Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/19 09:00:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618614.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_SRR618614 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618614_1.fastq.gz SRR618614_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Jan 19 09:00:14 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618614.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	29,708,384
Mapped reads	28,584,759 / 96.22%
Unmapped reads	1,123,625 / 3.78%
Mapped paired reads	28,584,759 / 96.22%
Mapped reads, first in pair	14,428,030 / 48.57%
Mapped reads, second in pair	14,156,729 / 47.65%
Mapped reads, both in pair	28,132,690 / 94.7%
Mapped reads, singletons	452,069 / 1.52%
Secondary alignments	0
Supplementary alignments	37,504 / 0.13%
Read min/max/mean length	30 / 100 / 100.05
Duplicated reads (estimated)	4,214,567 / 14.19%
Duplication rate	13.39%
Clipped reads	4,410,026 / 14.84%

2.2. ACGT Content

Number/percentage of A's	747,760,177 / 27.21%
Number/percentage of C's	609,605,786 / 22.18%
Number/percentage of T's	752,116,406 / 27.37%
Number/percentage of G's	638,640,903 / 23.24%
Number/percentage of N's	154,575 / 0.01%

GC Percentage	45.42%

2.3. Coverage

Mean	0.8884
Standard Deviation	3.7008

2.4. Mapping Quality

Mean Mapping Quality	52.54

2.5. Insert size

Mean	27,688.11
Standard Deviation	1,658,556.17
P25/Median/P75	194 / 223 / 261

2.6. Mismatches and indels

General error rate	1.18%
Mismatches	31,644,350
Insertions	477,069
Mapped reads with at least one insertion	1.65%
Deletions	1,328,571
Mapped reads with at least one deletion	4.54%
Homopolymer indels	53.12%

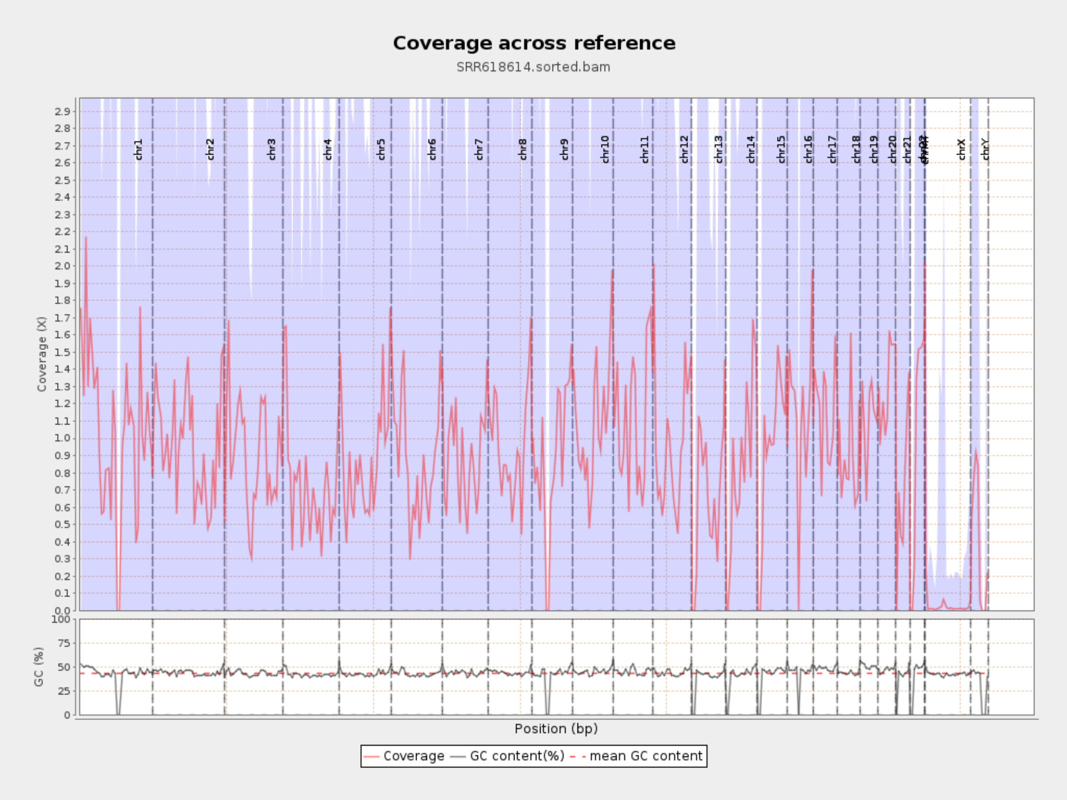
2.7. Chromosome stats

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

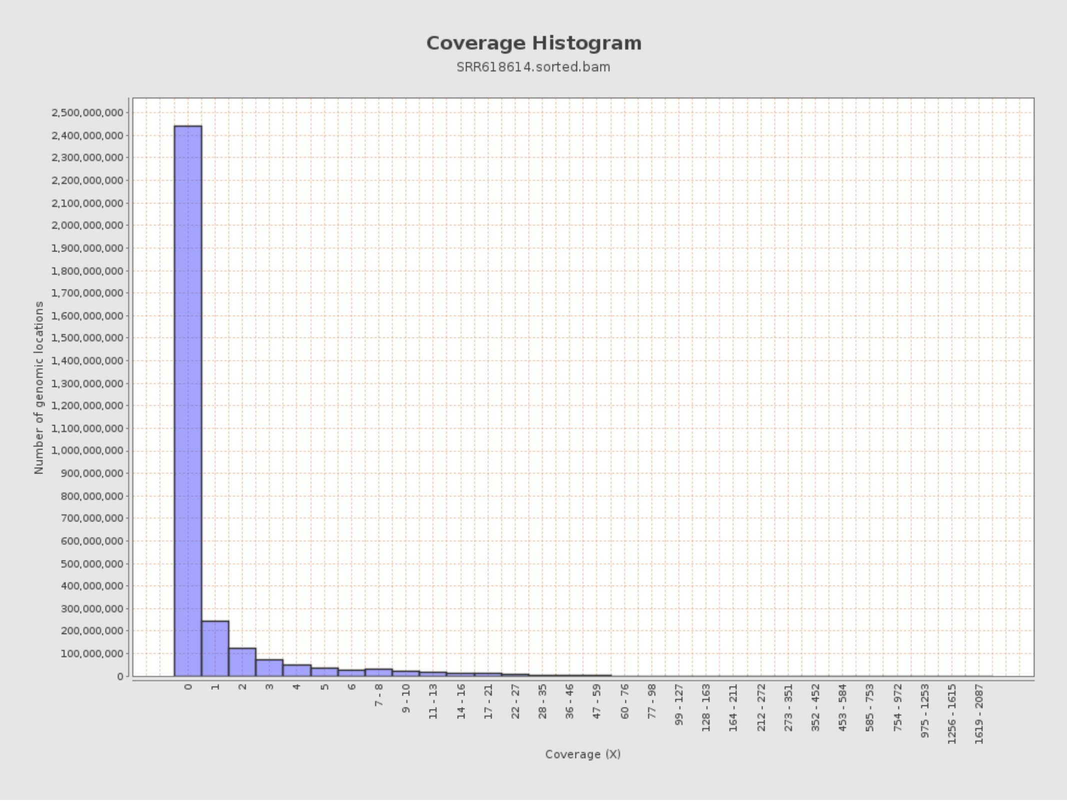
		bases	coverage	deviation
chr1	249250621	259936270	1.0429	4.6022
chr2	243199373	234885510	0.9658	3.7792
chr3	198022430	180306385	0.9105	3.2014
chr4	191154276	137575800	0.7197	3.2977
chr5	180915260	162003502	0.8955	3.1985
chr6	171115067	149790751	0.8754	3.2965
chr7	159138663	142445860	0.8951	3.3422
chr8	146364022	139317806	0.9519	3.4196
chr9	141213431	126302872	0.8944	4.1787
chr10	135534747	147536194	1.0885	3.8558
chr11	135006516	152562859	1.13	4.4064
chr12	133851895	128263222	0.9582	3.5097
chr13	115169878	74830361	0.6497	2.5819
chr14	107349540	89409601	0.8329	3.2575
chr15	102531392	94719929	0.9238	3.5528
chr16	90354753	102818353	1.1379	4.8156
chr17	81195210	94478284	1.1636	4.2108
chr18	78077248	70330033	0.9008	4.1044
chr19	59128983	65708034	1.1113	4.6214
chr20	63025520	82111999	1.3028	4.3236
chr21	48129895	34874634	0.7246	5.7509
chr22	51304566	51688647	1.0075	4.0493
chrMT	16571	33576	2.0262	2.8679
chrX	155270560	3768474	0.0243	0.7981

chrY	59373566	24392427	0.4108	2.5023

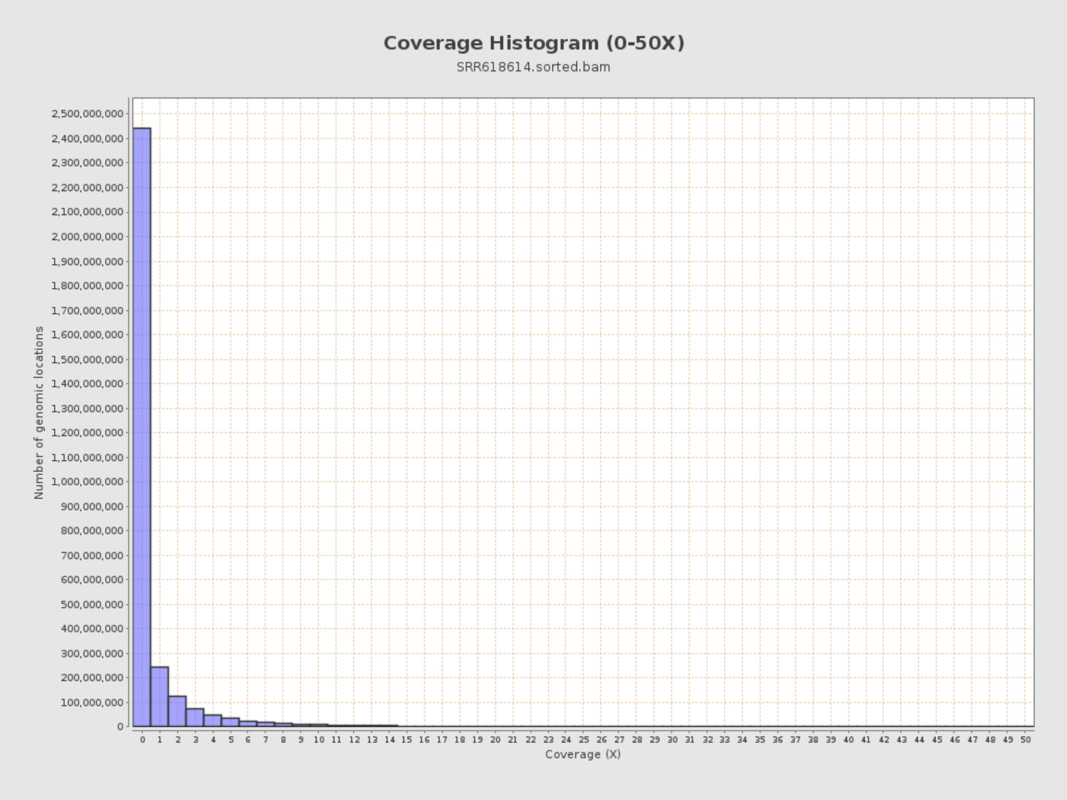
3. Results : Coverage across reference



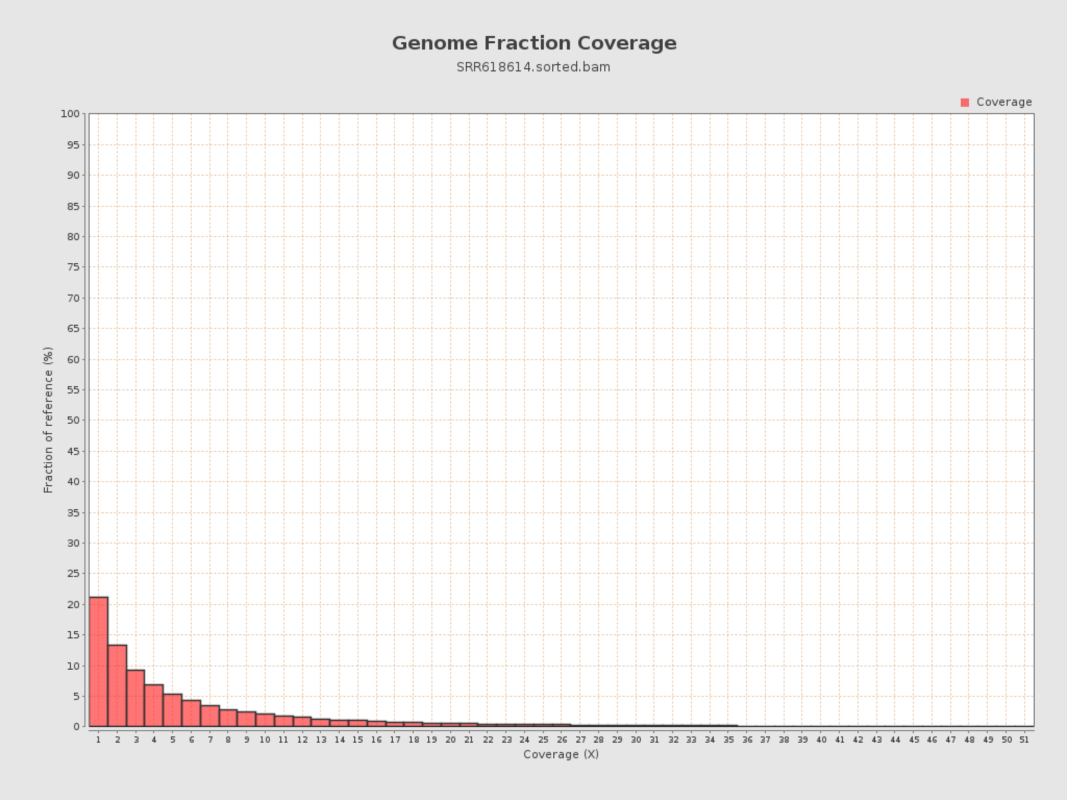
4. Results : Coverage Histogram



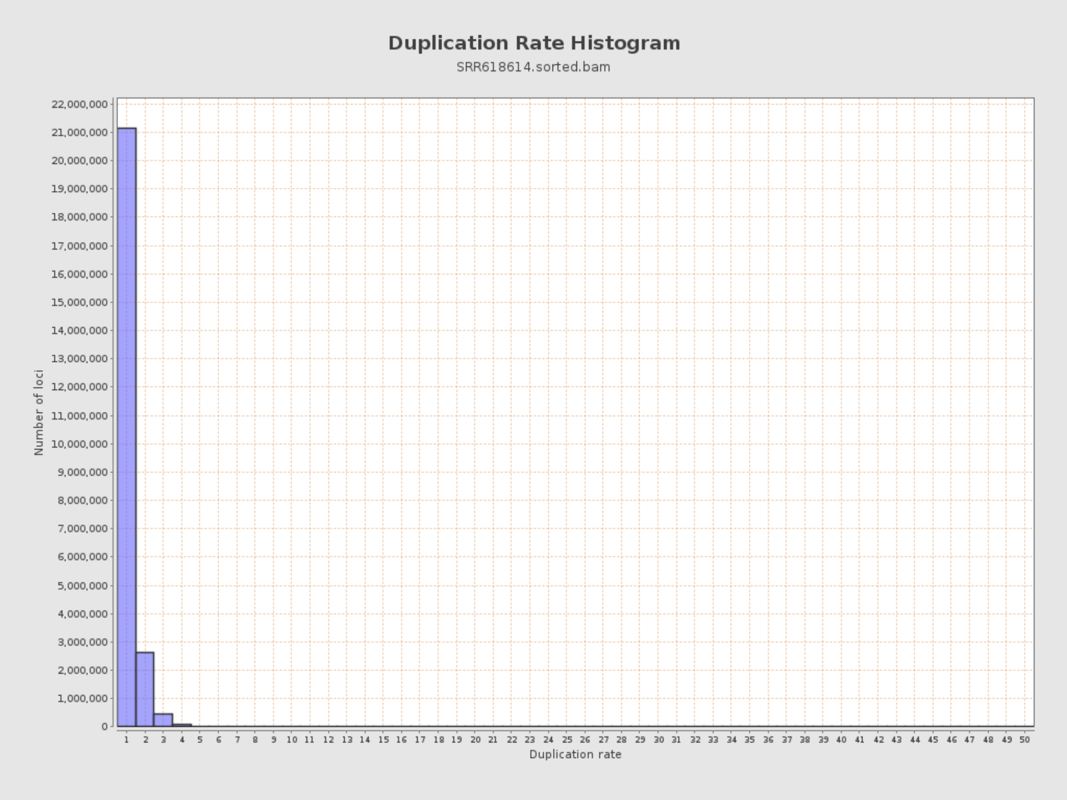
5. Results : Coverage Histogram (0-50X)



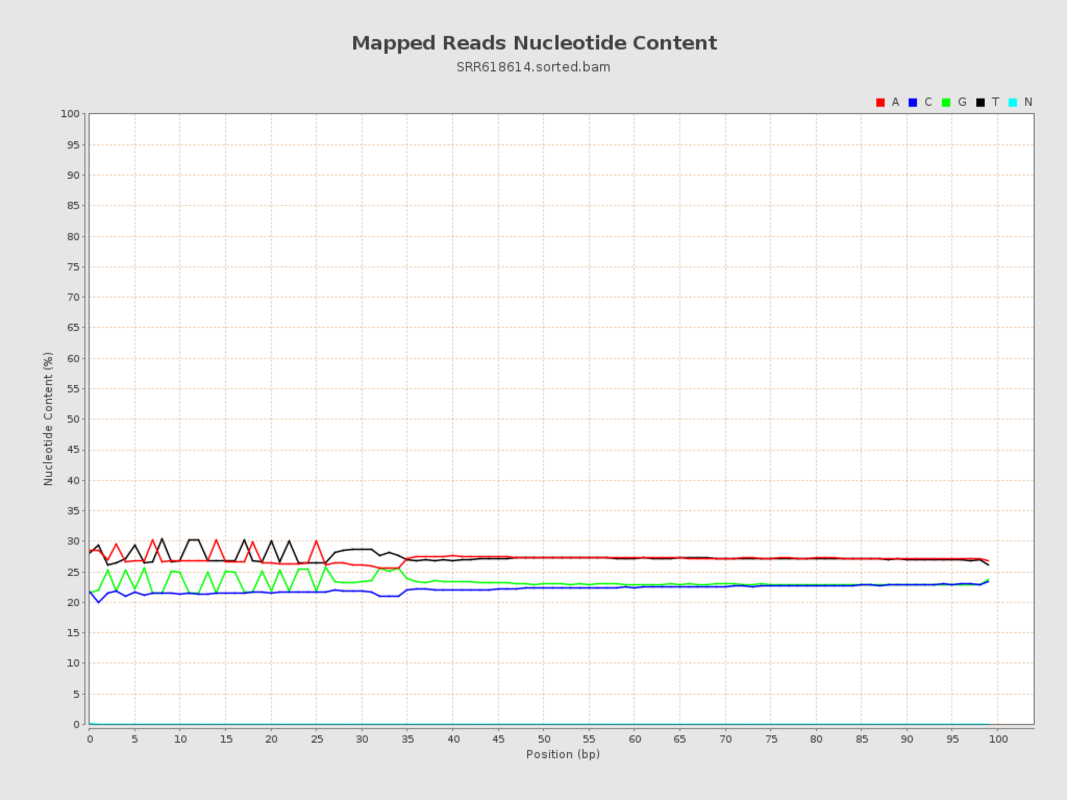
6. Results : Genome Fraction Coverage



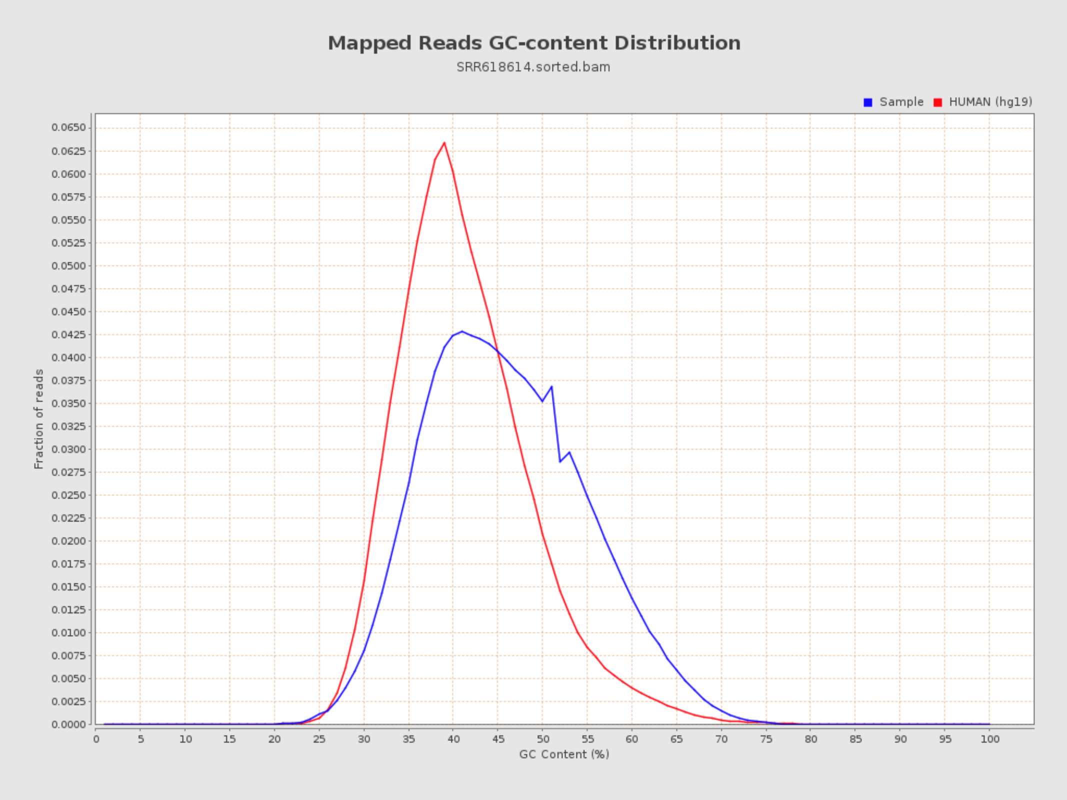
7. Results : Duplication Rate Histogram



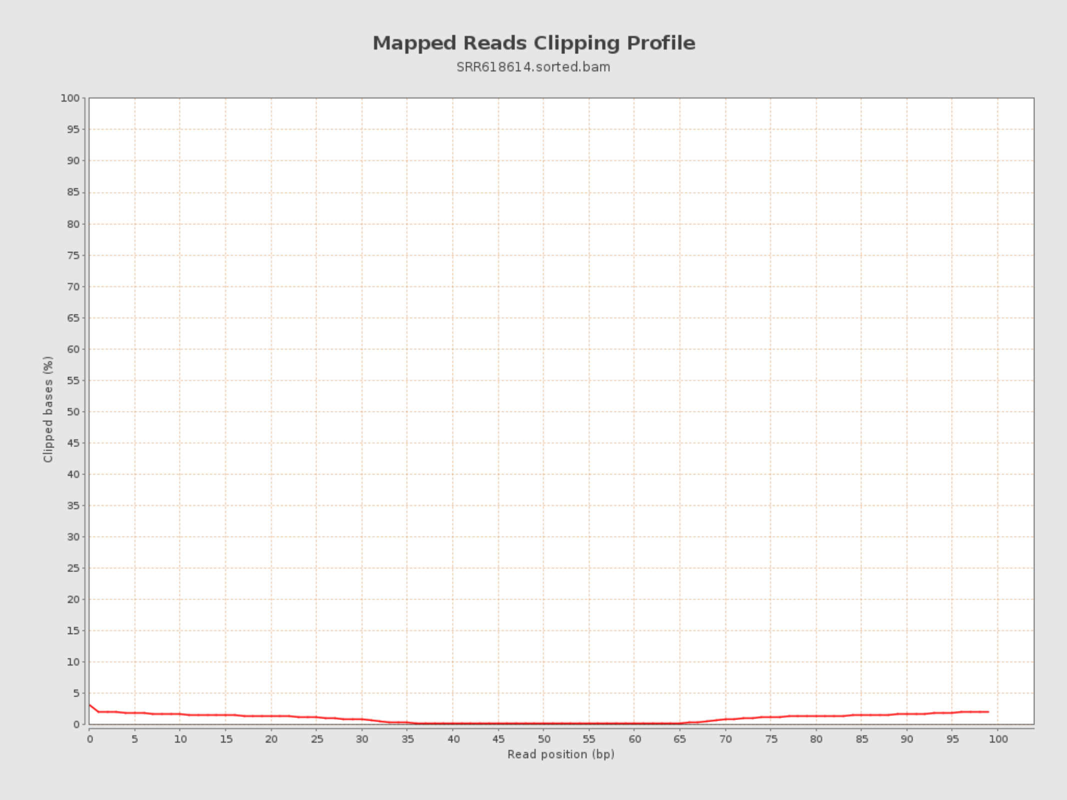
8. Results : Mapped Reads Nucleotide Content



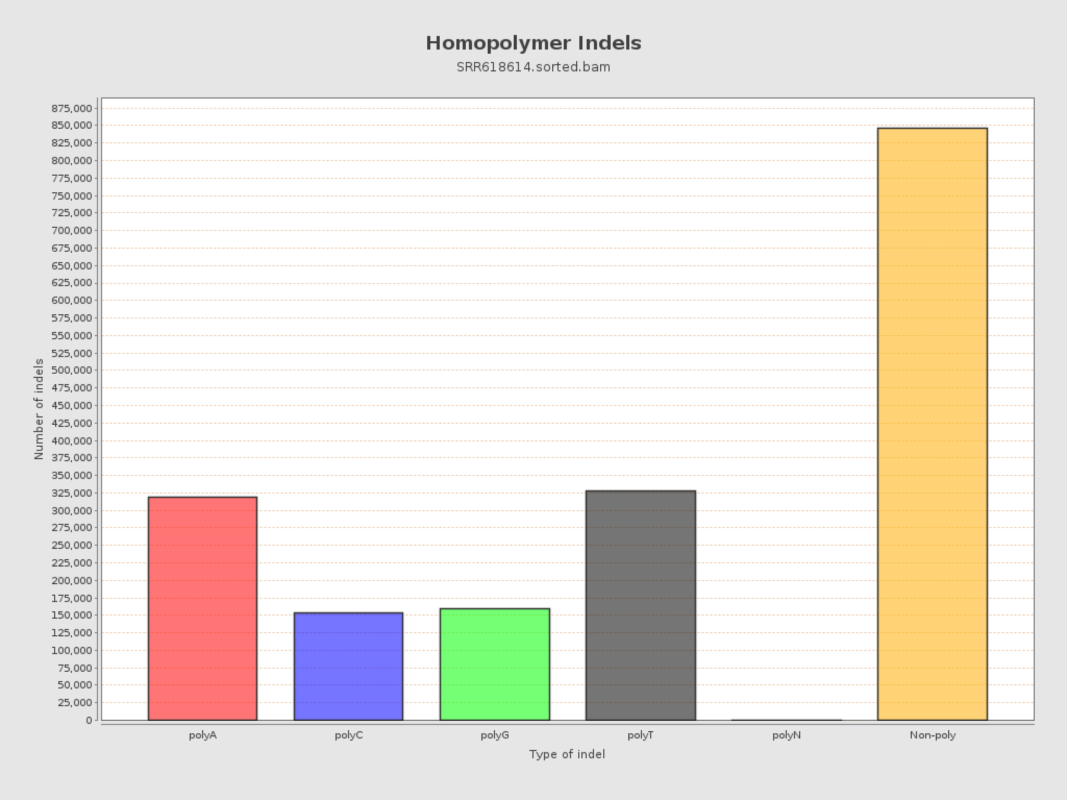
9. Results : Mapped Reads GC-content Distribution



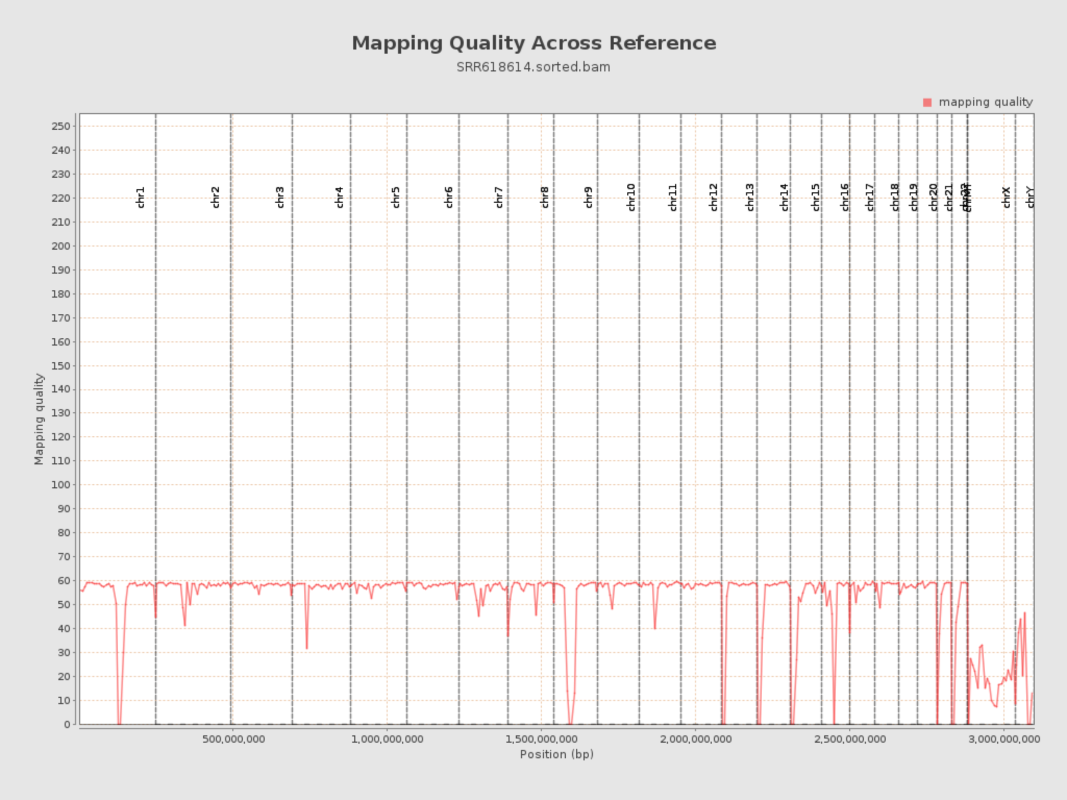
10. Results : Mapped Reads Clipping Profile



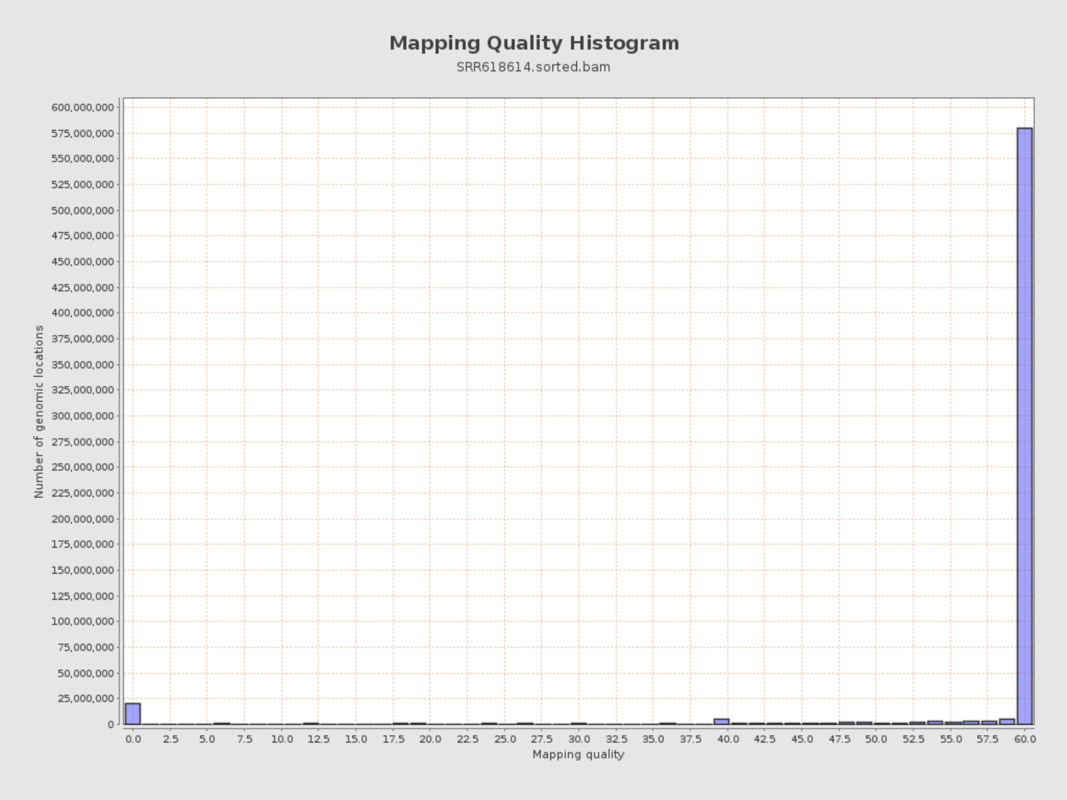
11. Results : Homopolymer Indels



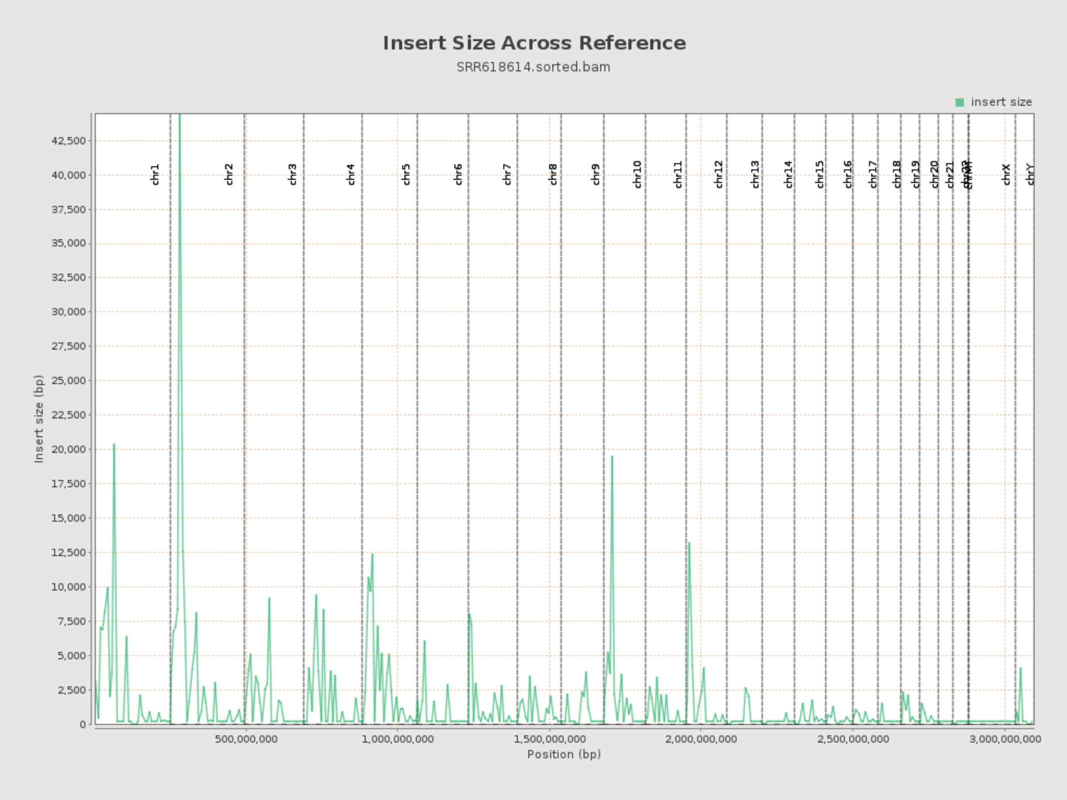
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram