Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/15 00:36:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038420.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_SRR5038420 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038420_1.fastq.gz SRR5038420_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 15 00:36:12 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038420.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	74,793,292
Mapped reads	74,310,262 / 99.35%
Unmapped reads	483,030 / 0.65%
Mapped paired reads	74,310,262 / 99.35%
Mapped reads, first in pair	37,319,936 / 49.9%
Mapped reads, second in pair	36,990,326 / 49.46%
Mapped reads, both in pair	73,938,498 / 98.86%
Mapped reads, singletons	371,764 / 0.5%
Secondary alignments	0
Supplementary alignments	109,908 / 0.15%
Read min/max/mean length	30 / 150 / 150.07
Duplicated reads (estimated)	27,659,529 / 36.98%
Duplication rate	35.3%
Clipped reads	4,666,307 / 6.24%

2.2. ACGT Content

Number/percentage of A's	2,778,662,101 / 25.17%
Number/percentage of C's	2,739,041,377 / 24.81%
Number/percentage of T's	2,802,844,491 / 25.39%
Number/percentage of G's	2,717,465,835 / 24.62%
Number/percentage of N's	996,044 / 0.01%

GC Percentage	49.43%

2.3. Coverage

Mean	3.5665
Standard Deviation	22.2598

2.4. Mapping Quality

Mean Mapping Quality	55.73

2.5. Insert size

Mean	18,585.1
Standard Deviation	1,414,329.94
P25/Median/P75	204 / 237 / 275

2.6. Mismatches and indels

General error rate	0.62%
Mismatches	67,504,091
Insertions	531,226
Mapped reads with at least one insertion	0.69%
Deletions	648,630
Mapped reads with at least one deletion	0.85%
Homopolymer indels	46.18%

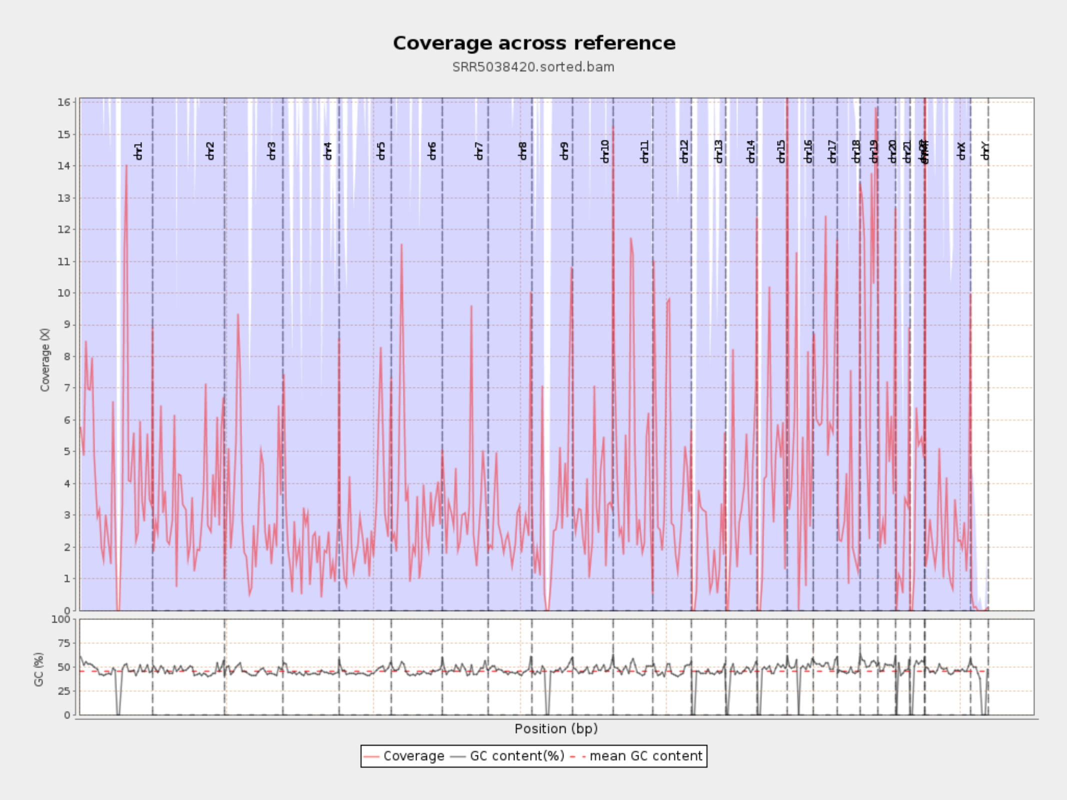
2.7. Chromosome stats

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

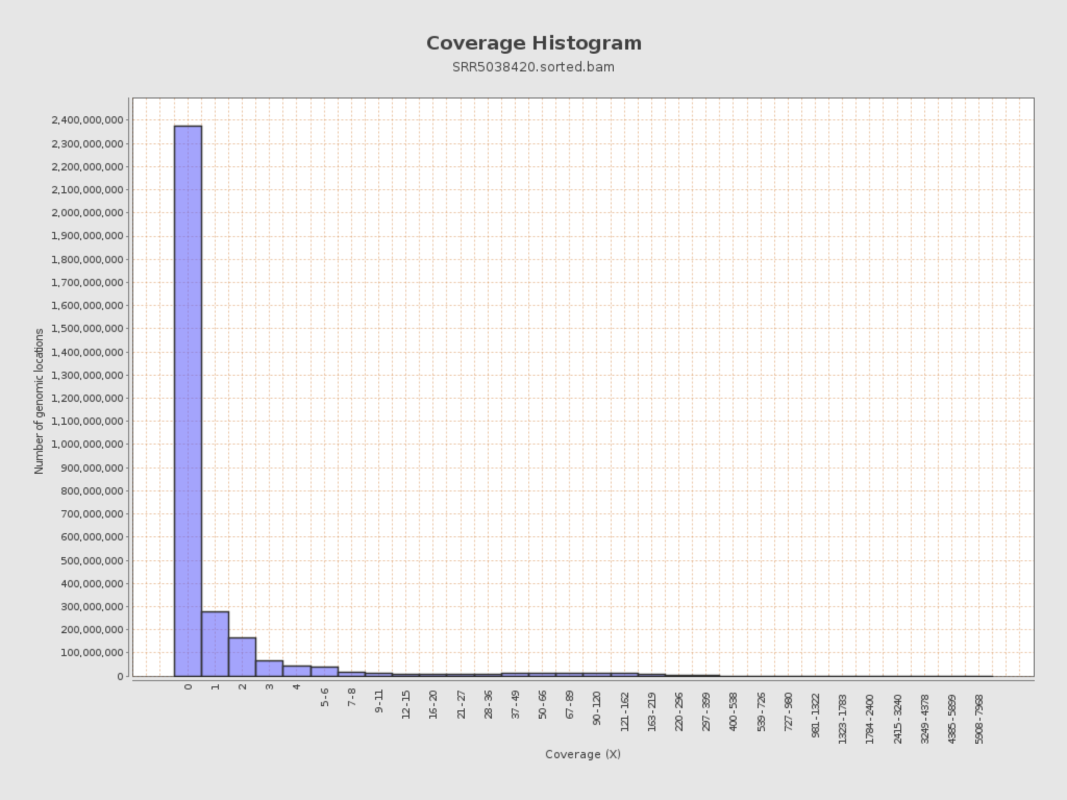
		bases	coverage	deviation
chr1	249250621	1124767908	4.5126	25.9925
chr2	243199373	822020090	3.38	22.0956
chr3	198022430	648908799	3.2769	21.0206
chr4	191154276	393516047	2.0586	15.3844
chr5	180915260	539606672	2.9826	20.5646
chr6	171115067	566495326	3.3106	21.3311
chr7	159138663	534508579	3.3588	21.454
chr8	146364022	420780400	2.8749	19.8722
chr9	141213431	451395252	3.1965	20.82
chr10	135534747	433099390	3.1955	19.8133
chr11	135006516	646173940	4.7862	27.0201
chr12	133851895	585214541	4.3721	24.2465
chr13	115169878	213925034	1.8575	15.2649
chr14	107349540	374569244	3.4892	22.0353
chr15	102531392	396727727	3.8693	22.421
chr16	90354753	465560576	5.1526	27.0636
chr17	81195210	602211955	7.4168	31.421
chr18	78077248	210941399	2.7017	21.8683
chr19	59128983	630518617	10.6634	38.1628
chr20	63025520	297224804	4.7159	26.4816
chr21	48129895	117127469	2.4336	21.2432
chr22	51304566	196149450	3.8232	20.0123
chrMT	16571	884965	53.4044	19.9008
chrX	155270560	363604787	2.3417	16.5963

chrY	59373566	4883532	0.0823	2.2401

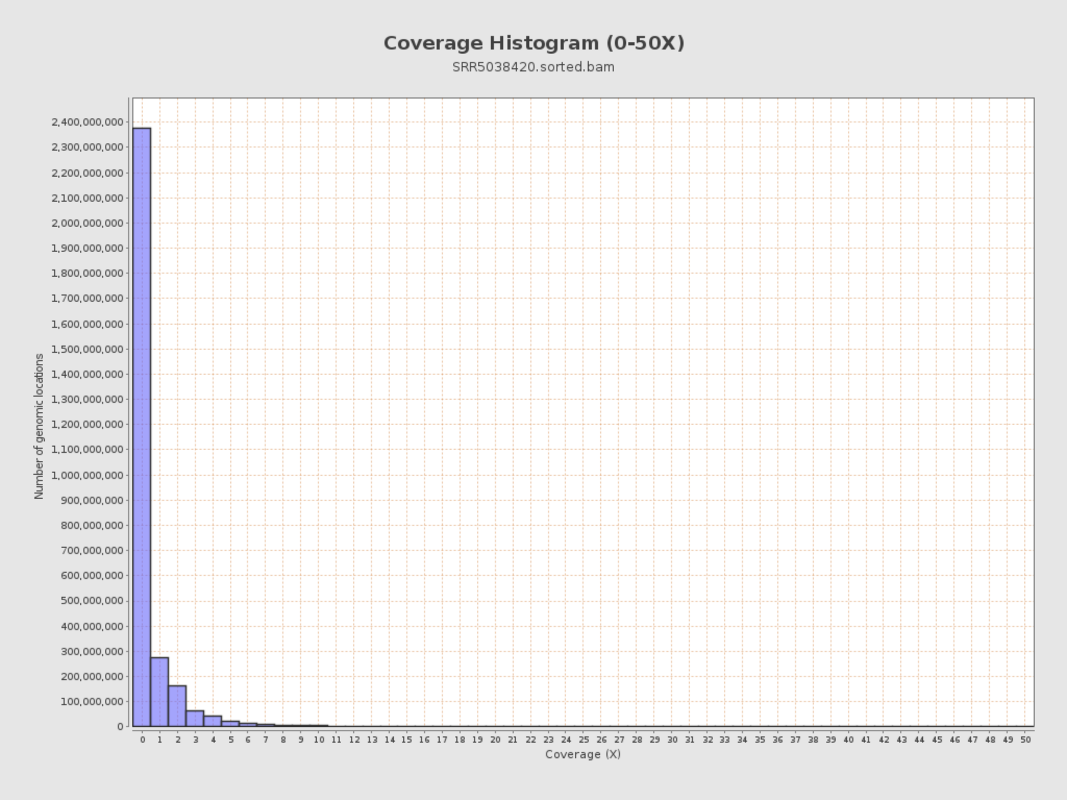
3. Results : Coverage across reference



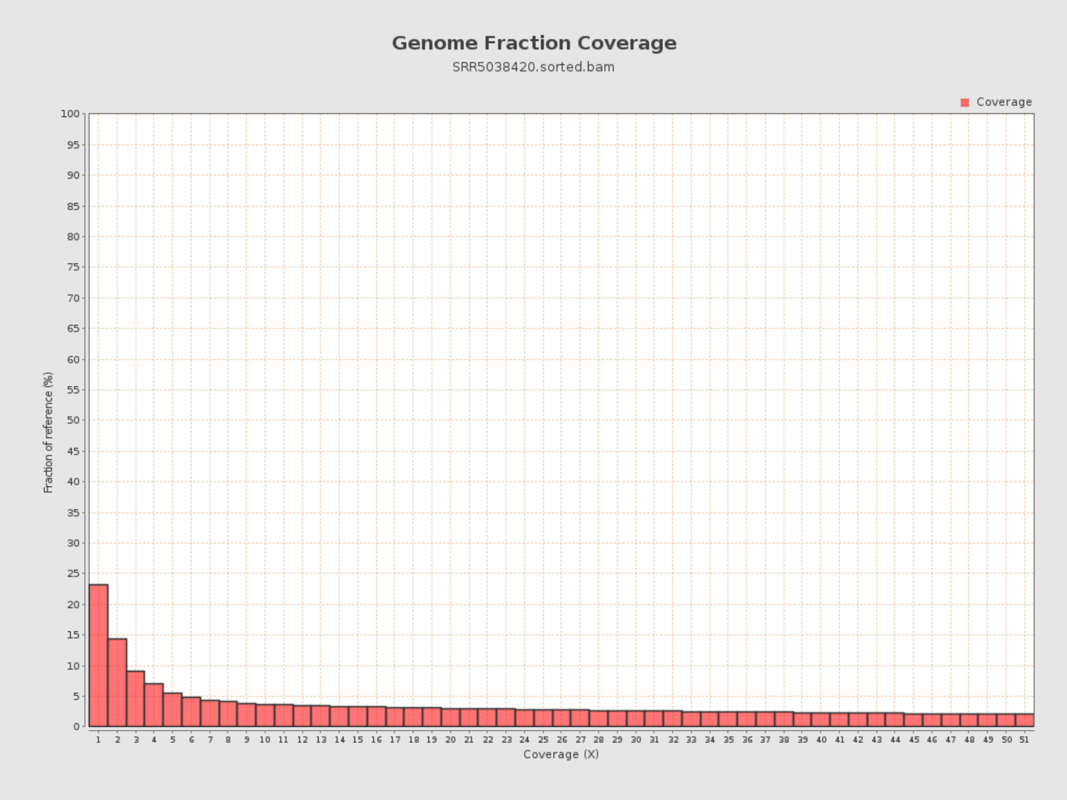
4. Results : Coverage Histogram



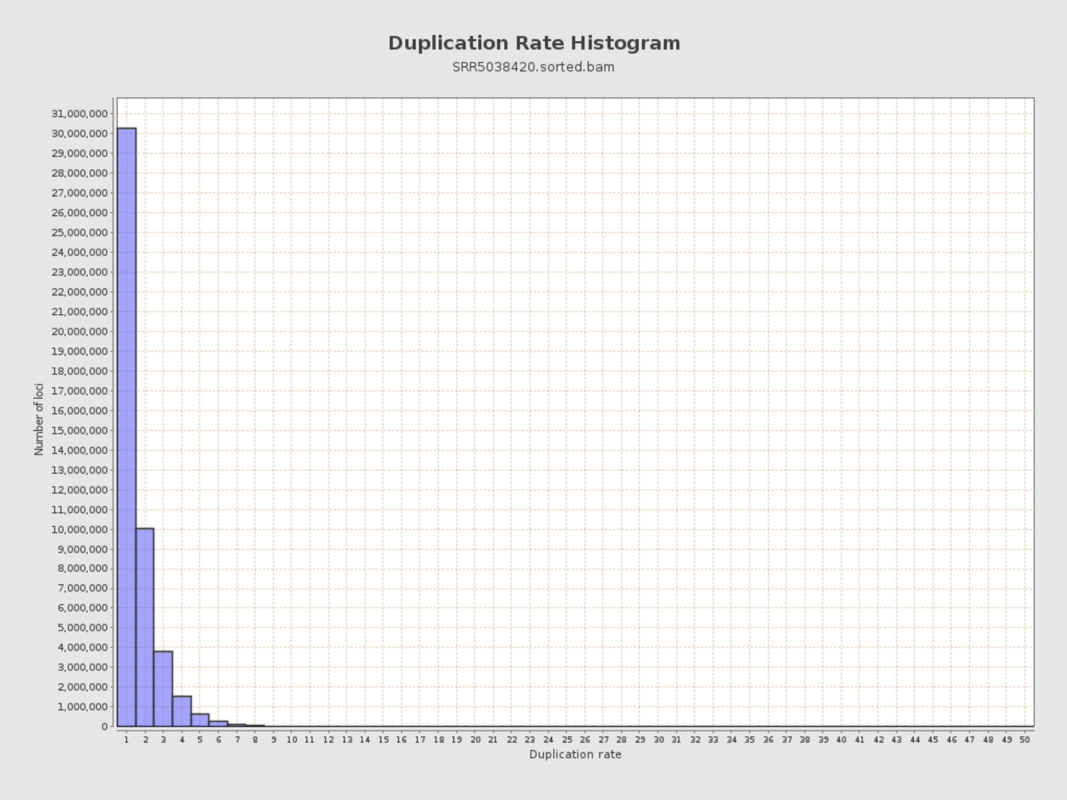
5. Results : Coverage Histogram (0-50X)



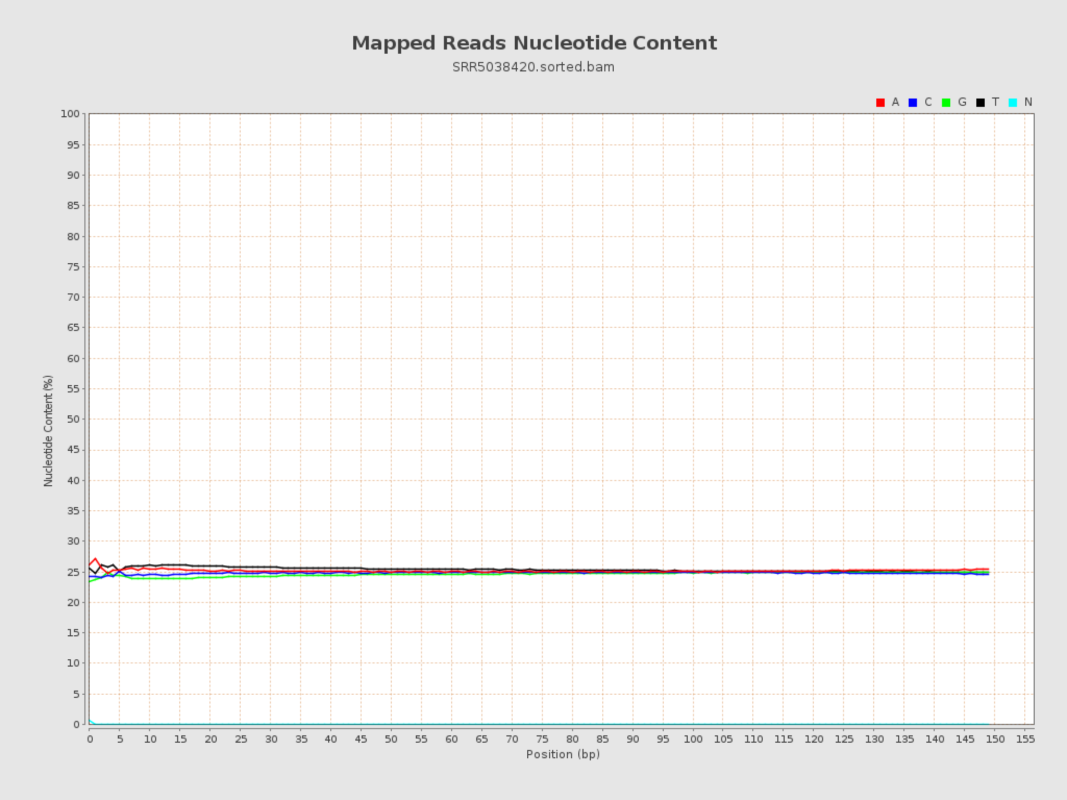
6. Results : Genome Fraction Coverage



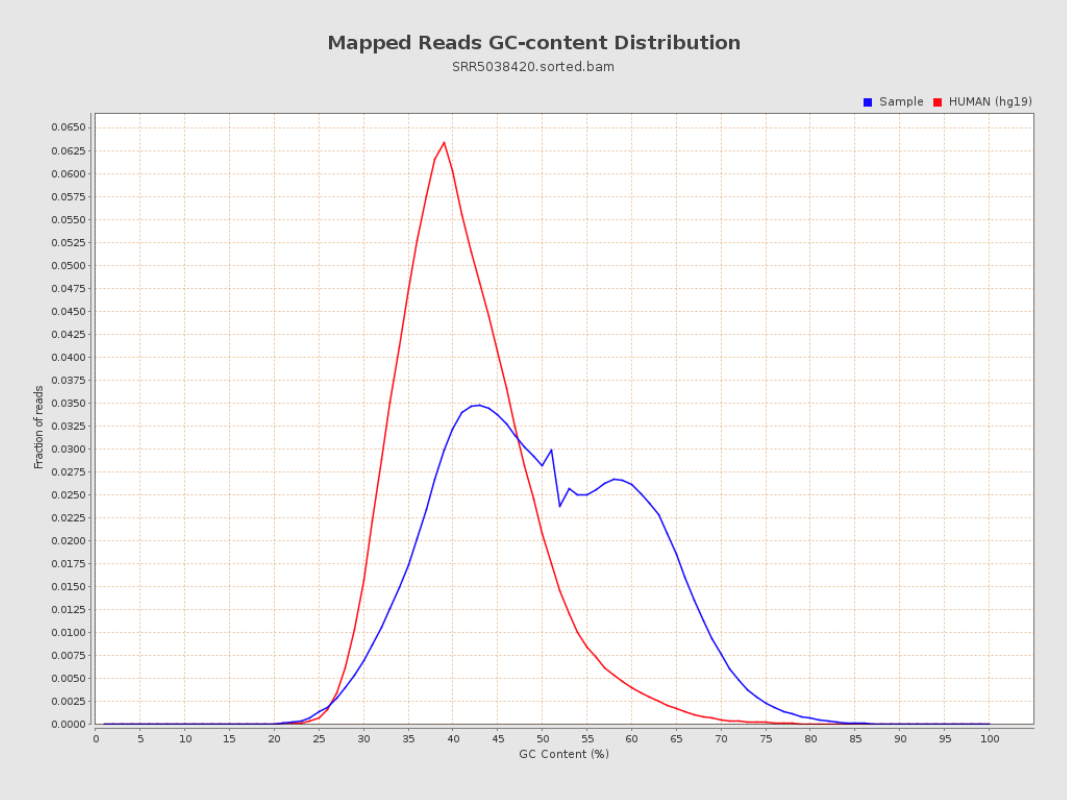
7. Results : Duplication Rate Histogram



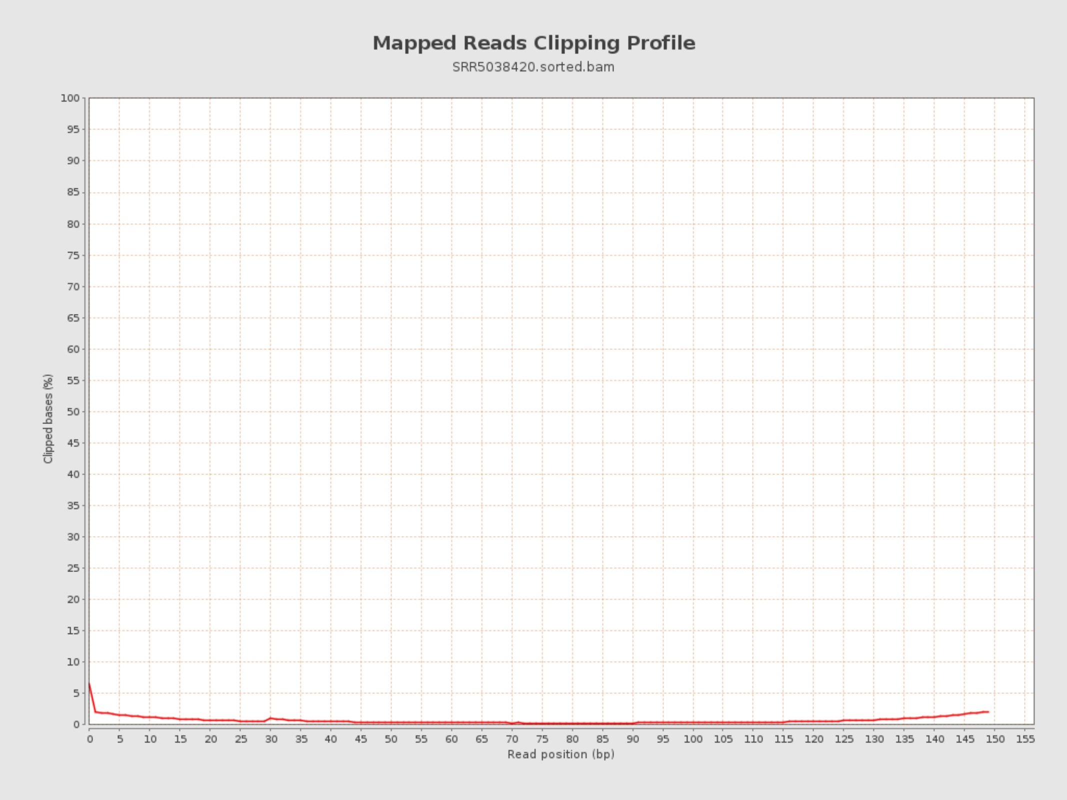
8. Results : Mapped Reads Nucleotide Content



9. Results : Mapped Reads GC-content Distribution



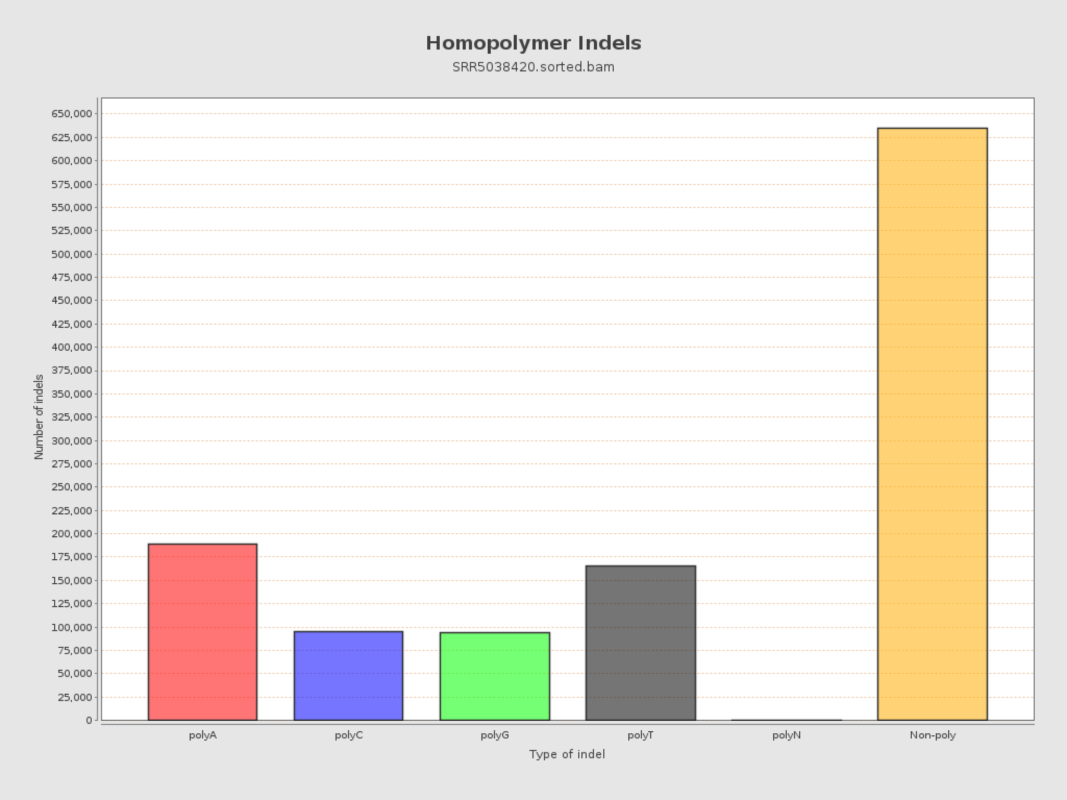
10. Results : Mapped Reads Clipping Profile



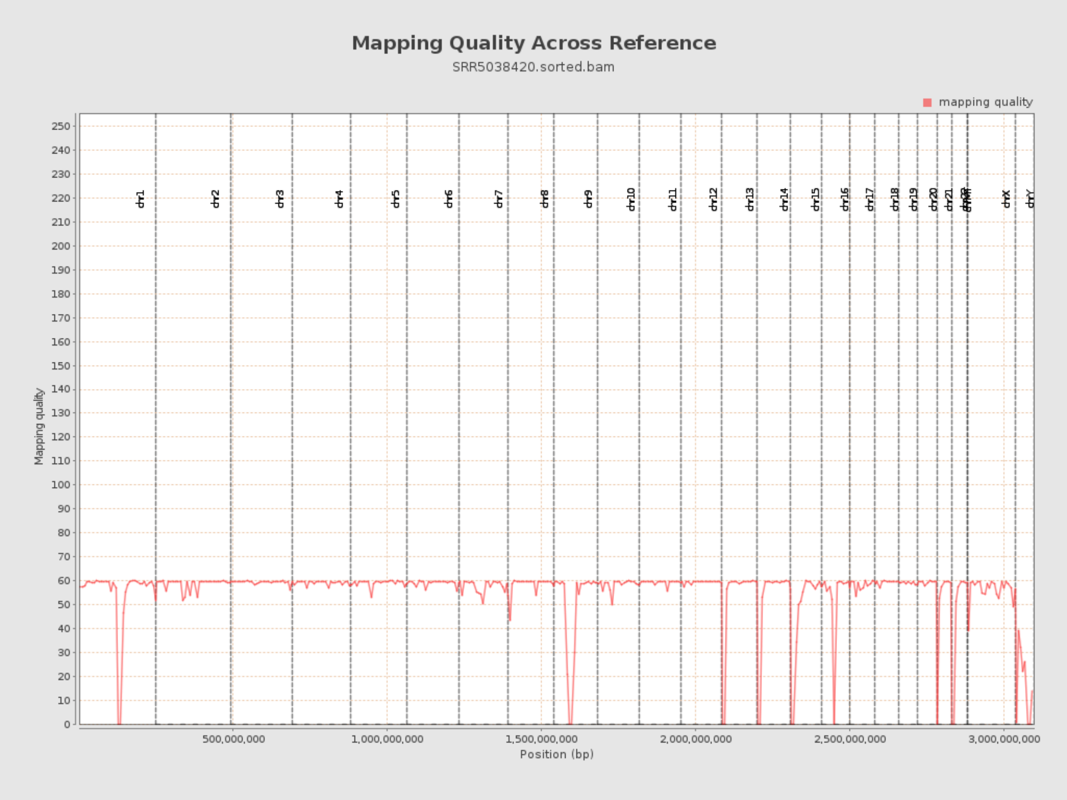
Mapped Reads Clipping Profile

SRR5038420.sorted.bam

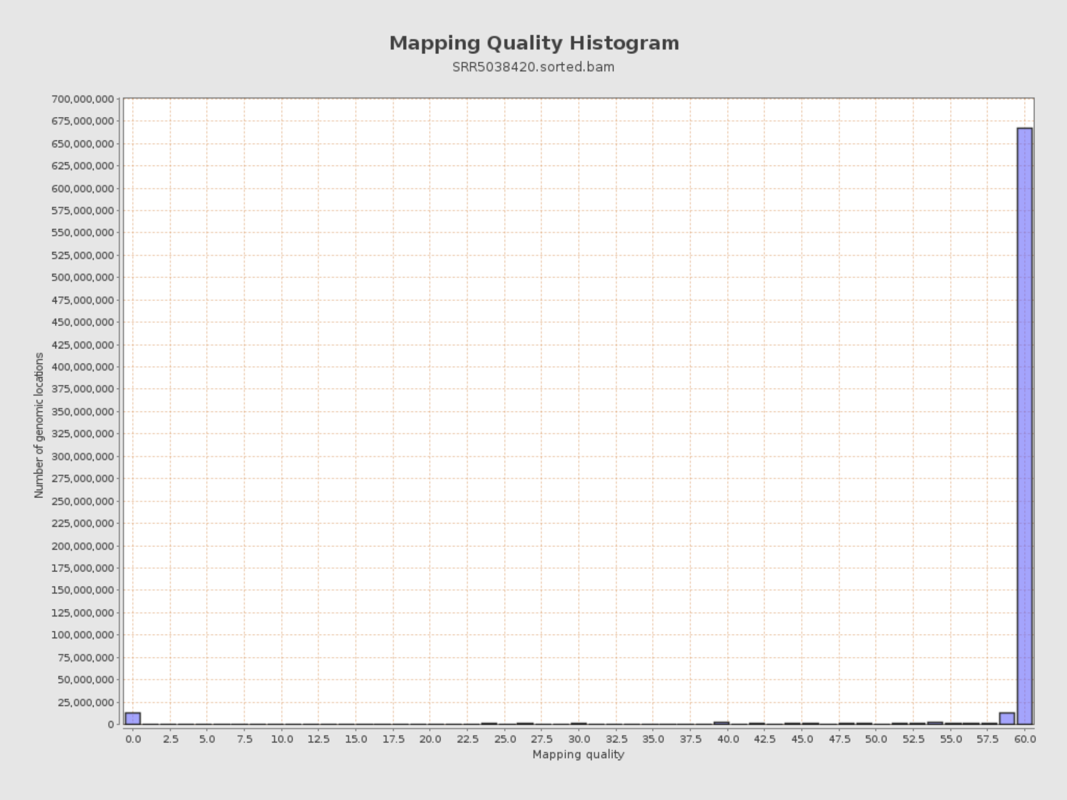
11. Results : Homopolymer Indels



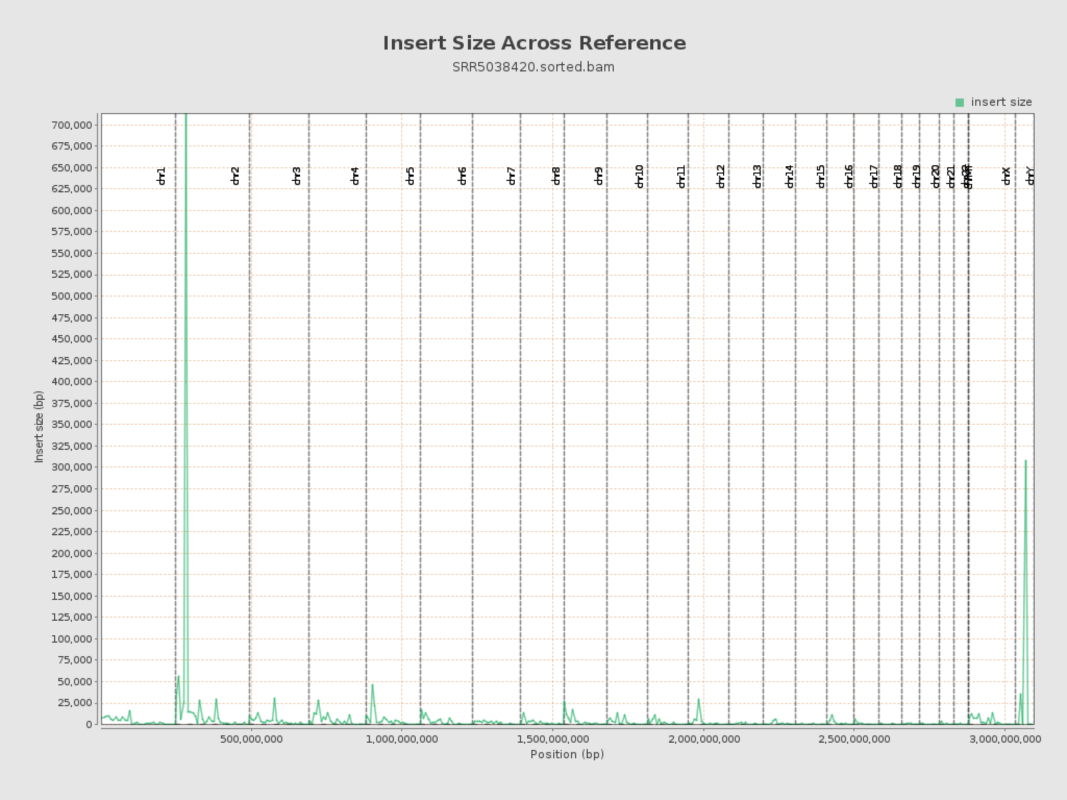
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram