

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/08 10:56:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779174.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_SRR1779174 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779174_1.fastq.gz SRR1779174_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 08 10:56:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779174.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	33,033,076
Mapped reads	32,255,950 / 97.65%
Unmapped reads	777,126 / 2.35%
Mapped paired reads	32,255,950 / 97.65%
Mapped reads, first in pair	16,220,126 / 49.1%
Mapped reads, second in pair	16,035,824 / 48.54%
Mapped reads, both in pair	31,968,656 / 96.78%
Mapped reads, singletons	287,294 / 0.87%
Secondary alignments	0
Supplementary alignments	195,976 / 0.59%
Read min/max/mean length	30 / 101 / 101.24
Duplicated reads (estimated)	1,414,145 / 4.28%
Duplication rate	3.74%
Clipped reads	2,117,984 / 6.41%

2.2. ACGT Content

Number/percentage of A's	982,638,984 / 30.5%
Number/percentage of C's	626,982,518 / 19.46%
Number/percentage of T's	972,784,744 / 30.2%
Number/percentage of G's	637,791,517 / 19.8%
Number/percentage of N's	1,301,370 / 0.04%

GC Percentage	39.26%
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2.3. Coverage

Mean	1.0409
Standard Deviation	3.0427

2.4. Mapping Quality

Mean Mapping Quality	53.43
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2.5. Insert size

Mean	79,462.52
Standard Deviation	2,699,427.76
P25/Median/P75	151 / 201 / 273

2.6. Mismatches and indels

General error rate	0.42%
Mismatches	12,983,827
Insertions	266,800
Mapped reads with at least one insertion	0.82%
Deletions	322,970
Mapped reads with at least one deletion	0.98%
Homopolymer indels	46.44%

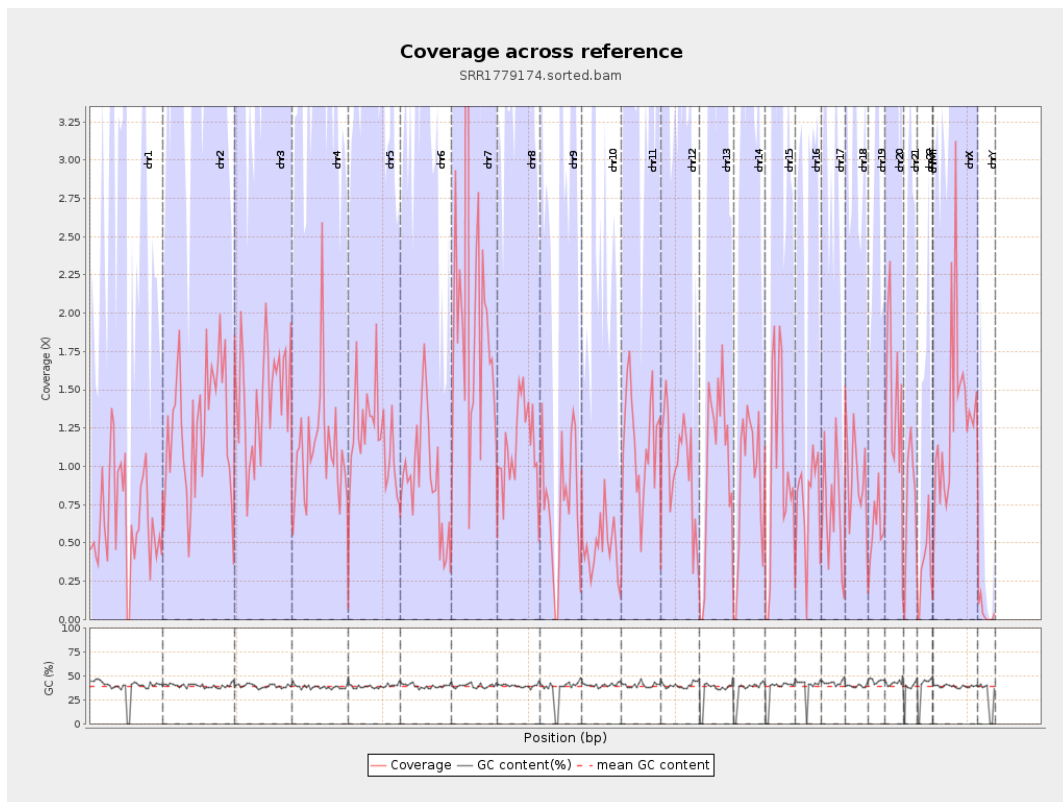
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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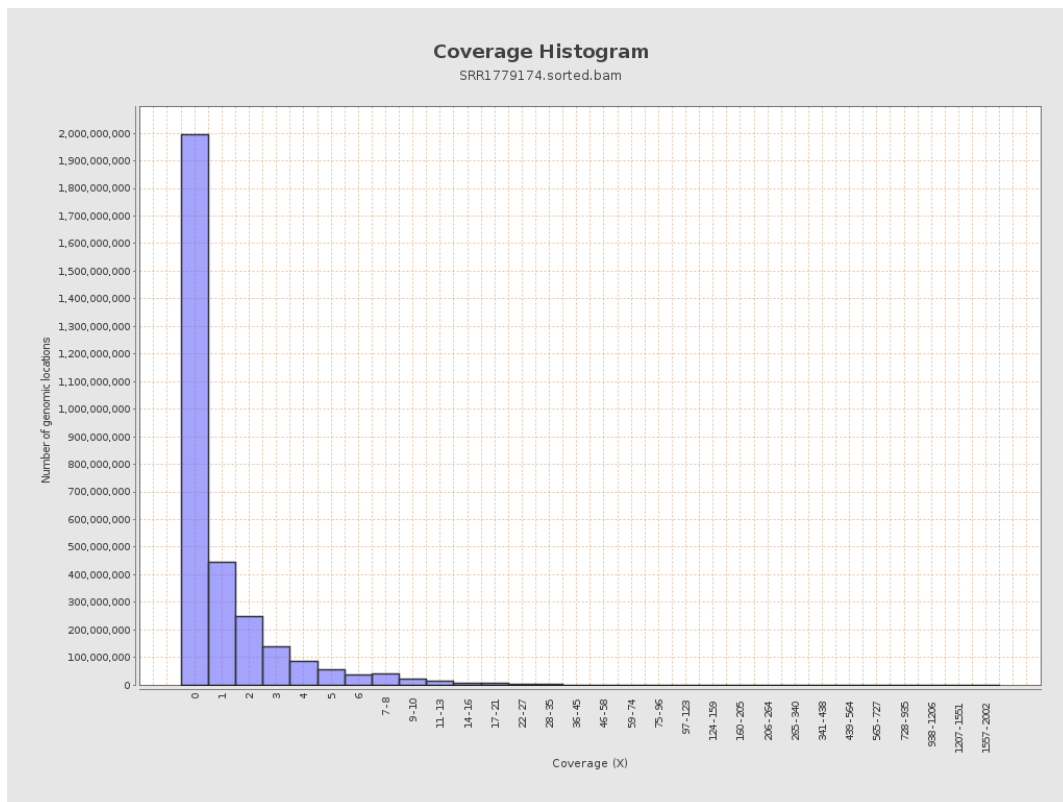
		bases	coverage	deviation
chr1	249250621	163020683	0.654	2.3471
chr2	243199373	306085755	1.2586	2.7194
chr3	198022430	288109636	1.4549	2.6231
chr4	191154276	212146724	1.1098	2.3247
chr5	180915260	213539557	1.1803	2.2924
chr6	171115067	158601270	0.9269	2.1313
chr7	159138663	350355775	2.2016	8.6571
chr8	146364022	166350955	1.1366	2.2469
chr9	141213431	106365726	0.7532	1.9019
chr10	135534747	64579726	0.4765	3.3214
chr11	135006516	156062381	1.156	2.3355
chr12	133851895	134885887	1.0077	2.1992
chr13	115169878	117130265	1.017	2.2351
chr14	107349540	96103593	0.8952	2.2441
chr15	102531392	98292206	0.9587	2.2851
chr16	90354753	67920642	0.7517	1.7961
chr17	81195210	58513080	0.7206	1.945
chr18	78077248	73420031	0.9404	1.9857
chr19	59128983	35662898	0.6031	1.9
chr20	63025520	91283718	1.4484	2.7579
chr21	48129895	36316715	0.7546	1.7148
chr22	51304566	18368632	0.358	1.1693
chrMT	16571	2322	0.1401	0.5052
chrX	155270560	206538063	1.3302	2.8989

chrY	59373566	2567915	0.0433	0.819
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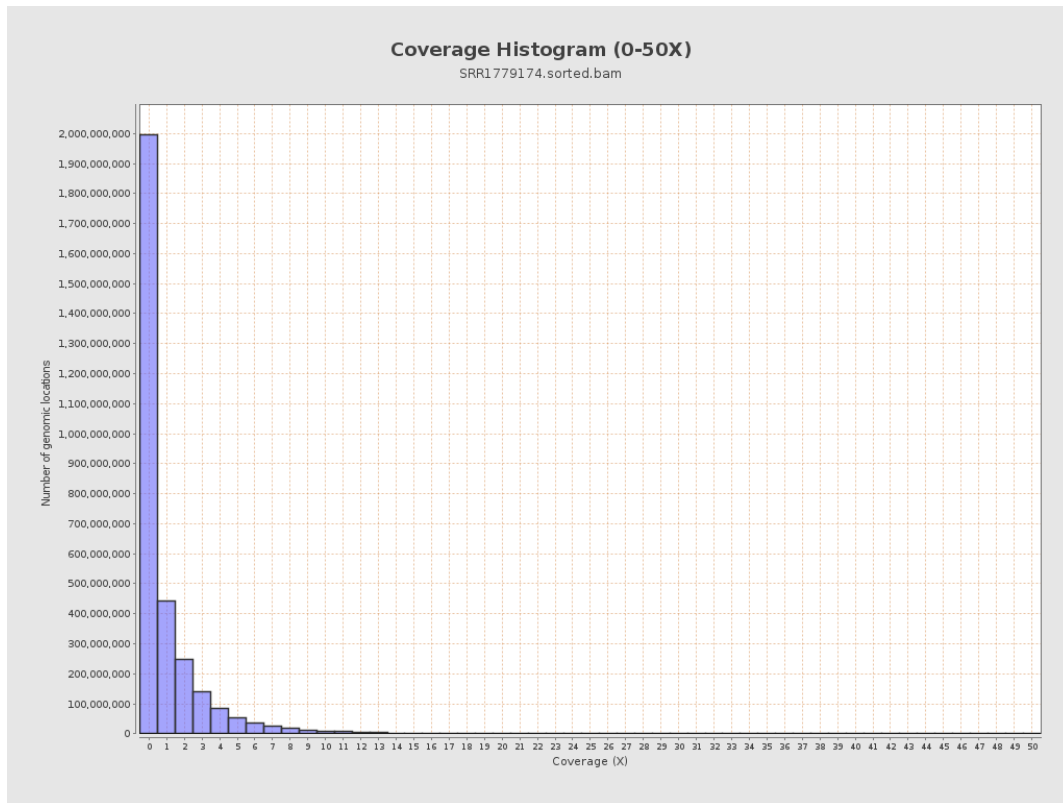
3. Results : Coverage across reference



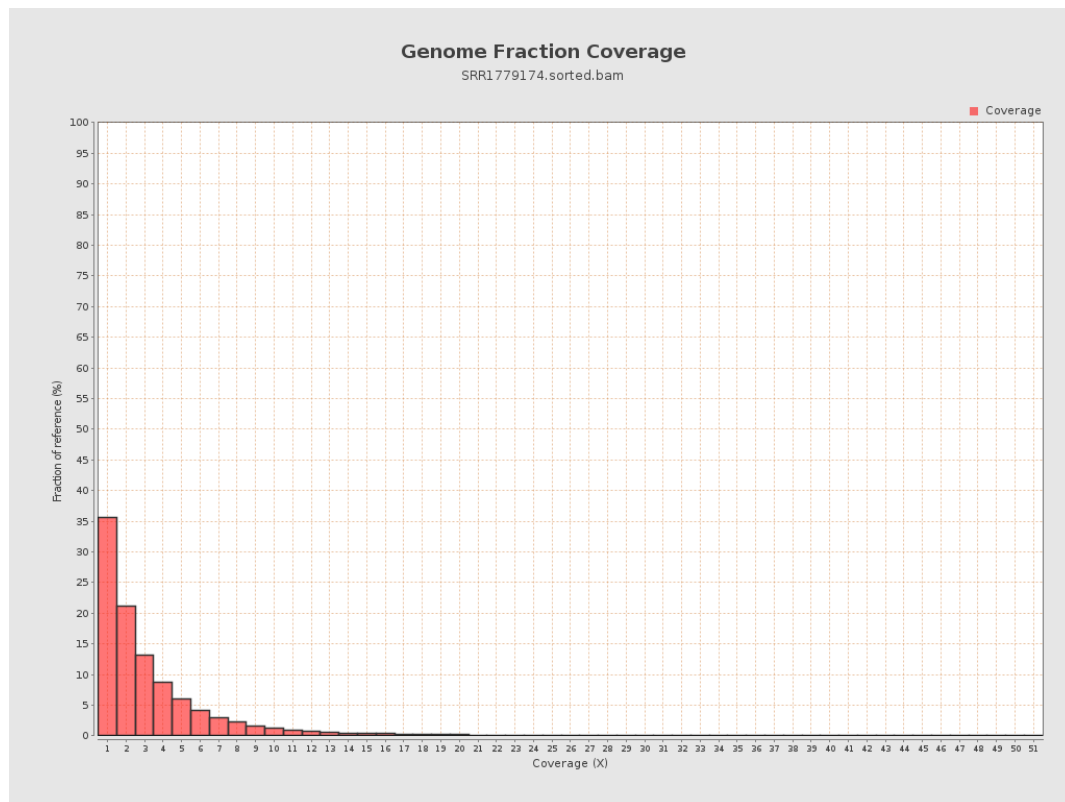
4. Results : Coverage Histogram



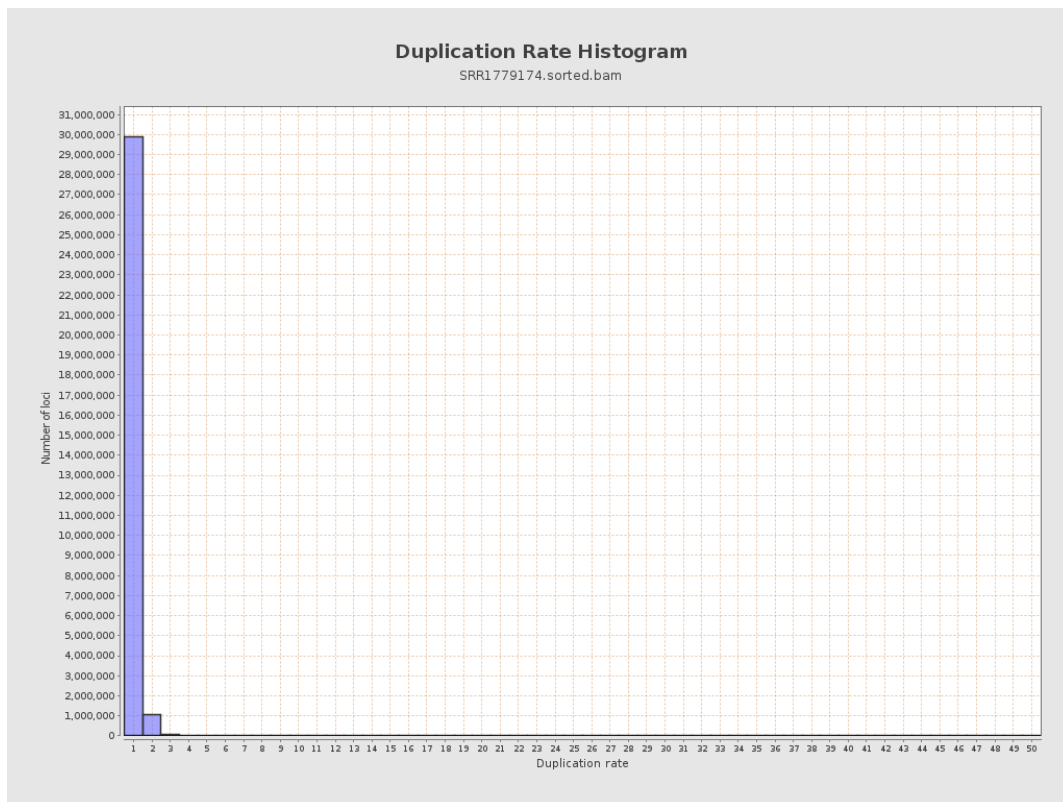
5. Results : Coverage Histogram (0-50X)



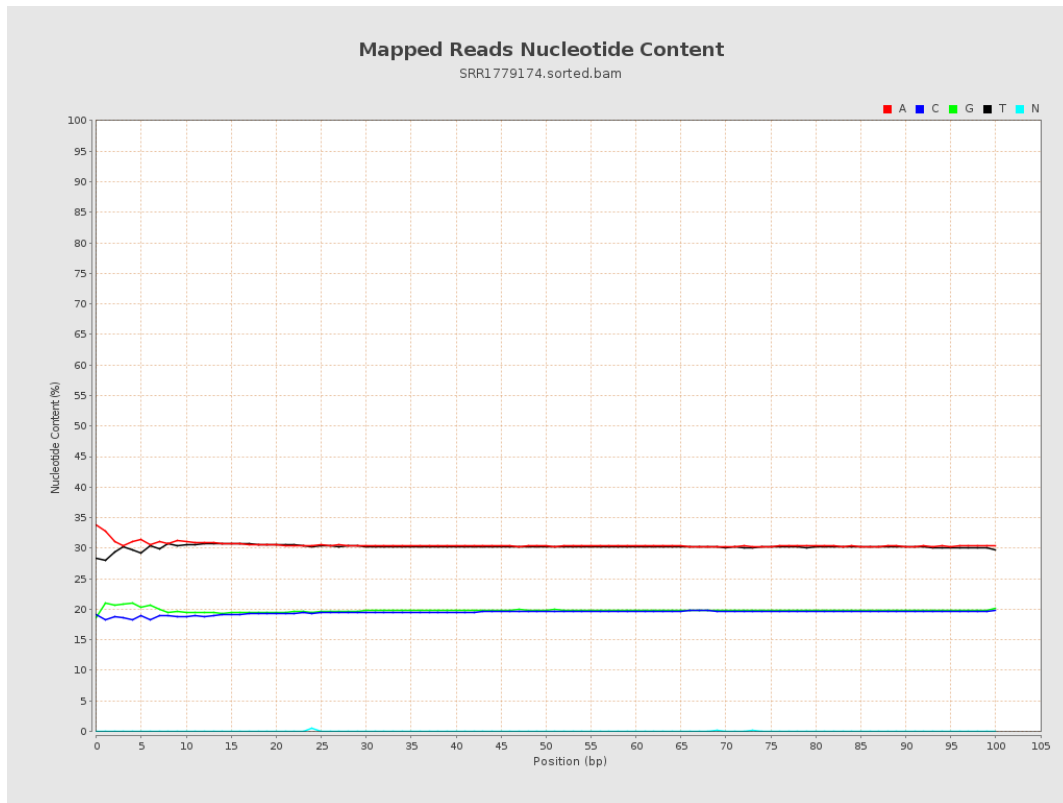
6. Results : Genome Fraction Coverage



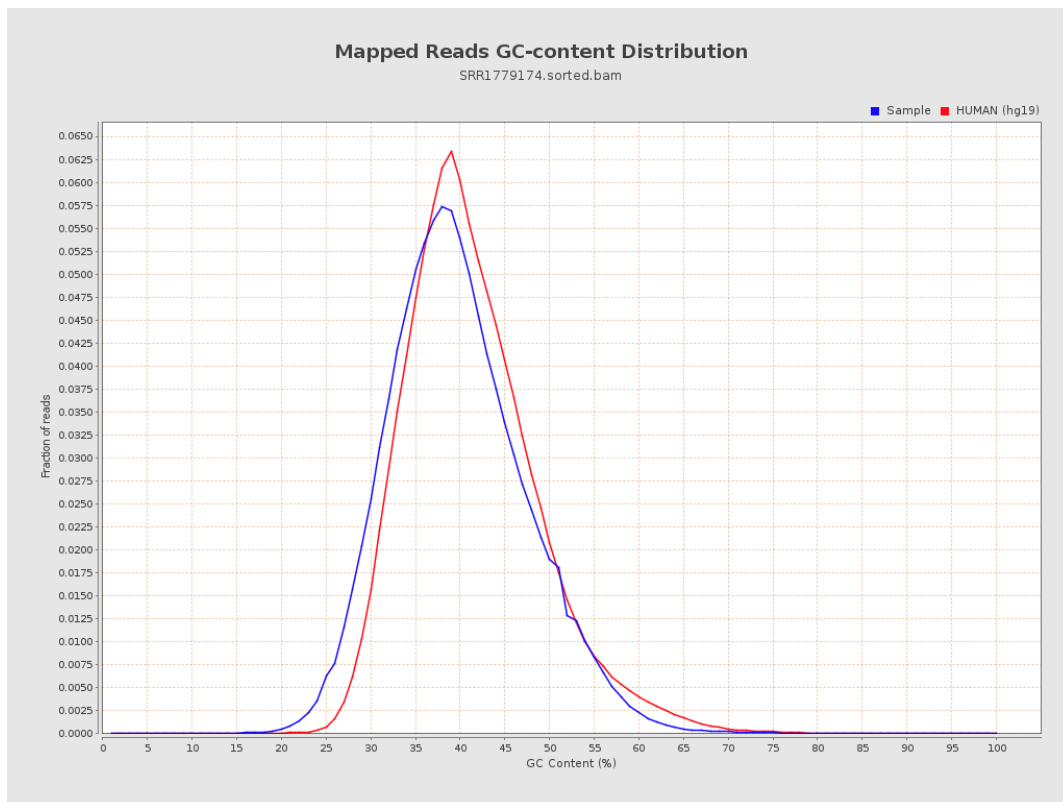
7. Results : Duplication Rate Histogram



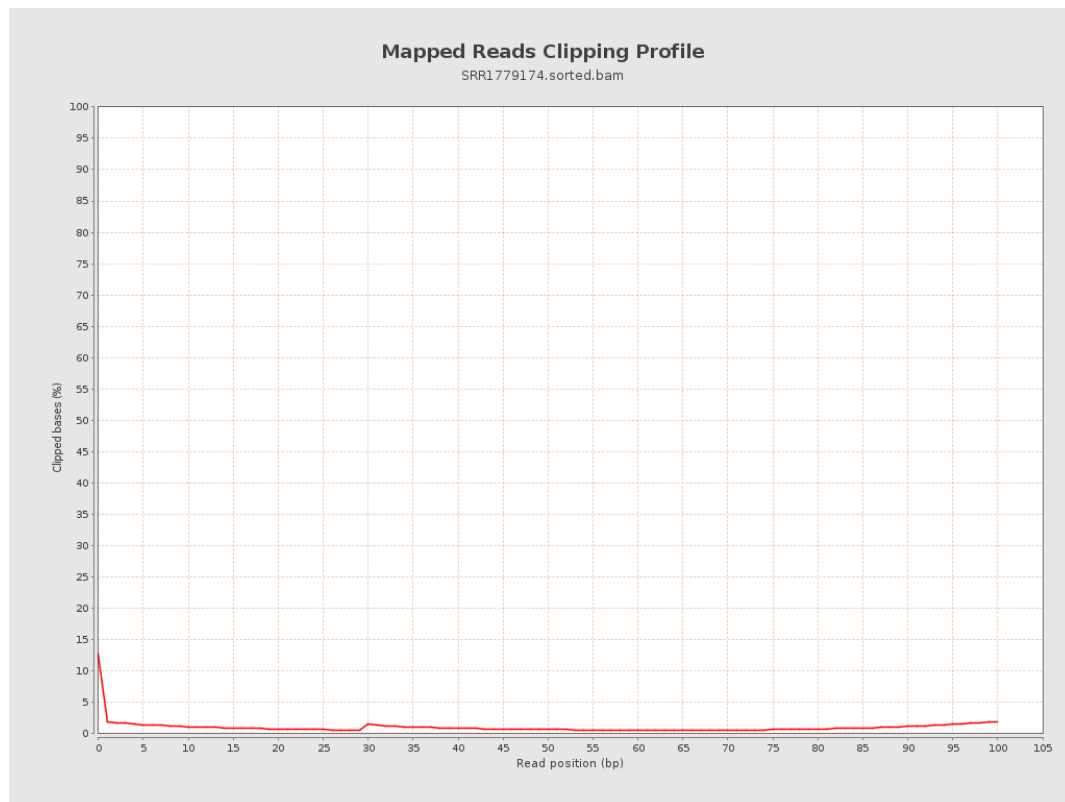
8. Results : Mapped Reads Nucleotide Content



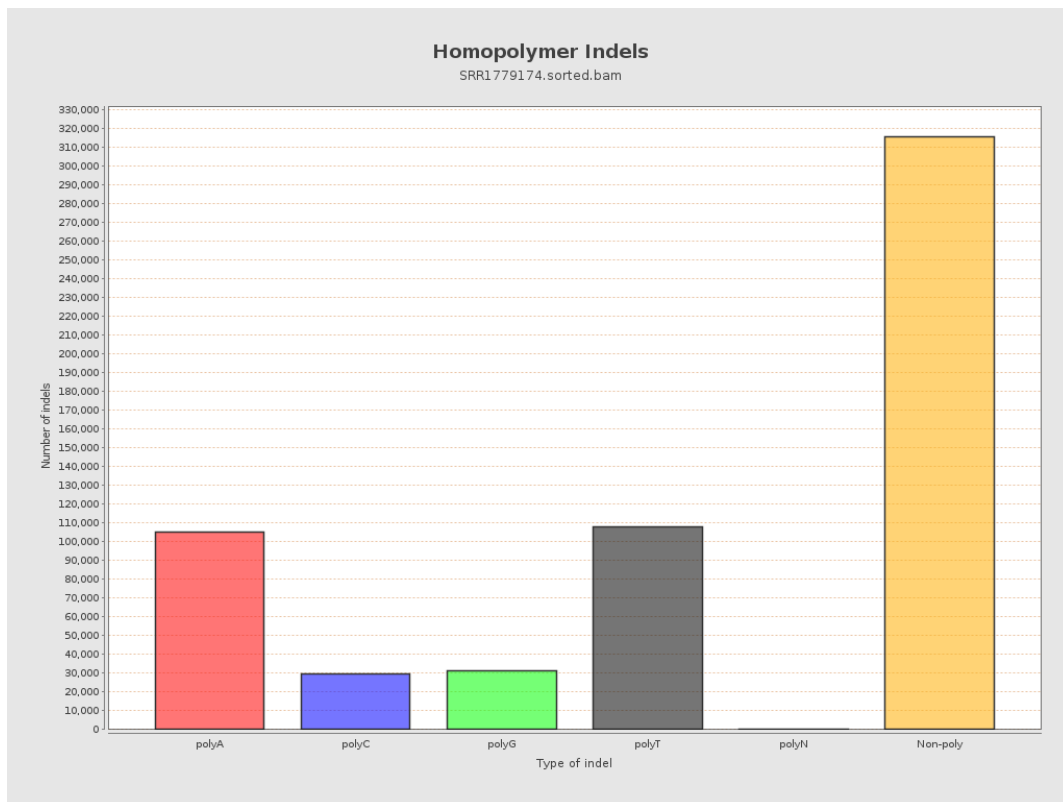
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



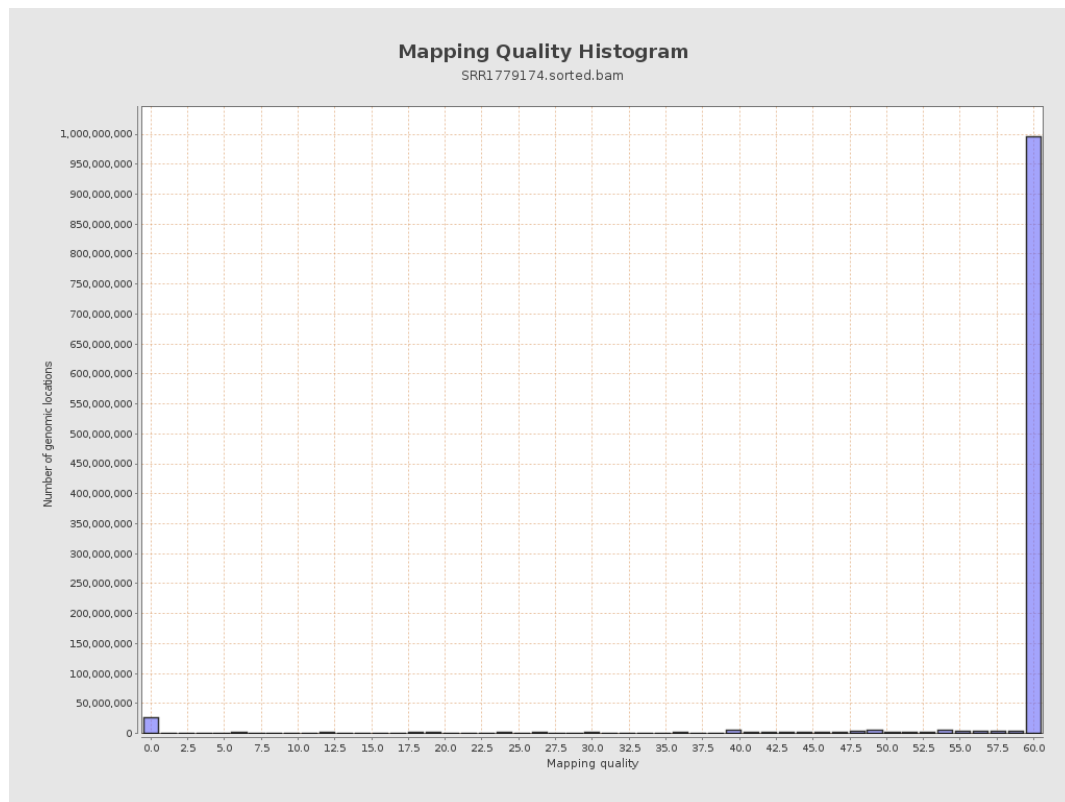
11. Results : Homopolymer Indels



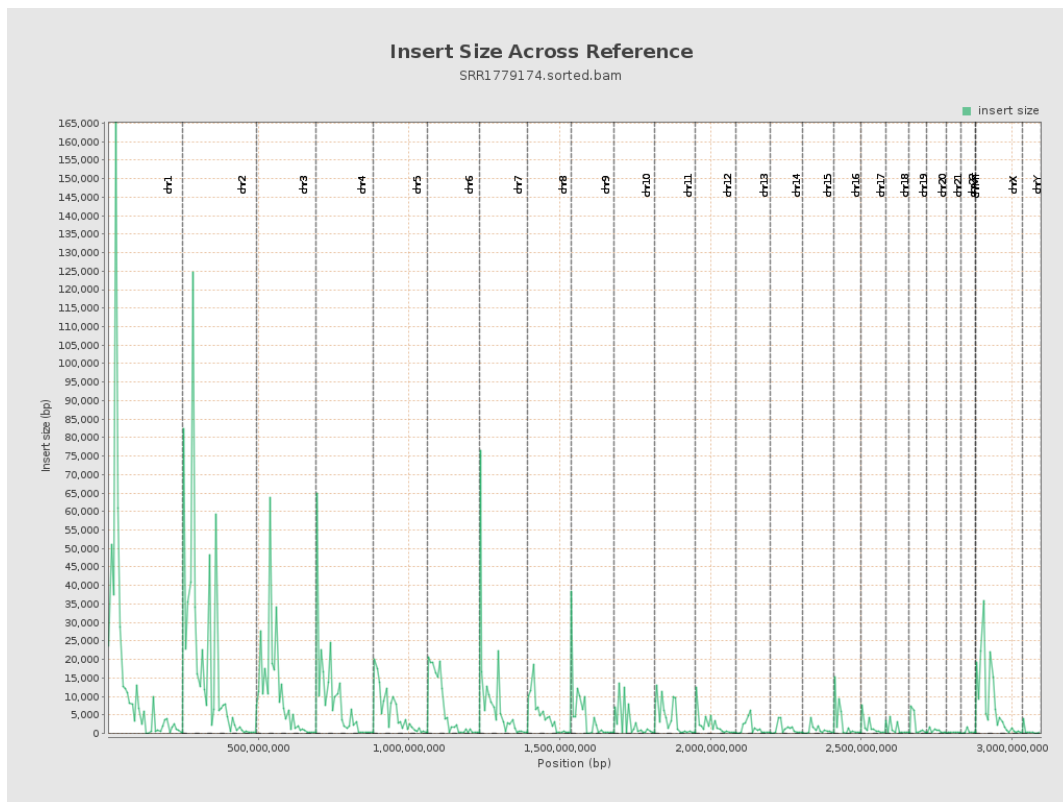
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

