

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/11 00:02:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779415.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_SRR1779415 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779415_1.fastq.gz SRR1779415_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Oct 11 00:02:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779415.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	13,687,070
Mapped reads	13,006,103 / 95.02%
Unmapped reads	680,967 / 4.98%
Mapped paired reads	13,006,103 / 95.02%
Mapped reads, first in pair	6,553,371 / 47.88%
Mapped reads, second in pair	6,452,732 / 47.14%
Mapped reads, both in pair	12,862,022 / 93.97%
Mapped reads, singletons	144,081 / 1.05%
Secondary alignments	0
Supplementary alignments	85,983 / 0.63%
Read min/max/mean length	30 / 80 / 80.23
Duplicated reads (estimated)	1,281,437 / 9.36%
Duplication rate	6.8%
Clipped reads	726,345 / 5.31%

2.2. ACGT Content

Number/percentage of A's	323,781,973 / 31.36%
Number/percentage of C's	191,993,145 / 18.6%
Number/percentage of T's	319,359,253 / 30.93%
Number/percentage of G's	197,121,093 / 19.09%
Number/percentage of N's	222,502 / 0.02%

GC Percentage	37.69%
---------------	--------

2.3. Coverage

Mean	0.3336
Standard Deviation	3.8468

2.4. Mapping Quality

Mean Mapping Quality	52.65
----------------------	-------

2.5. Insert size

Mean	73,723.74
Standard Deviation	2,556,715.4
P25/Median/P75	160 / 206 / 266

2.6. Mismatches and indels

General error rate	0.4%
Mismatches	4,004,363
Insertions	97,925
Mapped reads with at least one insertion	0.75%
Deletions	107,591
Mapped reads with at least one deletion	0.82%
Homopolymer indels	46.16%

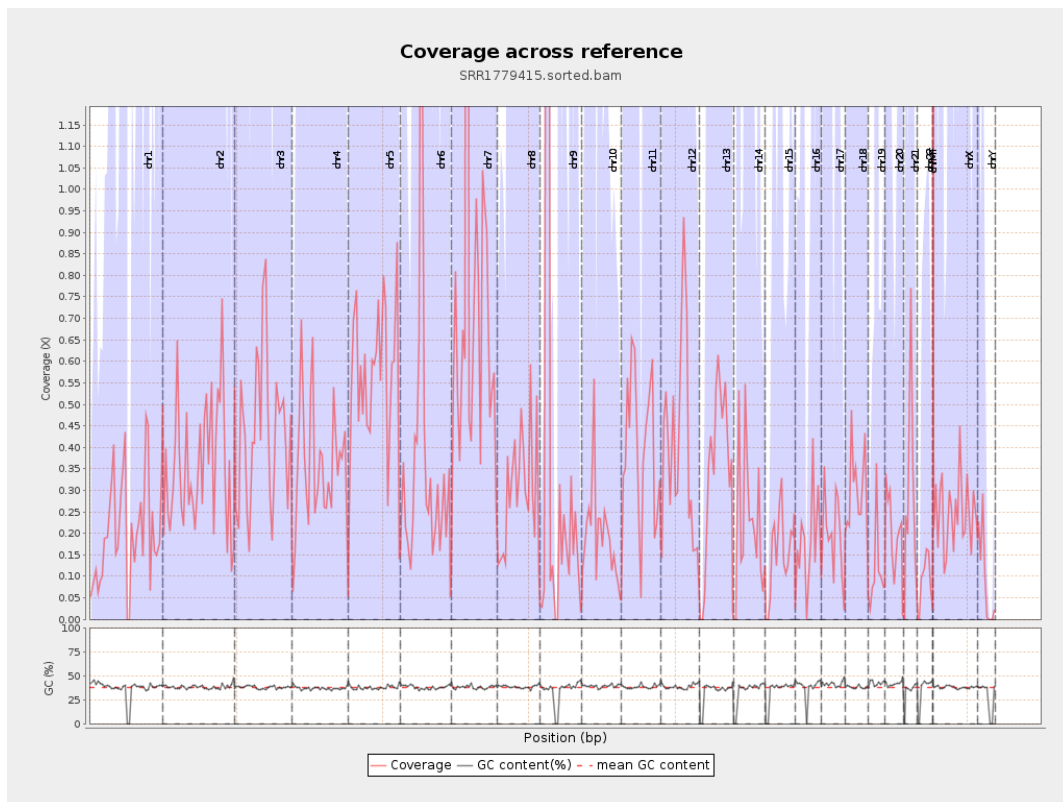
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
------	--------	--------	------	----------

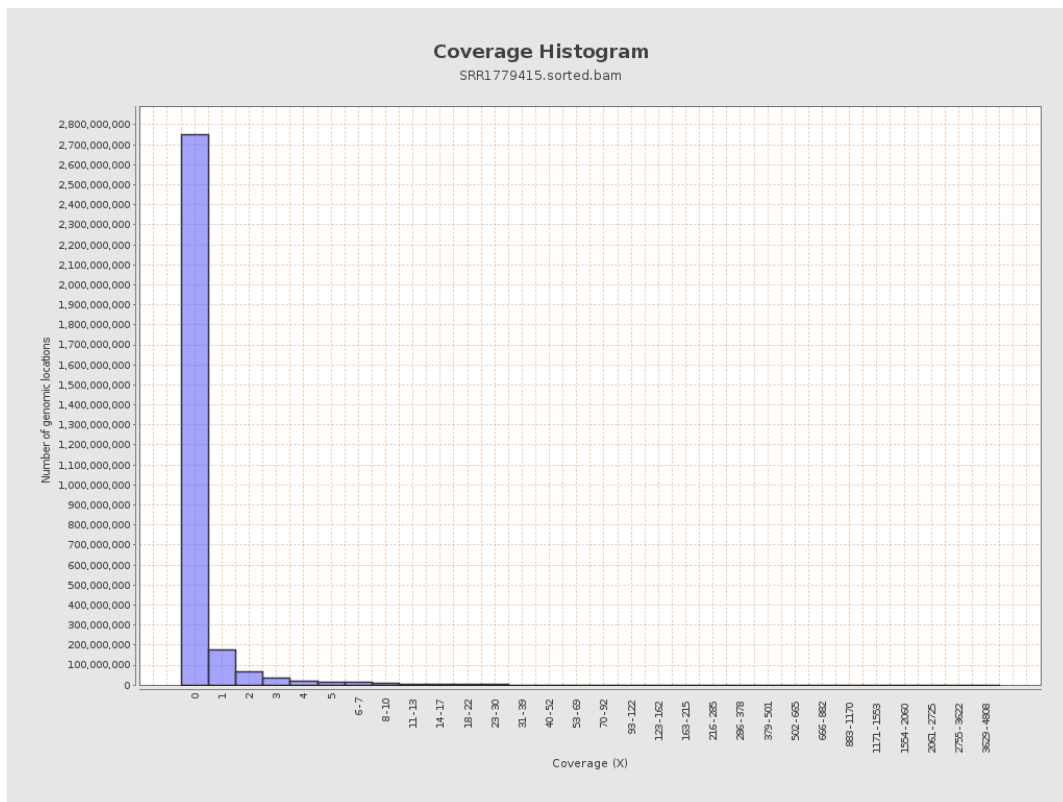
		bases	coverage	deviation
chr1	249250621	51628773	0.2071	5.1896
chr2	243199373	86244360	0.3546	6.4018
chr3	198022430	86207160	0.4353	2.5542
chr4	191154276	68754500	0.3597	2.3145
chr5	180915260	99880963	0.5521	2.8291
chr6	171115067	61225028	0.3578	4.8529
chr7	159138663	127772071	0.8029	5.5736
chr8	146364022	43983060	0.3005	2.0544
chr9	141213431	57023059	0.4038	2.8514
chr10	135534747	26298546	0.194	6.0827
chr11	135006516	53717820	0.3979	1.9395
chr12	133851895	52620571	0.3931	2.0744
chr13	115169878	40235462	0.3494	1.4537
chr14	107349540	23826252	0.222	4.903
chr15	102531392	15901701	0.1551	0.8614
chr16	90354753	15812686	0.175	2.6006
chr17	81195210	16239429	0.2	1.7806
chr18	78077248	23811347	0.305	2.778
chr19	59128983	6789306	0.1148	3.6581
chr20	63025520	13033616	0.2068	6.6912
chr21	48129895	13405751	0.2785	1.4987
chr22	51304566	4763862	0.0929	0.677
chrMT	16571	59544	3.5933	2.7357
chrX	155270560	37955388	0.2444	1.4106

chrY	59373566	5501979	0.0927	0.7069
------	----------	---------	--------	--------

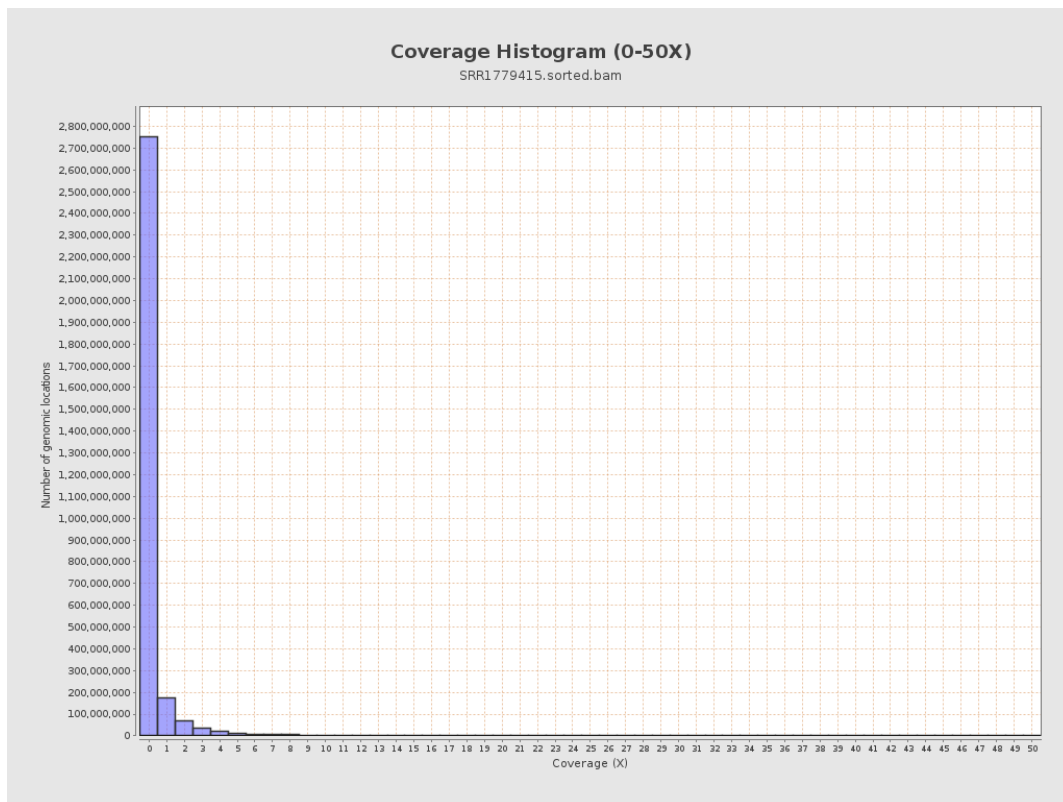
3. Results : Coverage across reference



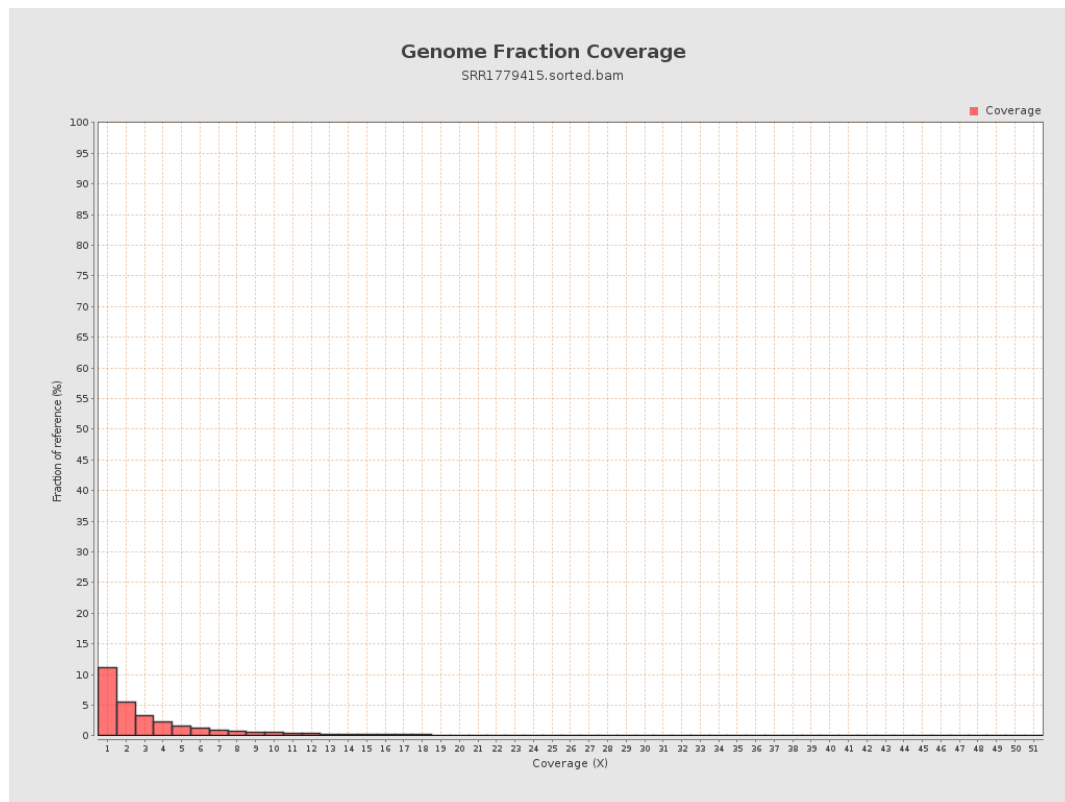
4. Results : Coverage Histogram



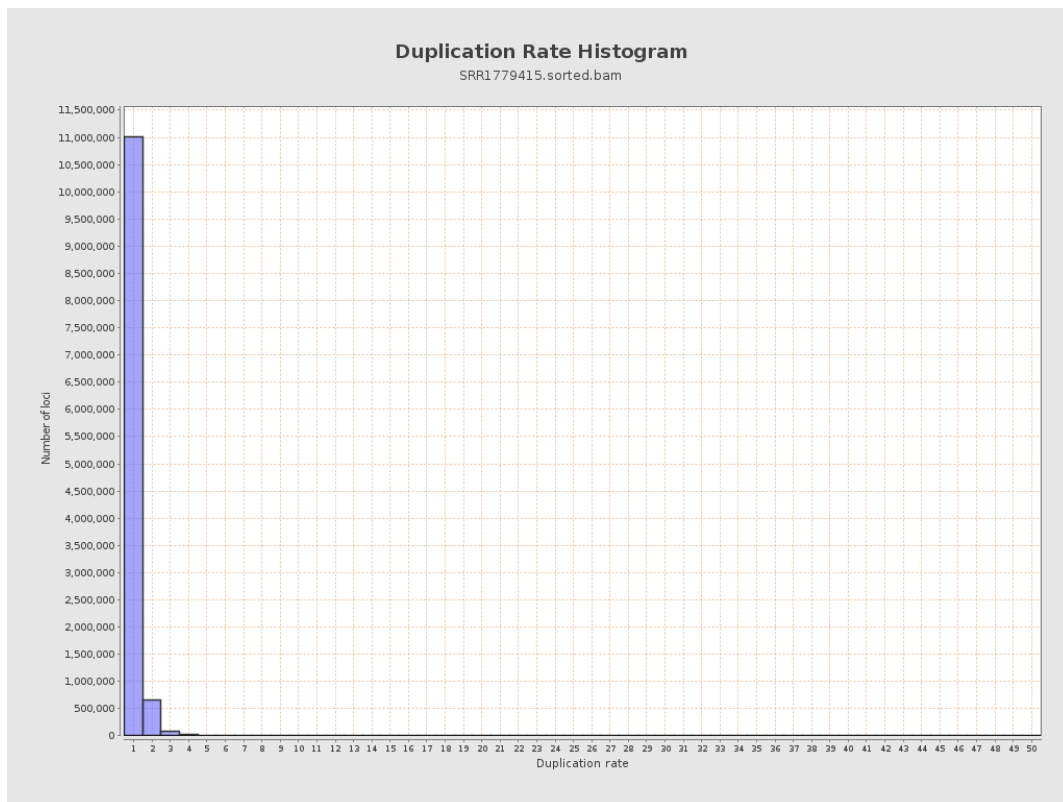
5. Results : Coverage Histogram (0-50X)



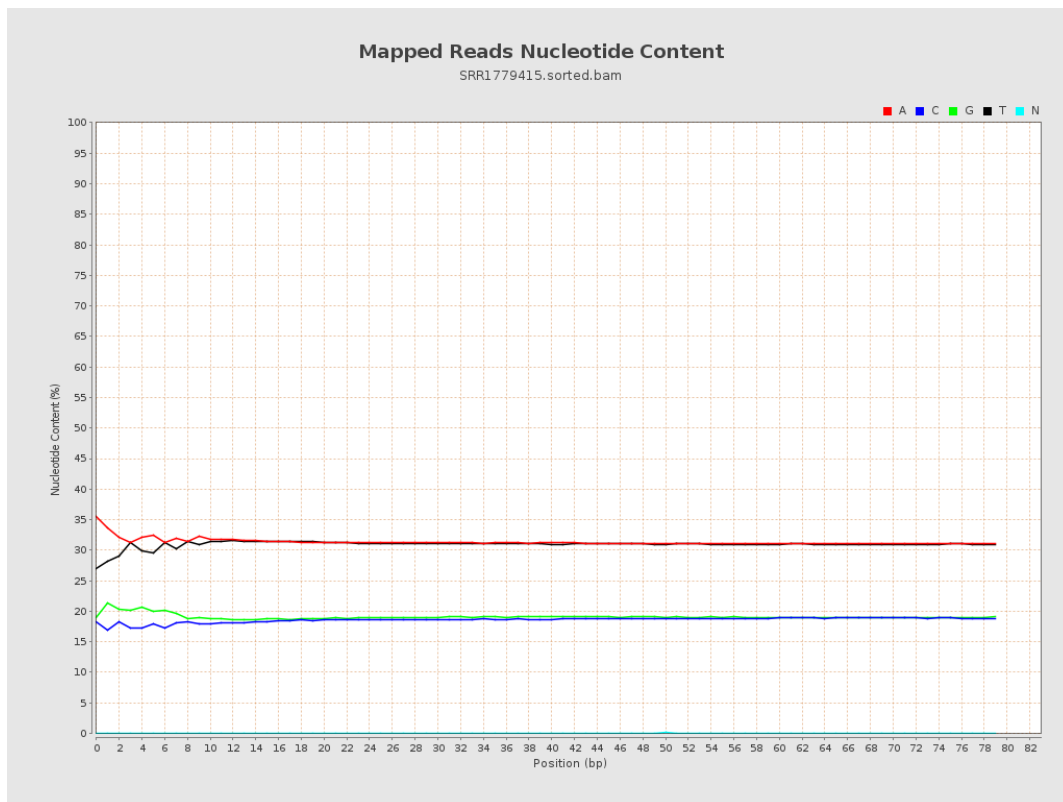
6. Results : Genome Fraction Coverage



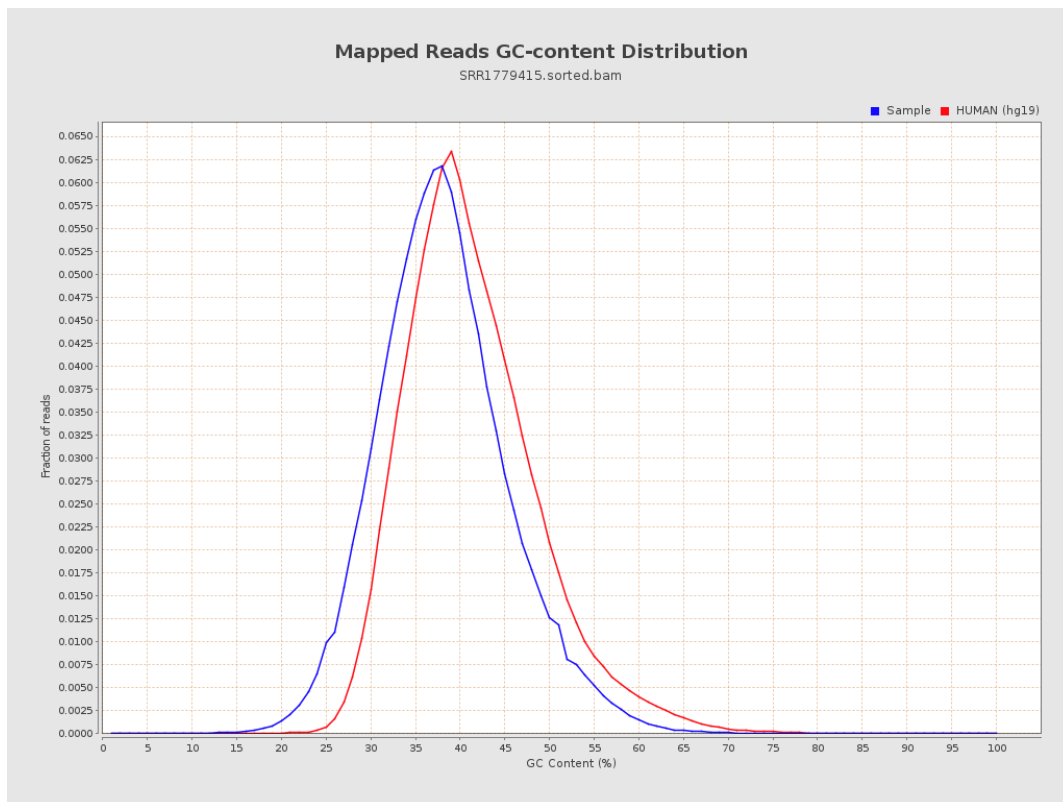
7. Results : Duplication Rate Histogram



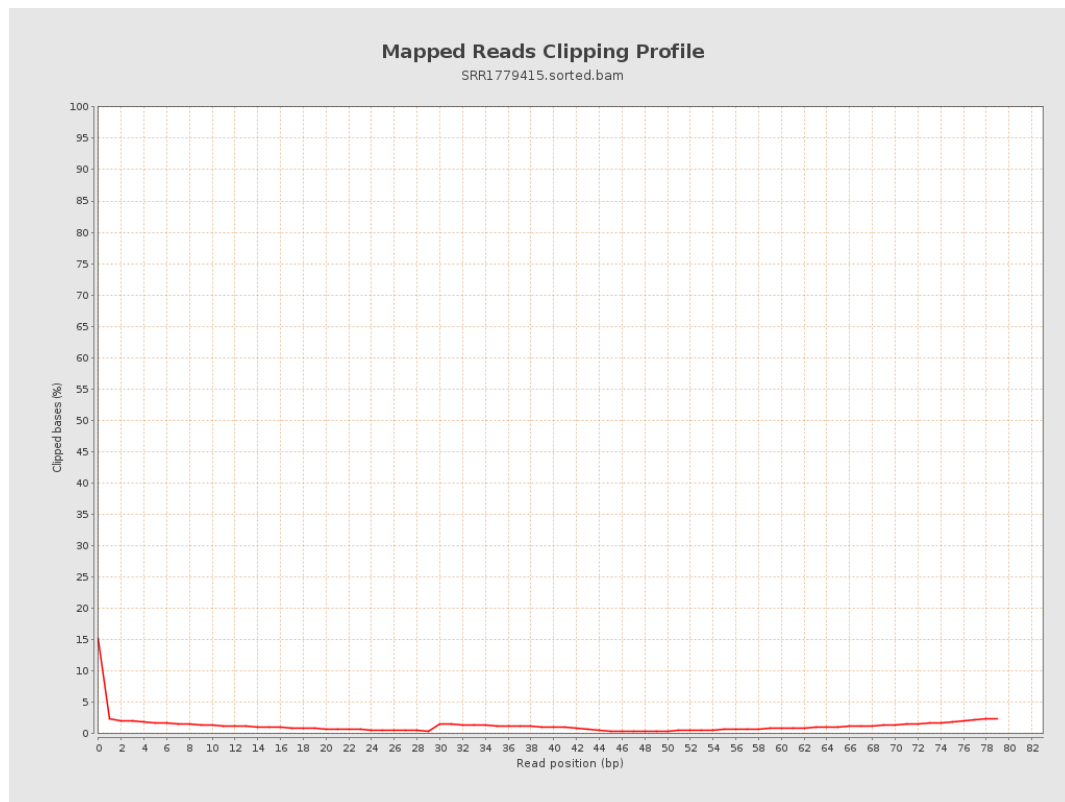
8. Results : Mapped Reads Nucleotide Content



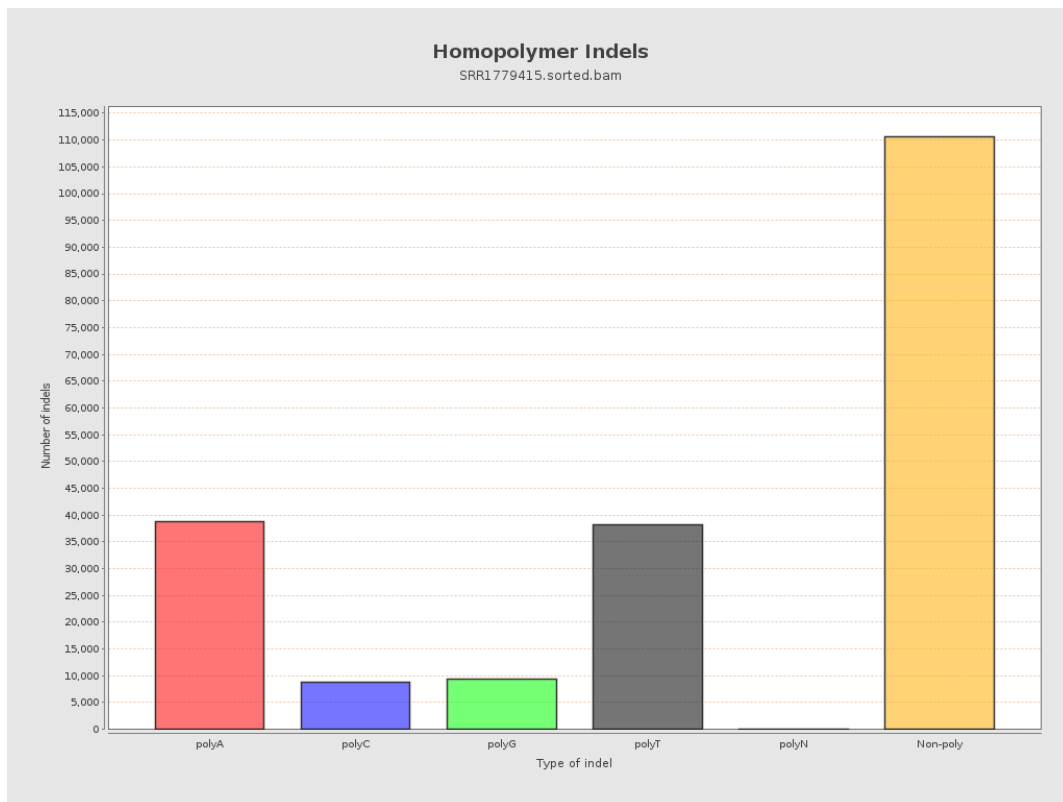
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



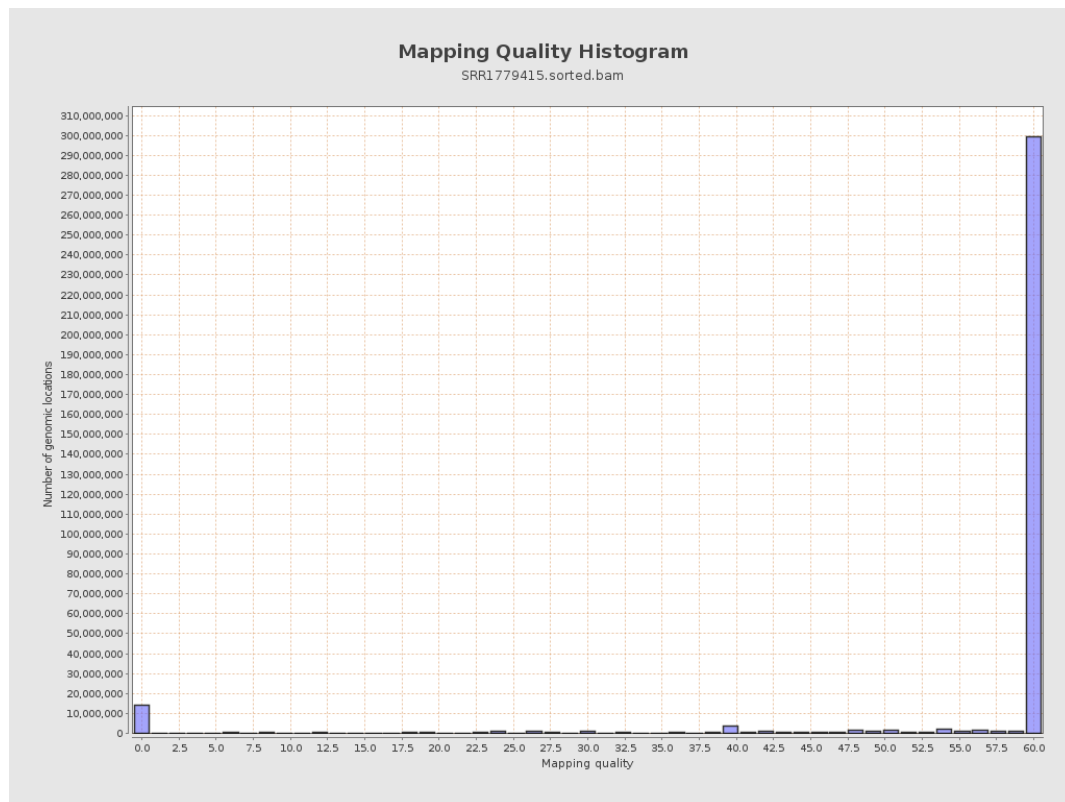
11. Results : Homopolymer Indels



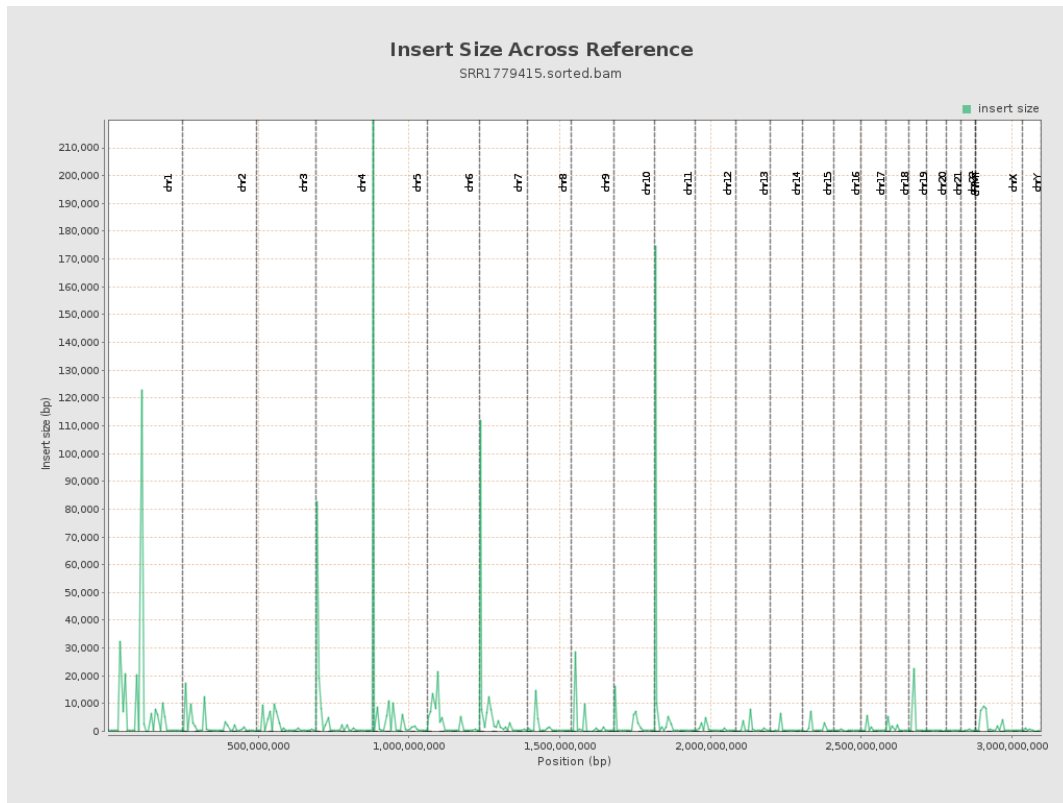
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

