

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 00:10:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124877.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_SRR3124877 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124877_1.fastq.gz SRR3124877_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 00:10:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124877.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,465,796
Mapped reads	3,420,091 / 98.68%
Unmapped reads	45,705 / 1.32%
Mapped paired reads	3,420,091 / 98.68%
Mapped reads, first in pair	1,710,682 / 49.36%
Mapped reads, second in pair	1,709,409 / 49.32%
Mapped reads, both in pair	3,409,556 / 98.38%
Mapped reads, singletons	10,535 / 0.3%
Secondary alignments	0
Supplementary alignments	16,212 / 0.47%
Read min/max/mean length	30 / 101 / 101.18
Duplicated reads (estimated)	182,902 / 5.28%
Duplication rate	3.86%
Clipped reads	1,377,564 / 39.75%

2.2. ACGT Content

Number/percentage of A's	87,521,922 / 28.22%
Number/percentage of C's	61,283,991 / 19.76%
Number/percentage of T's	90,042,111 / 29.03%
Number/percentage of G's	71,272,398 / 22.98%
Number/percentage of N's	4,519 / 0%

GC Percentage	42.74%
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2.3. Coverage

Mean	0.1002
Standard Deviation	0.7891

2.4. Mapping Quality

Mean Mapping Quality	53.31
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2.5. Insert size

Mean	91,159.42
Standard Deviation	2,919,171.05
P25/Median/P75	137 / 176 / 239

2.6. Mismatches and indels

General error rate	0.72%
Mismatches	2,139,705
Insertions	42,020
Mapped reads with at least one insertion	1.18%
Deletions	99,102
Mapped reads with at least one deletion	2.83%
Homopolymer indels	46.11%

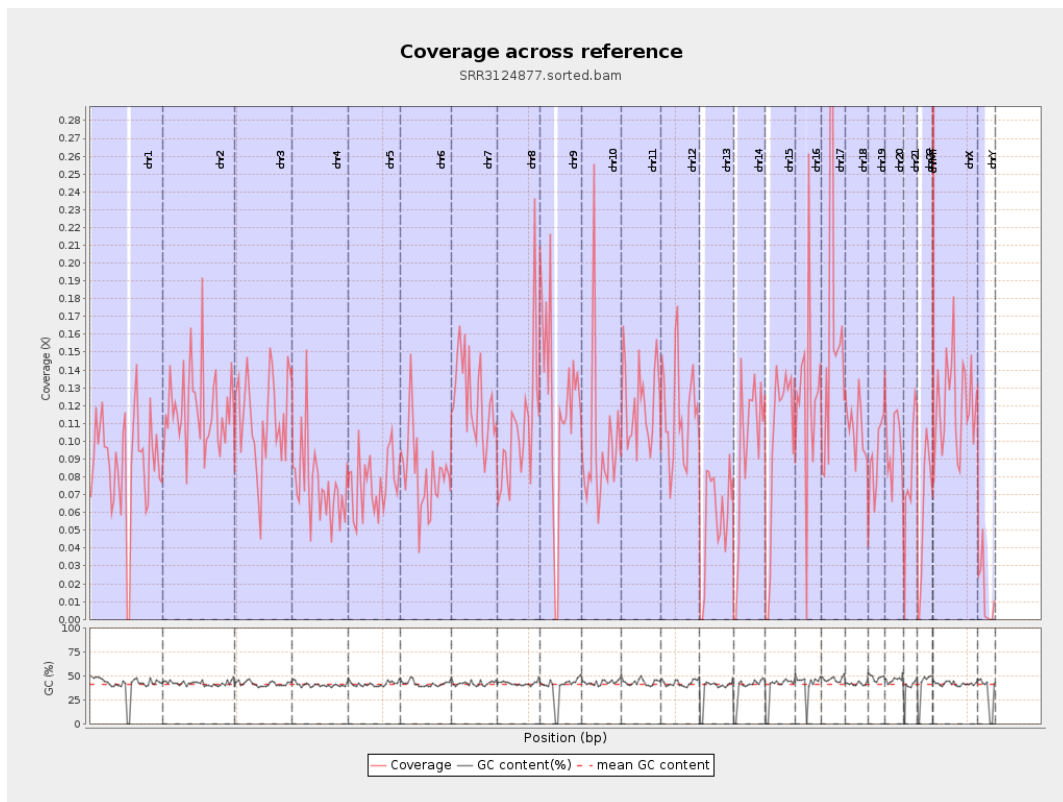
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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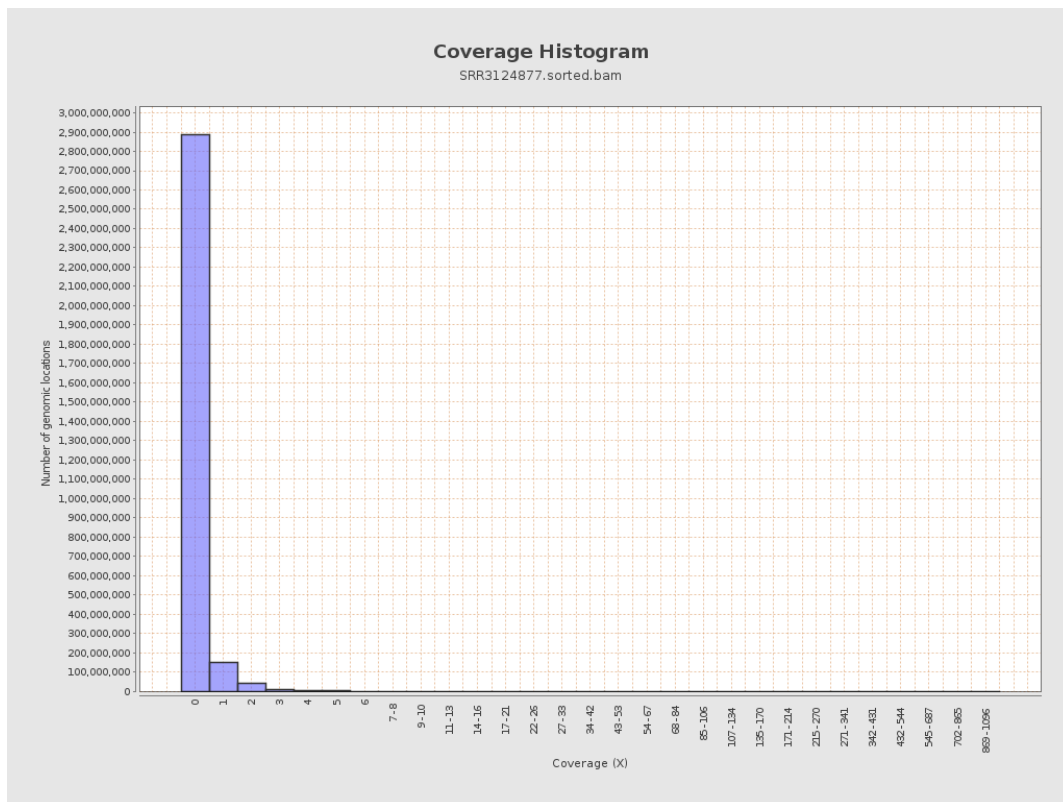
		bases	coverage	deviation
chr1	249250621	21797374	0.0875	0.6918
chr2	243199373	28779808	0.1183	1.143
chr3	198022430	22167149	0.1119	0.4521
chr4	191154276	14354150	0.0751	0.6491
chr5	180915260	13925105	0.077	0.4008
chr6	171115067	13997961	0.0818	0.4406
chr7	159138663	19661185	0.1235	1.1721
chr8	146364022	15446172	0.1055	0.4776
chr9	141213431	16954050	0.1201	0.805
chr10	135534747	12920929	0.0953	1.5021
chr11	135006516	16251747	0.1204	0.6042
chr12	133851895	15771023	0.1178	0.4825
chr13	115169878	6444175	0.056	0.3177
chr14	107349540	10262434	0.0956	0.4522
chr15	102531392	10023328	0.0978	0.426
chr16	90354753	11331350	0.1254	1.3428
chr17	81195210	13187968	0.1624	1.2965
chr18	78077248	8388349	0.1074	0.8827
chr19	59128983	5427511	0.0918	0.5439
chr20	63025520	6109973	0.0969	0.4935
chr21	48129895	4025317	0.0836	0.4573
chr22	51304566	3194810	0.0623	0.3791
chrMT	16571	299733	18.0878	10.1569
chrX	155270560	18739702	0.1207	0.5791

chrY	59373566	836368	0.0141	0.9511
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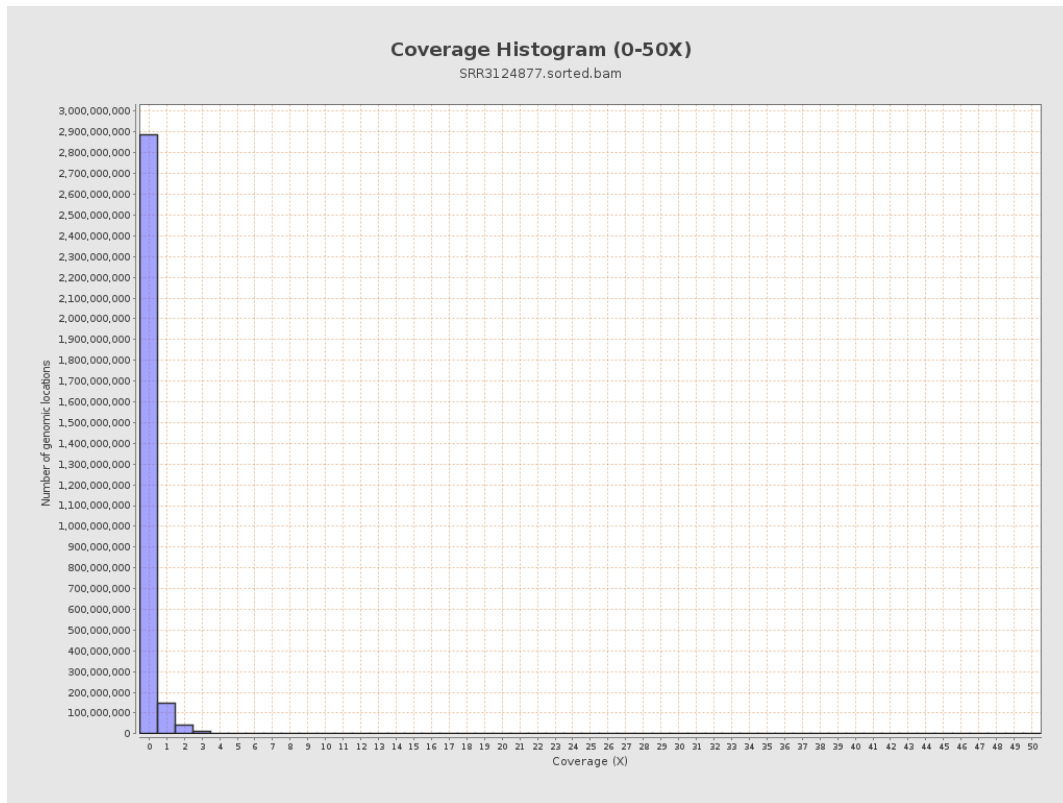
3. Results : Coverage across reference



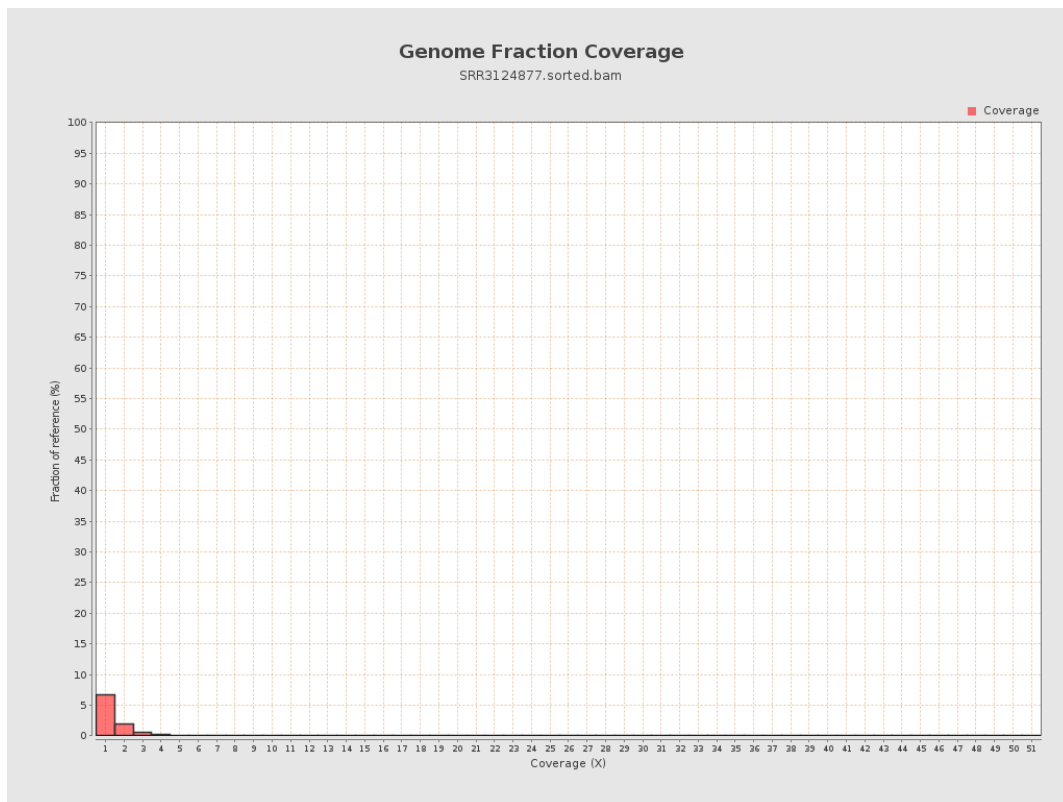
4. Results : Coverage Histogram



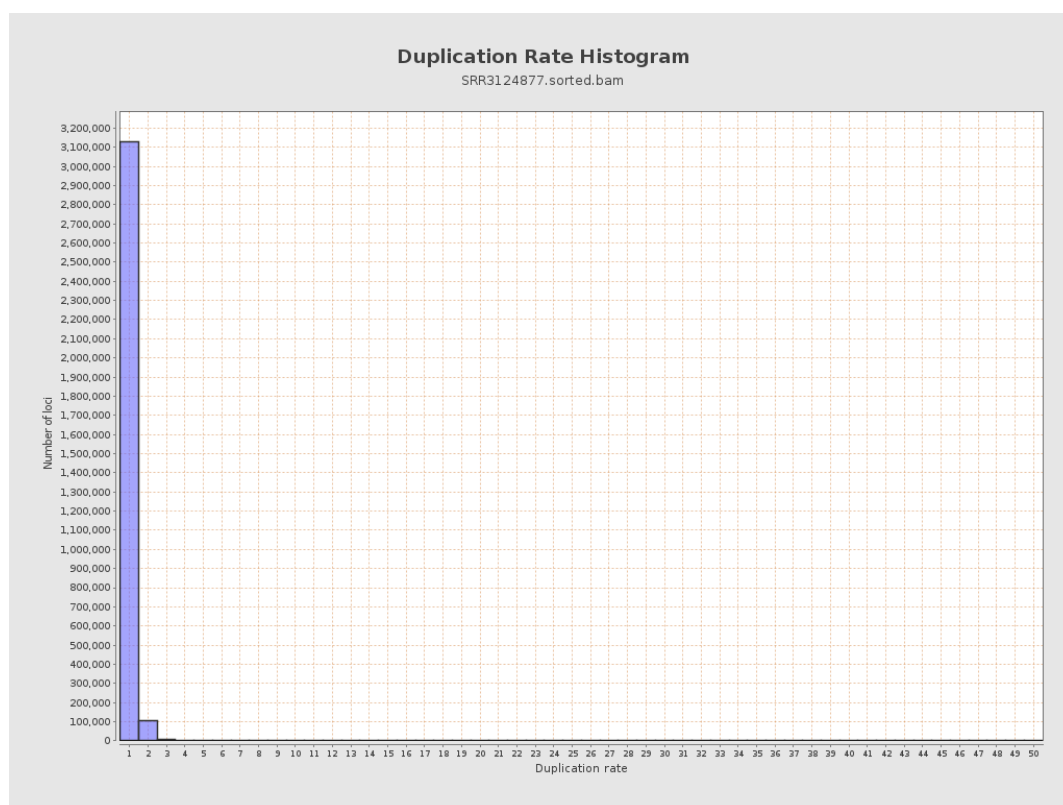
5. Results : Coverage Histogram (0-50X)



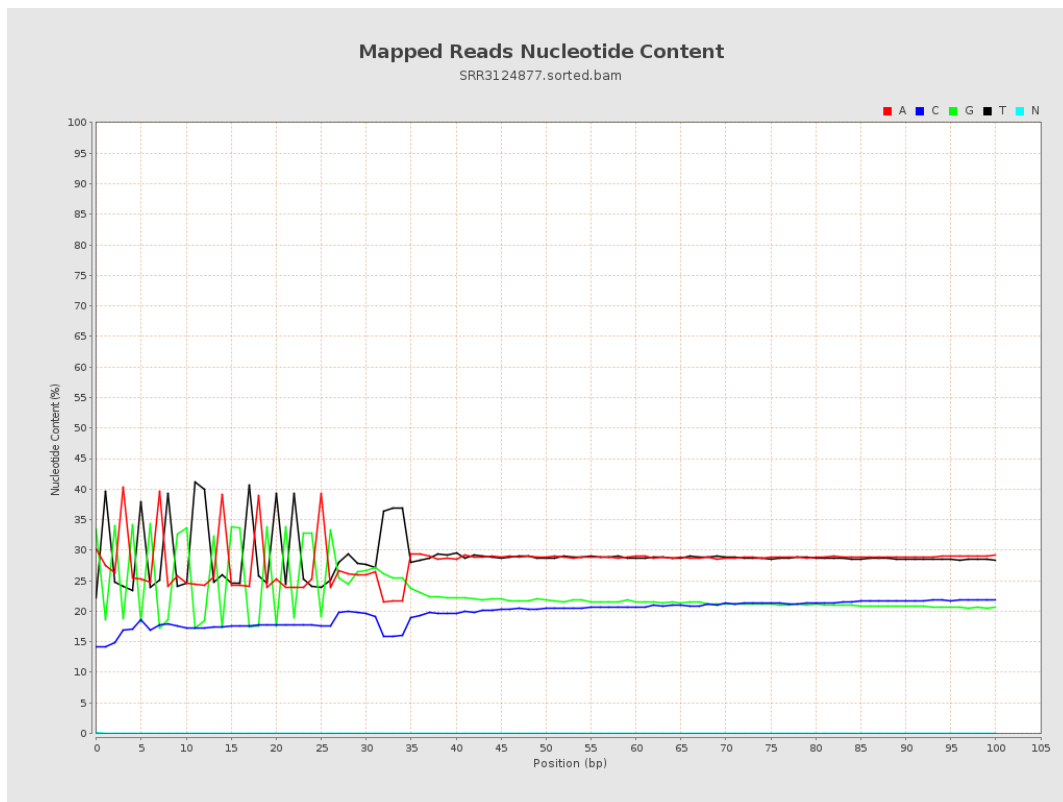
6. Results : Genome Fraction Coverage



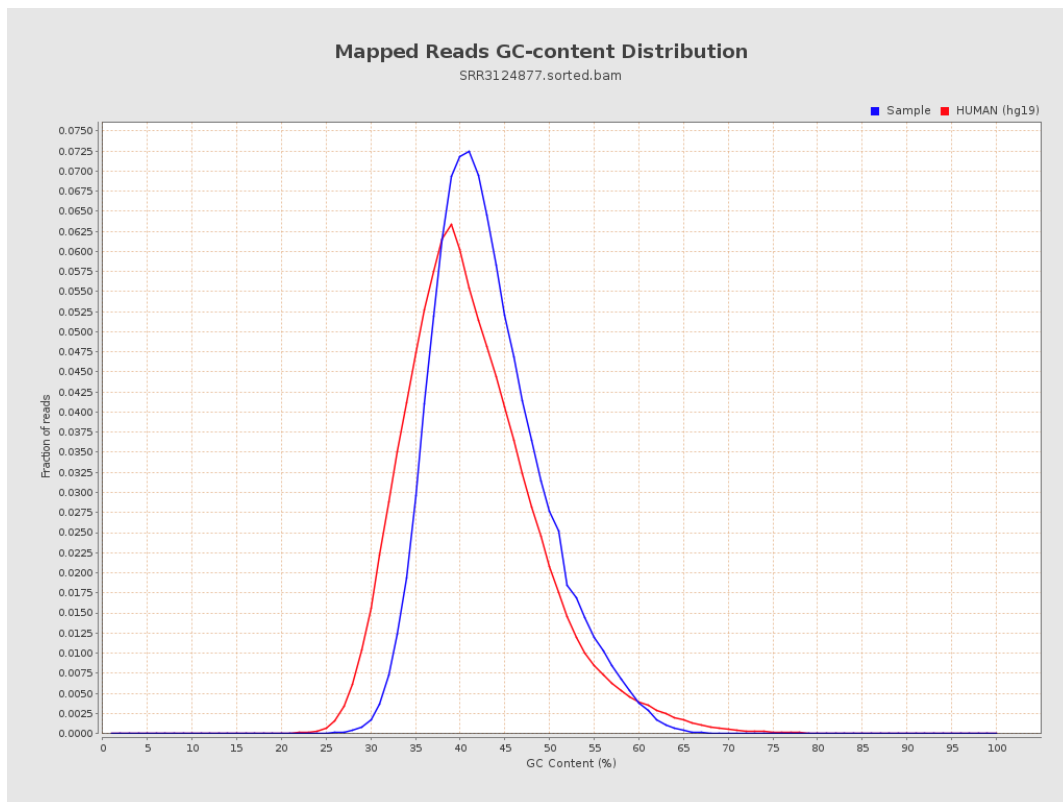
7. Results : Duplication Rate Histogram



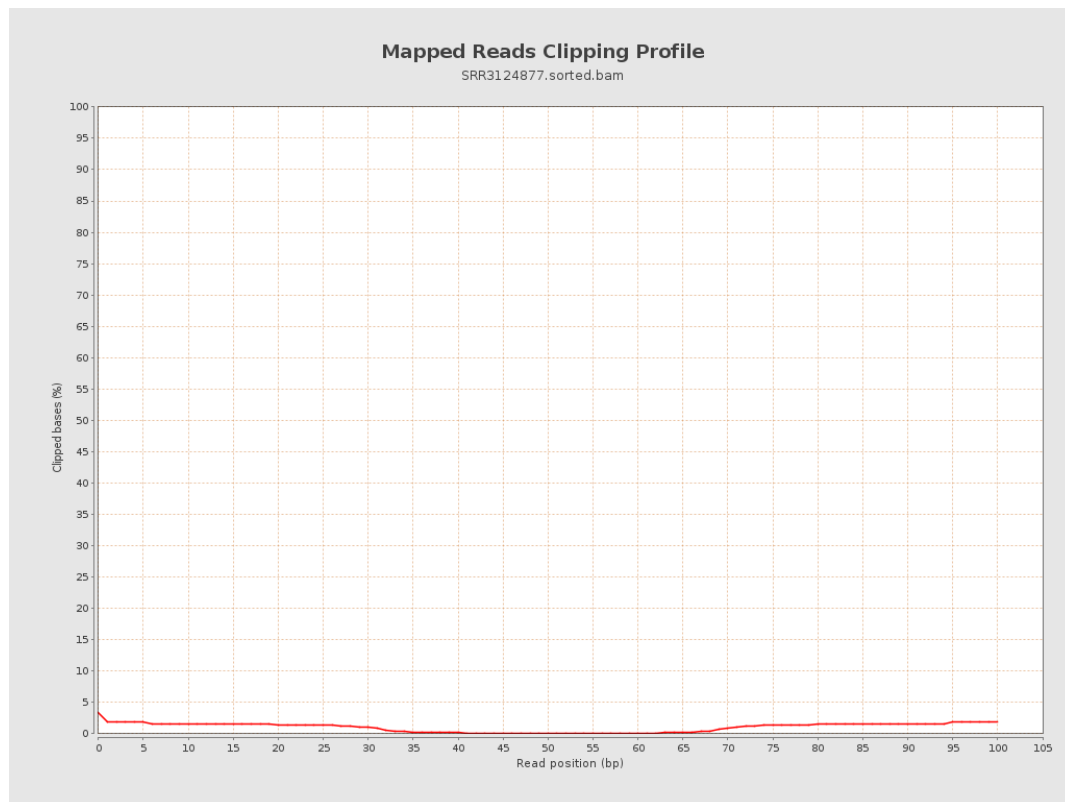
8. Results : Mapped Reads Nucleotide Content



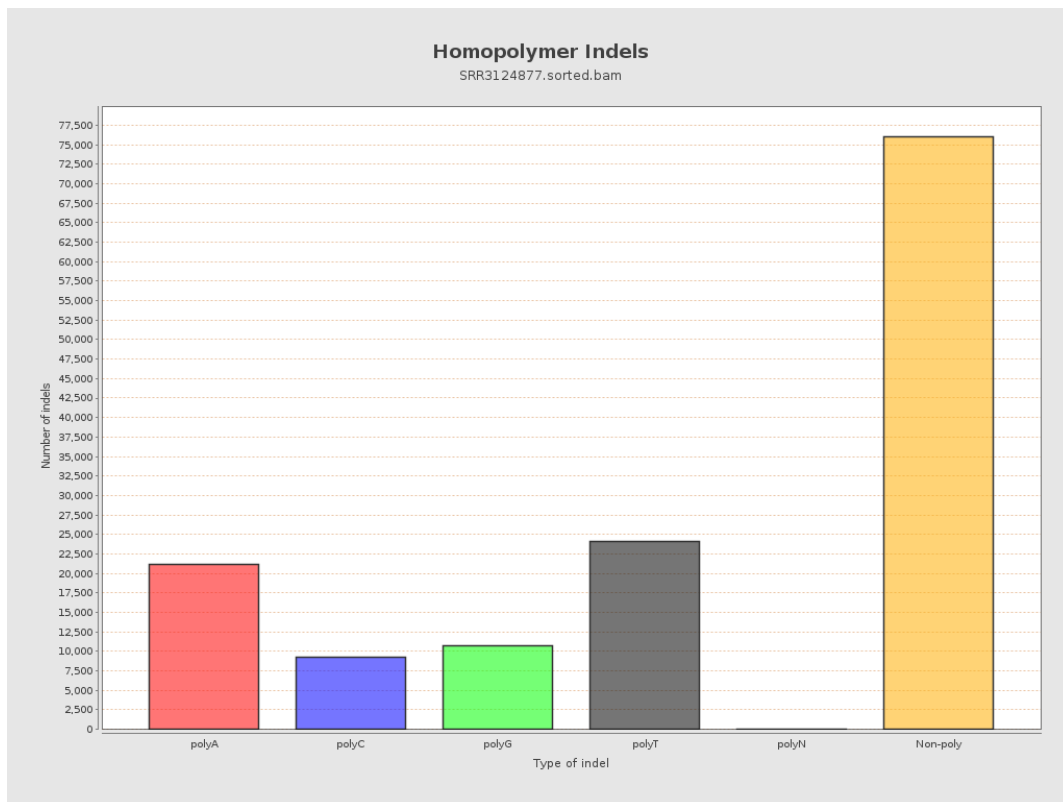
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



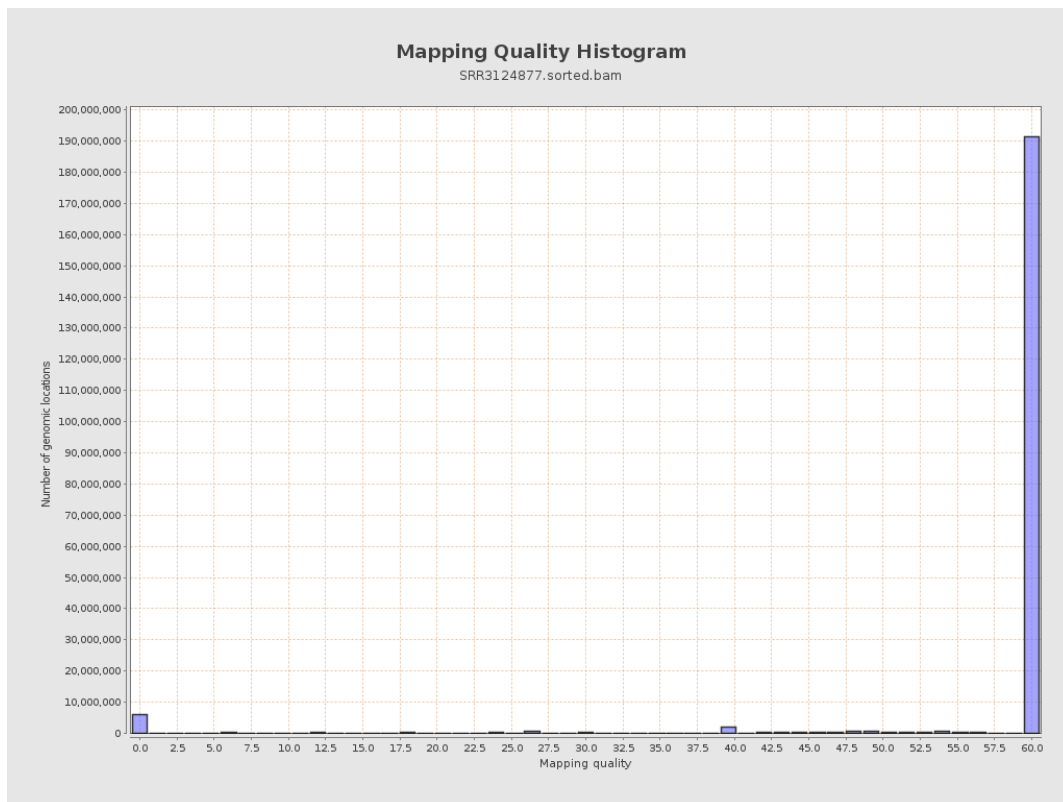
11. Results : Homopolymer Indels



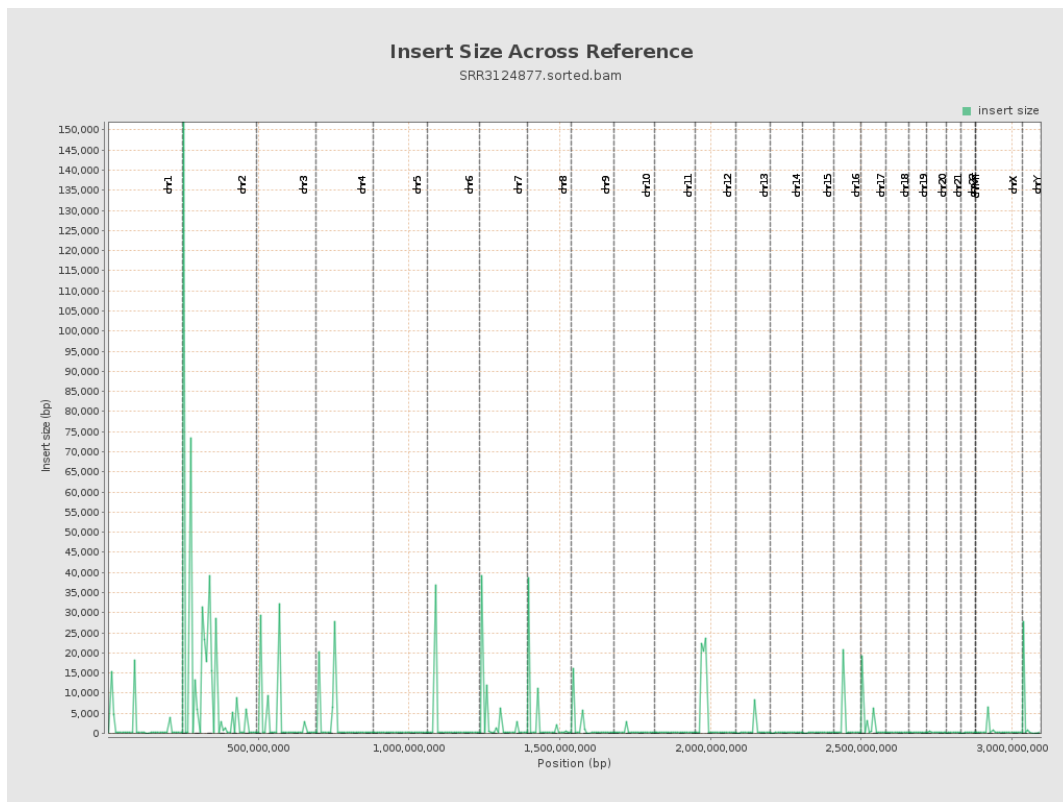
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

