Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/16 09:01:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038488.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_SRR5038488 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038488_1.fastq.gz SRR5038488_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Apr 16 09:01:35 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038488.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	18,623,262
Mapped reads	17,975,201 / 96.52%
Unmapped reads	648,061 / 3.48%
Mapped paired reads	17,975,201 / 96.52%
Mapped reads, first in pair	9,089,415 / 48.81%
Mapped reads, second in pair	8,885,786 / 47.71%
Mapped reads, both in pair	17,720,318 / 95.15%
Mapped reads, singletons	254,883 / 1.37%
Secondary alignments	0
Supplementary alignments	260,988 / 1.4%
Read min/max/mean length	30 / 150 / 150.7
Duplicated reads (estimated)	3,949,954 / 21.21%
Duplication rate	15.89%
Clipped reads	8,662,324 / 46.51%

2.2. ACGT Content

Number/percentage of A's	691,644,562 / 28.58%
Number/percentage of C's	478,625,405 / 19.78%
Number/percentage of T's	704,720,292 / 29.12%
Number/percentage of G's	544,509,976 / 22.5%
Number/percentage of N's	196,396 / 0.01%

GC Percentage	42.28%

2.3. Coverage

Mean	0.7822
Standard Deviation	9.9347

2.4. Mapping Quality

Mean Mapping Quality	53.41

2.5. Insert size

Mean	67,628.39
Standard Deviation	2,545,645.63
P25/Median/P75	194 / 242 / 305

2.6. Mismatches and indels

General error rate	1.27%
Mismatches	29,545,155
Insertions	417,712
Mapped reads with at least one insertion	2.21%
Deletions	831,111
Mapped reads with at least one deletion	4.46%
Homopolymer indels	47.82%

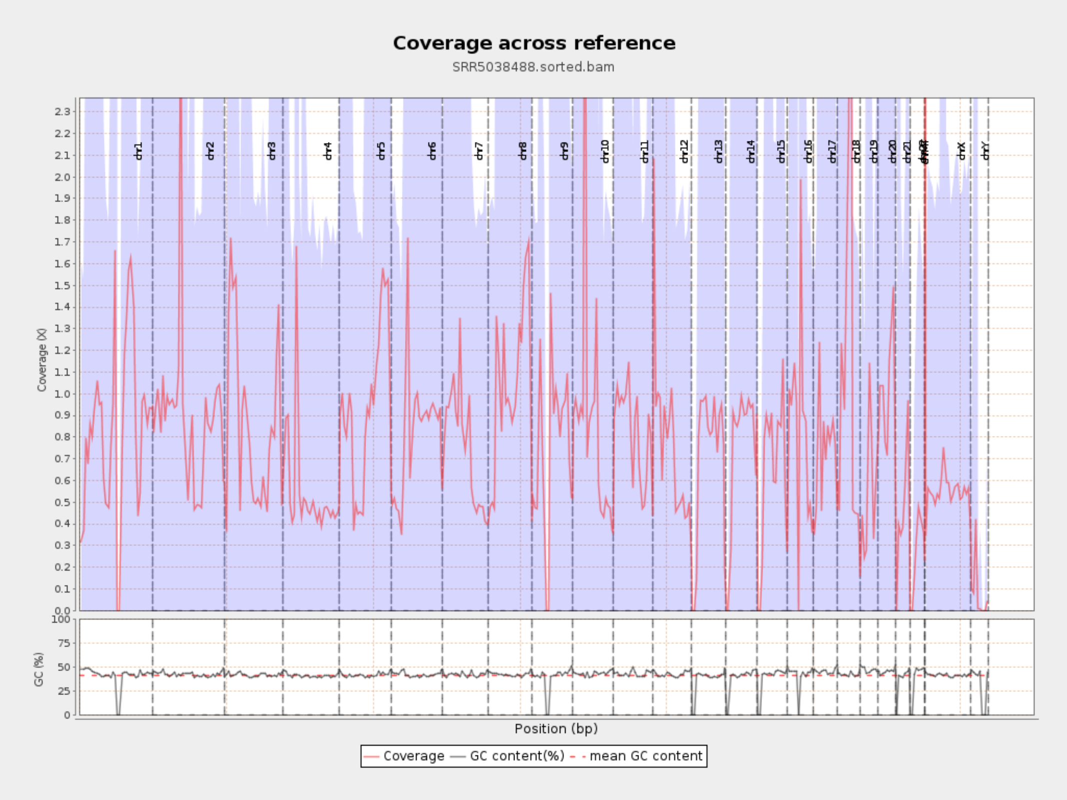
2.7. Chromosome stats

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

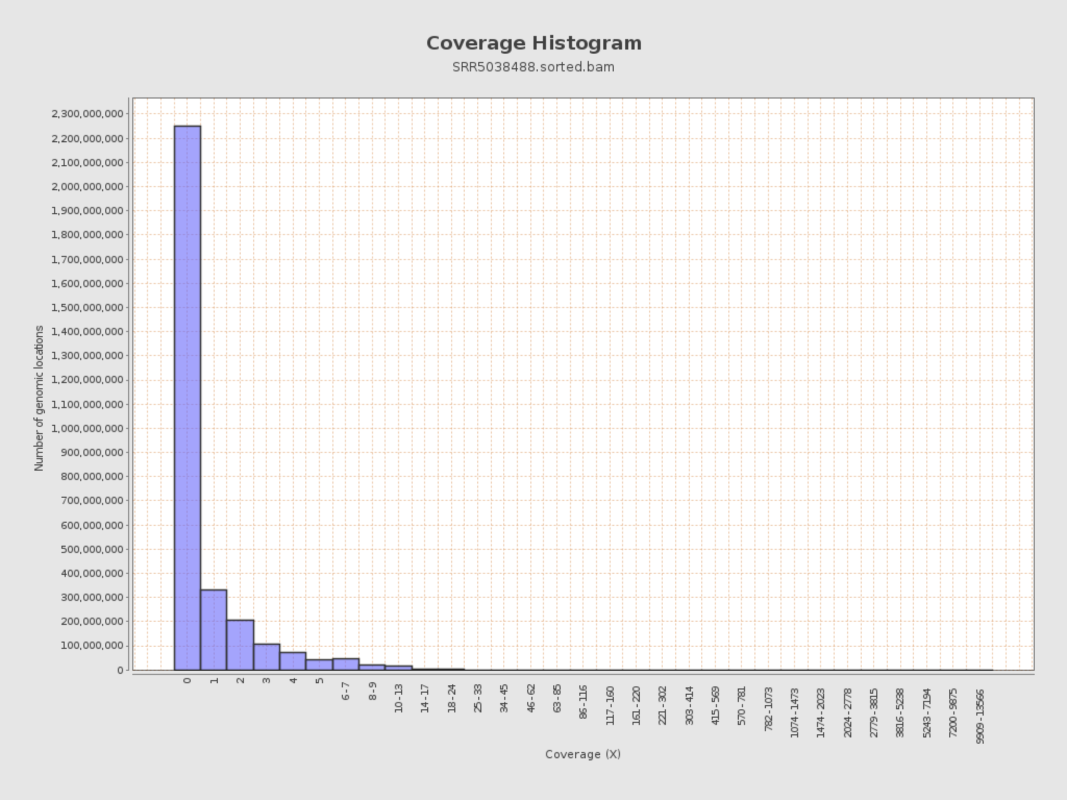
		bases	coverage	deviation
chr1	249250621	210713617	0.8454	13.6375
chr2	243199373	220773163	0.9078	12.4695
chr3	198022430	169862663	0.8578	1.9527
chr4	191154276	105335028	0.551	9.9181
chr5	180915260	169484844	0.9368	2.0011
chr6	171115067	143051811	0.836	8.6046
chr7	159138663	119323887	0.7498	10.6224
chr8	146364022	155725410	1.064	4.4849
chr9	141213431	103264993	0.7313	18.1
chr10	135534747	124768198	0.9206	21.823
chr11	135006516	110870596	0.8212	7.4098
chr12	133851895	103236350	0.7713	1.9749
chr13	115169878	83079018	0.7214	1.6991
chr14	107349540	78967548	0.7356	1.8486
chr15	102531392	65104522	0.635	1.6262
chr16	90354753	72209128	0.7992	8.6133
chr17	81195210	58941894	0.7259	12.9078
chr18	78077248	96565777	1.2368	12.5541
chr19	59128983	31450729	0.5319	6.1549
chr20	63025520	64901285	1.0298	3.7582
chr21	48129895	23213996	0.4823	4.7881
chr22	51304566	13821509	0.2694	1.0496
chrMT	16571	6713636	405.1437	260.8601
chrX	155270560	85119384	0.5482	2.2805

chrY	59373566	4807031	0.081	10.2325

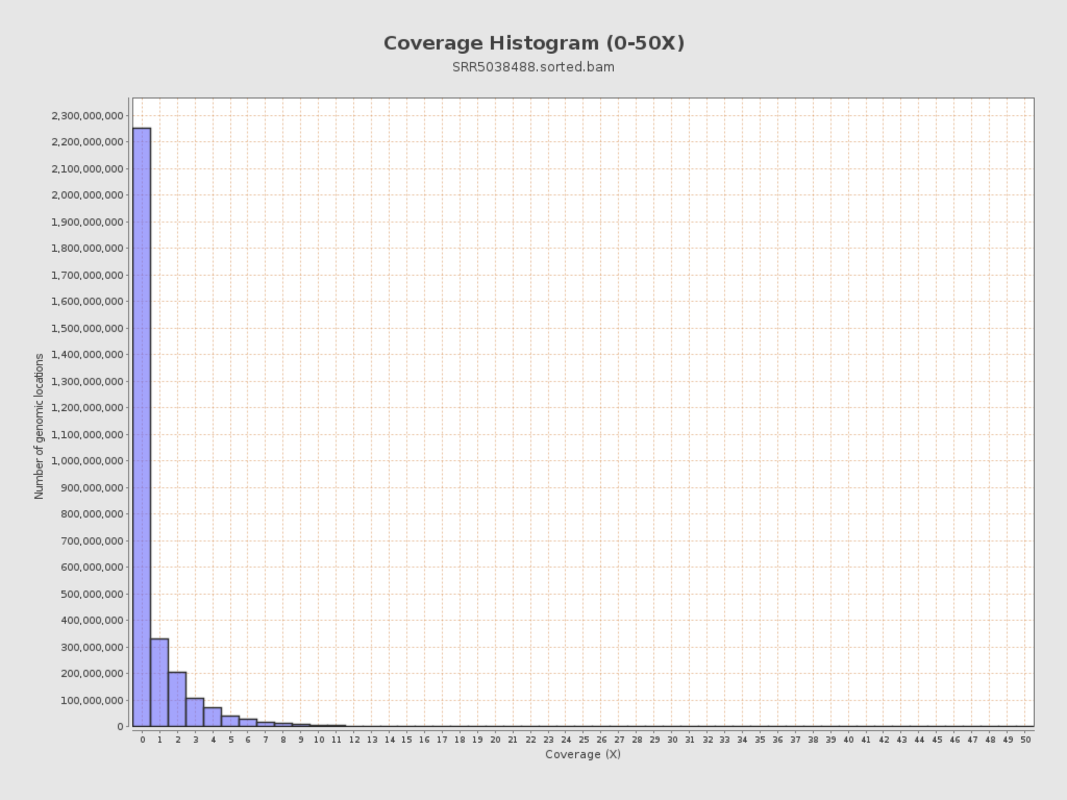
3. Results : Coverage across reference



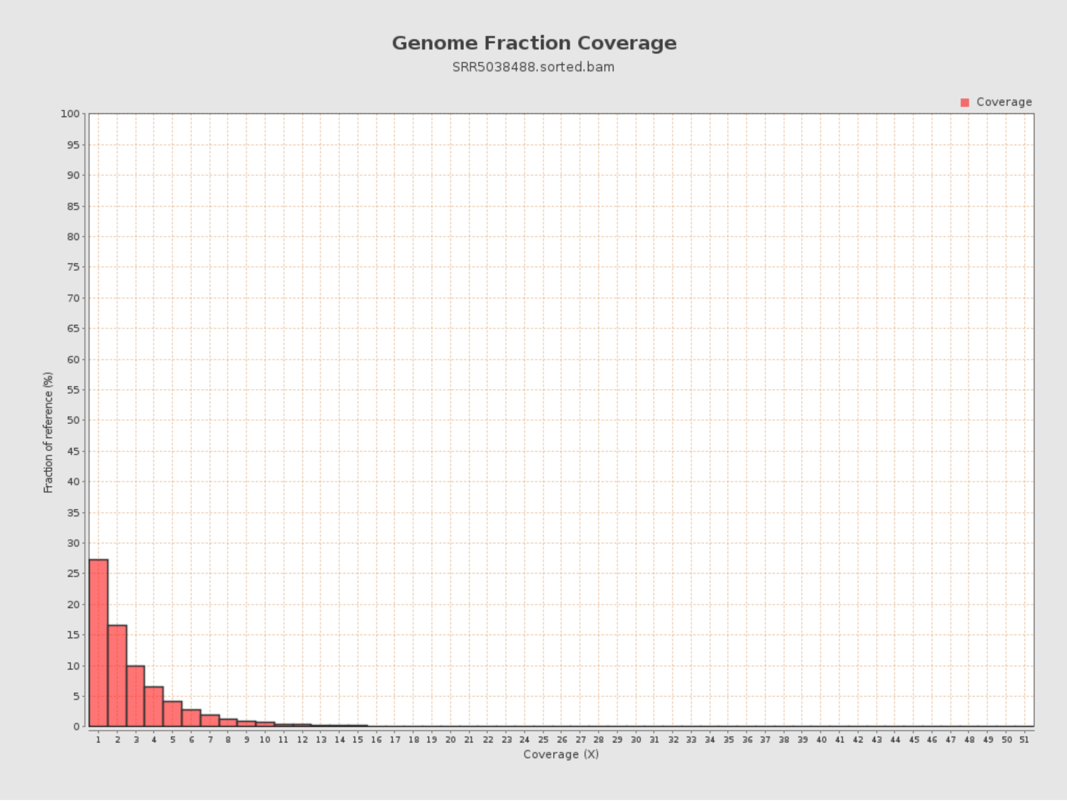
4. Results : Coverage Histogram



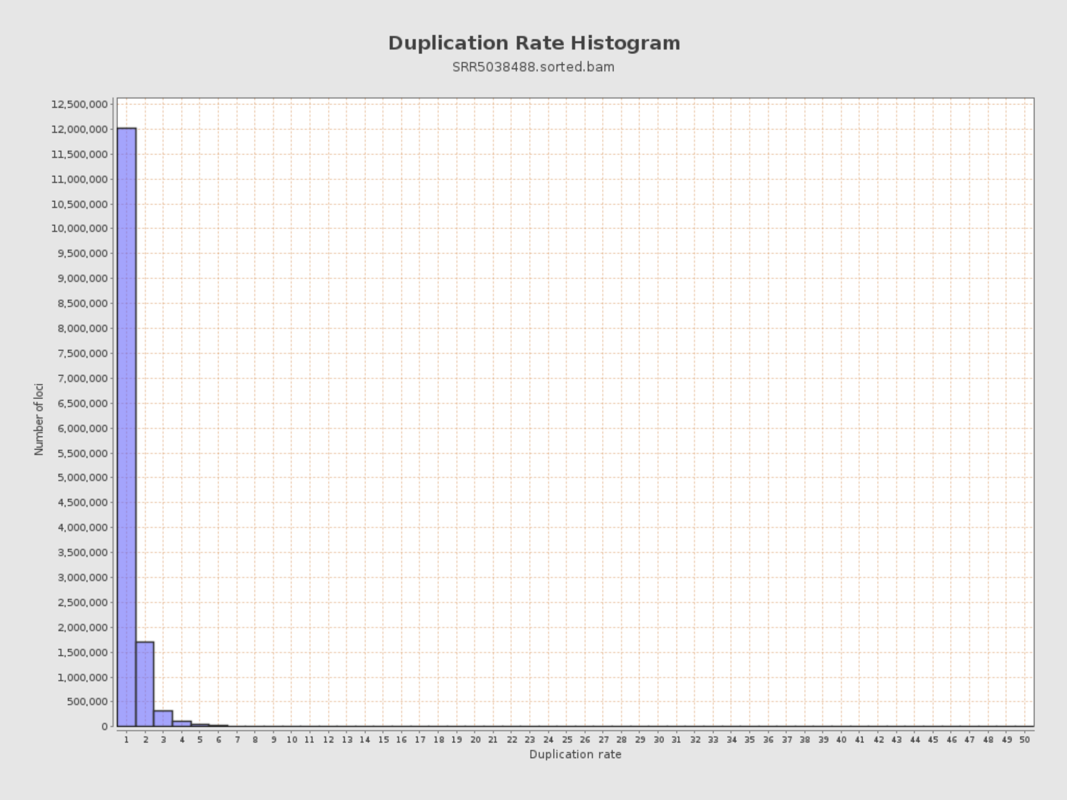
5. Results : Coverage Histogram (0-50X)



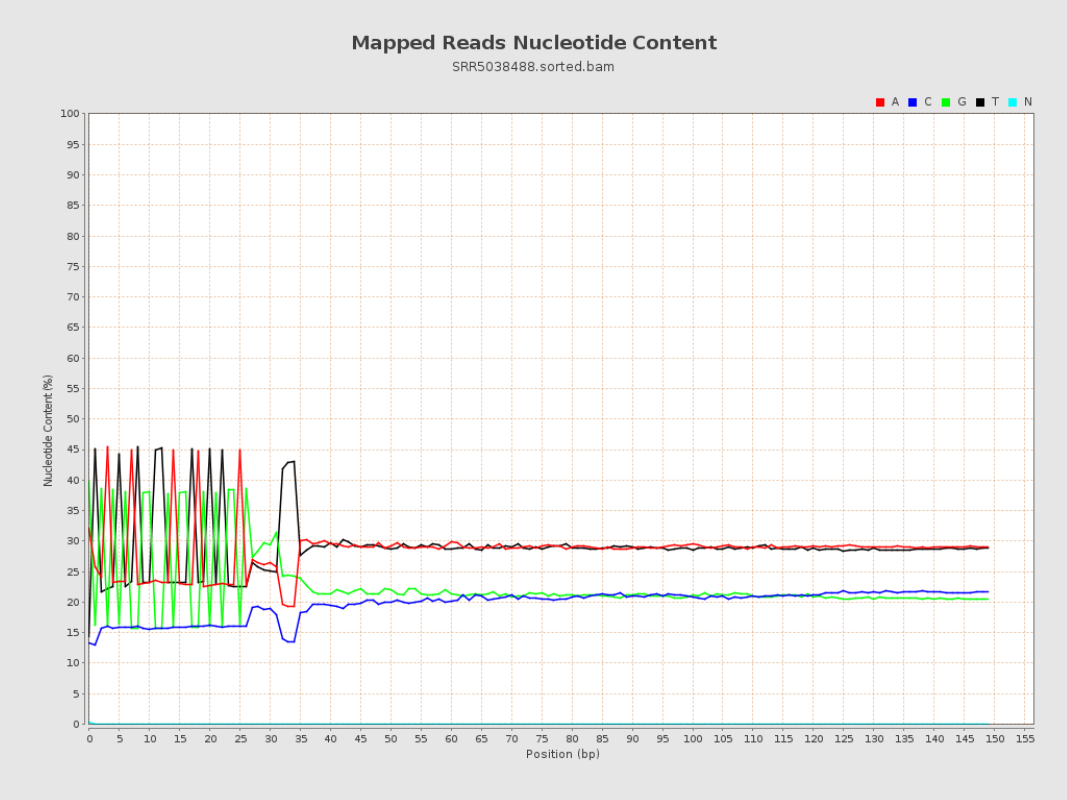
6. Results : Genome Fraction Coverage



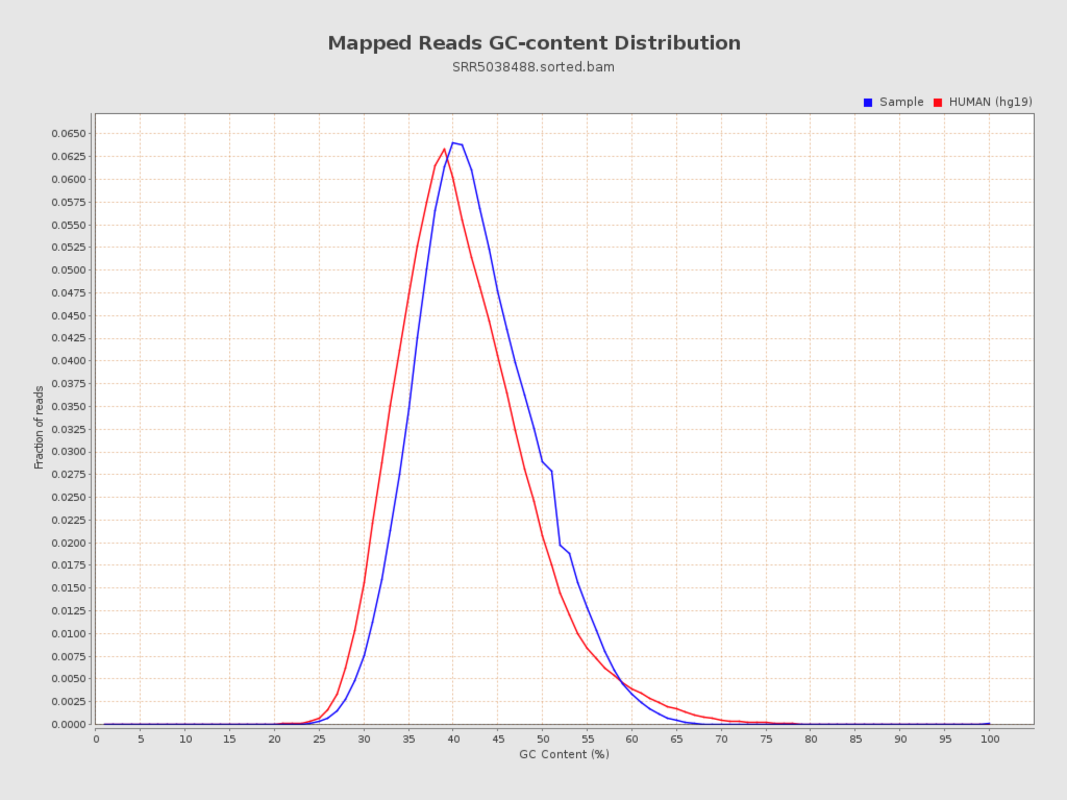
7. Results : Duplication Rate Histogram



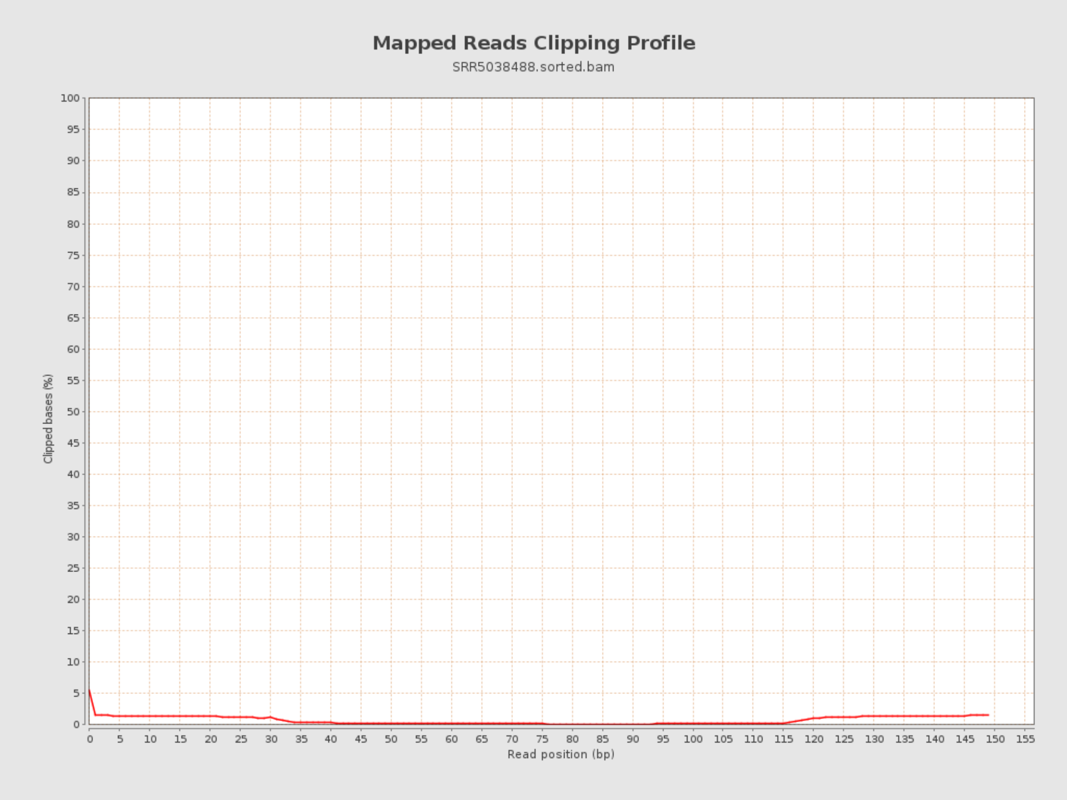
8. Results : Mapped Reads Nucleotide Content



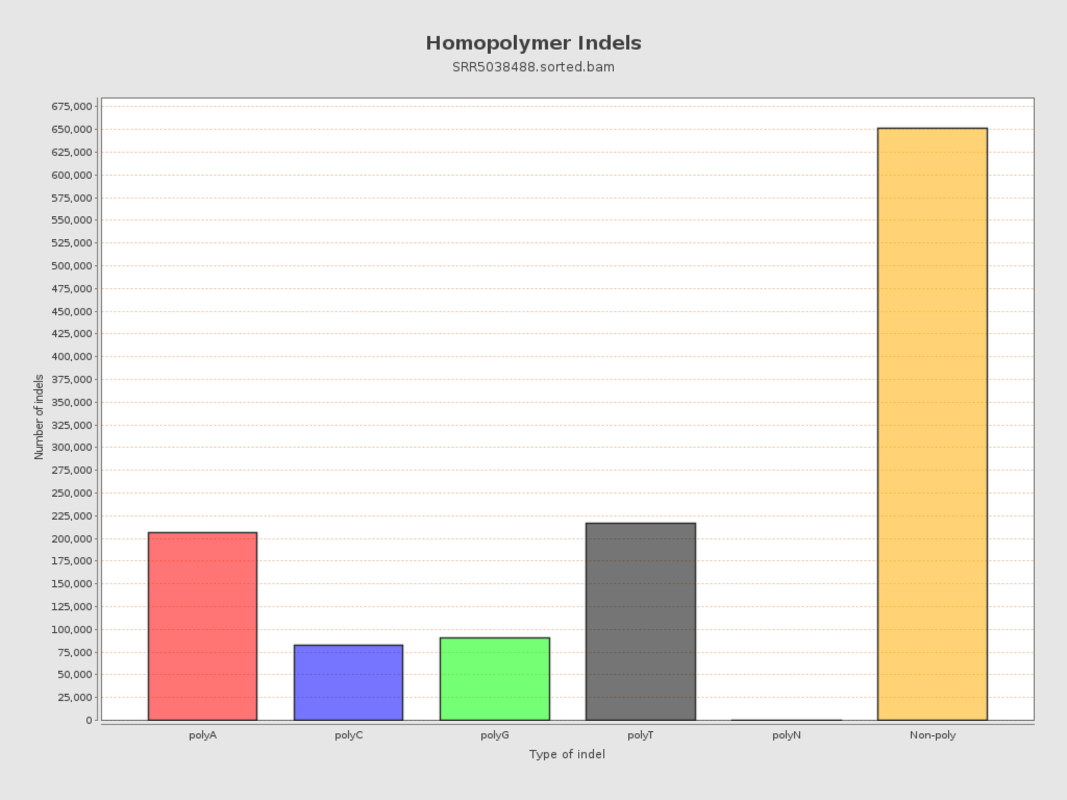
9. Results : Mapped Reads GC-content Distribution



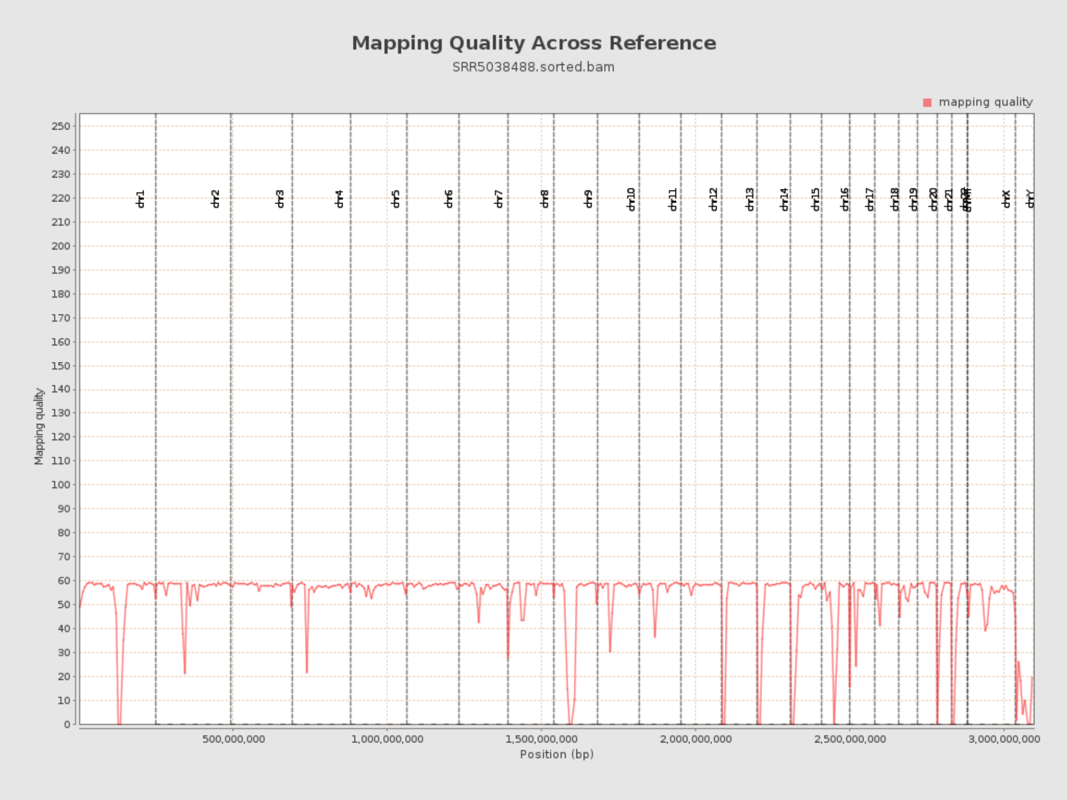
10. Results : Mapped Reads Clipping Profile



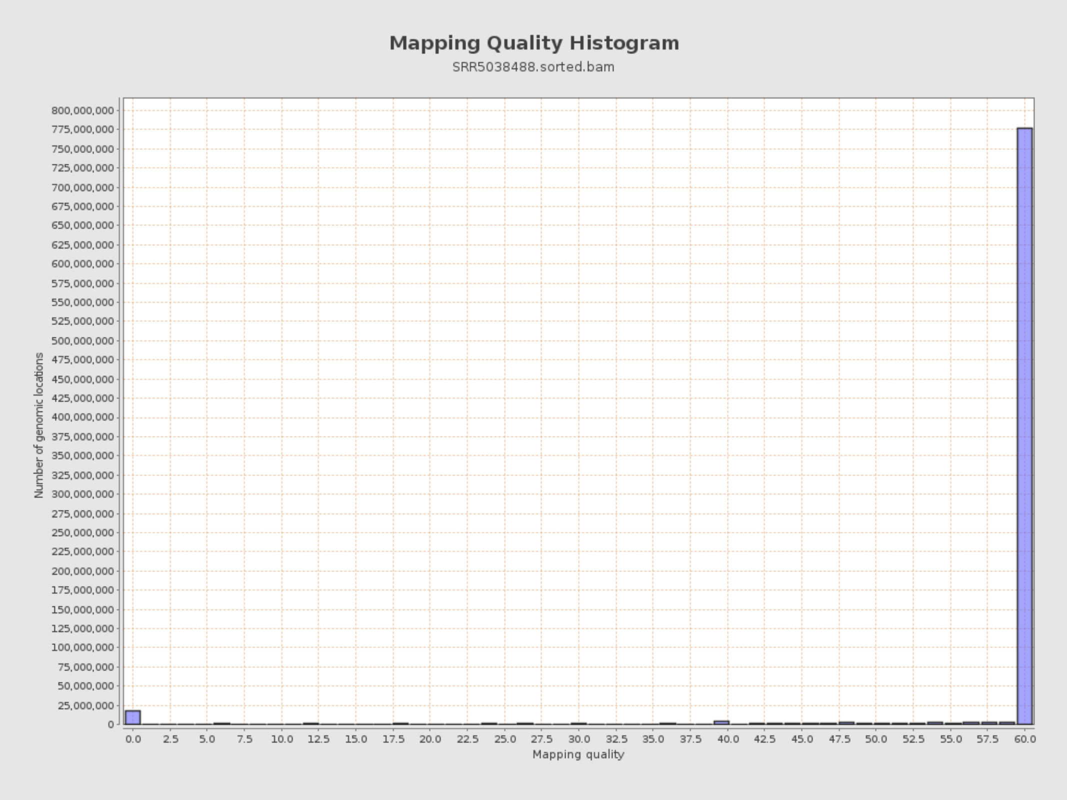
11. Results : Homopolymer Indels



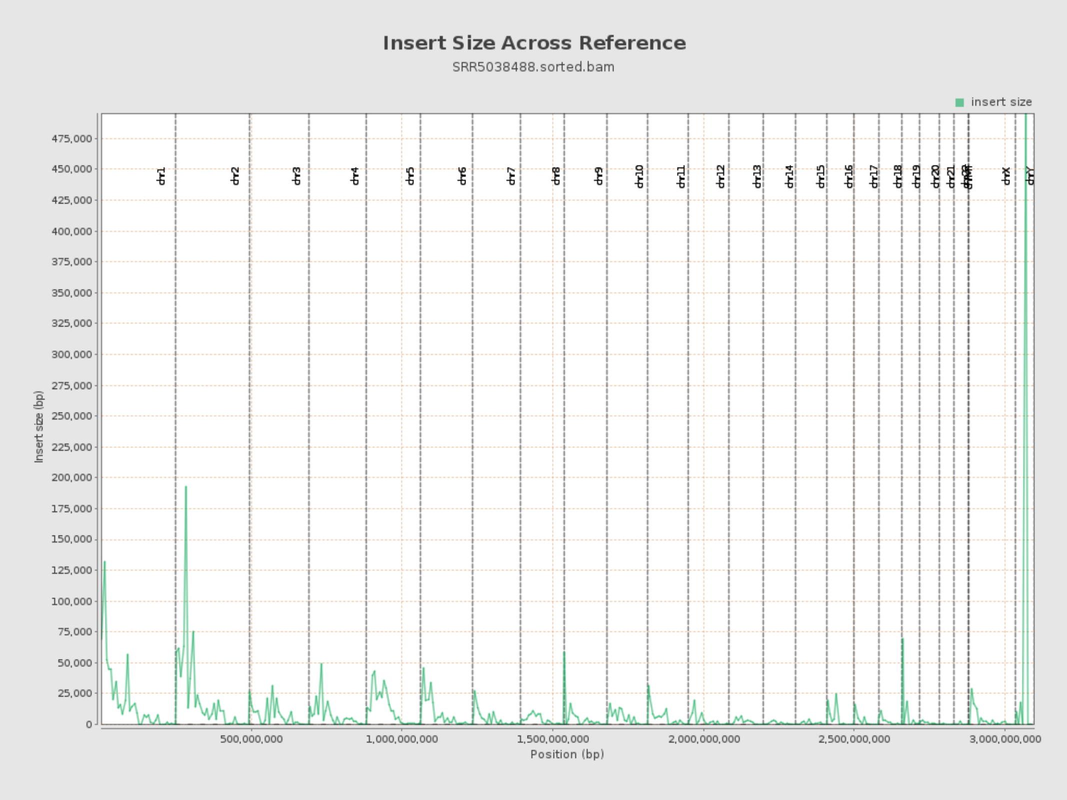
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram