

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/22 02:56:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926892.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_SRR926892 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926892_1.fastq.gz SRR926892_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 22 02:56:46 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926892.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	22,826,066
Mapped reads	22,371,459 / 98.01%
Unmapped reads	454,607 / 1.99%
Mapped paired reads	22,371,459 / 98.01%
Mapped reads, first in pair	11,240,896 / 49.25%
Mapped reads, second in pair	11,130,563 / 48.76%
Mapped reads, both in pair	22,208,310 / 97.29%
Mapped reads, singletons	163,149 / 0.71%
Secondary alignments	0
Supplementary alignments	50,243 / 0.22%
Read min/max/mean length	30 / 101 / 101.08
Duplicated reads (estimated)	1,365,139 / 5.98%
Duplication rate	5.21%
Clipped reads	3,971,075 / 17.4%

2.2. ACGT Content

Number/percentage of A's	605,825,649 / 28.12%
Number/percentage of C's	451,791,485 / 20.97%
Number/percentage of T's	605,619,554 / 28.11%
Number/percentage of G's	490,931,827 / 22.79%
Number/percentage of N's	214,458 / 0.01%

GC Percentage	43.76%
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2.3. Coverage

Mean	0.6964
Standard Deviation	2.2419

2.4. Mapping Quality

Mean Mapping Quality	54.15
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2.5. Insert size

Mean	30,977.32
Standard Deviation	1,725,725.28
P25/Median/P75	148 / 188 / 251

2.6. Mismatches and indels

General error rate	0.99%
Mismatches	20,907,406
Insertions	319,606
Mapped reads with at least one insertion	1.41%
Deletions	1,129,712
Mapped reads with at least one deletion	4.92%
Homopolymer indels	53.4%

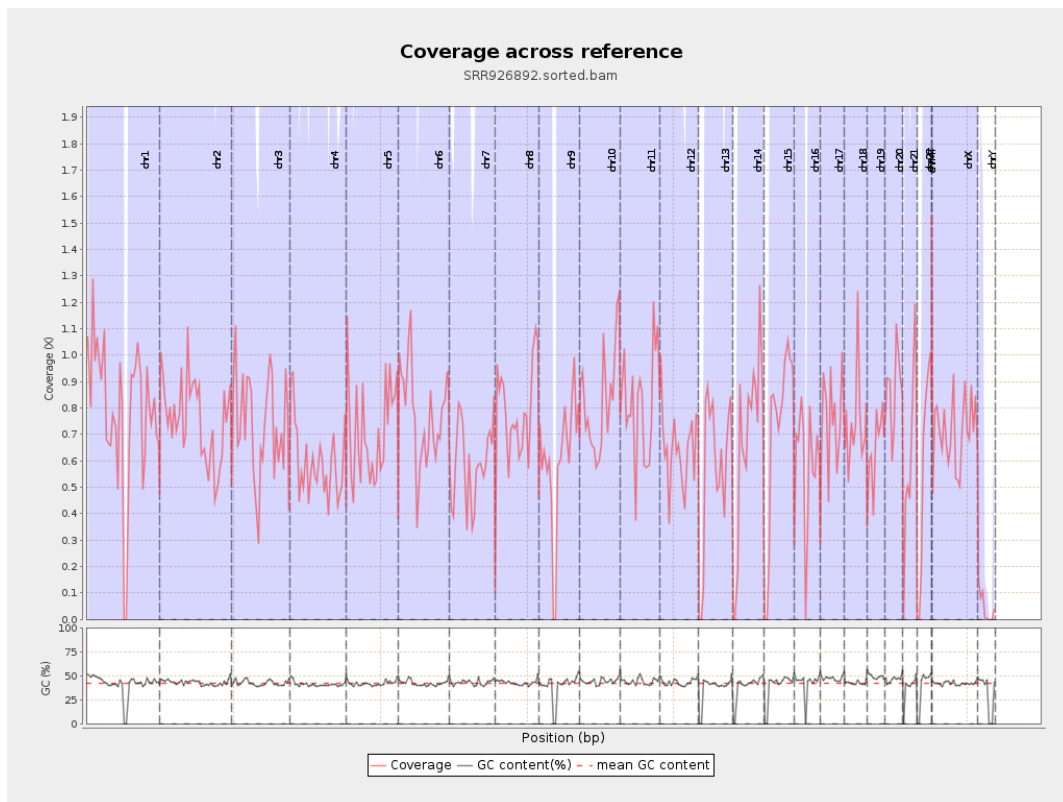
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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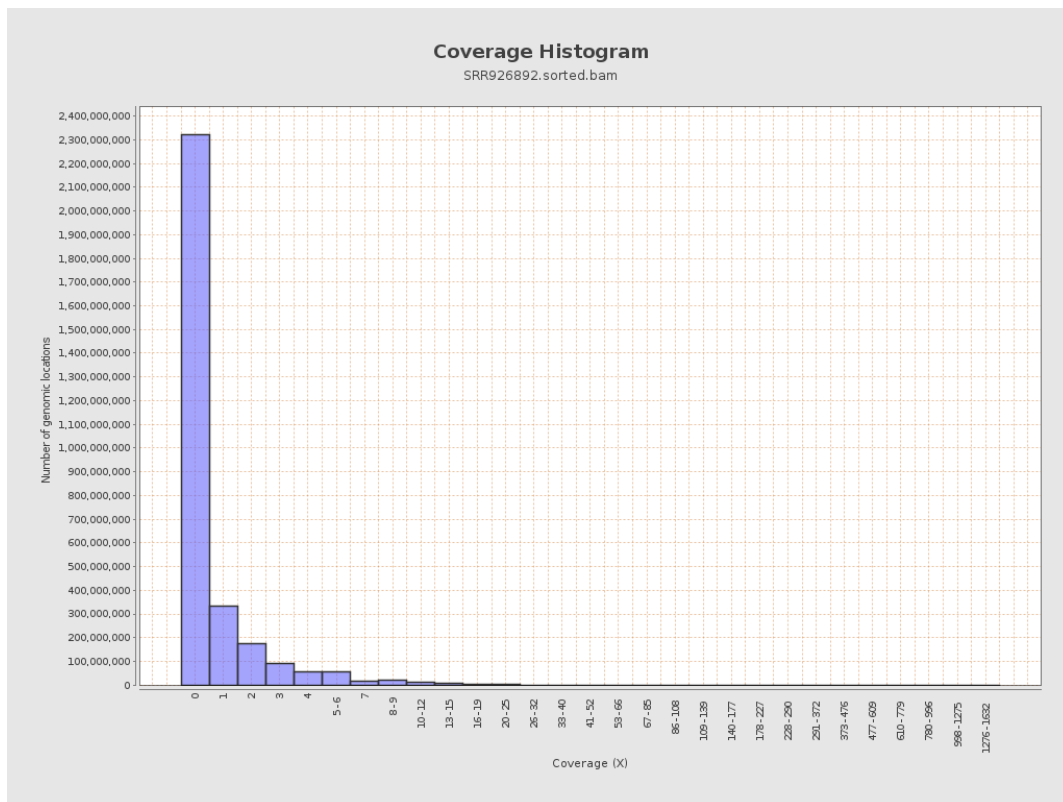
		bases	coverage	deviation
chr1	249250621	196353396	0.7878	2.5559
chr2	243199373	184079386	0.7569	3.2886
chr3	198022430	146606557	0.7404	1.9198
chr4	191154276	113552062	0.594	1.6841
chr5	180915260	128978470	0.7129	1.8806
chr6	171115067	132817507	0.7762	1.9821
chr7	159138663	93974783	0.5905	1.9002
chr8	146364022	116923355	0.7989	2.0965
chr9	141213431	85553727	0.6058	2.7353
chr10	135534747	111882927	0.8255	2.3128
chr11	135006516	110015817	0.8149	2.2127
chr12	133851895	86426305	0.6457	1.8925
chr13	115169878	65956334	0.5727	1.6655
chr14	107349540	71355537	0.6647	1.9207
chr15	102531392	72601573	0.7081	2.0123
chr16	90354753	51840427	0.5737	2.7688
chr17	81195210	61588180	0.7585	2.1571
chr18	78077248	58887375	0.7542	2.9524
chr19	59128983	38633997	0.6534	2.0777
chr20	63025520	55194519	0.8757	2.3246
chr21	48129895	30693110	0.6377	2.2297
chr22	51304566	29976353	0.5843	1.8882
chrMT	16571	25445	1.5355	2.2661
chrX	155270560	109428792	0.7048	1.928

chrY	59373566	2592961	0.0437	0.9451
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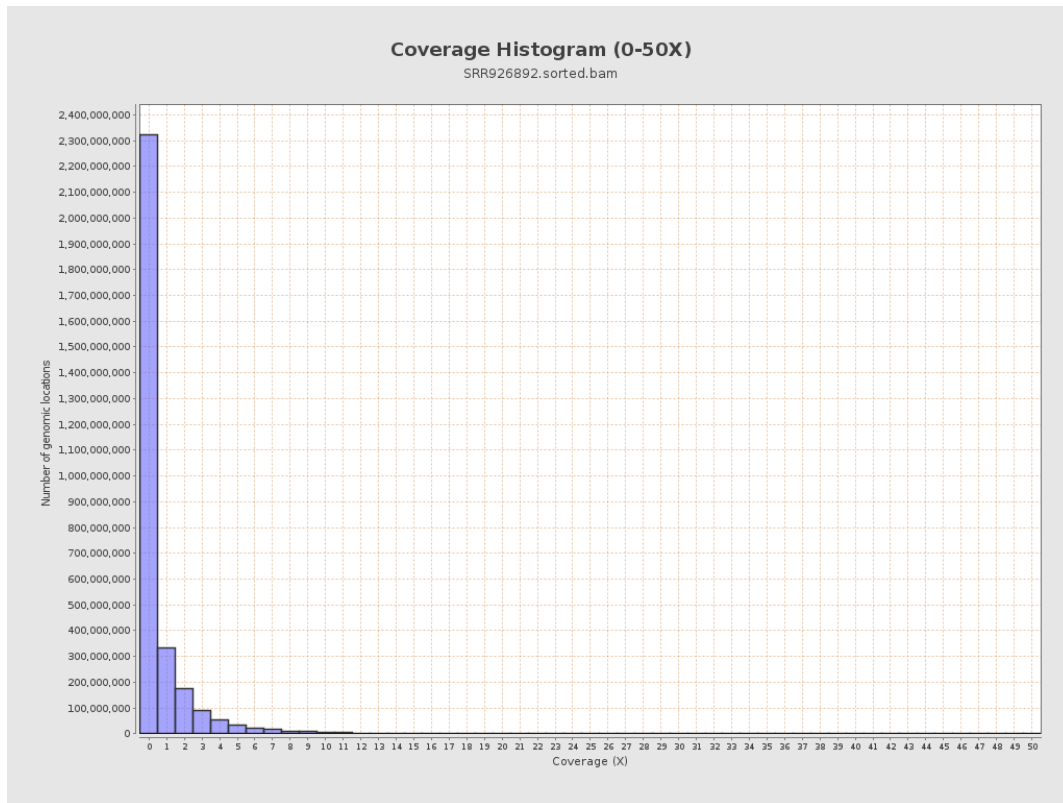
3. Results : Coverage across reference



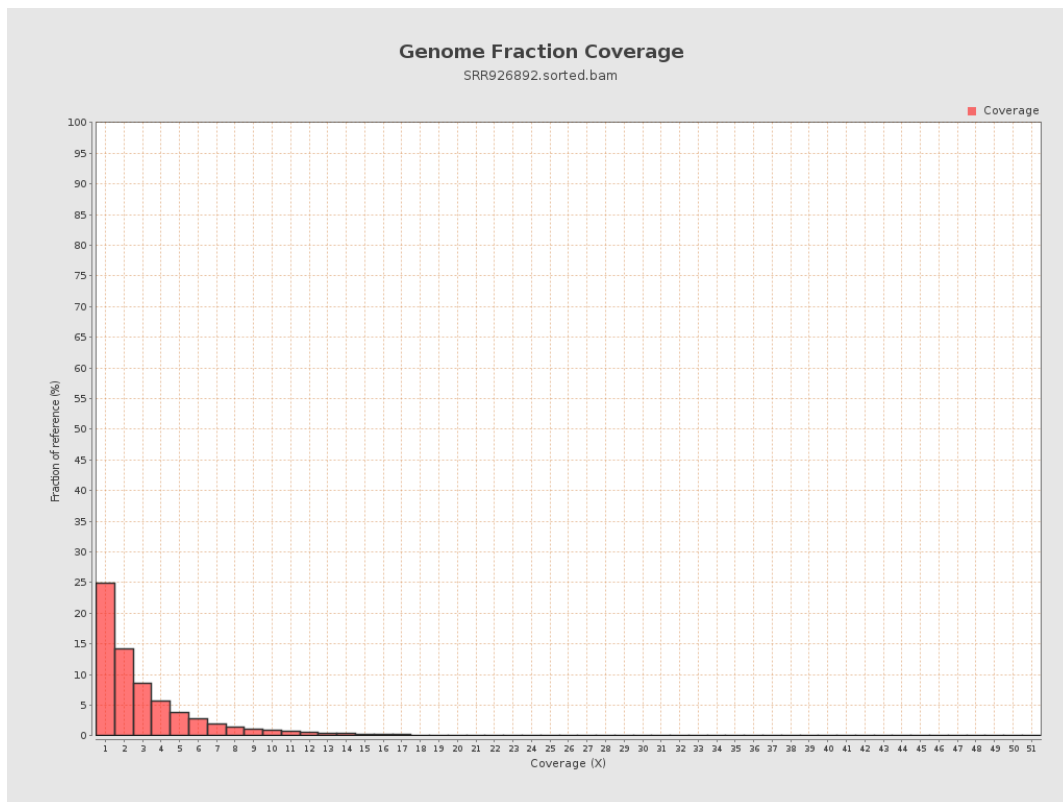
4. Results : Coverage Histogram



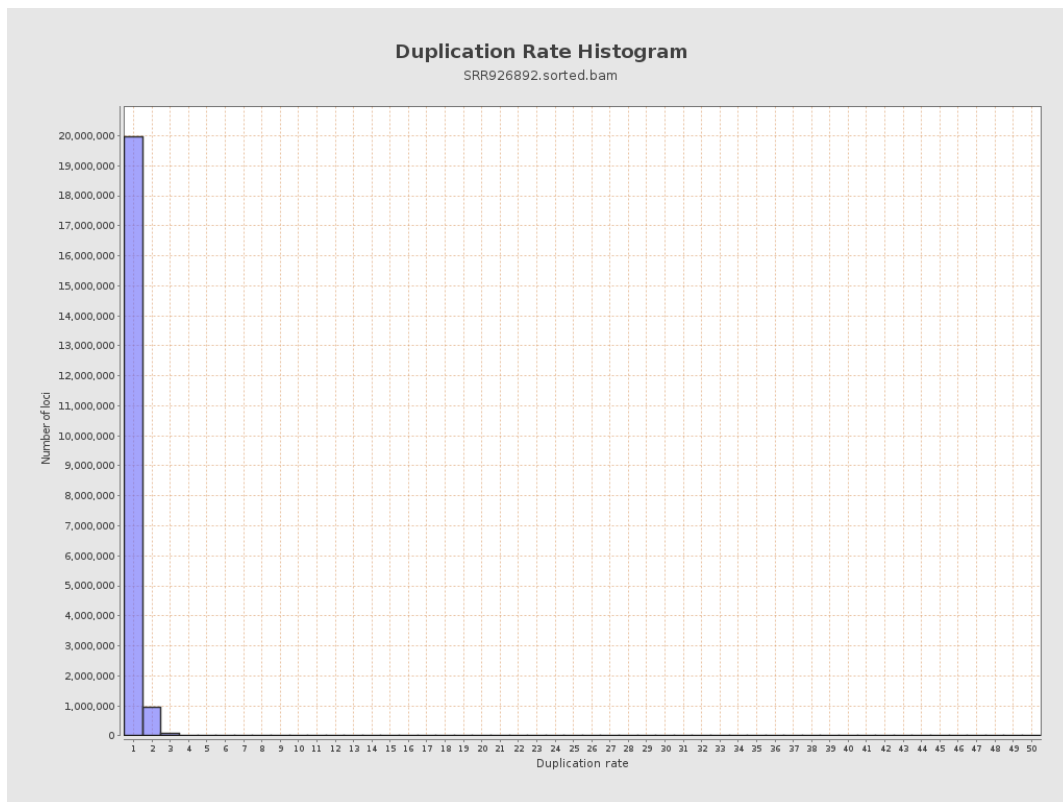
5. Results : Coverage Histogram (0-50X)



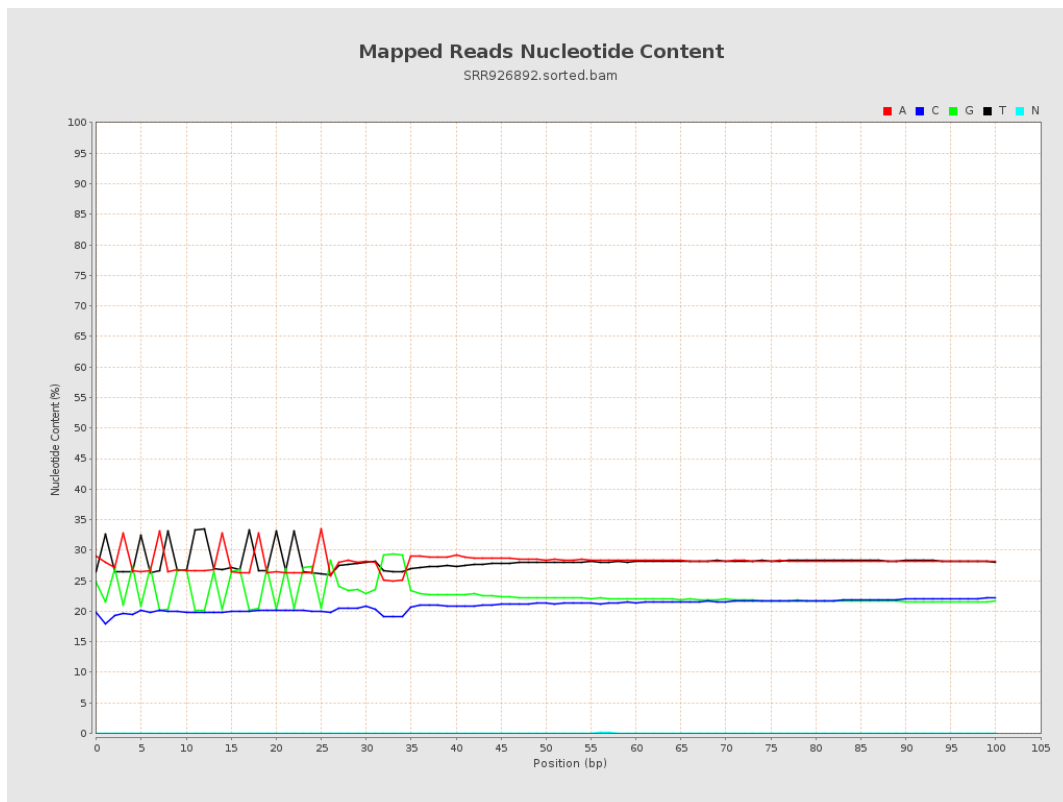
6. Results : Genome Fraction Coverage



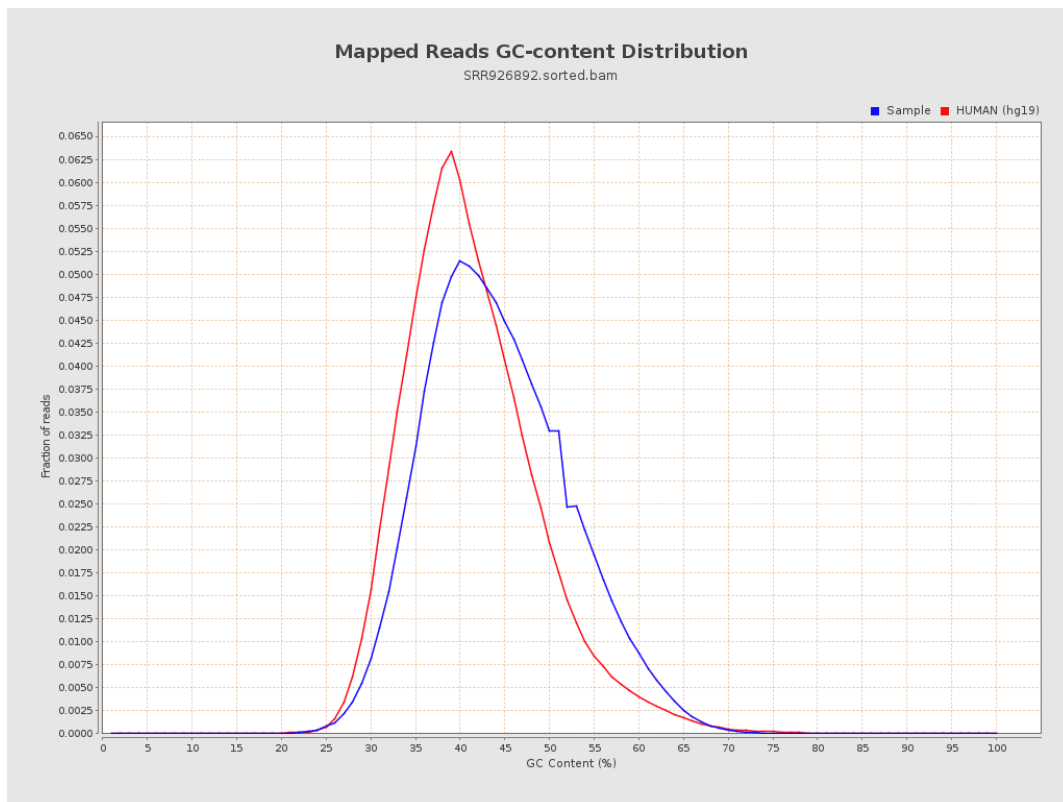
7. Results : Duplication Rate Histogram



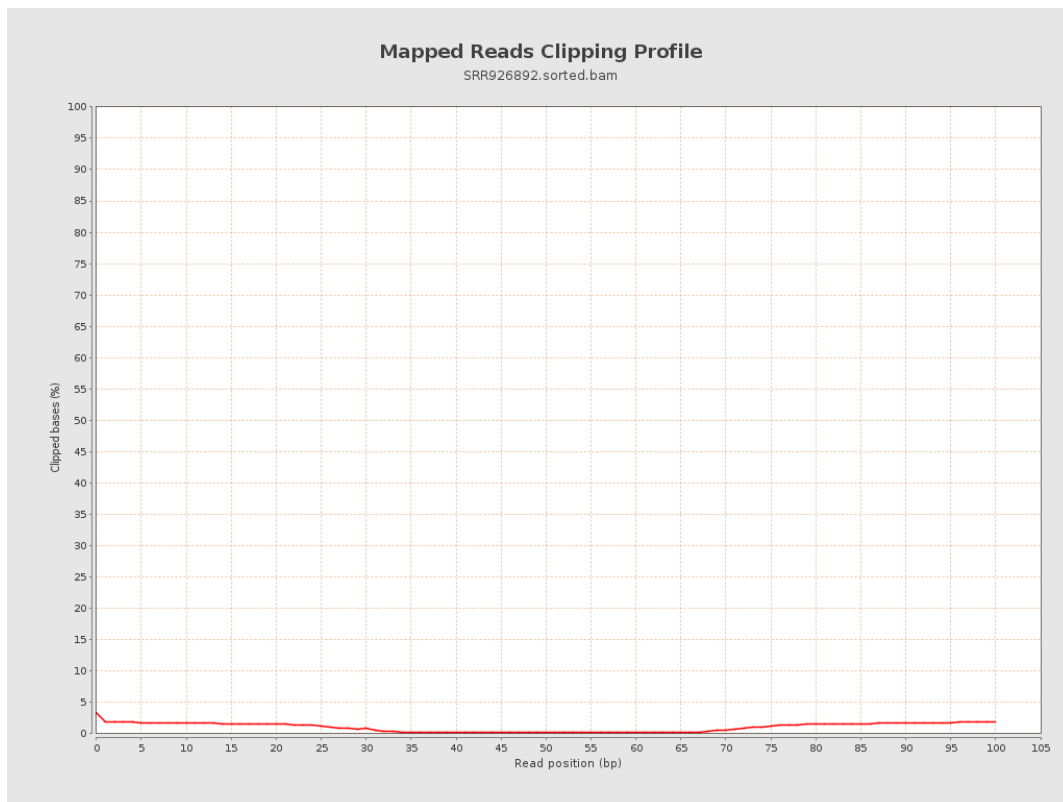
8. Results : Mapped Reads Nucleotide Content



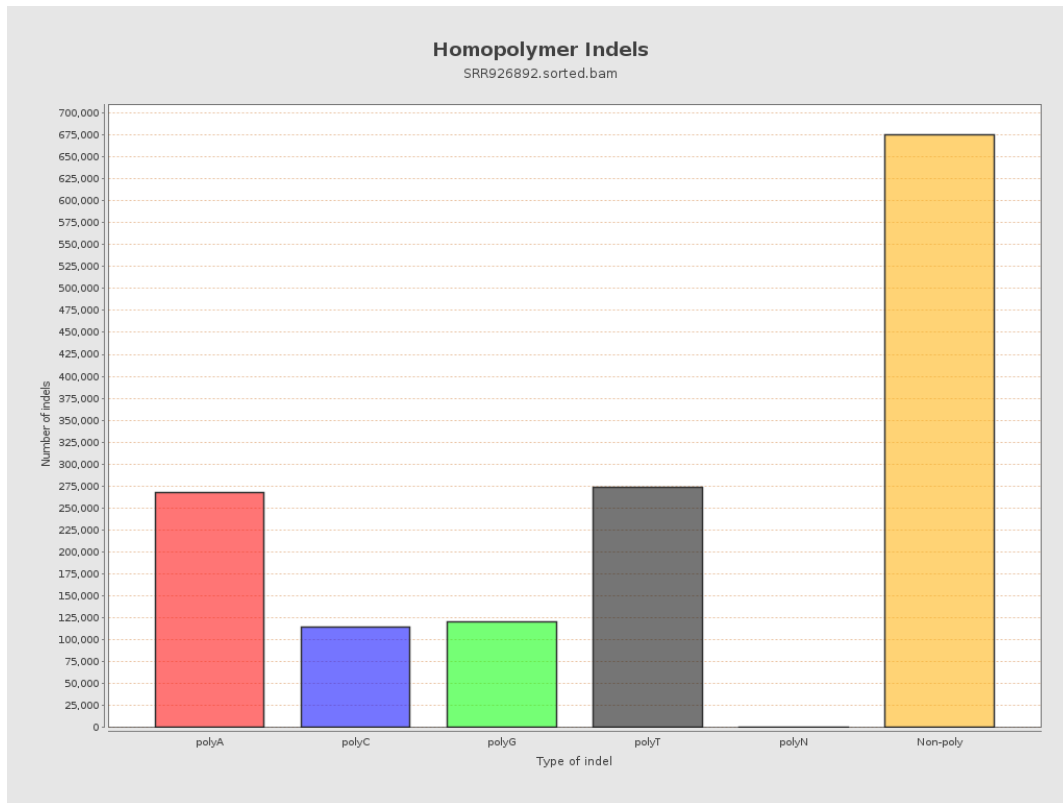
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



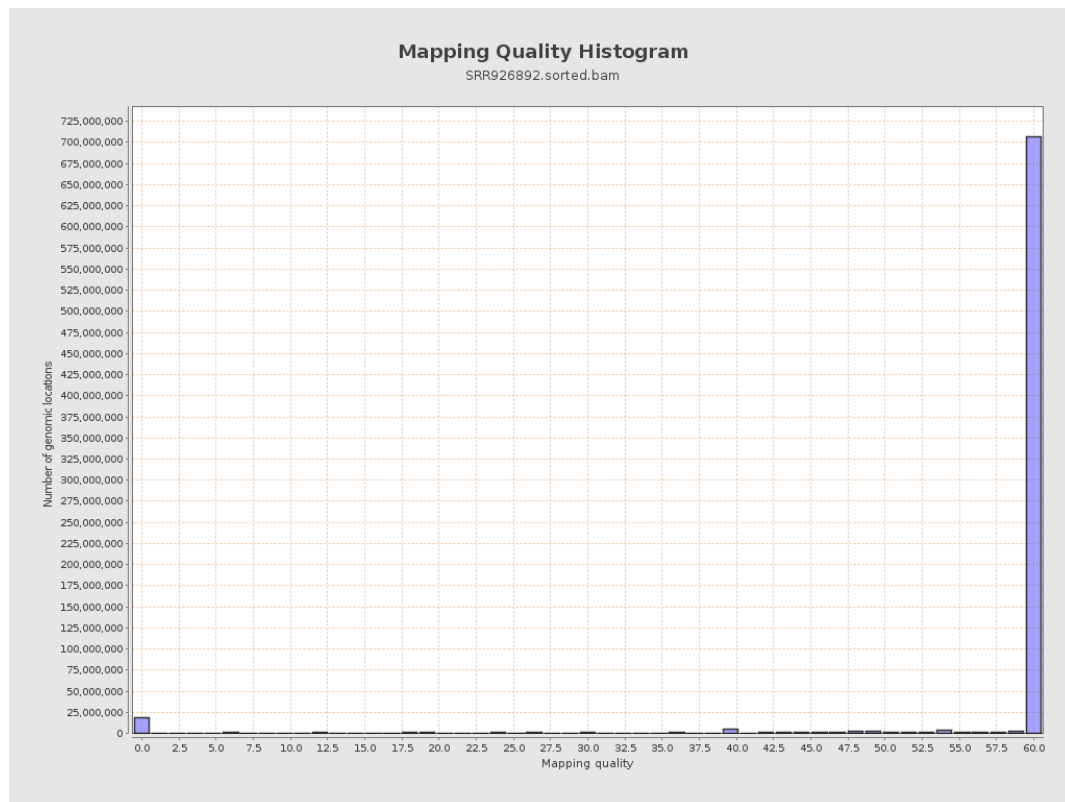
11. Results : Homopolymer Indels



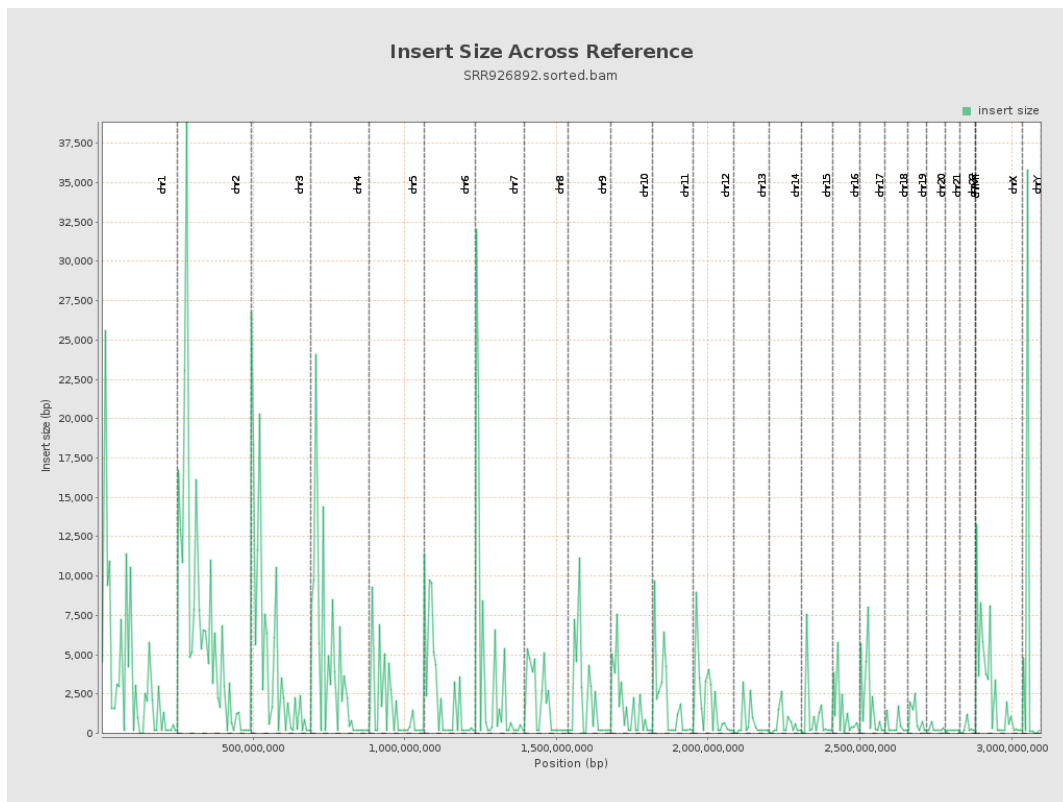
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

