Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/22 09:23:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926903.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_SRR926903 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926903_1.fastq.gz SRR926903_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 22 09:23:06 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926903.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	29,221,822
Mapped reads	27,331,032 / 93.53%
Unmapped reads	1,890,790 / 6.47%
Mapped paired reads	27,331,032 / 93.53%
Mapped reads, first in pair	13,750,372 / 47.06%
Mapped reads, second in pair	13,580,660 / 46.47%
Mapped reads, both in pair	27,023,114 / 92.48%
Mapped reads, singletons	307,918 / 1.05%
Secondary alignments	0
Supplementary alignments	198,865 / 0.68%
Read min/max/mean length	30 / 101 / 101.27
Duplicated reads (estimated)	1,810,359 / 6.2%
Duplication rate	5.35%
Clipped reads	7,240,520 / 24.78%

2.2. ACGT Content

Number/percentage of A's	730,313,652 / 28.49%
Number/percentage of C's	510,942,847 / 19.93%
Number/percentage of T's	735,133,510 / 28.67%
Number/percentage of G's	587,069,077 / 22.9%
Number/percentage of N's	243,521 / 0.01%

GC Percentage	42.83%

2.3. Coverage

Mean	0.8288
Standard Deviation	2.6465

2.4. Mapping Quality

Mean Mapping Quality	53.54

2.5. Insert size

Mean	110,390.45
Standard Deviation	3,289,651.43
P25/Median/P75	186 / 235 / 298

2.6. Mismatches and indels

General error rate	1.06%
Mismatches	26,521,015
Insertions	407,932
Mapped reads with at least one insertion	1.47%
Deletions	1,407,809
Mapped reads with at least one deletion	5.01%
Homopolymer indels	53.26%

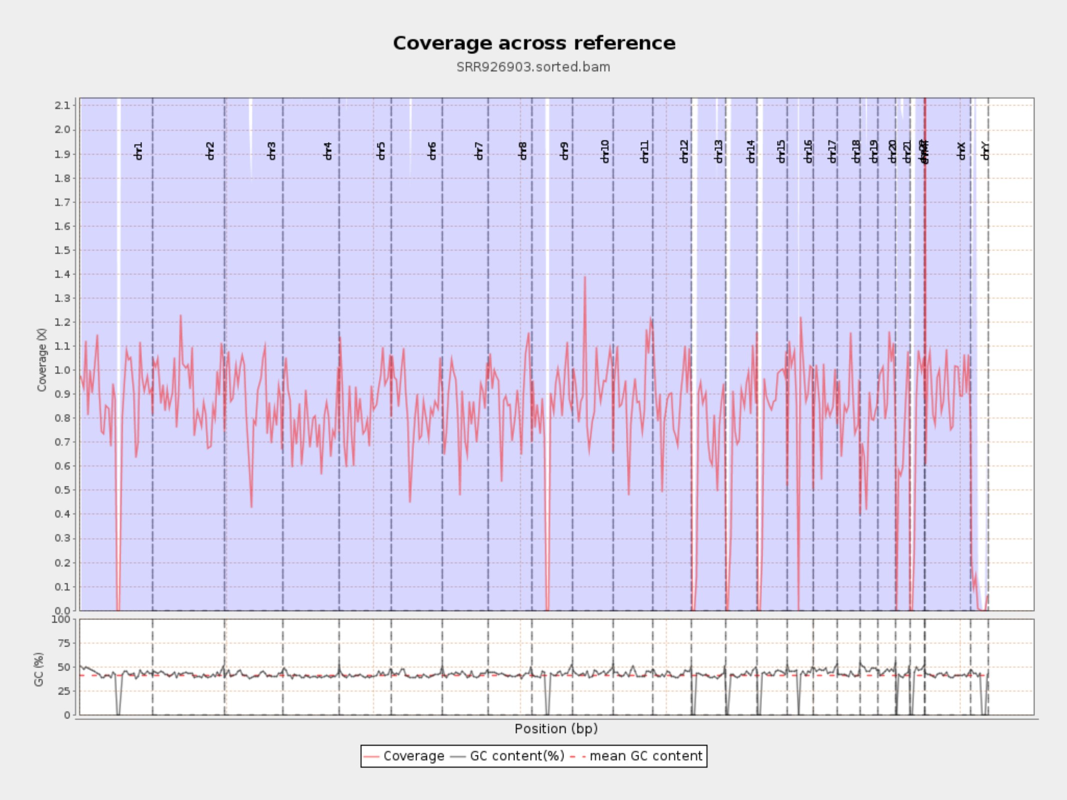
2.7. Chromosome stats

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

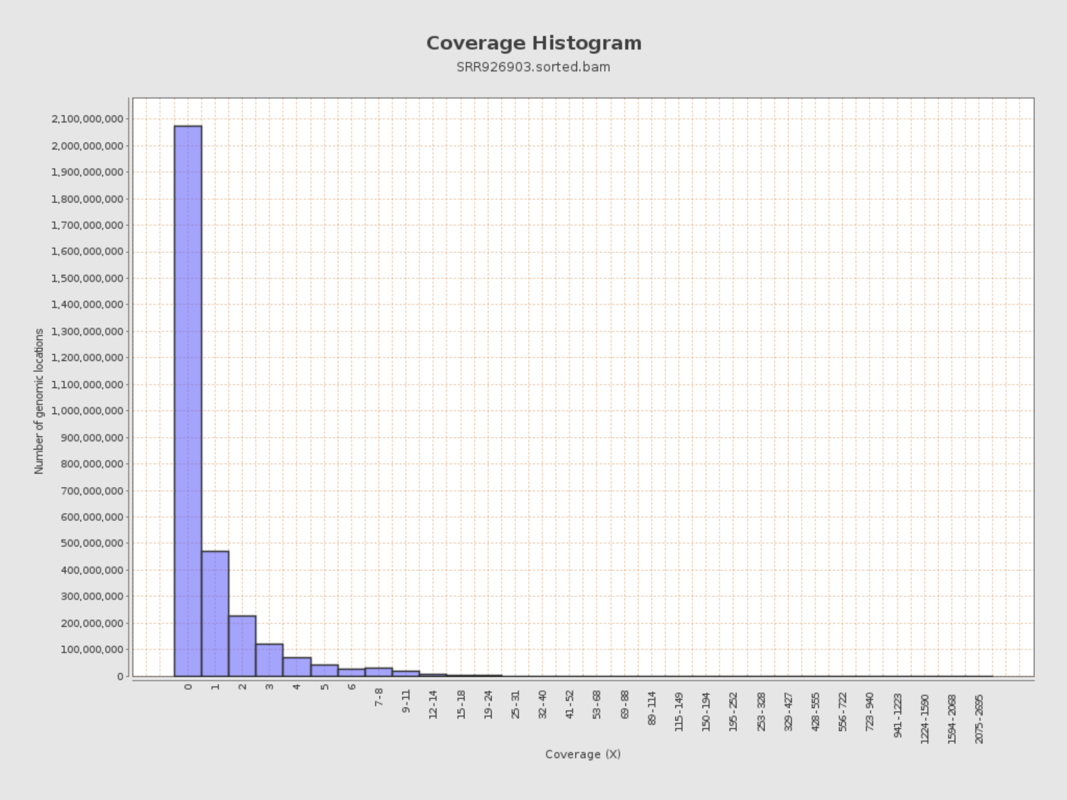
		bases	coverage	deviation
chr1	249250621	213682777	0.8573	2.7626
chr2	243199373	221880117	0.9123	3.4938
chr3	198022430	173754525	0.8774	1.8054
chr4	191154276	150256495	0.786	1.8596
chr5	180915260	155497399	0.8595	1.7816
chr6	171115067	145425055	0.8499	1.7873
chr7	159138663	132386579	0.8319	1.8665
chr8	146364022	130041621	0.8885	1.9253
chr9	141213431	111400722	0.7889	3.0651
chr10	135534747	126810717	0.9356	6.562
chr11	135006516	122385110	0.9065	2.1008
chr12	133851895	116310189	0.8689	1.8711
chr13	115169878	75840193	0.6585	1.5601
chr14	107349540	77450800	0.7215	1.7071
chr15	102531392	76709052	0.7482	1.7836
chr16	90354753	81306677	0.8999	3.9738
chr17	81195210	69748795	0.859	2.0182
chr18	78077248	67598260	0.8658	2.9838
chr19	59128983	42349171	0.7162	1.9938
chr20	63025520	61679081	0.9786	2.1708
chr21	48129895	32453642	0.6743	2.5236
chr22	51304566	34817930	0.6787	1.7642
chrMT	16571	137423	8.293	6.7537
chrX	155270560	142364105	0.9169	1.9055

chrY	59373566	3397693	0.0572	1.093

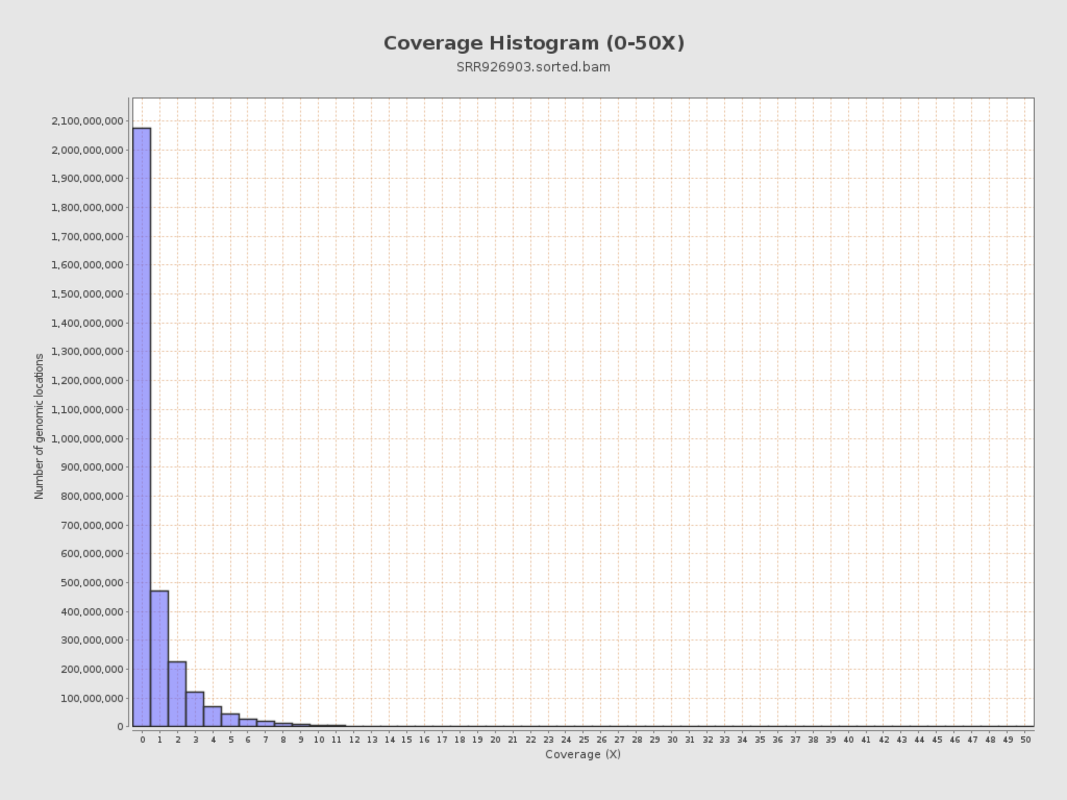
3. Results : Coverage across reference



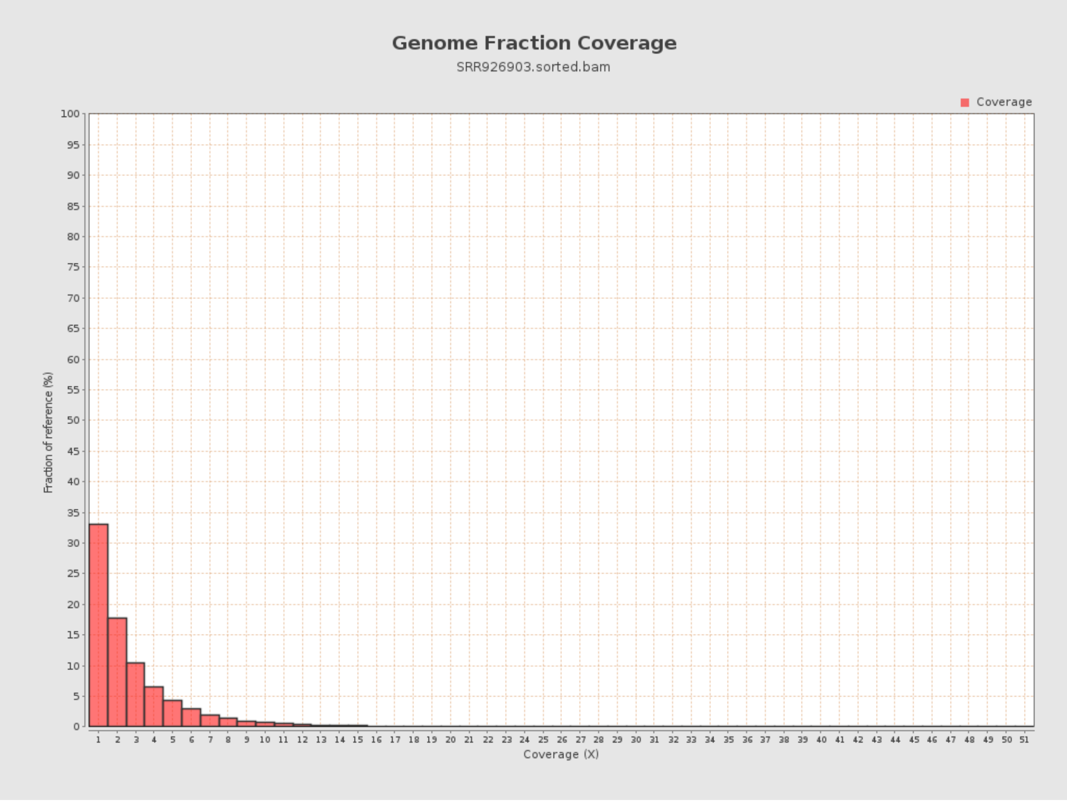
4. Results : Coverage Histogram



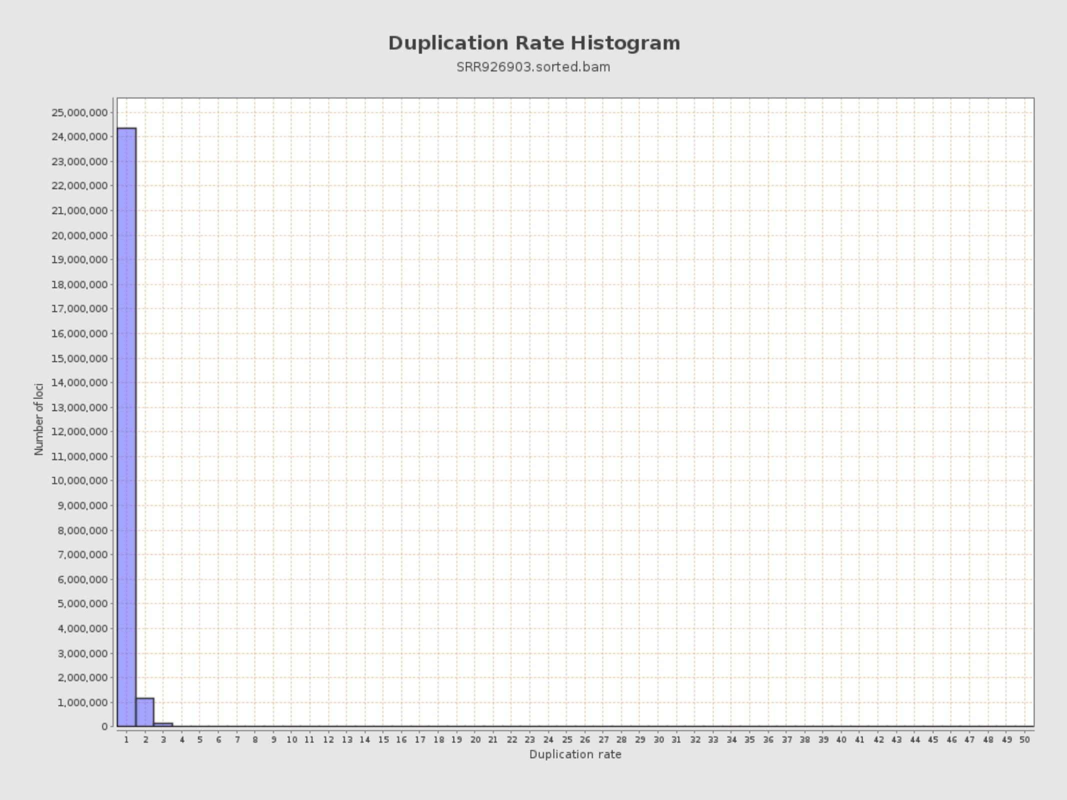
5. Results : Coverage Histogram (0-50X)



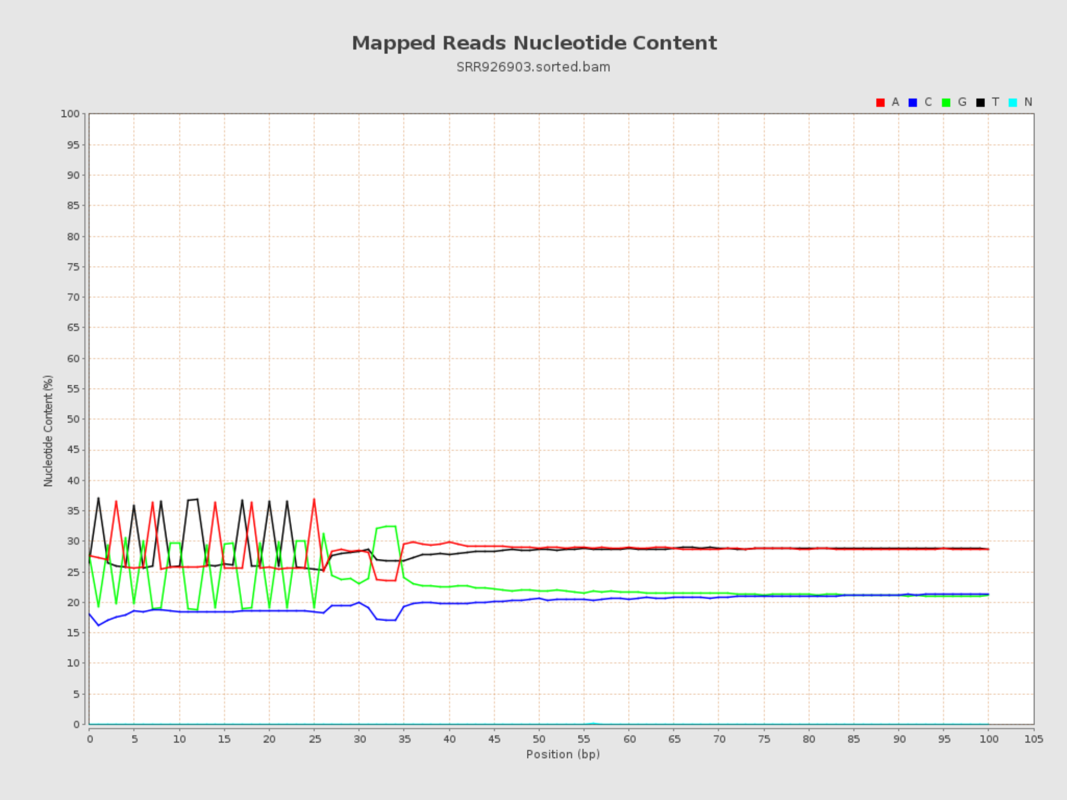
6. Results : Genome Fraction Coverage



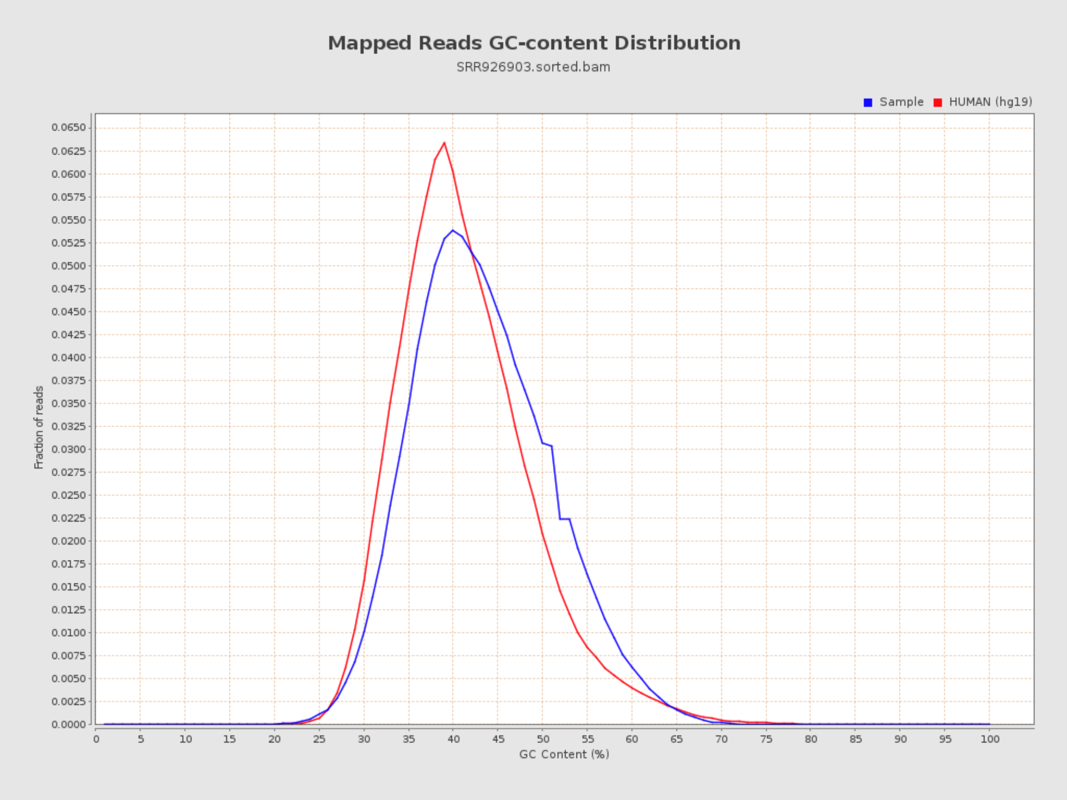
7. Results : Duplication Rate Histogram



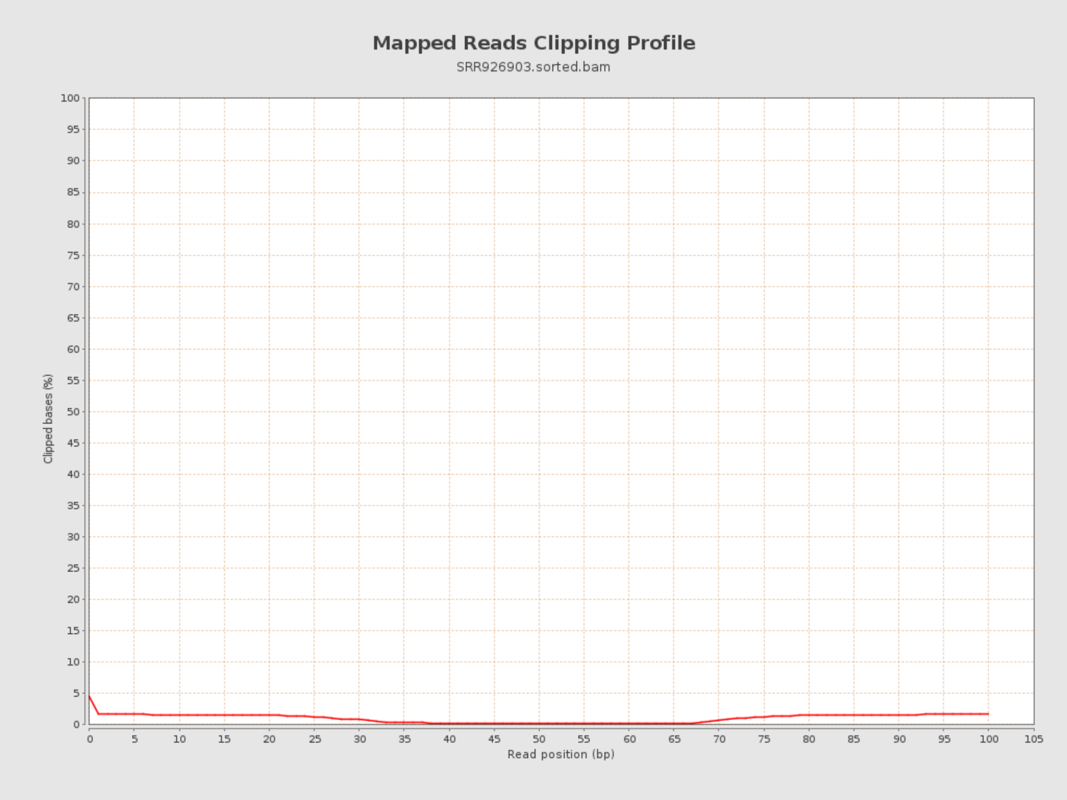
8. Results : Mapped Reads Nucleotide Content



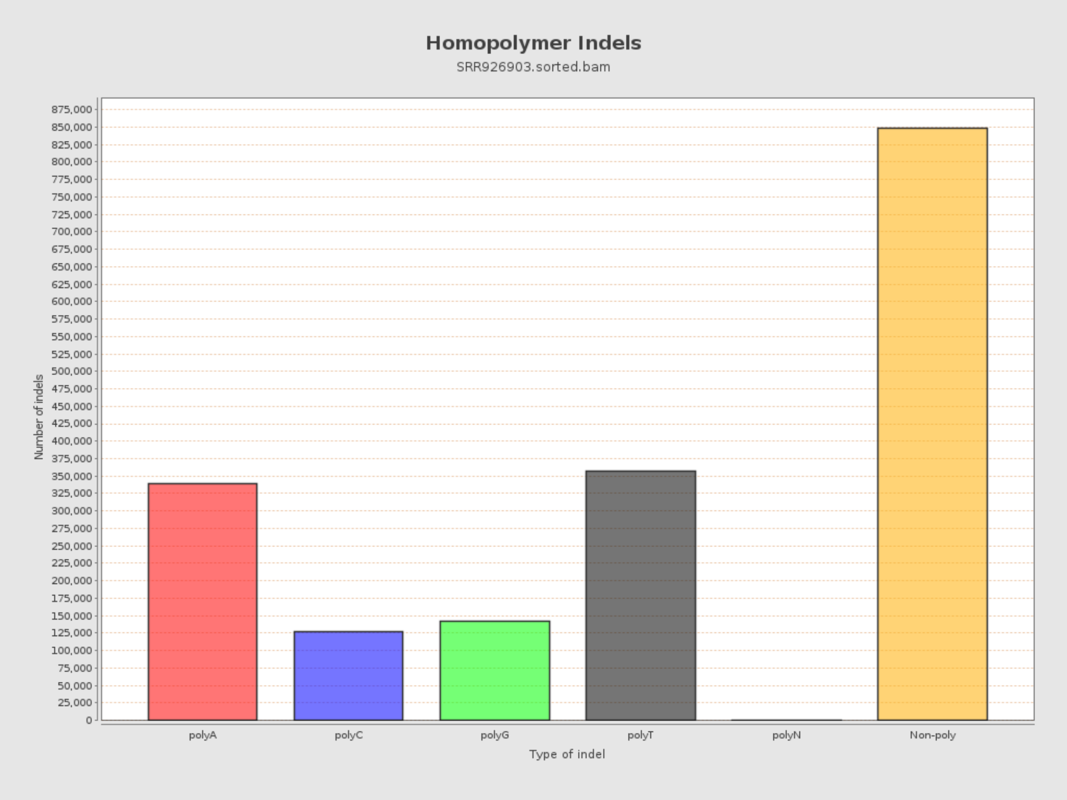
9. Results : Mapped Reads GC-content Distribution



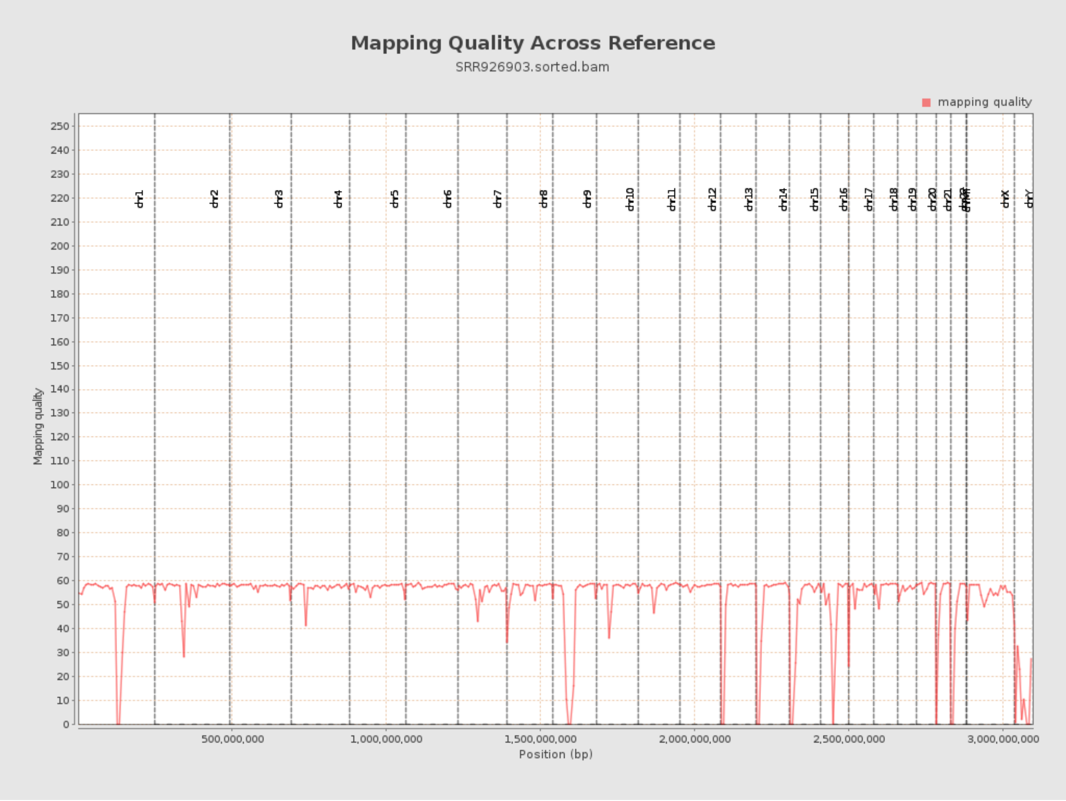
10. Results : Mapped Reads Clipping Profile



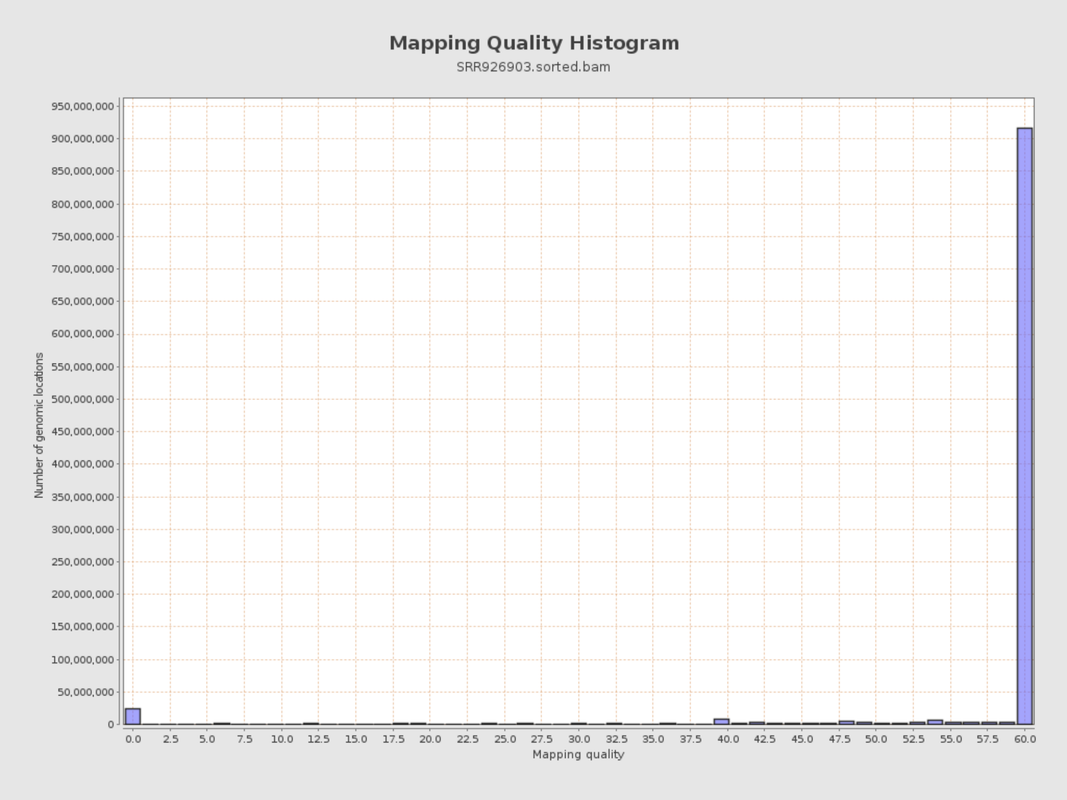
11. Results : Homopolymer Indels



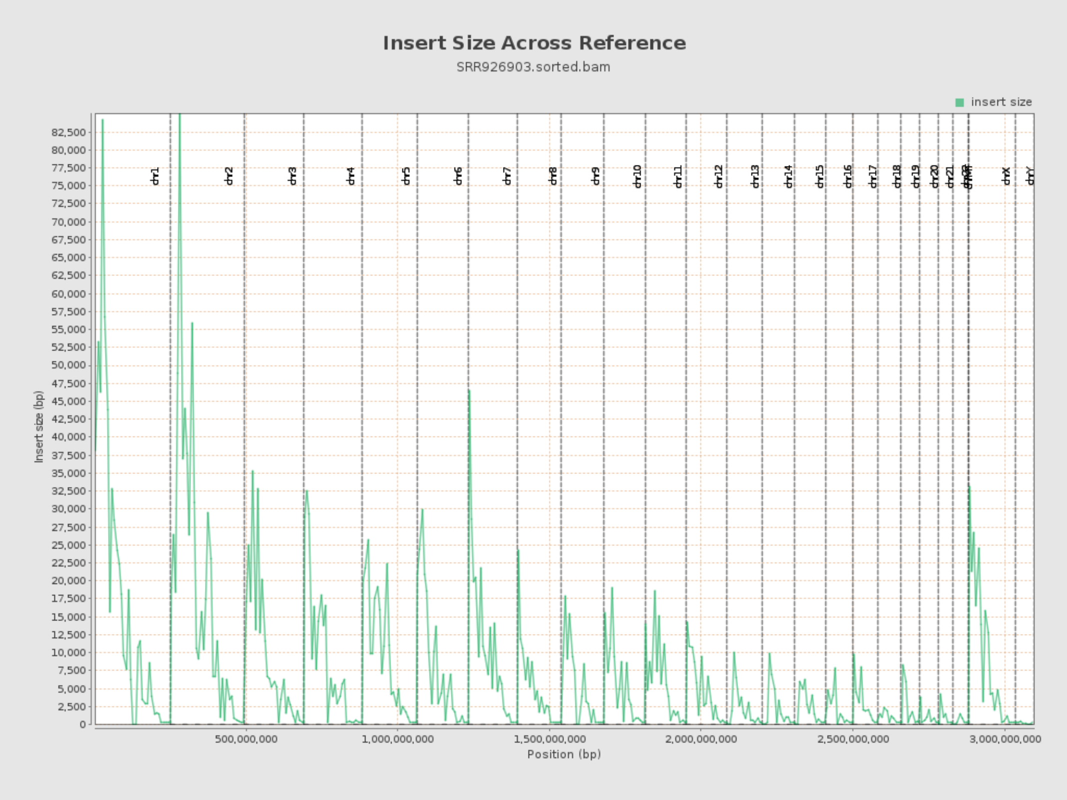
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram