Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/22 00:42:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926888.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_SRR926888 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926888_1.fastq.gz SRR926888_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 22 00:42:07 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926888.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	26,297,908
Mapped reads	22,933,588 / 87.21%
Unmapped reads	3,364,320 / 12.79%
Mapped paired reads	22,933,588 / 87.21%
Mapped reads, first in pair	11,536,735 / 43.87%
Mapped reads, second in pair	11,396,853 / 43.34%
Mapped reads, both in pair	22,474,094 / 85.46%
Mapped reads, singletons	459,494 / 1.75%
Secondary alignments	0
Supplementary alignments	607,434 / 2.31%
Read min/max/mean length	30 / 101 / 101.96
Duplicated reads (estimated)	2,016,661 / 7.67%
Duplication rate	7.08%
Clipped reads	10,049,139 / 38.21%

2.2. ACGT Content

Number/percentage of A's	584,860,349 / 28.21%
Number/percentage of C's	407,872,261 / 19.67%
Number/percentage of T's	594,103,584 / 28.65%
Number/percentage of G's	486,362,453 / 23.46%
Number/percentage of N's	170,270 / 0.01%

GC Percentage	43.13%

2.3. Coverage

Mean	0.6703
Standard Deviation	2.3245

2.4. Mapping Quality

Mean Mapping Quality	47.5

2.5. Insert size

Mean	292,778.67
Standard Deviation	5,190,681.94
P25/Median/P75	141 / 184 / 250

2.6. Mismatches and indels

General error rate	1.07%
Mismatches	21,644,258
Insertions	357,200
Mapped reads with at least one insertion	1.53%
Deletions	1,095,082
Mapped reads with at least one deletion	4.65%
Homopolymer indels	51.74%

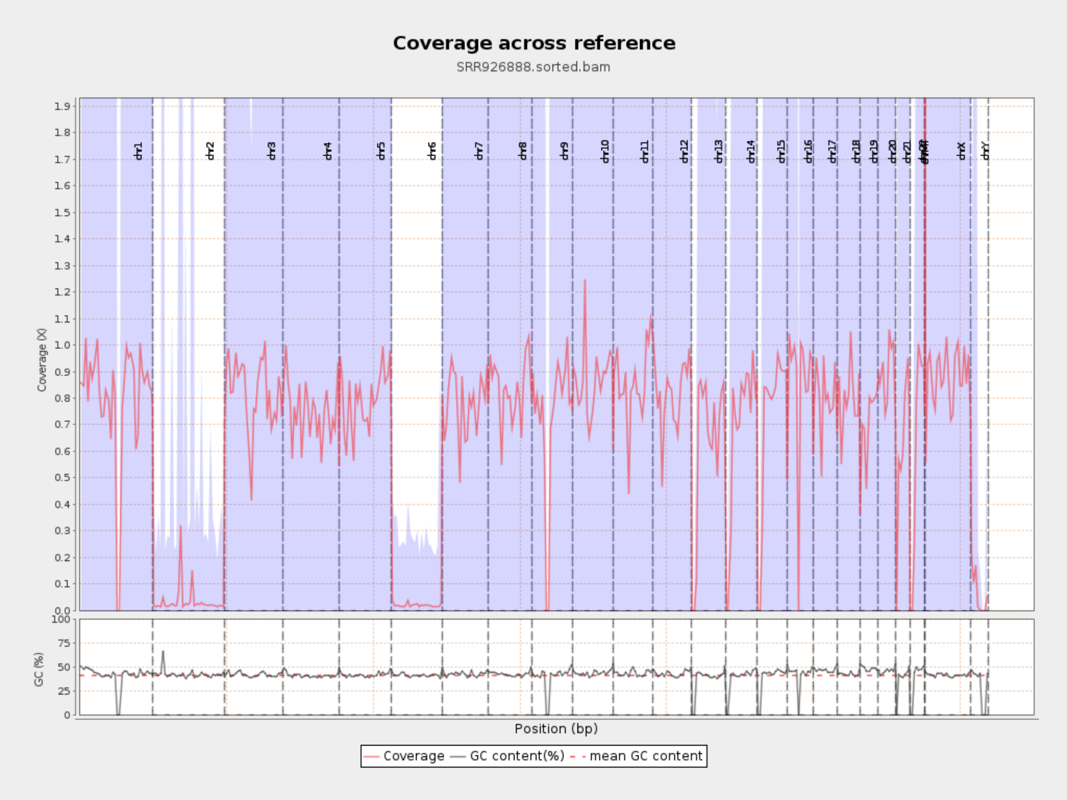
2.7. Chromosome stats

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

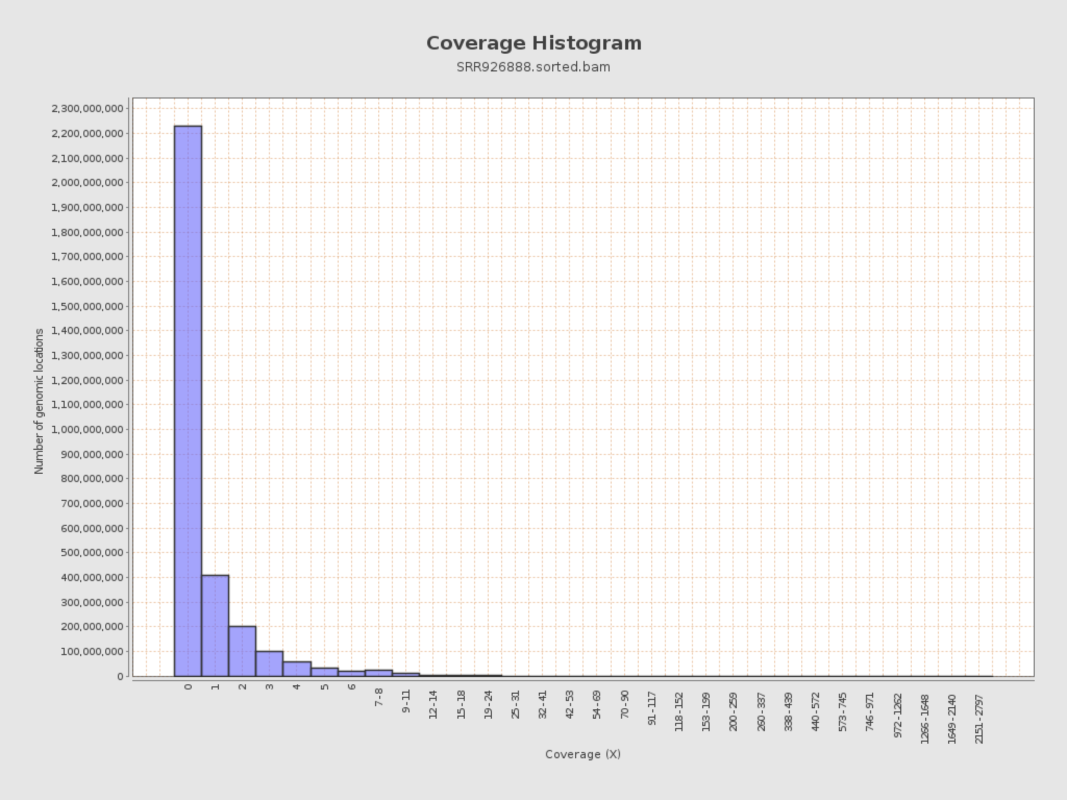
		bases	coverage	deviation
chr1	249250621	199745484	0.8014	2.4521
chr2	243199373	8867568	0.0365	2.0235
chr3	198022430	162938697	0.8228	1.7294
chr4	191154276	143585665	0.7512	1.9232
chr5	180915260	144444945	0.7984	1.6709
chr6	171115067	3411085	0.0199	0.3237
chr7	159138663	123920097	0.7787	1.8216
chr8	146364022	122489585	0.8369	1.8889
chr9	141213431	102379184	0.725	2.5889
chr10	135534747	118497960	0.8743	6.1926
chr11	135006516	115144740	0.8529	1.9921
chr12	133851895	109432355	0.8176	1.8288
chr13	115169878	71904047	0.6243	1.4848
chr14	107349540	72213066	0.6727	1.584
chr15	102531392	71699619	0.6993	1.6804
chr16	90354753	75866141	0.8396	3.2377
chr17	81195210	64956742	0.8	1.8511
chr18	78077248	63235694	0.8099	2.3961
chr19	59128983	41756901	0.7062	1.8568
chr20	63025520	56565477	0.8975	1.9189
chr21	48129895	30575642	0.6353	2.3049
chr22	51304566	31534903	0.6147	1.6141
chrMT	16571	72751	4.3903	3.7702
chrX	155270560	135988912	0.8758	1.8459

chrY	59373566	3753489	0.0632	1.598

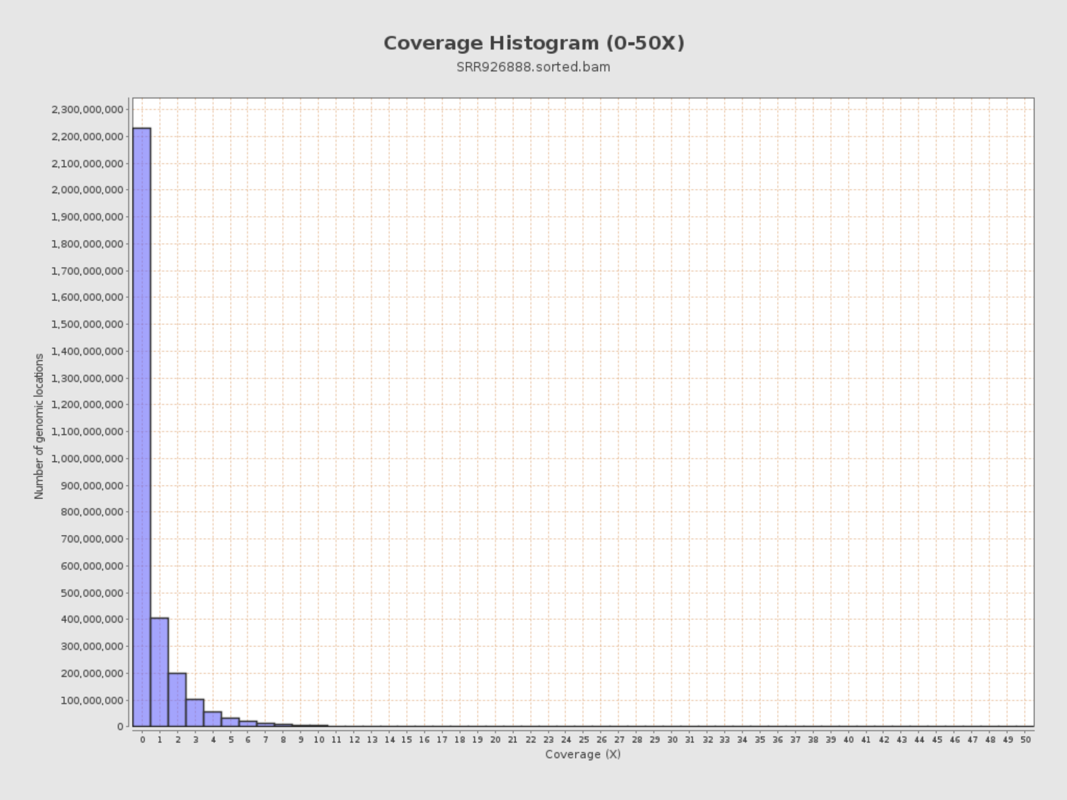
3. Results : Coverage across reference



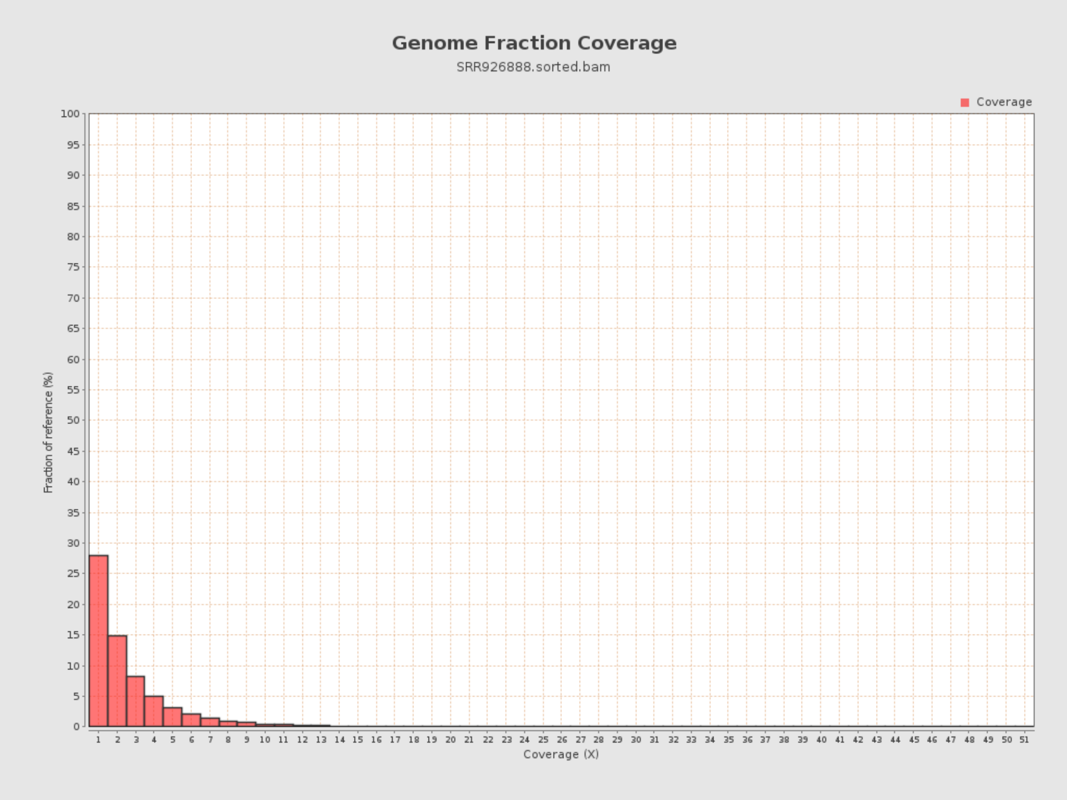
4. Results : Coverage Histogram



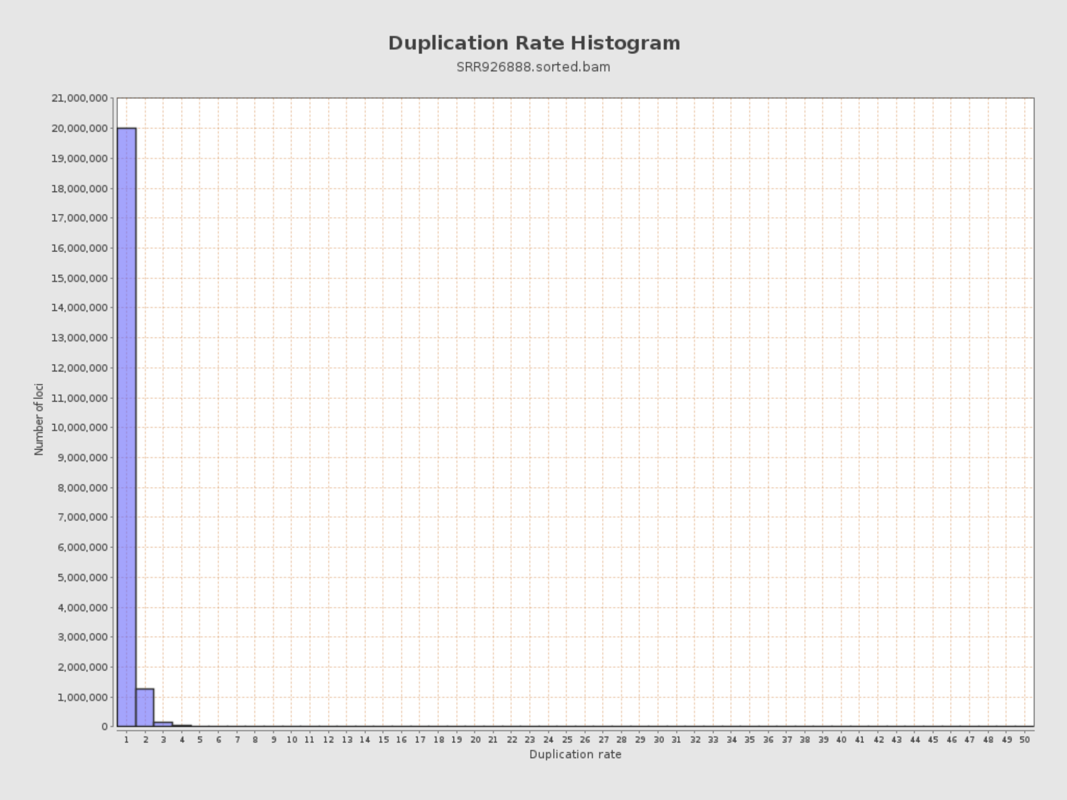
5. Results : Coverage Histogram (0-50X)



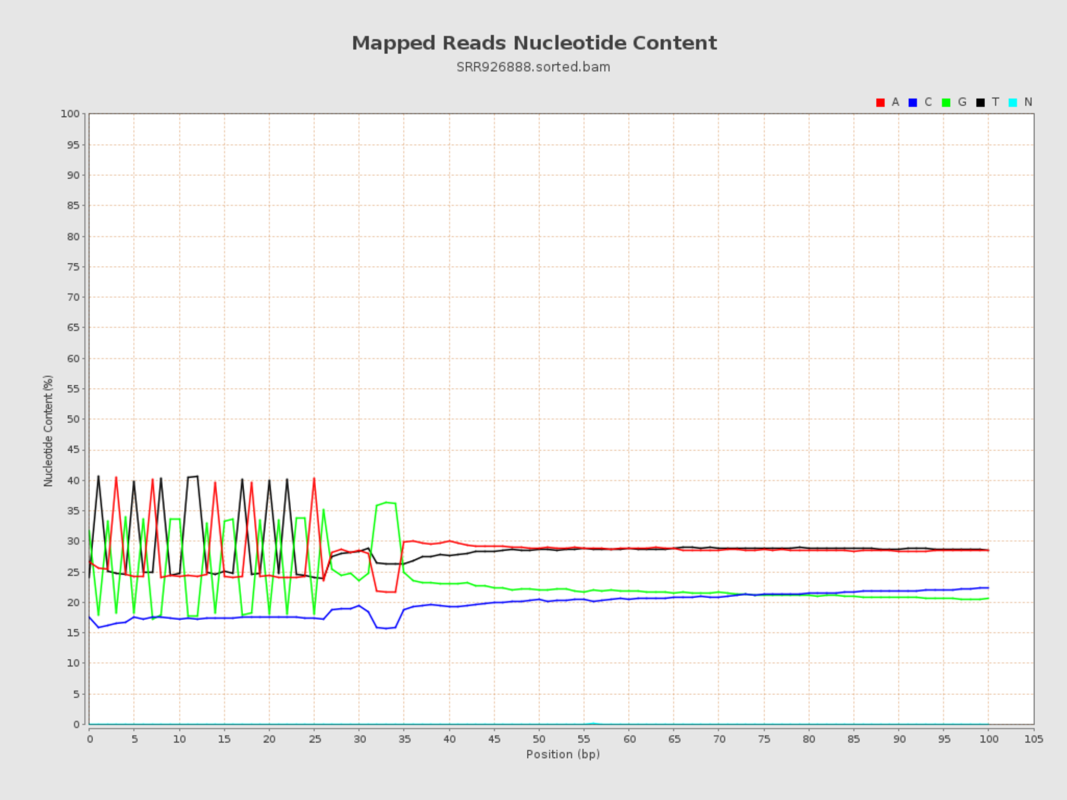
6. Results : Genome Fraction Coverage



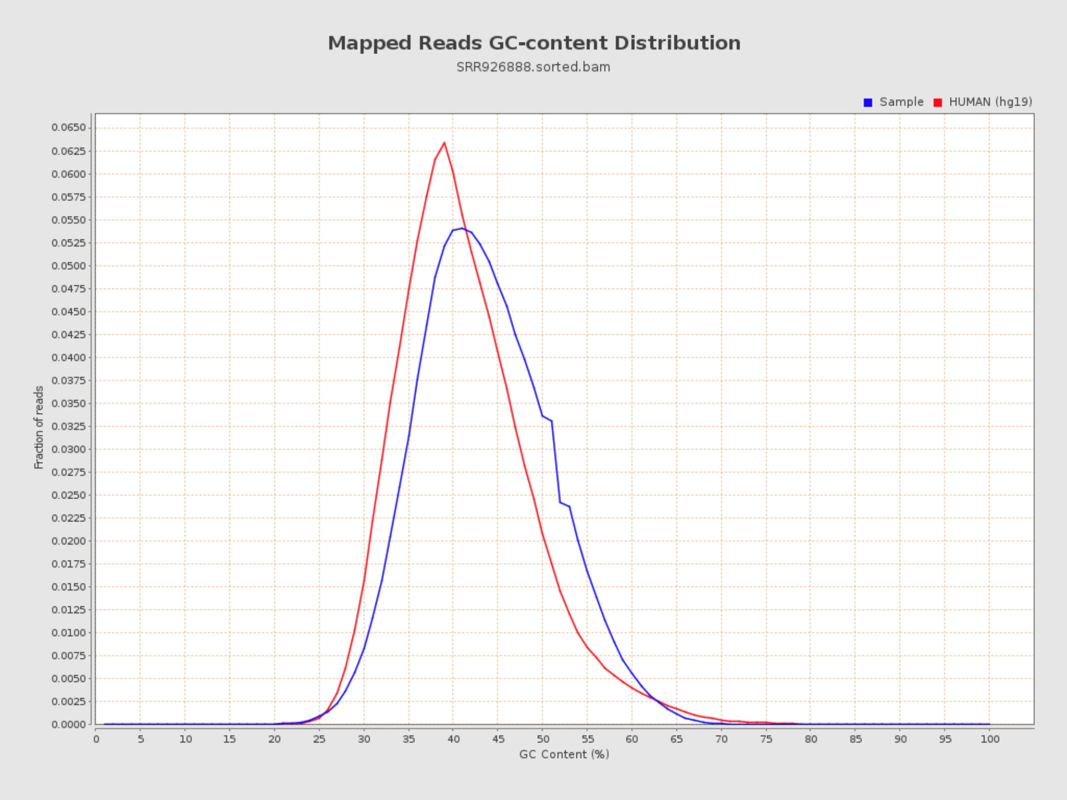
7. Results : Duplication Rate Histogram



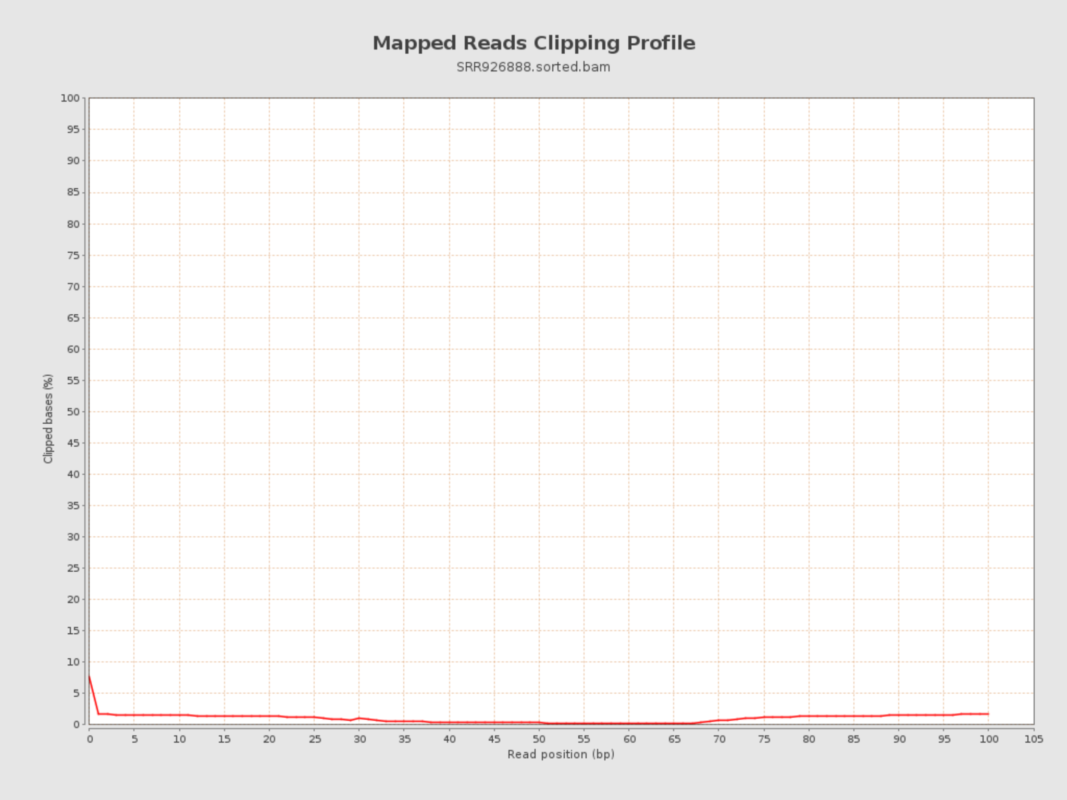
8. Results : Mapped Reads Nucleotide Content



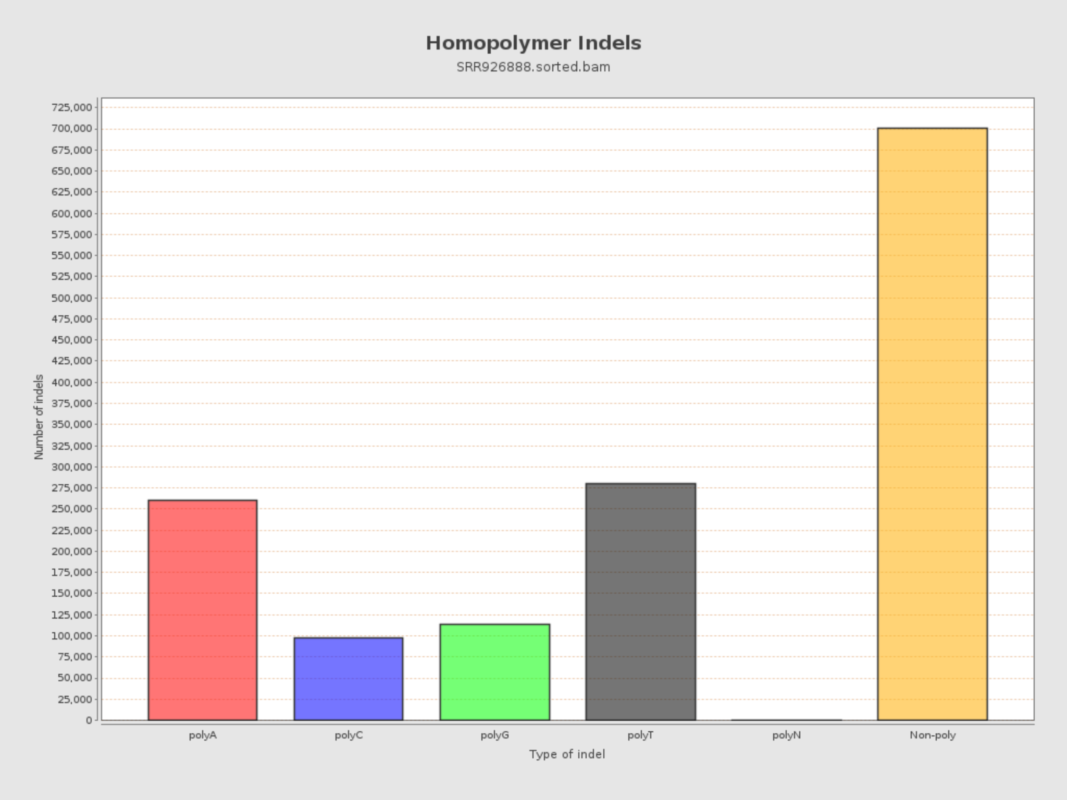
9. Results : Mapped Reads GC-content Distribution



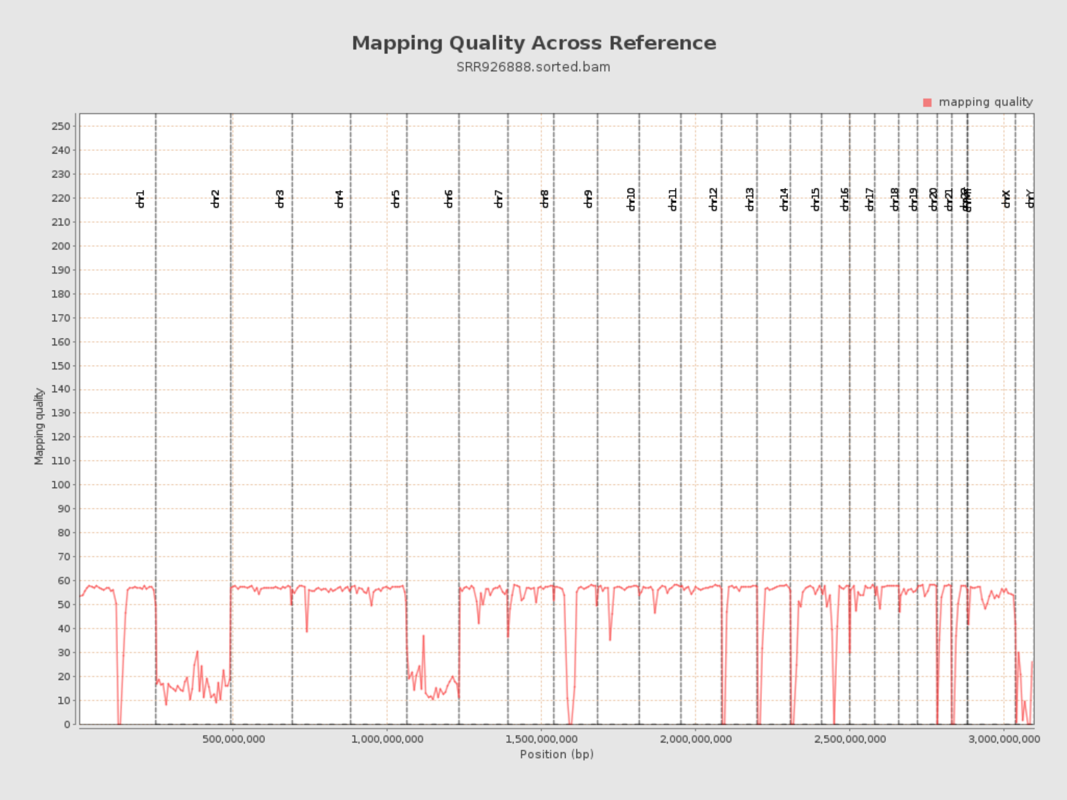
10. Results : Mapped Reads Clipping Profile



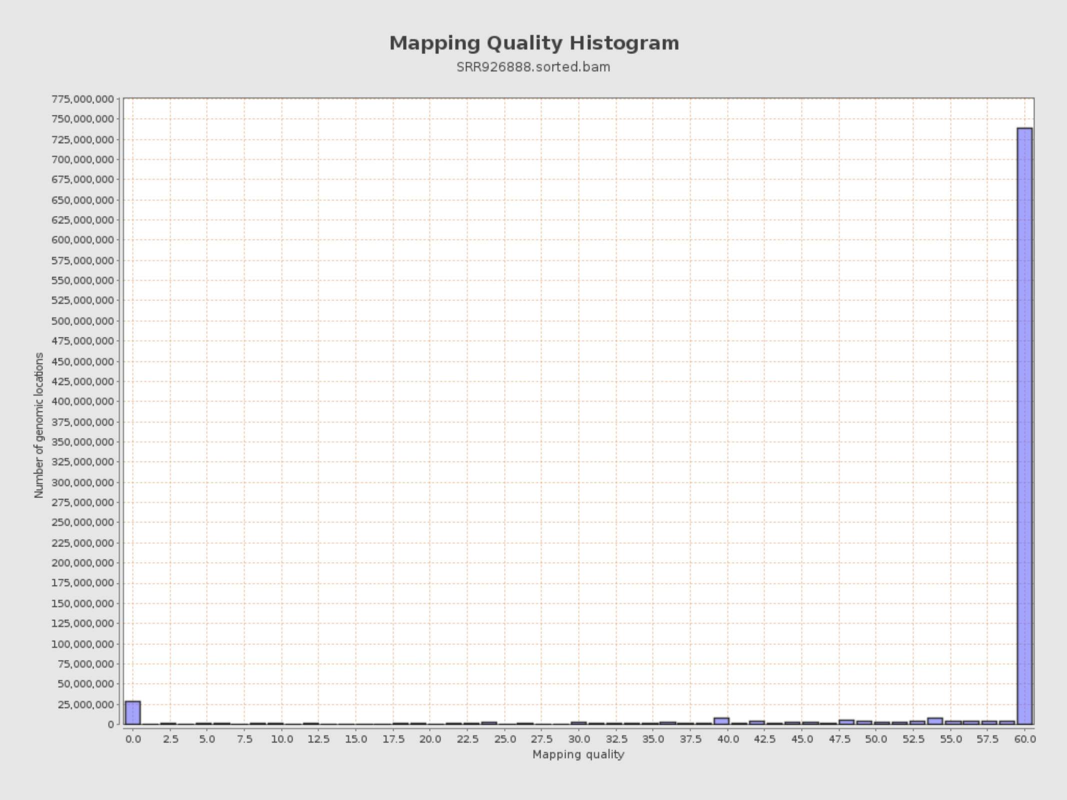
11. Results : Homopolymer Indels



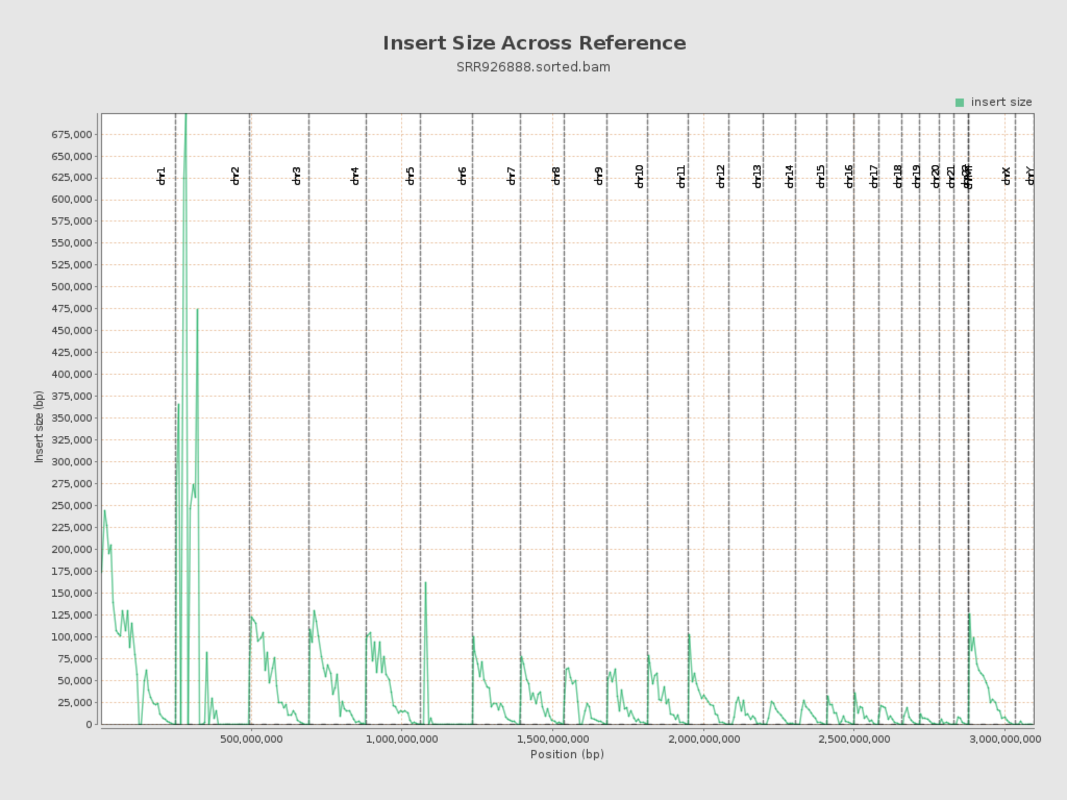
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram