Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/06 22:02:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975288.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_SRR975288 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975288_1.fastq.gz SRR975288_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 06 22:02:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975288.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,650,368
Mapped reads	5,590,106 / 98.93%
Unmapped reads	60,262 / 1.07%
Mapped paired reads	5,590,106 / 98.93%
Mapped reads, first in pair	2,793,390 / 49.44%
Mapped reads, second in pair	2,796,716 / 49.5%
Mapped reads, both in pair	5,563,968 / 98.47%
Mapped reads, singletons	26,138 / 0.46%
Secondary alignments	0
Supplementary alignments	37,980 / 0.67%
Read min/max/mean length	30 / 101 / 101.27
Duplicated reads (estimated)	406,925 / 7.2%
Duplication rate	3.07%
Clipped reads	3,290,311 / 58.23%

2.2. ACGT Content

Number/percentage of A's	155,737,059 / 30.01%
Number/percentage of C's	101,102,379 / 19.48%
Number/percentage of T's	154,653,463 / 29.8%
Number/percentage of G's	107,482,834 / 20.71%
Number/percentage of N's	13,986 / 0%

GC Percentage	40.19%

2.3. Coverage

Mean	0.1678
Standard Deviation	2.4016

2.4. Mapping Quality

Mean Mapping Quality	52.45

2.5. Insert size

Mean	78,447.26
Standard Deviation	2,630,319.74
P25/Median/P75	141 / 174 / 219

2.6. Mismatches and indels

General error rate	0.88%
Mismatches	4,359,630
Insertions	95,302
Mapped reads with at least one insertion	1.66%
Deletions	173,211
Mapped reads with at least one deletion	3.03%
Homopolymer indels	45.42%

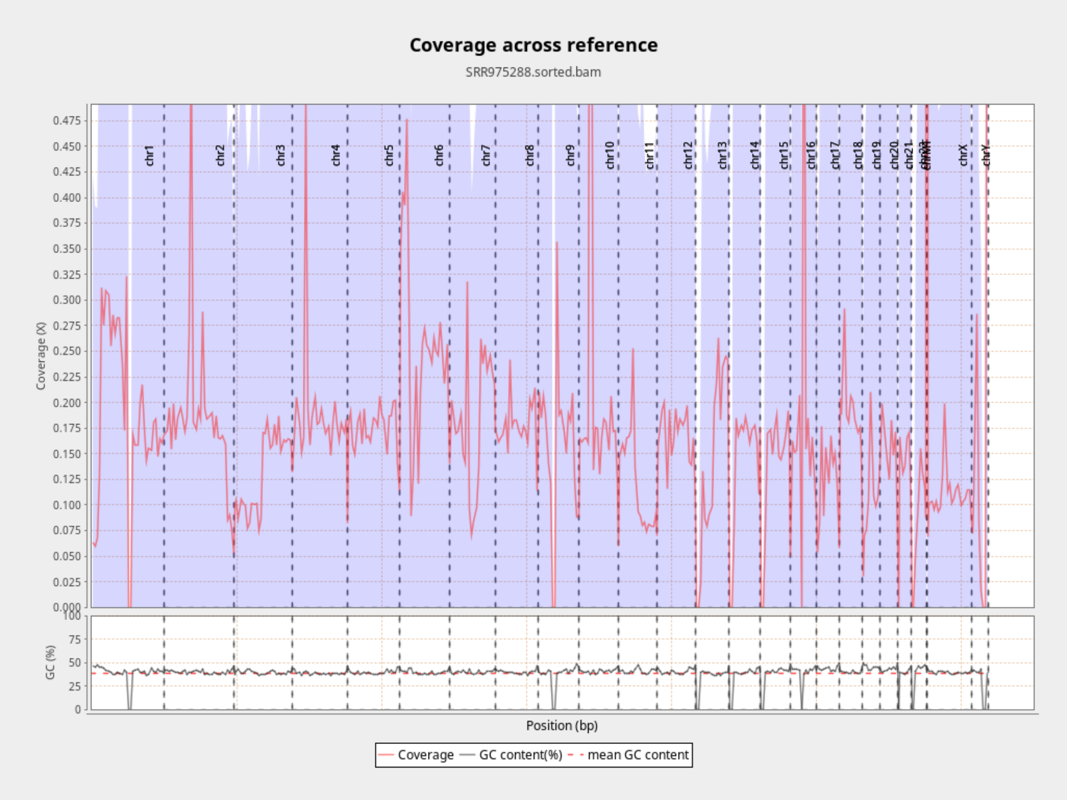
2.7. Chromosome stats

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

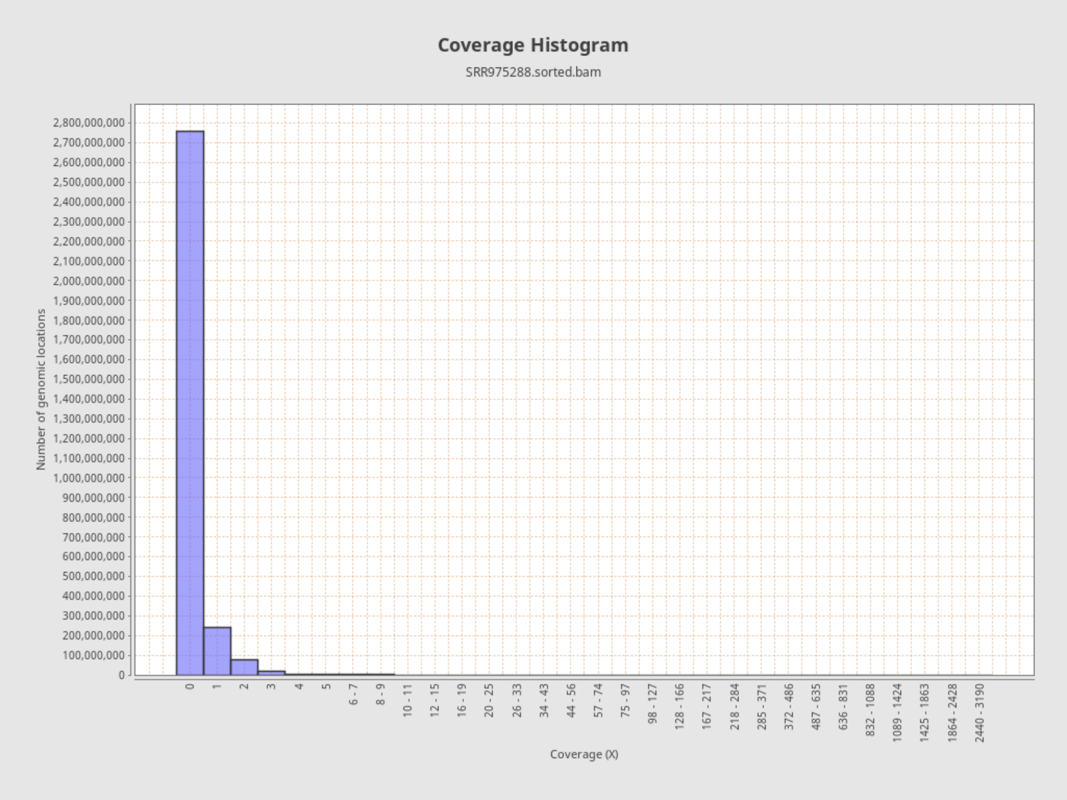
		bases	coverage	deviation
chr1	249250621	46641164	0.1871	2.5072
chr2	243199373	45170320	0.1857	2.49
chr3	198022430	25993324	0.1313	0.5782
chr4	191154276	36271691	0.1898	1.9192
chr5	180915260	31911556	0.1764	0.5689
chr6	171115067	44301300	0.2589	1.3691
chr7	159138663	29158603	0.1832	2.5232
chr8	146364022	25928070	0.1771	0.8933
chr9	141213431	22717824	0.1609	3.6137
chr10	135534747	29337597	0.2165	6.7669
chr11	135006516	16477385	0.122	1.7897
chr12	133851895	22650423	0.1692	0.5489
chr13	115169878	16415436	0.1425	0.4931
chr14	107349540	15046489	0.1402	0.6235
chr15	102531392	13960916	0.1362	0.4779
chr16	90354753	17347164	0.192	3.8859
chr17	81195210	9941894	0.1224	1.5758
chr18	78077248	15292237	0.1959	3.461
chr19	59128983	6328860	0.107	1.4395
chr20	63025520	9877447	0.1567	0.7056
chr21	48129895	6426223	0.1335	0.9269
chr22	51304566	4503655	0.0878	0.432
chrMT	16571	112139	6.7672	4.8613
chrX	155270560	17147022	0.1104	0.8775

chrY	59373566	10352975	0.1744	4.2134

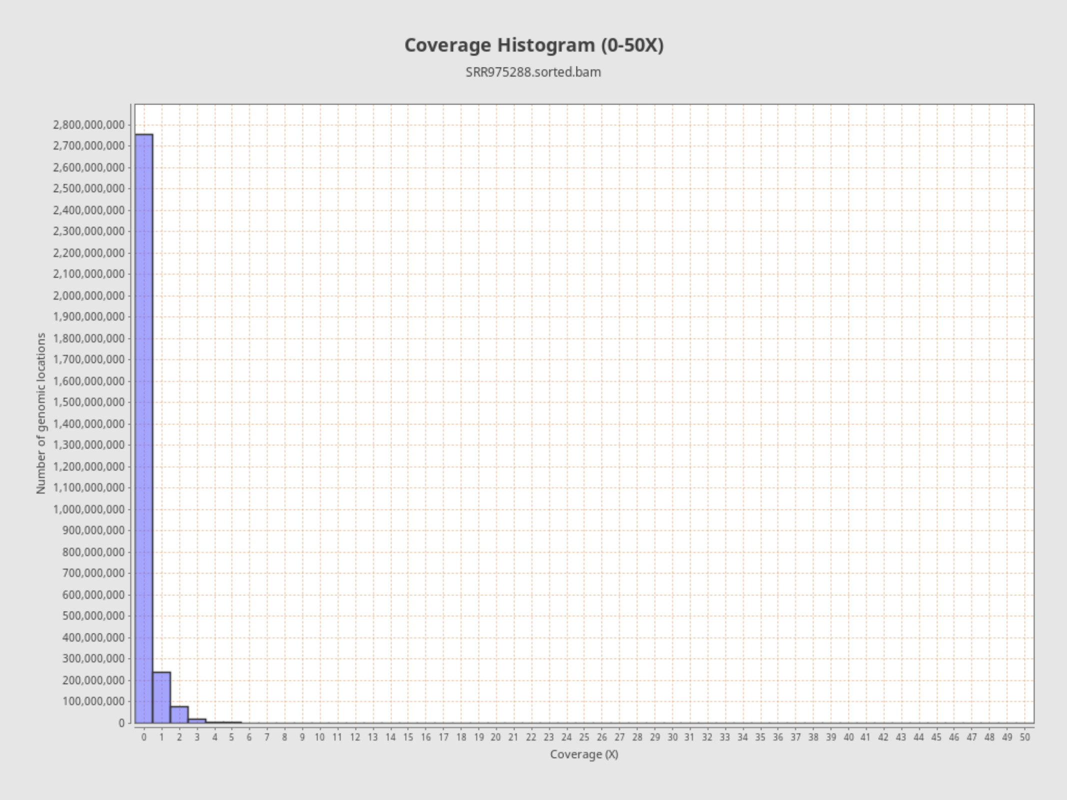
3. Results : Coverage across reference



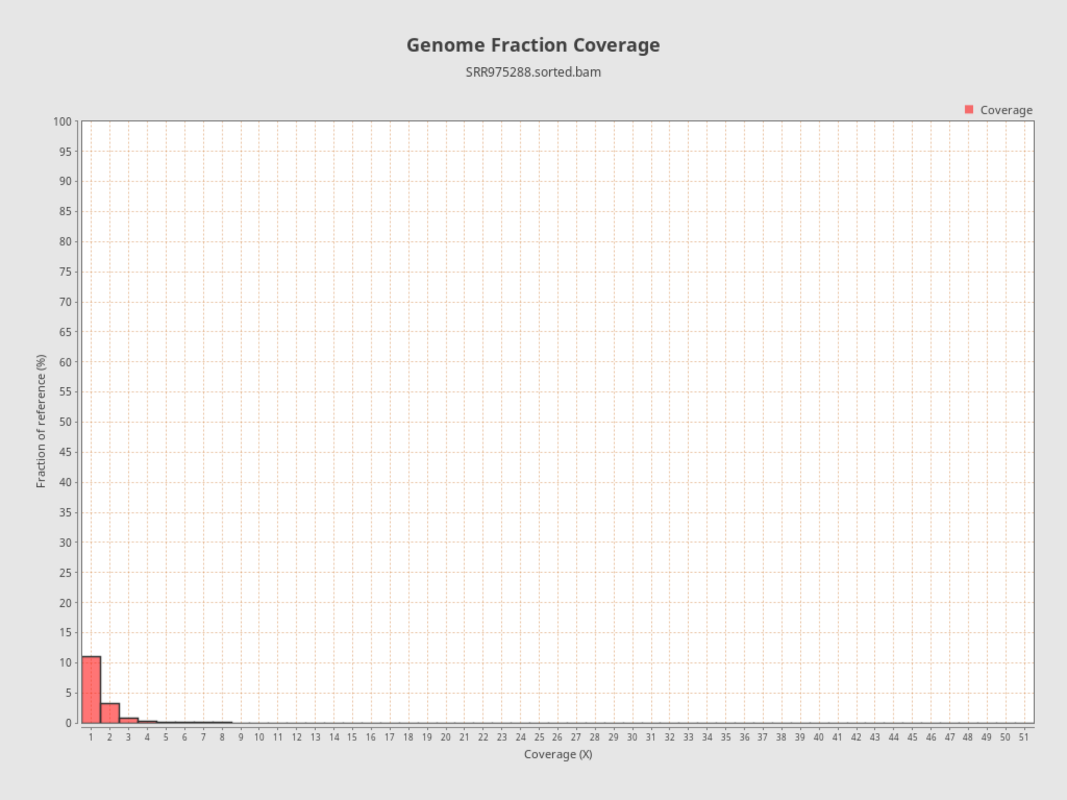
4. Results : Coverage Histogram



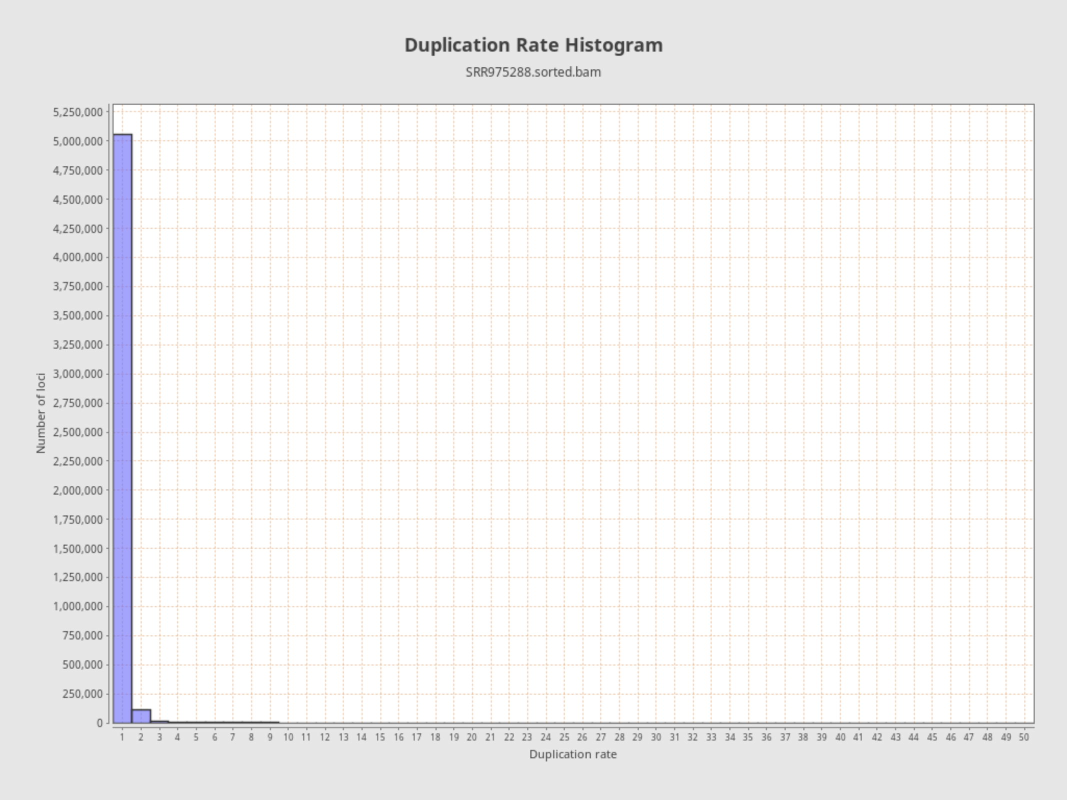
5. Results : Coverage Histogram (0-50X)



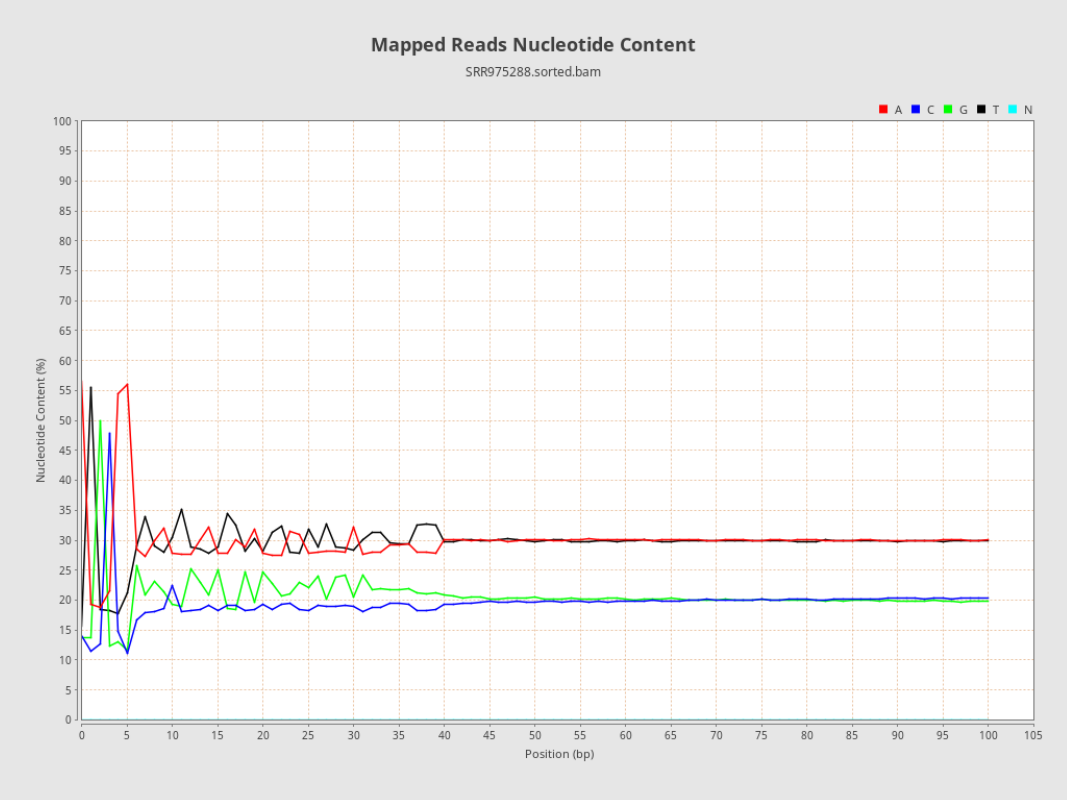
6. Results : Genome Fraction Coverage



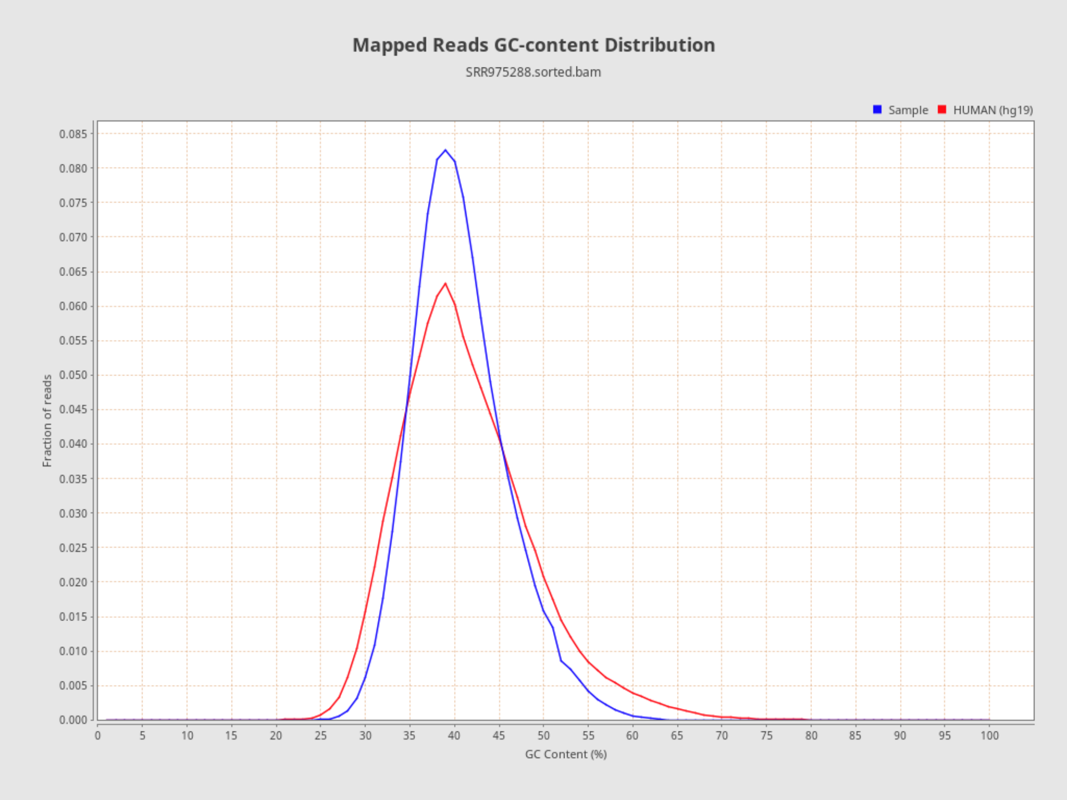
7. Results : Duplication Rate Histogram



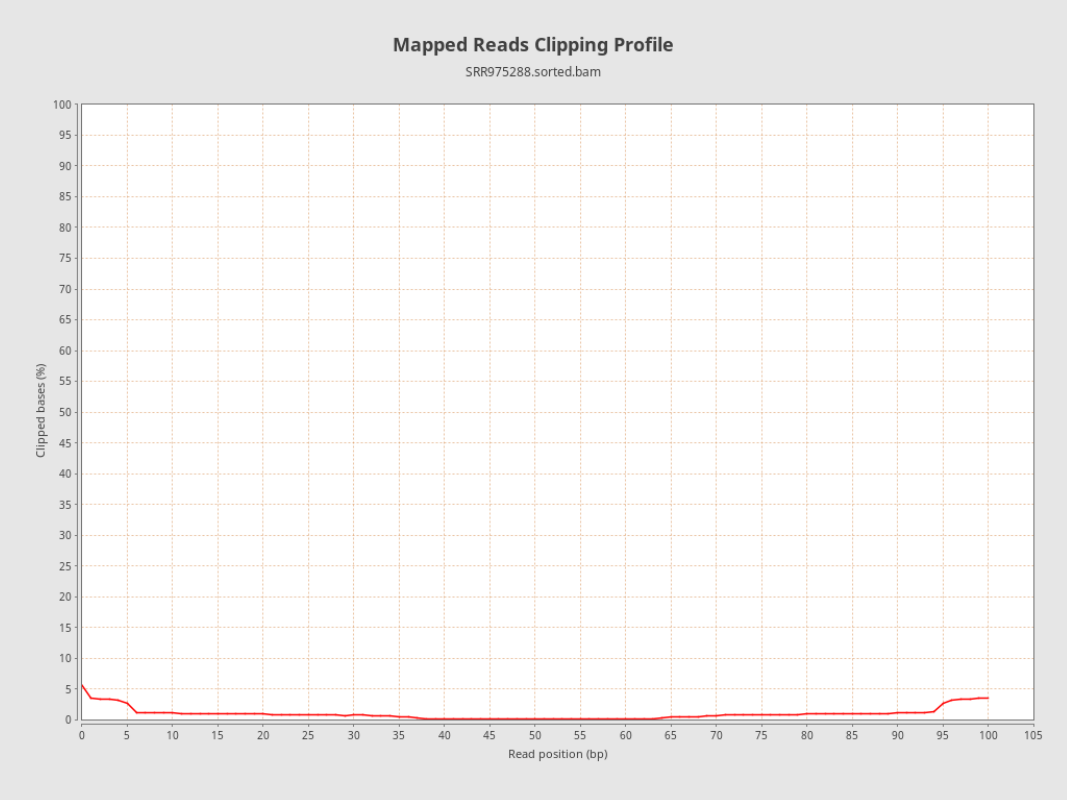
8. Results : Mapped Reads Nucleotide Content



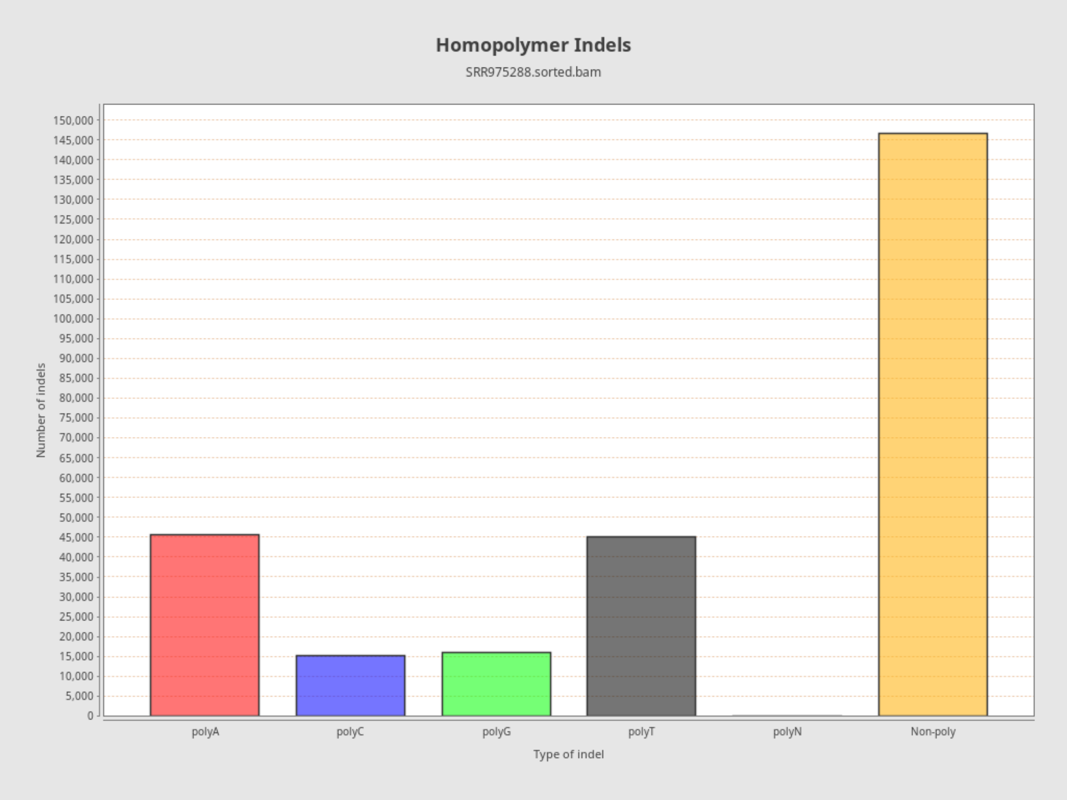
9. Results : Mapped Reads GC-content Distribution



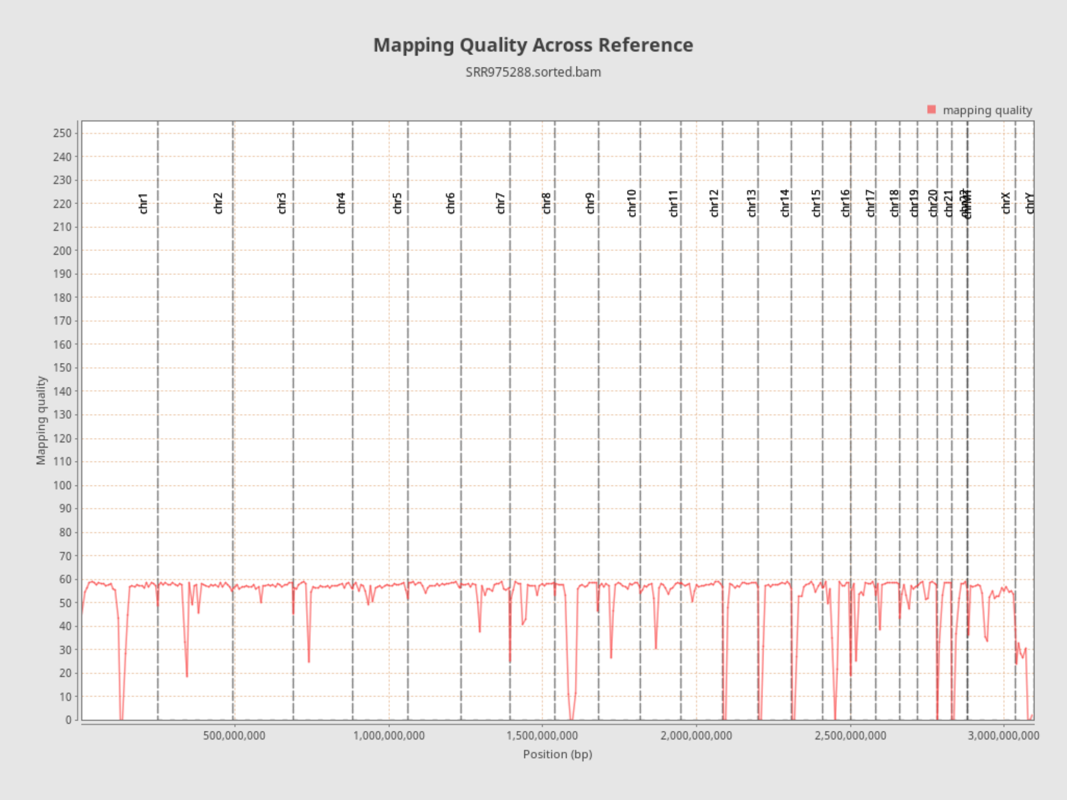
10. Results : Mapped Reads Clipping Profile



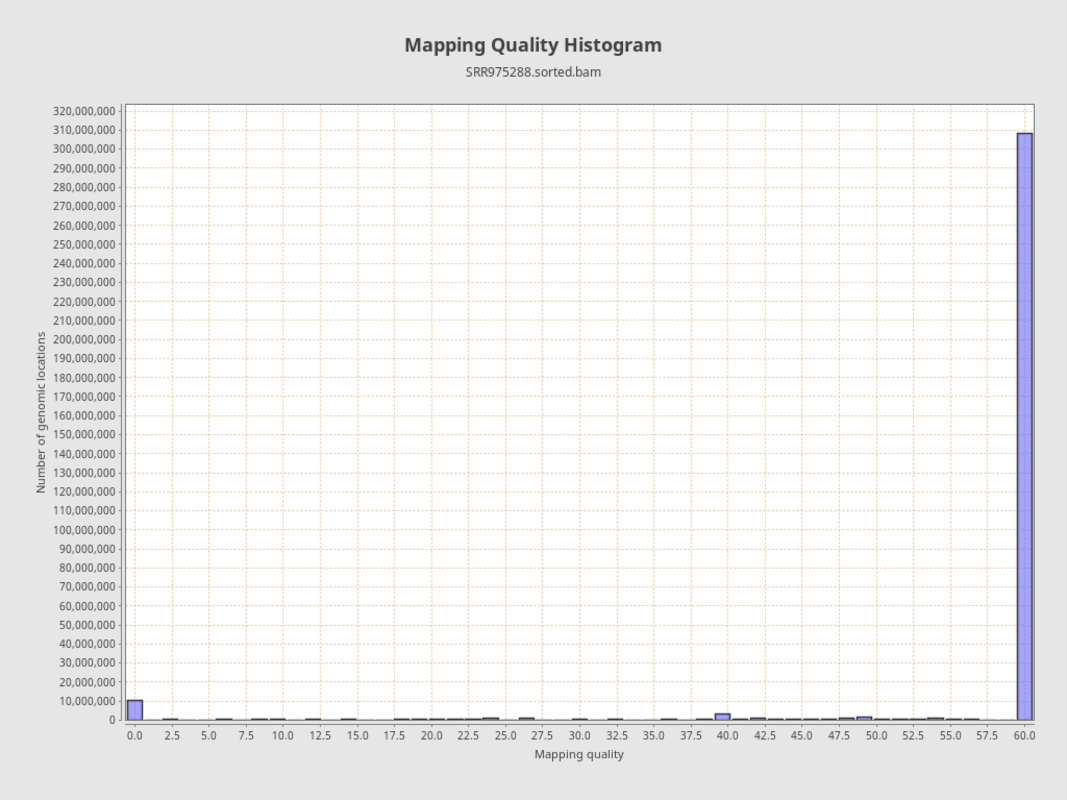
11. Results : Homopolymer Indels



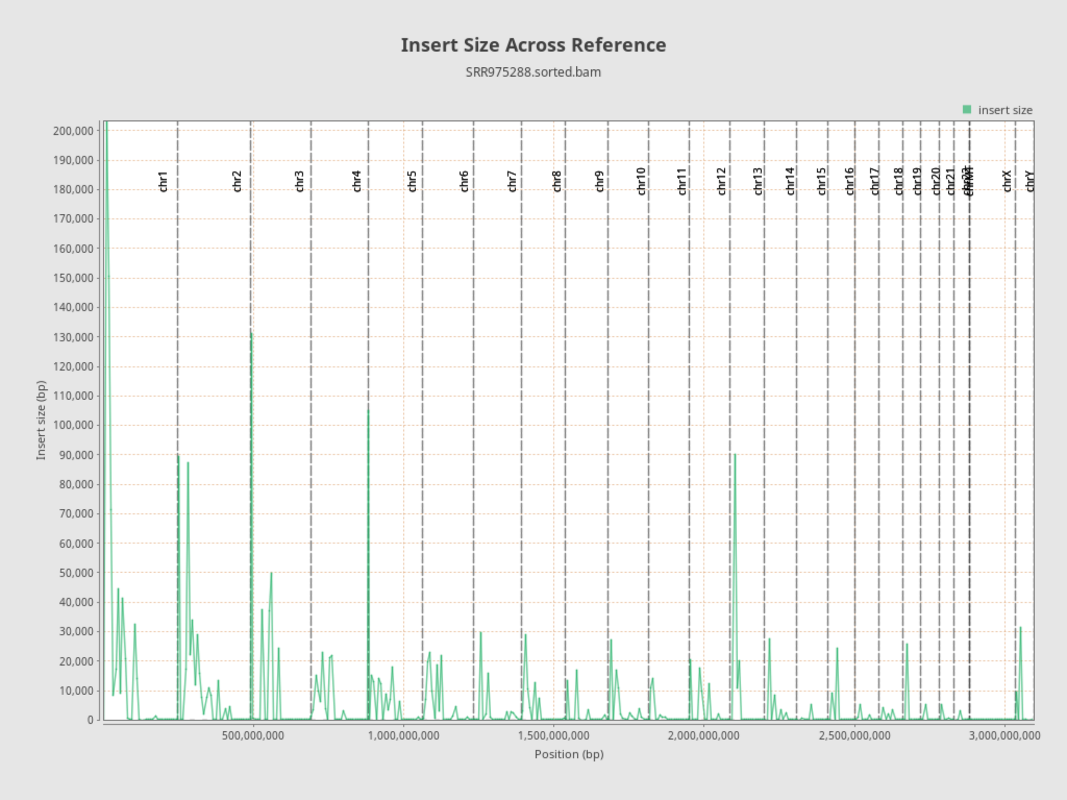
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram