Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/19 11:55:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618619.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_SRR618619 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618619_1.fastq.gz SRR618619_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Jan 19 11:55:00 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618619.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	38,074,480
Mapped reads	34,772,636 / 91.33%
Unmapped reads	3,301,844 / 8.67%
Mapped paired reads	34,772,636 / 91.33%
Mapped reads, first in pair	17,656,723 / 46.37%
Mapped reads, second in pair	17,115,913 / 44.95%
Mapped reads, both in pair	33,655,580 / 88.39%
Mapped reads, singletons	1,117,056 / 2.93%
Secondary alignments	0
Supplementary alignments	186,782 / 0.49%
Read min/max/mean length	30 / 100 / 100.2
Duplicated reads (estimated)	13,046,446 / 34.27%
Duplication rate	30.01%
Clipped reads	8,272,735 / 21.73%

2.2. ACGT Content

Number/percentage of A's	895,318,695 / 27.48%
Number/percentage of C's	705,174,194 / 21.64%
Number/percentage of T's	910,682,558 / 27.95%
Number/percentage of G's	744,485,558 / 22.85%
Number/percentage of N's	2,322,343 / 0.07%

GC Percentage	44.5%

2.3. Coverage

Mean	1.0532
Standard Deviation	4.5869

2.4. Mapping Quality

Mean Mapping Quality	52.07

2.5. Insert size

Mean	122,494.15
Standard Deviation	3,518,218.99
P25/Median/P75	181 / 213 / 255

2.6. Mismatches and indels

General error rate	1.4%
Mismatches	44,709,591
Insertions	628,266
Mapped reads with at least one insertion	1.78%
Deletions	1,701,198
Mapped reads with at least one deletion	4.77%
Homopolymer indels	52.6%

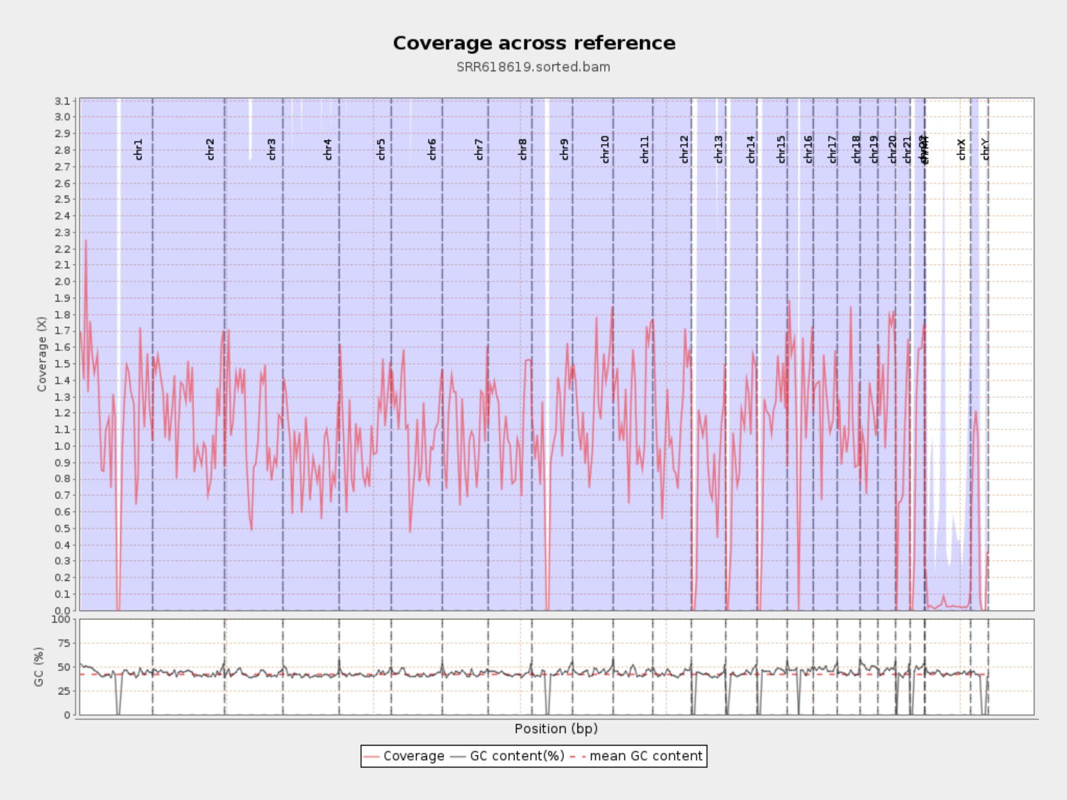
2.7. Chromosome stats

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

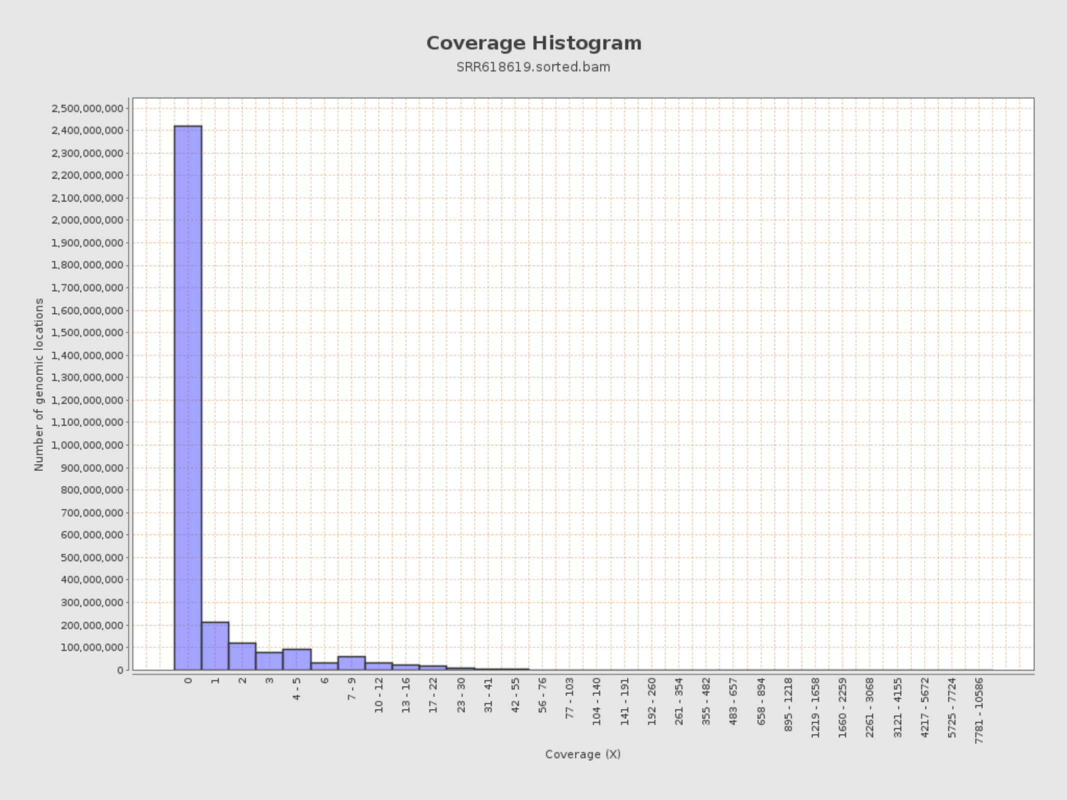
		bases	coverage	deviation
chr1	249250621	302275036	1.2127	8.2386
chr2	243199373	291134590	1.1971	4.7109
chr3	198022430	222590067	1.1241	3.7291
chr4	191154276	179044099	0.9366	3.4347
chr5	180915260	194581626	1.0755	3.6291
chr6	171115067	184842149	1.0802	4.0603
chr7	159138663	172965866	1.0869	4.0293
chr8	146364022	167044057	1.1413	3.9625
chr9	141213431	145122850	1.0277	5.3423
chr10	135534747	173493429	1.2801	4.3236
chr11	135006516	167997362	1.2444	4.6174
chr12	133851895	151679398	1.1332	4.1789
chr13	115169878	94007083	0.8162	3.1583
chr14	107349540	102795726	0.9576	3.6277
chr15	102531392	107371865	1.0472	3.7829
chr16	90354753	116480333	1.2891	5.0354
chr17	81195210	103643910	1.2765	4.5577
chr18	78077248	88542349	1.134	5.3364
chr19	59128983	64549606	1.0917	4.5373
chr20	63025520	93466288	1.483	4.8264
chr21	48129895	44412670	0.9228	4.9018
chr22	51304566	54080199	1.0541	4.2242
chrMT	16571	4212	0.2542	1.827
chrX	155270560	5766804	0.0371	1.0295

chrY	59373566	32399184	0.5457	3.0624

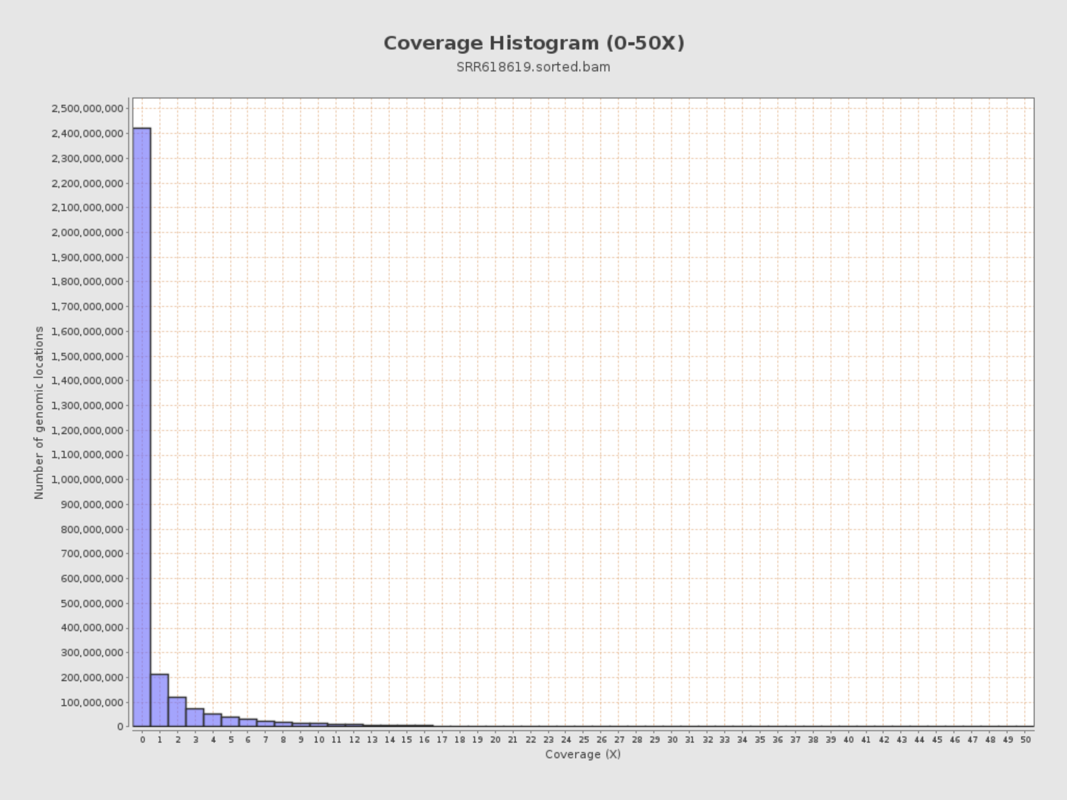
3. Results : Coverage across reference



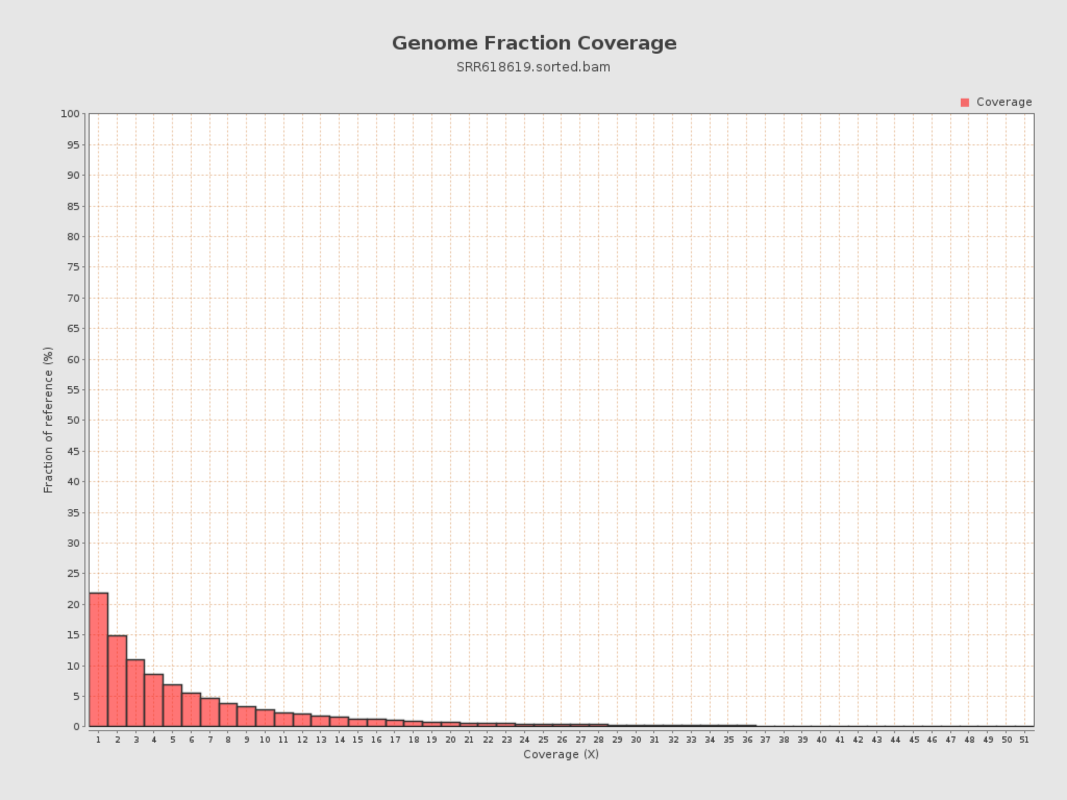
4. Results : Coverage Histogram



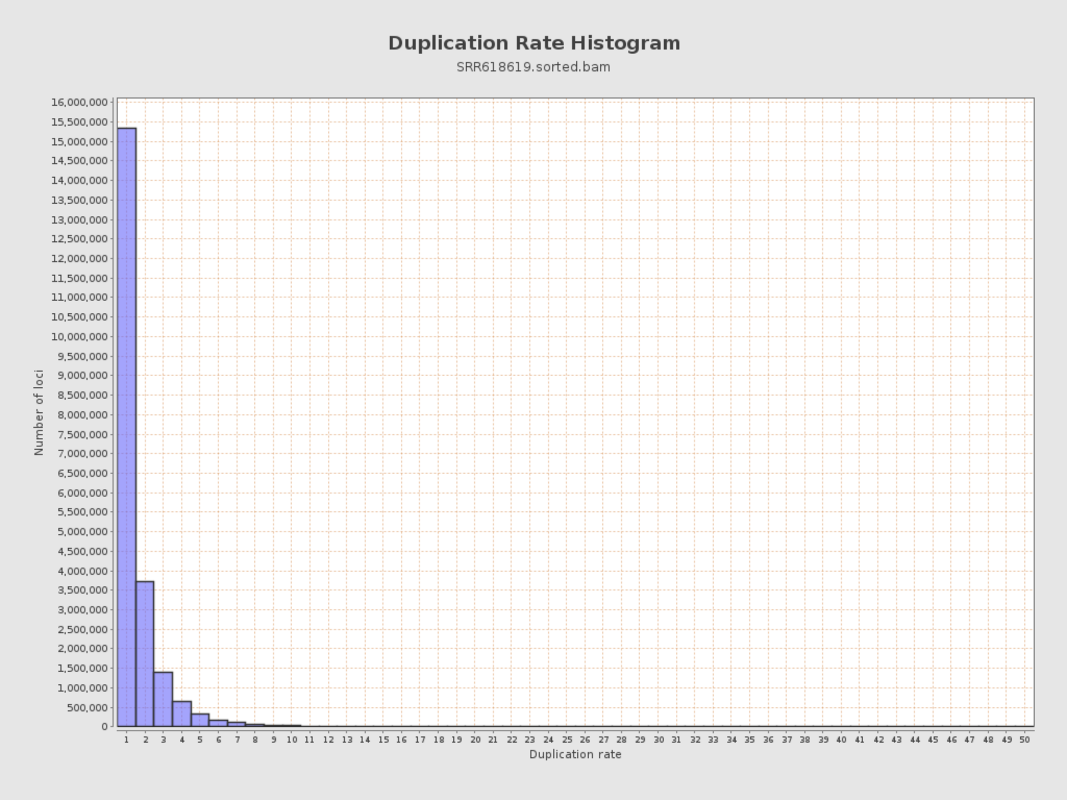
5. Results : Coverage Histogram (0-50X)



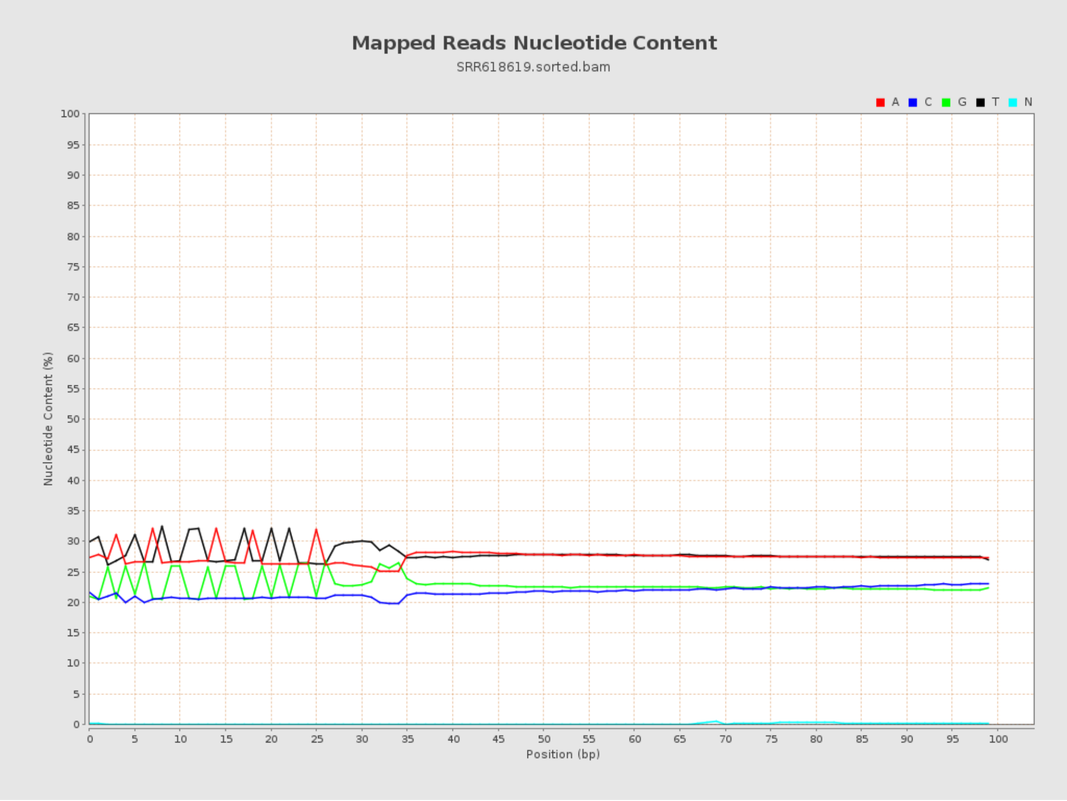
6. Results : Genome Fraction Coverage



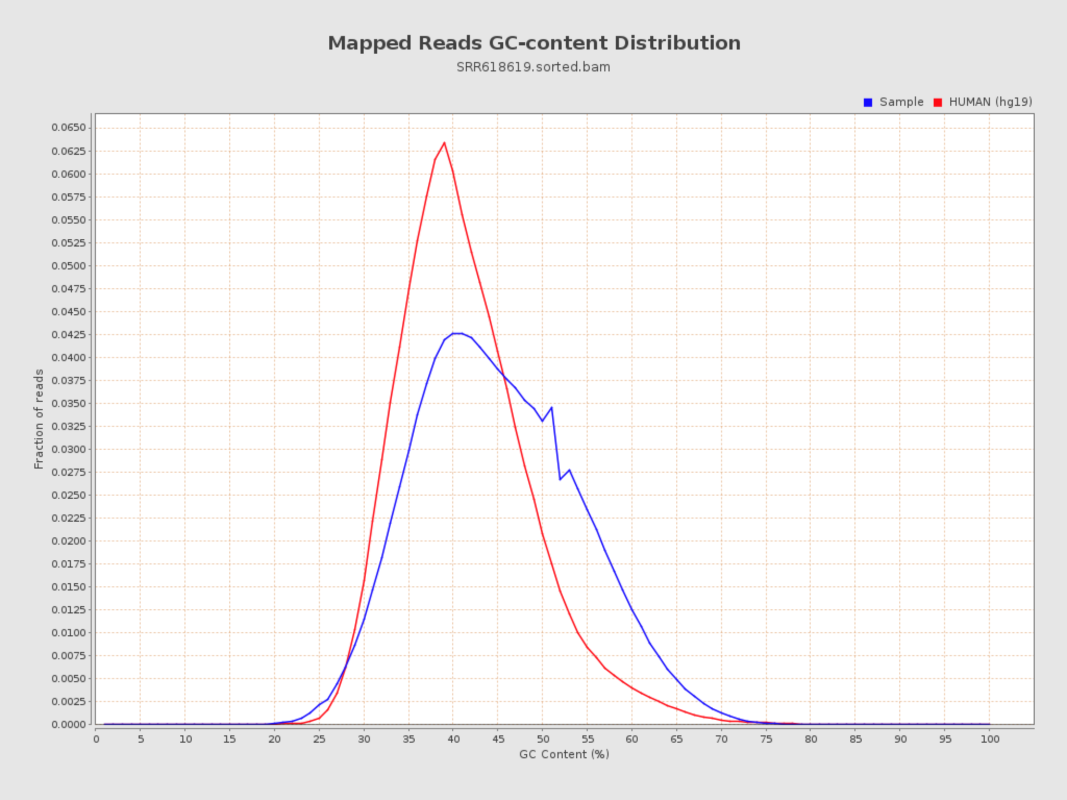
7. Results : Duplication Rate Histogram



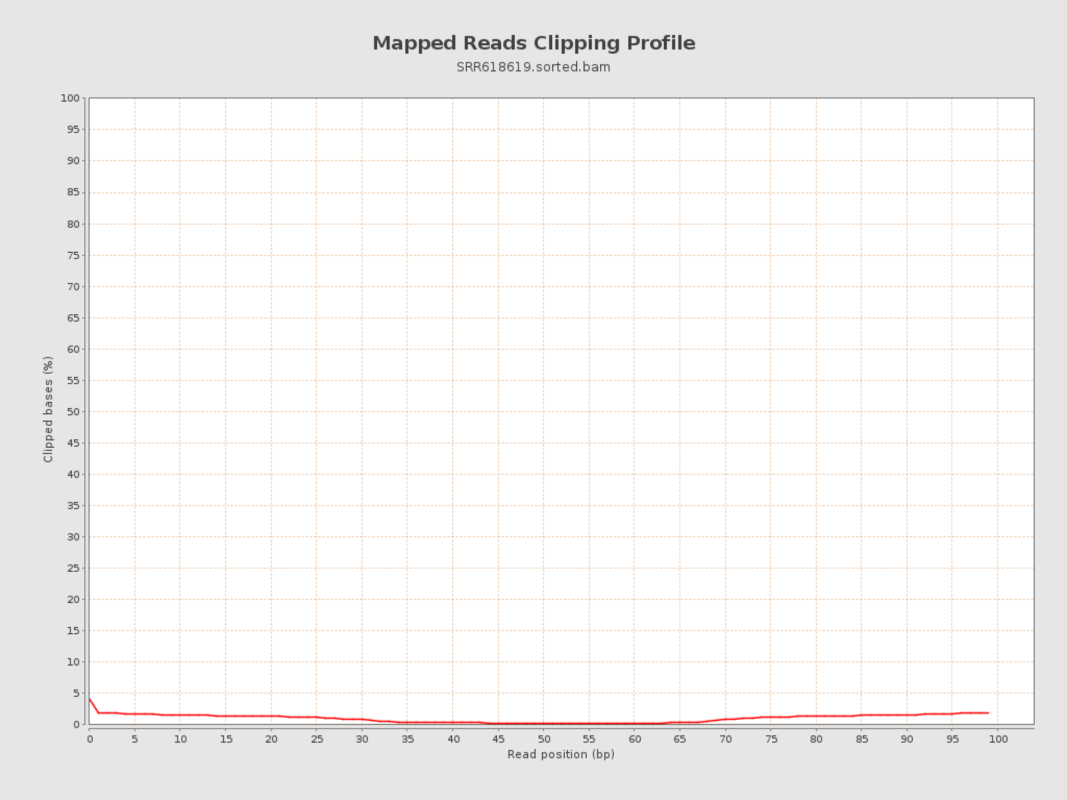
8. Results : Mapped Reads Nucleotide Content



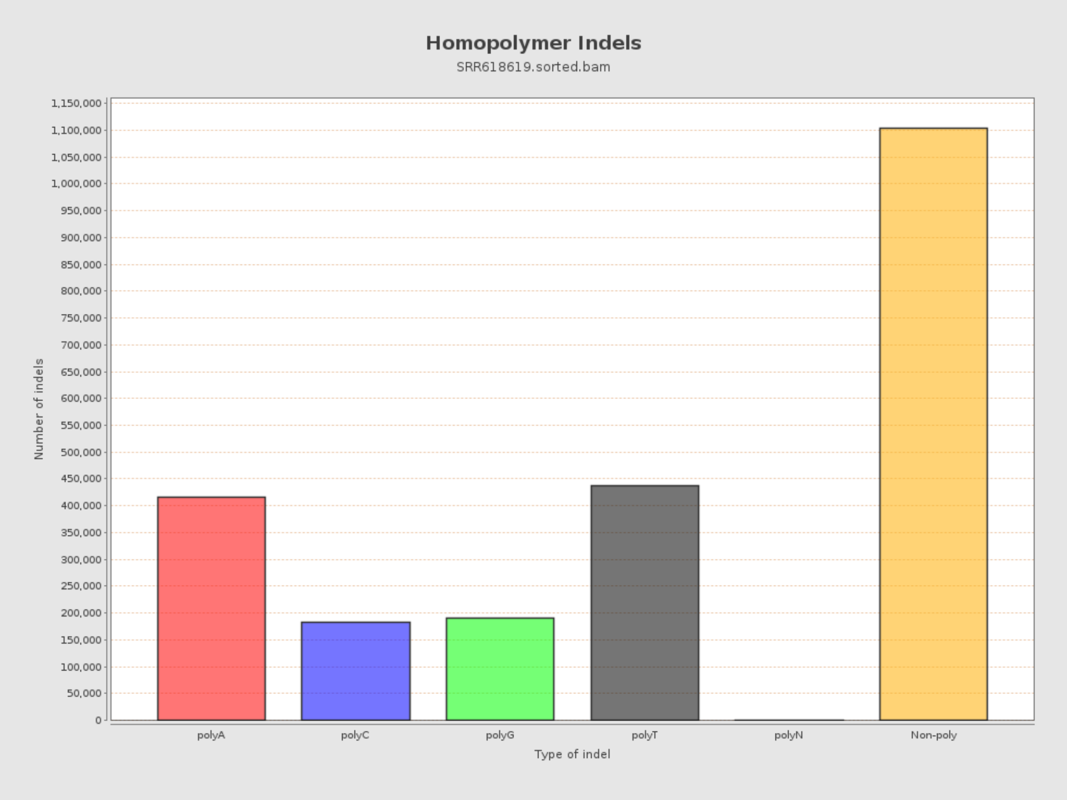
9. Results : Mapped Reads GC-content Distribution



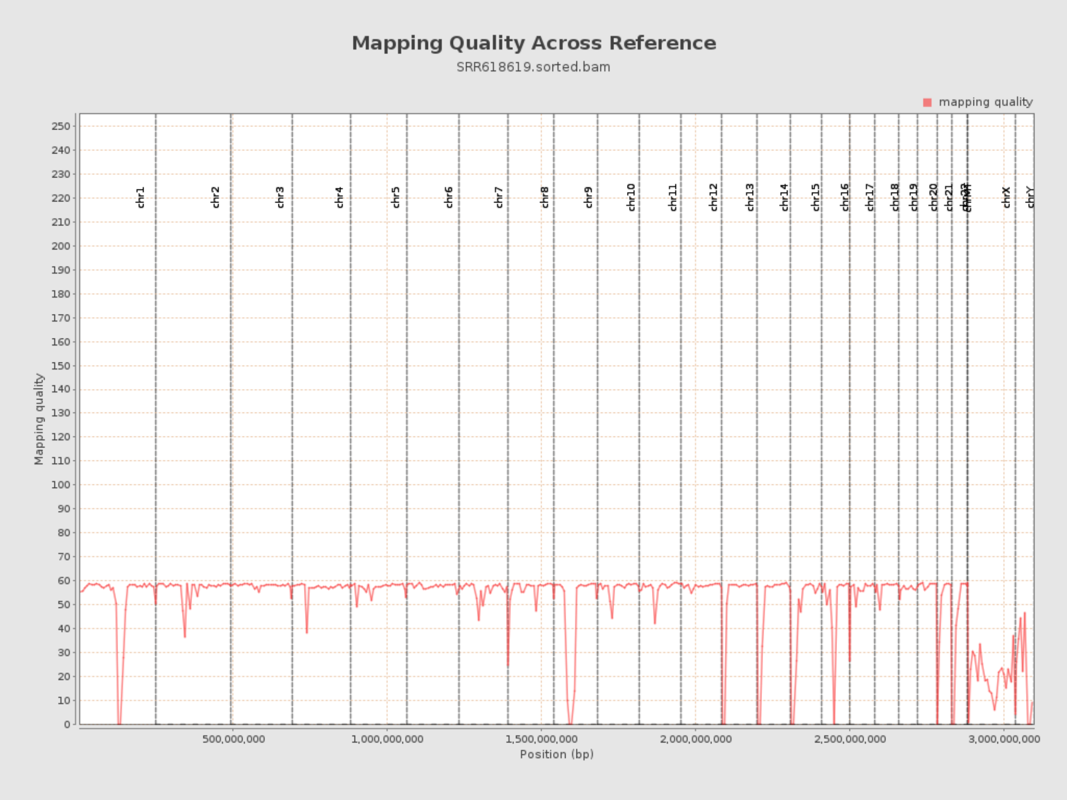
10. Results : Mapped Reads Clipping Profile



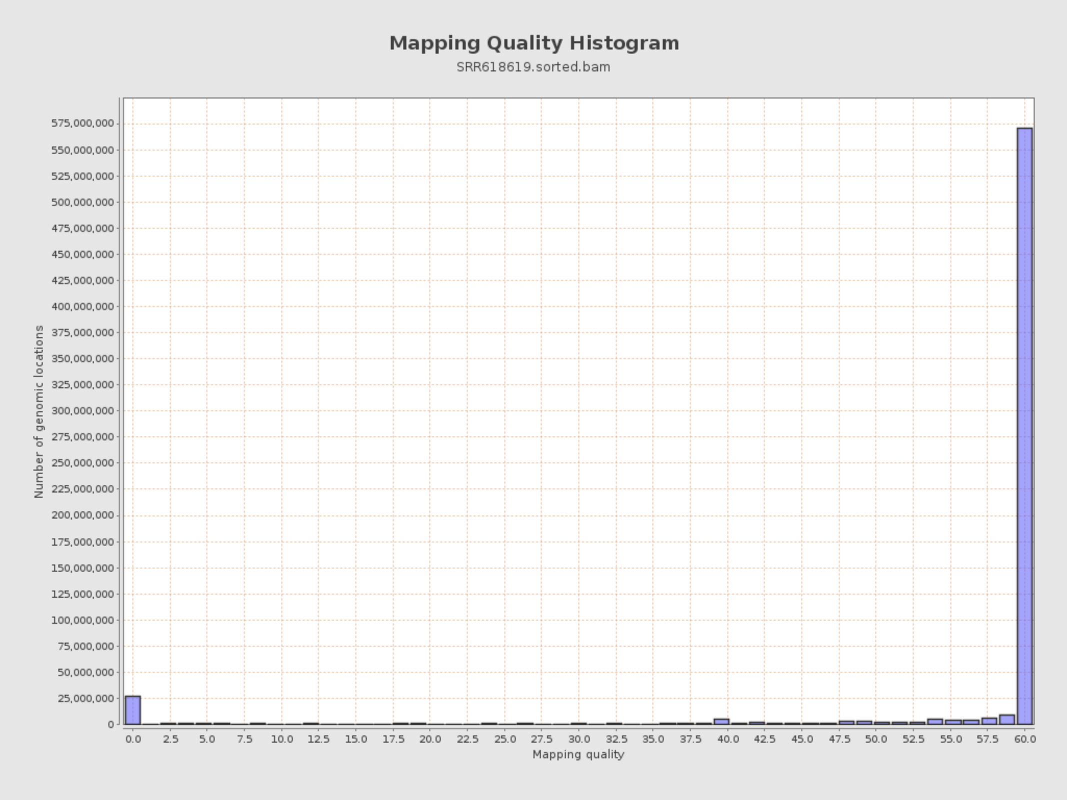
11. Results : Homopolymer Indels



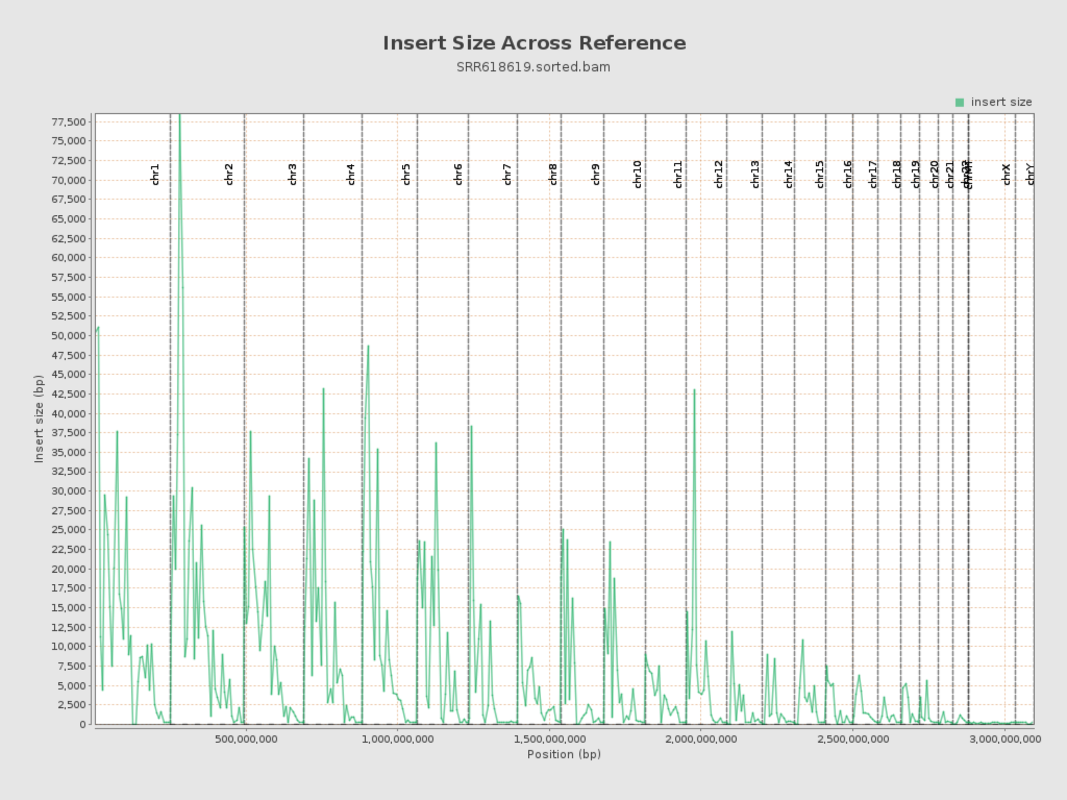
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram