Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/23 14:31:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR504605.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_SRR504605 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR504605_1.fastq.gz SRR504605_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Dec 23 14:31:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR504605.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	437,166,046
Mapped reads	375,488,696 / 85.89%
Unmapped reads	61,677,350 / 14.11%
Mapped paired reads	375,488,696 / 85.89%
Mapped reads, first in pair	187,986,104 / 43%
Mapped reads, second in pair	187,502,592 / 42.89%
Mapped reads, both in pair	373,163,068 / 85.36%
Mapped reads, singletons	2,325,628 / 0.53%
Secondary alignments	0
Supplementary alignments	1,931,911 / 0.44%
Read min/max/mean length	30 / 100 / 100.18
Duplicated reads (estimated)	93,541,564 / 21.4%
Duplication rate	22.22%
Clipped reads	18,120,109 / 4.14%

2.2. ACGT Content

Number/percentage of A's	9,811,335,694 / 26.33%
Number/percentage of C's	8,698,488,640 / 23.34%
Number/percentage of T's	9,837,199,913 / 26.4%
Number/percentage of G's	8,856,659,002 / 23.77%
Number/percentage of N's	63,917,380 / 0.17%

GC Percentage	47.11%

2.3. Coverage

Mean	12.0416
Standard Deviation	24.9808

2.4. Mapping Quality

Mean Mapping Quality	53.96

2.5. Insert size

Mean	29,653.49
Standard Deviation	1,680,575.12
P25/Median/P75	180 / 213 / 267

2.6. Mismatches and indels

General error rate	0.87%
Mismatches	316,673,903
Insertions	2,808,643
Mapped reads with at least one insertion	0.73%
Deletions	3,746,592
Mapped reads with at least one deletion	0.97%
Homopolymer indels	40.09%

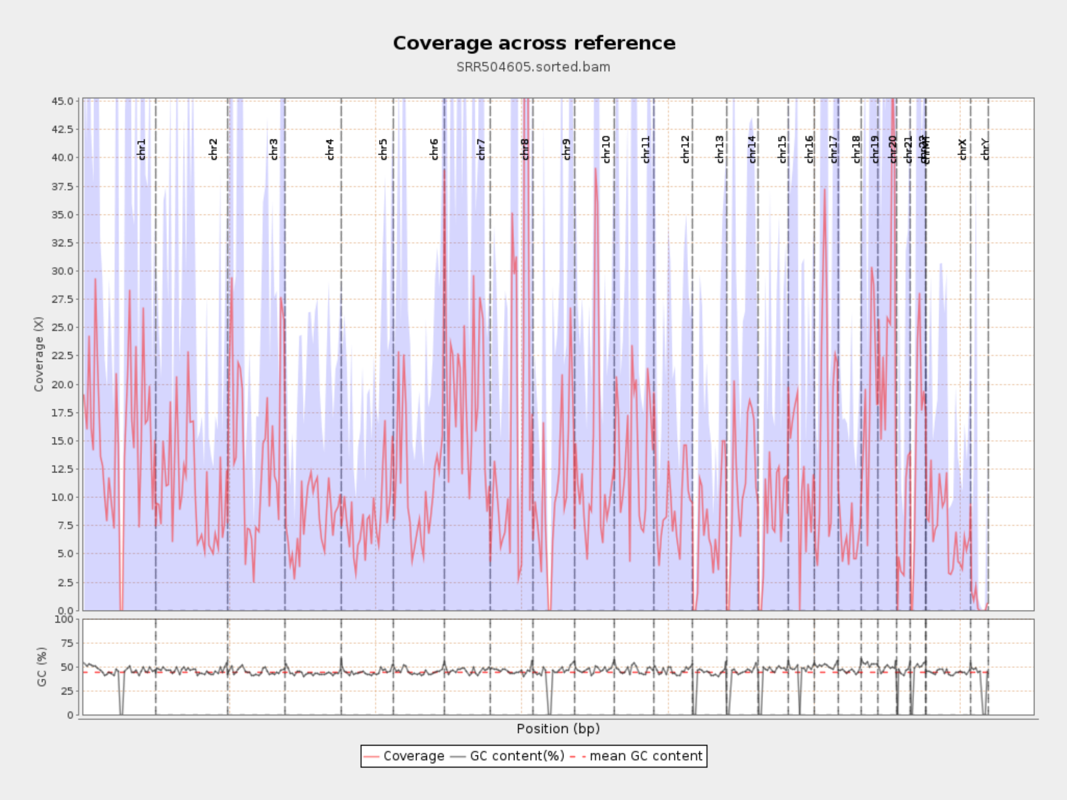
2.7. Chromosome stats

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

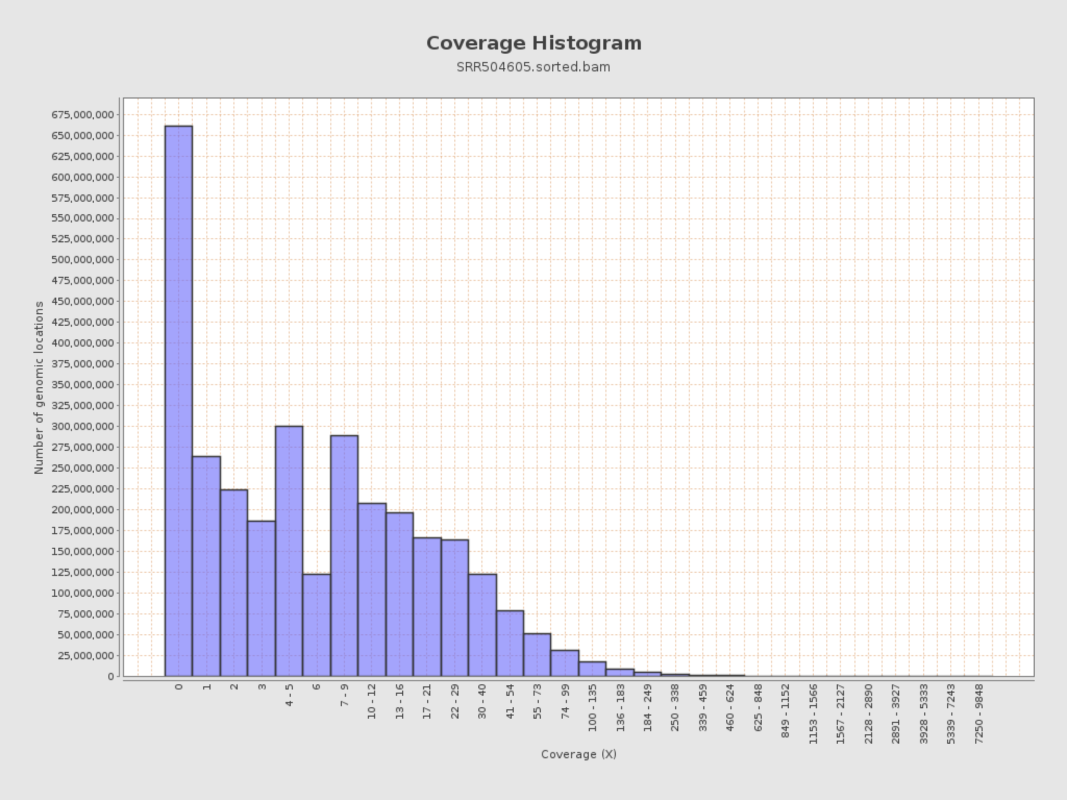
		bases	coverage	deviation
chr1	249250621	3831972159	15.374	26.0034
chr2	243199373	2558711591	10.521	19.1159
chr3	198022430	2758887669	13.9322	23.1483
chr4	191154276	1557605016	8.1484	13.0041
chr5	180915260	1515075272	8.3745	14.1345
chr6	171115067	1904490452	11.1299	18.2162
chr7	159138663	3031884854	19.0518	28.4686
chr8	146364022	2841351917	19.4129	47.834
chr9	141213431	1464755990	10.3726	20.2473
chr10	135534747	1754175378	12.9426	24.5148
chr11	135006516	1902480336	14.0918	23.9633
chr12	133851895	1270917235	9.495	16.1078
chr13	115169878	845417651	7.3406	13.8267
chr14	107349540	1244186856	11.5901	20.2326
chr15	102531392	830791501	8.1028	15.1633
chr16	90354753	1088825424	12.0506	20.7046
chr17	81195210	1354362492	16.6803	51.5753
chr18	78077248	487237612	6.2405	28.2485
chr19	59128983	1100283290	18.6082	32.3874
chr20	63025520	1678689052	26.6351	39.8701
chr21	48129895	353549028	7.3457	18.7239
chr22	51304566	767599853	14.9616	27.8985
chrMT	16571	246866	14.8975	11.9166
chrX	155270560	1096568801	7.0623	12.534

chrY	59373566	37152408	0.6257	14.7176

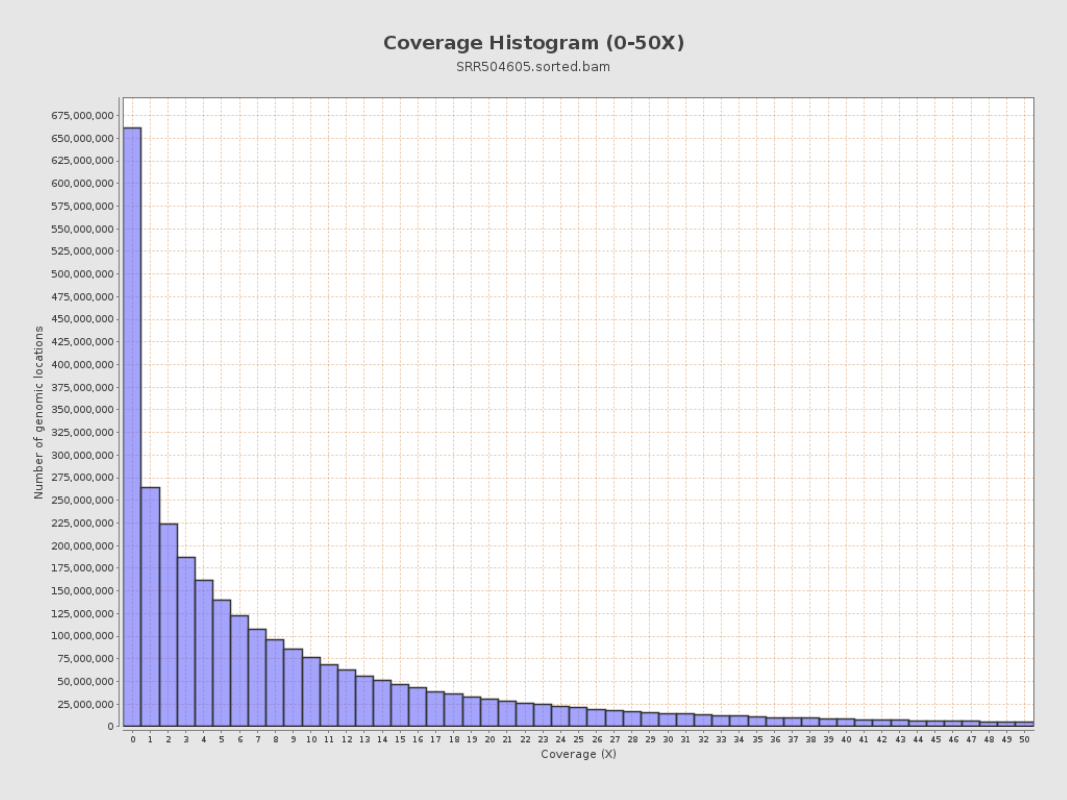
3. Results : Coverage across reference



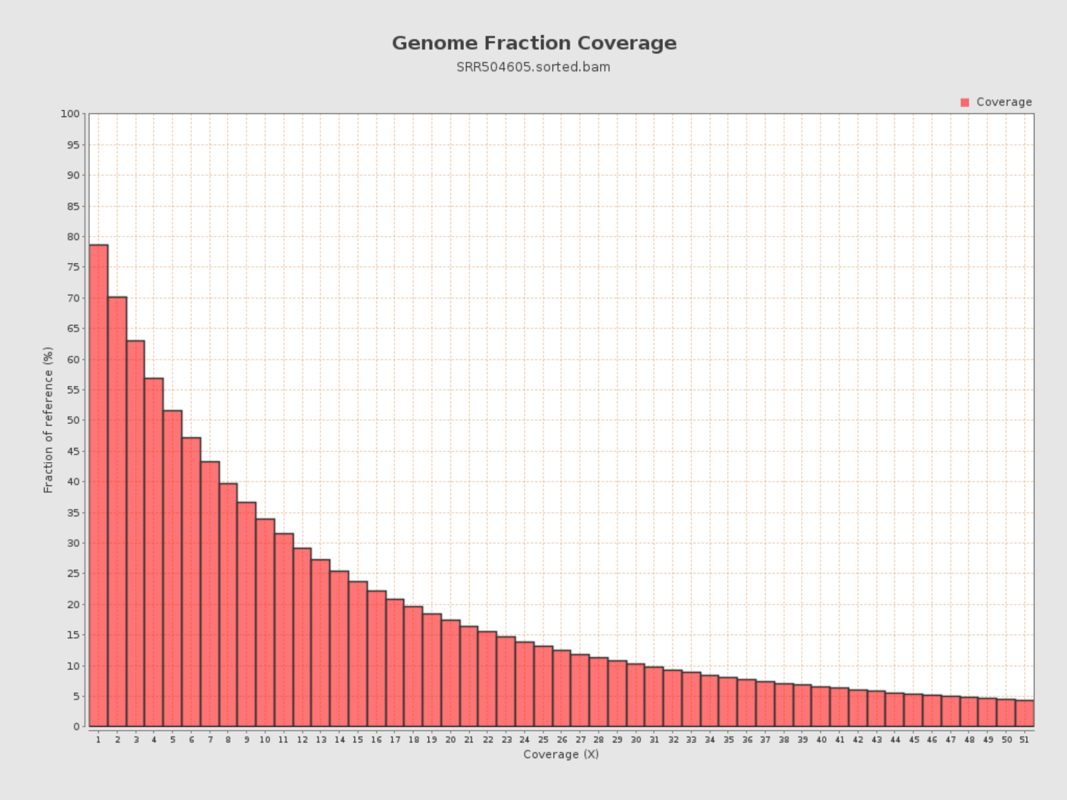
4. Results : Coverage Histogram



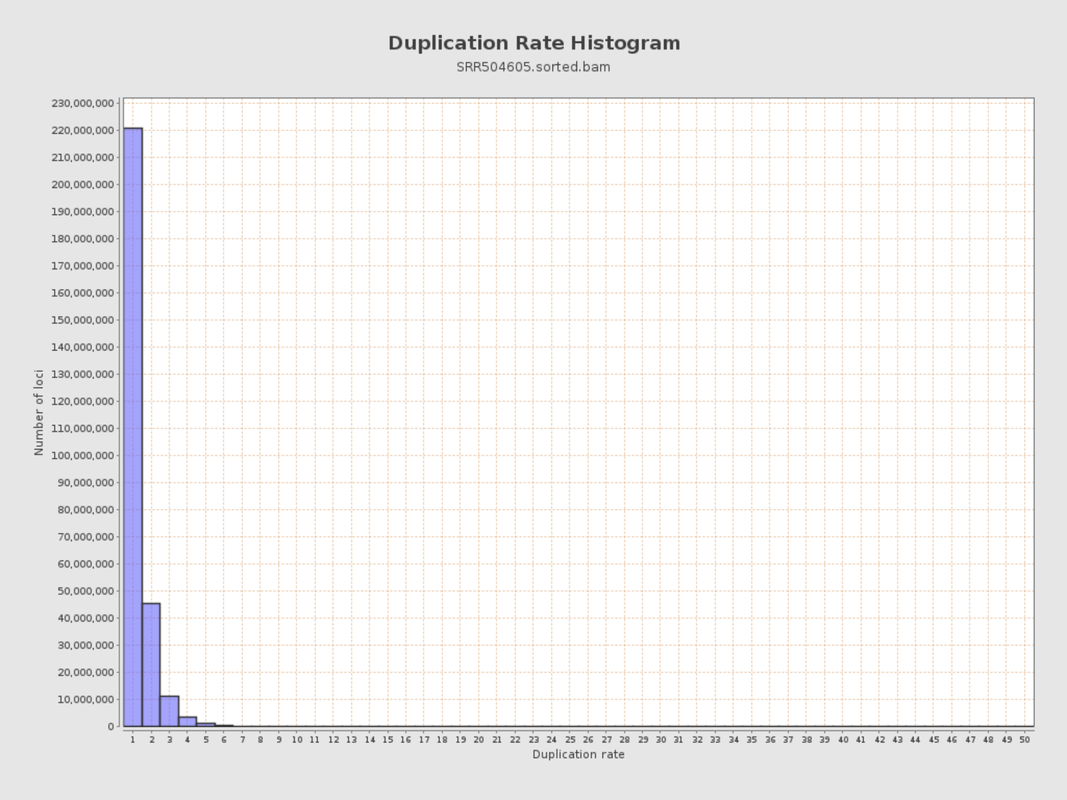
5. Results : Coverage Histogram (0-50X)



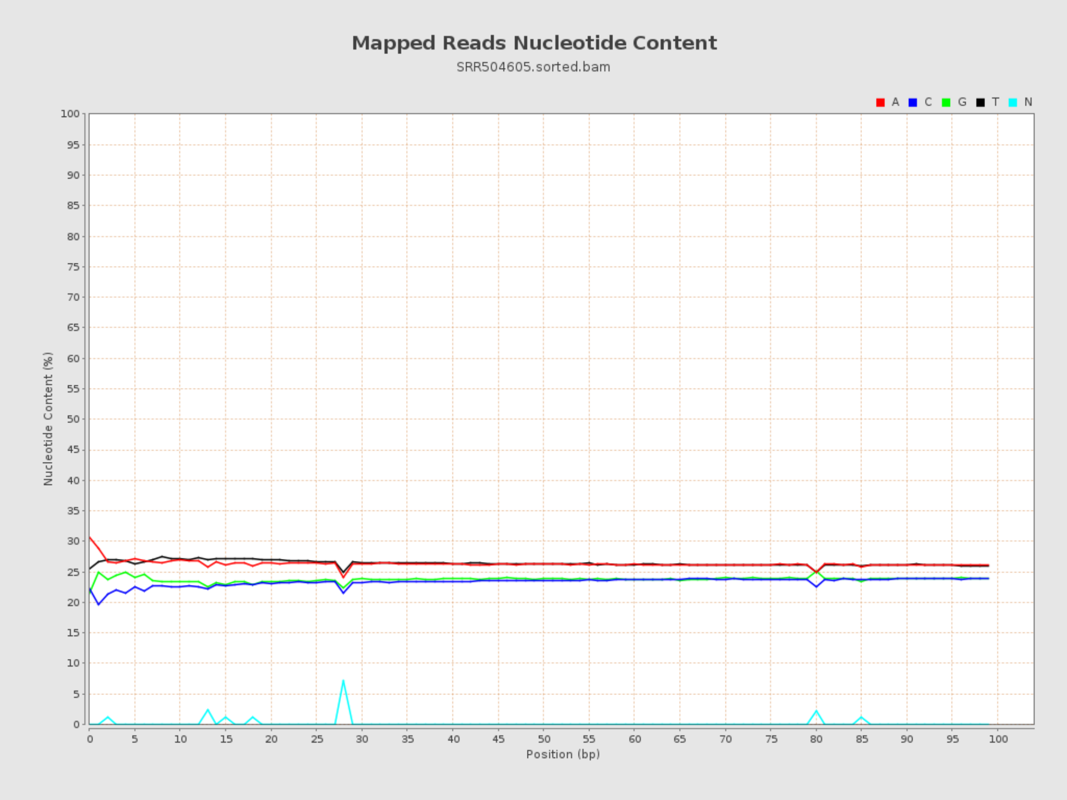
6. Results : Genome Fraction Coverage



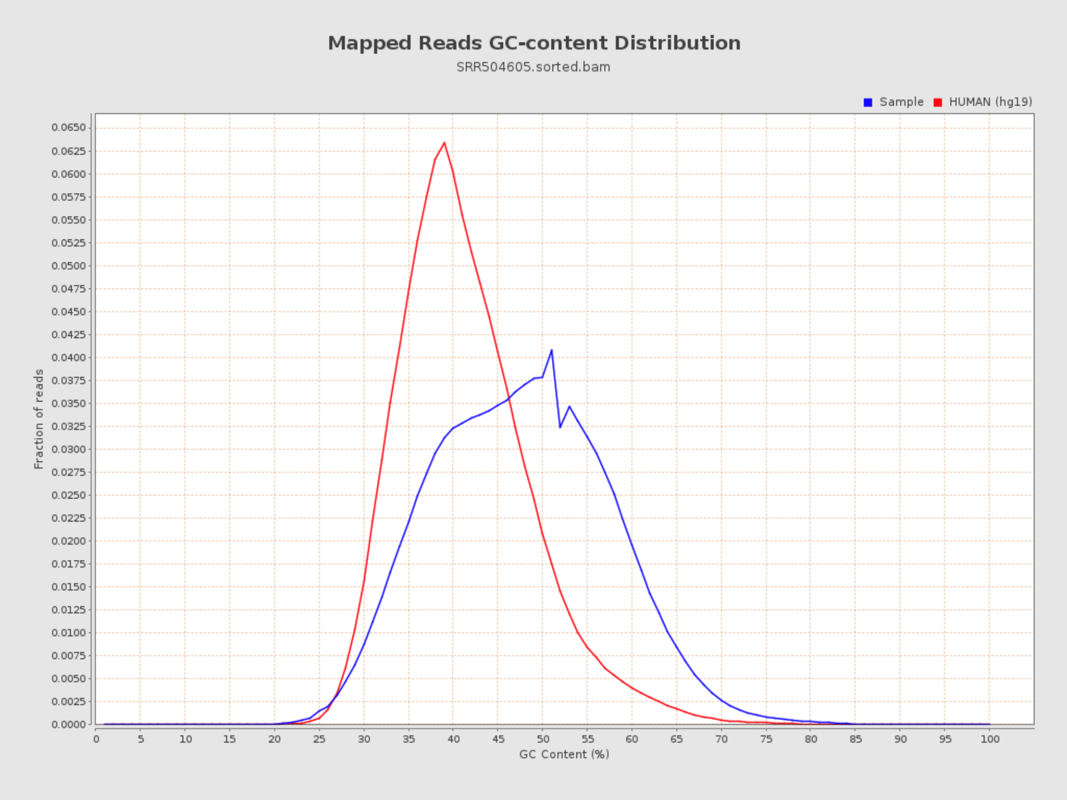
7. Results : Duplication Rate Histogram



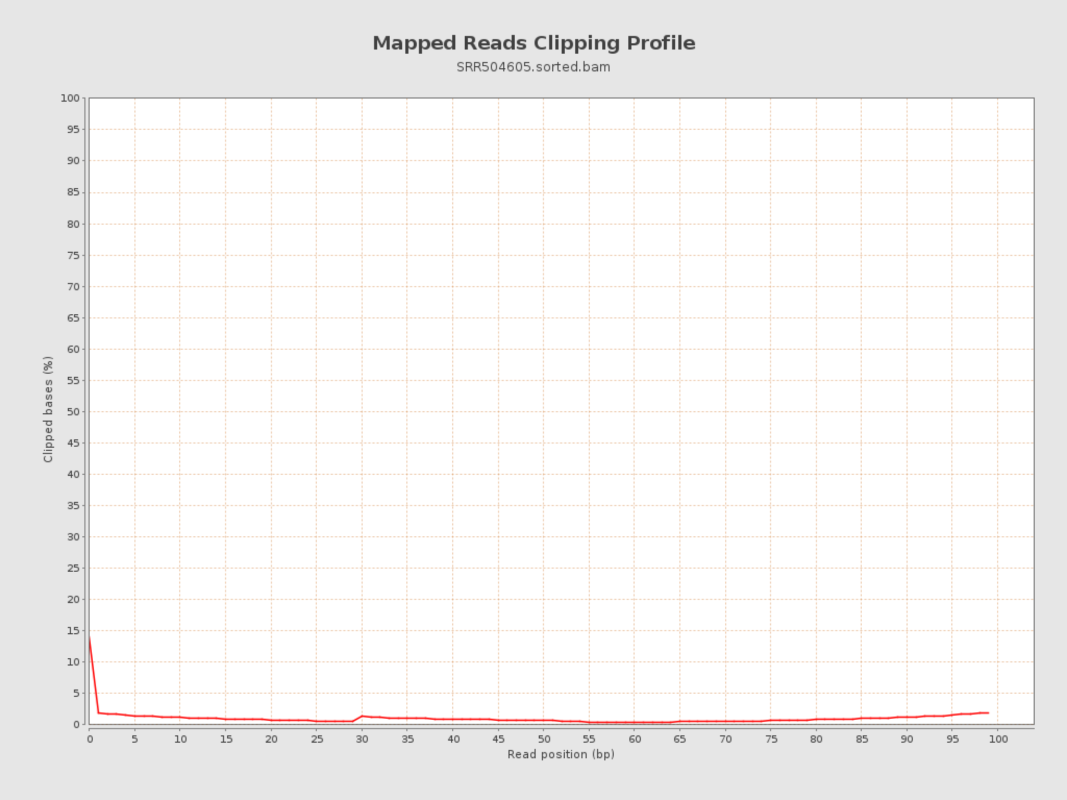
8. Results : Mapped Reads Nucleotide Content



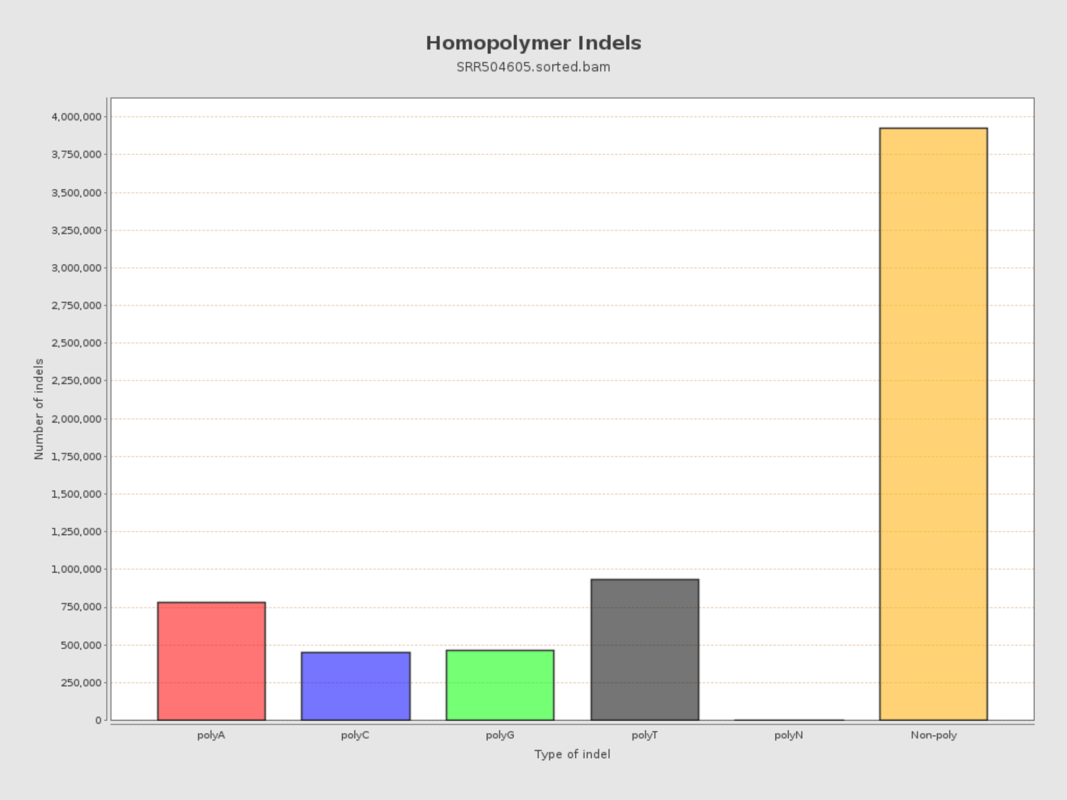
9. Results : Mapped Reads GC-content Distribution



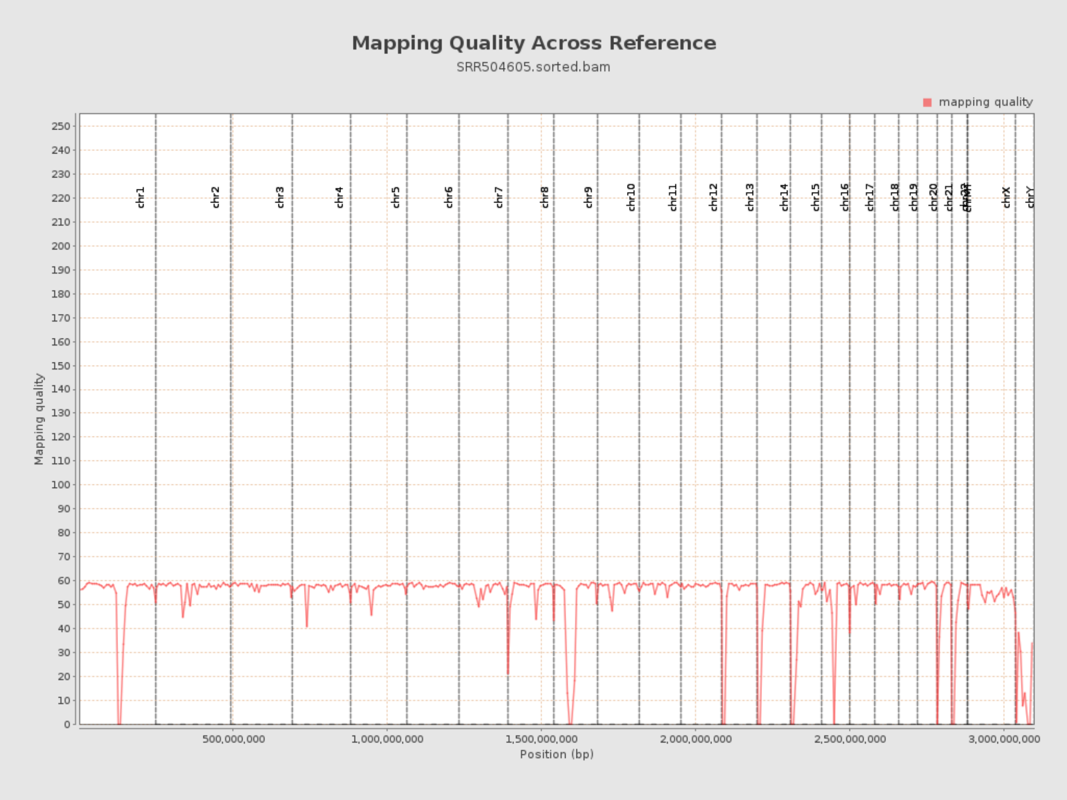
10. Results : Mapped Reads Clipping Profile



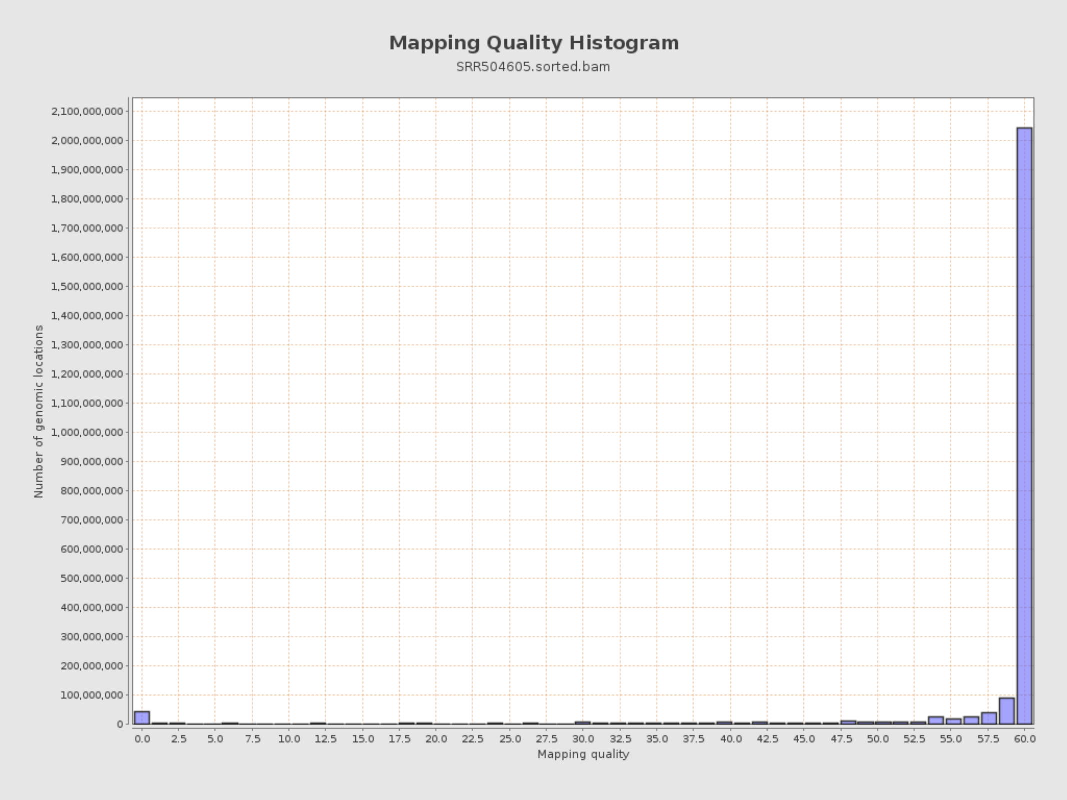
11. Results : Homopolymer Indels



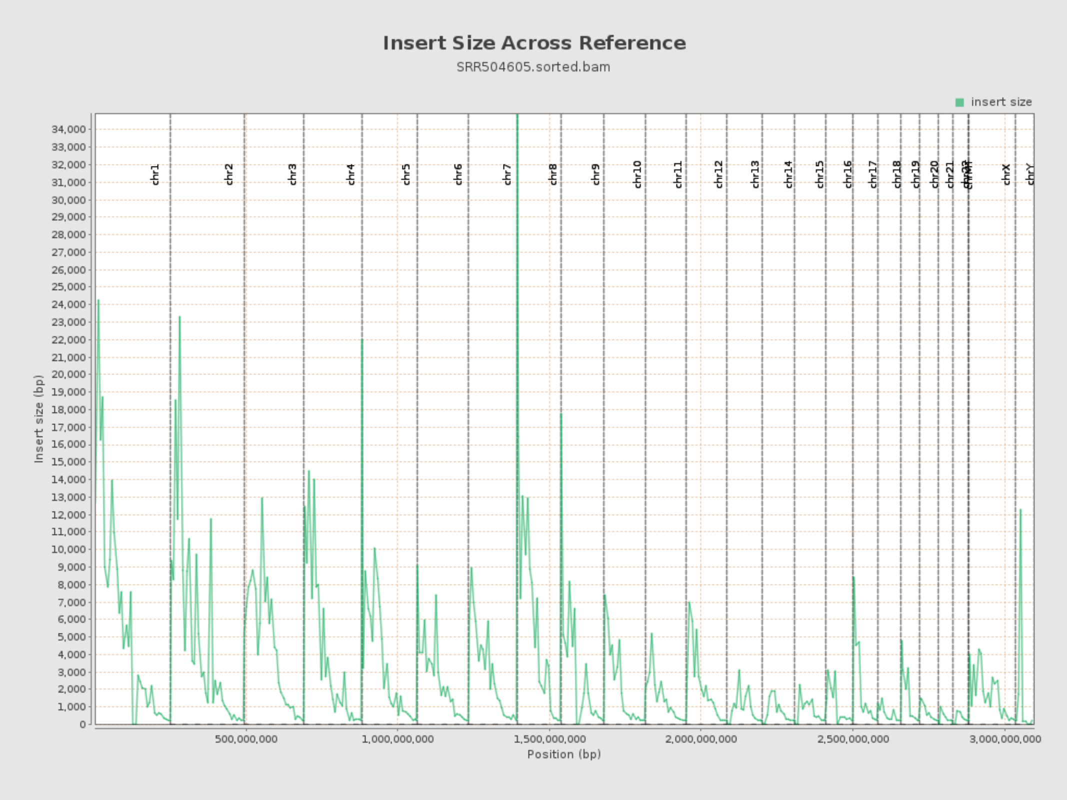
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram