Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 04:28:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975199.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_SRR975199 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975199_1.fastq.gz SRR975199_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 04:28:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975199.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,530,024
Mapped reads	2,503,957 / 98.97%
Unmapped reads	26,067 / 1.03%
Mapped paired reads	2,503,957 / 98.97%
Mapped reads, first in pair	1,253,717 / 49.55%
Mapped reads, second in pair	1,250,240 / 49.42%
Mapped reads, both in pair	2,495,600 / 98.64%
Mapped reads, singletons	8,357 / 0.33%
Secondary alignments	0
Supplementary alignments	22,966 / 0.91%
Read min/max/mean length	30 / 151 / 151.45
Duplicated reads (estimated)	376,162 / 14.87%
Duplication rate	14.51%
Clipped reads	1,823,286 / 72.07%

2.2. ACGT Content

Number/percentage of A's	100,092,676 / 29.28%
Number/percentage of C's	69,166,217 / 20.23%
Number/percentage of T's	100,689,875 / 29.45%
Number/percentage of G's	71,899,185 / 21.03%
Number/percentage of N's	18,963 / 0.01%

GC Percentage	41.26%

2.3. Coverage

Mean	0.1105
Standard Deviation	1.4167

2.4. Mapping Quality

Mean Mapping Quality	53.72

2.5. Insert size

Mean	72,158.15
Standard Deviation	2,567,769.26
P25/Median/P75	140 / 175 / 223

2.6. Mismatches and indels

General error rate	1.18%
Mismatches	3,906,550
Insertions	56,744
Mapped reads with at least one insertion	2.19%
Deletions	128,472
Mapped reads with at least one deletion	4.96%
Homopolymer indels	49.29%

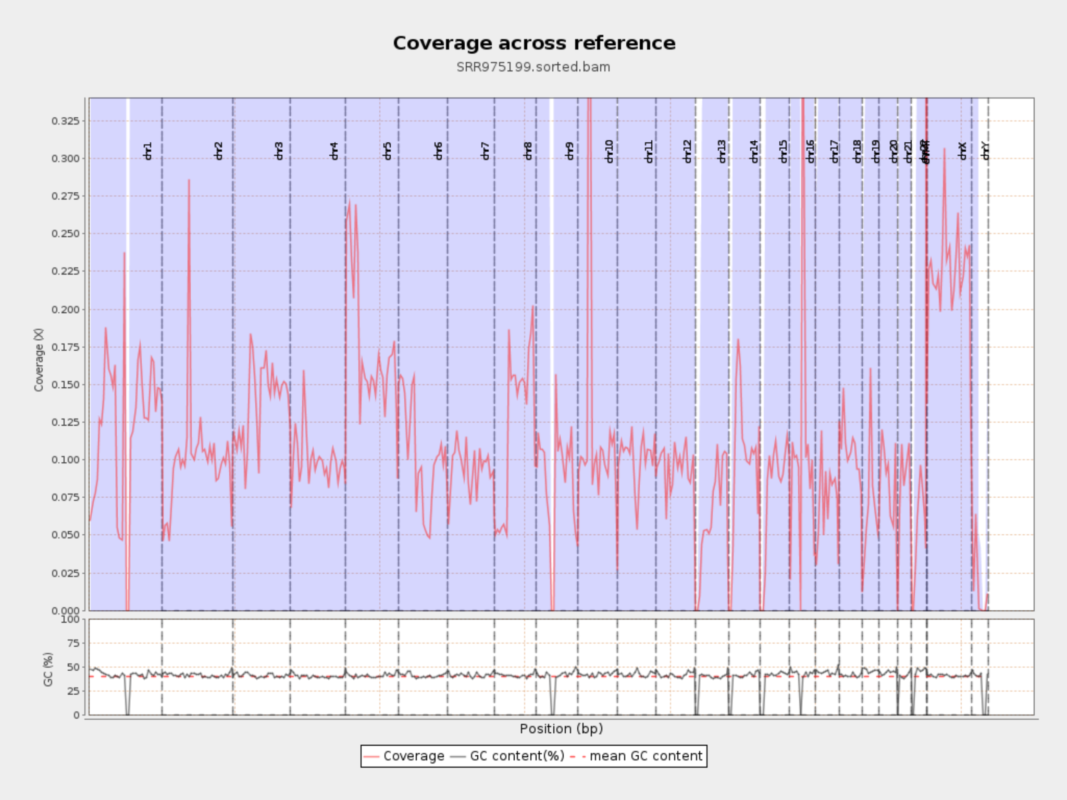
2.7. Chromosome stats

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

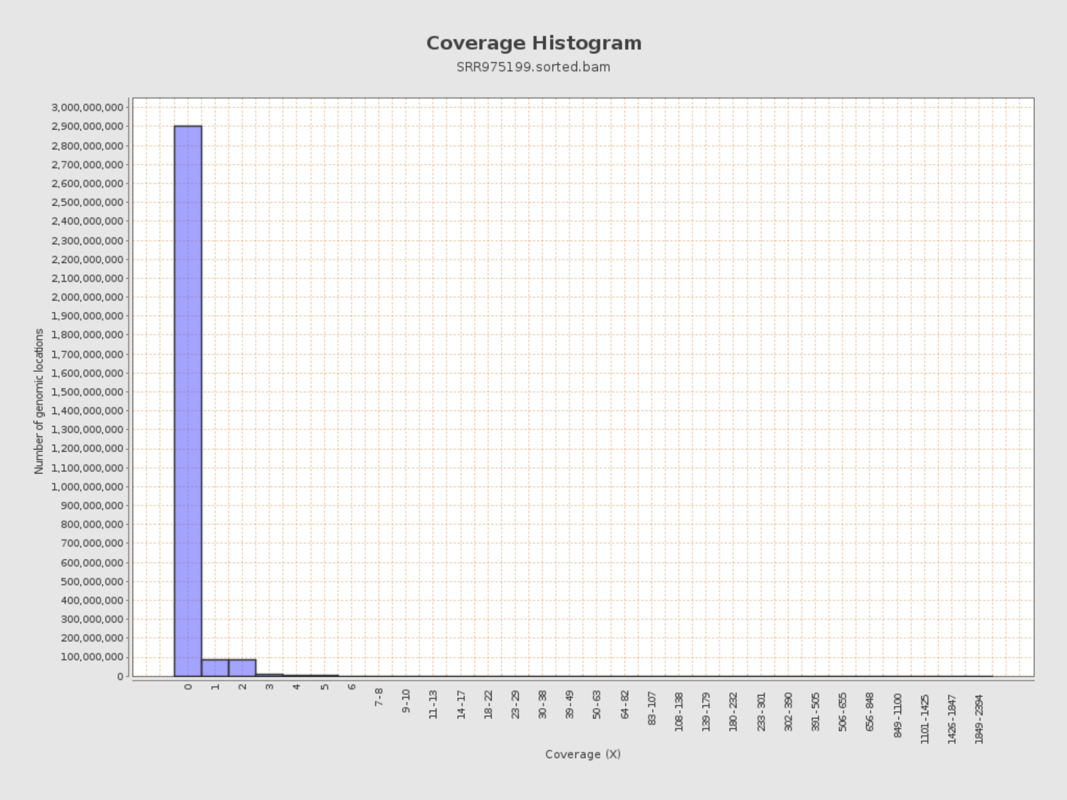
		bases	coverage	deviation
chr1	249250621	30347338	0.1218	1.9065
chr2	243199373	24466233	0.1006	1.2435
chr3	198022430	27436695	0.1386	0.5508
chr4	191154276	19078714	0.0998	0.6533
chr5	180915260	31849430	0.176	0.6059
chr6	171115067	17604295	0.1029	0.712
chr7	159138663	15130547	0.0951	0.8554
chr8	146364022	18214273	0.1244	0.6302
chr9	141213431	12403937	0.0878	1.7442
chr10	135534747	17004092	0.1255	4.5593
chr11	135006516	13473801	0.0998	0.9219
chr12	133851895	12710780	0.095	0.4298
chr13	115169878	7214653	0.0626	0.3465
chr14	107349540	10516469	0.098	0.4531
chr15	102531392	8068421	0.0787	0.392
chr16	90354753	9901721	0.1096	2.1183
chr17	81195210	5856236	0.0721	1.1727
chr18	78077248	8446581	0.1082	1.6615
chr19	59128983	4199313	0.071	1.0359
chr20	63025520	5594131	0.0888	0.4559
chr21	48129895	3901835	0.0811	0.4963
chr22	51304566	2628286	0.0512	0.3184
chrMT	16571	25347	1.5296	1.743
chrX	155270560	35110250	0.2261	0.9493

chrY	59373566	905658	0.0153	0.9402

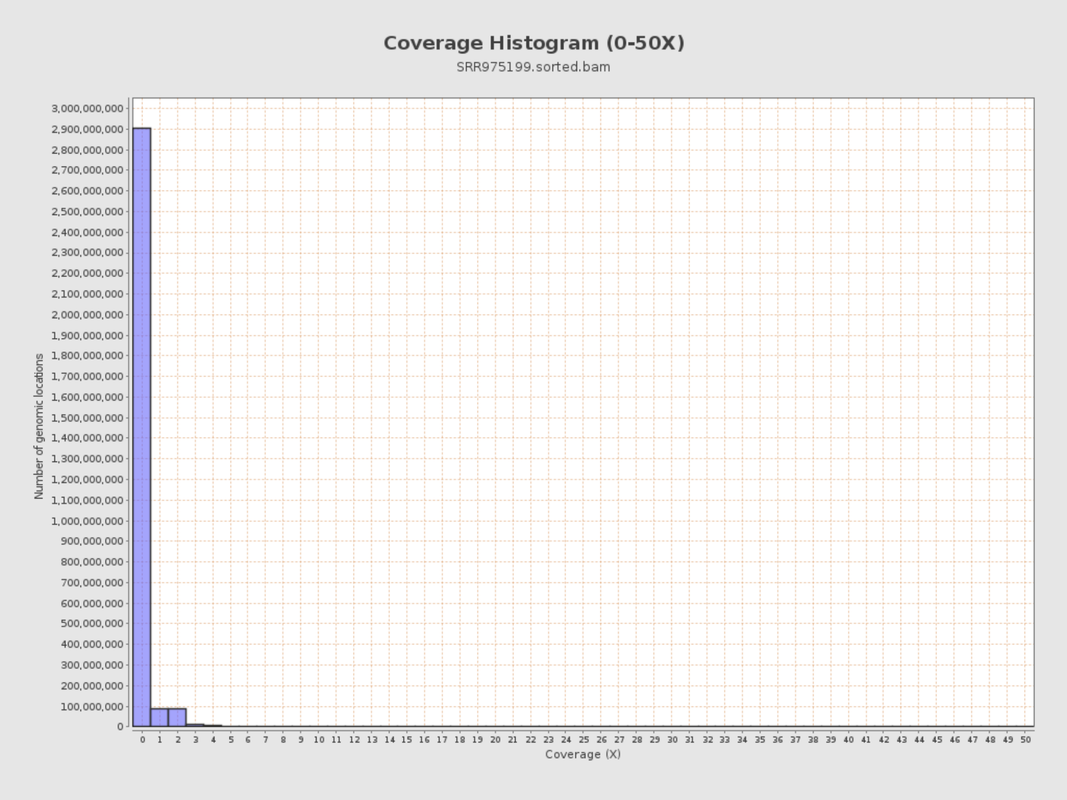
3. Results : Coverage across reference



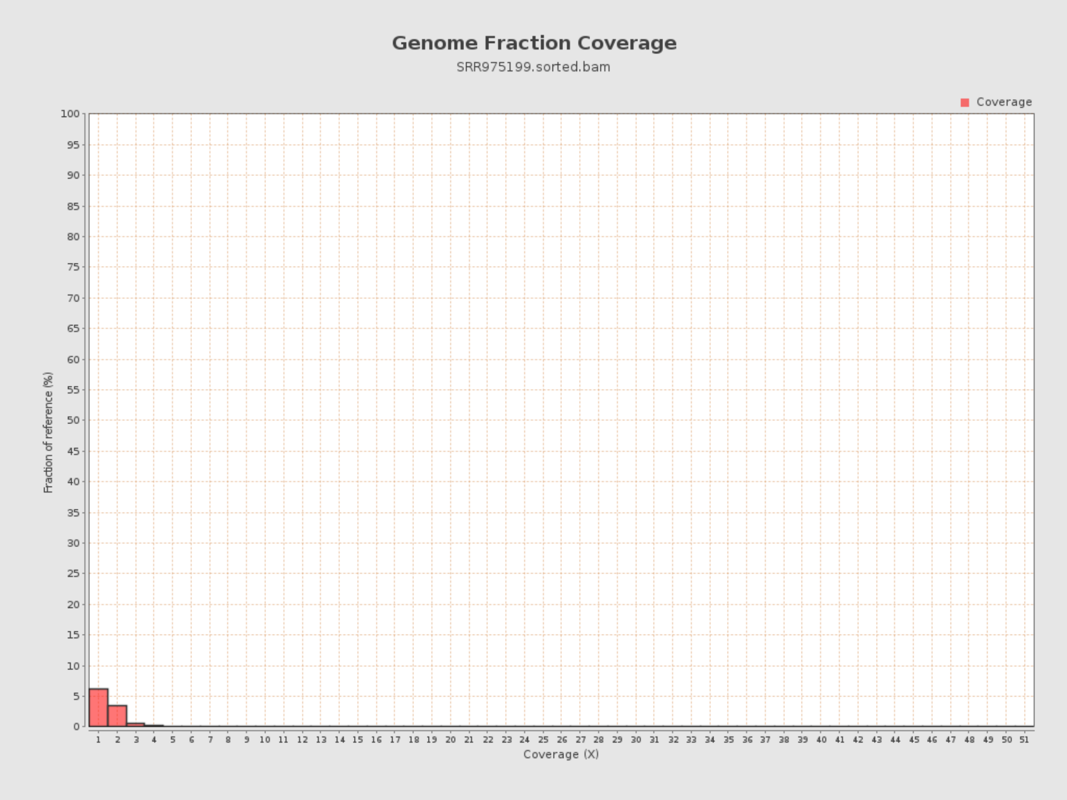
4. Results : Coverage Histogram



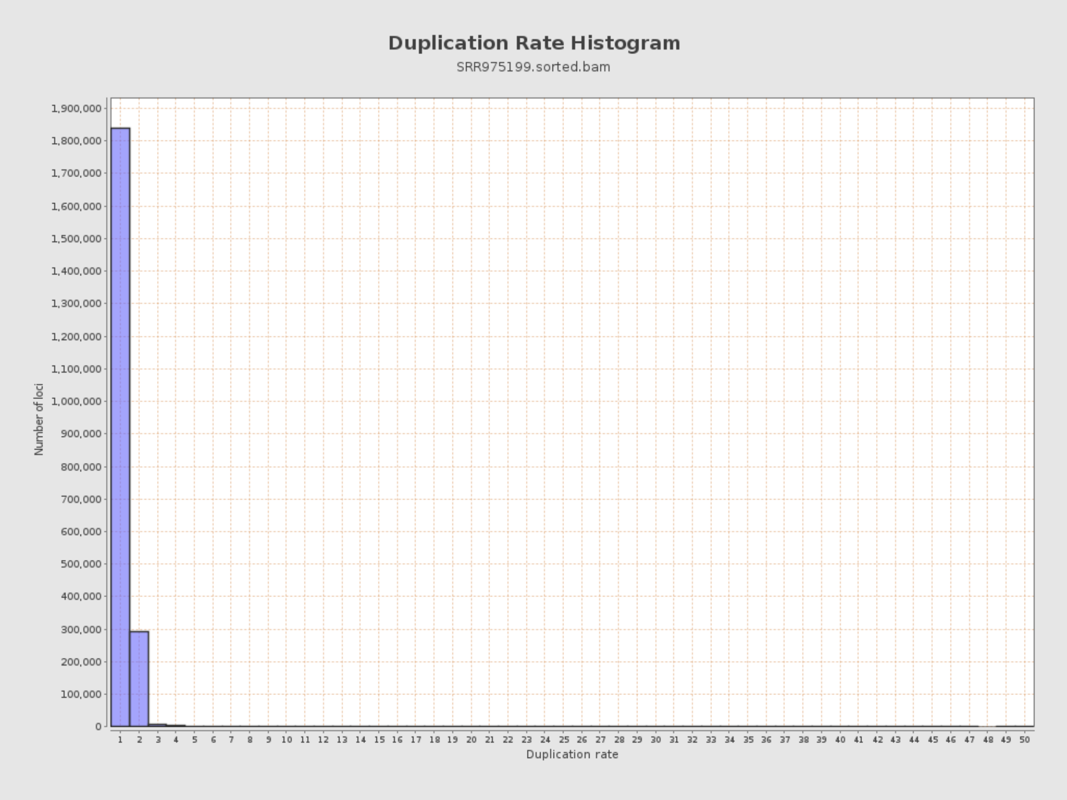
5. Results : Coverage Histogram (0-50X)



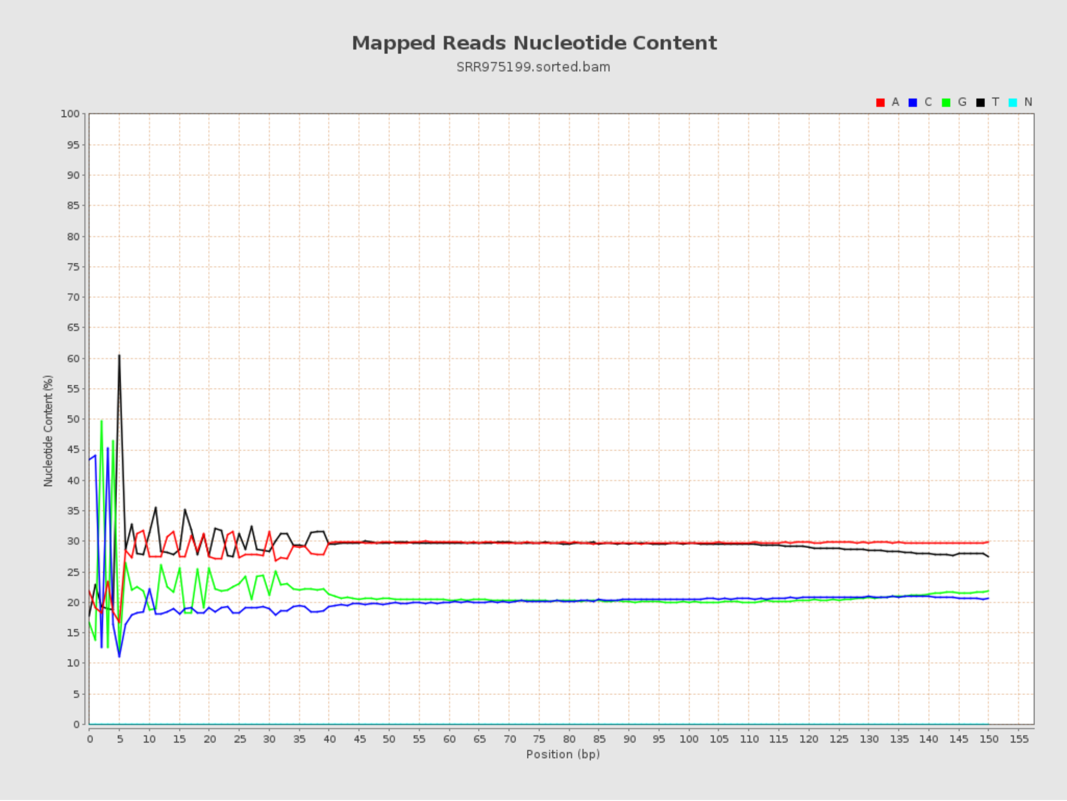
6. Results : Genome Fraction Coverage



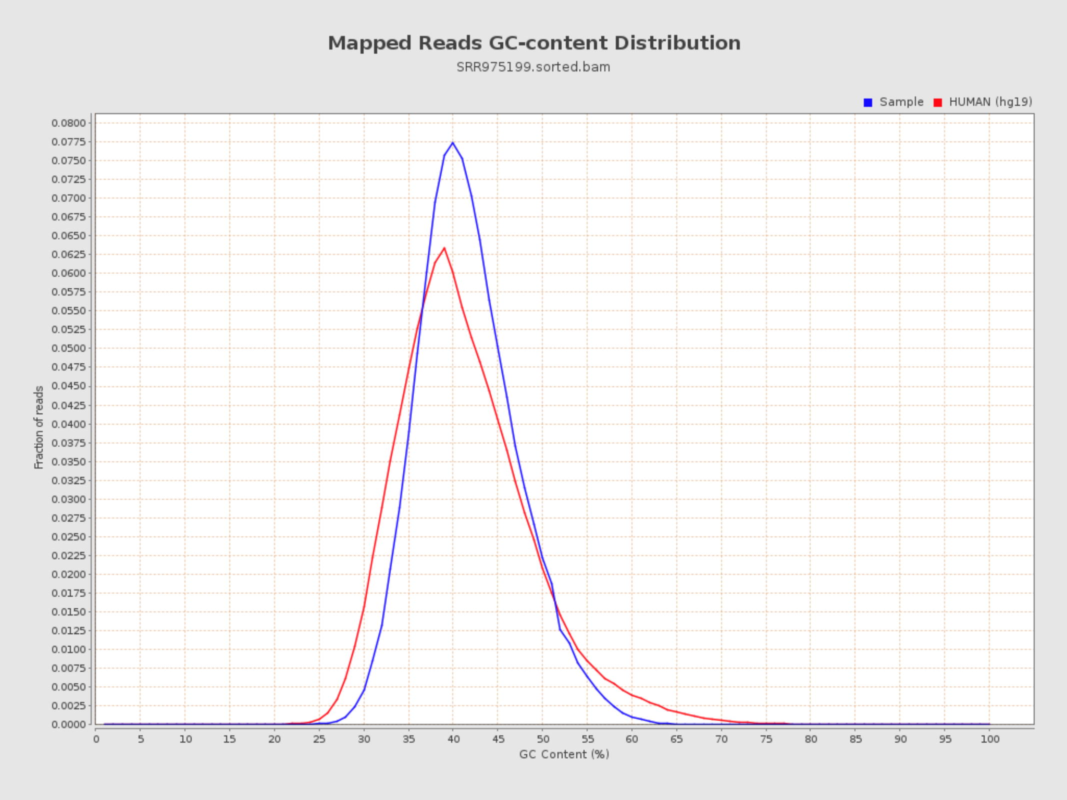
7. Results : Duplication Rate Histogram



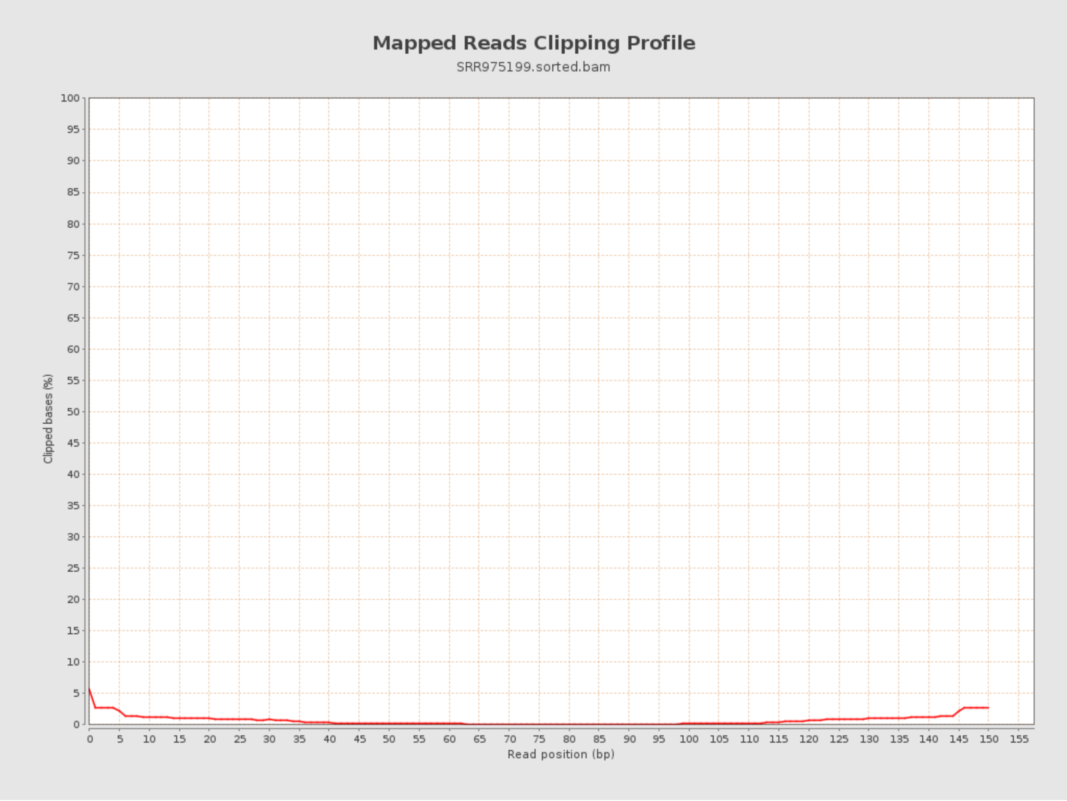
8. Results : Mapped Reads Nucleotide Content



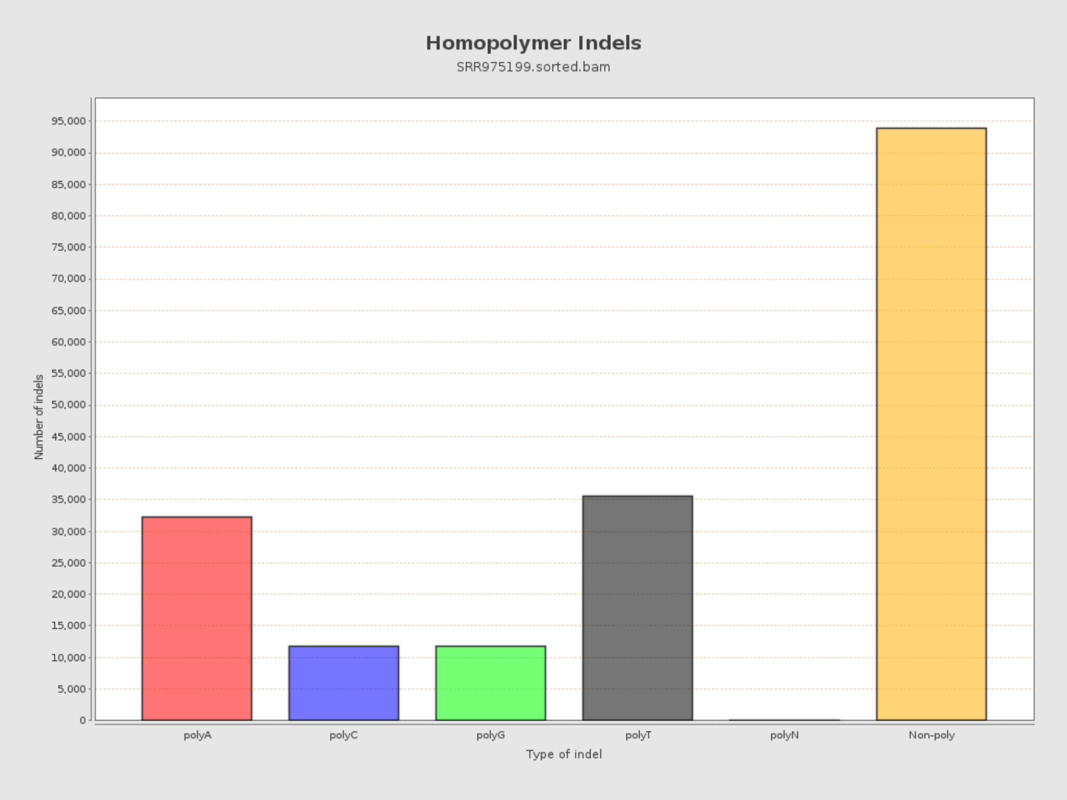
9. Results : Mapped Reads GC-content Distribution



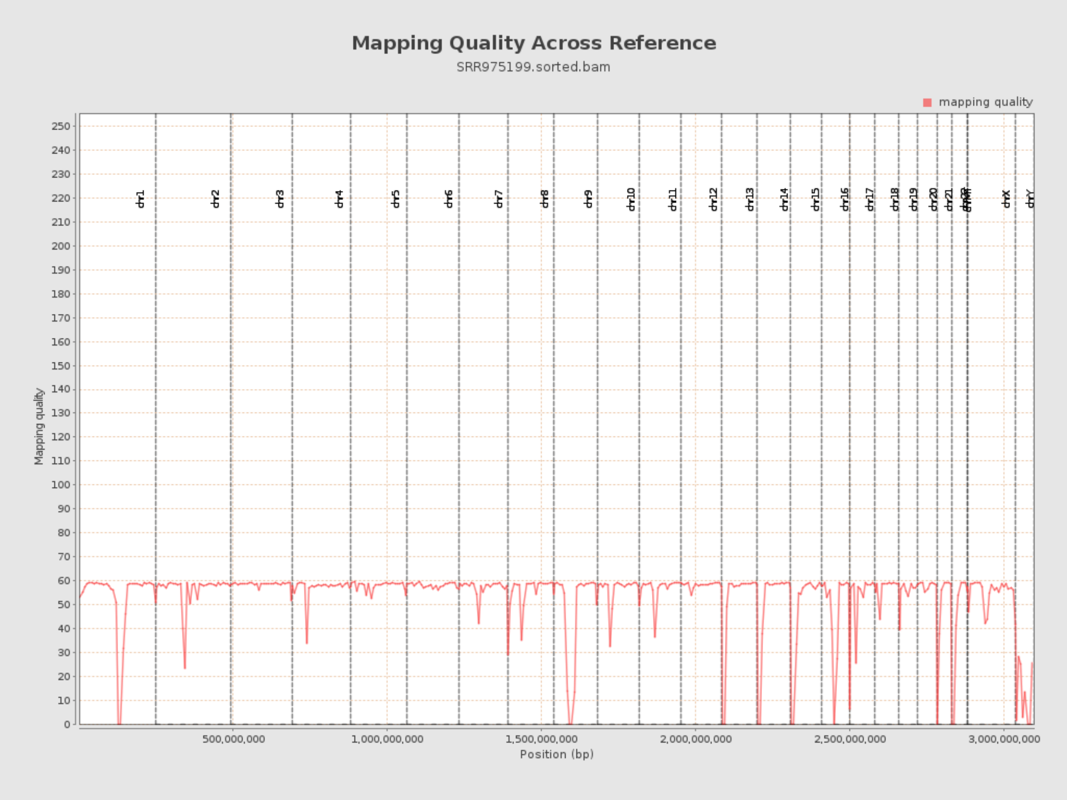
10. Results : Mapped Reads Clipping Profile



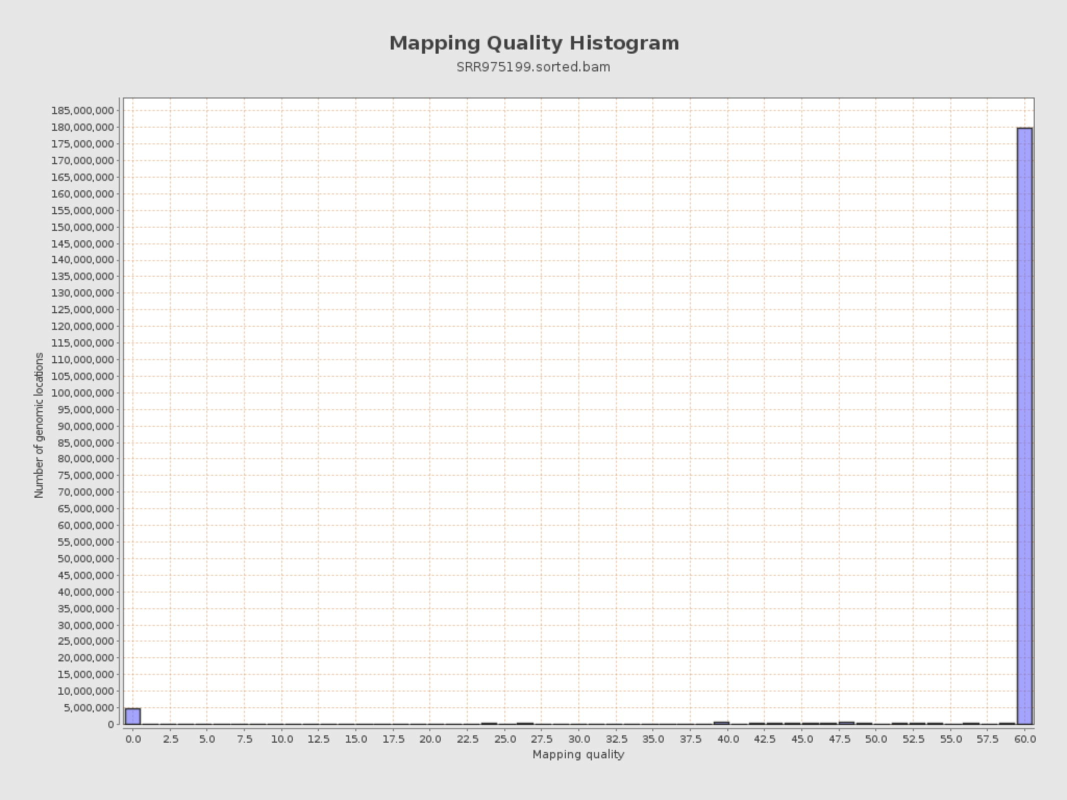
11. Results : Homopolymer Indels



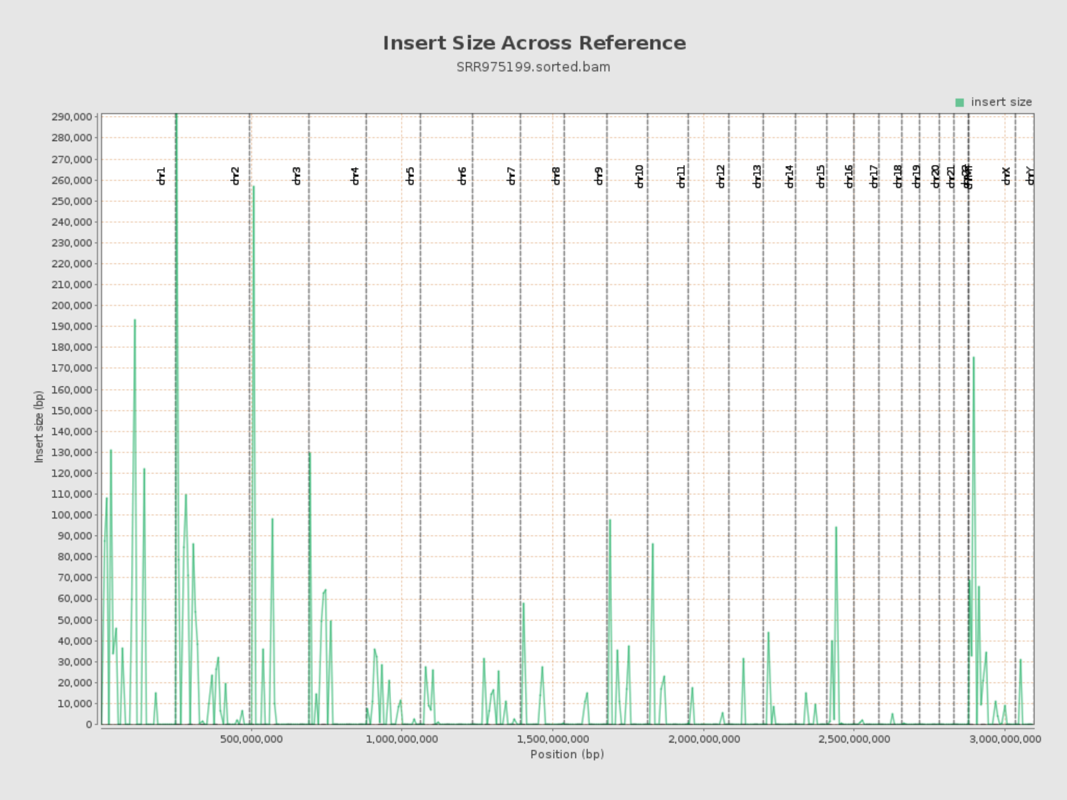
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram