

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/05 11:57:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR26104292.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_SRR26104292 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR26104292_1.fastq.gz SRR26104292_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Dec 05 11:57:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR26104292.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	522,209,866
Mapped reads	484,020,173 / 92.69%
Unmapped reads	38,189,693 / 7.31%
Mapped paired reads	484,020,173 / 92.69%
Mapped reads, first in pair	249,842,017 / 47.84%
Mapped reads, second in pair	234,178,156 / 44.84%
Mapped reads, both in pair	467,448,922 / 89.51%
Mapped reads, singletons	16,571,251 / 3.17%
Secondary alignments	0
Supplementary alignments	300,156 / 0.06%
Read min/max/mean length	30 / 97 / 91.02
Duplicated reads (estimated)	305,697,815 / 58.54%
Duplication rate	39.5%
Clipped reads	362,840,211 / 69.48%

2.2. ACGT Content

Number/percentage of A's	8,422,037,473 / 27.72%
Number/percentage of C's	7,020,133,233 / 23.1%
Number/percentage of T's	8,542,607,696 / 28.11%
Number/percentage of G's	6,393,275,200 / 21.04%
Number/percentage of N's	6,573,482 / 0.02%

GC Percentage	44.15%
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2.3. Coverage

Mean	9.8168
Standard Deviation	172.3024

2.4. Mapping Quality

Mean Mapping Quality	50.44
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2.5. Insert size

Mean	21,231.16
Standard Deviation	1,292,068.04
P25/Median/P75	45 / 57 / 90

2.6. Mismatches and indels

General error rate	0.52%
Mismatches	152,858,957
Insertions	2,219,067
Mapped reads with at least one insertion	0.45%
Deletions	2,460,790
Mapped reads with at least one deletion	0.5%
Homopolymer indels	40.16%

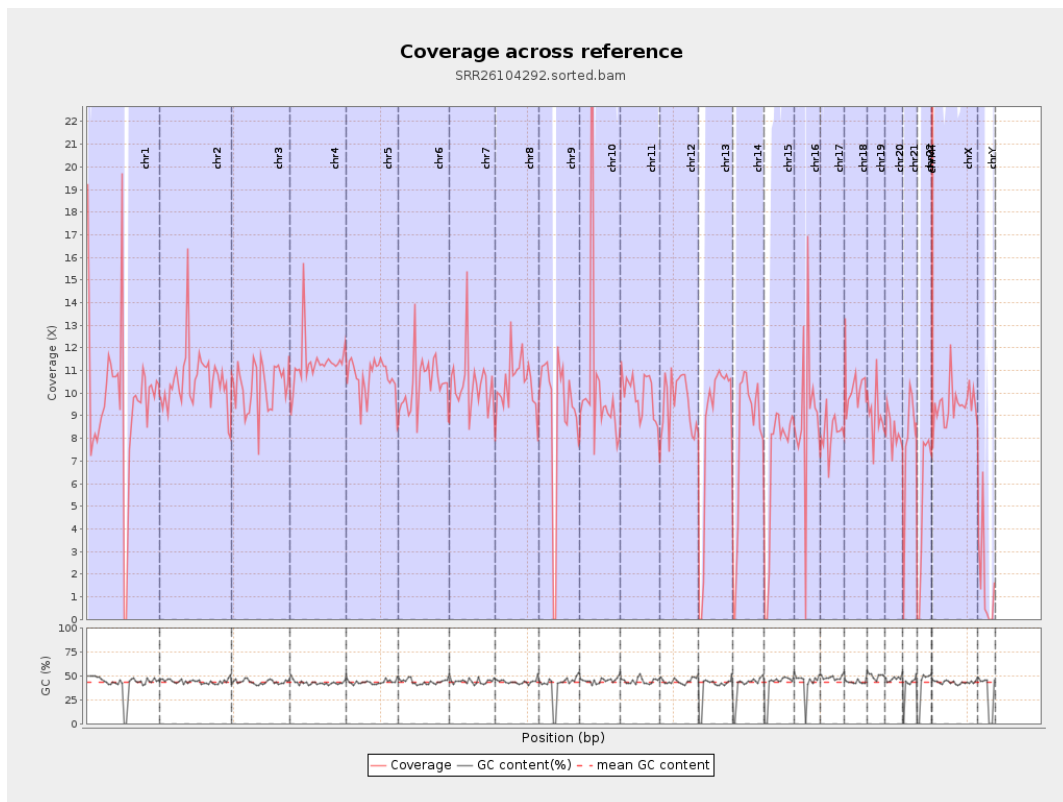
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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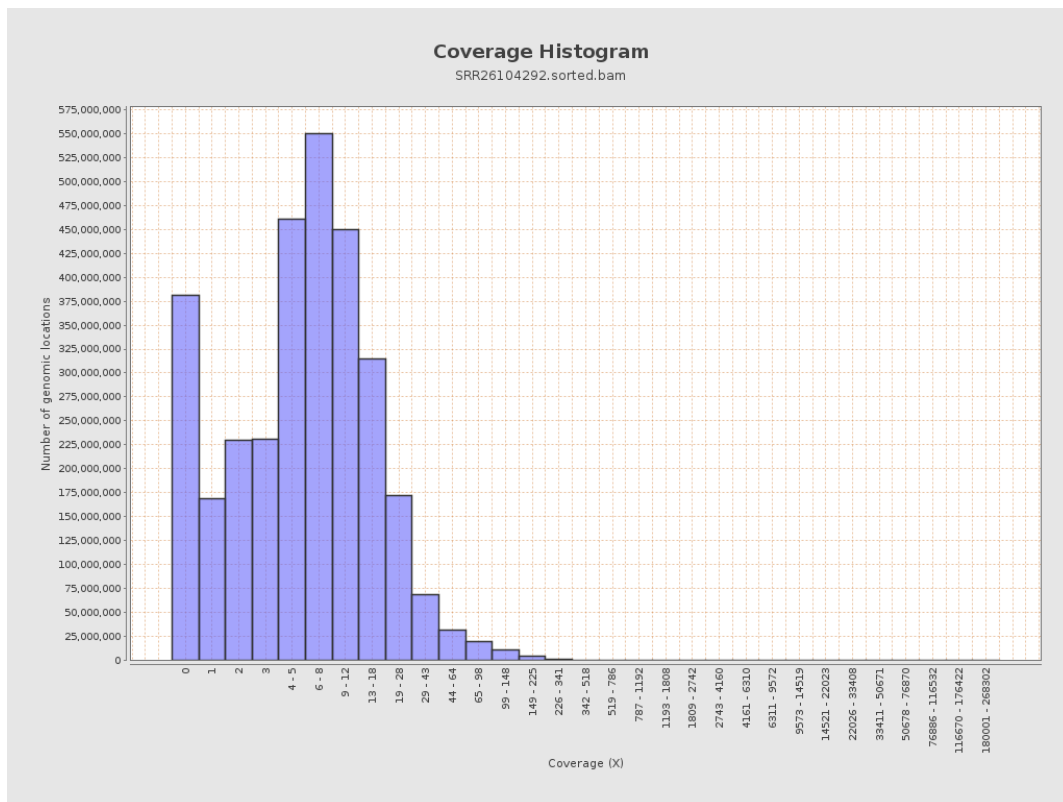
		bases	coverage	deviation
chr1	249250621	2404845330	9.6483	251.252
chr2	243199373	2568364153	10.5607	59.8349
chr3	198022430	2029308246	10.2479	31.0847
chr4	191154276	2160457049	11.3022	39.2866
chr5	180915260	1924691949	10.6386	45.6755
chr6	171115067	1789475372	10.4577	38.065
chr7	159138663	1648796322	10.3608	92.3249
chr8	146364022	1532645205	10.4715	51.6618
chr9	141213431	1269830689	8.9923	51.5606
chr10	135534747	1421833586	10.4905	161.1275
chr11	135006516	1338424532	9.9138	60.5685
chr12	133851895	1277385245	9.5433	25.3505
chr13	115169878	986183877	8.5629	35.8373
chr14	107349540	867207112	8.0783	25.4082
chr15	102531392	697453665	6.8023	14.3988
chr16	90354753	816295271	9.0343	63.5599
chr17	81195210	668193336	8.2295	34.6351
chr18	78077248	795780791	10.1922	87.256
chr19	59128983	533699432	9.026	151.3328
chr20	63025520	521167875	8.2692	19.7379
chr21	48129895	385909275	8.0181	34.6776
chr22	51304566	276785540	5.3949	68.6065
chrMT	16571	905058602	54,617.0178	30,327.9516
chrX	155270560	1473460197	9.4896	27.7531

chrY	59373566	96559139	1.6263	59.5872
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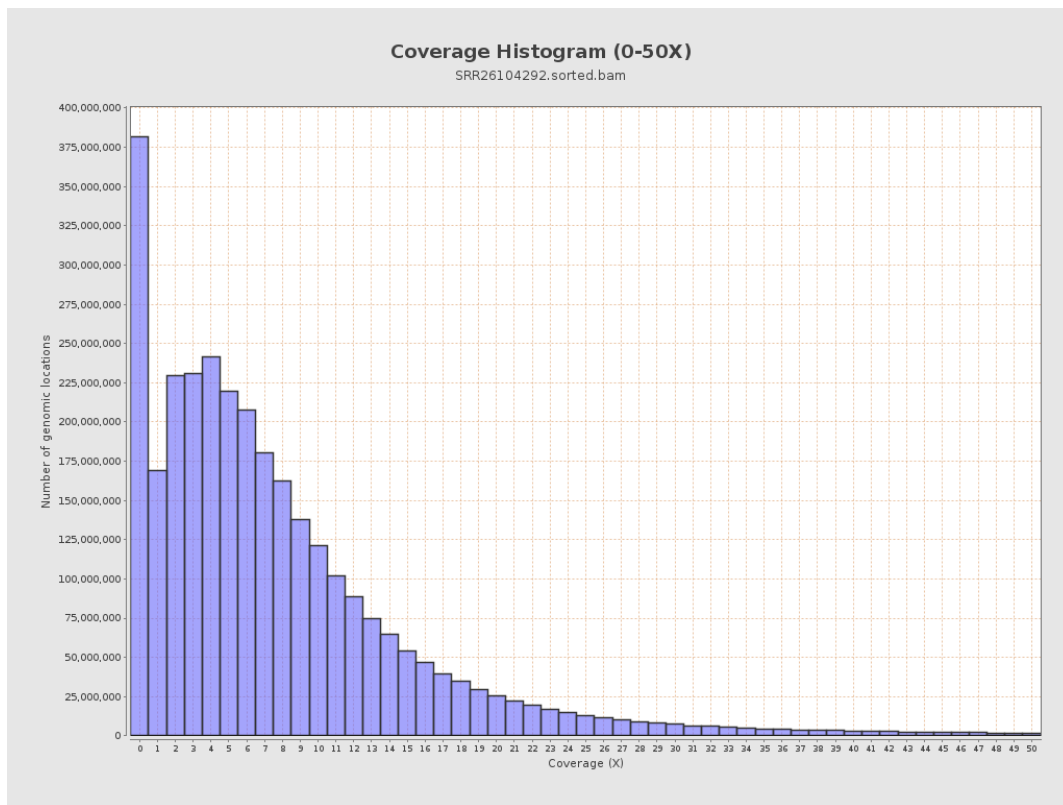
3. Results : Coverage across reference



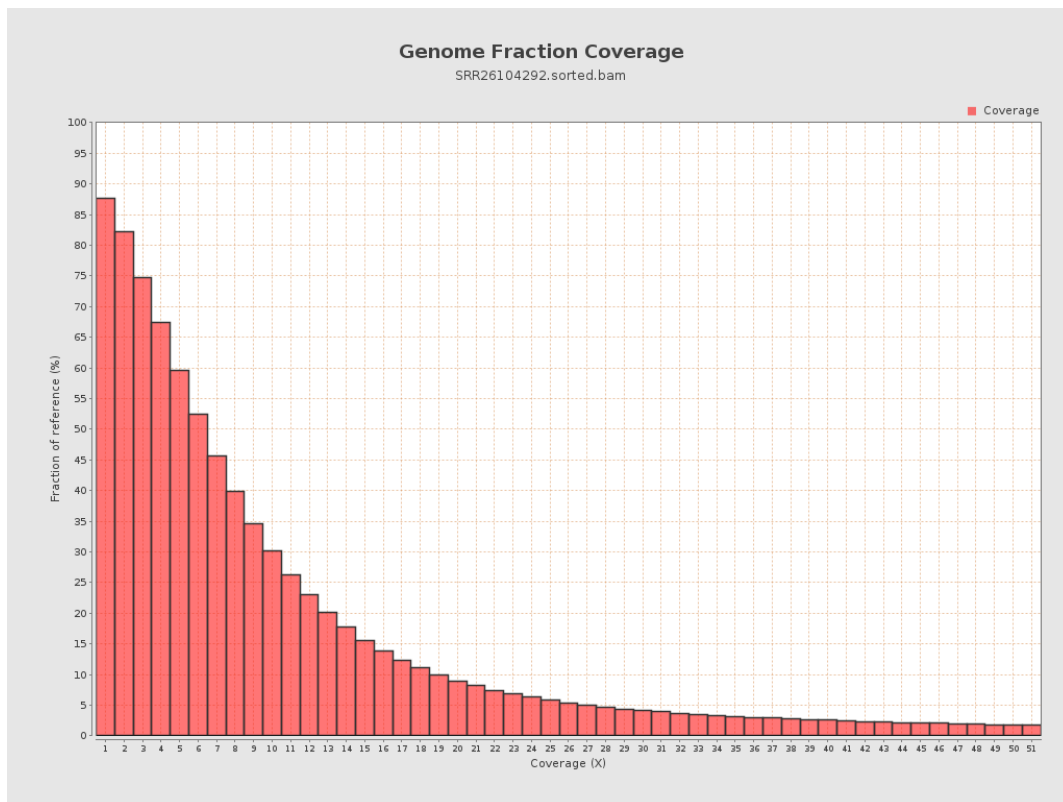
4. Results : Coverage Histogram



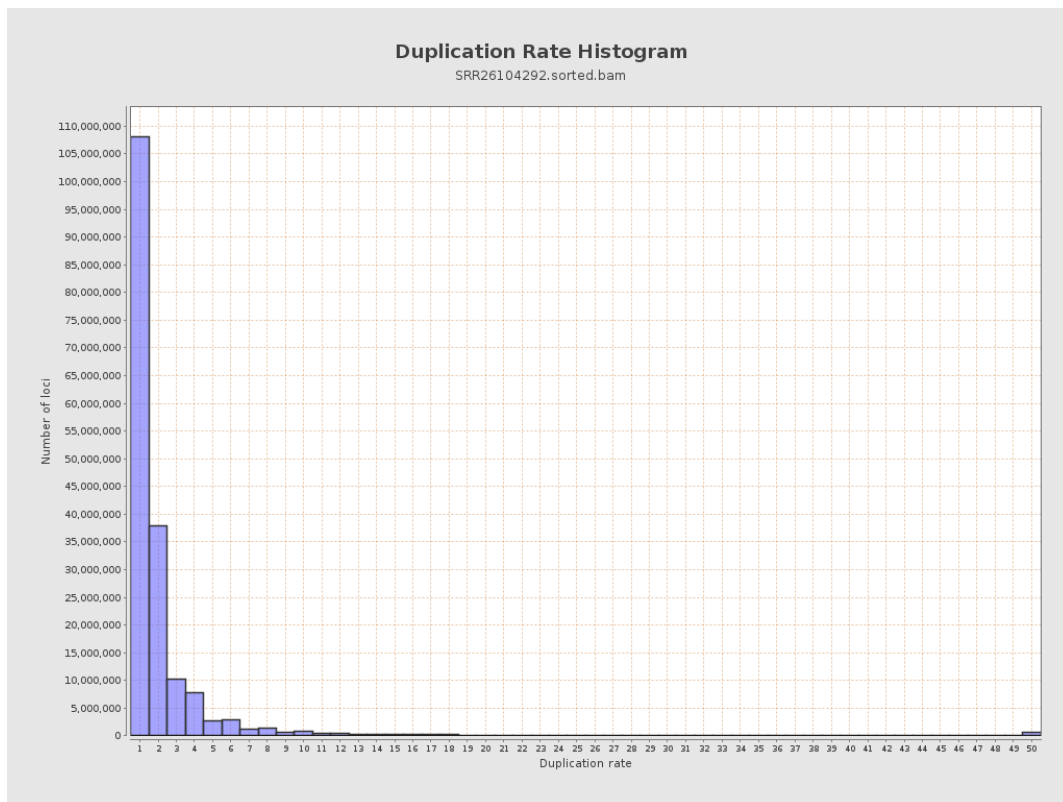
5. Results : Coverage Histogram (0-50X)



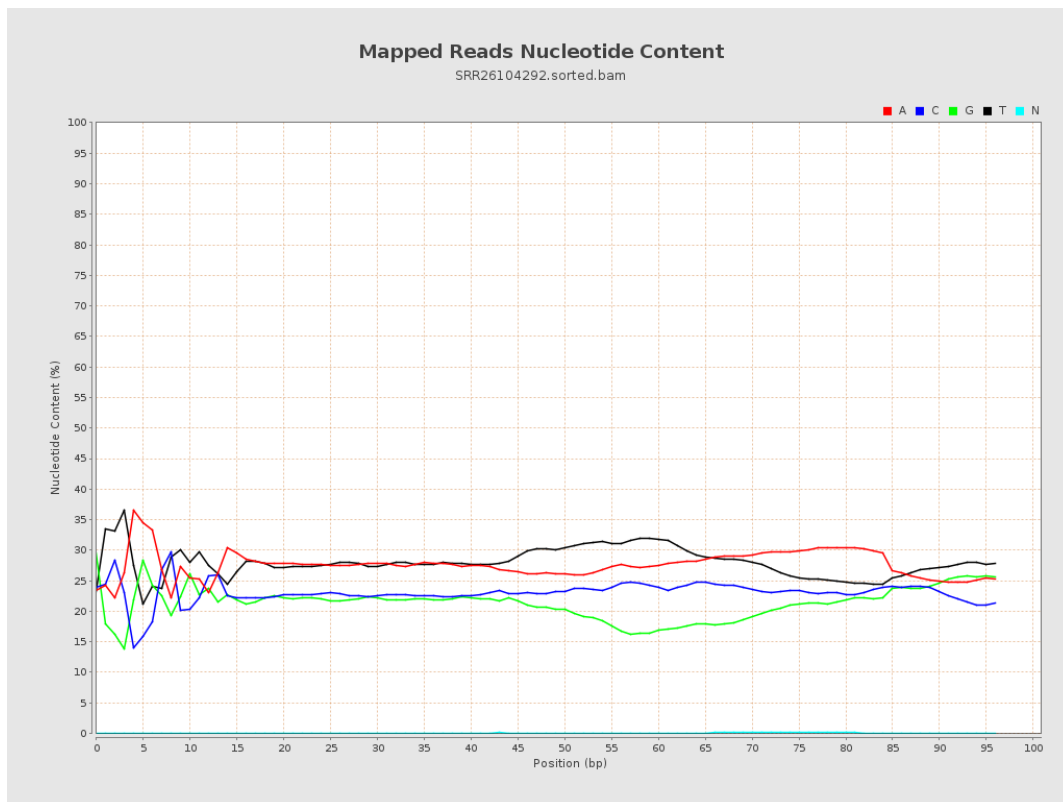
6. Results : Genome Fraction Coverage



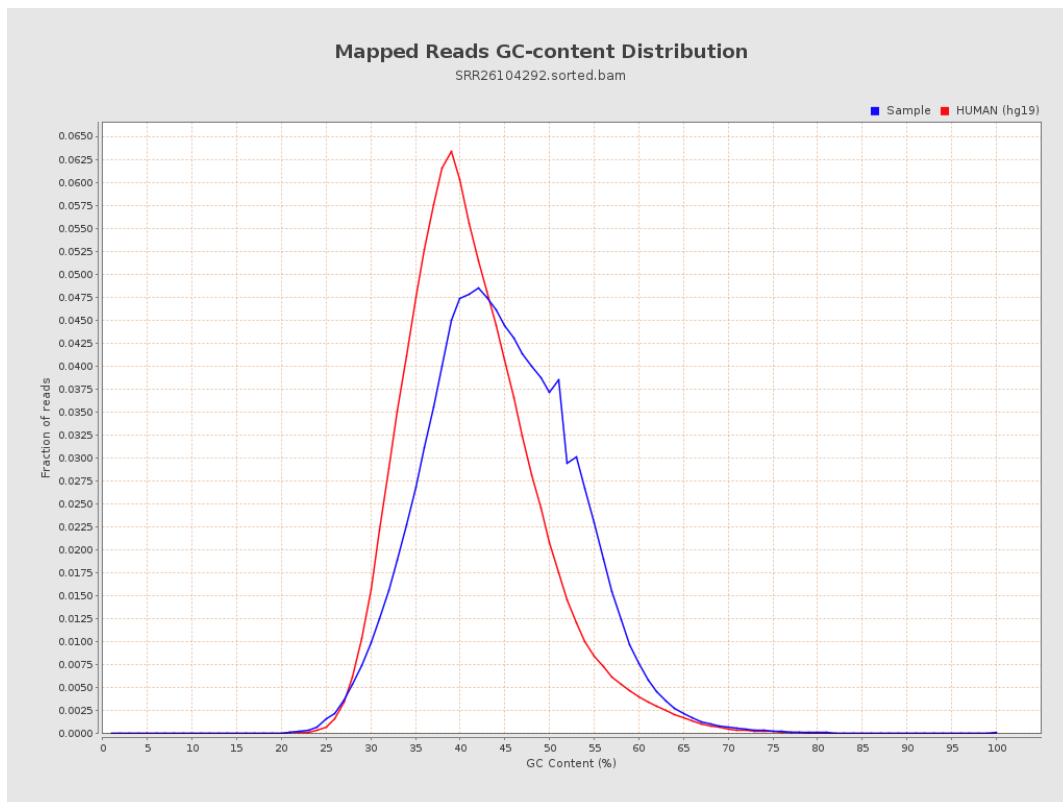
7. Results : Duplication Rate Histogram



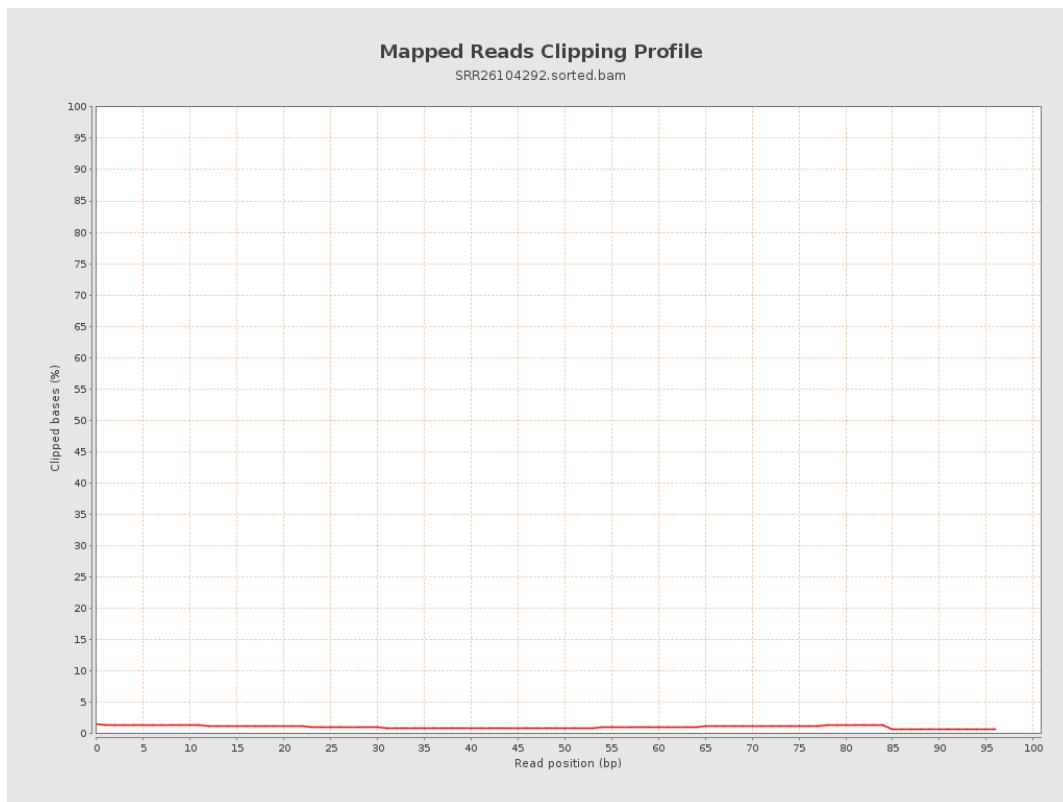
8. Results : Mapped Reads Nucleotide Content



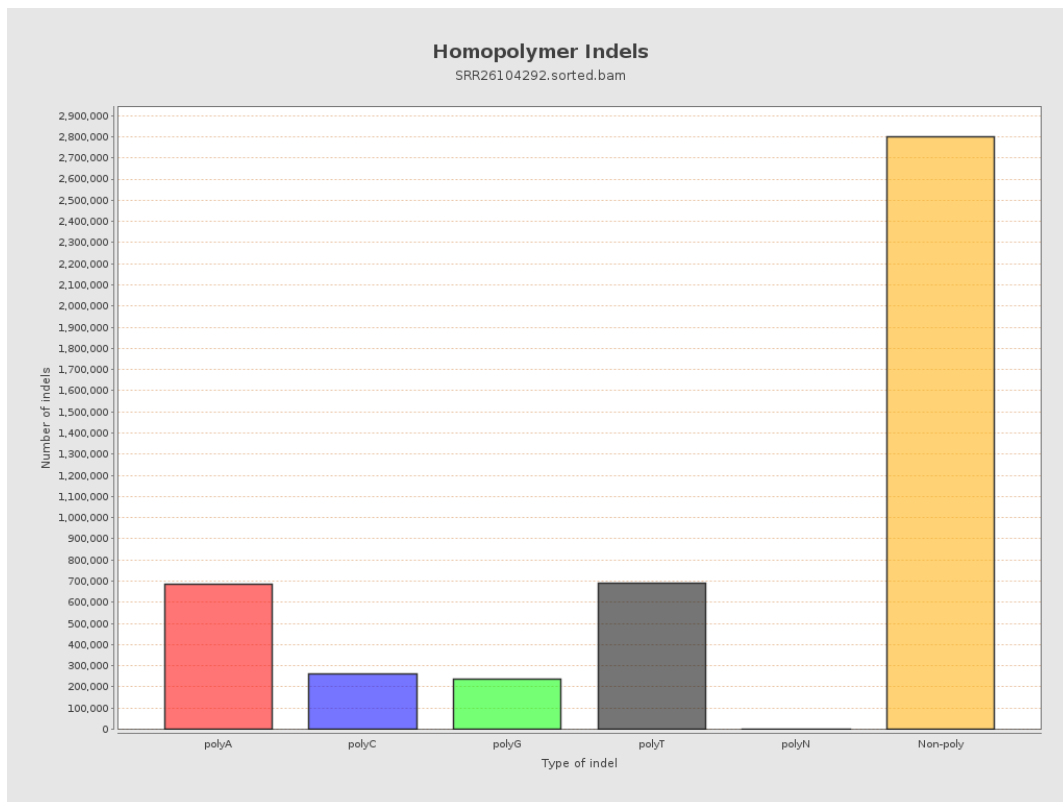
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



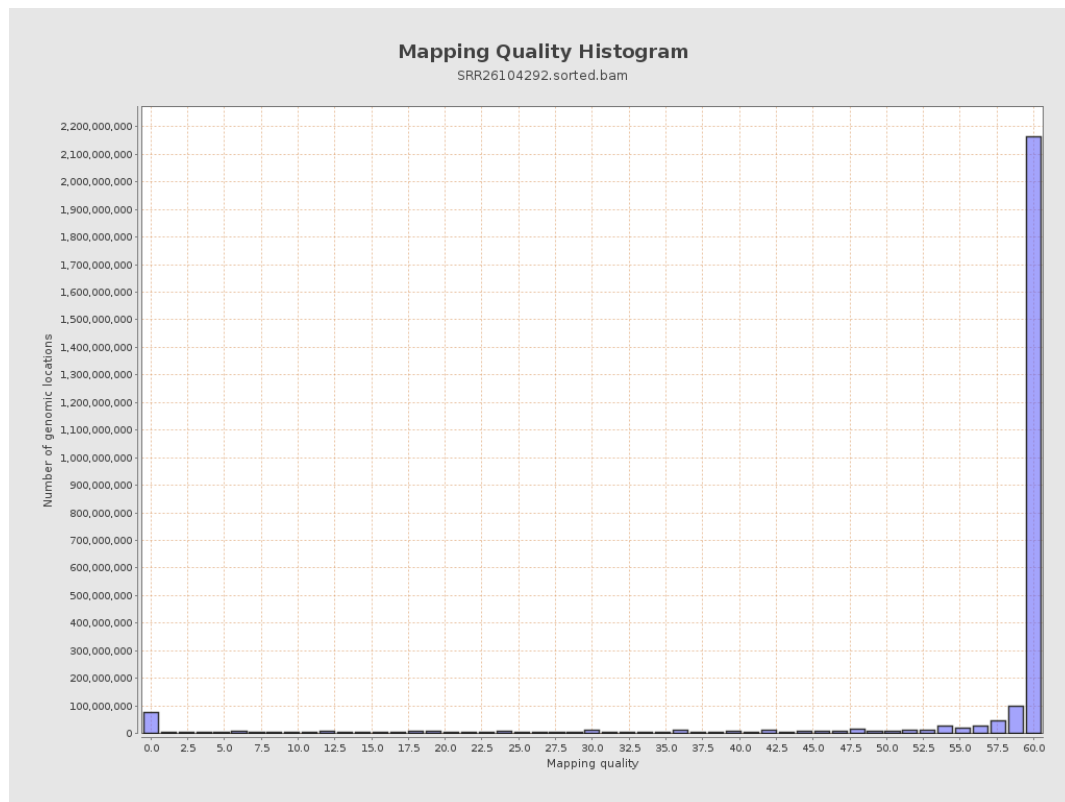
11. Results : Homopolymer Indels



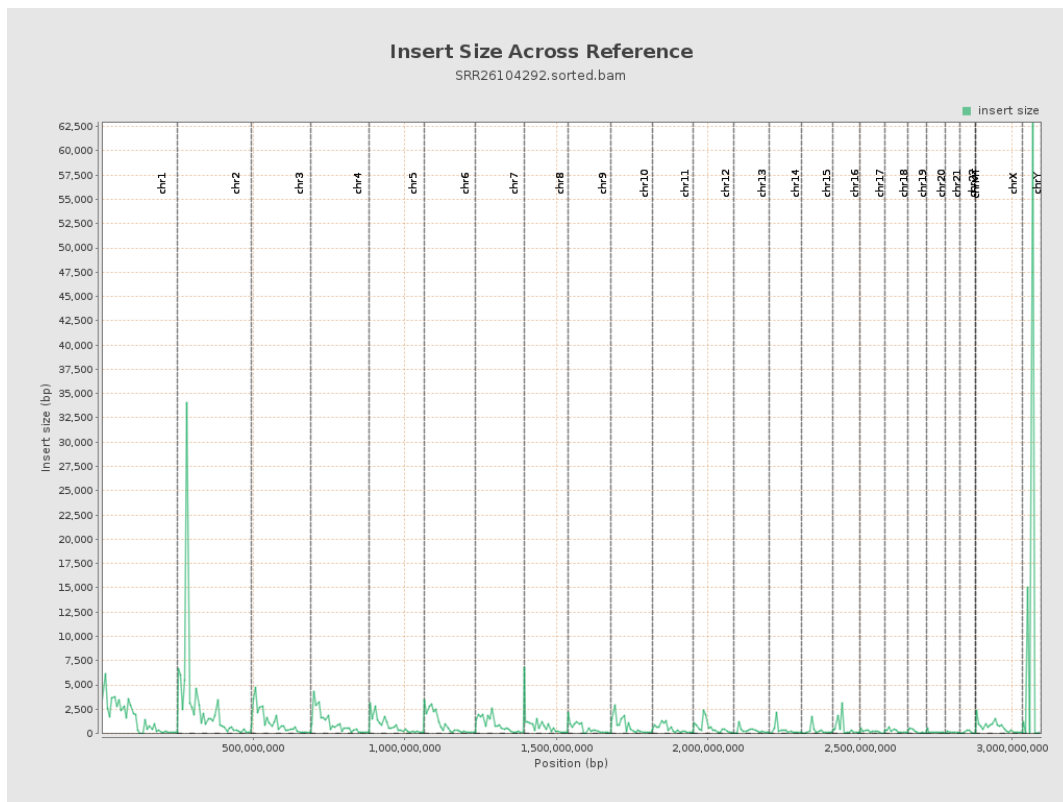
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

