Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/16 10:44:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038492.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_SRR5038492 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038492_1.fastq.gz SRR5038492_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Apr 16 10:44:43 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038492.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	72,356,550
Mapped reads	71,911,407 / 99.38%
Unmapped reads	445,143 / 0.62%
Mapped paired reads	71,911,407 / 99.38%
Mapped reads, first in pair	36,094,352 / 49.88%
Mapped reads, second in pair	35,817,055 / 49.5%
Mapped reads, both in pair	71,596,820 / 98.95%
Mapped reads, singletons	314,587 / 0.43%
Secondary alignments	0
Supplementary alignments	141,916 / 0.2%
Read min/max/mean length	30 / 150 / 150.09
Duplicated reads (estimated)	26,994,667 / 37.31%
Duplication rate	35.25%
Clipped reads	4,870,299 / 6.73%

2.2. ACGT Content

Number/percentage of A's	2,659,874,312 / 24.92%
Number/percentage of C's	2,675,749,871 / 25.07%
Number/percentage of T's	2,679,022,313 / 25.1%
Number/percentage of G's	2,658,329,442 / 24.91%
Number/percentage of N's	405,830 / 0%

GC Percentage	49.98%

2.3. Coverage

Mean	3.4484
Standard Deviation	22.0569

2.4. Mapping Quality

Mean Mapping Quality	55.84

2.5. Insert size

Mean	19,111.98
Standard Deviation	1,449,498.11
P25/Median/P75	204 / 239 / 281

2.6. Mismatches and indels

General error rate	0.58%
Mismatches	60,097,565
Insertions	547,674
Mapped reads with at least one insertion	0.73%
Deletions	655,946
Mapped reads with at least one deletion	0.89%
Homopolymer indels	46.06%

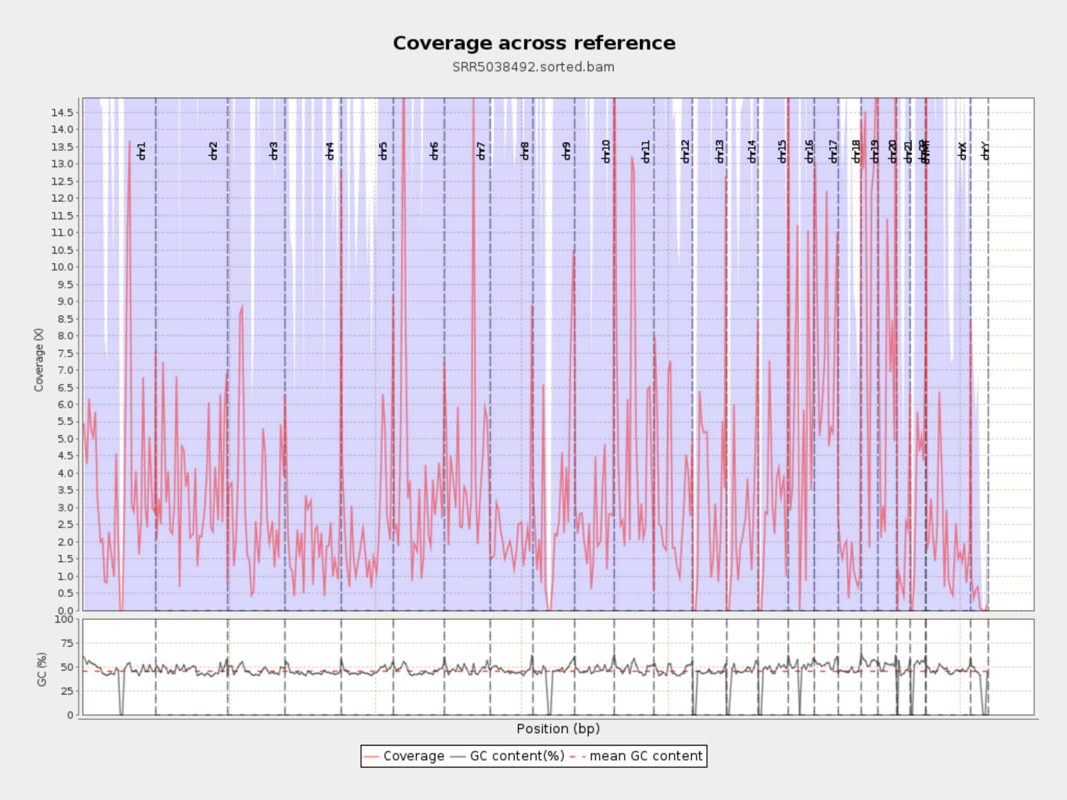
2.7. Chromosome stats

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

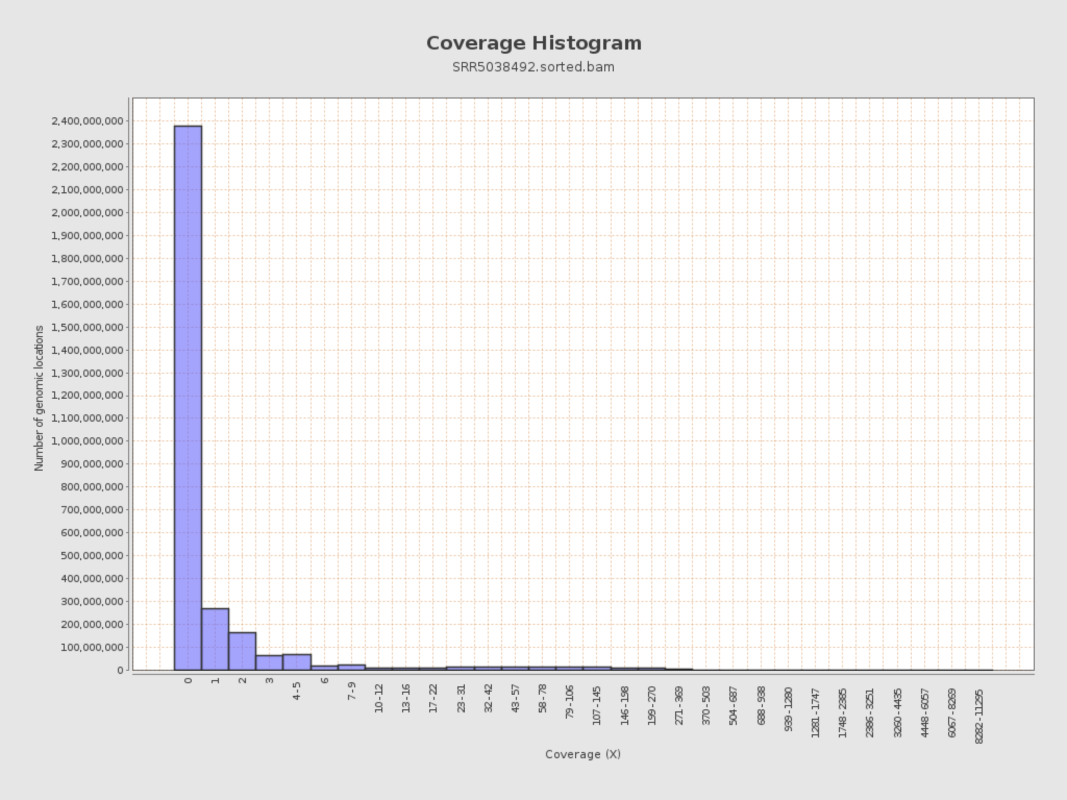
		bases	coverage	deviation
chr1	249250621	924387806	3.7087	21.7546
chr2	243199373	866161319	3.5615	23.0098
chr3	198022430	608637206	3.0736	19.6371
chr4	191154276	369049455	1.9306	14.2997
chr5	180915260	466622722	2.5792	18.5742
chr6	171115067	621793704	3.6338	23.7065
chr7	159138663	696940529	4.3795	29.1888
chr8	146364022	338106655	2.31	16.0953
chr9	141213431	421902199	2.9877	19.4315
chr10	135534747	340730803	2.514	15.3731
chr11	135006516	708869303	5.2506	29.9124
chr12	133851895	469433132	3.5071	19.3258
chr13	115169878	363671989	3.1577	25.6878
chr14	107349540	260444549	2.4261	15.3115
chr15	102531392	284691170	2.7766	16.1878
chr16	90354753	515083135	5.7007	29.463
chr17	81195210	627768817	7.7316	32.9789
chr18	78077248	110091211	1.41	10.3892
chr19	59128983	662227610	11.1997	39.2852
chr20	63025520	402868644	6.3922	35.4476
chr21	48129895	87966137	1.8277	19.6729
chr22	51304566	177615289	3.462	18.0419
chrMT	16571	1408123	84.9751	28.5211
chrX	155270560	328872445	2.1181	15.2915

chrY	59373566	19858705	0.3345	4.5187

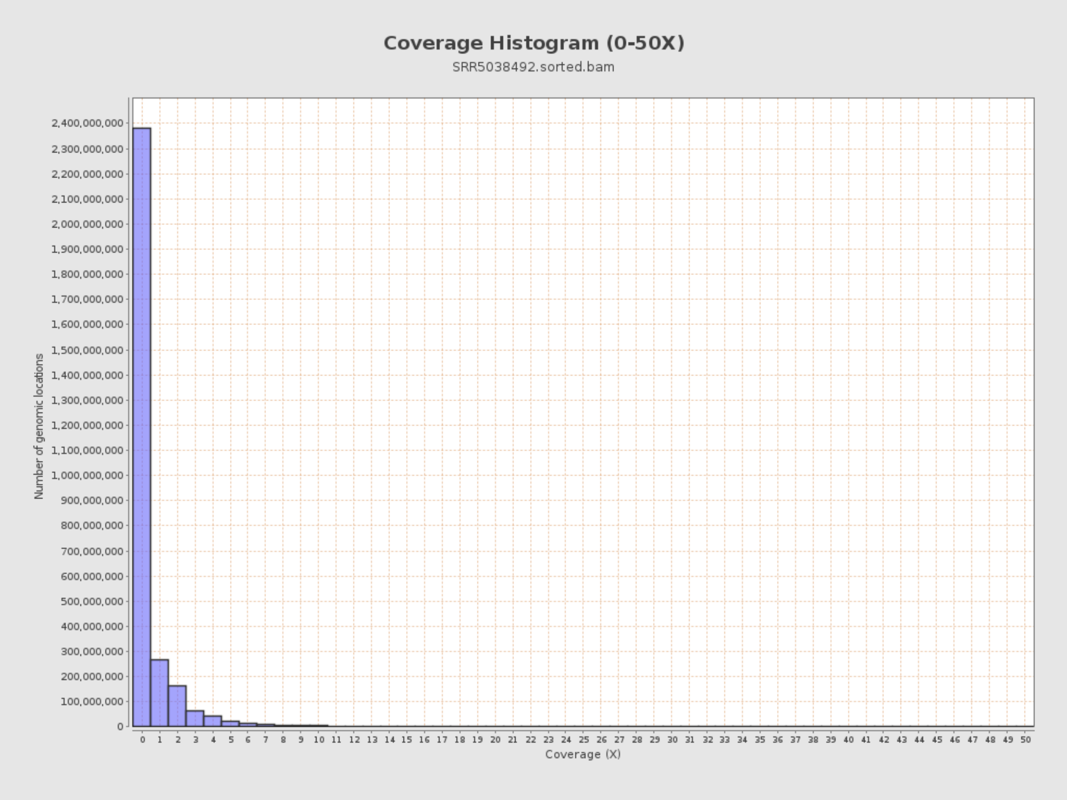
3. Results : Coverage across reference



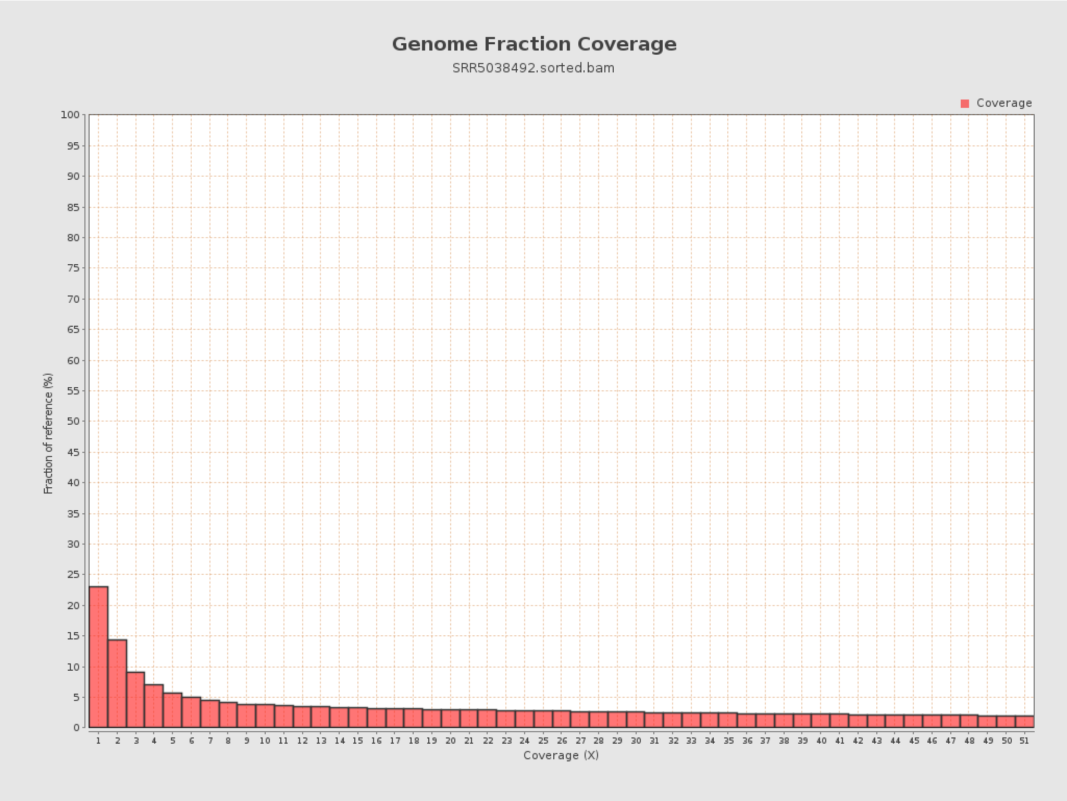
4. Results : Coverage Histogram



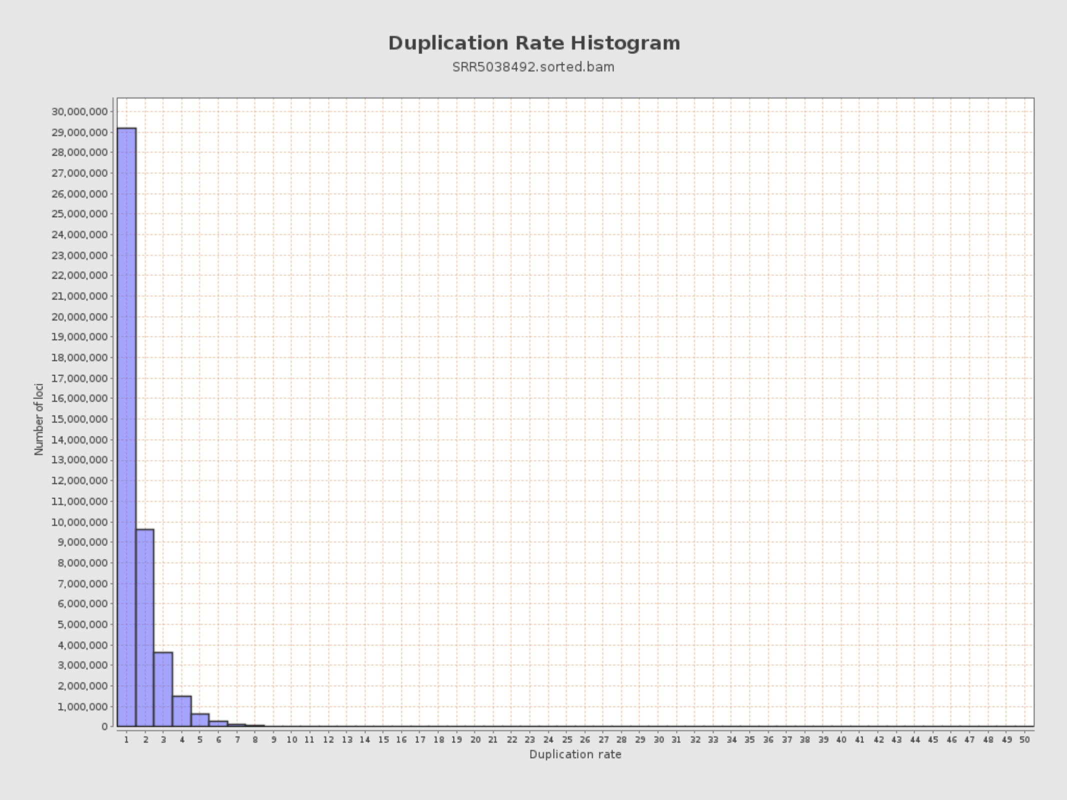
5. Results : Coverage Histogram (0-50X)



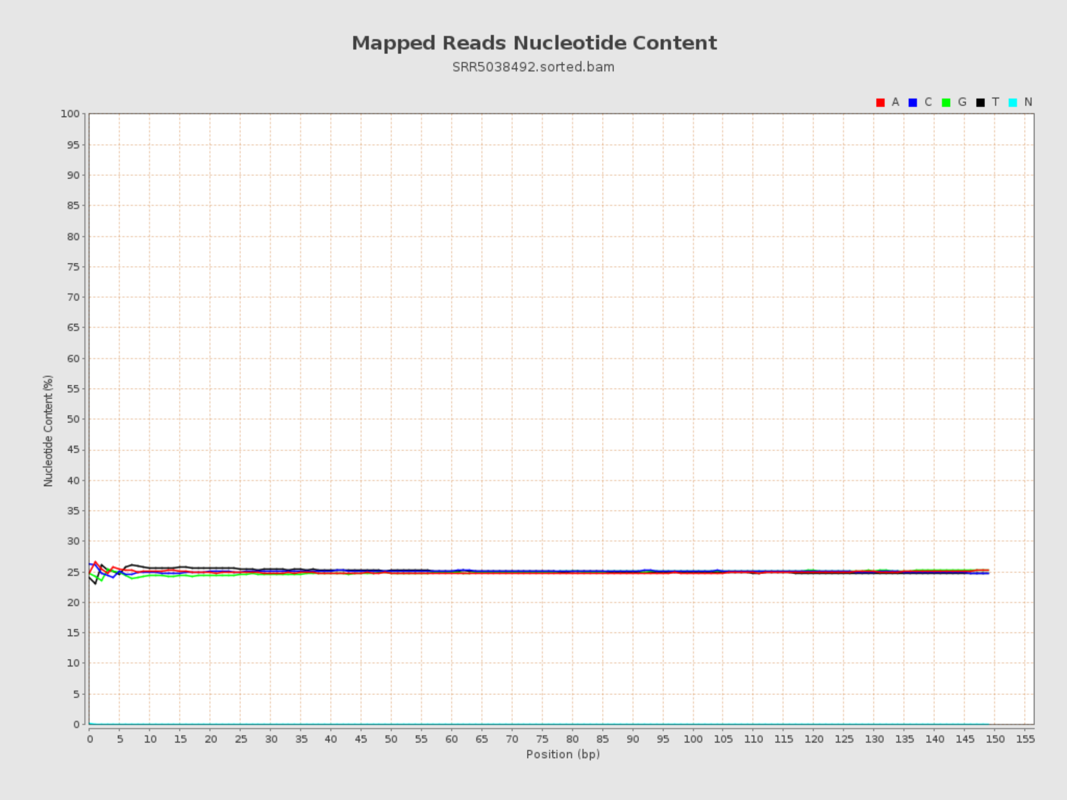
6. Results : Genome Fraction Coverage



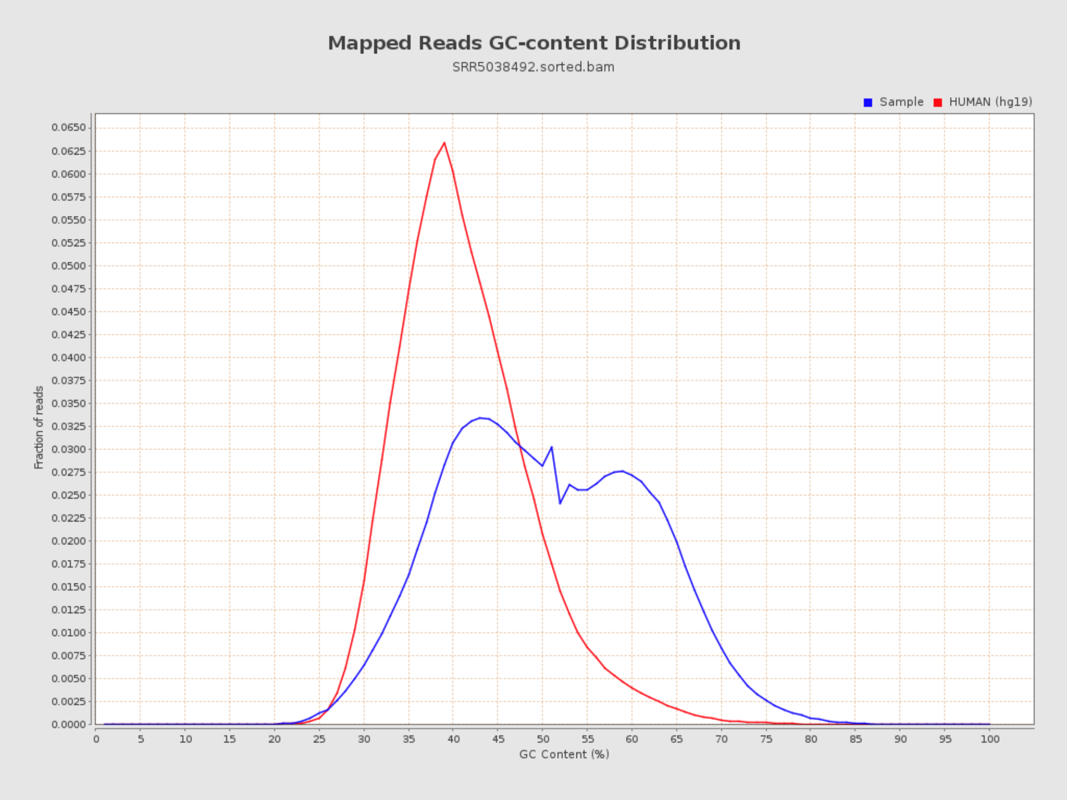
7. Results : Duplication Rate Histogram



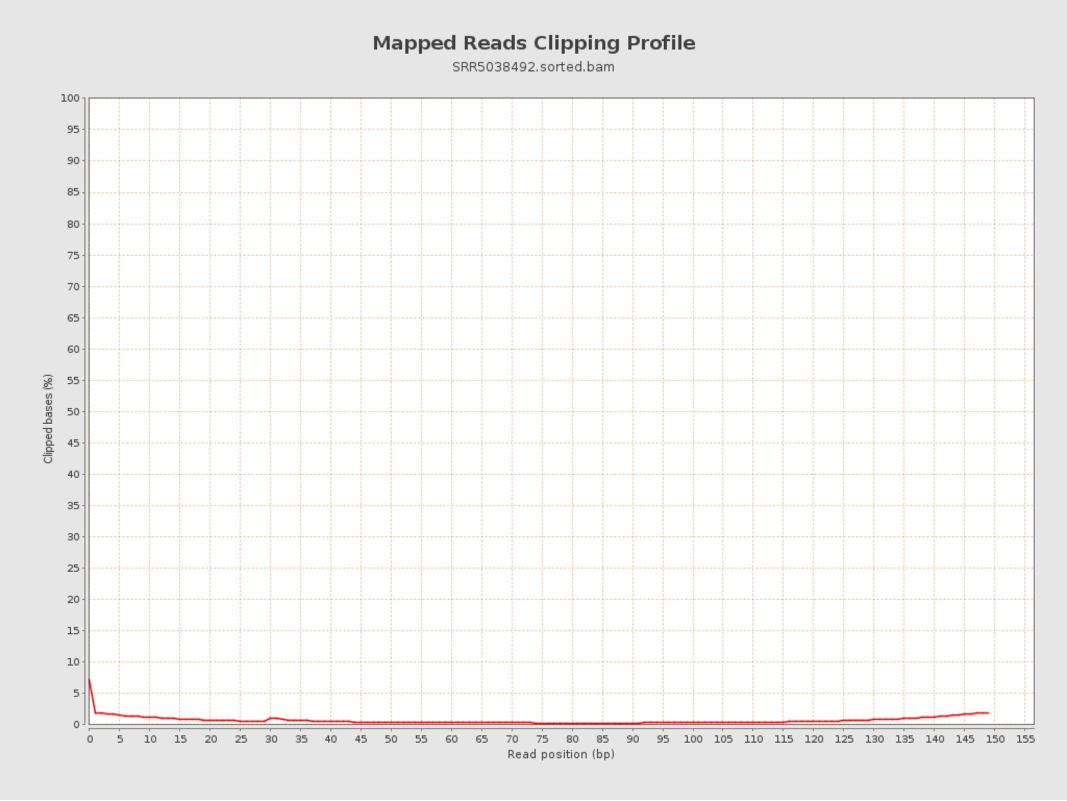
8. Results : Mapped Reads Nucleotide Content



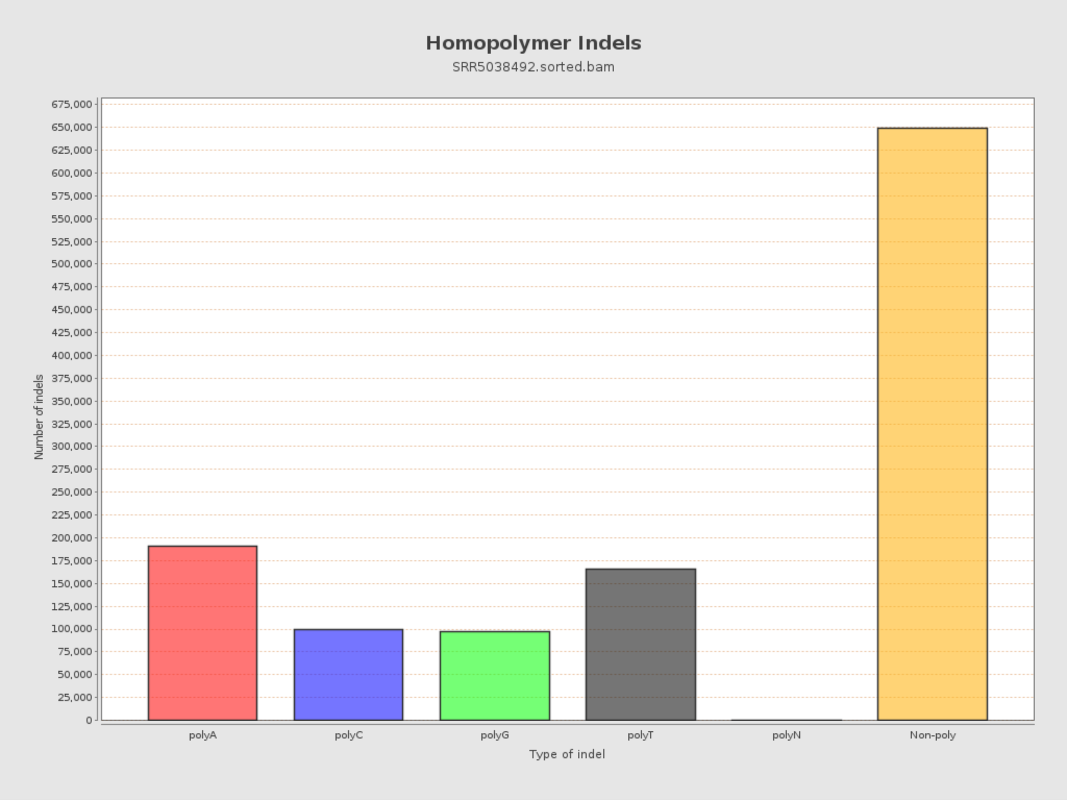
9. Results : Mapped Reads GC-content Distribution



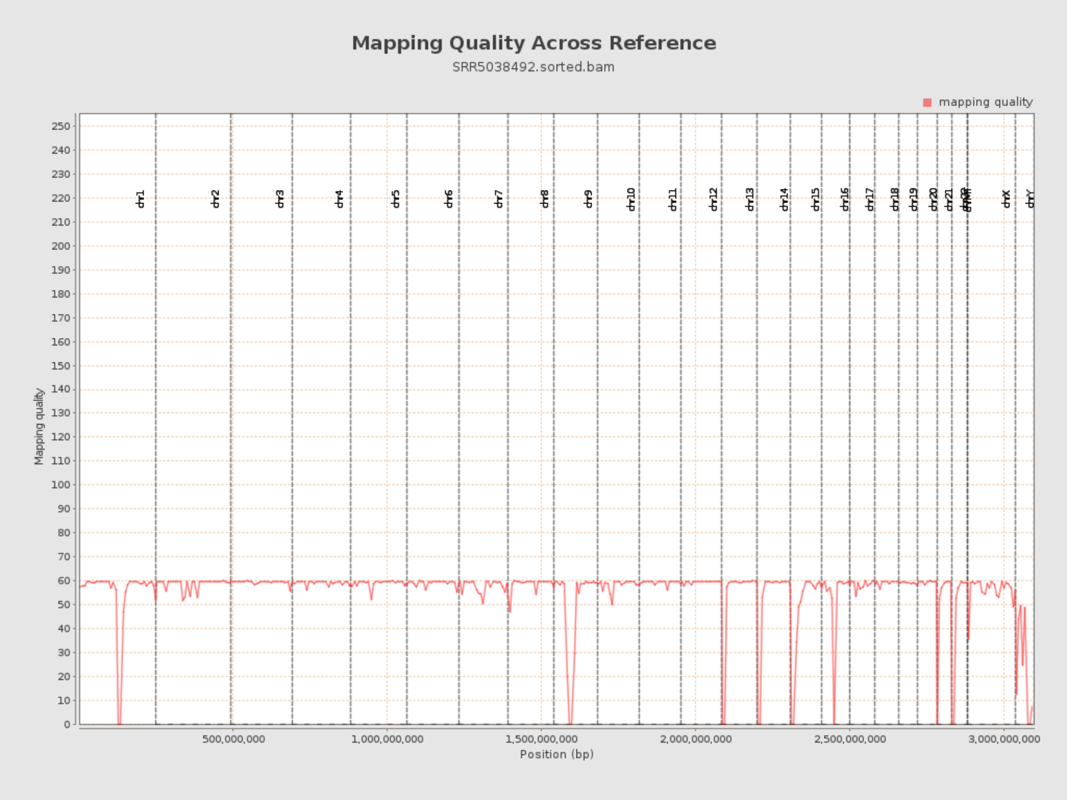
10. Results : Mapped Reads Clipping Profile



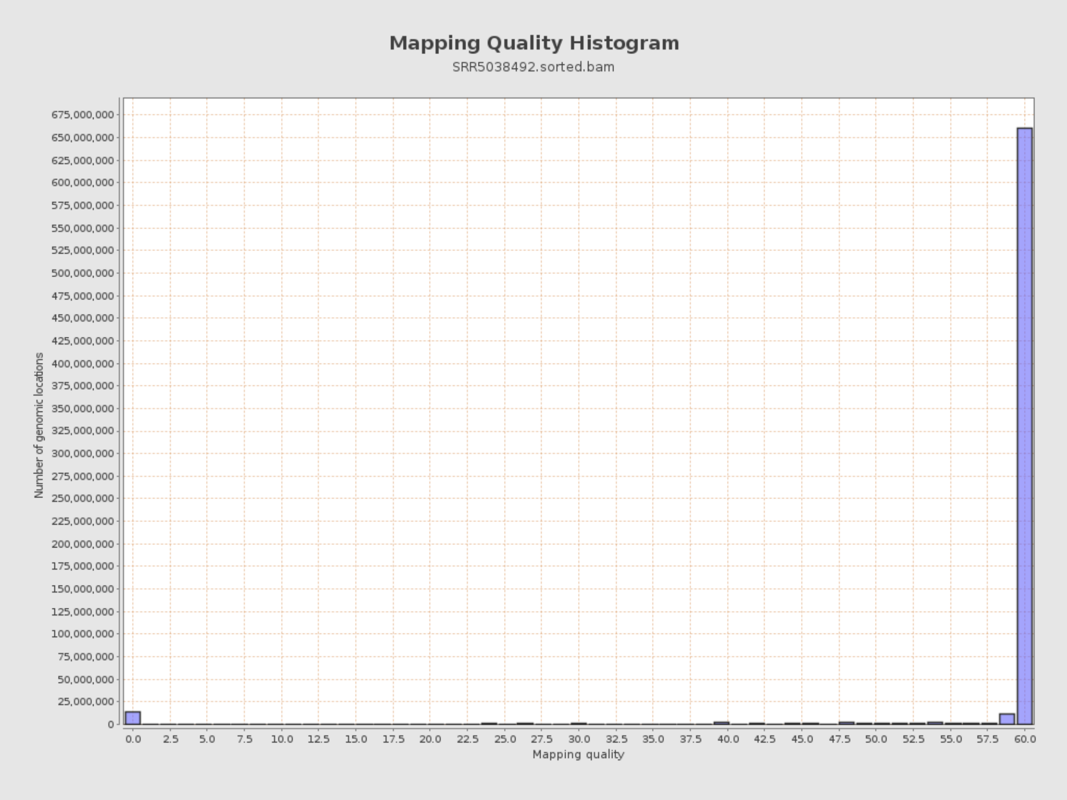
11. Results : Homopolymer Indels



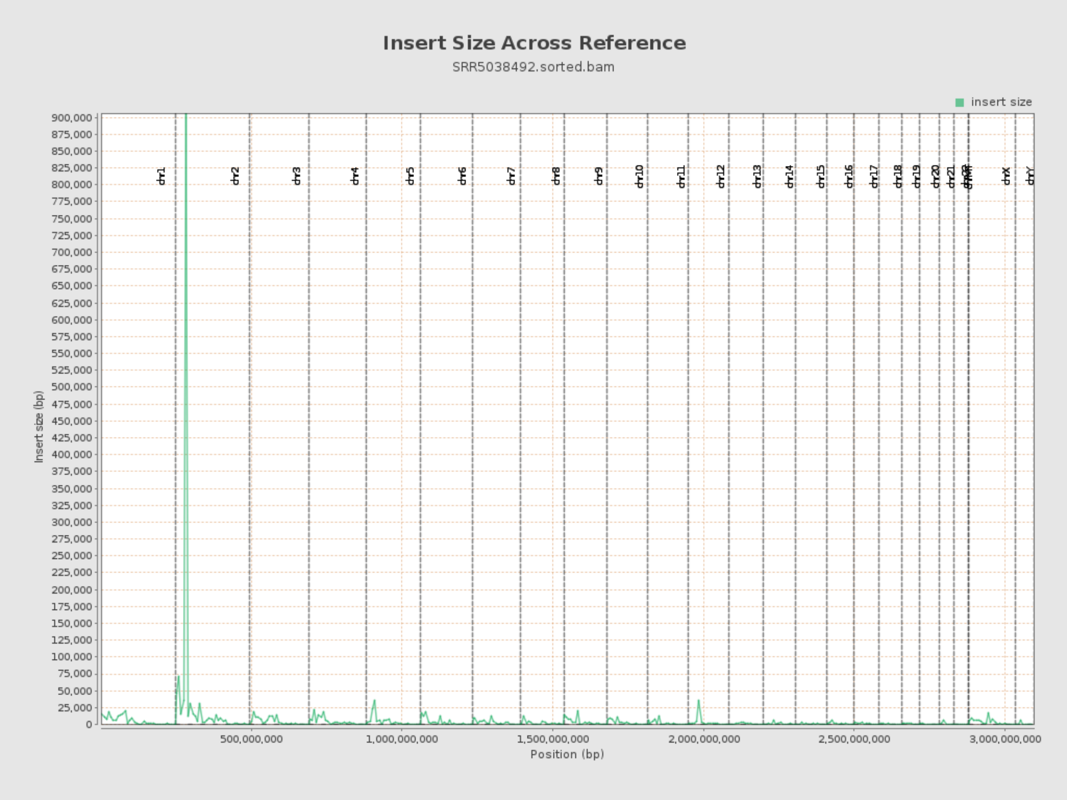
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram