

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/10 16:11:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779389.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_SRR1779389 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779389_1.fastq.gz SRR1779389_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 10 16:11:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779389.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,745,044
Mapped reads	5,090,418 / 65.72%
Unmapped reads	2,654,626 / 34.28%
Mapped paired reads	5,090,418 / 65.72%
Mapped reads, first in pair	2,603,284 / 33.61%
Mapped reads, second in pair	2,487,134 / 32.11%
Mapped reads, both in pair	4,912,812 / 63.43%
Mapped reads, singletons	177,606 / 2.29%
Secondary alignments	0
Supplementary alignments	23,027 / 0.3%
Read min/max/mean length	30 / 80 / 80.11
Duplicated reads (estimated)	186,309 / 2.41%
Duplication rate	2.98%
Clipped reads	434,757 / 5.61%

2.2. ACGT Content

Number/percentage of A's	124,179,101 / 30.84%
Number/percentage of C's	74,024,885 / 18.39%
Number/percentage of T's	118,963,670 / 29.55%
Number/percentage of G's	85,370,242 / 21.2%
Number/percentage of N's	83,817 / 0.02%

GC Percentage	39.59%
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2.3. Coverage

Mean	0.1301
Standard Deviation	0.6923

2.4. Mapping Quality

Mean Mapping Quality	51.91
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2.5. Insert size

Mean	69,165.81
Standard Deviation	2,516,495.27
P25/Median/P75	275 / 385 / 548

2.6. Mismatches and indels

General error rate	0.68%
Mismatches	2,673,477
Insertions	38,996
Mapped reads with at least one insertion	0.76%
Deletions	44,348
Mapped reads with at least one deletion	0.86%
Homopolymer indels	46.52%

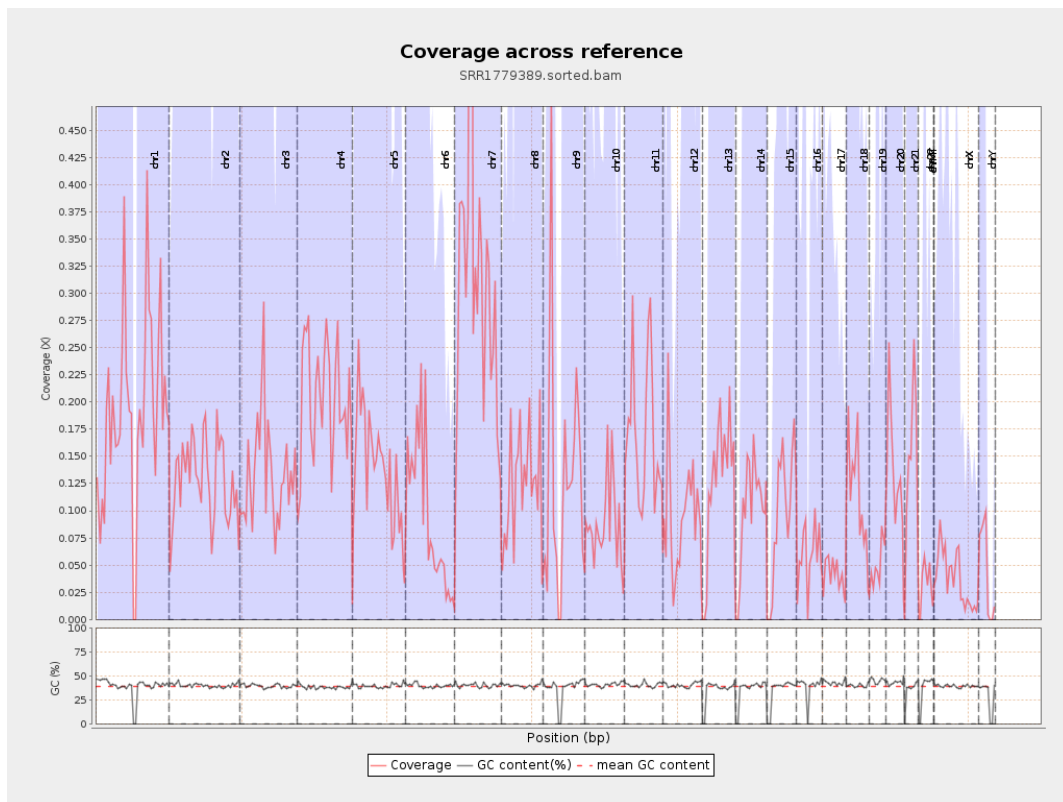
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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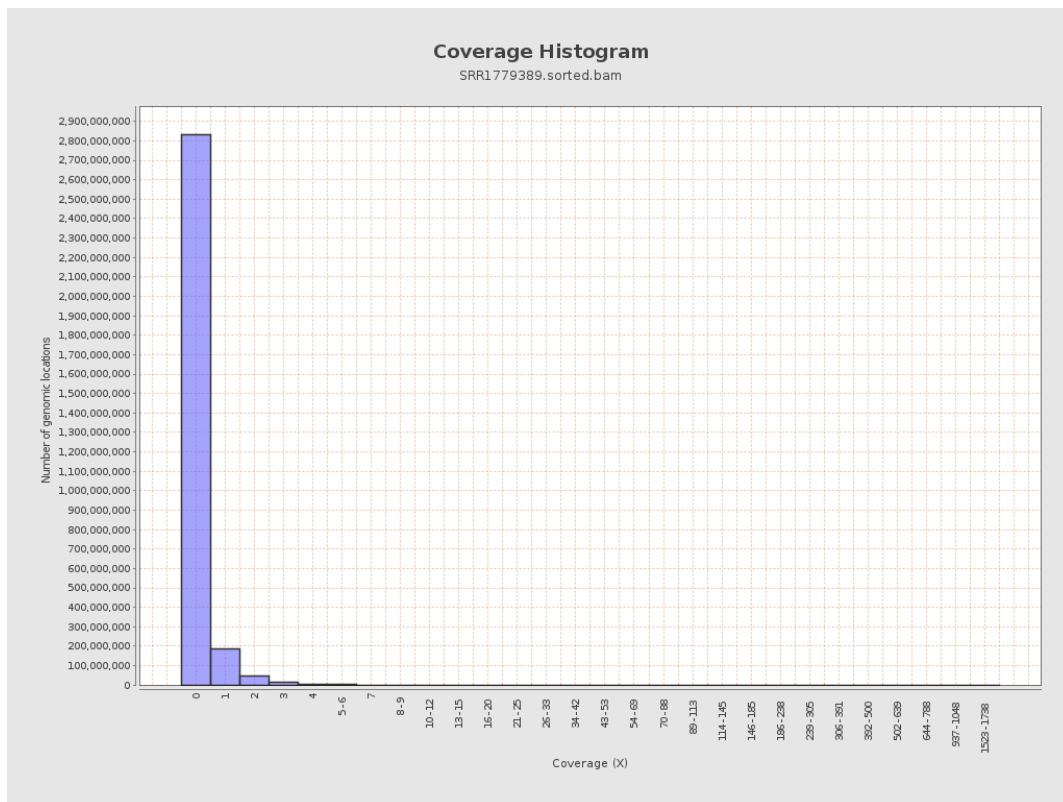
		bases	coverage	deviation
chr1	249250621	47840559	0.1919	1.1362
chr2	243199373	31487699	0.1295	0.7179
chr3	198022430	26421441	0.1334	0.5414
chr4	191154276	39153329	0.2048	0.6661
chr5	180915260	25147642	0.139	0.5307
chr6	171115067	15921371	0.093	0.5534
chr7	159138663	51986880	0.3267	1.4526
chr8	146364022	17881120	0.1222	0.5216
chr9	141213431	18755365	0.1328	0.6347
chr10	135534747	11889635	0.0877	0.5608
chr11	135006516	22962937	0.1701	0.6195
chr12	133851895	12440754	0.0929	0.4394
chr13	115169878	14425199	0.1253	0.5355
chr14	107349540	10597260	0.0987	0.4483
chr15	102531392	9882953	0.0964	0.4447
chr16	90354753	5386113	0.0596	0.4252
chr17	81195210	3244159	0.04	0.3266
chr18	78077248	9027270	0.1156	0.8039
chr19	59128983	2984296	0.0505	0.4958
chr20	63025520	8587783	0.1363	0.553
chr21	48129895	6814178	0.1416	0.59
chr22	51304566	1633562	0.0318	0.3119
chrMT	16571	369	0.0223	0.1612
chrX	155270560	5651470	0.0364	0.2926

chrY	59373566	2588951	0.0436	0.2955
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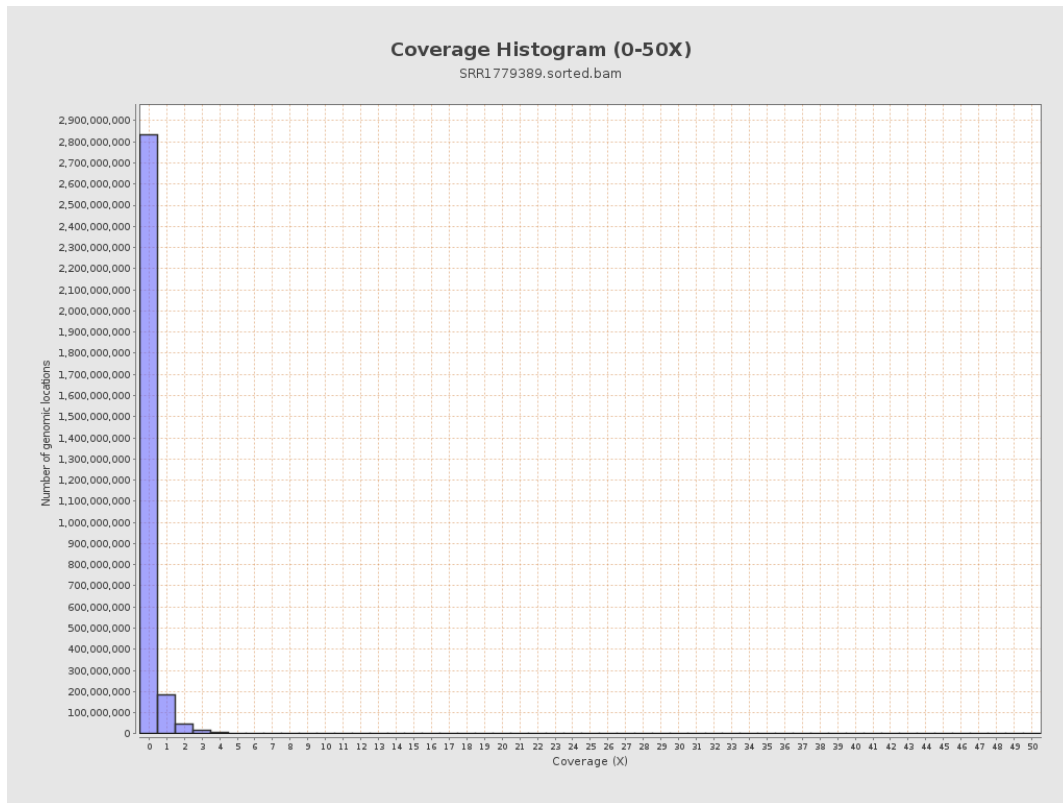
3. Results : Coverage across reference



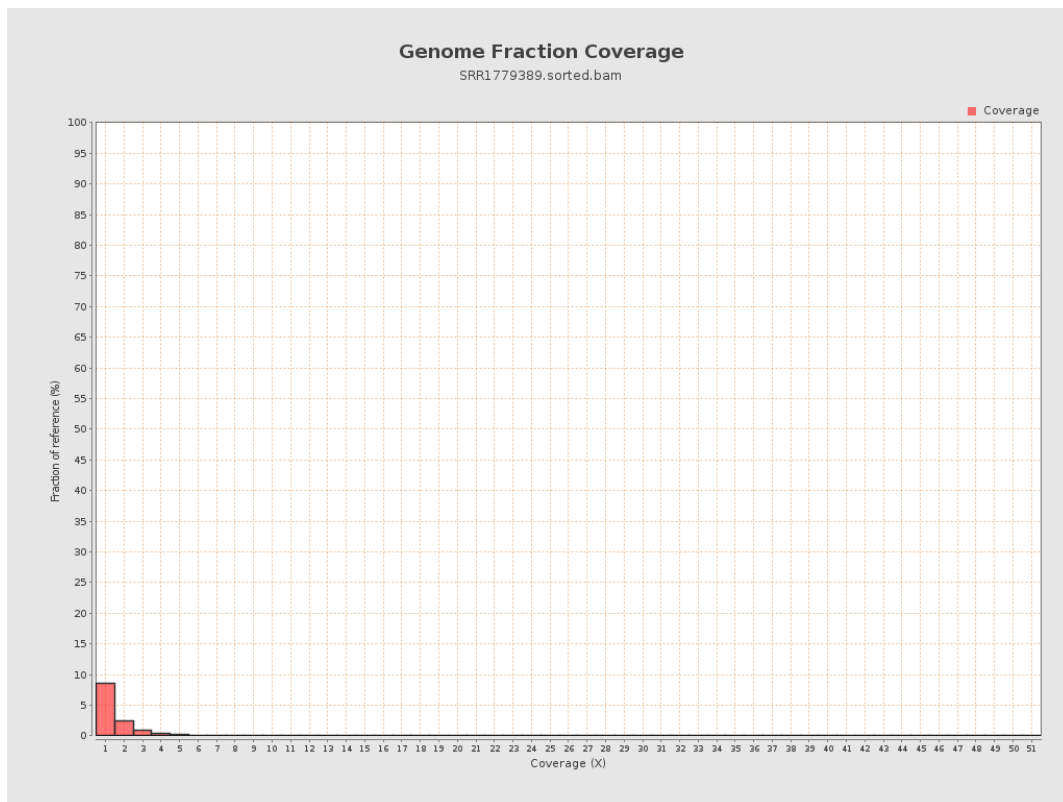
4. Results : Coverage Histogram



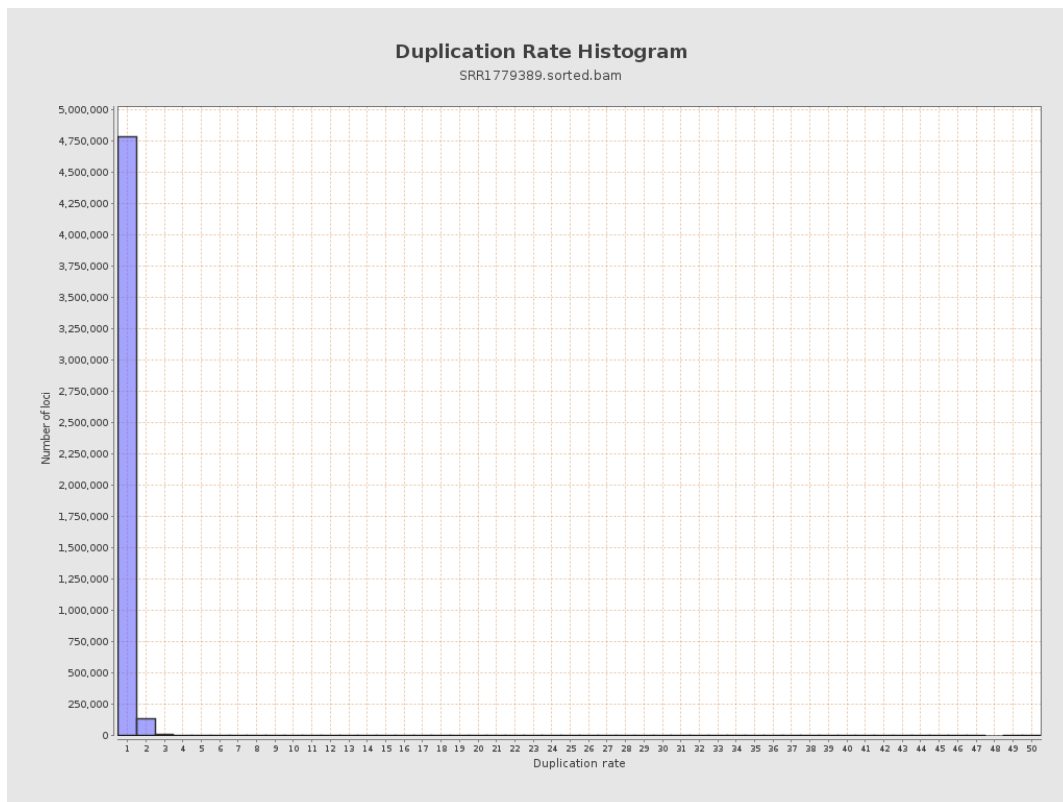
5. Results : Coverage Histogram (0-50X)



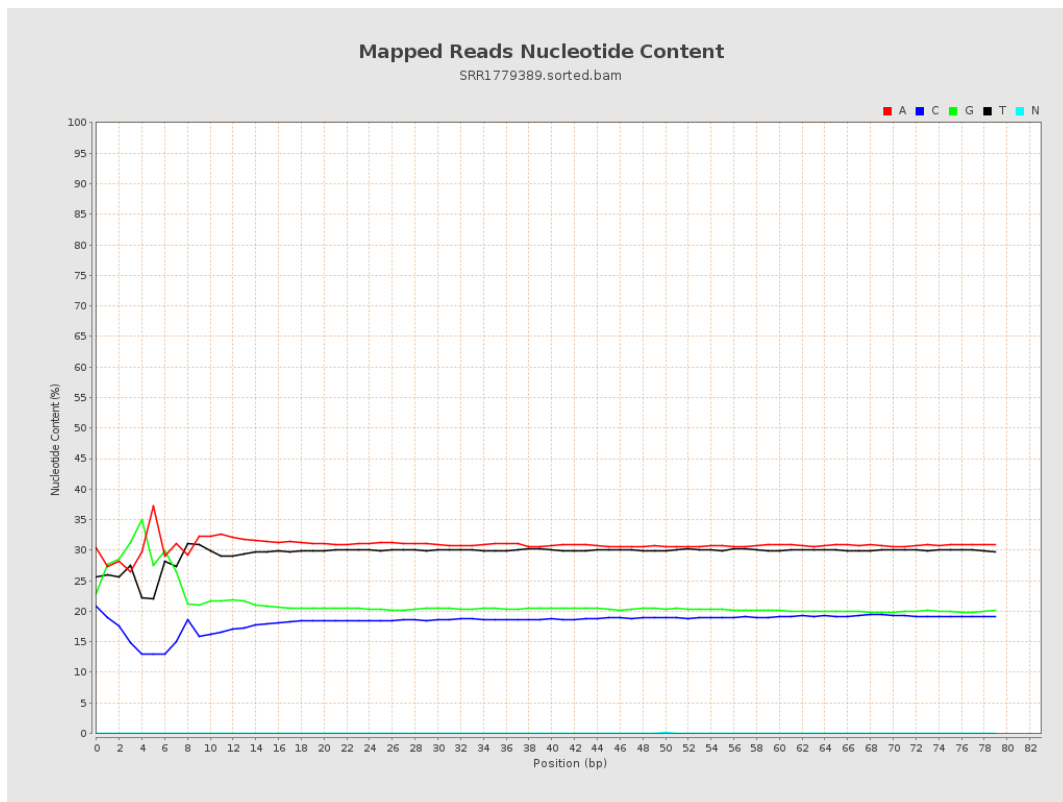
6. Results : Genome Fraction Coverage



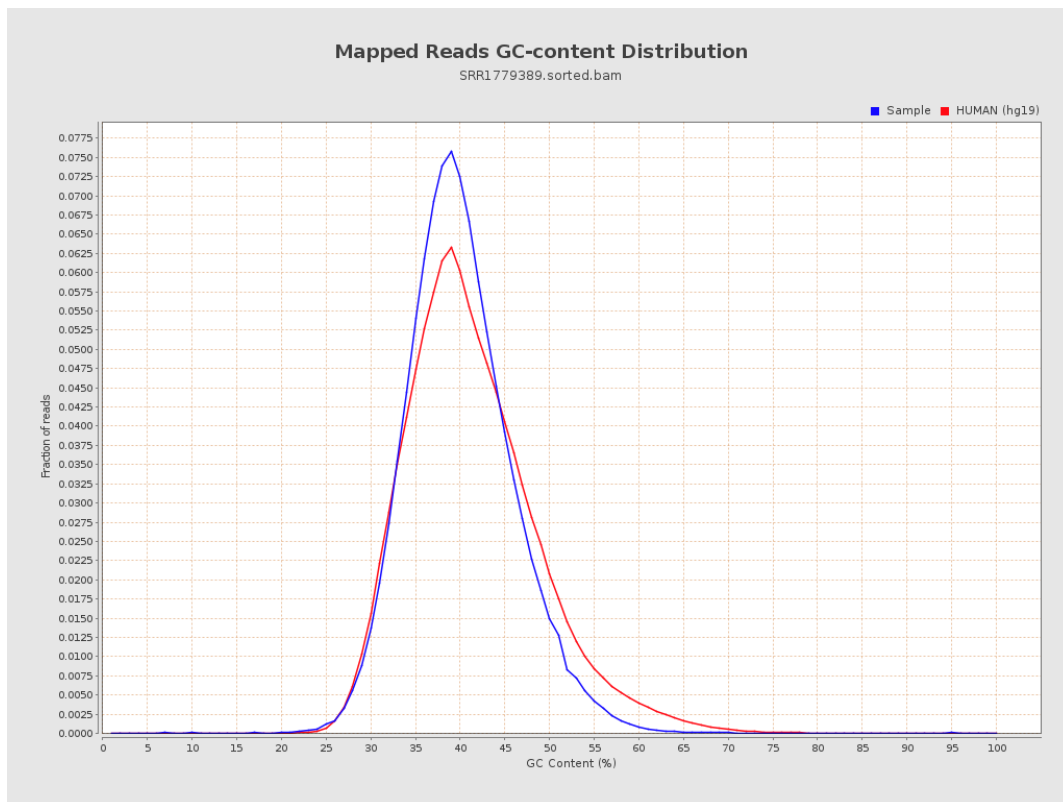
7. Results : Duplication Rate Histogram



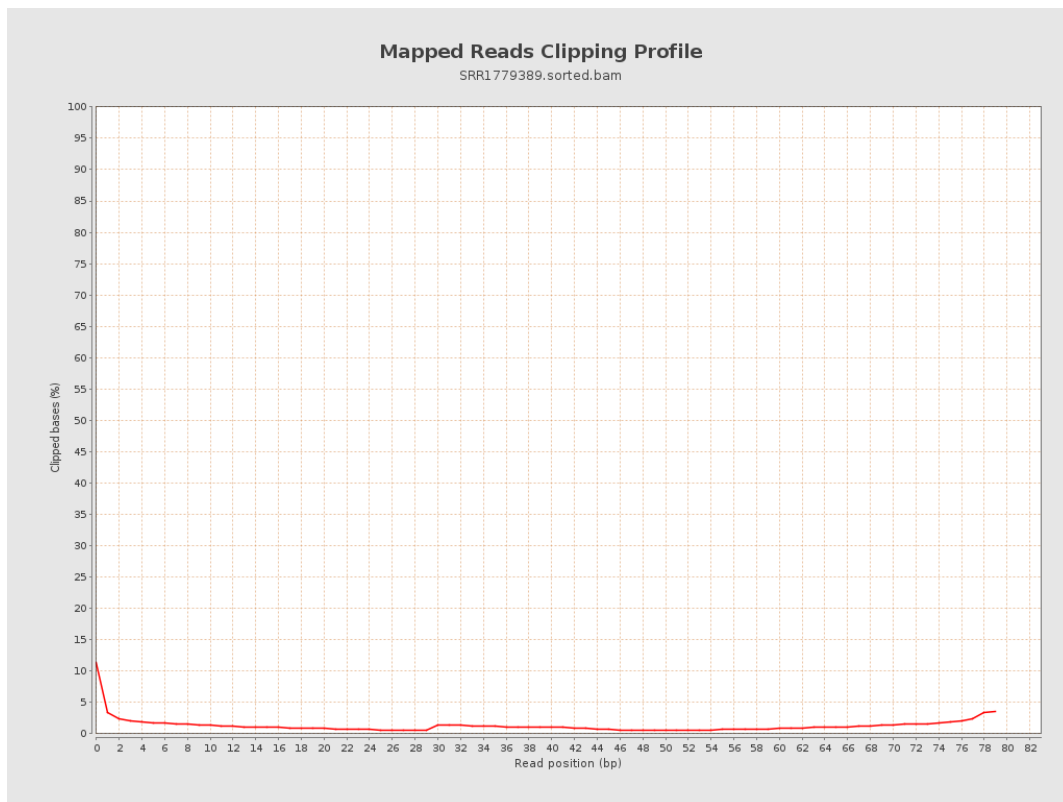
8. Results : Mapped Reads Nucleotide Content



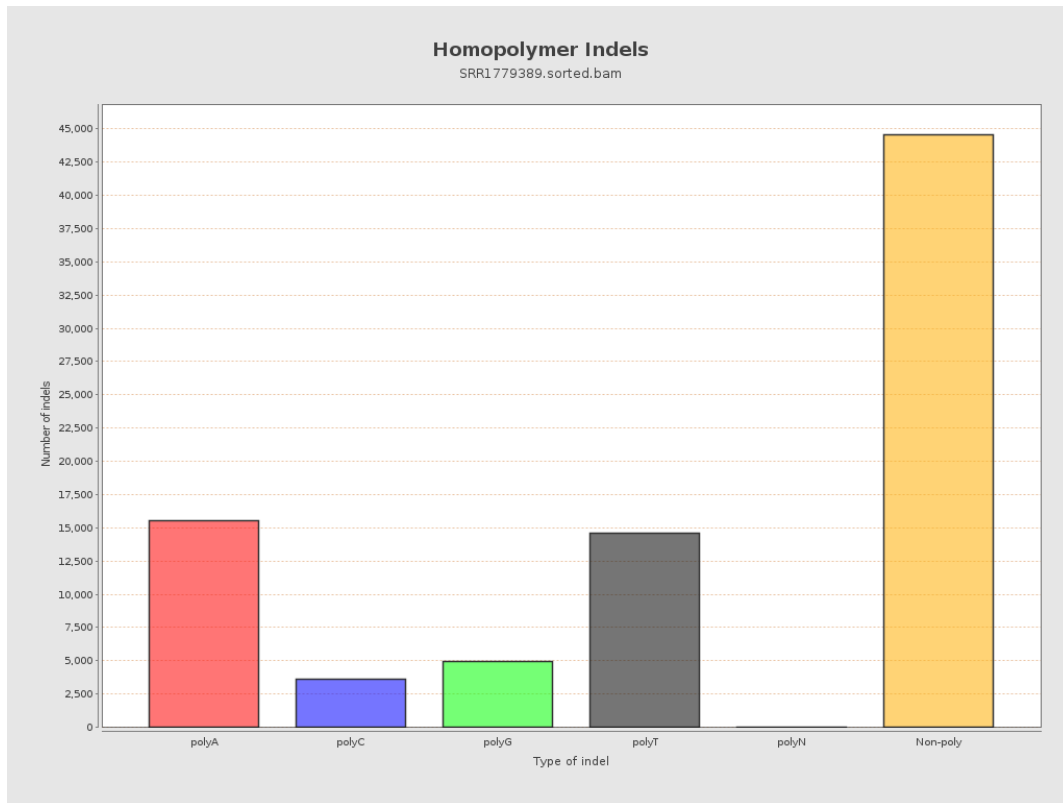
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



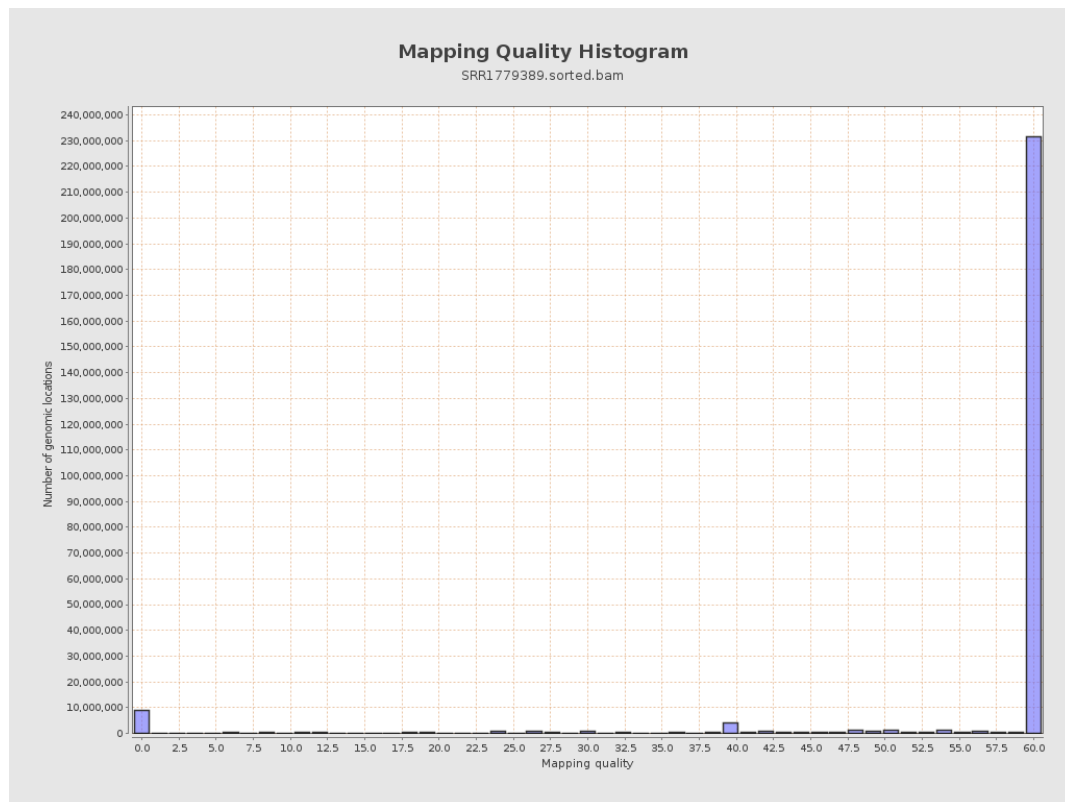
11. Results : Homopolymer Indels



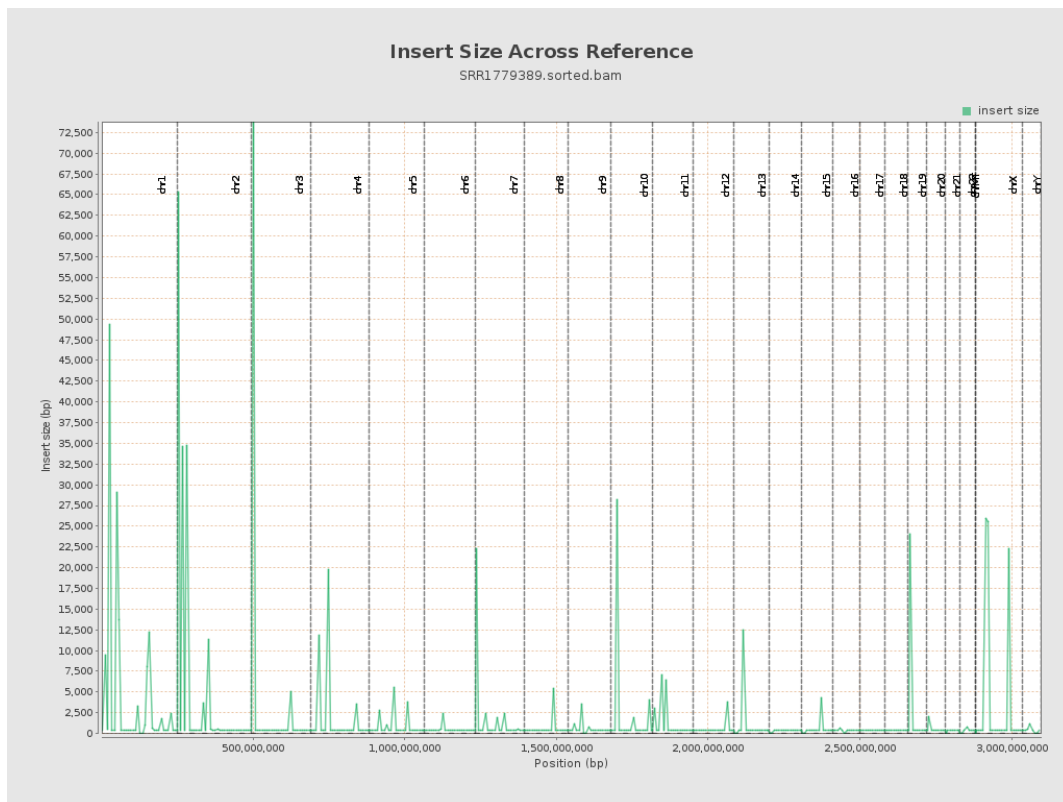
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

