Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/16 11:31:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038493.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_SRR5038493 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038493_1.fastq.gz SRR5038493_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Apr 16 11:31:27 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038493.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	12,578,636
Mapped reads	12,226,776 / 97.2%
Unmapped reads	351,860 / 2.8%
Mapped paired reads	12,226,776 / 97.2%
Mapped reads, first in pair	6,169,815 / 49.05%
Mapped reads, second in pair	6,056,961 / 48.15%
Mapped reads, both in pair	12,096,840 / 96.17%
Mapped reads, singletons	129,936 / 1.03%
Secondary alignments	0
Supplementary alignments	267,244 / 2.12%
Read min/max/mean length	30 / 150 / 151.04
Duplicated reads (estimated)	1,950,592 / 15.51%
Duplication rate	10.45%
Clipped reads	3,076,869 / 24.46%

2.2. ACGT Content

Number/percentage of A's	516,858,555 / 29.62%
Number/percentage of C's	347,245,699 / 19.9%
Number/percentage of T's	519,376,717 / 29.77%
Number/percentage of G's	361,272,970 / 20.71%
Number/percentage of N's	35,348 / 0%

GC Percentage	40.61%

2.3. Coverage

Mean	0.5641
Standard Deviation	7.9593

2.4. Mapping Quality

Mean Mapping Quality	53.59

2.5. Insert size

Mean	109,932.63
Standard Deviation	3,191,091.91
P25/Median/P75	210 / 255 / 313

2.6. Mismatches and indels

General error rate	1.46%
Mismatches	24,316,222
Insertions	409,030
Mapped reads with at least one insertion	3.04%
Deletions	756,913
Mapped reads with at least one deletion	5.85%
Homopolymer indels	45.34%

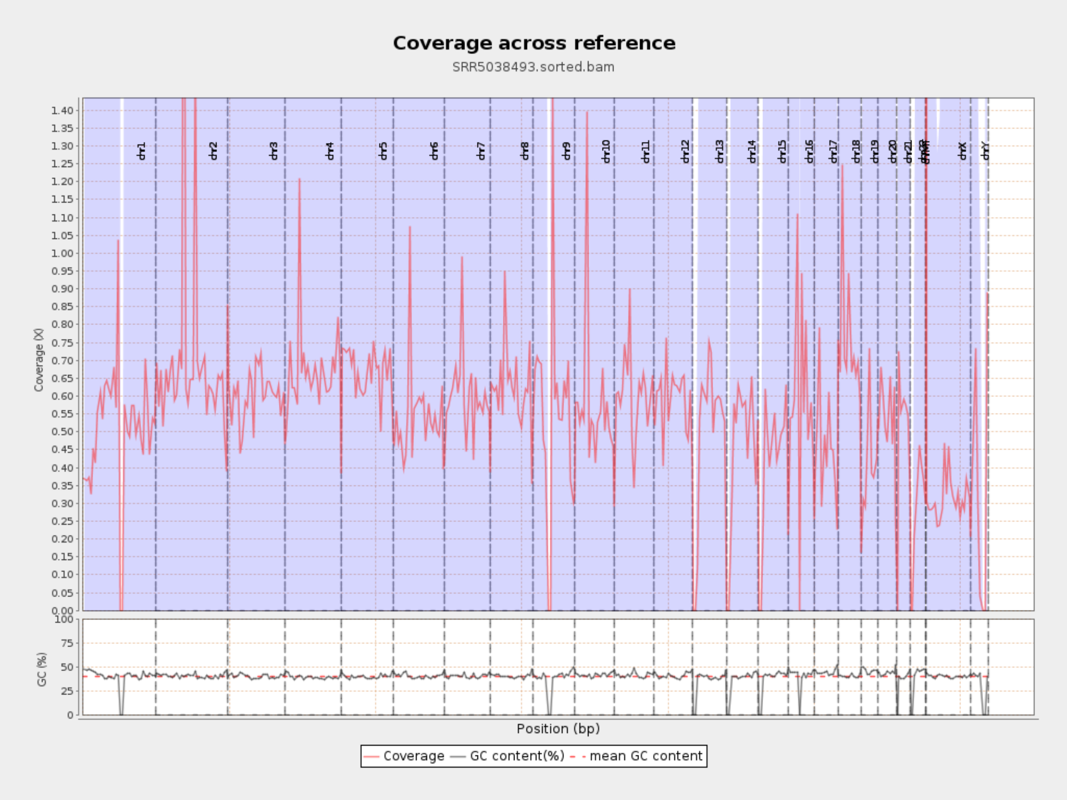
2.7. Chromosome stats

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

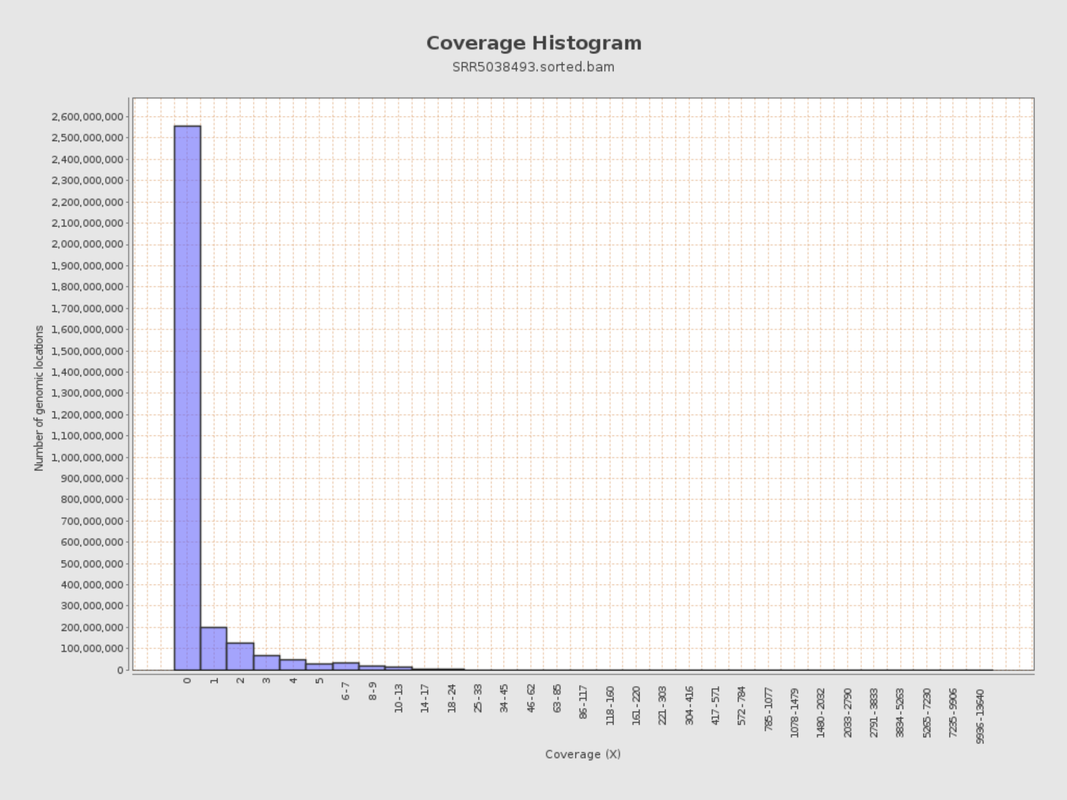
		bases	coverage	deviation
chr1	249250621	126739263	0.5085	7.9778
chr2	243199373	173926464	0.7152	14.9826
chr3	198022430	119916407	0.6056	1.8587
chr4	191154276	129142638	0.6756	4.9763
chr5	180915260	120918336	0.6684	2.3112
chr6	171115067	93618347	0.5471	6.1466
chr7	159138663	95481270	0.6	6.9041
chr8	146364022	91549187	0.6255	2.8131
chr9	141213431	78645802	0.5569	16.8949
chr10	135534747	78452871	0.5788	11.0614
chr11	135006516	81044874	0.6003	4.9259
chr12	133851895	79208346	0.5918	1.9432
chr13	115169878	57211415	0.4968	1.6469
chr14	107349540	49196744	0.4583	2.1795
chr15	102531392	42724584	0.4167	1.4934
chr16	90354753	52053508	0.5761	9.0687
chr17	81195210	37899985	0.4668	5.5516
chr18	78077248	59465637	0.7616	14.0939
chr19	59128983	24697350	0.4177	4.6721
chr20	63025520	34829405	0.5526	2.3032
chr21	48129895	24759083	0.5144	2.9231
chr22	51304566	14557966	0.2838	2.1494
chrMT	16571	10770015	649.9315	384.0894
chrX	155270560	48673276	0.3135	1.9118

chrY	59373566	20879717	0.3517	8.7967

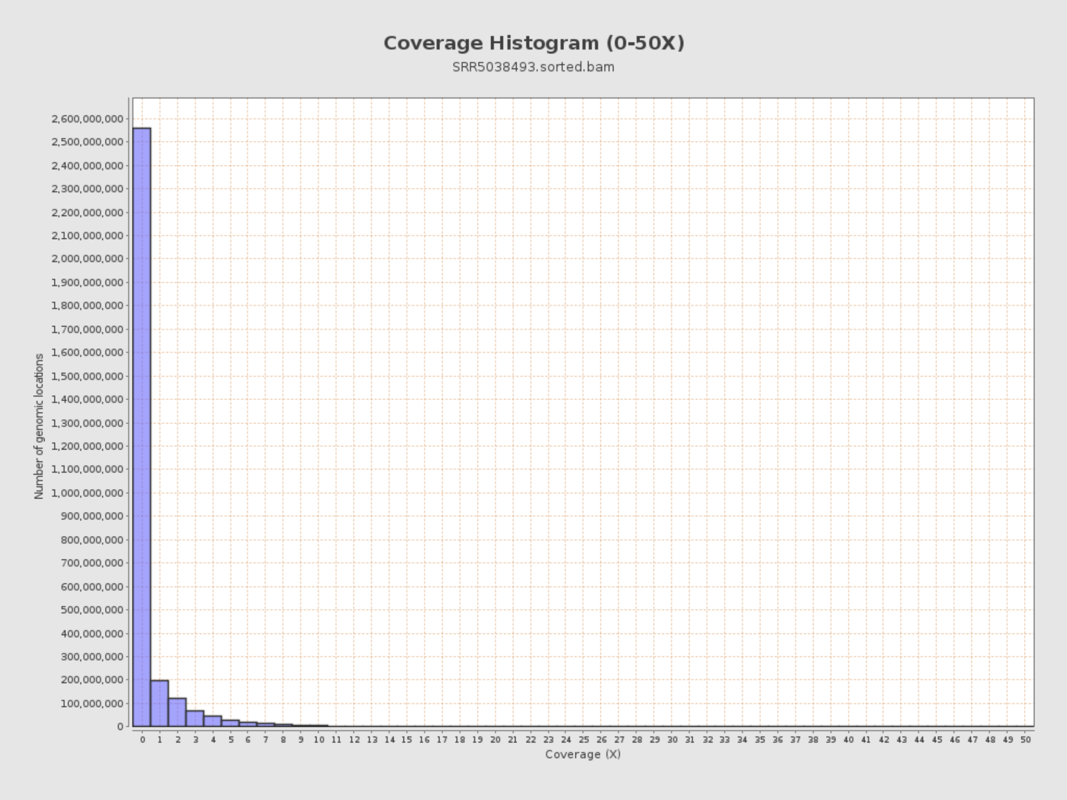
3. Results : Coverage across reference



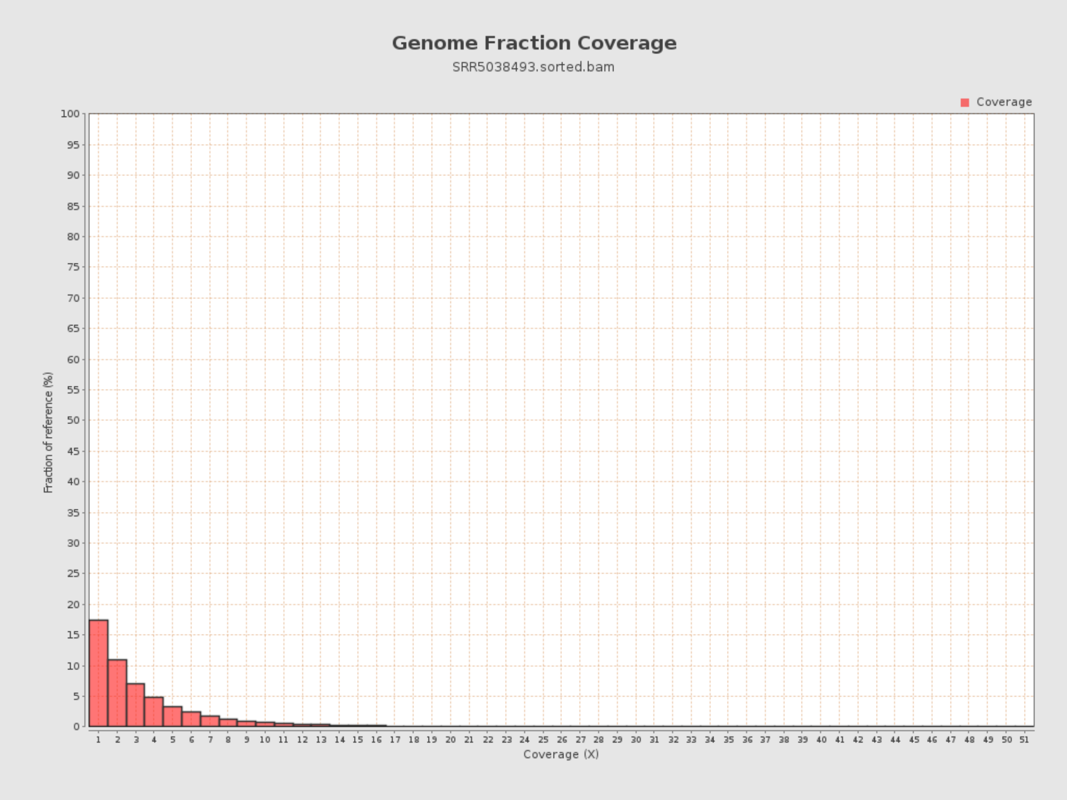
4. Results : Coverage Histogram



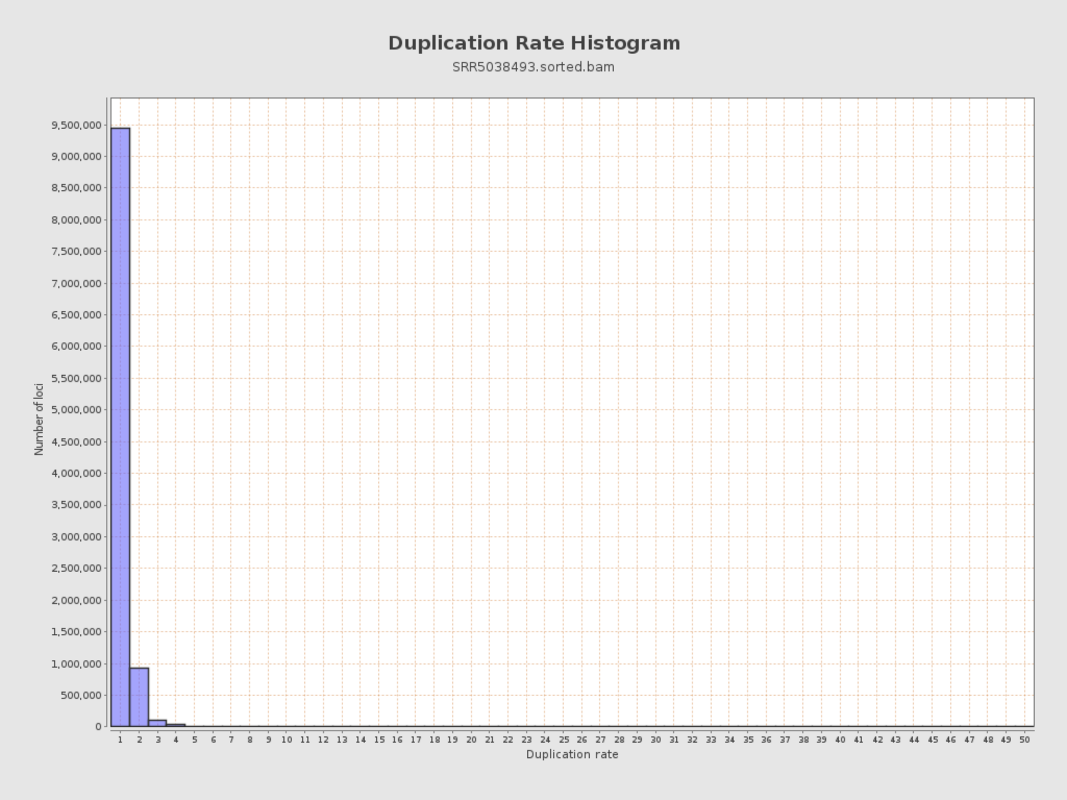
5. Results : Coverage Histogram (0-50X)



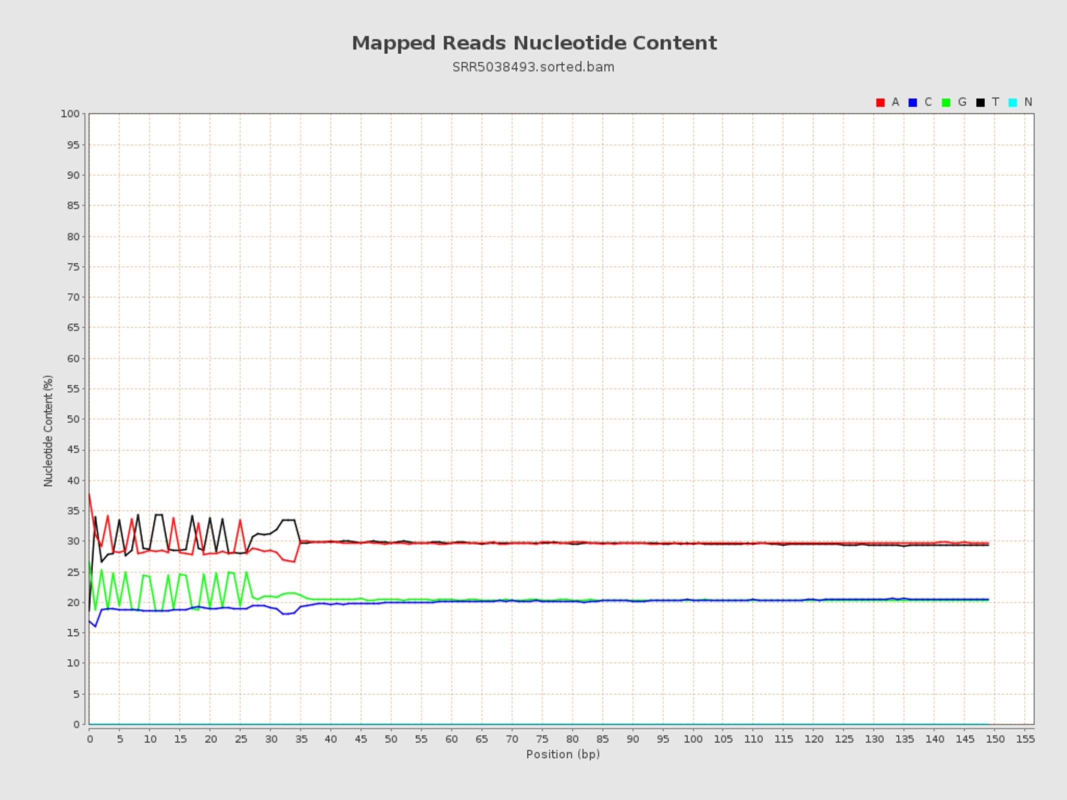
6. Results : Genome Fraction Coverage



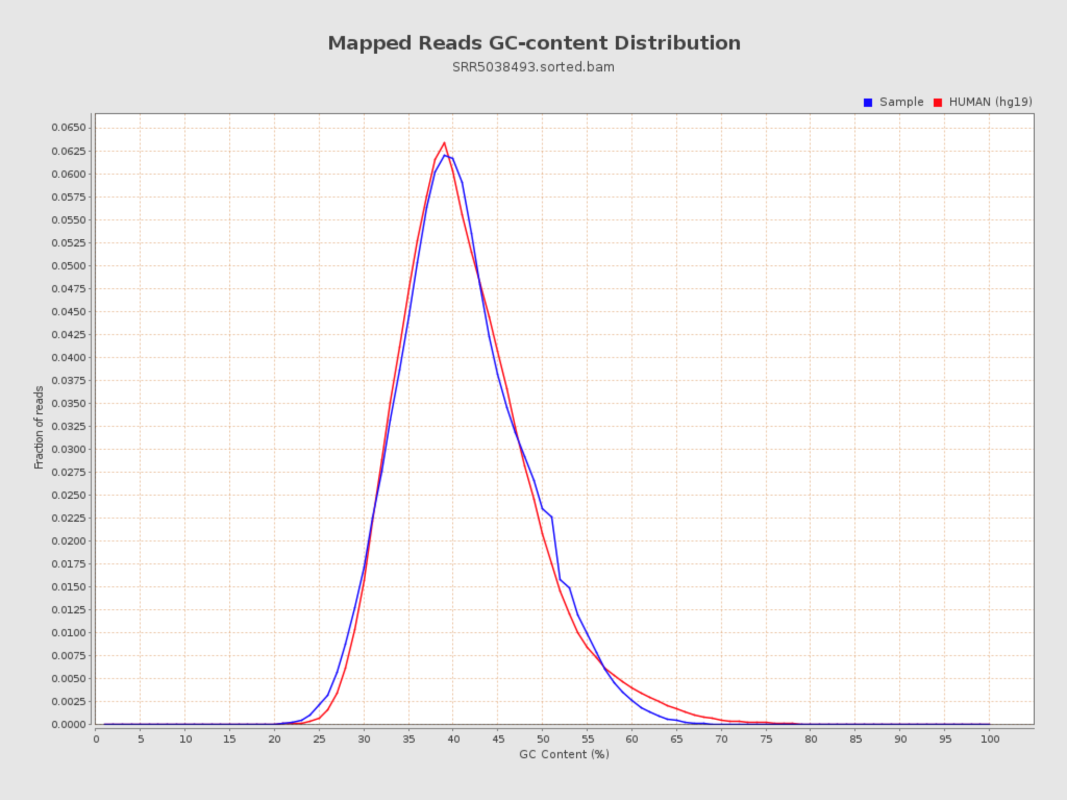
7. Results : Duplication Rate Histogram



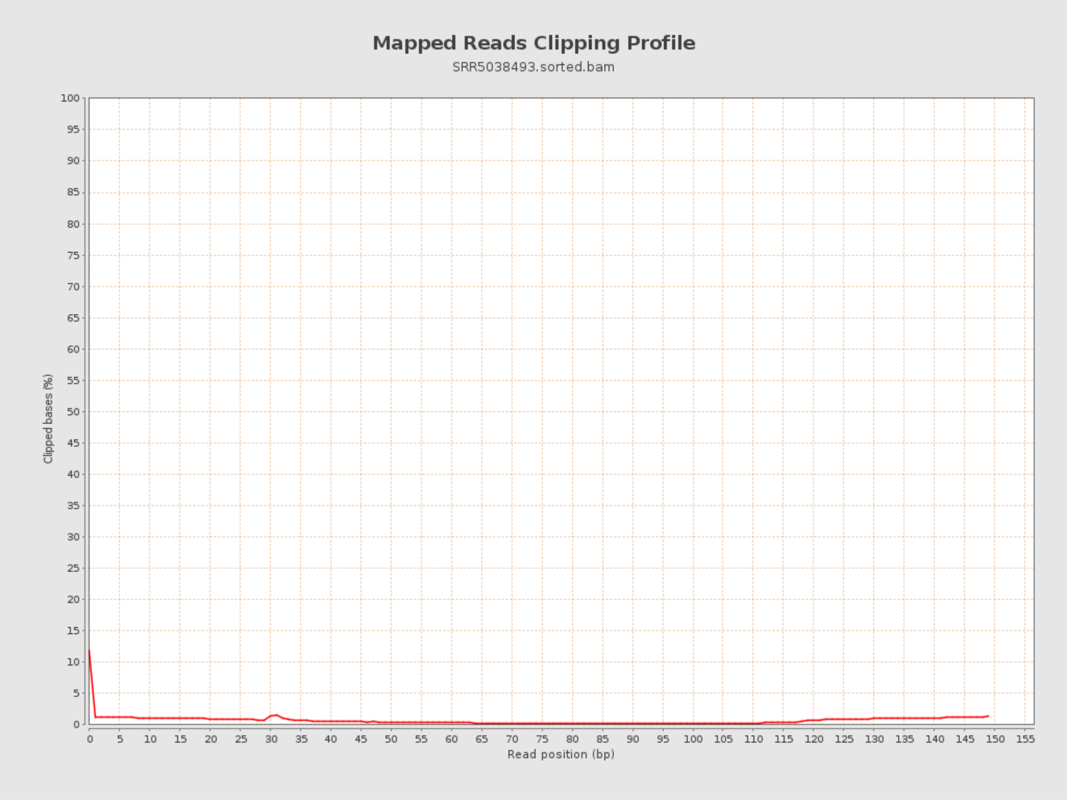
8. Results : Mapped Reads Nucleotide Content



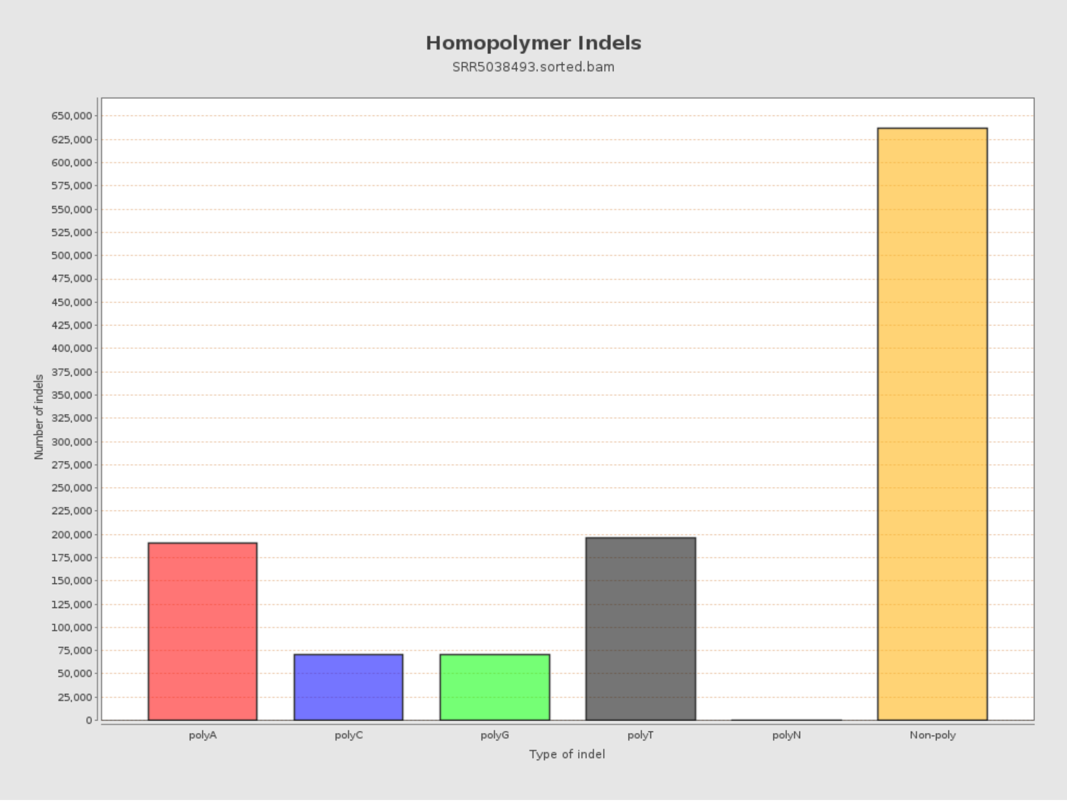
9. Results : Mapped Reads GC-content Distribution



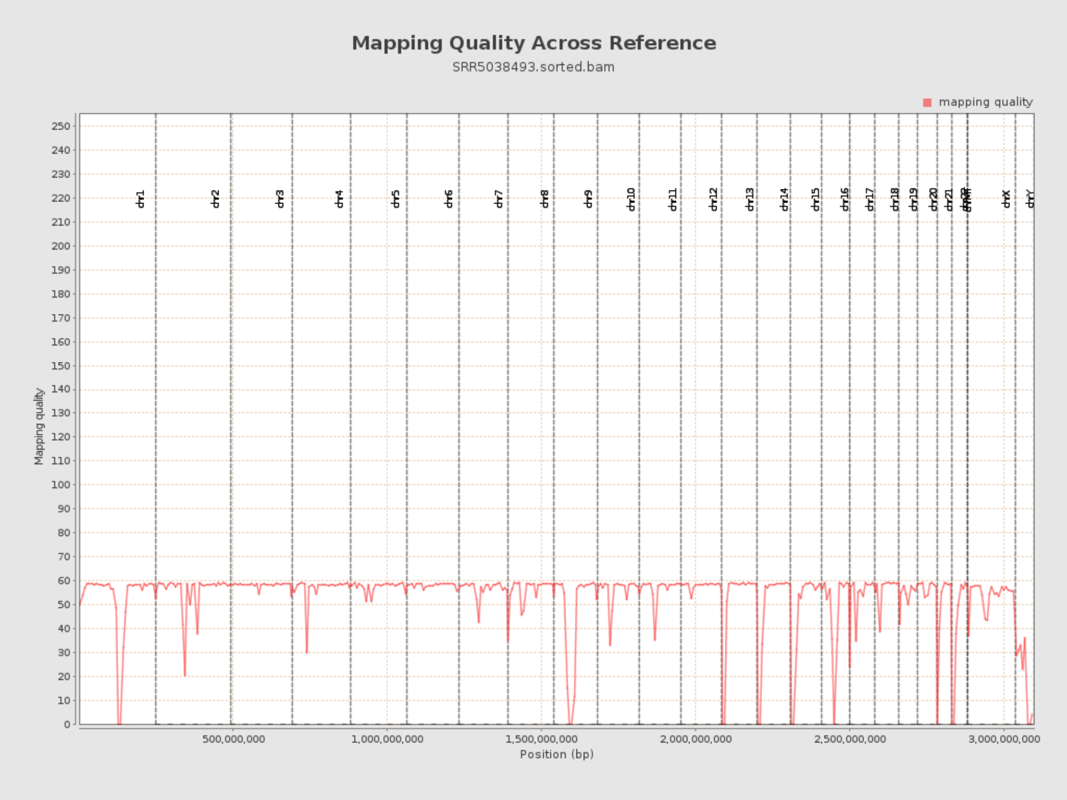
10. Results : Mapped Reads Clipping Profile



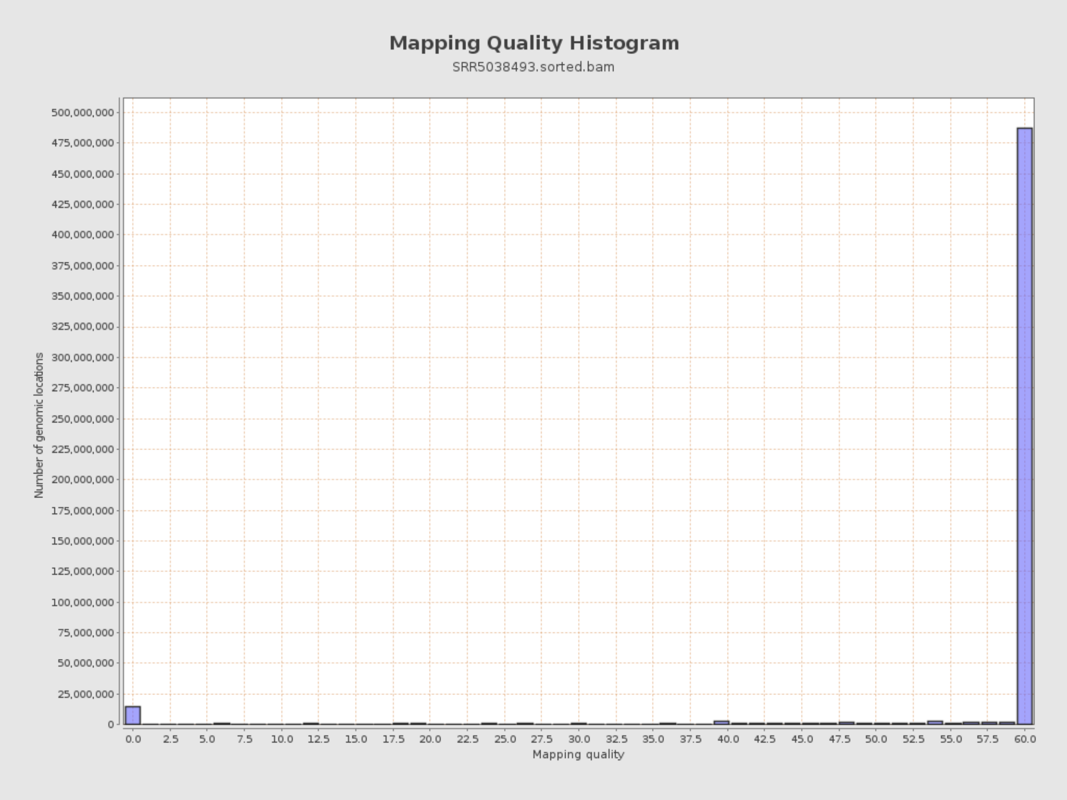
11. Results : Homopolymer Indels



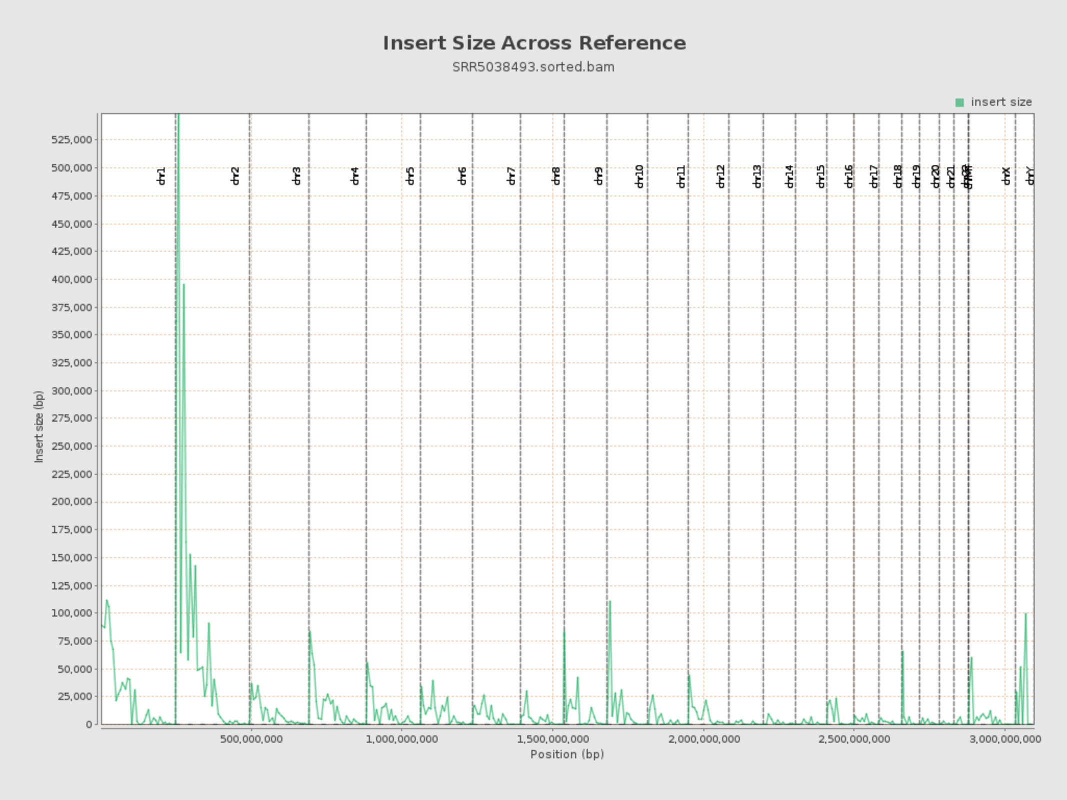
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram