Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/22 08:26:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926901.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_SRR926901 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926901_1.fastq.gz SRR926901_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 22 08:26:08 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926901.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	31,285,914
Mapped reads	30,390,101 / 97.14%
Unmapped reads	895,813 / 2.86%
Mapped paired reads	30,390,101 / 97.14%
Mapped reads, first in pair	15,232,488 / 48.69%
Mapped reads, second in pair	15,157,613 / 48.45%
Mapped reads, both in pair	29,989,934 / 95.86%
Mapped reads, singletons	400,167 / 1.28%
Secondary alignments	0
Supplementary alignments	1,002,670 / 3.2%
Read min/max/mean length	30 / 101 / 102.32
Duplicated reads (estimated)	2,710,569 / 8.66%
Duplication rate	7.25%
Clipped reads	11,740,170 / 37.53%

2.2. ACGT Content

Number/percentage of A's	801,553,007 / 28.5%
Number/percentage of C's	563,951,683 / 20.05%
Number/percentage of T's	807,233,076 / 28.7%
Number/percentage of G's	639,334,160 / 22.73%
Number/percentage of N's	182,251 / 0.01%

GC Percentage	42.79%

2.3. Coverage

Mean	0.9091
Standard Deviation	3.2476

2.4. Mapping Quality

Mean Mapping Quality	52.59

2.5. Insert size

Mean	296,897.16
Standard Deviation	5,358,211.76
P25/Median/P75	127 / 164 / 220

2.6. Mismatches and indels

General error rate	0.95%
Mismatches	26,015,235
Insertions	461,543
Mapped reads with at least one insertion	1.49%
Deletions	1,487,408
Mapped reads with at least one deletion	4.77%
Homopolymer indels	52.4%

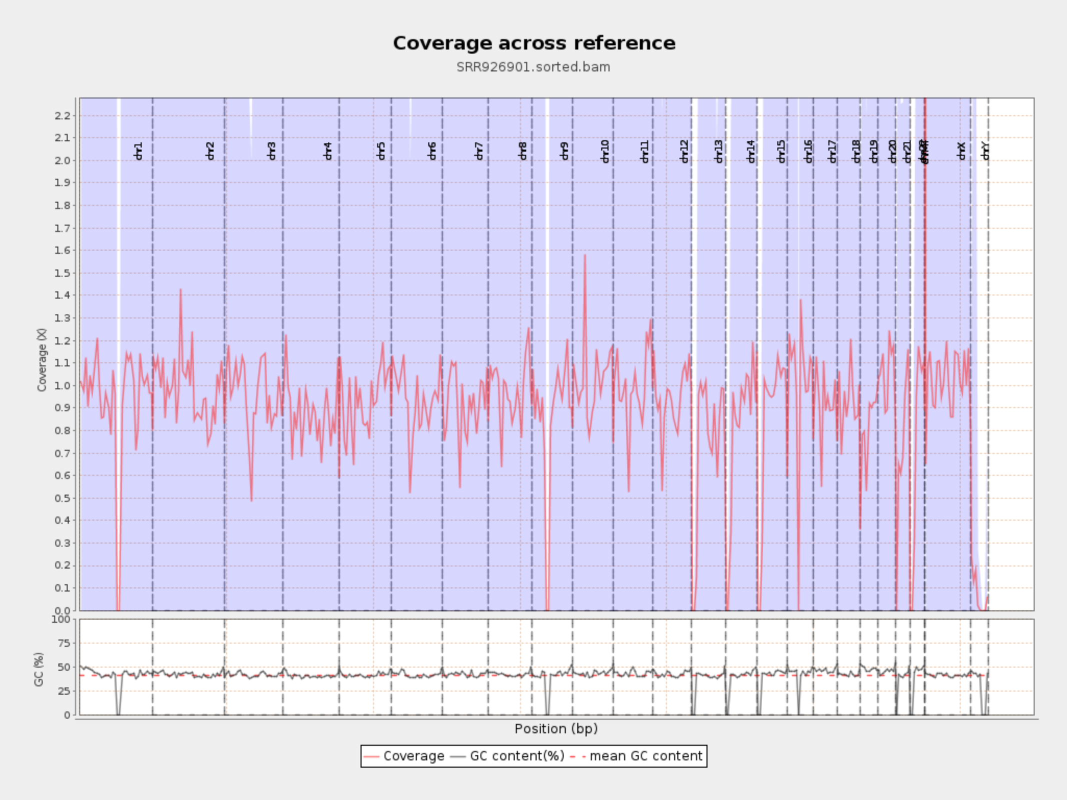
2.7. Chromosome stats

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

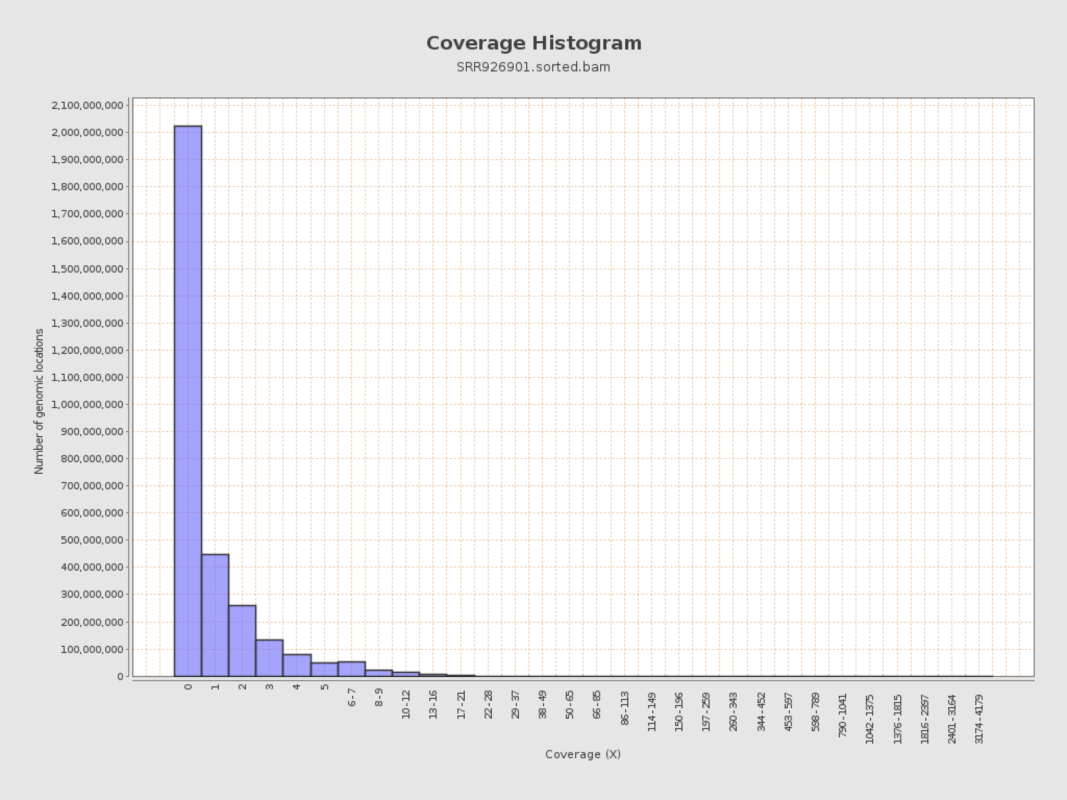
		bases	coverage	deviation
chr1	249250621	231699076	0.9296	2.936
chr2	243199373	241510524	0.9931	5.2196
chr3	198022430	190414010	0.9616	1.9867
chr4	191154276	167852475	0.8781	2.1448
chr5	180915260	169516601	0.937	1.8873
chr6	171115067	160927879	0.9405	1.9105
chr7	159138663	145924950	0.917	2.3886
chr8	146364022	143615464	0.9812	2.148
chr9	141213431	119837481	0.8486	3.2809
chr10	135534747	140848716	1.0392	8.5698
chr11	135006516	133882841	0.9917	2.4883
chr12	133851895	125905842	0.9406	2.1352
chr13	115169878	83991630	0.7293	1.7329
chr14	107349540	84816508	0.7901	1.8216
chr15	102531392	84286421	0.8221	1.9098
chr16	90354753	89863056	0.9946	4.8303
chr17	81195210	74512161	0.9177	2.1878
chr18	78077248	73791798	0.9451	3.3008
chr19	59128983	47771755	0.8079	2.1213
chr20	63025520	66747543	1.0591	2.1985
chr21	48129895	36188335	0.7519	2.6675
chr22	51304566	37304722	0.7271	1.8728
chrMT	16571	603069	36.393	25.5599
chrX	155270560	158360010	1.0199	2.1215

chrY	59373566	4221570	0.0711	1.4947

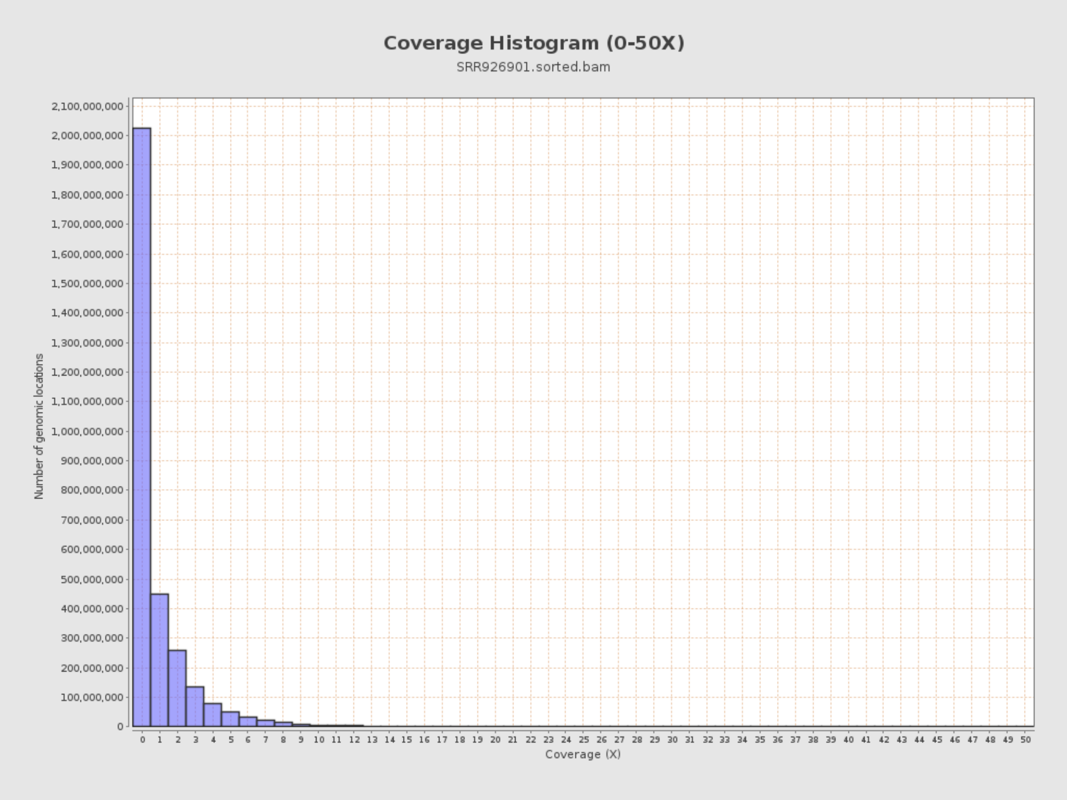
3. Results : Coverage across reference



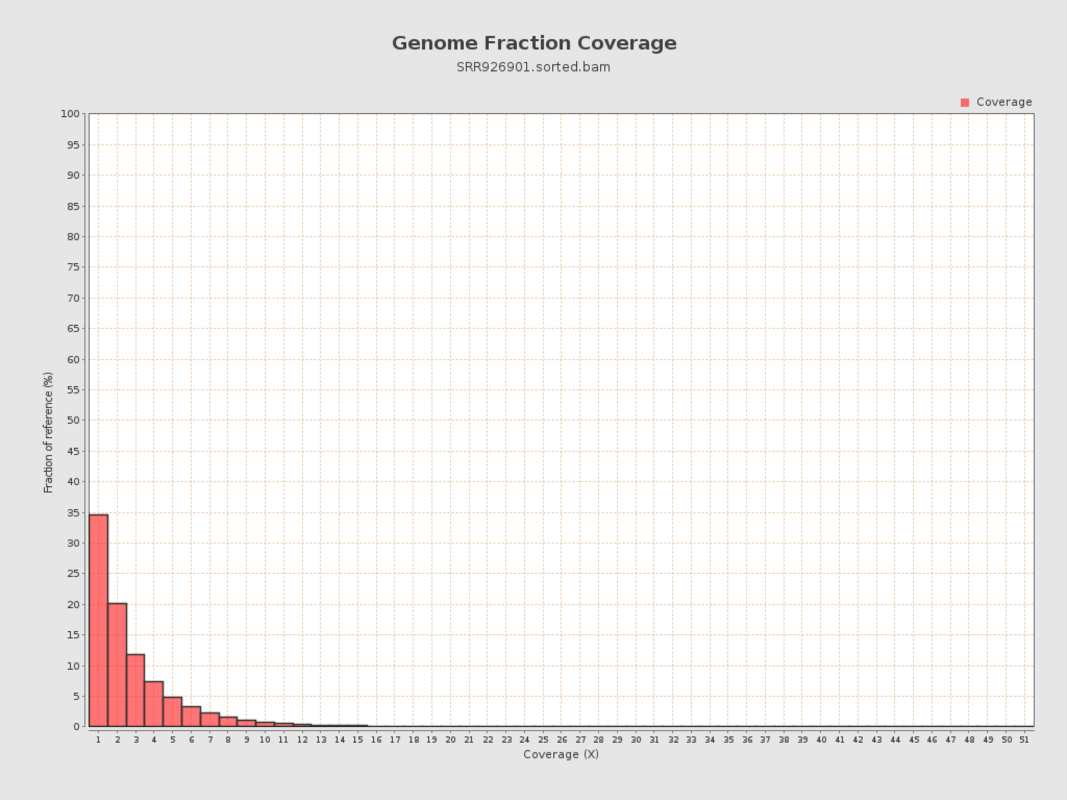
4. Results : Coverage Histogram



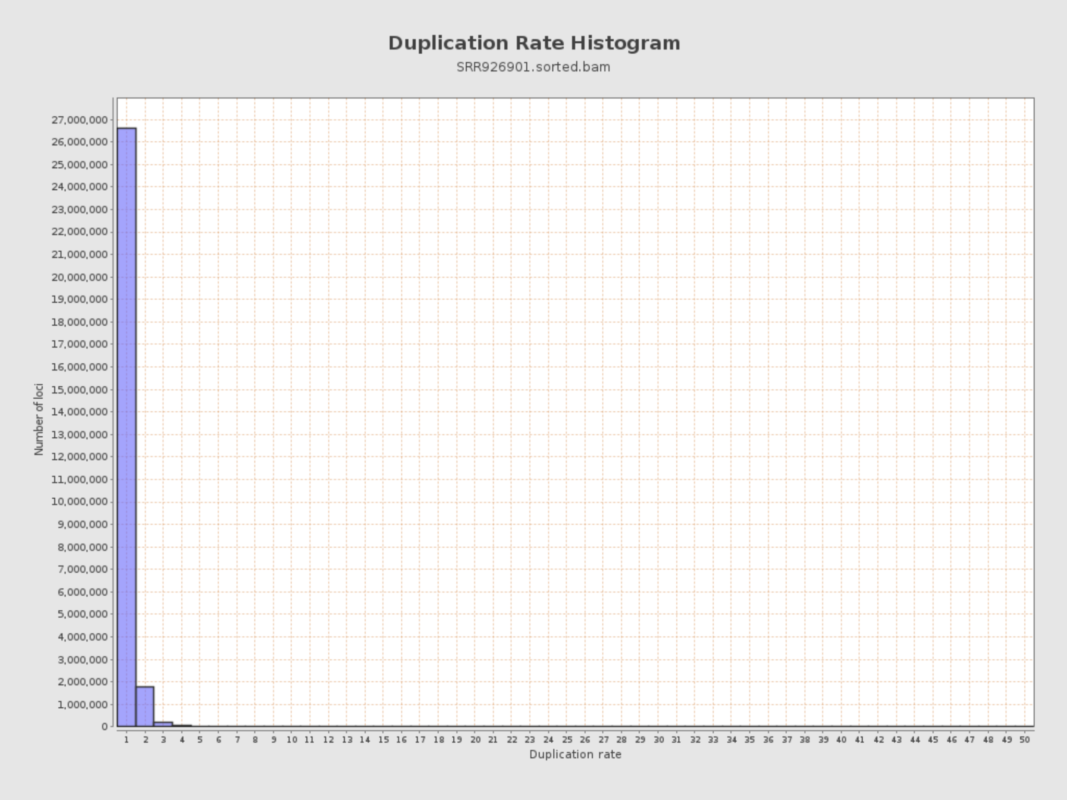
5. Results : Coverage Histogram (0-50X)



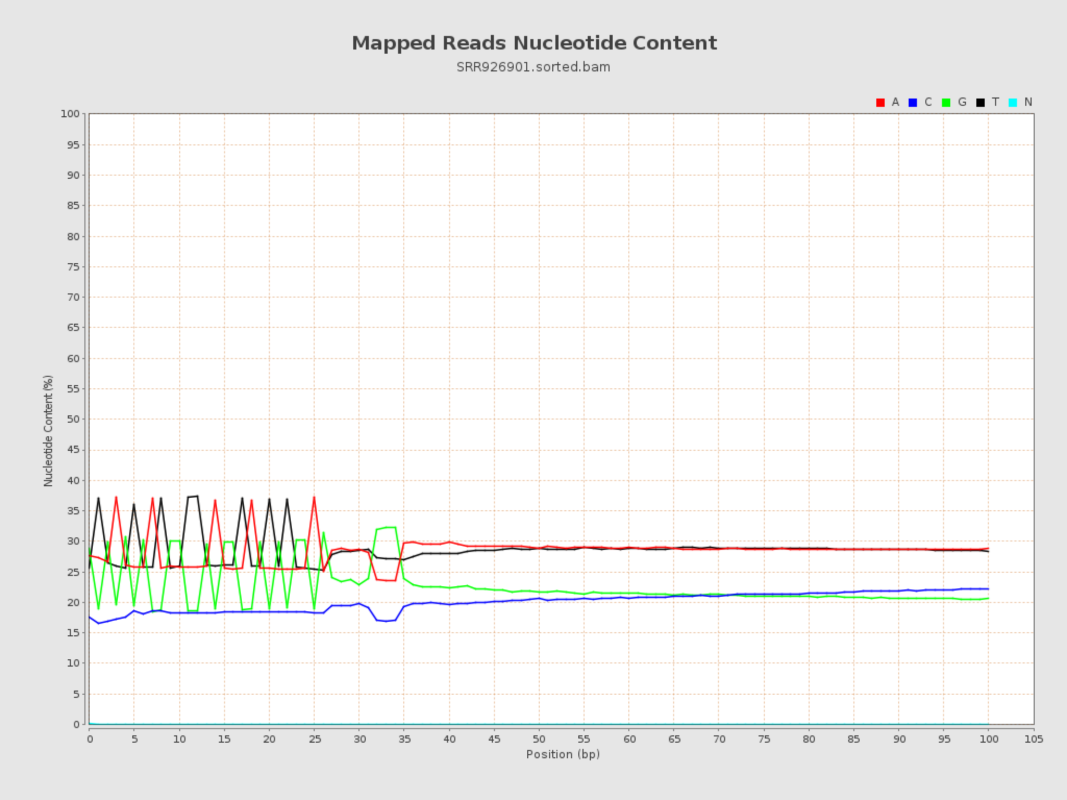
6. Results : Genome Fraction Coverage



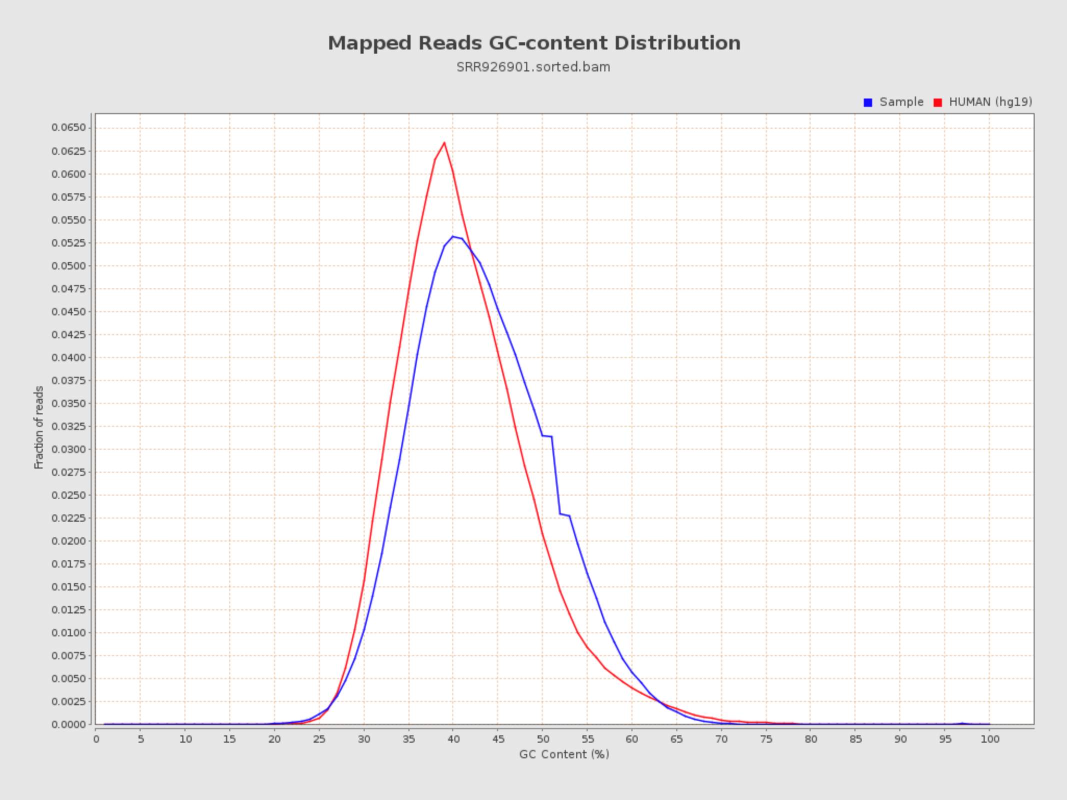
7. Results : Duplication Rate Histogram



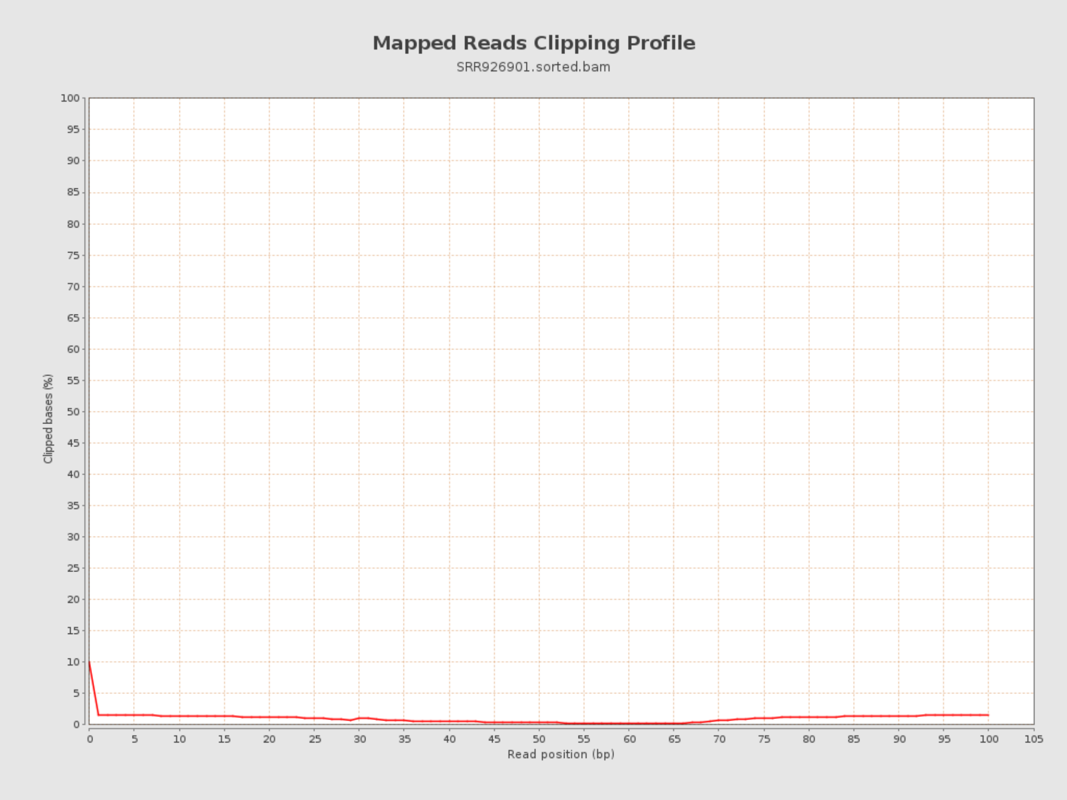
8. Results : Mapped Reads Nucleotide Content



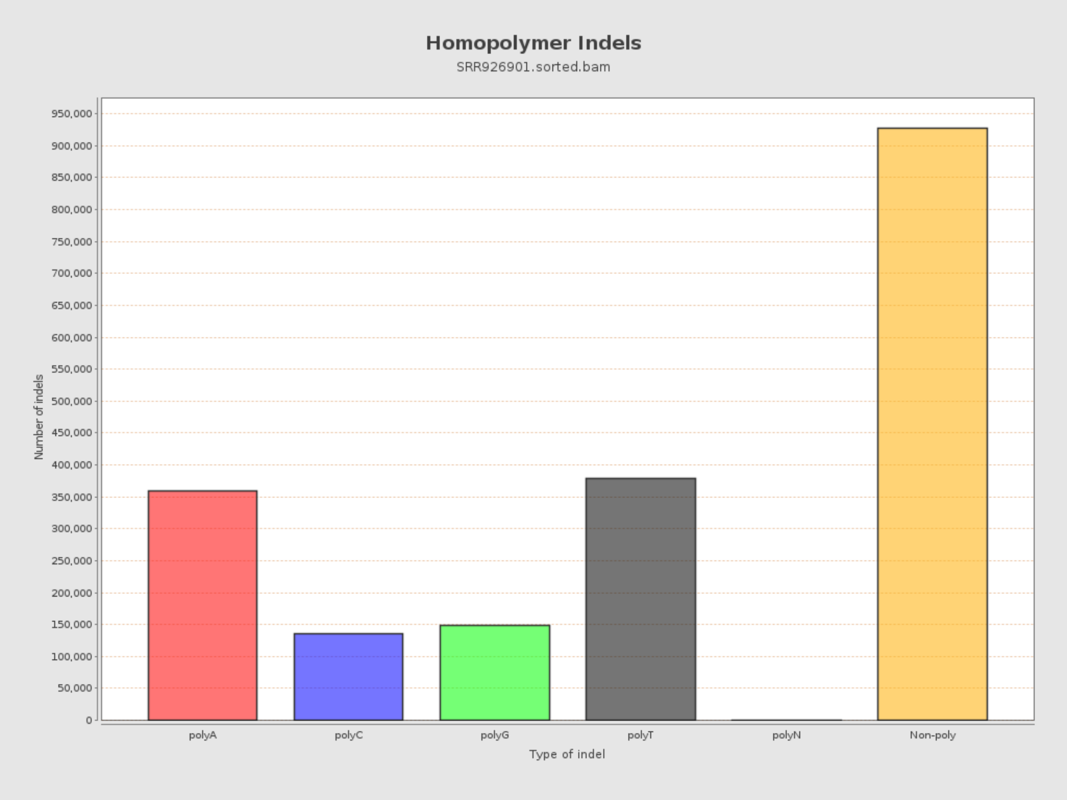
9. Results : Mapped Reads GC-content Distribution



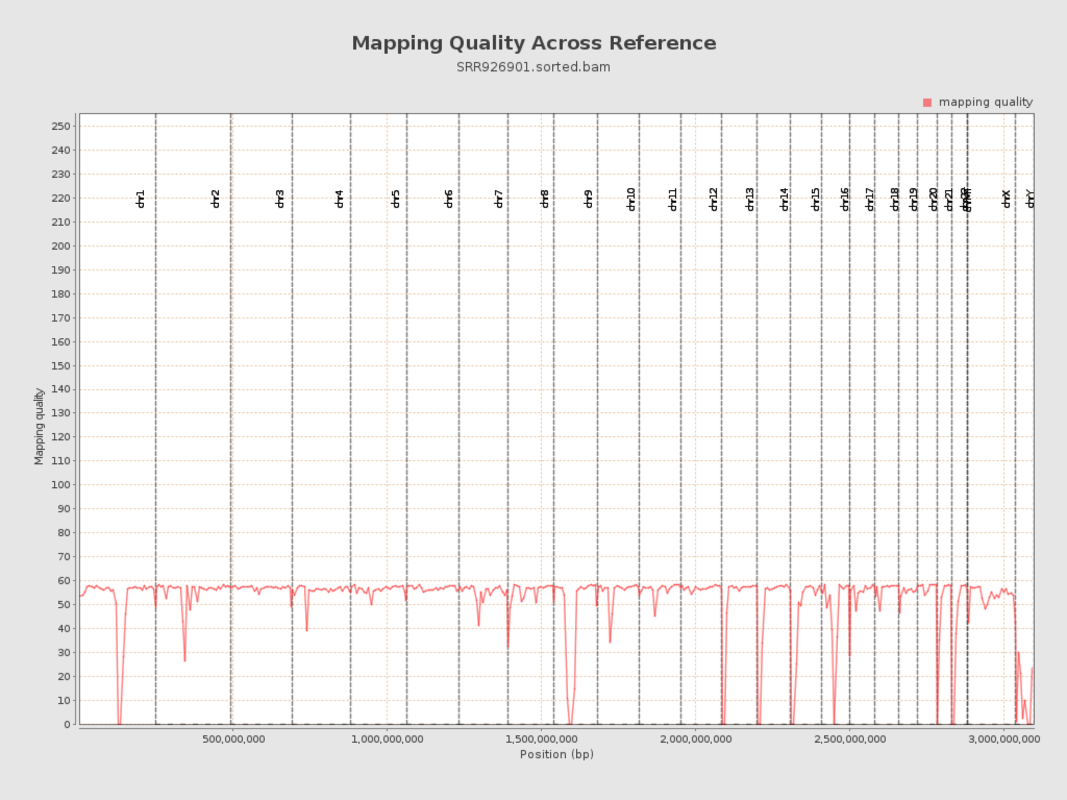
10. Results : Mapped Reads Clipping Profile



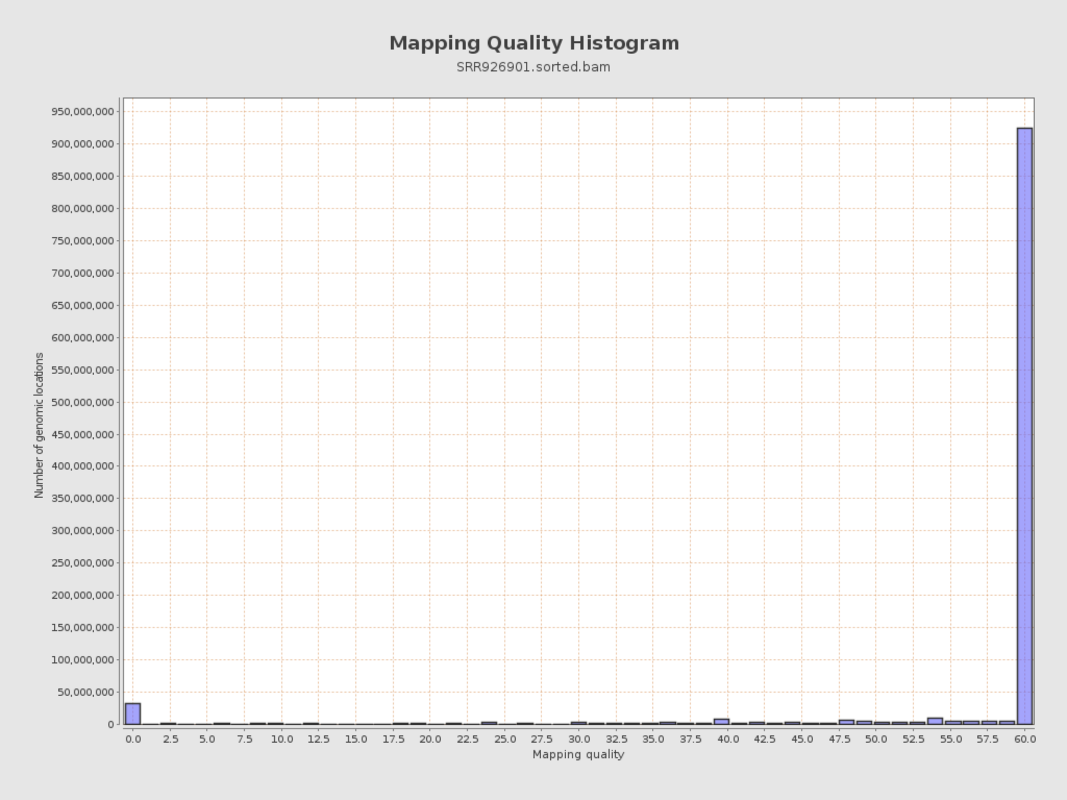
11. Results : Homopolymer Indels



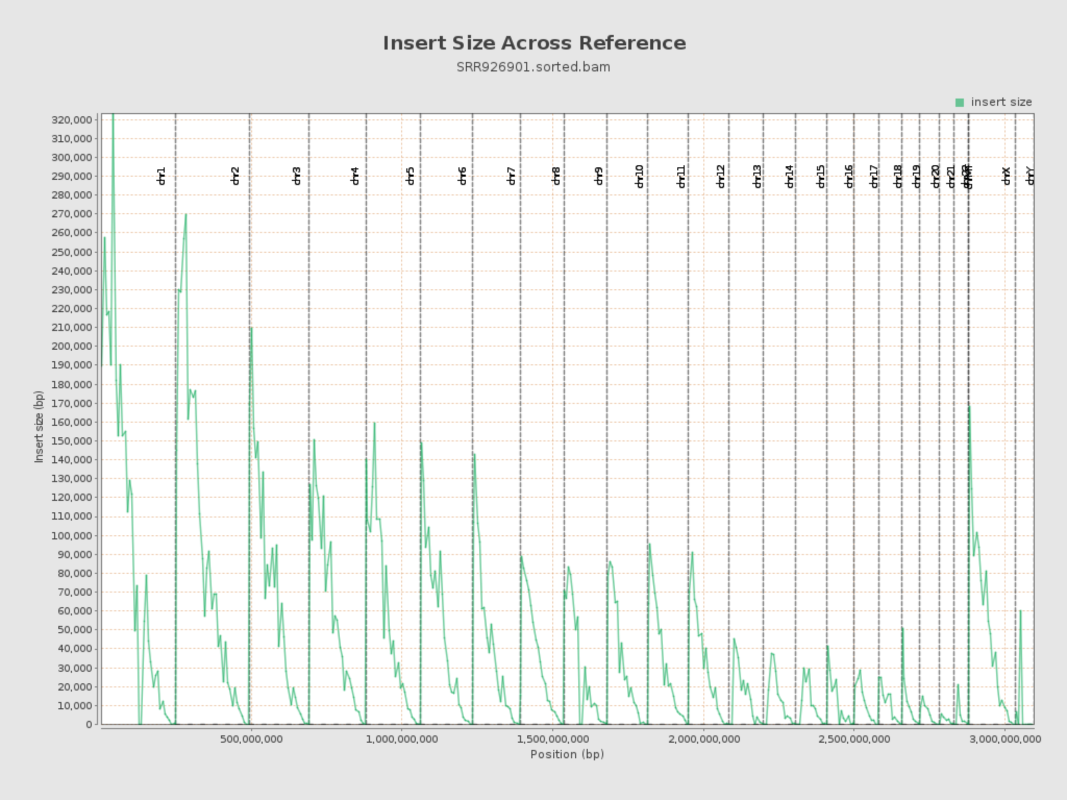
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram