

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/07 16:08:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779086.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_SRR1779086 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779086_1.fastq.gz SRR1779086_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Oct 07 16:08:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779086.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,829,940
Mapped reads	5,645,628 / 96.84%
Unmapped reads	184,312 / 3.16%
Mapped paired reads	5,645,628 / 96.84%
Mapped reads, first in pair	2,846,200 / 48.82%
Mapped reads, second in pair	2,799,428 / 48.02%
Mapped reads, both in pair	5,577,656 / 95.67%
Mapped reads, singletons	67,972 / 1.17%
Secondary alignments	0
Supplementary alignments	31,160 / 0.53%
Read min/max/mean length	30 / 101 / 101.21
Duplicated reads (estimated)	82,029 / 1.41%
Duplication rate	1.33%
Clipped reads	370,843 / 6.36%

2.2. ACGT Content

Number/percentage of A's	170,906,092 / 30.32%
Number/percentage of C's	110,369,171 / 19.58%
Number/percentage of T's	170,067,438 / 30.17%
Number/percentage of G's	112,082,520 / 19.89%
Number/percentage of N's	191,729 / 0.03%

GC Percentage	39.47%
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2.3. Coverage

Mean	0.1821
Standard Deviation	0.62

2.4. Mapping Quality

Mean Mapping Quality	53.64
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2.5. Insert size

Mean	65,506.4
Standard Deviation	2,469,791.54
P25/Median/P75	157 / 207 / 278

2.6. Mismatches and indels

General error rate	0.47%
Mismatches	2,572,537
Insertions	47,106
Mapped reads with at least one insertion	0.82%
Deletions	57,523
Mapped reads with at least one deletion	1%
Homopolymer indels	46.65%

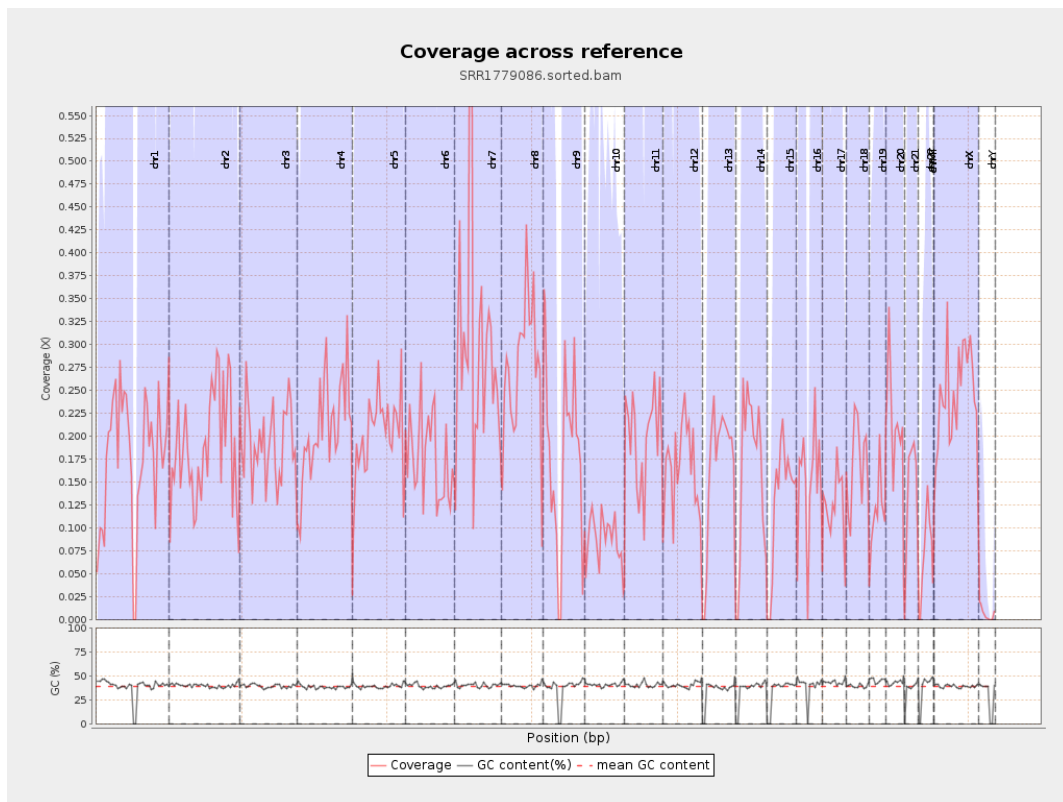
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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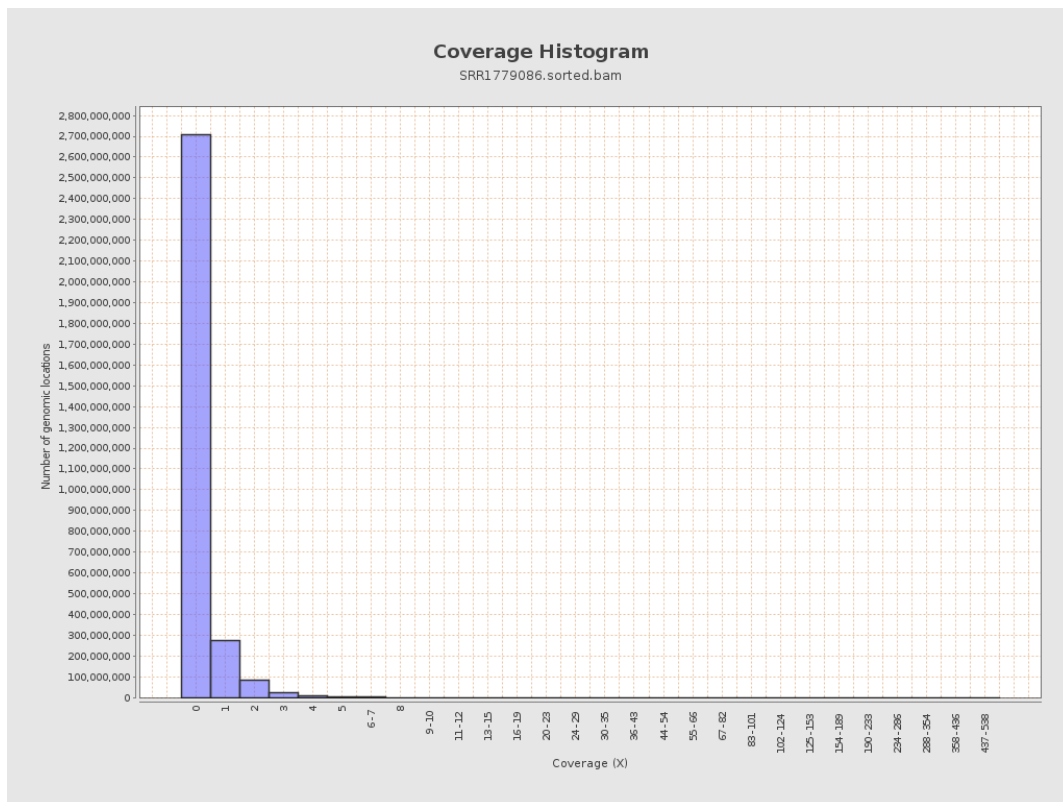
		bases	coverage	deviation
chr1	249250621	43753135	0.1755	0.7734
chr2	243199373	45458094	0.1869	0.6068
chr3	198022430	38318077	0.1935	0.5783
chr4	191154276	39887648	0.2087	0.6005
chr5	180915260	36513241	0.2018	0.5804
chr6	171115067	30322863	0.1772	0.5503
chr7	159138663	48312749	0.3036	0.9988
chr8	146364022	40147293	0.2743	0.6888
chr9	141213431	24580431	0.1741	0.5738
chr10	135534747	12043660	0.0889	0.6497
chr11	135006516	26485700	0.1962	0.5816
chr12	133851895	22190908	0.1658	0.5338
chr13	115169878	18816963	0.1634	0.5303
chr14	107349540	17535501	0.1633	0.5372
chr15	102531392	13458326	0.1313	0.471
chr16	90354753	13564756	0.1501	0.5015
chr17	81195210	9960754	0.1227	0.4647
chr18	78077248	13114407	0.168	0.547
chr19	59128983	7199373	0.1218	0.5802
chr20	63025520	13497547	0.2142	0.6028
chr21	48129895	6563809	0.1364	0.484
chr22	51304566	3679871	0.0717	0.3357
chrMT	16571	1398	0.0844	0.2892
chrX	155270560	37941367	0.2444	0.662

chrY	59373566	397100	0.0067	0.1239
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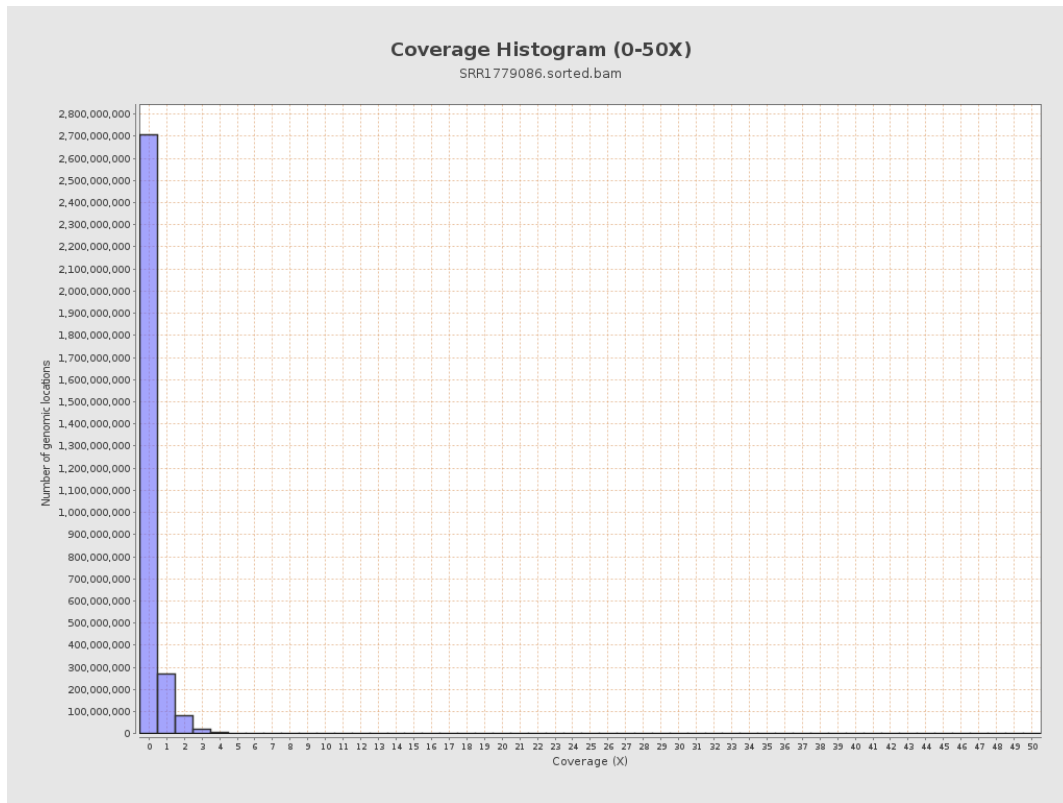
3. Results : Coverage across reference



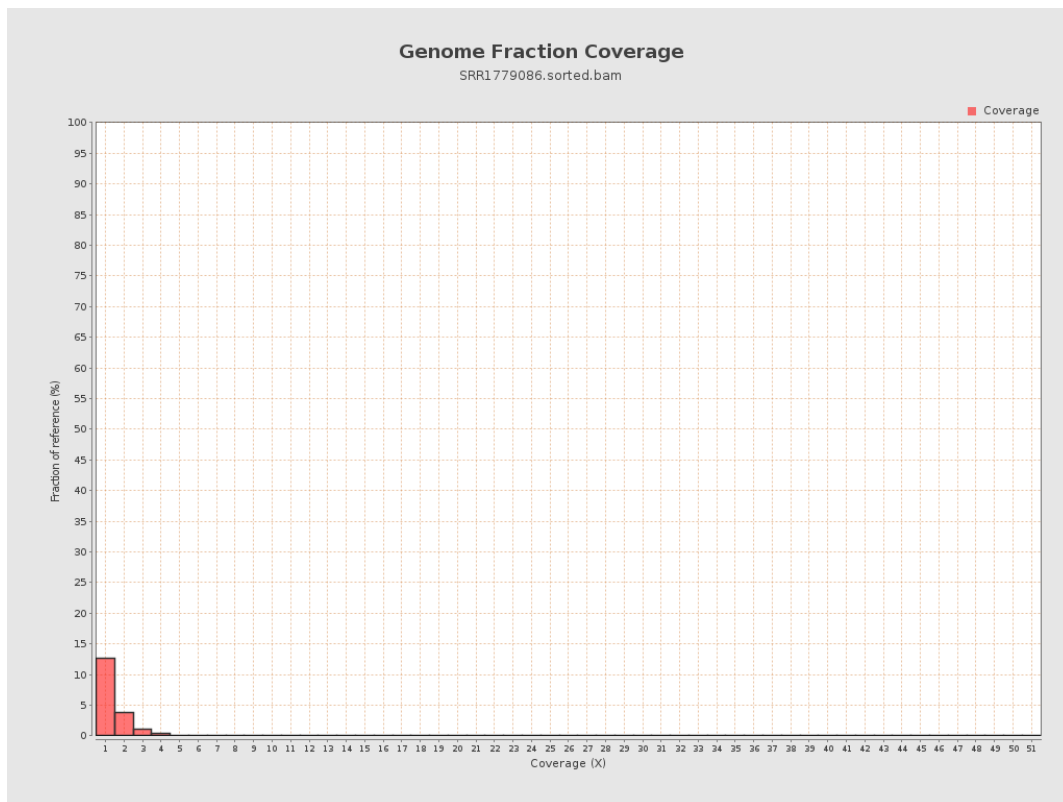
4. Results : Coverage Histogram



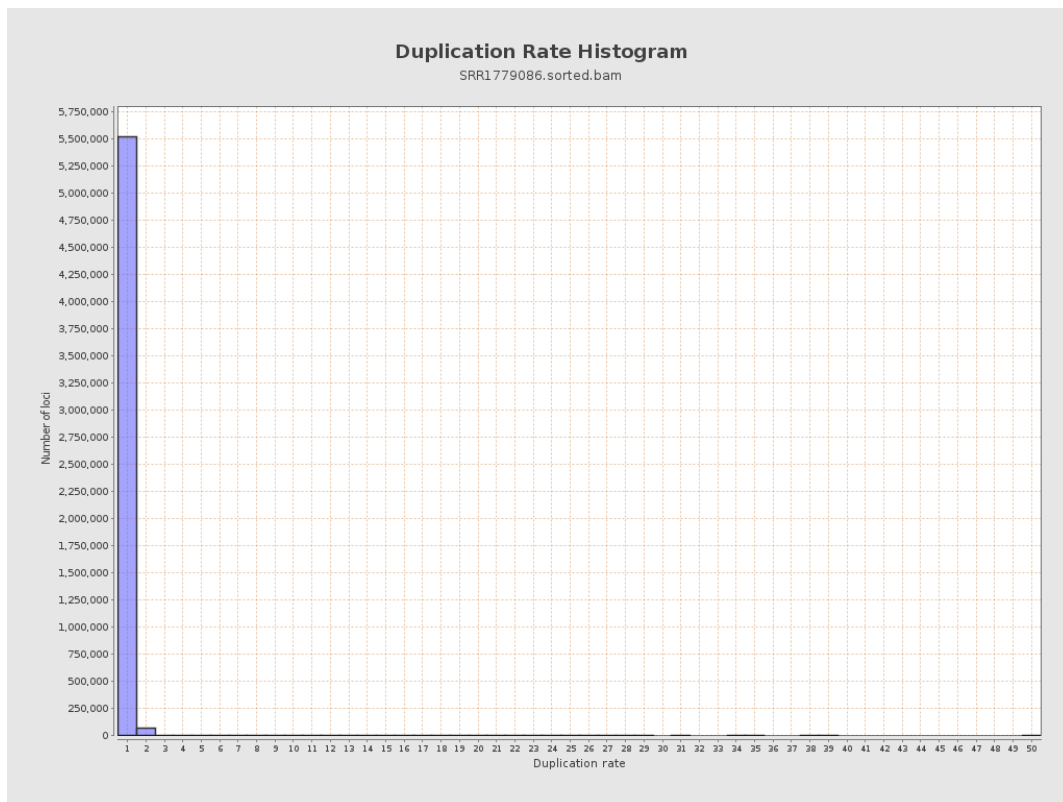
5. Results : Coverage Histogram (0-50X)



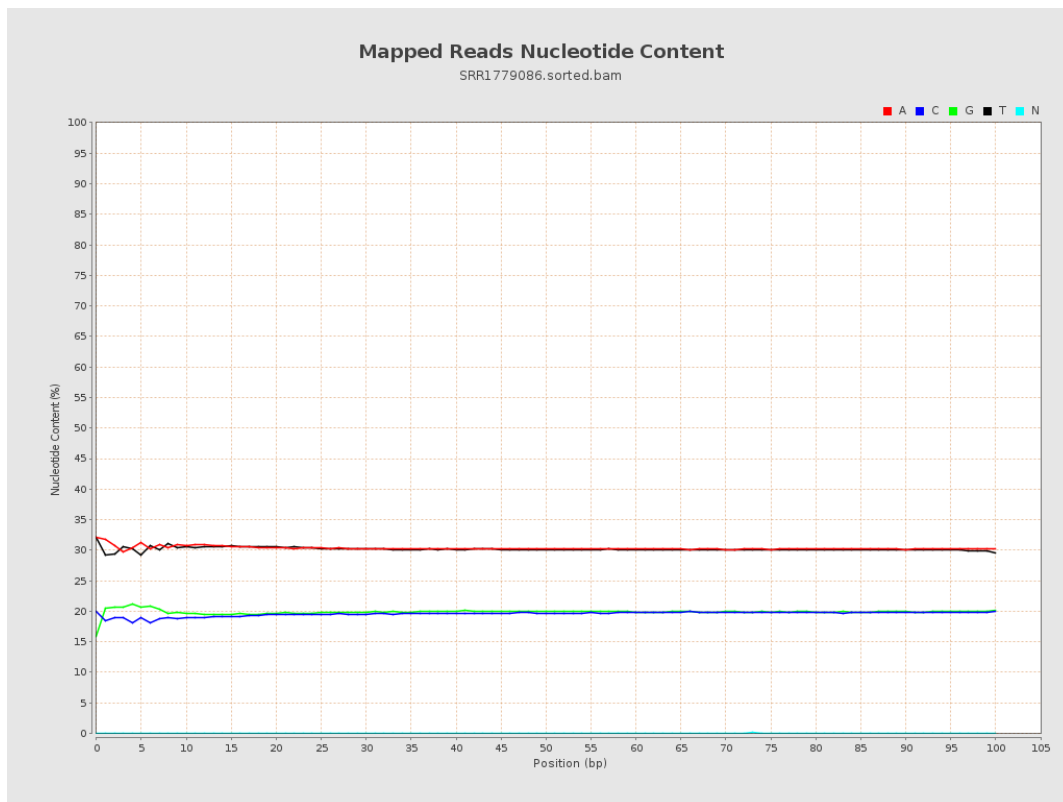
6. Results : Genome Fraction Coverage



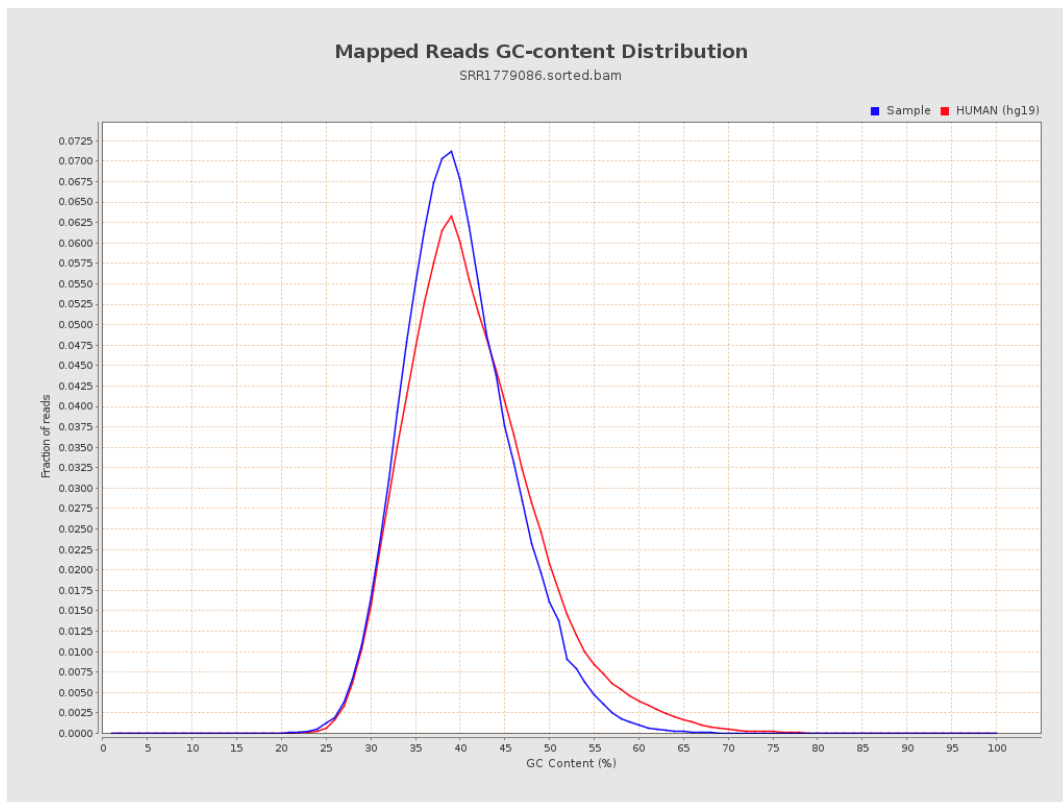
7. Results : Duplication Rate Histogram



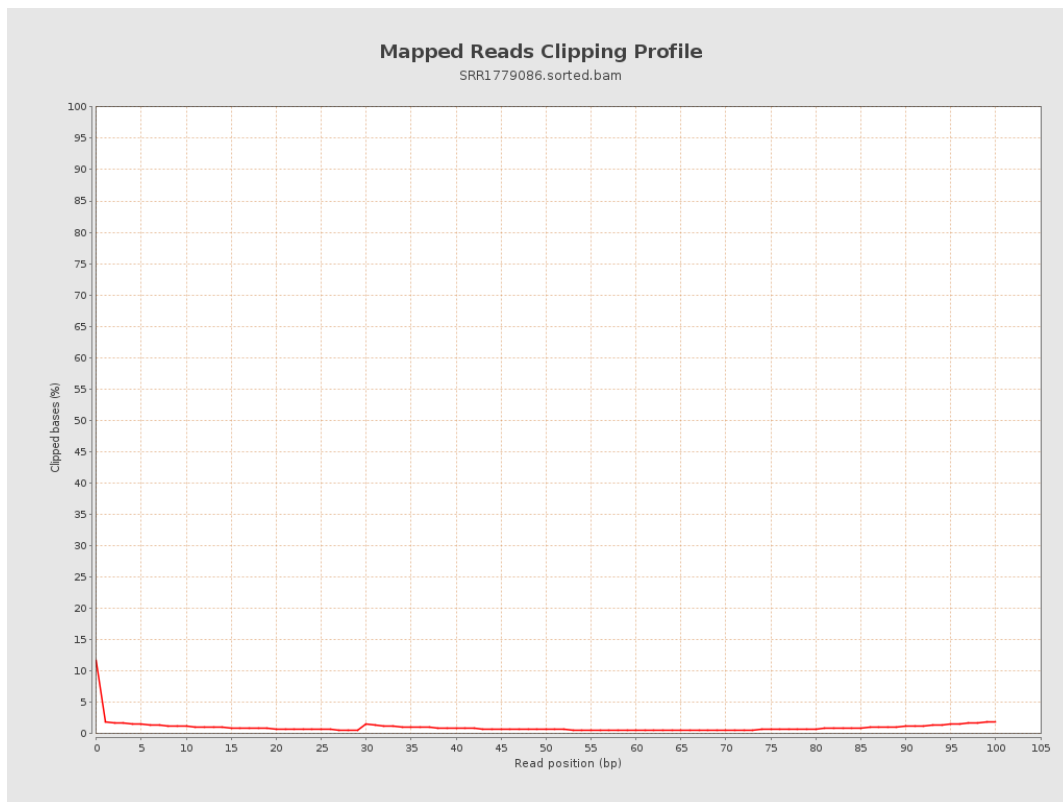
8. Results : Mapped Reads Nucleotide Content



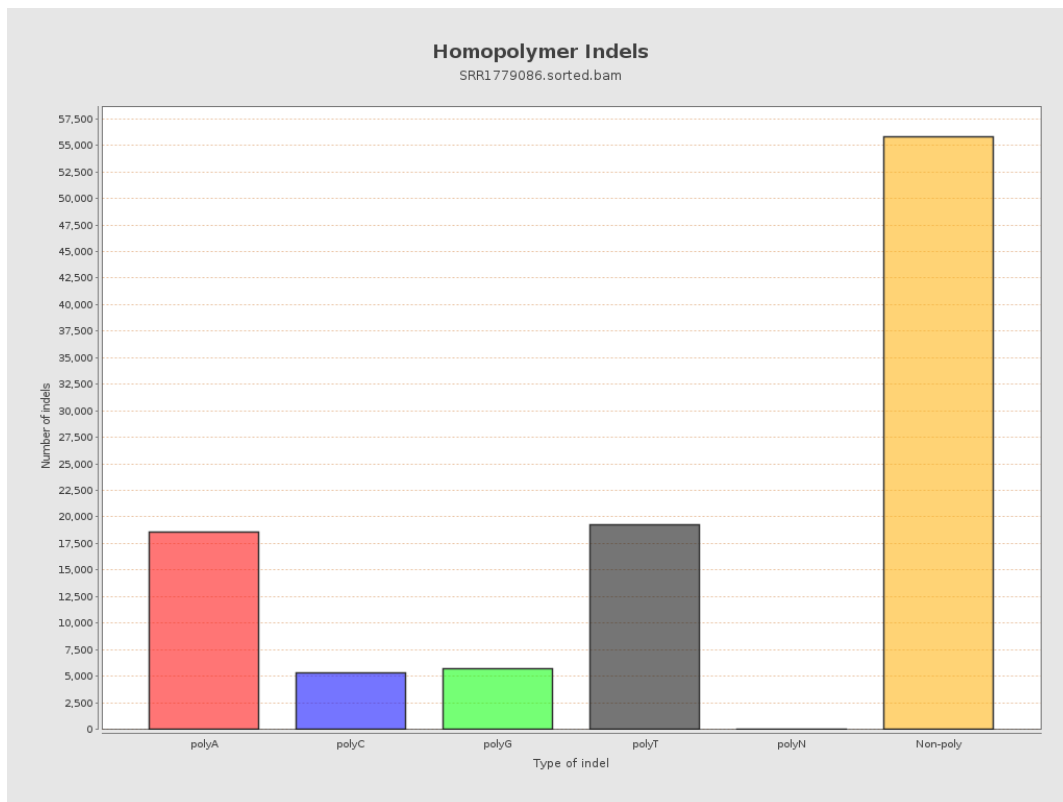
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



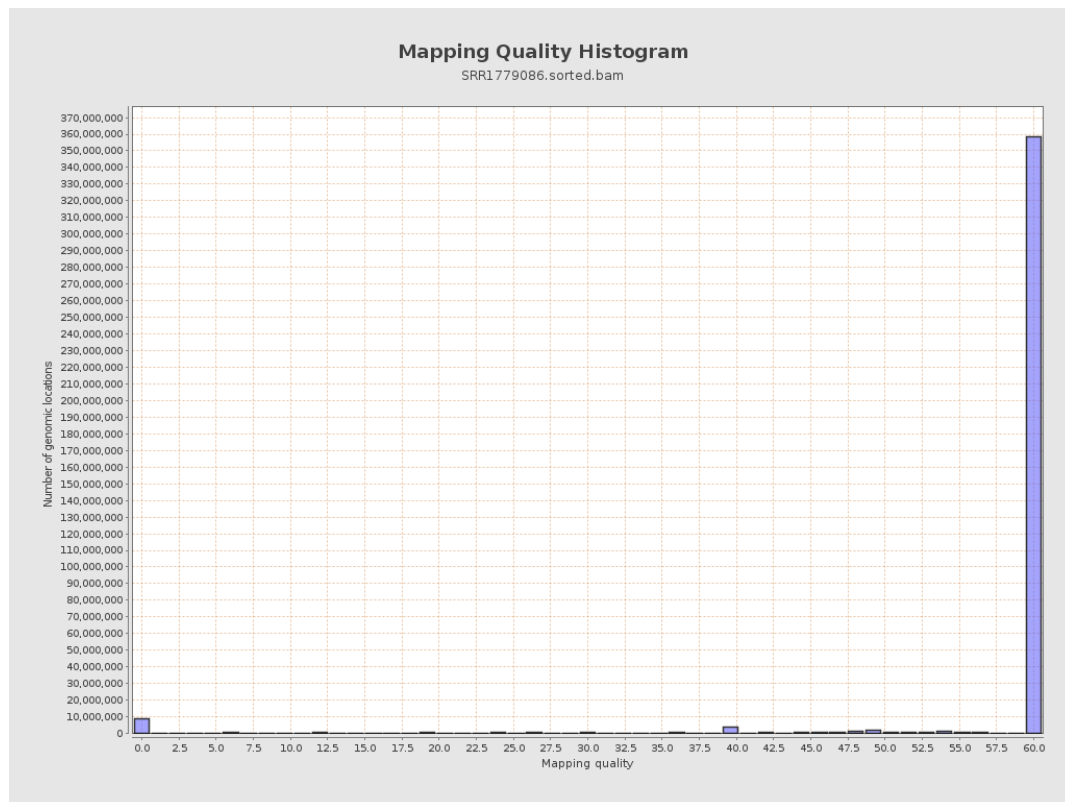
11. Results : Homopolymer Indels



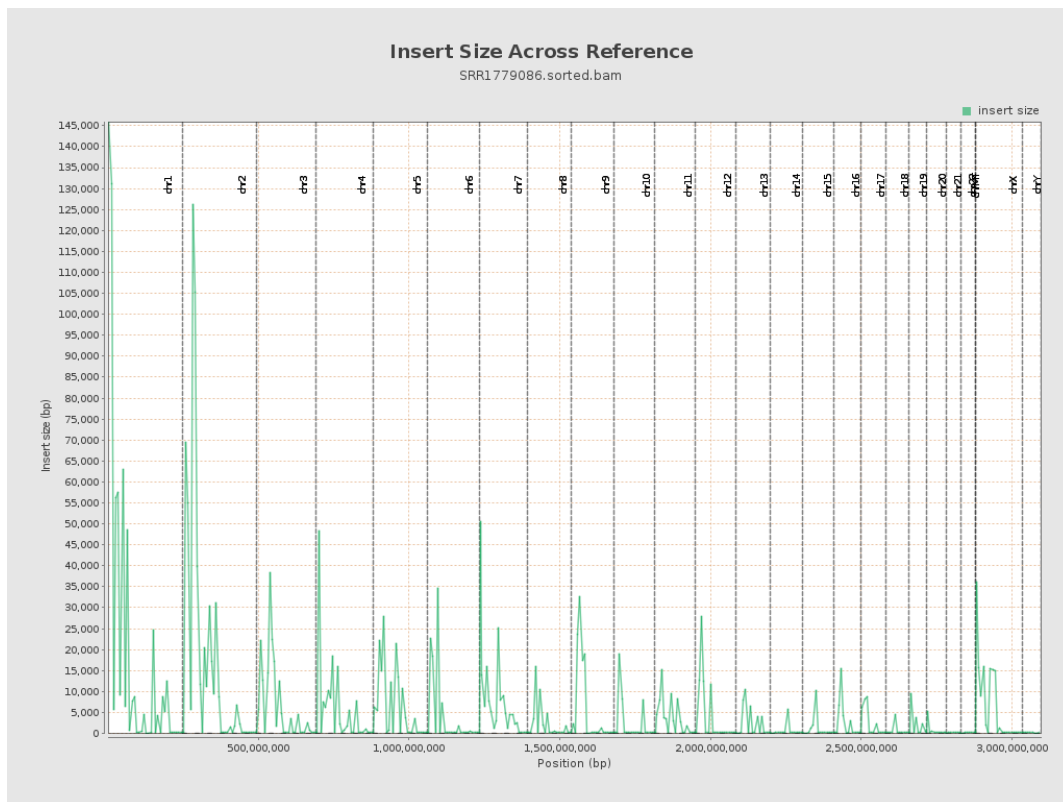
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

