Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/16 07:31:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038484.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_SRR5038484 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038484_1.fastq.gz SRR5038484_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Apr 16 07:31:10 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038484.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	19,380,598
Mapped reads	18,666,711 / 96.32%
Unmapped reads	713,887 / 3.68%
Mapped paired reads	18,666,711 / 96.32%
Mapped reads, first in pair	9,418,019 / 48.6%
Mapped reads, second in pair	9,248,692 / 47.72%
Mapped reads, both in pair	18,473,848 / 95.32%
Mapped reads, singletons	192,863 / 1%
Secondary alignments	0
Supplementary alignments	169,627 / 0.88%
Read min/max/mean length	30 / 150 / 150.45
Duplicated reads (estimated)	2,172,025 / 11.21%
Duplication rate	8.27%
Clipped reads	2,155,245 / 11.12%

2.2. ACGT Content

Number/percentage of A's	789,430,633 / 28.83%
Number/percentage of C's	582,620,318 / 21.28%
Number/percentage of T's	784,374,849 / 28.65%
Number/percentage of G's	581,121,786 / 21.23%
Number/percentage of N's	248,911 / 0.01%

GC Percentage	42.51%

2.3. Coverage

Mean	0.8847
Standard Deviation	11.6903

2.4. Mapping Quality

Mean Mapping Quality	54.25

2.5. Insert size

Mean	81,612.31
Standard Deviation	2,828,171.02
P25/Median/P75	219 / 272 / 343

2.6. Mismatches and indels

General error rate	1.07%
Mismatches	28,257,366
Insertions	348,045
Mapped reads with at least one insertion	1.75%
Deletions	368,071
Mapped reads with at least one deletion	1.88%
Homopolymer indels	43.43%

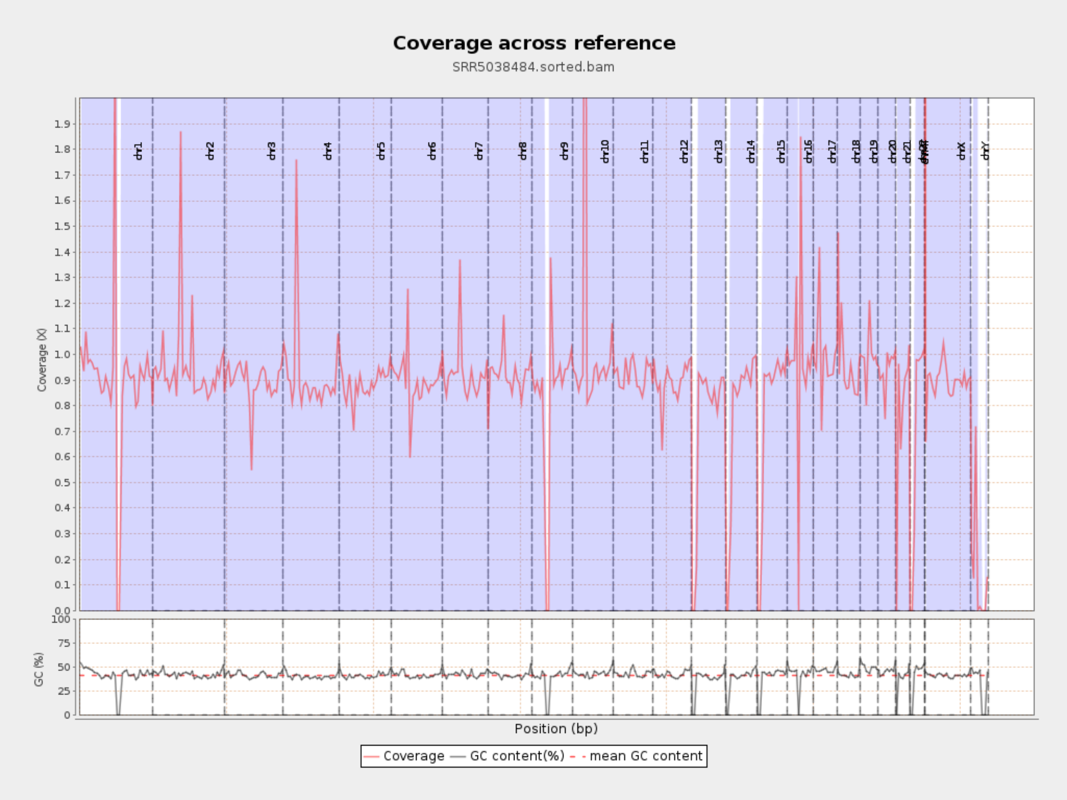
2.7. Chromosome stats

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

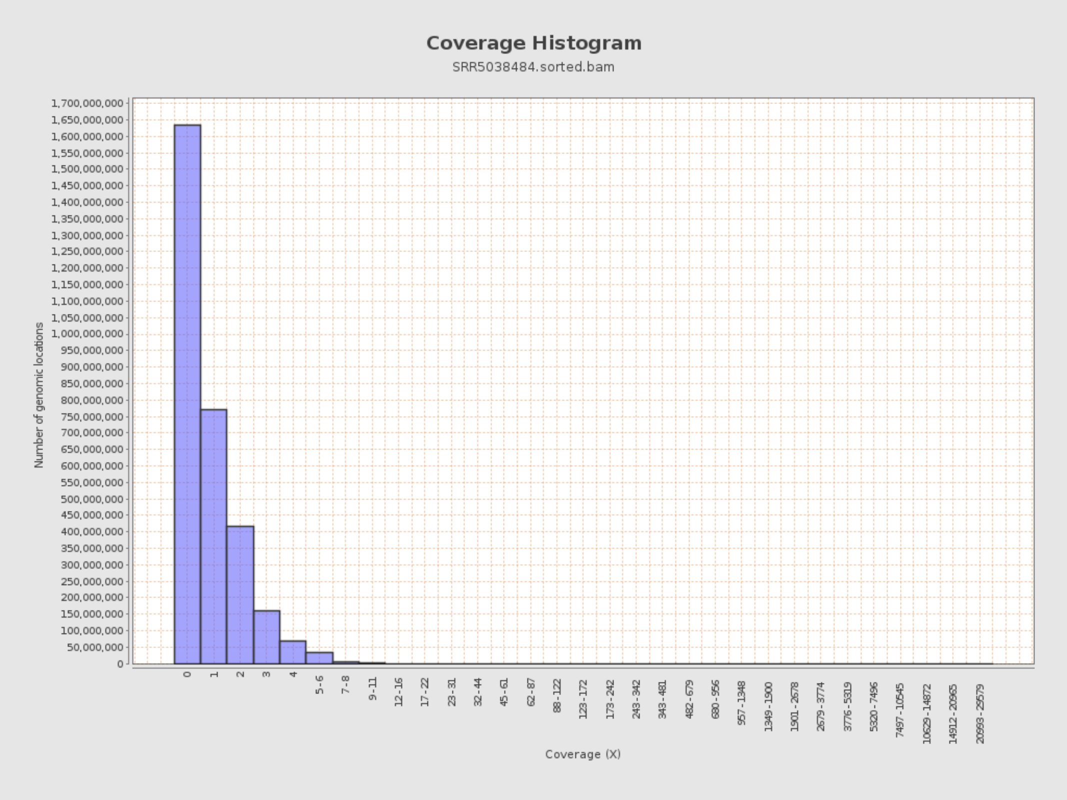
		bases	coverage	deviation
chr1	249250621	225845693	0.9061	29.8524
chr2	243199373	232288097	0.9551	8.3663
chr3	198022430	176651506	0.8921	1.3526
chr4	191154276	174926662	0.9151	7.3702
chr5	180915260	160208802	0.8855	1.268
chr6	171115067	153820666	0.8989	4.5448
chr7	159138663	147457505	0.9266	9.1657
chr8	146364022	135722522	0.9273	7.5808
chr9	141213431	115591203	0.8186	13.0049
chr10	135534747	147331176	1.087	25.5295
chr11	135006516	124395147	0.9214	4.4083
chr12	133851895	119156814	0.8902	1.4753
chr13	115169878	83837356	0.7279	1.1222
chr14	107349540	80974208	0.7543	1.2314
chr15	102531392	77176054	0.7527	1.1499
chr16	90354753	89232143	0.9876	7.2405
chr17	81195210	80173314	0.9874	6.0462
chr18	78077248	74253375	0.951	10.5815
chr19	59128983	58786227	0.9942	12.5323
chr20	63025520	59038004	0.9367	2.5631
chr21	48129895	37976131	0.789	4.0138
chr22	51304566	35034303	0.6829	1.168
chrMT	16571	1272388	76.784	13.3042
chrX	155270560	138773686	0.8938	2.6435

chrY	59373566	8885345	0.1497	7.9594

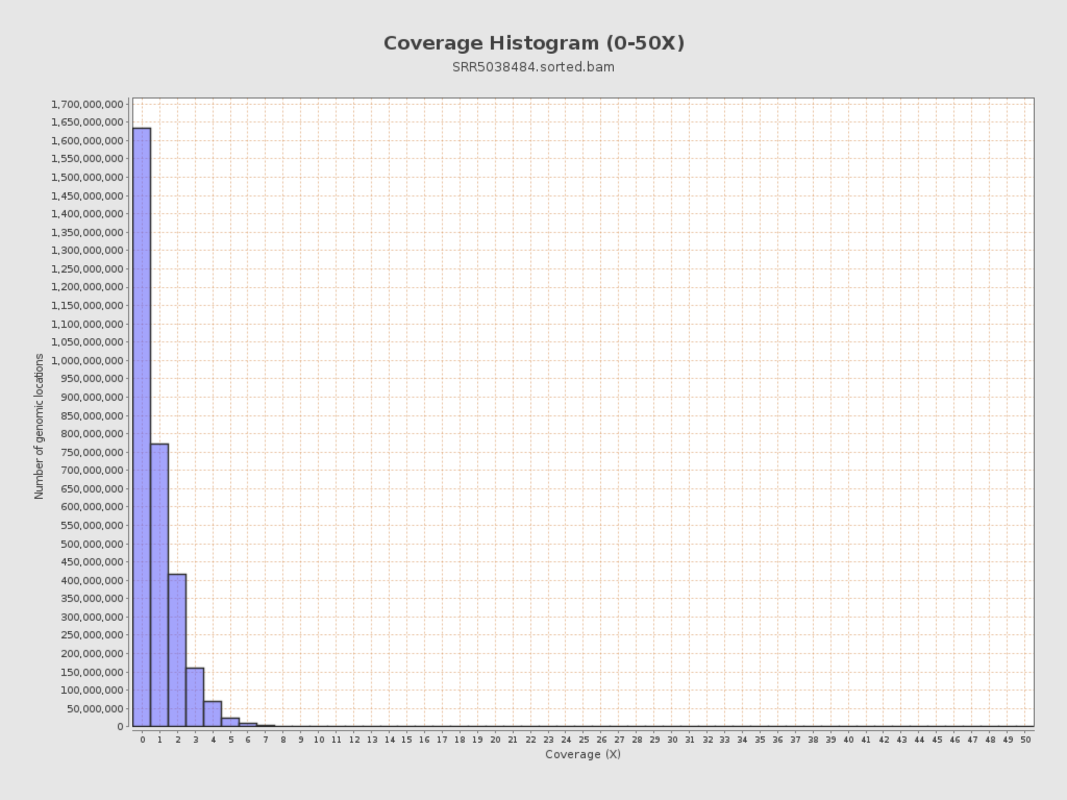
3. Results : Coverage across reference



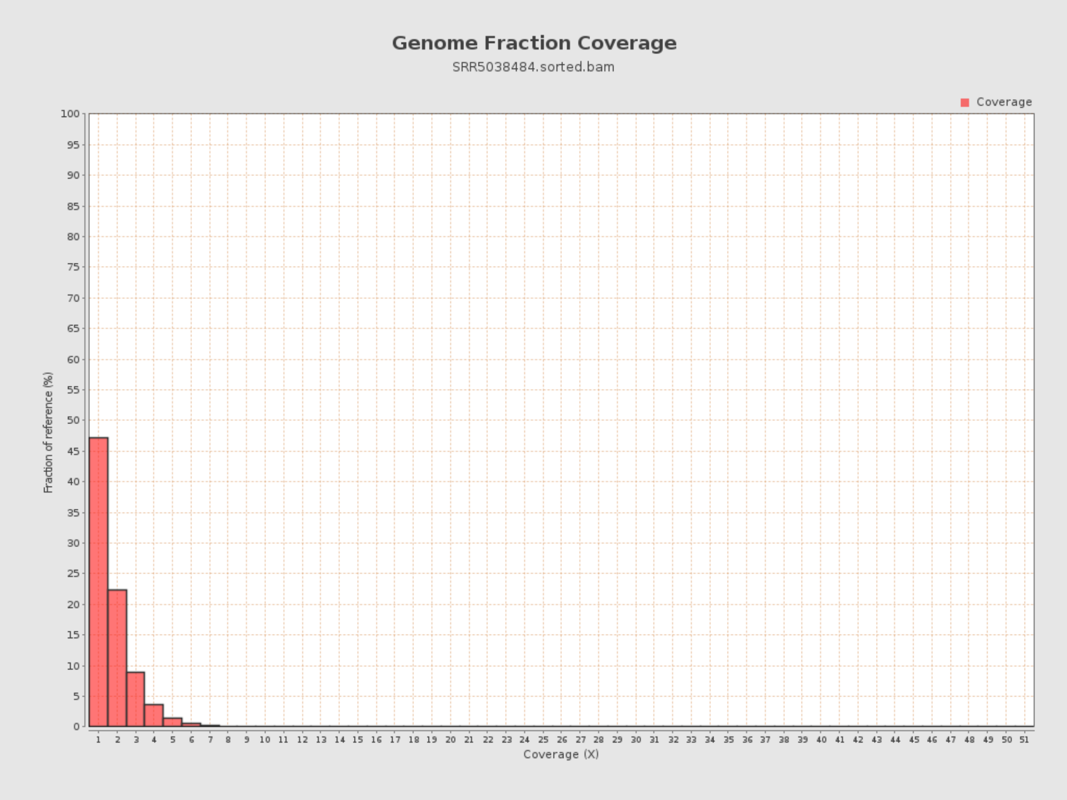
4. Results : Coverage Histogram



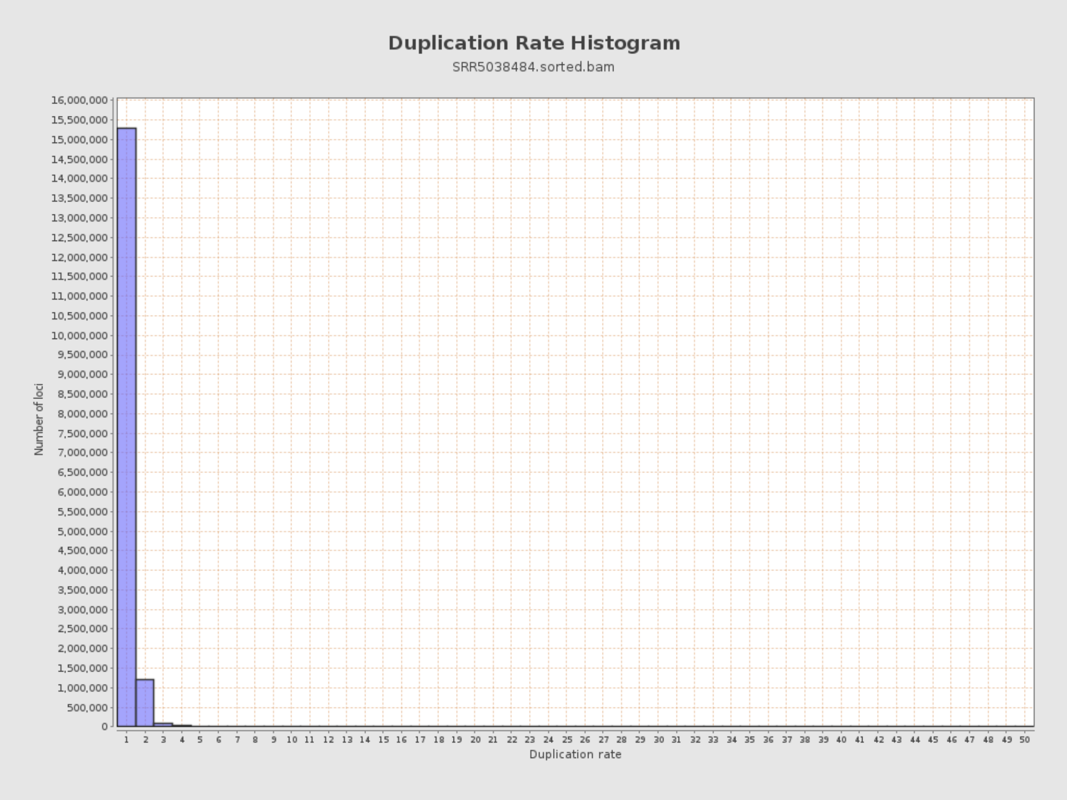
5. Results : Coverage Histogram (0-50X)



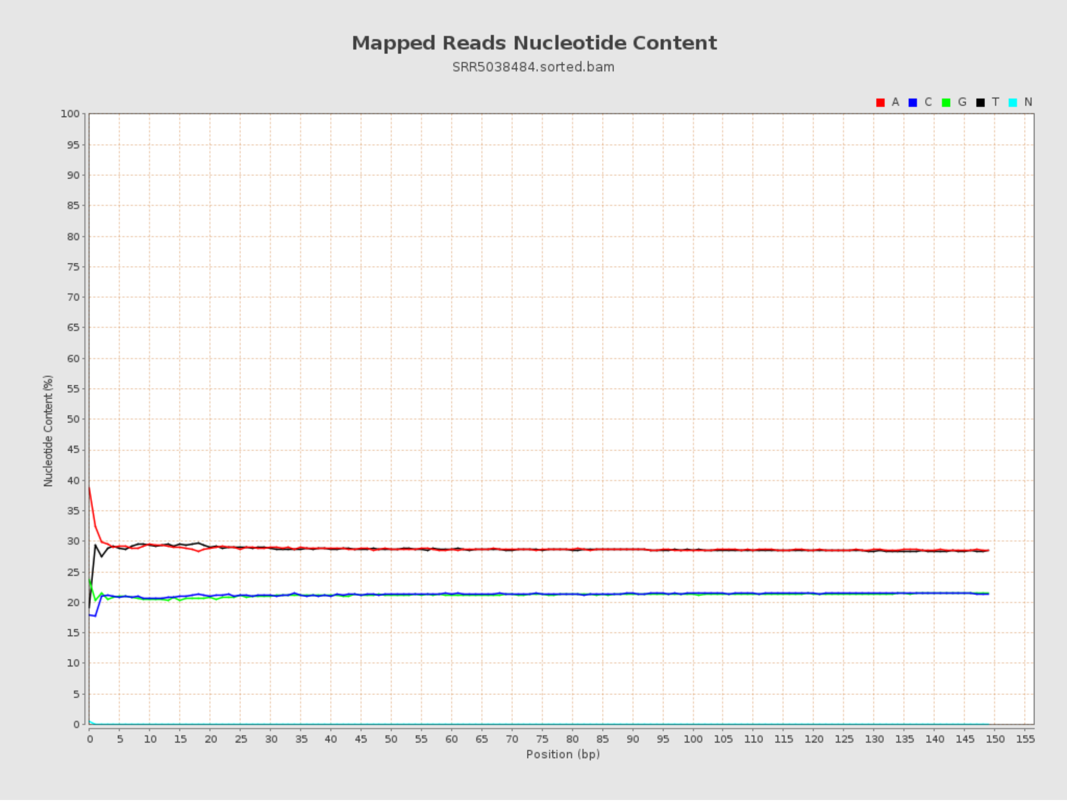
6. Results : Genome Fraction Coverage



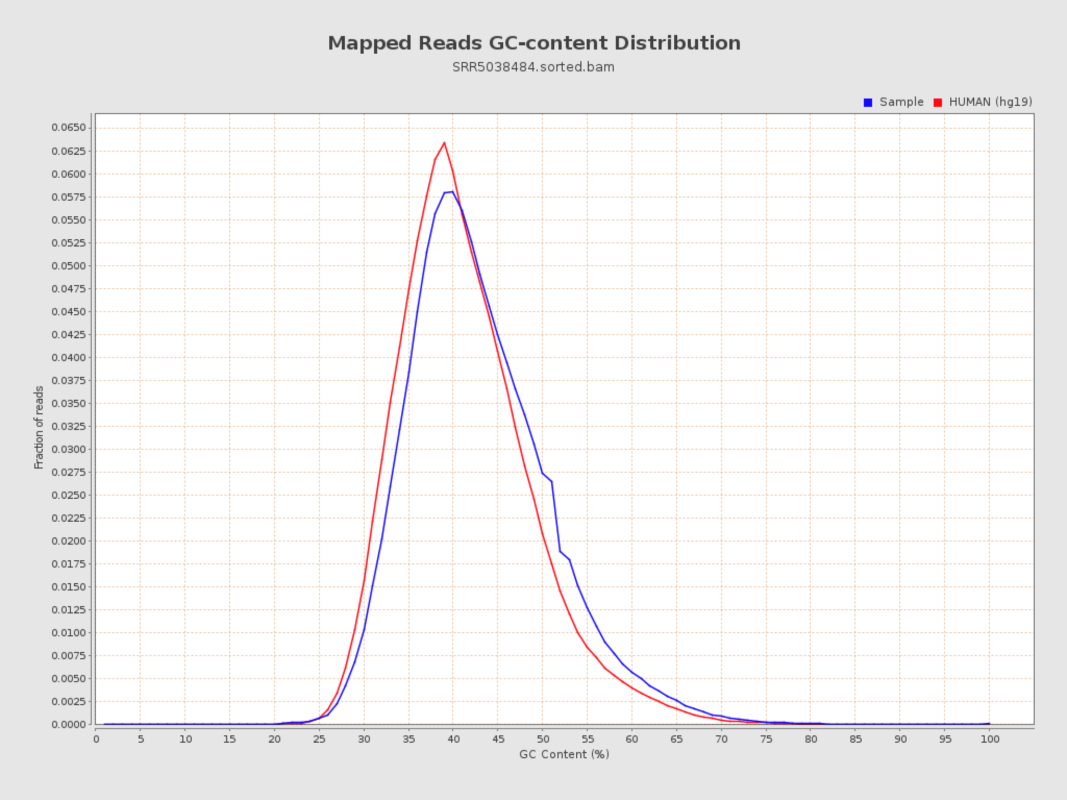
7. Results : Duplication Rate Histogram



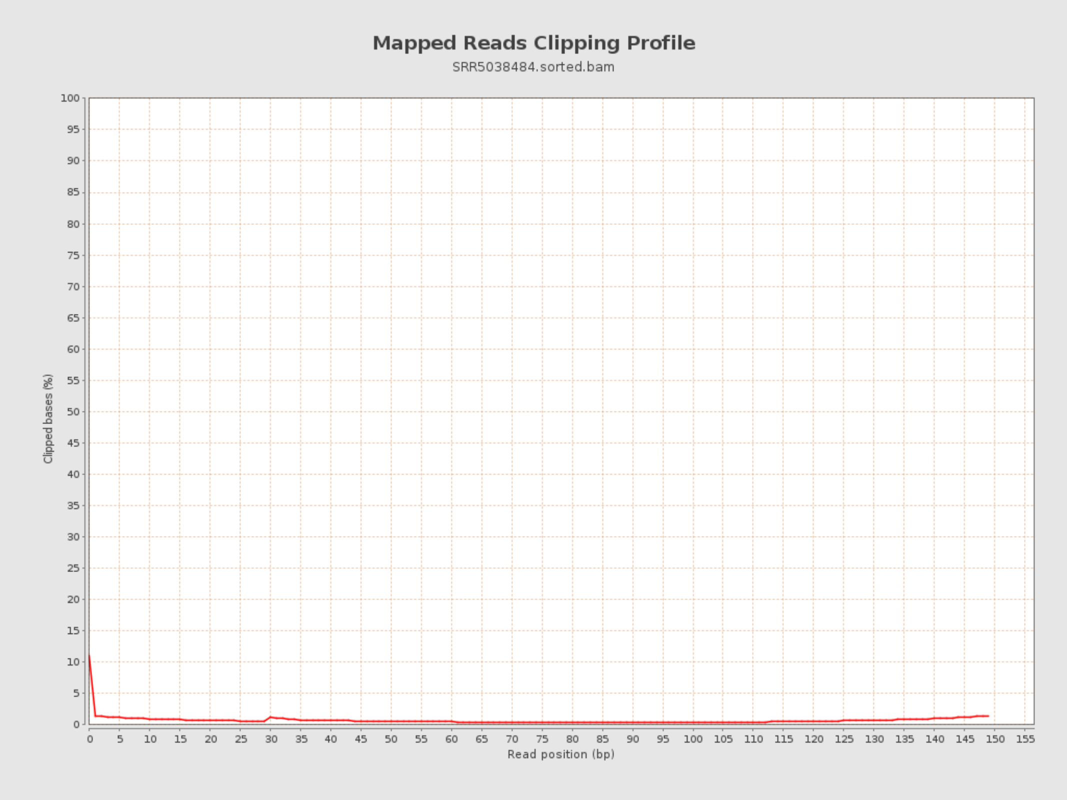
8. Results : Mapped Reads Nucleotide Content



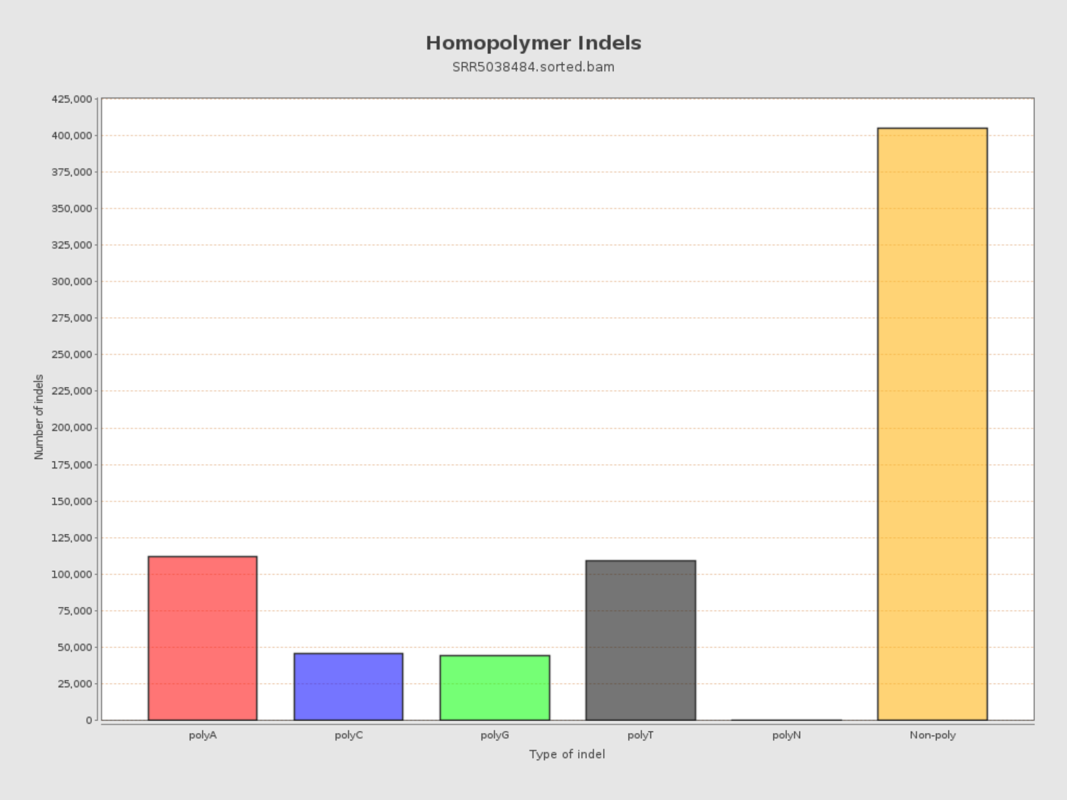
9. Results : Mapped Reads GC-content Distribution



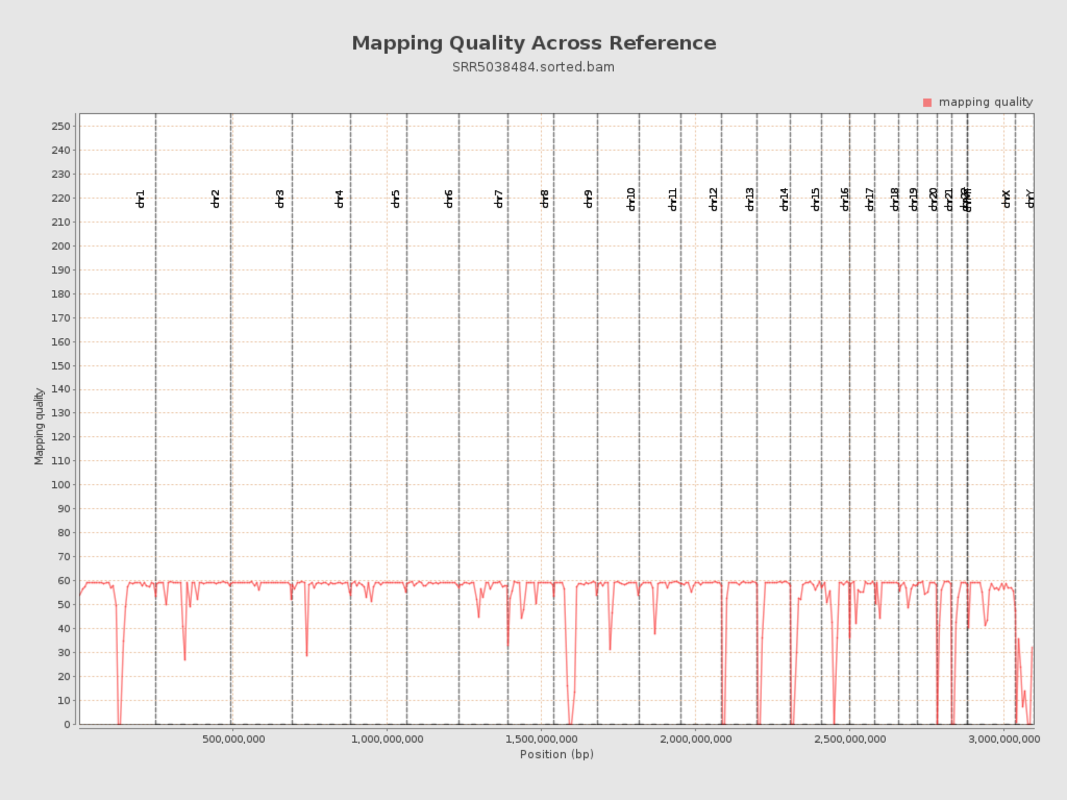
10. Results : Mapped Reads Clipping Profile



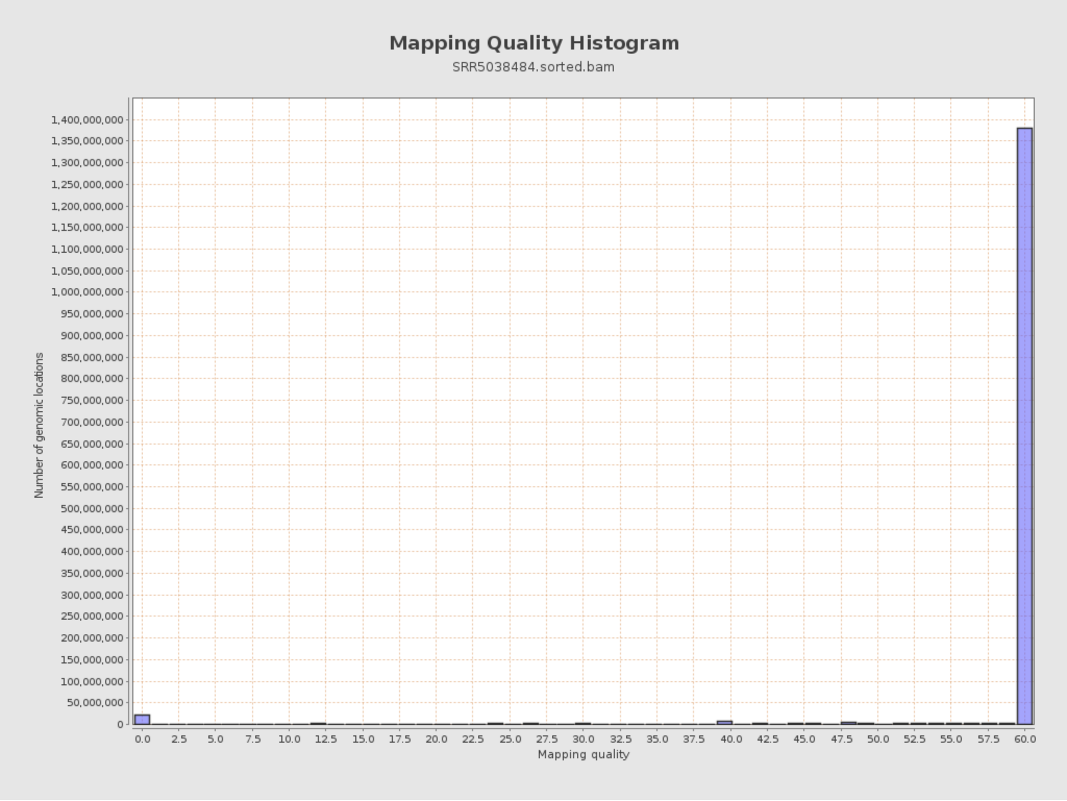
11. Results : Homopolymer Indels



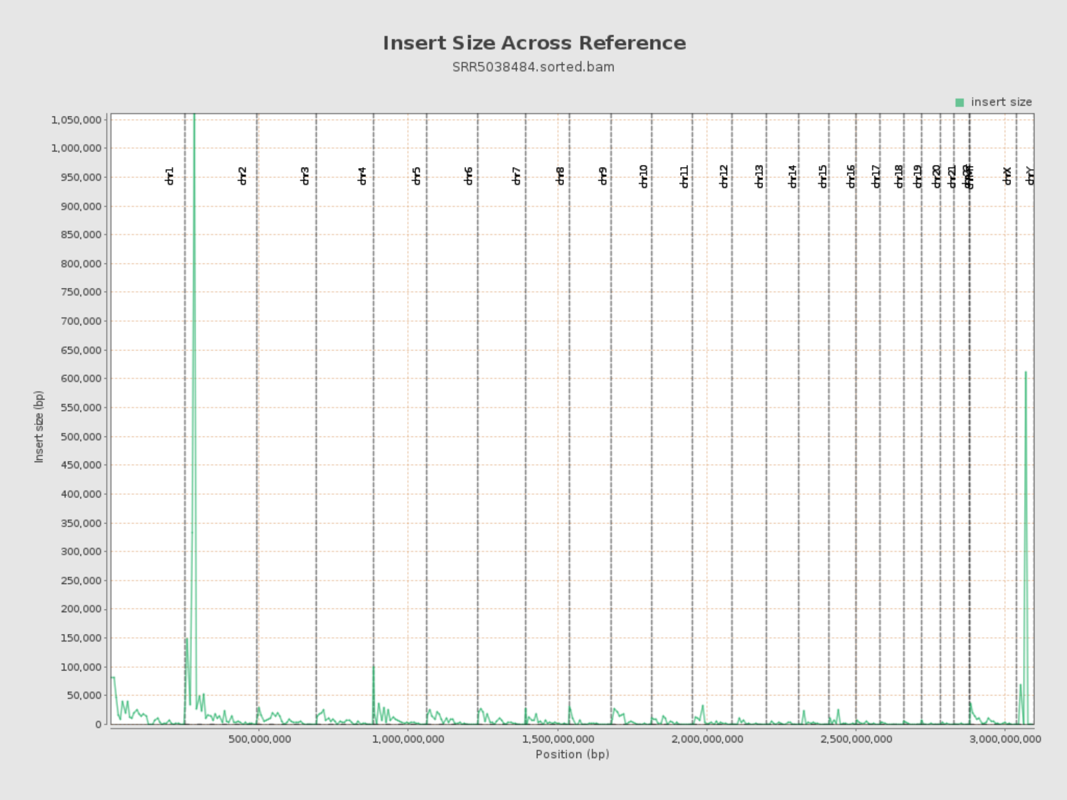
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram