Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 02:51:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124900.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_SRR3124900 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124900_1.fastq.gz SRR3124900_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 02:51:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124900.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,859,862
Mapped reads	6,772,848 / 98.73%
Unmapped reads	87,014 / 1.27%
Mapped paired reads	6,772,848 / 98.73%
Mapped reads, first in pair	3,392,988 / 49.46%
Mapped reads, second in pair	3,379,860 / 49.27%
Mapped reads, both in pair	6,745,632 / 98.33%
Mapped reads, singletons	27,216 / 0.4%
Secondary alignments	0
Supplementary alignments	31,964 / 0.47%
Read min/max/mean length	30 / 101 / 101.18
Duplicated reads (estimated)	560,426 / 8.17%
Duplication rate	5.74%
Clipped reads	3,285,375 / 47.89%

2.2. ACGT Content

Number/percentage of A's	165,299,733 / 28.18%
Number/percentage of C's	109,172,247 / 18.61%
Number/percentage of T's	175,296,729 / 29.88%
Number/percentage of G's	136,887,181 / 23.33%
Number/percentage of N's	8,303 / 0%

GC Percentage	41.94%

2.3. Coverage

Mean	0.1896
Standard Deviation	1.6914

2.4. Mapping Quality

Mean Mapping Quality	52.76

2.5. Insert size

Mean	41,901.85
Standard Deviation	1,942,396.24
P25/Median/P75	142 / 196 / 278

2.6. Mismatches and indels

General error rate	0.78%
Mismatches	4,400,500
Insertions	78,424
Mapped reads with at least one insertion	1.13%
Deletions	196,555
Mapped reads with at least one deletion	2.85%
Homopolymer indels	47.7%

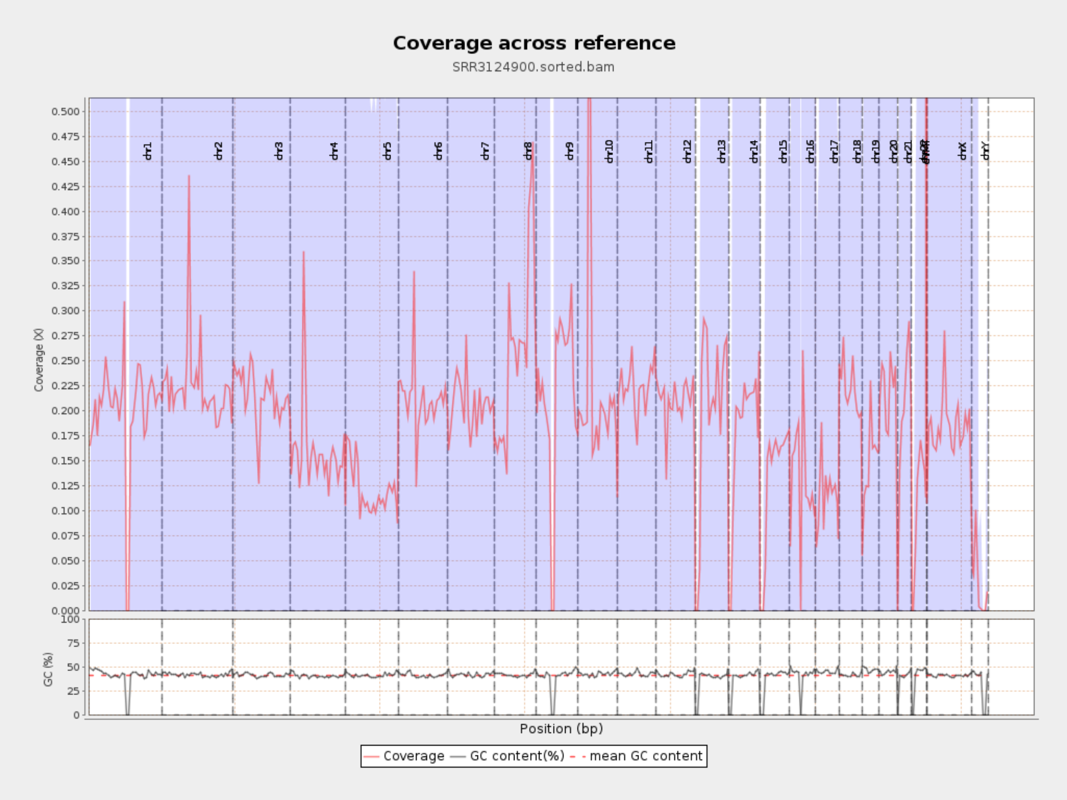
2.7. Chromosome stats

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

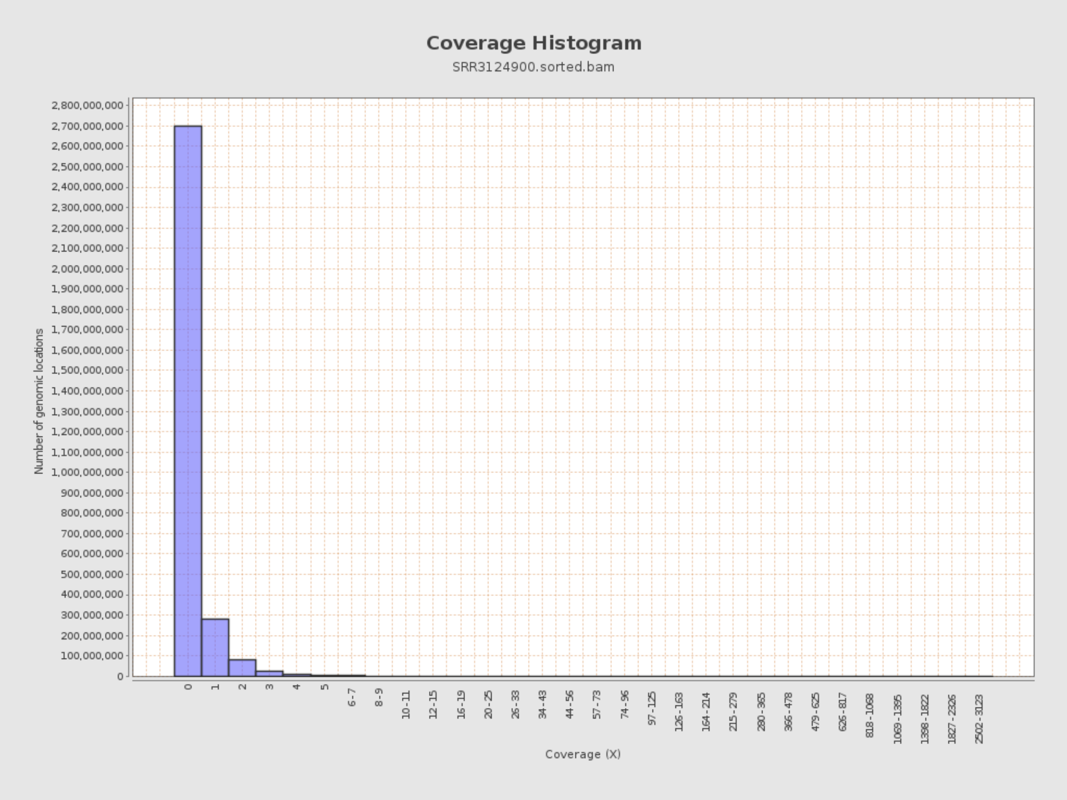
		bases	coverage	deviation
chr1	249250621	49884276	0.2001	1.594
chr2	243199373	54917315	0.2258	1.7956
chr3	198022430	42762997	0.216	0.6303
chr4	191154276	30220517	0.1581	1.2599
chr5	180915260	21840406	0.1207	0.4594
chr6	171115067	36316426	0.2122	1.6382
chr7	159138663	32895028	0.2067	2.1272
chr8	146364022	38443669	0.2627	0.9374
chr9	141213431	30803664	0.2181	2.0947
chr10	135534747	30093453	0.222	4.7888
chr11	135006516	29930562	0.2217	2.025
chr12	133851895	27963384	0.2089	0.6089
chr13	115169878	22713451	0.1972	0.5963
chr14	107349540	18729349	0.1745	0.6328
chr15	102531392	13518854	0.1319	0.4881
chr16	90354753	11853897	0.1312	1.3833
chr17	81195210	9180611	0.1131	1.5094
chr18	78077248	17472492	0.2238	2.5845
chr19	59128983	8863763	0.1499	0.9609
chr20	63025520	13763636	0.2184	0.6936
chr21	48129895	9372742	0.1947	0.8191
chr22	51304566	5285604	0.103	0.4462
chrMT	16571	127945	7.721	5.1686
chrX	155270560	28584098	0.1841	0.9877

chrY	59373566	1449162	0.0244	1.3333

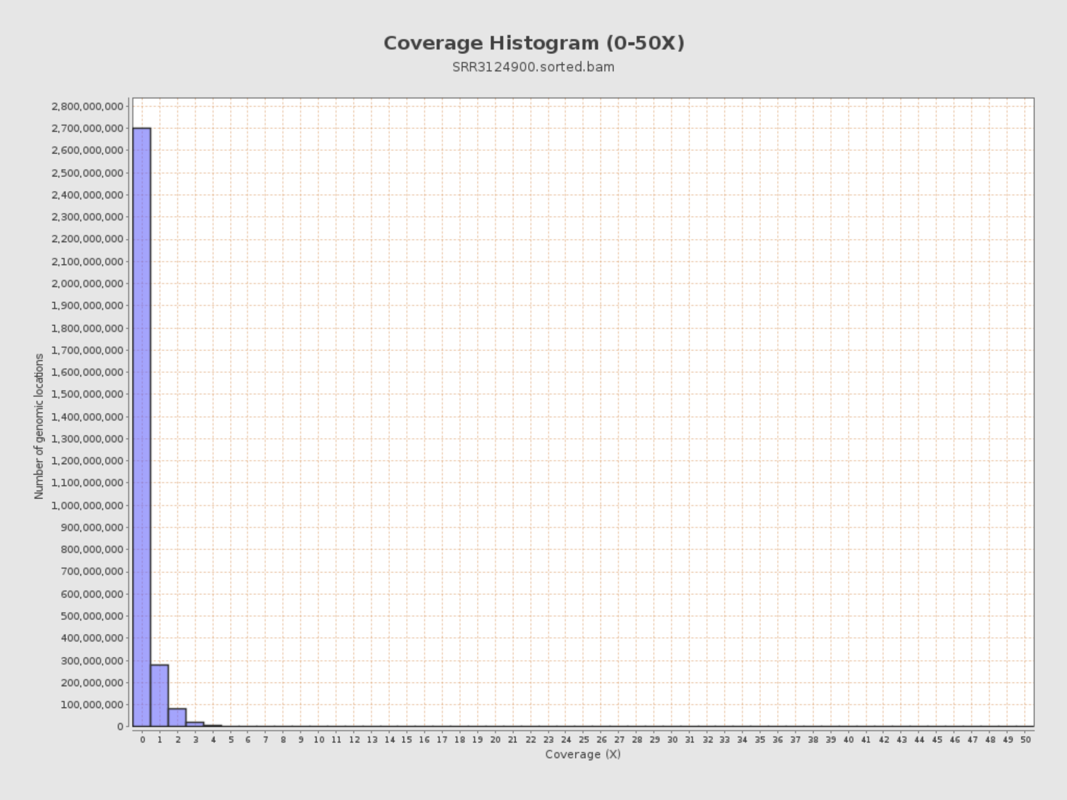
3. Results : Coverage across reference



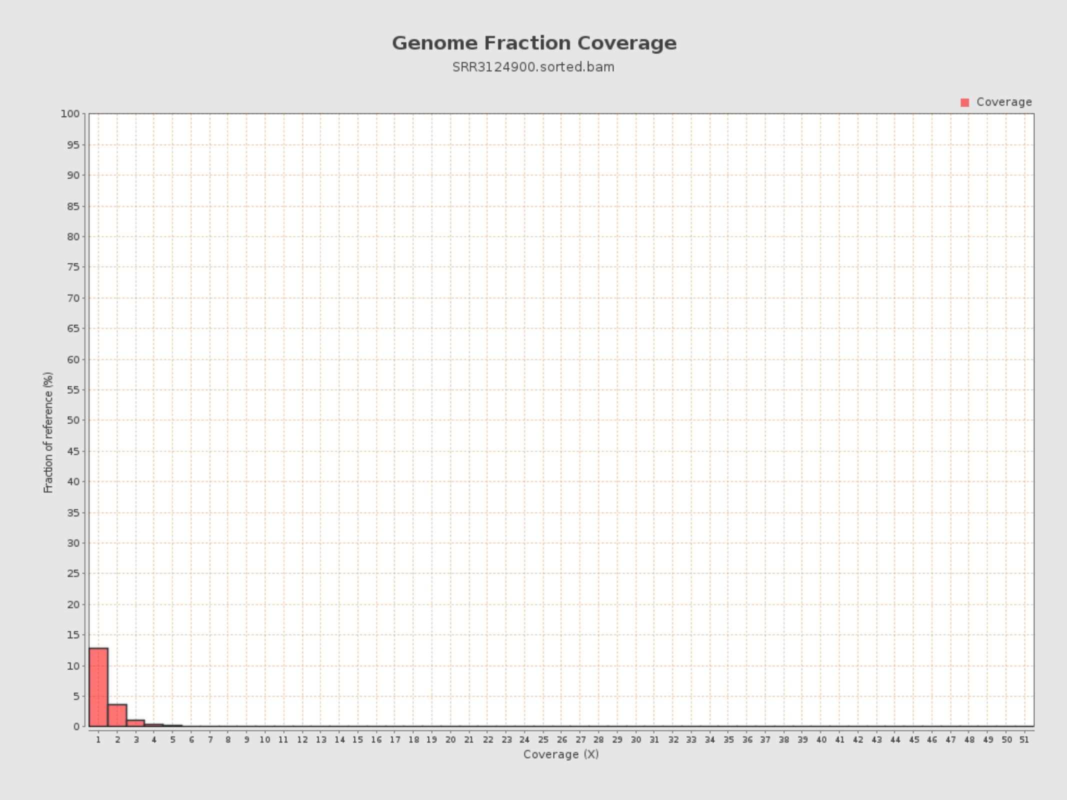
4. Results : Coverage Histogram



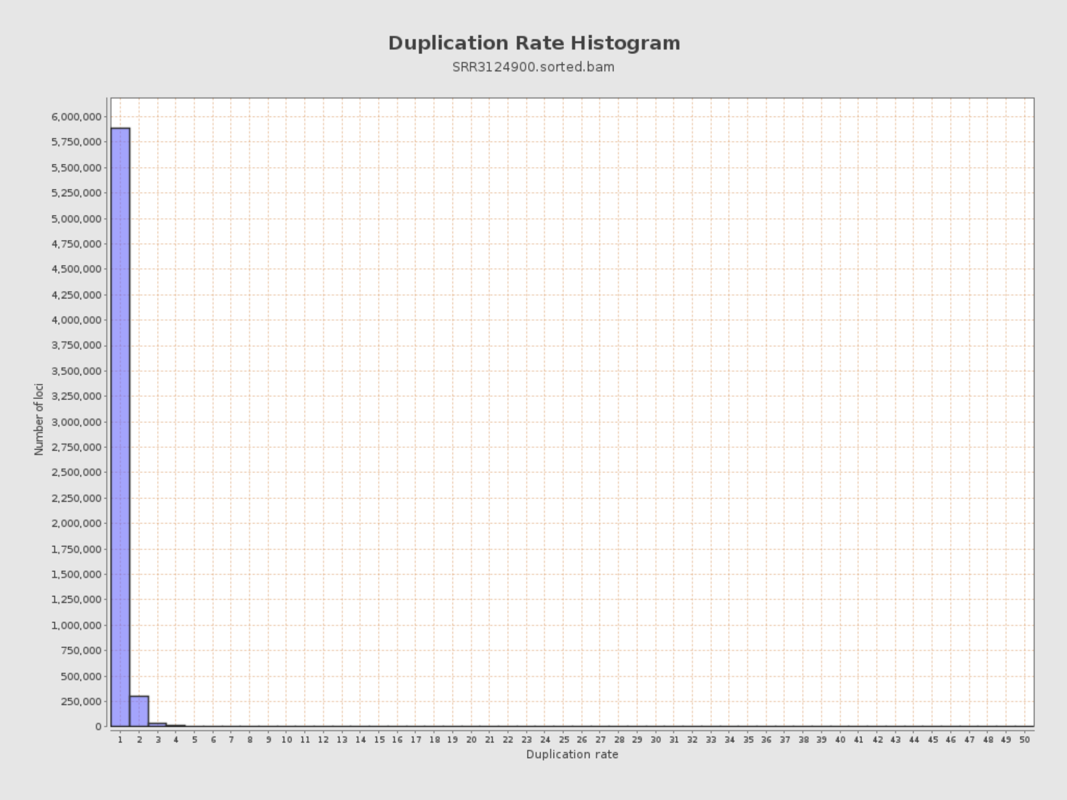
5. Results : Coverage Histogram (0-50X)



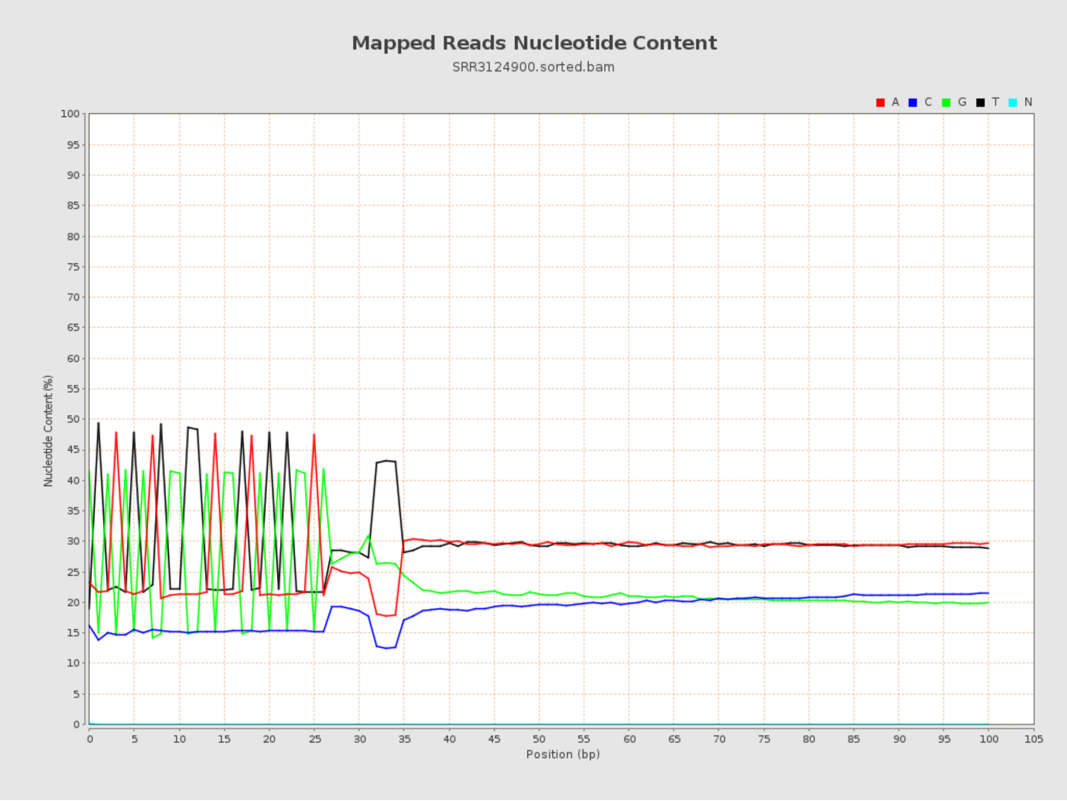
6. Results : Genome Fraction Coverage



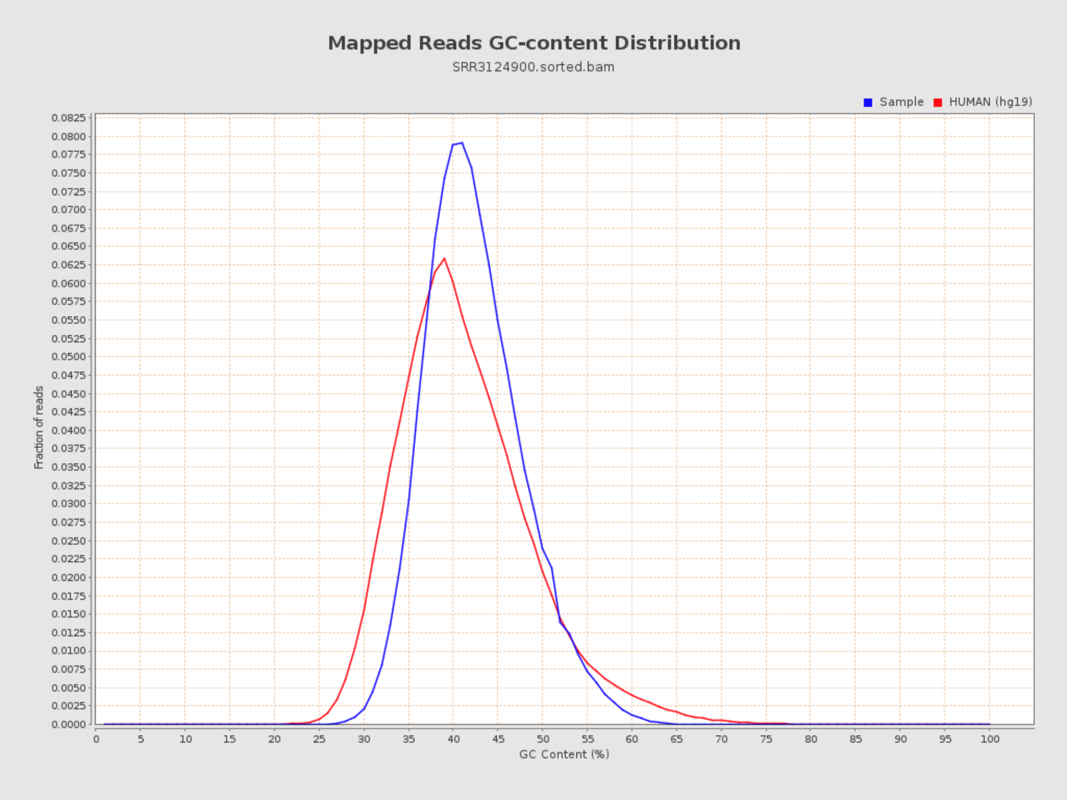
7. Results : Duplication Rate Histogram



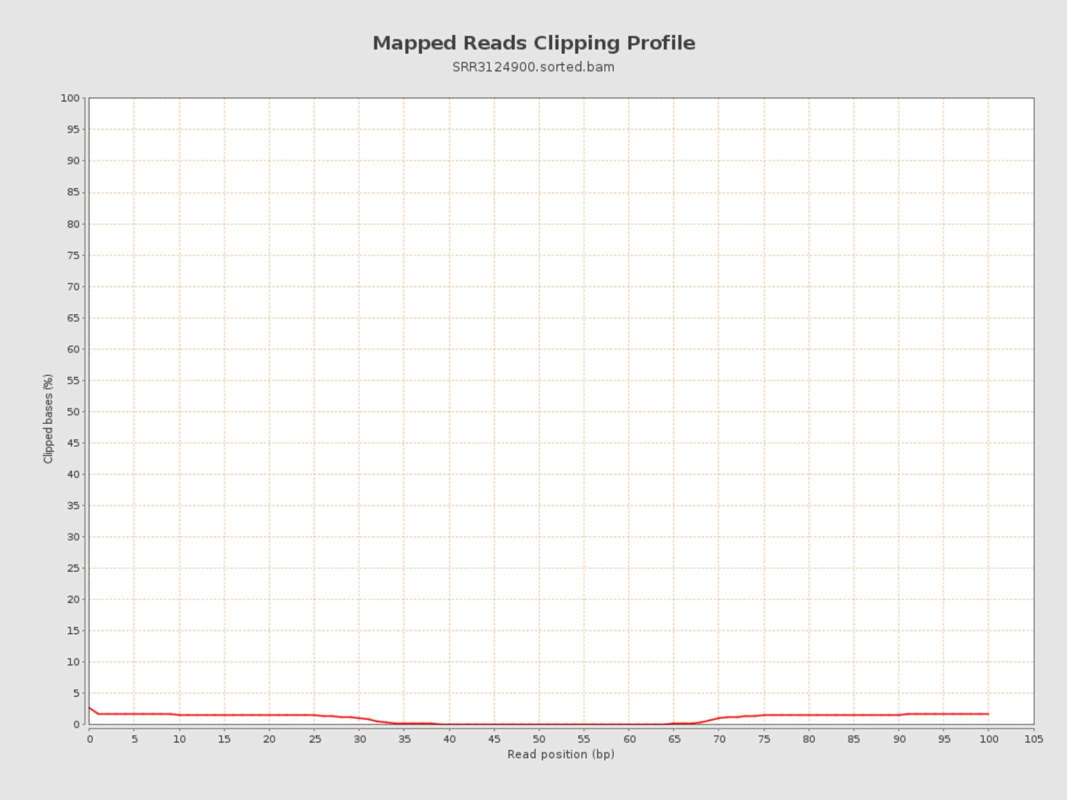
8. Results : Mapped Reads Nucleotide Content



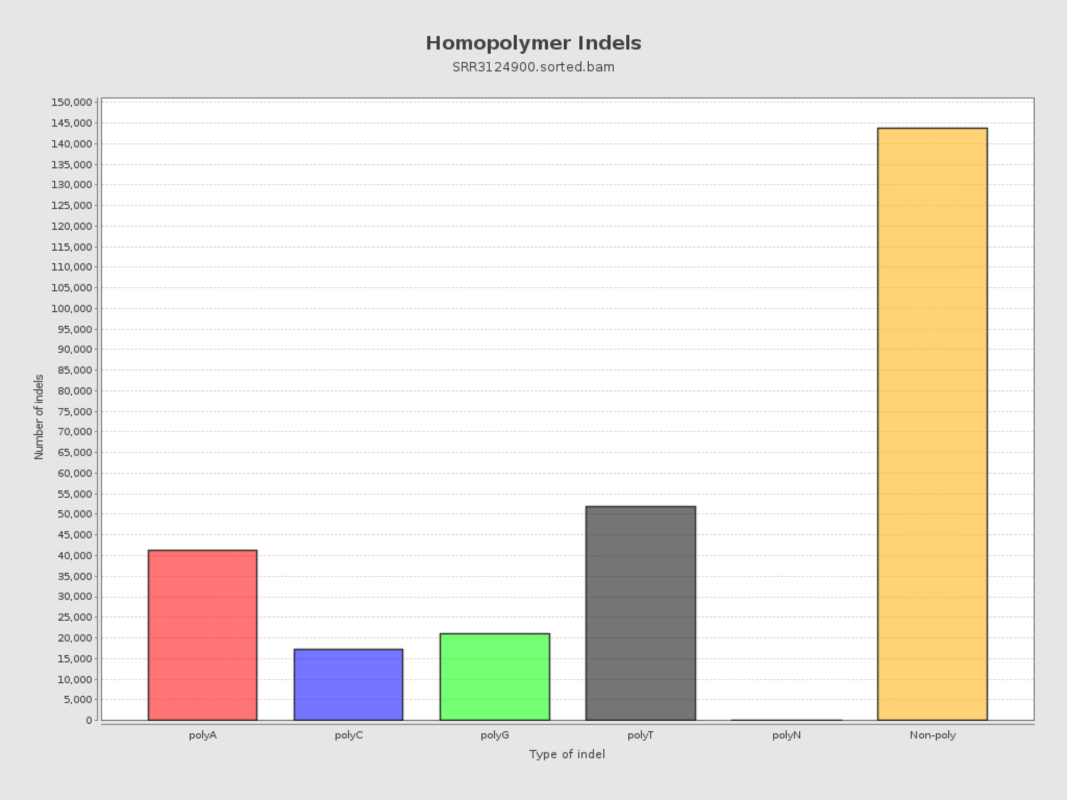
9. Results : Mapped Reads GC-content Distribution



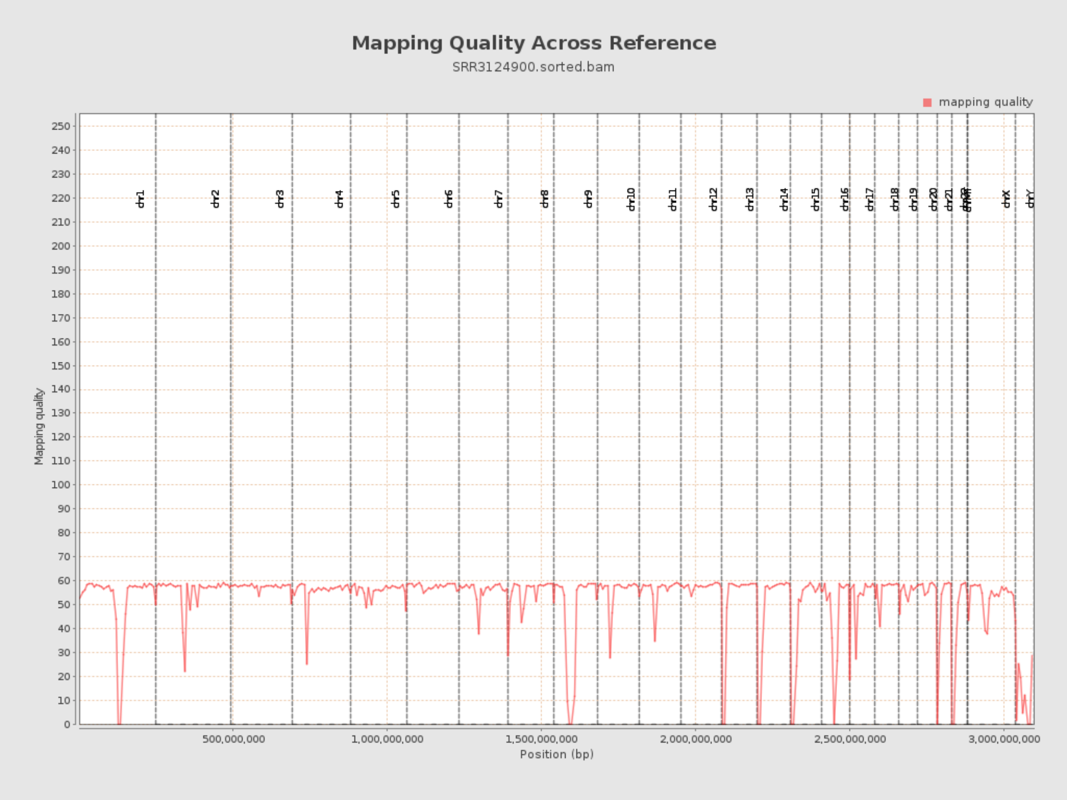
10. Results : Mapped Reads Clipping Profile



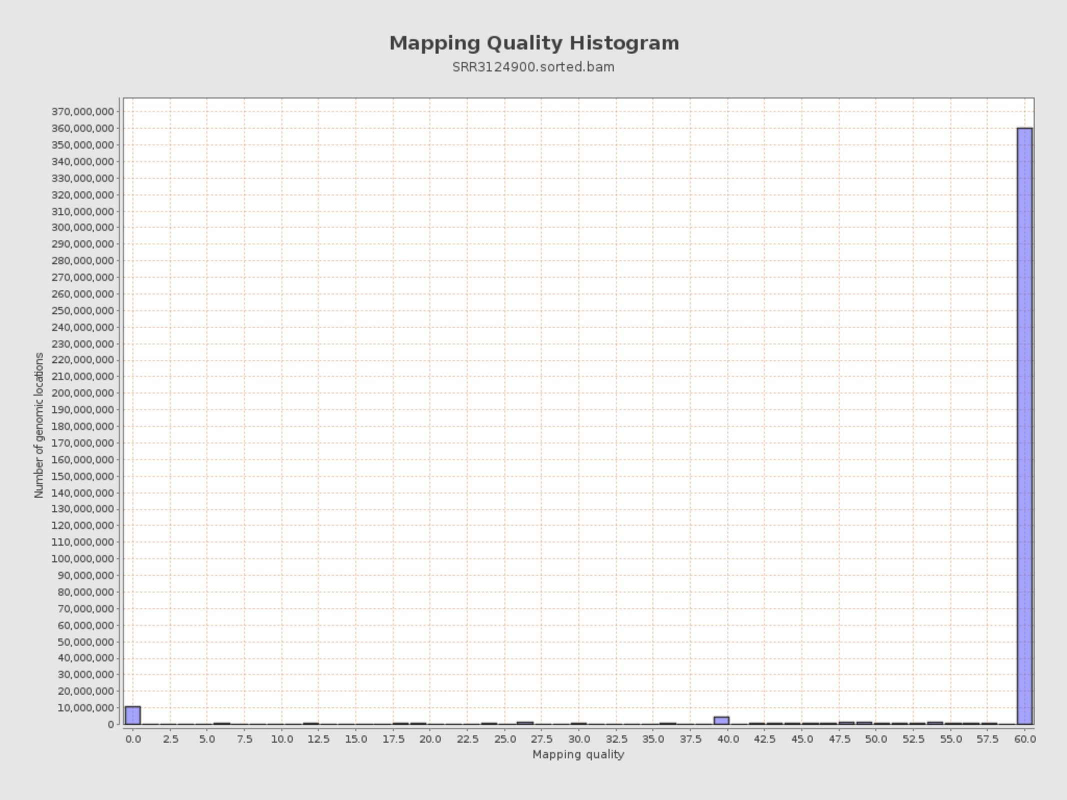
11. Results : Homopolymer Indels



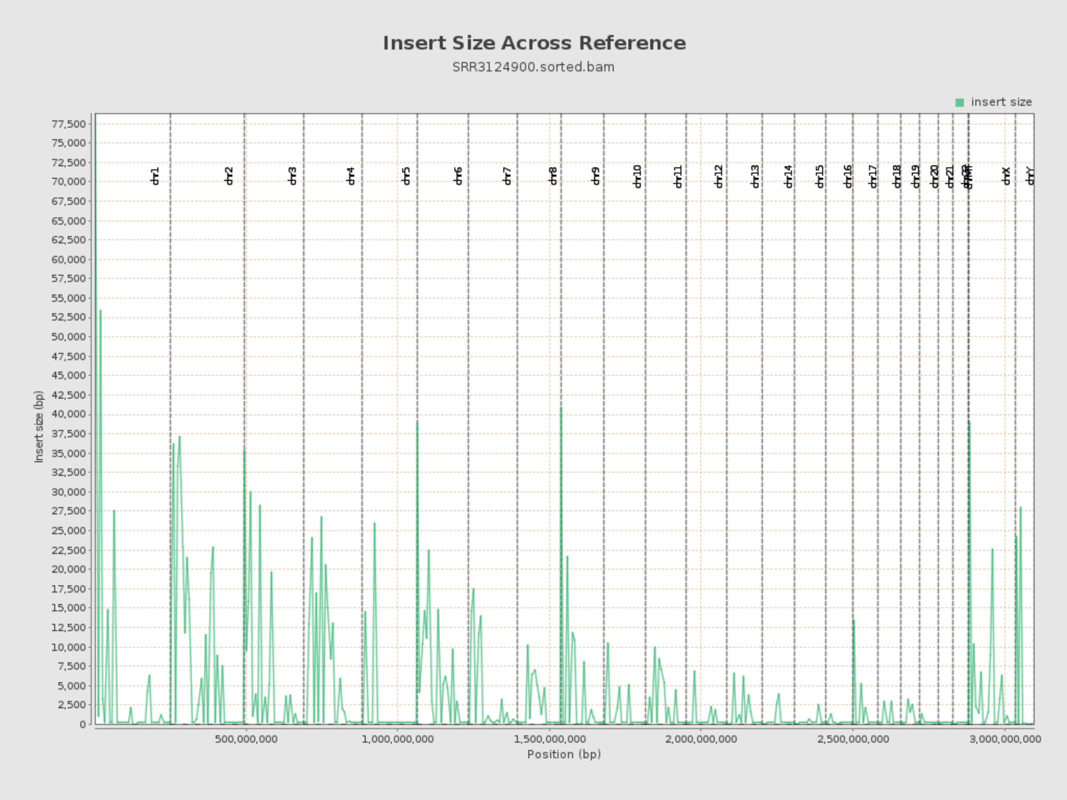
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram