Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/14 15:56:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038403.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_SRR5038403 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038403_1.fastq.gz SRR5038403_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Apr 14 15:56:40 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038403.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	18,103,366
Mapped reads	16,907,169 / 93.39%
Unmapped reads	1,196,197 / 6.61%
Mapped paired reads	16,907,169 / 93.39%
Mapped reads, first in pair	8,609,673 / 47.56%
Mapped reads, second in pair	8,297,496 / 45.83%
Mapped reads, both in pair	16,510,012 / 91.2%
Mapped reads, singletons	397,157 / 2.19%
Secondary alignments	0
Supplementary alignments	306,529 / 1.69%
Read min/max/mean length	30 / 150 / 150.83
Duplicated reads (estimated)	4,362,717 / 24.1%
Duplication rate	17.93%
Clipped reads	9,700,957 / 53.59%

2.2. ACGT Content

Number/percentage of A's	646,559,584 / 29.09%
Number/percentage of C's	419,668,436 / 18.88%
Number/percentage of T's	665,973,455 / 29.96%
Number/percentage of G's	490,320,637 / 22.06%
Number/percentage of N's	171,707 / 0.01%

GC Percentage	40.94%

2.3. Coverage

Mean	0.7185
Standard Deviation	10.338

2.4. Mapping Quality

Mean Mapping Quality	53.1

2.5. Insert size

Mean	84,782.42
Standard Deviation	2,751,593.41
P25/Median/P75	186 / 230 / 282

2.6. Mismatches and indels

General error rate	1.33%
Mismatches	28,578,915
Insertions	394,448
Mapped reads with at least one insertion	2.23%
Deletions	735,166
Mapped reads with at least one deletion	4.2%
Homopolymer indels	47.9%

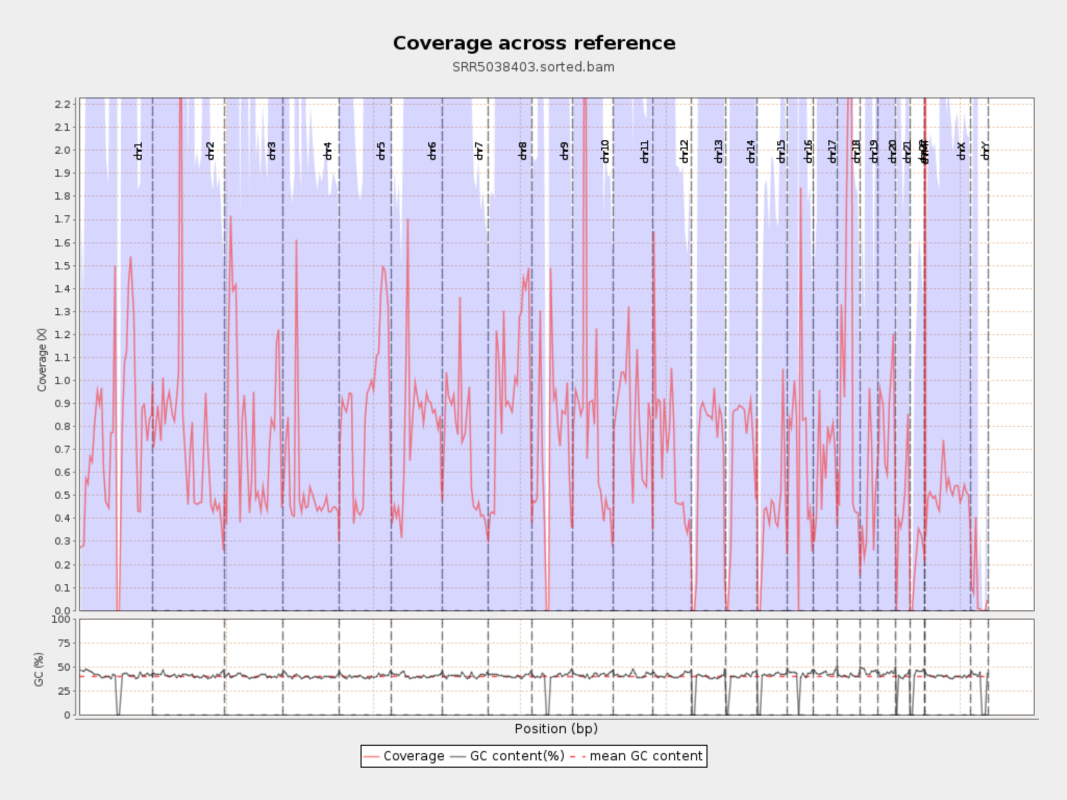
2.7. Chromosome stats

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

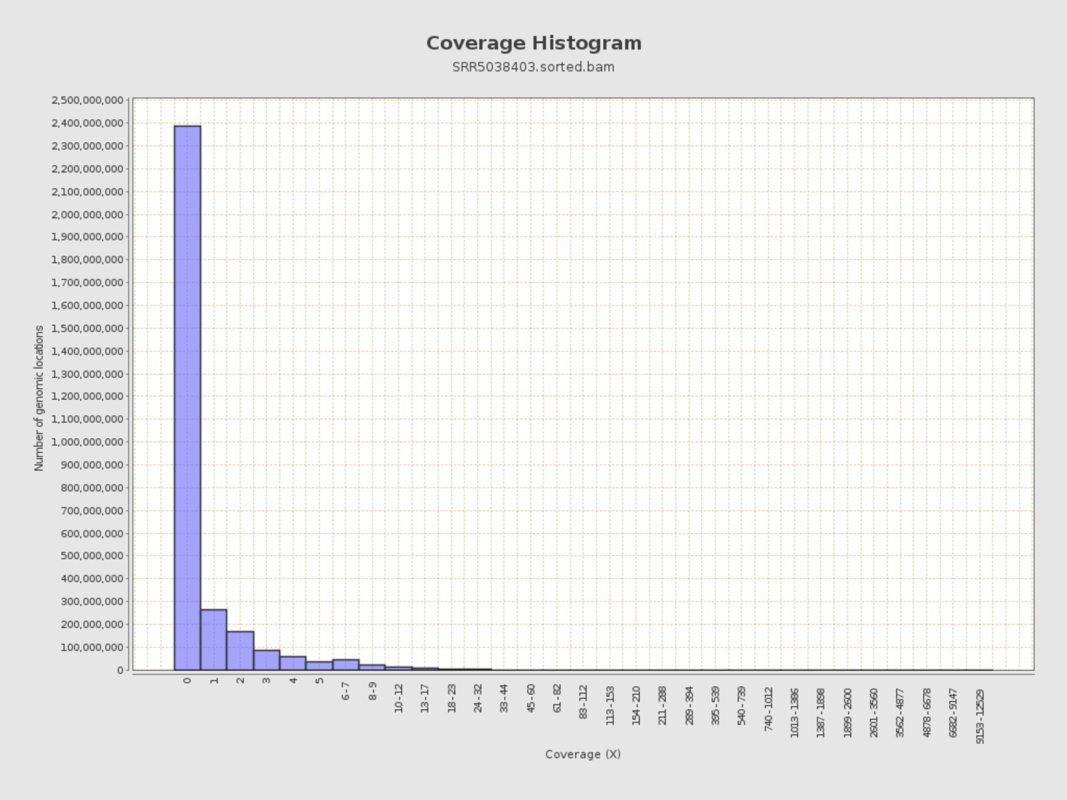
		bases	coverage	deviation
chr1	249250621	189855294	0.7617	12.5008
chr2	243199373	184352572	0.758	14.1411
chr3	198022430	158295019	0.7994	2.1437
chr4	191154276	101799230	0.5326	9.4997
chr5	180915260	162129912	0.8962	2.2442
chr6	171115067	136115257	0.7955	8.9989
chr7	159138663	112808431	0.7089	11.4058
chr8	146364022	145194401	0.992	4.7663
chr9	141213431	96213539	0.6813	17.7908
chr10	135534747	120661077	0.8903	24.7709
chr11	135006516	112831251	0.8357	8.915
chr12	133851895	93660930	0.6997	2.0618
chr13	115169878	79188391	0.6876	1.8619
chr14	107349540	72826644	0.6784	2.0152
chr15	102531392	41938452	0.409	1.402
chr16	90354753	63867124	0.7068	8.6777
chr17	81195210	51223153	0.6309	10.5463
chr18	78077248	96839560	1.2403	13.9985
chr19	59128983	28047973	0.4744	5.9988
chr20	63025520	53460457	0.8482	3.673
chr21	48129895	21626595	0.4493	4.5076
chr22	51304566	10693640	0.2084	1.2398
chrMT	16571	6161527	371.8259	337.001
chrX	155270560	79643474	0.5129	2.3699

chrY	59373566	4720132	0.0795	9.8806

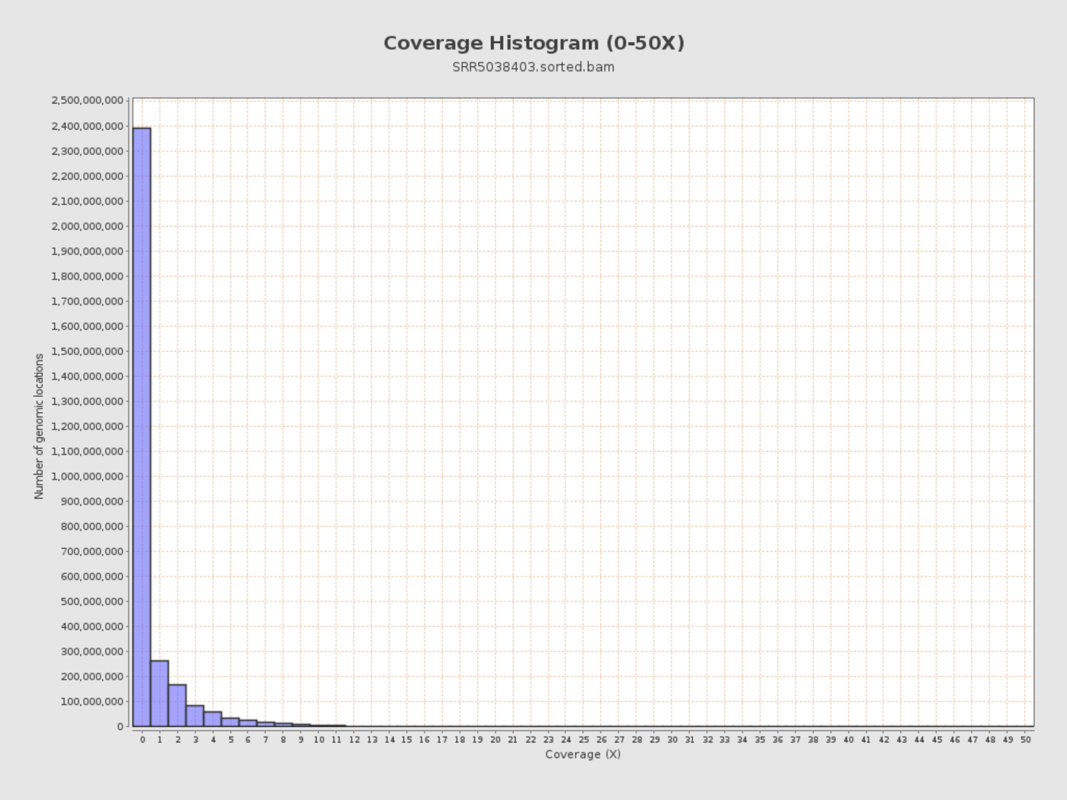
3. Results : Coverage across reference



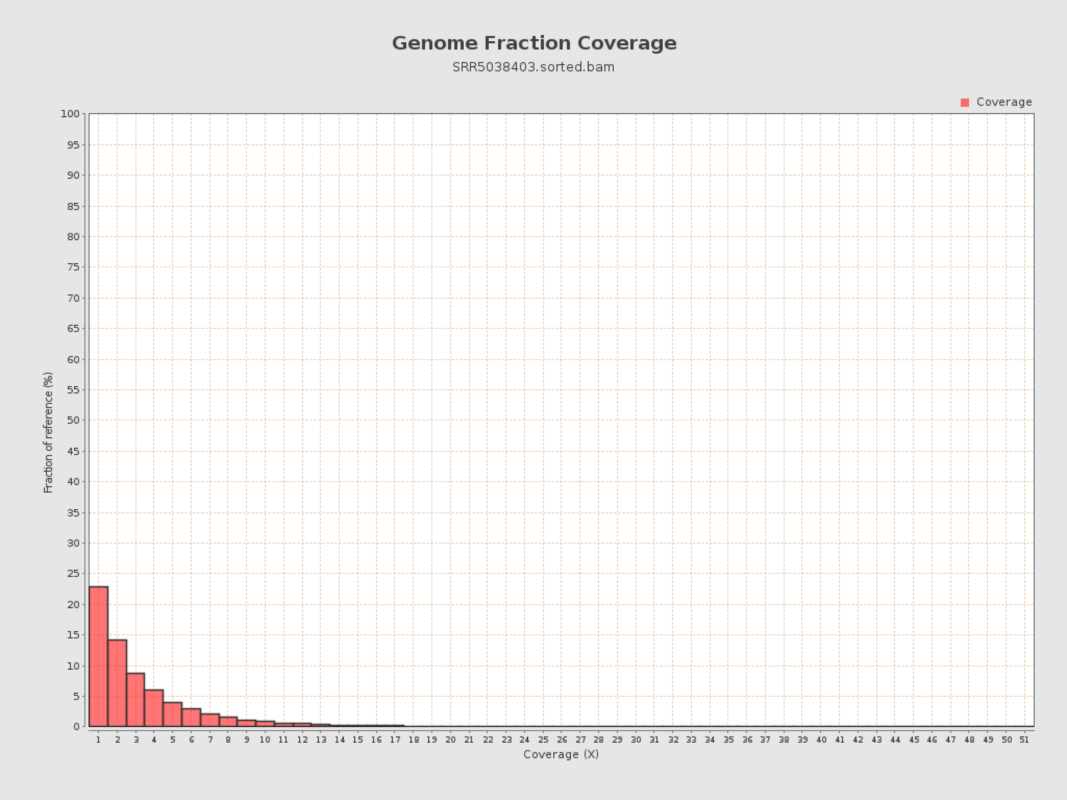
4. Results : Coverage Histogram



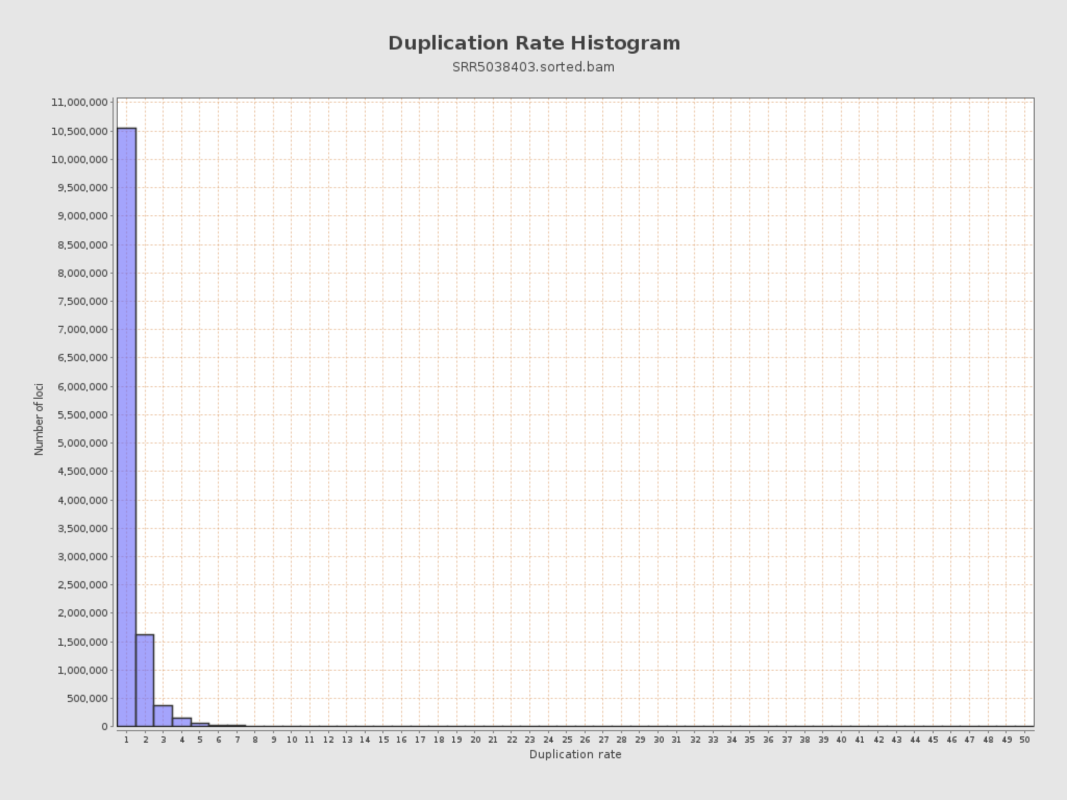
5. Results : Coverage Histogram (0-50X)



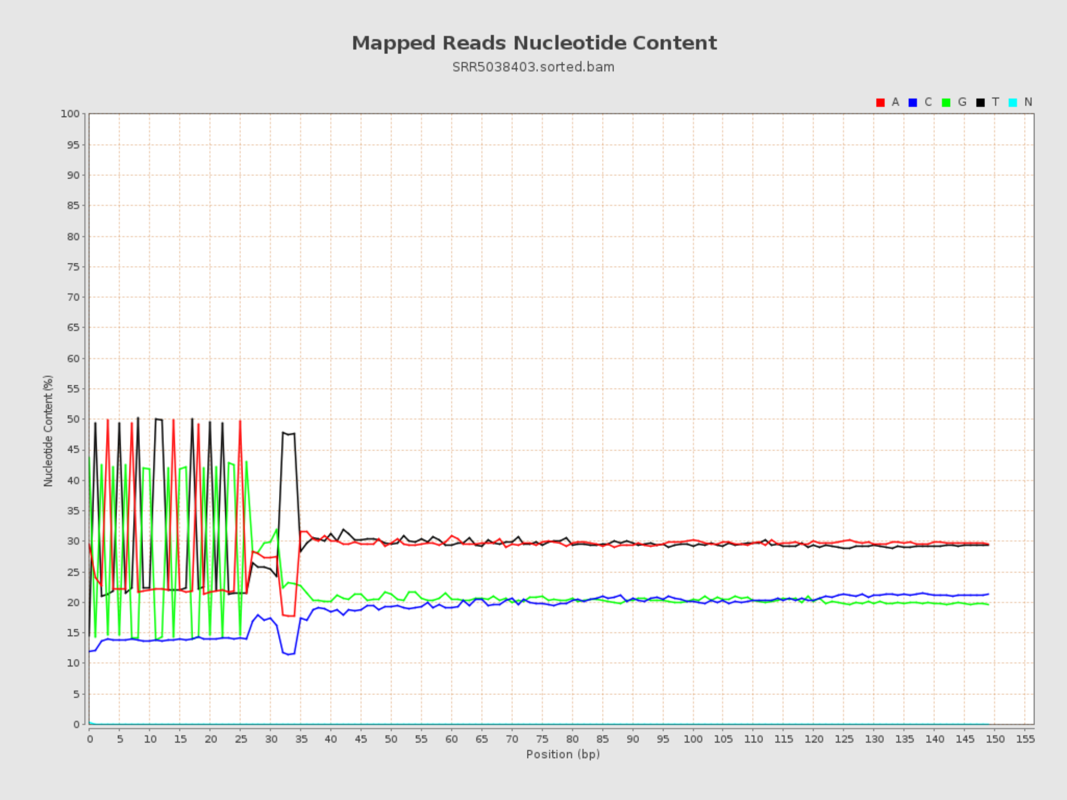
6. Results : Genome Fraction Coverage



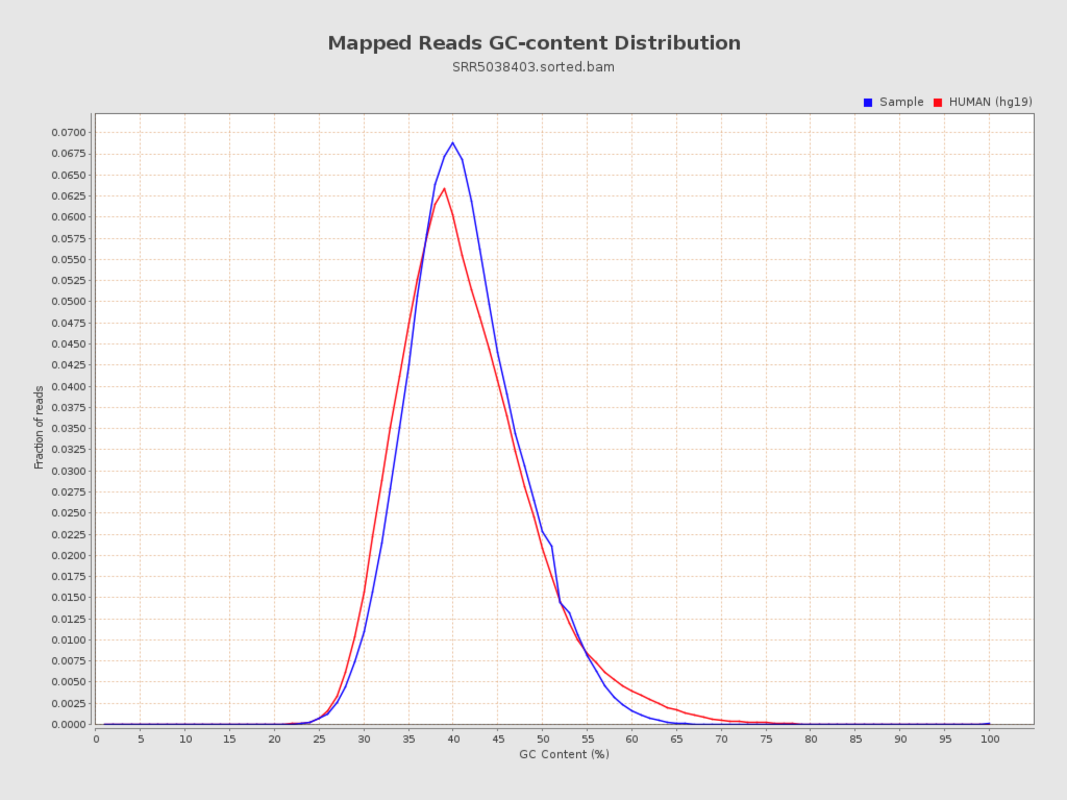
7. Results : Duplication Rate Histogram



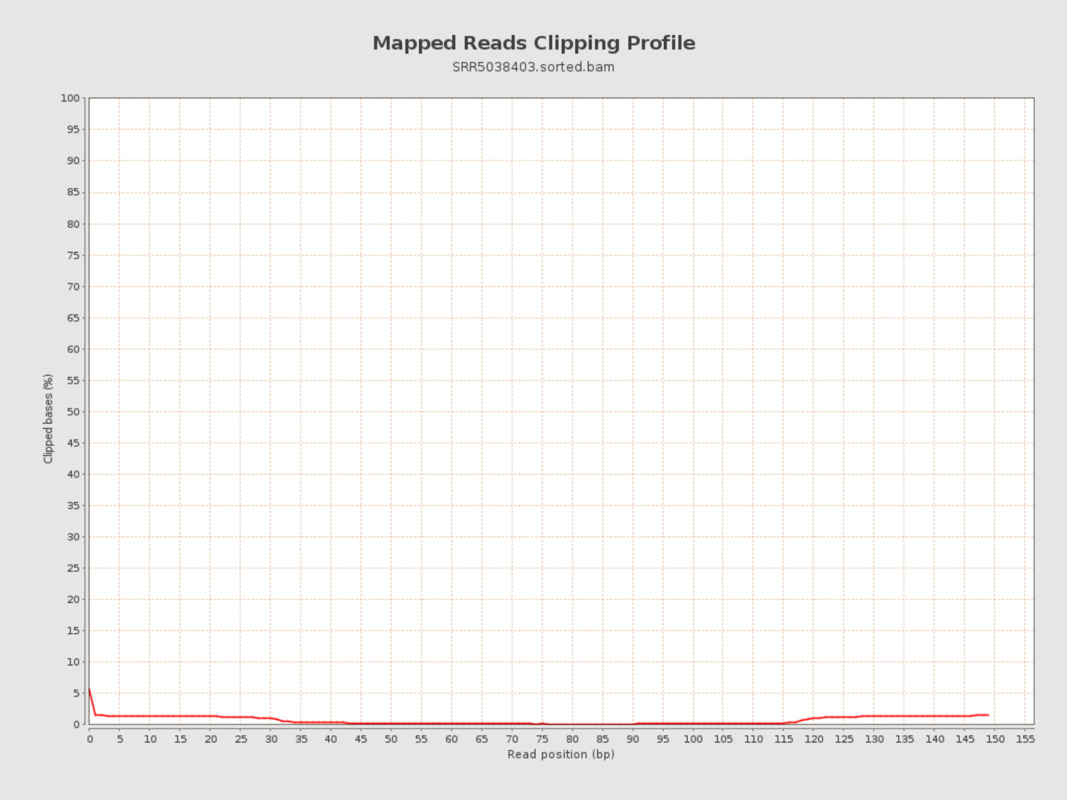
8. Results : Mapped Reads Nucleotide Content



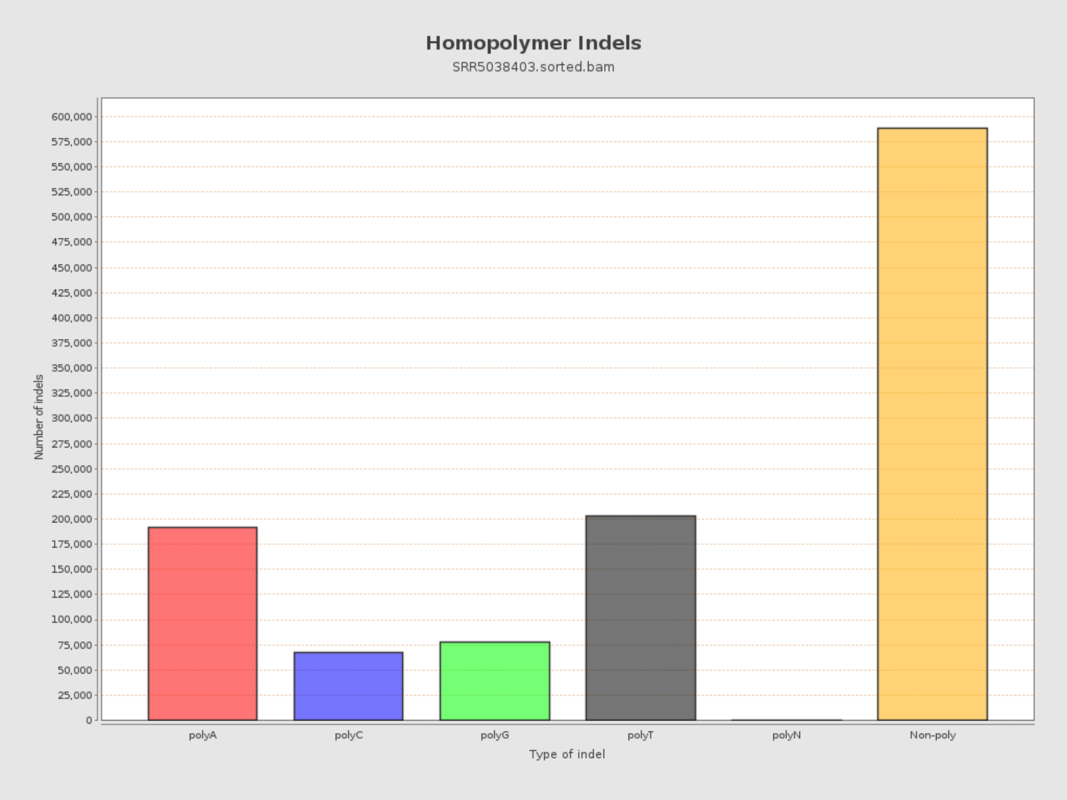
9. Results : Mapped Reads GC-content Distribution



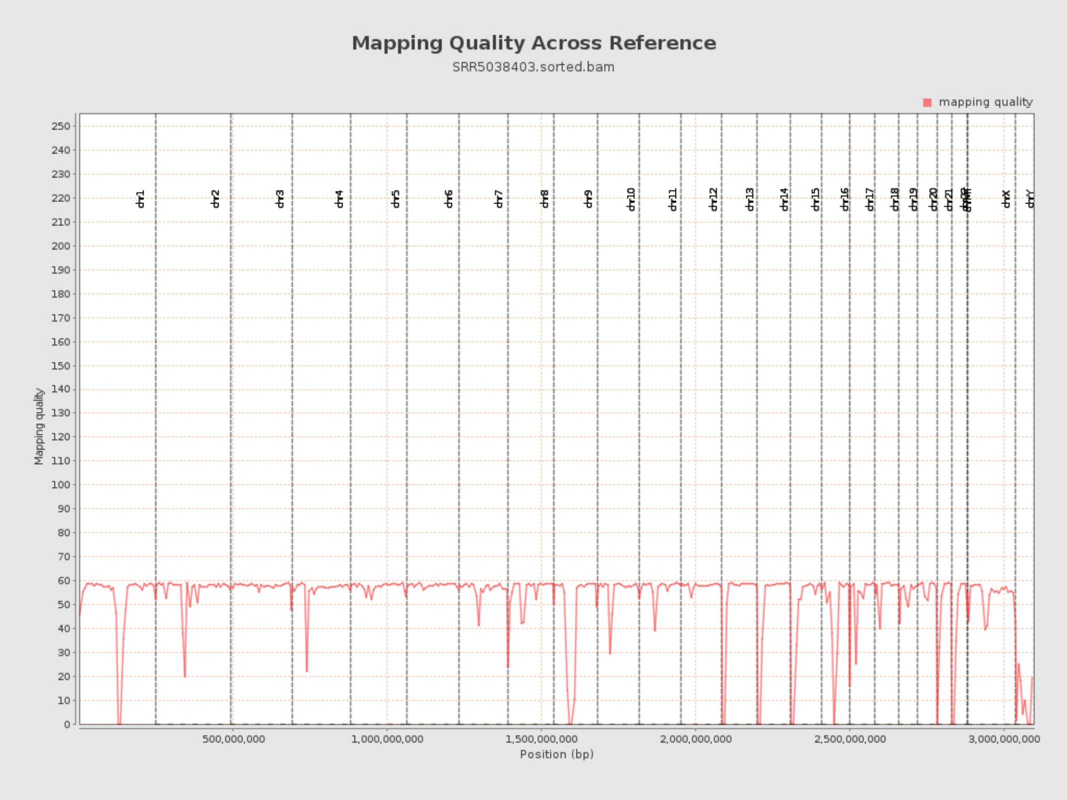
10. Results : Mapped Reads Clipping Profile



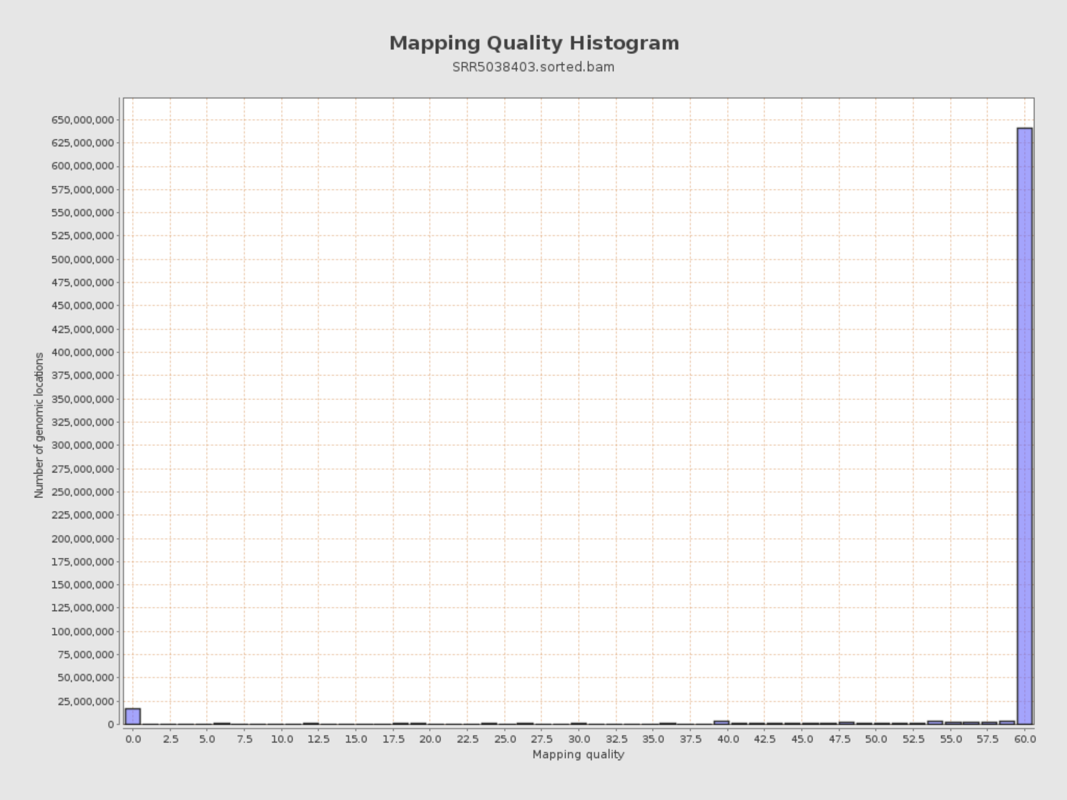
11. Results : Homopolymer Indels



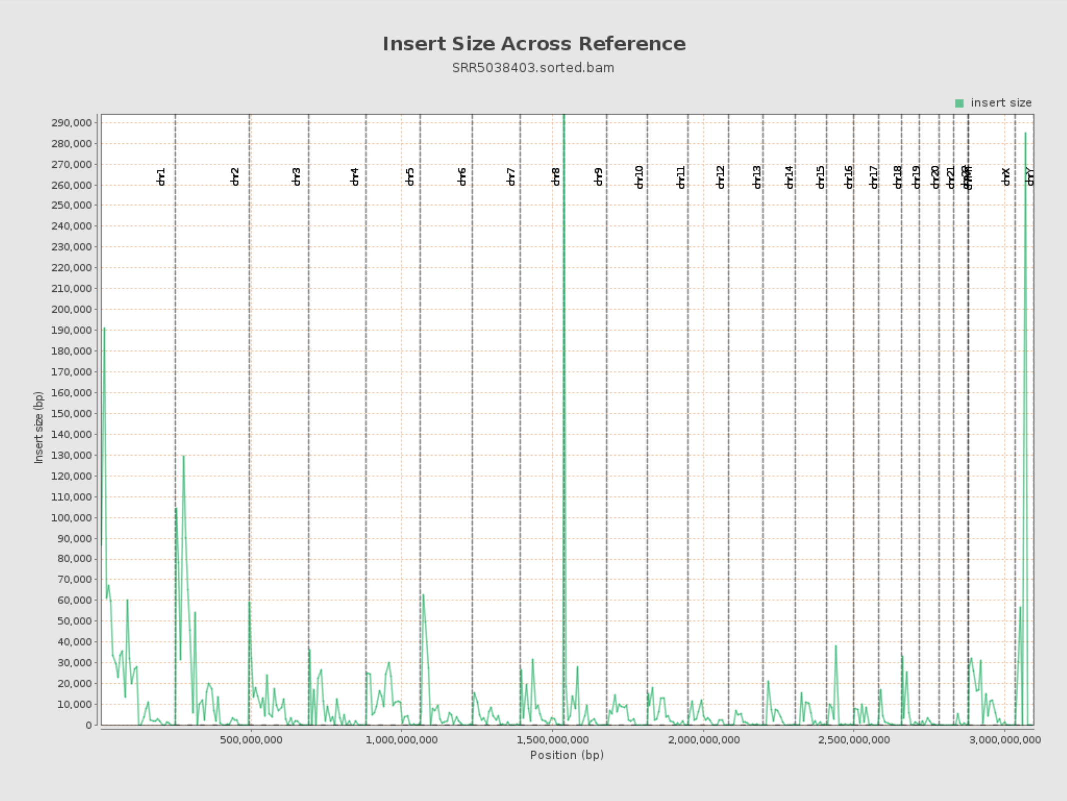
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram