Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/17 23:11:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006190.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_SRR1006190 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006190_1.fastq.gz SRR1006190_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 17 23:11:39 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006190.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,474,868
Mapped reads	4,619,099 / 54.5%
Unmapped reads	3,855,769 / 45.5%
Mapped paired reads	4,619,099 / 54.5%
Mapped reads, first in pair	2,326,876 / 27.46%
Mapped reads, second in pair	2,292,223 / 27.05%
Mapped reads, both in pair	4,240,986 / 50.04%
Mapped reads, singletons	378,113 / 4.46%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	146,873 / 1.73%
Duplication rate	2.68%
Clipped reads	263,426 / 3.11%

2.2. ACGT Content

Number/percentage of A's	49,099,801 / 27.46%
Number/percentage of C's	39,137,667 / 21.89%
Number/percentage of T's	50,065,002 / 28%
Number/percentage of G's	40,456,837 / 22.63%
Number/percentage of N's	20,949 / 0.01%
GC Percentage	44.52%

2.3. Coverage

Mean	0.0578
Standard Deviation	0.3854

2.4. Mapping Quality

Mean Mapping Quality	47.85

2.5. Insert size

Mean	55,363.46
Standard Deviation	2,256,560.79
P25/Median/P75	78 / 114 / 153

2.6. Mismatches and indels

General error rate	0.32%
Mismatches	558,502
Insertions	5,366
Mapped reads with at least one insertion	0.12%
Deletions	18,590
Mapped reads with at least one deletion	0.4%
Homopolymer indels	42.23%

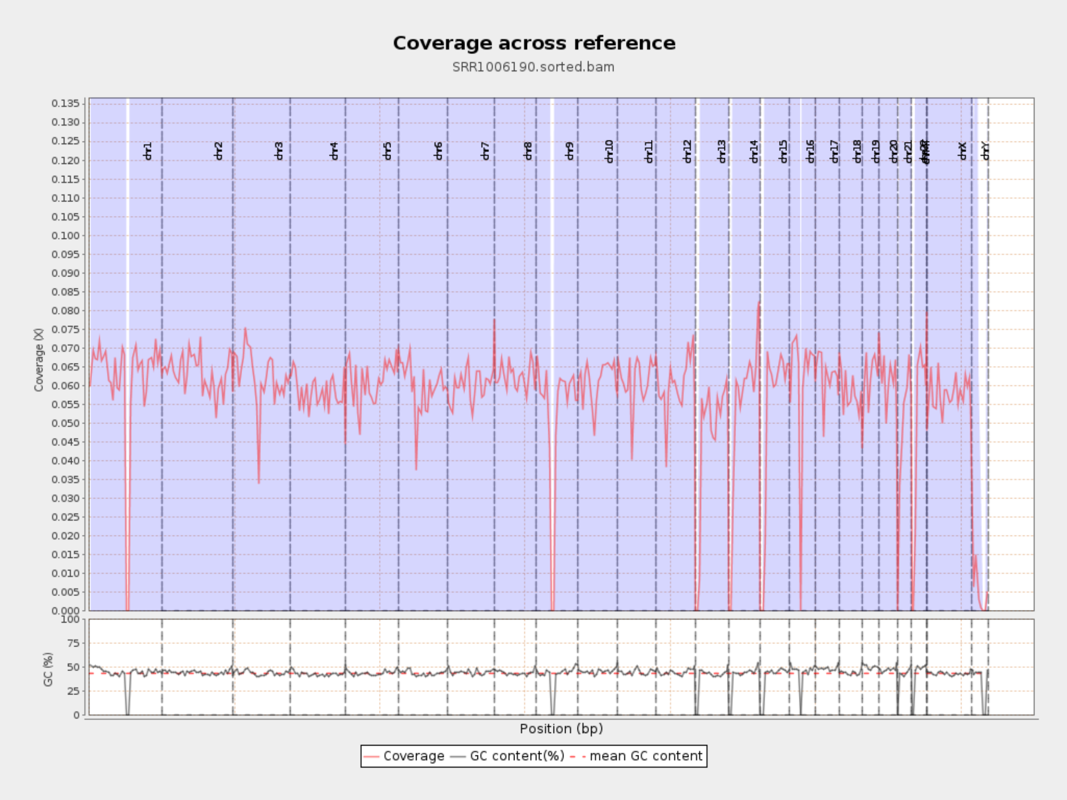
2.7. Chromosome stats

Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**

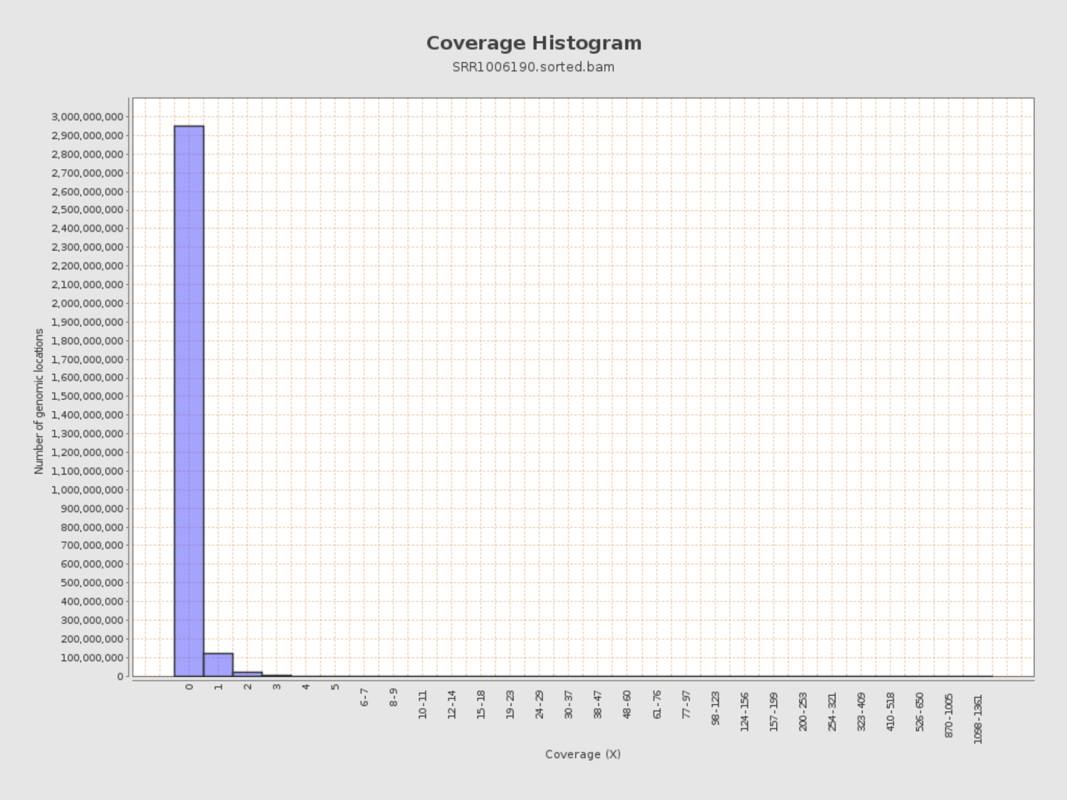
chr1	249250621	15184815	0.0609	0.4445
chr2	243199373	15412090	0.0634	0.4044
chr3	198022430	12291427	0.0621	0.2956
chr4	191154276	11168831	0.0584	0.289
chr5	180915260	11044443	0.061	0.3992
chr6	171115067	10227954	0.0598	0.327
chr7	159138663	9497098	0.0597	0.405
chr8	146364022	9134848	0.0624	0.7271
chr9	141213431	7322978	0.0519	0.3044
chr10	135534747	8303889	0.0613	0.3299
chr11	135006516	8272185	0.0613	0.3425
chr12	133851895	8071109	0.0603	0.2949
chr13	115169878	5191851	0.0451	0.2534
chr14	107349540	5654832	0.0527	0.6673
chr15	102531392	5319456	0.0519	0.2719
chr16	90354753	5563829	0.0616	0.3216
chr17	81195210	5062975	0.0624	0.3182
chr18	78077248	4540204	0.0582	0.4303
chr19	59128983	3692892	0.0625	0.376
chr20	63025520	3882029	0.0616	0.3023
chr21	48129895	2297864	0.0477	0.2786
chr22	51304566	2343501	0.0457	0.2755
chrMT	16571	1318	0.0795	0.4106
chrX	155270560	8977976	0.0578	0.2986

chrY	59373566	344948	0.0058	0.1271

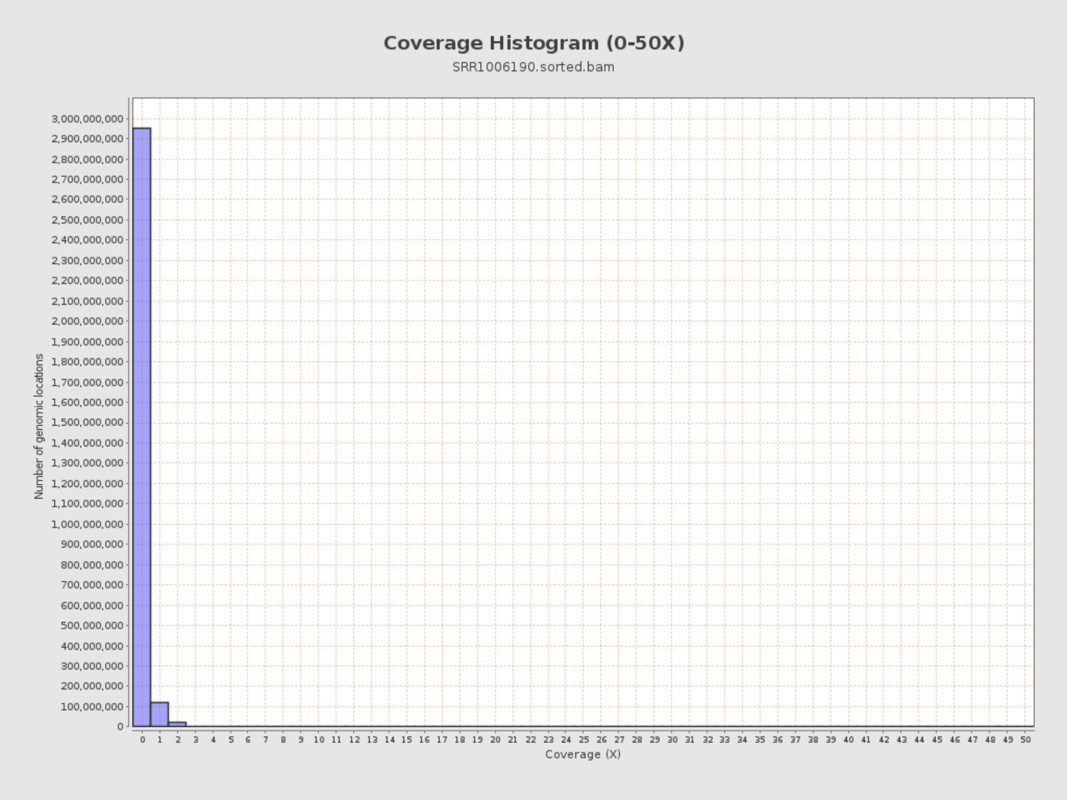
3. Results : Coverage across reference



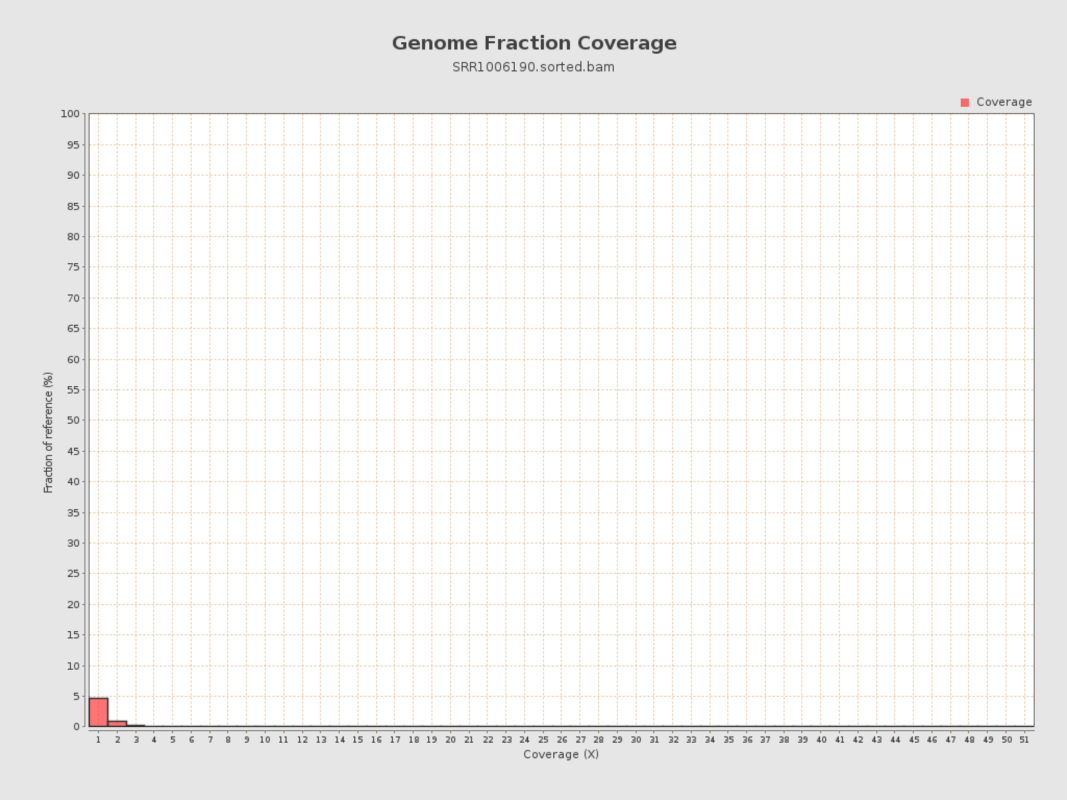
4. Results : Coverage Histogram



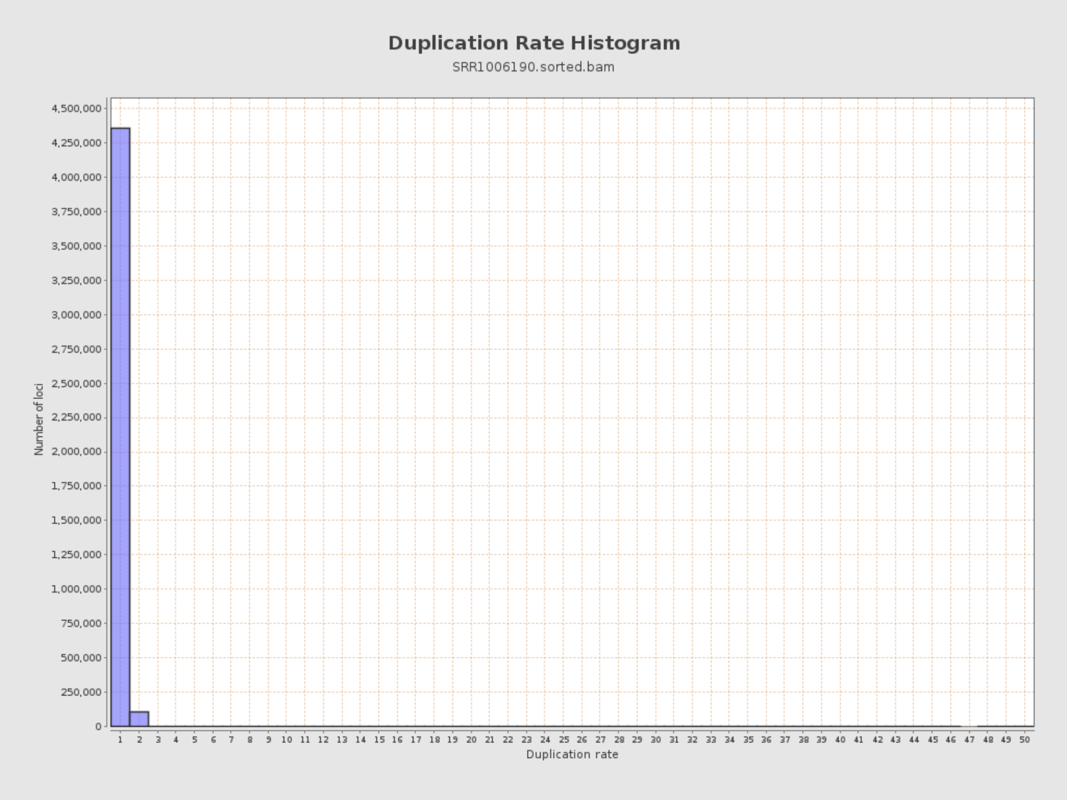
5. Results : Coverage Histogram (0-50X)



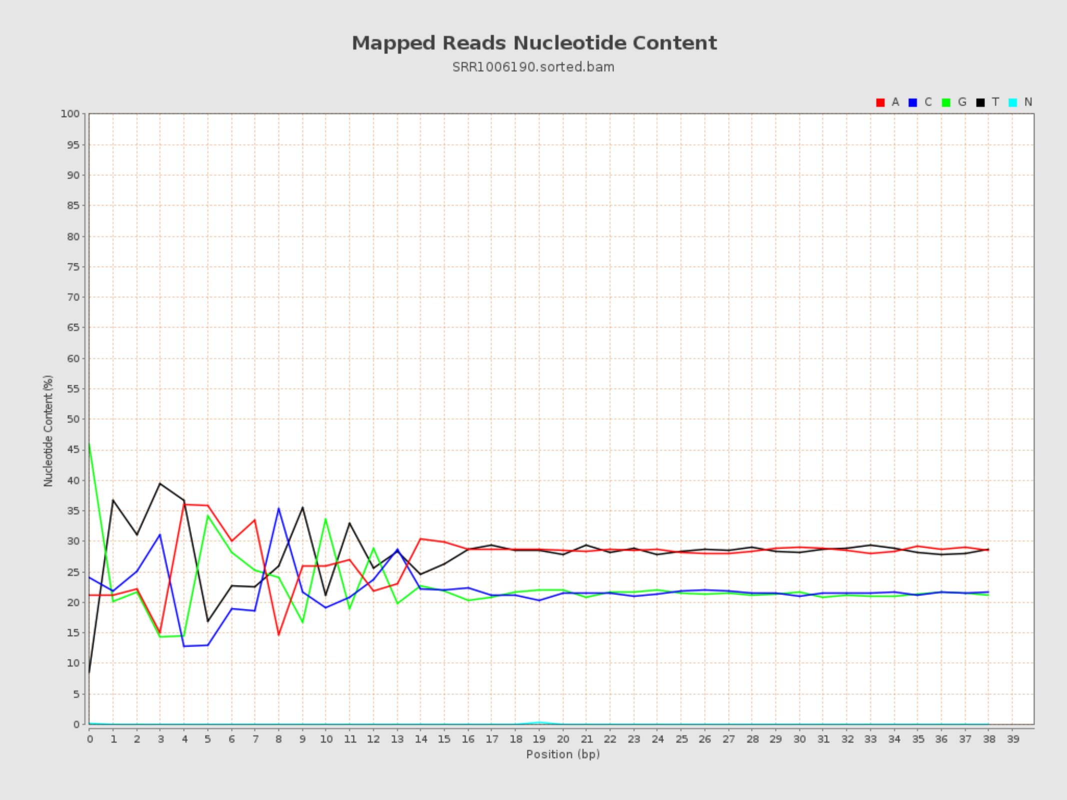
6. Results : Genome Fraction Coverage



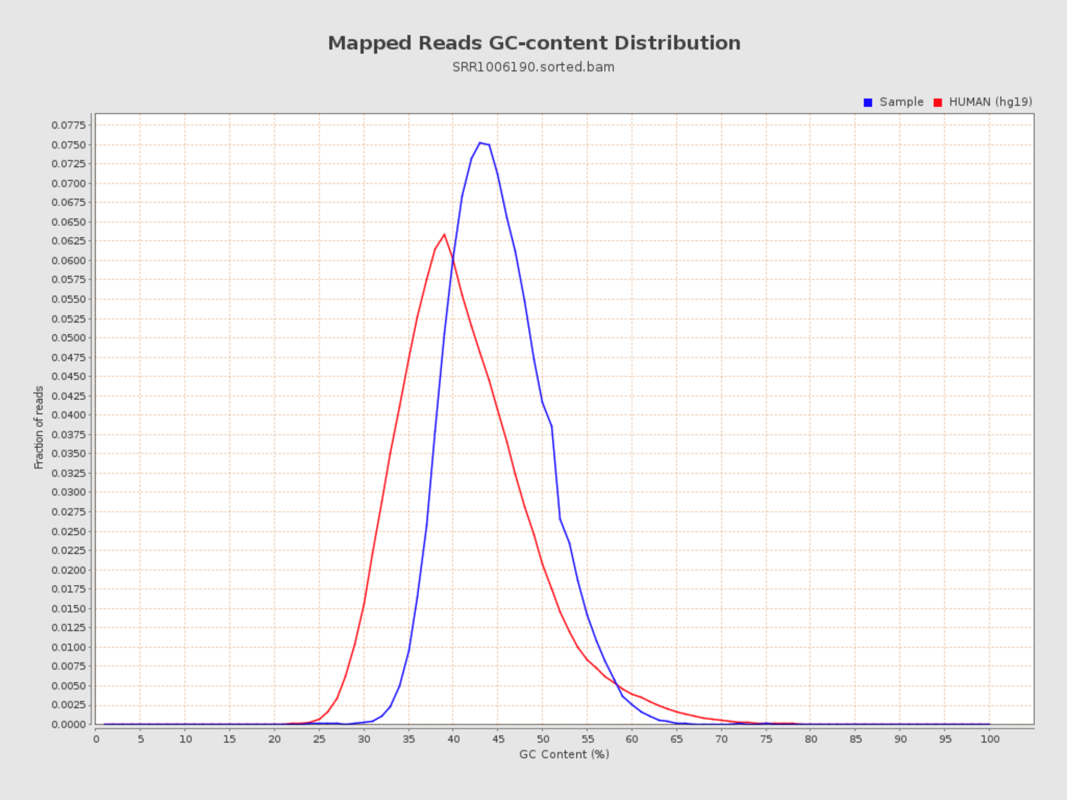
7. Results : Duplication Rate Histogram



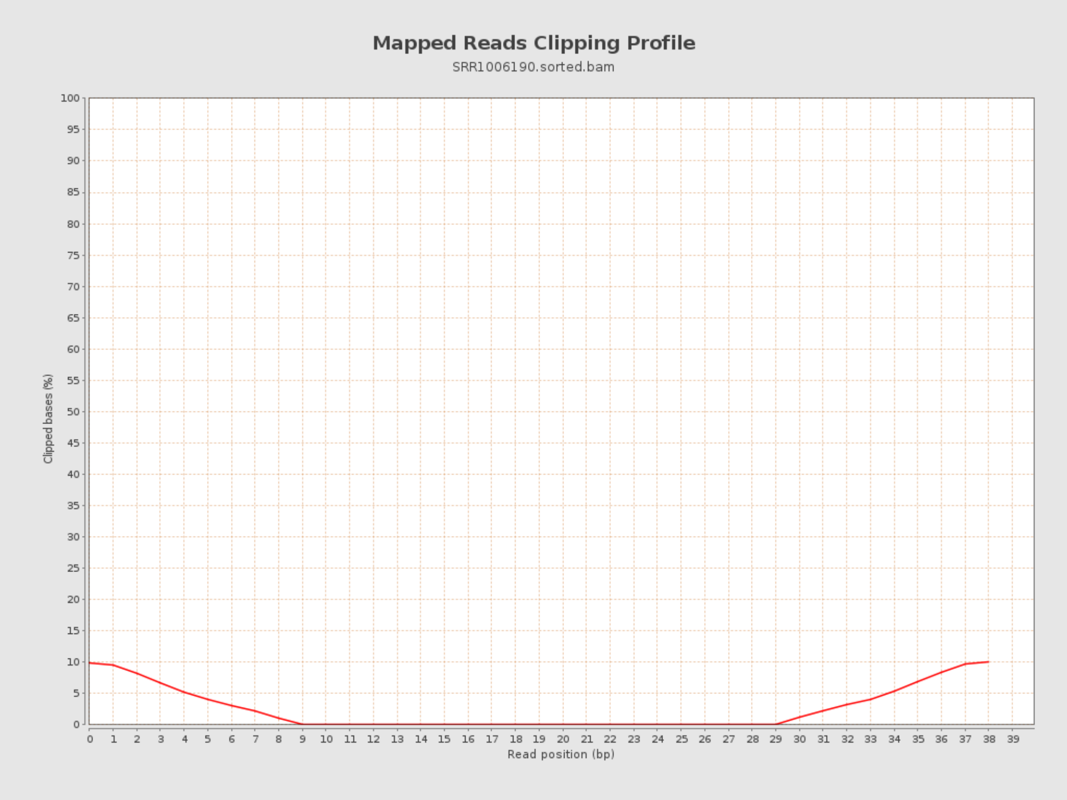
8. Results : Mapped Reads Nucleotide Content



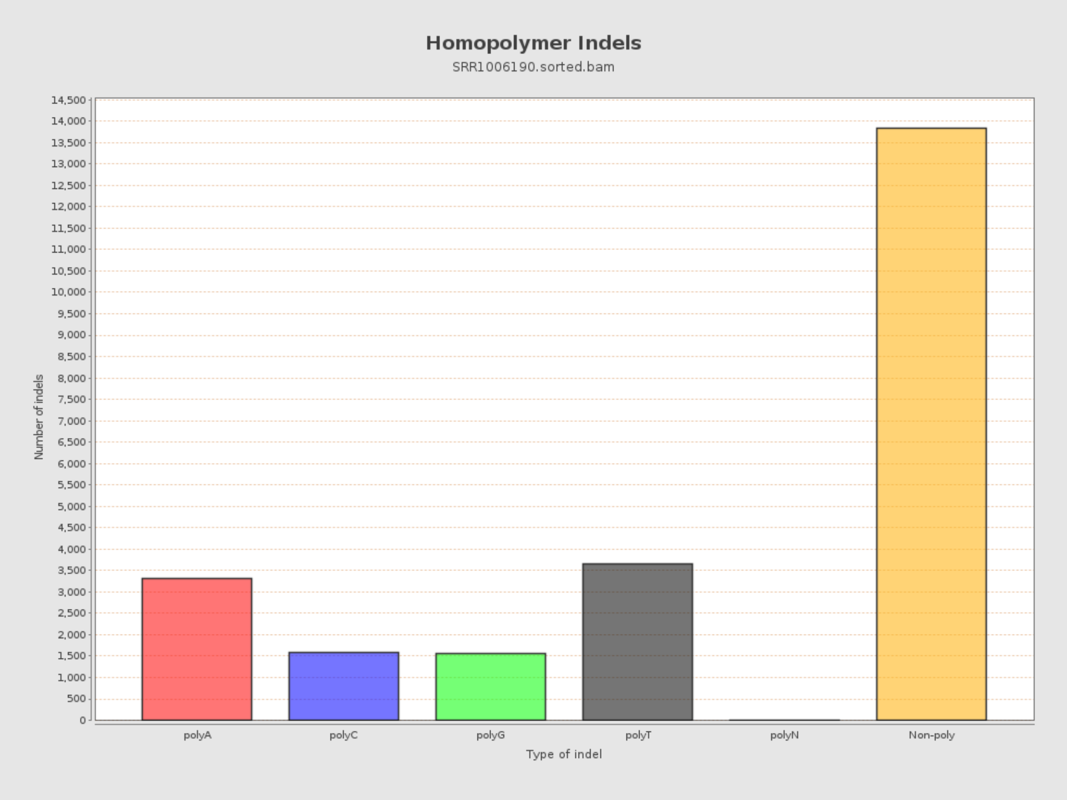
9. Results : Mapped Reads GC-content Distribution



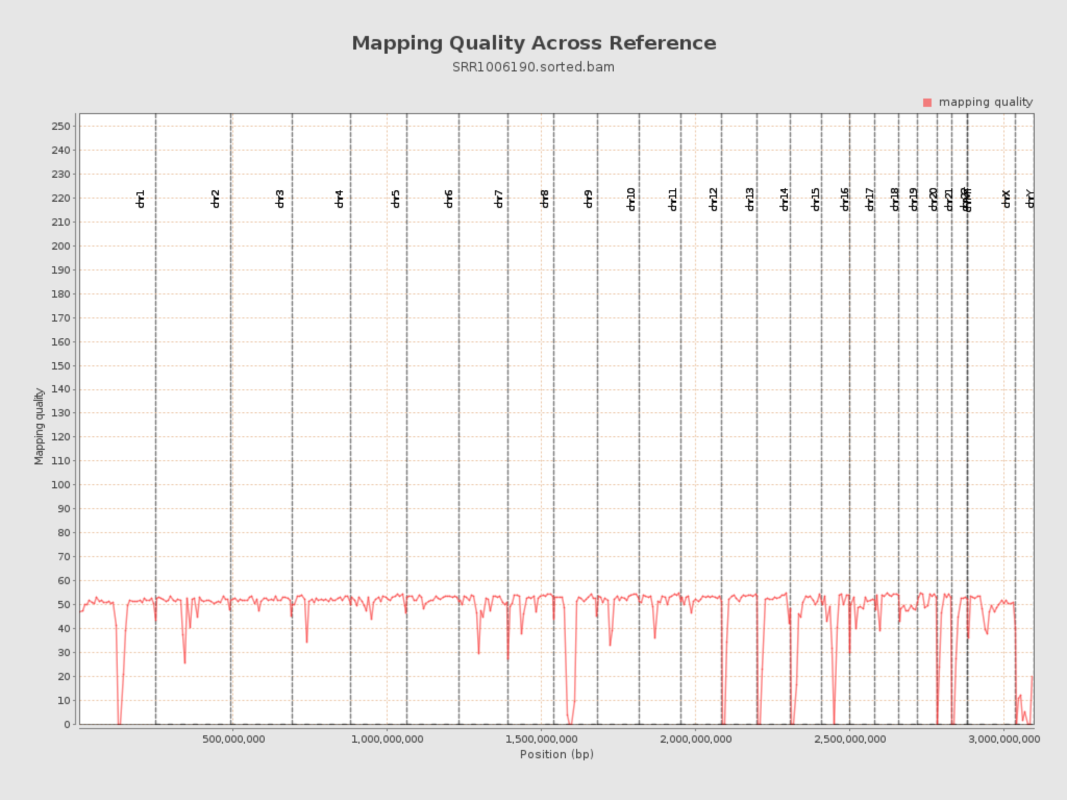
10. Results : Mapped Reads Clipping Profile



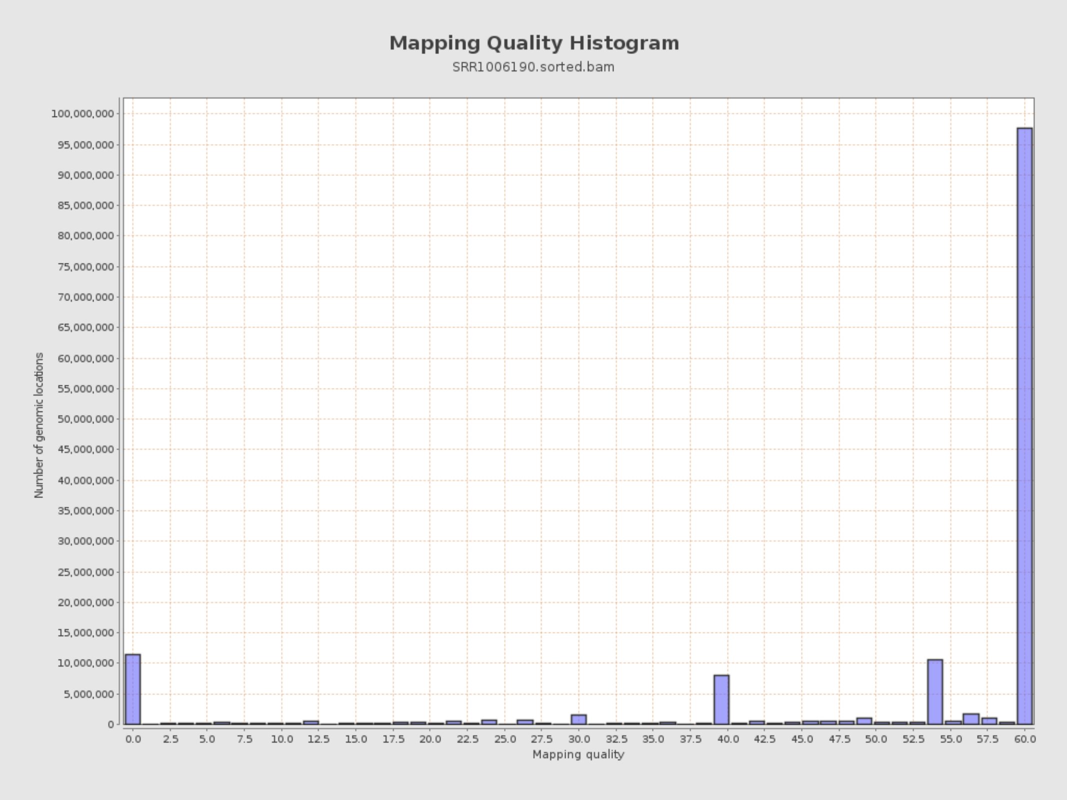
11. Results : Homopolymer Indels



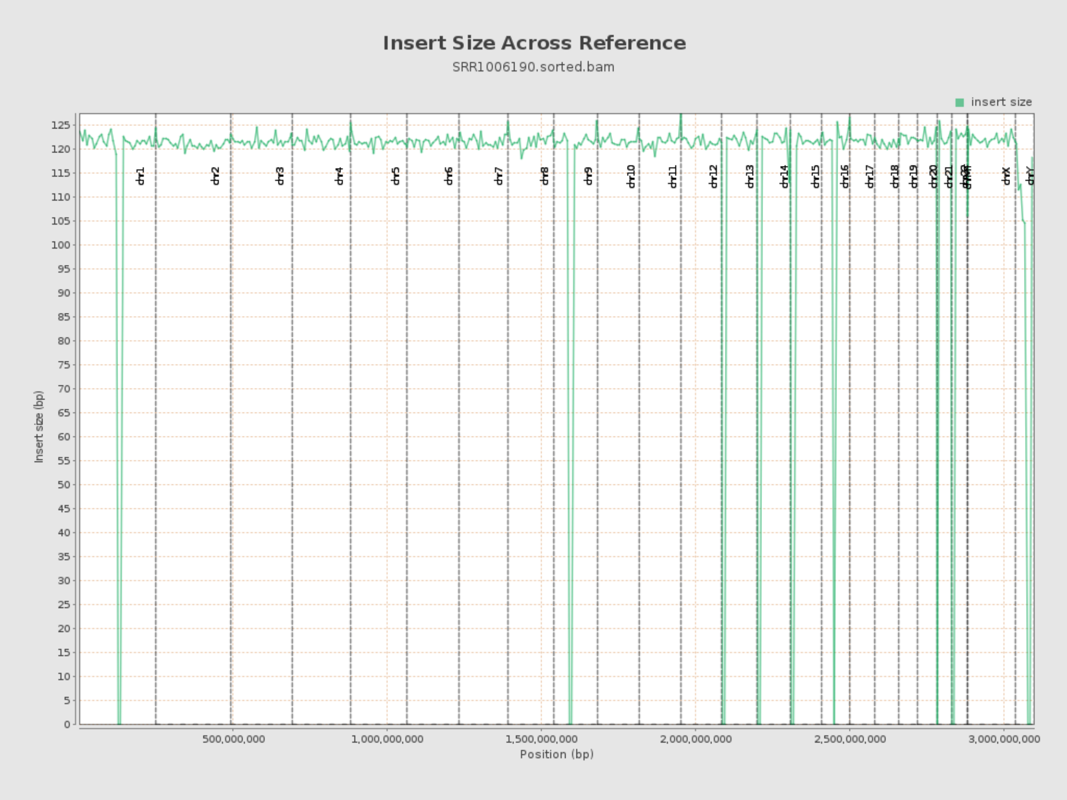
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram