Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/05 01:03:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124822.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_SRR3124822 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124822_1.fastq.gz SRR3124822_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Dec 05 01:03:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124822.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	29,890,158
Mapped reads	28,381,380 / 94.95%
Unmapped reads	1,508,778 / 5.05%
Mapped paired reads	28,381,380 / 94.95%
Mapped reads, first in pair	14,524,865 / 48.59%
Mapped reads, second in pair	13,856,515 / 46.36%
Mapped reads, both in pair	27,579,718 / 92.27%
Mapped reads, singletons	801,662 / 2.68%
Secondary alignments	0
Supplementary alignments	92,361 / 0.31%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	5,811,889 / 19.44%
Duplication rate	12.97%
Clipped reads	13,370,648 / 44.73%

2.2. ACGT Content

Number/percentage of A's	492,698,668 / 27.89%
Number/percentage of C's	314,931,782 / 17.83%
Number/percentage of T's	534,253,561 / 30.25%
Number/percentage of G's	424,420,761 / 24.03%
Number/percentage of N's	35 / 0%

GC Percentage	41.86%

2.3. Coverage

Mean	0.5708
Standard Deviation	4.7868

2.4. Mapping Quality

Mean Mapping Quality	51.48

2.5. Insert size

Mean	98,569.47
Standard Deviation	3,021,362.87
P25/Median/P75	133 / 176 / 237

2.6. Mismatches and indels

General error rate	0.85%
Mismatches	14,600,951
Insertions	197,591
Mapped reads with at least one insertion	0.69%
Deletions	524,501
Mapped reads with at least one deletion	1.83%
Homopolymer indels	48.5%

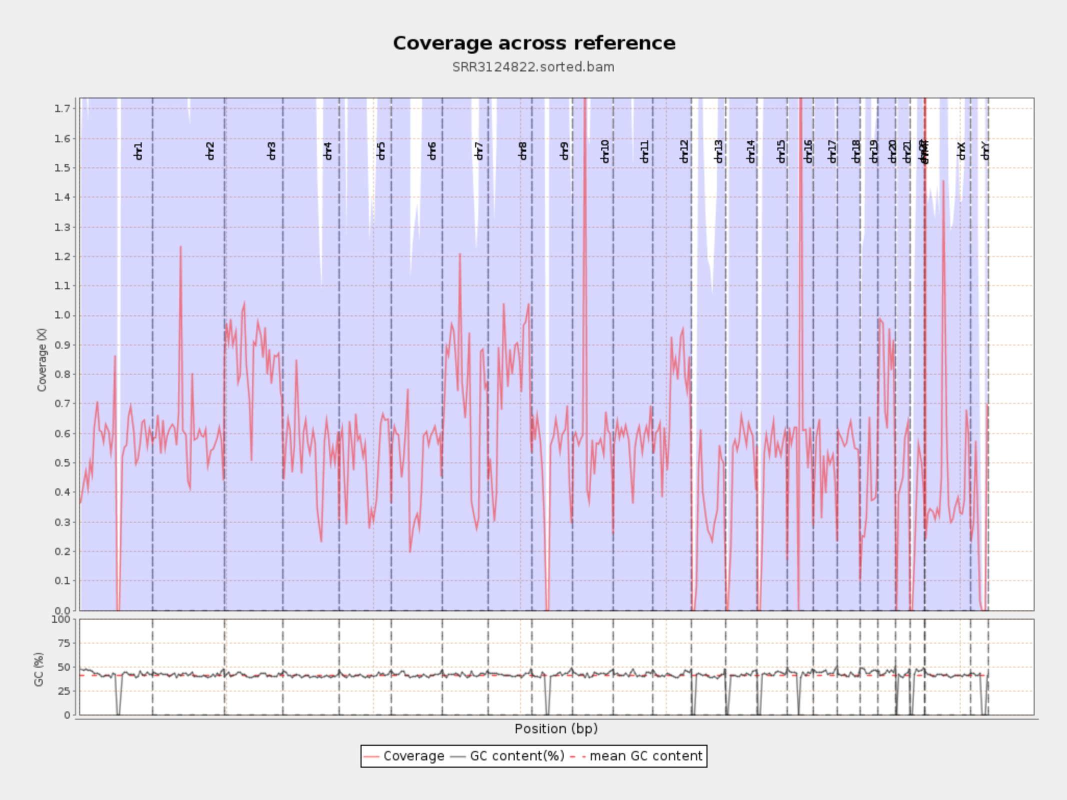
2.7. Chromosome stats

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

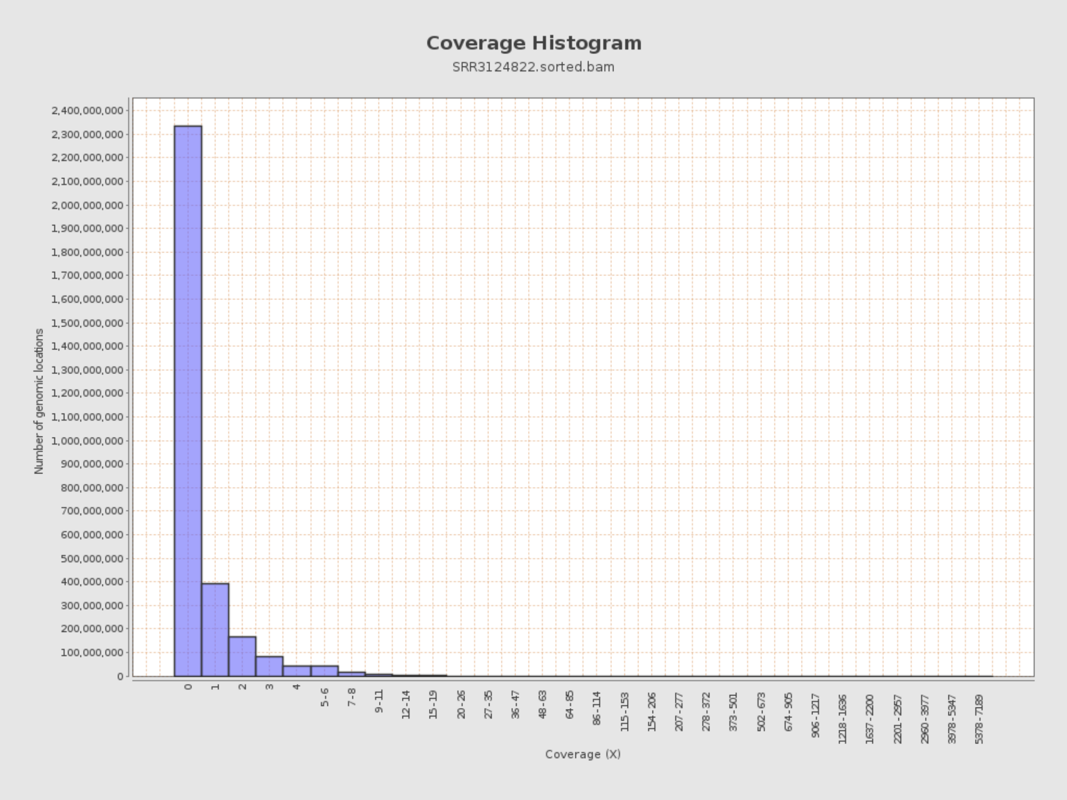
		bases	coverage	deviation
chr1	249250621	134220693	0.5385	4.7463
chr2	243199373	147015463	0.6045	4.9076
chr3	198022430	171649454	0.8668	2.0399
chr4	191154276	103747599	0.5427	2.1049
chr5	180915260	93040229	0.5143	1.4094
chr6	171115067	87258132	0.5099	3.4048
chr7	159138663	117564794	0.7388	9.3094
chr8	146364022	111924614	0.7647	2.5331
chr9	141213431	69107339	0.4894	3.7372
chr10	135534747	85493032	0.6308	11.2828
chr11	135006516	77418443	0.5734	3.2143
chr12	133851895	94894388	0.709	1.7319
chr13	115169878	38188266	0.3316	1.0515
chr14	107349540	51098332	0.476	1.8059
chr15	102531392	47428647	0.4626	1.5634
chr16	90354753	58851924	0.6513	11.4837
chr17	81195210	38621004	0.4757	3.9145
chr18	78077248	45167435	0.5785	5.3447
chr19	59128983	21379134	0.3616	4.2514
chr20	63025520	51550743	0.8179	1.9782
chr21	48129895	20877156	0.4338	1.674
chr22	51304566	16073799	0.3133	1.145
chrMT	16571	625244	37.7312	22.1327
chrX	155270560	67829732	0.4368	2.5188

chrY	59373566	16052478	0.2704	4.0641

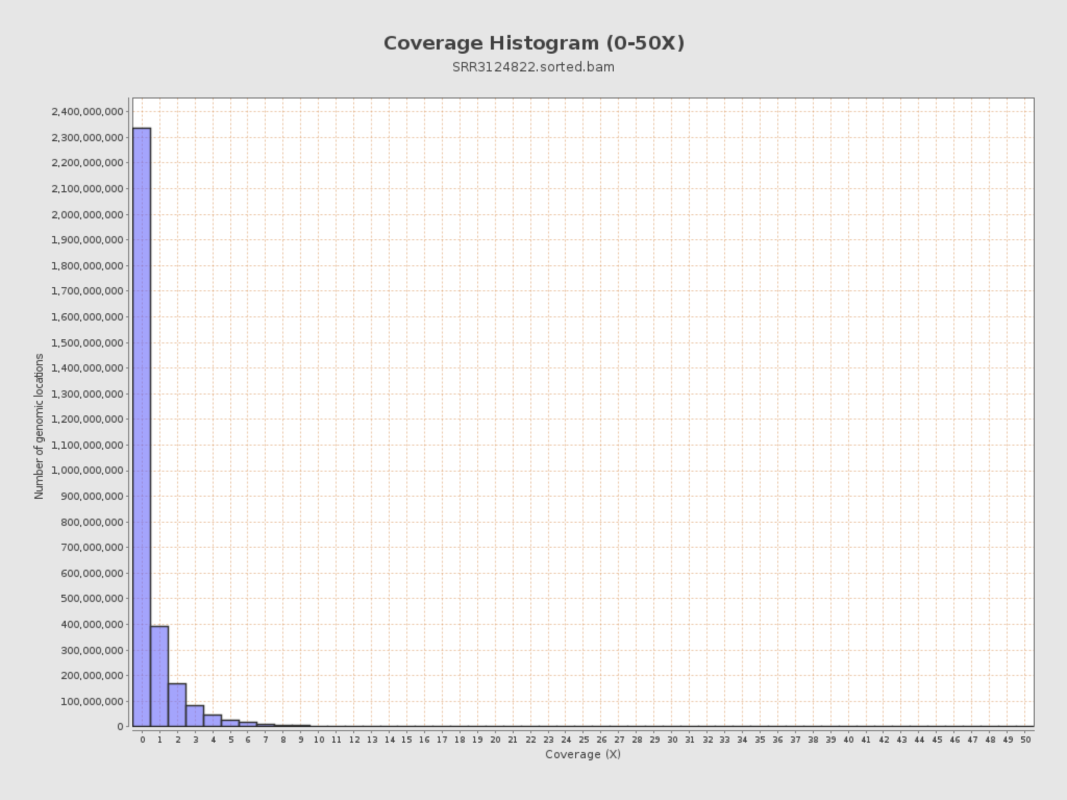
3. Results : Coverage across reference



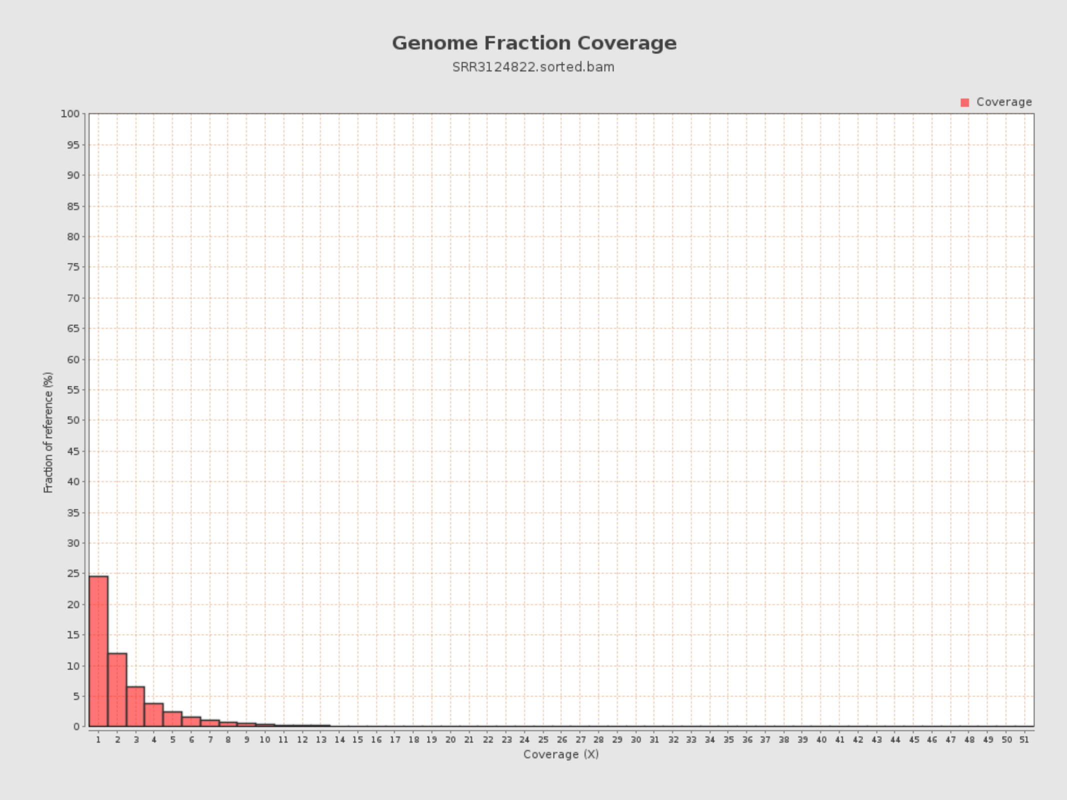
4. Results : Coverage Histogram



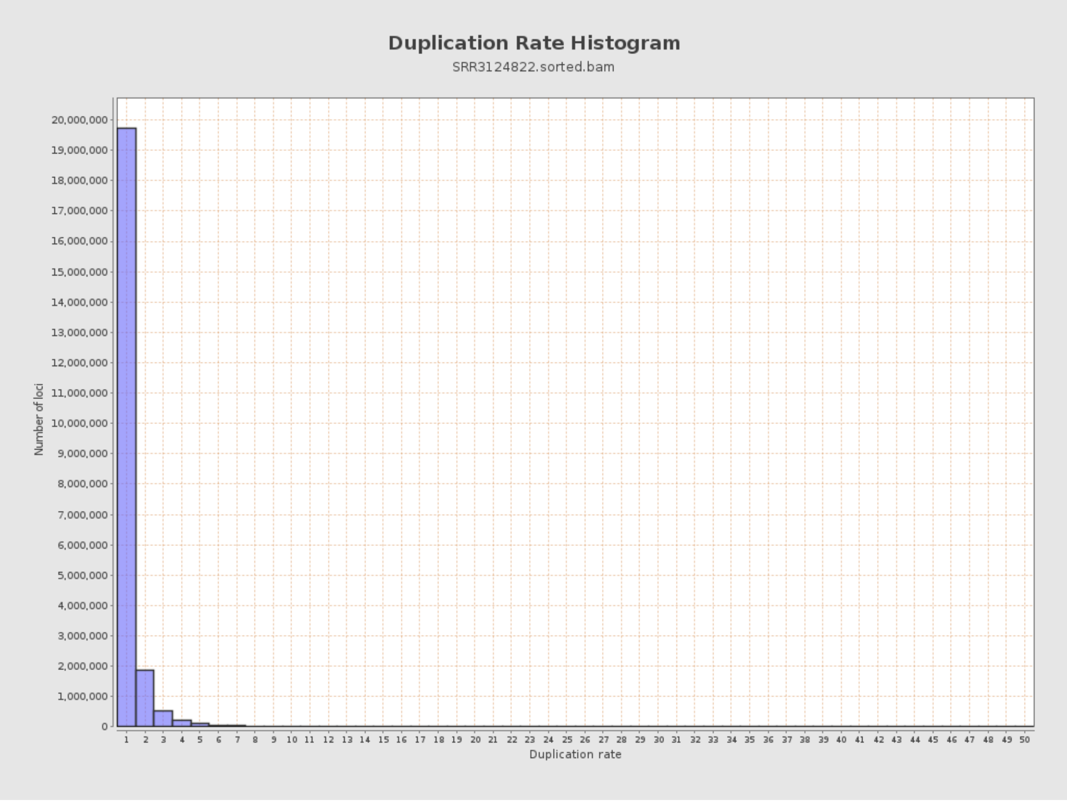
5. Results : Coverage Histogram (0-50X)



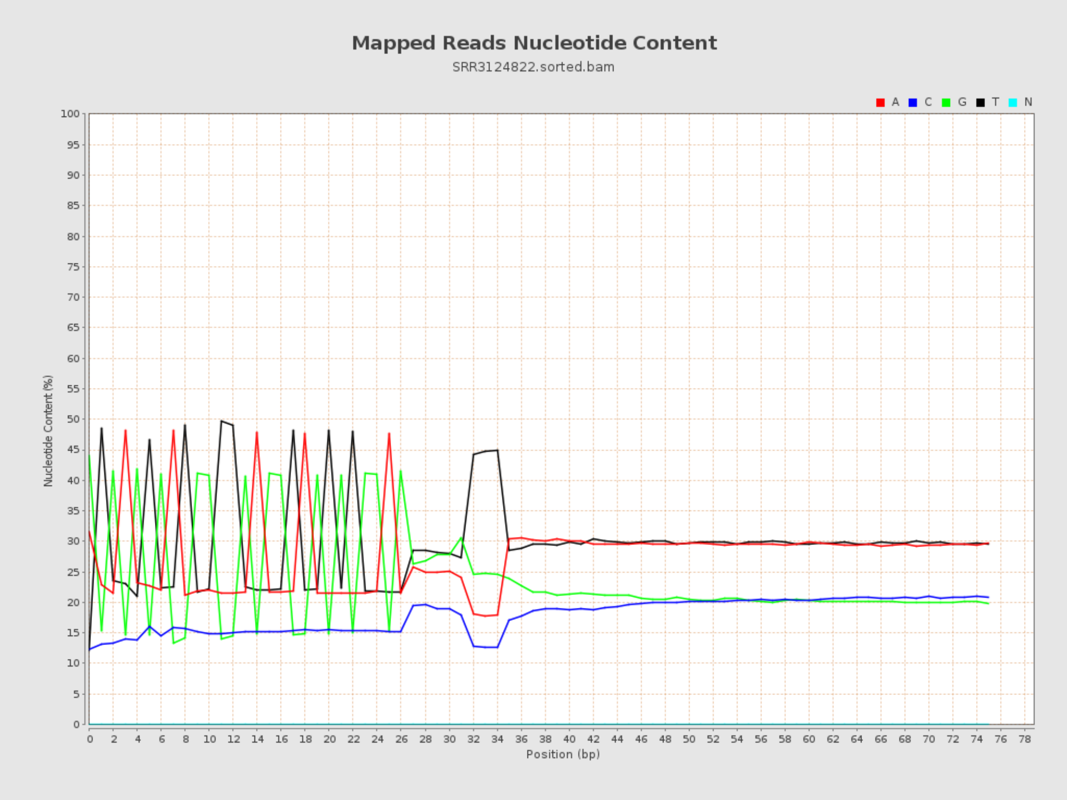
6. Results : Genome Fraction Coverage



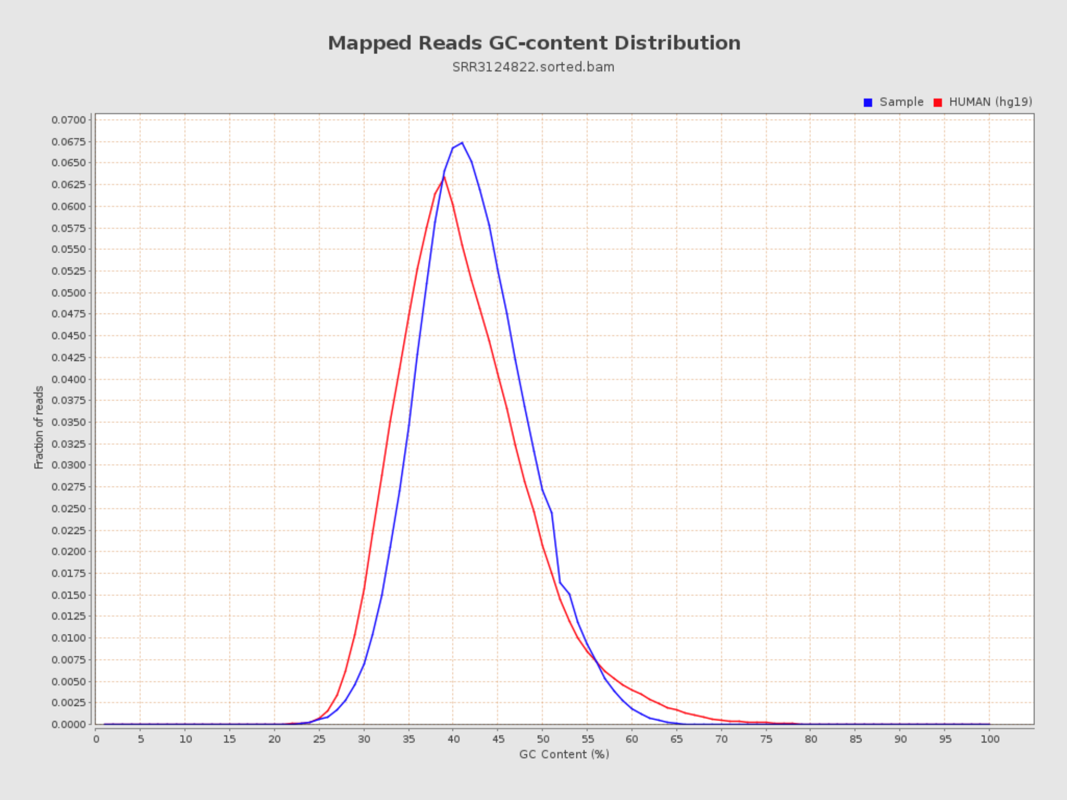
7. Results : Duplication Rate Histogram



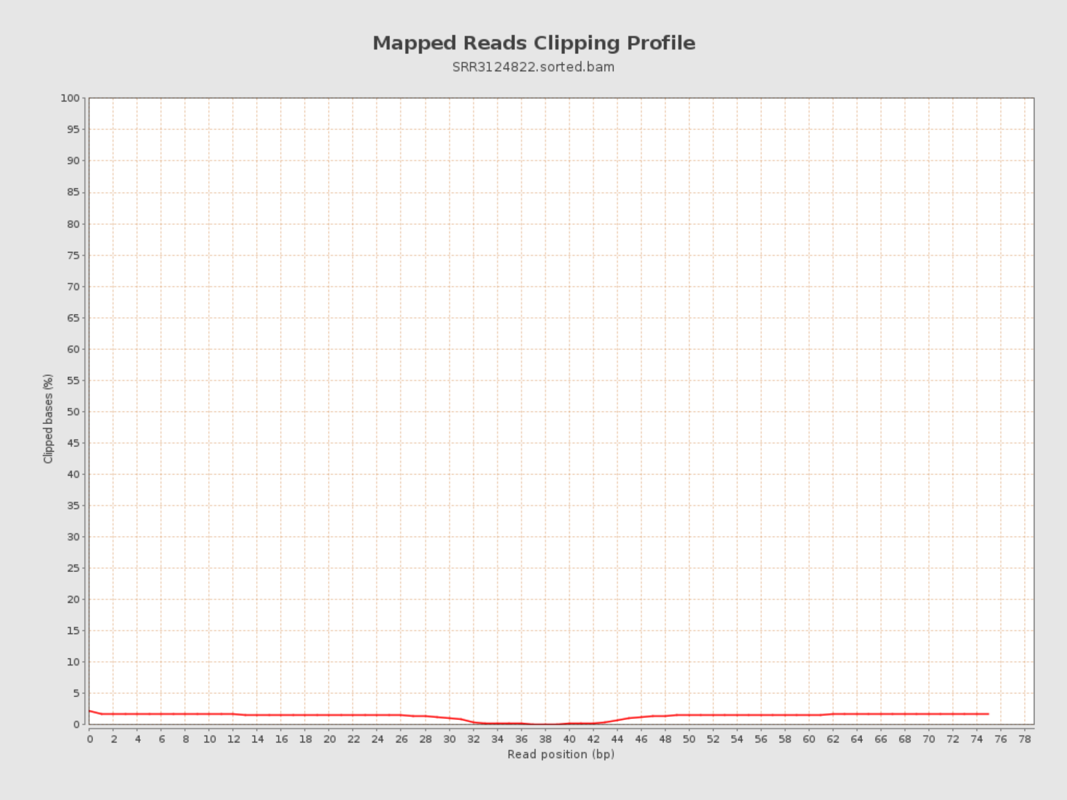
8. Results : Mapped Reads Nucleotide Content



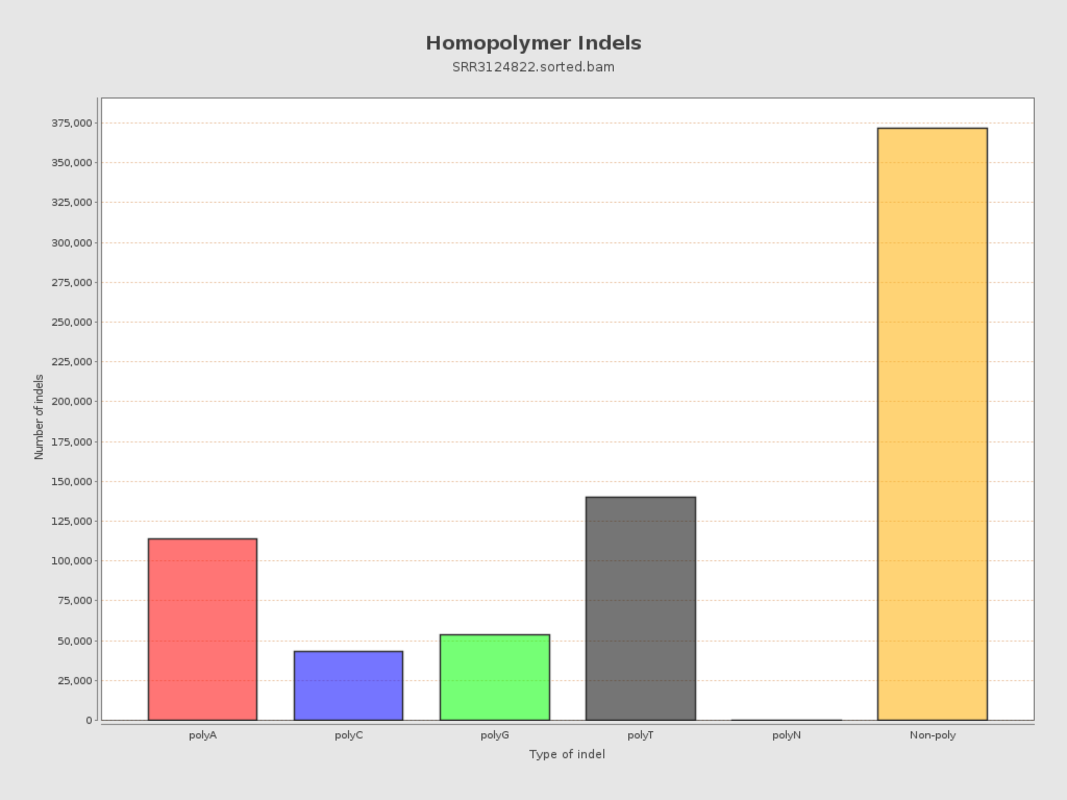
9. Results : Mapped Reads GC-content Distribution



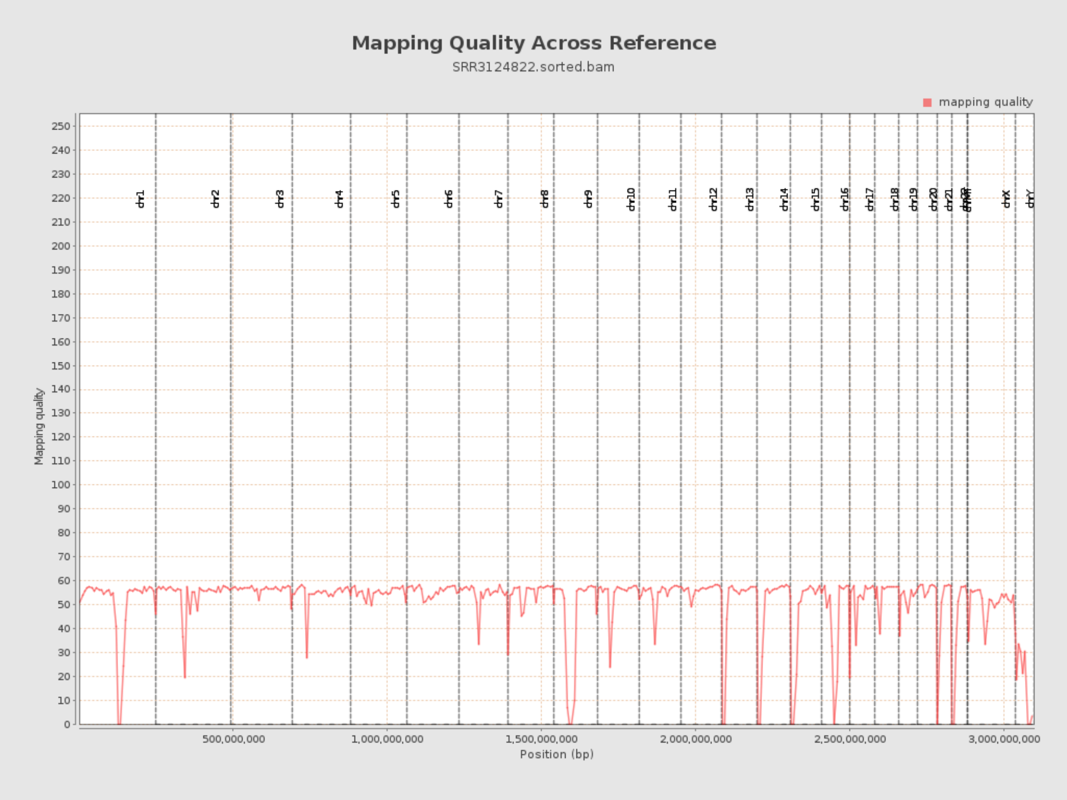
10. Results : Mapped Reads Clipping Profile



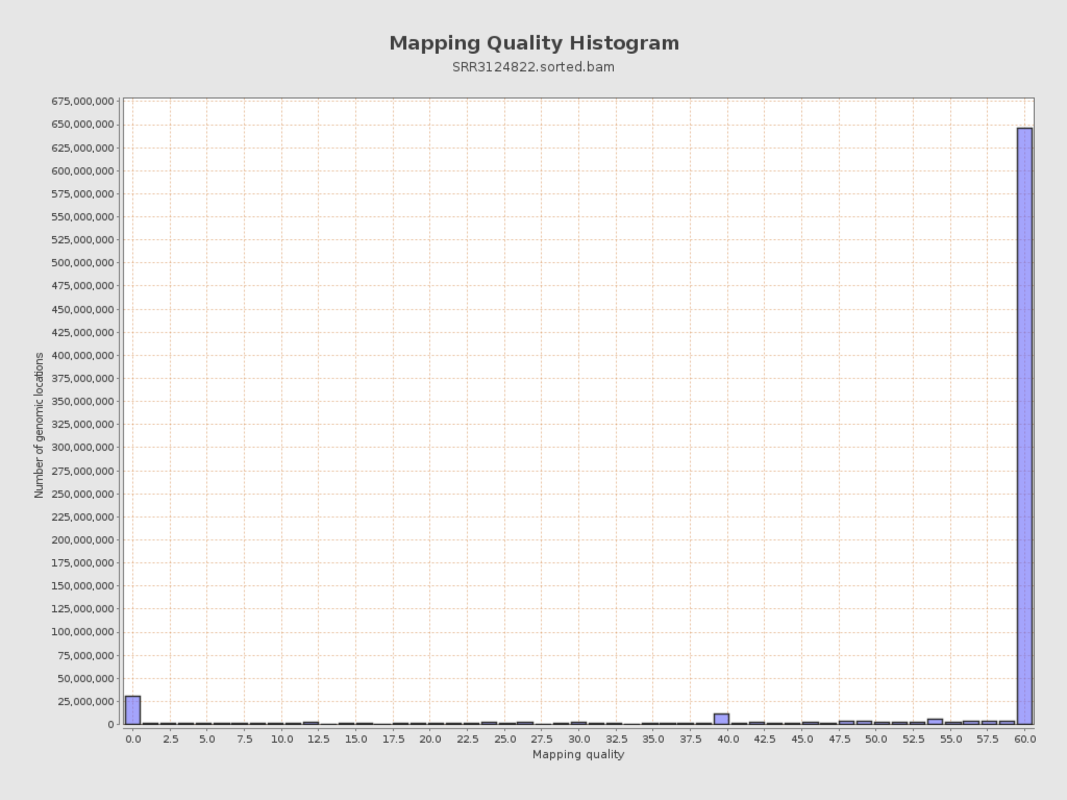
11. Results : Homopolymer Indels



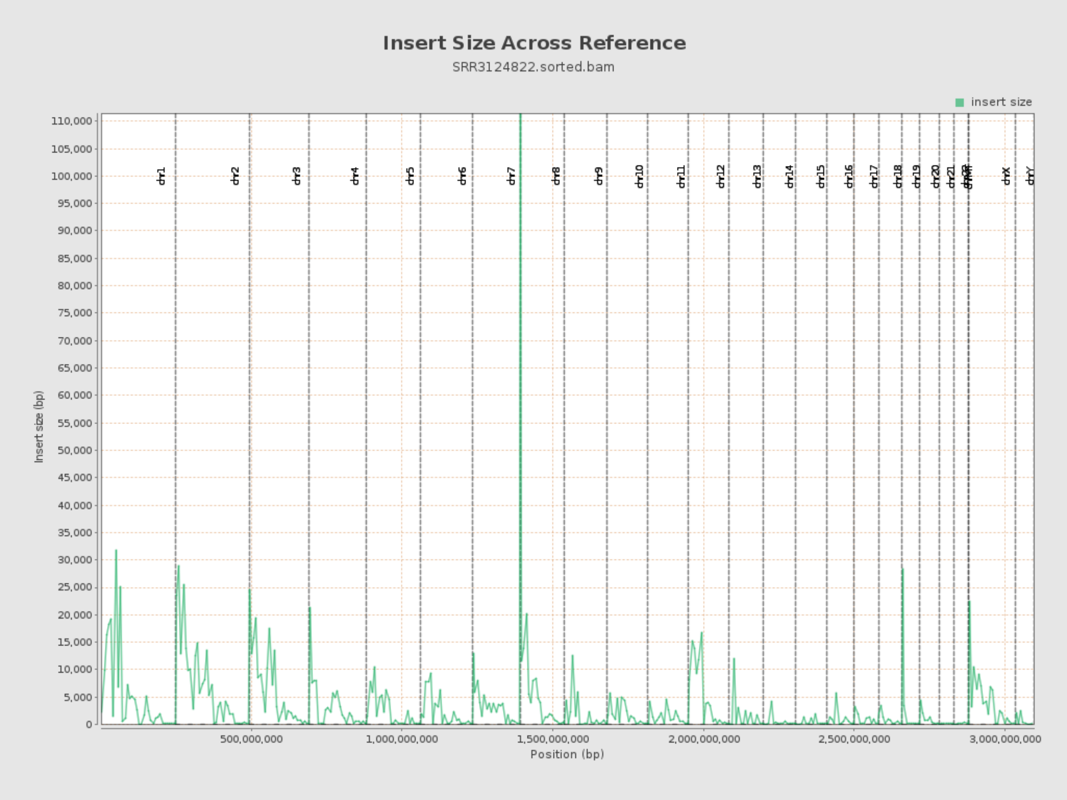
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram