Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/17 15:37:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006040.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_SRR1006040 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006040_1.fastq.gz SRR1006040_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 17 15:37:34 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006040.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	24,488,990
Mapped reads	17,402,452 / 71.06%
Unmapped reads	7,086,538 / 28.94%
Mapped paired reads	17,402,452 / 71.06%
Mapped reads, first in pair	8,733,929 / 35.66%
Mapped reads, second in pair	8,668,523 / 35.4%
Mapped reads, both in pair	15,705,052 / 64.13%
Mapped reads, singletons	1,697,400 / 6.93%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	1,024,214 / 4.18%
Duplication rate	4.91%
Clipped reads	1,783,496 / 7.28%

2.2. ACGT Content

Number/percentage of A's	191,413,882 / 28.56%
Number/percentage of C's	142,179,899 / 21.21%
Number/percentage of T's	193,430,264 / 28.86%
Number/percentage of G's	143,122,413 / 21.35%
Number/percentage of N's	83,720 / 0.01%
GC Percentage	42.57%

2.3. Coverage

Mean	0.2165
Standard Deviation	1.2438

2.4. Mapping Quality

Mean Mapping Quality	46.29

2.5. Insert size

Mean	60,268.29
Standard Deviation	2,380,886.41
P25/Median/P75	51 / 68 / 95

2.6. Mismatches and indels

General error rate	0.59%
Mismatches	3,930,193
Insertions	24,430
Mapped reads with at least one insertion	0.14%
Deletions	69,345
Mapped reads with at least one deletion	0.4%
Homopolymer indels	42.18%

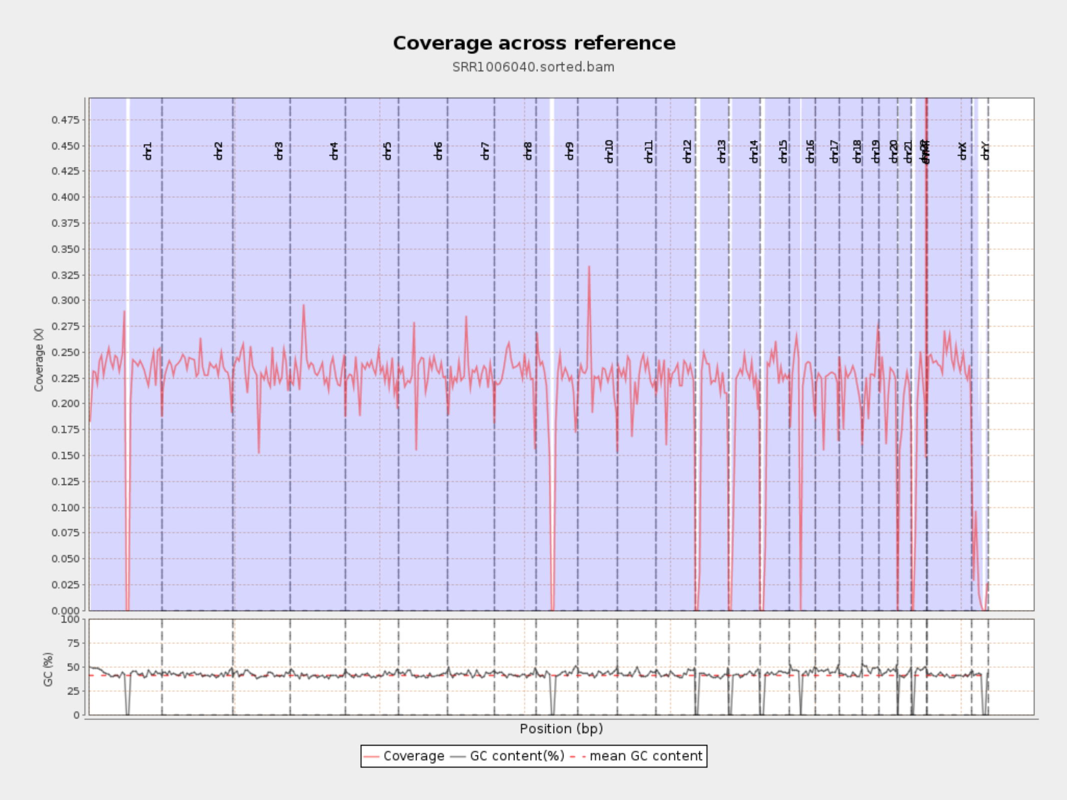
2.7. Chromosome stats

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

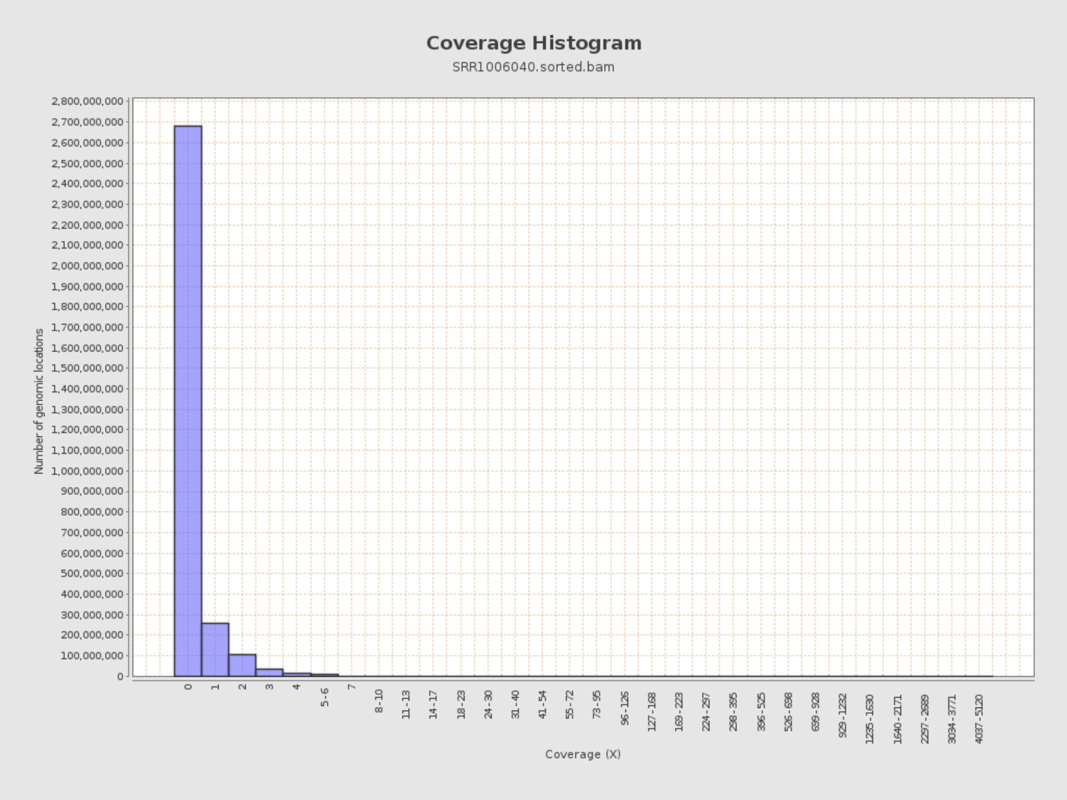
chr1	249250621	55304457	0.2219	1.8546
chr2	243199373	57286118	0.2356	0.9657
chr3	198022430	45649175	0.2305	0.6876
chr4	191154276	44683653	0.2338	0.8102
chr5	180915260	41374518	0.2287	0.6817
chr6	171115067	39269694	0.2295	0.9362
chr7	159138663	36574879	0.2298	1.3387
chr8	146364022	33716393	0.2304	2.5926
chr9	141213431	27648984	0.1958	0.8109
chr10	135534747	31213020	0.2303	1.2621
chr11	135006516	30377077	0.225	0.8723
chr12	133851895	30086827	0.2248	0.6921
chr13	115169878	21662360	0.1881	0.6158
chr14	107349540	20169177	0.1879	0.7164
chr15	102531392	19413873	0.1893	0.6239
chr16	90354753	19057715	0.2109	0.8621
chr17	81195210	17589968	0.2166	0.7191
chr18	78077248	17192979	0.2202	1.2725
chr19	59128983	13172552	0.2228	3.9543
chr20	63025520	13450572	0.2134	0.6996
chr21	48129895	8529301	0.1772	0.7258
chr22	51304566	7632795	0.1488	0.7601
chrMT	16571	113176	6.8298	5.2221
chrX	155270560	37364254	0.2406	0.7916

chrY	59373566	1787091	0.0301	0.5946

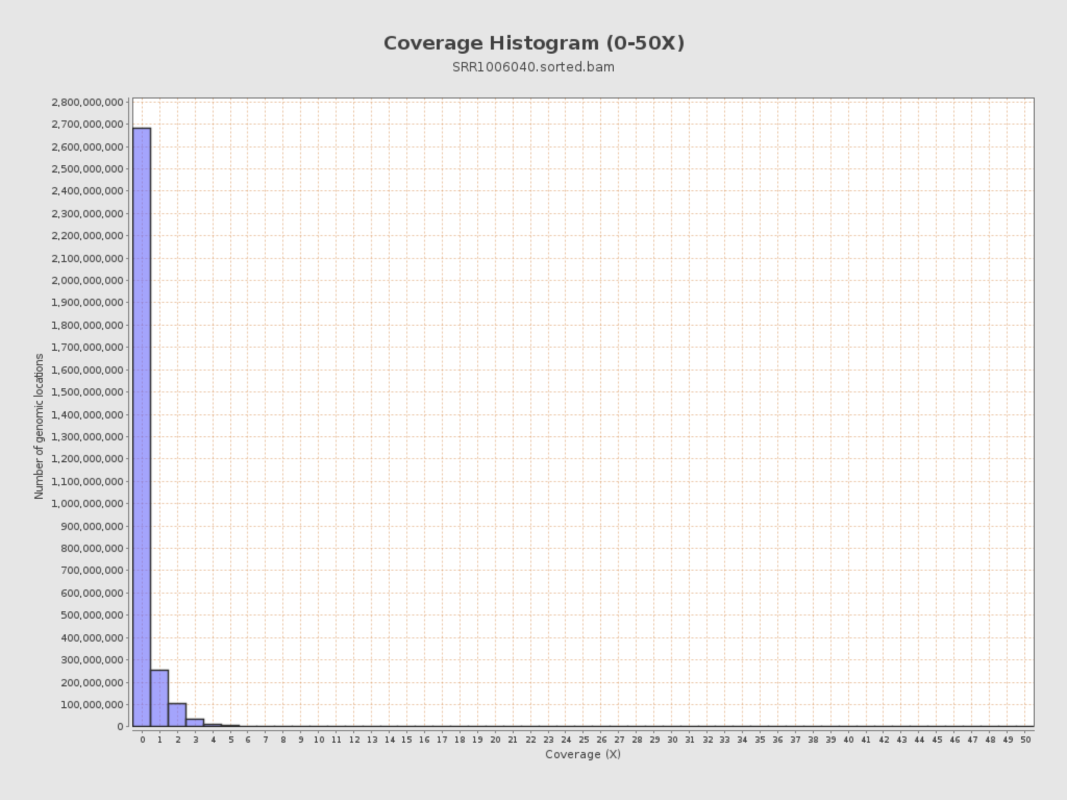
3. Results : Coverage across reference



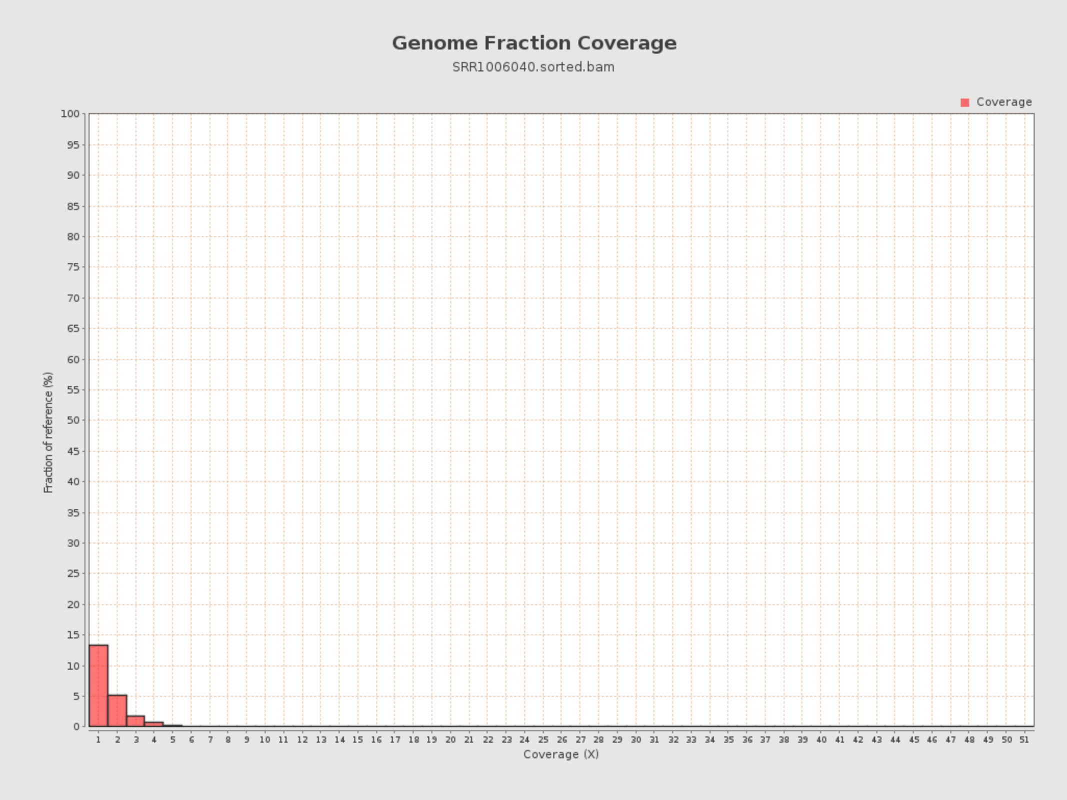
4. Results : Coverage Histogram



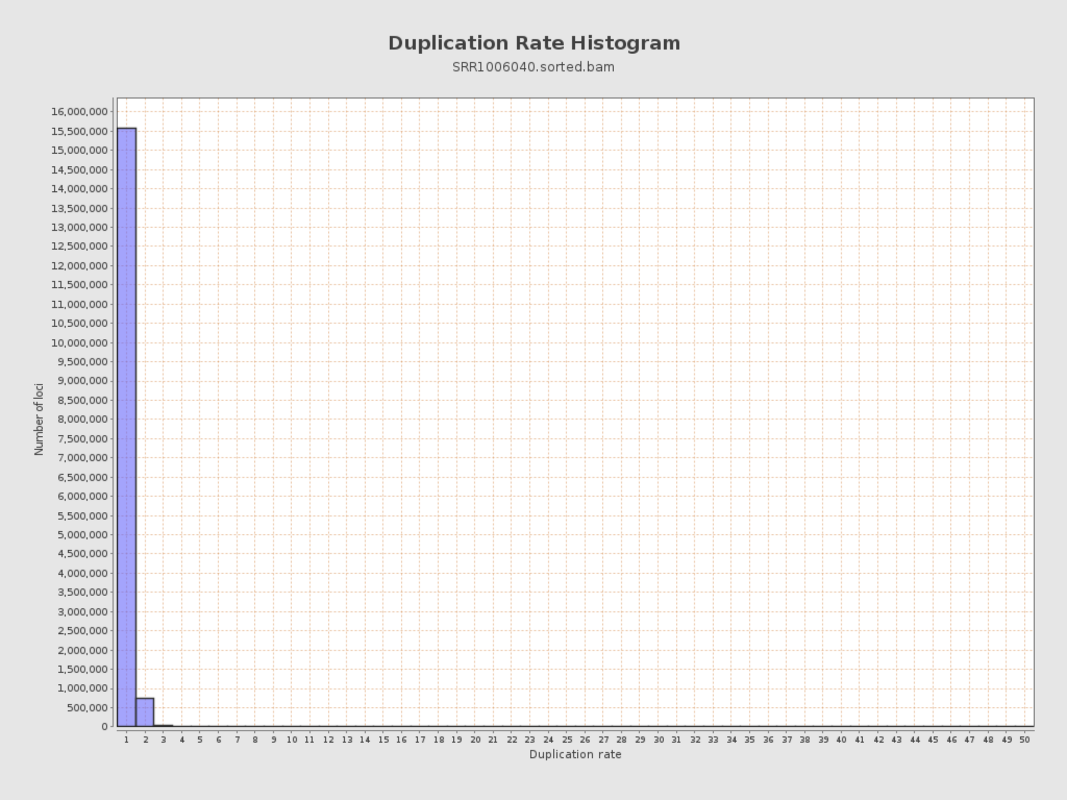
5. Results : Coverage Histogram (0-50X)



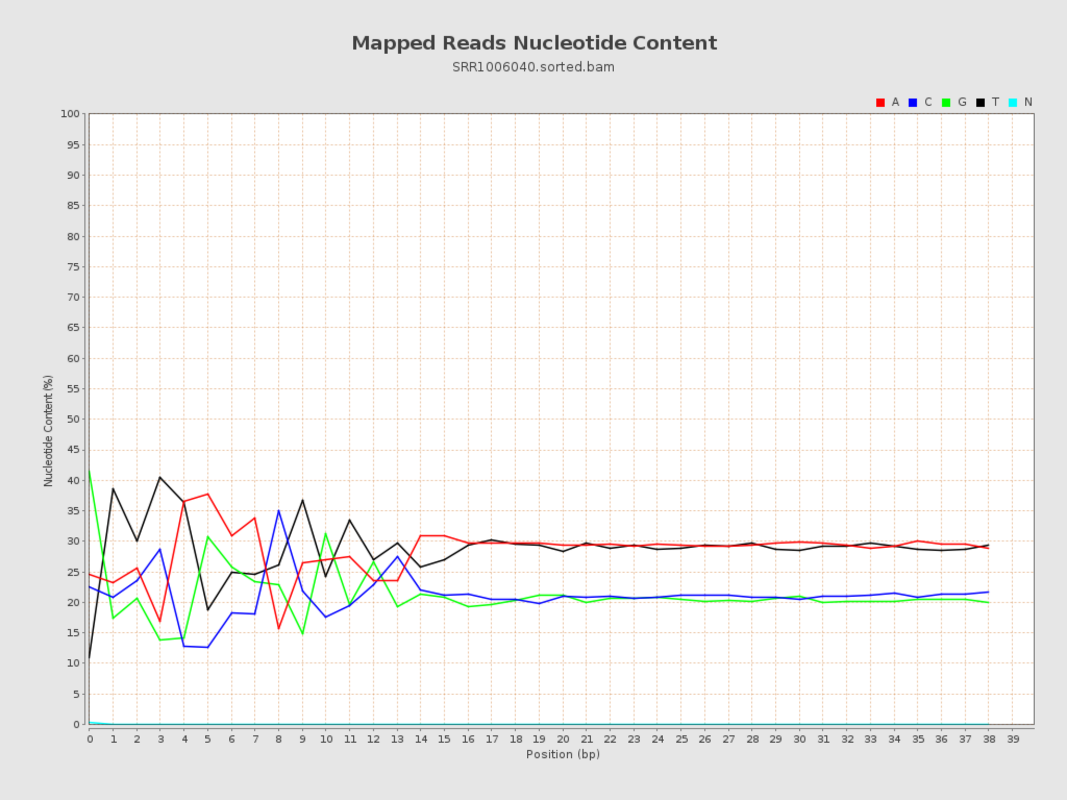
6. Results : Genome Fraction Coverage



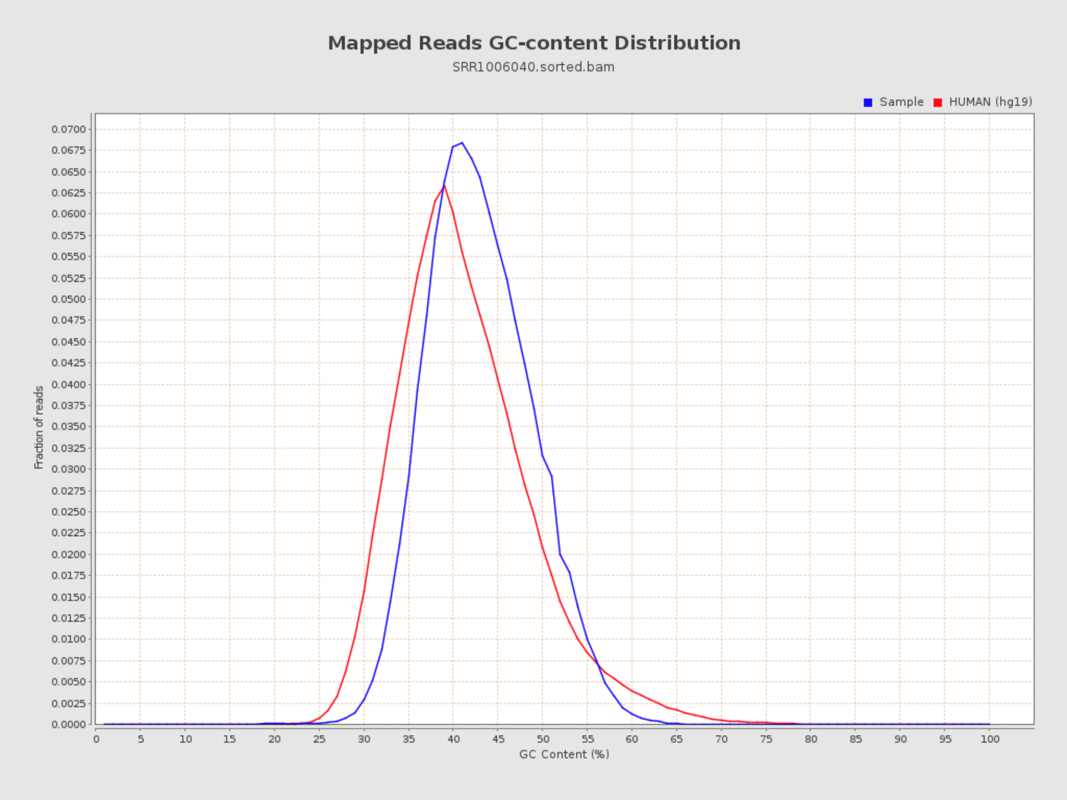
7. Results : Duplication Rate Histogram



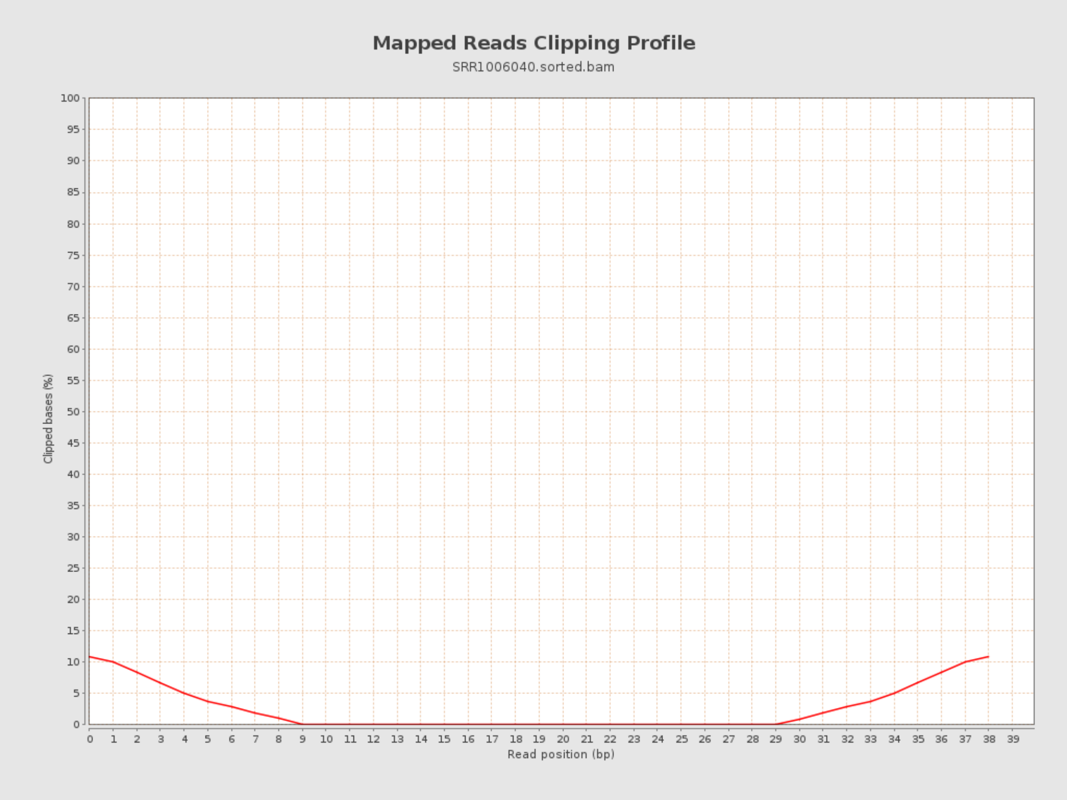
8. Results : Mapped Reads Nucleotide Content



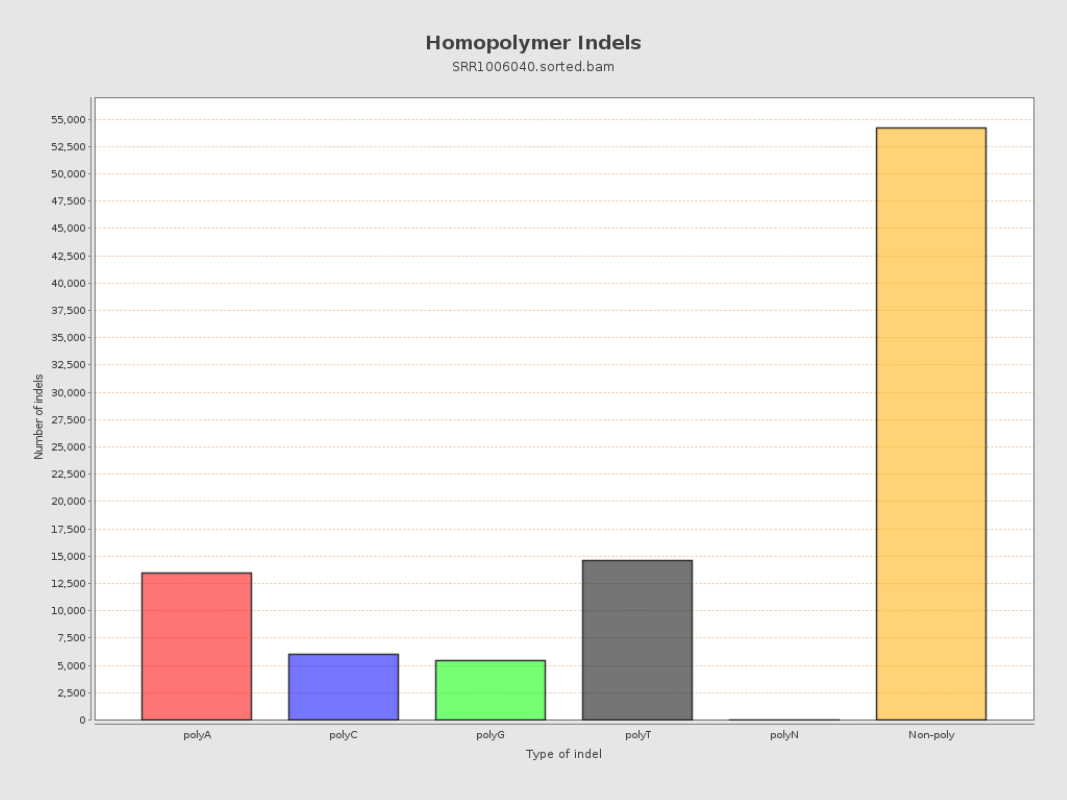
9. Results : Mapped Reads GC-content Distribution



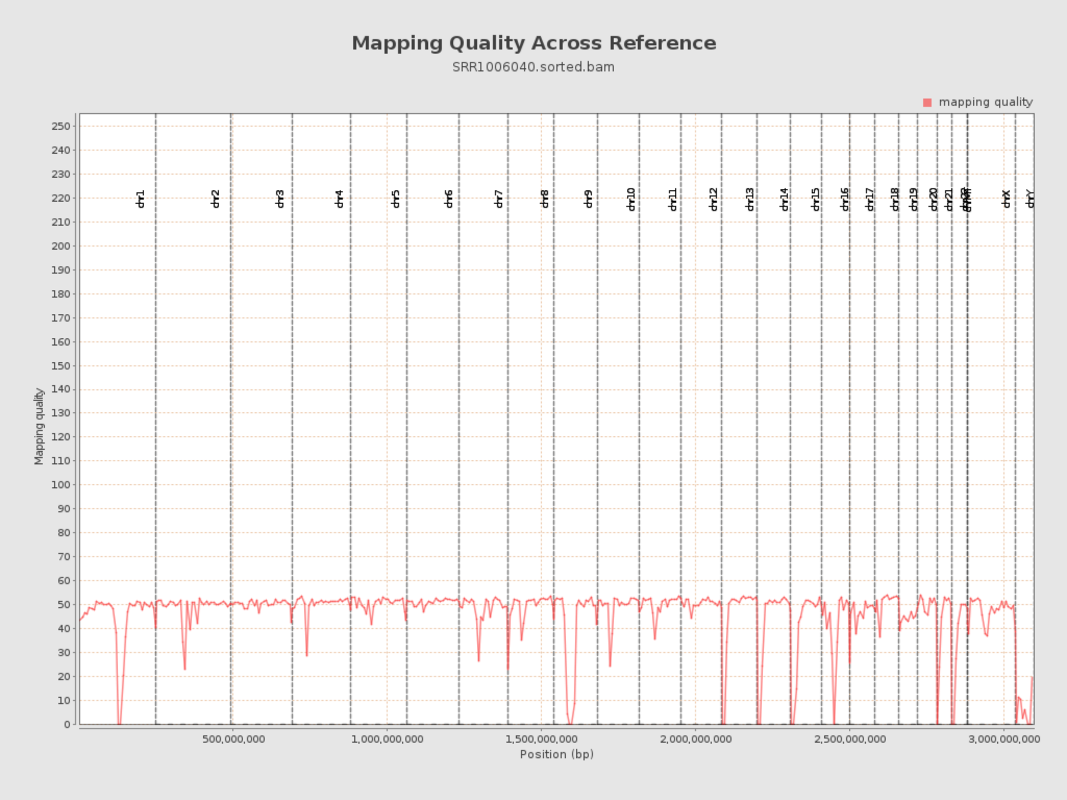
10. Results : Mapped Reads Clipping Profile



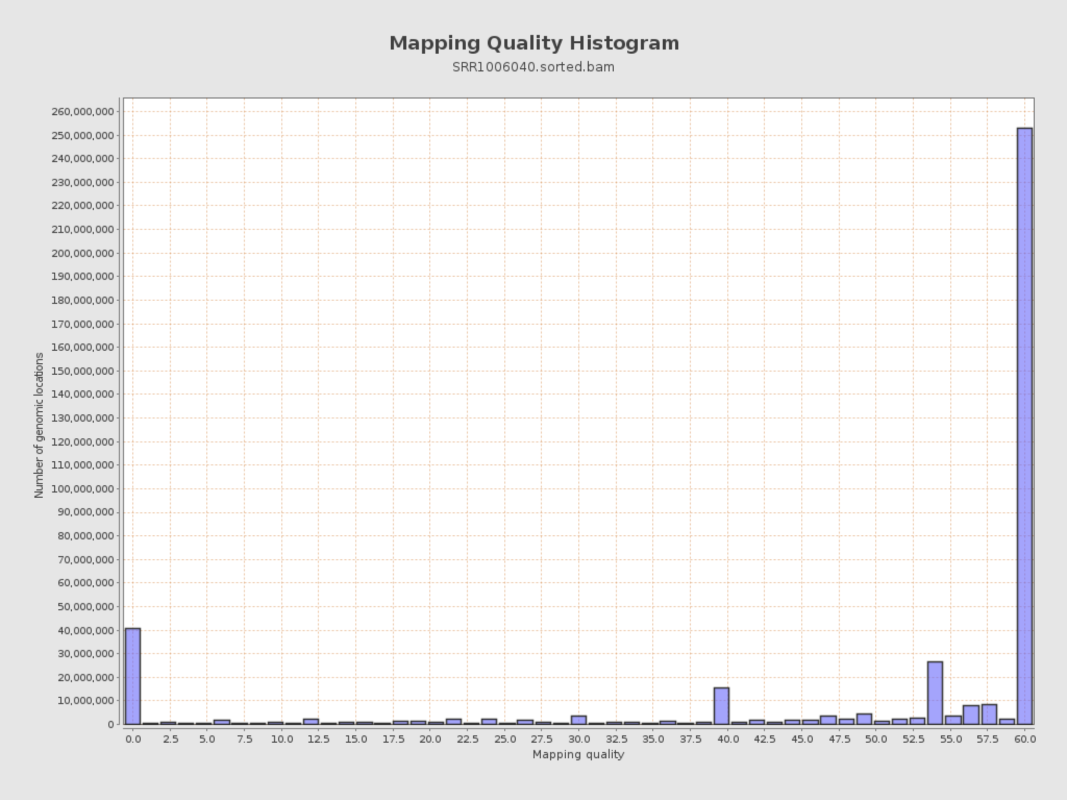
11. Results : Homopolymer Indels



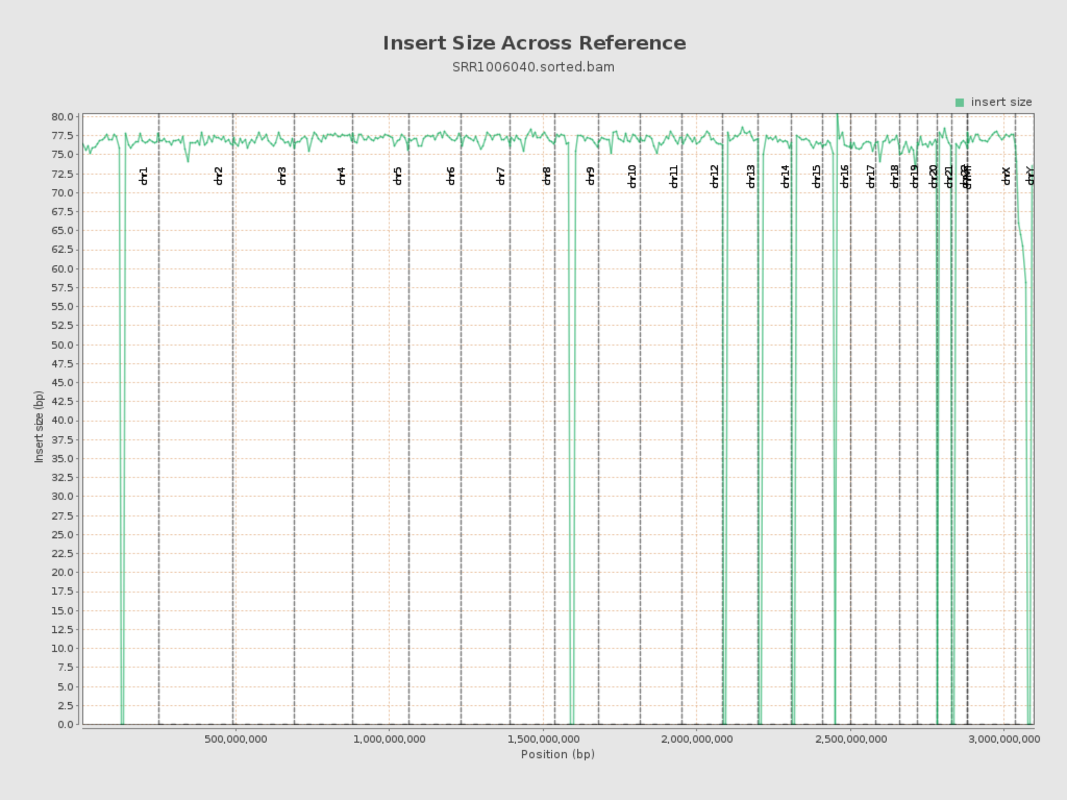
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram