

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/22 01:17:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926889.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_SRR926889 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926889_1.fastq.gz SRR926889_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 22 01:17:22 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926889.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	38,351,548
Mapped reads	35,904,899 / 93.62%
Unmapped reads	2,446,649 / 6.38%
Mapped paired reads	35,904,899 / 93.62%
Mapped reads, first in pair	17,997,767 / 46.93%
Mapped reads, second in pair	17,907,132 / 46.69%
Mapped reads, both in pair	35,556,876 / 92.71%
Mapped reads, singletons	348,023 / 0.91%
Secondary alignments	0
Supplementary alignments	362,247 / 0.94%
Read min/max/mean length	30 / 101 / 101.38
Duplicated reads (estimated)	3,089,915 / 8.06%
Duplication rate	6.85%
Clipped reads	9,344,814 / 24.37%

2.2. ACGT Content

Number/percentage of A's	964,763,185 / 28.44%
Number/percentage of C's	692,358,037 / 20.41%
Number/percentage of T's	968,981,289 / 28.56%
Number/percentage of G's	766,062,685 / 22.58%
Number/percentage of N's	233,214 / 0.01%

GC Percentage	42.99%
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2.3. Coverage

Mean	1.0967
Standard Deviation	4.8335

2.4. Mapping Quality

Mean Mapping Quality	53.46
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2.5. Insert size

Mean	82,468.94
Standard Deviation	2,845,716.14
P25/Median/P75	133 / 170 / 224

2.6. Mismatches and indels

General error rate	0.95%
Mismatches	31,421,140
Insertions	532,221
Mapped reads with at least one insertion	1.46%
Deletions	1,846,434
Mapped reads with at least one deletion	5.01%
Homopolymer indels	53.05%

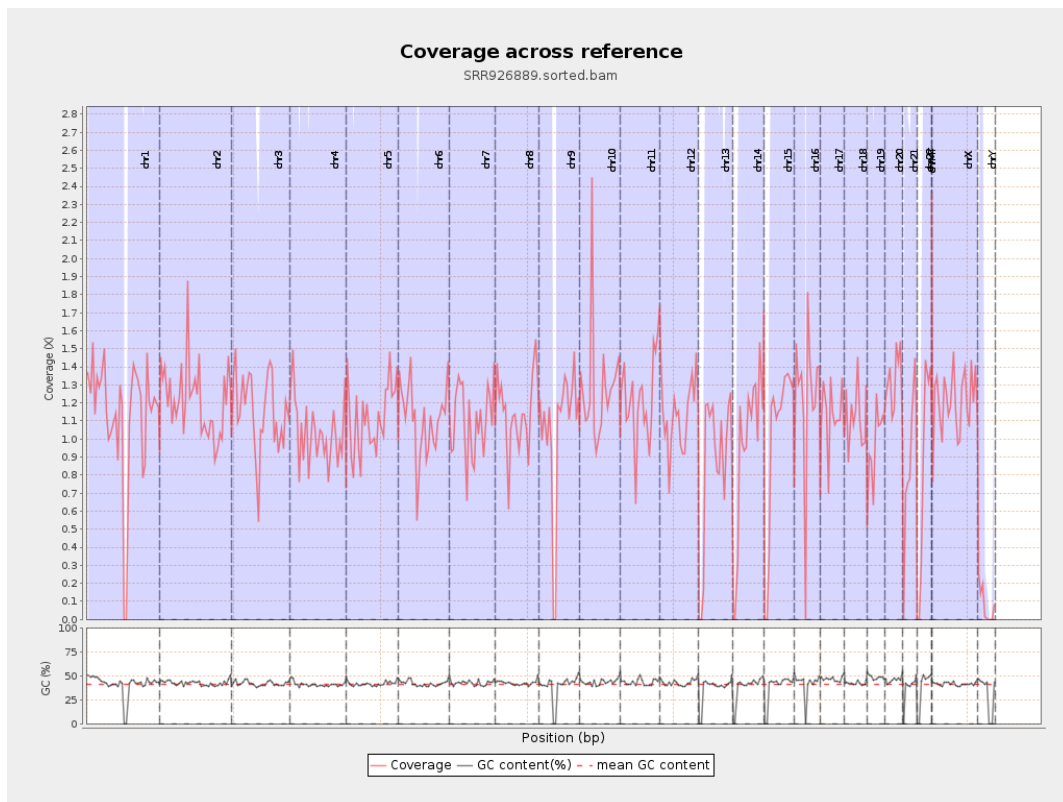
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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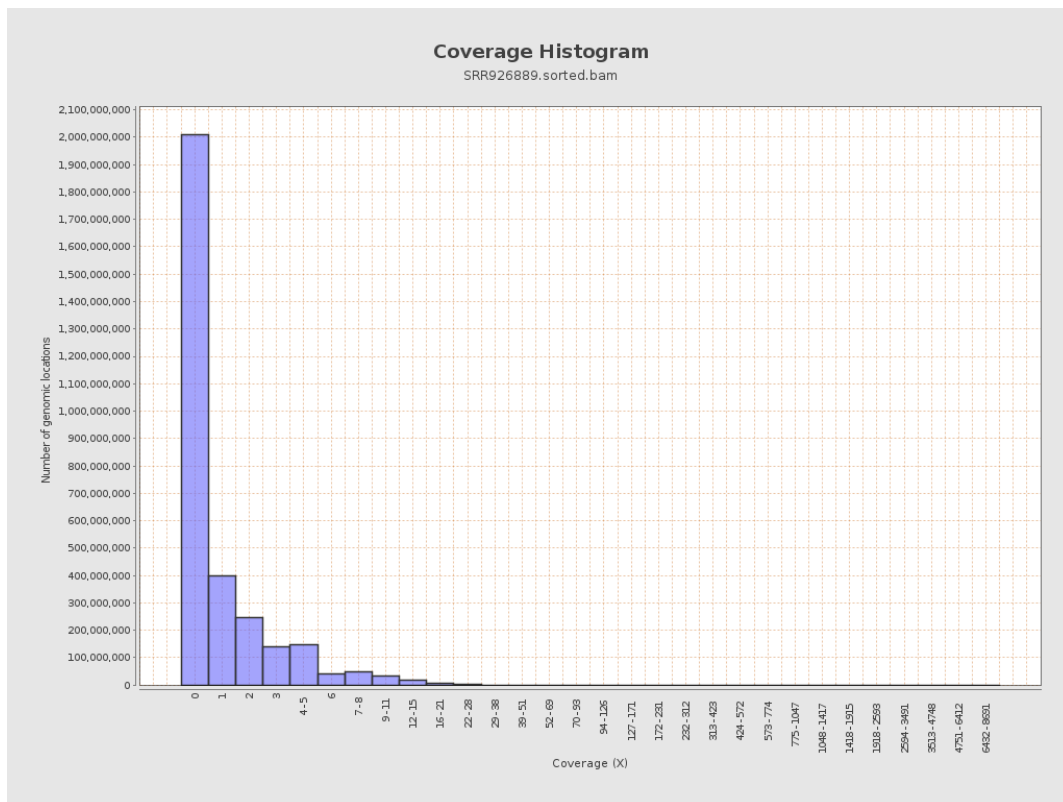
		bases	coverage	deviation
chr1	249250621	282621790	1.1339	3.9677
chr2	243199373	295571076	1.2153	6.0728
chr3	198022430	228789376	1.1554	2.5313
chr4	191154276	197980223	1.0357	2.439
chr5	180915260	202862838	1.1213	2.3309
chr6	171115067	190635536	1.1141	2.9187
chr7	159138663	175300704	1.1016	2.8851
chr8	146364022	167772956	1.1463	2.6272
chr9	141213431	148245704	1.0498	4.4844
chr10	135534747	174737701	1.2892	16.3313
chr11	135006516	163937319	1.2143	3.0941
chr12	133851895	151667664	1.1331	2.5544
chr13	115169878	99920677	0.8676	2.1345
chr14	107349540	102445615	0.9543	2.2764
chr15	102531392	102867647	1.0033	2.371
chr16	90354753	109968011	1.2171	6.6635
chr17	81195210	91938456	1.1323	2.8307
chr18	78077248	88315030	1.1311	4.7214
chr19	59128983	57656586	0.9751	2.8294
chr20	63025520	83331497	1.3222	2.8157
chr21	48129895	43028781	0.894	3.0985
chr22	51304566	44040855	0.8584	2.311
chrMT	16571	39110	2.3601	2.504
chrX	155270560	186602703	1.2018	2.611

chrY	59373566	4716376	0.0794	1.6953
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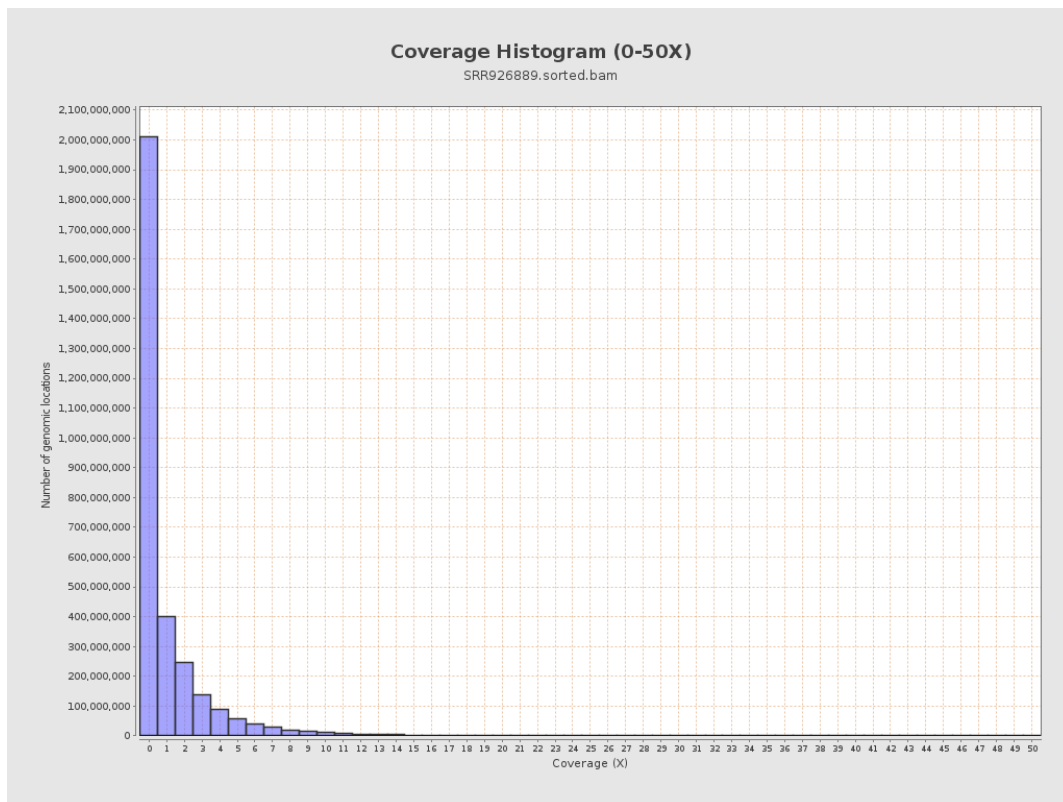
3. Results : Coverage across reference



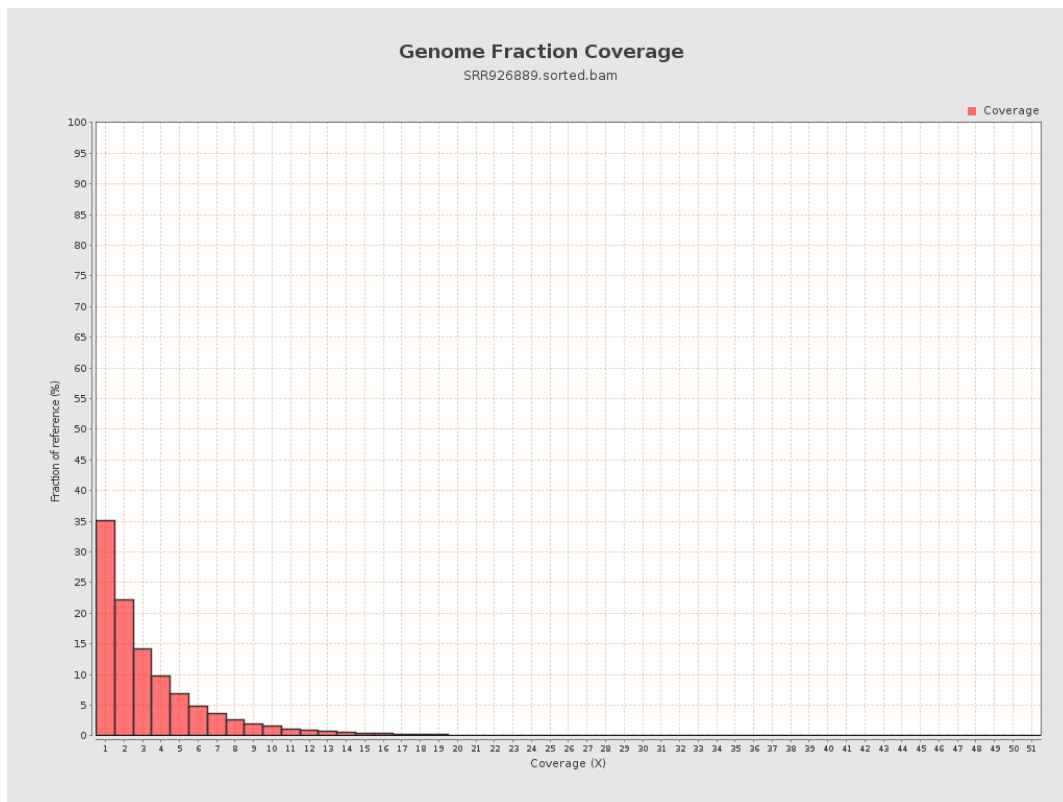
4. Results : Coverage Histogram



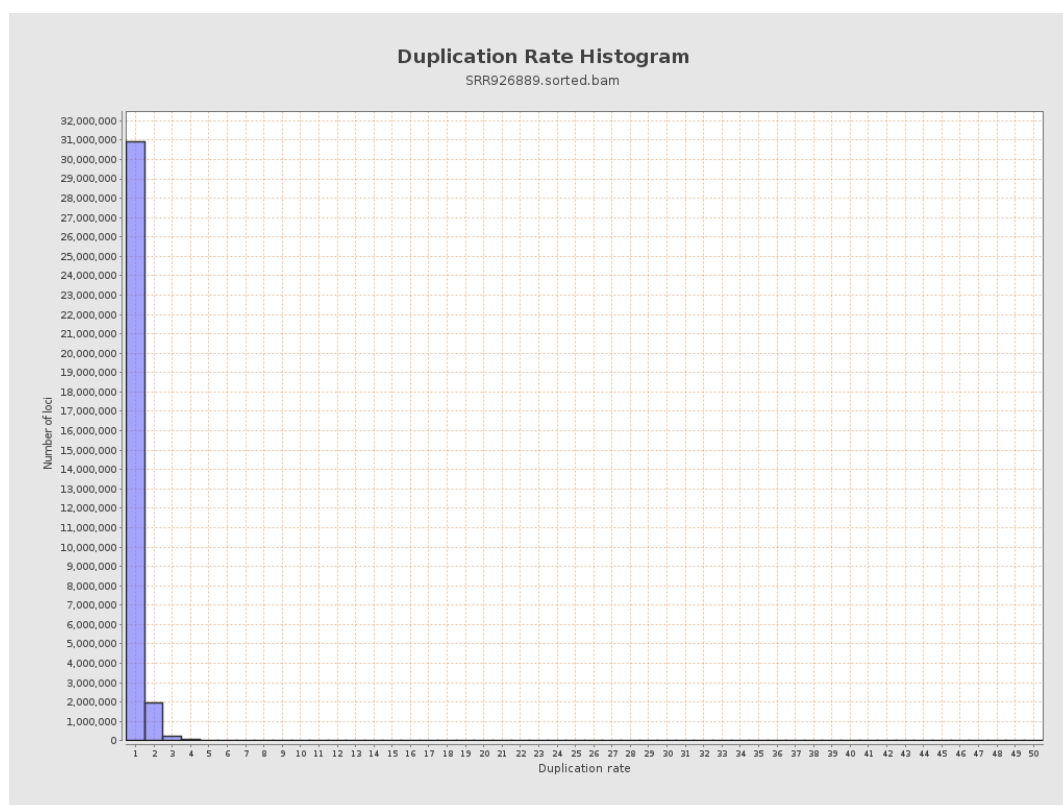
5. Results : Coverage Histogram (0-50X)



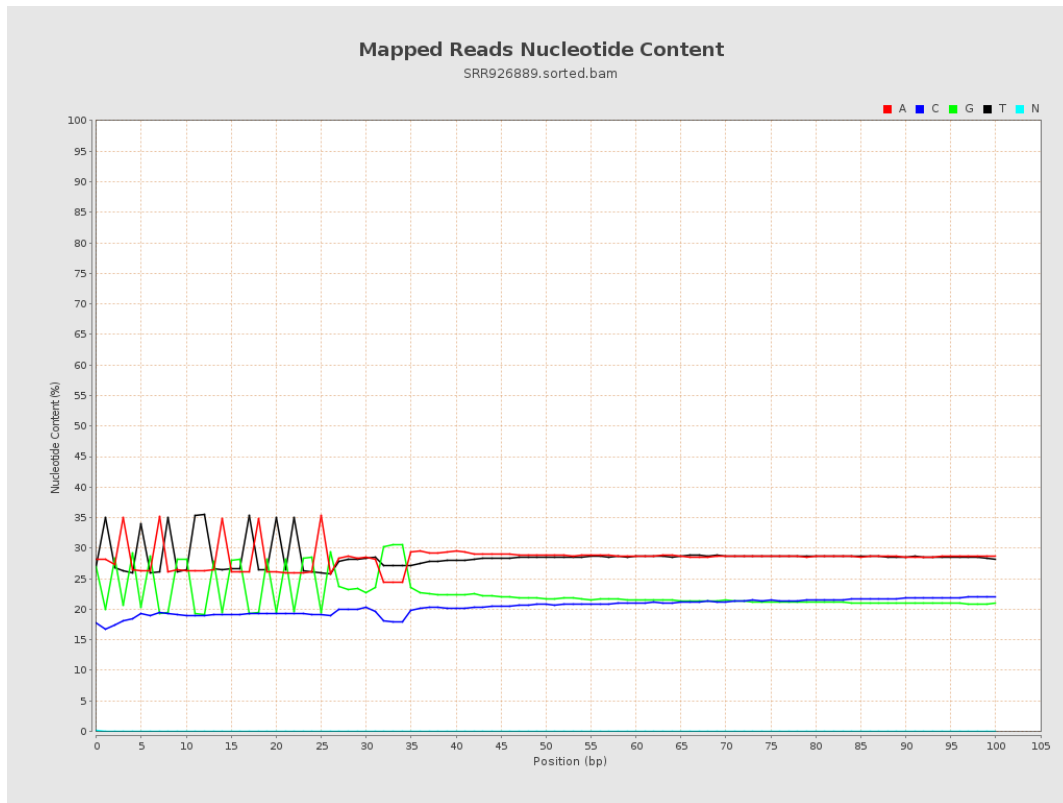
6. Results : Genome Fraction Coverage



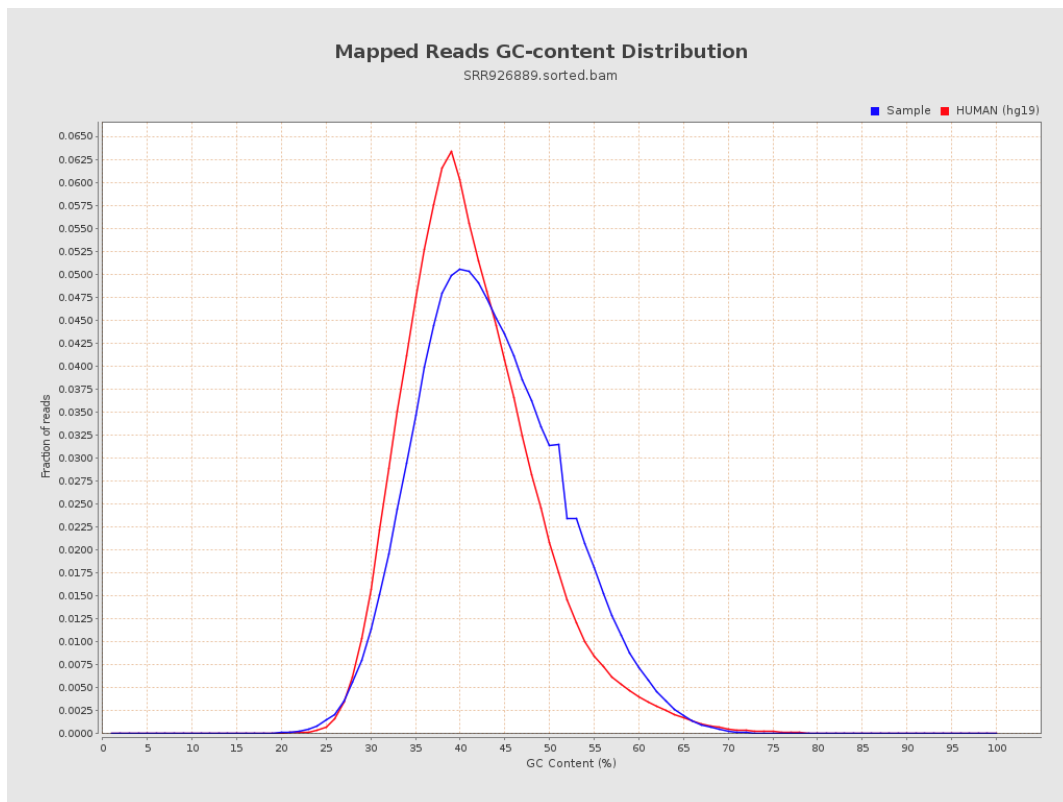
7. Results : Duplication Rate Histogram



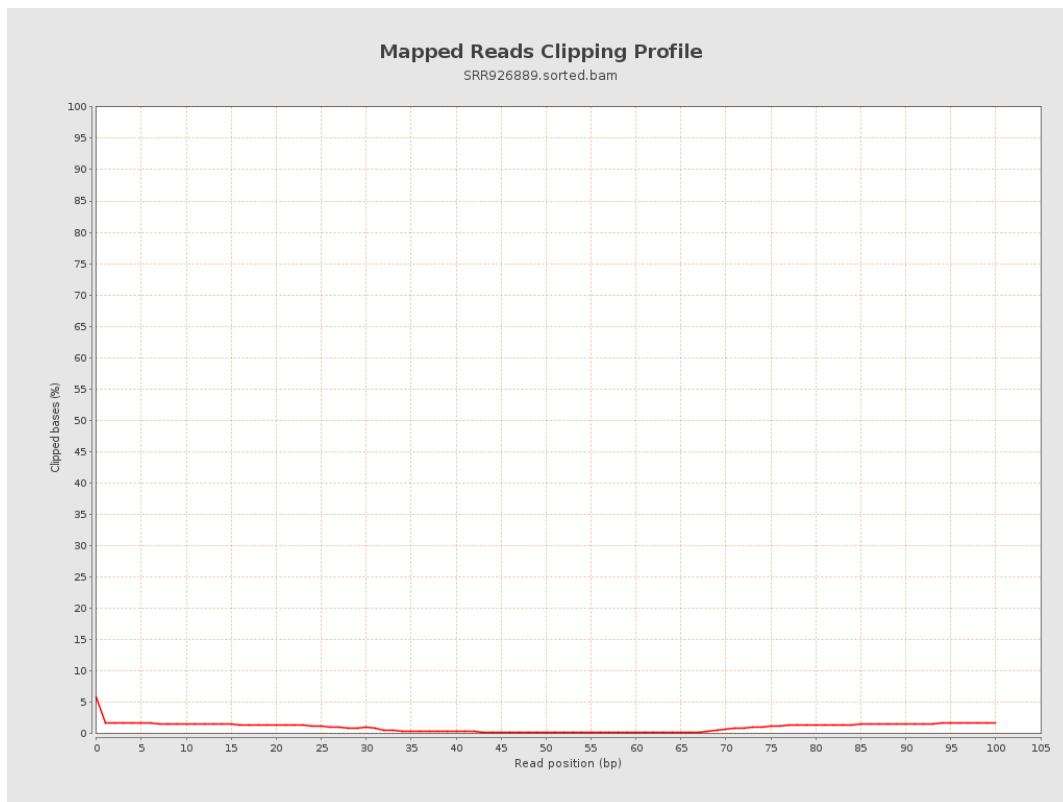
8. Results : Mapped Reads Nucleotide Content



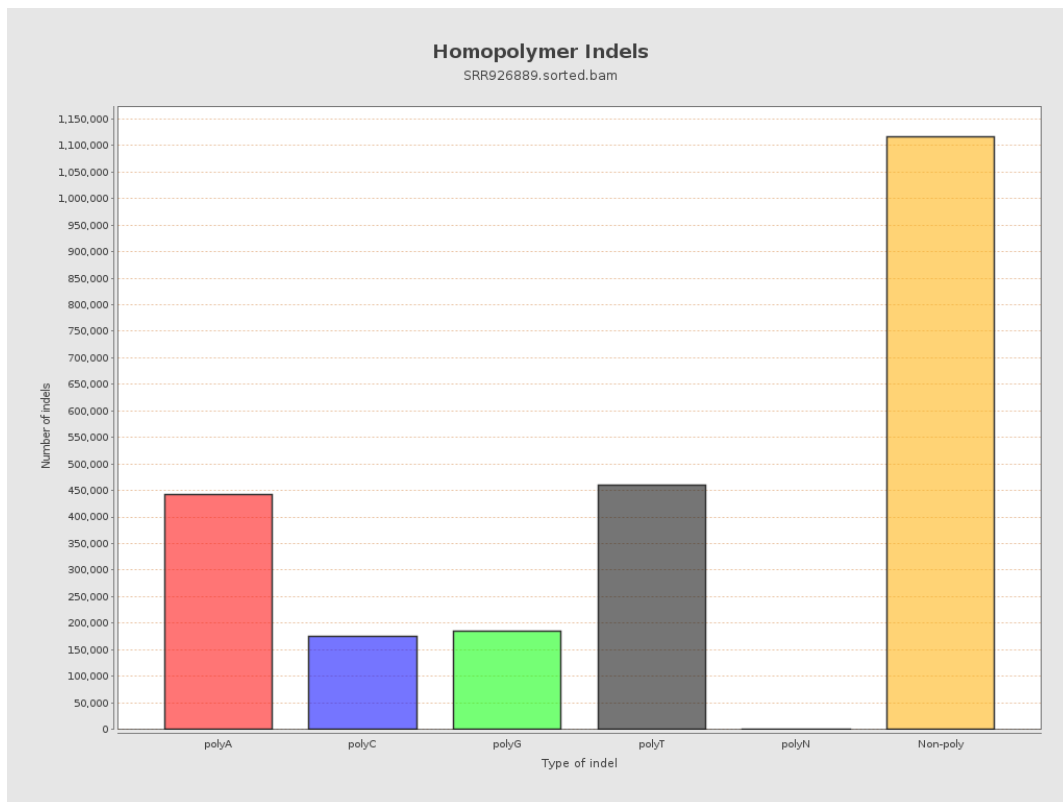
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



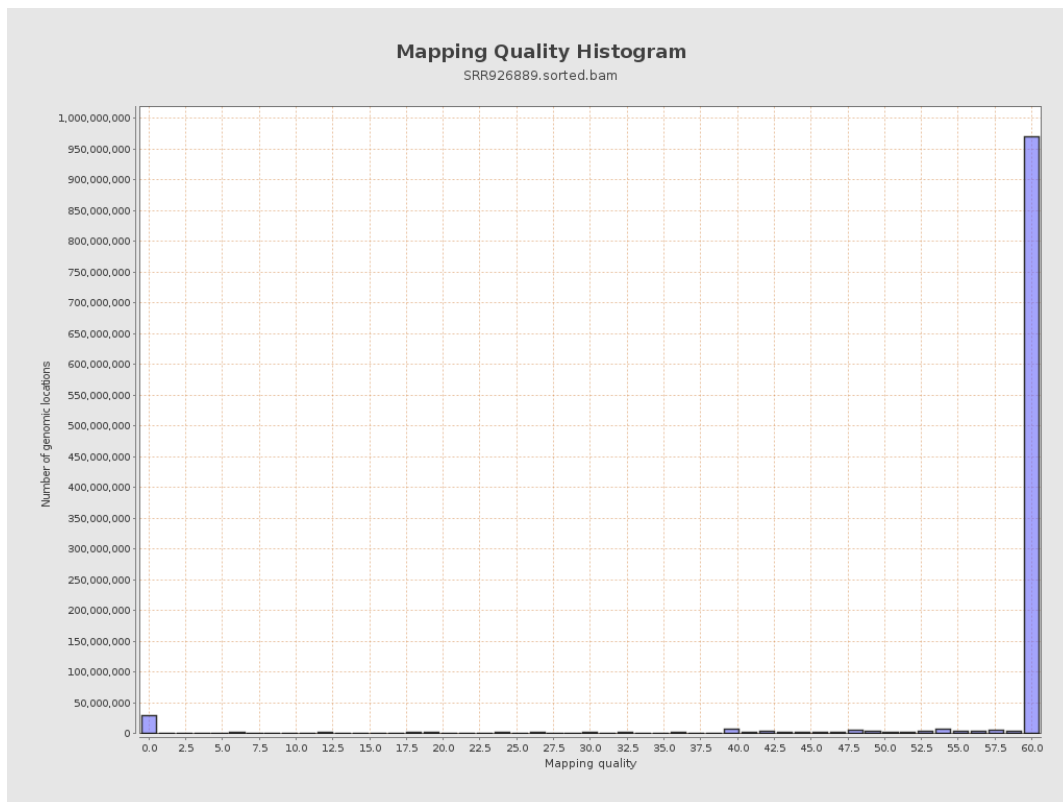
11. Results : Homopolymer Indels



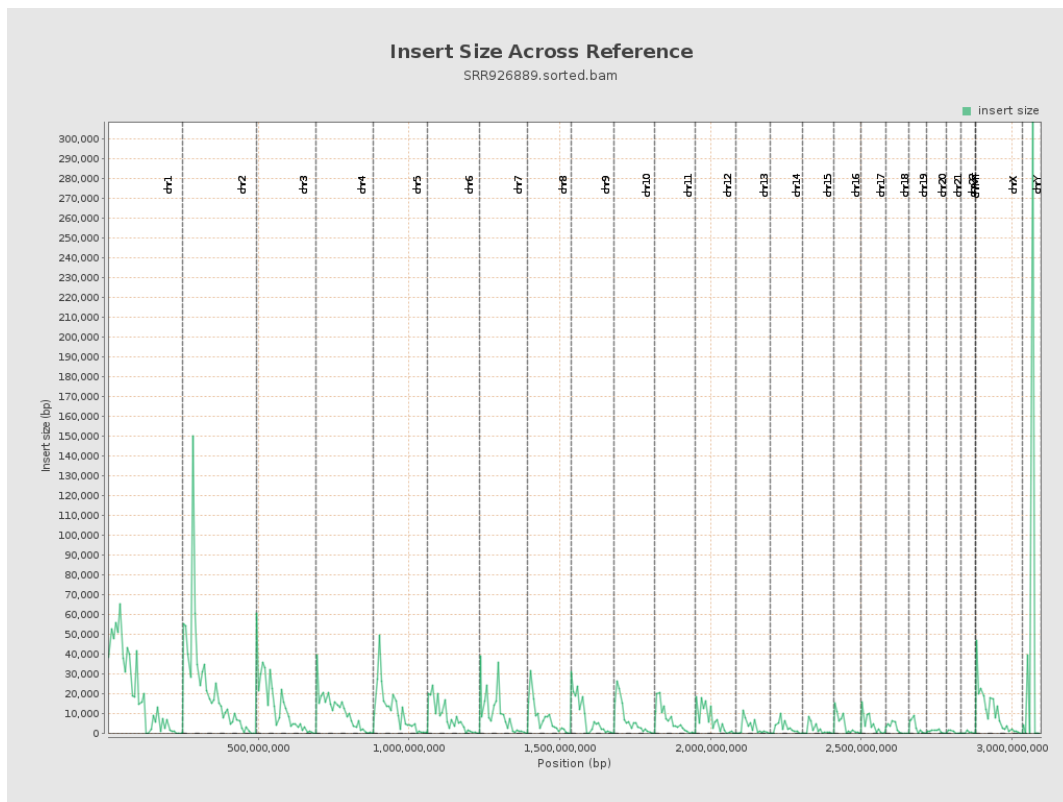
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

