Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/11/13 11:51:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5365356.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_SRR5365356 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5365356_1.fastq.gz SRR5365356_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Nov 13 11:51:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5365356.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	568,335,354
Mapped reads	534,860,976 / 94.11%
Unmapped reads	33,474,378 / 5.89%
Mapped paired reads	534,860,976 / 94.11%
Mapped reads, first in pair	268,042,799 / 47.16%
Mapped reads, second in pair	266,818,177 / 46.95%
Mapped reads, both in pair	532,063,754 / 93.62%
Mapped reads, singletons	2,797,222 / 0.49%
Secondary alignments	0
Supplementary alignments	2,501,403 / 0.44%
Read min/max/mean length	30 / 125 / 125.18
Duplicated reads (estimated)	327,401,715 / 57.61%
Duplication rate	31.14%
Clipped reads	342,363,909 / 60.24%

2.2. ACGT Content

Number/percentage of A's	16,851,699,432 / 30.29%
Number/percentage of C's	10,795,479,245 / 19.4%
Number/percentage of T's	16,386,042,054 / 29.45%
Number/percentage of G's	11,597,053,974 / 20.84%
Number/percentage of N's	9,439,322 / 0.02%

GC Percentage	40.25%

2.3. Coverage

Mean	17.9796
Standard Deviation	228.4189

2.4. Mapping Quality

Mean Mapping Quality	53.72

2.5. Insert size

Mean	51,887.47
Standard Deviation	2,190,045.78
P25/Median/P75	113 / 161 / 228

2.6. Mismatches and indels

General error rate	0.65%
Mismatches	331,903,431
Insertions	16,928,085
Mapped reads with at least one insertion	3.09%
Deletions	9,163,568
Mapped reads with at least one deletion	1.67%
Homopolymer indels	49.66%

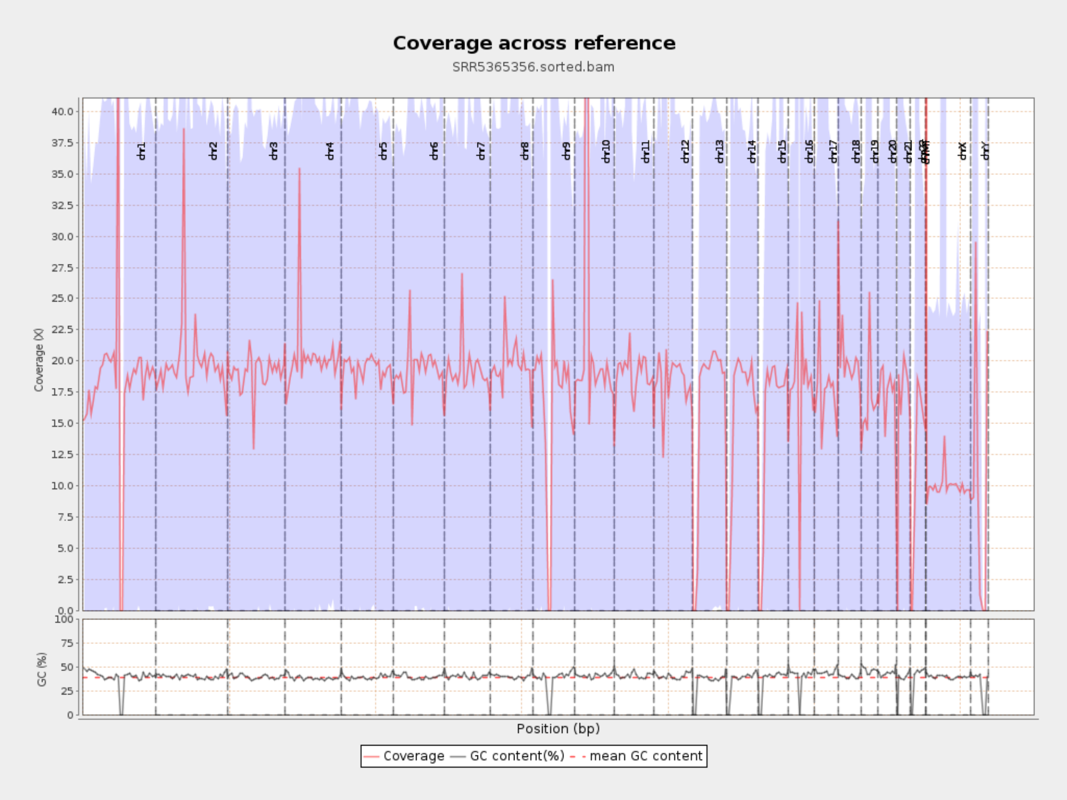
2.7. Chromosome stats

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

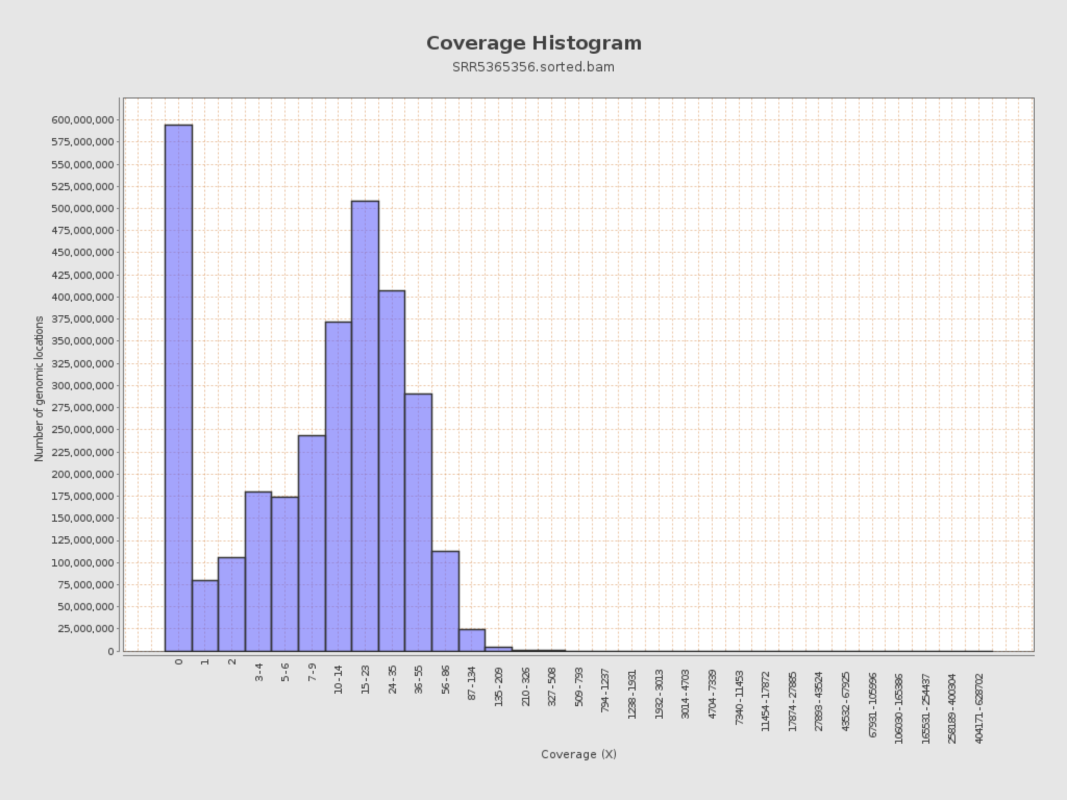
		bases	coverage	deviation
chr1	249250621	4577543127	18.3652	603.0991
chr2	243199373	4878192370	20.0584	133.6496
chr3	198022430	3773507178	19.056	38.9688
chr4	191154276	3901937703	20.4125	127.0051
chr5	180915260	3484270816	19.2591	24.147
chr6	171115067	3319677853	19.4003	80.8225
chr7	159138663	3059673707	19.2265	167.2491
chr8	146364022	2870479535	19.6119	71.8481
chr9	141213431	2362252237	16.7282	198.6329
chr10	135534747	3004593095	22.1684	498.6062
chr11	135006516	2561915733	18.9762	123.5445
chr12	133851895	2466111649	18.4242	37.4906
chr13	115169878	1883727914	16.3561	19.3957
chr14	107349540	1686568672	15.711	25.6194
chr15	102531392	1525338218	14.8768	23.1501
chr16	90354753	1569380327	17.3691	77.1435
chr17	81195210	1434934826	17.6727	101.5411
chr18	78077248	1586467989	20.3192	230.9283
chr19	59128983	1002140236	16.9484	295.5503
chr20	63025520	1102556482	17.4938	39.9842
chr21	48129895	792241661	16.4605	71.8254
chr22	51304566	610447669	11.8985	54.2047
chrMT	16571	49543216	2,989.7541	606.5154
chrX	155270560	1550640546	9.9867	49.778

chrY	59373566	605167681	10.1925	234.0158

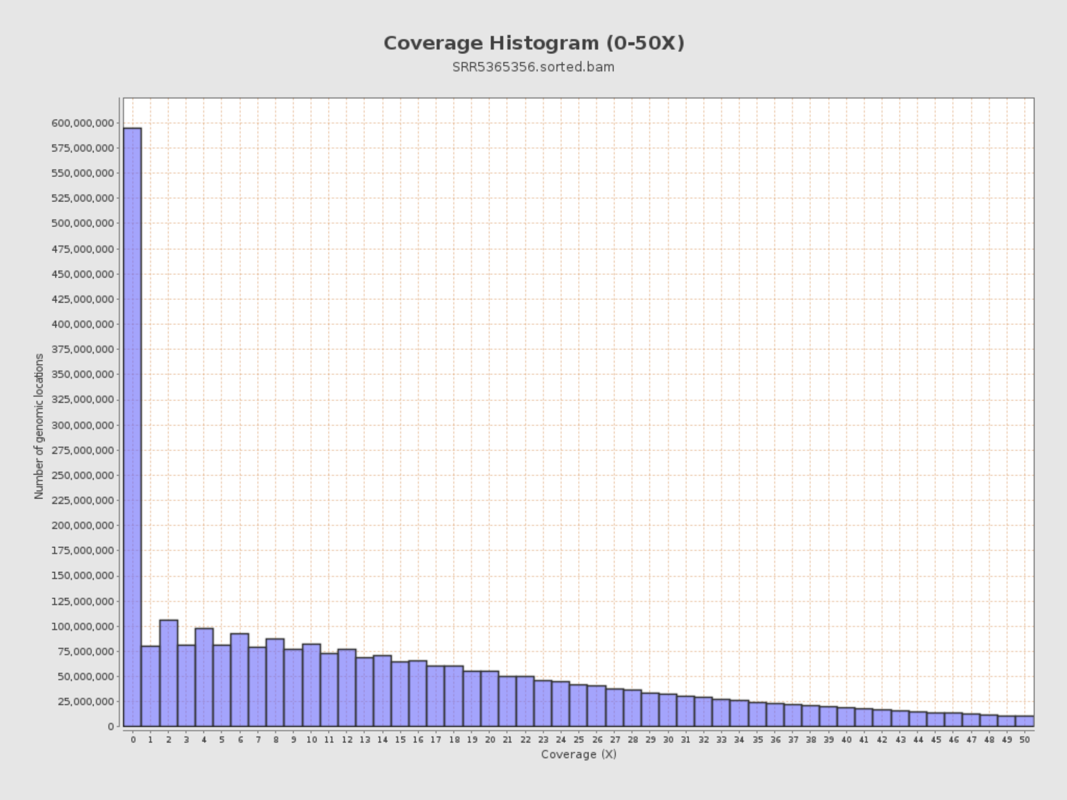
3. Results : Coverage across reference



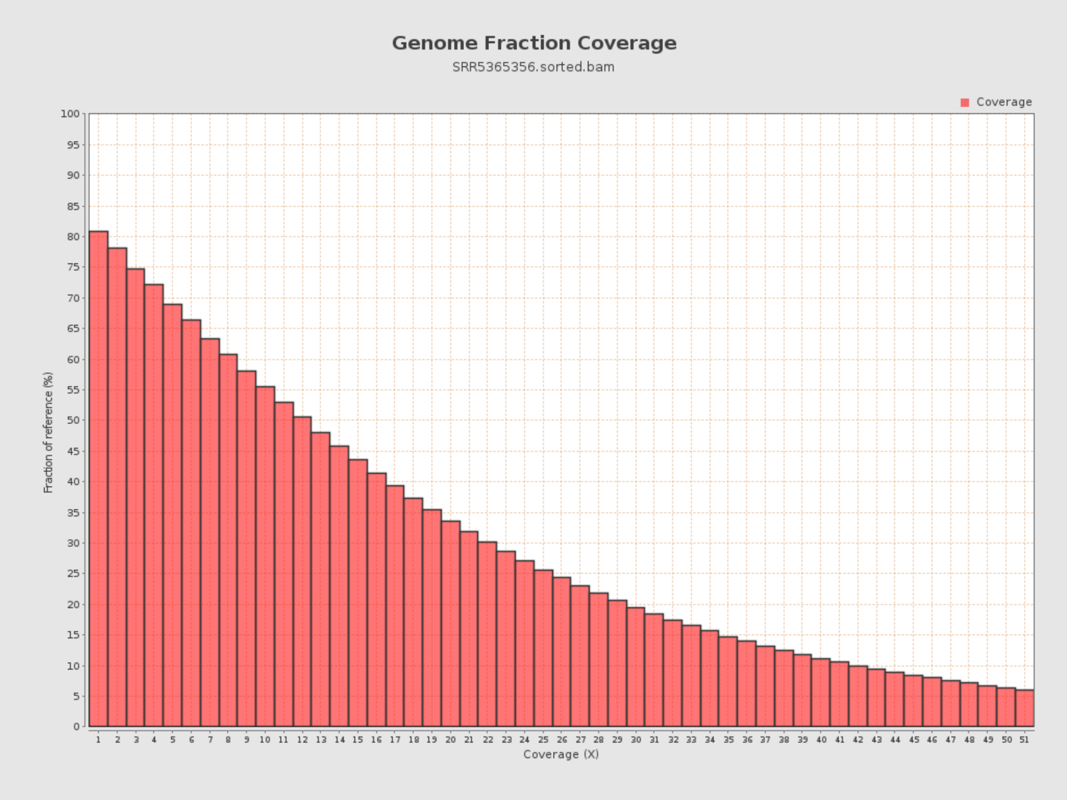
4. Results : Coverage Histogram



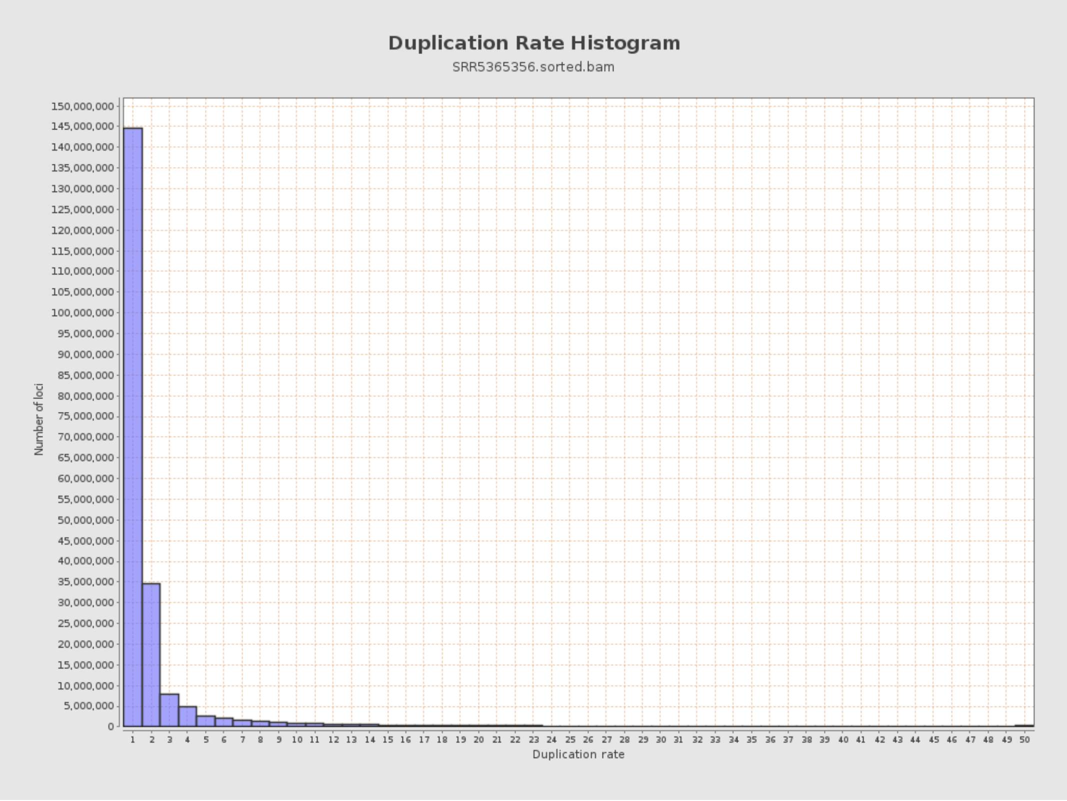
5. Results : Coverage Histogram (0-50X)



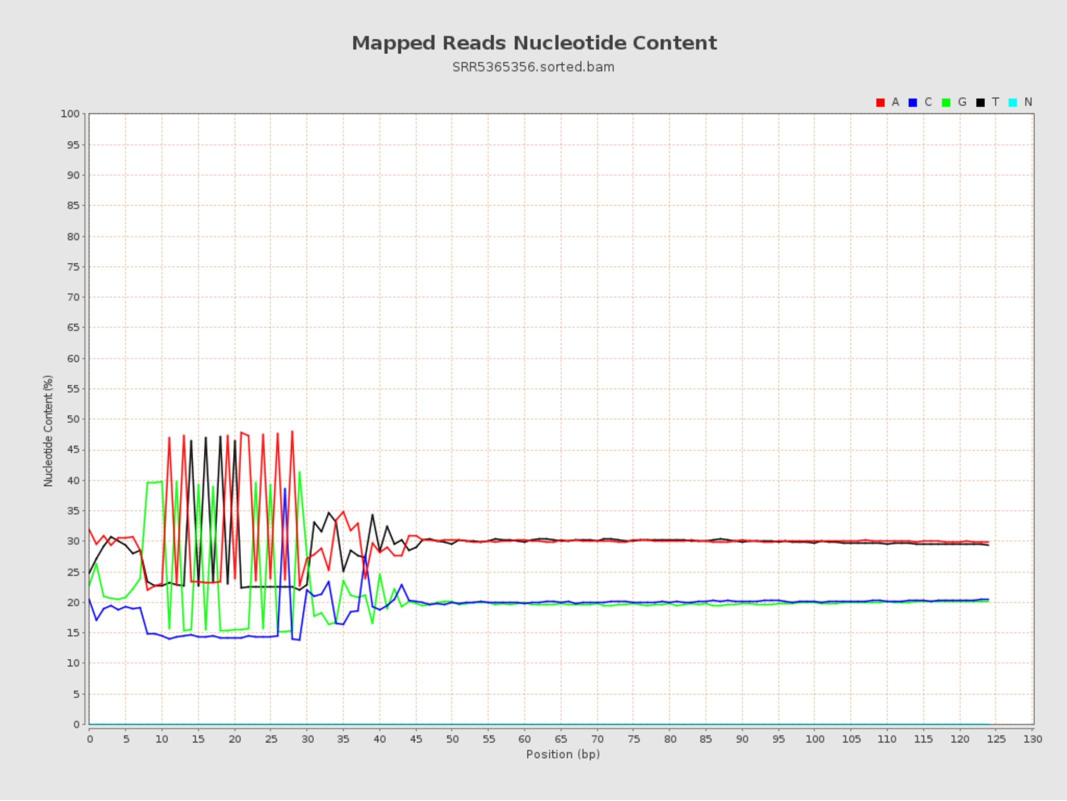
6. Results : Genome Fraction Coverage



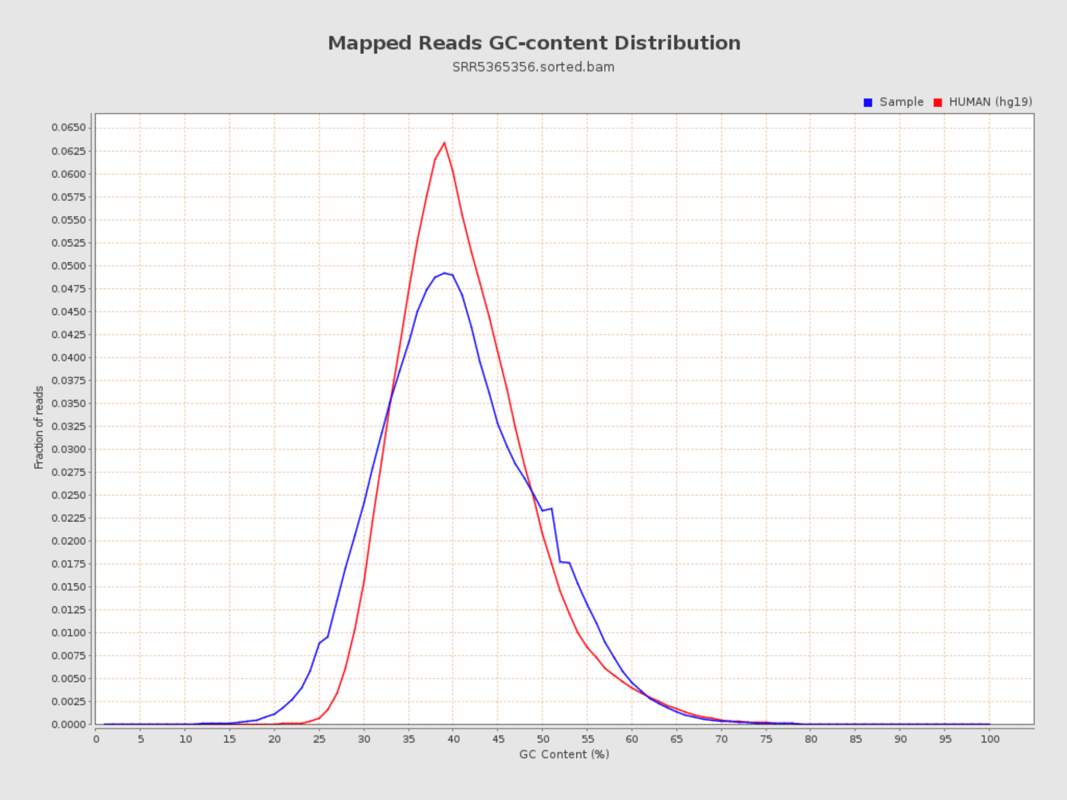
7. Results : Duplication Rate Histogram



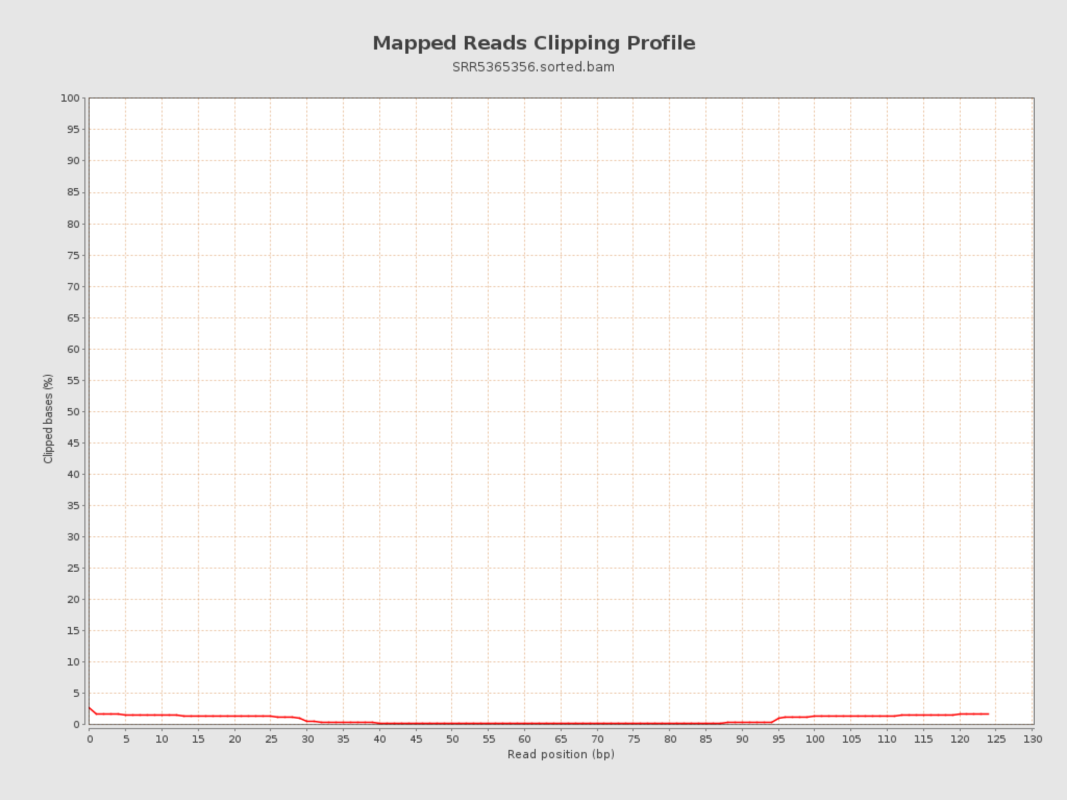
8. Results : Mapped Reads Nucleotide Content



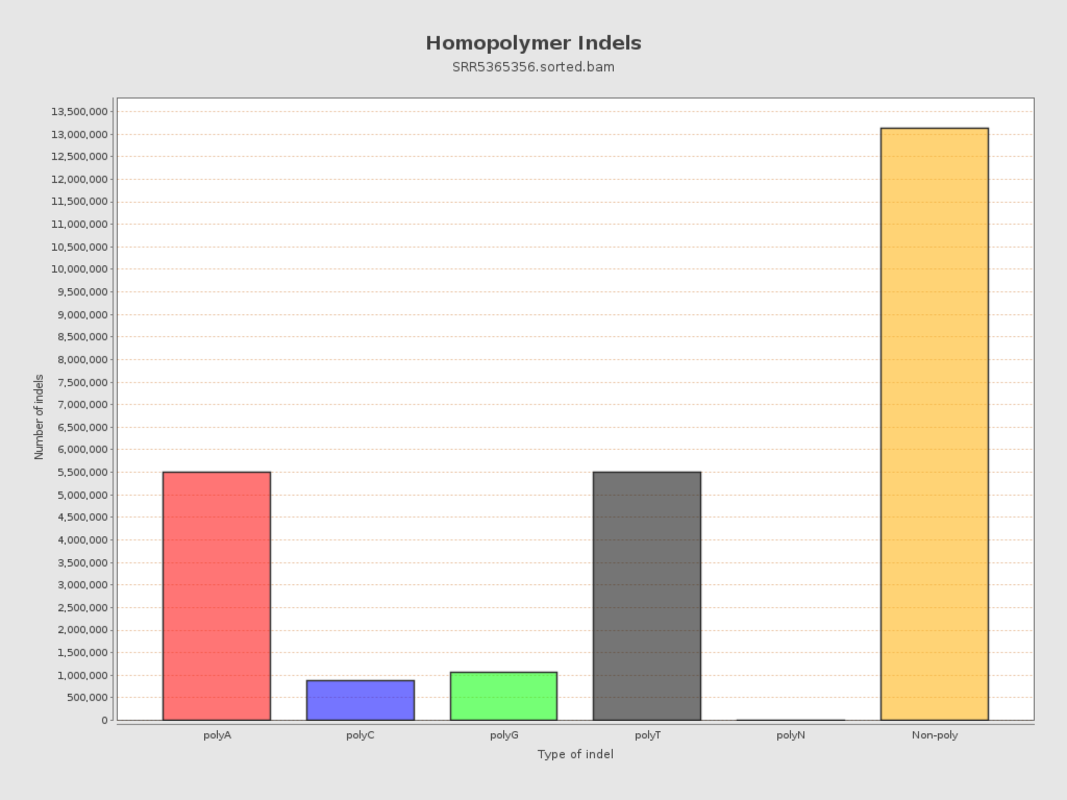
9. Results : Mapped Reads GC-content Distribution



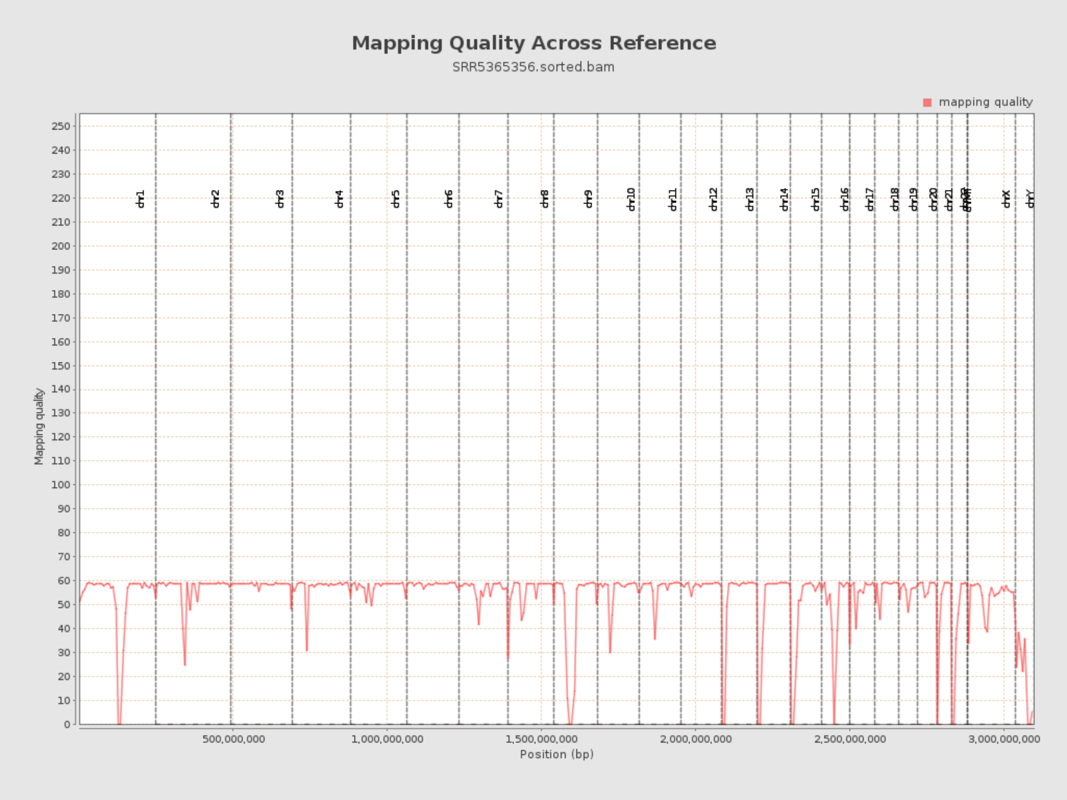
10. Results : Mapped Reads Clipping Profile



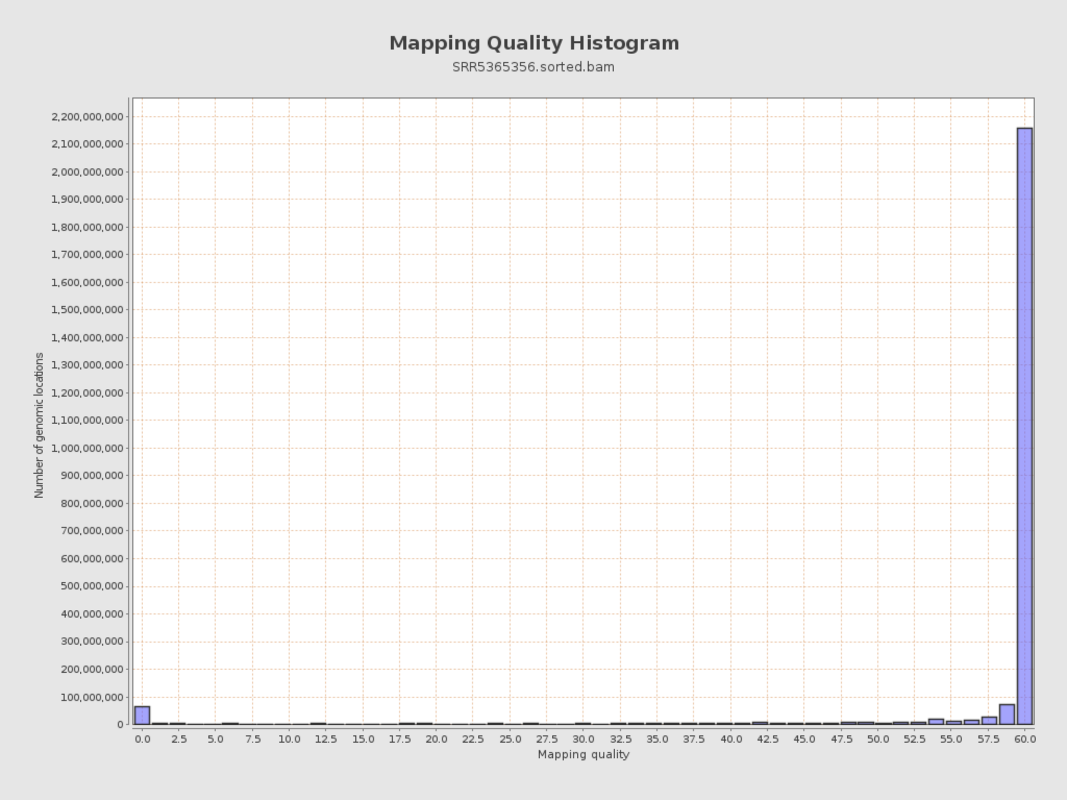
11. Results : Homopolymer Indels



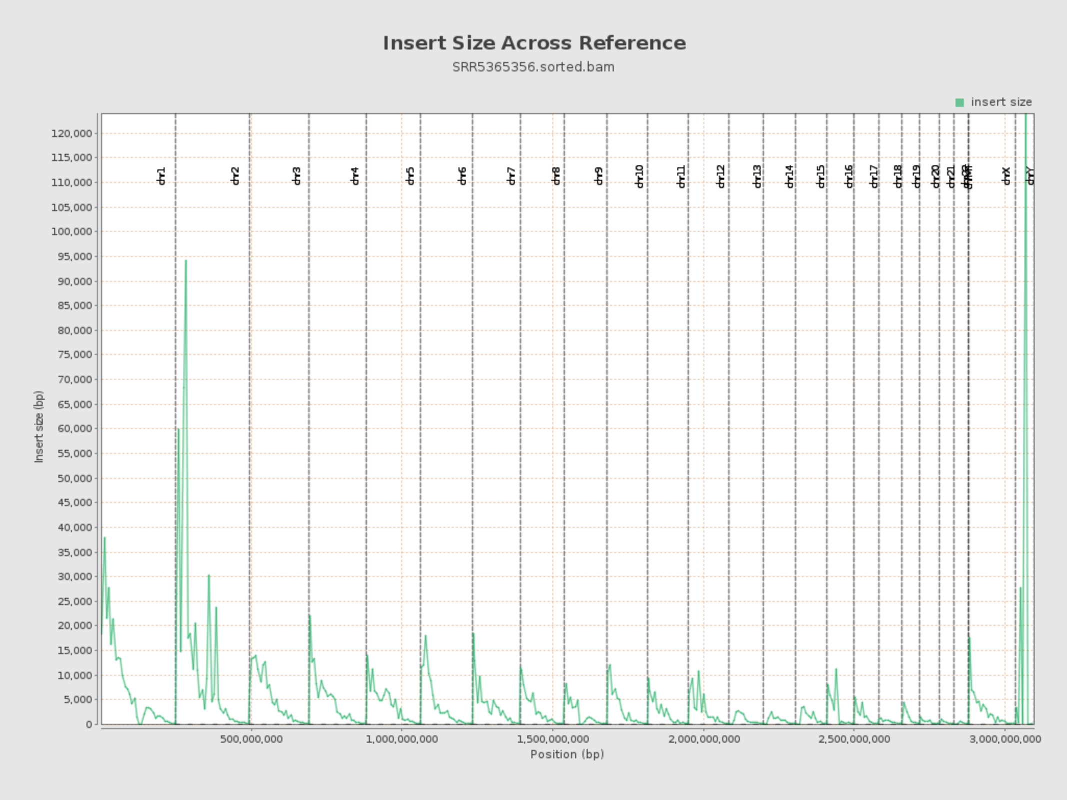
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram