Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/05 14:23:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR611511.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_SRR611511 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR611511_1.fastq.gz SRR611511_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Oct 05 14:23:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR611511.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,127,379,558
Mapped reads	1,098,821,716 / 97.47%
Unmapped reads	28,557,842 / 2.53%
Mapped paired reads	1,098,821,716 / 97.47%
Mapped reads, first in pair	551,187,316 / 48.89%
Mapped reads, second in pair	547,634,400 / 48.58%
Mapped reads, both in pair	1,087,372,276 / 96.45%
Mapped reads, singletons	11,449,440 / 1.02%
Secondary alignments	0
Supplementary alignments	11,016,486 / 0.98%
Read min/max/mean length	30 / 90 / 90.38
Duplicated reads (estimated)	436,311,124 / 38.7%
Duplication rate	31.78%
Clipped reads	180,328,454 / 16%

2.2. ACGT Content

Number/percentage of A's	27,033,387,773 / 28.5%
Number/percentage of C's	19,803,216,610 / 20.88%
Number/percentage of T's	27,160,715,864 / 28.63%
Number/percentage of G's	20,848,652,970 / 21.98%
Number/percentage of N's	8,302,130 / 0.01%

GC Percentage	42.86%

2.3. Coverage

Mean	30.6644
Standard Deviation	352.999

2.4. Mapping Quality

Mean Mapping Quality	52.07

2.5. Insert size

Mean	146,464.47
Standard Deviation	3,658,832.98
P25/Median/P75	178 / 187 / 195

2.6. Mismatches and indels

General error rate	1.11%
Mismatches	1,014,370,303
Insertions	17,479,762
Mapped reads with at least one insertion	1.55%
Deletions	44,345,302
Mapped reads with at least one deletion	3.94%
Homopolymer indels	48.19%

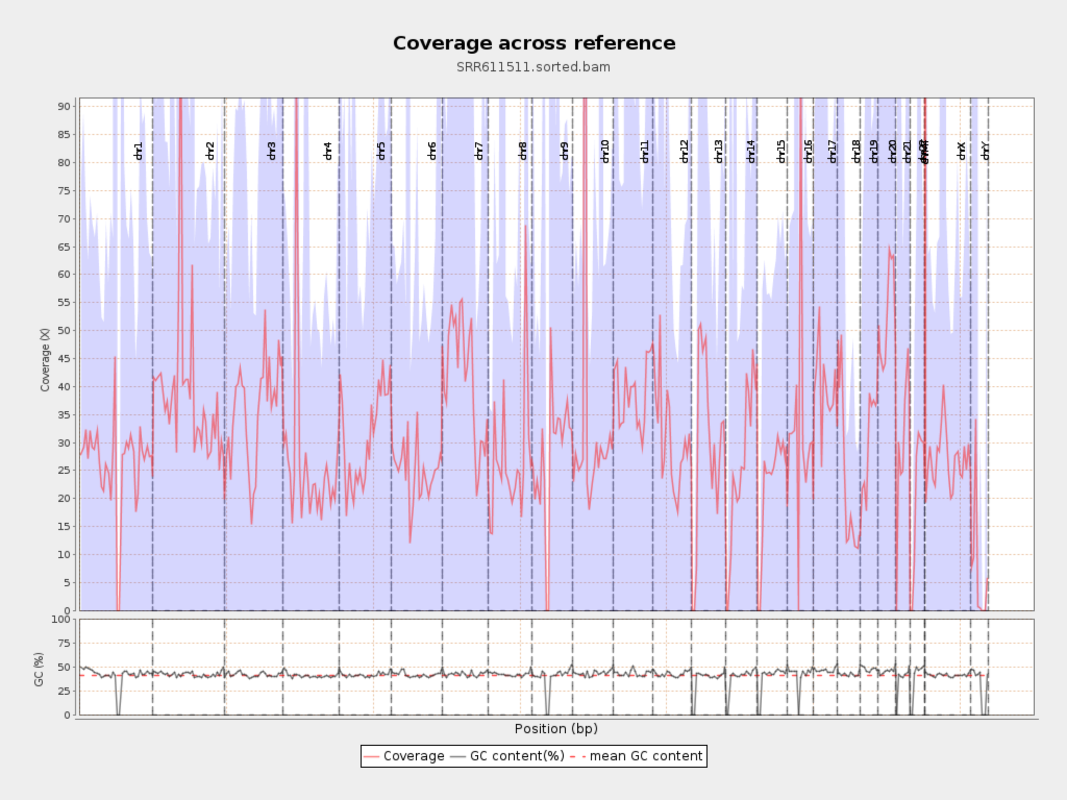
2.7. Chromosome stats

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

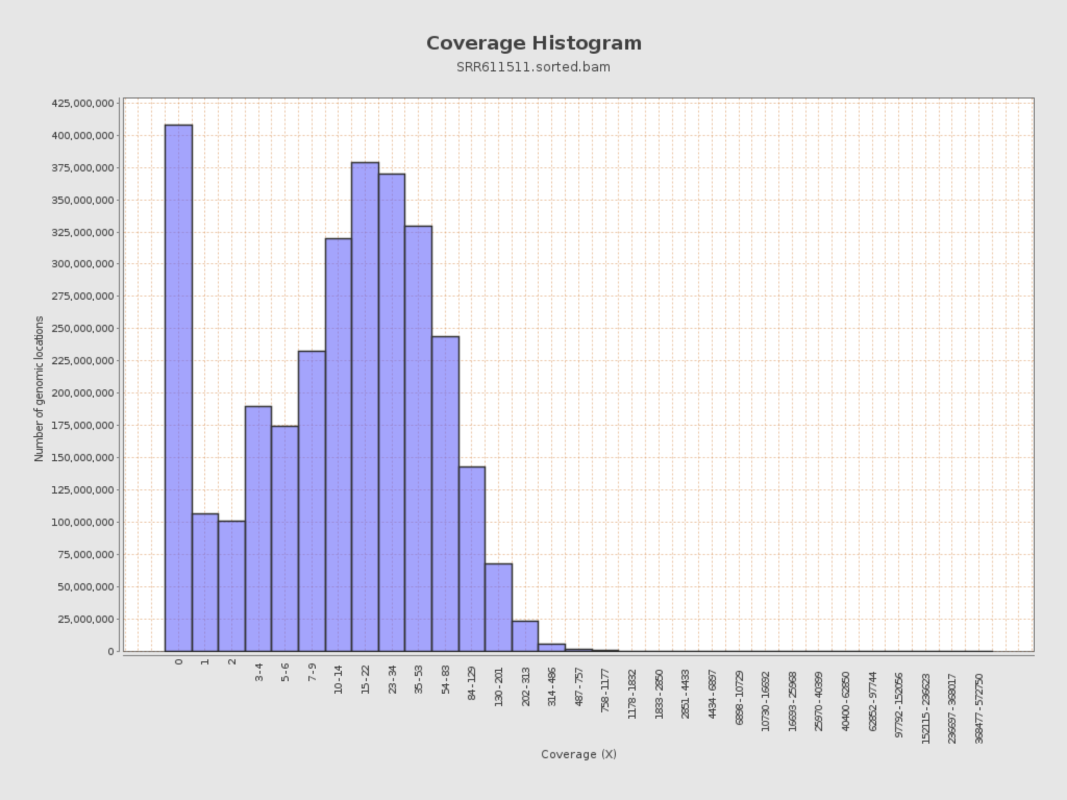
		bases	coverage	deviation
chr1	249250621	6538059395	26.2309	348.6871
chr2	243199373	9522729682	39.1561	465.2399
chr3	198022430	7016714299	35.4339	59.7977
chr4	191154276	4938327451	25.8343	301.3186
chr5	180915260	5641038305	31.1806	56.2198
chr6	171115067	4267230227	24.9378	129.8944
chr7	159138663	6596649607	41.4522	306.1311
chr8	146364022	3927451446	26.8334	128.4869
chr9	141213431	3872990718	27.4265	419.5128
chr10	135534747	4659795663	34.3808	1,110.9245
chr11	135006516	5199623514	38.5139	213.1234
chr12	133851895	4091002918	30.5637	54.3849
chr13	115169878	3401145609	29.5316	47.3014
chr14	107349540	2729523972	25.4265	68.1301
chr15	102531392	2262167947	22.0632	35.0946
chr16	90354753	3003986818	33.2466	497.893
chr17	81195210	3215318025	39.5998	246.6054
chr18	78077248	1729678368	22.1534	442.1528
chr19	59128983	1757752866	29.7274	199.3339
chr20	63025520	3361609340	53.3373	151.0871
chr21	48129895	1461327806	30.3622	181.1762
chr22	51304566	1041788261	20.306	57.8663
chrMT	16571	84646800	5,108.1287	2,028.523
chrX	155270560	4175832244	26.8939	119.2011

chrY	59373566	431187916	7.2623	475.2755

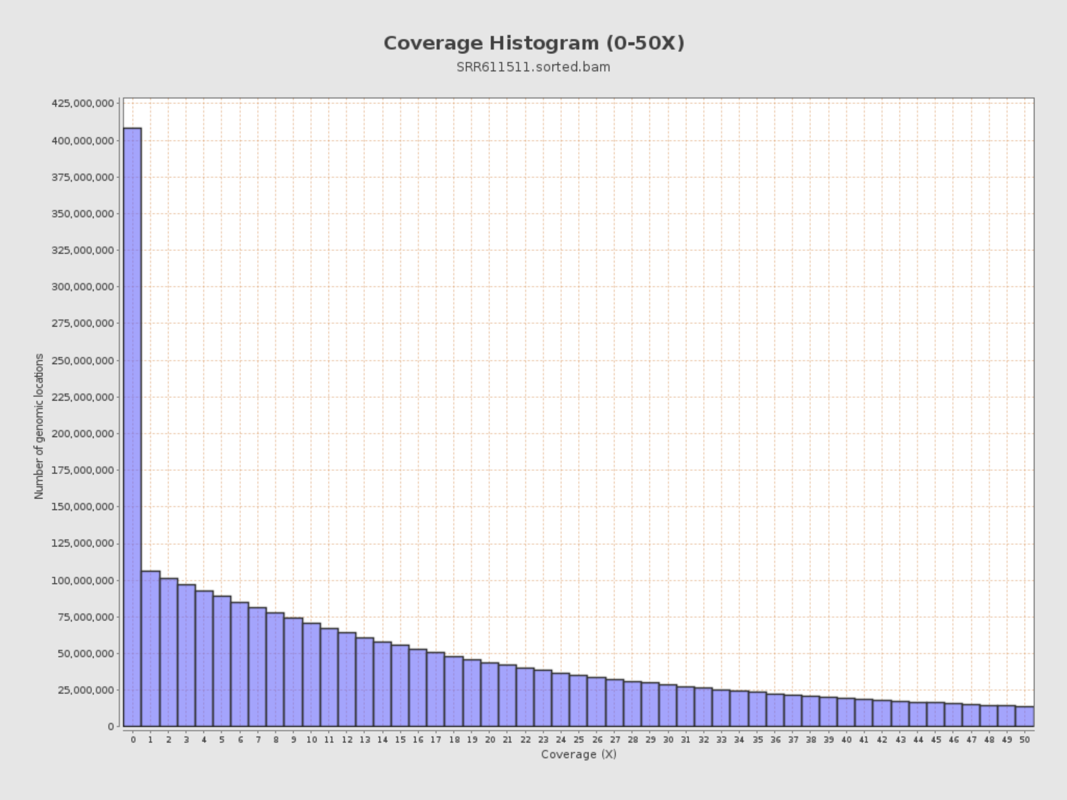
3. Results : Coverage across reference



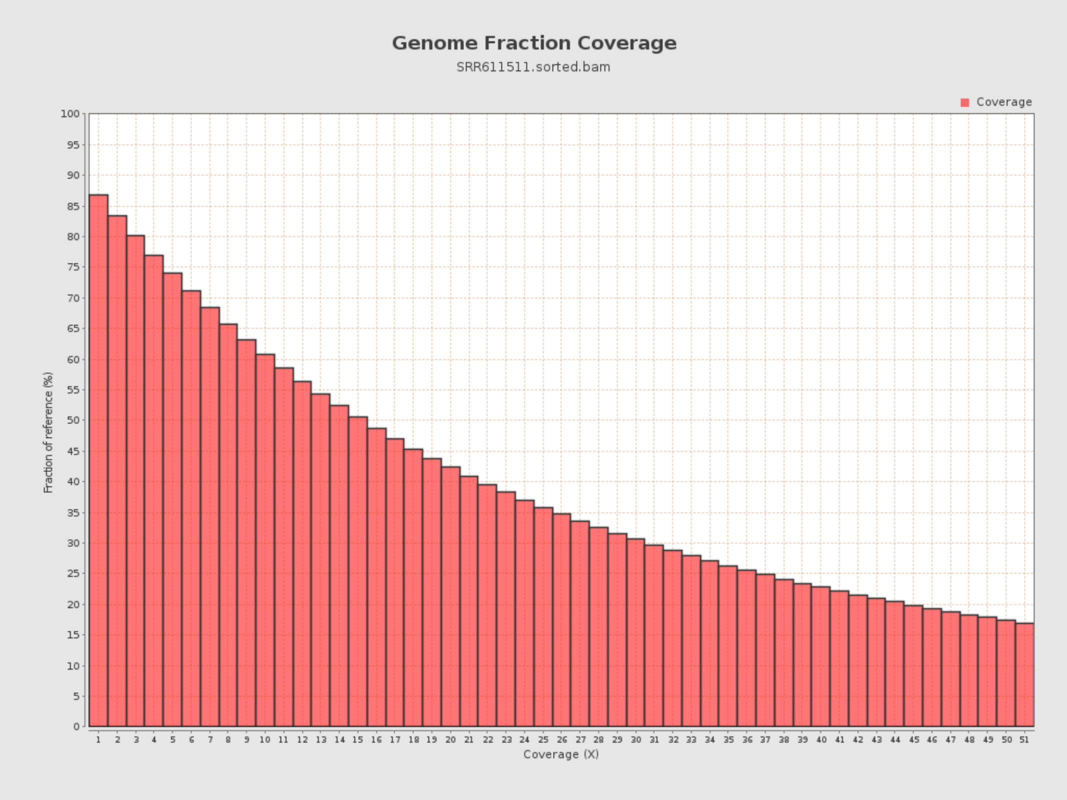
4. Results : Coverage Histogram



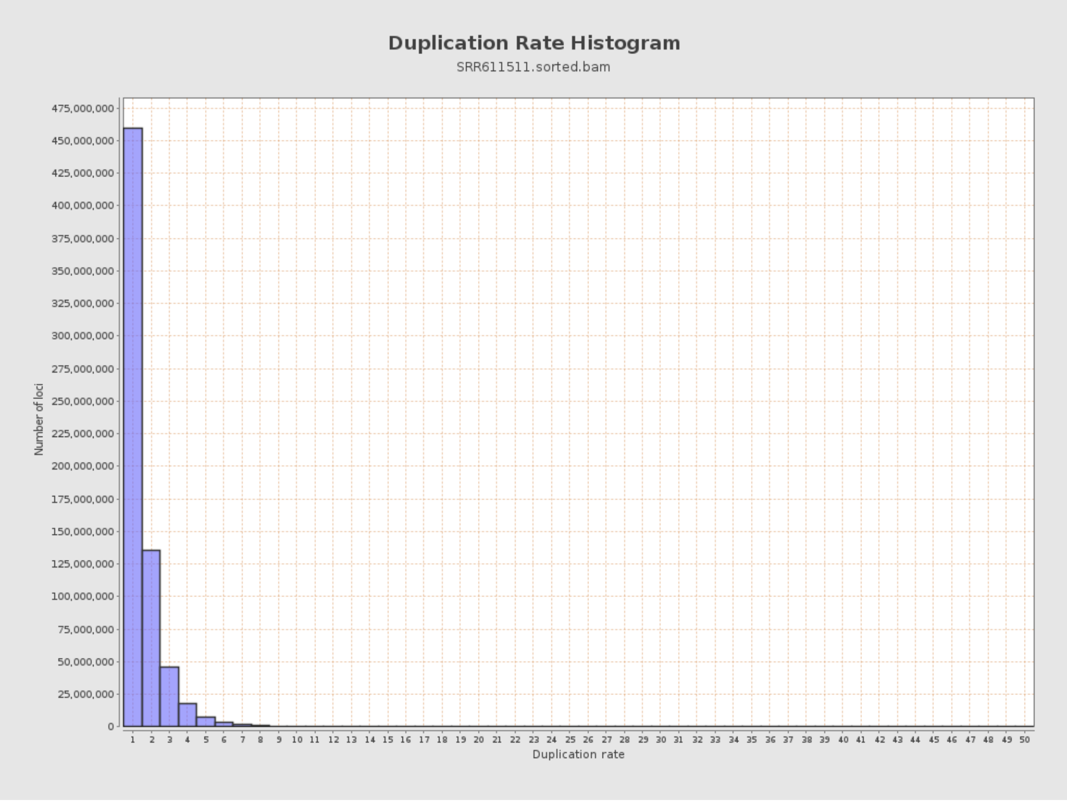
5. Results : Coverage Histogram (0-50X)



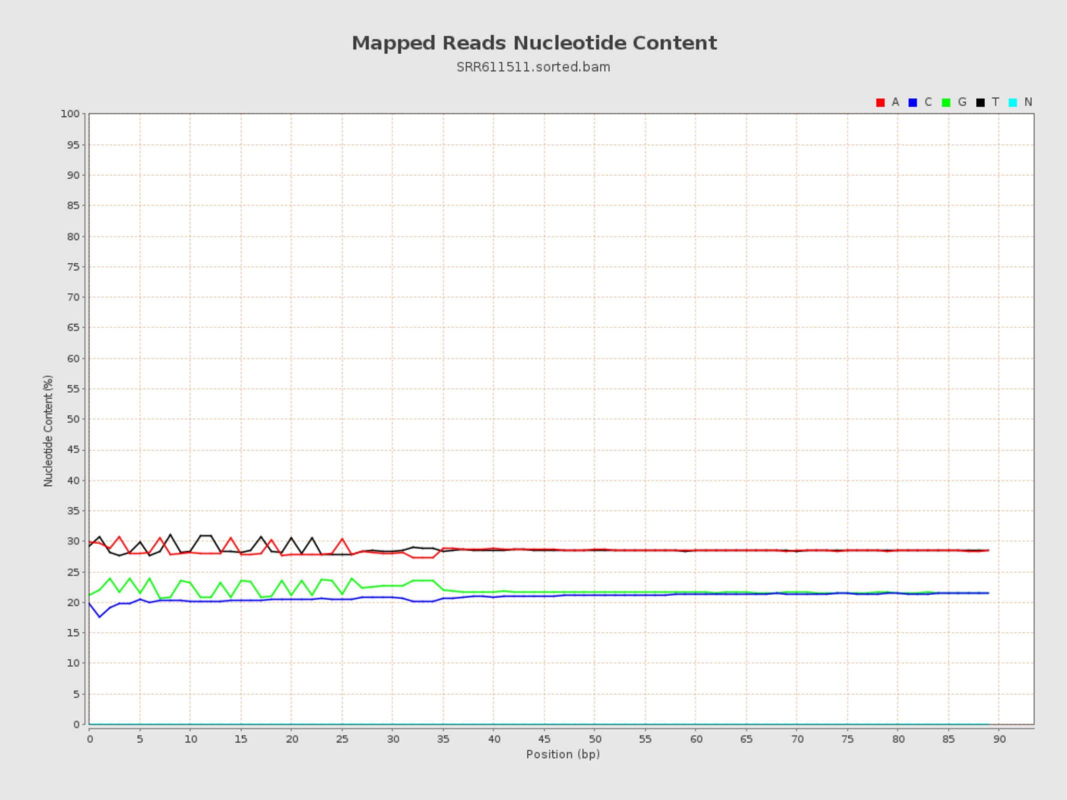
6. Results : Genome Fraction Coverage



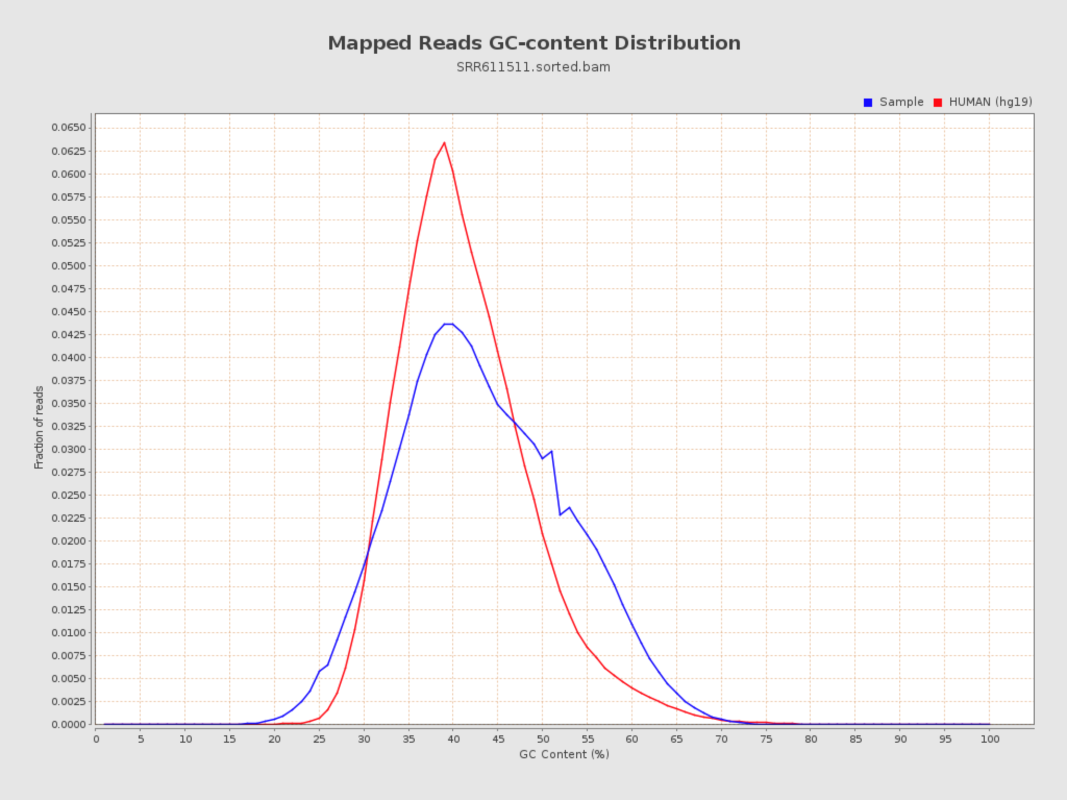
7. Results : Duplication Rate Histogram



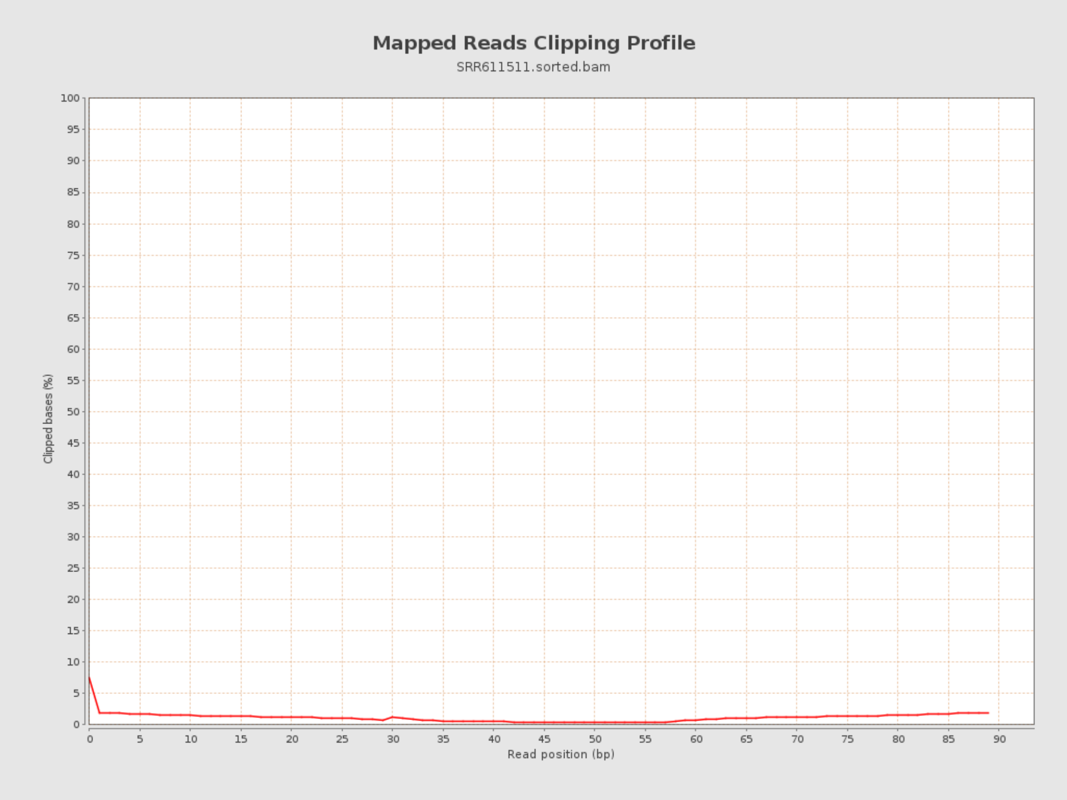
8. Results : Mapped Reads Nucleotide Content



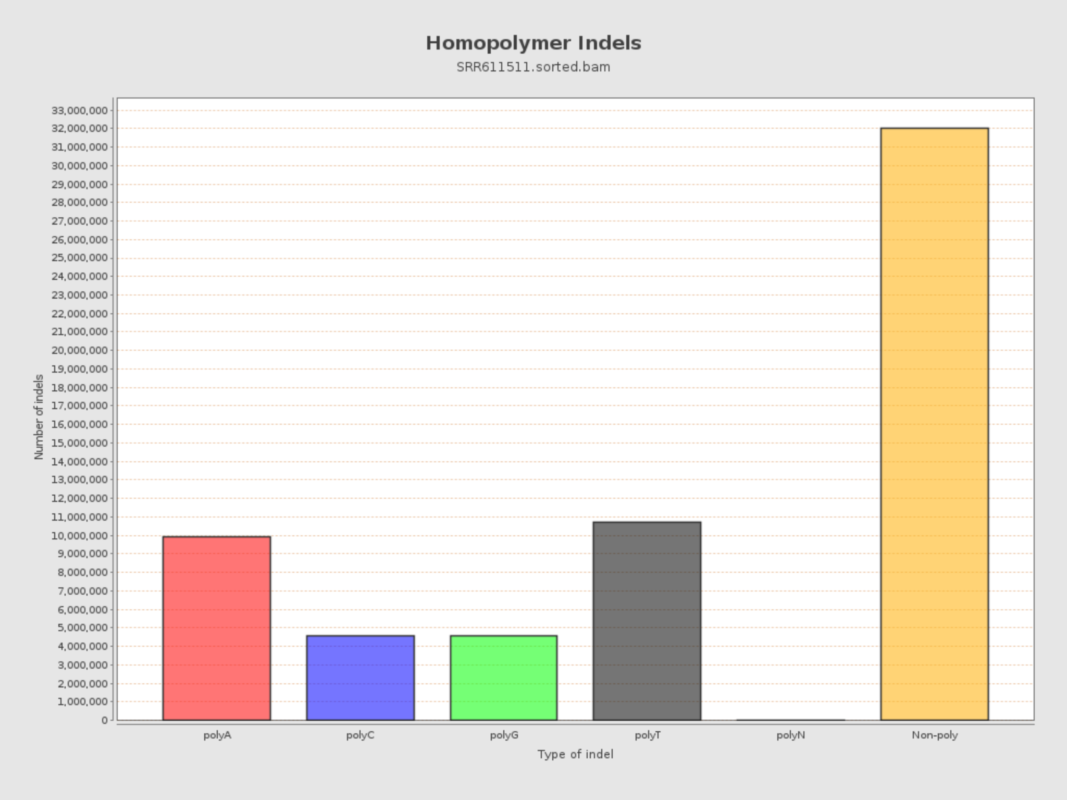
9. Results : Mapped Reads GC-content Distribution



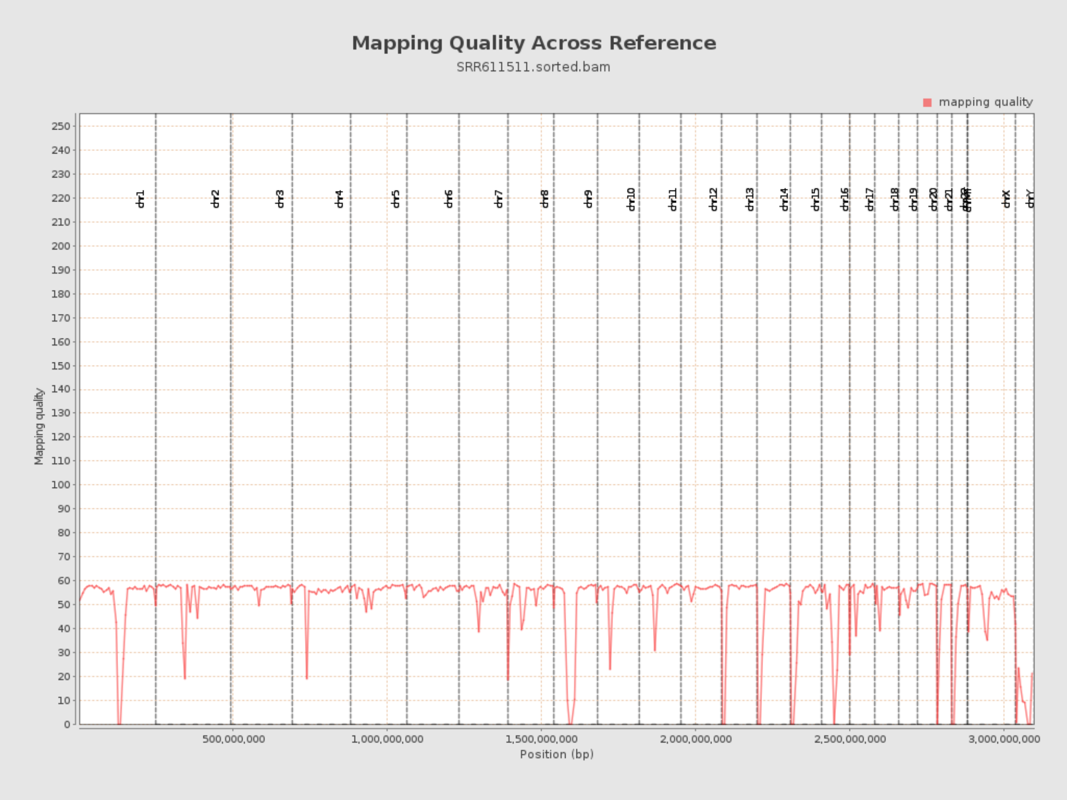
10. Results : Mapped Reads Clipping Profile



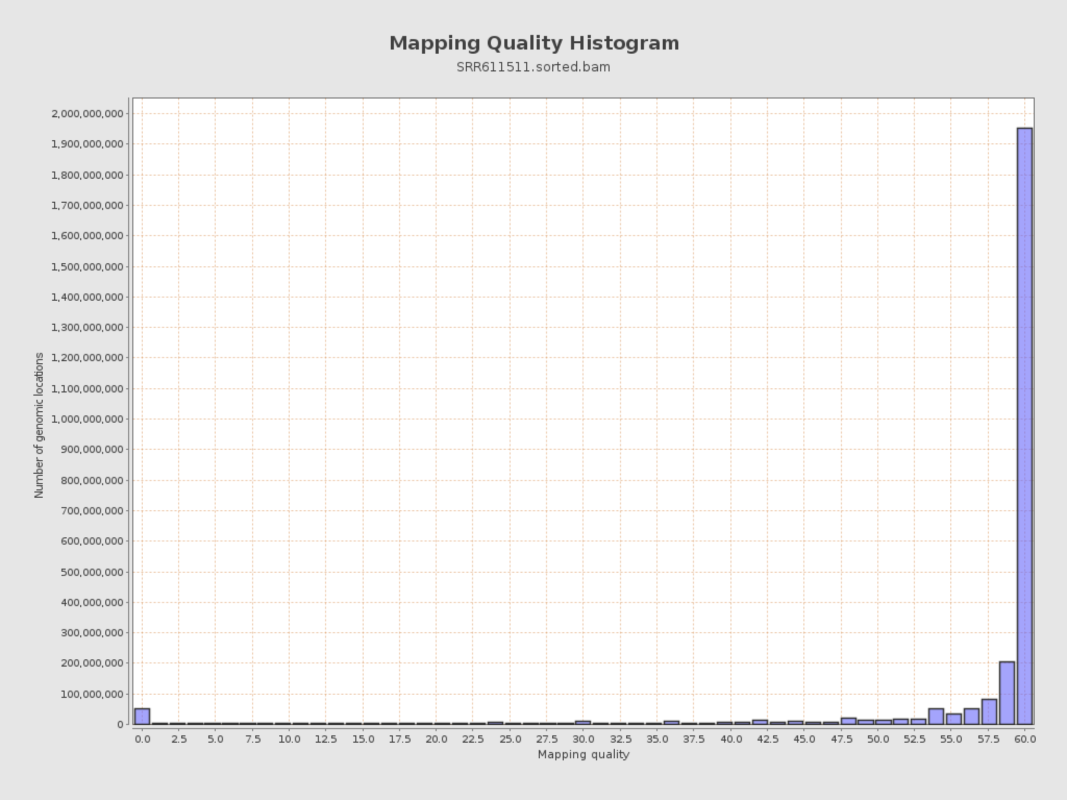
11. Results : Homopolymer Indels



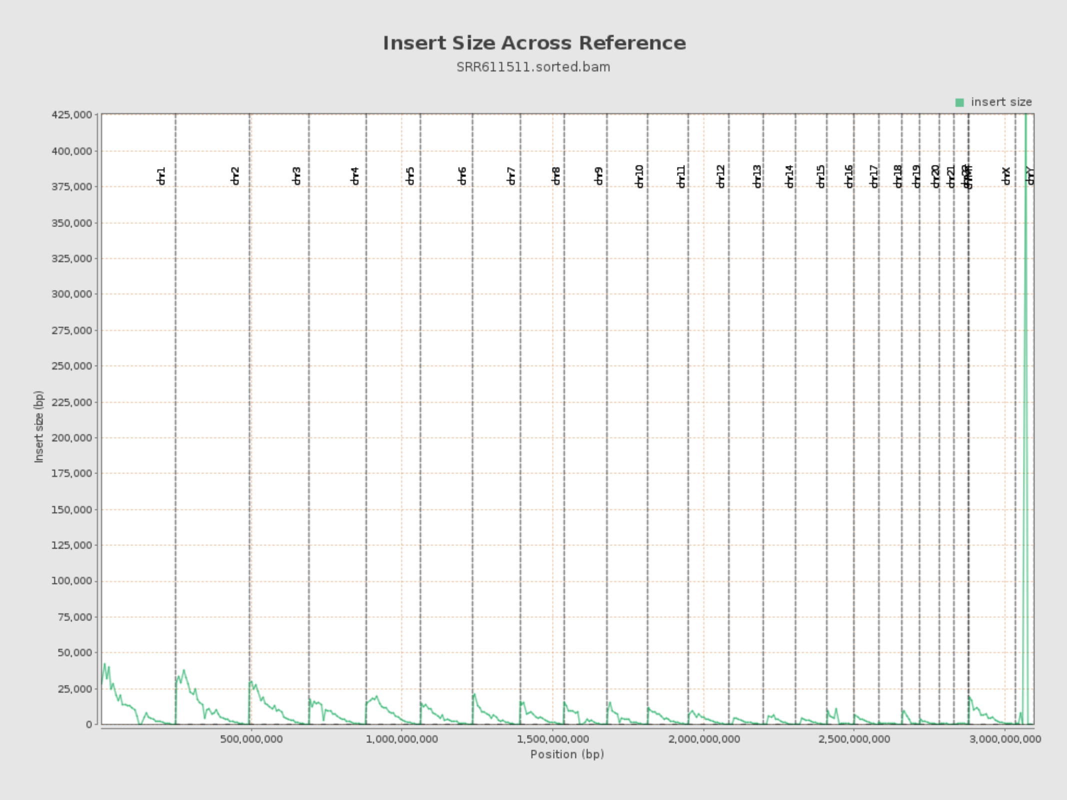
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram