Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/22 12:04:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2976561.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_SRR2976561 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2976561_1.fastq.gz SRR2976561_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 22 12:04:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2976561.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	530,130,538
Mapped reads	511,163,888 / 96.42%
Unmapped reads	18,966,650 / 3.58%
Mapped paired reads	511,163,888 / 96.42%
Mapped reads, first in pair	259,216,119 / 48.9%
Mapped reads, second in pair	251,947,769 / 47.53%
Mapped reads, both in pair	501,965,782 / 94.69%
Mapped reads, singletons	9,198,106 / 1.74%
Secondary alignments	0
Supplementary alignments	5,264,665 / 0.99%
Read min/max/mean length	20 / 249 / 204.16
Duplicated reads (estimated)	98,173,916 / 18.52%
Duplication rate	11.22%
Clipped reads	71,442,748 / 13.48%

2.2. ACGT Content

Number/percentage of A's	31,183,288,984 / 30.14%
Number/percentage of C's	20,728,214,818 / 20.04%
Number/percentage of T's	31,170,161,790 / 30.13%
Number/percentage of G's	20,288,228,001 / 19.61%
Number/percentage of N's	79,291,610 / 0.08%

GC Percentage	39.65%

2.3. Coverage

Mean	33.4336
Standard Deviation	616.5514

2.4. Mapping Quality

Mean Mapping Quality	54.51

2.5. Insert size

Mean	37,027.5
Standard Deviation	1,729,625.74
P25/Median/P75	530 / 588 / 664

2.6. Mismatches and indels

General error rate	2.16%
Mismatches	2,186,888,584
Insertions	15,486,861
Mapped reads with at least one insertion	2.7%
Deletions	17,116,166
Mapped reads with at least one deletion	3.06%
Homopolymer indels	40.53%

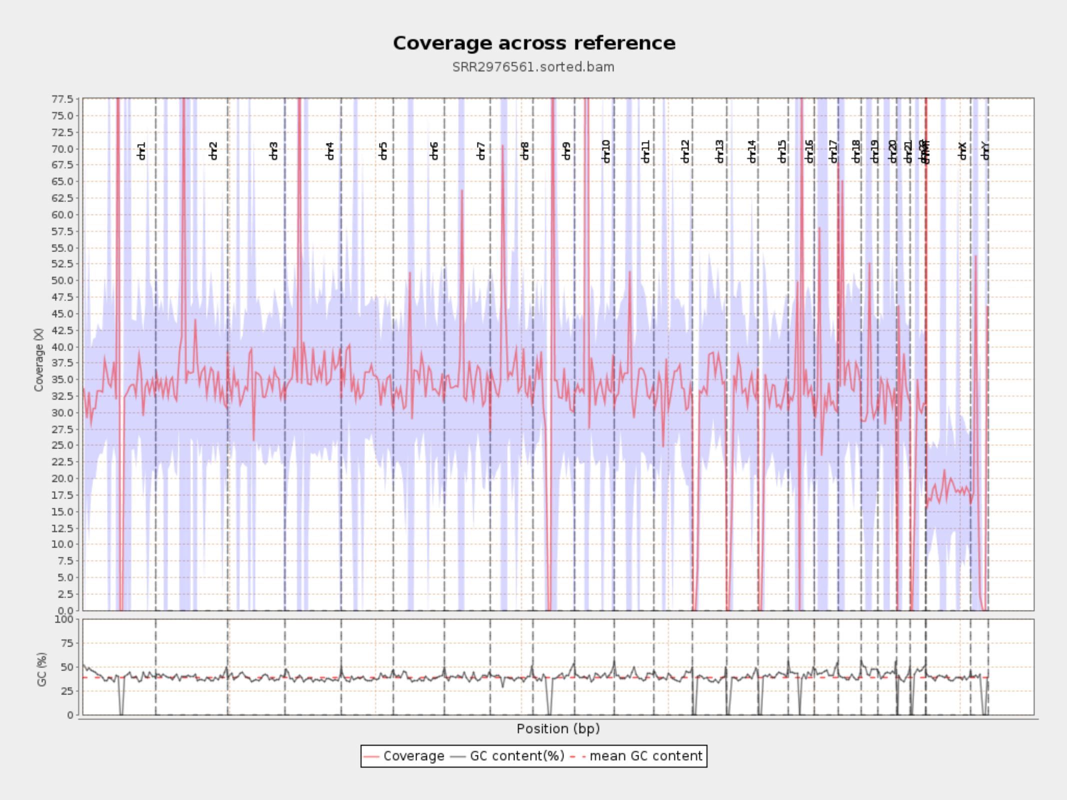
2.7. Chromosome stats

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

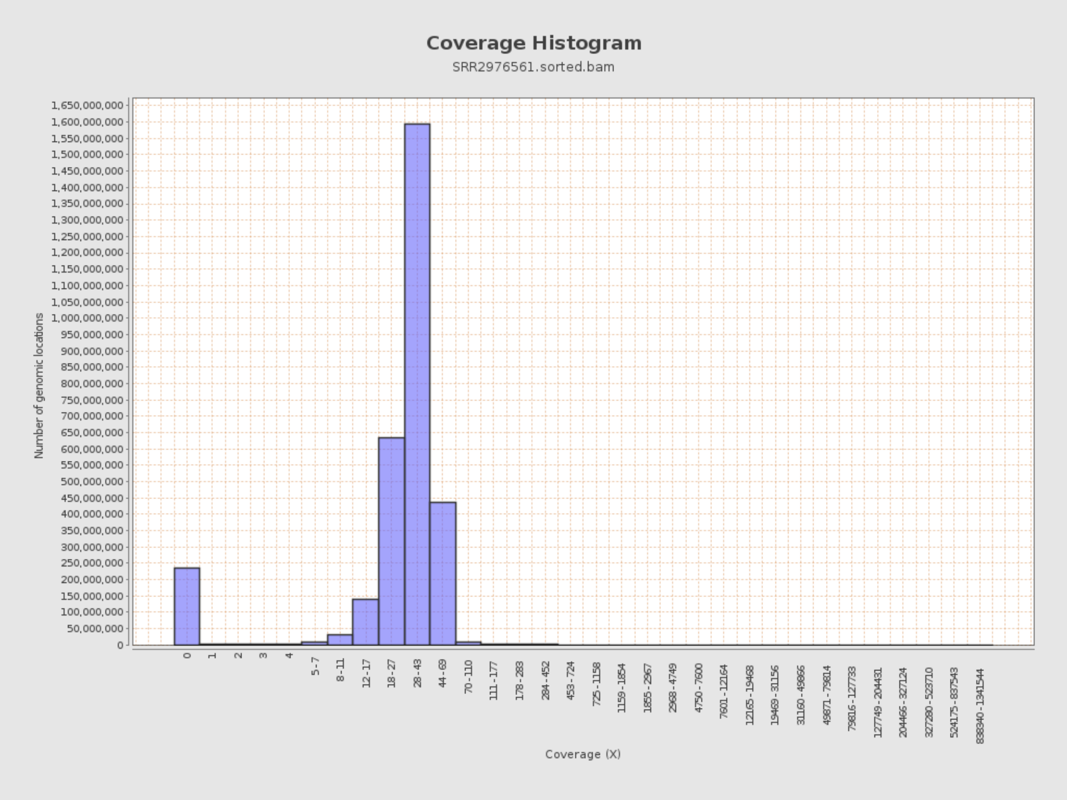
		bases	coverage	deviation
chr1	249250621	8355564390	33.5227	1,336.782
chr2	243199373	8931066207	36.7232	294.4777
chr3	198022430	6789264448	34.2853	23.8027
chr4	191154276	7385918080	38.6385	488.9656
chr5	180915260	6303232906	34.8408	34.274
chr6	171115067	5971427780	34.8971	193.1181
chr7	159138663	5708969042	35.8742	511.6454
chr8	146364022	5504601178	37.609	1,017.9262
chr9	141213431	4682357380	33.158	1,162.9965
chr10	135534747	5633948929	41.5683	1,056.4516
chr11	135006516	4742701733	35.1294	284.1167
chr12	133851895	4455038121	33.2833	23.1634
chr13	115169878	3434086077	29.8176	17.3028
chr14	107349540	3081918142	28.7092	24.8418
chr15	102531392	2749879359	26.8199	19.0073
chr16	90354753	3219668576	35.6336	335.7577
chr17	81195210	2697378649	33.2209	314.3503
chr18	78077248	3110374227	39.8371	727.5017
chr19	59128983	1938627911	32.7864	674.8099
chr20	63025520	2051579574	32.5516	213.0031
chr21	48129895	1549866063	32.2017	288.4661
chr22	51304566	1139637312	22.2132	94.7468
chrMT	16571	78726871	4,750.8823	896.7148
chrX	155270560	2816222456	18.1375	46.6724

chrY	59373566	1168105967	19.6738	528.6393

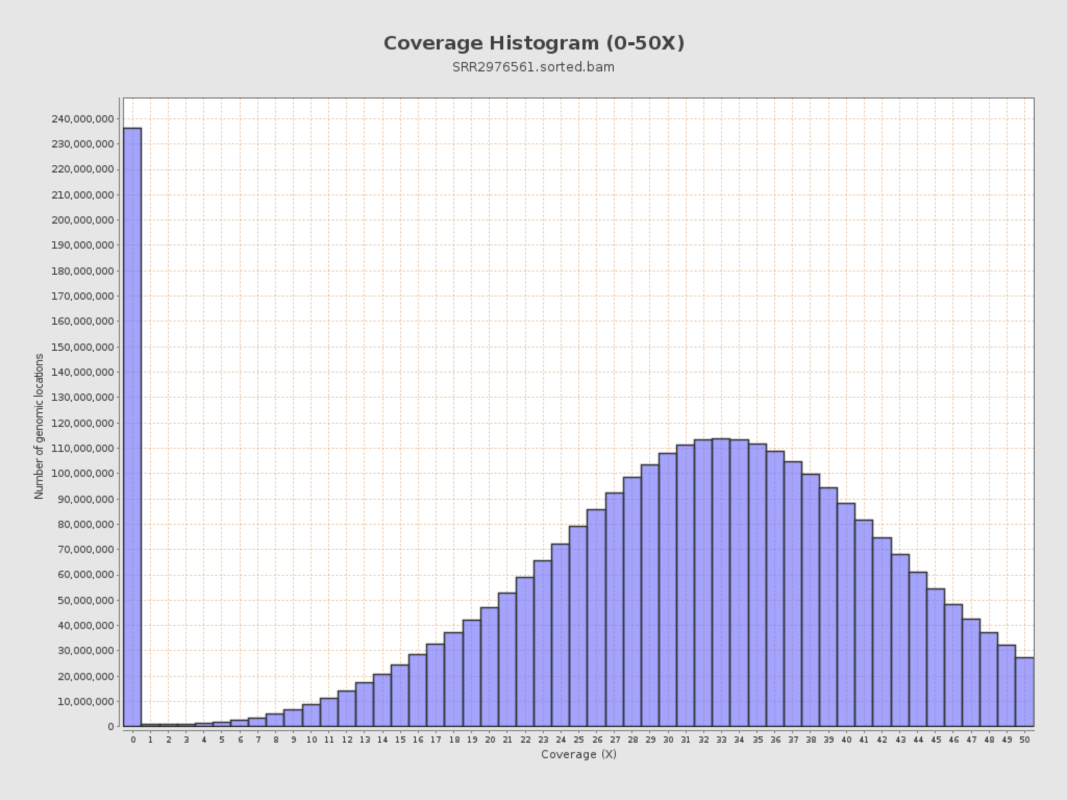
3. Results : Coverage across reference



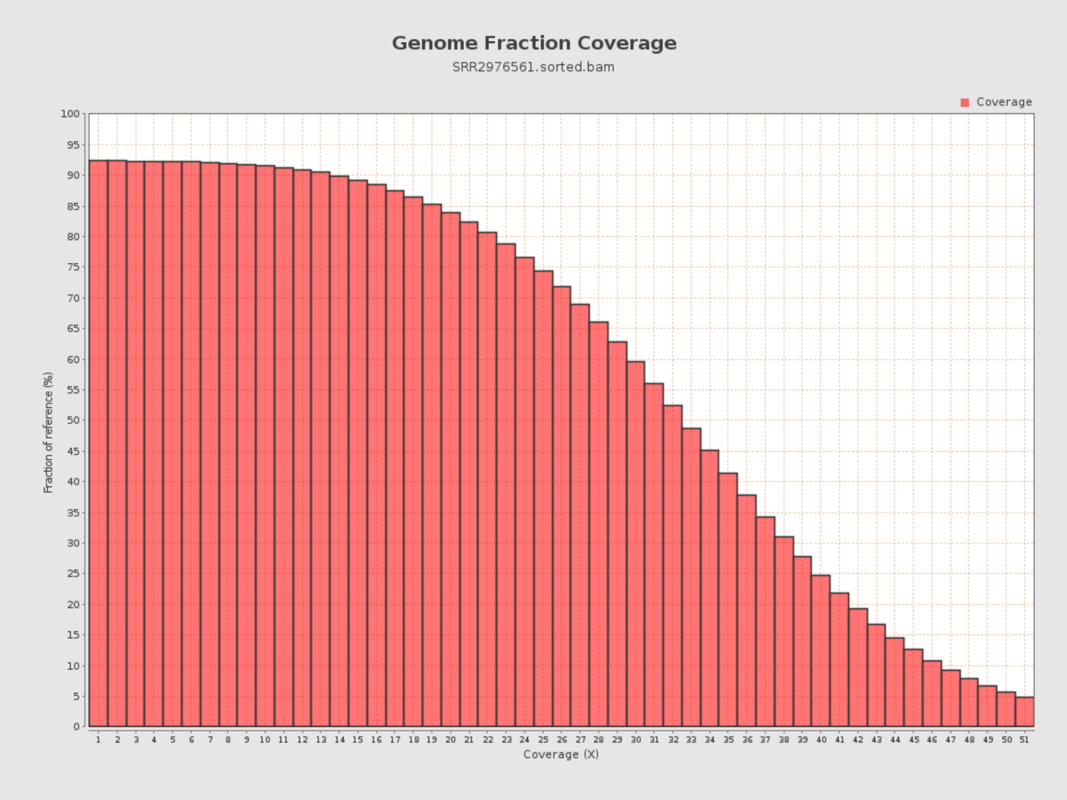
4. Results : Coverage Histogram



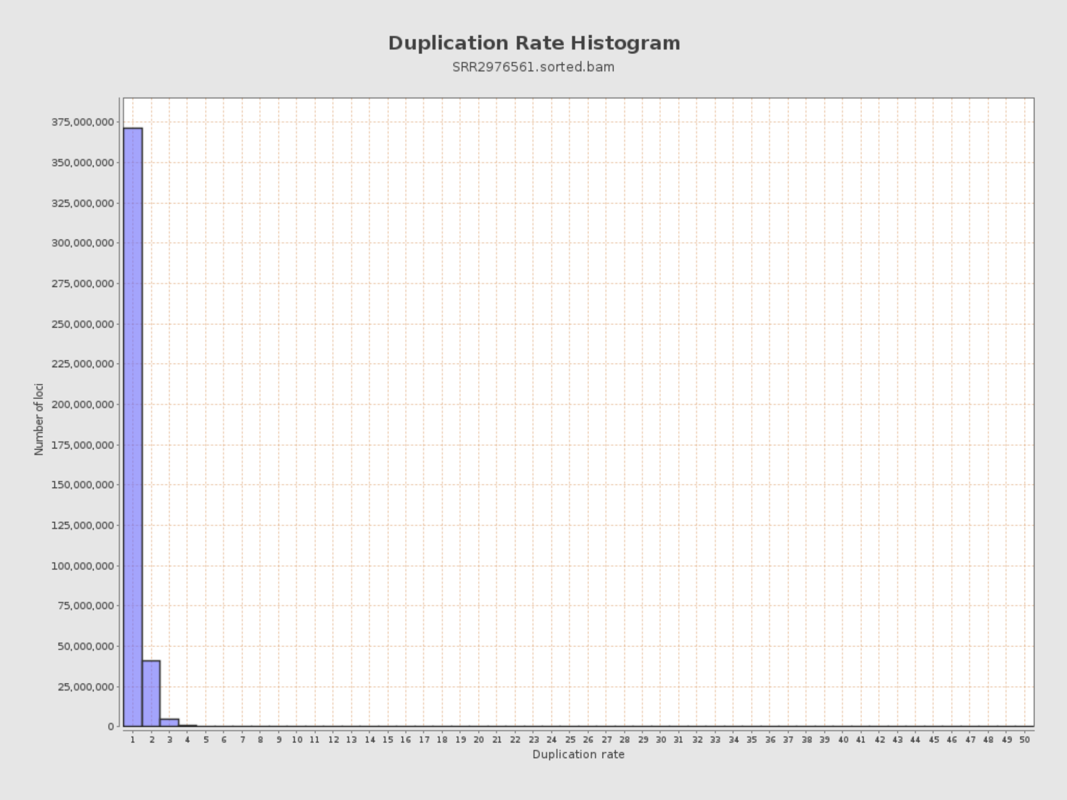
5. Results : Coverage Histogram (0-50X)



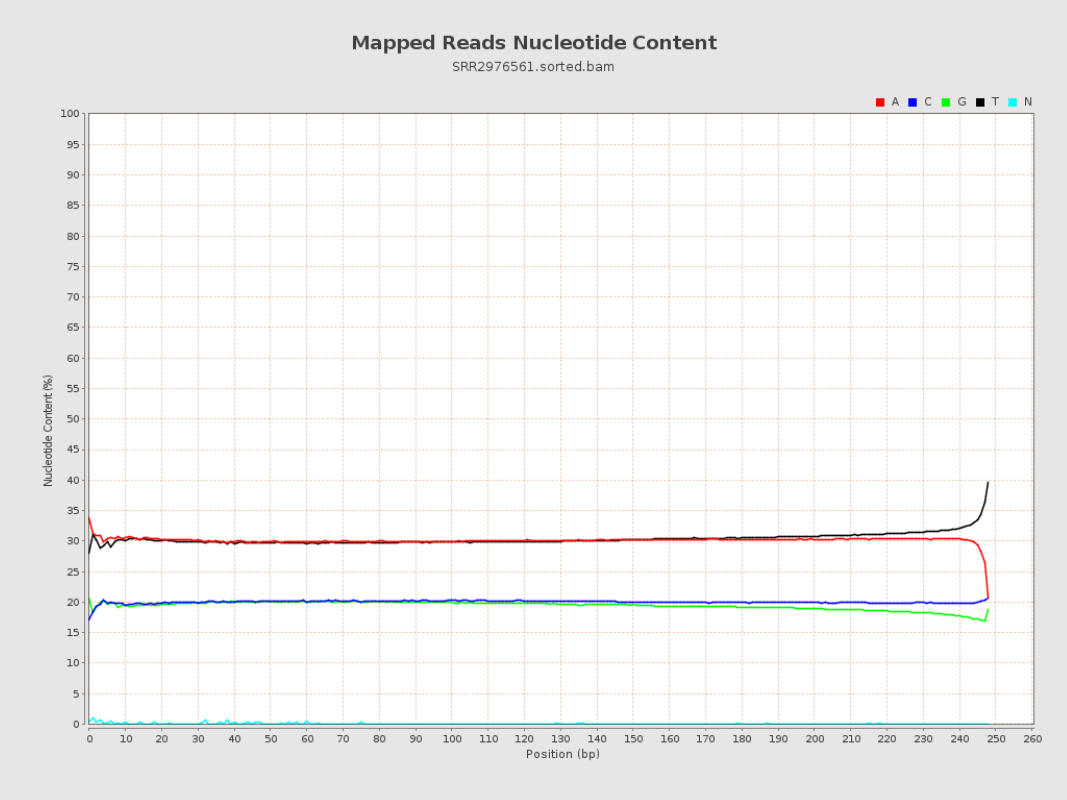
6. Results : Genome Fraction Coverage



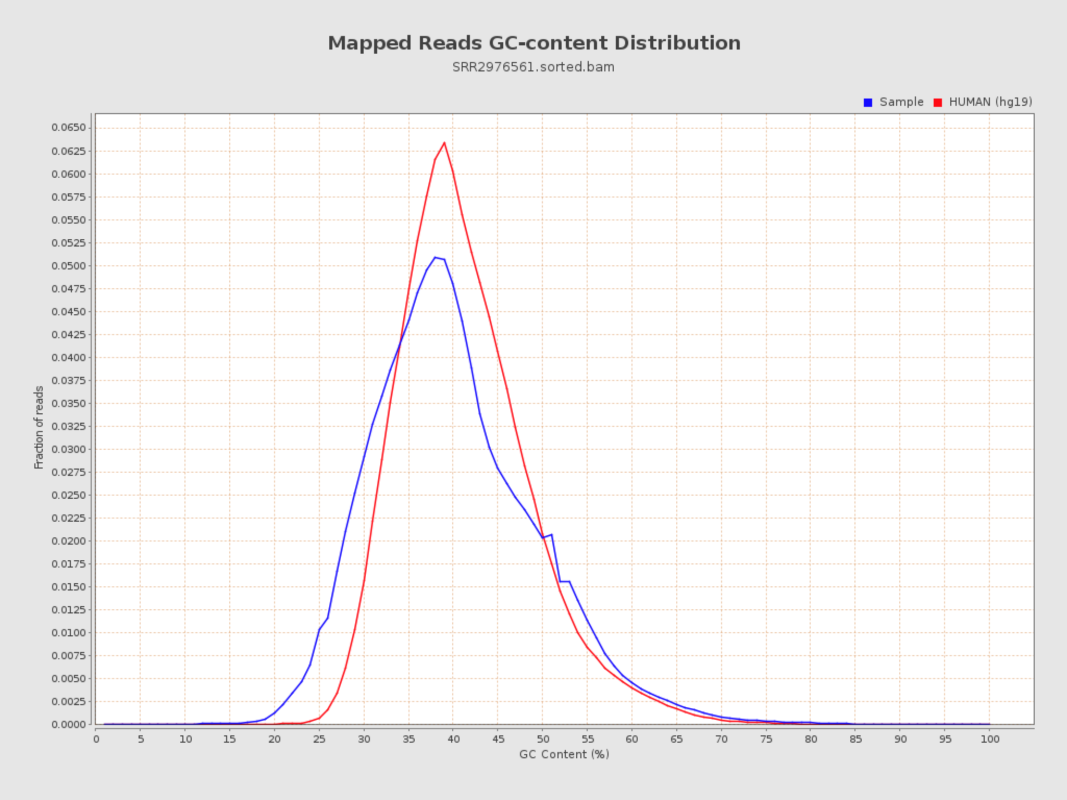
7. Results : Duplication Rate Histogram



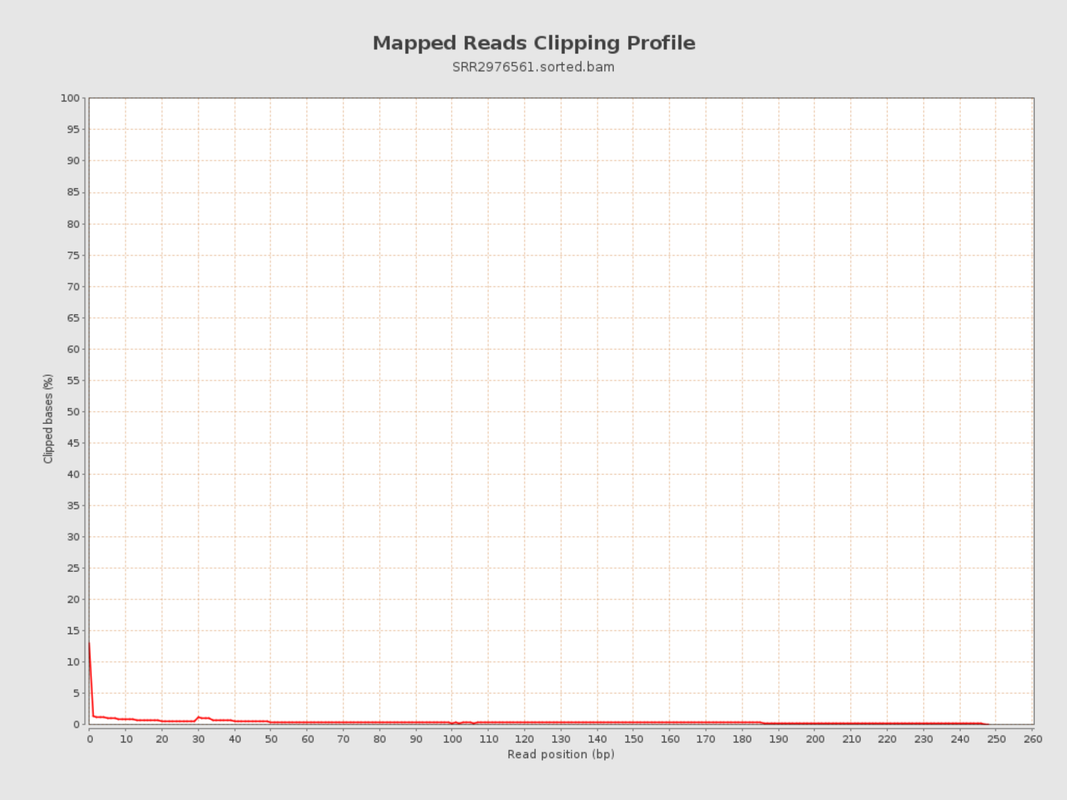
8. Results : Mapped Reads Nucleotide Content



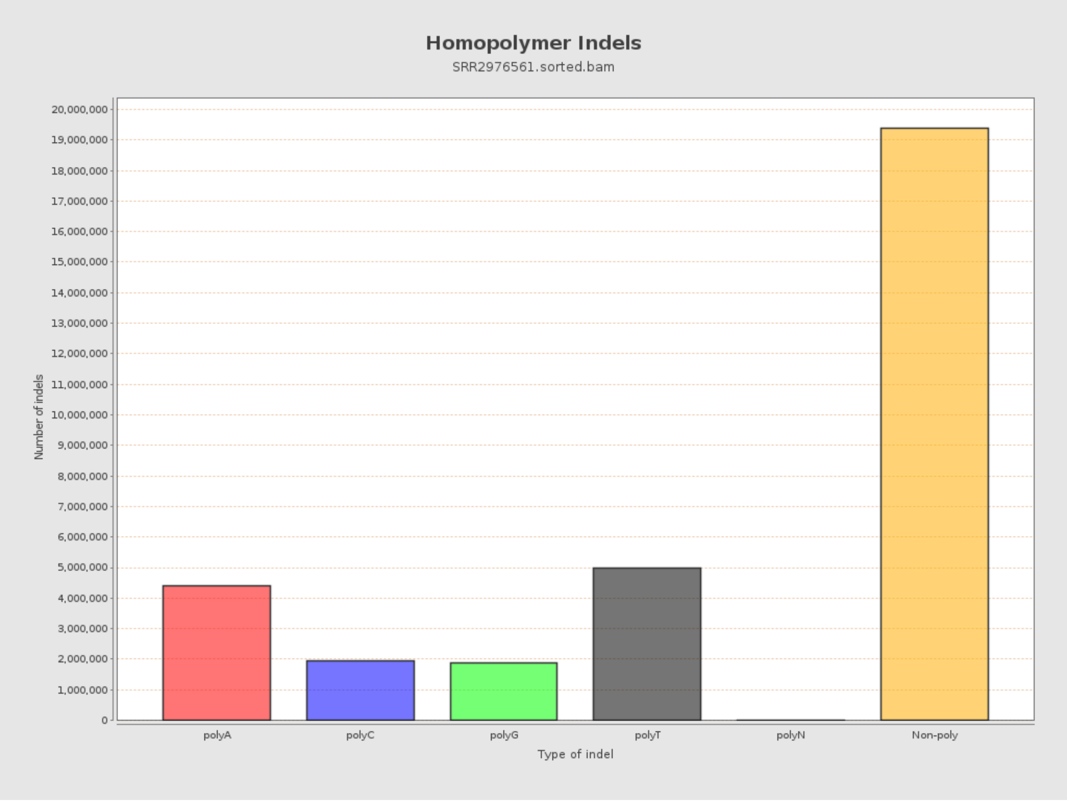
9. Results : Mapped Reads GC-content Distribution



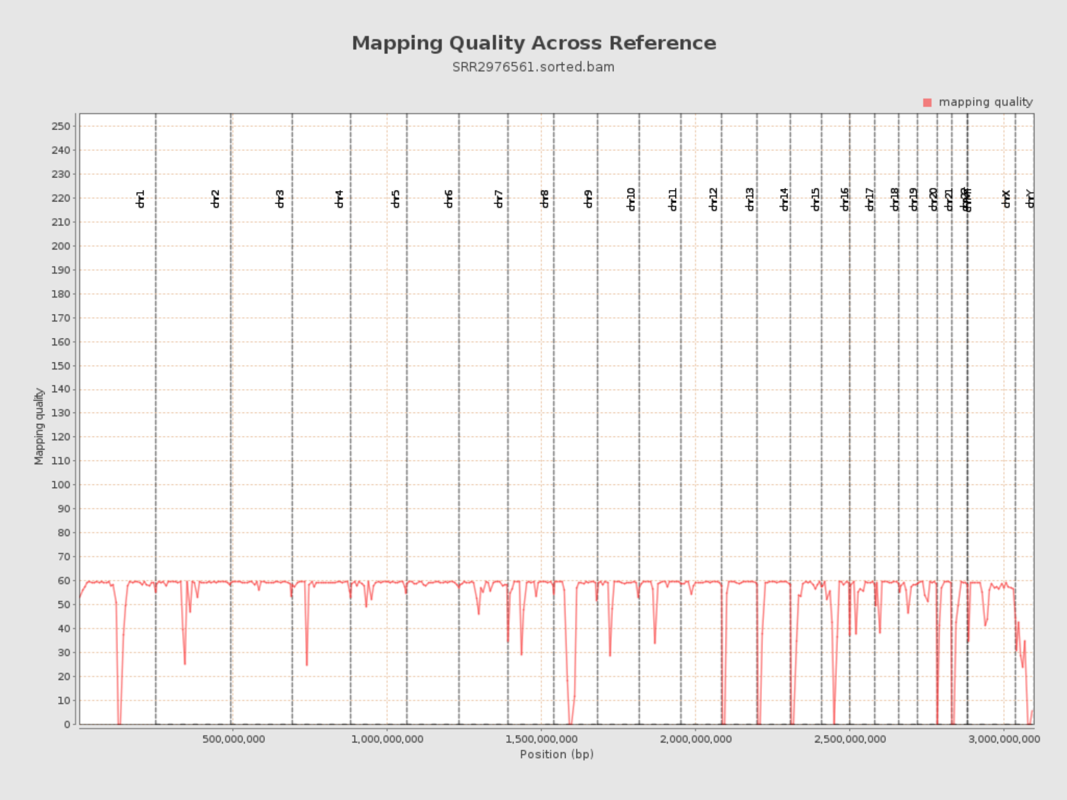
10. Results : Mapped Reads Clipping Profile



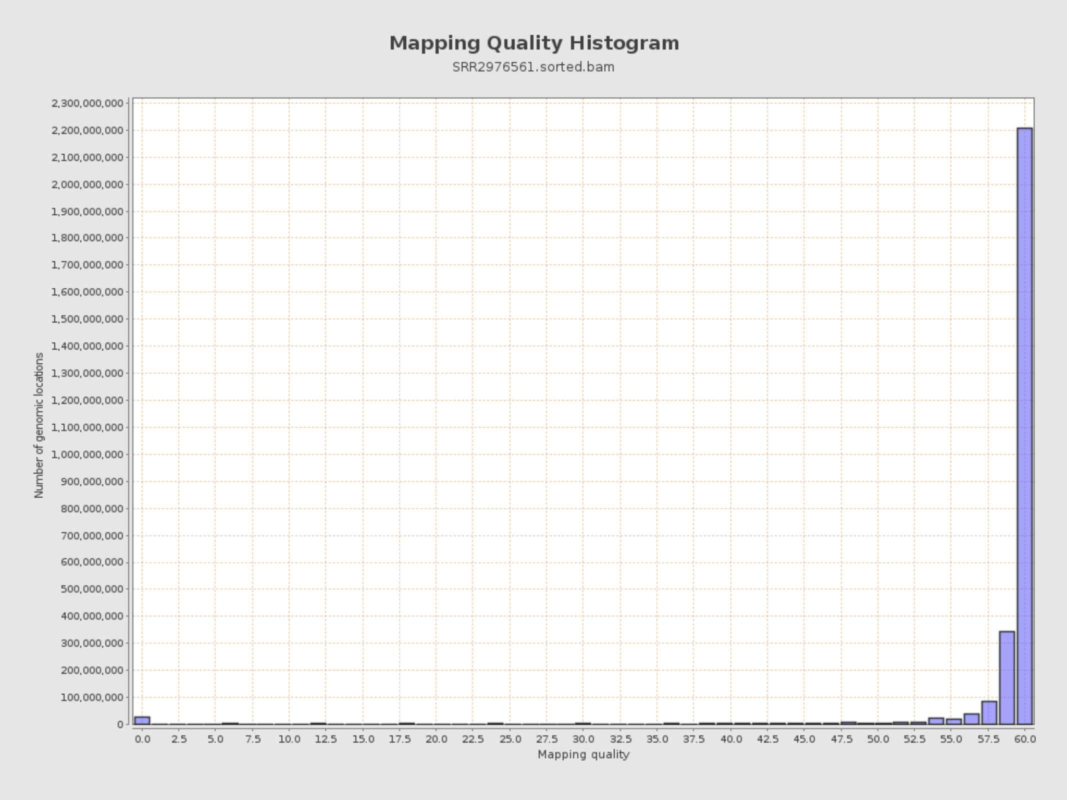
11. Results : Homopolymer Indels



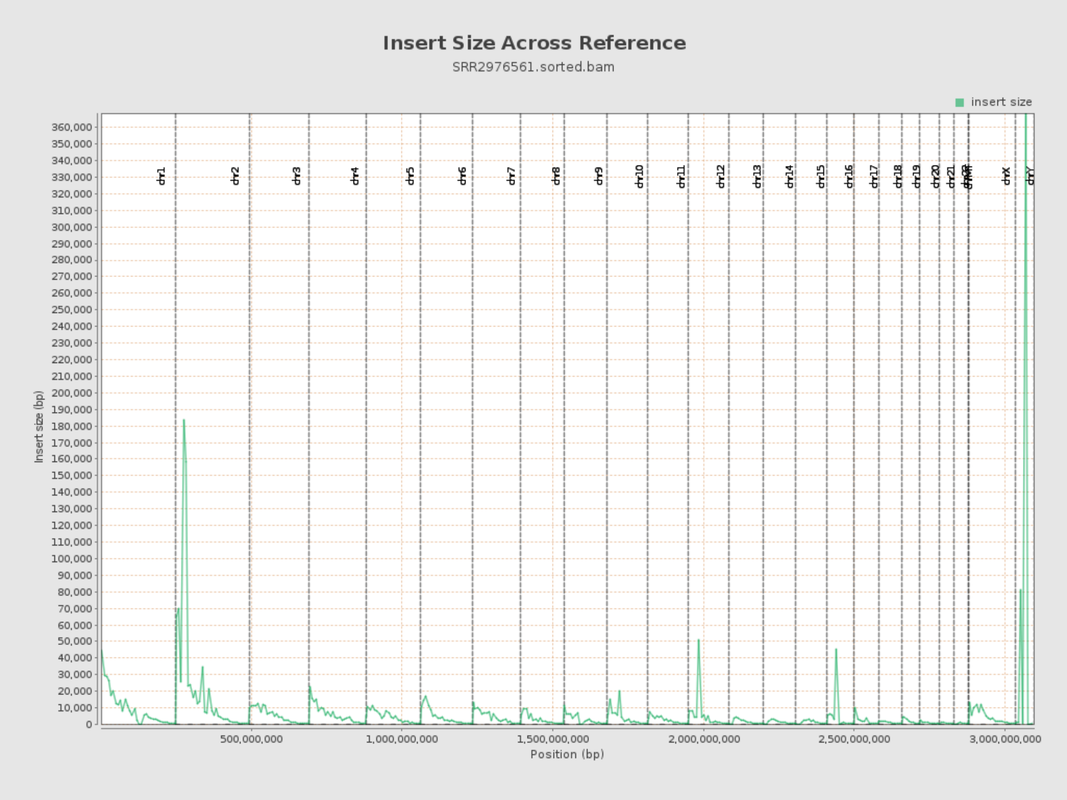
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram