Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/04 05:27:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR504705.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_SRR504705 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR504705_1.fastq.gz SRR504705_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Jan 04 05:27:01 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR504705.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	506,077,902
Mapped reads	456,025,762 / 90.11%
Unmapped reads	50,052,140 / 9.89%
Mapped paired reads	456,025,762 / 90.11%
Mapped reads, first in pair	229,998,561 / 45.45%
Mapped reads, second in pair	226,027,201 / 44.66%
Mapped reads, both in pair	448,458,090 / 88.61%
Mapped reads, singletons	7,567,672 / 1.5%
Secondary alignments	0
Supplementary alignments	2,331,874 / 0.46%
Read min/max/mean length	30 / 100 / 100.19
Duplicated reads (estimated)	121,601,365 / 24.03%
Duplication rate	23.44%
Clipped reads	41,496,704 / 8.2%

2.2. ACGT Content

Number/percentage of A's	11,855,873,584 / 26.5%
Number/percentage of C's	10,400,620,563 / 23.25%
Number/percentage of T's	11,873,749,101 / 26.54%
Number/percentage of G's	10,582,390,605 / 23.65%
Number/percentage of N's	27,179,305 / 0.06%

GC Percentage	46.9%

2.3. Coverage

Mean	14.4553
Standard Deviation	34.2975

2.4. Mapping Quality

Mean Mapping Quality	53.77

2.5. Insert size

Mean	43,774.52
Standard Deviation	1,955,475.01
P25/Median/P75	374 / 409 / 449

2.6. Mismatches and indels

General error rate	0.8%
Mismatches	349,685,423
Insertions	3,085,760
Mapped reads with at least one insertion	0.66%
Deletions	3,851,812
Mapped reads with at least one deletion	0.82%
Homopolymer indels	40.97%

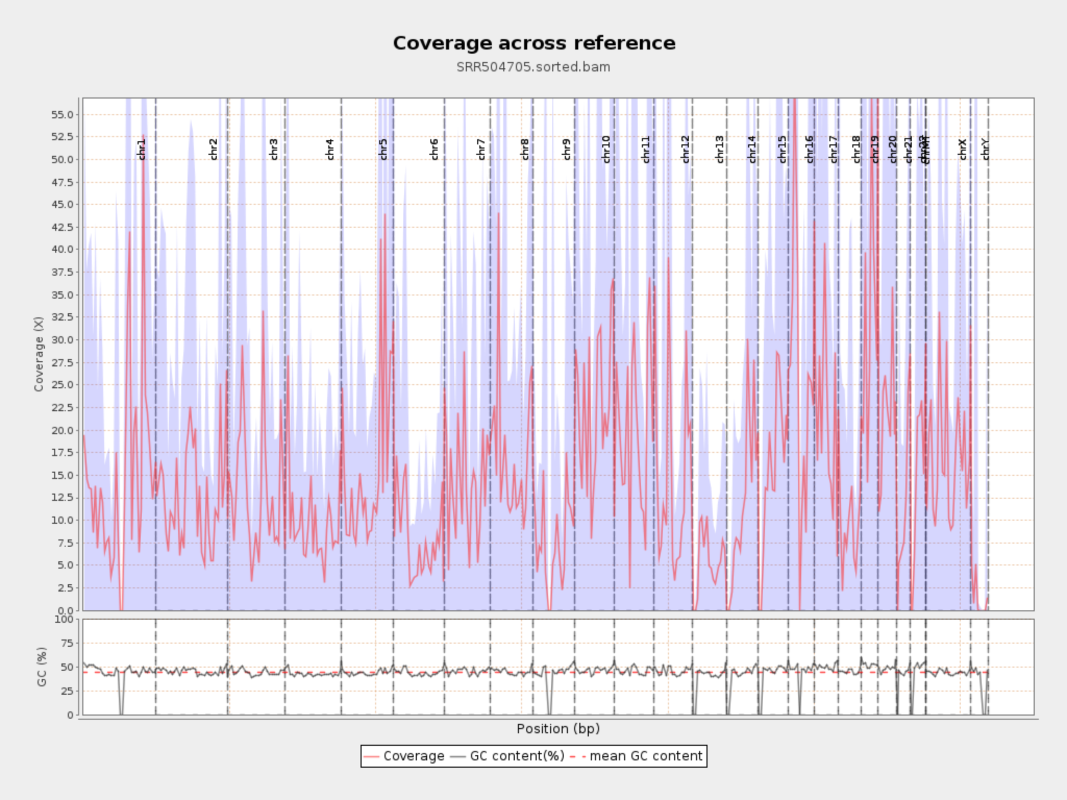
2.7. Chromosome stats

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

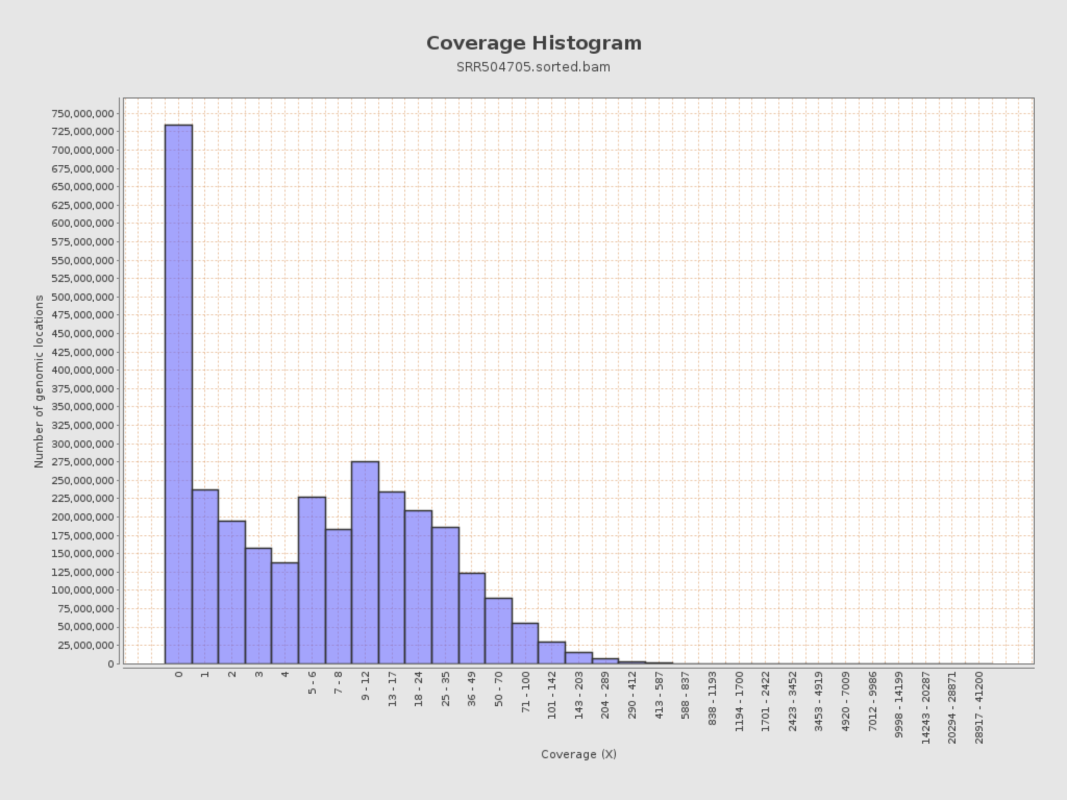
		bases	coverage	deviation
chr1	249250621	3684900240	14.7839	31.4125
chr2	243199373	3059220864	12.5791	23.8506
chr3	198022430	2609227054	13.1764	24.9499
chr4	191154276	1923643375	10.0633	17.9555
chr5	180915260	2925797015	16.1722	31.1559
chr6	171115067	1351818256	7.9001	15.7498
chr7	159138663	2292675478	14.4068	24.7687
chr8	146364022	2516803236	17.1955	33.8224
chr9	141213431	1071827135	7.5901	27.8511
chr10	135534747	3039929915	22.4292	35.7894
chr11	135006516	2682629904	19.8704	36.2514
chr12	133851895	2036344084	15.2134	35.8285
chr13	115169878	626936774	5.4436	11.0136
chr14	107349540	1292954229	12.0443	23.7259
chr15	102531392	1587079170	15.479	30.1966
chr16	90354753	2246864508	24.8671	41.8971
chr17	81195210	1746906824	21.5149	40.8586
chr18	78077248	697930890	8.939	98.6396
chr19	59128983	1922294304	32.5102	60.4797
chr20	63025520	1377182023	21.8512	35.6153
chr21	48129895	571090322	11.8656	25.5466
chr22	51304566	736936591	14.364	29.7537
chrMT	16571	199134	12.017	16.9981
chrX	155270560	2664002944	17.1572	28.5842

chrY	59373566	84056641	1.4157	48.8084

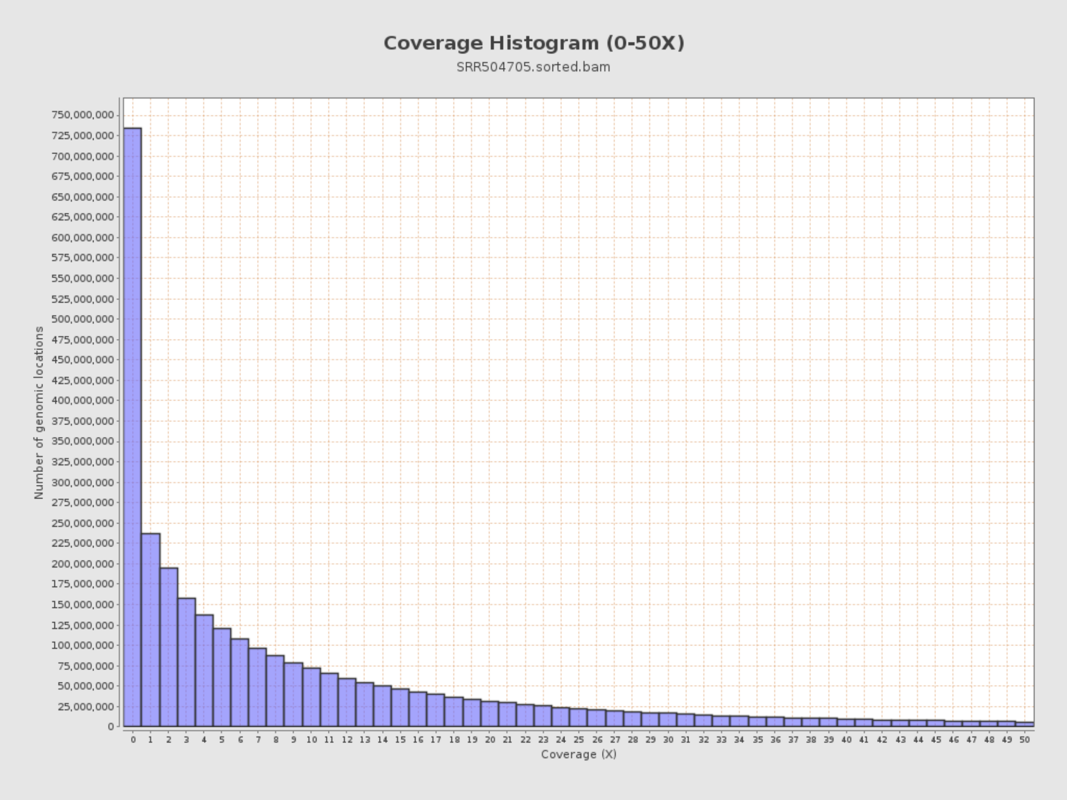
3. Results : Coverage across reference



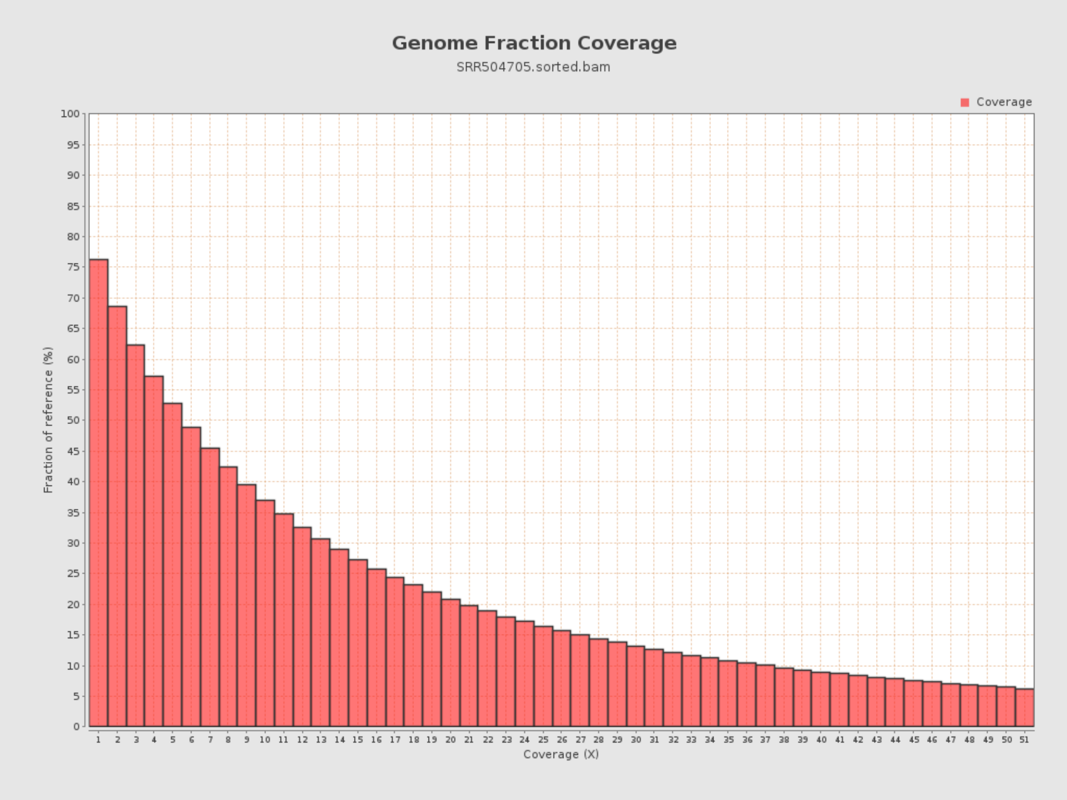
4. Results : Coverage Histogram



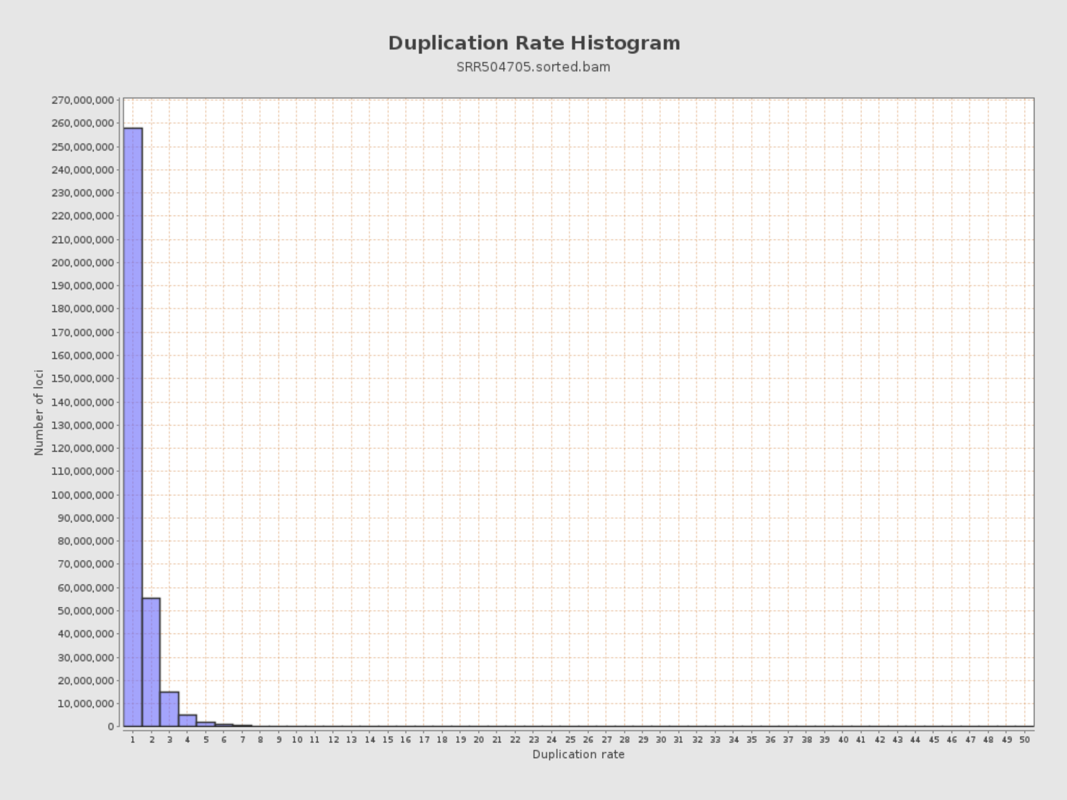
5. Results : Coverage Histogram (0-50X)



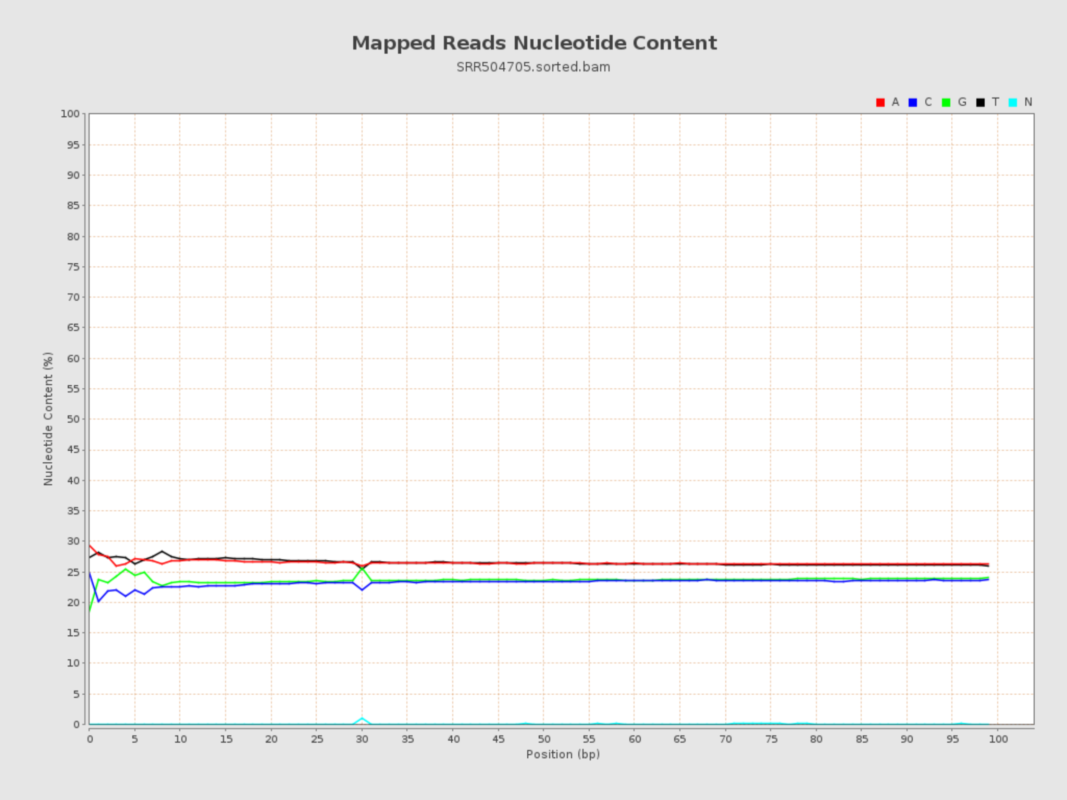
6. Results : Genome Fraction Coverage



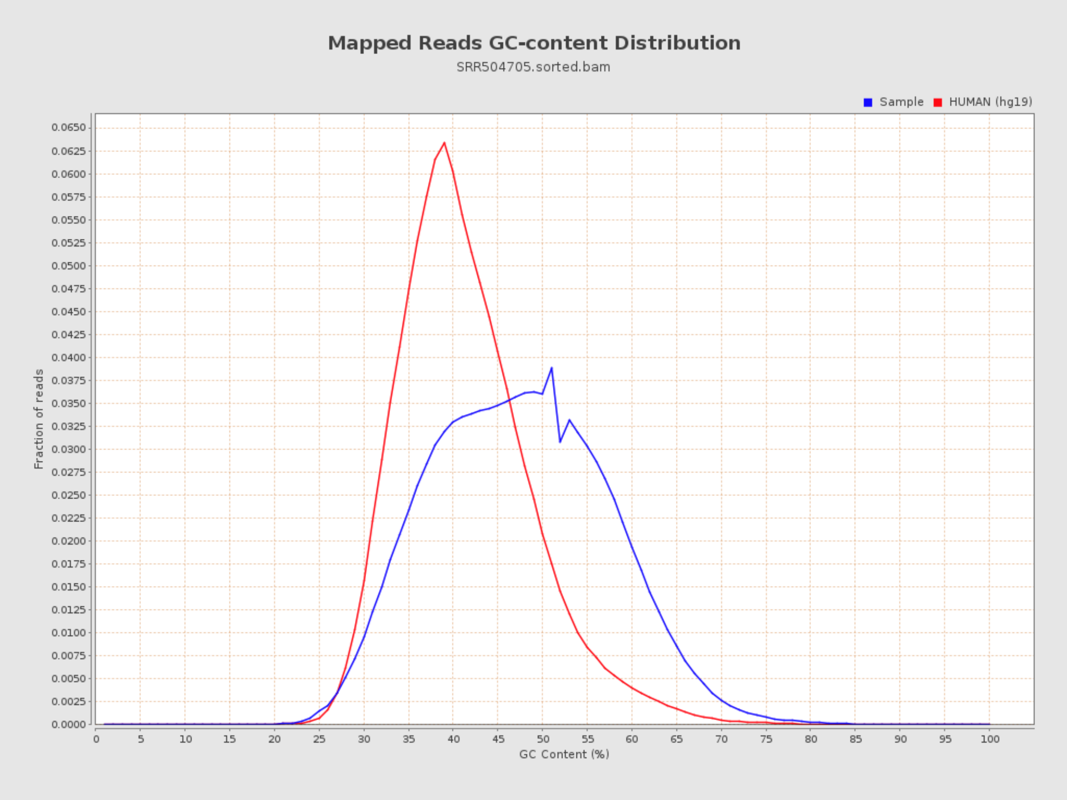
7. Results : Duplication Rate Histogram



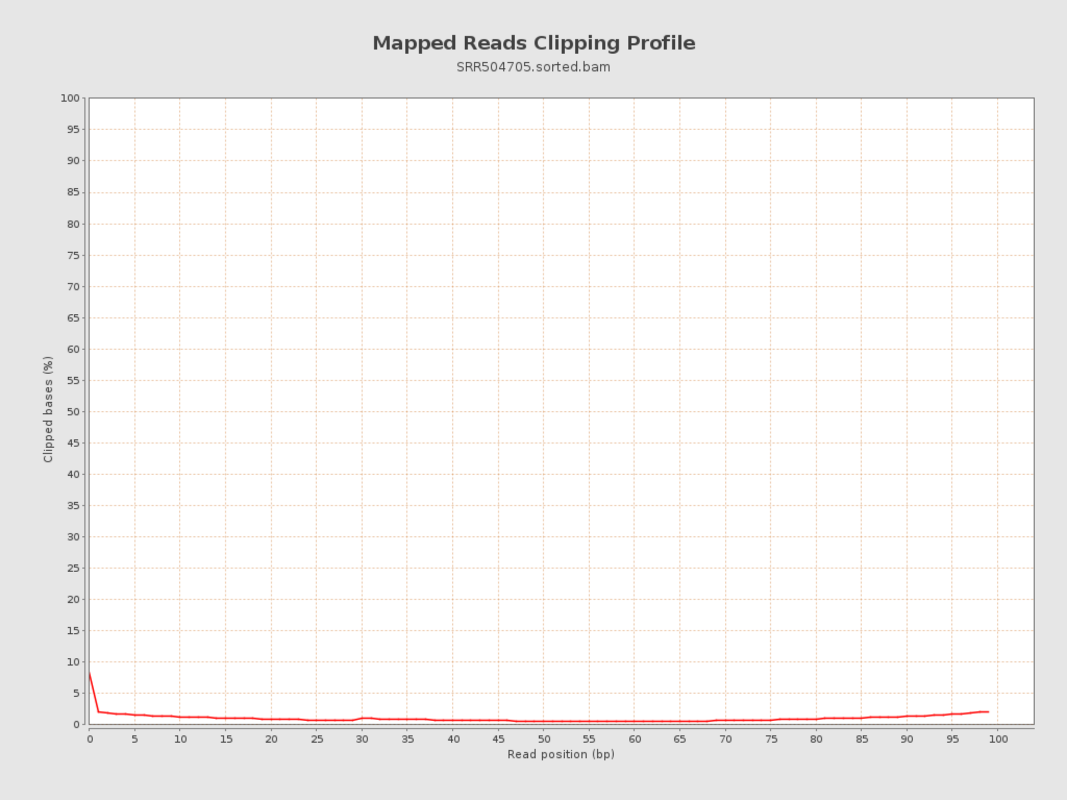
8. Results : Mapped Reads Nucleotide Content



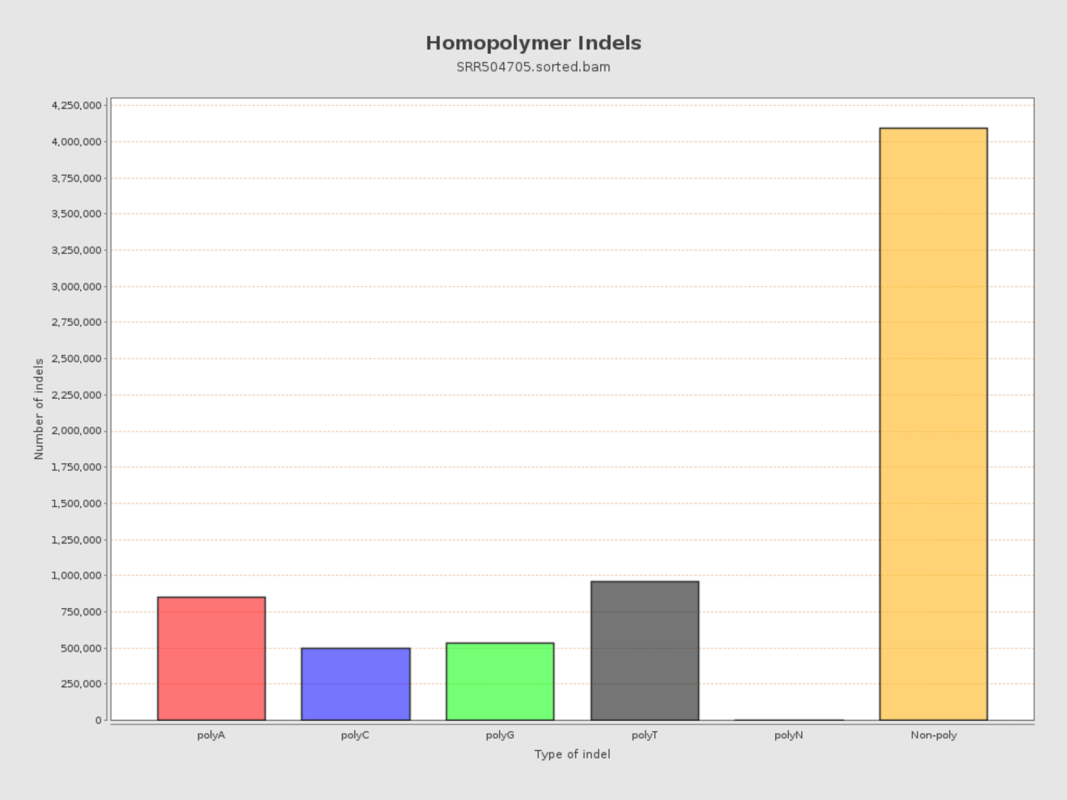
9. Results : Mapped Reads GC-content Distribution



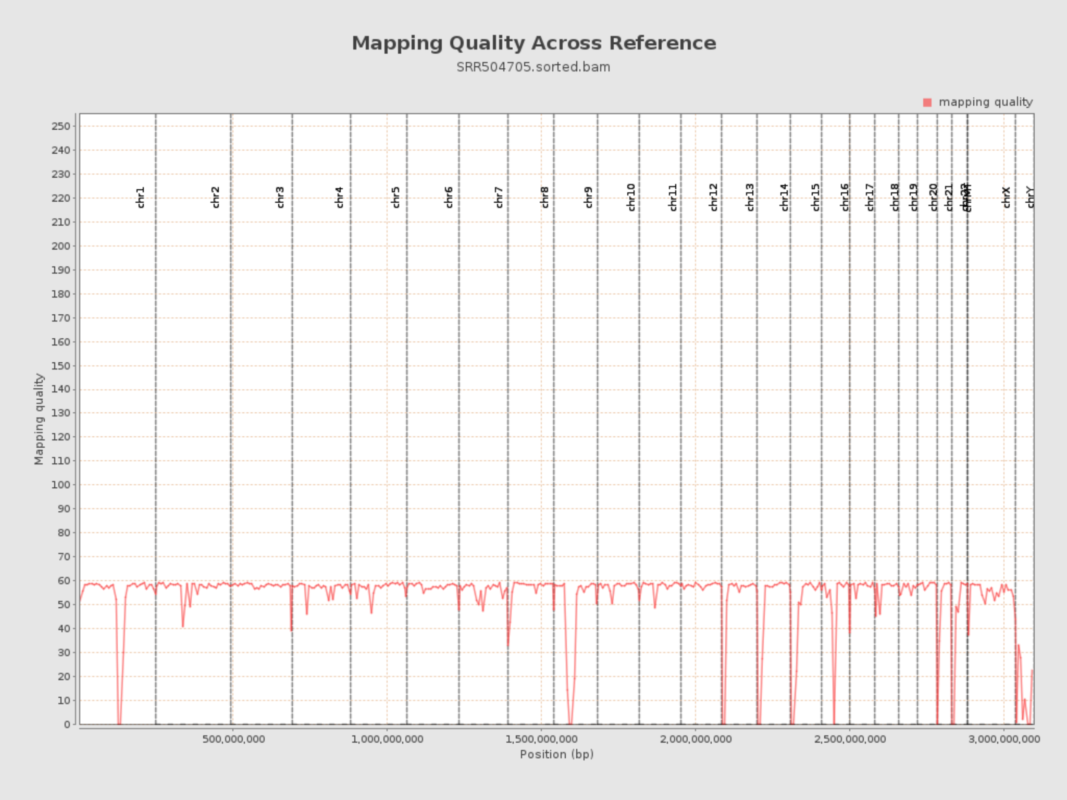
10. Results : Mapped Reads Clipping Profile



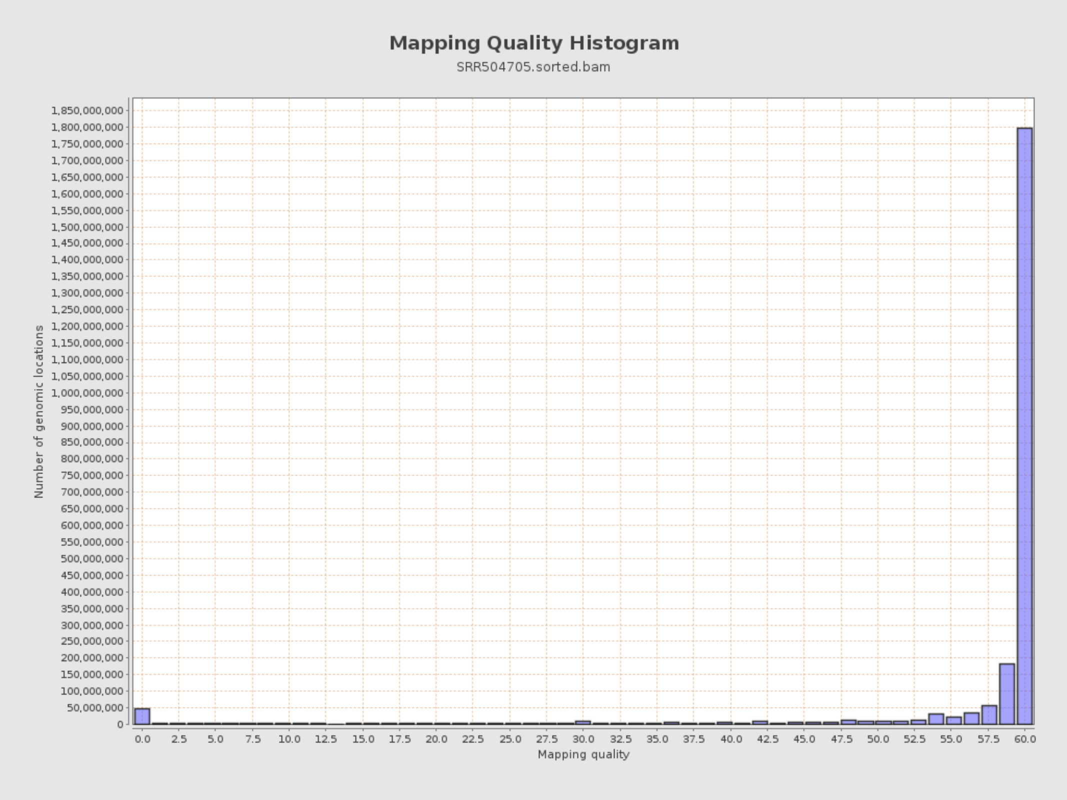
11. Results : Homopolymer Indels



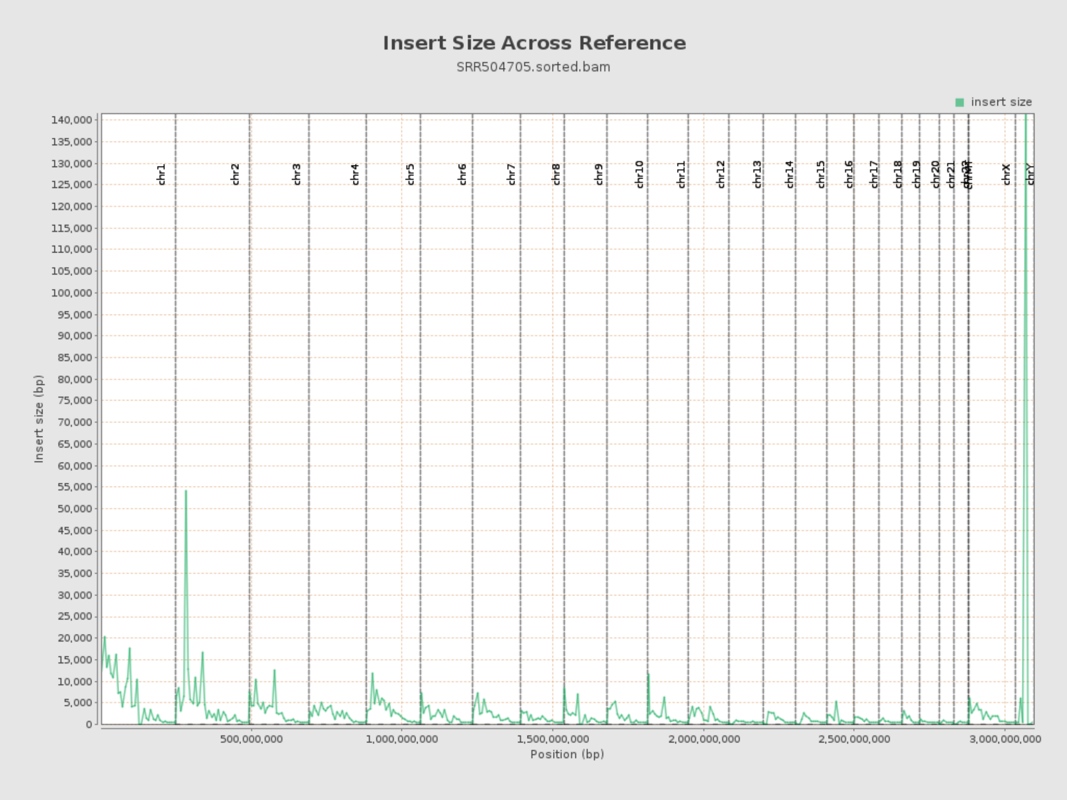
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram