Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/15 16:55:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038453.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_SRR5038453 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038453_1.fastq.gz SRR5038453_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 15 16:54:58 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038453.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	16,842,540
Mapped reads	15,939,433 / 94.64%
Unmapped reads	903,107 / 5.36%
Mapped paired reads	15,939,433 / 94.64%
Mapped reads, first in pair	8,101,523 / 48.1%
Mapped reads, second in pair	7,837,910 / 46.54%
Mapped reads, both in pair	15,630,582 / 92.8%
Mapped reads, singletons	308,851 / 1.83%
Secondary alignments	0
Supplementary alignments	260,705 / 1.55%
Read min/max/mean length	30 / 150 / 150.77
Duplicated reads (estimated)	2,674,518 / 15.88%
Duplication rate	11.72%
Clipped reads	7,543,769 / 44.79%

2.2. ACGT Content

Number/percentage of A's	614,515,145 / 28.61%
Number/percentage of C's	425,299,836 / 19.8%
Number/percentage of T's	627,316,169 / 29.2%
Number/percentage of G's	480,862,421 / 22.38%
Number/percentage of N's	170,081 / 0.01%

GC Percentage	42.18%

2.3. Coverage

Mean	0.6944
Standard Deviation	9.3751

2.4. Mapping Quality

Mean Mapping Quality	53.39

2.5. Insert size

Mean	96,421.62
Standard Deviation	3,024,131.01
P25/Median/P75	205 / 255 / 320

2.6. Mismatches and indels

General error rate	1.35%
Mismatches	27,898,177
Insertions	374,046
Mapped reads with at least one insertion	2.22%
Deletions	714,211
Mapped reads with at least one deletion	4.31%
Homopolymer indels	46.91%

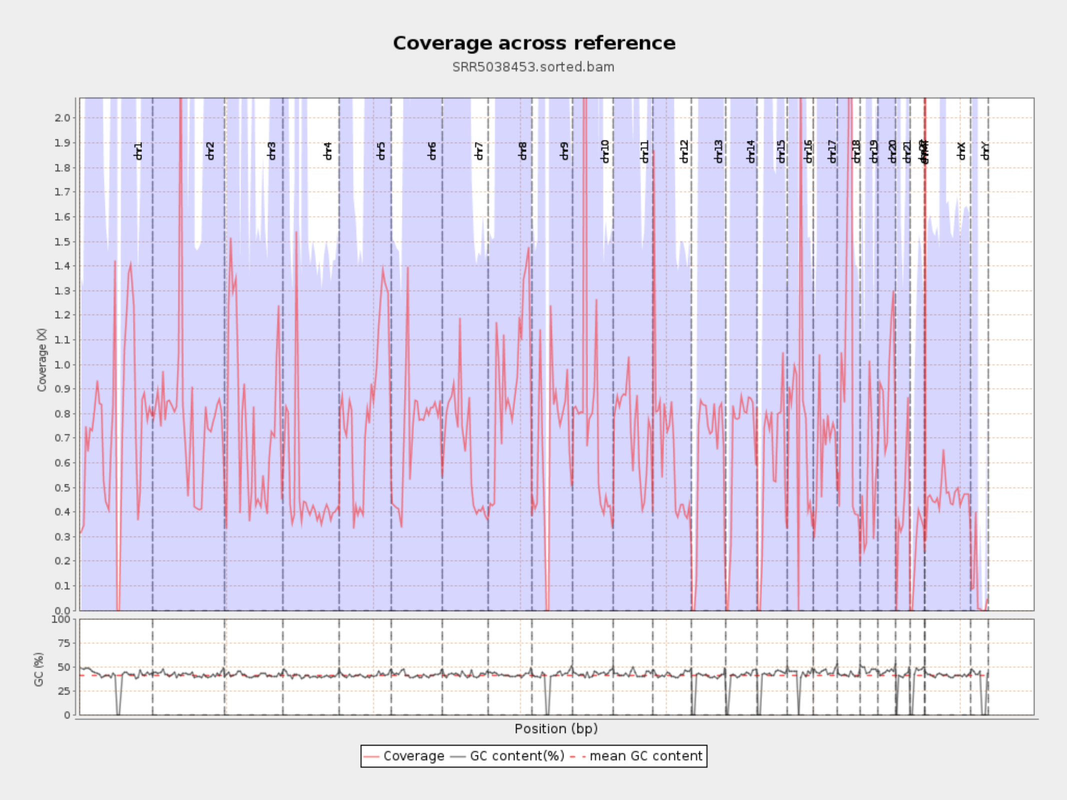
2.7. Chromosome stats

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

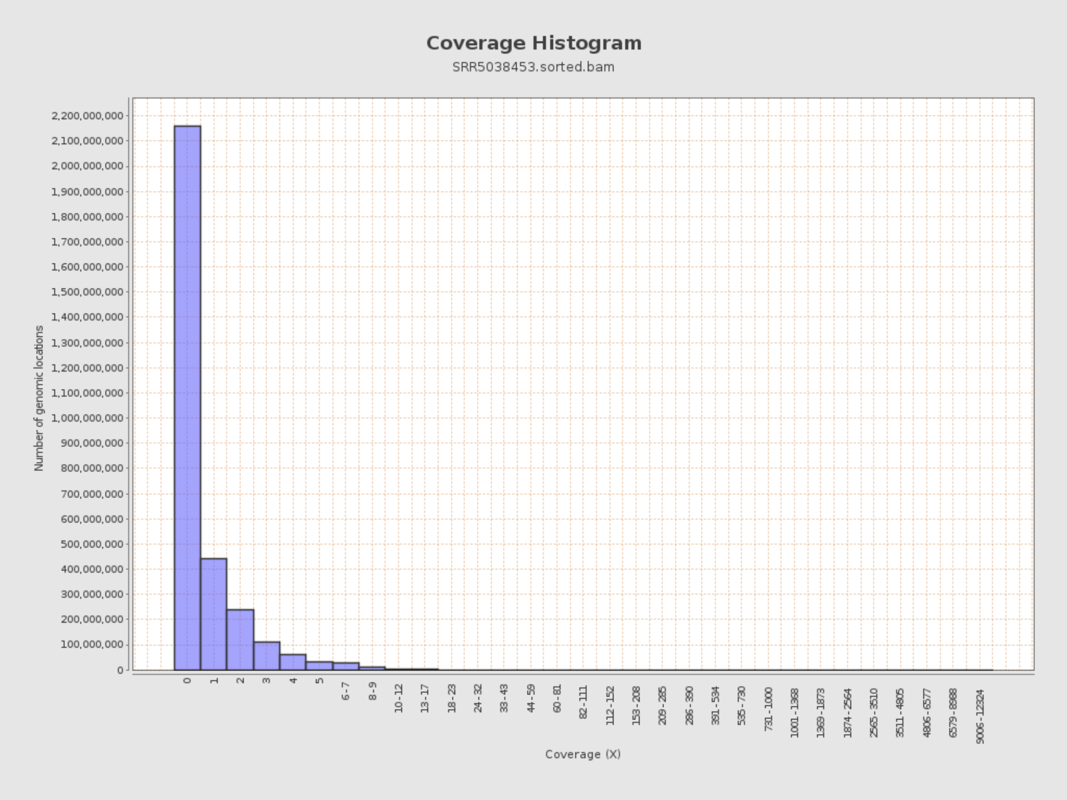
		bases	coverage	deviation
chr1	249250621	186411871	0.7479	12.202
chr2	243199373	193861347	0.7971	10.3134
chr3	198022430	148650219	0.7507	1.6291
chr4	191154276	93495130	0.4891	9.2496
chr5	180915260	149156712	0.8245	1.5682
chr6	171115067	125995302	0.7363	6.7627
chr7	159138663	104709161	0.658	9.2194
chr8	146364022	136961640	0.9358	3.5232
chr9	141213431	92374541	0.6541	14.4912
chr10	135534747	117901701	0.8699	26.8494
chr11	135006516	98567971	0.7301	6.6638
chr12	133851895	89286388	0.6671	1.5478
chr13	115169878	73496035	0.6382	1.3286
chr14	107349540	71119675	0.6625	1.4489
chr15	102531392	59233875	0.5777	1.2811
chr16	90354753	69640082	0.7707	10.1312
chr17	81195210	53370716	0.6573	10.1203
chr18	78077248	86046293	1.1021	10.0369
chr19	59128983	29608656	0.5007	5.1623
chr20	63025520	57690762	0.9154	3.2823
chr21	48129895	21133526	0.4391	4.1477
chr22	51304566	12514378	0.2439	0.8438
chrMT	16571	1924164	116.1163	63.8866
chrX	155270560	71765115	0.4622	1.9389

chrY	59373566	4713924	0.0794	8.9943

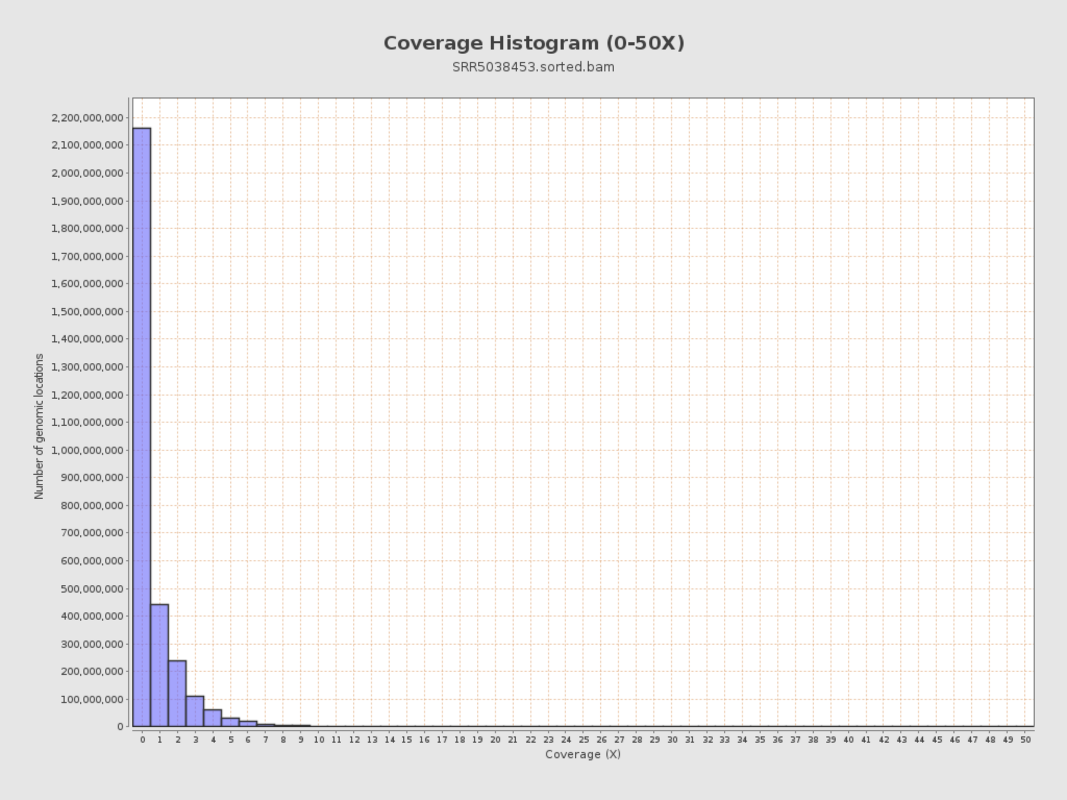
3. Results : Coverage across reference



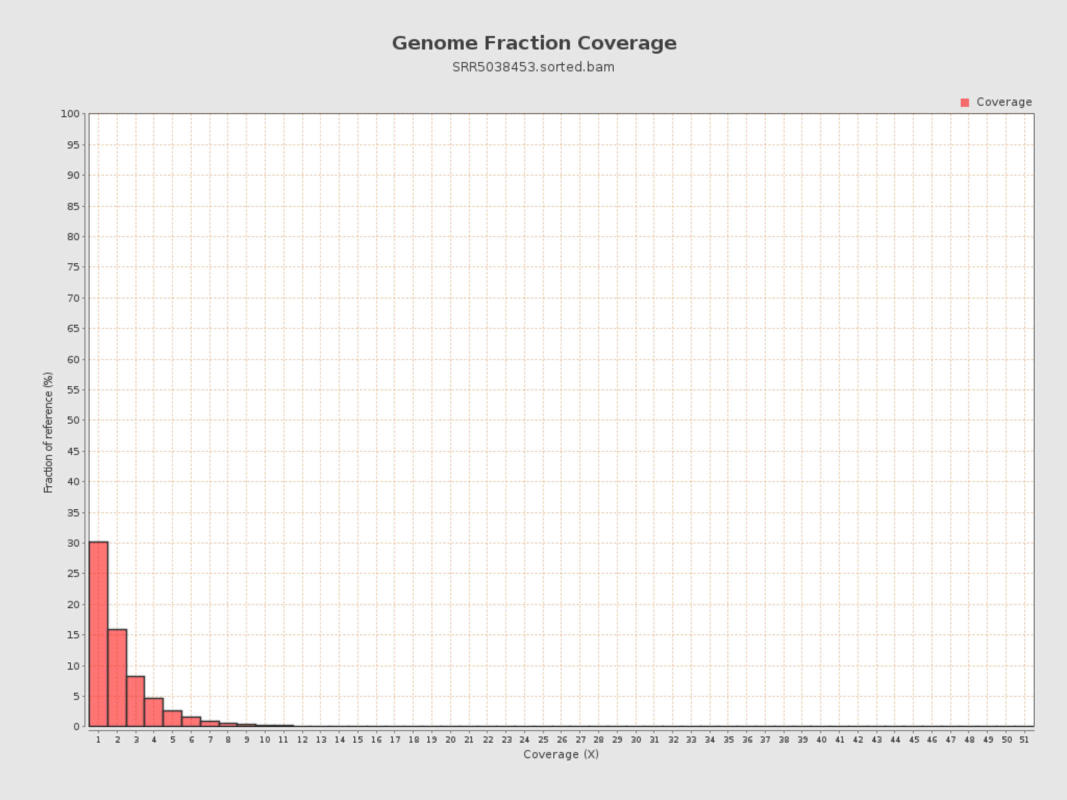
4. Results : Coverage Histogram



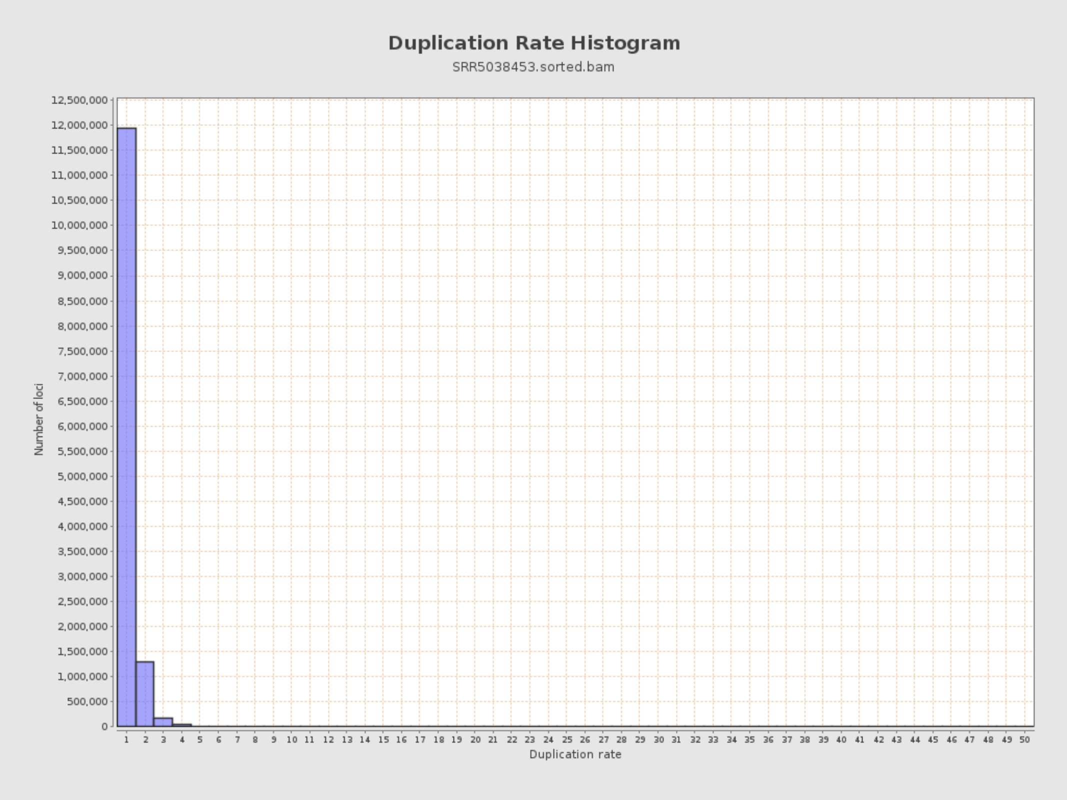
5. Results : Coverage Histogram (0-50X)



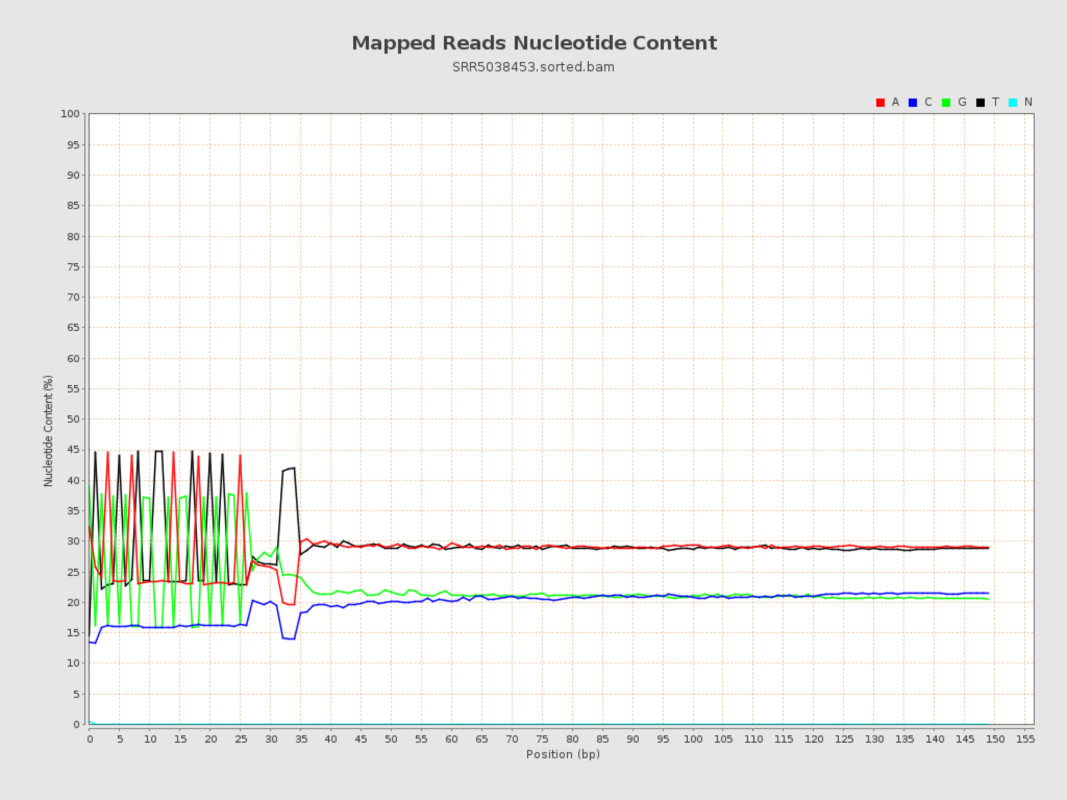
6. Results : Genome Fraction Coverage



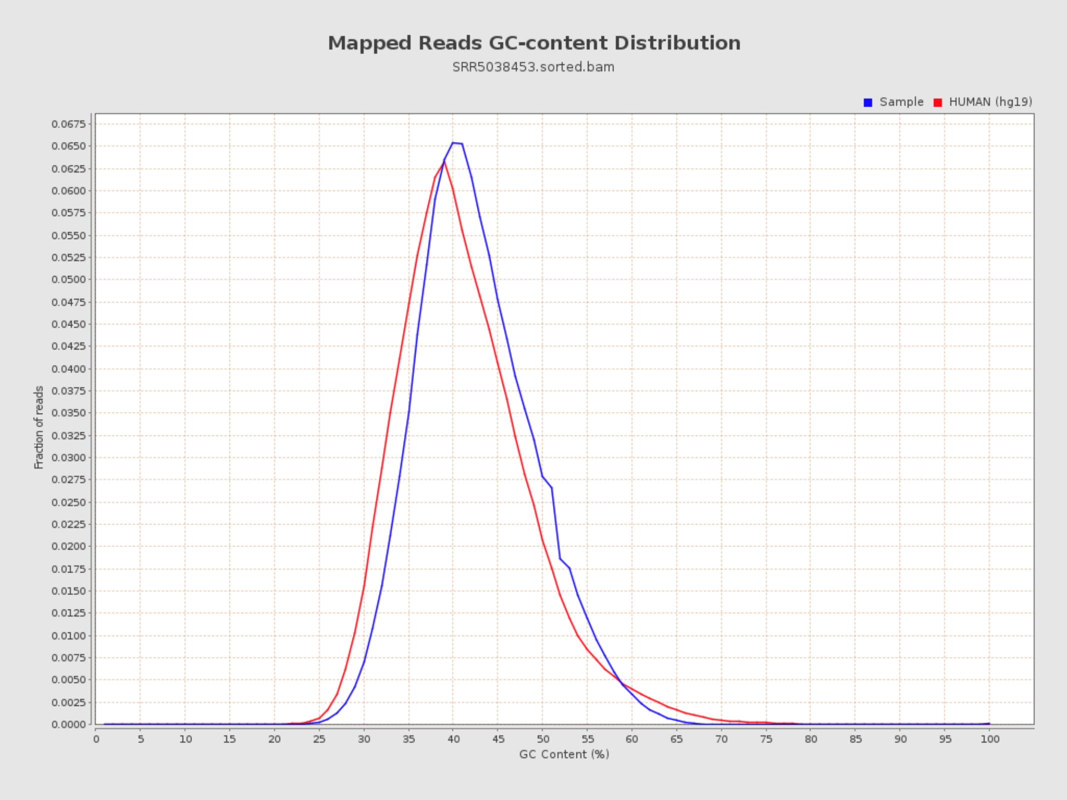
7. Results : Duplication Rate Histogram



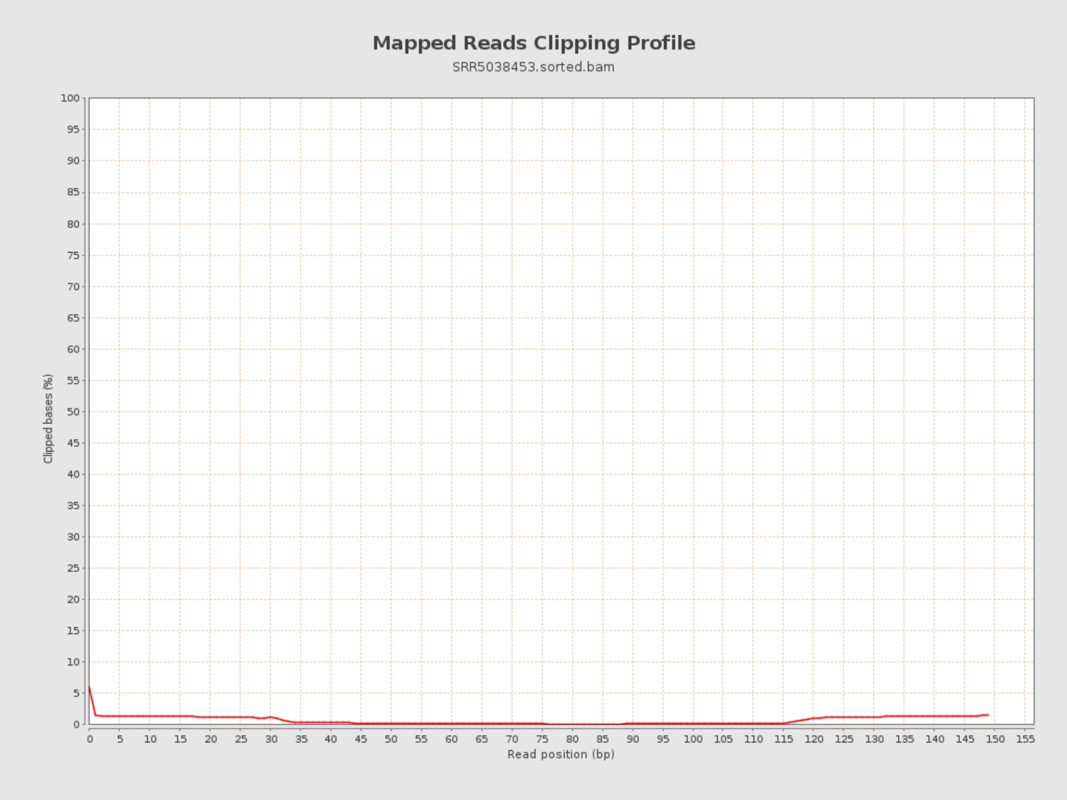
8. Results : Mapped Reads Nucleotide Content



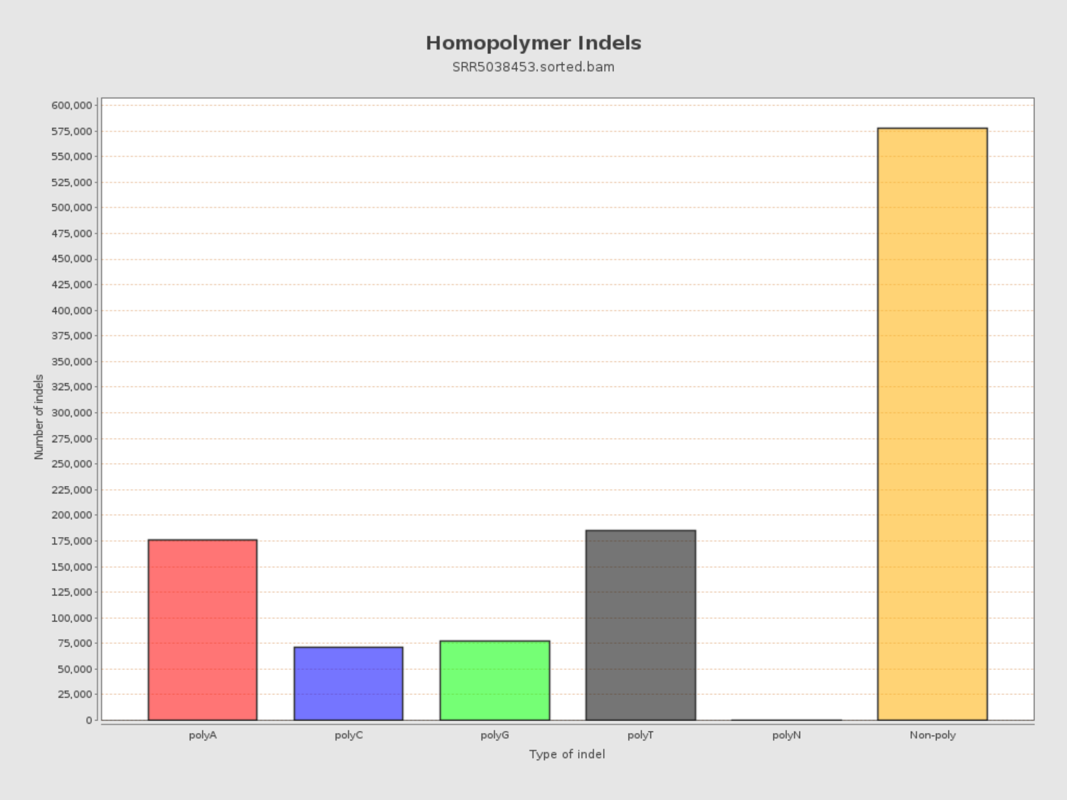
9. Results : Mapped Reads GC-content Distribution



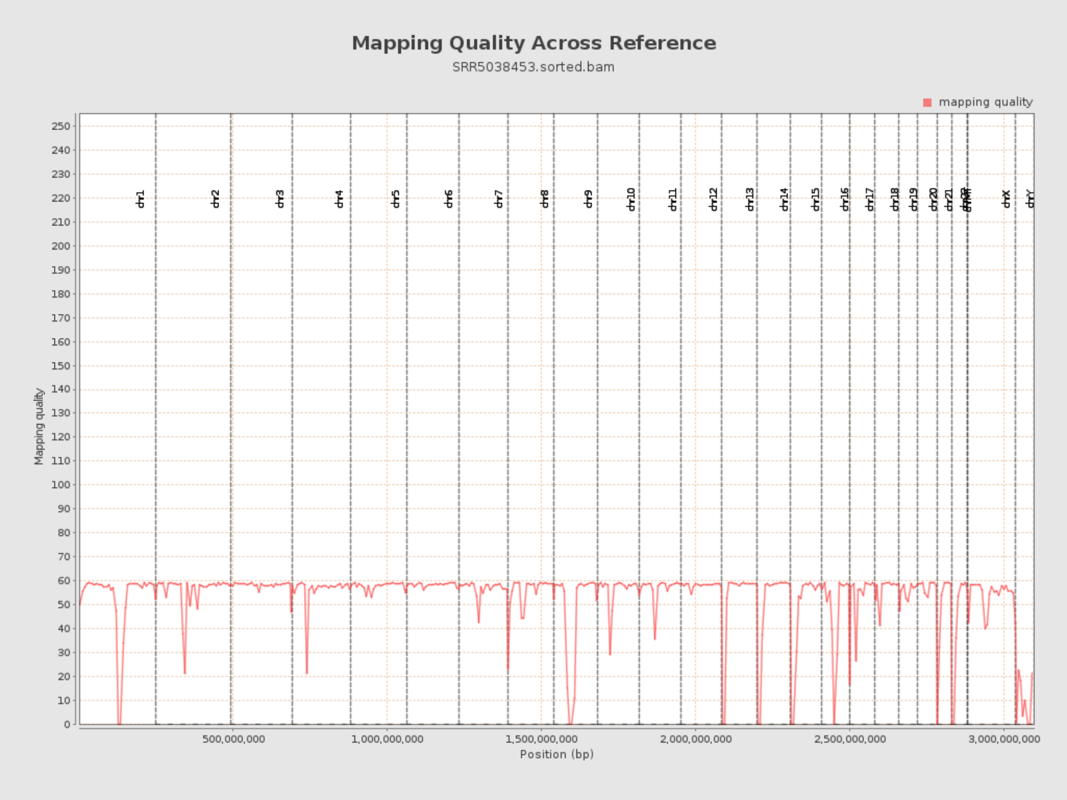
10. Results : Mapped Reads Clipping Profile



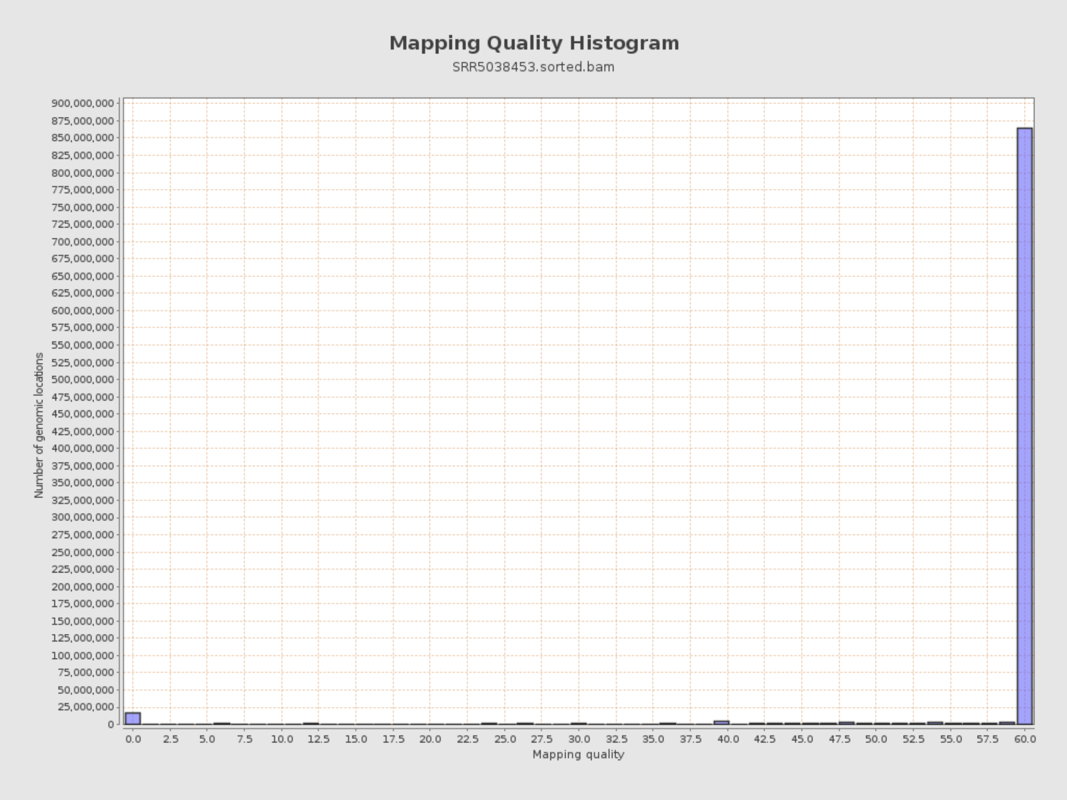
11. Results : Homopolymer Indels



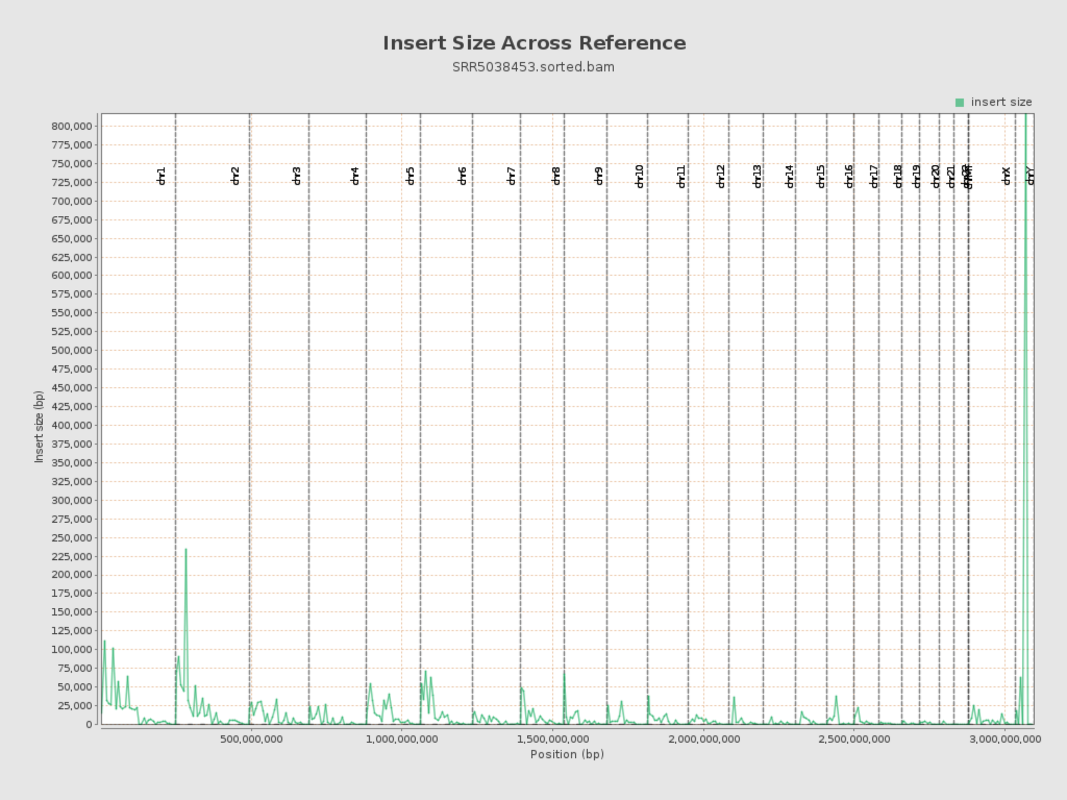
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram