Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/22 23:59:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926942.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_SRR926942 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926942_1.fastq.gz SRR926942_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 22 23:59:09 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926942.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	11,891,978
Mapped reads	11,688,158 / 98.29%
Unmapped reads	203,820 / 1.71%
Mapped paired reads	11,688,158 / 98.29%
Mapped reads, first in pair	5,872,176 / 49.38%
Mapped reads, second in pair	5,815,982 / 48.91%
Mapped reads, both in pair	11,570,500 / 97.3%
Mapped reads, singletons	117,658 / 0.99%
Secondary alignments	0
Supplementary alignments	75,390 / 0.63%
Read min/max/mean length	30 / 101 / 101.26
Duplicated reads (estimated)	536,548 / 4.51%
Duplication rate	3.79%
Clipped reads	3,077,902 / 25.88%

2.2. ACGT Content

Number/percentage of A's	312,063,873 / 28.41%
Number/percentage of C's	221,061,997 / 20.12%
Number/percentage of T's	315,704,872 / 28.74%
Number/percentage of G's	249,610,500 / 22.72%
Number/percentage of N's	59,290 / 0.01%

GC Percentage	42.85%

2.3. Coverage

Mean	0.3551
Standard Deviation	1.4057

2.4. Mapping Quality

Mean Mapping Quality	53.71

2.5. Insert size

Mean	67,760.43
Standard Deviation	2,588,033.23
P25/Median/P75	149 / 192 / 258

2.6. Mismatches and indels

General error rate	0.91%
Mismatches	9,701,856
Insertions	170,880
Mapped reads with at least one insertion	1.44%
Deletions	570,783
Mapped reads with at least one deletion	4.76%
Homopolymer indels	53.49%

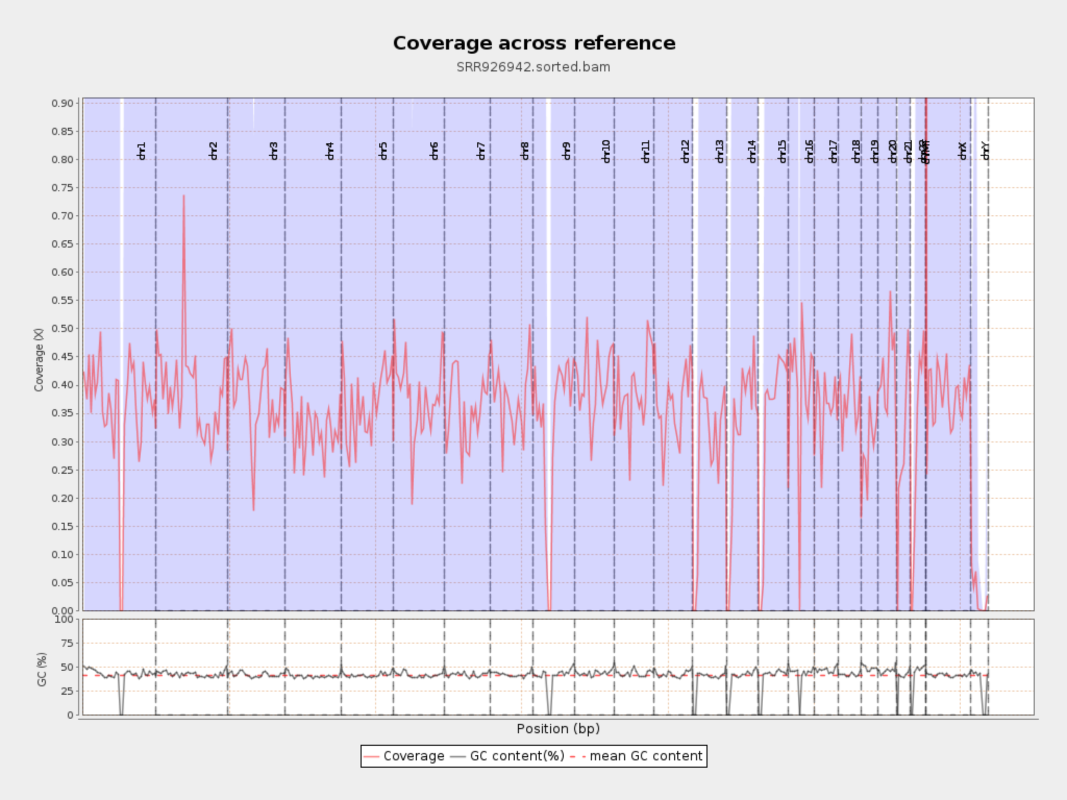
2.7. Chromosome stats

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

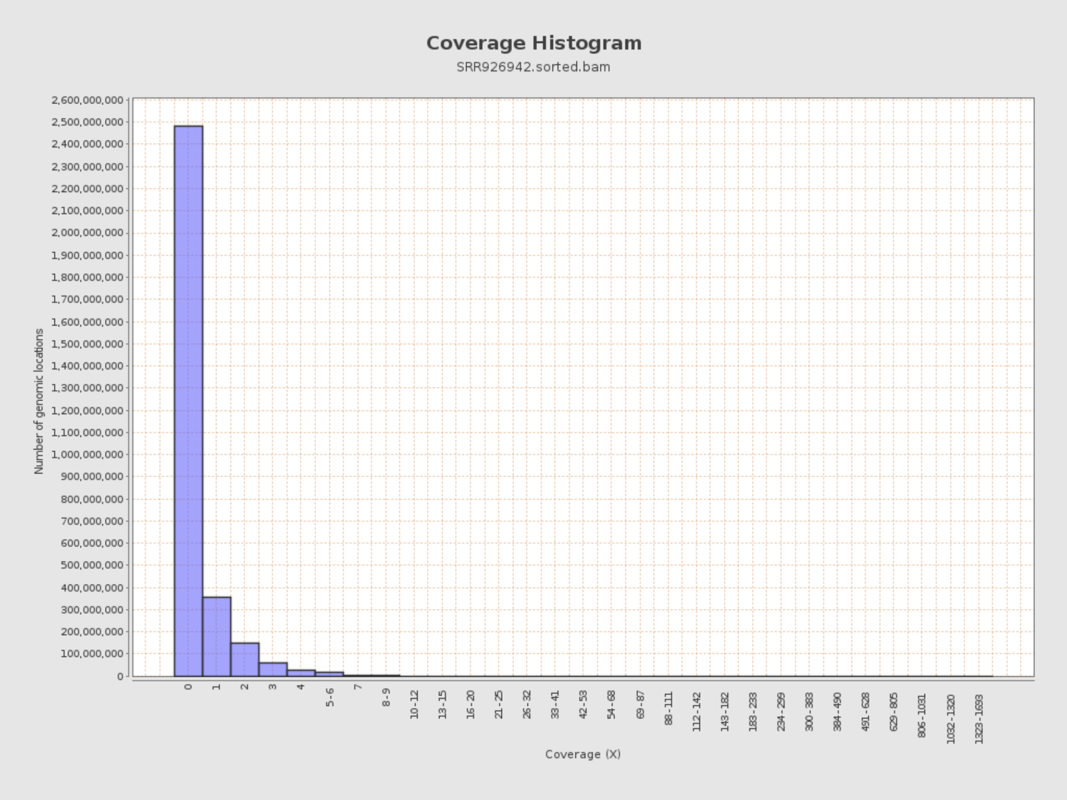
		bases	coverage	deviation
chr1	249250621	89692797	0.3598	1.6438
chr2	243199373	95257849	0.3917	2.765
chr3	198022430	74821023	0.3778	0.9324
chr4	191154276	63384284	0.3316	0.9323
chr5	180915260	66995345	0.3703	0.916
chr6	171115067	64766936	0.3785	1.0636
chr7	159138663	57148917	0.3591	1.0487
chr8	146364022	55017074	0.3759	1.0289
chr9	141213431	46831626	0.3316	1.5787
chr10	135534747	54450715	0.4017	2.0696
chr11	135006516	52380060	0.388	1.2876
chr12	133851895	49525961	0.37	0.9377
chr13	115169878	32844506	0.2852	0.804
chr14	107349540	34070794	0.3174	0.8875
chr15	102531392	33369874	0.3255	0.8852
chr16	90354753	35139622	0.3889	1.8633
chr17	81195210	29347334	0.3614	1.048
chr18	78077248	29550731	0.3785	1.6694
chr19	59128983	17402986	0.2943	1.1573
chr20	63025520	27235363	0.4321	1.0633
chr21	48129895	14374887	0.2987	1.1187
chr22	51304566	15134727	0.295	0.8798
chrMT	16571	95610	5.7697	5.1341
chrX	155270560	58960520	0.3797	1.0066

chrY	59373566	1507172	0.0254	0.5588

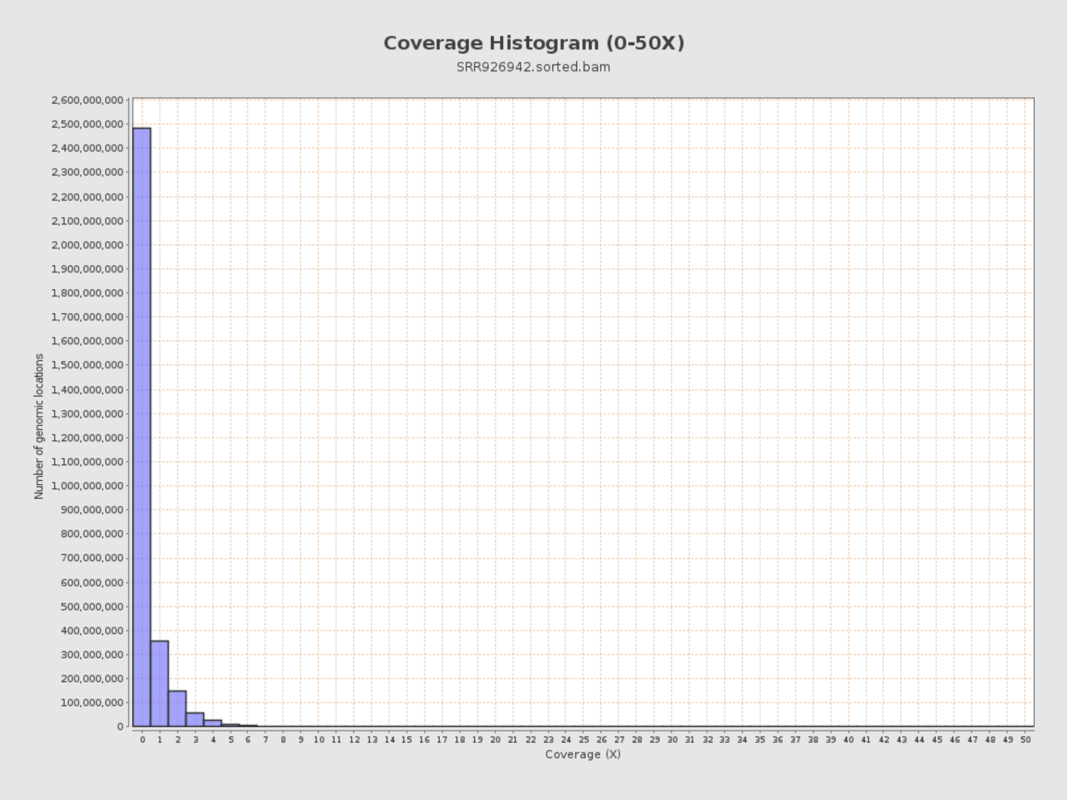
3. Results : Coverage across reference



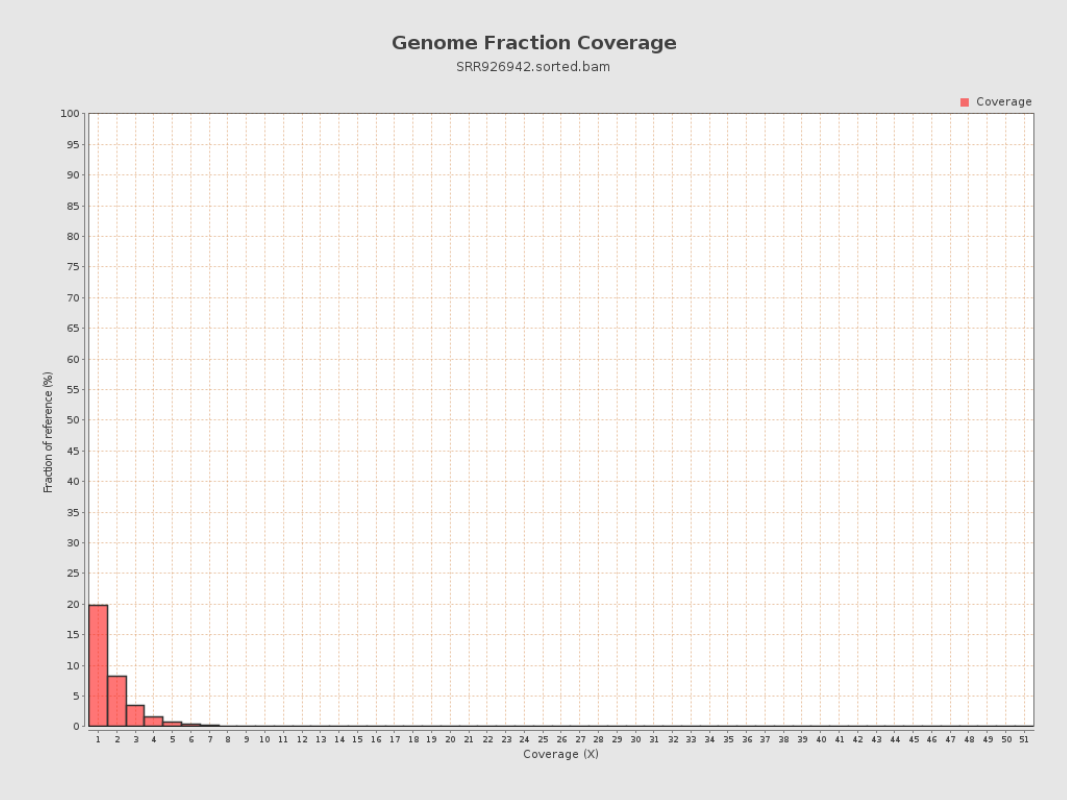
4. Results : Coverage Histogram



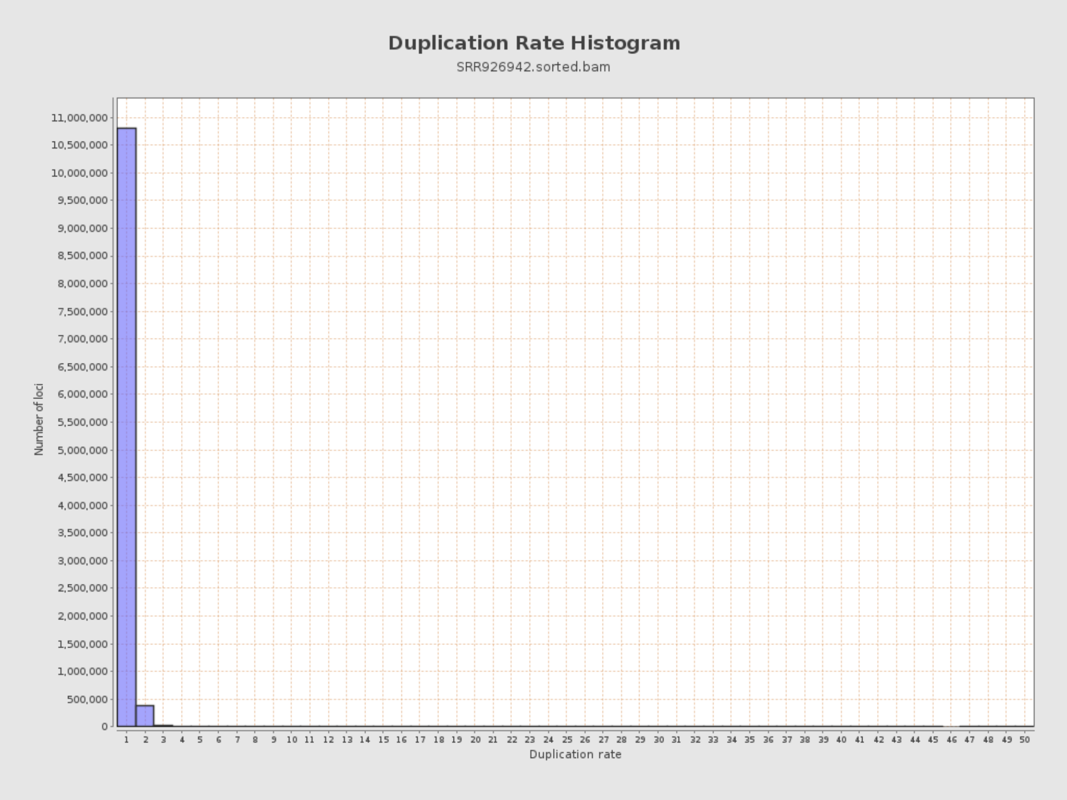
5. Results : Coverage Histogram (0-50X)



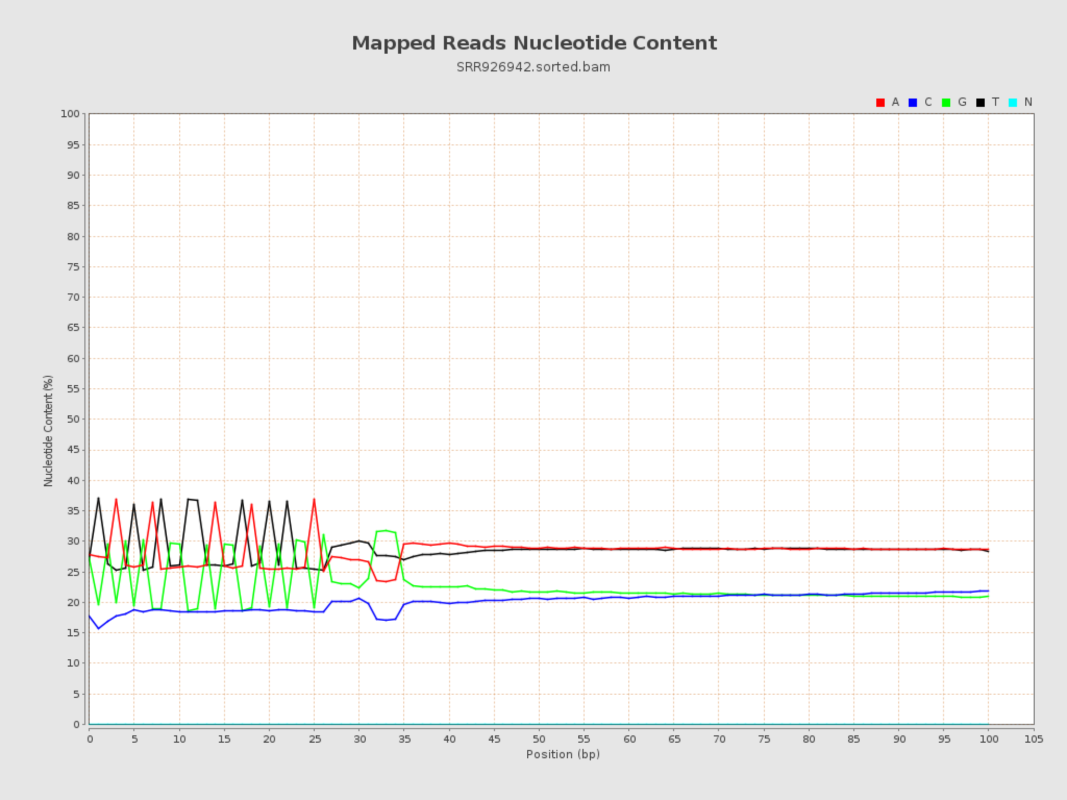
6. Results : Genome Fraction Coverage



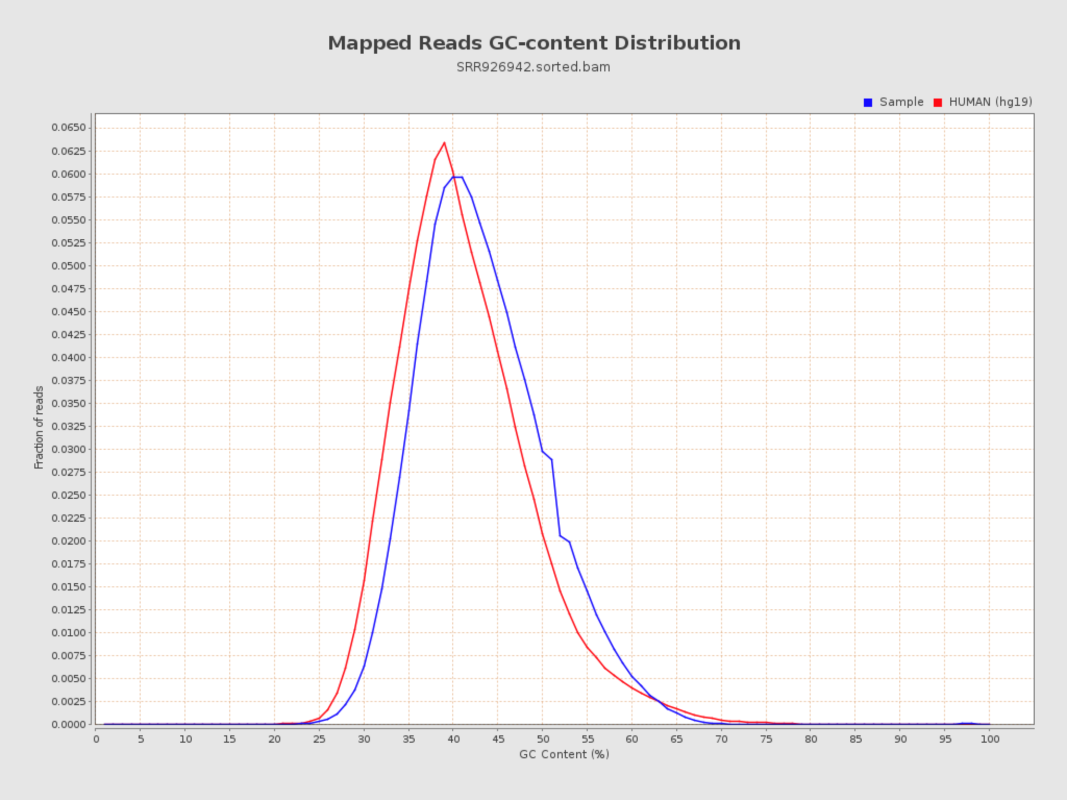
7. Results : Duplication Rate Histogram



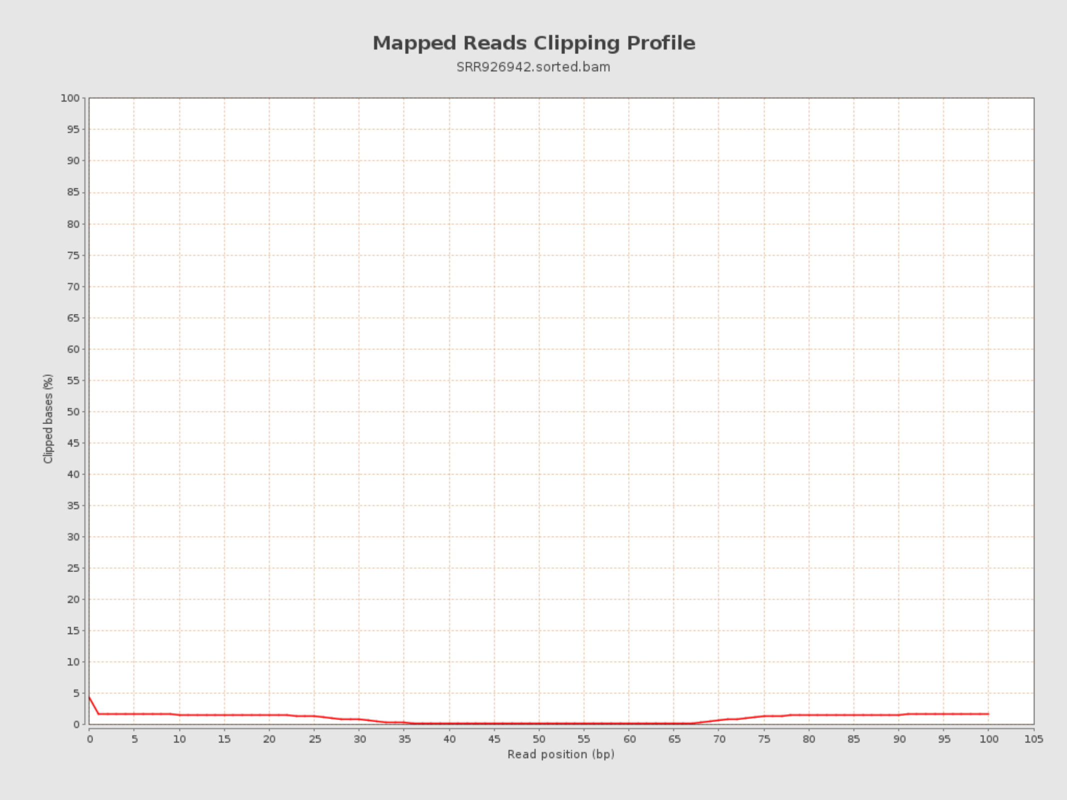
8. Results : Mapped Reads Nucleotide Content



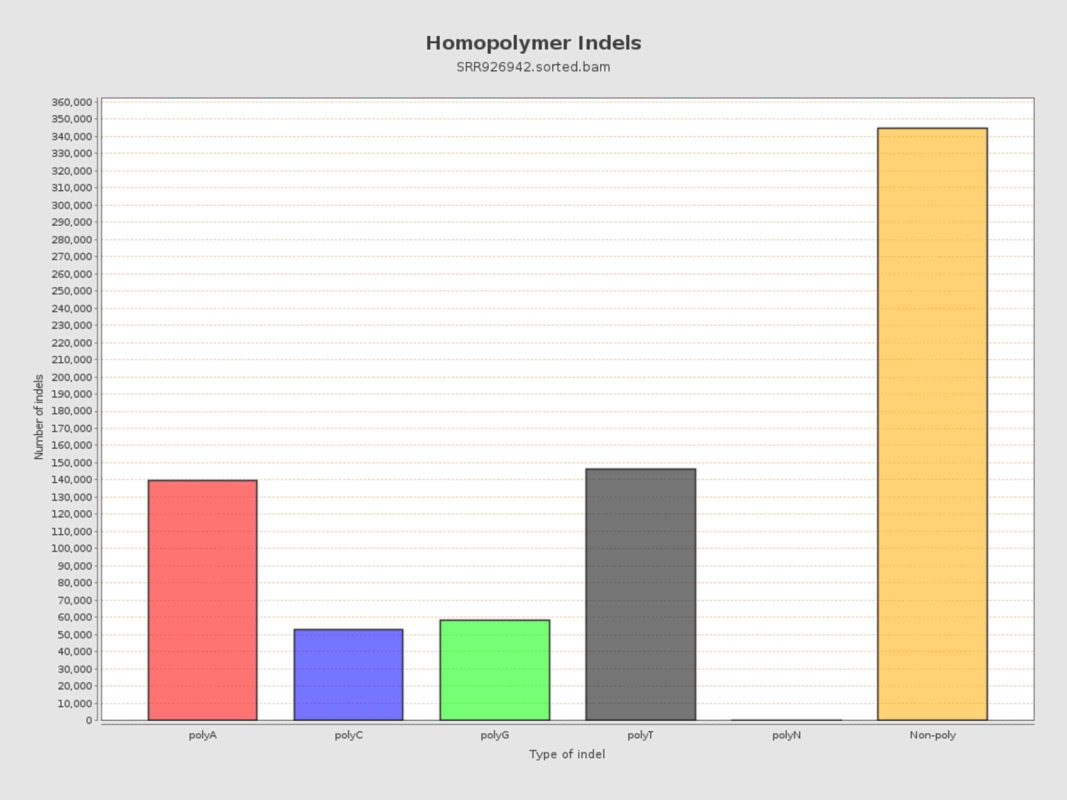
9. Results : Mapped Reads GC-content Distribution



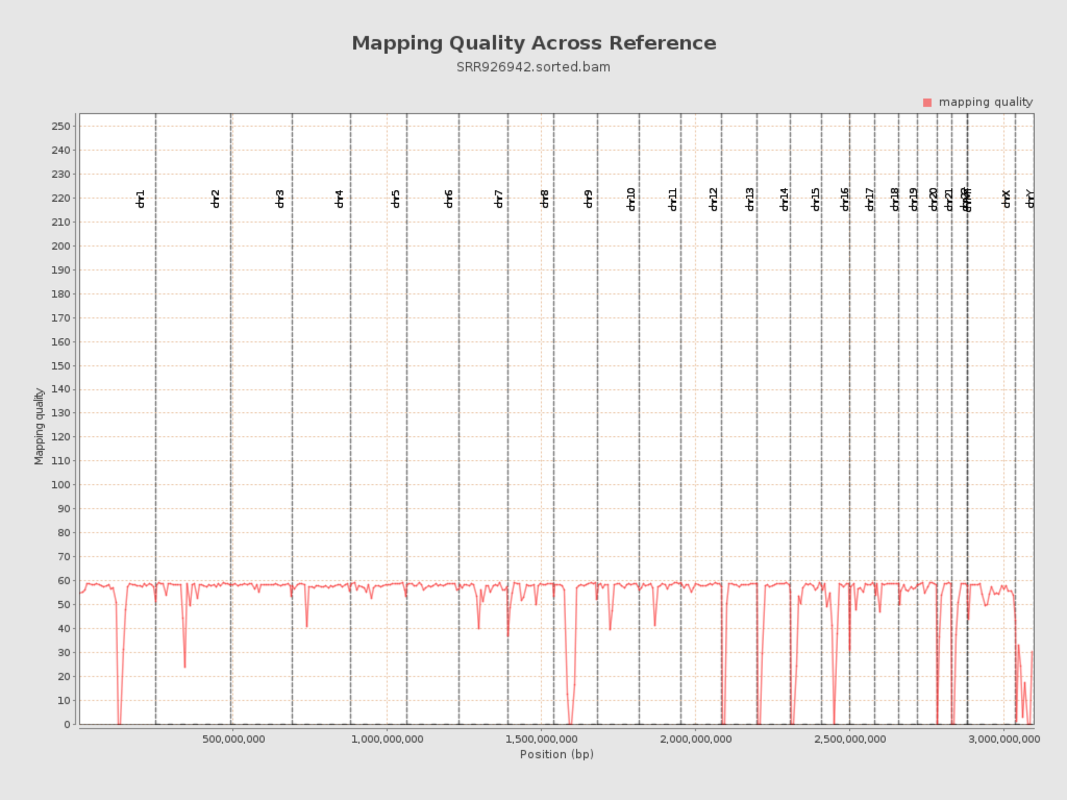
10. Results : Mapped Reads Clipping Profile



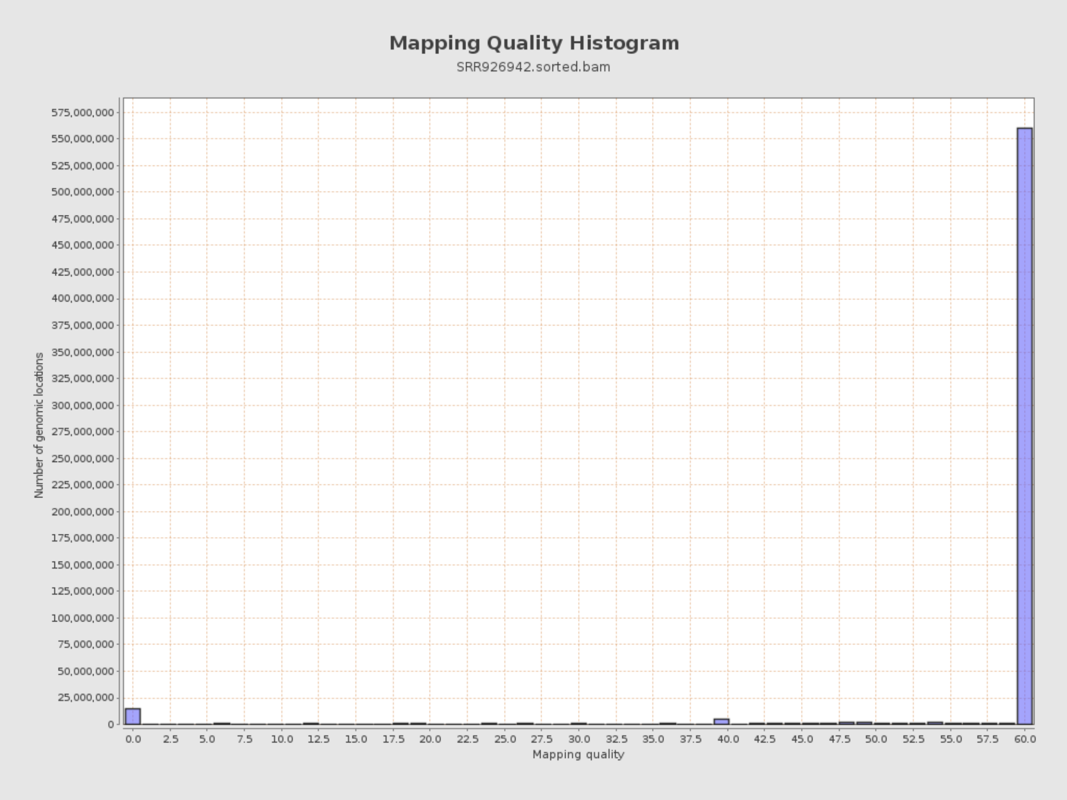
11. Results : Homopolymer Indels



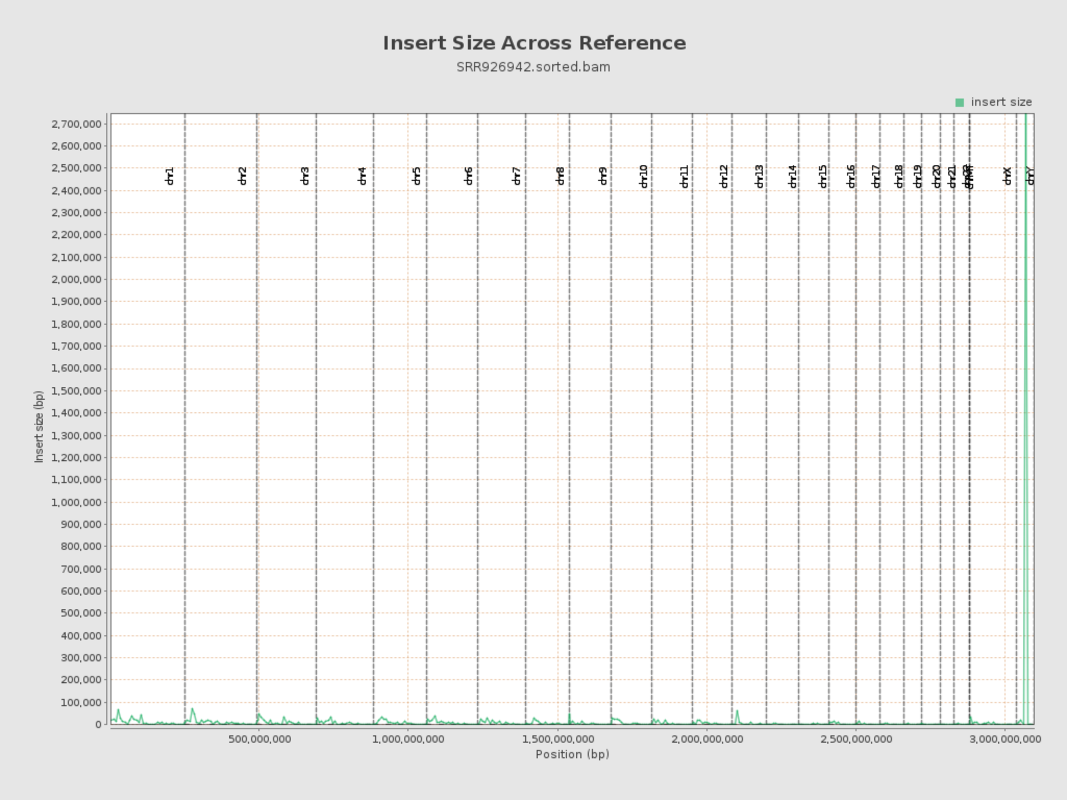
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram