

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 08:15:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472415.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_SRR3472415 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472415_1.fastq.gz SRR3472415_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 08:15:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472415.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	18,140,012
Mapped reads	17,981,689 / 99.13%
Unmapped reads	158,323 / 0.87%
Mapped paired reads	17,981,689 / 99.13%
Mapped reads, first in pair	9,016,804 / 49.71%
Mapped reads, second in pair	8,964,885 / 49.42%
Mapped reads, both in pair	17,887,816 / 98.61%
Mapped reads, singletons	93,873 / 0.52%
Secondary alignments	0
Supplementary alignments	71,937 / 0.4%
Read min/max/mean length	30 / 100 / 99.36
Duplicated reads (estimated)	11,579,857 / 63.84%
Duplication rate	47.35%
Clipped reads	1,231,470 / 6.79%

2.2. ACGT Content

Number/percentage of A's	474,022,625 / 26.88%
Number/percentage of C's	409,156,020 / 23.2%
Number/percentage of T's	475,066,328 / 26.94%
Number/percentage of G's	404,948,991 / 22.96%
Number/percentage of N's	211,972 / 0.01%

GC Percentage	46.17%
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2.3. Coverage

Mean	0.5697
Standard Deviation	19.9493

2.4. Mapping Quality

Mean Mapping Quality	55.12
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2.5. Insert size

Mean	17,909.39
Standard Deviation	1,291,779.74
P25/Median/P75	155 / 216 / 291

2.6. Mismatches and indels

General error rate	0.55%
Mismatches	9,431,877
Insertions	100,070
Mapped reads with at least one insertion	0.55%
Deletions	86,359
Mapped reads with at least one deletion	0.48%
Homopolymer indels	46.64%

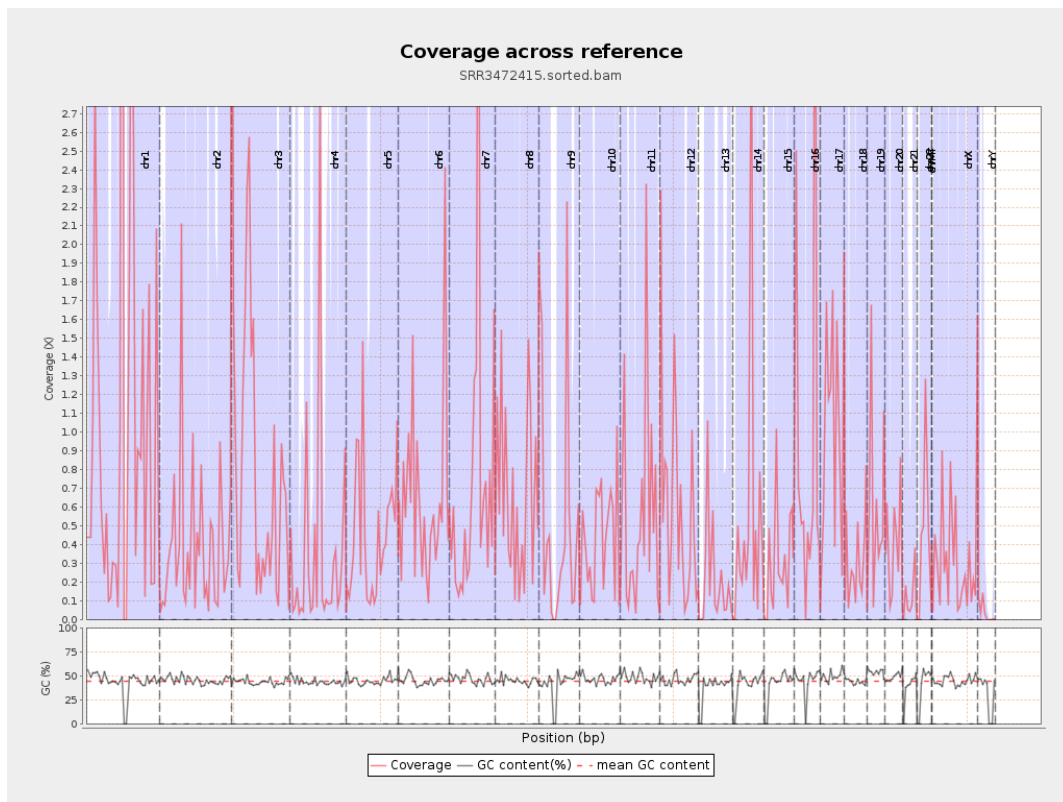
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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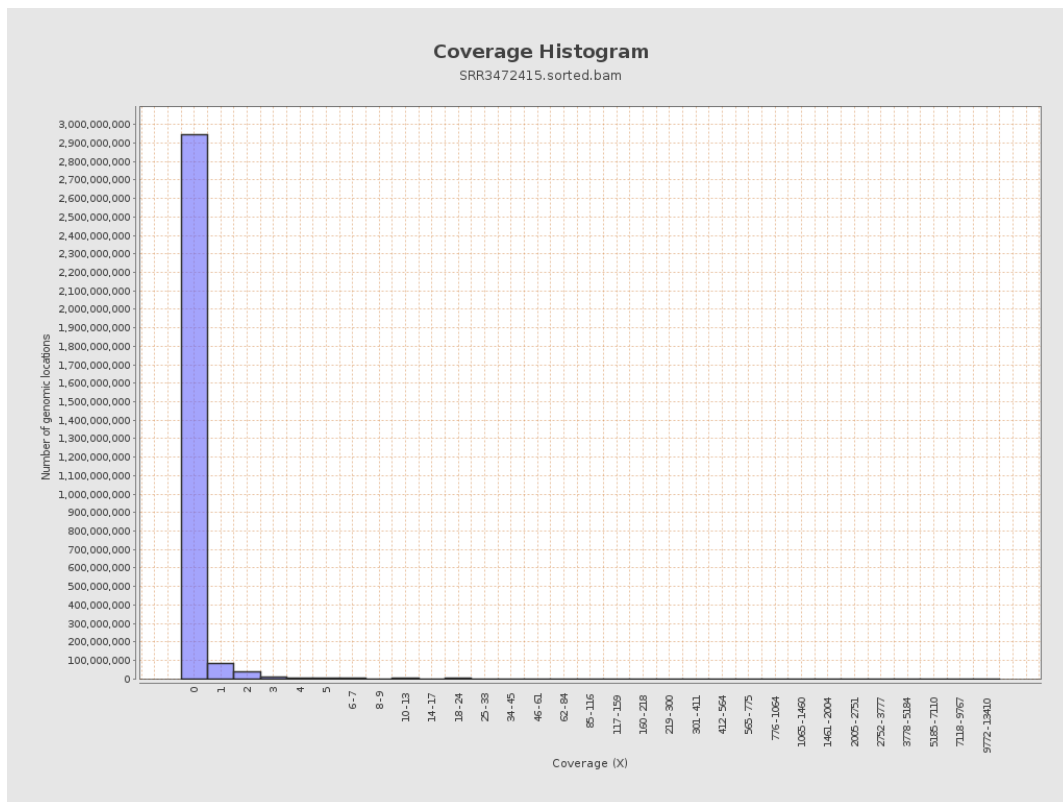
		bases	coverage	deviation
chr1	249250621	292650731	1.1741	41.1416
chr2	243199373	95578229	0.393	14.7602
chr3	198022430	167499113	0.8459	18.5455
chr4	191154276	63658178	0.333	22.3435
chr5	180915260	82605718	0.4566	12.3867
chr6	171115067	109428399	0.6395	15.6762
chr7	159138663	122336393	0.7687	22.2317
chr8	146364022	98557929	0.6734	20.567
chr9	141213431	74901618	0.5304	18.9974
chr10	135534747	57416356	0.4236	14.9249
chr11	135006516	73155429	0.5419	18.0176
chr12	133851895	82440999	0.6159	16.0524
chr13	115169878	23524480	0.2043	8.052
chr14	107349540	55579439	0.5177	19.7284
chr15	102531392	31230184	0.3046	9.0877
chr16	90354753	87715052	0.9708	28.3889
chr17	81195210	82668418	1.0181	22.0873
chr18	78077248	24438587	0.313	9.1899
chr19	59128983	34341797	0.5808	14.3399
chr20	63025520	25299758	0.4014	11.7439
chr21	48129895	6064220	0.126	4.6776
chr22	51304566	22138767	0.4315	13.0155
chrMT	16571	6708	0.4048	0.8476
chrX	155270560	48087532	0.3097	10.0249

chrY	59373566	2280027	0.0384	3.1092
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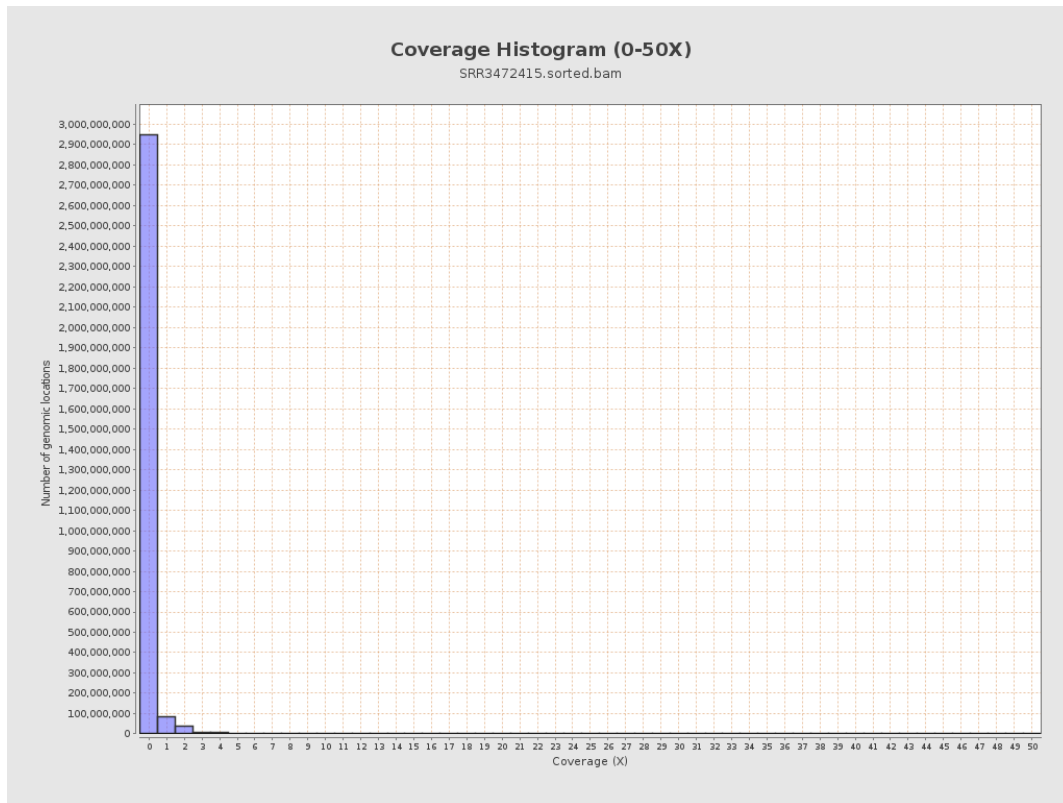
3. Results : Coverage across reference



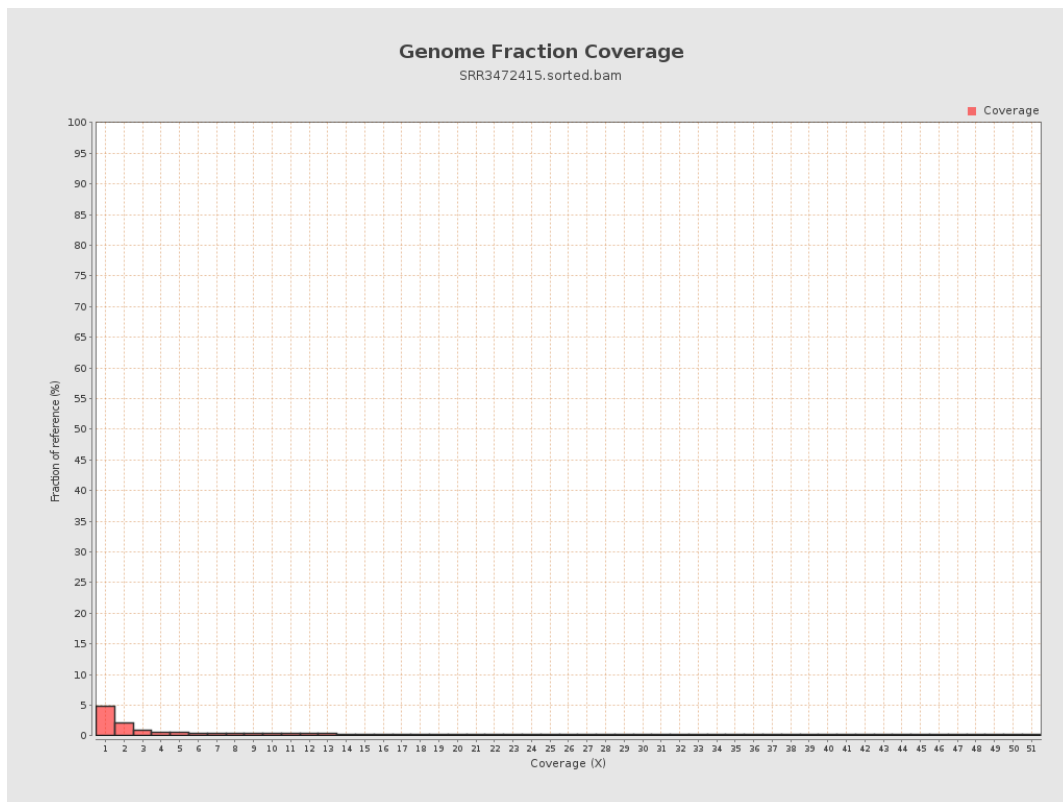
4. Results : Coverage Histogram



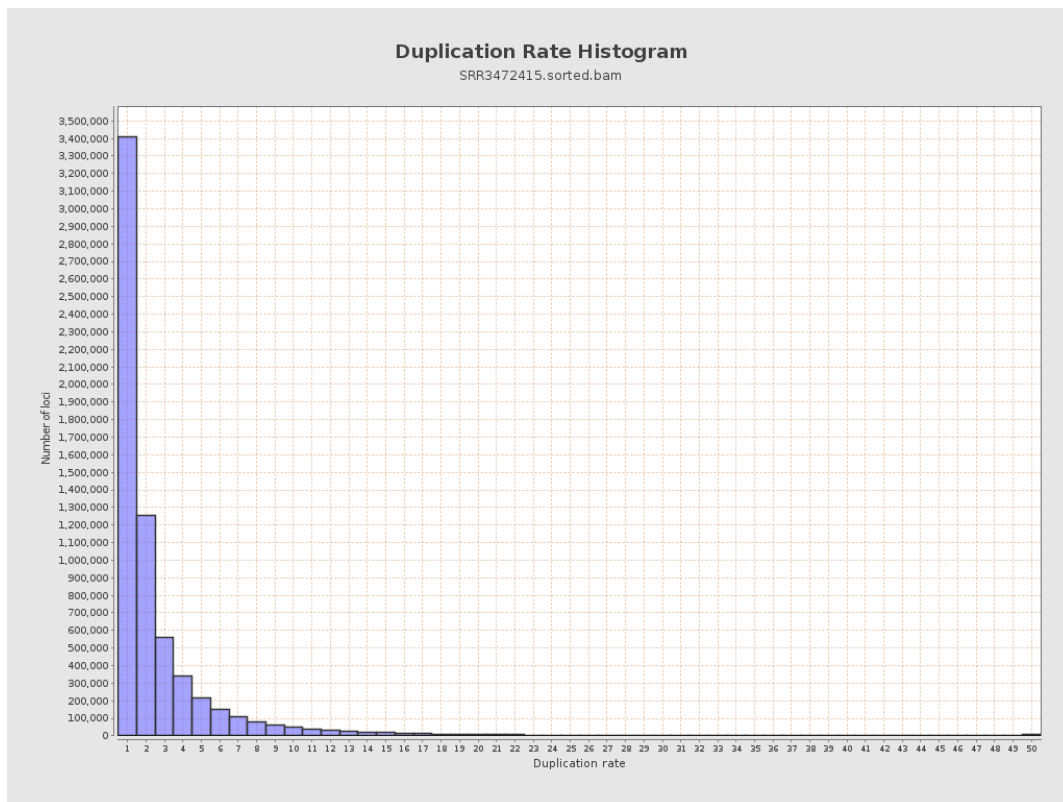
5. Results : Coverage Histogram (0-50X)



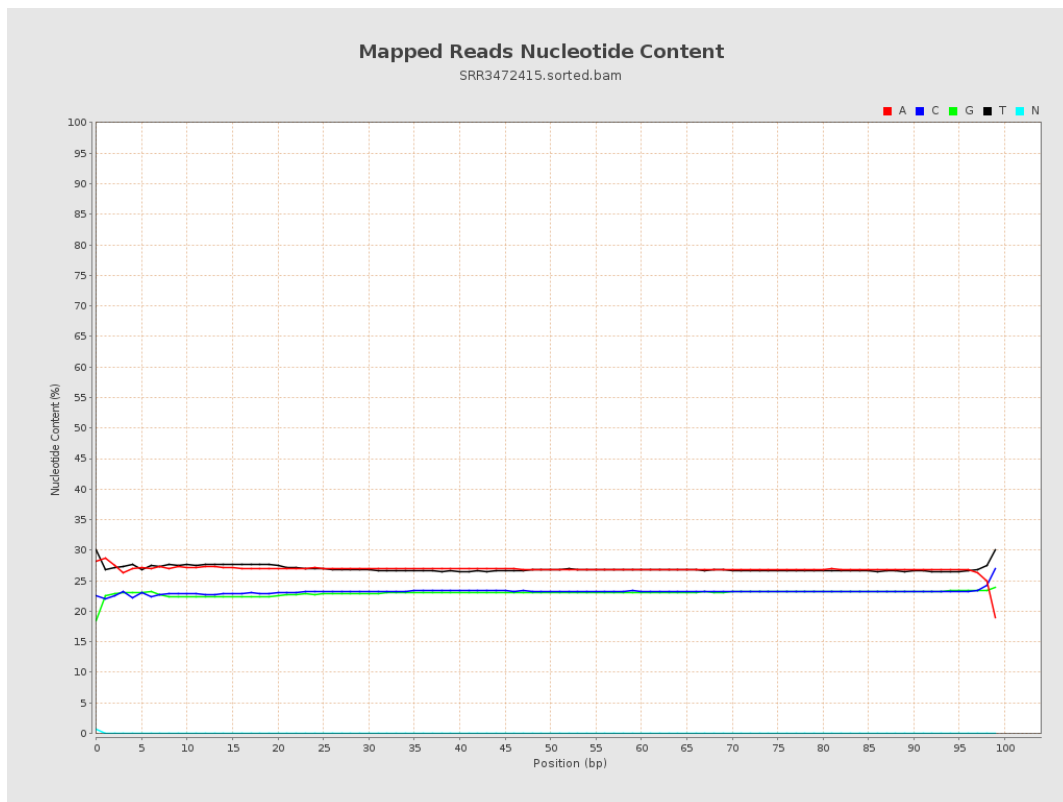
6. Results : Genome Fraction Coverage



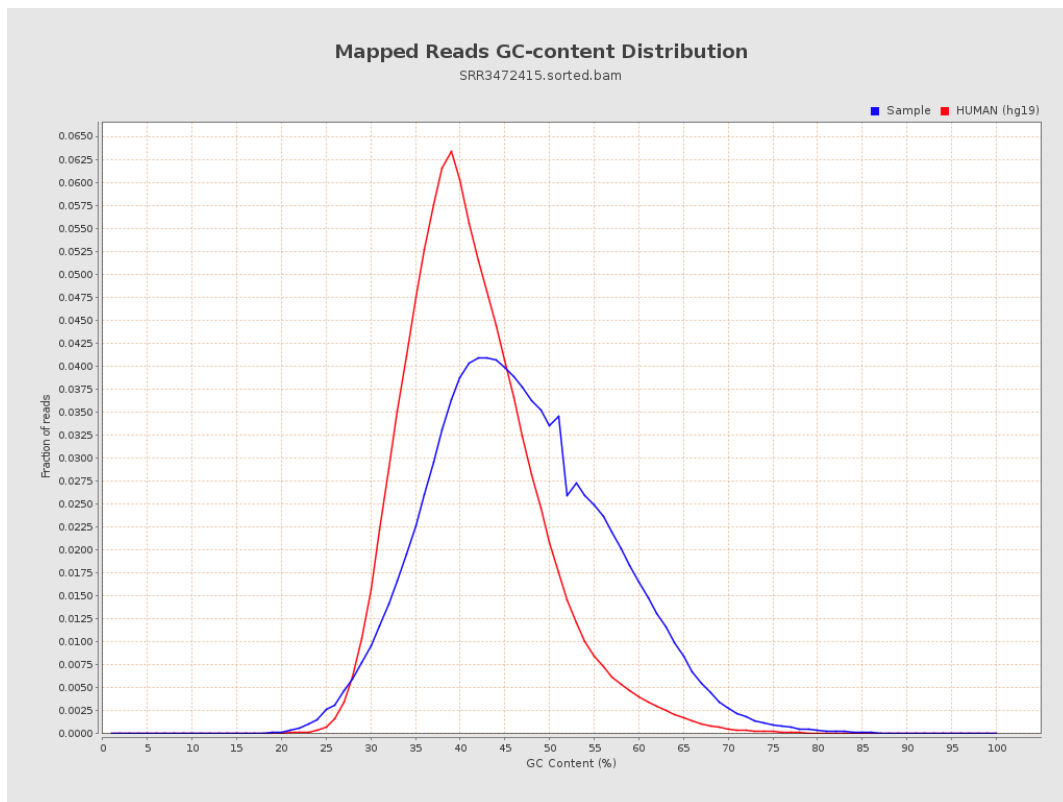
7. Results : Duplication Rate Histogram



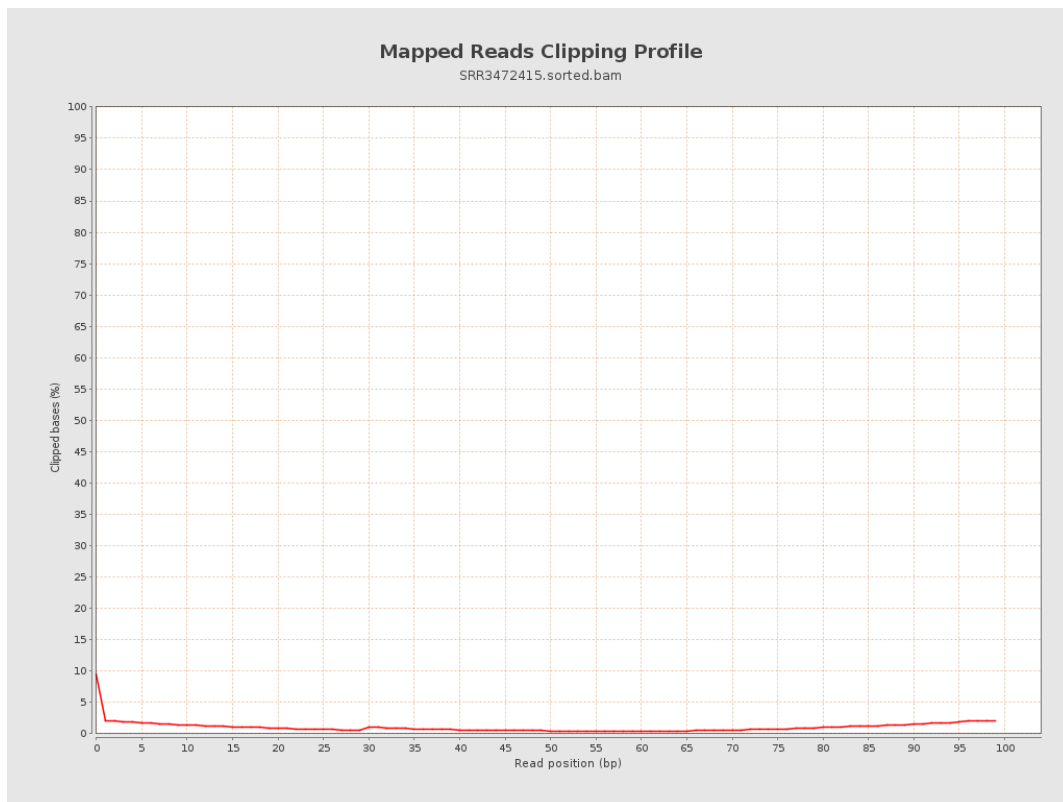
8. Results : Mapped Reads Nucleotide Content



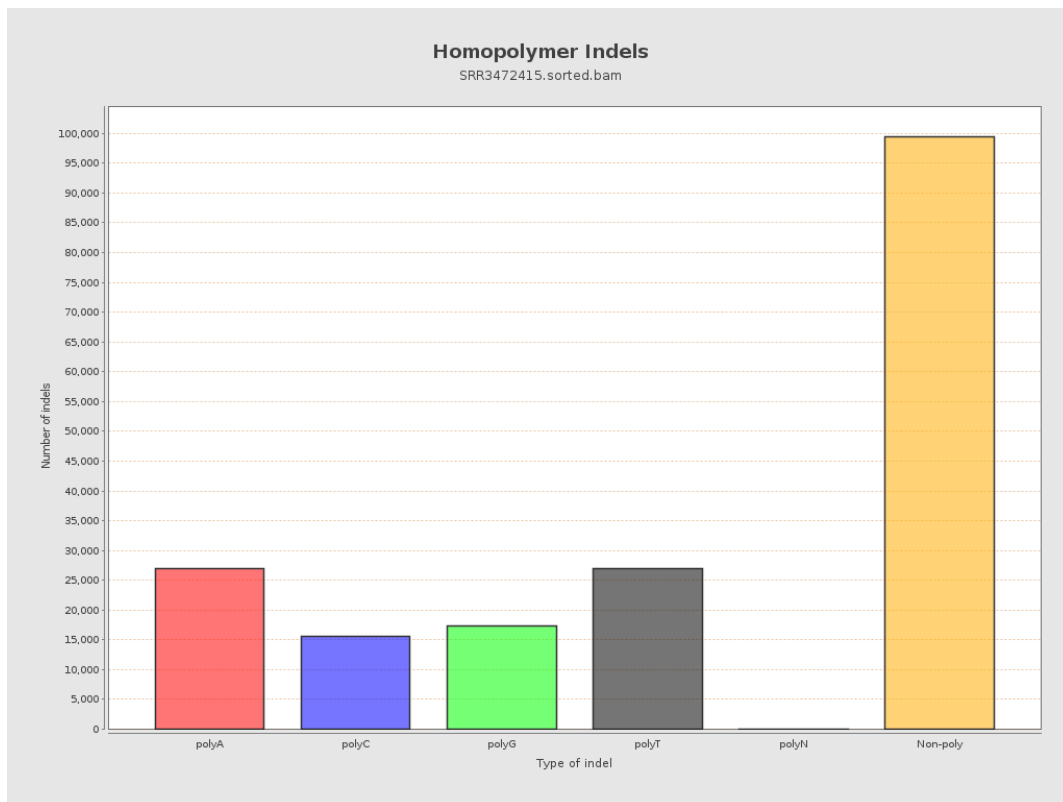
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



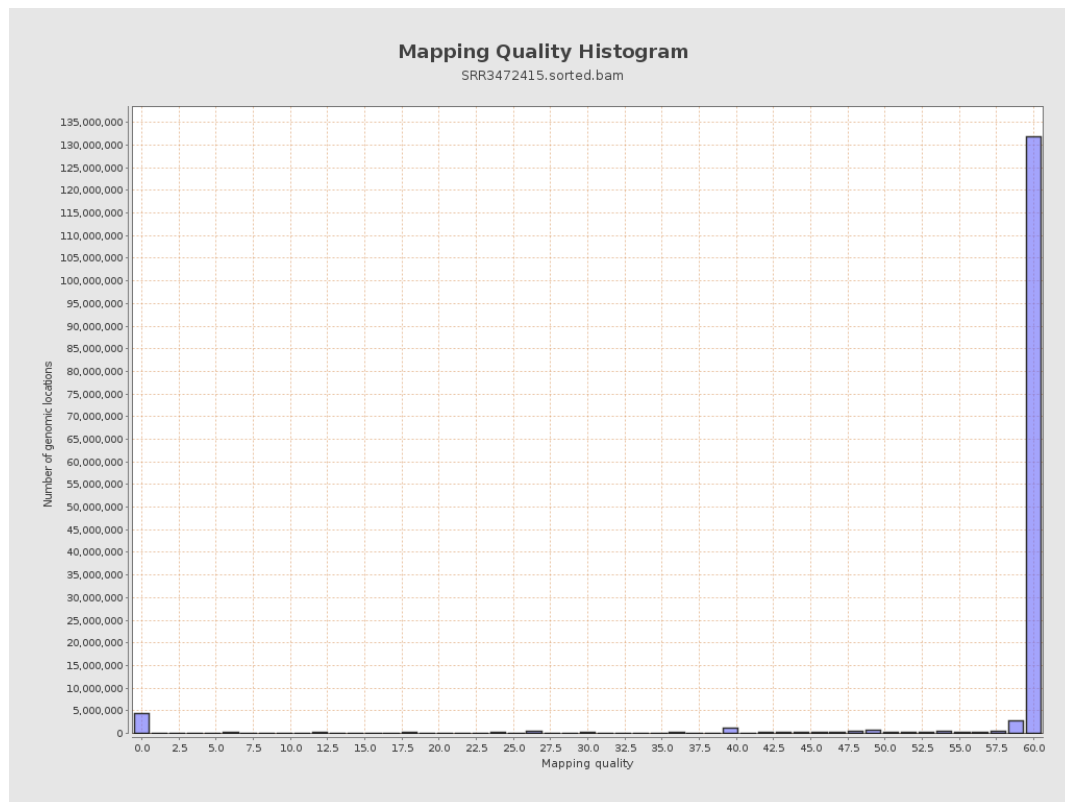
11. Results : Homopolymer Indels



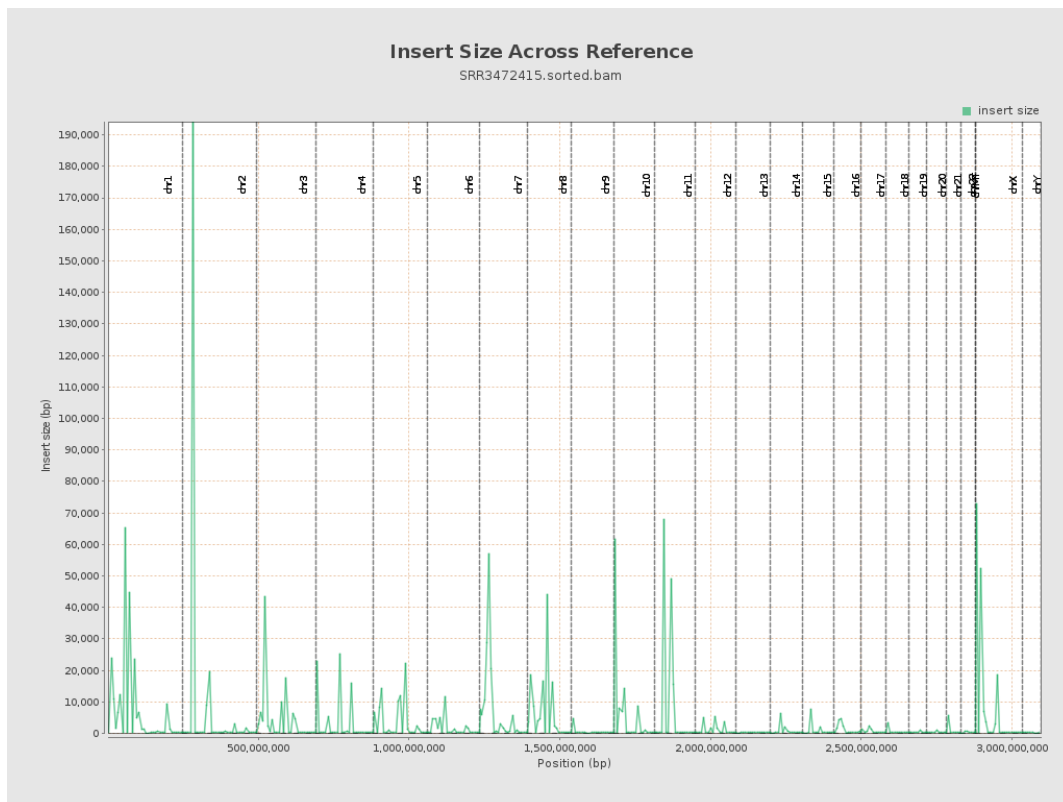
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

