Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/02 16:44:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR504699.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_SRR504699 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR504699_1.fastq.gz SRR504699_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Jan 02 16:44:07 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR504699.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	504,585,878
Mapped reads	457,360,252 / 90.64%
Unmapped reads	47,225,626 / 9.36%
Mapped paired reads	457,360,252 / 90.64%
Mapped reads, first in pair	230,213,658 / 45.62%
Mapped reads, second in pair	227,146,594 / 45.02%
Mapped reads, both in pair	450,714,394 / 89.32%
Mapped reads, singletons	6,645,858 / 1.32%
Secondary alignments	0
Supplementary alignments	2,361,568 / 0.47%
Read min/max/mean length	30 / 100 / 100.19
Duplicated reads (estimated)	111,131,987 / 22.02%
Duplication rate	22.06%
Clipped reads	58,588,508 / 11.61%

2.2. ACGT Content

Number/percentage of A's	11,799,856,739 / 26.55%
Number/percentage of C's	10,297,792,924 / 23.17%
Number/percentage of T's	11,761,551,800 / 26.47%
Number/percentage of G's	10,562,067,819 / 23.77%
Number/percentage of N's	15,053,245 / 0.03%

GC Percentage	46.94%

2.3. Coverage

Mean	14.3573
Standard Deviation	29.1368

2.4. Mapping Quality

Mean Mapping Quality	53.97

2.5. Insert size

Mean	29,776.07
Standard Deviation	1,635,753.13
P25/Median/P75	204 / 435 / 483

2.6. Mismatches and indels

General error rate	0.73%
Mismatches	317,077,897
Insertions	3,077,413
Mapped reads with at least one insertion	0.66%
Deletions	3,833,824
Mapped reads with at least one deletion	0.81%
Homopolymer indels	40.39%

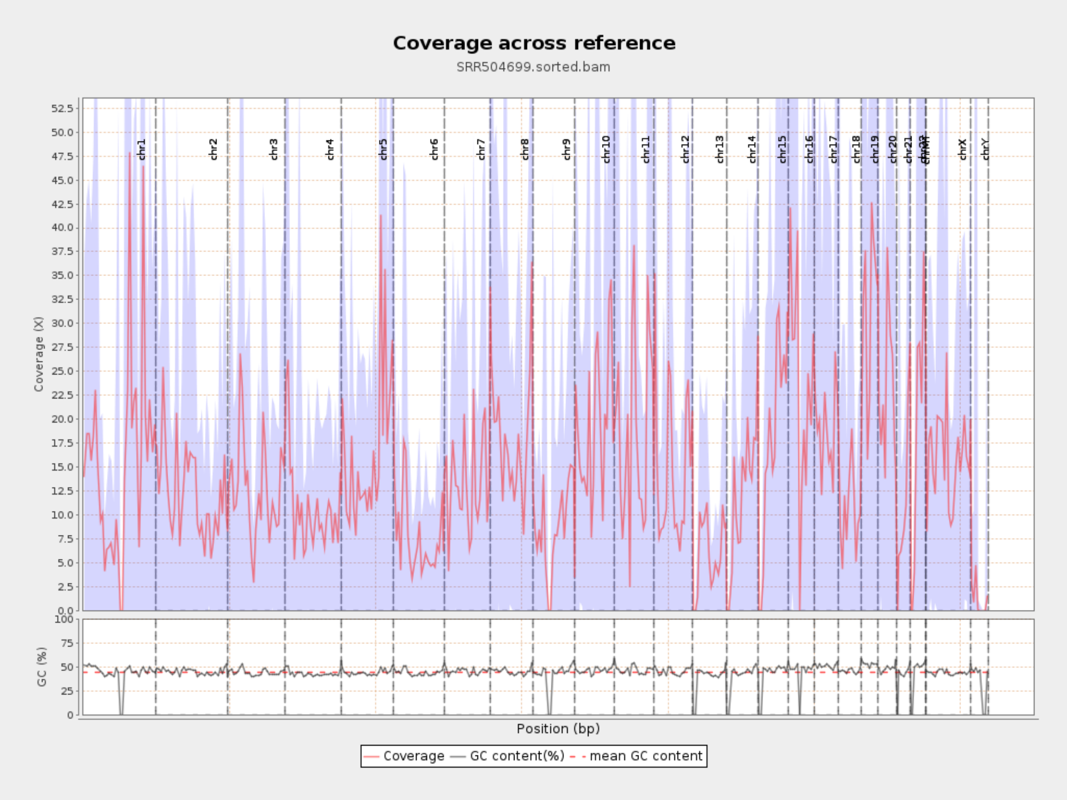
2.7. Chromosome stats

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

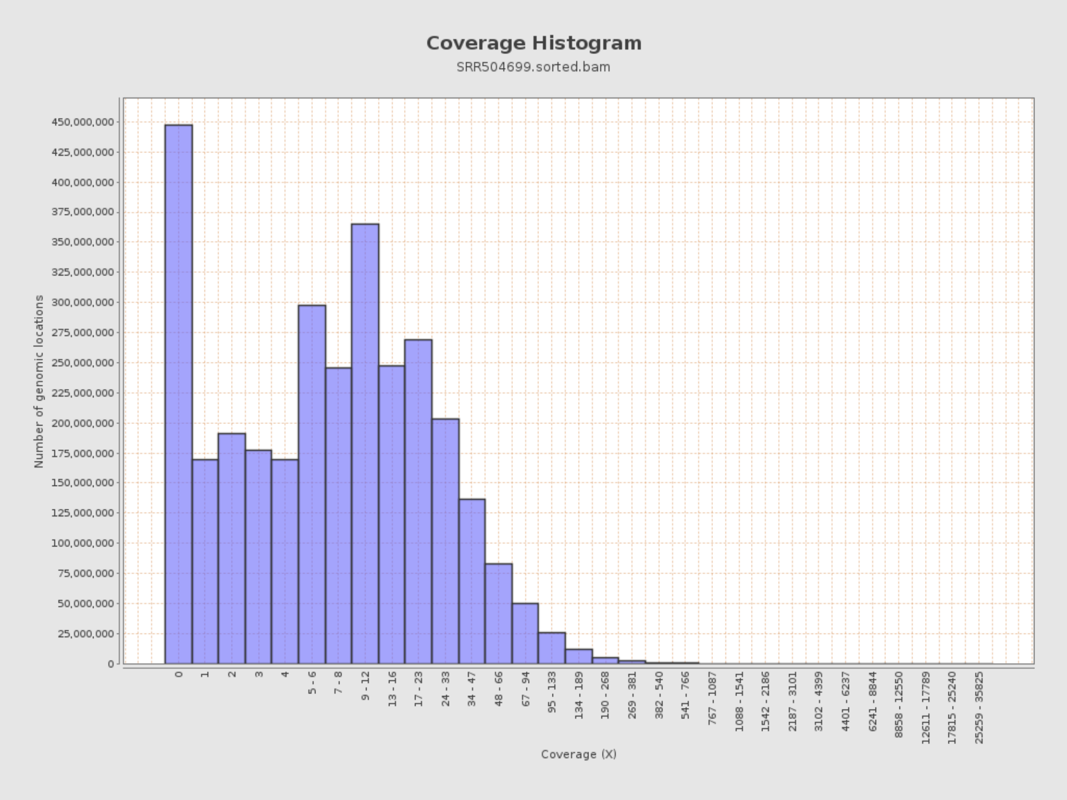
		bases	coverage	deviation
chr1	249250621	3895478369	15.6288	31.2178
chr2	243199373	2953332931	12.1437	19.1586
chr3	198022430	2512169436	12.6863	18.9634
chr4	191154276	2058413511	10.7683	18.2907
chr5	180915260	3052946911	16.875	25.4381
chr6	171115067	1274121443	7.446	13.0478
chr7	159138663	2102427752	13.2113	19.6502
chr8	146364022	2603458190	17.7876	31.3979
chr9	141213431	1210239165	8.5703	17.9704
chr10	135534747	2640160714	19.4796	28.7972
chr11	135006516	2543254841	18.838	31.4651
chr12	133851895	2007017927	14.9943	25.2479
chr13	115169878	684586199	5.9441	9.8146
chr14	107349540	1251708606	11.6601	17.8527
chr15	102531392	1799543708	17.5511	27.9725
chr16	90354753	2132572982	23.6022	35.8392
chr17	81195210	1526561727	18.8011	29.9786
chr18	78077248	820790983	10.5126	85.6035
chr19	59128983	1854428431	31.3624	46.2514
chr20	63025520	1435499375	22.7765	31.2392
chr21	48129895	558268757	11.5992	26.9329
chr22	51304566	972633659	18.958	34.909
chrMT	16571	324834	19.6026	7.6093
chrX	155270560	2485788590	16.0094	22.7476

chrY	59373566	70037984	1.1796	40.6825

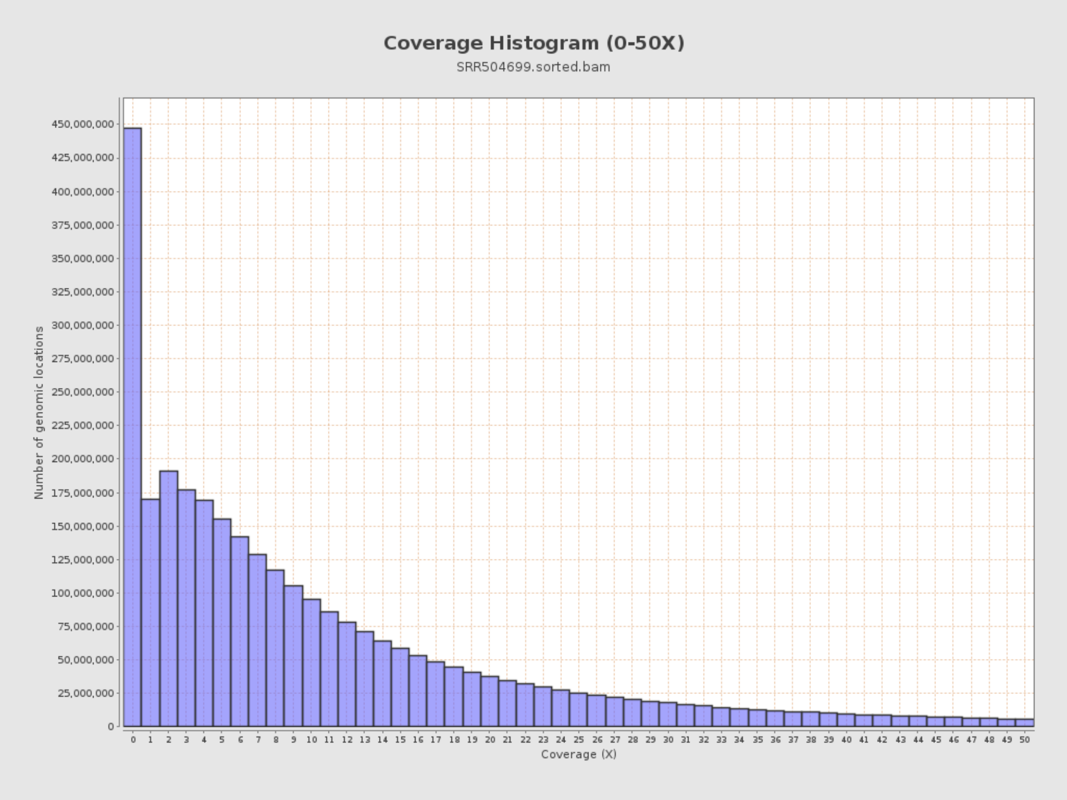
3. Results : Coverage across reference



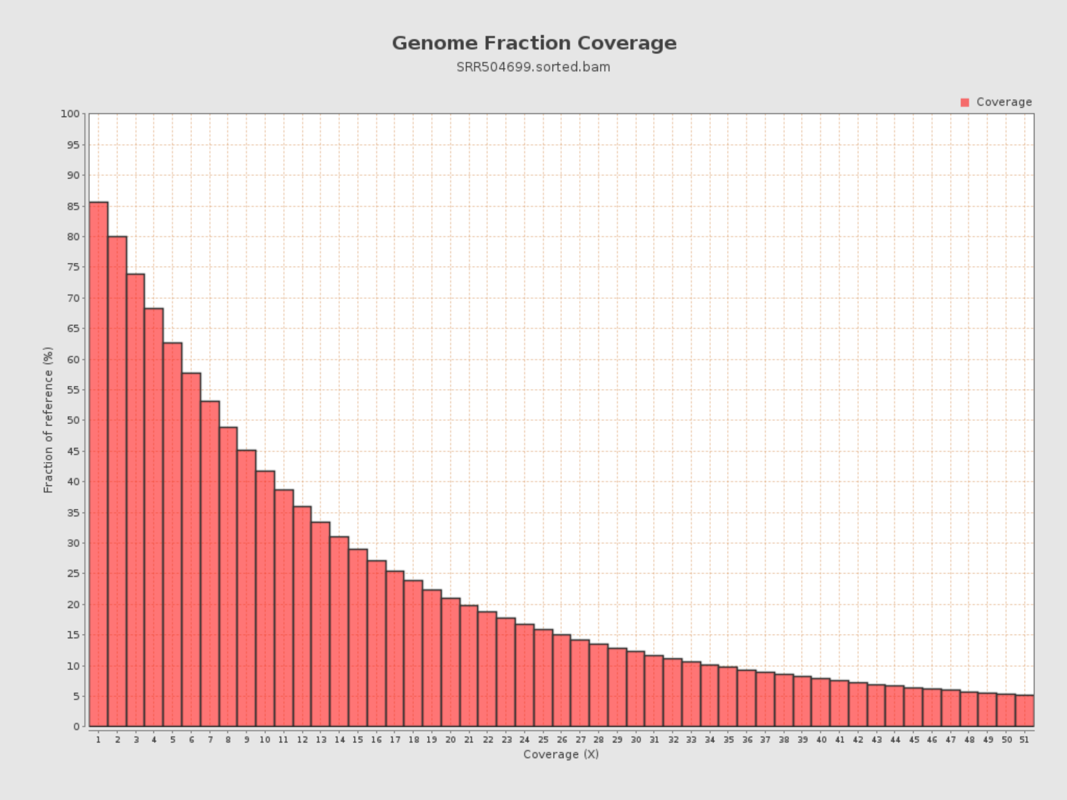
4. Results : Coverage Histogram



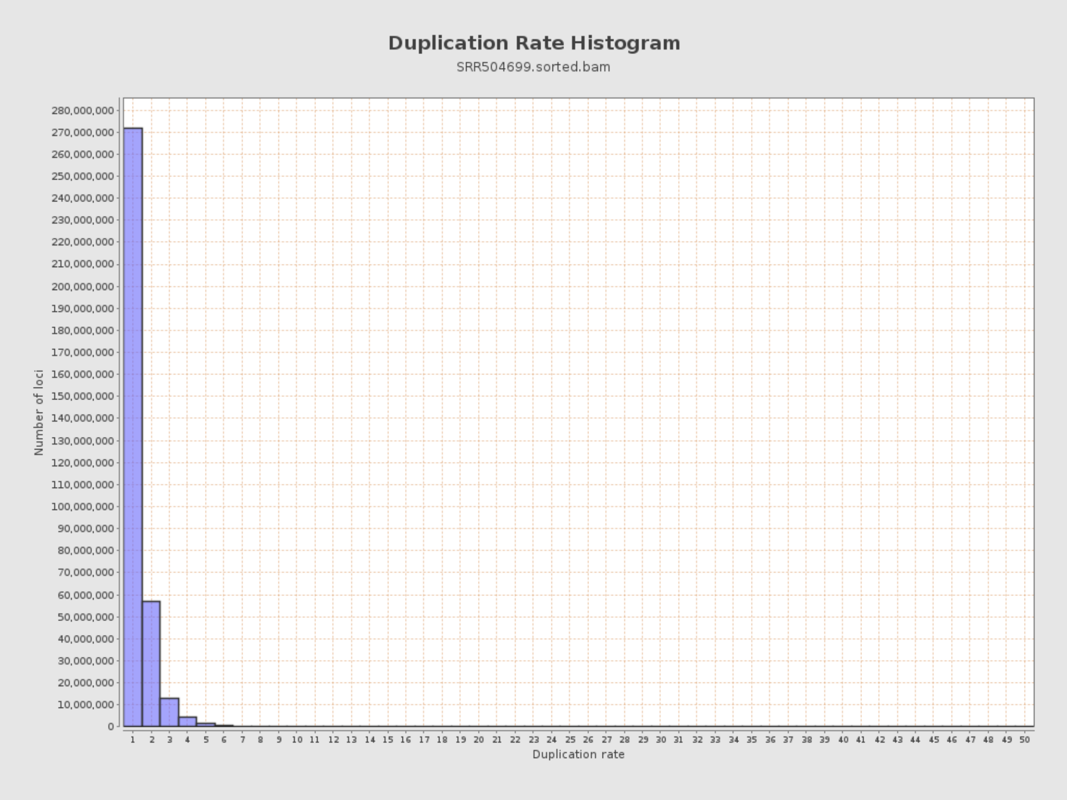
5. Results : Coverage Histogram (0-50X)



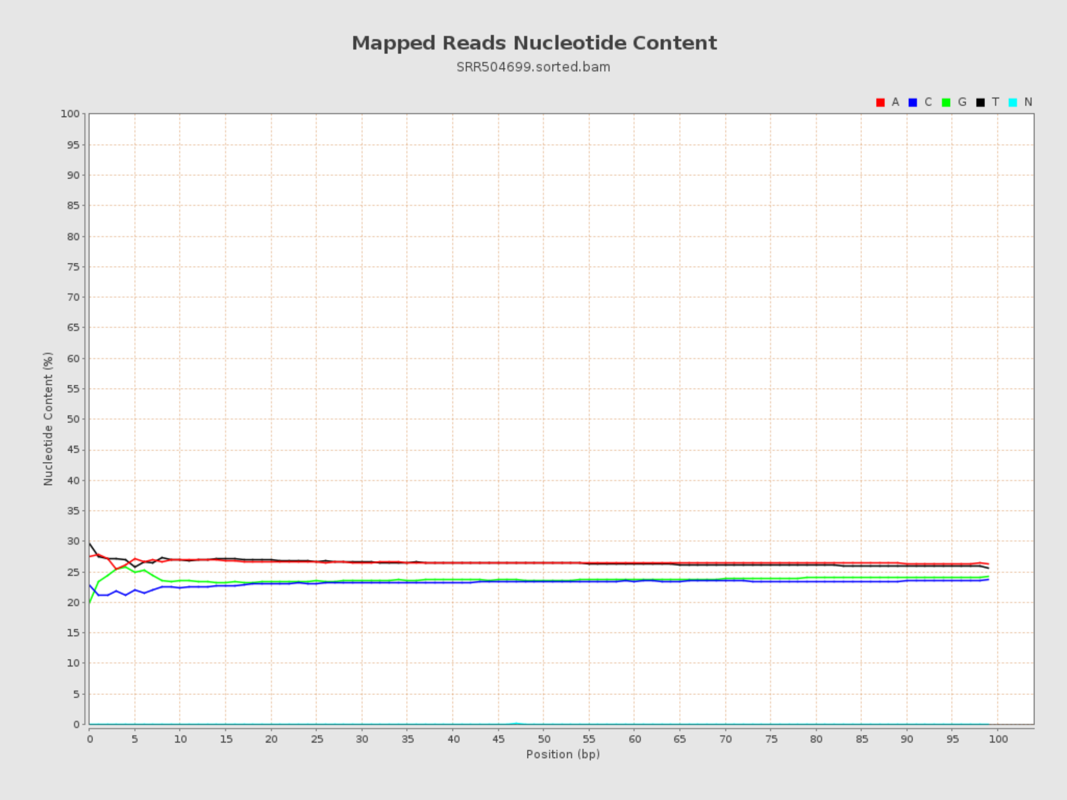
6. Results : Genome Fraction Coverage



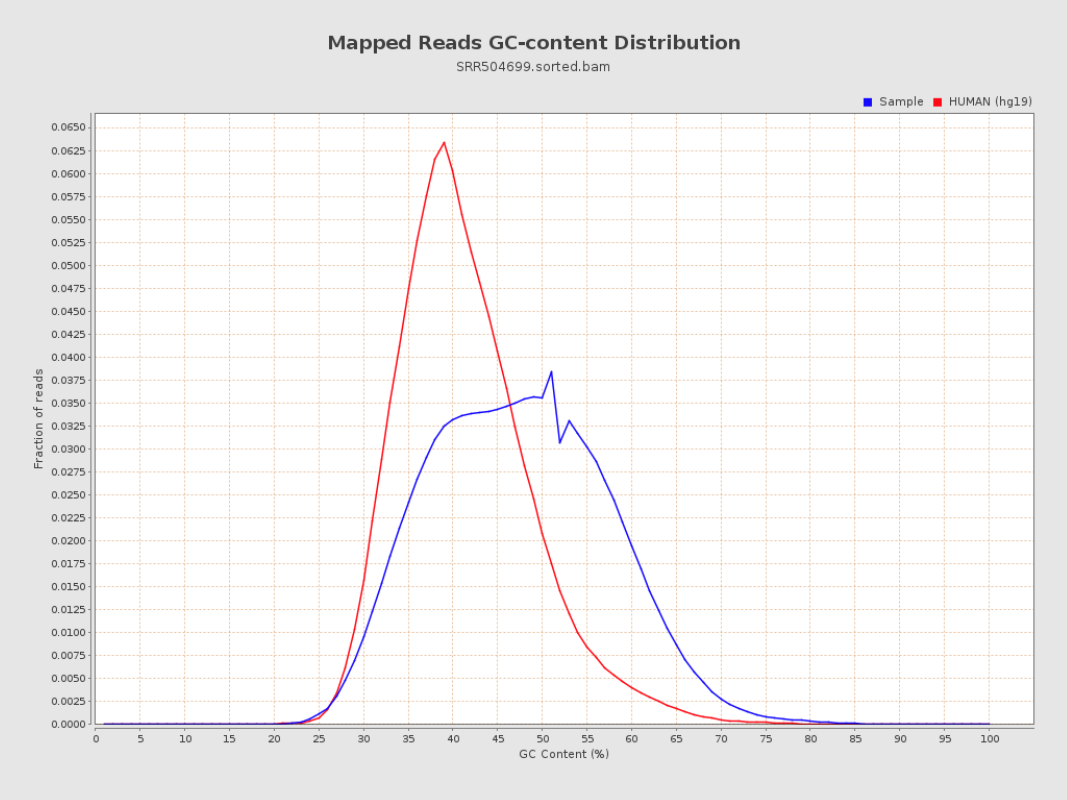
7. Results : Duplication Rate Histogram



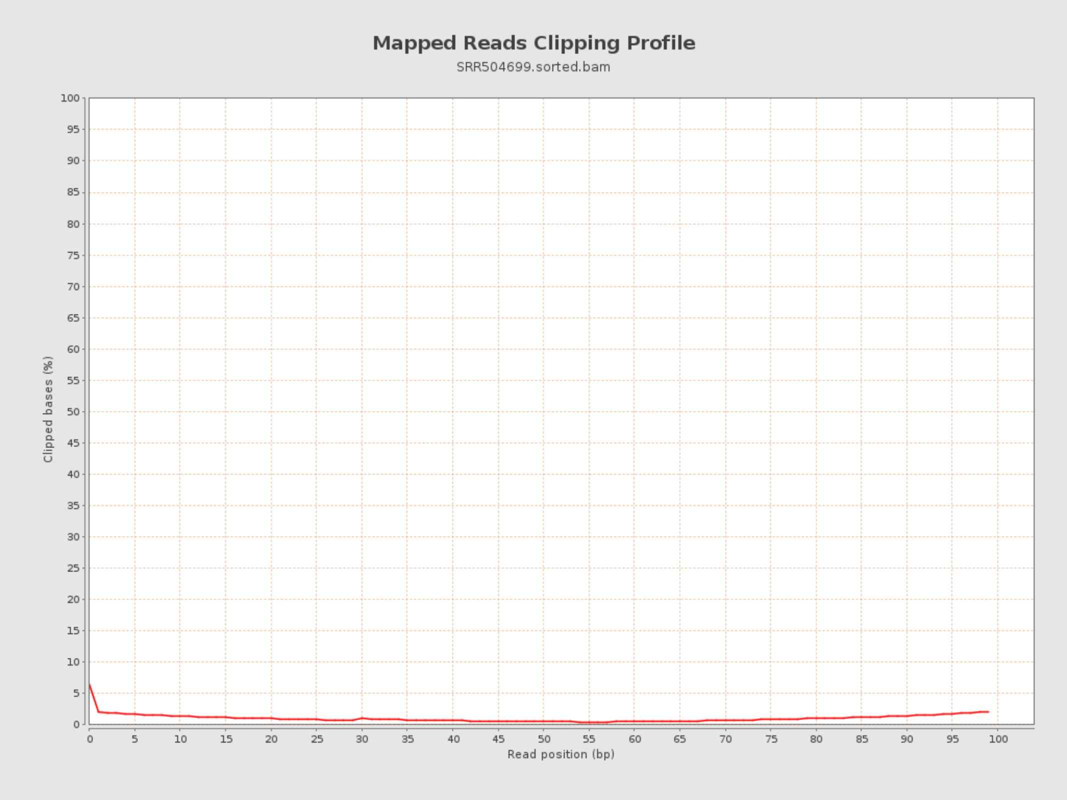
8. Results : Mapped Reads Nucleotide Content



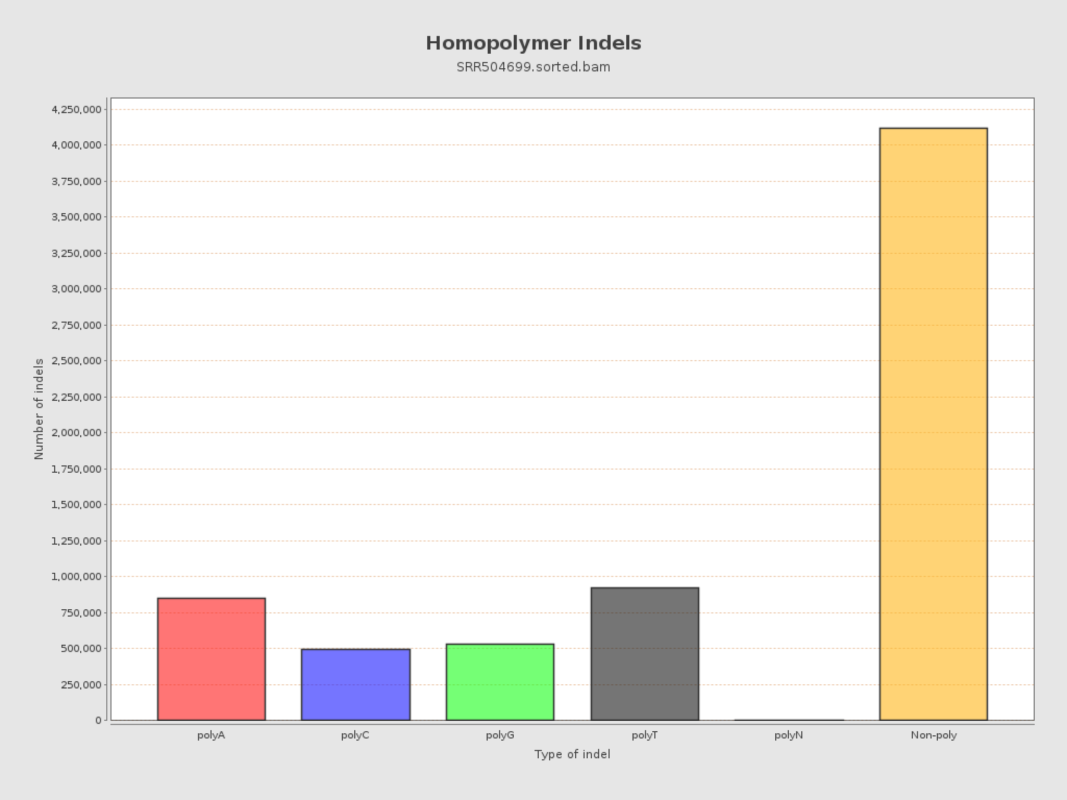
9. Results : Mapped Reads GC-content Distribution



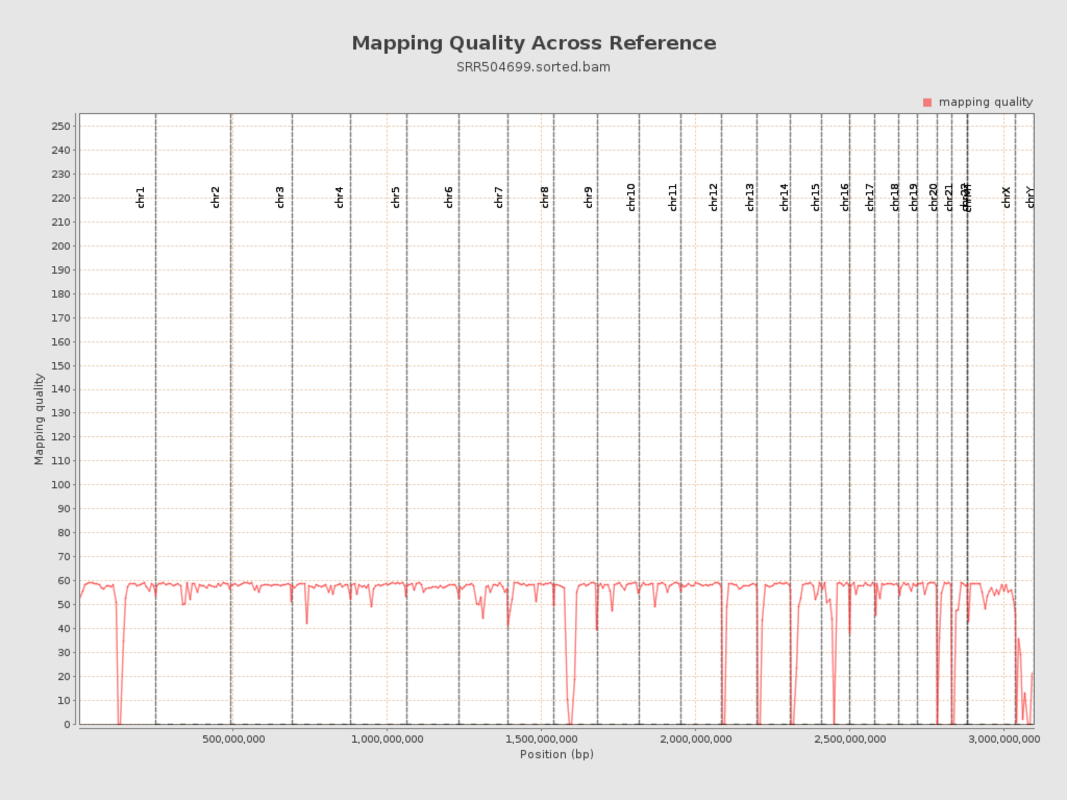
10. Results : Mapped Reads Clipping Profile



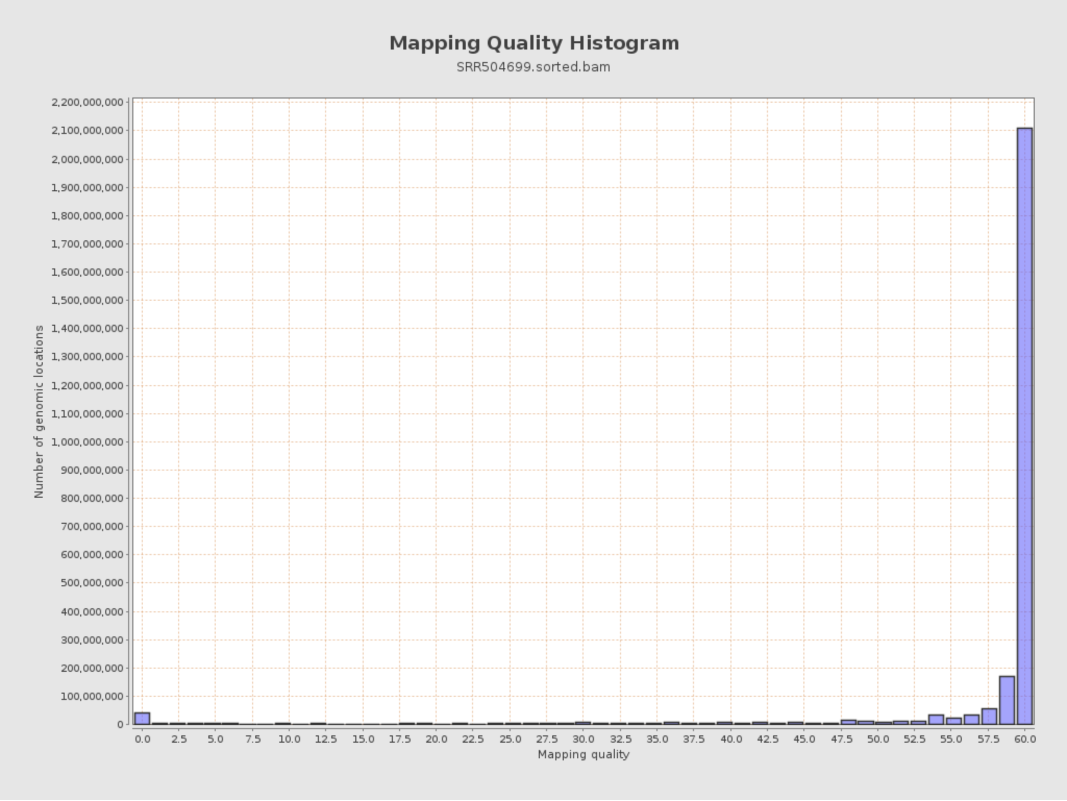
11. Results : Homopolymer Indels



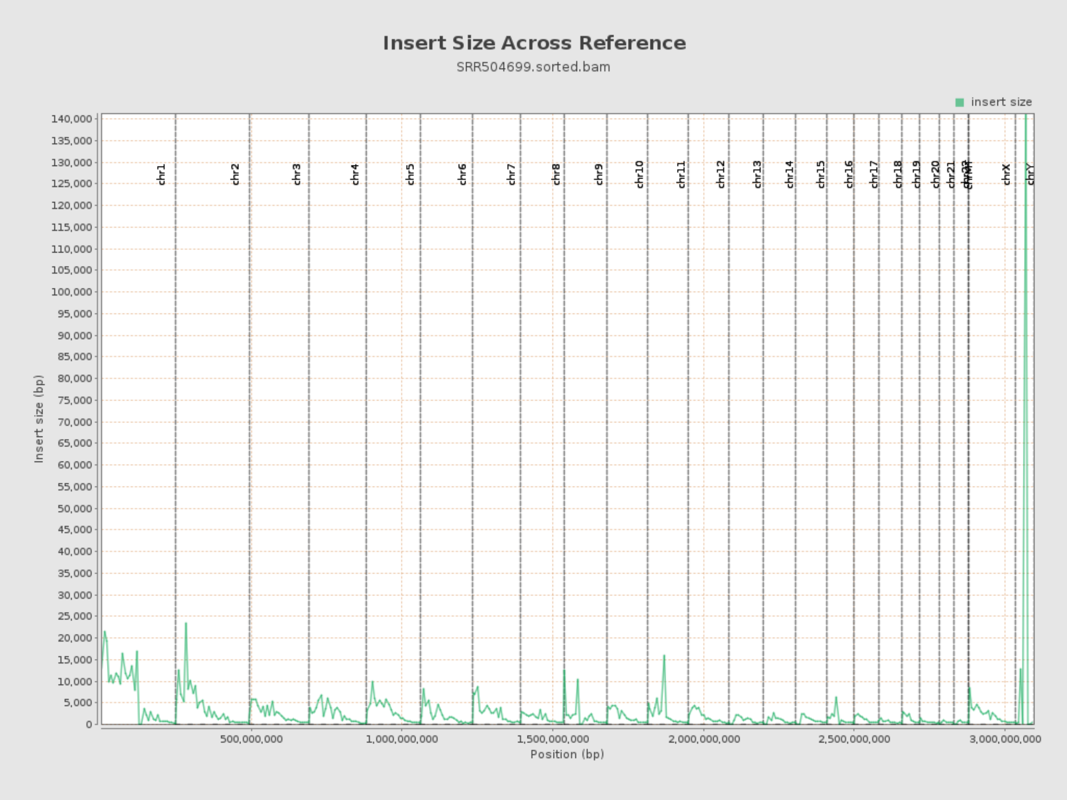
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram