Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/23 00:25:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926944.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_SRR926944 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926944_1.fastq.gz SRR926944_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Apr 23 00:25:26 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926944.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	11,572,714
Mapped reads	11,297,218 / 97.62%
Unmapped reads	275,496 / 2.38%
Mapped paired reads	11,297,218 / 97.62%
Mapped reads, first in pair	5,673,595 / 49.03%
Mapped reads, second in pair	5,623,623 / 48.59%
Mapped reads, both in pair	11,159,802 / 96.43%
Mapped reads, singletons	137,416 / 1.19%
Secondary alignments	0
Supplementary alignments	146,799 / 1.27%
Read min/max/mean length	30 / 101 / 101.52
Duplicated reads (estimated)	601,436 / 5.2%
Duplication rate	4.27%
Clipped reads	3,610,018 / 31.19%

2.2. ACGT Content

Number/percentage of A's	300,307,617 / 28.65%
Number/percentage of C's	206,414,095 / 19.69%
Number/percentage of T's	304,964,875 / 29.1%
Number/percentage of G's	236,415,416 / 22.56%
Number/percentage of N's	55,536 / 0.01%

GC Percentage	42.25%

2.3. Coverage

Mean	0.3388
Standard Deviation	1.4561

2.4. Mapping Quality

Mean Mapping Quality	53.33

2.5. Insert size

Mean	142,347.45
Standard Deviation	3,763,543.45
P25/Median/P75	144 / 188 / 254

2.6. Mismatches and indels

General error rate	0.93%
Mismatches	9,419,214
Insertions	176,289
Mapped reads with at least one insertion	1.53%
Deletions	557,989
Mapped reads with at least one deletion	4.81%
Homopolymer indels	52.97%

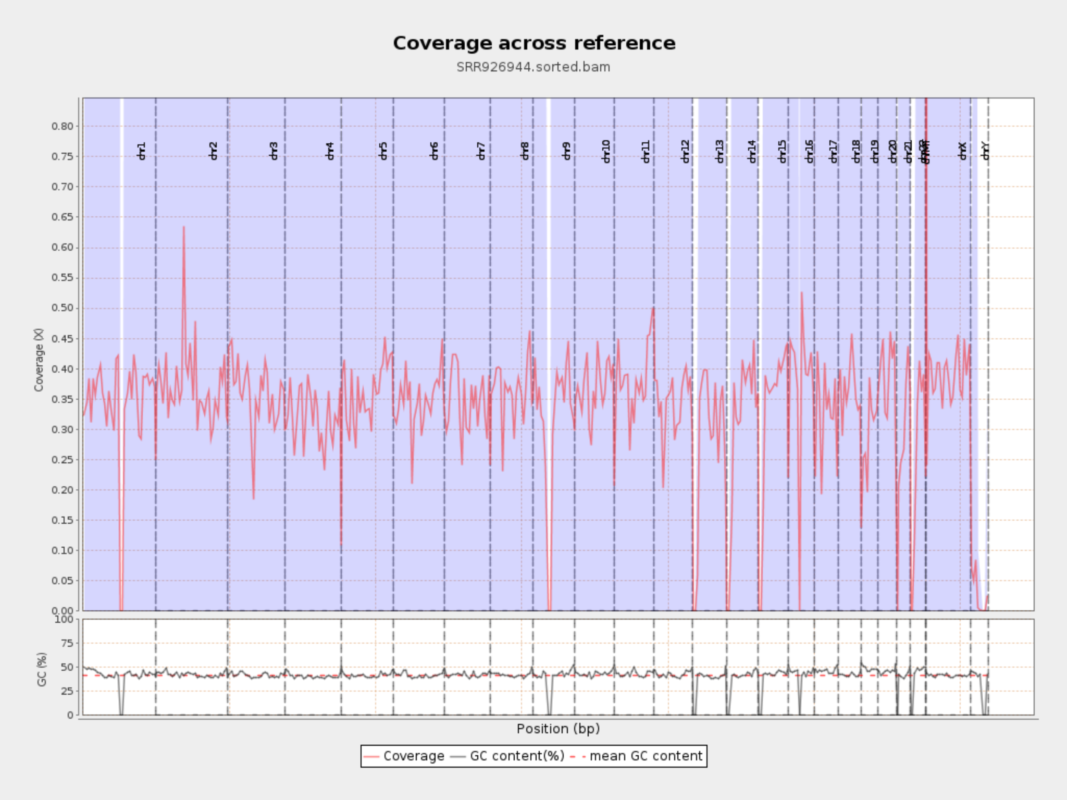
2.7. Chromosome stats

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

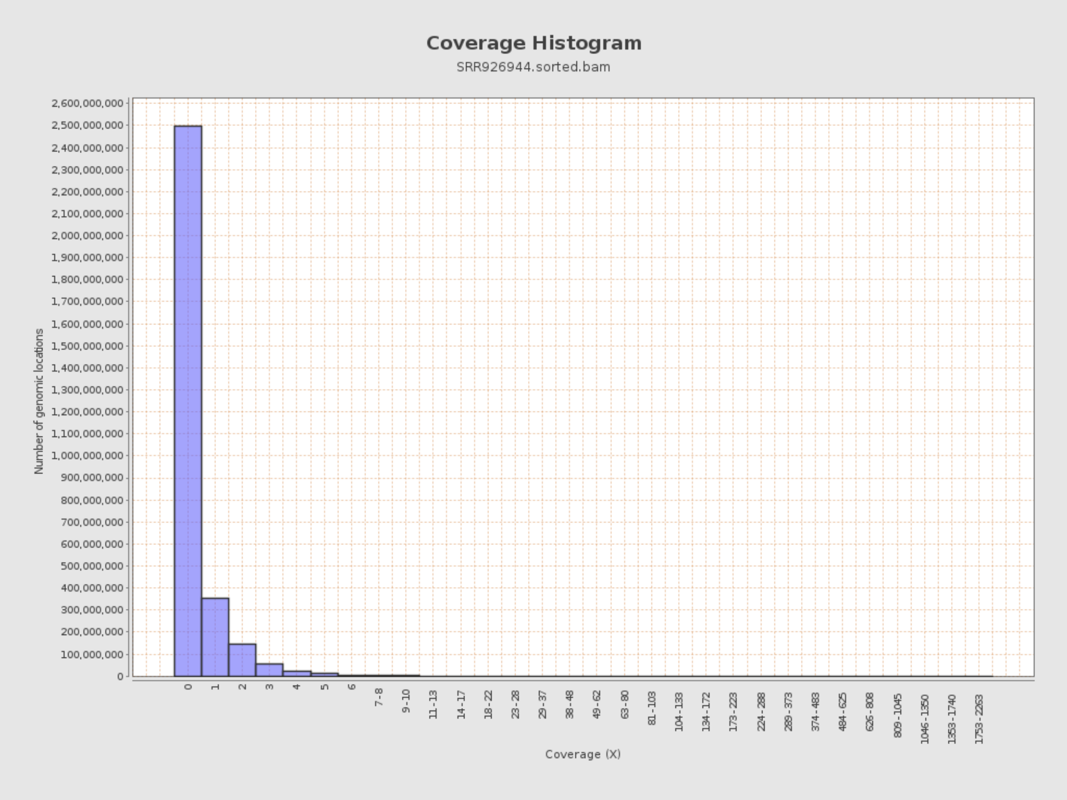
		bases	coverage	deviation
chr1	249250621	84410096	0.3387	1.8461
chr2	243199373	90709186	0.373	2.8059
chr3	198022430	70801165	0.3575	0.8933
chr4	191154276	61289545	0.3206	1.1567
chr5	180915260	65551738	0.3623	0.8871
chr6	171115067	59376084	0.347	1.0266
chr7	159138663	54783218	0.3442	1.0984
chr8	146364022	53311360	0.3642	0.9845
chr9	141213431	44273340	0.3135	1.5219
chr10	135534747	49803093	0.3675	1.9613
chr11	135006516	51285749	0.3799	1.7523
chr12	133851895	46277285	0.3457	0.8952
chr13	115169878	31985995	0.2777	0.7833
chr14	107349540	32974501	0.3072	0.8605
chr15	102531392	32727104	0.3192	0.8722
chr16	90354753	33803837	0.3741	1.9542
chr17	81195210	26531495	0.3268	1.0964
chr18	78077248	28682446	0.3674	1.6625
chr19	59128983	17177112	0.2905	1.2035
chr20	63025520	24970702	0.3962	0.9915
chr21	48129895	13645667	0.2835	1.032
chr22	51304566	12943234	0.2523	0.787
chrMT	16571	102353	6.1766	5.5606
chrX	155270560	59920042	0.3859	1.0672

chrY	59373566	1622093	0.0273	0.9595

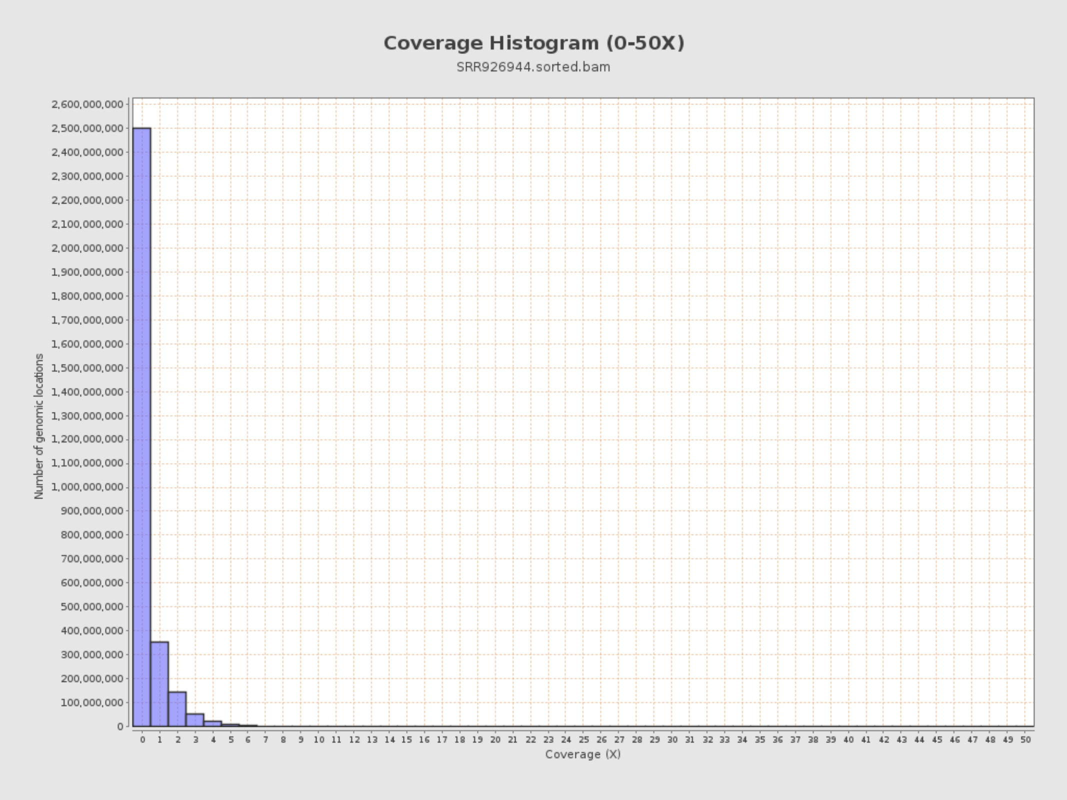
3. Results : Coverage across reference



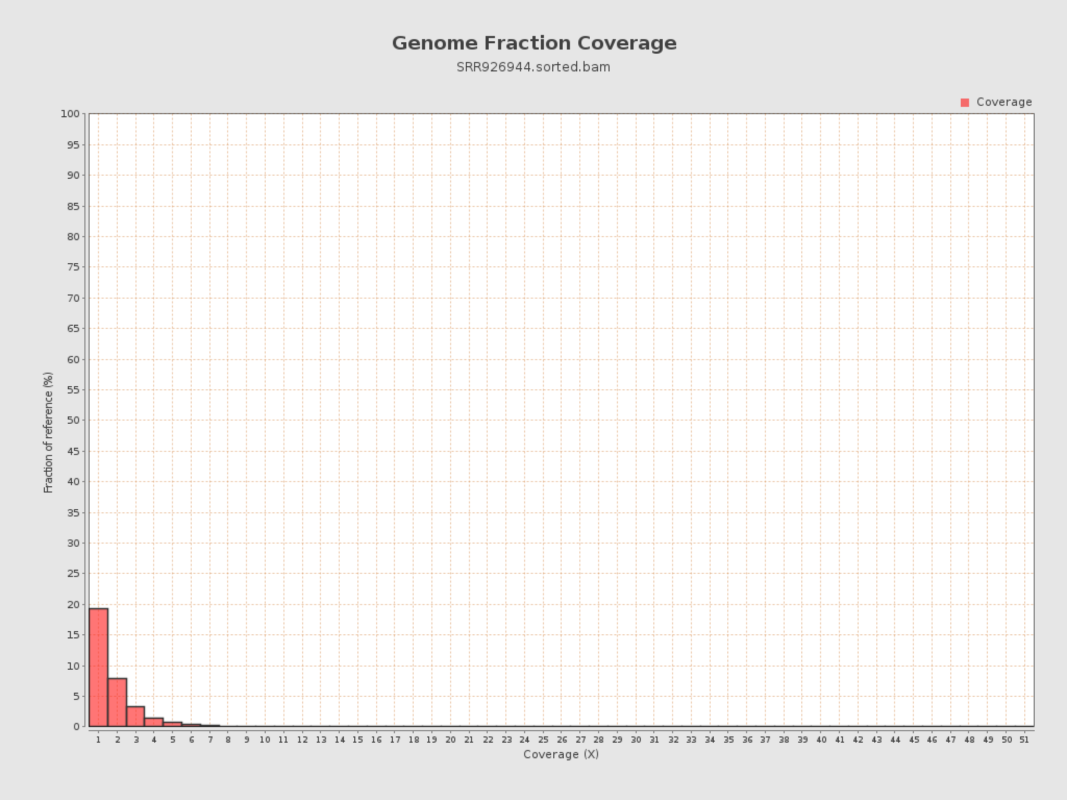
4. Results : Coverage Histogram



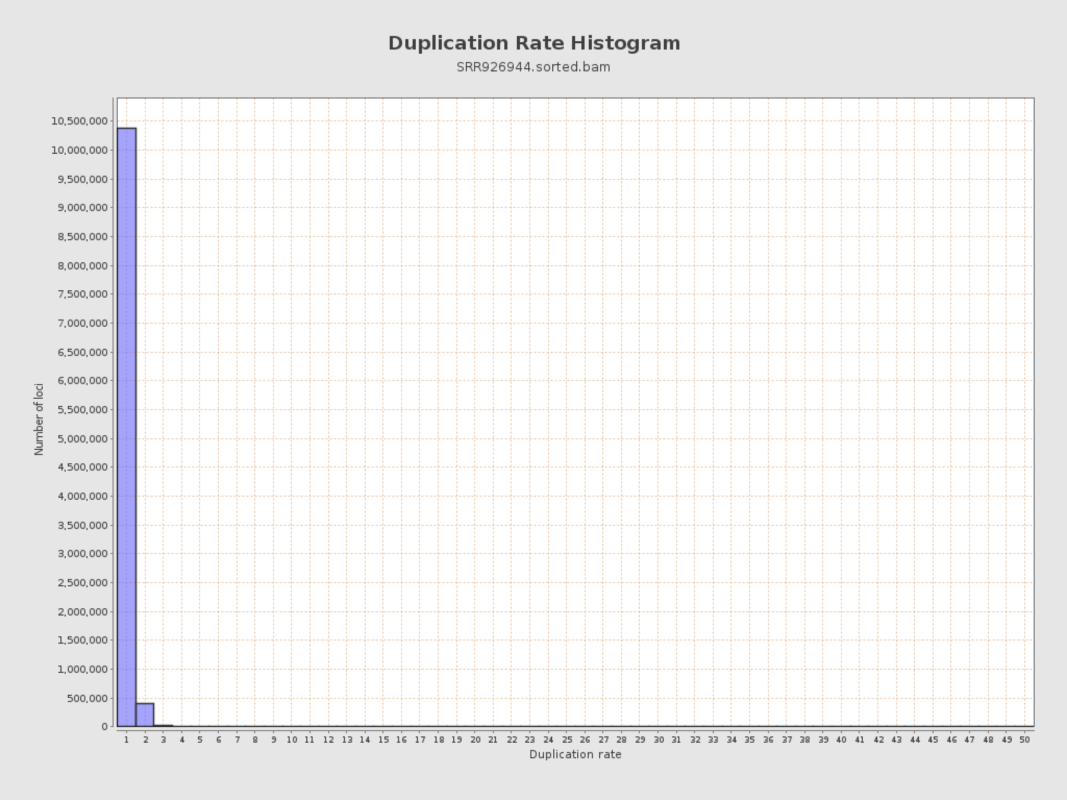
5. Results : Coverage Histogram (0-50X)



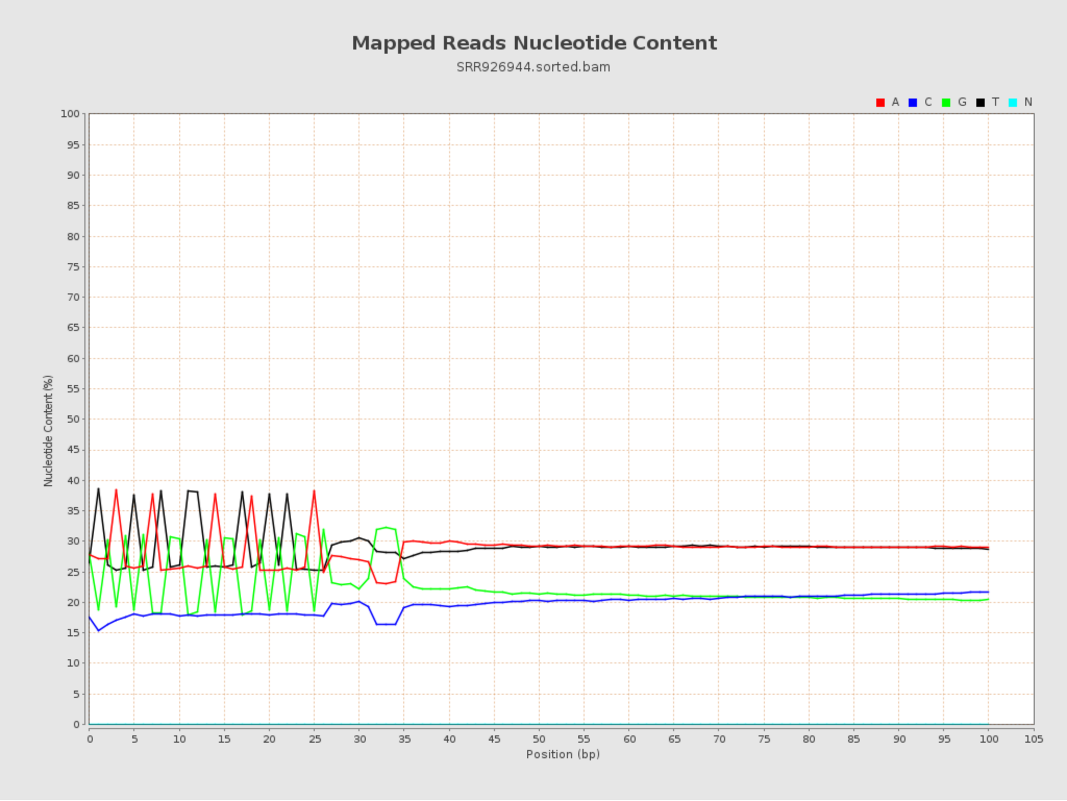
6. Results : Genome Fraction Coverage



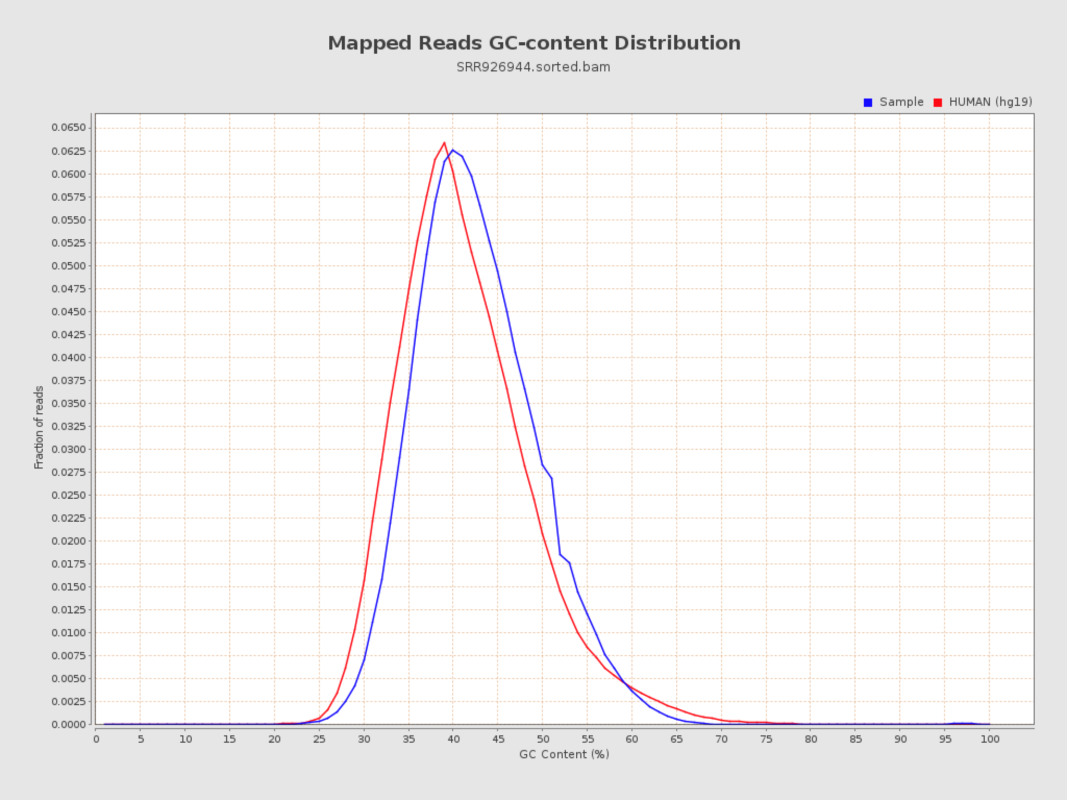
7. Results : Duplication Rate Histogram



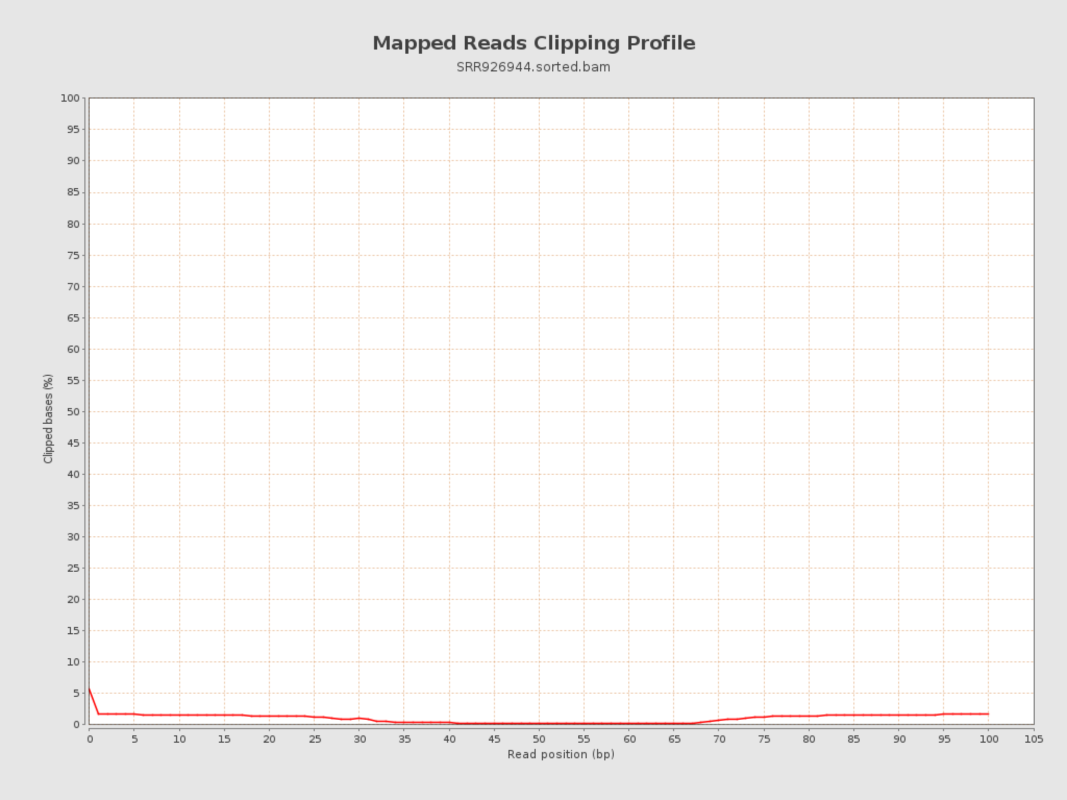
8. Results : Mapped Reads Nucleotide Content



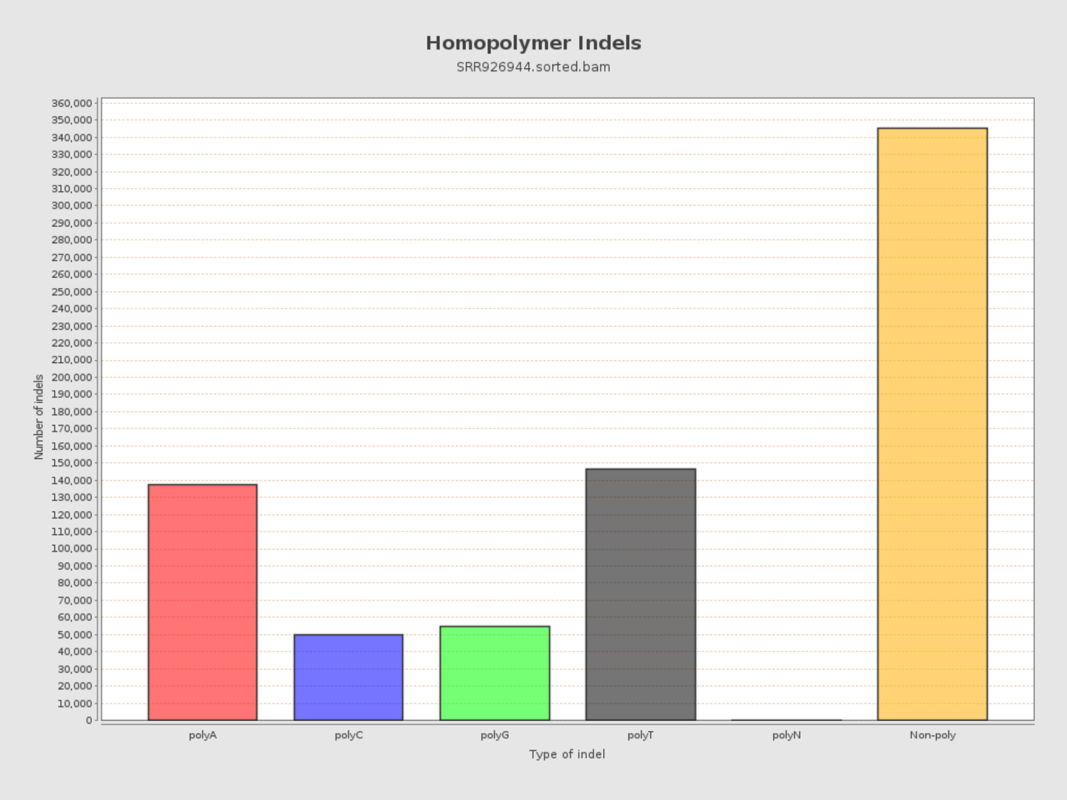
9. Results : Mapped Reads GC-content Distribution



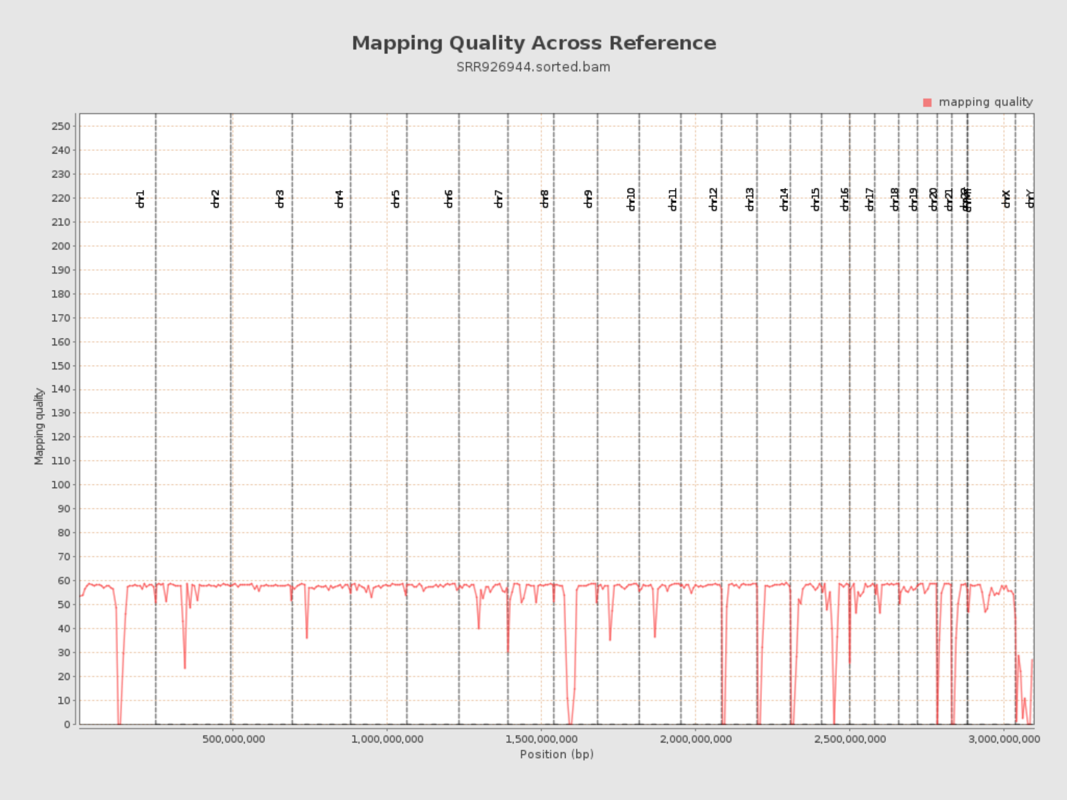
10. Results : Mapped Reads Clipping Profile



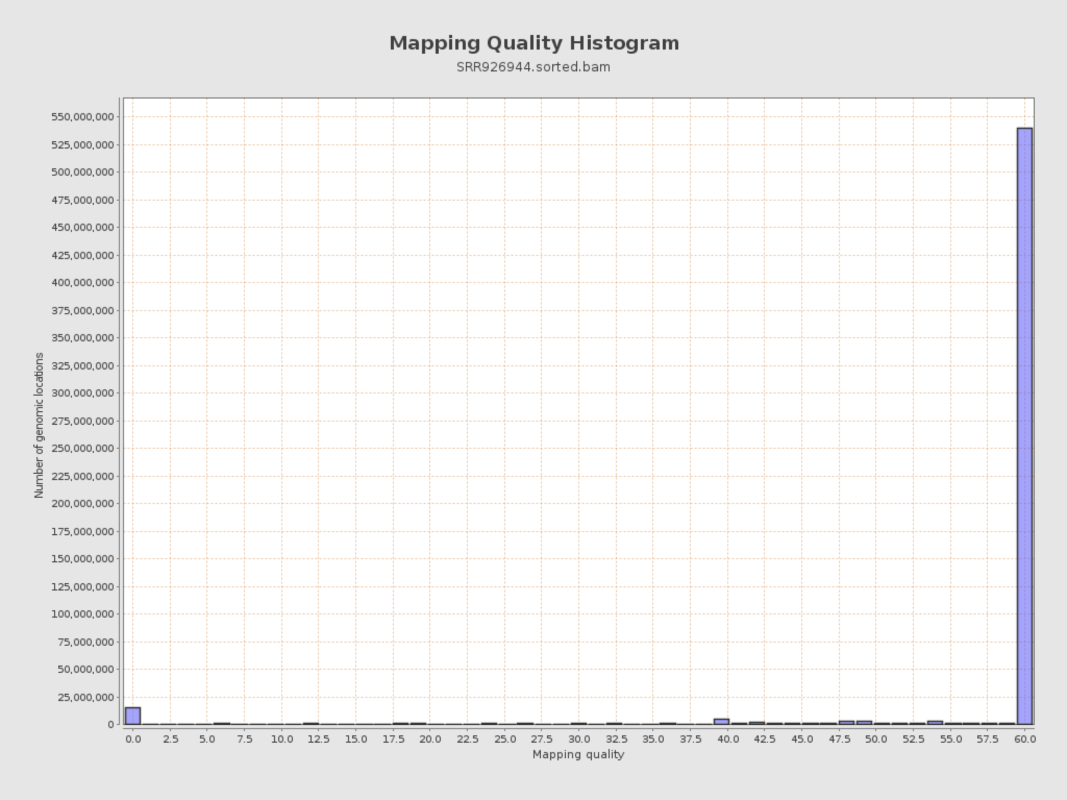
11. Results : Homopolymer Indels



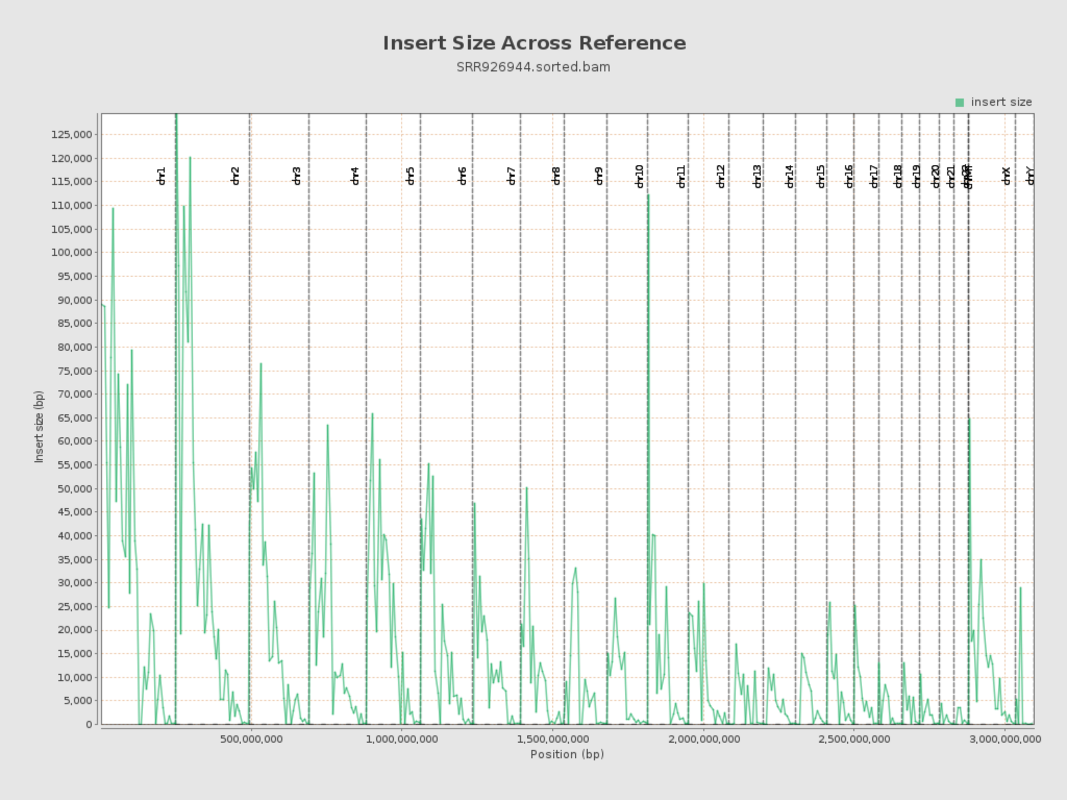
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram