

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/08 10:06:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR22354884.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_SRR22354884 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR22354884_1.fastq.gz SRR22354884_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 08 10:06:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR22354884.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	18,330,356
Mapped reads	17,830,243 / 97.27%
Unmapped reads	500,113 / 2.73%
Mapped paired reads	17,830,243 / 97.27%
Mapped reads, first in pair	8,934,911 / 48.74%
Mapped reads, second in pair	8,895,332 / 48.53%
Mapped reads, both in pair	17,755,348 / 96.86%
Mapped reads, singletons	74,895 / 0.41%
Secondary alignments	0
Supplementary alignments	668,142 / 3.65%
Read min/max/mean length	30 / 150 / 151.72
Duplicated reads (estimated)	9,738,352 / 53.13%
Duplication rate	52.61%
Clipped reads	6,057,505 / 33.05%

2.2. ACGT Content

Number/percentage of A's	674,816,793 / 27.01%
Number/percentage of C's	556,577,905 / 22.28%
Number/percentage of T's	669,111,801 / 26.79%
Number/percentage of G's	597,533,774 / 23.92%
Number/percentage of N's	11,750 / 0%

GC Percentage	46.2%
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2.3. Coverage

Mean	0.8076
Standard Deviation	19.043

2.4. Mapping Quality

Mean Mapping Quality	53.56
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2.5. Insert size

Mean	281,097.09
Standard Deviation	5,899,452.47
P25/Median/P75	182 / 295 / 443

2.6. Mismatches and indels

General error rate	1.24%
Mismatches	29,908,428
Insertions	559,043
Mapped reads with at least one insertion	3.04%
Deletions	1,338,576
Mapped reads with at least one deletion	7.2%
Homopolymer indels	51.84%

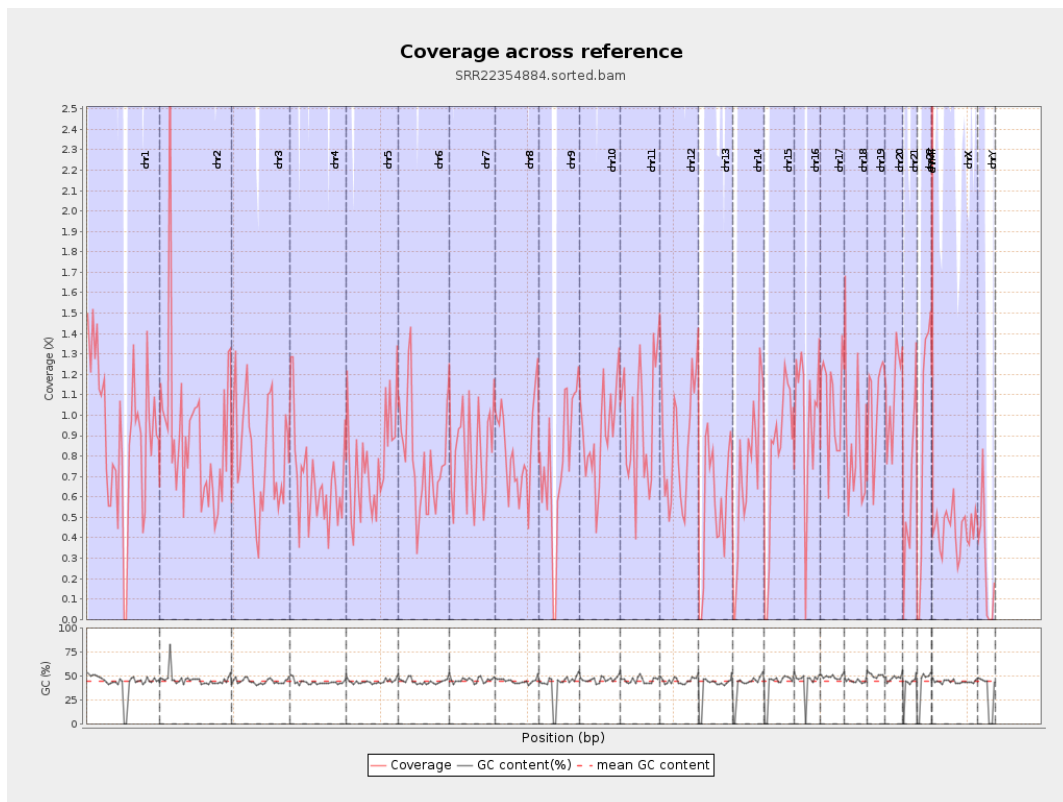
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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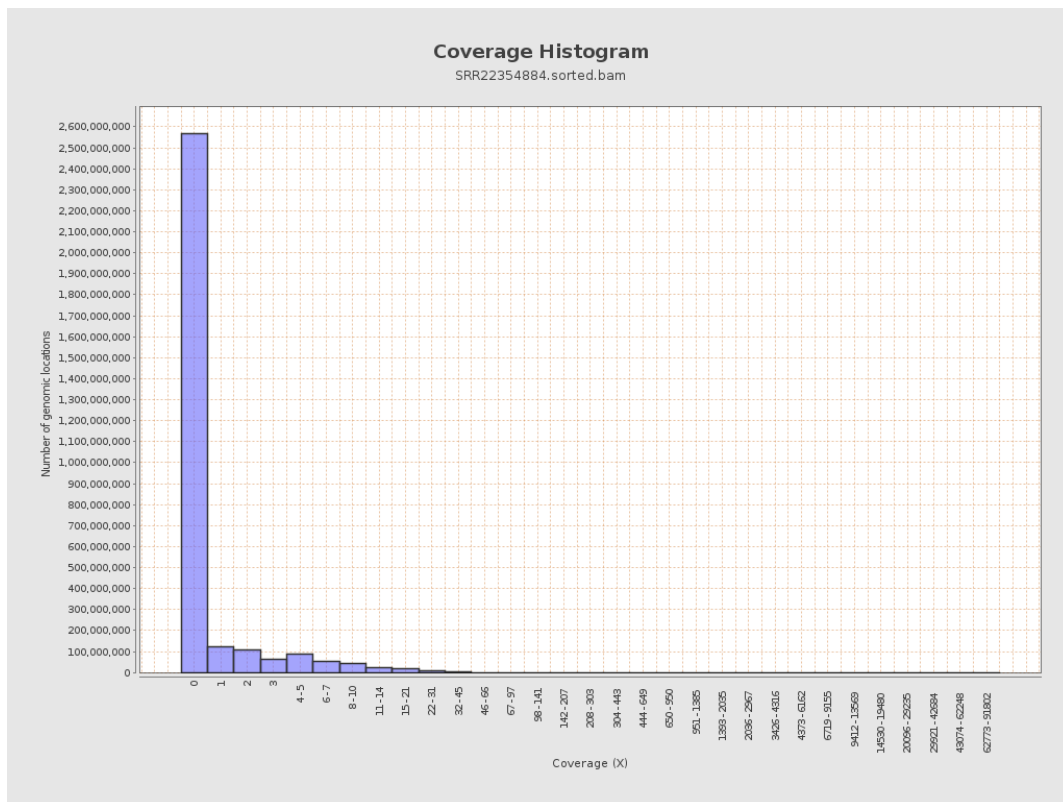
		bases	coverage	deviation
chr1	249250621	226156754	0.9073	3.1241
chr2	243199373	220427432	0.9064	66.0456
chr3	198022430	161025046	0.8132	2.7369
chr4	191154276	129342448	0.6766	2.8151
chr5	180915260	140340653	0.7757	2.6625
chr6	171115067	133446629	0.7799	2.6513
chr7	159138663	130830682	0.8221	13.0716
chr8	146364022	121222366	0.8282	2.7723
chr9	141213431	108523305	0.7685	2.9056
chr10	135534747	123140832	0.9086	3.089
chr11	135006516	130407503	0.9659	3.2722
chr12	133851895	115696865	0.8644	2.8664
chr13	115169878	65265591	0.5667	2.2686
chr14	107349540	76160716	0.7095	8.6185
chr15	102531392	80750599	0.7876	2.772
chr16	90354753	89632470	0.992	3.3423
chr17	81195210	86449409	1.0647	3.6997
chr18	78077248	65306874	0.8364	8.1566
chr19	59128983	62971790	1.065	3.3461
chr20	63025520	69646449	1.1051	3.3123
chr21	48129895	30919482	0.6424	2.9153
chr22	51304566	47343906	0.9228	3.0938
chrMT	16571	305098	18.4116	13.1802
chrX	155270560	68234313	0.4395	1.7661

chrY	59373566	16585938	0.2793	4.1171
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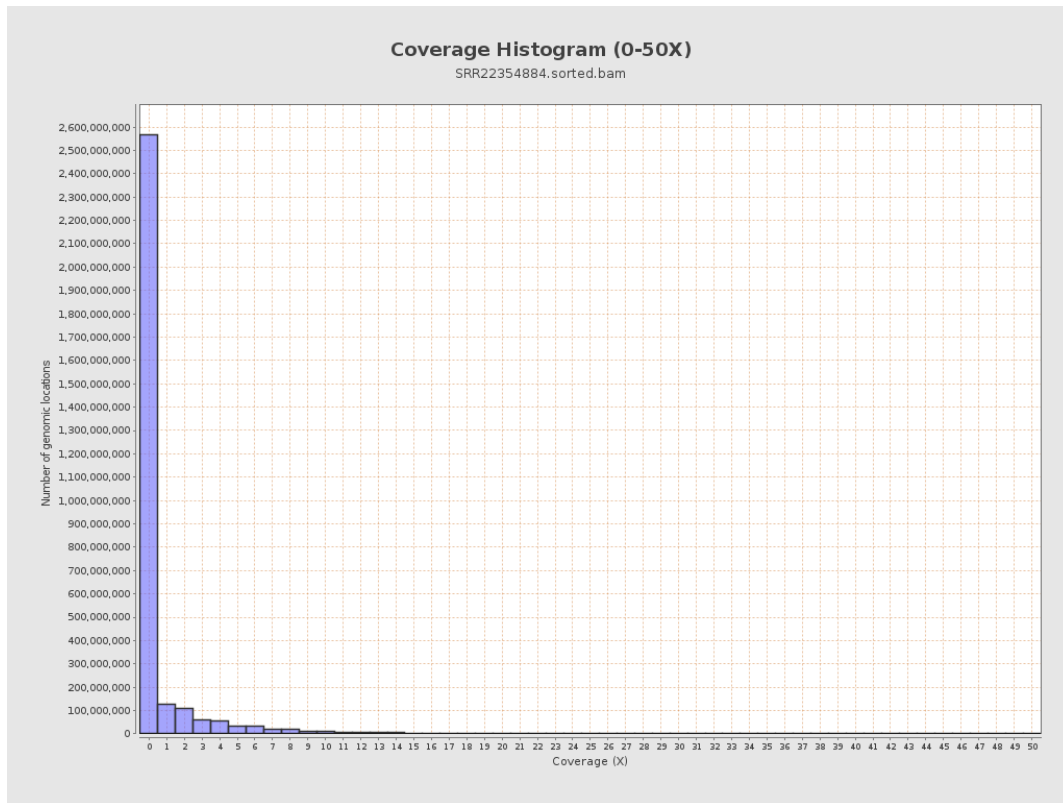
3. Results : Coverage across reference



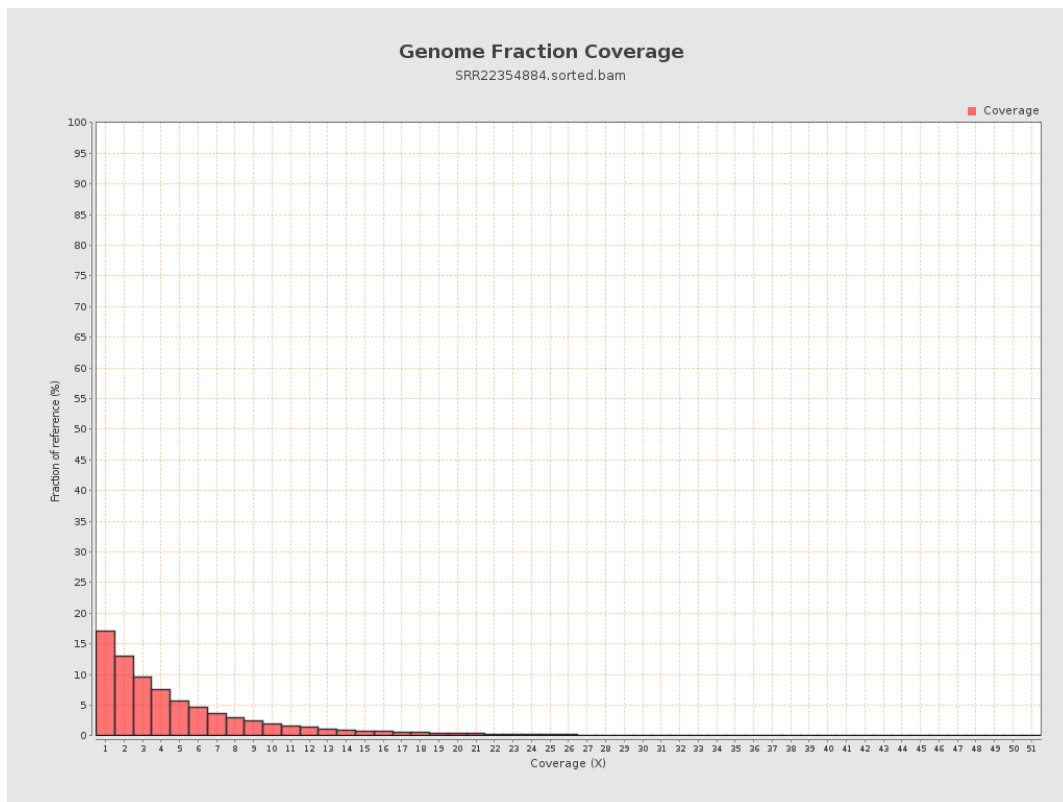
4. Results : Coverage Histogram



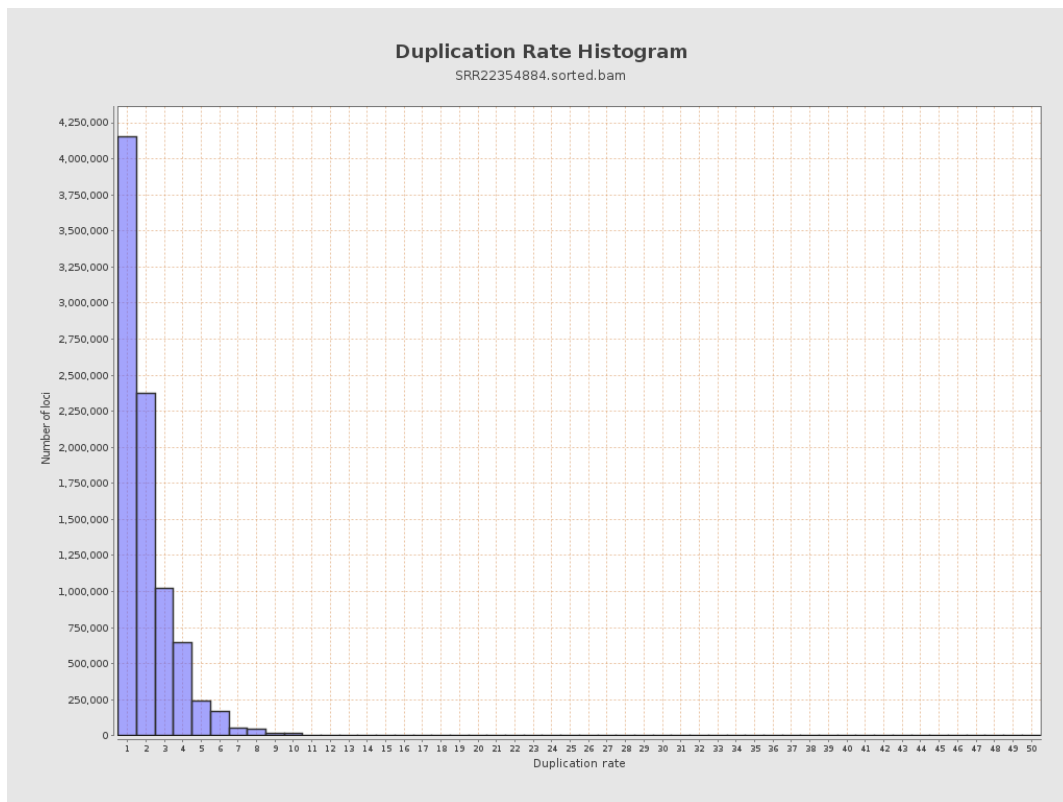
5. Results : Coverage Histogram (0-50X)



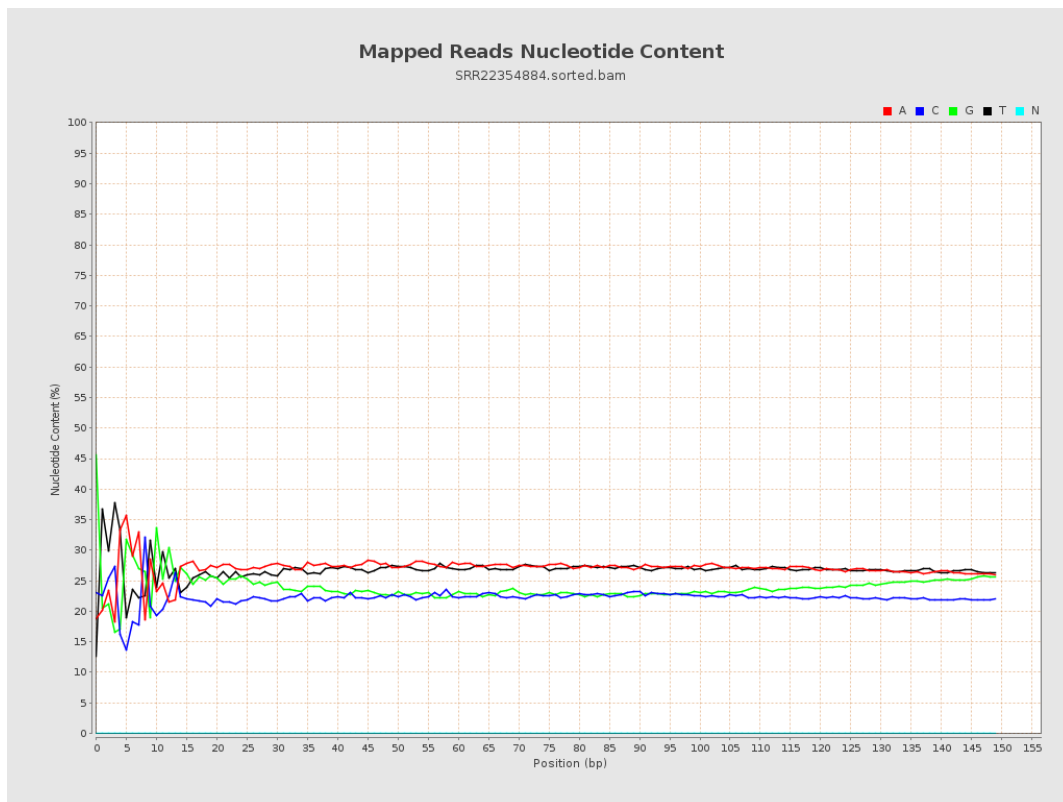
6. Results : Genome Fraction Coverage



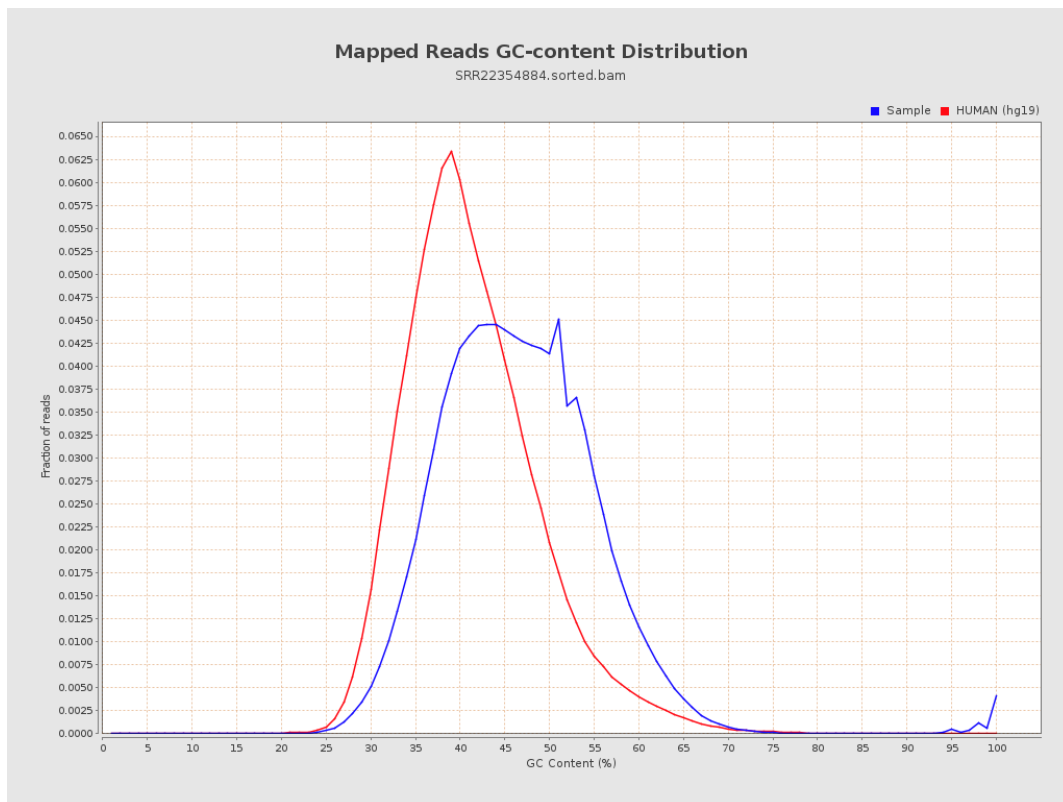
7. Results : Duplication Rate Histogram



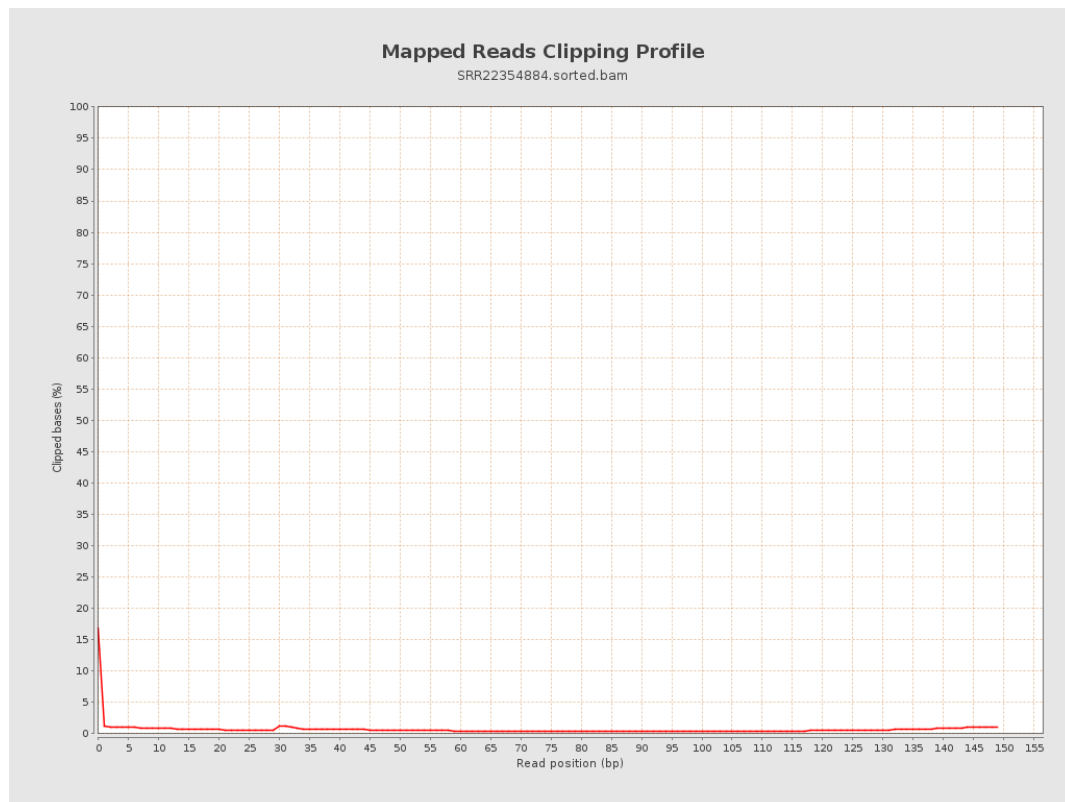
8. Results : Mapped Reads Nucleotide Content



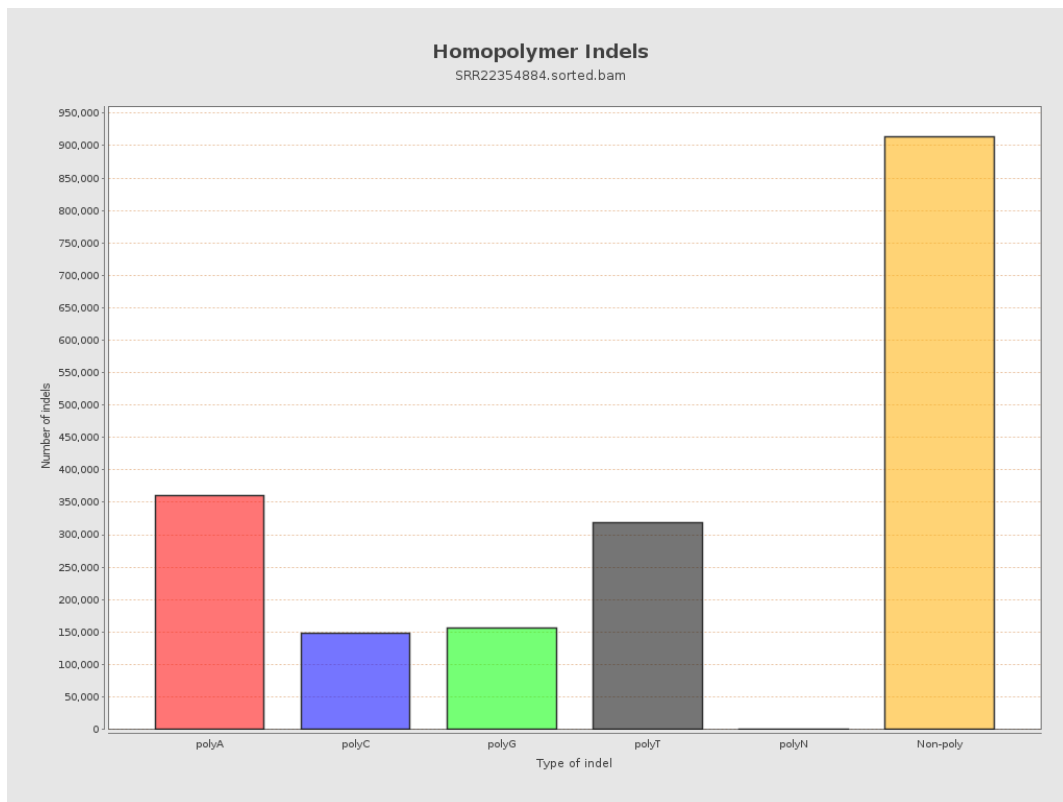
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



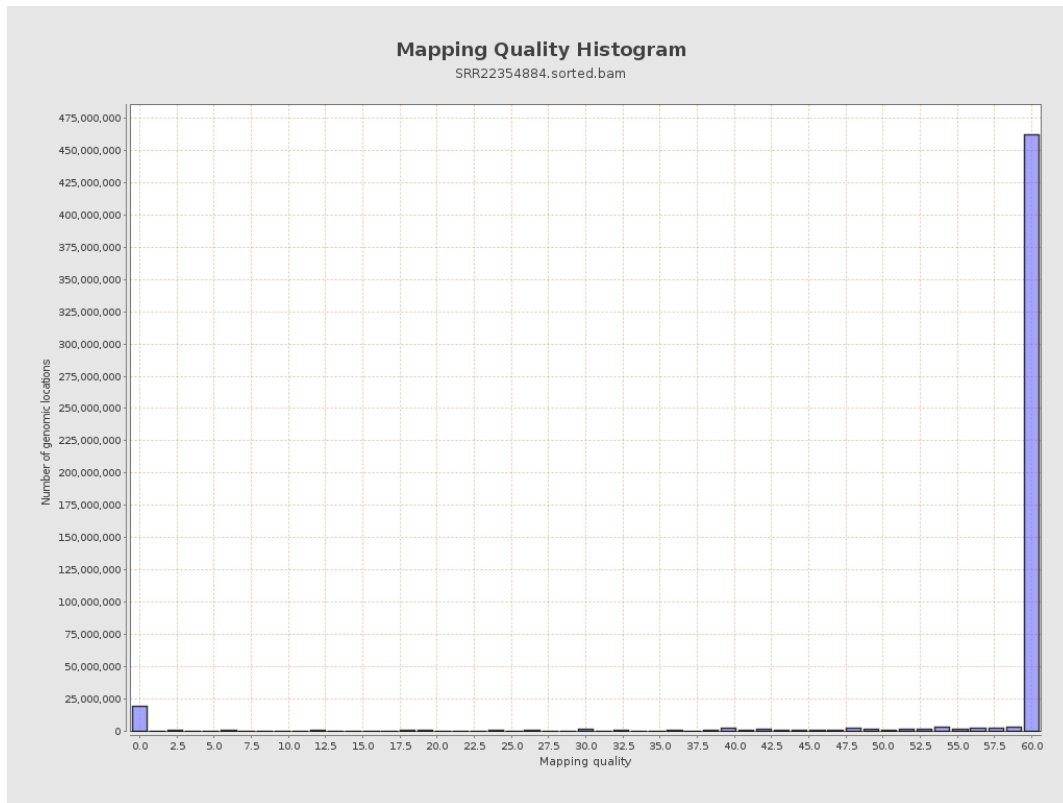
11. Results : Homopolymer Indels



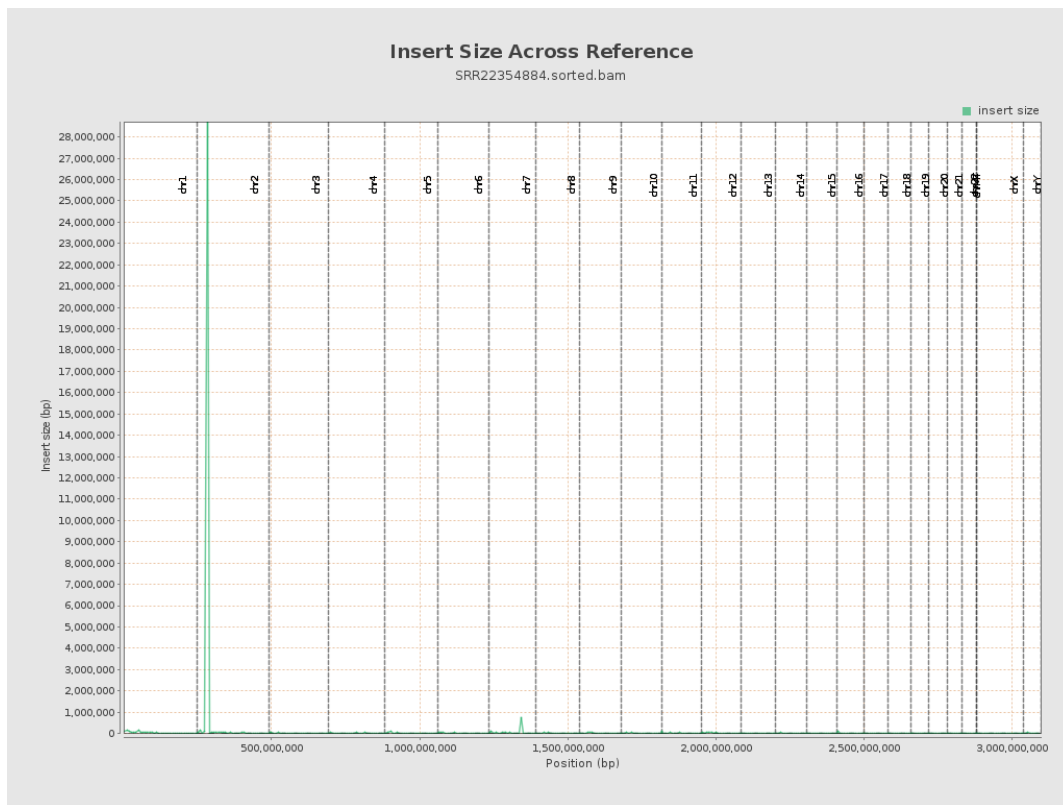
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

