Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/22 19:21:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926922.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_SRR926922 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926922_1.fastq.gz SRR926922_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 22 19:21:42 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926922.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	15,472,624
Mapped reads	15,126,256 / 97.76%
Unmapped reads	346,368 / 2.24%
Mapped paired reads	15,126,256 / 97.76%
Mapped reads, first in pair	7,580,519 / 48.99%
Mapped reads, second in pair	7,545,737 / 48.77%
Mapped reads, both in pair	14,963,412 / 96.71%
Mapped reads, singletons	162,844 / 1.05%
Secondary alignments	0
Supplementary alignments	193,674 / 1.25%
Read min/max/mean length	30 / 101 / 101.52
Duplicated reads (estimated)	816,875 / 5.28%
Duplication rate	4.17%
Clipped reads	4,428,540 / 28.62%

2.2. ACGT Content

Number/percentage of A's	402,941,379 / 28.47%
Number/percentage of C's	282,995,702 / 19.99%
Number/percentage of T's	408,523,919 / 28.86%
Number/percentage of G's	320,658,573 / 22.65%
Number/percentage of N's	295,175 / 0.02%

GC Percentage	42.65%

2.3. Coverage

Mean	0.4576
Standard Deviation	1.9998

2.4. Mapping Quality

Mean Mapping Quality	53.33

2.5. Insert size

Mean	125,076.59
Standard Deviation	3,443,028.14
P25/Median/P75	152 / 196 / 261

2.6. Mismatches and indels

General error rate	0.98%
Mismatches	13,463,083
Insertions	234,335
Mapped reads with at least one insertion	1.52%
Deletions	774,054
Mapped reads with at least one deletion	4.98%
Homopolymer indels	52.69%

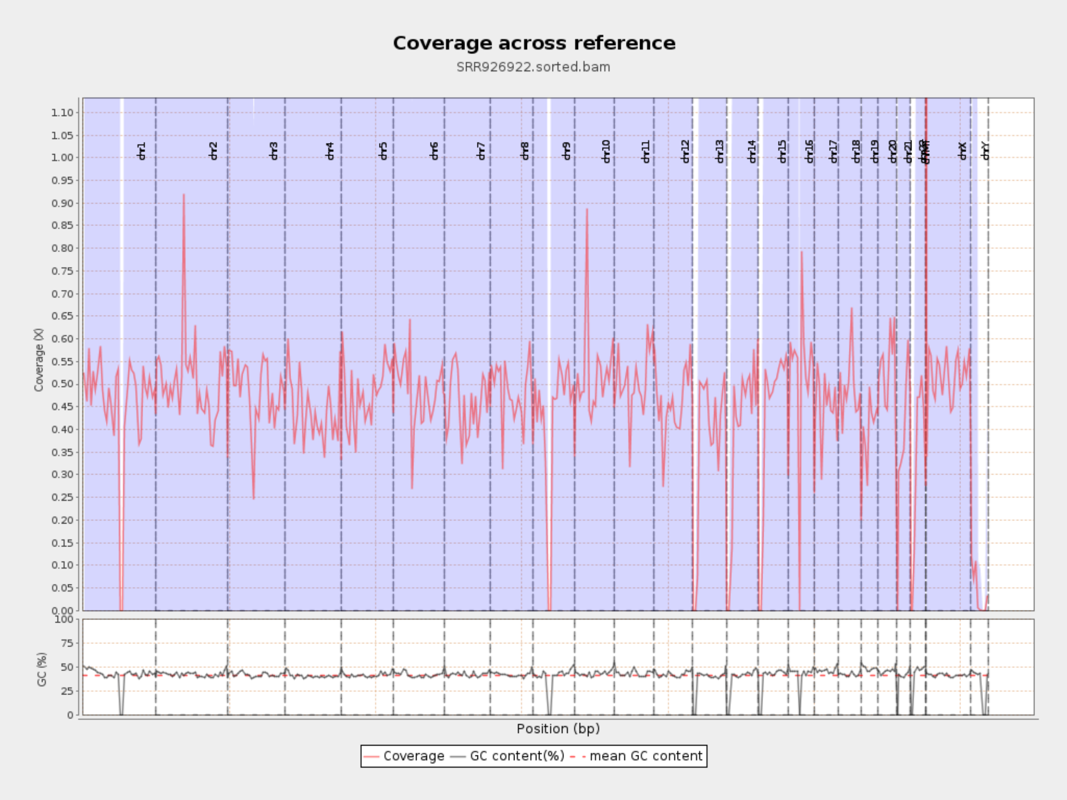
2.7. Chromosome stats

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

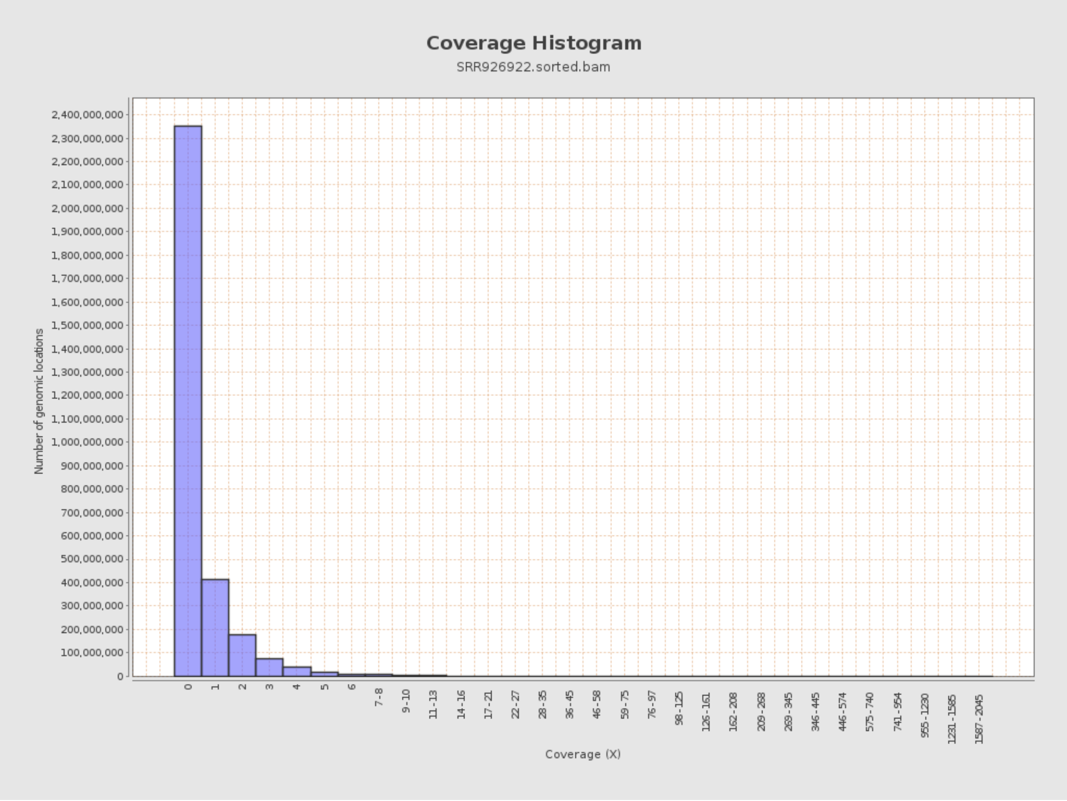
		bases	coverage	deviation
chr1	249250621	113643994	0.4559	2.2015
chr2	243199373	123488045	0.5078	3.1229
chr3	198022430	95375131	0.4816	1.0958
chr4	191154276	84875916	0.444	1.767
chr5	180915260	87123330	0.4816	1.0776
chr6	171115067	83412634	0.4875	2.3552
chr7	159138663	72401845	0.455	1.4876
chr8	146364022	70820057	0.4839	1.2459
chr9	141213431	59632872	0.4223	2.1795
chr10	135534747	70374791	0.5192	4.4181
chr11	135006516	68181274	0.505	1.5695
chr12	133851895	61823807	0.4619	1.0797
chr13	115169878	42915244	0.3726	0.9451
chr14	107349540	42070322	0.3919	1.0026
chr15	102531392	43265351	0.422	1.054
chr16	90354753	46406795	0.5136	2.9898
chr17	81195210	37046038	0.4563	1.3518
chr18	78077248	38271925	0.4902	2.1382
chr19	59128983	23434623	0.3963	1.5836
chr20	63025520	34229748	0.5431	1.2742
chr21	48129895	18532216	0.385	1.3897
chr22	51304566	16374983	0.3192	0.9499
chrMT	16571	518688	31.3009	24.7103
chrX	155270560	79987252	0.5151	1.2411

chrY	59373566	2318474	0.039	1.3759

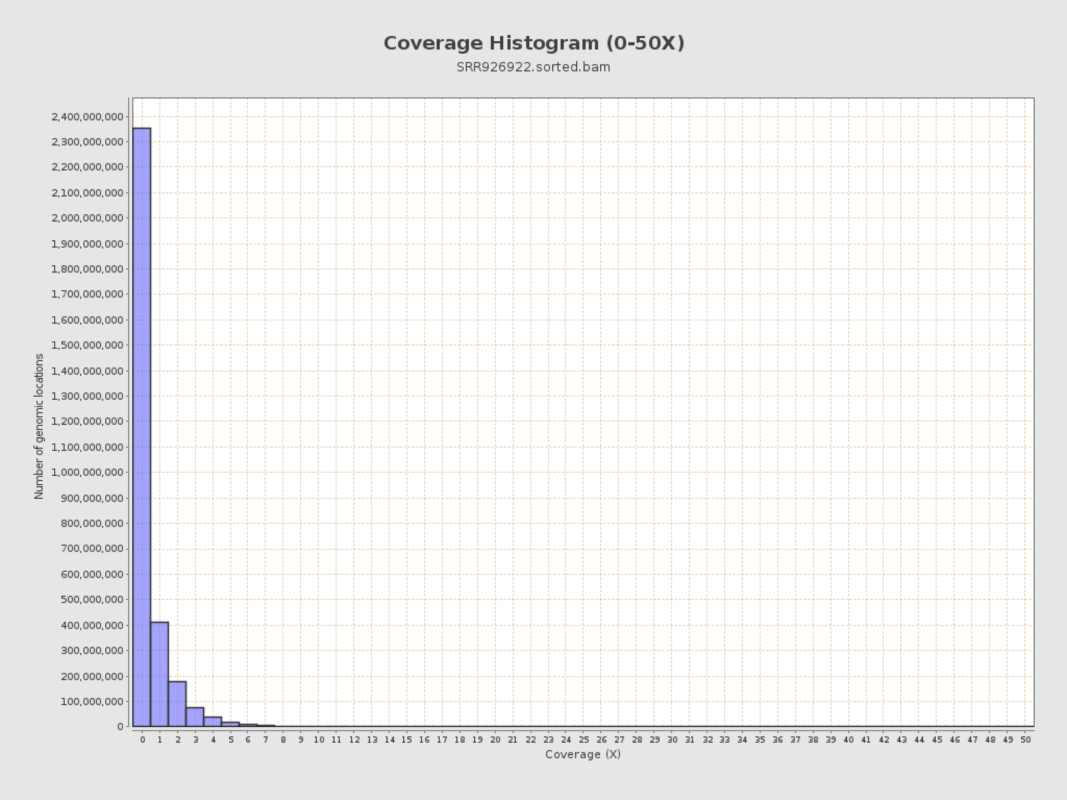
3. Results : Coverage across reference



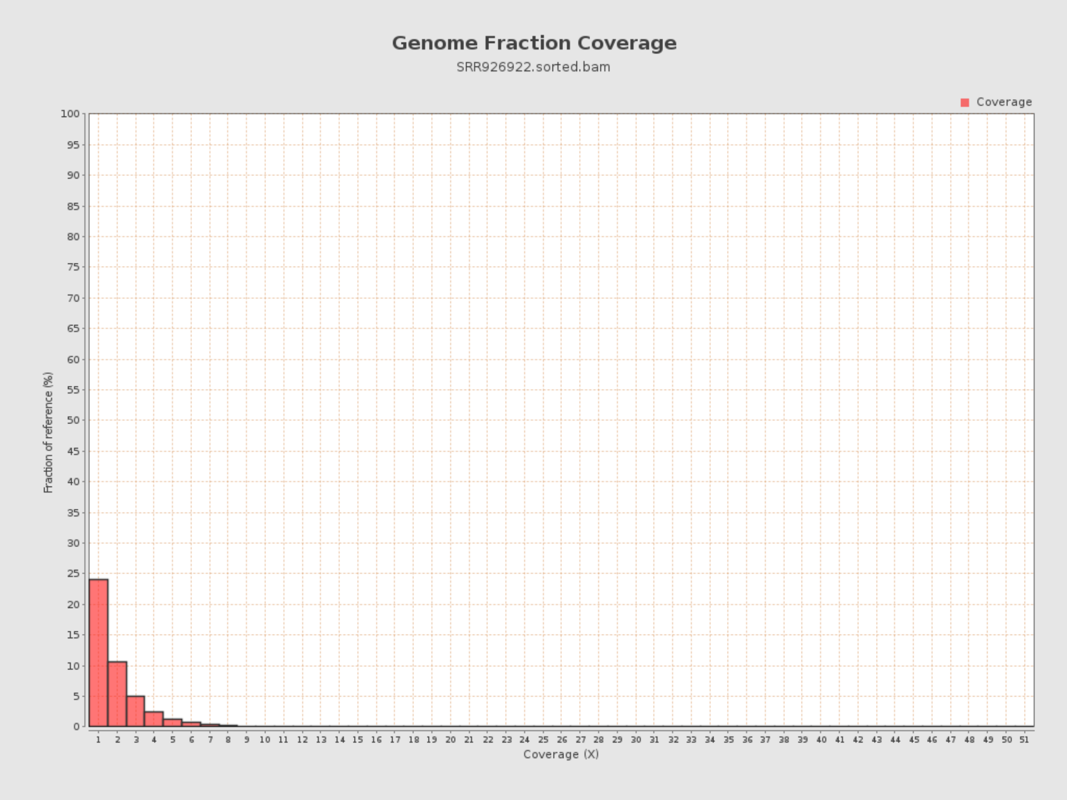
4. Results : Coverage Histogram



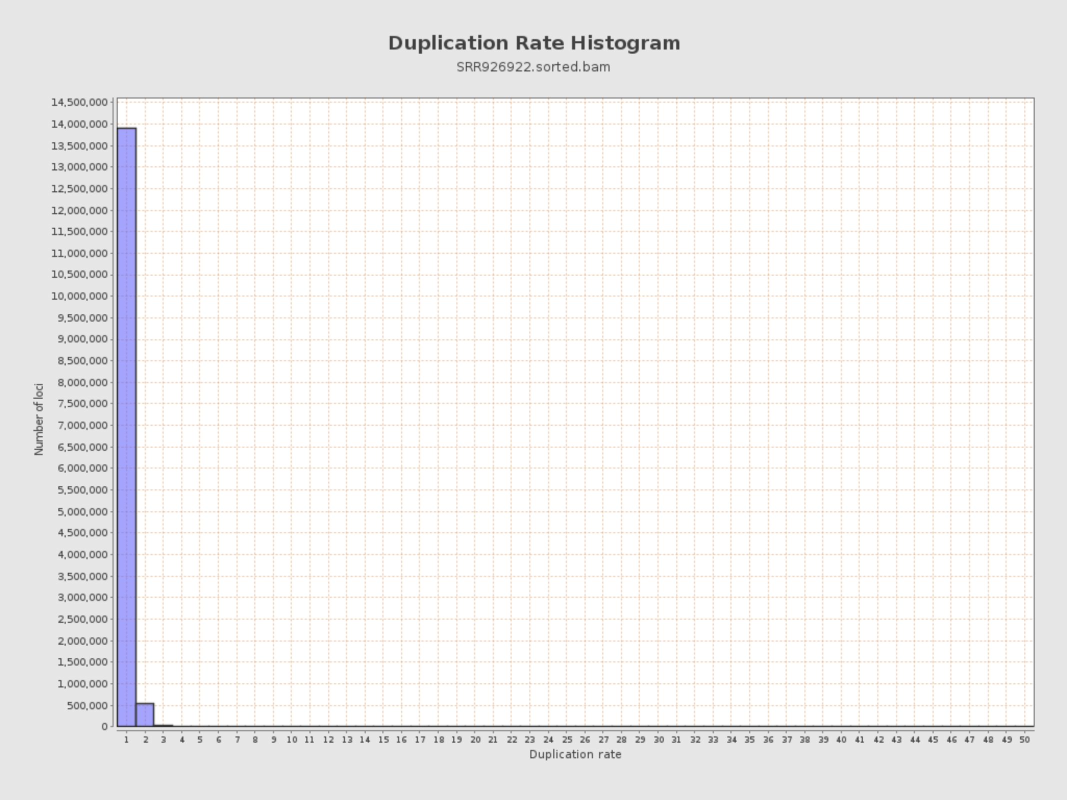
5. Results : Coverage Histogram (0-50X)



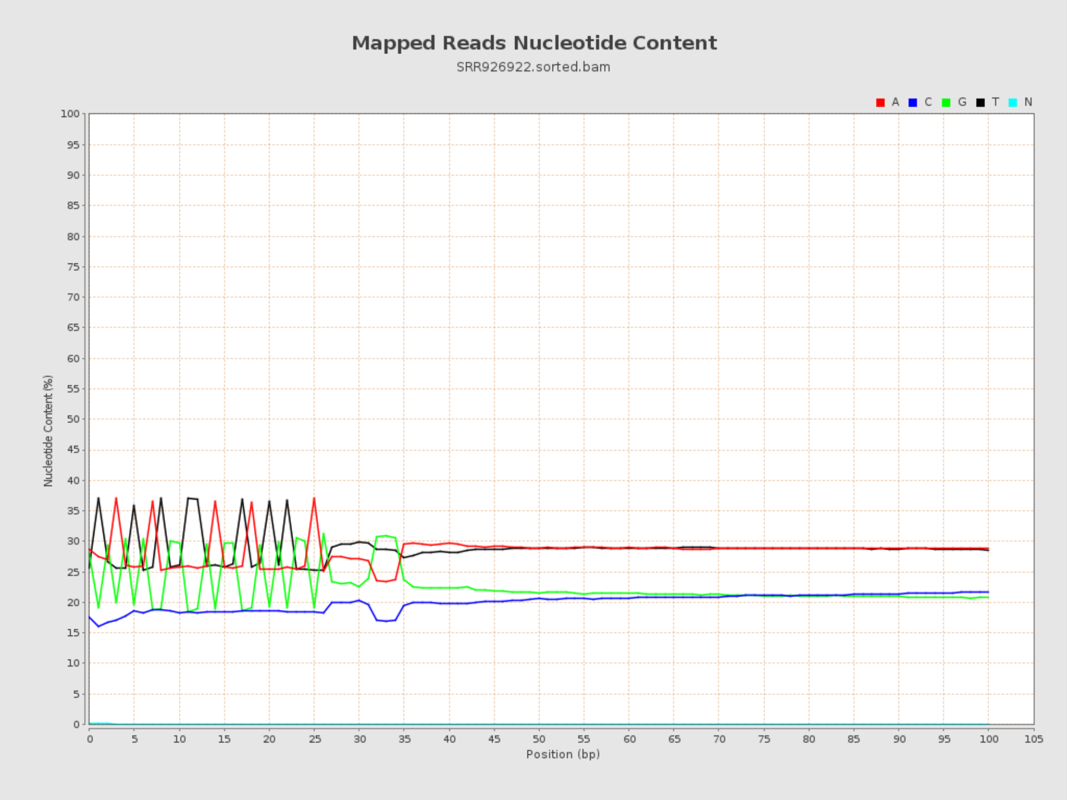
6. Results : Genome Fraction Coverage



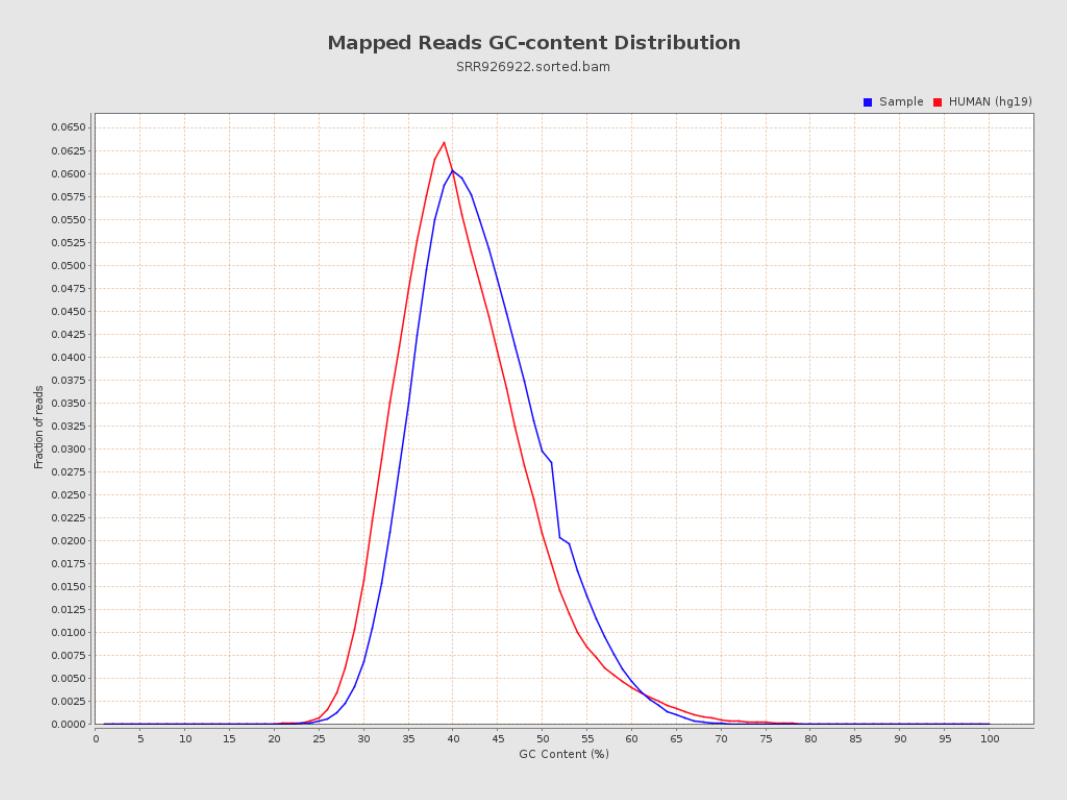
7. Results : Duplication Rate Histogram



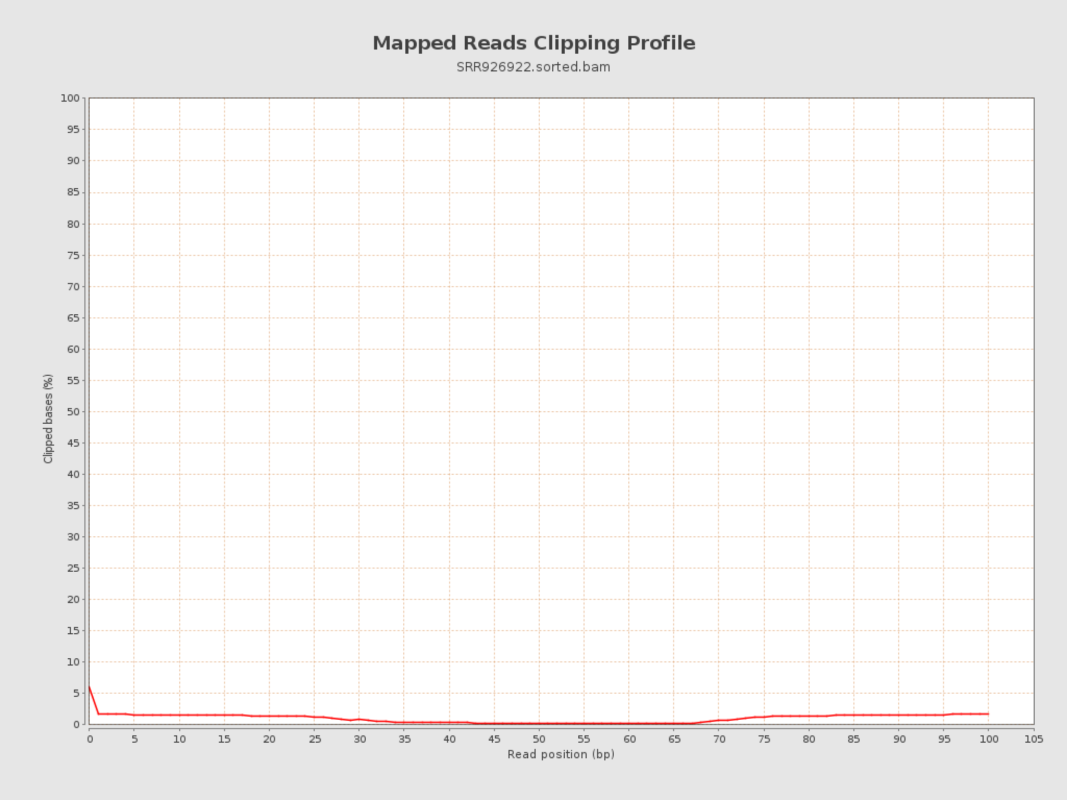
8. Results : Mapped Reads Nucleotide Content



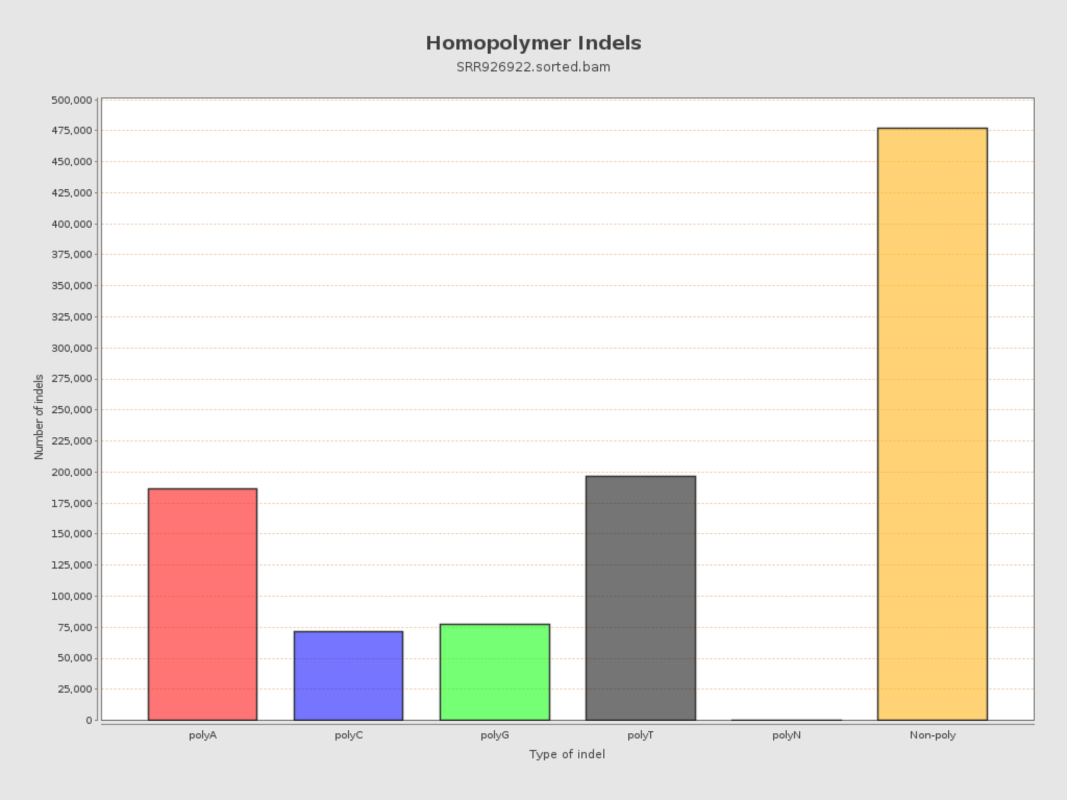
9. Results : Mapped Reads GC-content Distribution



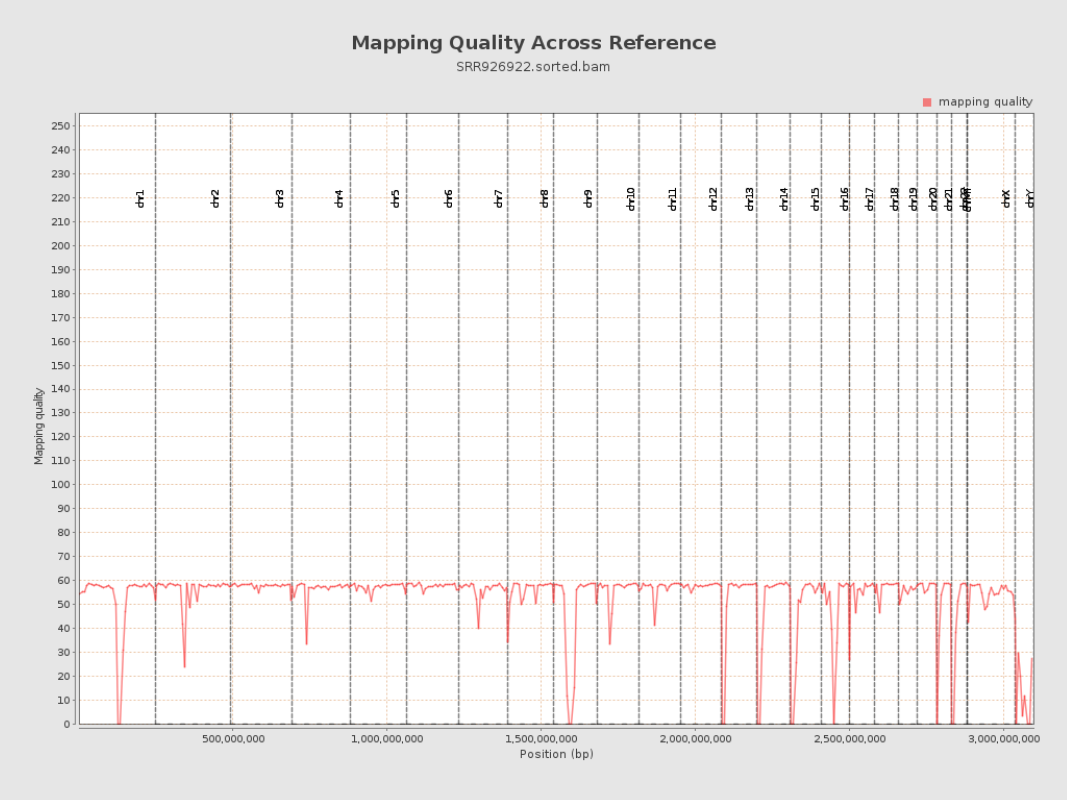
10. Results : Mapped Reads Clipping Profile



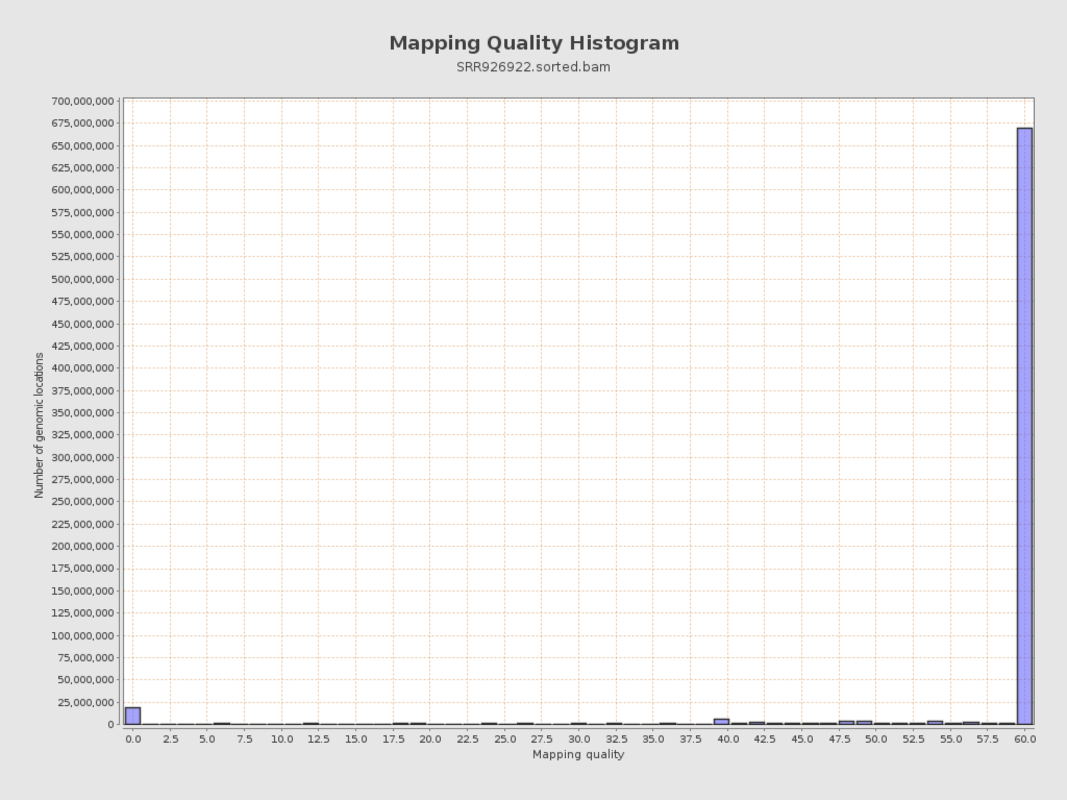
11. Results : Homopolymer Indels



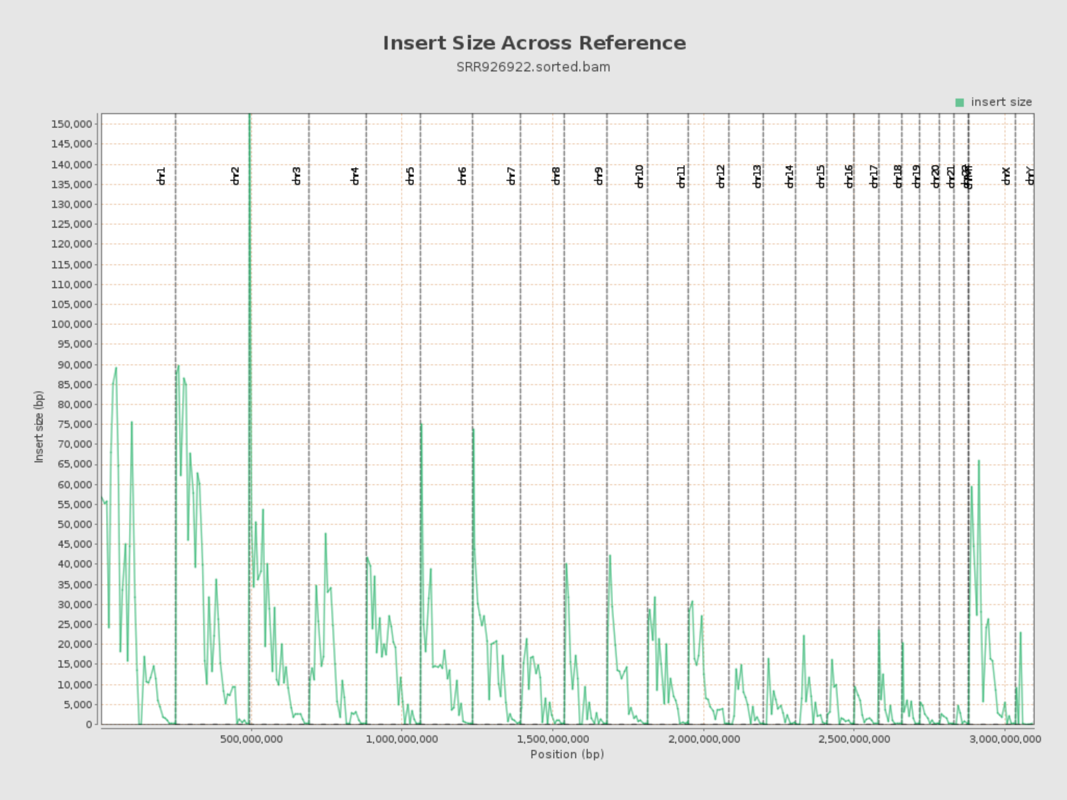
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram