Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 03:44:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975234.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_SRR975234 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975234_1.fastq.gz SRR975234_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 03:44:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975234.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	33,656,898
Mapped reads	33,574,269 / 99.75%
Unmapped reads	82,629 / 0.25%
Mapped paired reads	33,574,269 / 99.75%
Mapped reads, first in pair	16,787,496 / 49.88%
Mapped reads, second in pair	16,786,773 / 49.88%
Mapped reads, both in pair	33,515,138 / 99.58%
Mapped reads, singletons	59,131 / 0.18%
Secondary alignments	0
Supplementary alignments	169,493 / 0.5%
Read min/max/mean length	30 / 101 / 101.2
Duplicated reads (estimated)	20,682,716 / 61.45%
Duplication rate	42.61%
Clipped reads	19,695,732 / 58.52%

2.2. ACGT Content

Number/percentage of A's	824,972,062 / 26.03%
Number/percentage of C's	723,183,031 / 22.81%
Number/percentage of T's	858,415,283 / 27.08%
Number/percentage of G's	763,238,906 / 24.08%
Number/percentage of N's	88,477 / 0%

GC Percentage	46.89%

2.3. Coverage

Mean	1.0244
Standard Deviation	16.9499

2.4. Mapping Quality

Mean Mapping Quality	55.9

2.5. Insert size

Mean	205,590.98
Standard Deviation	4,425,240.59
P25/Median/P75	192 / 236 / 286

2.6. Mismatches and indels

General error rate	0.77%
Mismatches	23,644,472
Insertions	365,959
Mapped reads with at least one insertion	1.08%
Deletions	896,985
Mapped reads with at least one deletion	2.62%
Homopolymer indels	47.11%

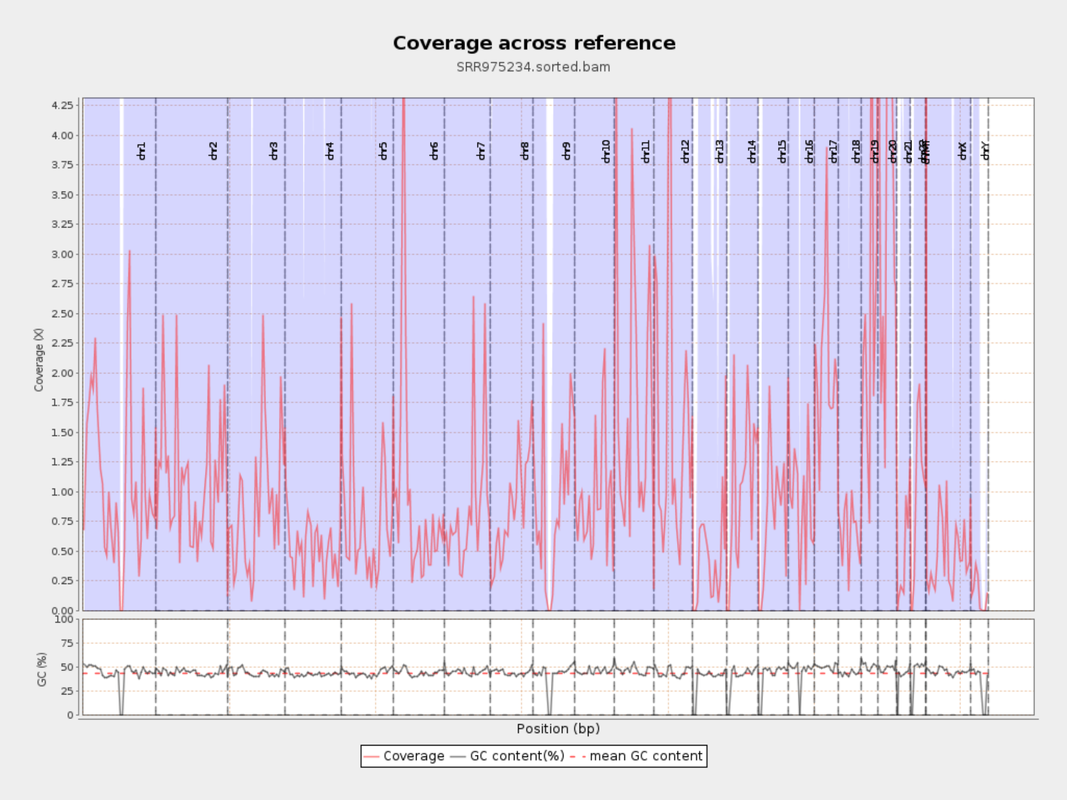
2.7. Chromosome stats

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

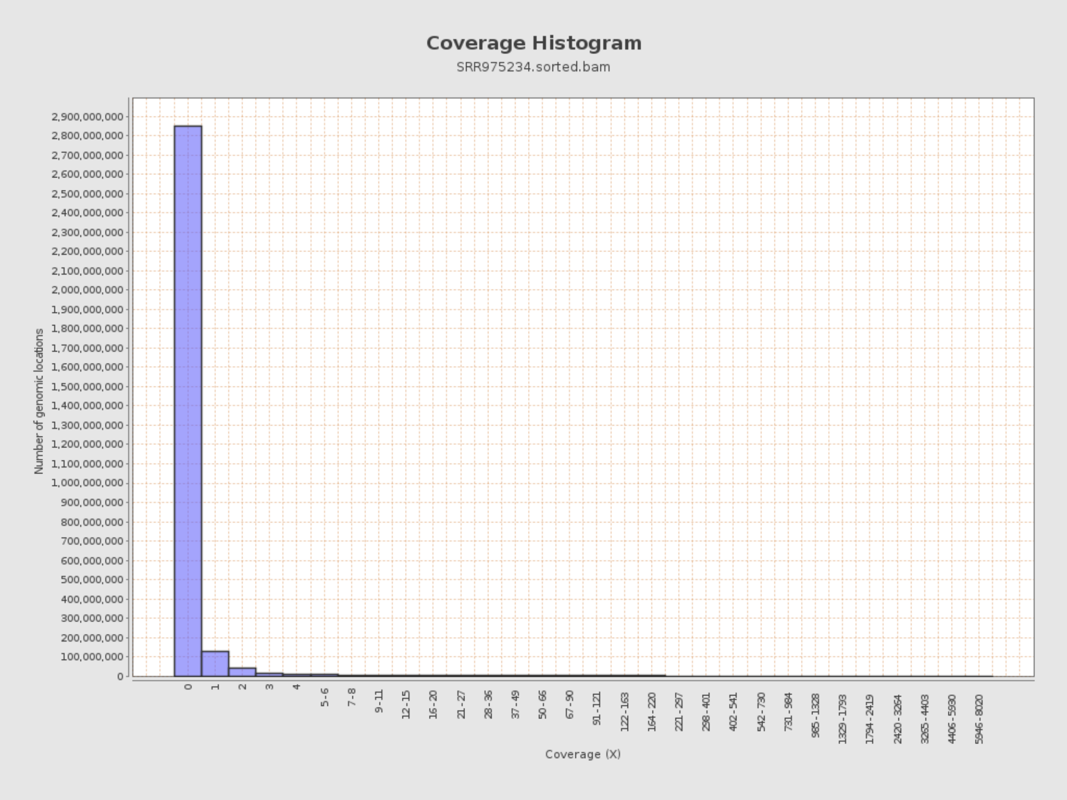
		bases	coverage	deviation
chr1	249250621	269166478	1.0799	15.6186
chr2	243199373	267818571	1.1012	16.8051
chr3	198022430	173866510	0.878	14.5246
chr4	191154276	98398744	0.5148	9.5846
chr5	180915260	142432077	0.7873	13.8718
chr6	171115067	159872684	0.9343	16.0097
chr7	159138663	139518141	0.8767	14.8569
chr8	146364022	127114620	0.8685	14.5478
chr9	141213431	126153505	0.8934	13.4112
chr10	135534747	129799865	0.9577	15.2916
chr11	135006516	242625443	1.7971	23.8063
chr12	133851895	226369706	1.6912	23.8247
chr13	115169878	49389691	0.4288	8.4055
chr14	107349540	112458234	1.0476	16.1308
chr15	102531392	79160080	0.7721	11.5592
chr16	90354753	81763920	0.9049	14.1118
chr17	81195210	170810484	2.1037	27.3174
chr18	78077248	52303772	0.6699	12.5718
chr19	59128983	153974987	2.6041	33.7664
chr20	63025520	214288128	3.4	40.84
chr21	48129895	22601984	0.4696	8.8824
chr22	51304566	50884578	0.9918	14.9611
chrMT	16571	180857	10.9141	15.7303
chrX	155270560	71679880	0.4616	9.9729

chrY	59373566	8593164	0.1447	4.6133

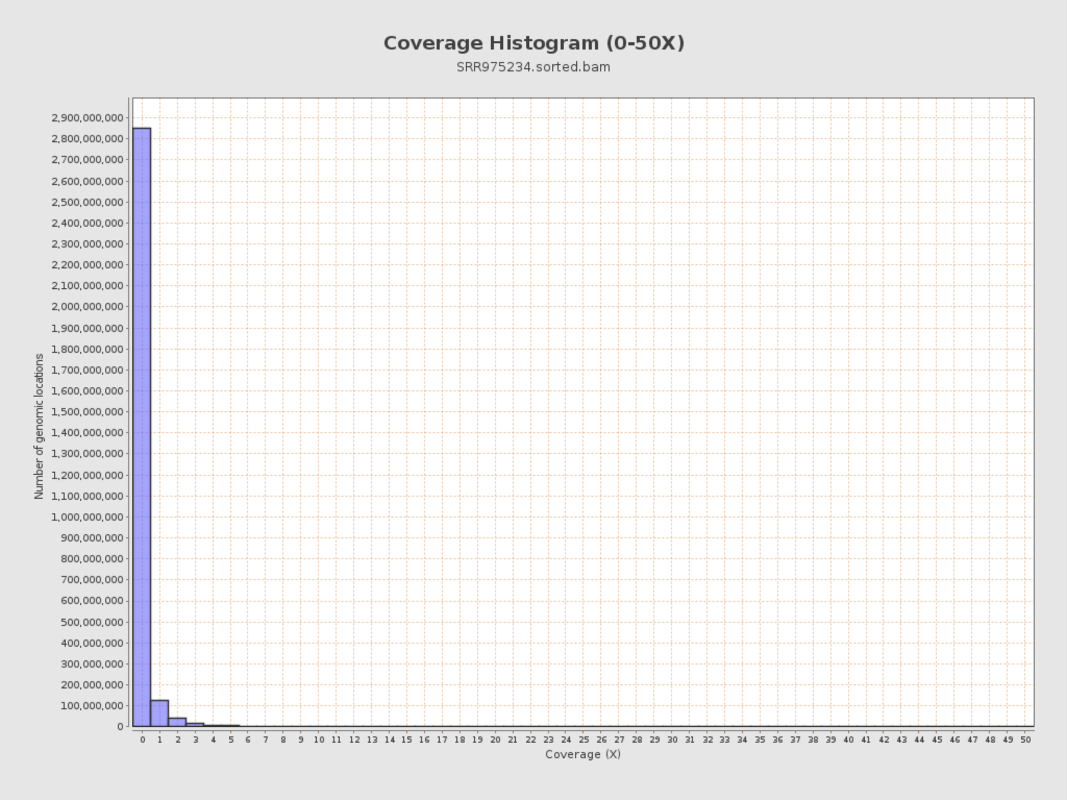
3. Results : Coverage across reference



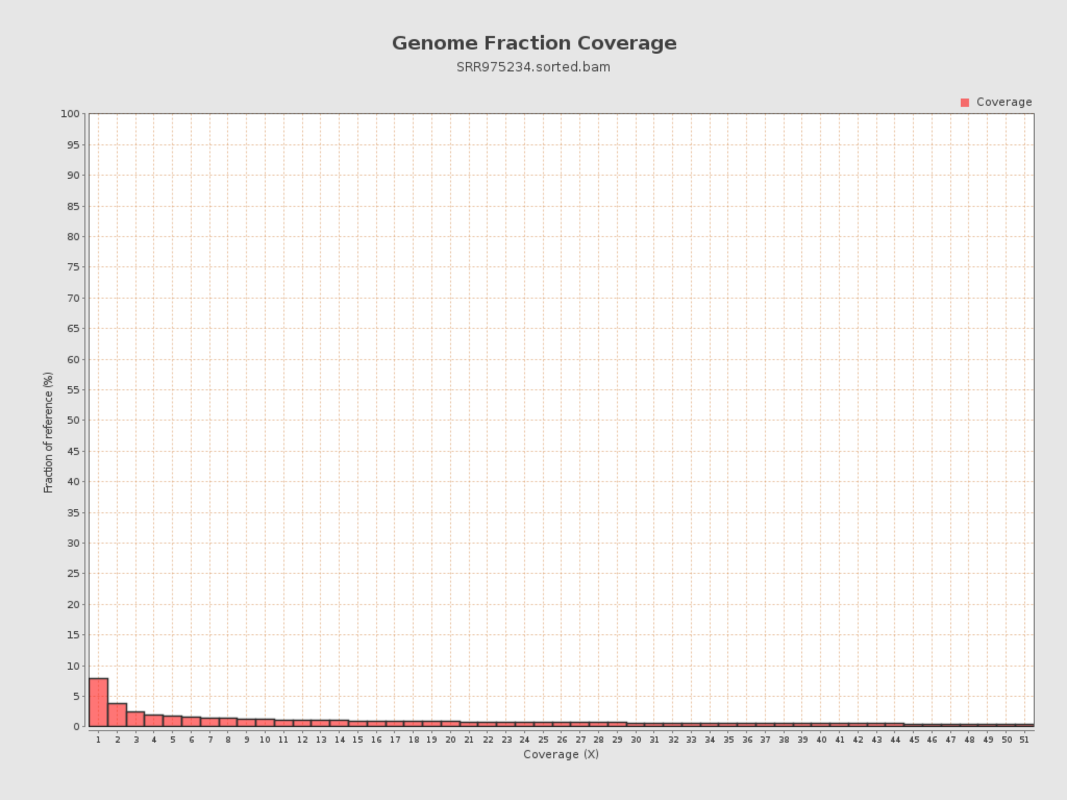
4. Results : Coverage Histogram



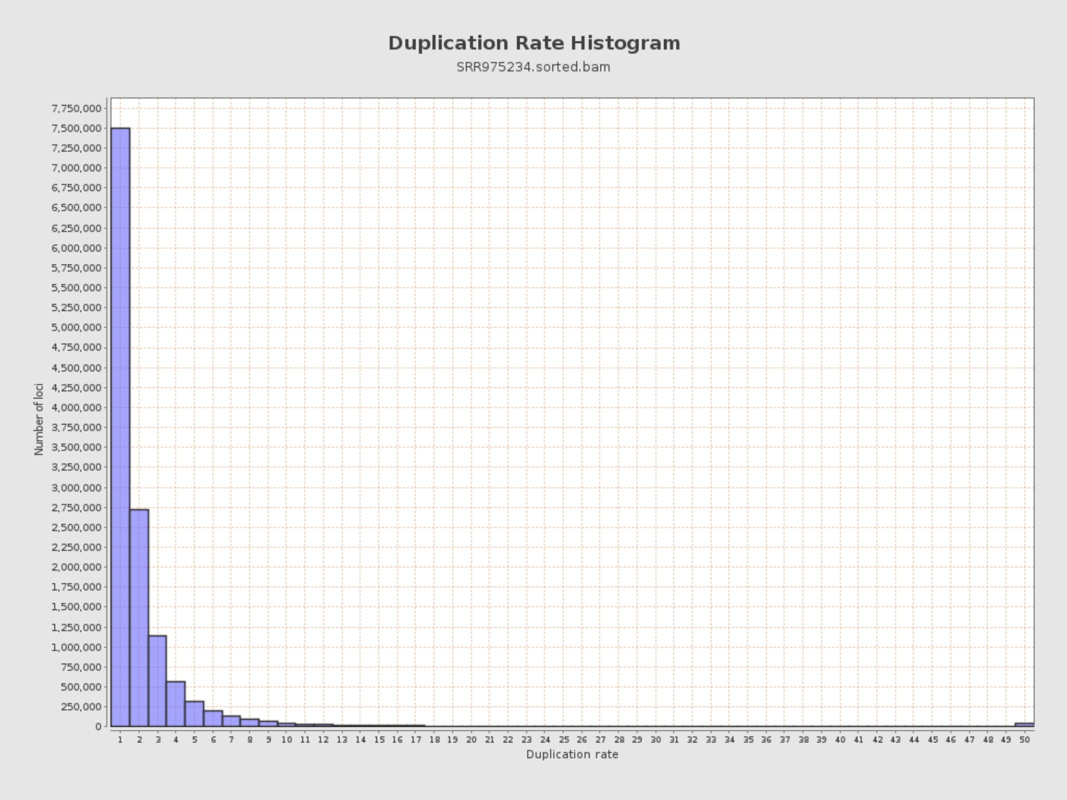
5. Results : Coverage Histogram (0-50X)



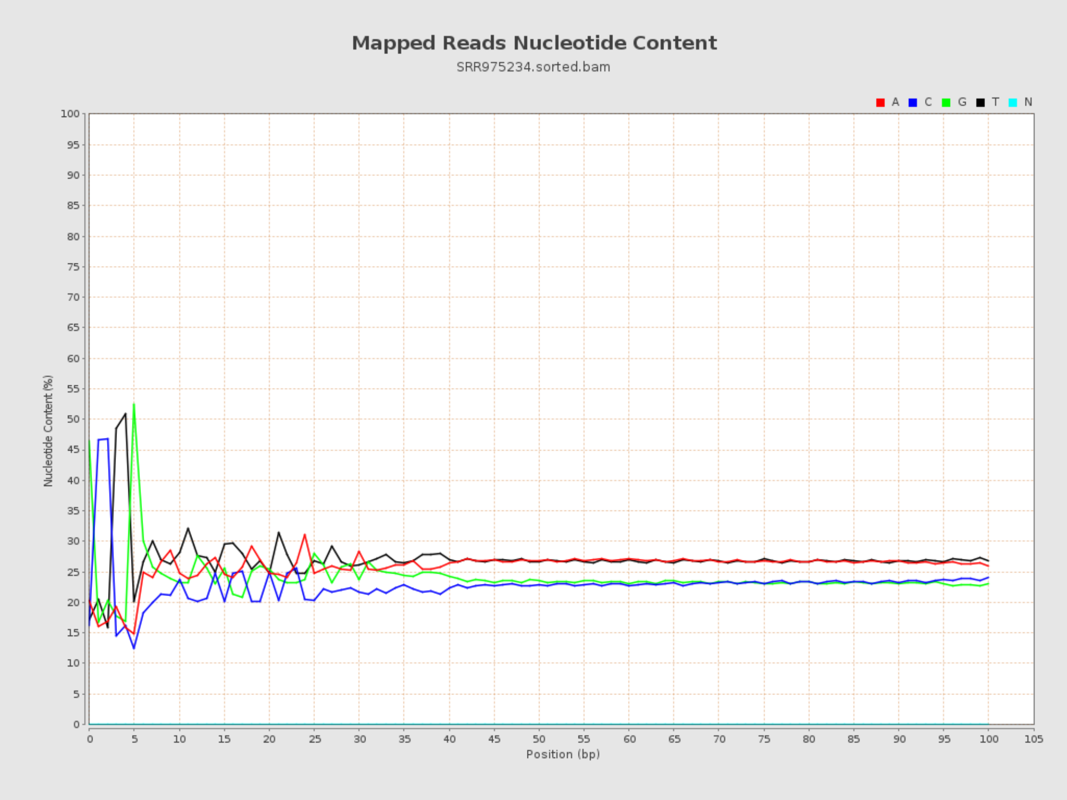
6. Results : Genome Fraction Coverage



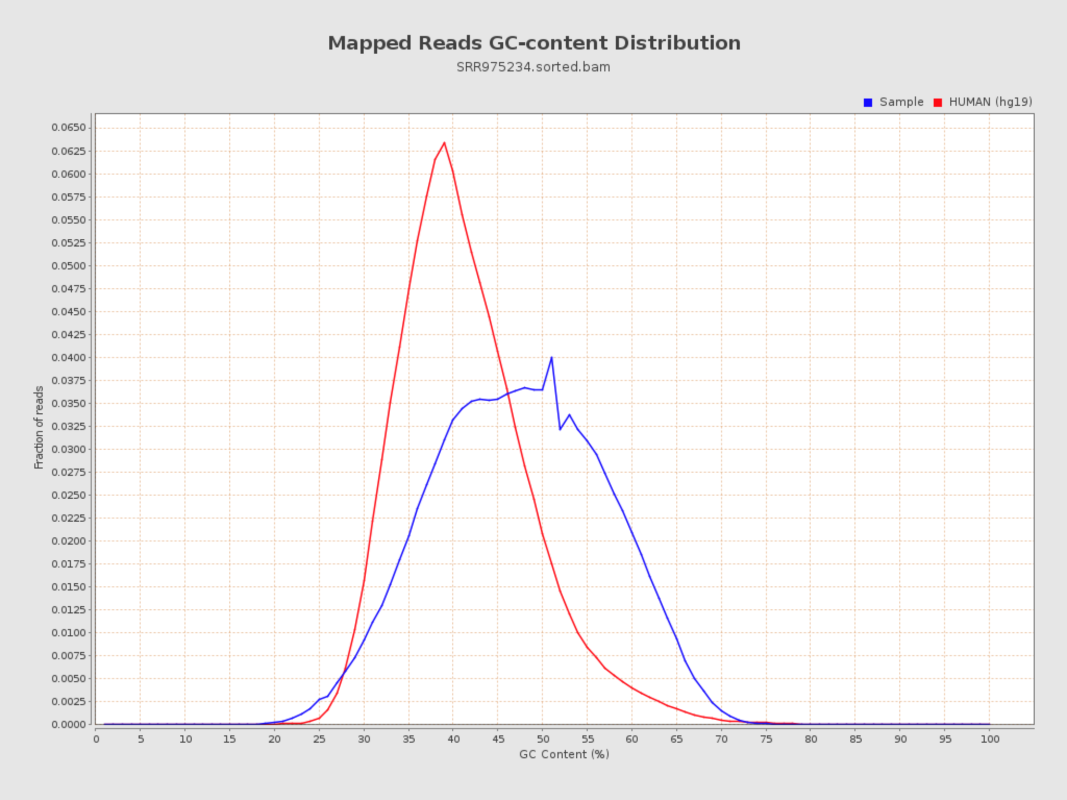
7. Results : Duplication Rate Histogram



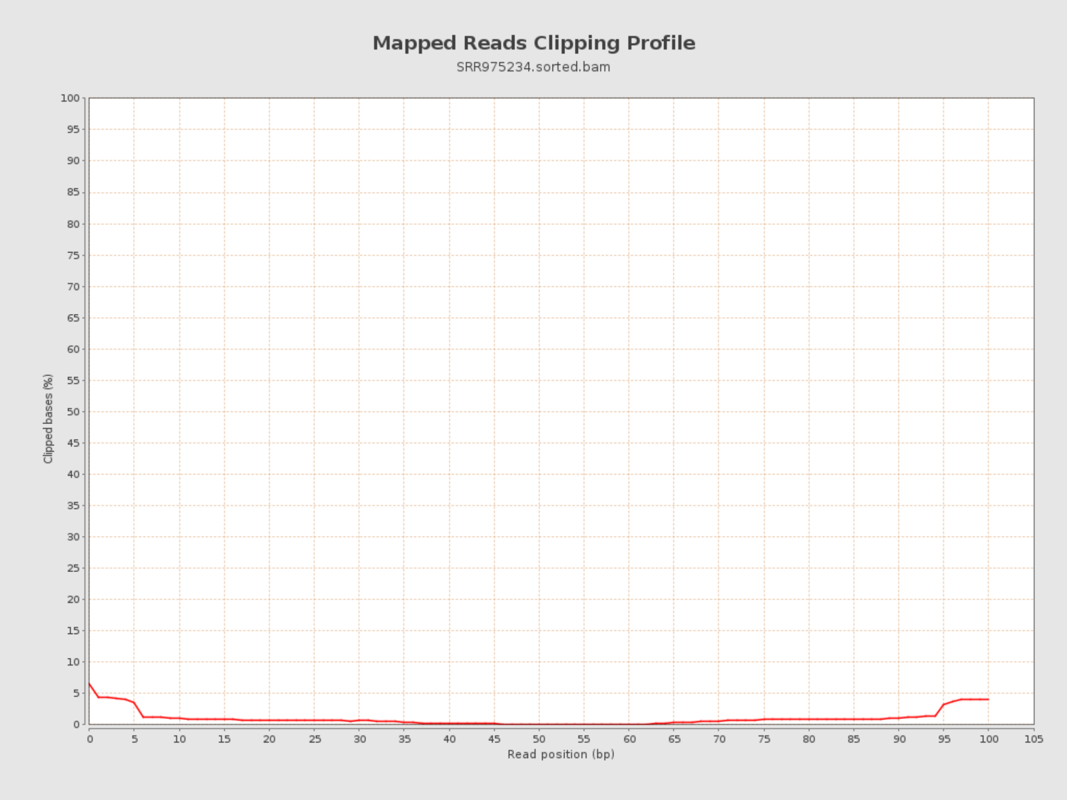
8. Results : Mapped Reads Nucleotide Content



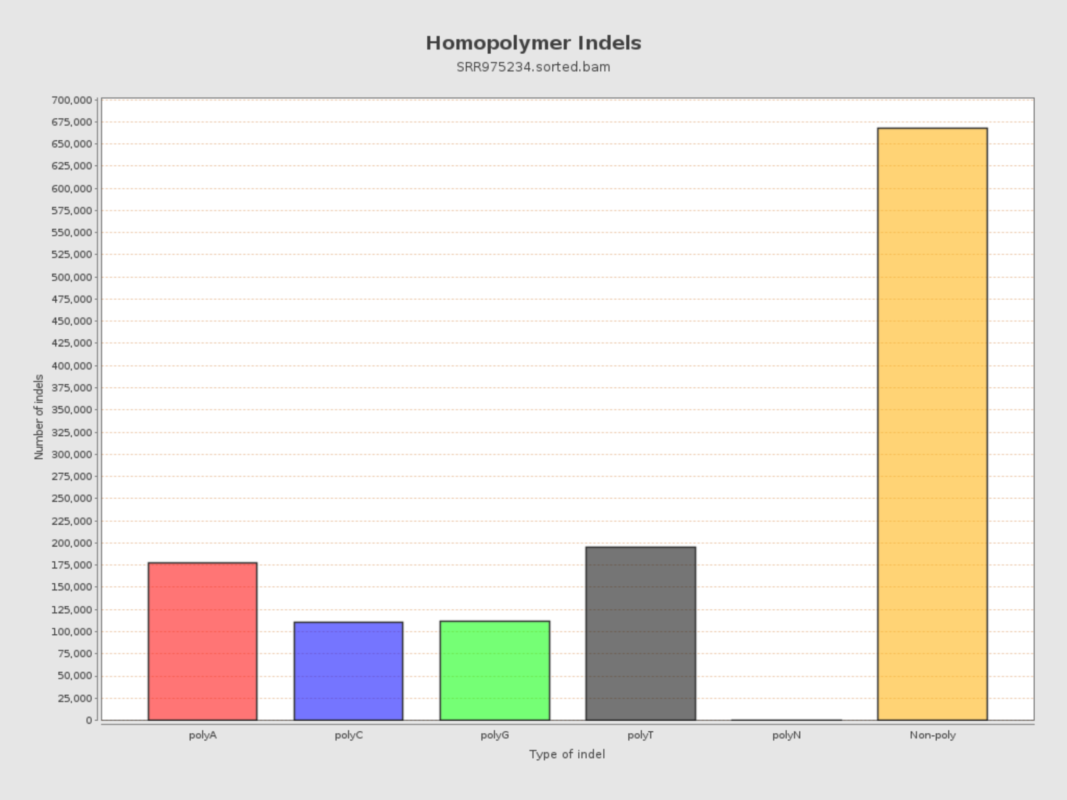
9. Results : Mapped Reads GC-content Distribution



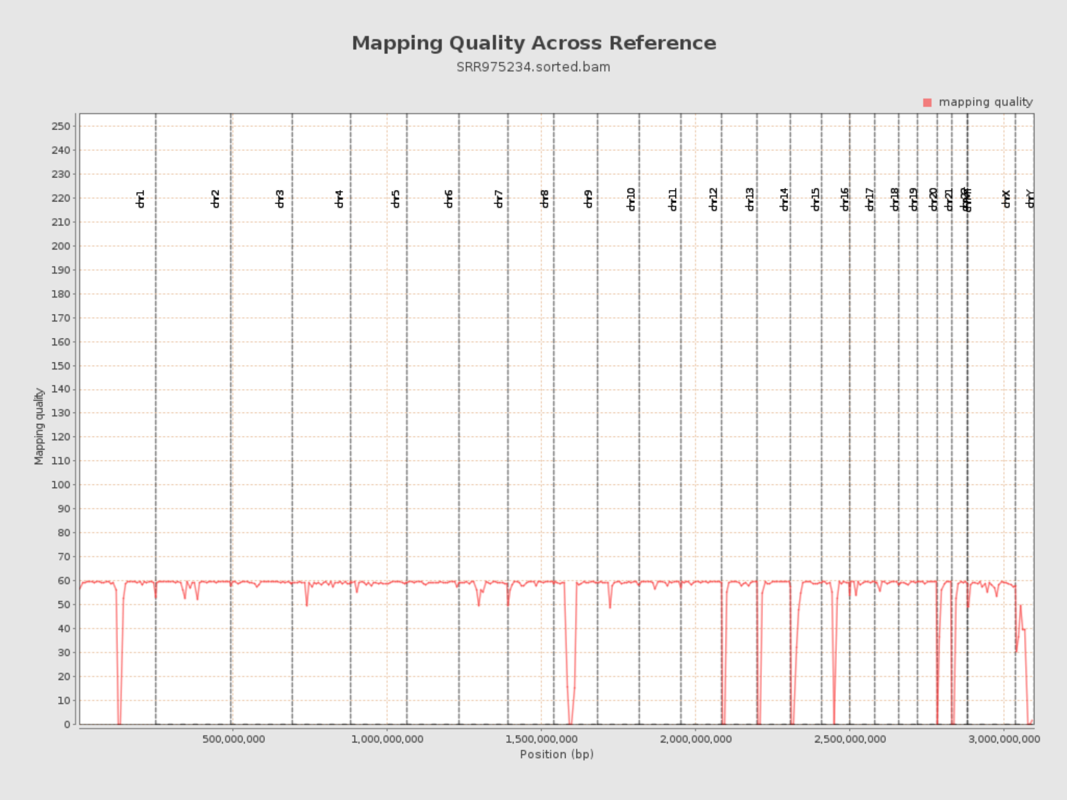
10. Results : Mapped Reads Clipping Profile



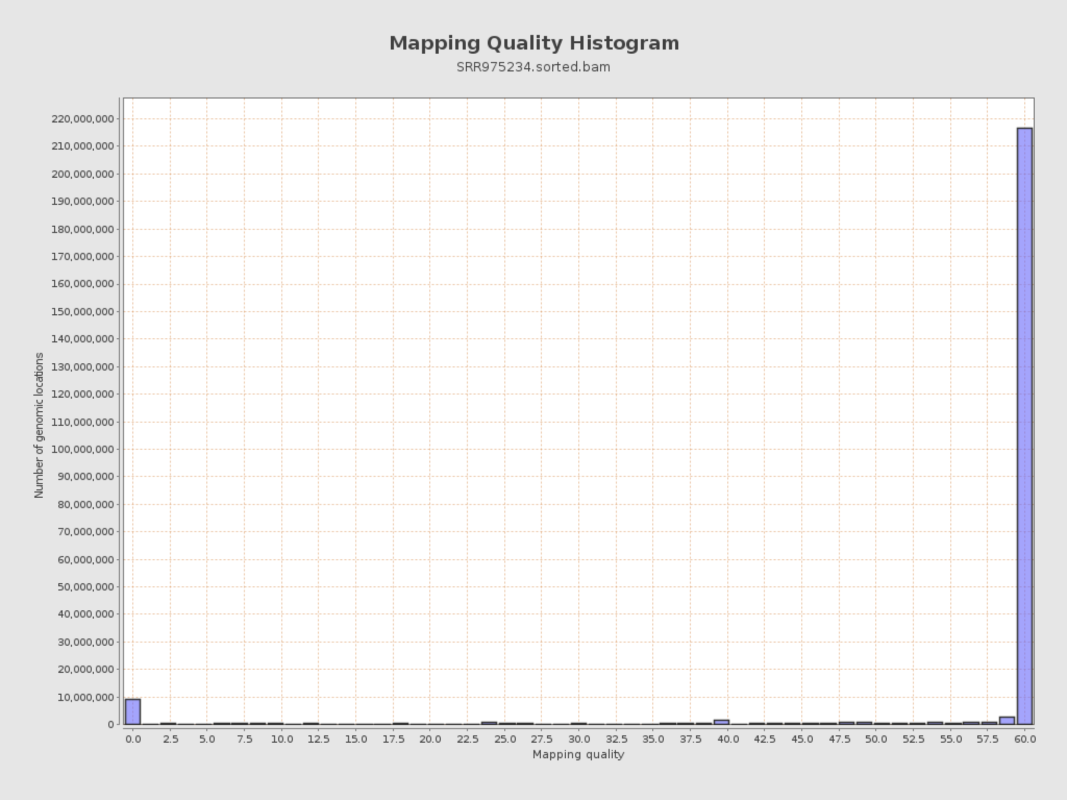
11. Results : Homopolymer Indels



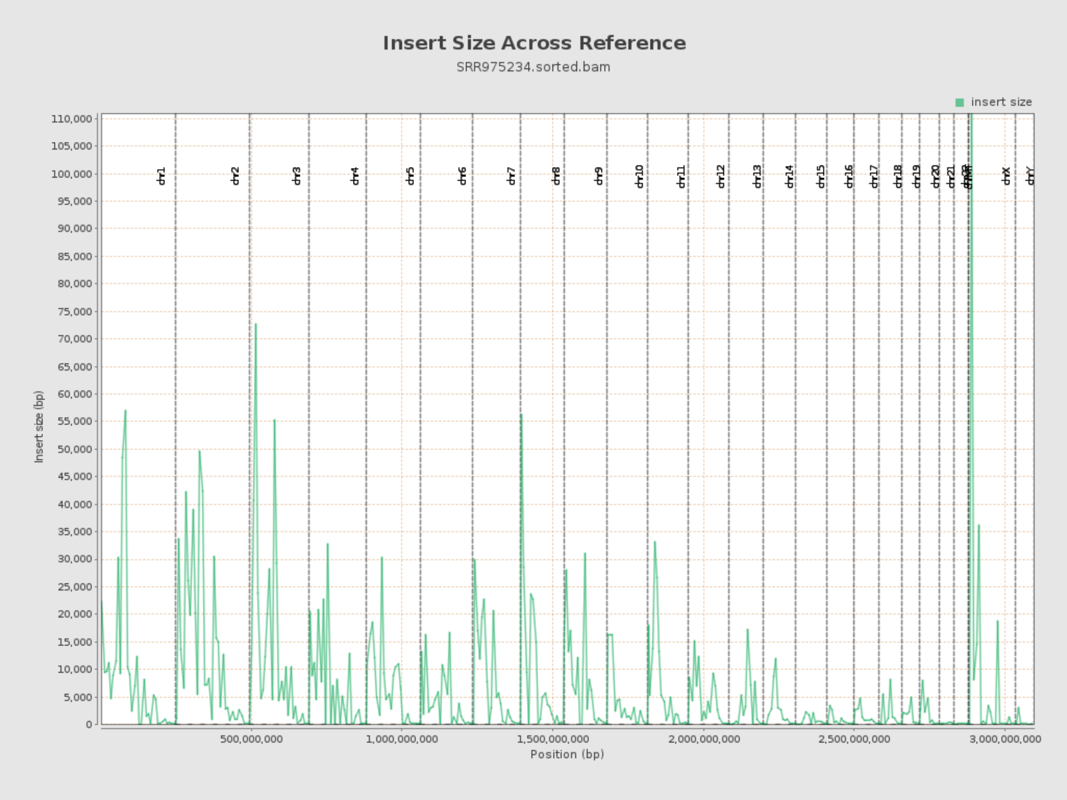
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram