

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 01:42:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173884.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_SRR10173884 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173884_1.fastq.gz SRR10173884_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 01:42:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173884.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,198,740
Mapped reads	4,085,973 / 97.31%
Unmapped reads	112,767 / 2.69%
Mapped paired reads	4,085,973 / 97.31%
Mapped reads, first in pair	2,045,817 / 48.72%
Mapped reads, second in pair	2,040,156 / 48.59%
Mapped reads, both in pair	4,014,948 / 95.62%
Mapped reads, singletons	71,025 / 1.69%
Secondary alignments	0
Supplementary alignments	405,288 / 9.65%
Read min/max/mean length	30 / 133 / 127.6
Duplicated reads (estimated)	2,995,113 / 71.33%
Duplication rate	62.29%
Clipped reads	1,656,795 / 39.46%

2.2. ACGT Content

Number/percentage of A's	145,583,270 / 30.3%
Number/percentage of C's	93,354,862 / 19.43%
Number/percentage of T's	145,026,595 / 30.18%
Number/percentage of G's	96,525,113 / 20.09%
Number/percentage of N's	5,568 / 0%

GC Percentage	39.52%
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2.3. Coverage

Mean	0.1553
Standard Deviation	2.3526

2.4. Mapping Quality

Mean Mapping Quality	52.75
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2.5. Insert size

Mean	690,147.89
Standard Deviation	7,525,664.45
P25/Median/P75	136 / 189 / 270

2.6. Mismatches and indels

General error rate	1.03%
Mismatches	4,825,348
Insertions	50,096
Mapped reads with at least one insertion	1.18%
Deletions	107,362
Mapped reads with at least one deletion	2.57%
Homopolymer indels	43.36%

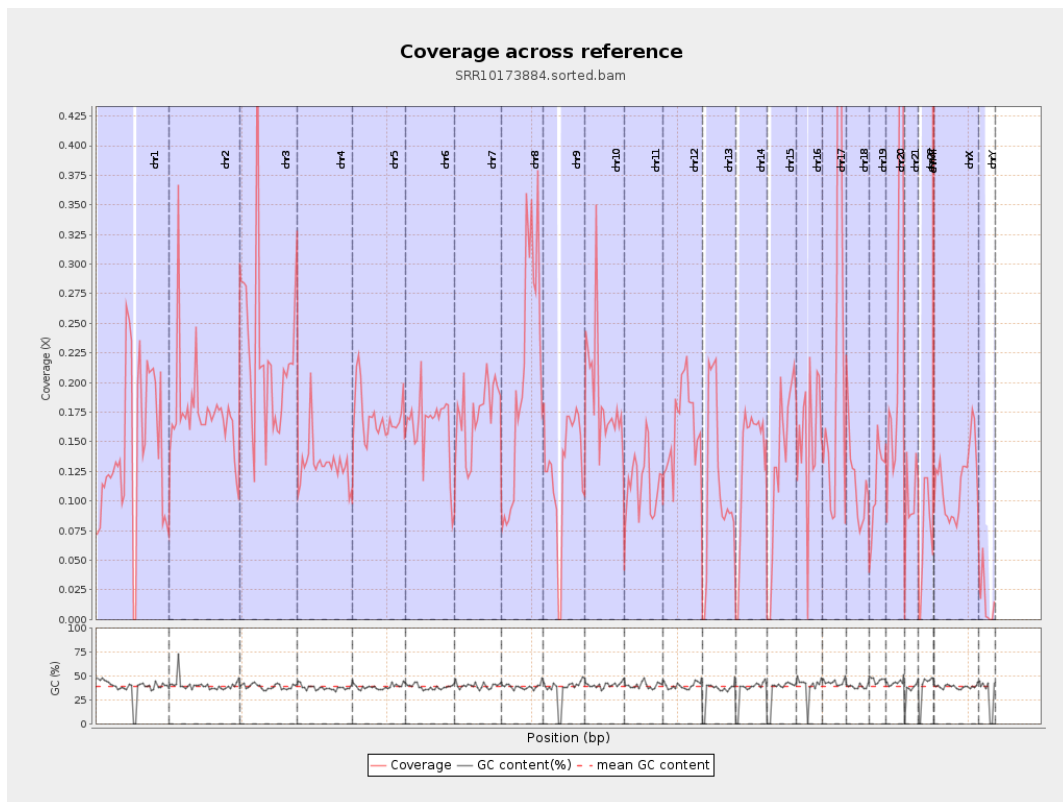
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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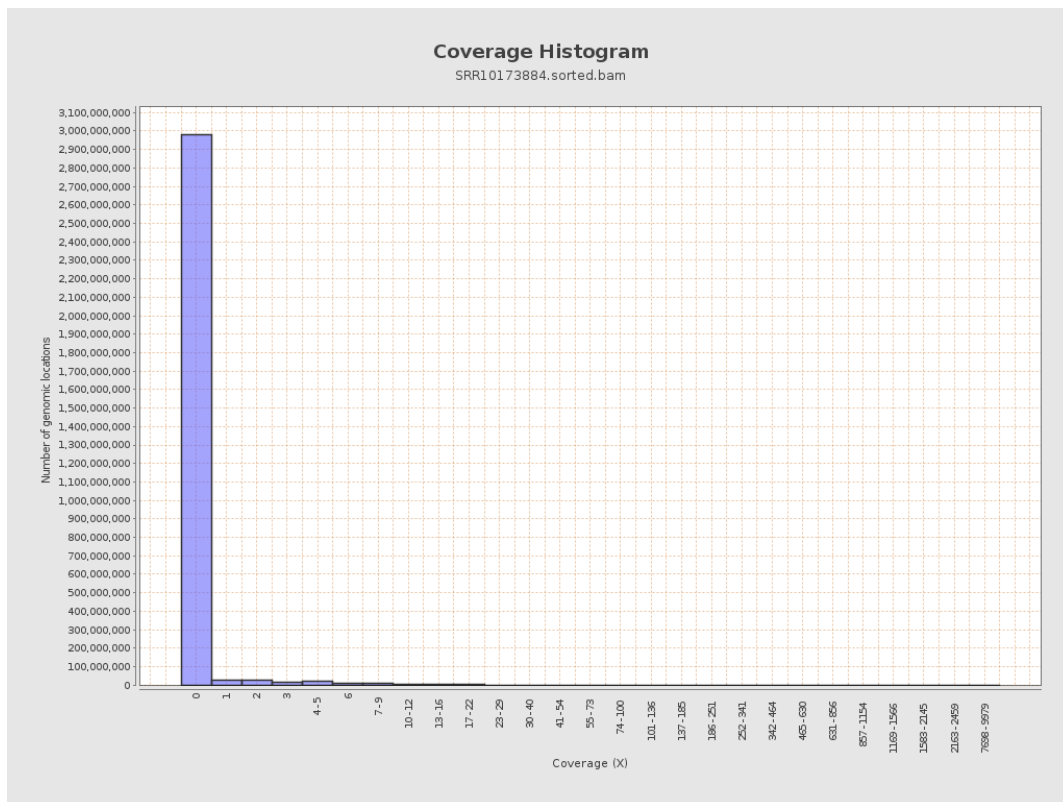
		bases	coverage	deviation
chr1	249250621	35521239	0.1425	1.4733
chr2	243199373	42495560	0.1747	7.0094
chr3	198022430	43674473	0.2206	1.2992
chr4	191154276	24996719	0.1308	1.1709
chr5	180915260	30883275	0.1707	1.1274
chr6	171115067	27755774	0.1622	1.2281
chr7	159138663	27825353	0.1748	1.4606
chr8	146364022	29537791	0.2018	1.5526
chr9	141213431	17956072	0.1272	1.1707
chr10	135534747	25495976	0.1881	2.271
chr11	135006516	15516812	0.1149	0.924
chr12	133851895	21820077	0.163	1.0959
chr13	115169878	12908938	0.1121	0.9173
chr14	107349540	14374913	0.1339	0.9871
chr15	102531392	13762069	0.1342	0.9851
chr16	90354753	13883025	0.1537	1.403
chr17	81195210	18724724	0.2306	1.4249
chr18	78077248	9148716	0.1172	1.6716
chr19	59128983	6837852	0.1156	1.2094
chr20	63025520	18451329	0.2928	1.5931
chr21	48129895	4803747	0.0998	0.9357
chr22	51304566	3499500	0.0682	0.6884
chrMT	16571	1980801	119.5342	87.7696
chrX	155270560	18026923	0.1161	0.9232

chrY	59373566	874739	0.0147	0.5956
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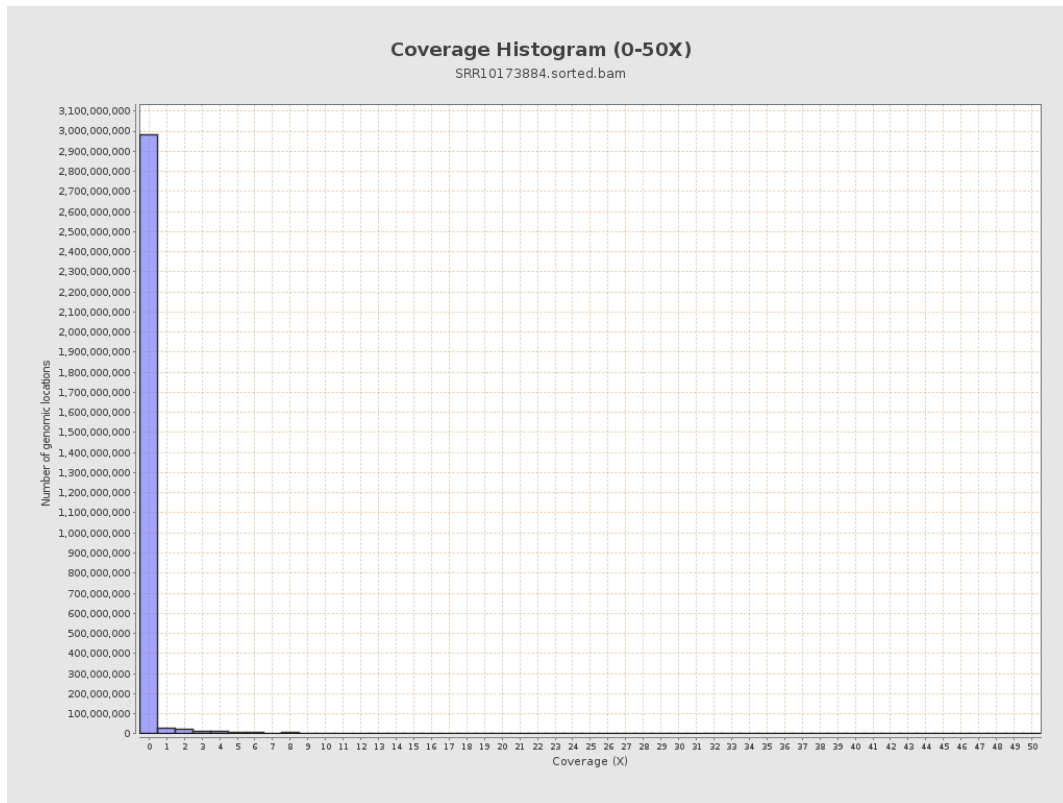
3. Results : Coverage across reference



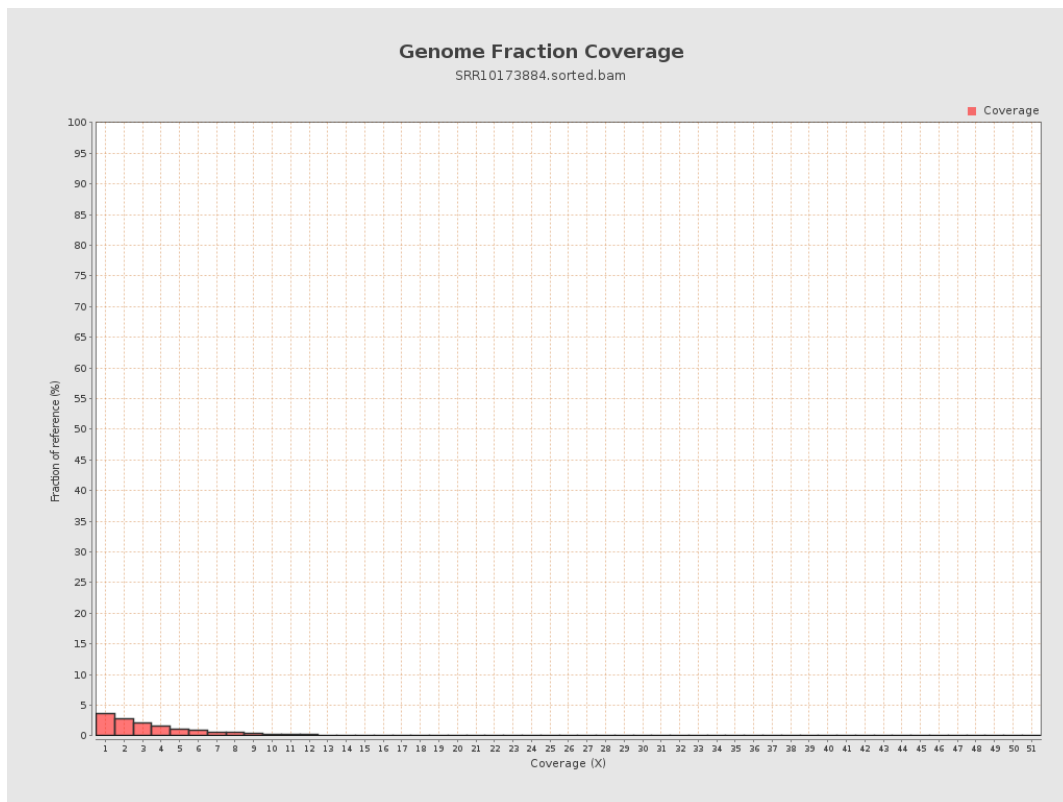
4. Results : Coverage Histogram



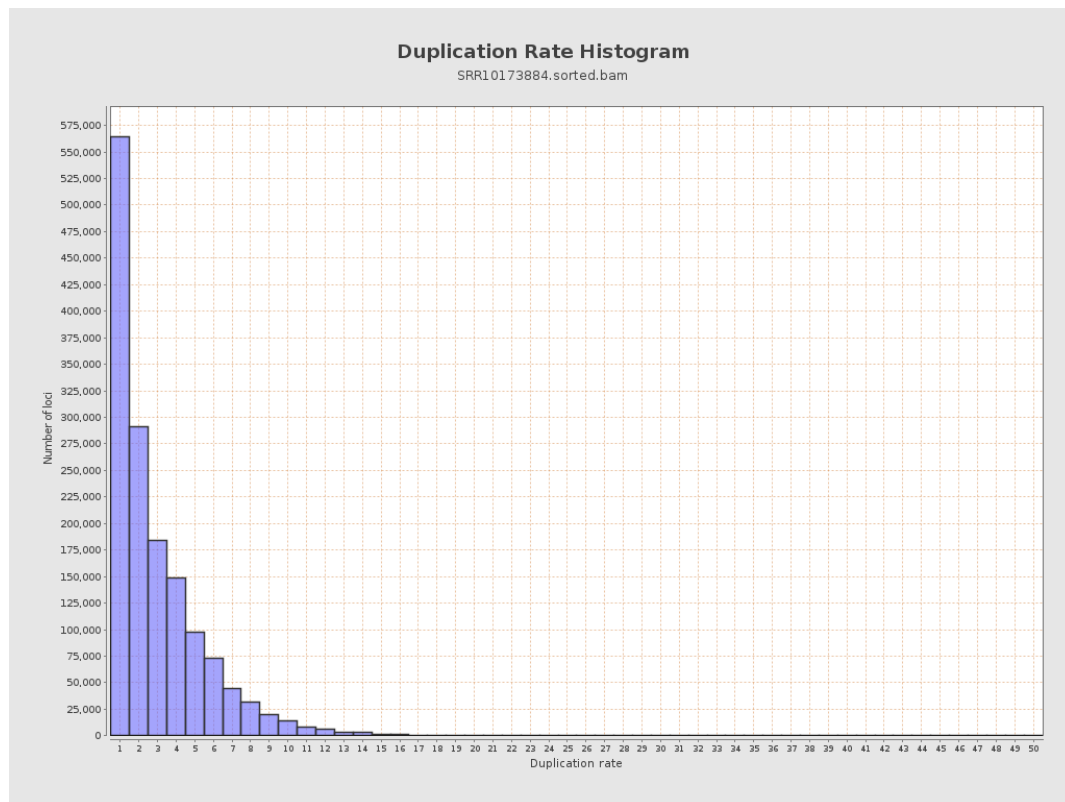
5. Results : Coverage Histogram (0-50X)



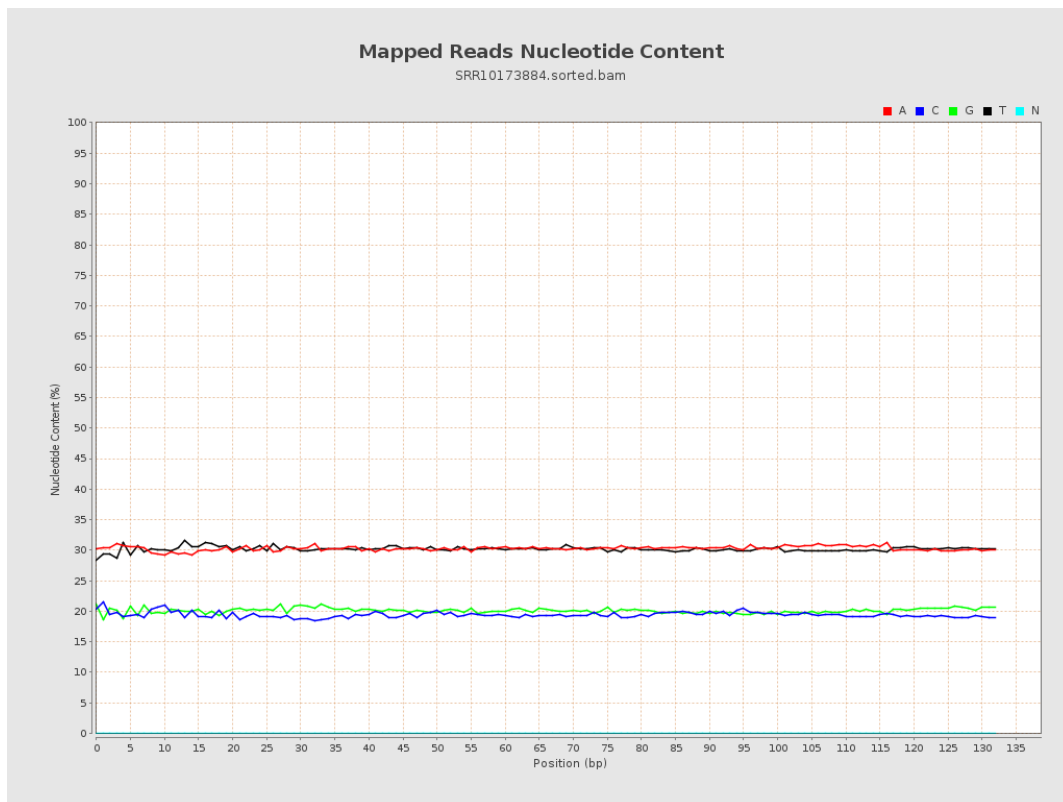
6. Results : Genome Fraction Coverage



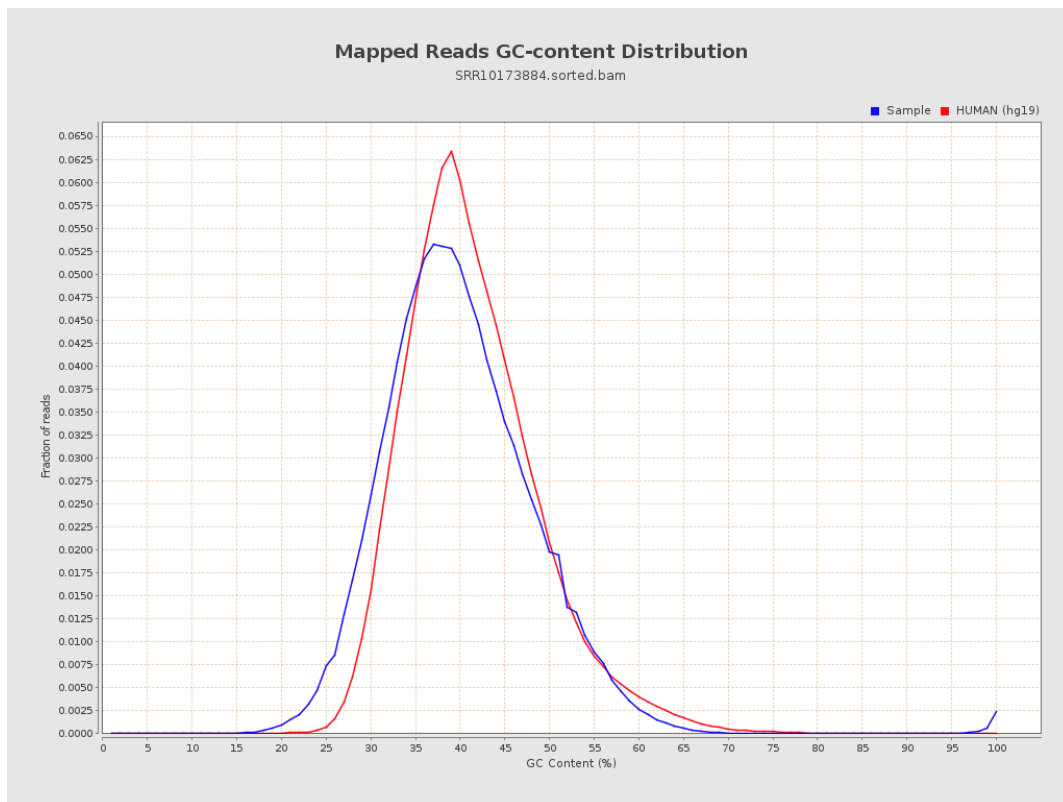
7. Results : Duplication Rate Histogram



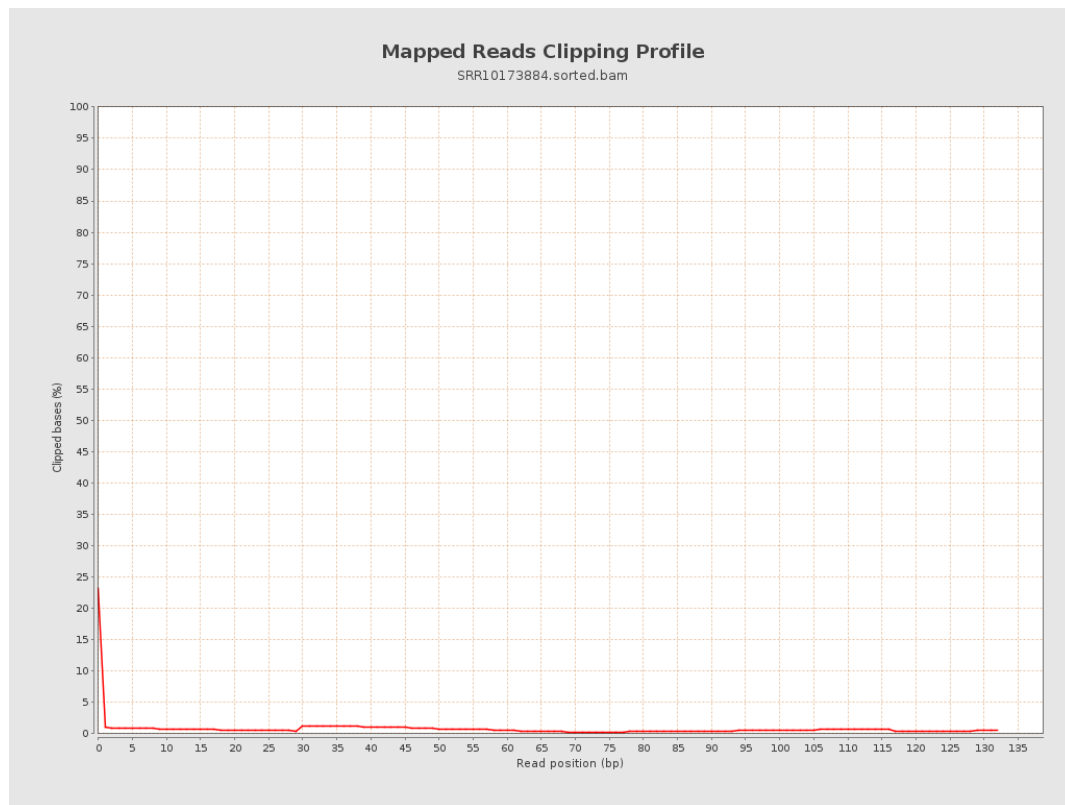
8. Results : Mapped Reads Nucleotide Content



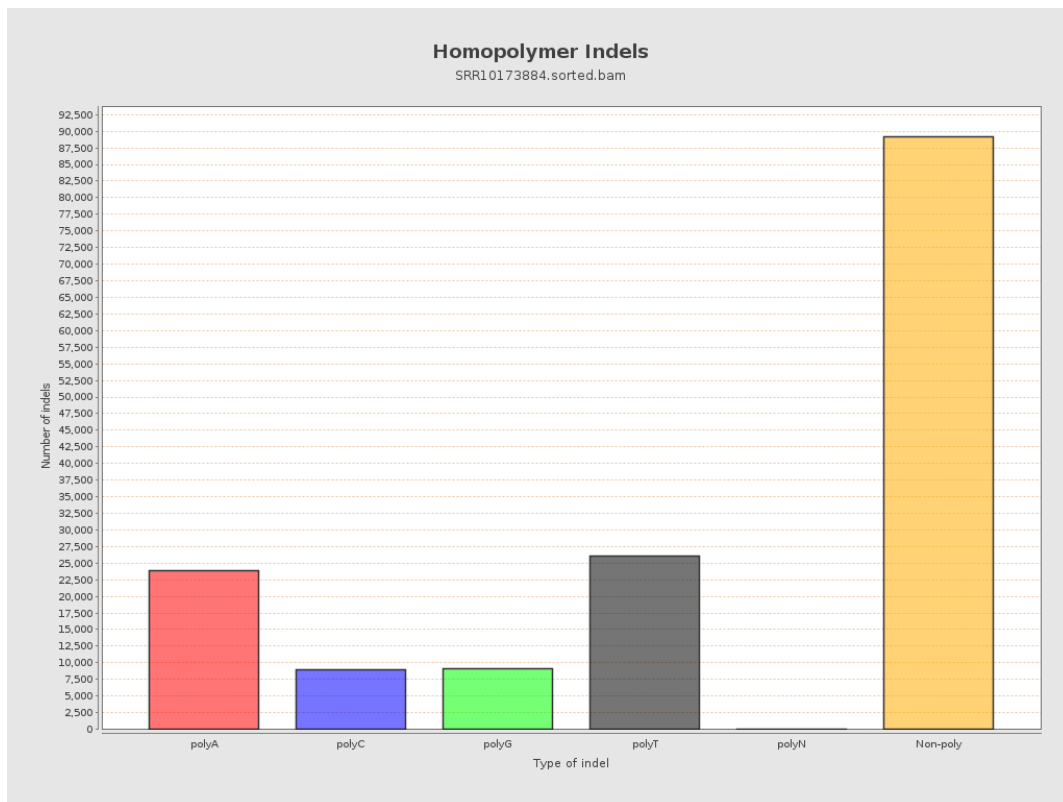
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



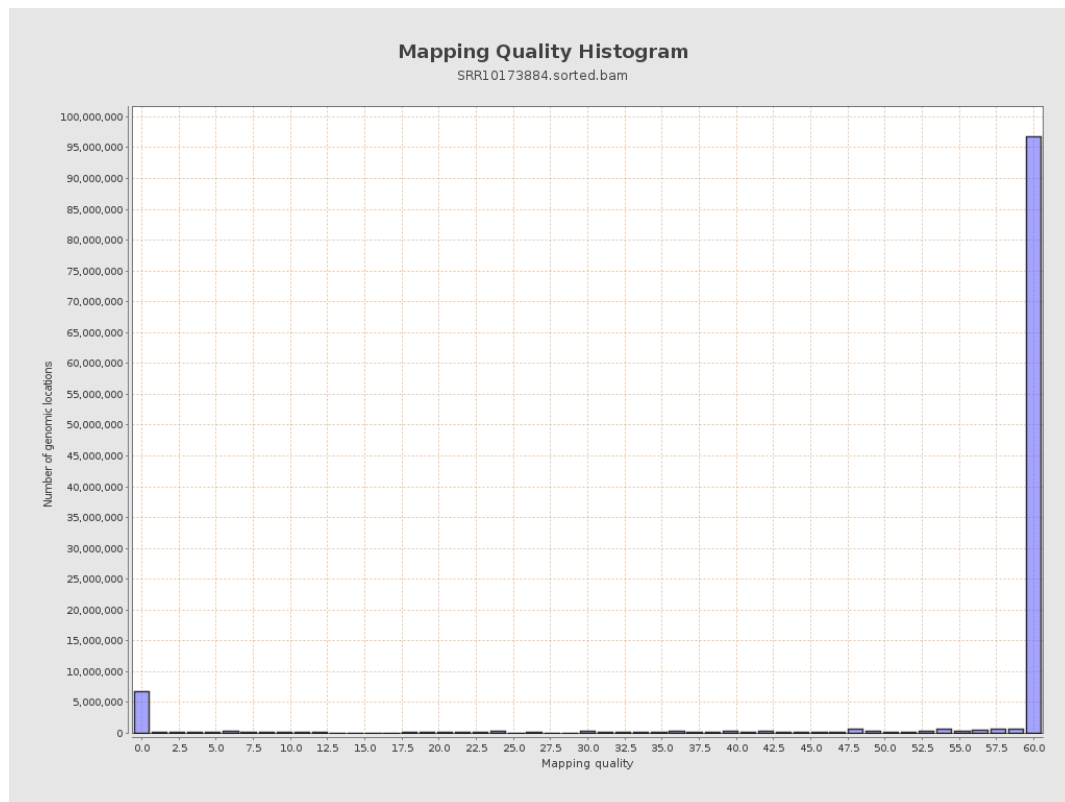
11. Results : Homopolymer Indels



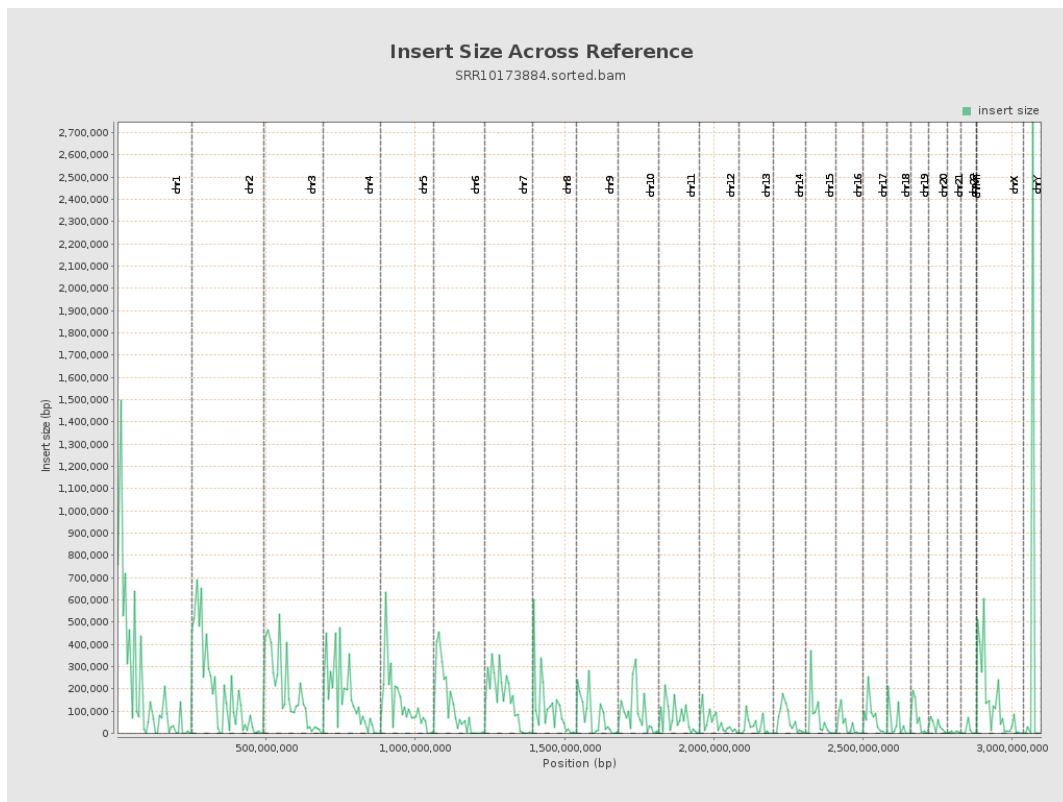
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

