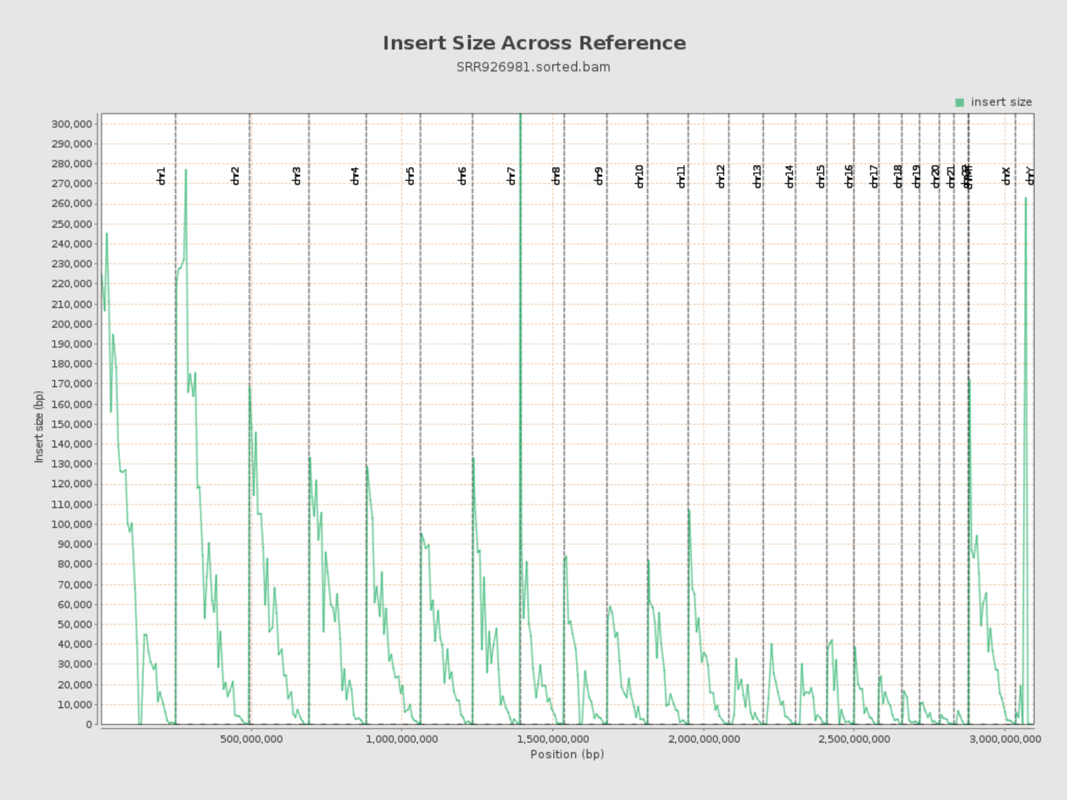
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram