Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/02 04:40:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR504639.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_SRR504639 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR504639_1.fastq.gz SRR504639_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Jan 02 04:40:56 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR504639.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	398,288,092
Mapped reads	362,310,969 / 90.97%
Unmapped reads	35,977,123 / 9.03%
Mapped paired reads	362,310,969 / 90.97%
Mapped reads, first in pair	184,434,499 / 46.31%
Mapped reads, second in pair	177,876,470 / 44.66%
Mapped reads, both in pair	352,769,380 / 88.57%
Mapped reads, singletons	9,541,589 / 2.4%
Secondary alignments	0
Supplementary alignments	2,830,674 / 0.71%
Read min/max/mean length	30 / 100 / 100.27
Duplicated reads (estimated)	93,992,765 / 23.6%
Duplication rate	22.92%
Clipped reads	198,033,435 / 49.72%

2.2. ACGT Content

Number/percentage of A's	8,106,868,715 / 26.39%
Number/percentage of C's	7,122,116,062 / 23.18%
Number/percentage of T's	8,145,010,672 / 26.51%
Number/percentage of G's	7,214,420,938 / 23.48%
Number/percentage of N's	133,494,286 / 0.43%

GC Percentage	46.67%

2.3. Coverage

Mean	9.927
Standard Deviation	22.8495

2.4. Mapping Quality

Mean Mapping Quality	53.29

2.5. Insert size

Mean	57,682.27
Standard Deviation	2,312,898.72
P25/Median/P75	314 / 348 / 384

2.6. Mismatches and indels

General error rate	1.01%
Mismatches	291,706,358
Insertions	15,017,026
Mapped reads with at least one insertion	3.14%
Deletions	4,232,772
Mapped reads with at least one deletion	1.09%
Homopolymer indels	24.64%

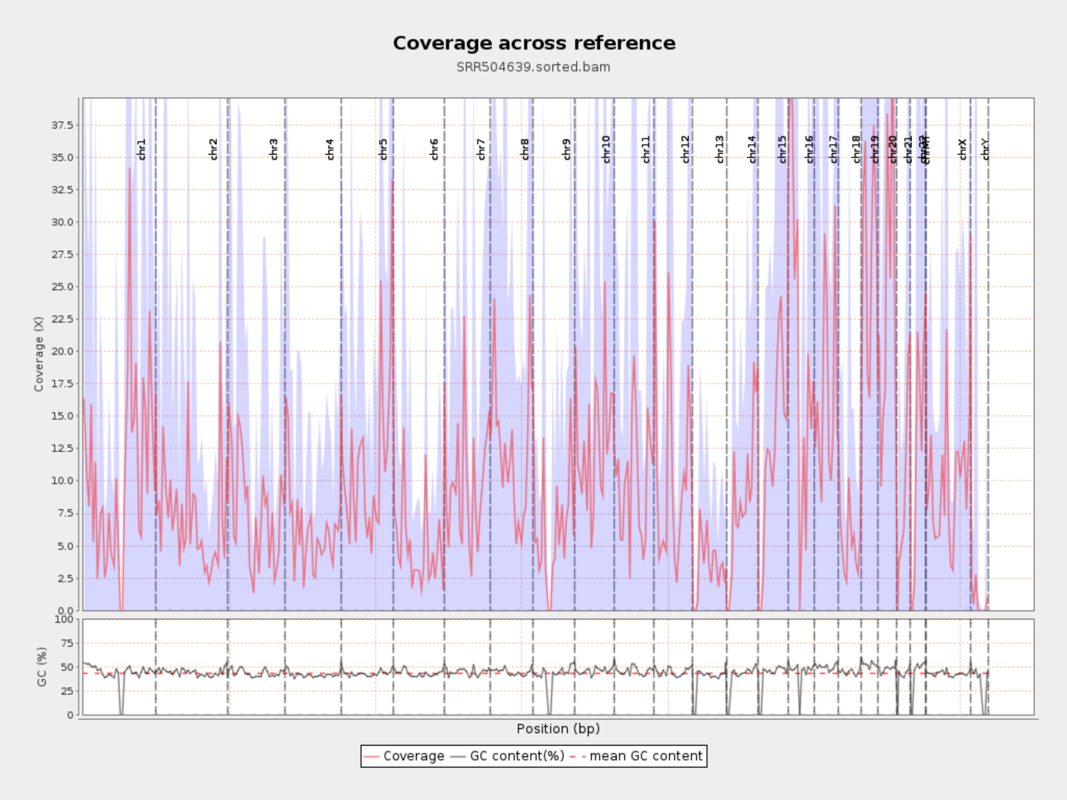
2.7. Chromosome stats

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

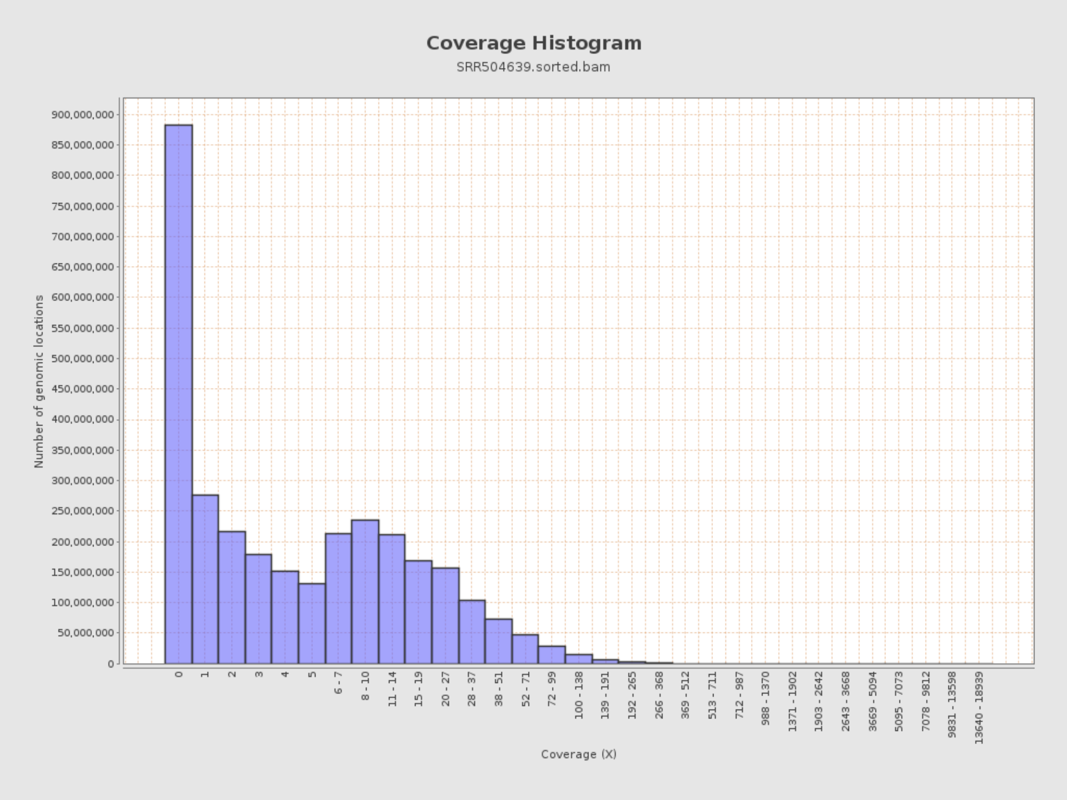
		bases	coverage	deviation
chr1	249250621	2594724634	10.4101	21.4833
chr2	243199373	1720446222	7.0742	17.4872
chr3	198022430	1518458113	7.6681	15.1196
chr4	191154276	1185273509	6.2006	10.975
chr5	180915260	2085214204	11.5259	19.3638
chr6	171115067	811226695	4.7408	10.6608
chr7	159138663	1577754321	9.9143	16.6092
chr8	146364022	1789486302	12.2263	32.1344
chr9	141213431	848645684	6.0097	13.3367
chr10	135534747	1773023712	13.0817	21.7868
chr11	135006516	1358889274	10.0654	18.6896
chr12	133851895	1472360084	10.9999	23.1765
chr13	115169878	400473329	3.4772	6.734
chr14	107349540	927548473	8.6405	15.8181
chr15	102531392	1250845979	12.1996	22.8893
chr16	90354753	1822609072	20.1717	32.3575
chr17	81195210	1359510135	16.7437	29.2811
chr18	78077248	415724424	5.3245	44.7264
chr19	59128983	1596529749	27.0008	54.0021
chr20	63025520	1543207730	24.4854	34.8185
chr21	48129895	466457518	9.6916	18.8282
chr22	51304566	626602613	12.2134	25.9633
chrMT	16571	371020	22.3897	18.3008
chrX	155270560	1541719707	9.9292	17.8295

chrY	59373566	43808117	0.7378	26.0241

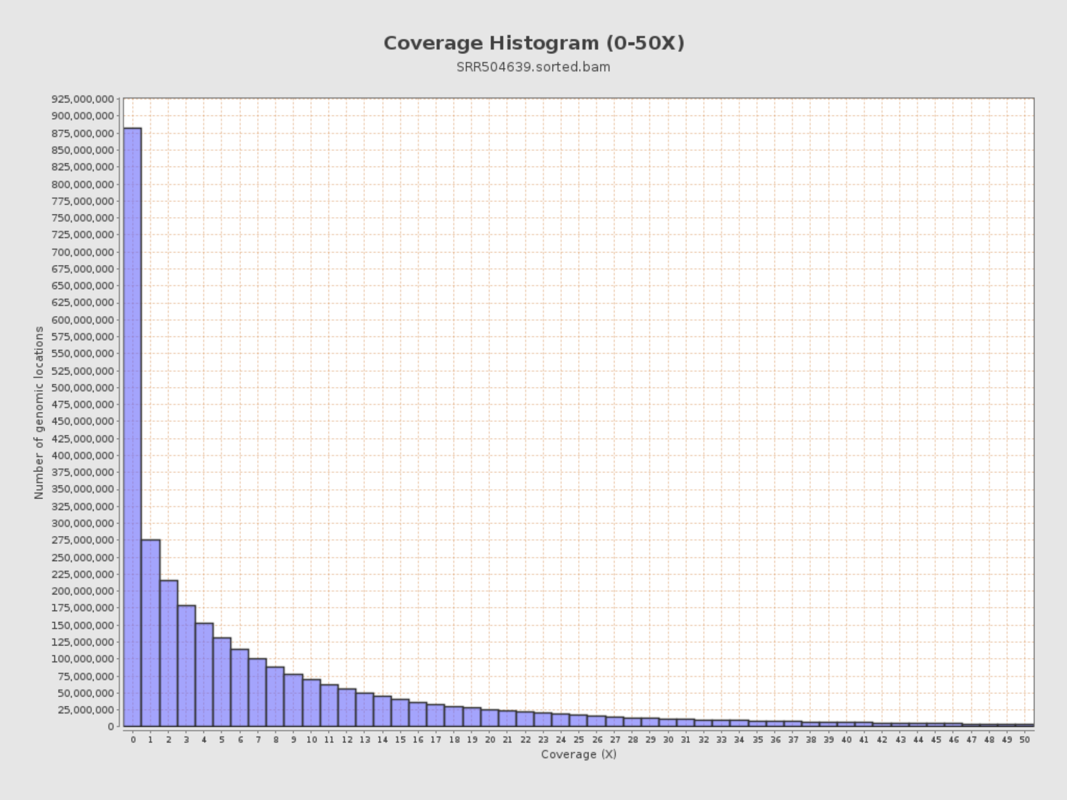
3. Results : Coverage across reference



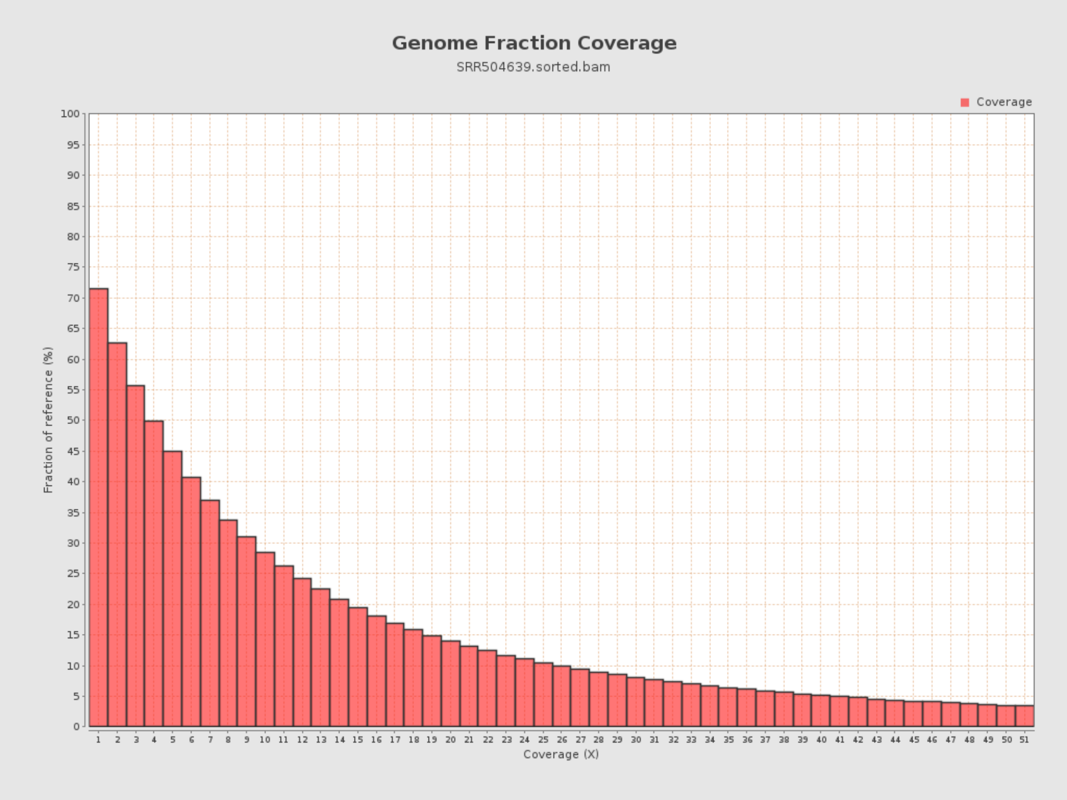
4. Results : Coverage Histogram



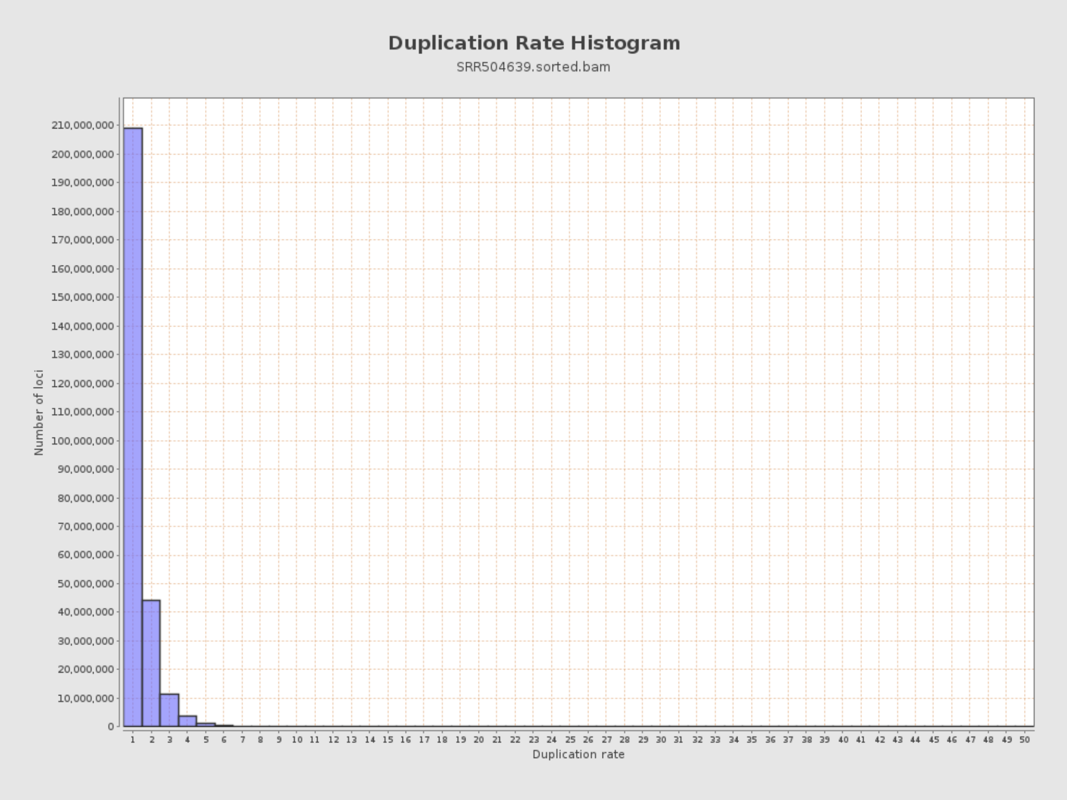
5. Results : Coverage Histogram (0-50X)



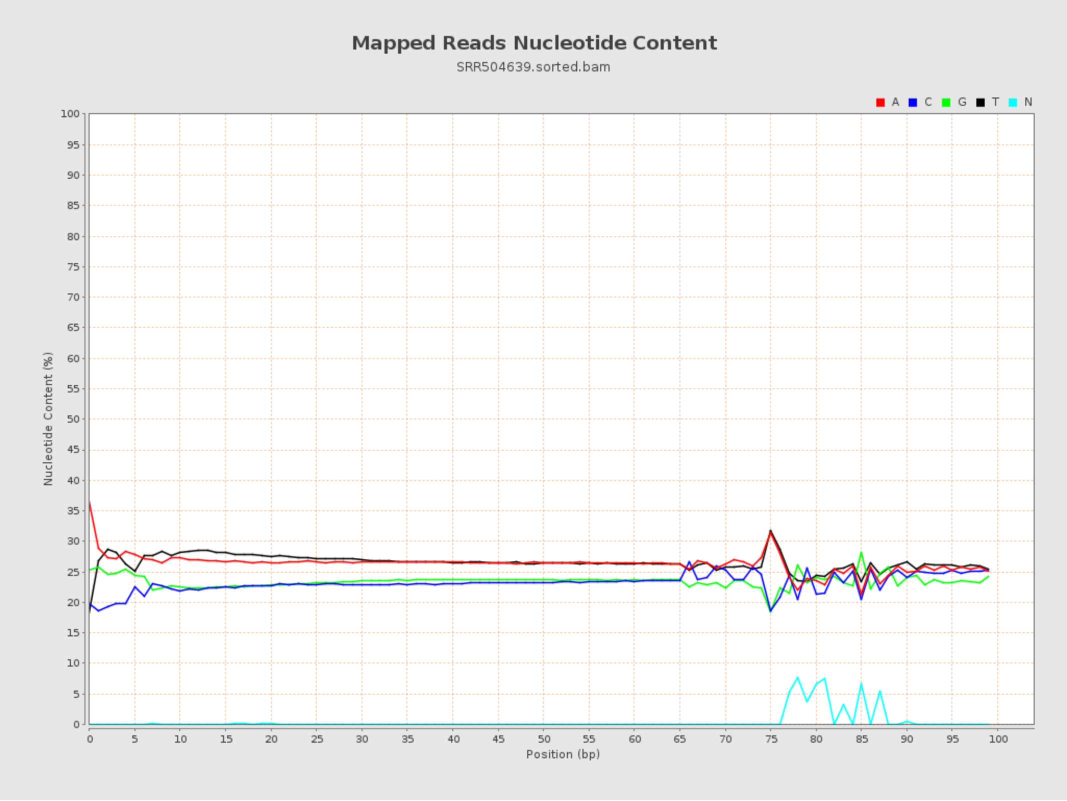
6. Results : Genome Fraction Coverage



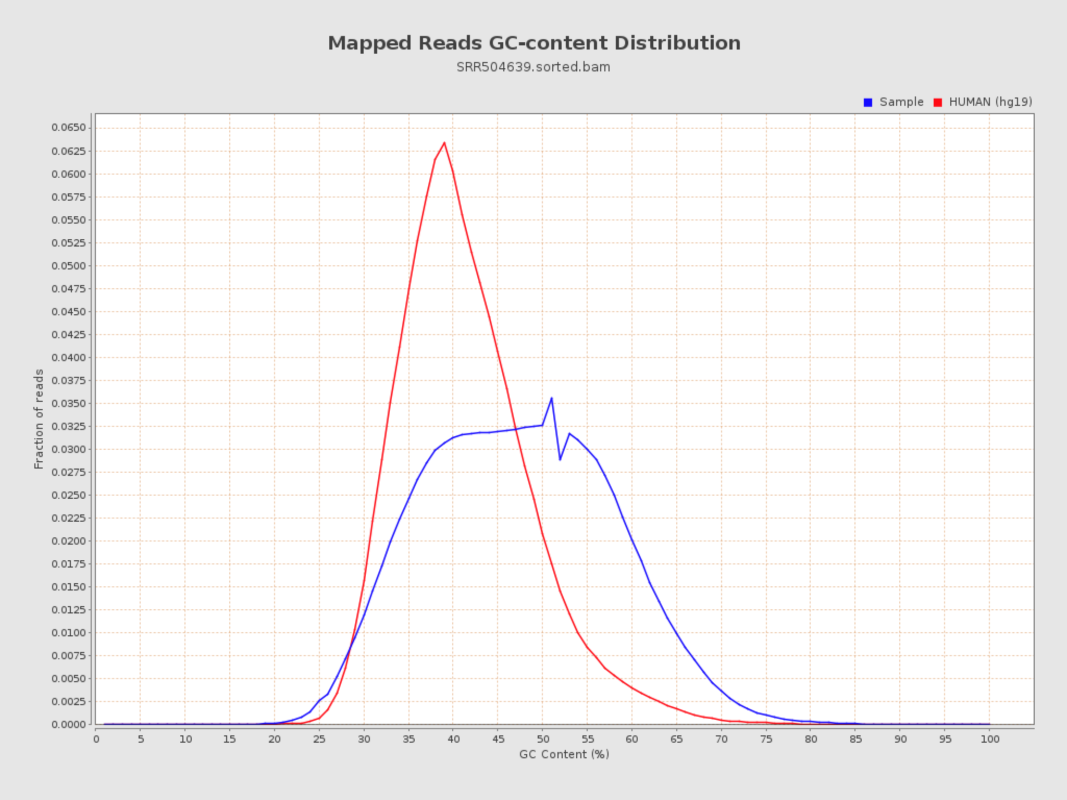
7. Results : Duplication Rate Histogram



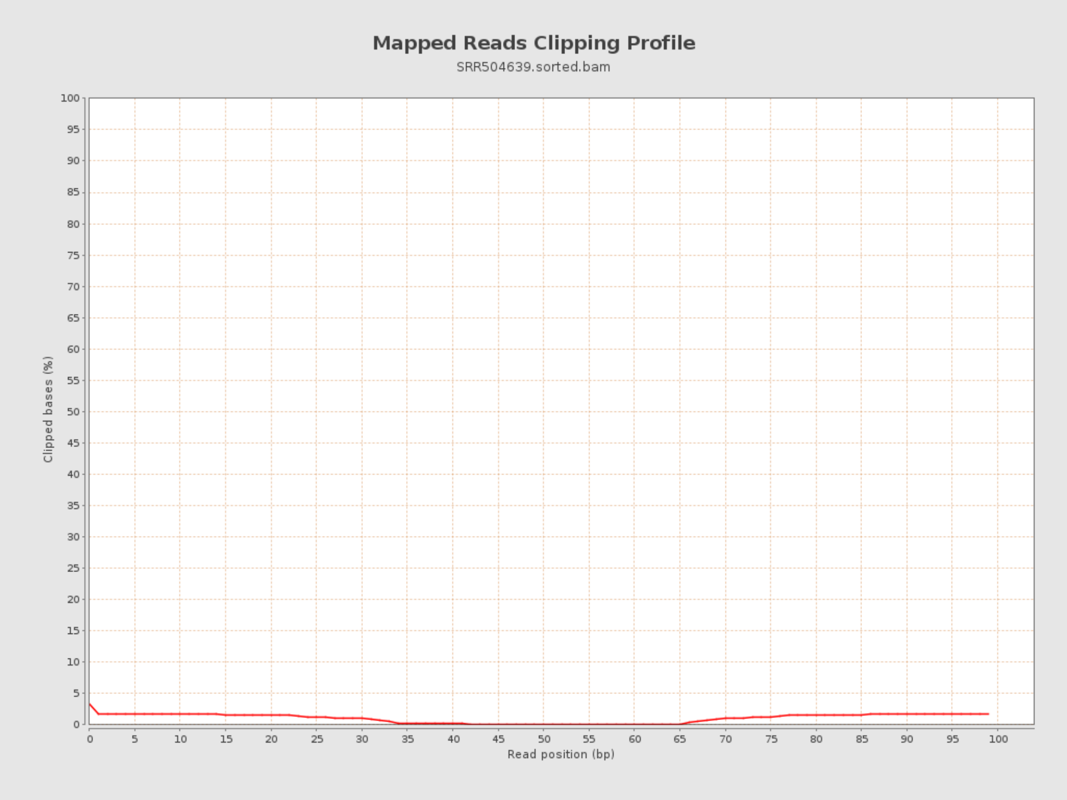
8. Results : Mapped Reads Nucleotide Content



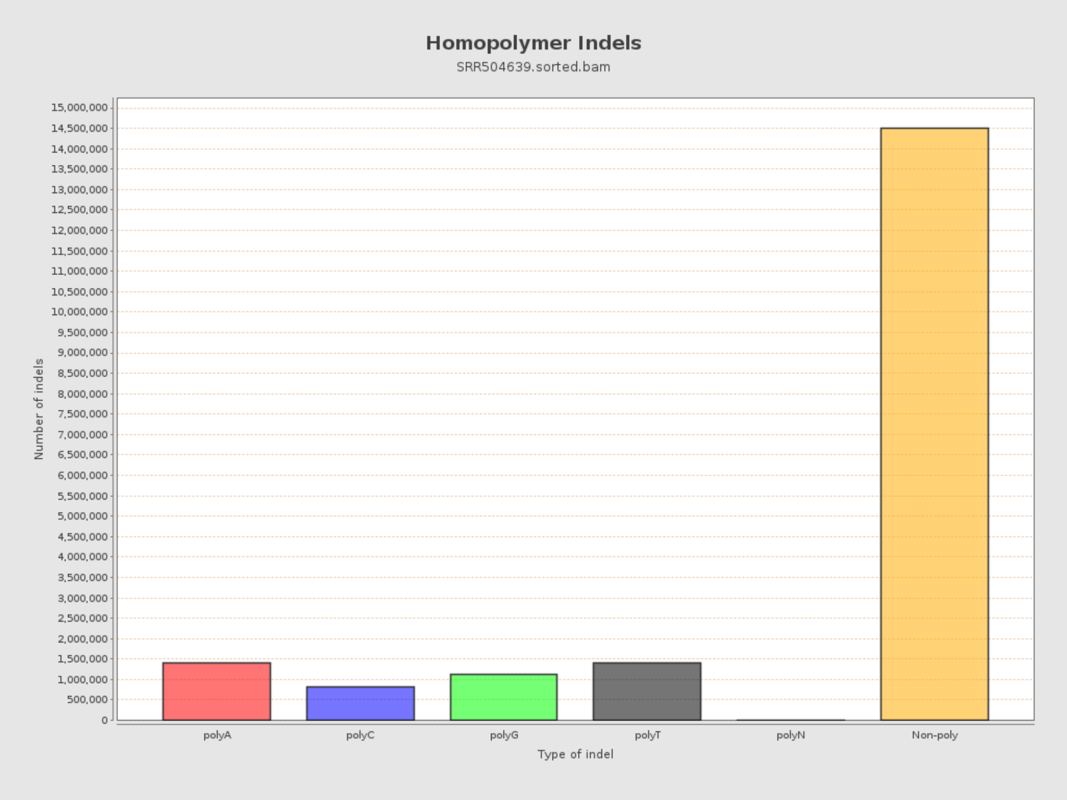
9. Results : Mapped Reads GC-content Distribution



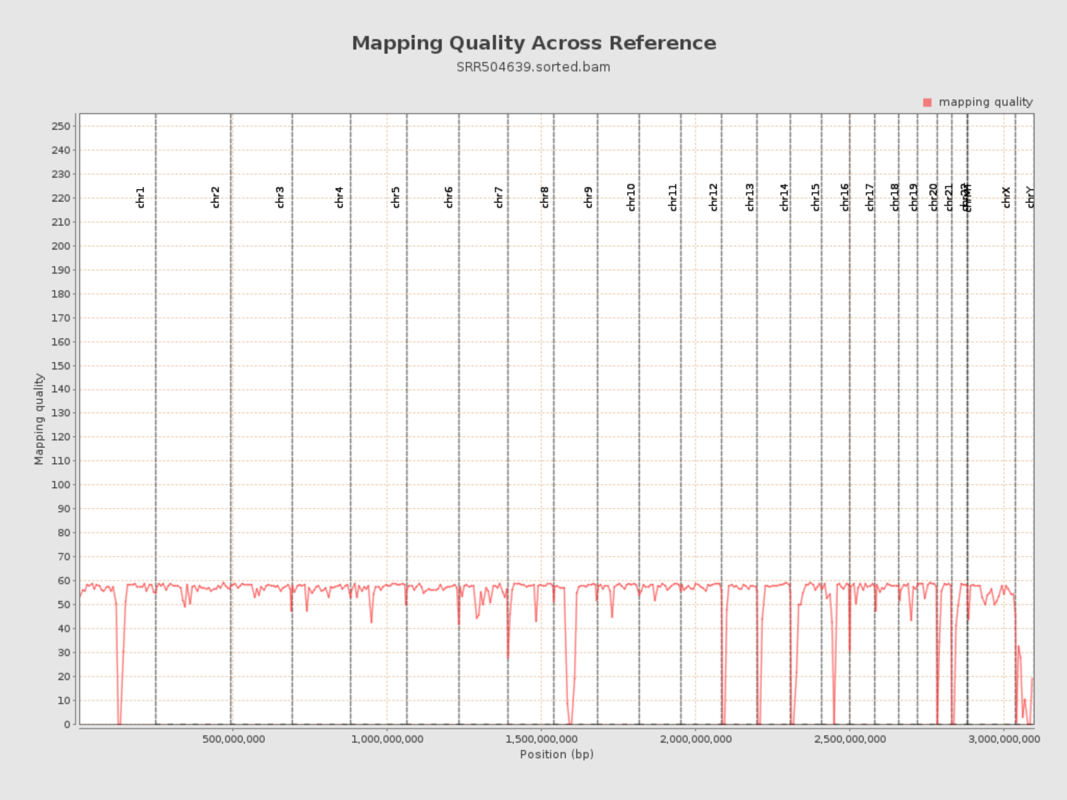
10. Results : Mapped Reads Clipping Profile



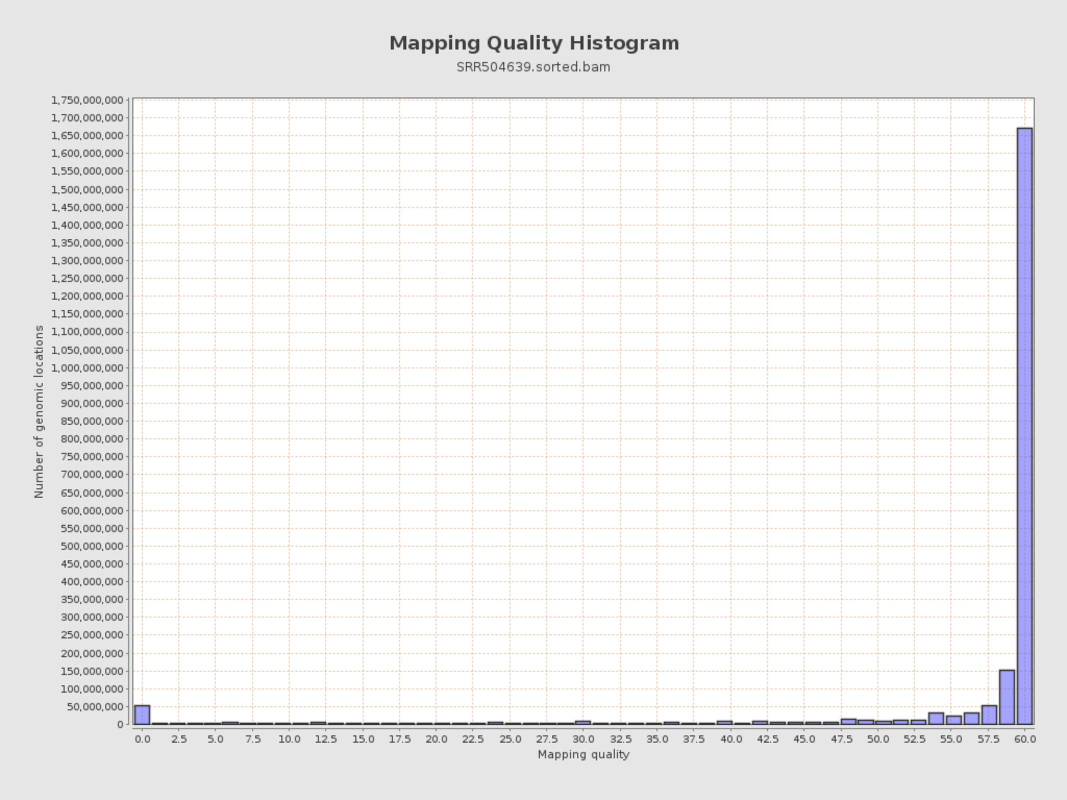
11. Results : Homopolymer Indels



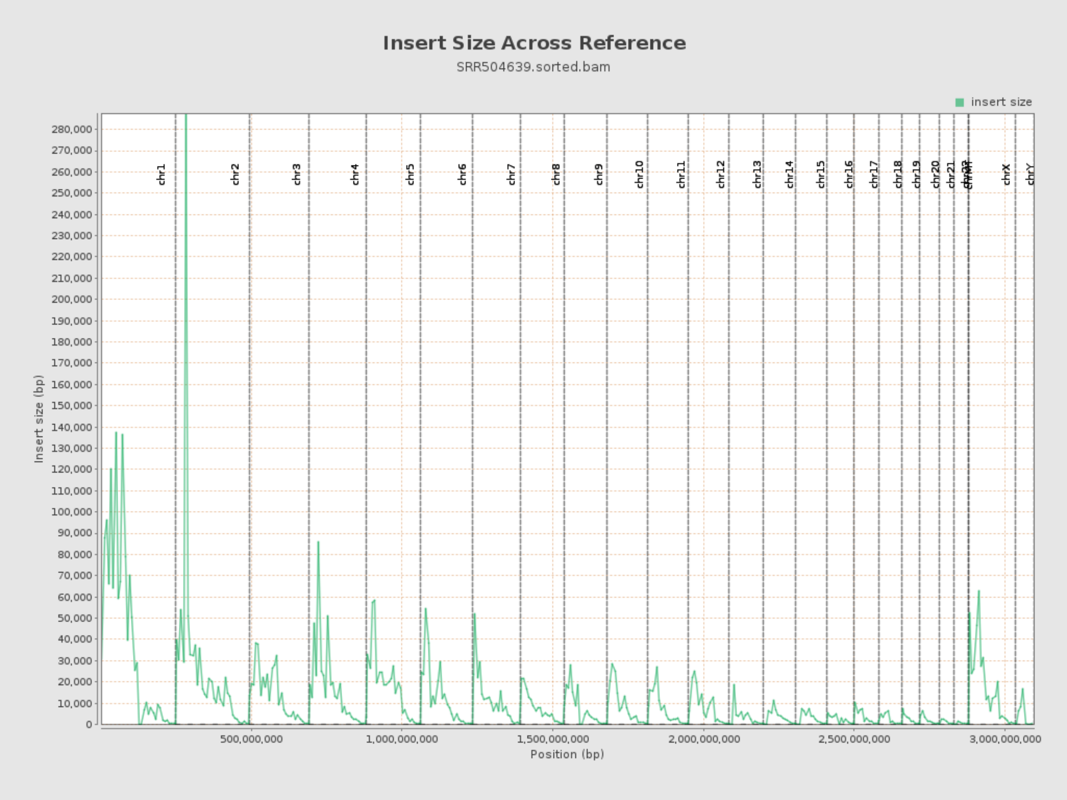
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram