Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/25 12:33:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2976566.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_SRR2976566 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2976566_1.fastq.gz SRR2976566_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Oct 25 12:33:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2976566.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	640,855,848
Mapped reads	631,956,424 / 98.61%
Unmapped reads	8,899,424 / 1.39%
Mapped paired reads	631,956,424 / 98.61%
Mapped reads, first in pair	317,262,663 / 49.51%
Mapped reads, second in pair	314,693,761 / 49.11%
Mapped reads, both in pair	627,492,554 / 97.91%
Mapped reads, singletons	4,463,870 / 0.7%
Secondary alignments	0
Supplementary alignments	1,999,630 / 0.31%
Read min/max/mean length	20 / 150 / 143.36
Duplicated reads (estimated)	110,556,499 / 17.25%
Duplication rate	12.75%
Clipped reads	30,685,921 / 4.79%

2.2. ACGT Content

Number/percentage of A's	26,520,071,251 / 29.38%
Number/percentage of C's	18,550,173,254 / 20.55%
Number/percentage of T's	26,657,490,319 / 29.53%
Number/percentage of G's	18,543,334,691 / 20.54%
Number/percentage of N's	2,043,357 / 0%

GC Percentage	41.09%

2.3. Coverage

Mean	29.1708
Standard Deviation	308.6545

2.4. Mapping Quality

Mean Mapping Quality	54.41

2.5. Insert size

Mean	23,343.86
Standard Deviation	1,445,066.45
P25/Median/P75	344 / 392 / 446

2.6. Mismatches and indels

General error rate	0.86%
Mismatches	748,747,131
Insertions	9,685,627
Mapped reads with at least one insertion	1.44%
Deletions	11,034,052
Mapped reads with at least one deletion	1.67%
Homopolymer indels	42.14%

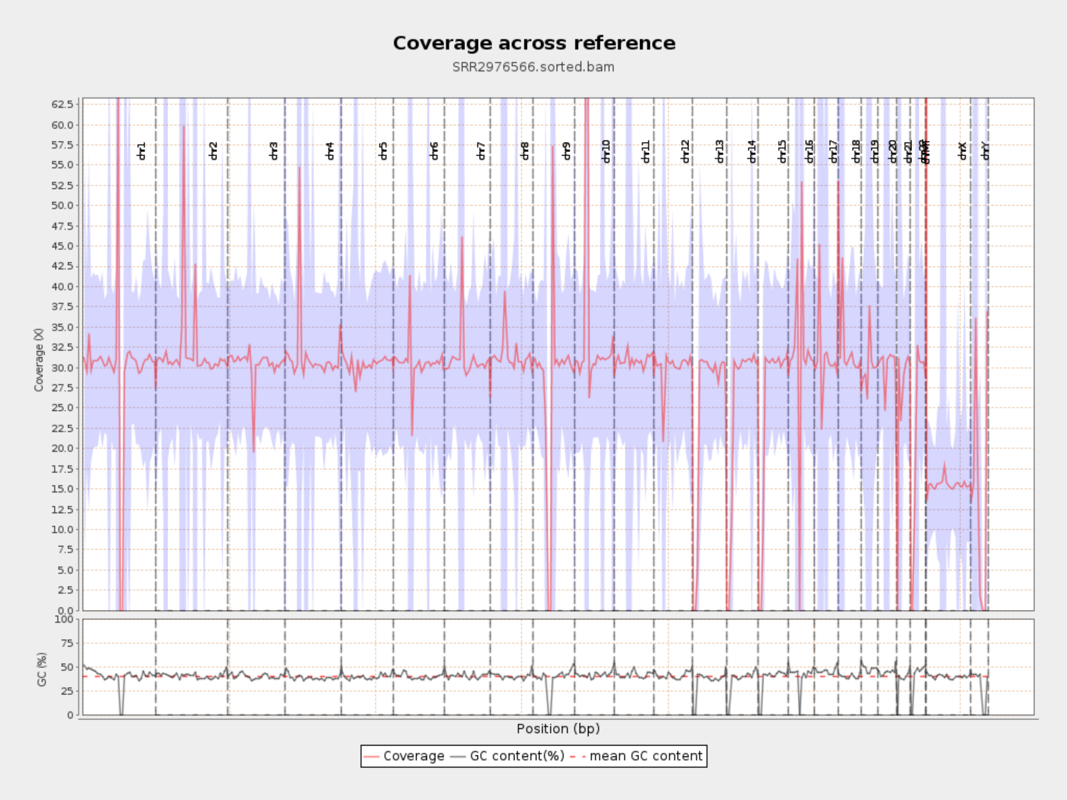
2.7. Chromosome stats

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

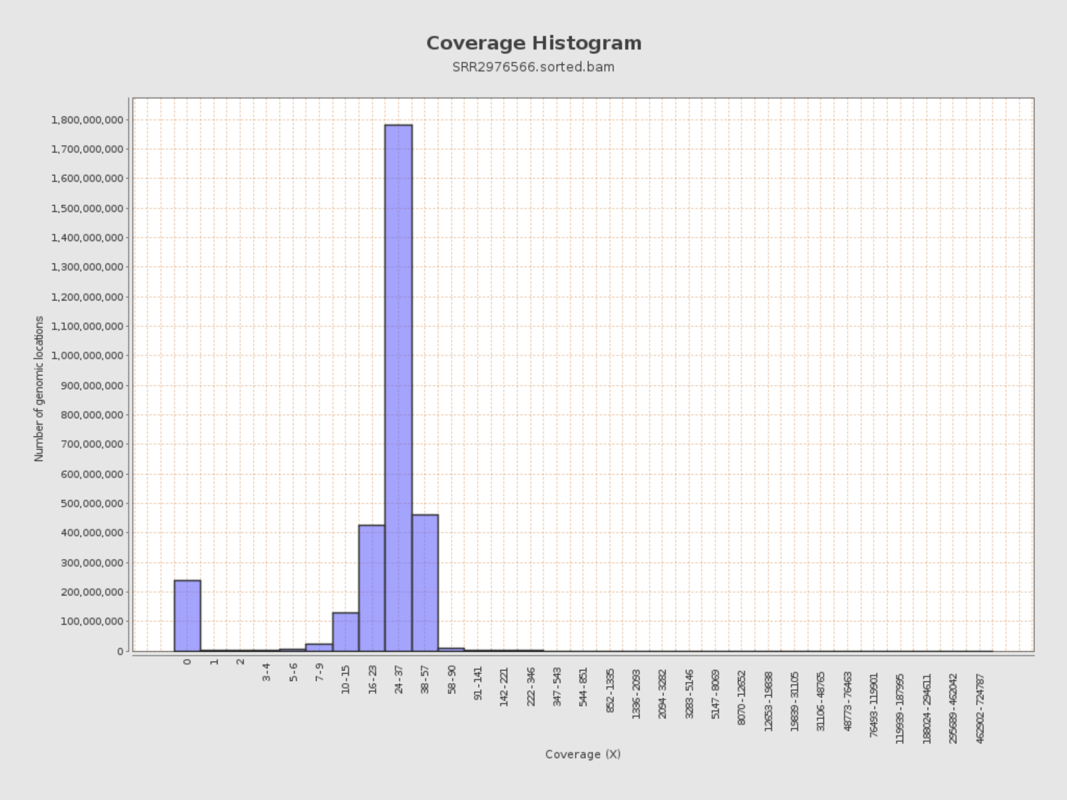
		bases	coverage	deviation
chr1	249250621	7450045562	29.8898	723.6813
chr2	243199373	7820383658	32.1563	182.9641
chr3	198022430	6013670113	30.3686	15.4765
chr4	191154276	6042865436	31.6125	213.9248
chr5	180915260	5504446297	30.4256	27.5826
chr6	171115067	5250716975	30.6853	127.5067
chr7	159138663	4967333232	31.2139	313.7153
chr8	146364022	4600922627	31.4348	222.9328
chr9	141213431	3992592473	28.2735	571.3966
chr10	135534747	4698516254	34.6665	551.9227
chr11	135006516	4166805723	30.8637	121.0642
chr12	133851895	4019527147	30.0297	17.6027
chr13	115169878	2900543323	25.1849	15.1002
chr14	107349540	2740042215	25.5245	20.8533
chr15	102531392	2567306223	25.0392	16.1417
chr16	90354753	2831885293	31.3419	180.9093
chr17	81195210	2533824661	31.2066	176.4065
chr18	78077248	2575593747	32.9878	416.0994
chr19	59128983	1785117269	30.1902	300.499
chr20	63025520	1909778104	30.3017	51.3511
chr21	48129895	1277337365	26.5394	85.3948
chr22	51304566	1106086215	21.5592	61.9691
chrMT	16571	236650648	14,281.0119	1,654.3392
chrX	155270560	2411744118	15.5325	36.4665

chrY	59373566	900199057	15.1616	237.3523

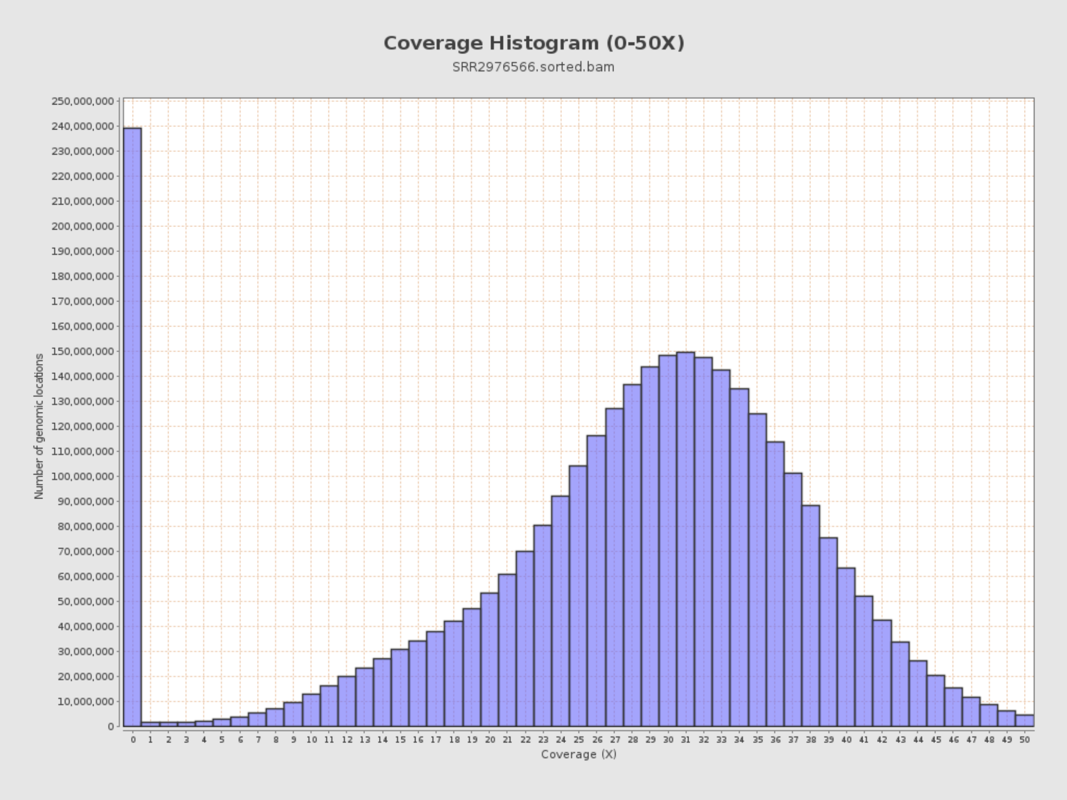
3. Results : Coverage across reference



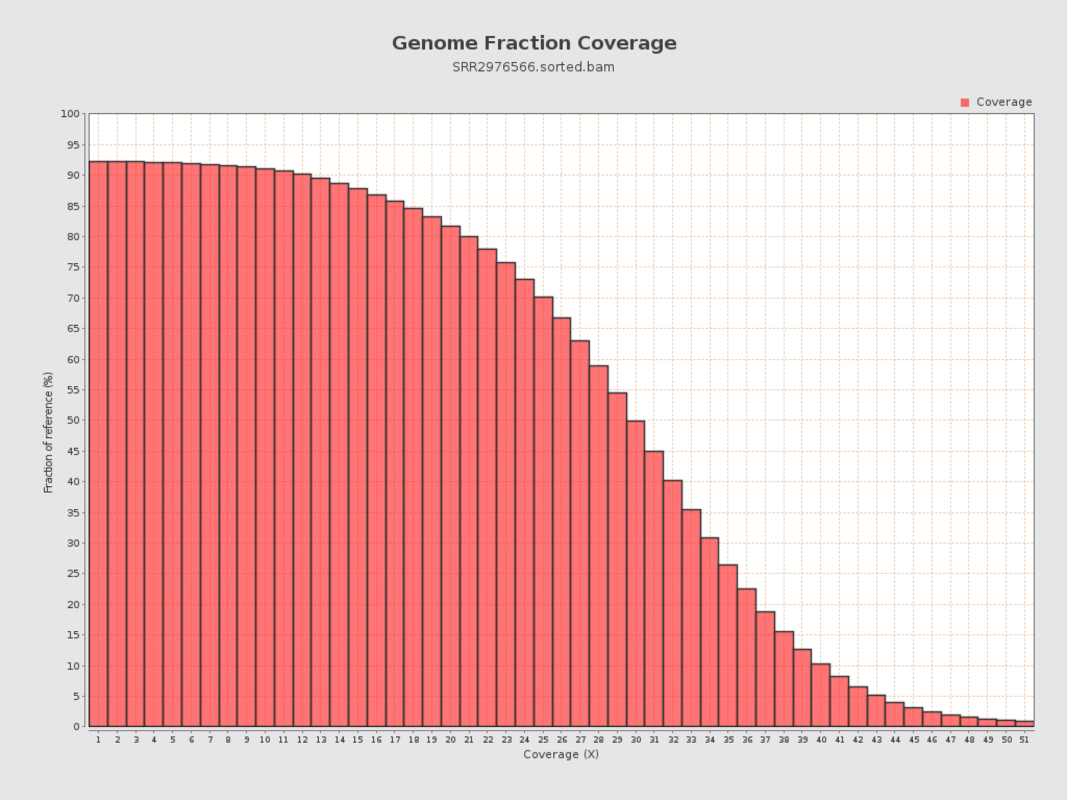
4. Results : Coverage Histogram



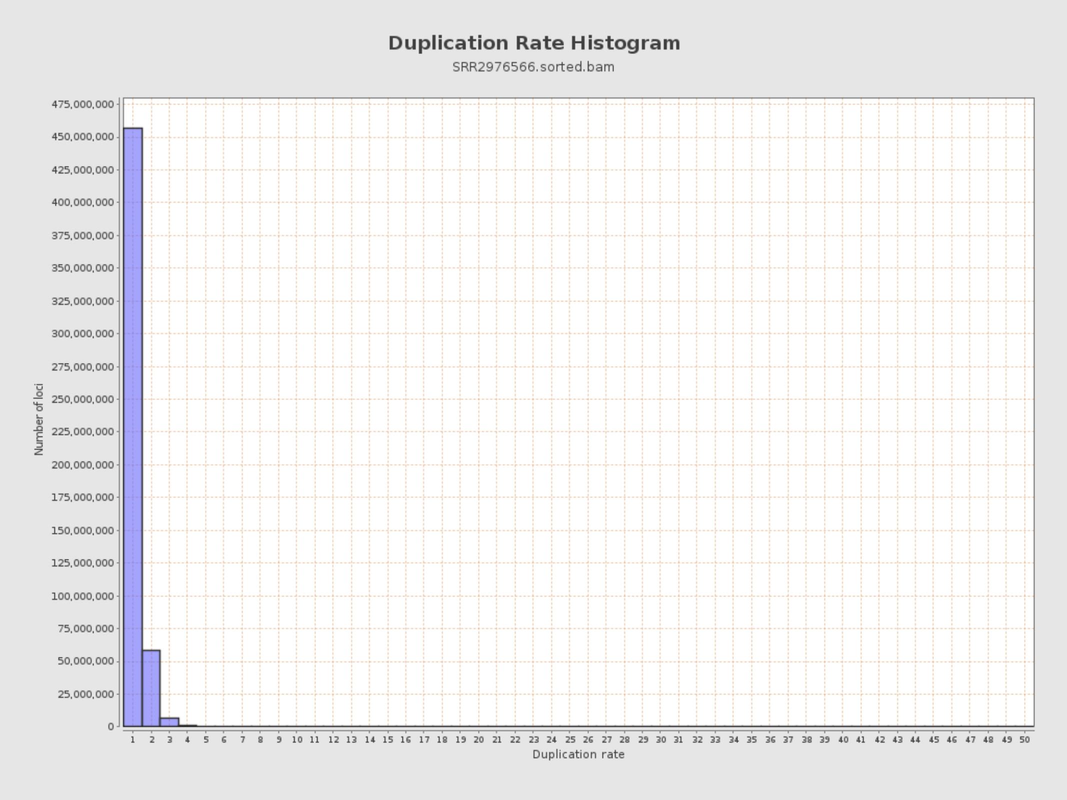
5. Results : Coverage Histogram (0-50X)



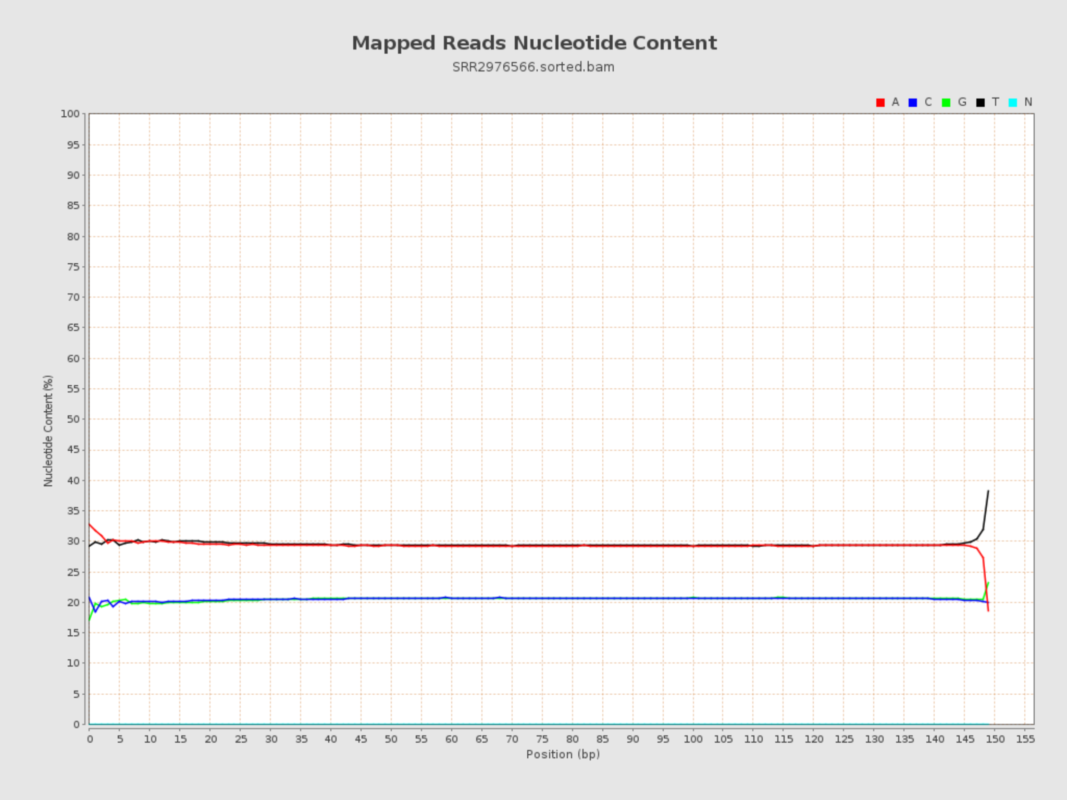
6. Results : Genome Fraction Coverage



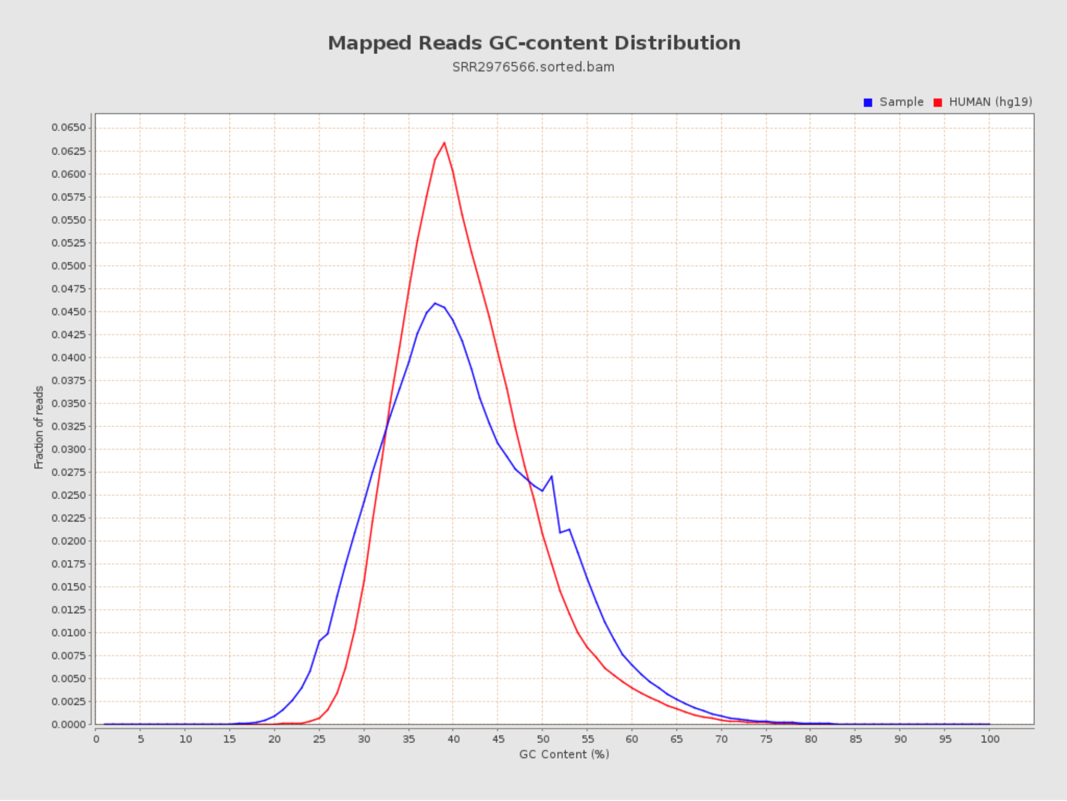
7. Results : Duplication Rate Histogram



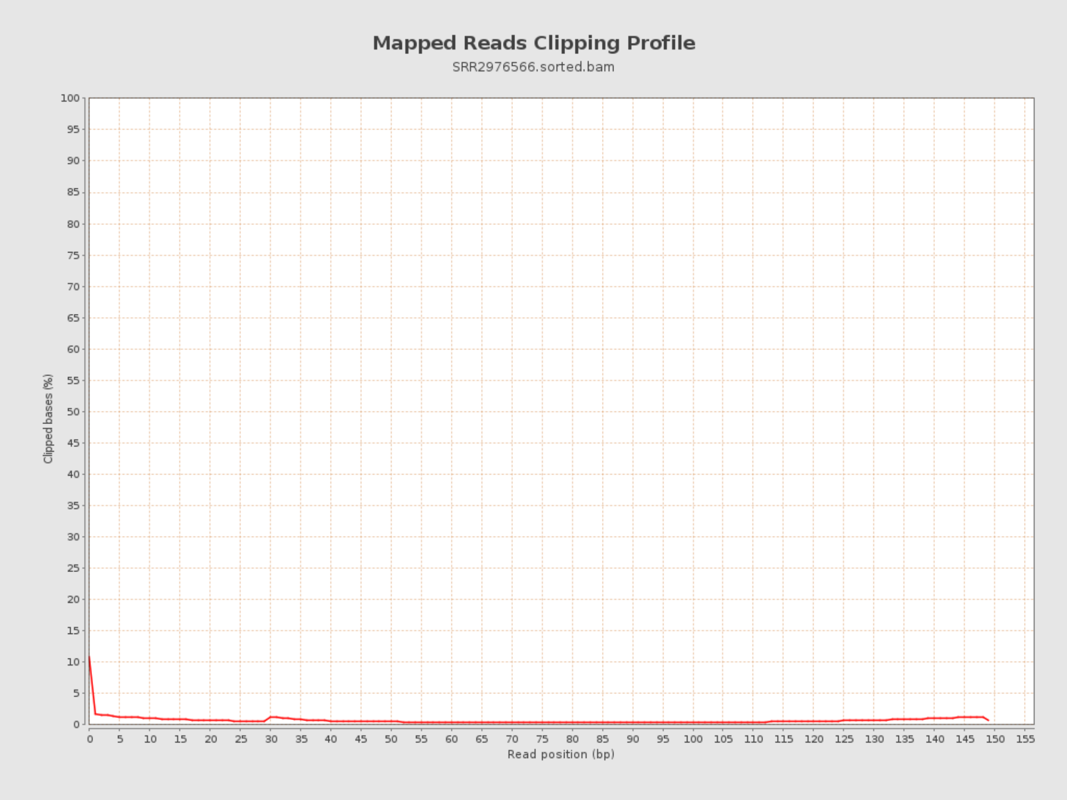
8. Results : Mapped Reads Nucleotide Content



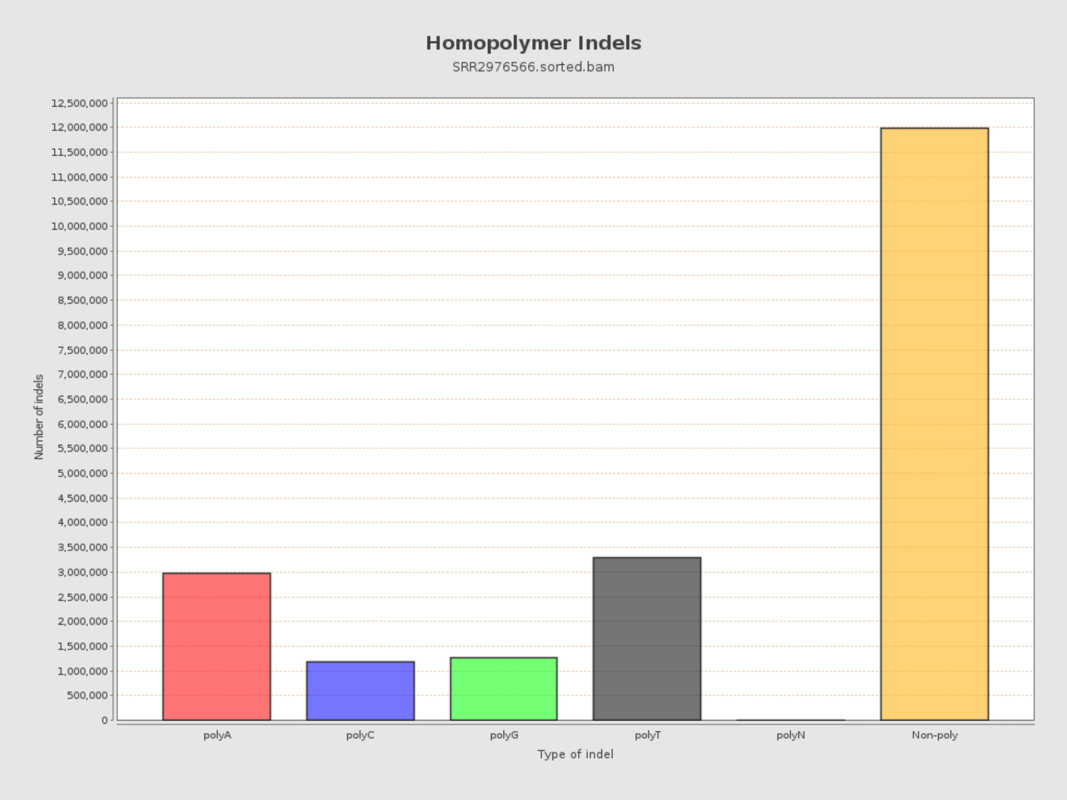
9. Results : Mapped Reads GC-content Distribution



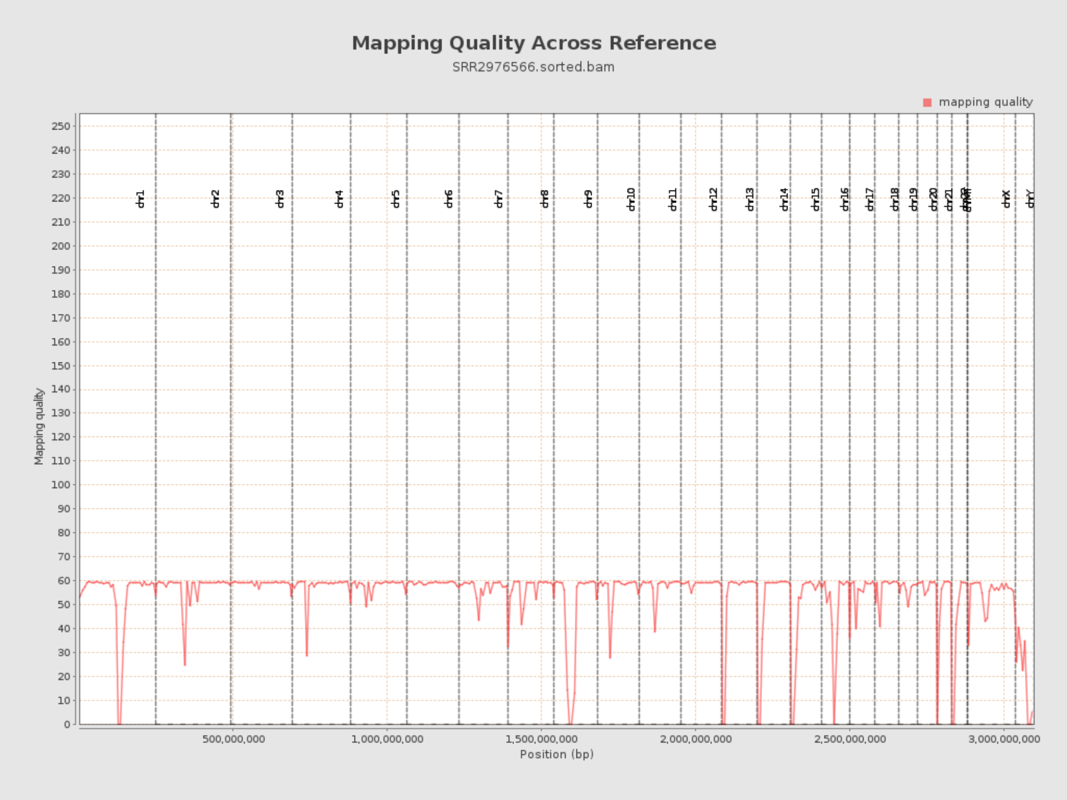
10. Results : Mapped Reads Clipping Profile



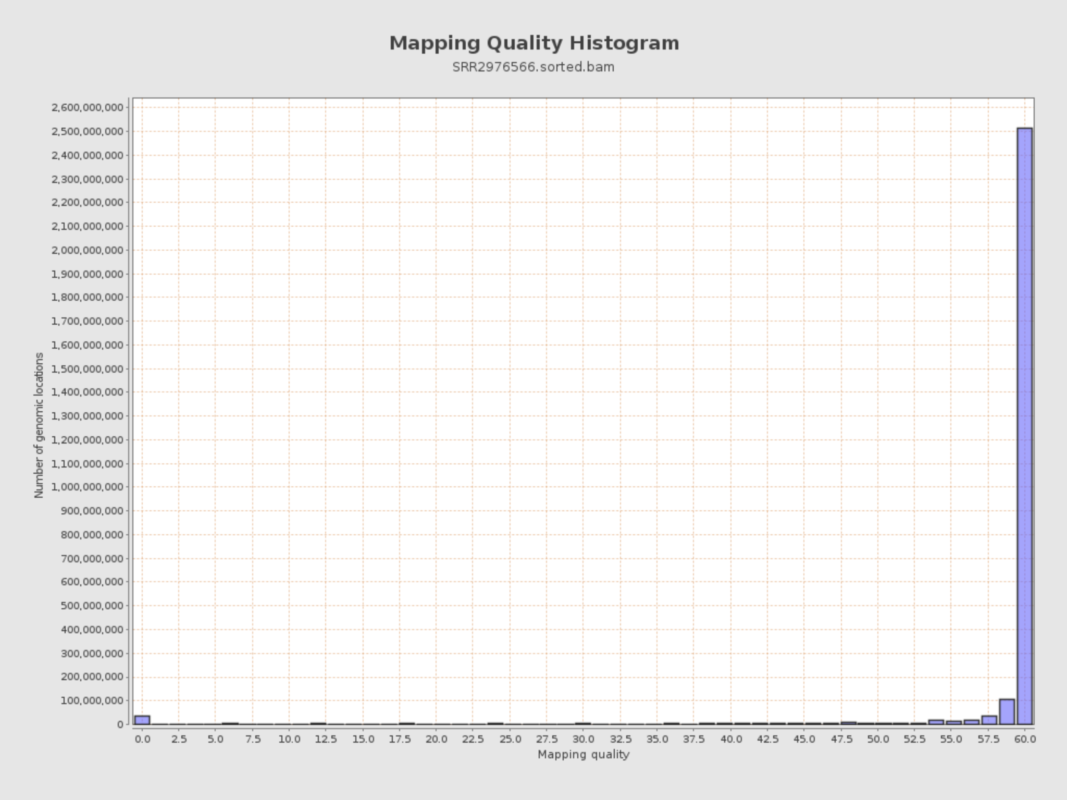
11. Results : Homopolymer Indels



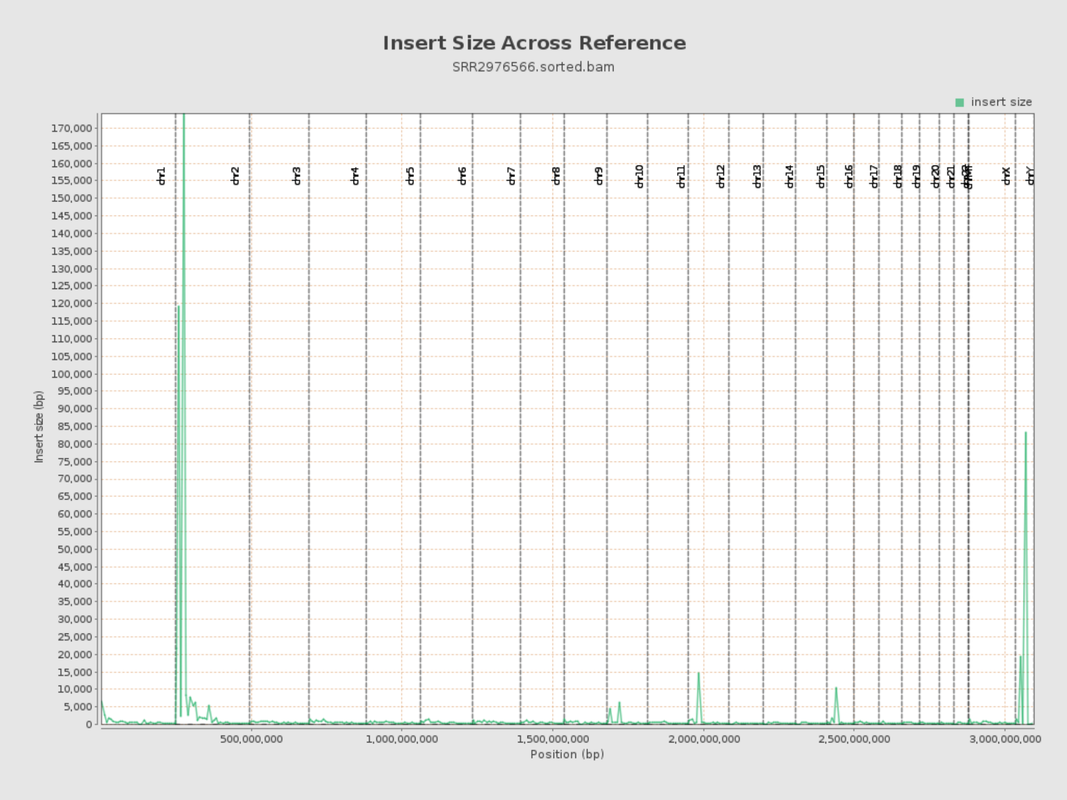
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram