

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/09 23:58:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124875.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_SRR3124875 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124875_1.fastq.gz SRR3124875_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Dec 09 23:58:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124875.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,810,972
Mapped reads	3,701,695 / 97.13%
Unmapped reads	109,277 / 2.87%
Mapped paired reads	3,701,695 / 97.13%
Mapped reads, first in pair	1,851,891 / 48.59%
Mapped reads, second in pair	1,849,804 / 48.54%
Mapped reads, both in pair	3,688,104 / 96.78%
Mapped reads, singletons	13,591 / 0.36%
Secondary alignments	0
Supplementary alignments	15,837 / 0.42%
Read min/max/mean length	30 / 101 / 101.16
Duplicated reads (estimated)	210,135 / 5.51%
Duplication rate	4%
Clipped reads	1,550,687 / 40.69%

2.2. ACGT Content

Number/percentage of A's	93,897,878 / 28.34%
Number/percentage of C's	63,545,289 / 19.18%
Number/percentage of T's	97,818,075 / 29.52%
Number/percentage of G's	76,102,638 / 22.97%
Number/percentage of N's	4,706 / 0%

GC Percentage	42.14%
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2.3. Coverage

Mean	0.1071
Standard Deviation	0.8174

2.4. Mapping Quality

Mean Mapping Quality	53.19
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2.5. Insert size

Mean	41,082
Standard Deviation	1,902,686.22
P25/Median/P75	144 / 188 / 256

2.6. Mismatches and indels

General error rate	0.75%
Mismatches	2,392,076
Insertions	44,641
Mapped reads with at least one insertion	1.17%
Deletions	111,305
Mapped reads with at least one deletion	2.94%
Homopolymer indels	46.89%

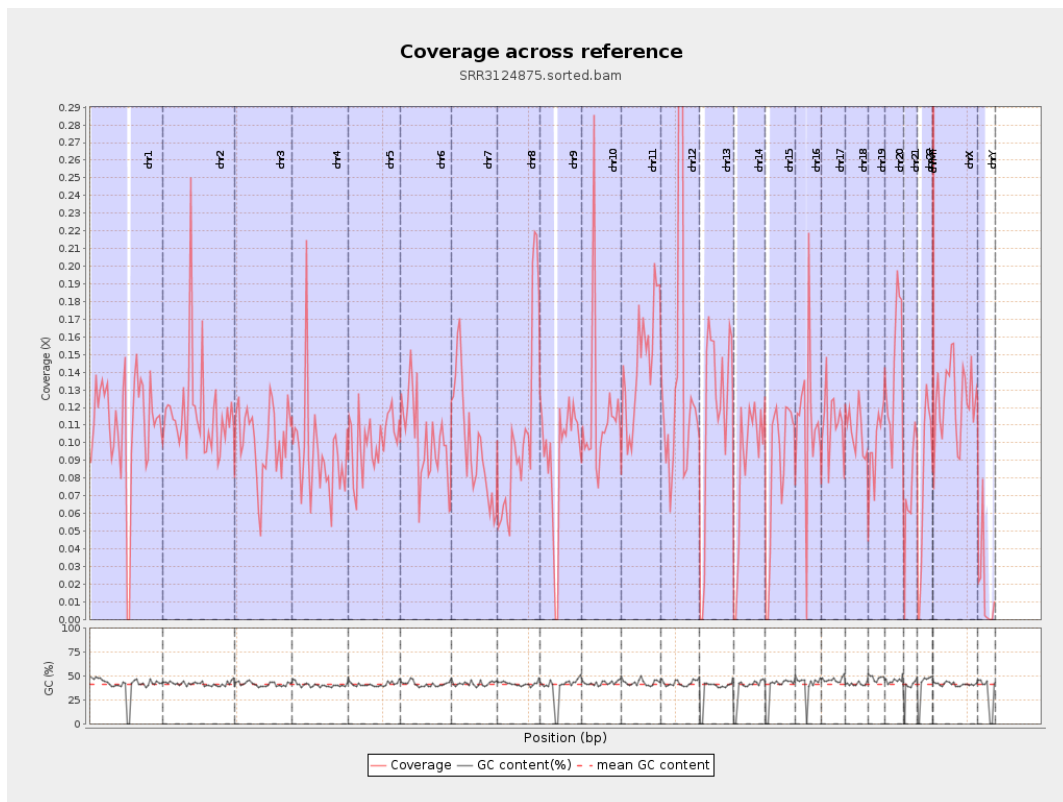
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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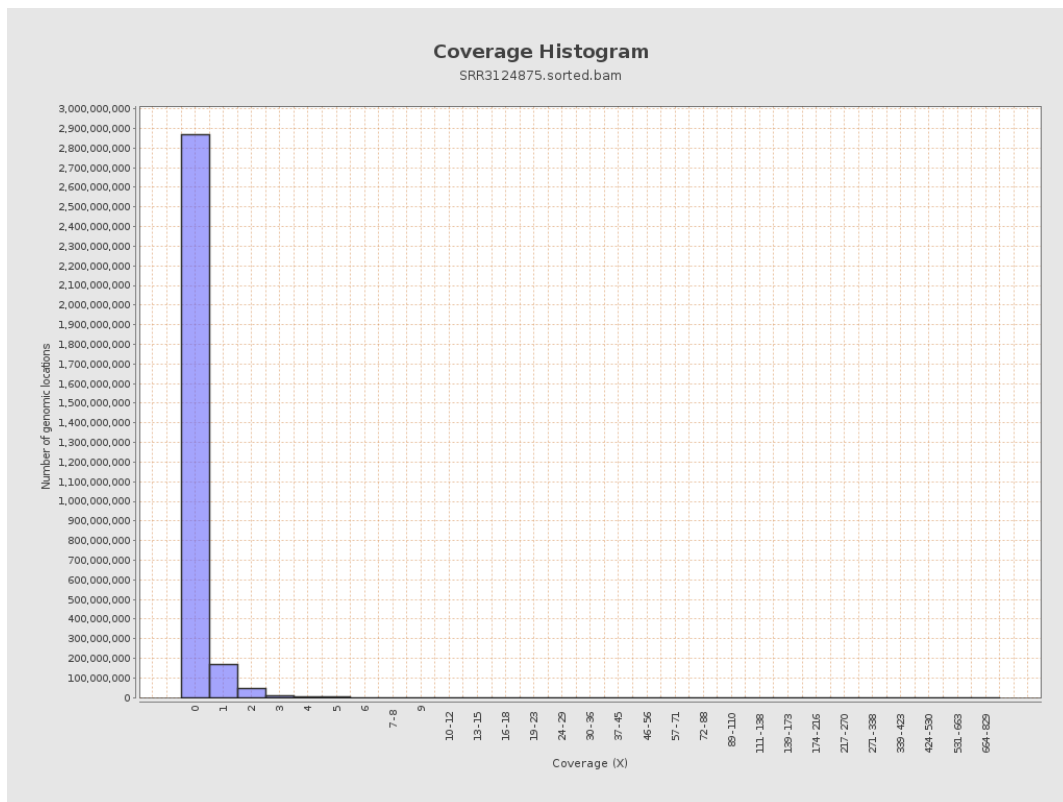
		bases	coverage	deviation
chr1	249250621	27399488	0.1099	0.8034
chr2	243199373	28500135	0.1172	1.1497
chr3	198022430	20039362	0.1012	0.4123
chr4	191154276	17949513	0.0939	0.8658
chr5	180915260	18354610	0.1015	0.4207
chr6	171115067	17436894	0.1019	0.5429
chr7	159138663	15816969	0.0994	0.8506
chr8	146364022	15542498	0.1062	0.4922
chr9	141213431	13054187	0.0924	0.9556
chr10	135534747	15585177	0.115	1.535
chr11	135006516	19658776	0.1456	0.9709
chr12	133851895	19915117	0.1488	0.6607
chr13	115169878	13535121	0.1175	0.4457
chr14	107349540	9522534	0.0887	0.4167
chr15	102531392	8825052	0.0861	0.3842
chr16	90354753	10009144	0.1108	1.1299
chr17	81195210	9145642	0.1126	0.8937
chr18	78077248	8300843	0.1063	1.0801
chr19	59128983	5941879	0.1005	0.5824
chr20	63025520	8970299	0.1423	0.5536
chr21	48129895	3587423	0.0745	0.514
chr22	51304566	4080537	0.0795	0.3871
chrMT	16571	57429	3.4656	2.2829
chrX	155270560	19316271	0.1244	0.6076

chrY	59373566	1009702	0.017	1.2664
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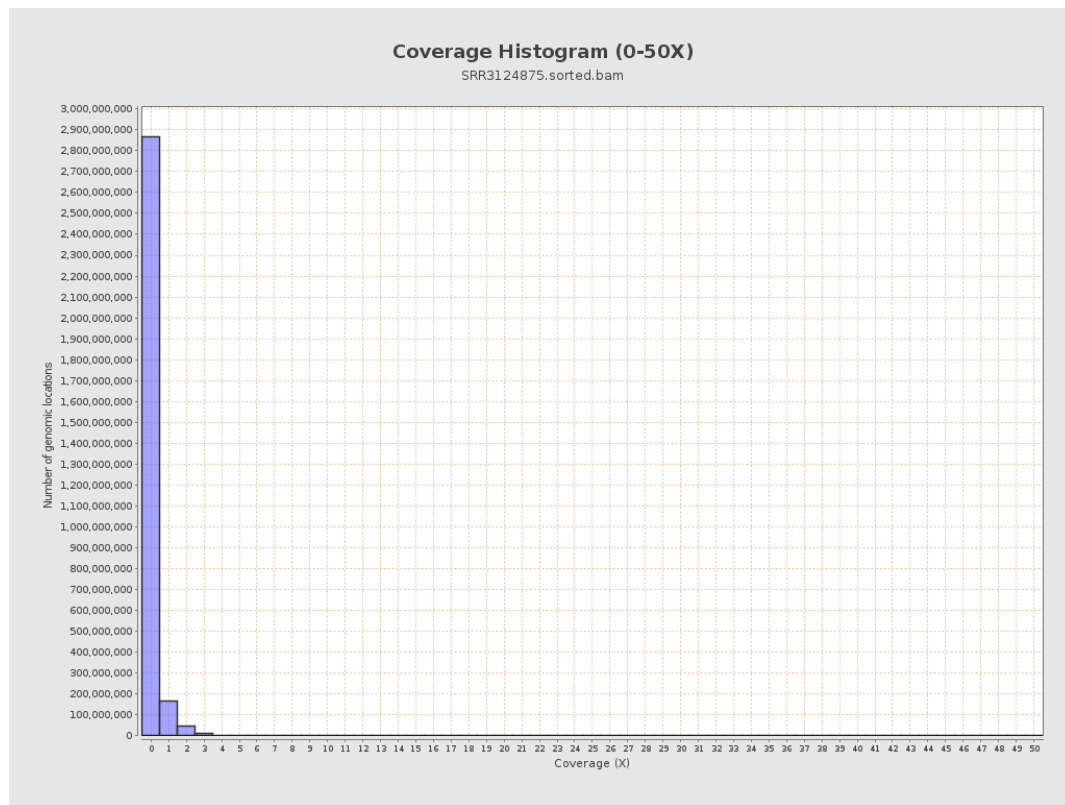
3. Results : Coverage across reference



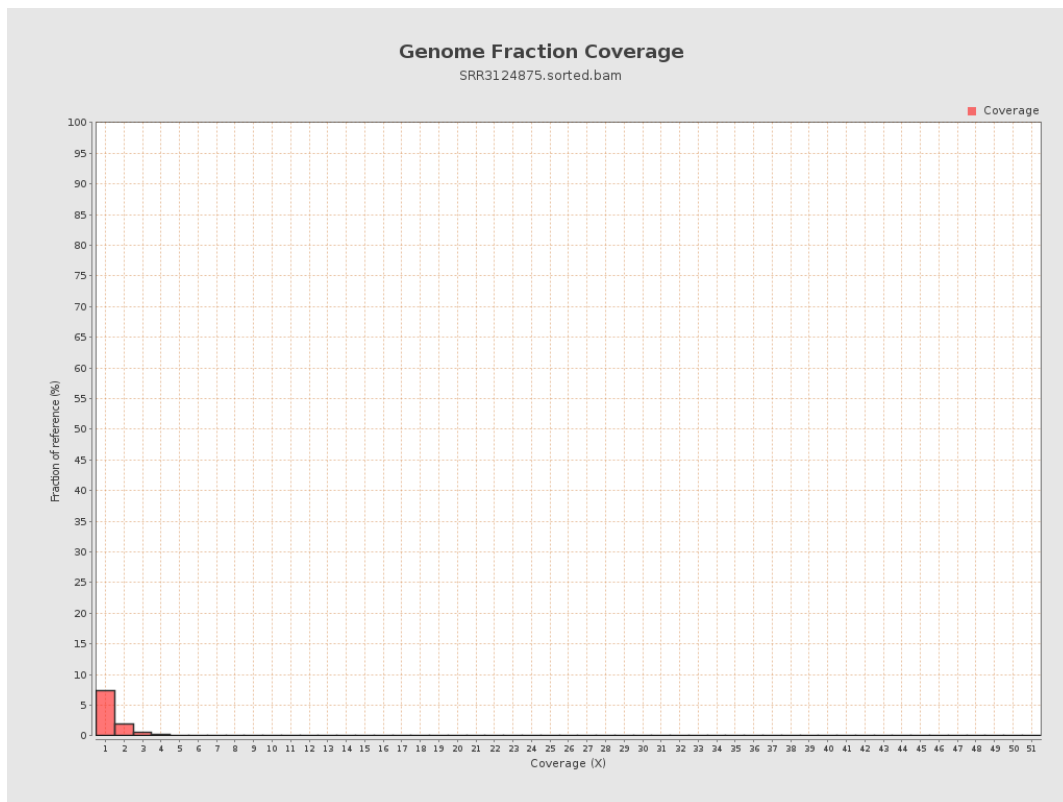
4. Results : Coverage Histogram



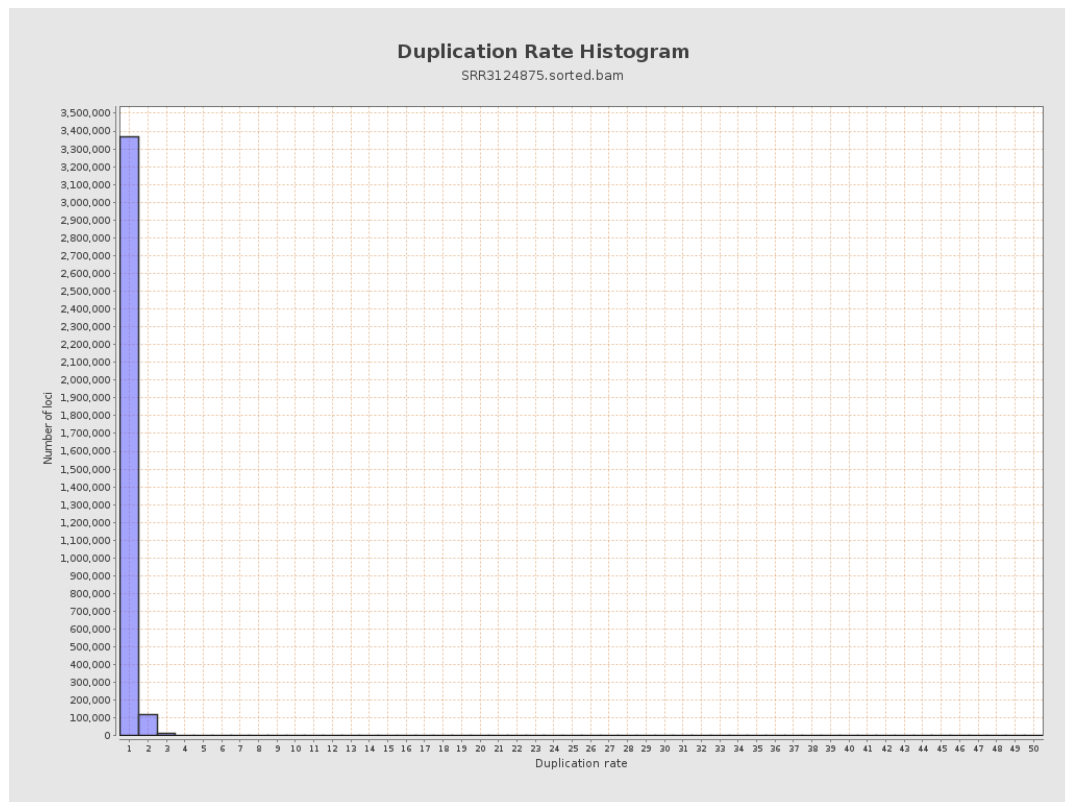
5. Results : Coverage Histogram (0-50X)



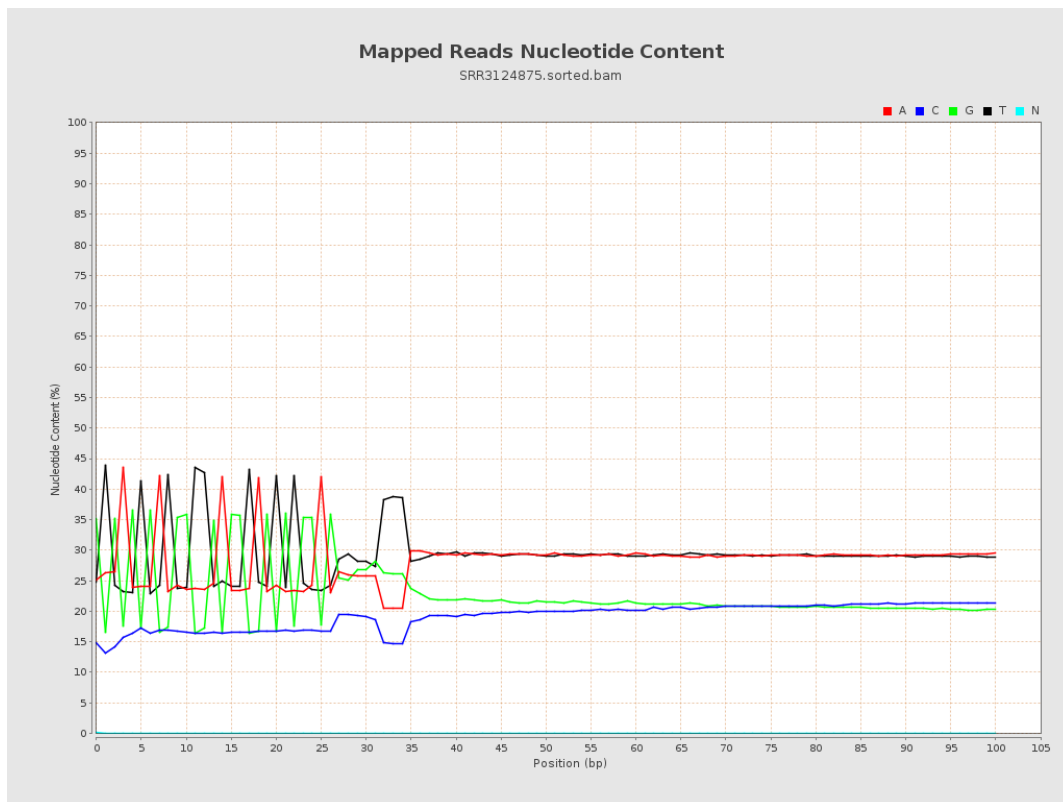
6. Results : Genome Fraction Coverage



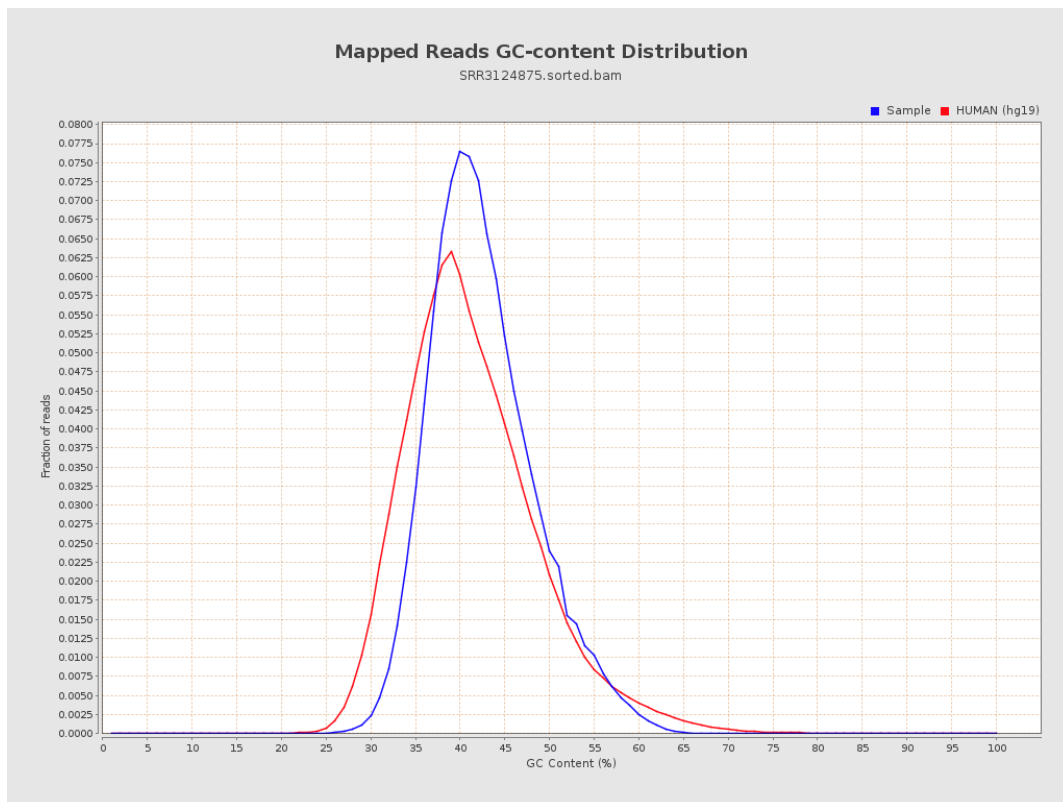
7. Results : Duplication Rate Histogram



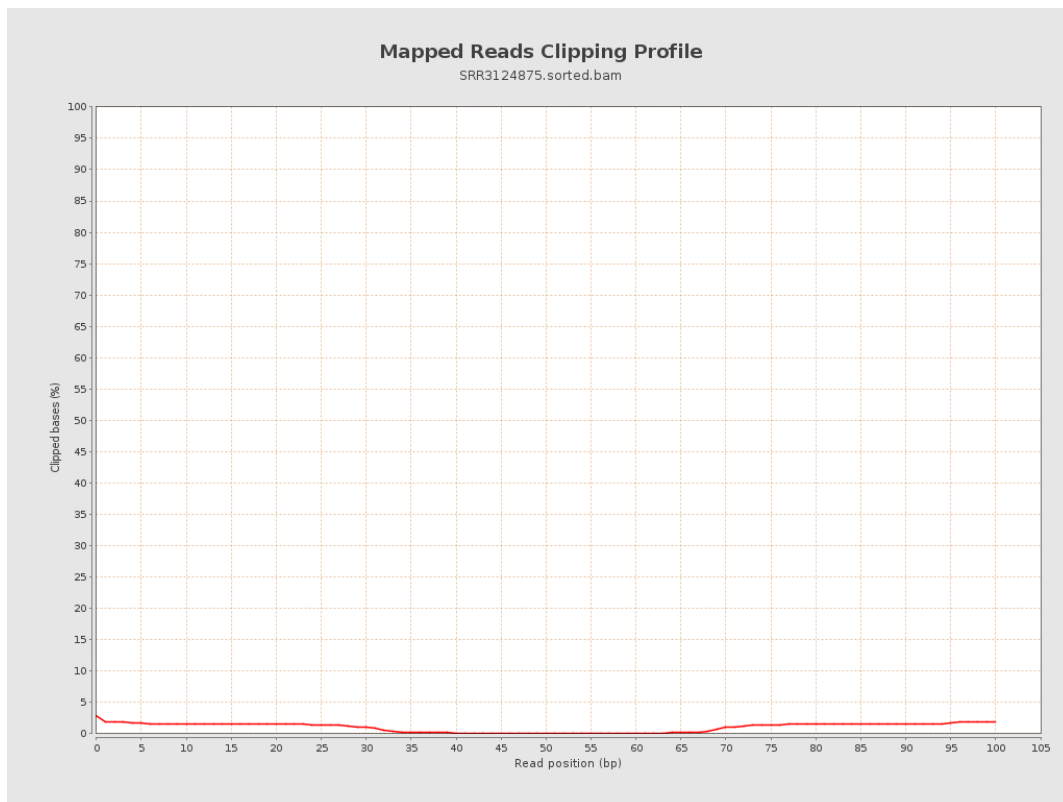
8. Results : Mapped Reads Nucleotide Content



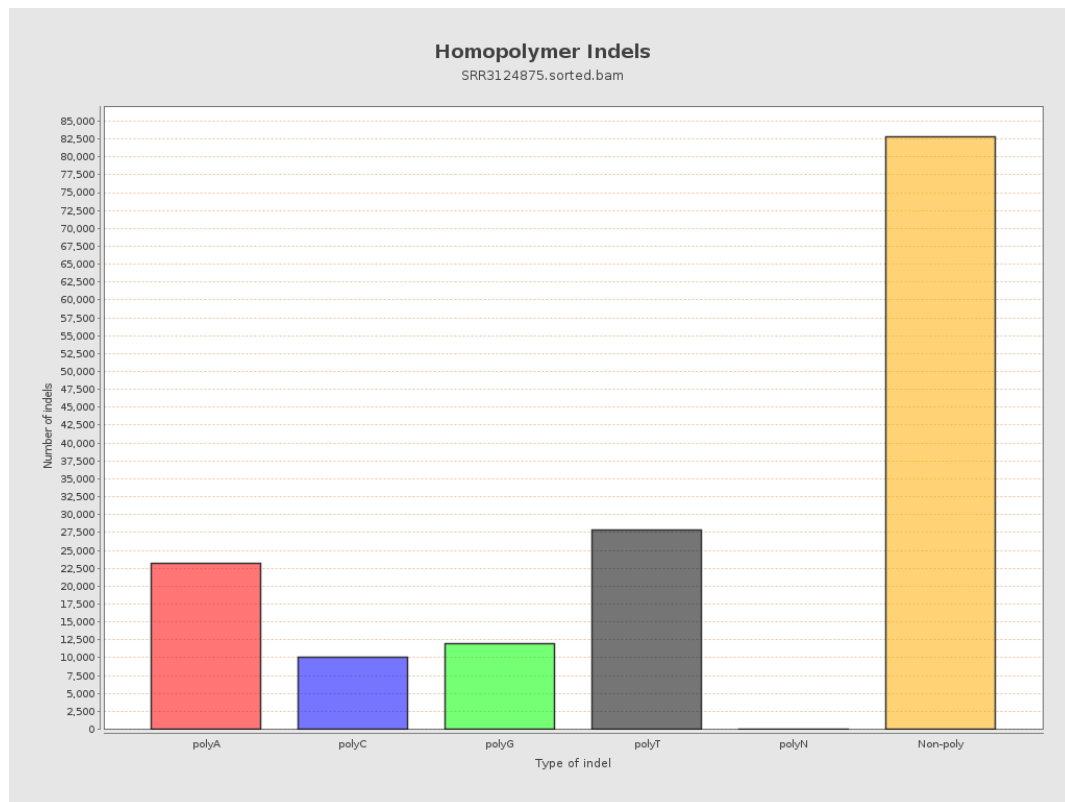
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



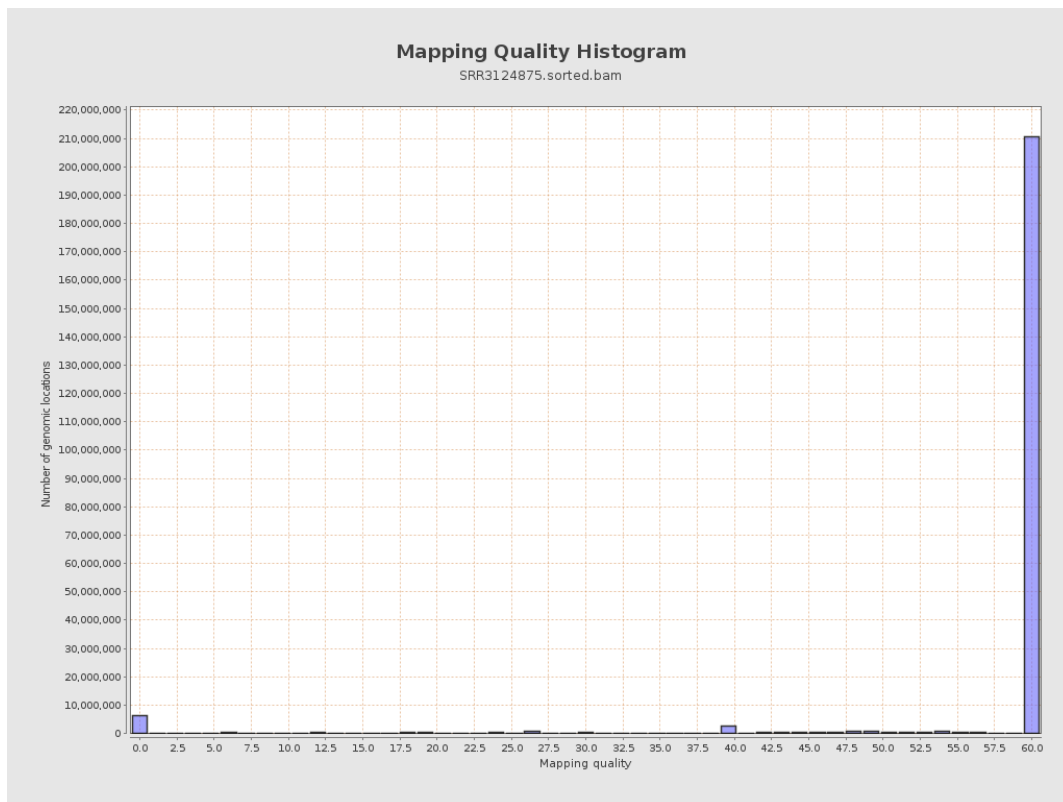
11. Results : Homopolymer Indels



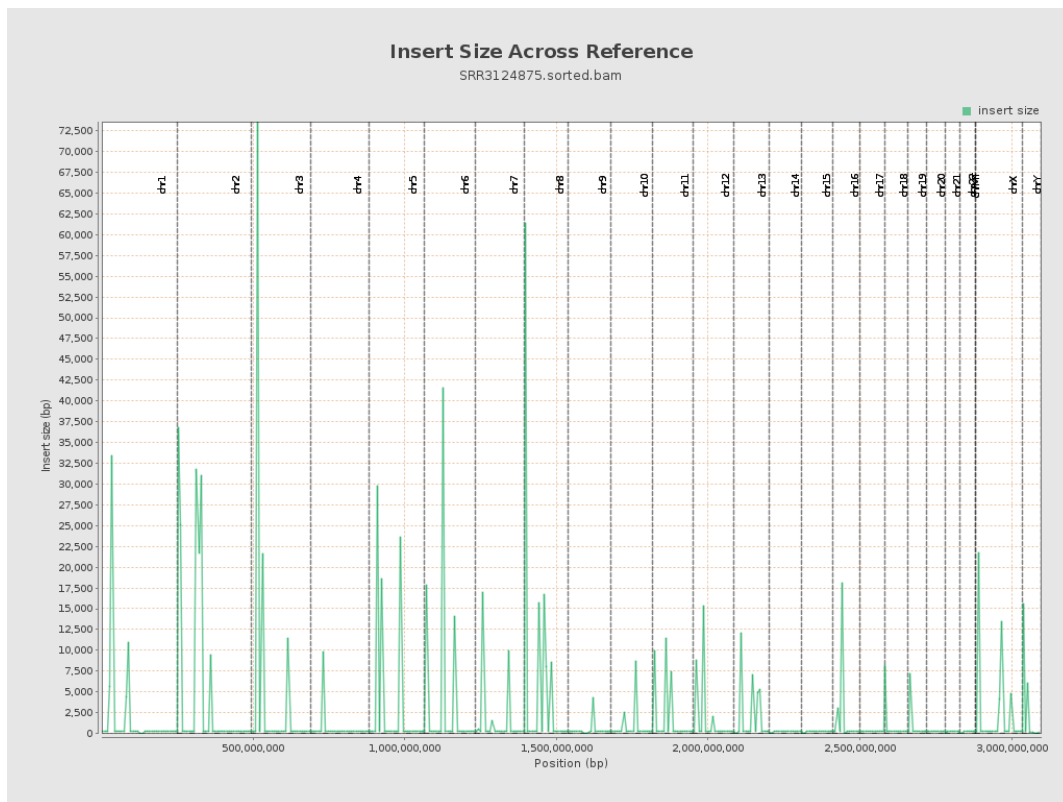
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

