Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/09 03:20:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617415.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_SRR617415 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617415_1.fastq.gz SRR617415_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 09 03:20:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617415.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	29,069,856 / 90.84%
Unmapped reads	2,930,144 / 9.16%
Mapped paired reads	29,069,856 / 90.84%
Mapped reads, first in pair	14,690,923 / 45.91%
Mapped reads, second in pair	14,378,933 / 44.93%
Mapped reads, both in pair	28,423,716 / 88.82%
Mapped reads, singletons	646,140 / 2.02%
Secondary alignments	0
Supplementary alignments	418,136 / 1.31%
Read min/max/mean length	30 / 100 / 100.54
Duplicated reads (estimated)	1,275,921 / 3.99%
Duplication rate	4.02%
Clipped reads	3,535,225 / 11.05%

2.2. ACGT Content

Number/percentage of A's	853,766,691 / 29.94%
Number/percentage of C's	570,716,312 / 20.01%
Number/percentage of T's	844,369,273 / 29.61%
Number/percentage of G's	581,640,057 / 20.4%
Number/percentage of N's	1,010,256 / 0.04%

GC Percentage	40.41%

2.3. Coverage

Mean	0.9213
Standard Deviation	2.8105

2.4. Mapping Quality

Mean Mapping Quality	53.8

2.5. Insert size

Mean	47,570.68
Standard Deviation	2,082,652.61
P25/Median/P75	168 / 205 / 263

2.6. Mismatches and indels

General error rate	1.45%
Mismatches	40,938,600
Insertions	241,325
Mapped reads with at least one insertion	0.82%
Deletions	282,754
Mapped reads with at least one deletion	0.95%
Homopolymer indels	43.67%

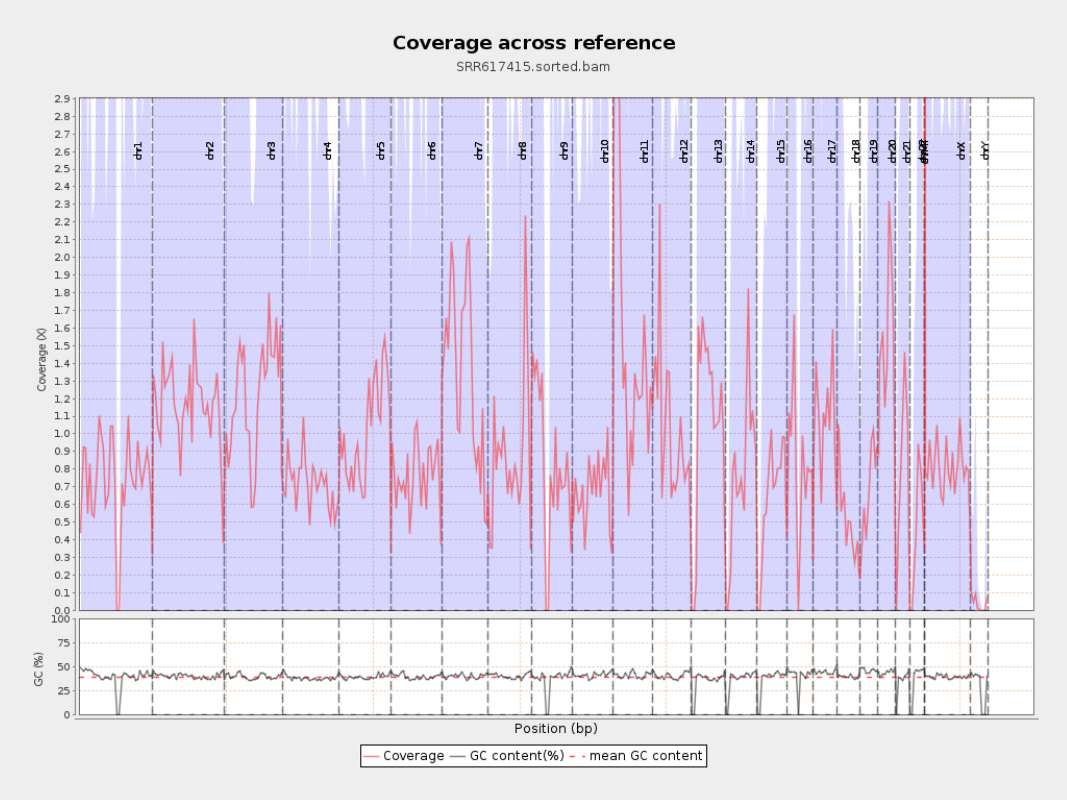
2.7. Chromosome stats

Name	**Length**	**Mapped**	**Mean**	**Standard**

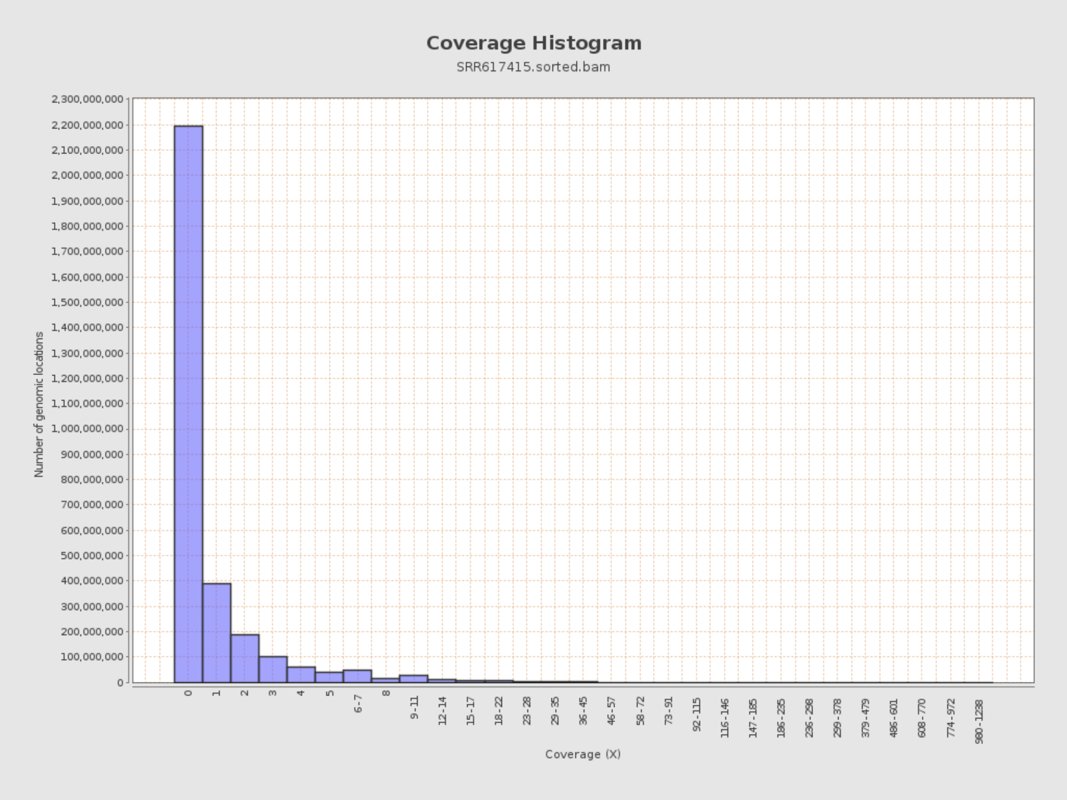
		bases	coverage	deviation
chr1	249250621	183770788	0.7373	2.6459
chr2	243199373	284761561	1.1709	2.9564
chr3	198022430	241128378	1.2177	3.2659
chr4	191154276	138347612	0.7237	2.2074
chr5	180915260	183162187	1.0124	2.7762
chr6	171115067	131408607	0.768	2.5154
chr7	159138663	213978410	1.3446	3.1262
chr8	146364022	126261105	0.8627	3.1124
chr9	141213431	113978639	0.8071	2.5141
chr10	135534747	91235136	0.6731	2.3122
chr11	135006516	211056419	1.5633	3.6878
chr12	133851895	136072206	1.0166	2.685
chr13	115169878	124413764	1.0803	2.6913
chr14	107349540	82650158	0.7699	2.7758
chr15	102531392	65126427	0.6352	2.2631
chr16	90354753	71023689	0.7861	3.177
chr17	81195210	86758994	1.0685	3.4968
chr18	78077248	40926169	0.5242	1.9257
chr19	59128983	39862250	0.6742	2.2132
chr20	63025520	96160185	1.5257	4.492
chr21	48129895	38986700	0.81	2.4291
chr22	51304566	22586479	0.4402	1.9779
chrMT	16571	176496	10.6509	5.789
chrX	155270560	126018692	0.8116	2.4825

chrY	59373566	2277786	0.0384	0.5444

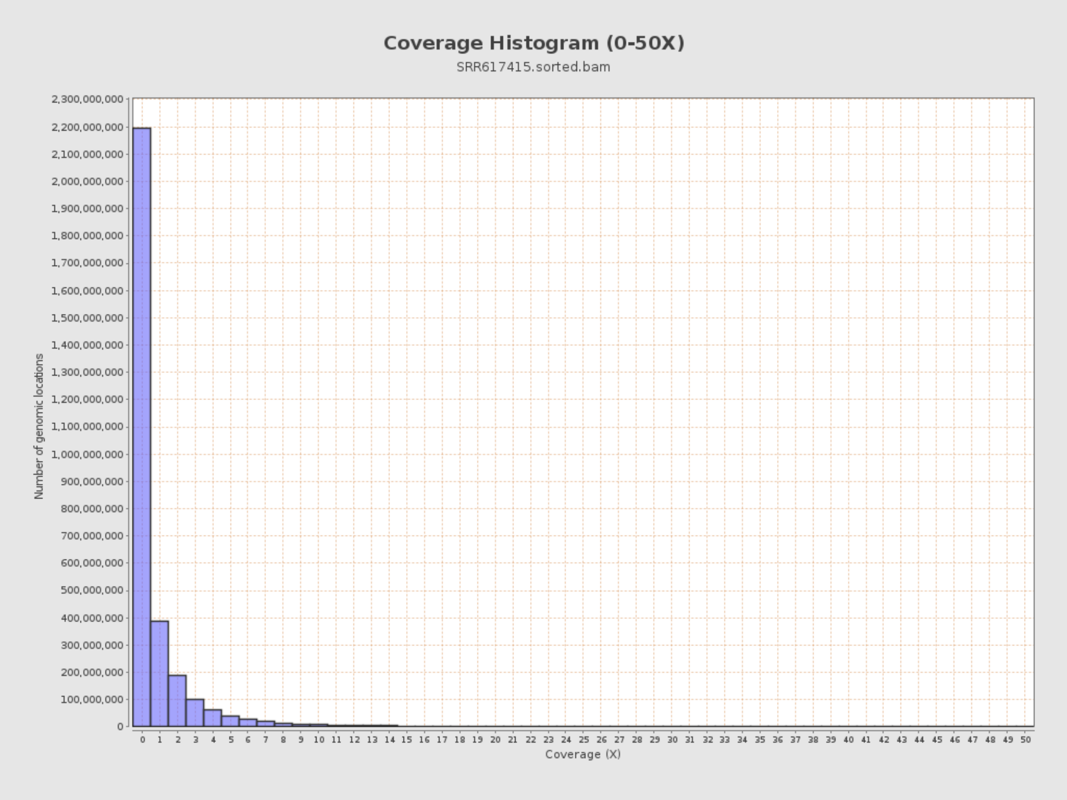
3. Results : Coverage across reference



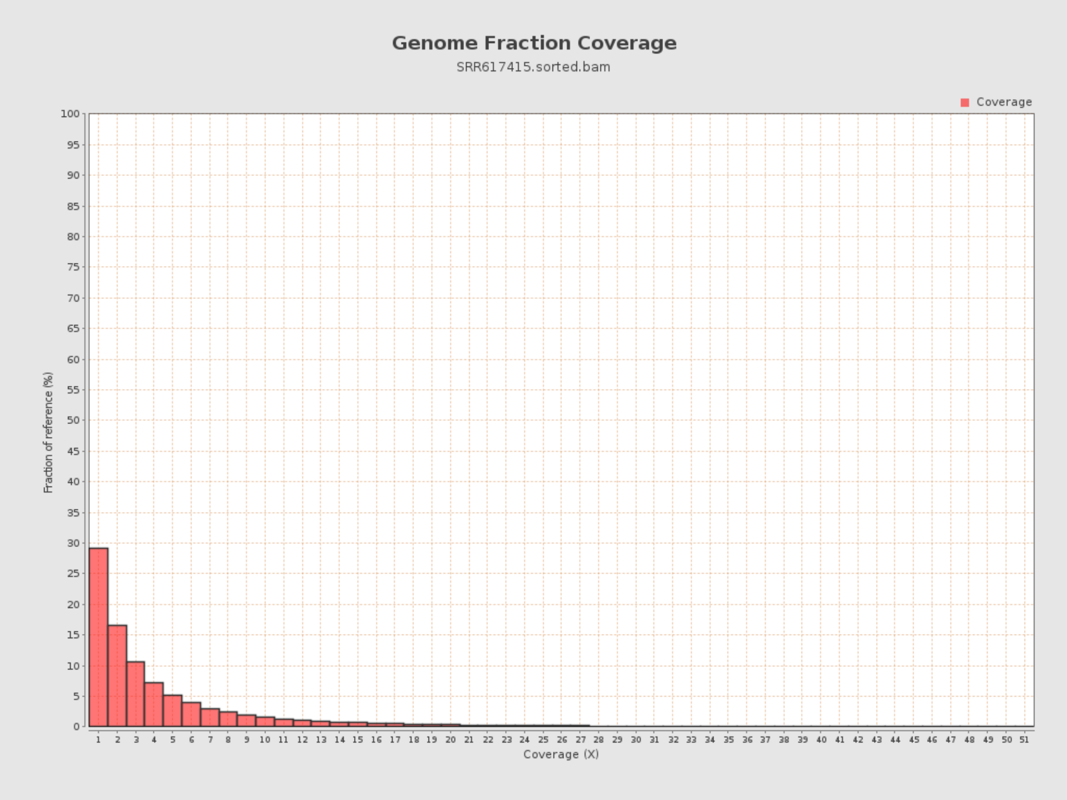
4. Results : Coverage Histogram



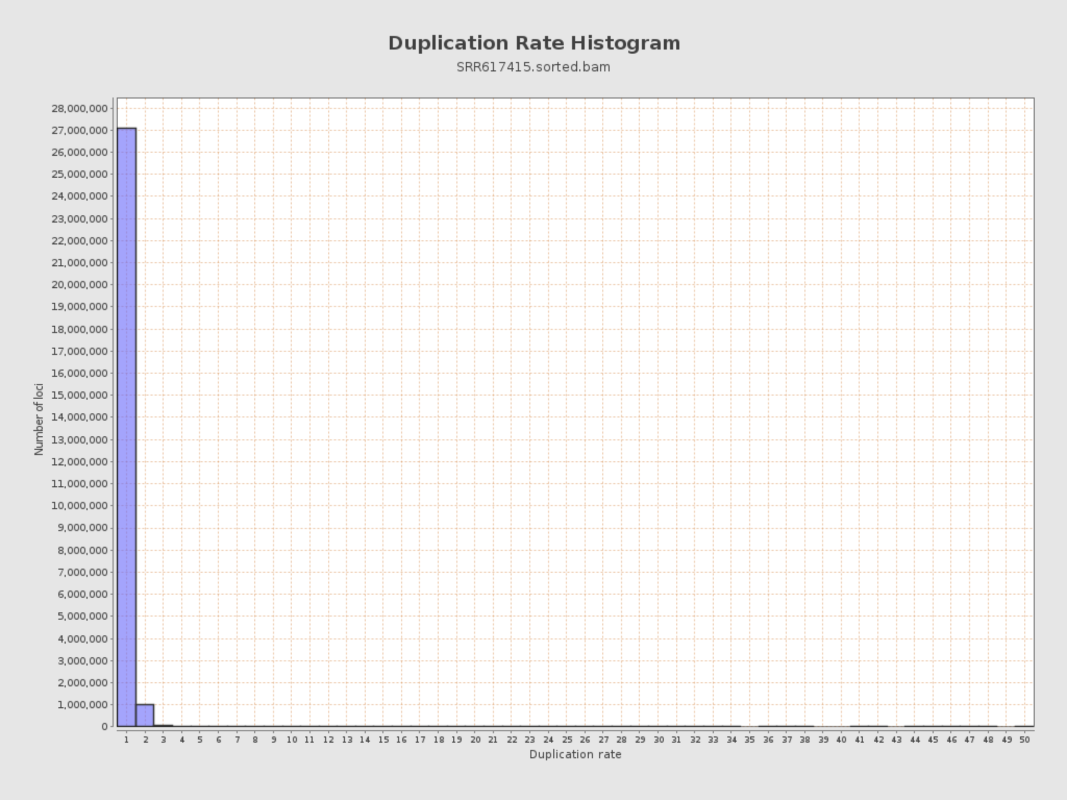
5. Results : Coverage Histogram (0-50X)



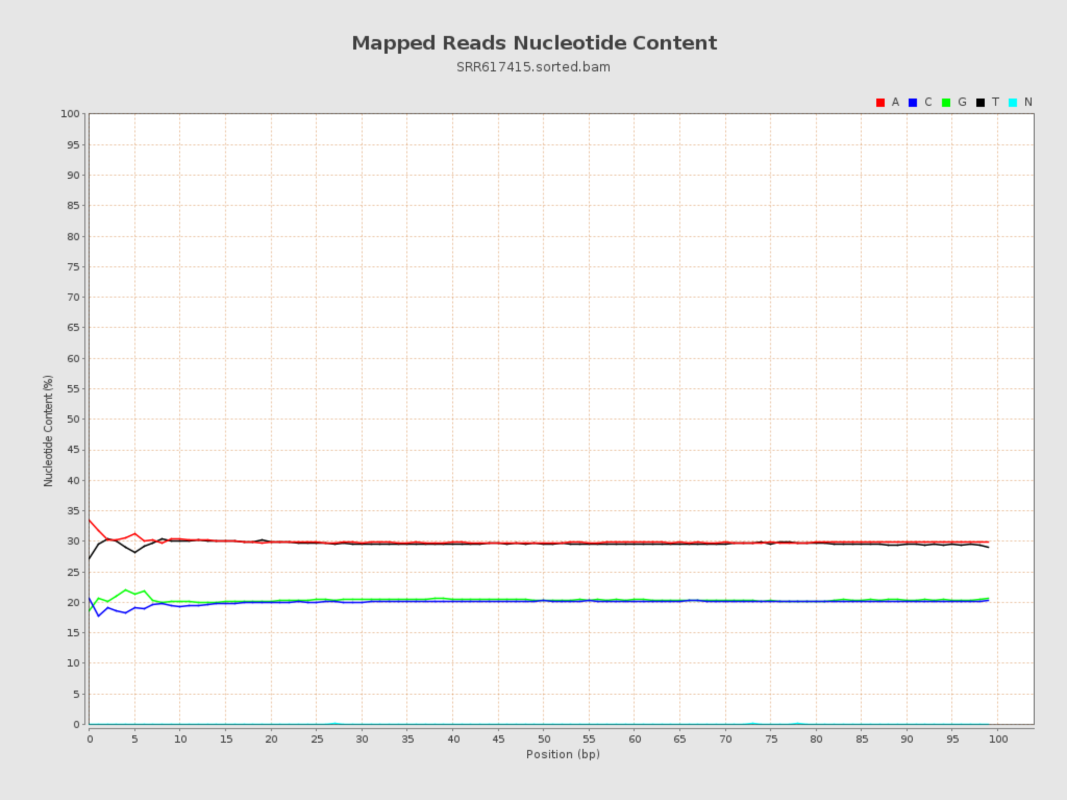
6. Results : Genome Fraction Coverage



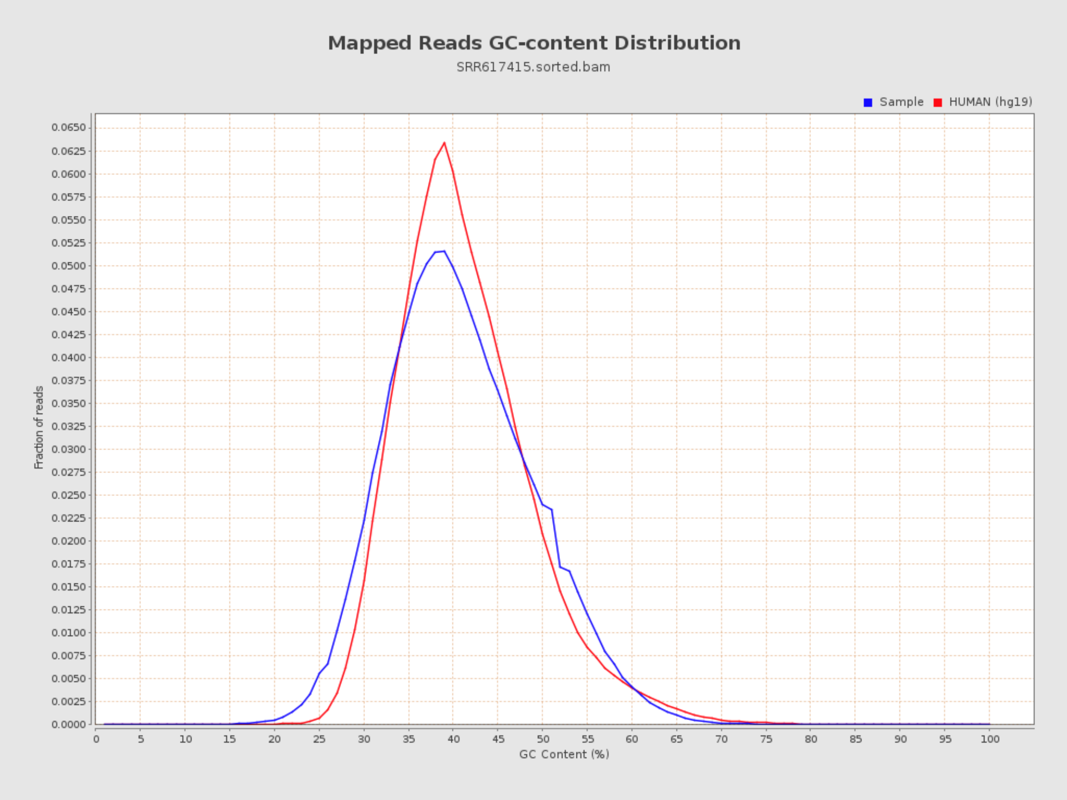
7. Results : Duplication Rate Histogram



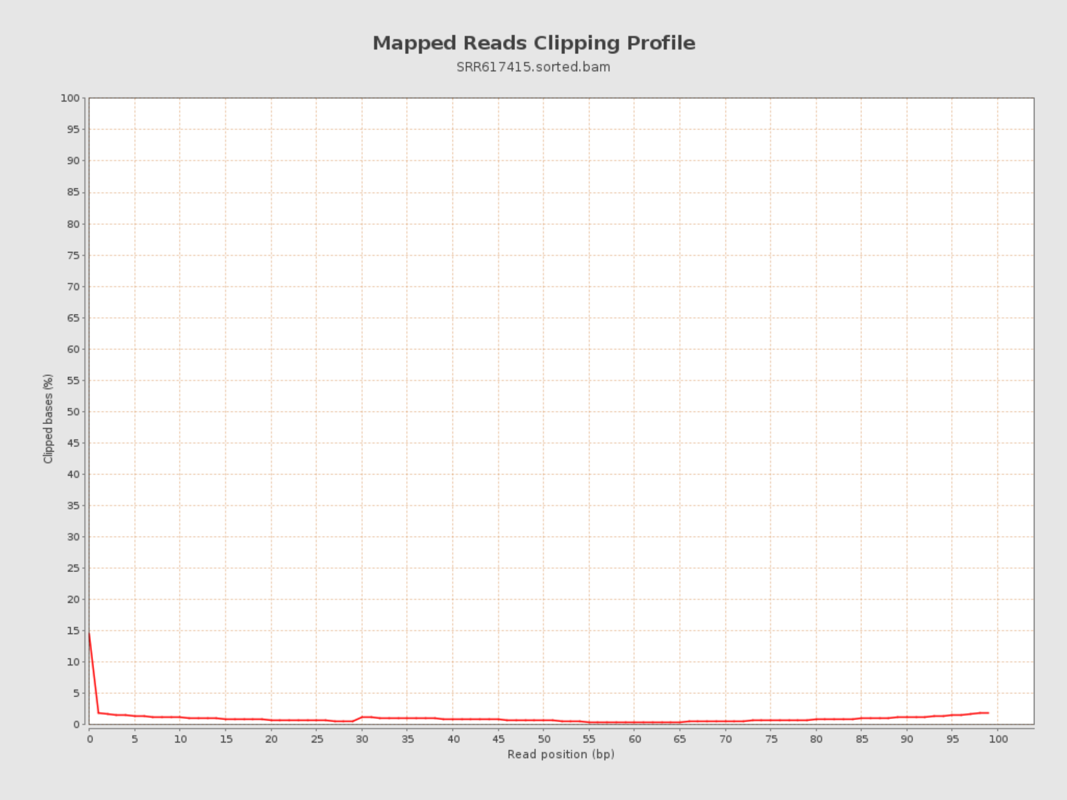
8. Results : Mapped Reads Nucleotide Content



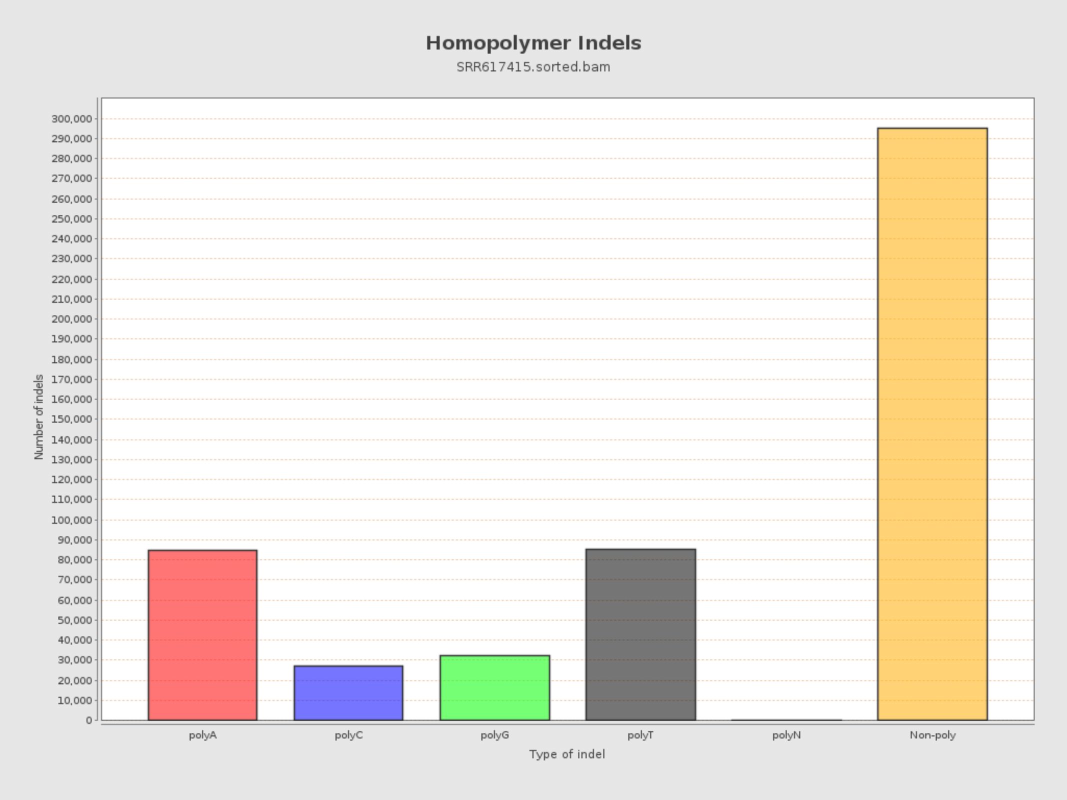
9. Results : Mapped Reads GC-content Distribution



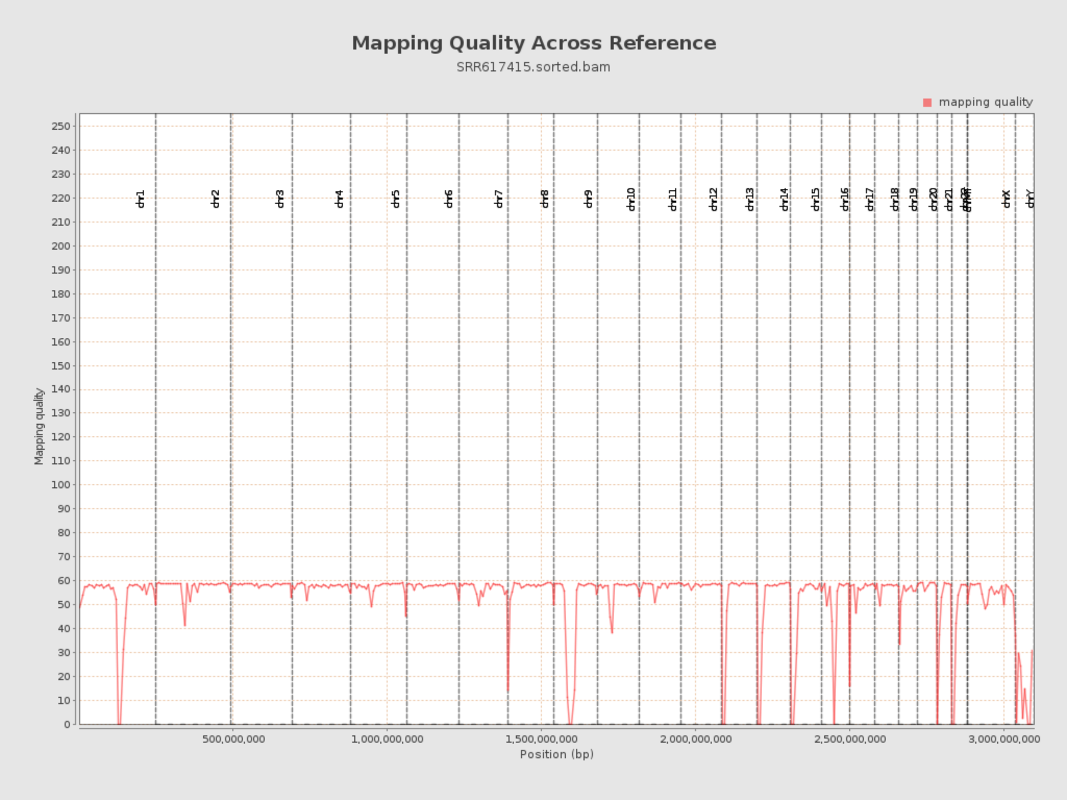
10. Results : Mapped Reads Clipping Profile



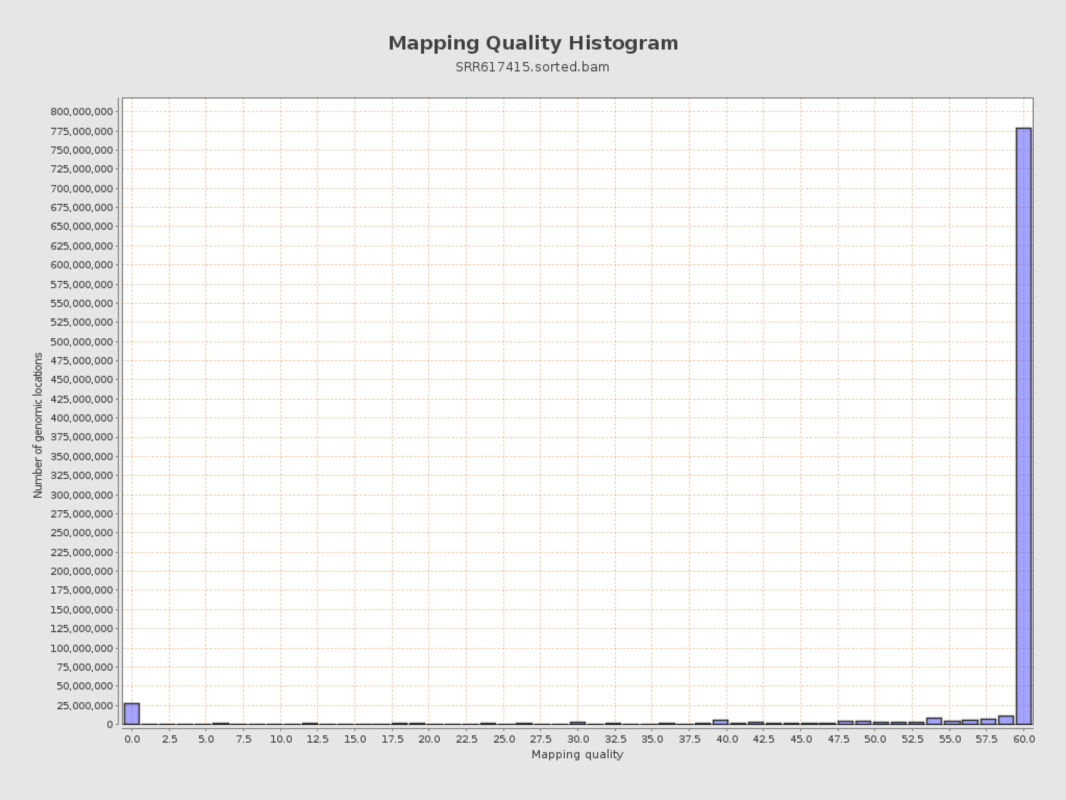
11. Results : Homopolymer Indels



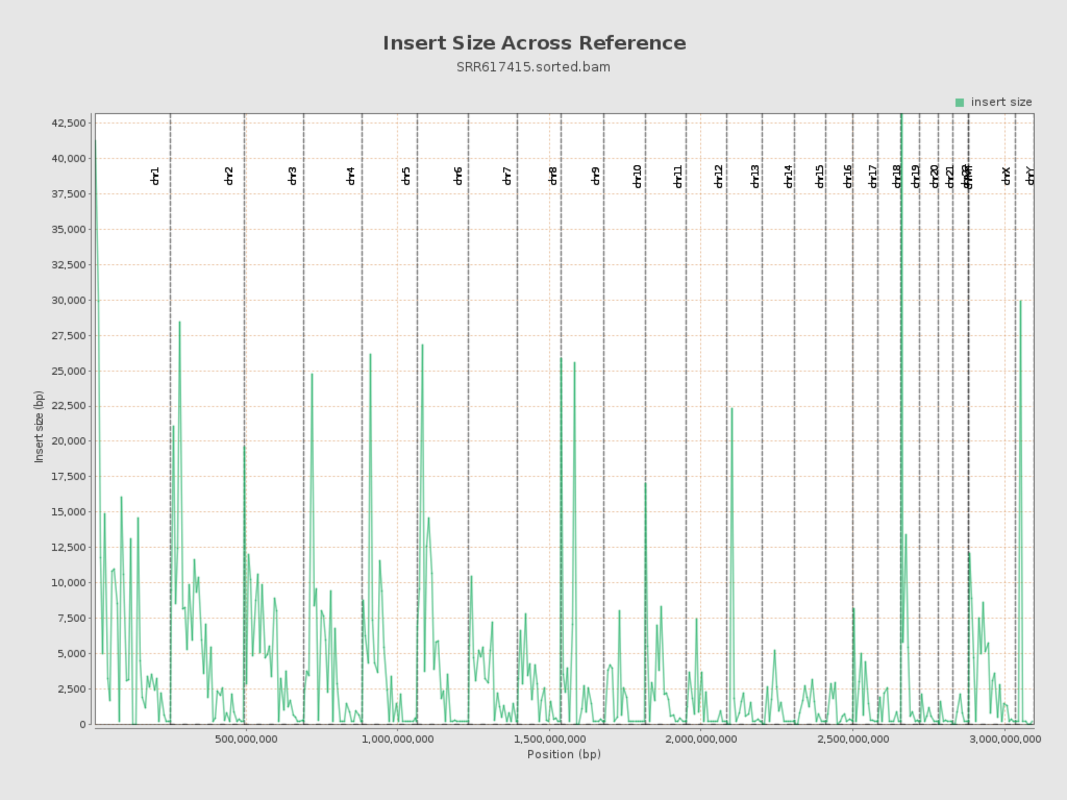
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram