Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/09 22:57:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124866.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_SRR3124866 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124866_1.fastq.gz SRR3124866_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Dec 09 22:57:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124866.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,370,902
Mapped reads	4,299,120 / 98.36%
Unmapped reads	71,782 / 1.64%
Mapped paired reads	4,299,120 / 98.36%
Mapped reads, first in pair	2,154,860 / 49.3%
Mapped reads, second in pair	2,144,260 / 49.06%
Mapped reads, both in pair	4,274,496 / 97.79%
Mapped reads, singletons	24,624 / 0.56%
Secondary alignments	0
Supplementary alignments	20,578 / 0.47%
Read min/max/mean length	30 / 101 / 101.19
Duplicated reads (estimated)	379,199 / 8.68%
Duplication rate	5.29%
Clipped reads	2,092,602 / 47.88%

2.2. ACGT Content

Number/percentage of A's	106,535,229 / 28.4%
Number/percentage of C's	69,558,182 / 18.54%
Number/percentage of T's	113,147,811 / 30.17%
Number/percentage of G's	85,838,335 / 22.88%
Number/percentage of N's	11,567 / 0%

GC Percentage	41.43%

2.3. Coverage

Mean	0.1212
Standard Deviation	1.5019

2.4. Mapping Quality

Mean Mapping Quality	52.56

2.5. Insert size

Mean	36,322.98
Standard Deviation	1,748,228.58
P25/Median/P75	146 / 194 / 268

2.6. Mismatches and indels

General error rate	0.81%
Mismatches	2,919,602
Insertions	53,726
Mapped reads with at least one insertion	1.22%
Deletions	118,676
Mapped reads with at least one deletion	2.7%
Homopolymer indels	46.72%

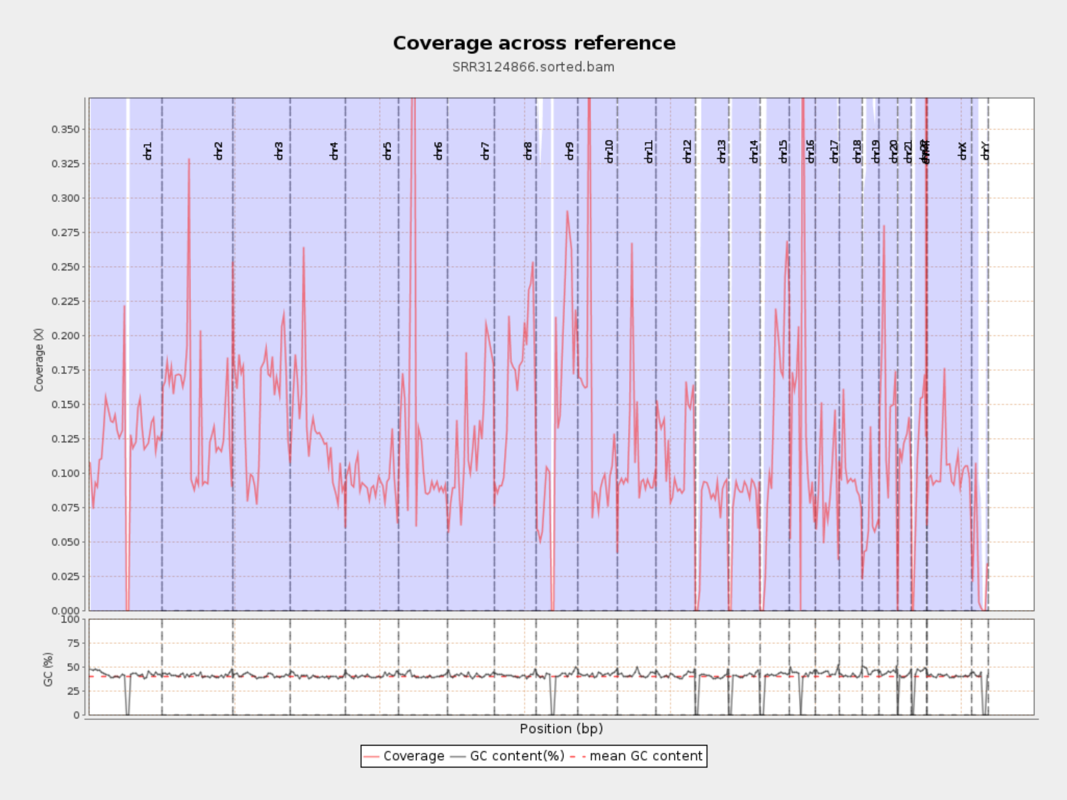
2.7. Chromosome stats

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

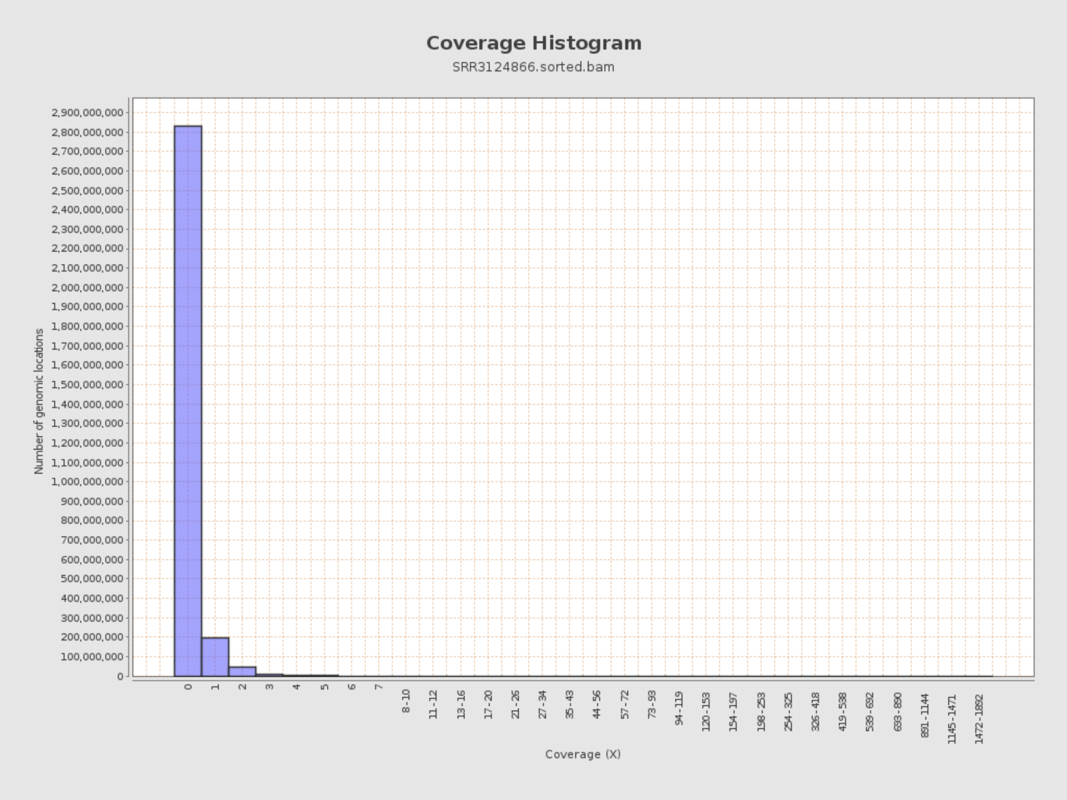
		bases	coverage	deviation
chr1	249250621	30007615	0.1204	1.5065
chr2	243199373	35399778	0.1456	1.5665
chr3	198022430	30594196	0.1545	0.5176
chr4	191154276	24781900	0.1296	0.8782
chr5	180915260	16924919	0.0936	0.4899
chr6	171115067	24016524	0.1404	3.1959
chr7	159138663	20365150	0.128	1.431
chr8	146364022	24234832	0.1656	0.7029
chr9	141213431	20291443	0.1437	1.9649
chr10	135534747	18207350	0.1343	2.7567
chr11	135006516	14683404	0.1088	1.66
chr12	133851895	15787188	0.1179	0.5402
chr13	115169878	8305497	0.0721	0.3279
chr14	107349540	8092617	0.0754	0.442
chr15	102531392	13887328	0.1354	0.4901
chr16	90354753	13009635	0.144	2.5605
chr17	81195210	7025418	0.0865	1.1526
chr18	78077248	7789888	0.0998	1.9457
chr19	59128983	3781126	0.0639	1.0872
chr20	63025520	9867510	0.1566	0.5644
chr21	48129895	5278386	0.1097	0.7411
chr22	51304566	5254292	0.1024	0.4285
chrMT	16571	127767	7.7103	4.6457
chrX	155270560	15971312	0.1029	0.7641

chrY	59373566	1609676	0.0271	1.6947

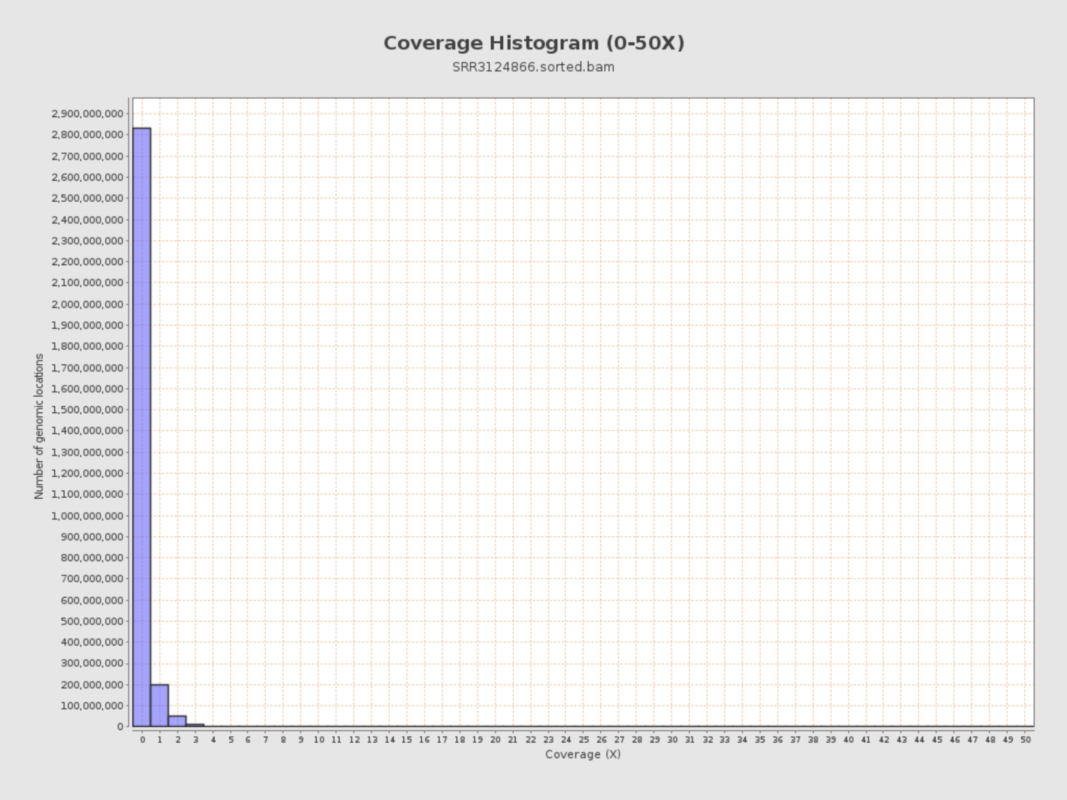
3. Results : Coverage across reference



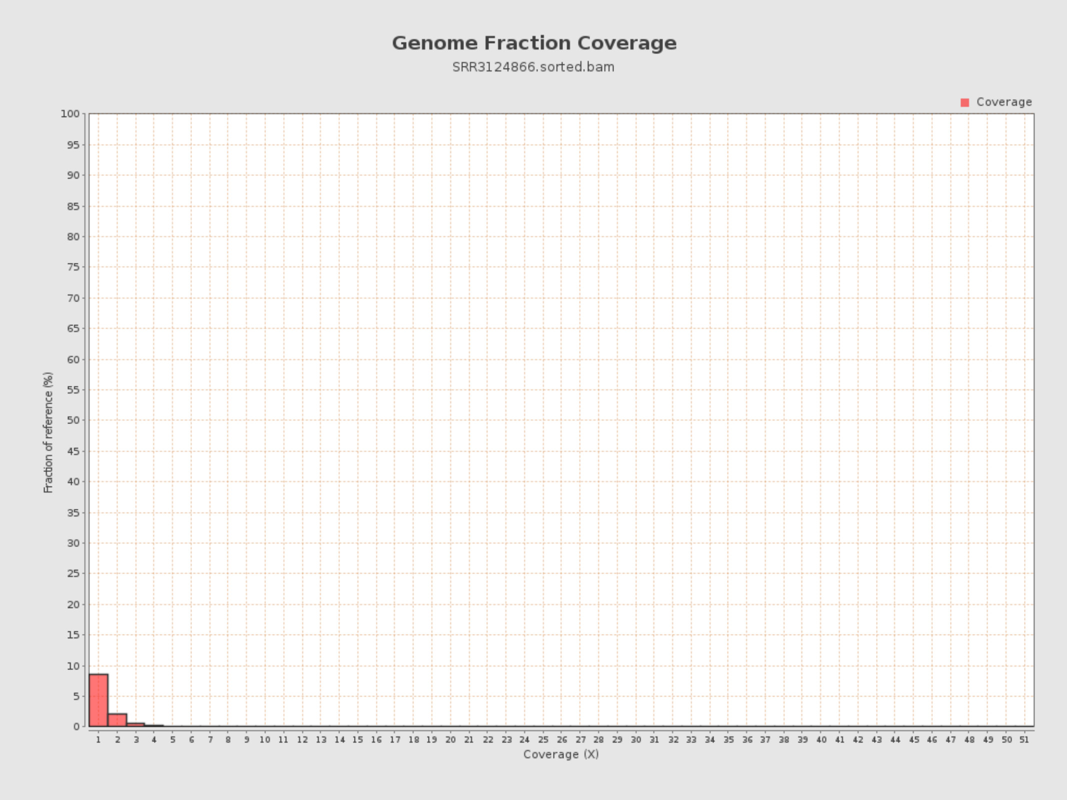
4. Results : Coverage Histogram



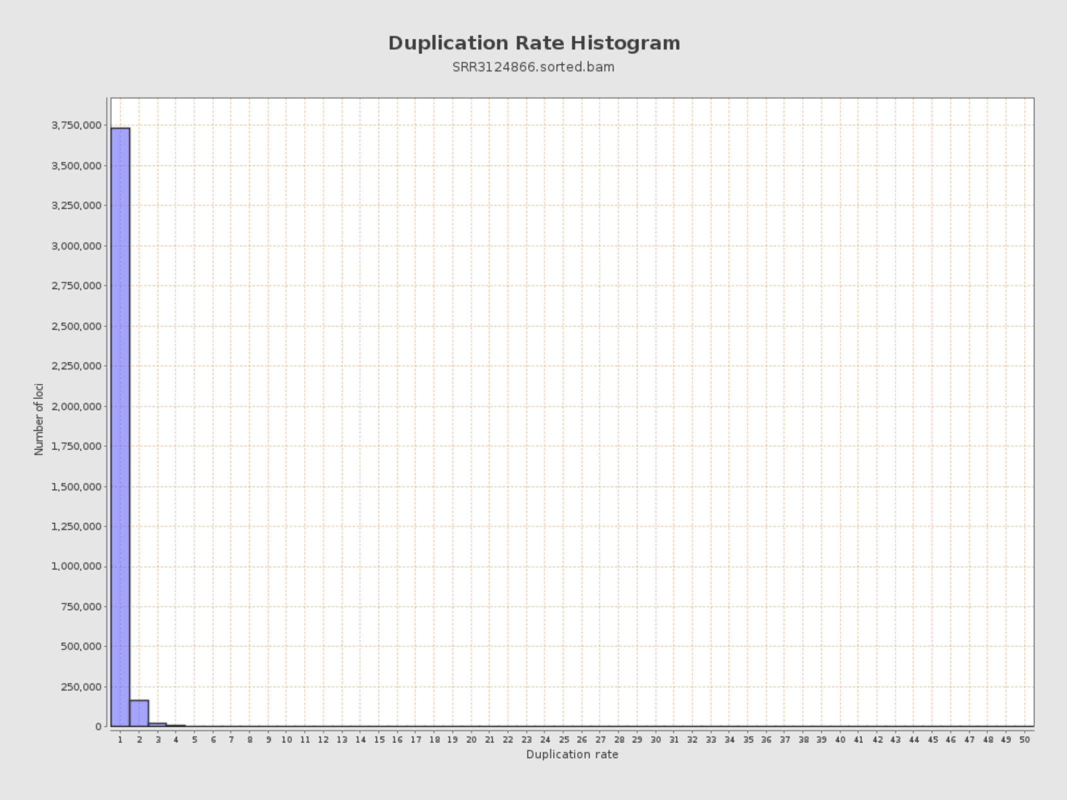
5. Results : Coverage Histogram (0-50X)



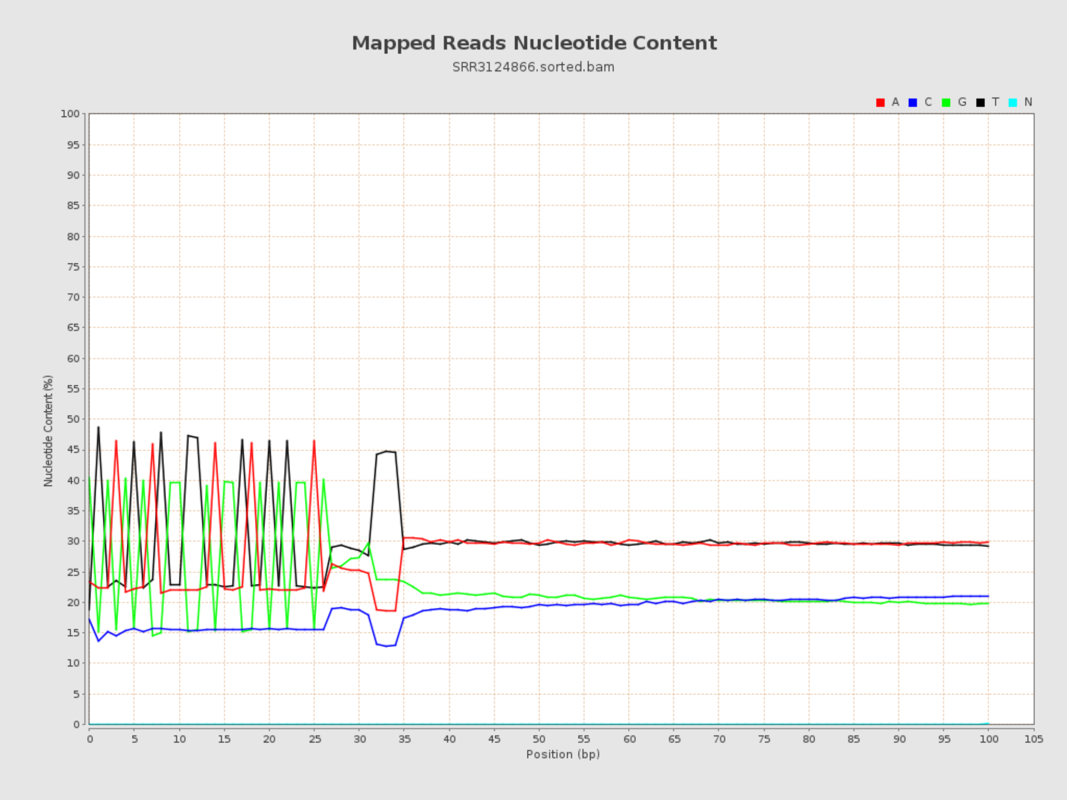
6. Results : Genome Fraction Coverage



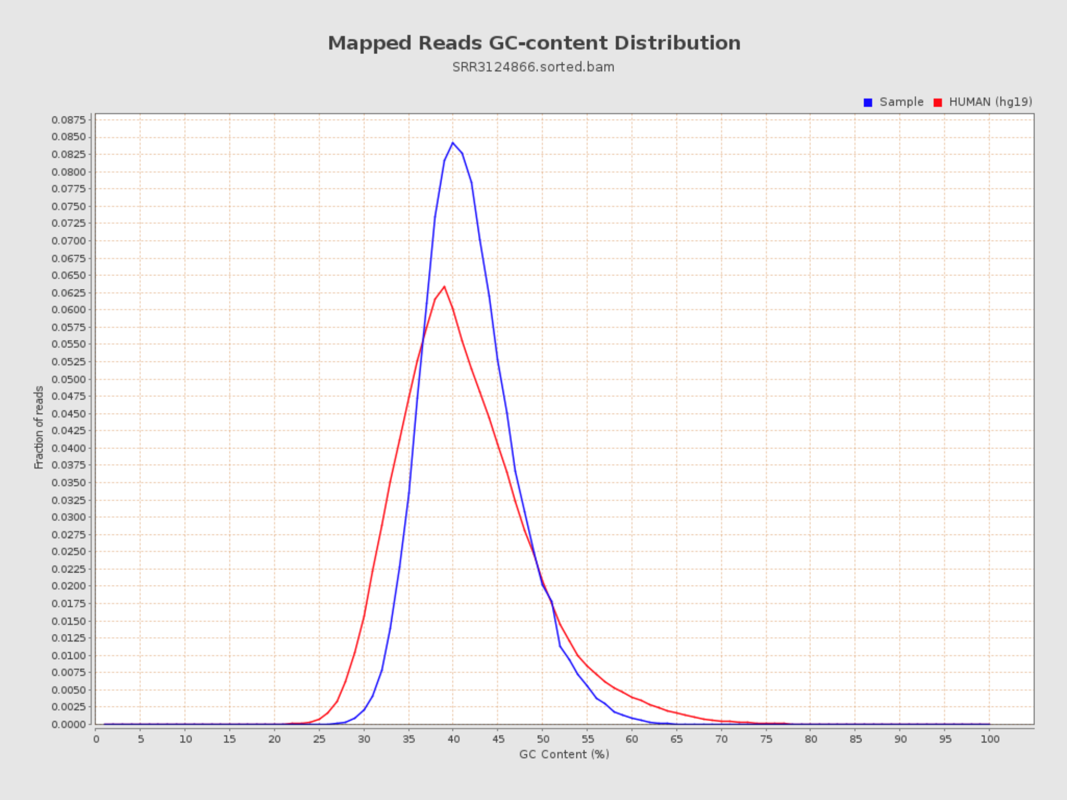
7. Results : Duplication Rate Histogram



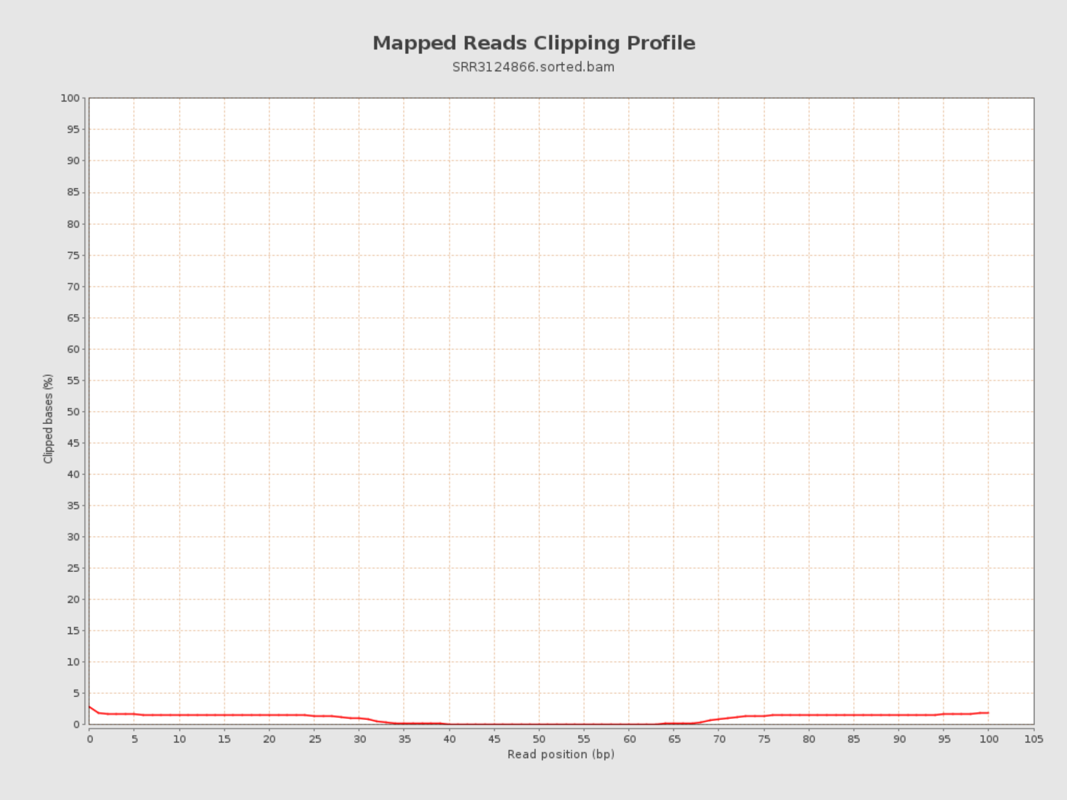
8. Results : Mapped Reads Nucleotide Content



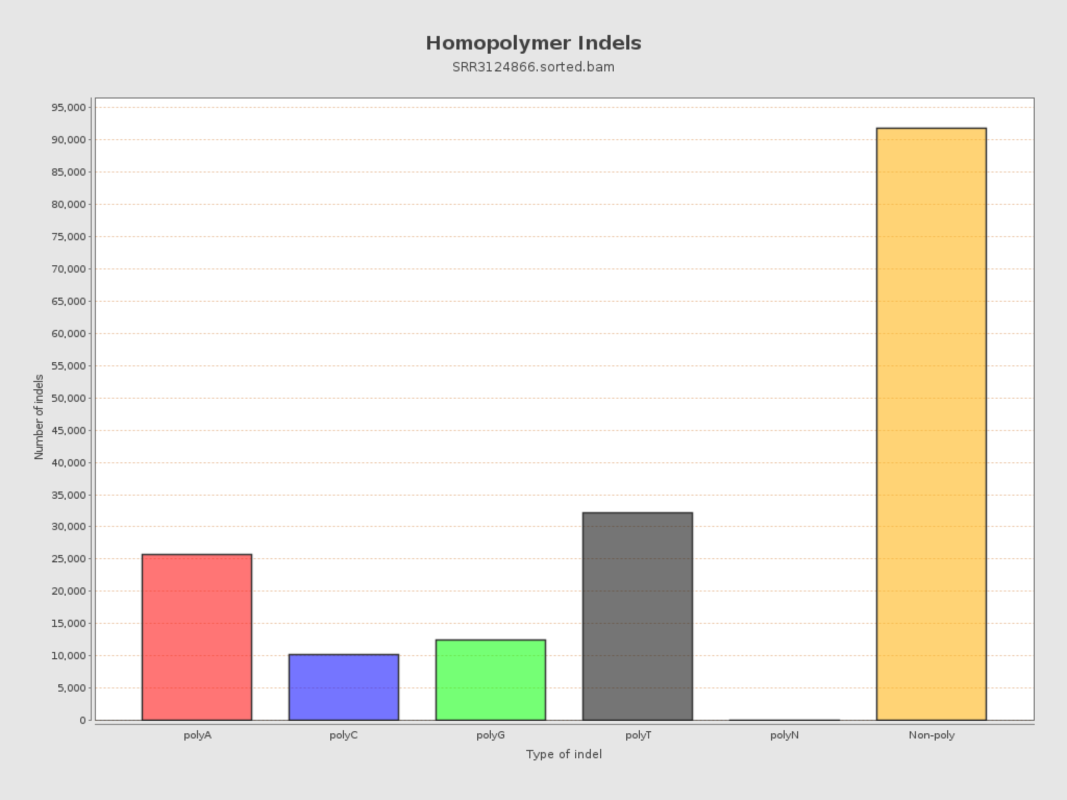
9. Results : Mapped Reads GC-content Distribution



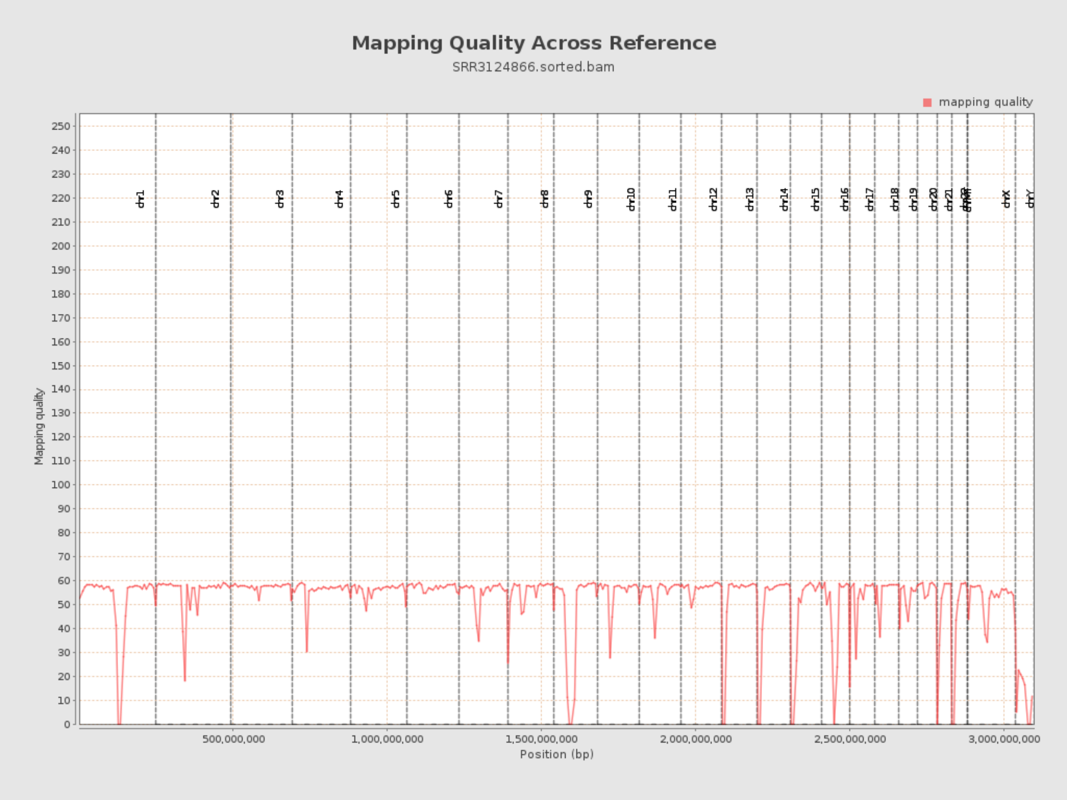
10. Results : Mapped Reads Clipping Profile



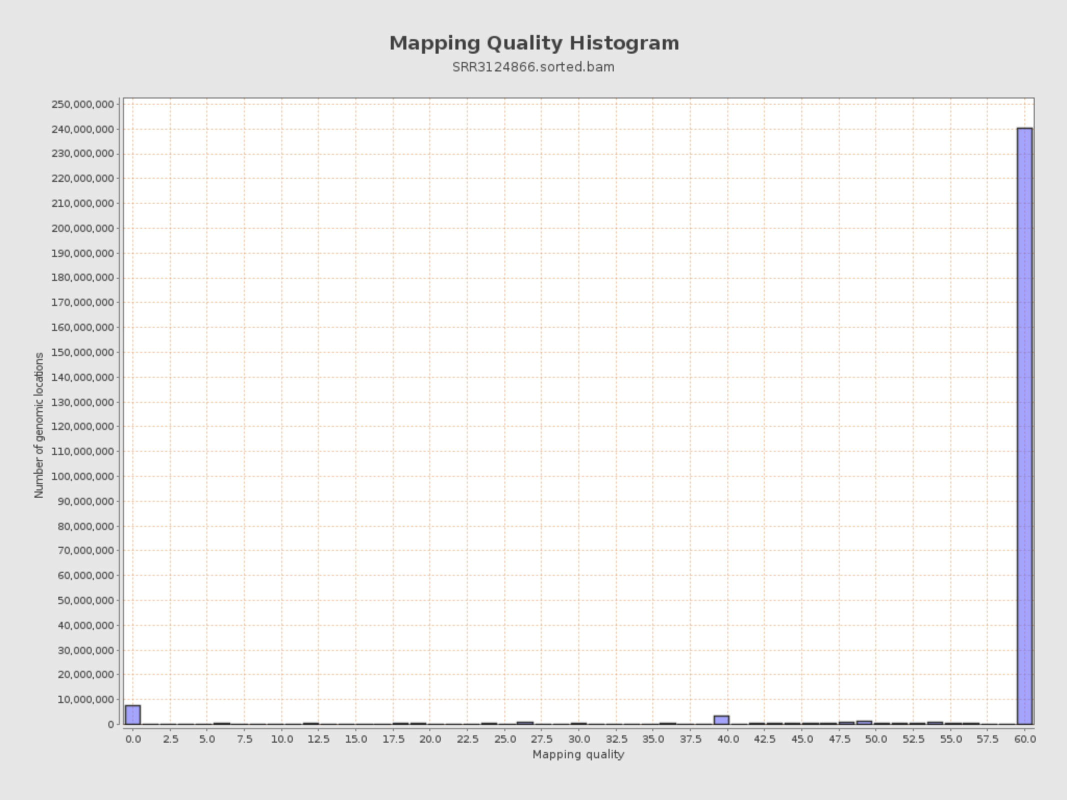
11. Results : Homopolymer Indels



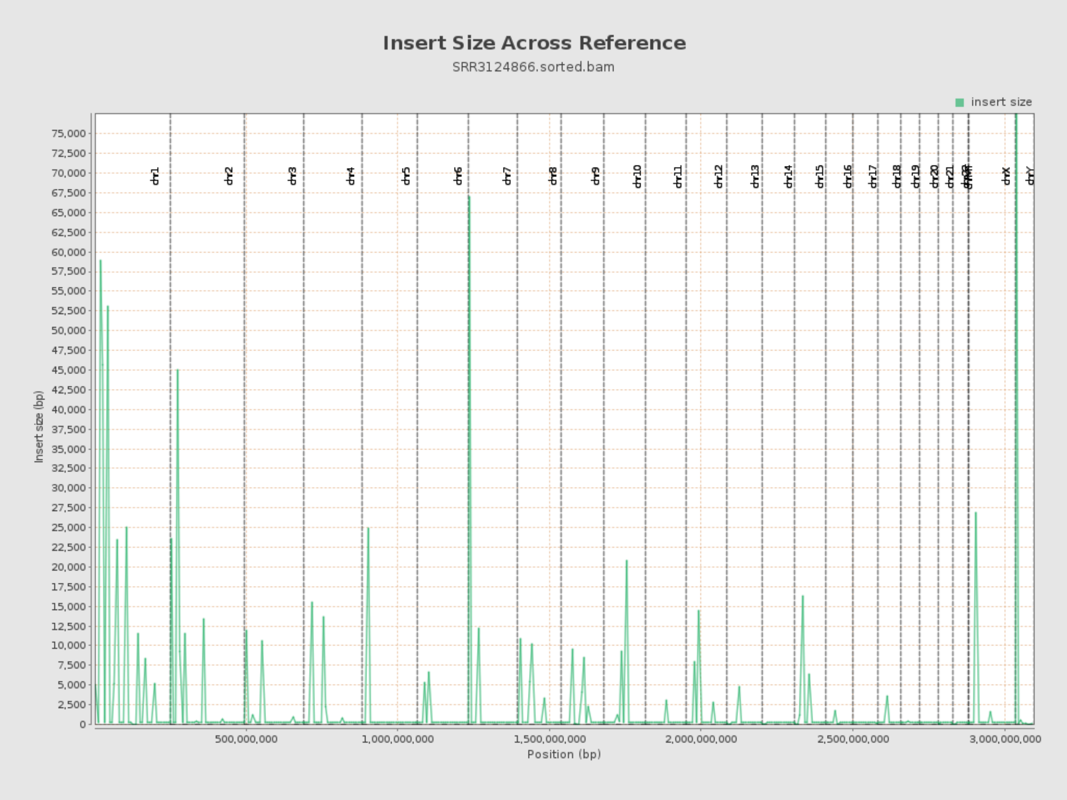
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram