Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/07 09:47:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617365.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_SRR617365 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617365_1.fastq.gz SRR617365_2.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Oct 07 09:47:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617365.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	30,640,623 / 95.75%
Unmapped reads	1,359,377 / 4.25%
Mapped paired reads	30,640,623 / 95.75%
Mapped reads, first in pair	15,397,012 / 48.12%
Mapped reads, second in pair	15,243,611 / 47.64%
Mapped reads, both in pair	30,136,354 / 94.18%
Mapped reads, singletons	504,269 / 1.58%
Secondary alignments	0
Supplementary alignments	104,265 / 0.33%
Read min/max/mean length	30 / 100 / 100.12
Duplicated reads (estimated)	1,642,251 / 5.13%
Duplication rate	1.53%
Clipped reads	2,321,560 / 7.25%

2.2. ACGT Content

Number/percentage of A's	908,086,515 / 30.21%
Number/percentage of C's	598,042,282 / 19.9%
Number/percentage of T's	897,927,041 / 29.87%
Number/percentage of G's	600,423,490 / 19.98%
Number/percentage of N's	1,308,323 / 0.04%

GC Percentage	39.87%

2.3. Coverage

Mean	0.9713
Standard Deviation	9.9255

2.4. Mapping Quality

Mean Mapping Quality	53.43

2.5. Insert size

Mean	73,737.95
Standard Deviation	2,607,406.32
P25/Median/P75	174 / 216 / 283

2.6. Mismatches and indels

General error rate	0.9%
Mismatches	26,268,450
Insertions	310,493
Mapped reads with at least one insertion	0.98%
Deletions	374,875
Mapped reads with at least one deletion	1.19%
Homopolymer indels	41.43%

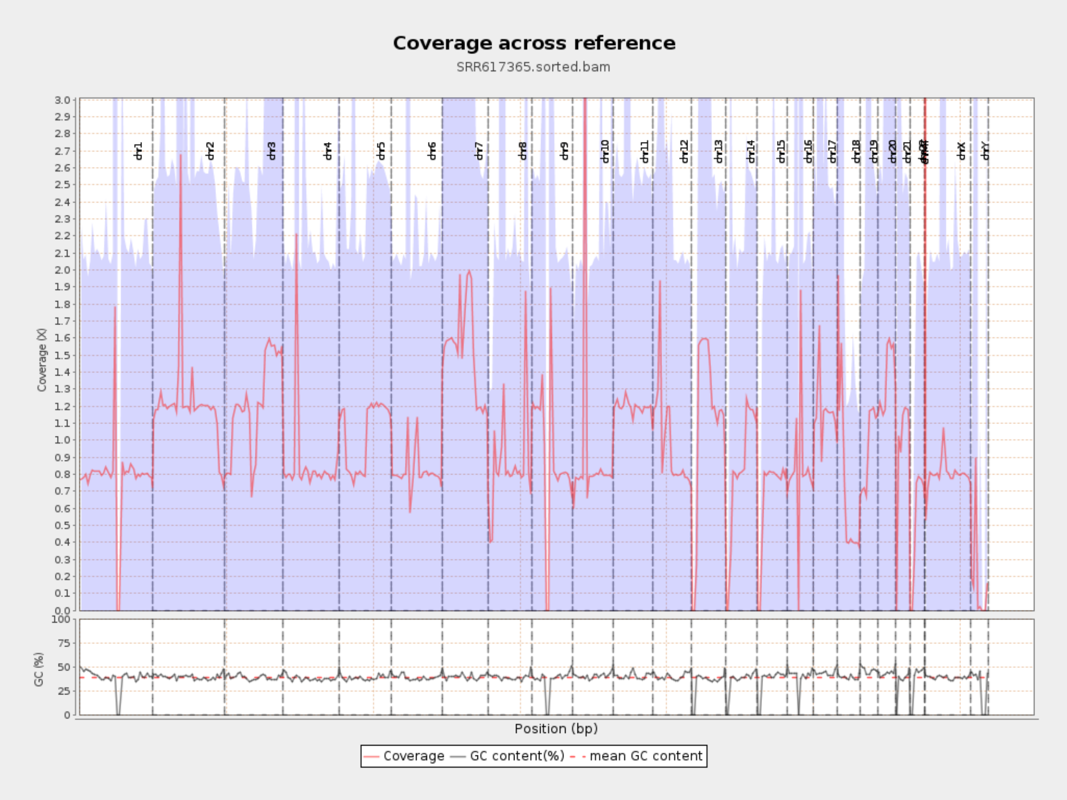
2.7. Chromosome stats

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

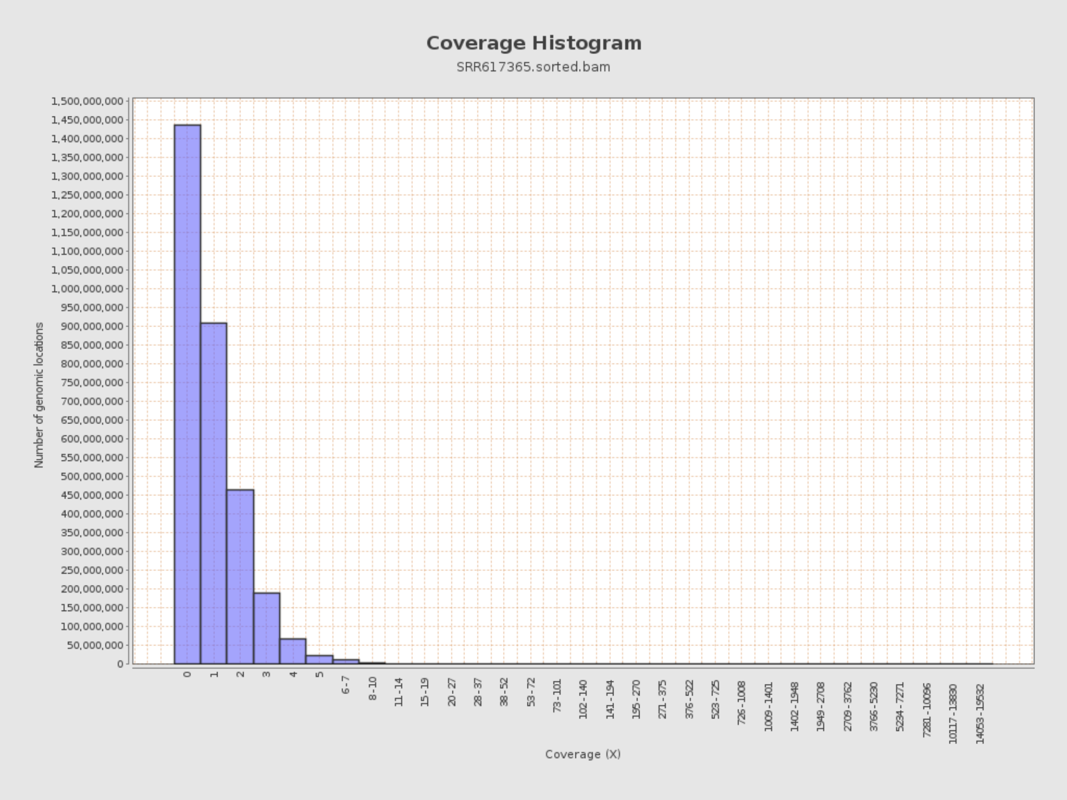
		bases	coverage	deviation
chr1	249250621	195752650	0.7854	20.1302
chr2	243199373	296680335	1.2199	9.0311
chr3	198022430	238683610	1.2053	1.5122
chr4	191154276	163997469	0.8579	9.8128
chr5	180915260	187594962	1.0369	1.481
chr6	171115067	140636590	0.8219	3.6359
chr7	159138663	243960651	1.533	10.974
chr8	146364022	126372658	0.8634	7.8238
chr9	141213431	126584549	0.8964	15.1273
chr10	135534747	126560631	0.9338	20.1952
chr11	135006516	161235229	1.1943	5.7096
chr12	133851895	132677457	0.9912	1.4176
chr13	115169878	130426391	1.1325	1.3574
chr14	107349540	87225128	0.8125	1.4031
chr15	102531392	67917603	0.6624	1.181
chr16	90354753	75778836	0.8387	7.7833
chr17	81195210	94659578	1.1658	7.2172
chr18	78077248	54455104	0.6975	15.6194
chr19	59128983	56729656	0.9594	9.6899
chr20	63025520	86905295	1.3789	2.5377
chr21	48129895	47700321	0.9911	3.2753
chr22	51304566	27066667	0.5276	0.9422
chrMT	16571	2124221	128.1891	23.0905
chrX	155270560	124515808	0.8019	3.0577

chrY	59373566	10457123	0.1761	8.6835

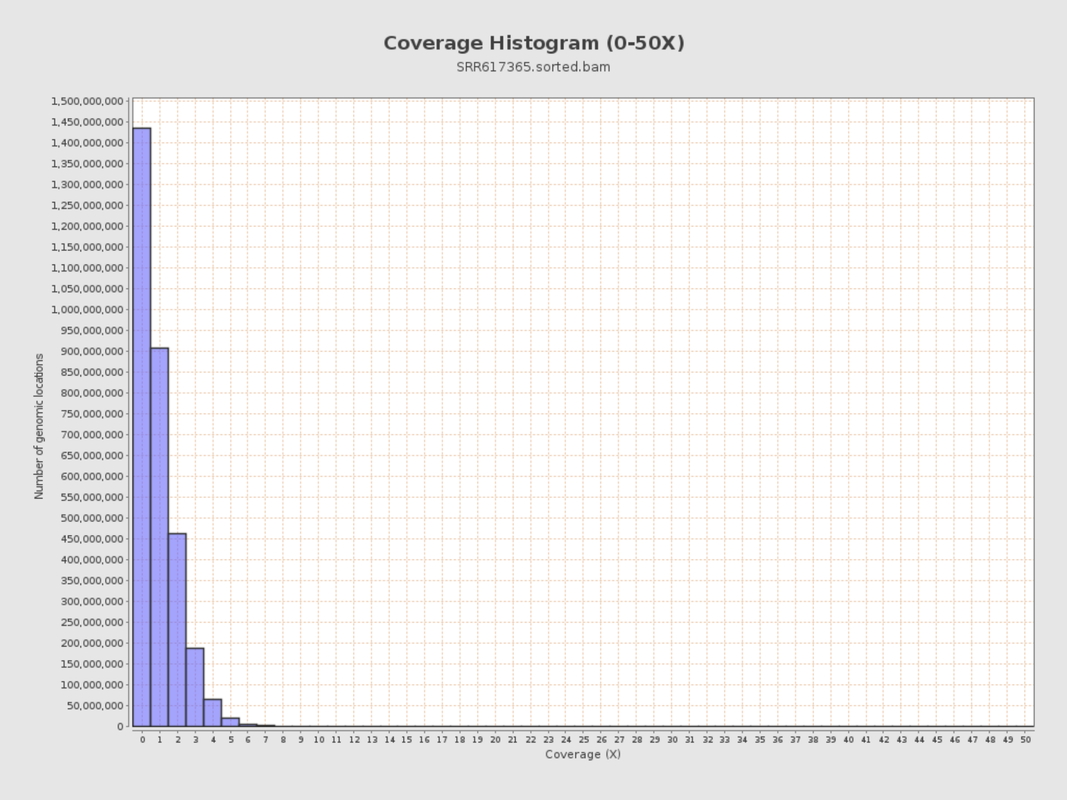
3. Results : Coverage across reference



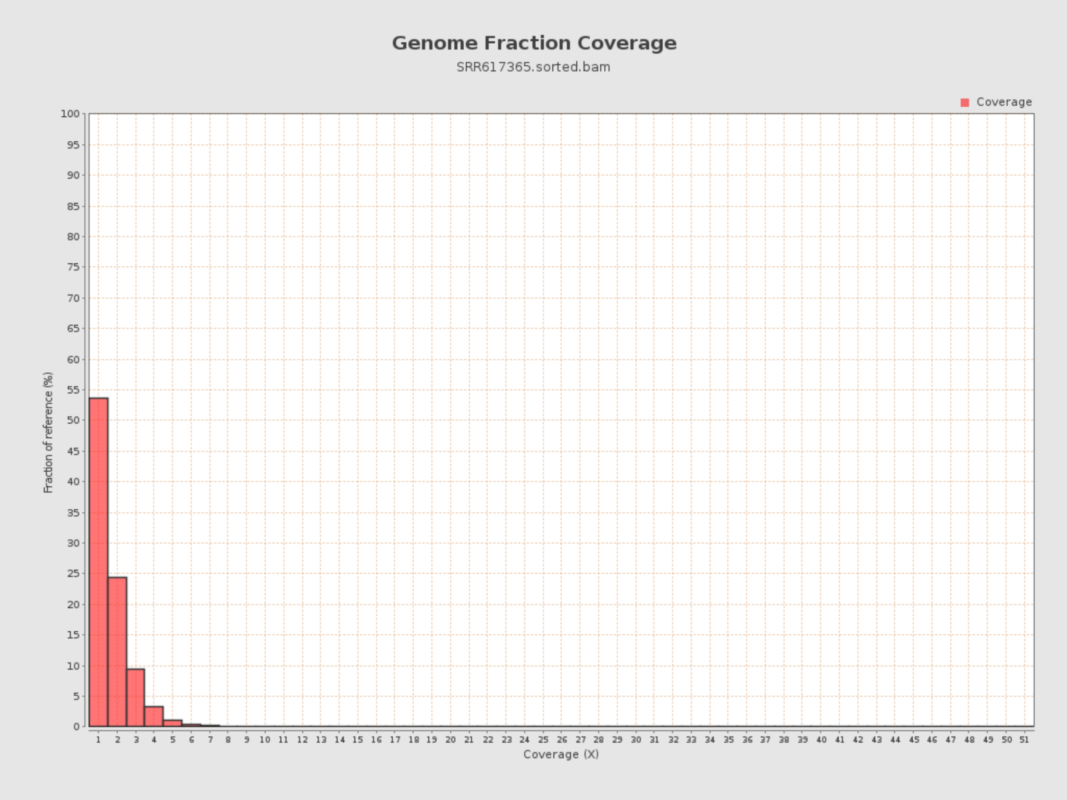
4. Results : Coverage Histogram



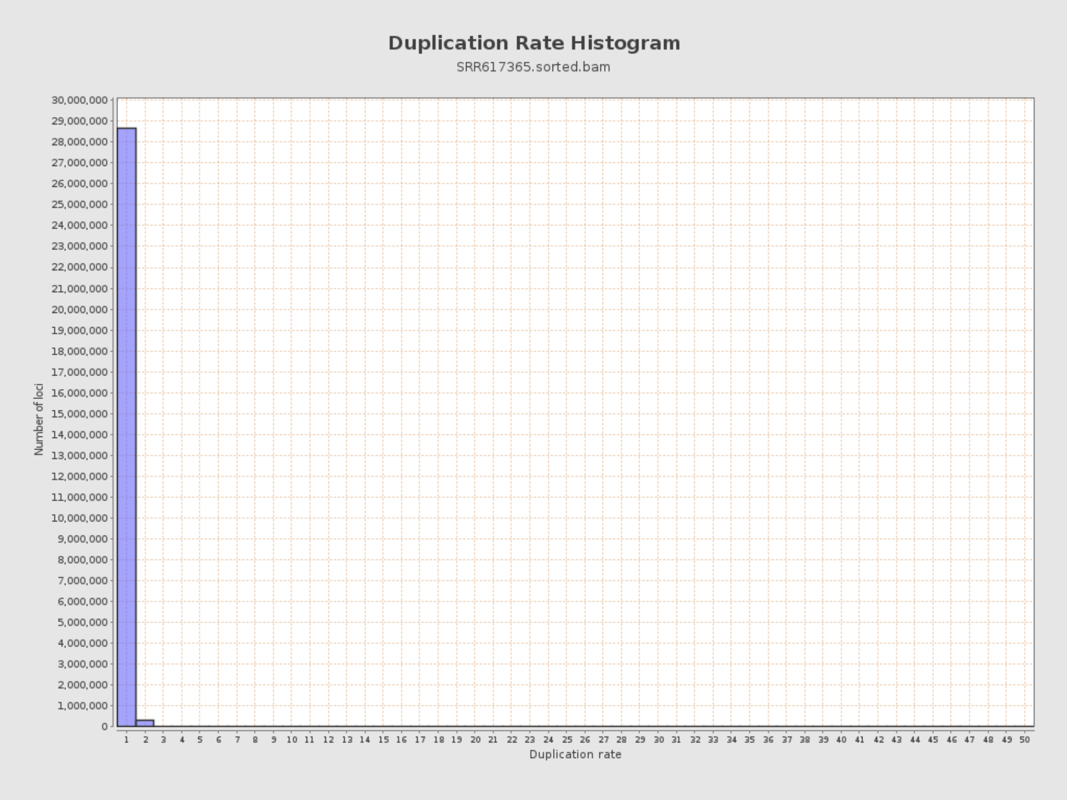
5. Results : Coverage Histogram (0-50X)



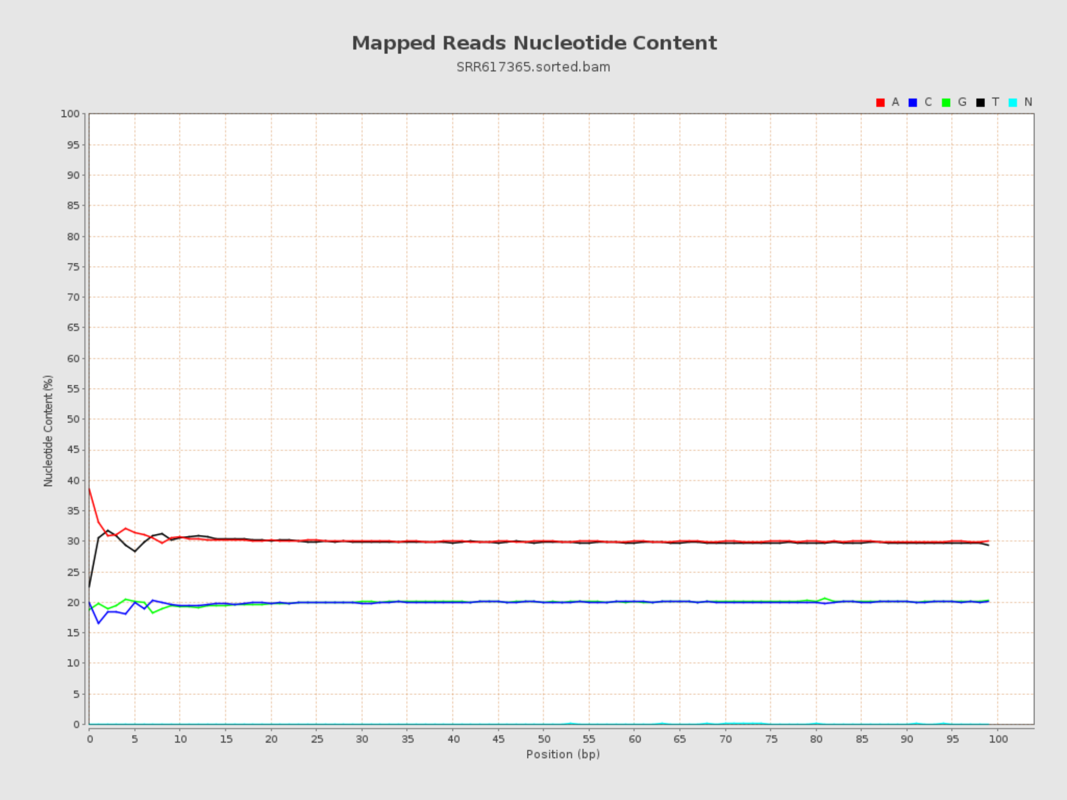
6. Results : Genome Fraction Coverage



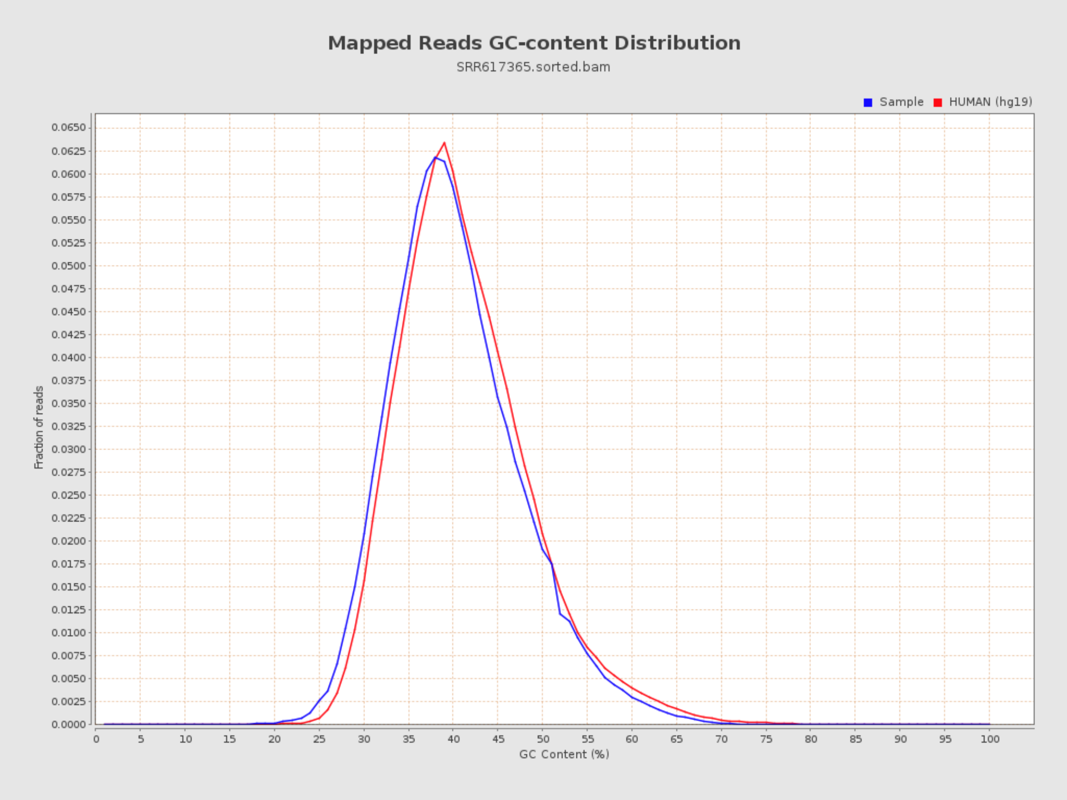
7. Results : Duplication Rate Histogram



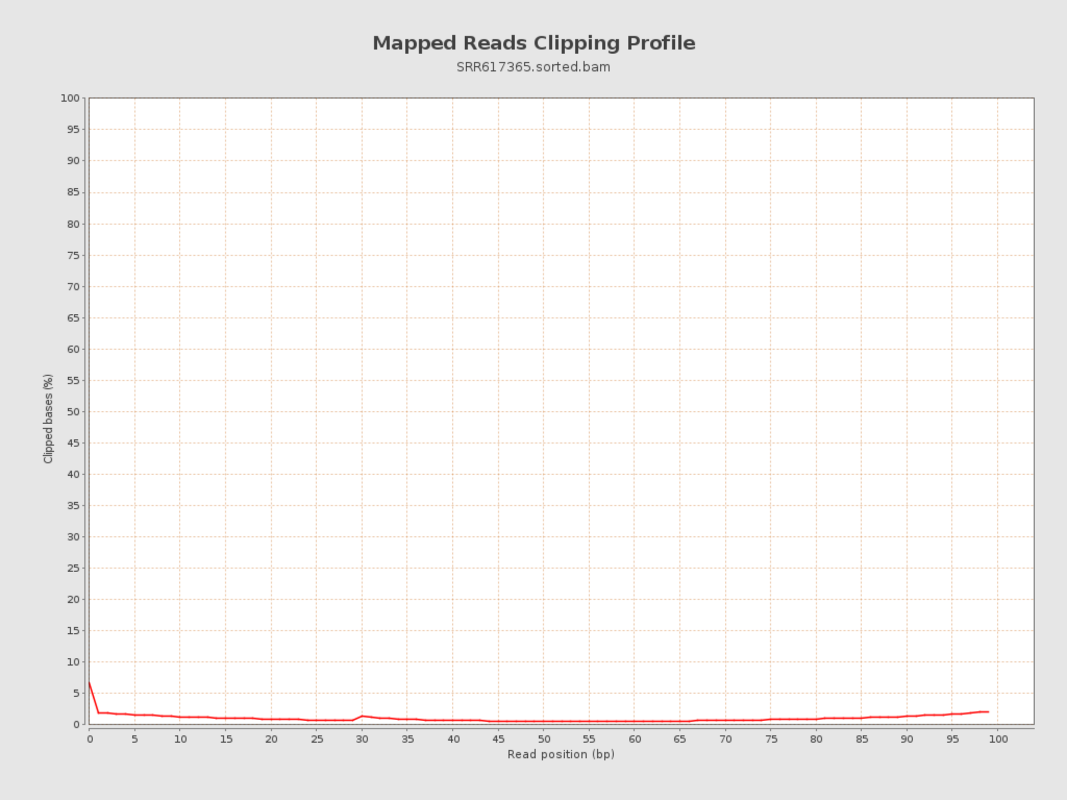
8. Results : Mapped Reads Nucleotide Content



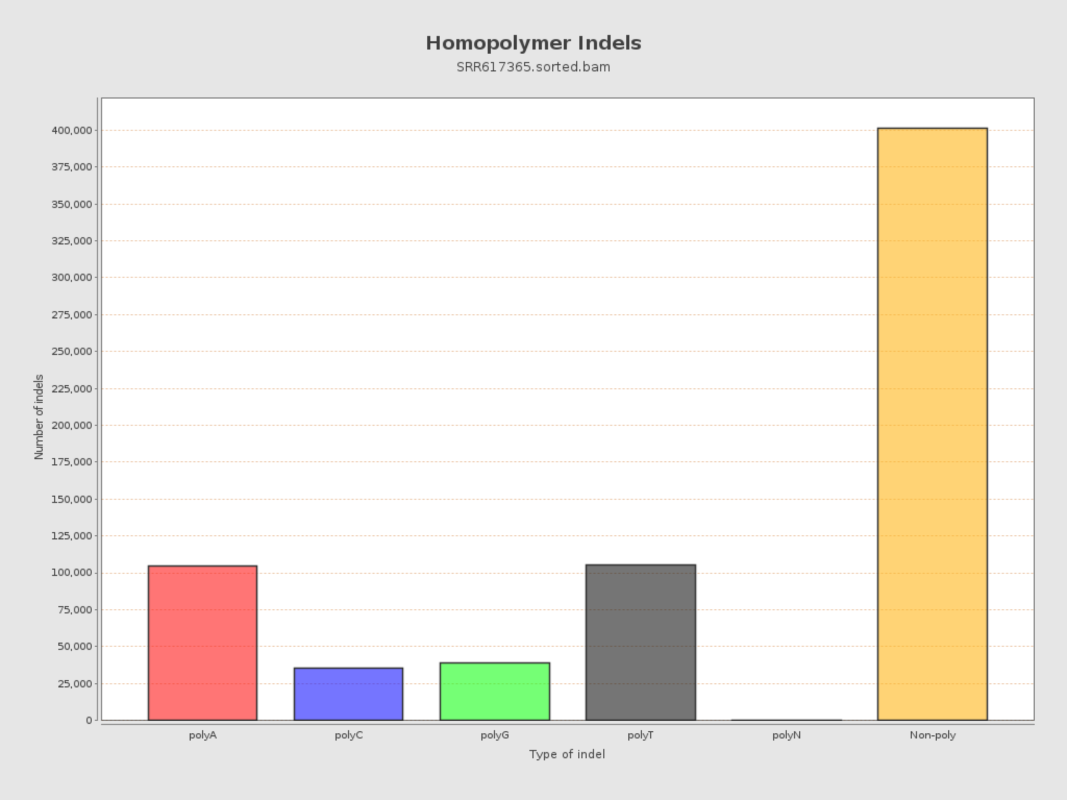
9. Results : Mapped Reads GC-content Distribution



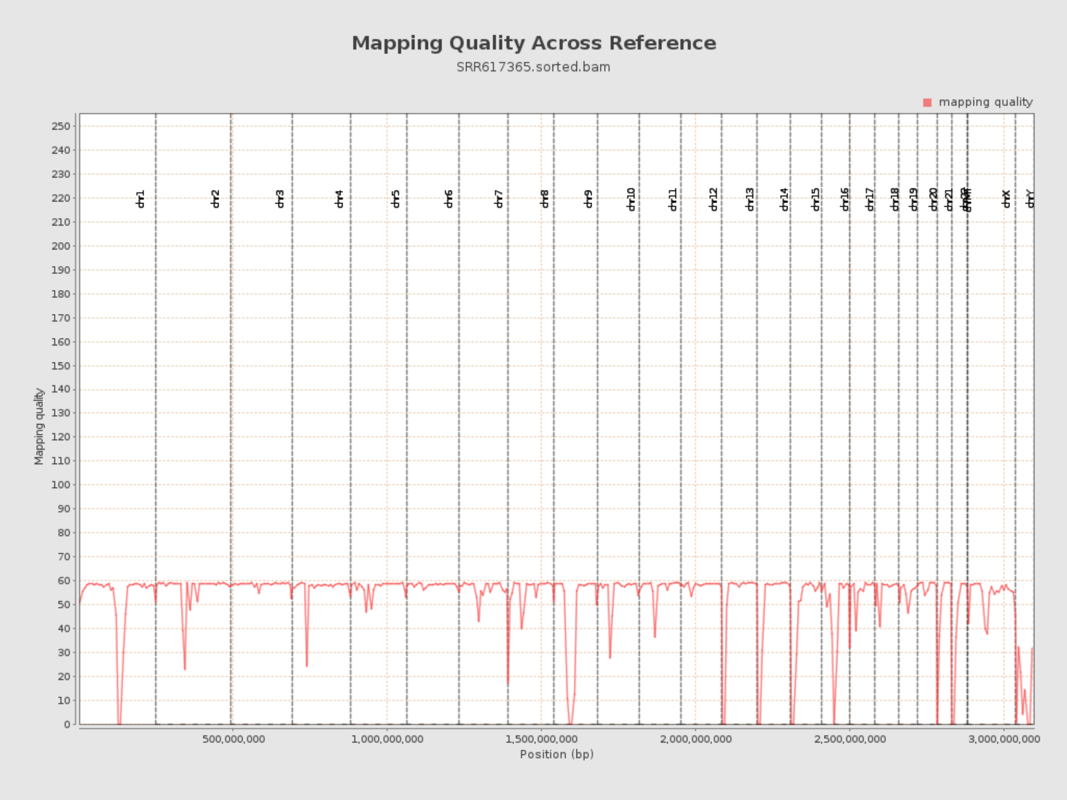
10. Results : Mapped Reads Clipping Profile



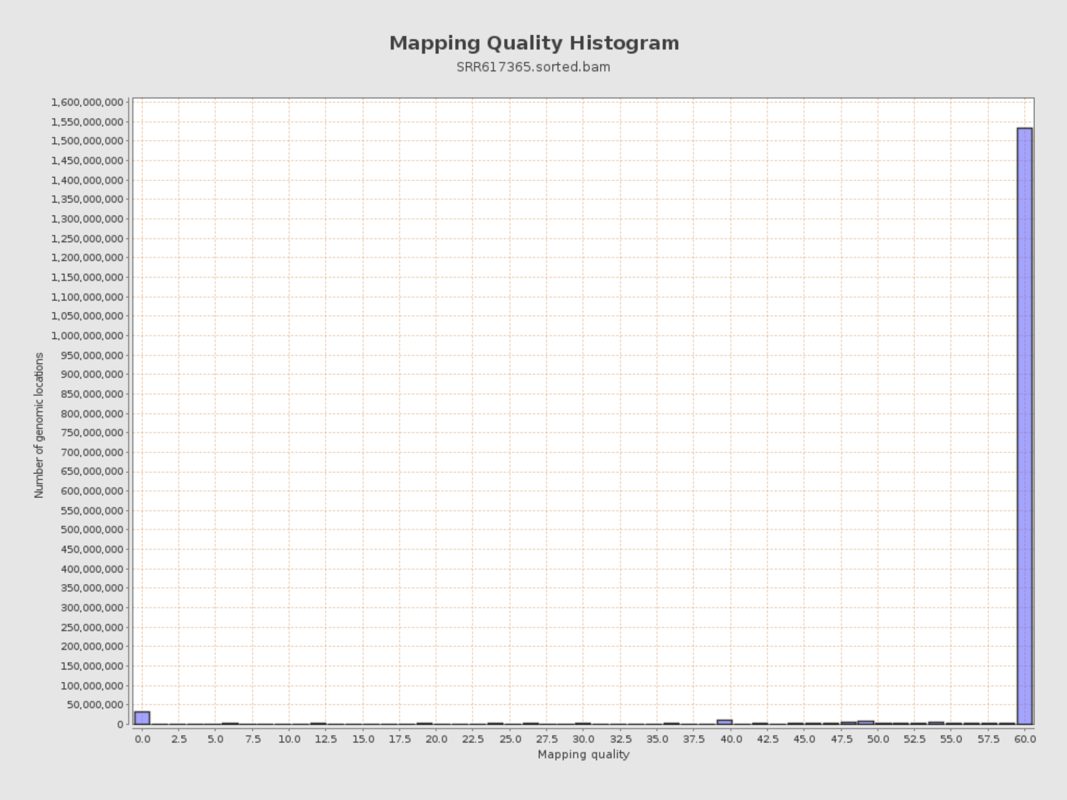
11. Results : Homopolymer Indels



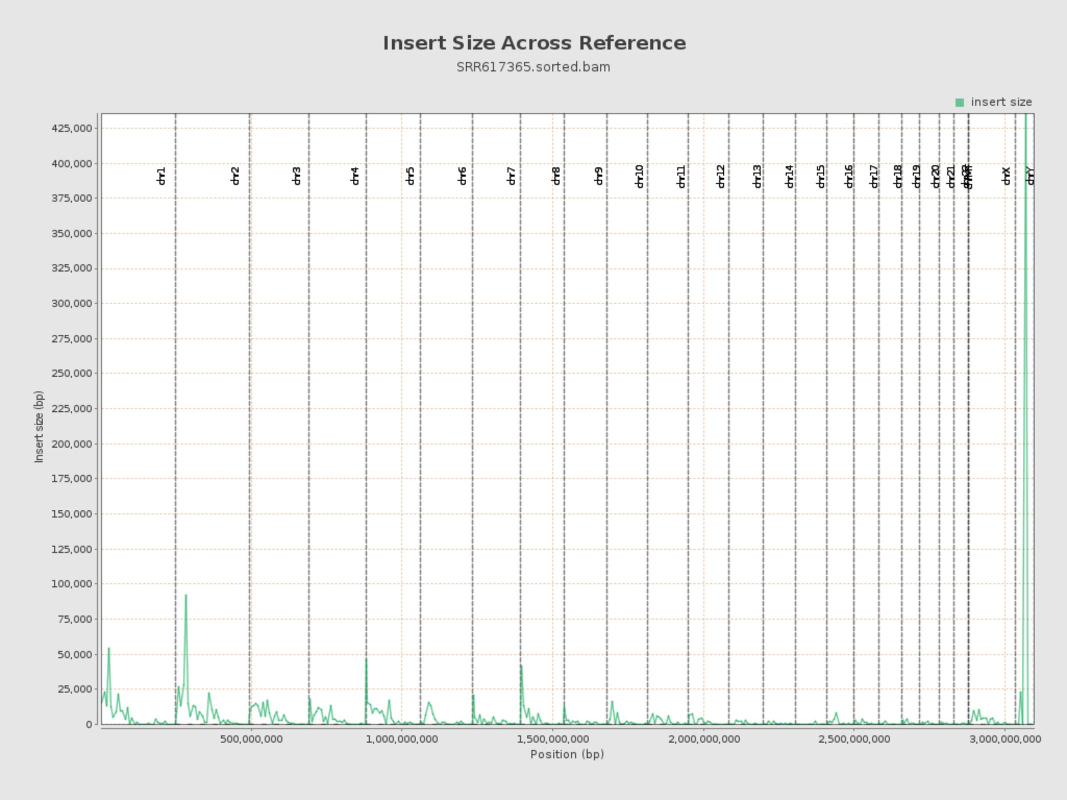
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram