

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/07 12:50:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779080.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_SRR1779080 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779080_1.fastq.gz SRR1779080_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Oct 07 12:50:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779080.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	26,301,926
Mapped reads	25,640,951 / 97.49%
Unmapped reads	660,975 / 2.51%
Mapped paired reads	25,640,951 / 97.49%
Mapped reads, first in pair	12,920,080 / 49.12%
Mapped reads, second in pair	12,720,871 / 48.36%
Mapped reads, both in pair	25,356,090 / 96.4%
Mapped reads, singletons	284,861 / 1.08%
Secondary alignments	0
Supplementary alignments	136,763 / 0.52%
Read min/max/mean length	30 / 101 / 101.21
Duplicated reads (estimated)	950,820 / 3.62%
Duplication rate	3.05%
Clipped reads	1,698,344 / 6.46%

2.2. ACGT Content

Number/percentage of A's	780,339,320 / 30.48%
Number/percentage of C's	497,694,381 / 19.44%
Number/percentage of T's	775,955,581 / 30.3%
Number/percentage of G's	505,684,876 / 19.75%
Number/percentage of N's	847,036 / 0.03%

GC Percentage	39.19%
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2.3. Coverage

Mean	0.8273
Standard Deviation	2.6126

2.4. Mapping Quality

Mean Mapping Quality	53.64
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2.5. Insert size

Mean	58,402.37
Standard Deviation	2,291,464.8
P25/Median/P75	154 / 210 / 288

2.6. Mismatches and indels

General error rate	0.47%
Mismatches	11,715,660
Insertions	211,203
Mapped reads with at least one insertion	0.81%
Deletions	259,570
Mapped reads with at least one deletion	0.99%
Homopolymer indels	46.43%

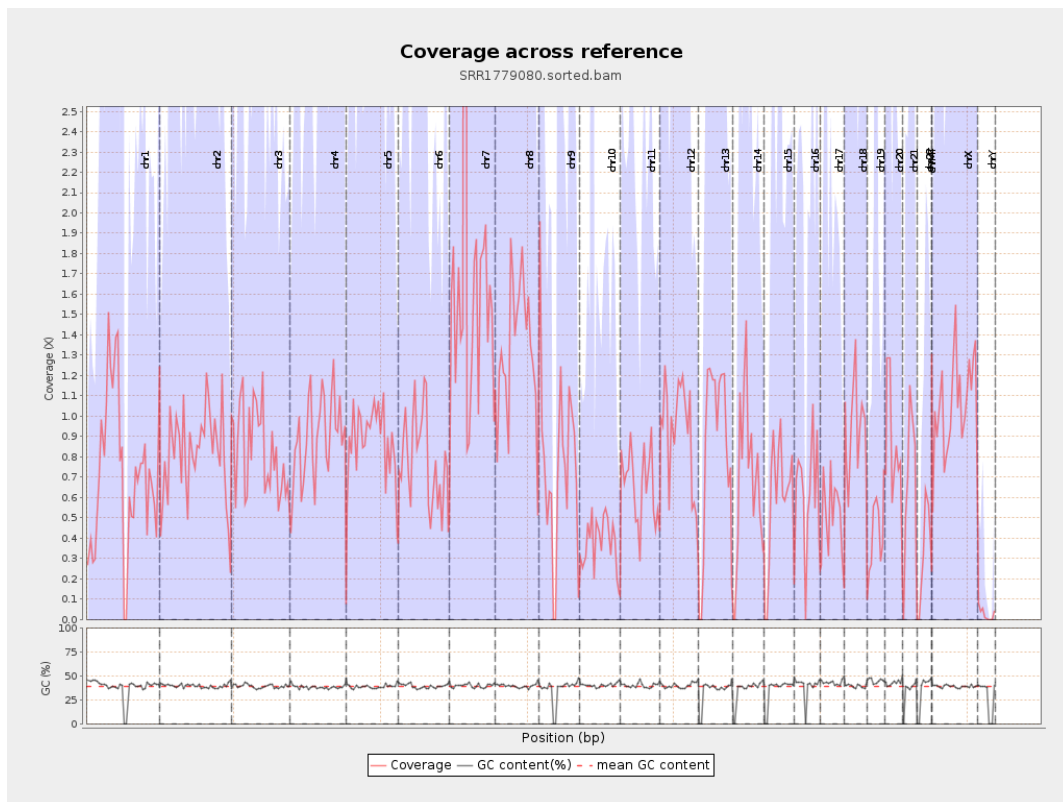
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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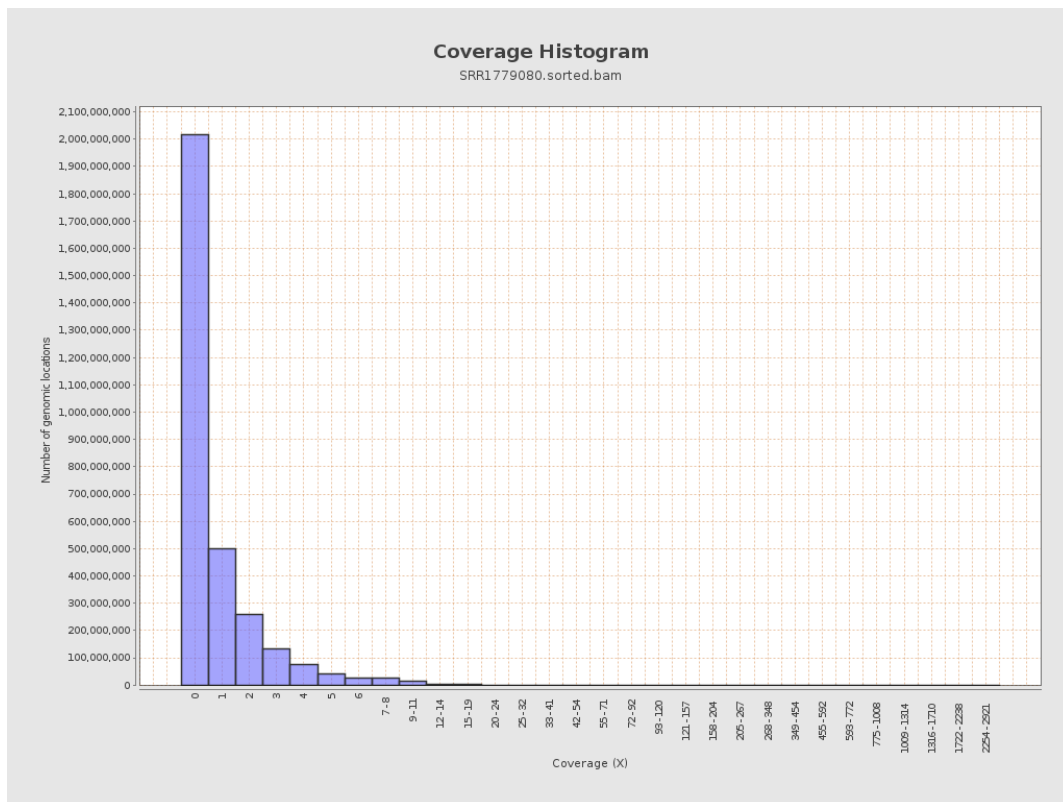
		bases	coverage	deviation
chr1	249250621	178590242	0.7165	3.3516
chr2	243199373	198740130	0.8172	1.7871
chr3	198022430	164197339	0.8292	1.5709
chr4	191154276	172115687	0.9004	1.6639
chr5	180915260	157664297	0.8715	1.6241
chr6	171115067	135403460	0.7913	1.66
chr7	159138663	292828516	1.8401	7.626
chr8	146364022	195583821	1.3363	2.1198
chr9	141213431	104716243	0.7415	1.8318
chr10	135534747	52145569	0.3847	3.4443
chr11	135006516	88204257	0.6533	1.4019
chr12	133851895	124025308	0.9266	1.7402
chr13	115169878	99142433	0.8608	1.6907
chr14	107349540	73794088	0.6874	1.4875
chr15	102531392	60739198	0.5924	1.4519
chr16	90354753	54113966	0.5989	1.3495
chr17	81195210	40670575	0.5009	1.5168
chr18	78077248	74284379	0.9514	1.8569
chr19	59128983	23977421	0.4055	1.9237
chr20	63025520	52814422	0.838	1.6702
chr21	48129895	34255927	0.7117	1.5409
chr22	51304566	16389255	0.3195	0.9508
chrMT	16571	21662	1.3072	1.2604
chrX	155270560	165143921	1.0636	2.0036

chrY	59373566	1539007	0.0259	0.3728
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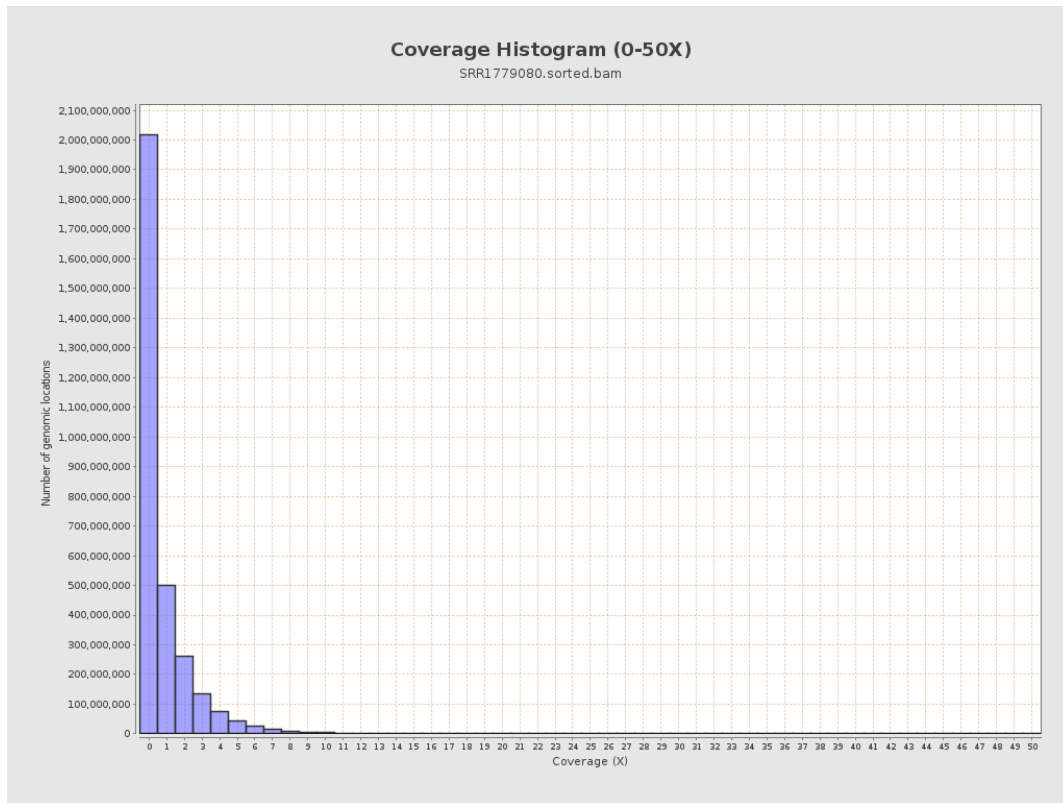
3. Results : Coverage across reference



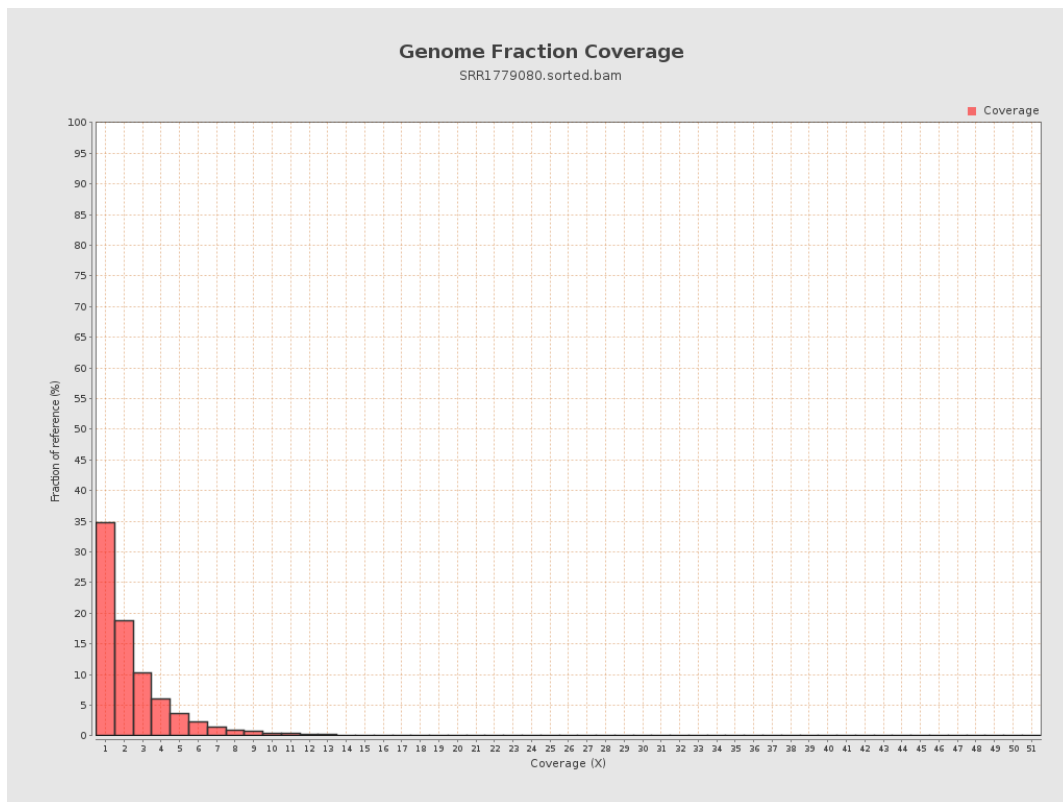
4. Results : Coverage Histogram



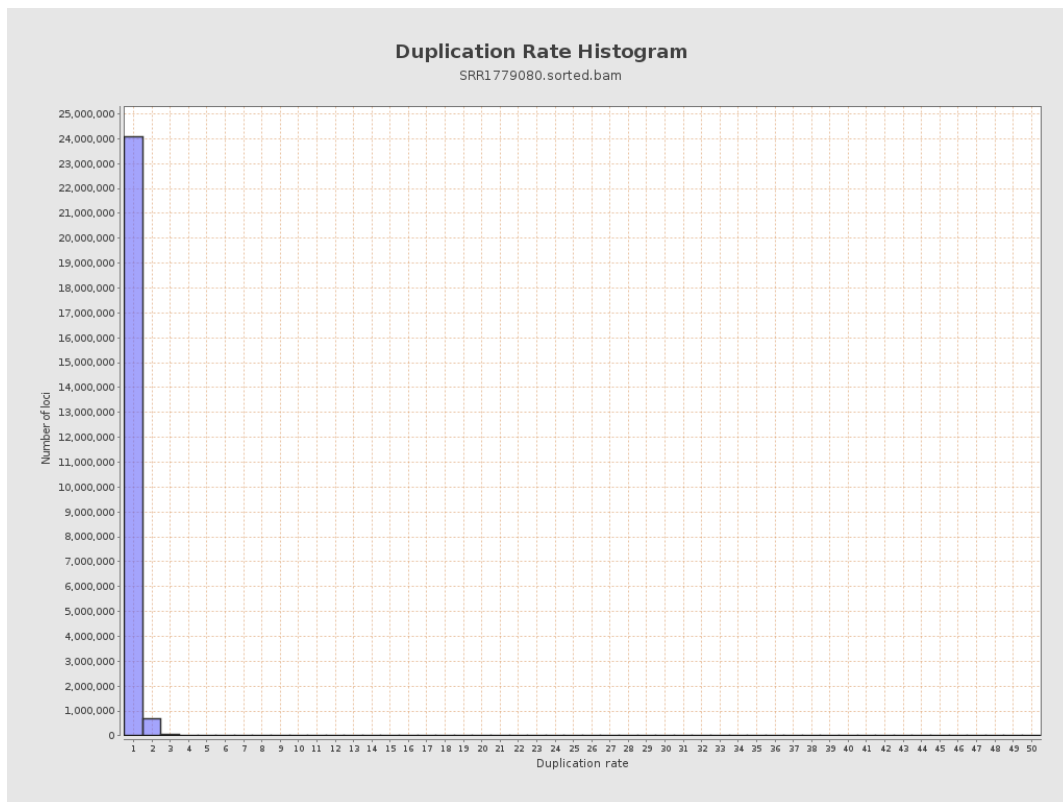
5. Results : Coverage Histogram (0-50X)



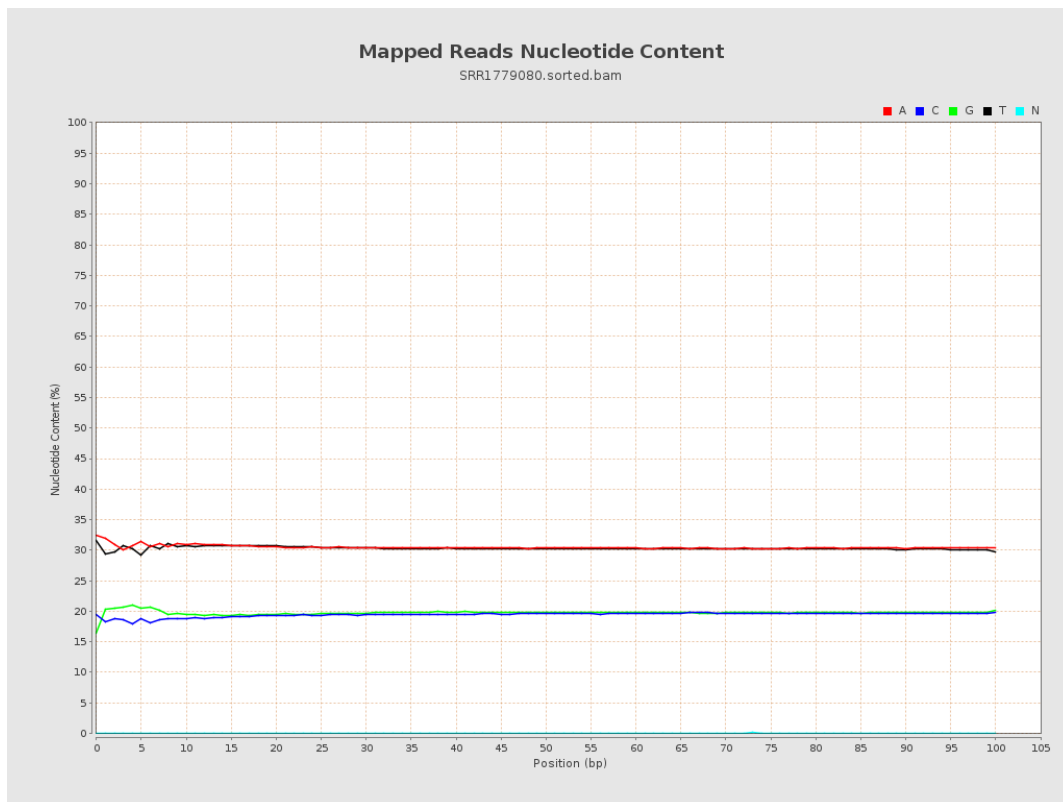
6. Results : Genome Fraction Coverage



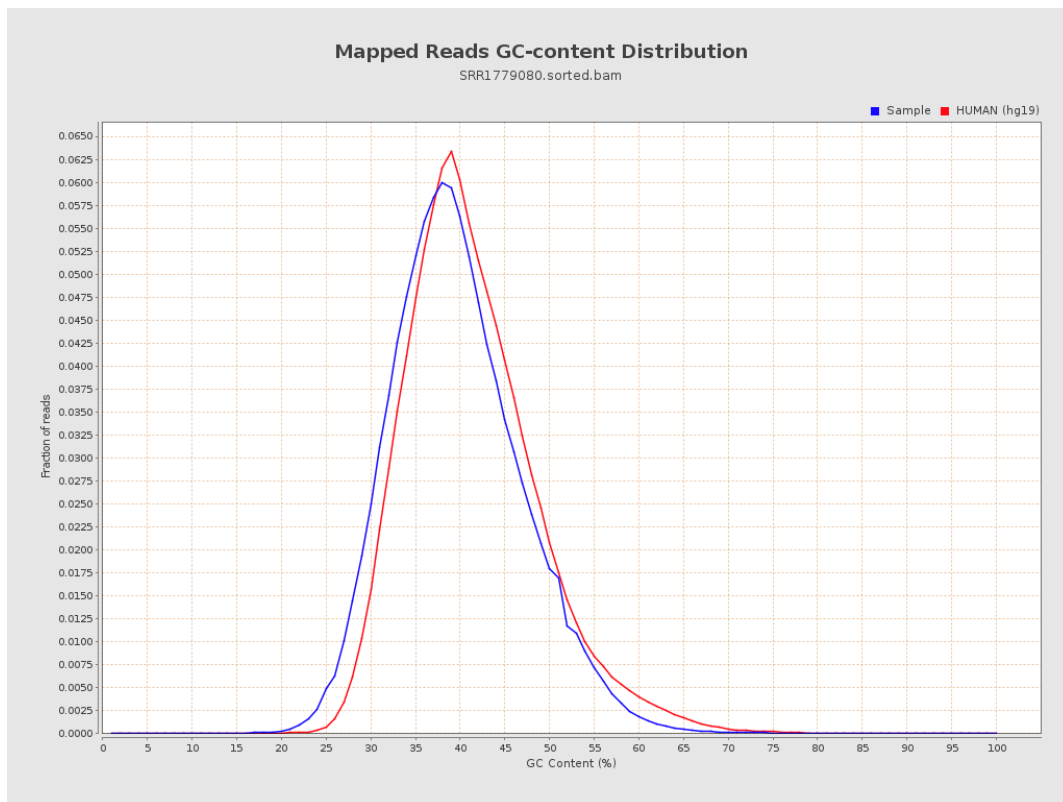
7. Results : Duplication Rate Histogram



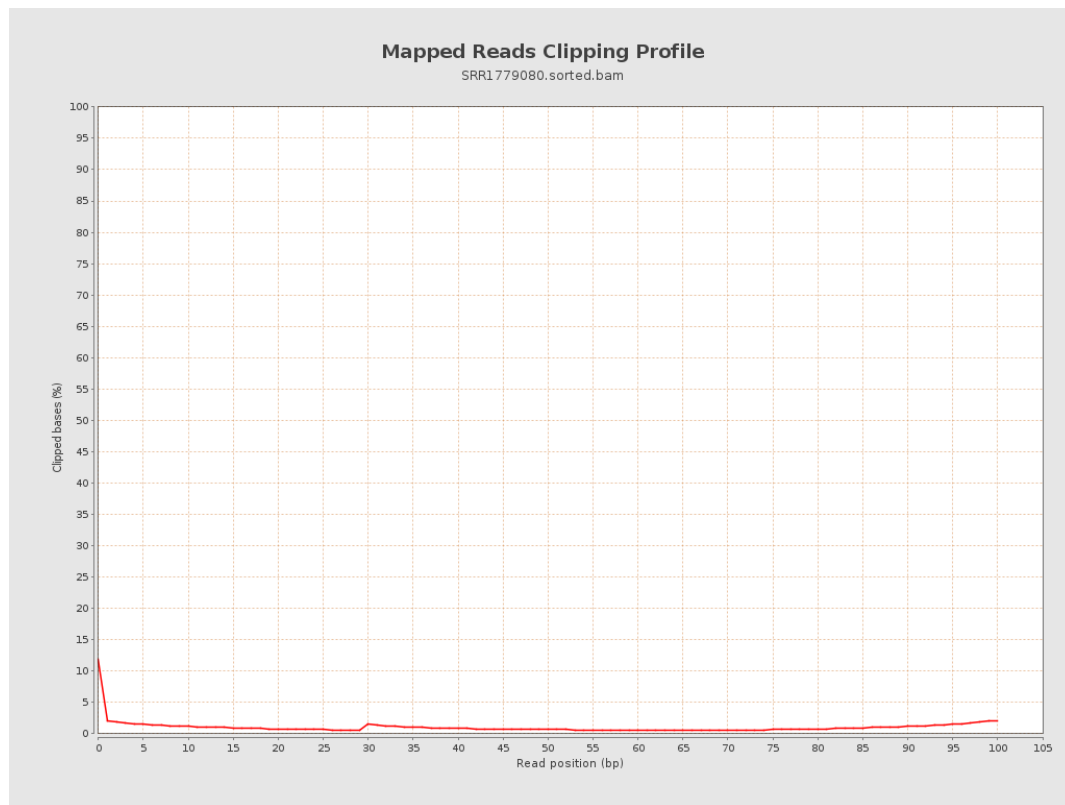
8. Results : Mapped Reads Nucleotide Content



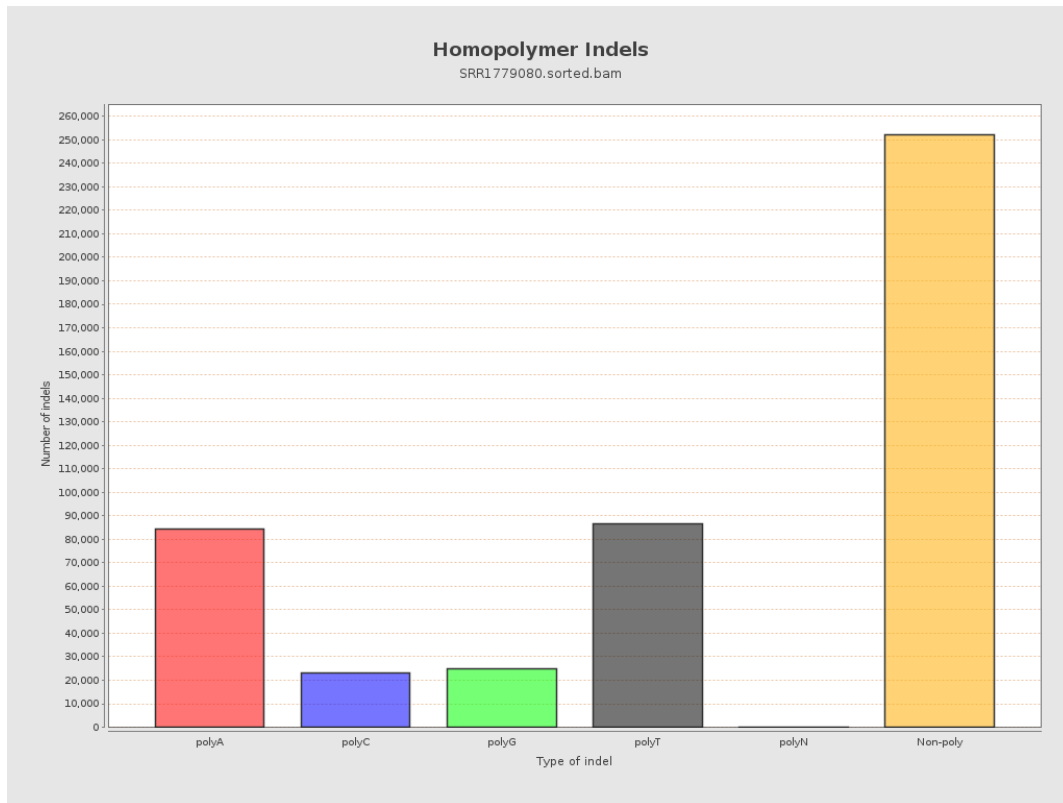
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



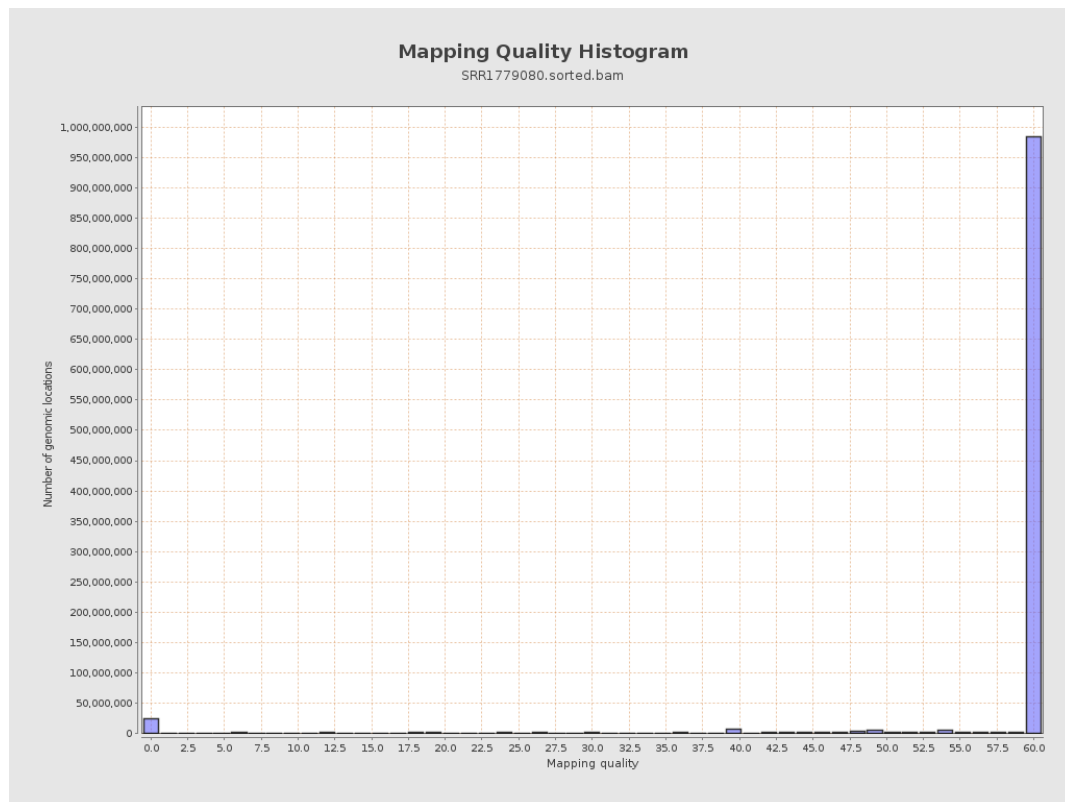
11. Results : Homopolymer Indels



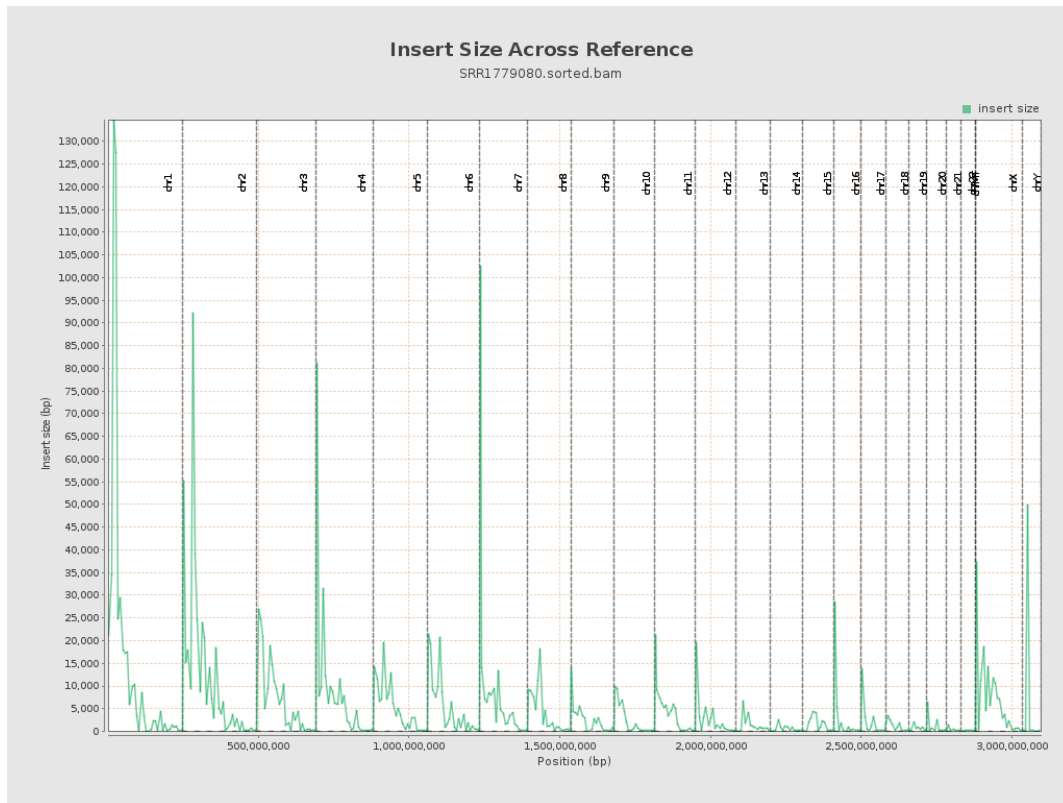
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

