Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/05 09:04:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124834.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_SRR3124834 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124834_1.fastq.gz SRR3124834_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Dec 05 09:04:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124834.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	26,097,260
Mapped reads	25,826,586 / 98.96%
Unmapped reads	270,674 / 1.04%
Mapped paired reads	25,826,586 / 98.96%
Mapped reads, first in pair	12,940,452 / 49.59%
Mapped reads, second in pair	12,886,134 / 49.38%
Mapped reads, both in pair	25,723,776 / 98.57%
Mapped reads, singletons	102,810 / 0.39%
Secondary alignments	0
Supplementary alignments	98,799 / 0.38%
Read min/max/mean length	30 / 101 / 101.15
Duplicated reads (estimated)	3,591,456 / 13.76%
Duplication rate	9.2%
Clipped reads	12,305,459 / 47.15%

2.2. ACGT Content

Number/percentage of A's	635,385,013 / 28.25%
Number/percentage of C's	418,229,485 / 18.6%
Number/percentage of T's	673,124,327 / 29.93%
Number/percentage of G's	522,189,676 / 23.22%
Number/percentage of N's	20,932 / 0%

GC Percentage	41.82%

2.3. Coverage

Mean	0.7268
Standard Deviation	6.4877

2.4. Mapping Quality

Mean Mapping Quality	52.77

2.5. Insert size

Mean	30,690.7
Standard Deviation	1,634,792.27
P25/Median/P75	145 / 198 / 279

2.6. Mismatches and indels

General error rate	0.76%
Mismatches	16,570,256
Insertions	280,563
Mapped reads with at least one insertion	1.07%
Deletions	709,537
Mapped reads with at least one deletion	2.7%
Homopolymer indels	48.09%

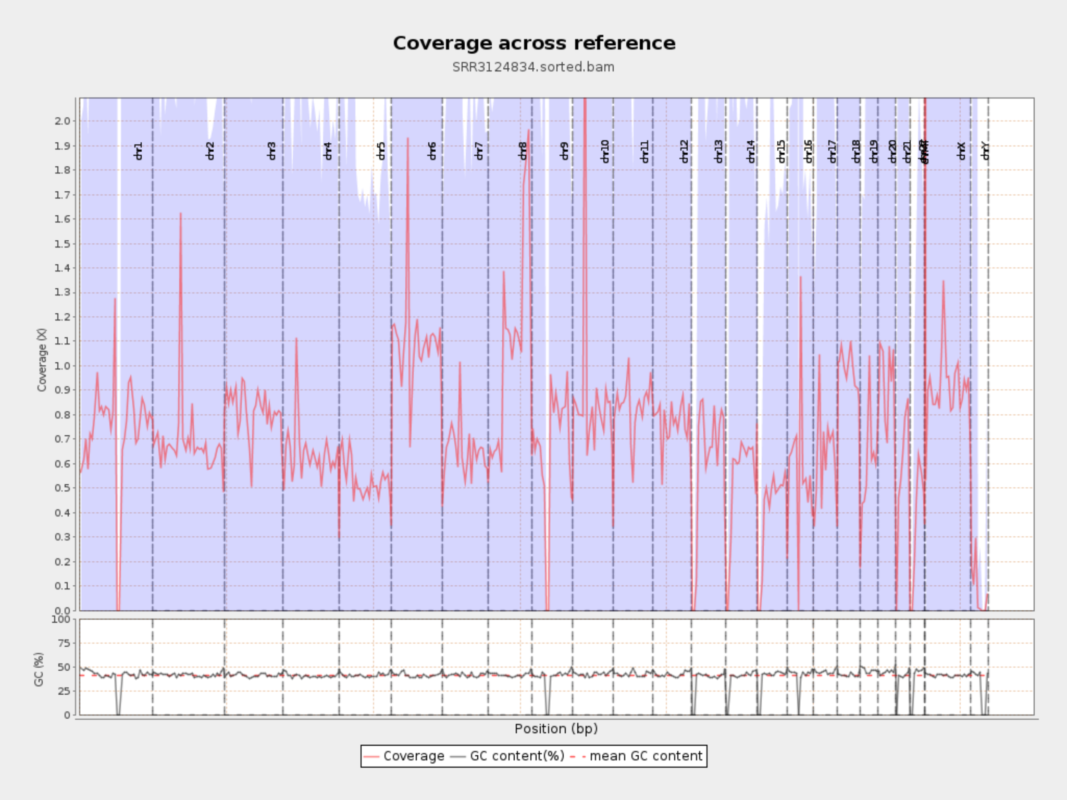
2.7. Chromosome stats

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

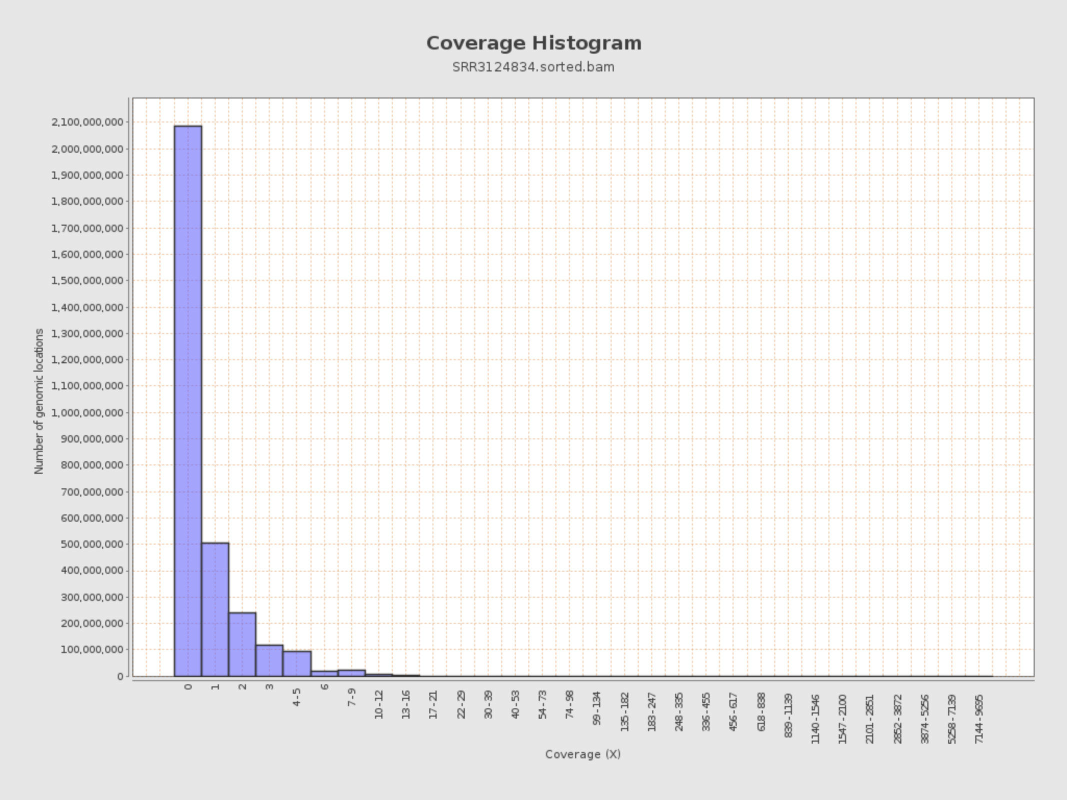
		bases	coverage	deviation
chr1	249250621	184262392	0.7393	7.41
chr2	243199373	168728100	0.6938	6.5089
chr3	198022430	161829378	0.8172	1.6153
chr4	191154276	122747818	0.6421	3.4948
chr5	180915260	96640241	0.5342	1.2747
chr6	171115067	189825521	1.1093	9.8294
chr7	159138663	103708911	0.6517	7.9826
chr8	146364022	160079355	1.0937	3.4651
chr9	141213431	92321790	0.6538	8.0405
chr10	135534747	123123332	0.9084	15.9396
chr11	135006516	110948078	0.8218	7.5645
chr12	133851895	102732469	0.7675	1.5482
chr13	115169878	70145238	0.6091	1.3249
chr14	107349540	56358463	0.525	1.6636
chr15	102531392	41096807	0.4008	1.1204
chr16	90354753	51425552	0.5692	6.6486
chr17	81195210	50521659	0.6222	8.6524
chr18	78077248	77321911	0.9903	9.5924
chr19	59128983	35159221	0.5946	4.5547
chr20	63025520	58119814	0.9222	1.9248
chr21	48129895	28022632	0.5822	2.0965
chr22	51304566	18716248	0.3648	1.0836
chrMT	16571	355431	21.449	13.5785
chrX	155270560	141217018	0.9095	4.1387

chrY	59373566	4675926	0.0788	3.4549

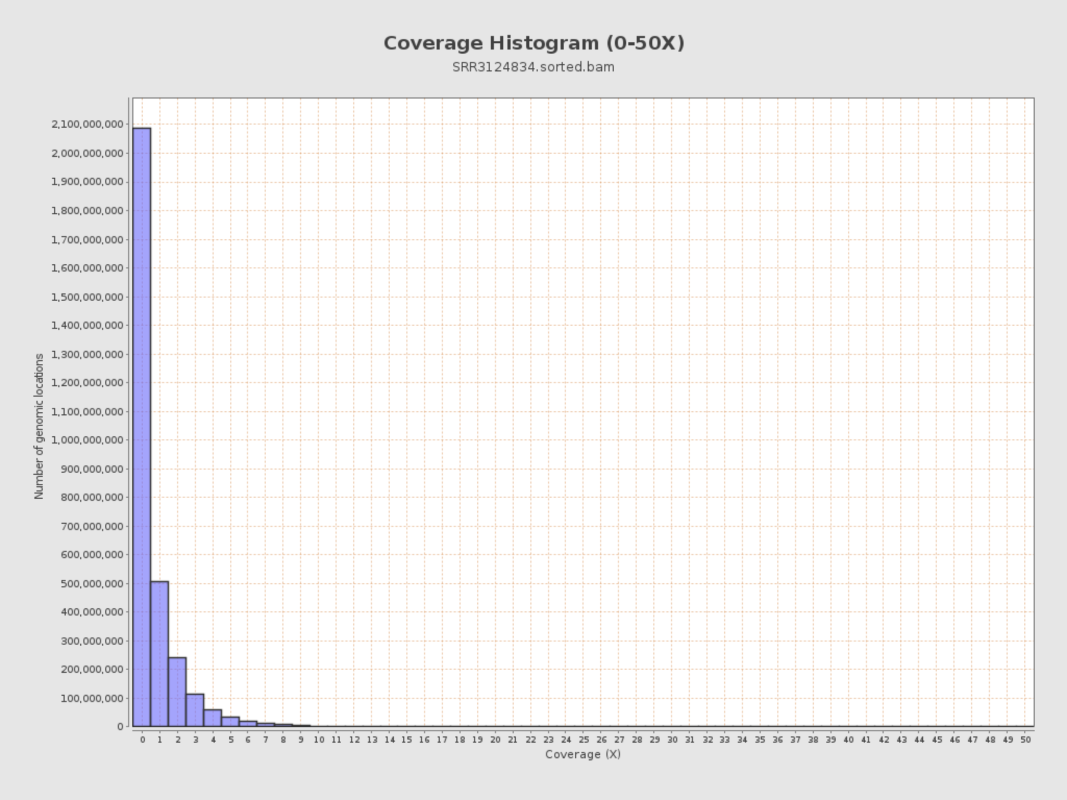
3. Results : Coverage across reference



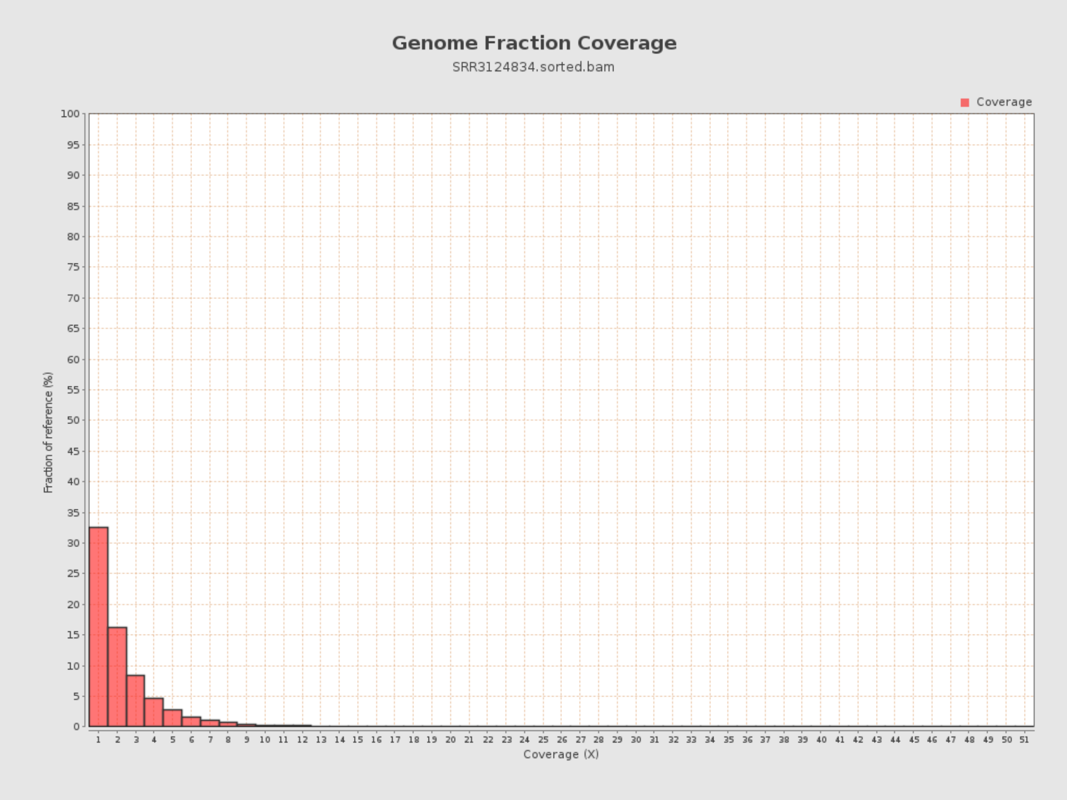
4. Results : Coverage Histogram



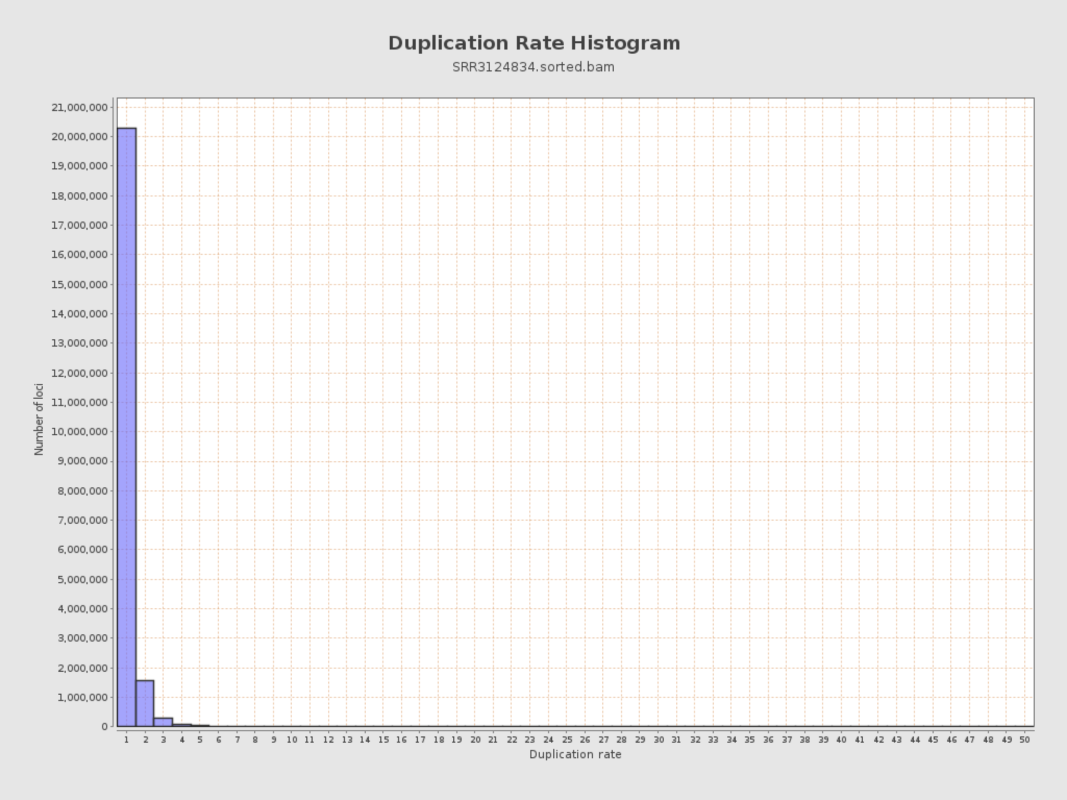
5. Results : Coverage Histogram (0-50X)



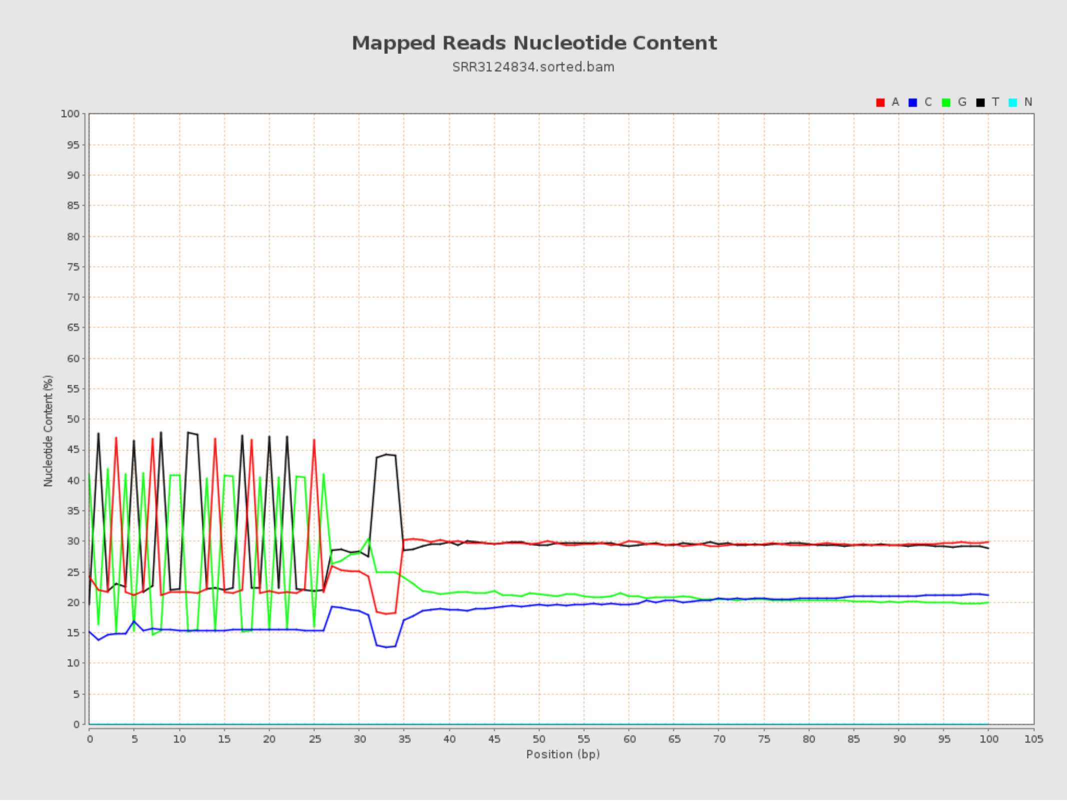
6. Results : Genome Fraction Coverage



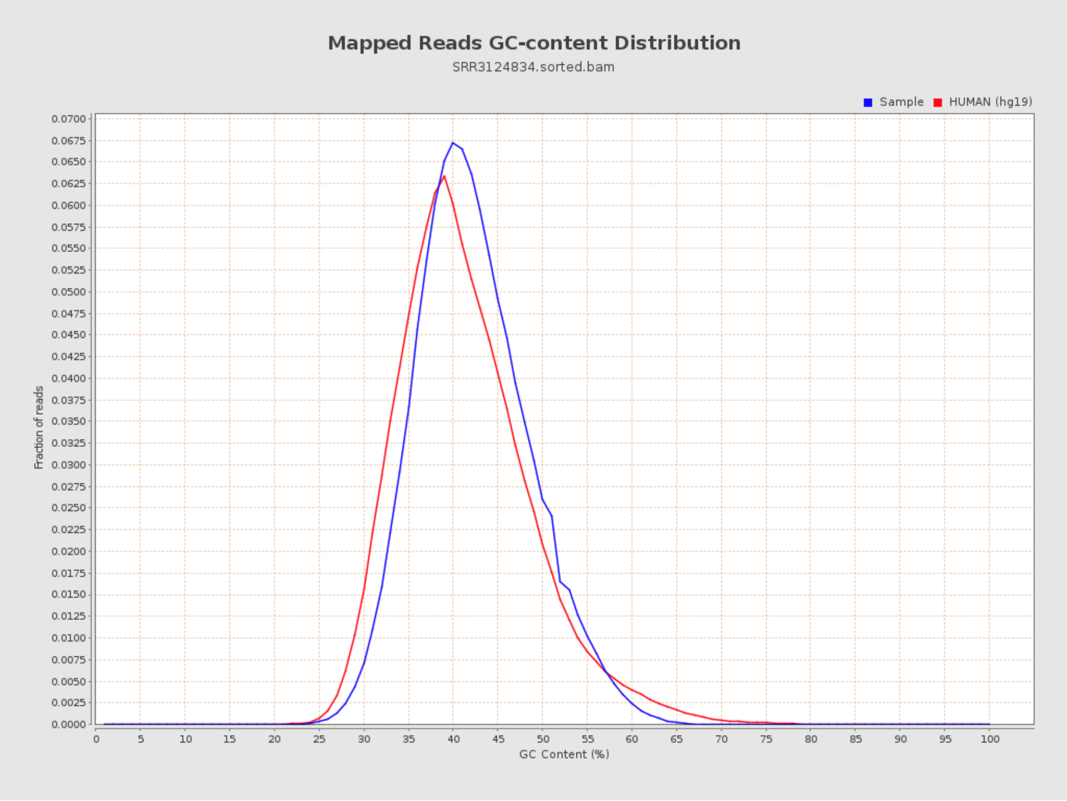
7. Results : Duplication Rate Histogram



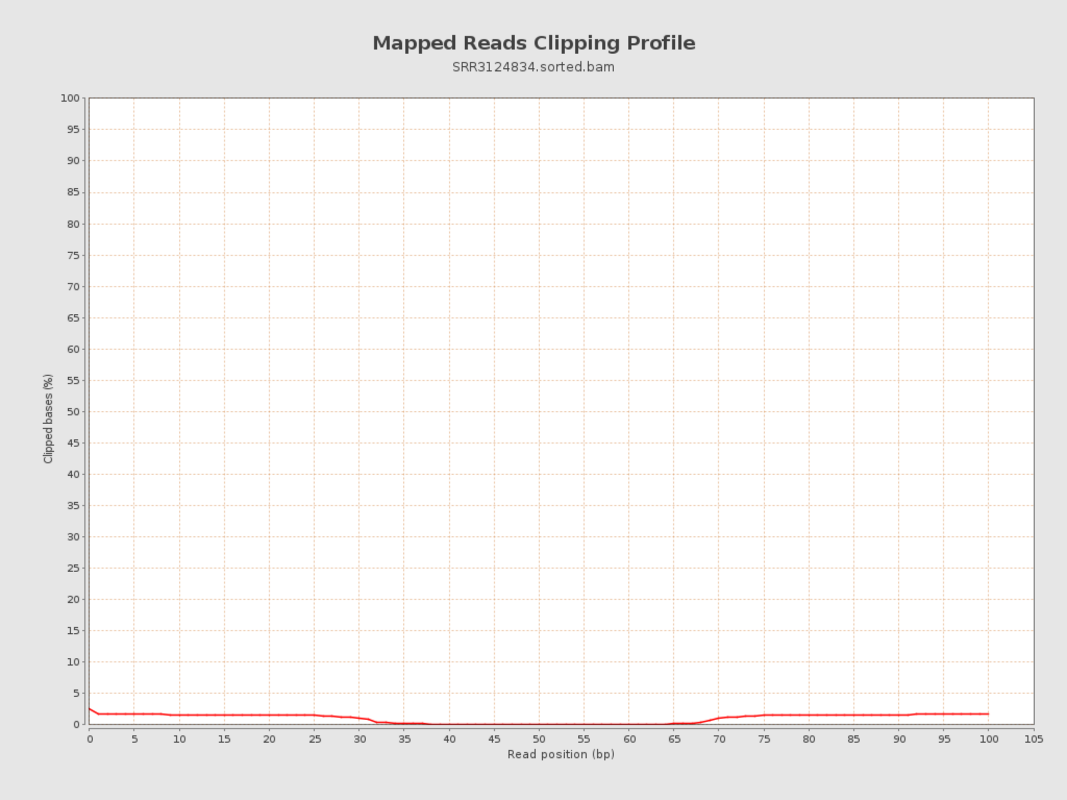
8. Results : Mapped Reads Nucleotide Content



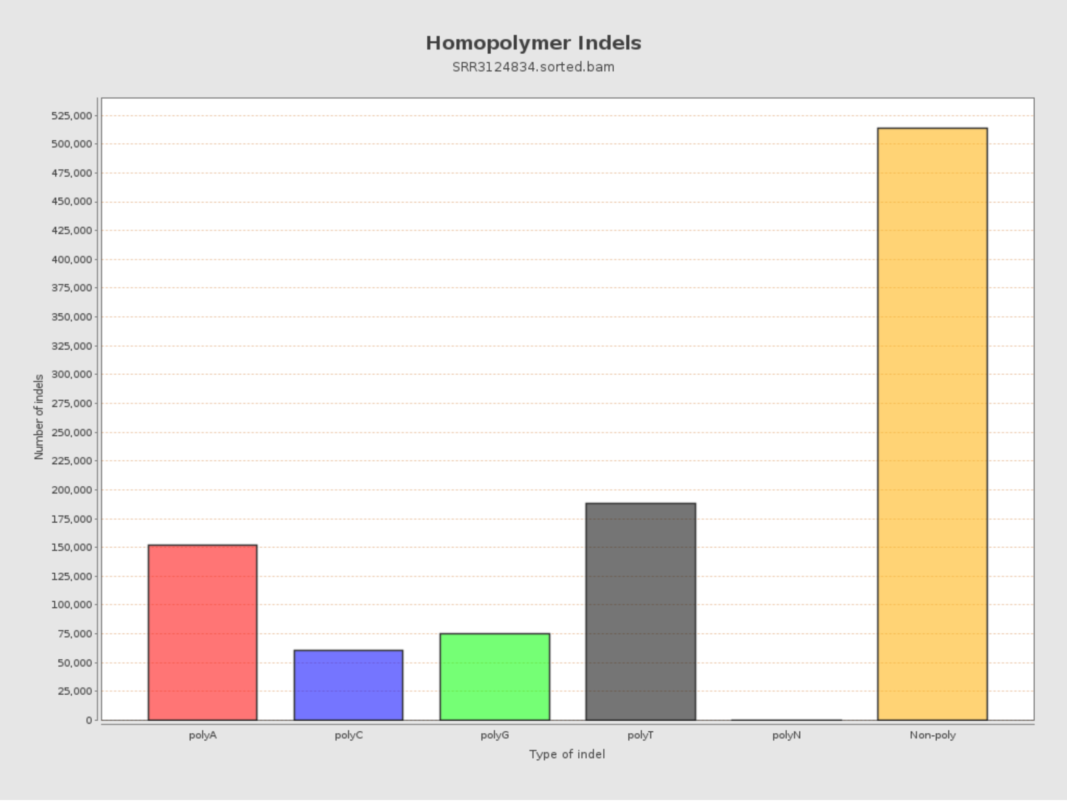
9. Results : Mapped Reads GC-content Distribution



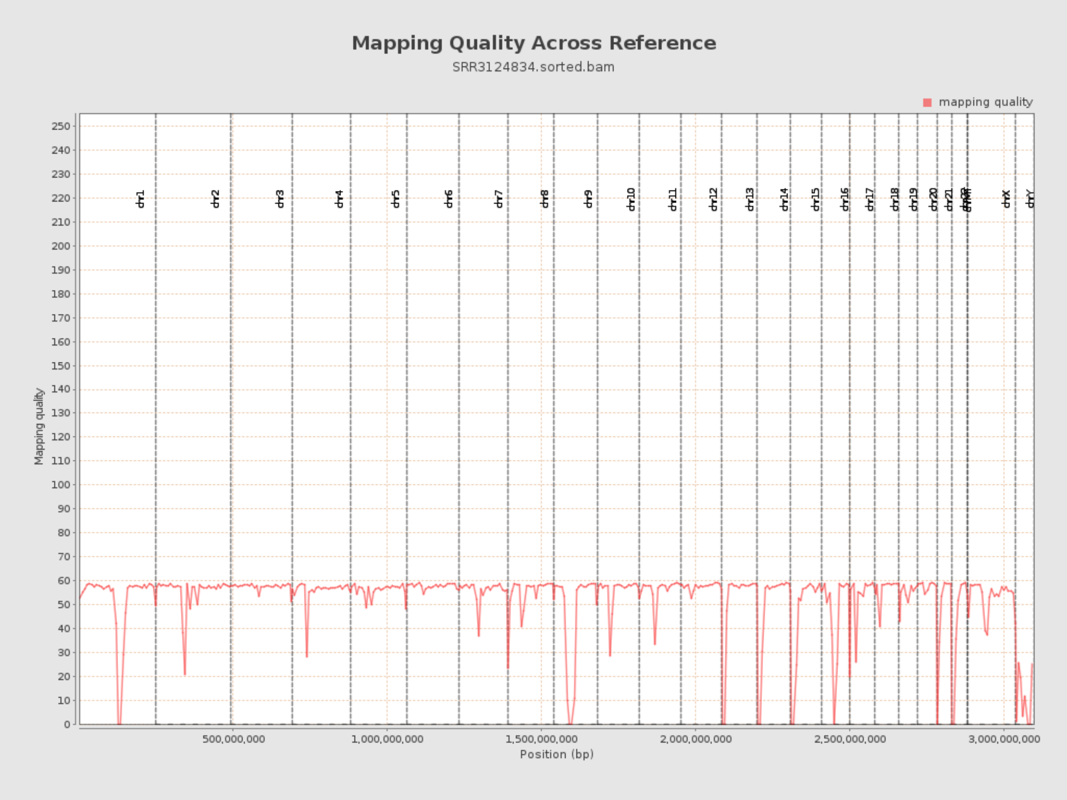
10. Results : Mapped Reads Clipping Profile



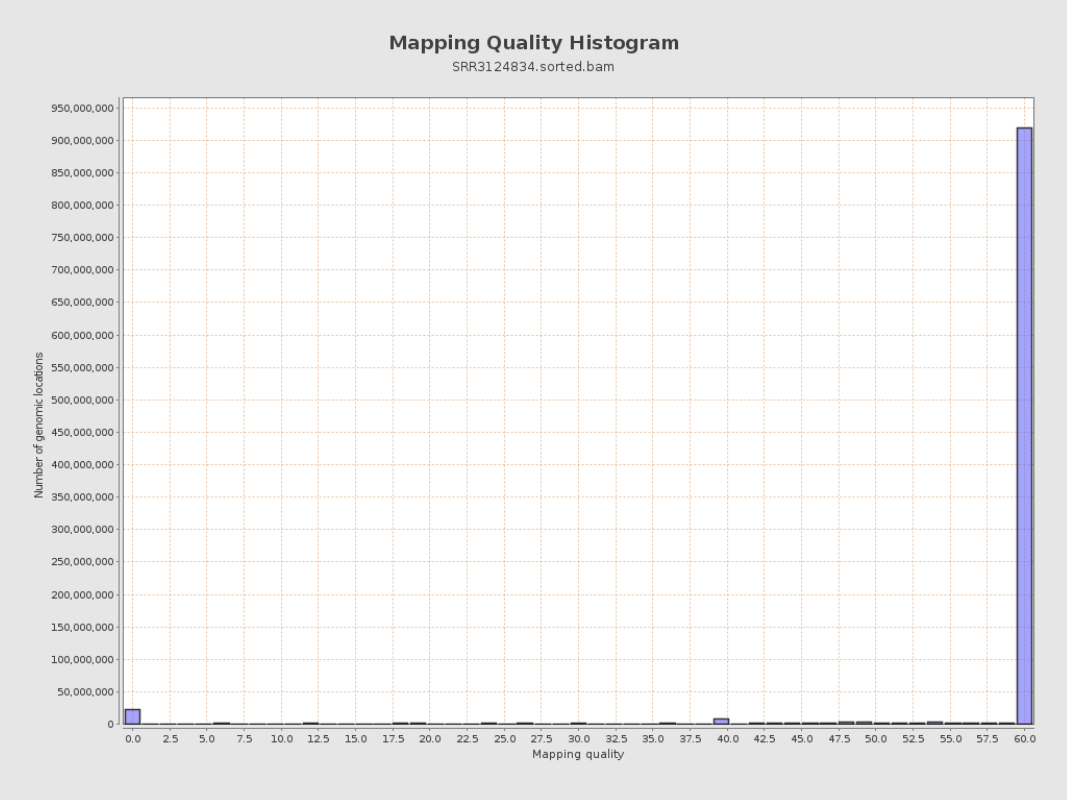
11. Results : Homopolymer Indels



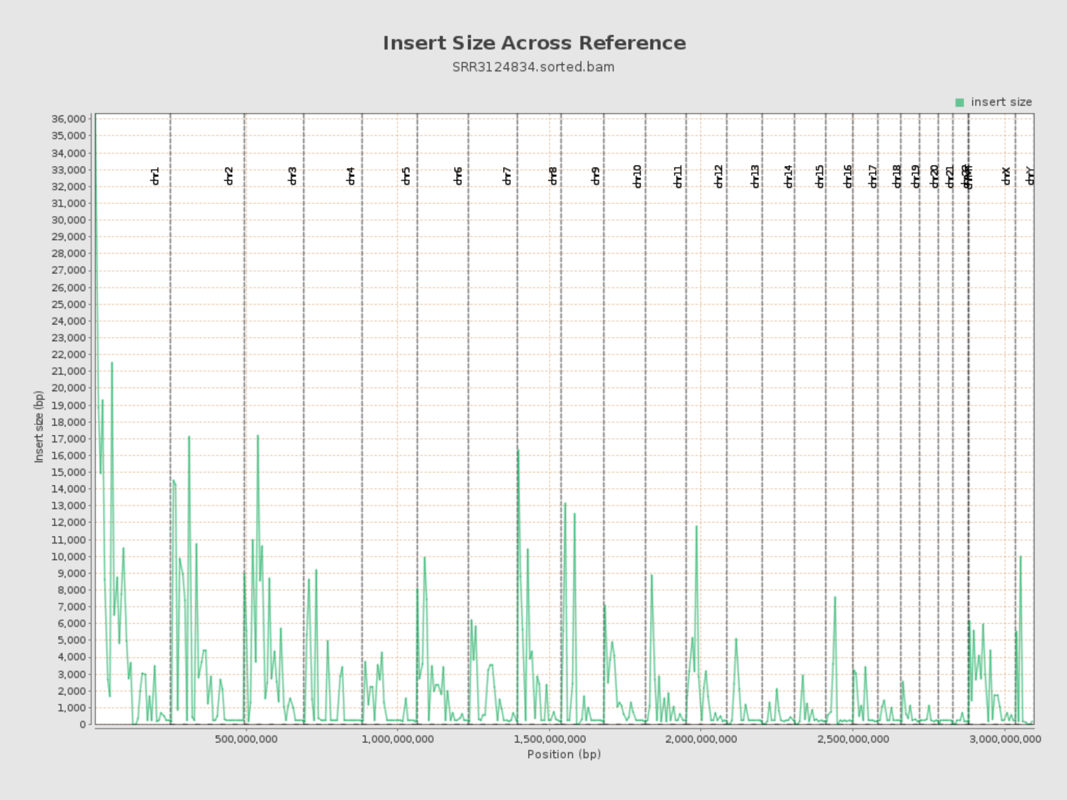
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram