Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/22 08:54:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926902.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_SRR926902 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926902_1.fastq.gz SRR926902_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 22 08:54:17 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926902.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	21,190,182
Mapped reads	19,082,400 / 90.05%
Unmapped reads	2,107,782 / 9.95%
Mapped paired reads	19,082,400 / 90.05%
Mapped reads, first in pair	9,585,590 / 45.24%
Mapped reads, second in pair	9,496,810 / 44.82%
Mapped reads, both in pair	18,589,284 / 87.73%
Mapped reads, singletons	493,116 / 2.33%
Secondary alignments	0
Supplementary alignments	586,181 / 2.77%
Read min/max/mean length	30 / 101 / 102.14
Duplicated reads (estimated)	1,358,529 / 6.41%
Duplication rate	5.75%
Clipped reads	8,635,966 / 40.75%

2.2. ACGT Content

Number/percentage of A's	489,731,194 / 28.46%
Number/percentage of C's	331,057,769 / 19.24%
Number/percentage of T's	497,390,073 / 28.91%
Number/percentage of G's	402,229,455 / 23.38%
Number/percentage of N's	140,555 / 0.01%

GC Percentage	42.62%

2.3. Coverage

Mean	0.5562
Standard Deviation	1.9644

2.4. Mapping Quality

Mean Mapping Quality	52.42

2.5. Insert size

Mean	419,596.05
Standard Deviation	6,372,620.32
P25/Median/P75	172 / 224 / 291

2.6. Mismatches and indels

General error rate	1.11%
Mismatches	18,664,437
Insertions	295,575
Mapped reads with at least one insertion	1.52%
Deletions	915,263
Mapped reads with at least one deletion	4.67%
Homopolymer indels	52.07%

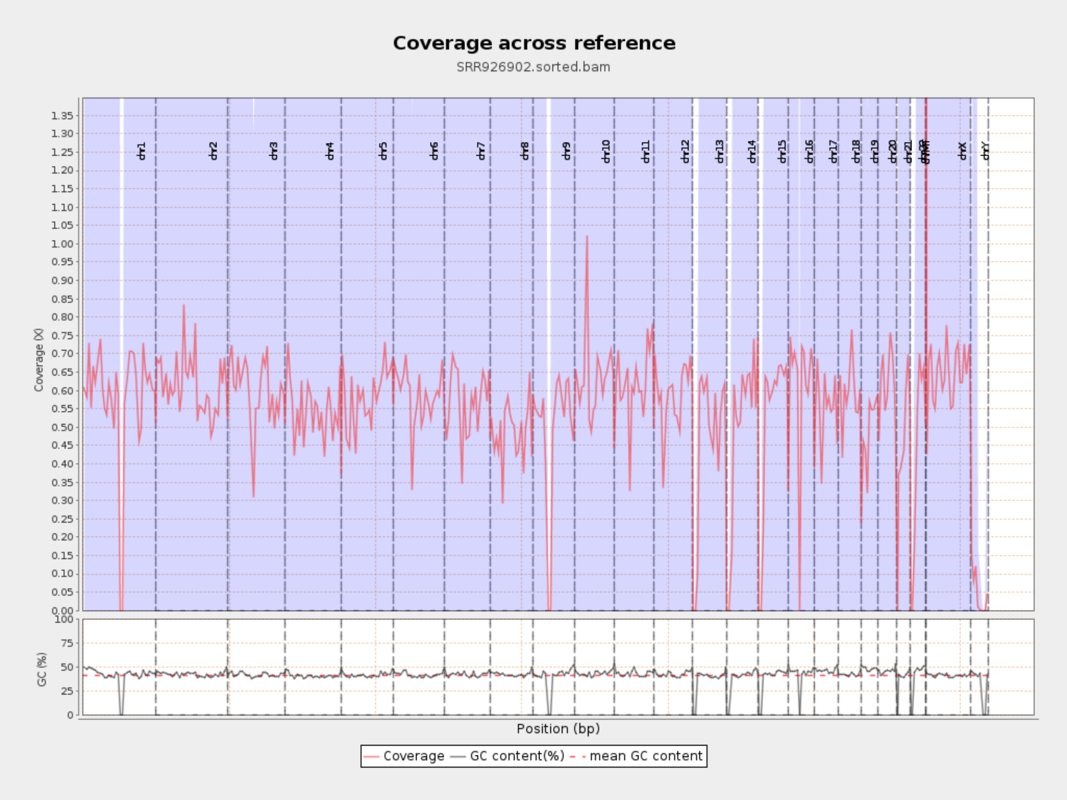
2.7. Chromosome stats

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

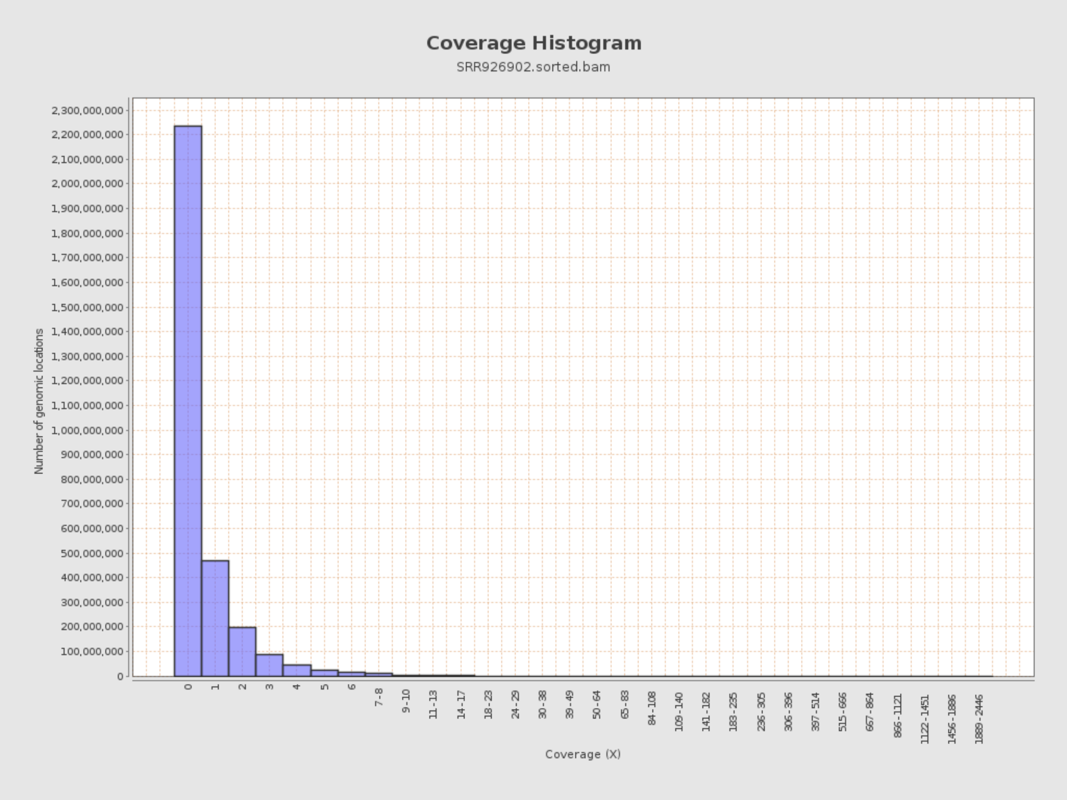
		bases	coverage	deviation
chr1	249250621	144691333	0.5805	1.7601
chr2	243199373	149838974	0.6161	2.5747
chr3	198022430	118083410	0.5963	1.2975
chr4	191154276	104923363	0.5489	1.3397
chr5	180915260	105976741	0.5858	1.2637
chr6	171115067	100368933	0.5866	1.4227
chr7	159138663	90370450	0.5679	1.4875
chr8	146364022	71095238	0.4857	1.1837
chr9	141213431	69244810	0.4904	1.8813
chr10	135534747	86189131	0.6359	5.6079
chr11	135006516	83251419	0.6166	1.568
chr12	133851895	79115594	0.5911	1.3887
chr13	115169878	52901860	0.4593	1.1236
chr14	107349540	52510336	0.4892	1.1843
chr15	102531392	52379427	0.5109	1.2809
chr16	90354753	54236437	0.6003	2.5821
chr17	81195210	45429085	0.5595	1.3553
chr18	78077248	46217684	0.5919	1.9151
chr19	59128983	28772464	0.4866	1.3715
chr20	63025520	39252413	0.6228	1.4003
chr21	48129895	22050858	0.4582	1.5416
chr22	51304566	21934613	0.4275	1.1871
chrMT	16571	112377	6.7815	4.9431
chrX	155270560	100122024	0.6448	1.3974

chrY	59373566	2818921	0.0475	1.2169

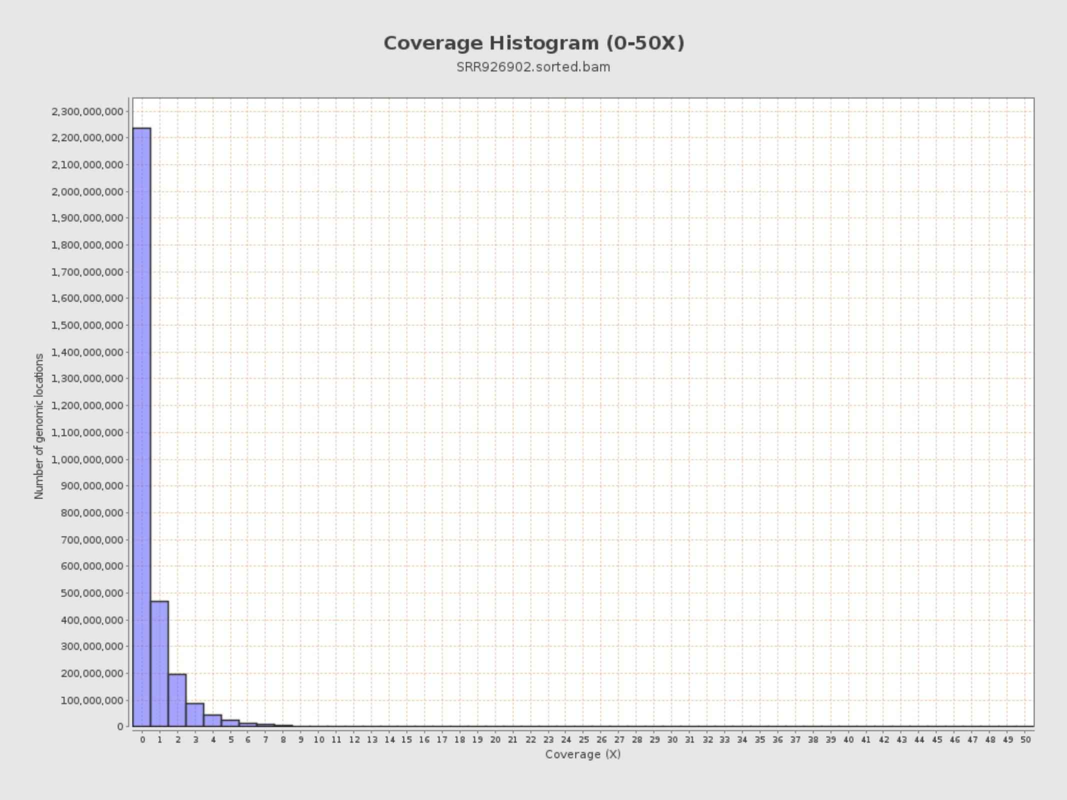
3. Results : Coverage across reference



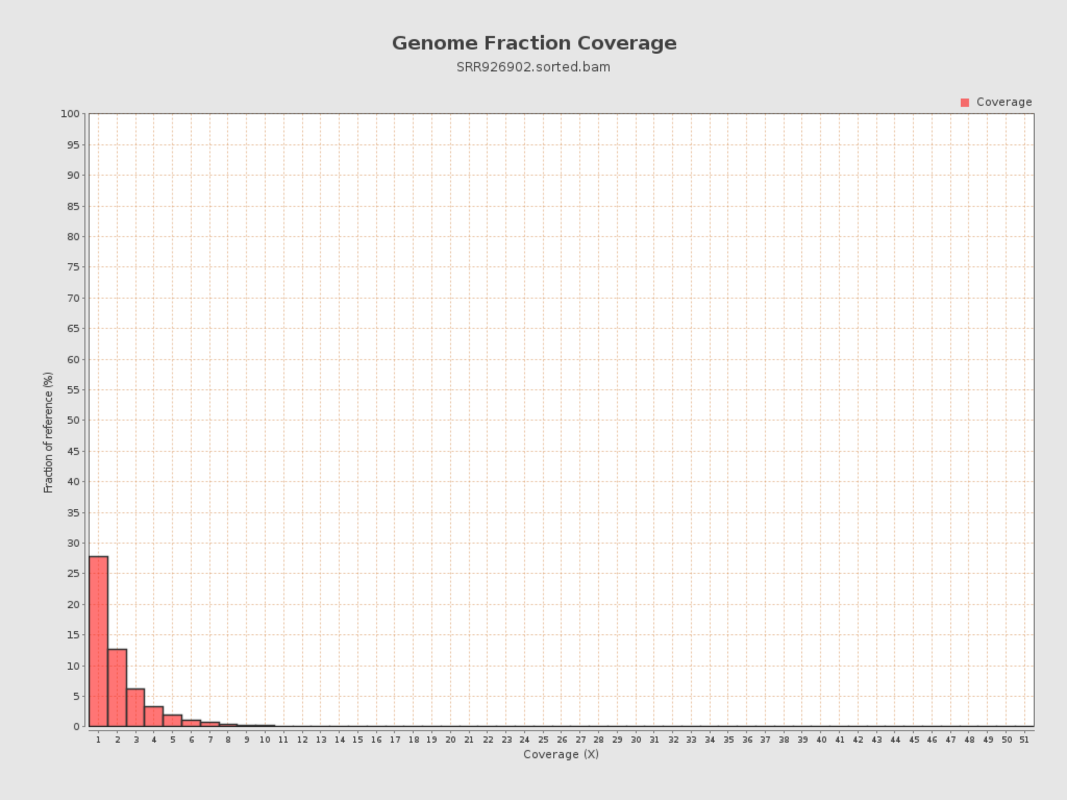
4. Results : Coverage Histogram



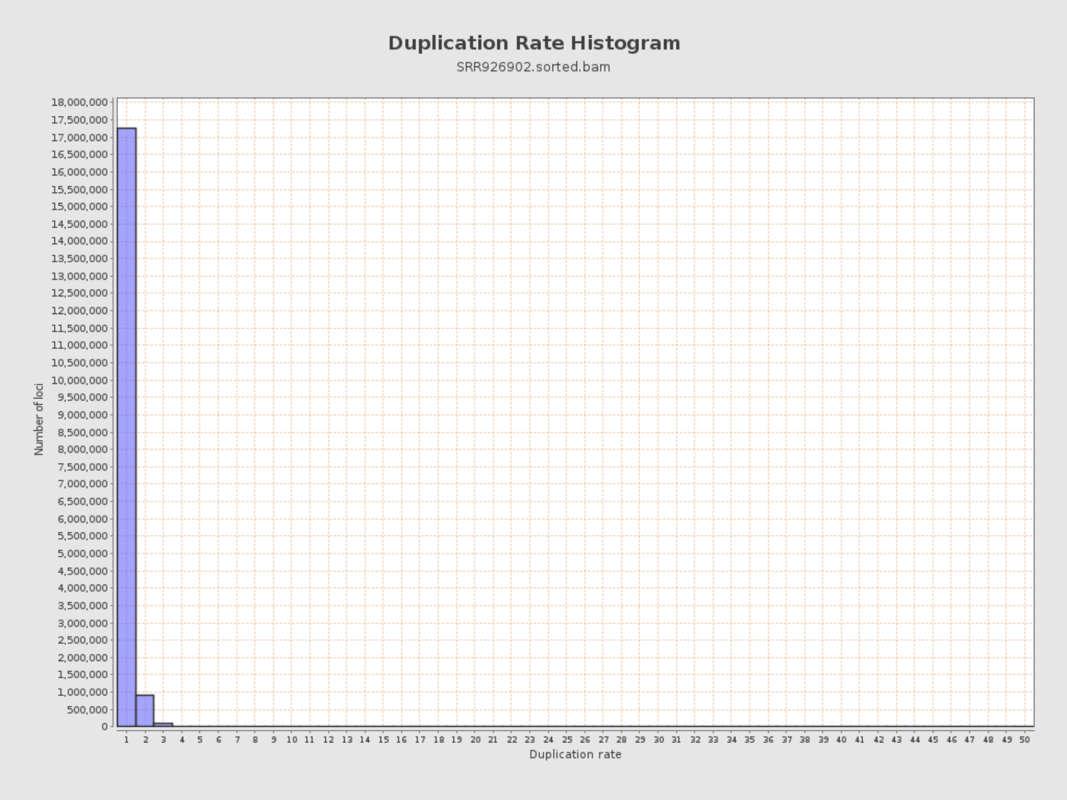
5. Results : Coverage Histogram (0-50X)



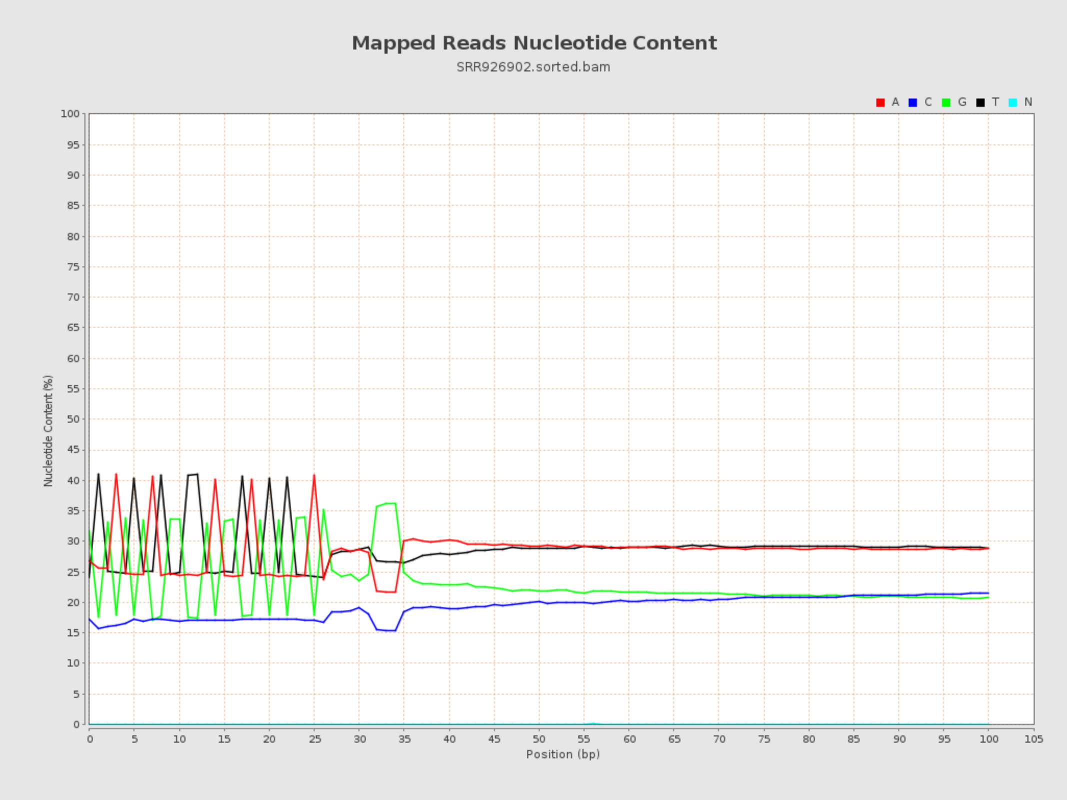
6. Results : Genome Fraction Coverage



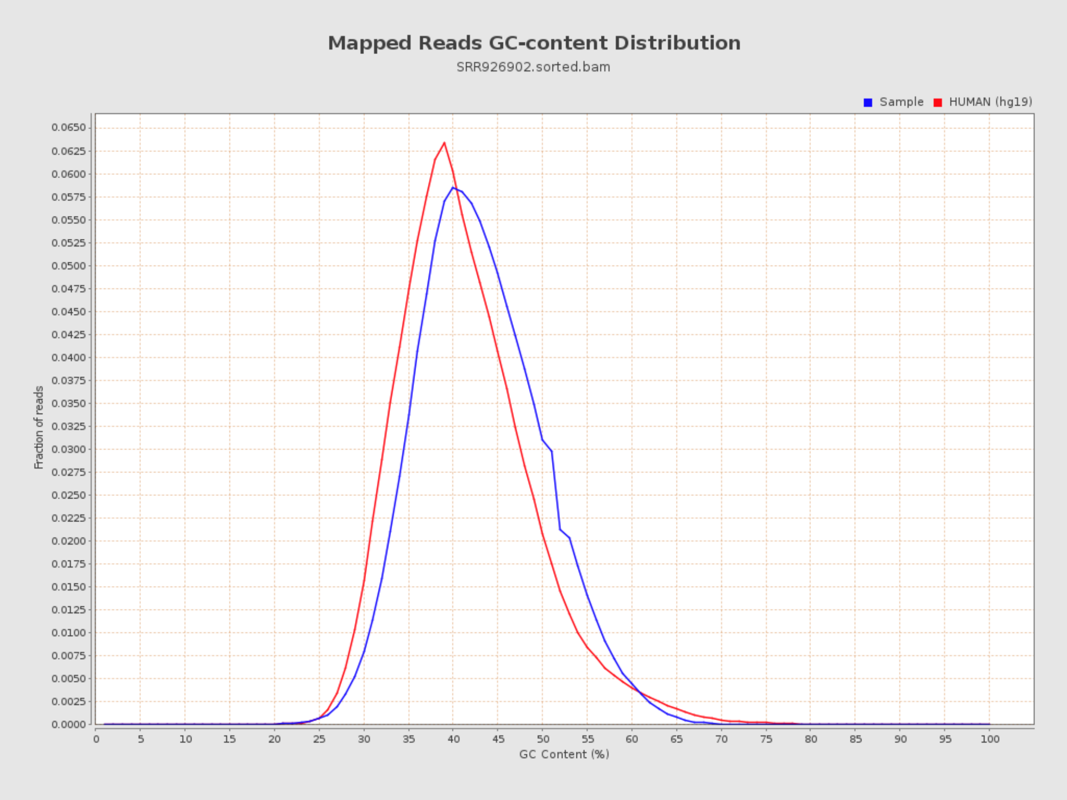
7. Results : Duplication Rate Histogram



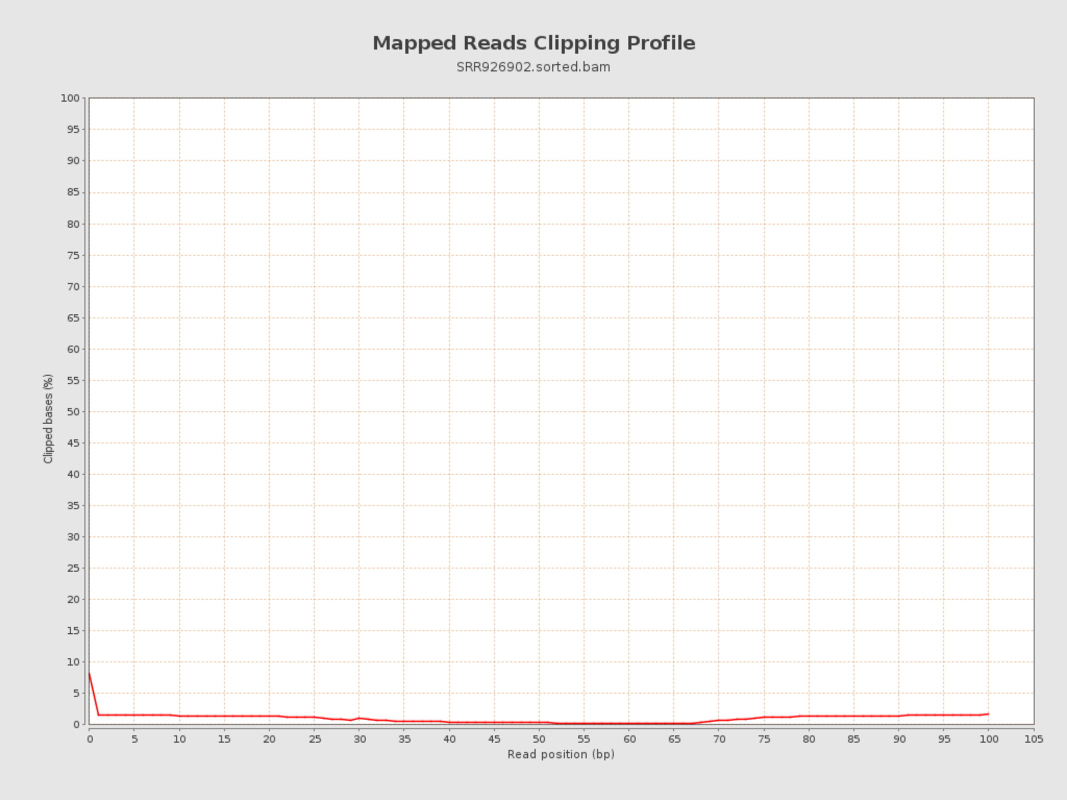
8. Results : Mapped Reads Nucleotide Content



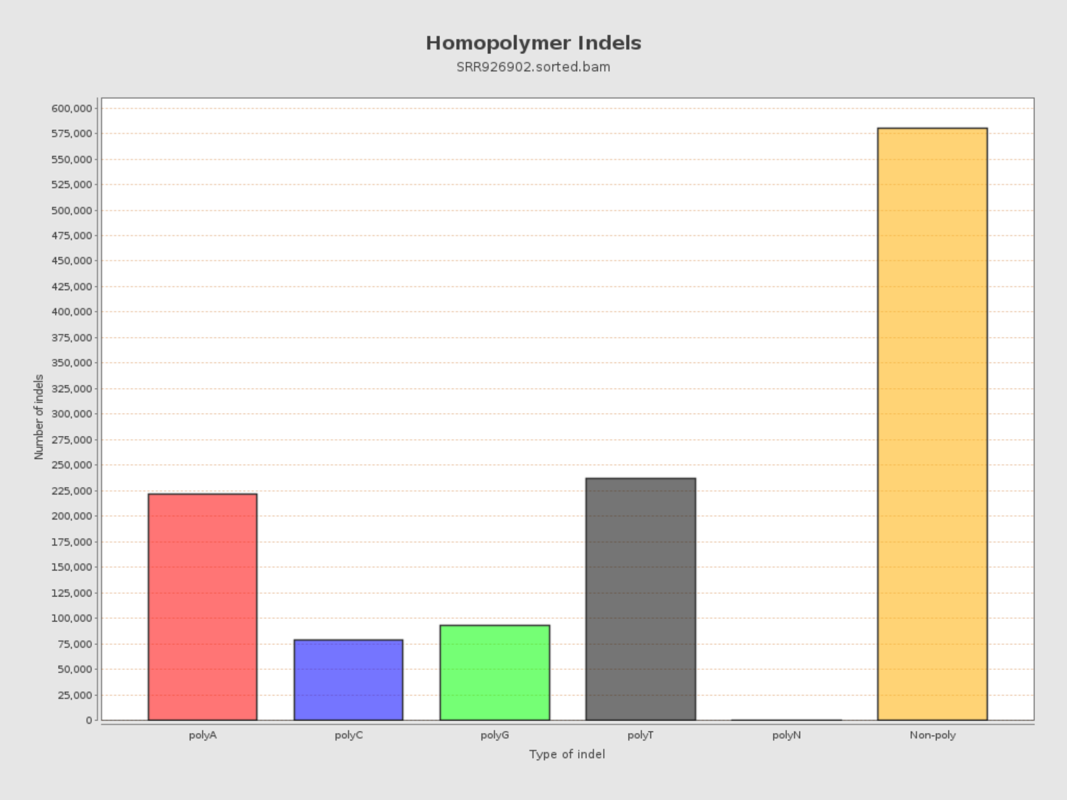
9. Results : Mapped Reads GC-content Distribution



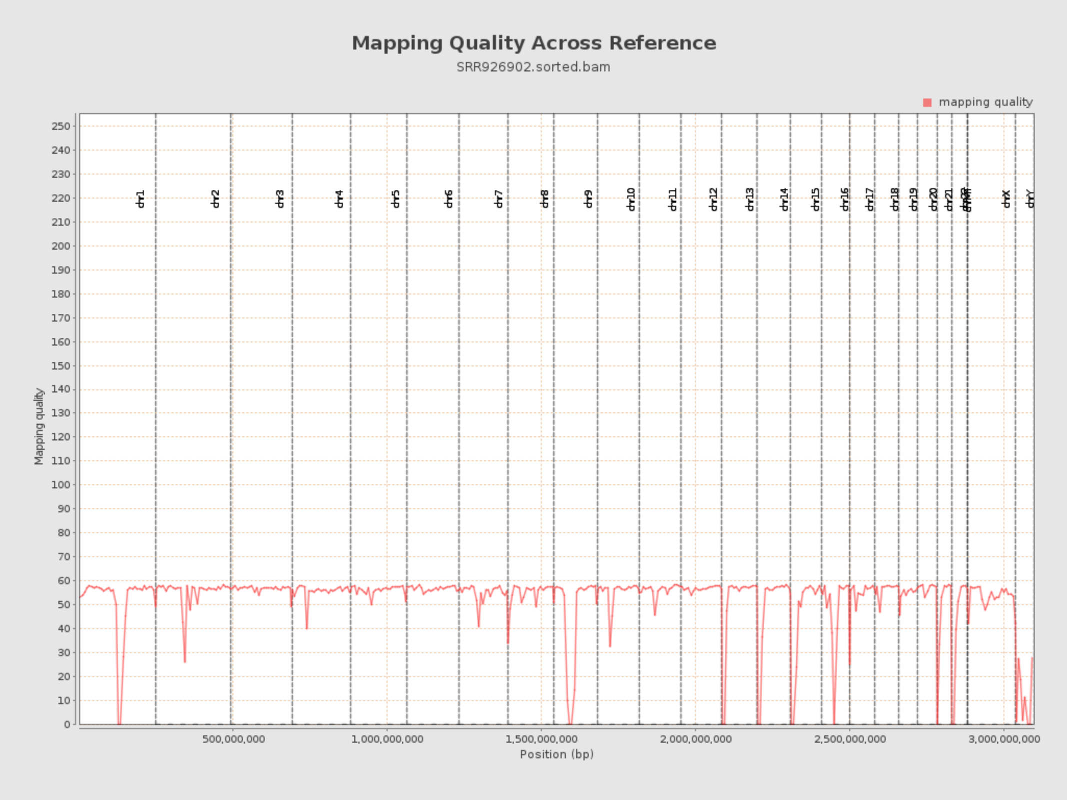
10. Results : Mapped Reads Clipping Profile



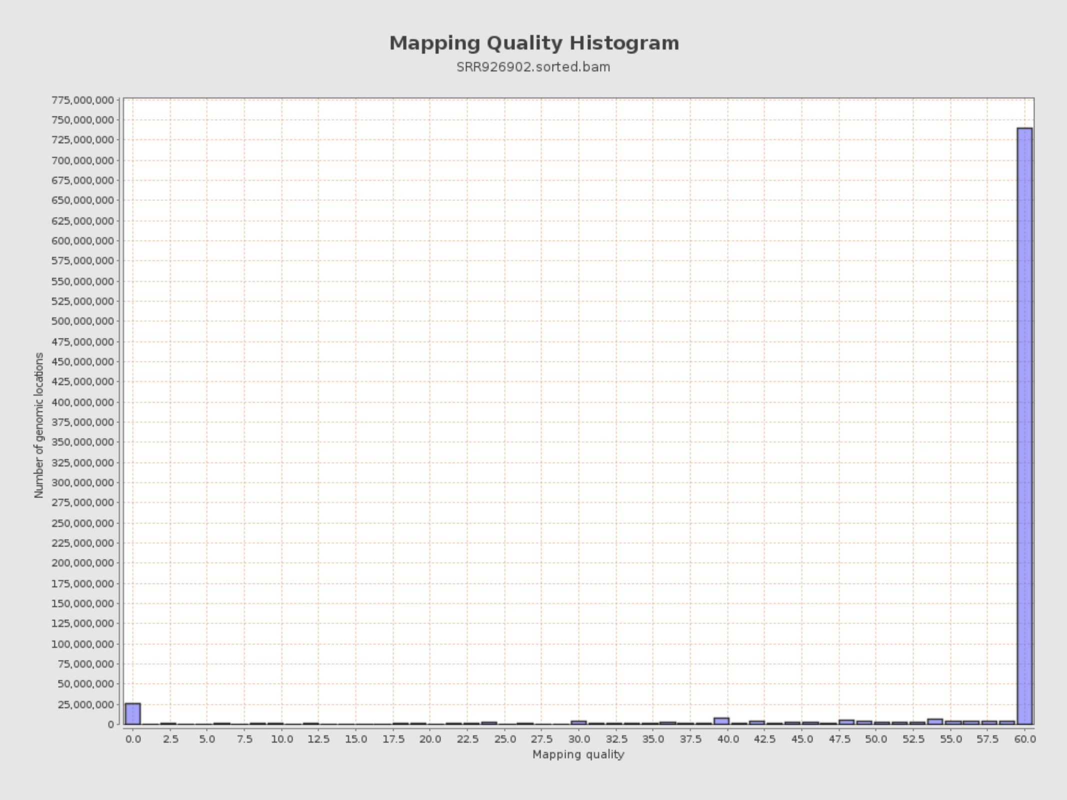
11. Results : Homopolymer Indels



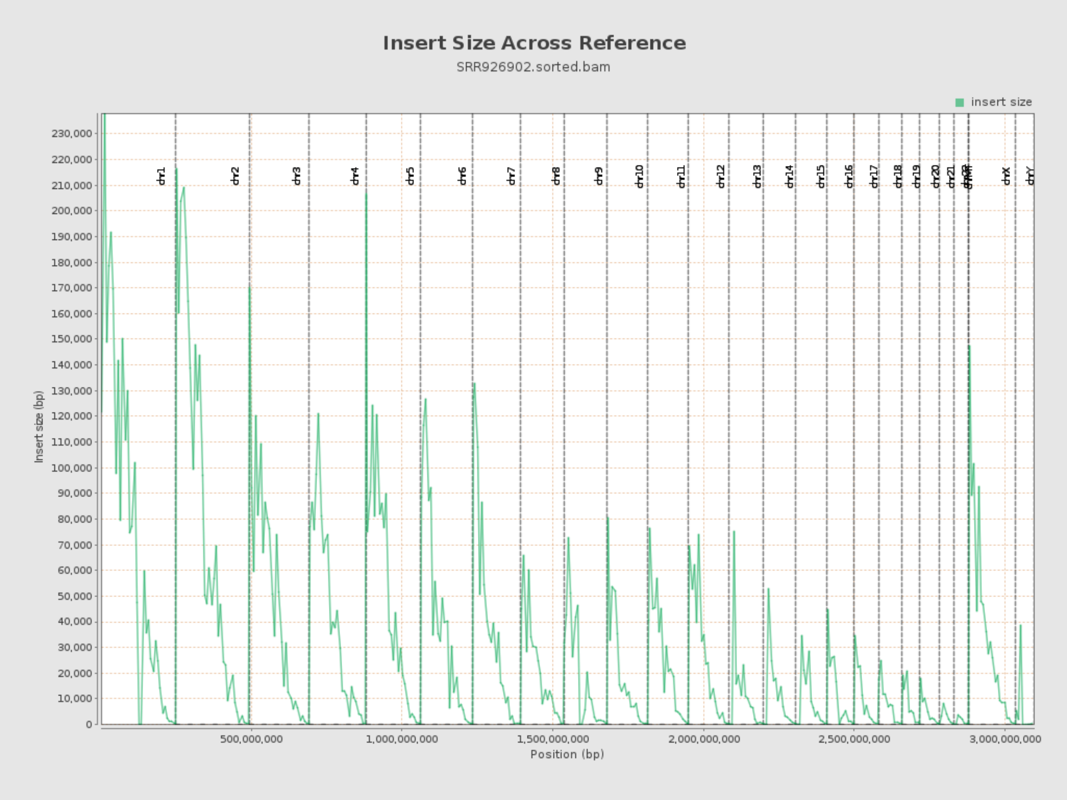
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram