Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/14 13:32:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038397.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_SRR5038397 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038397_1.fastq.gz SRR5038397_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Apr 14 13:32:54 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038397.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	17,527,258
Mapped reads	16,248,191 / 92.7%
Unmapped reads	1,279,067 / 7.3%
Mapped paired reads	16,248,191 / 92.7%
Mapped reads, first in pair	8,235,721 / 46.99%
Mapped reads, second in pair	8,012,470 / 45.71%
Mapped reads, both in pair	15,963,576 / 91.08%
Mapped reads, singletons	284,615 / 1.62%
Secondary alignments	0
Supplementary alignments	288,182 / 1.64%
Read min/max/mean length	30 / 150 / 150.82
Duplicated reads (estimated)	3,324,820 / 18.97%
Duplication rate	13.76%
Clipped reads	7,802,257 / 44.51%

2.2. ACGT Content

Number/percentage of A's	626,425,951 / 28.73%
Number/percentage of C's	430,769,705 / 19.76%
Number/percentage of T's	635,746,722 / 29.16%
Number/percentage of G's	487,320,841 / 22.35%
Number/percentage of N's	175,294 / 0.01%

GC Percentage	42.11%

2.3. Coverage

Mean	0.7049
Standard Deviation	10.5247

2.4. Mapping Quality

Mean Mapping Quality	53.51

2.5. Insert size

Mean	86,931.82
Standard Deviation	2,825,482.23
P25/Median/P75	199 / 252 / 321

2.6. Mismatches and indels

General error rate	1.38%
Mismatches	28,842,328
Insertions	430,128
Mapped reads with at least one insertion	2.49%
Deletions	809,377
Mapped reads with at least one deletion	4.79%
Homopolymer indels	46.72%

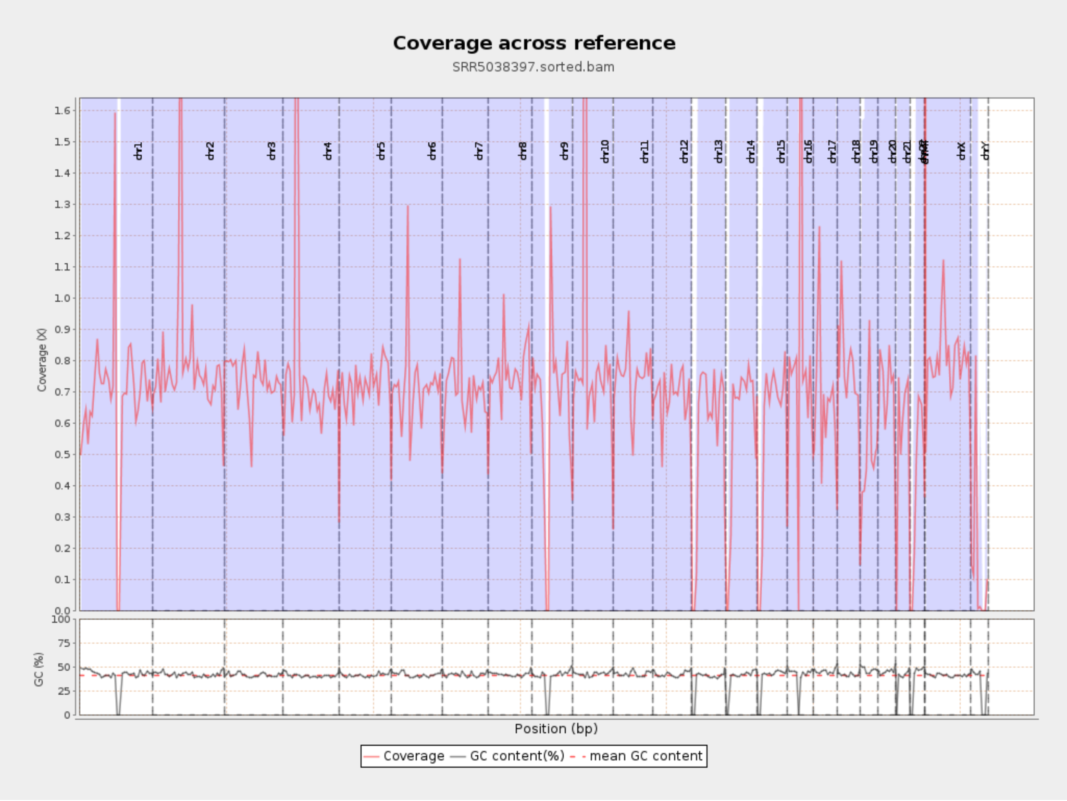
2.7. Chromosome stats

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

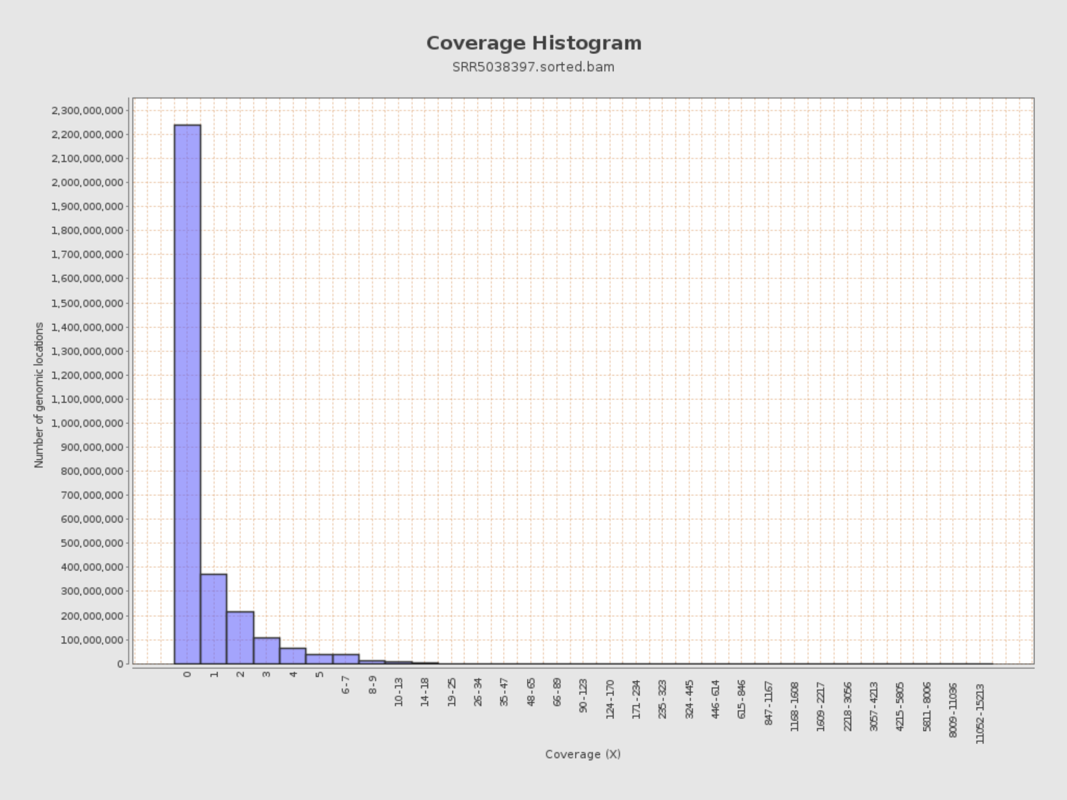
		bases	coverage	deviation
chr1	249250621	171007293	0.6861	15.1632
chr2	243199373	196485324	0.8079	10.3321
chr3	198022430	145980567	0.7372	1.691
chr4	191154276	148454325	0.7766	13.8933
chr5	180915260	130346056	0.7205	1.5685
chr6	171115067	123688953	0.7228	6.2859
chr7	159138663	112697097	0.7082	8.265
chr8	146364022	111003598	0.7584	3.1827
chr9	141213431	90249412	0.6391	15.2126
chr10	135534747	125377597	0.9251	28.0568
chr11	135006516	99800976	0.7392	6.7314
chr12	133851895	91876216	0.6864	1.6475
chr13	115169878	65560092	0.5692	1.3642
chr14	107349540	62127297	0.5787	1.5279
chr15	102531392	58961364	0.5751	1.3889
chr16	90354753	74208133	0.8213	13.4147
chr17	81195210	53722746	0.6616	9.8875
chr18	78077248	60985700	0.7811	11.7754
chr19	59128983	29306972	0.4956	7.3082
chr20	63025520	44638426	0.7083	4.3621
chr21	48129895	27625148	0.574	6.1523
chr22	51304566	20339353	0.3964	1.2264
chrMT	16571	4478079	270.2359	151.6123
chrX	155270560	124341844	0.8008	3.1765

chrY	59373566	8841449	0.1489	13.9923

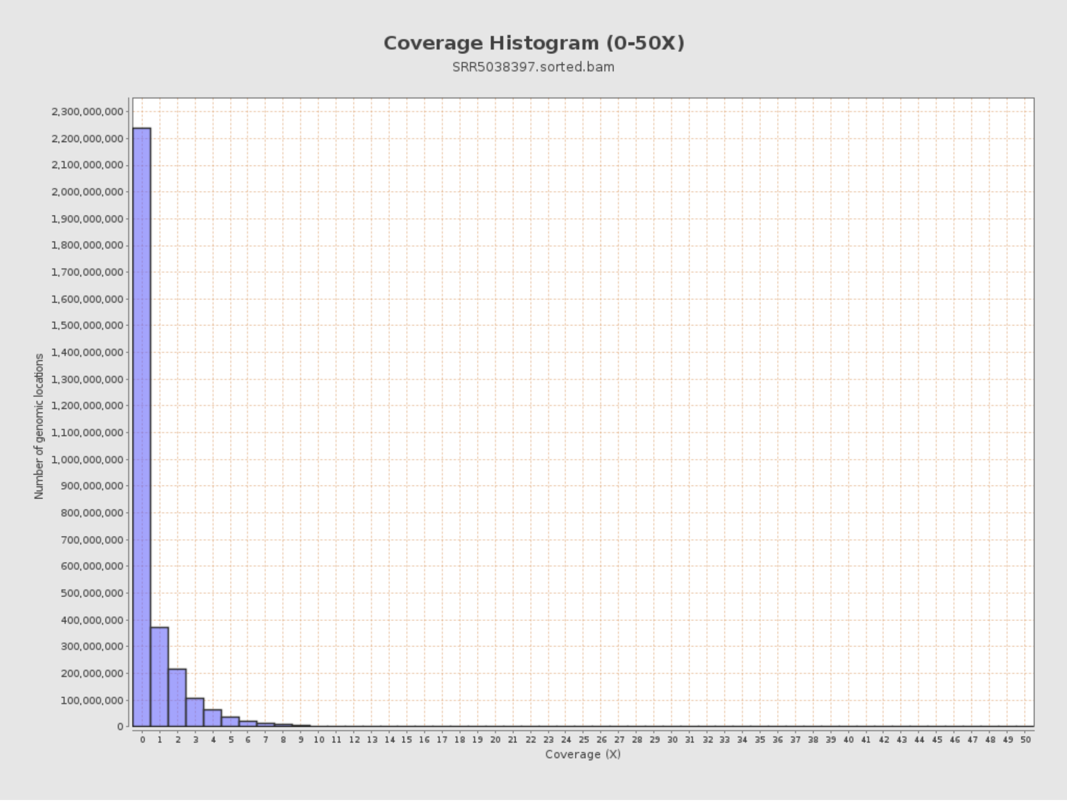
3. Results : Coverage across reference



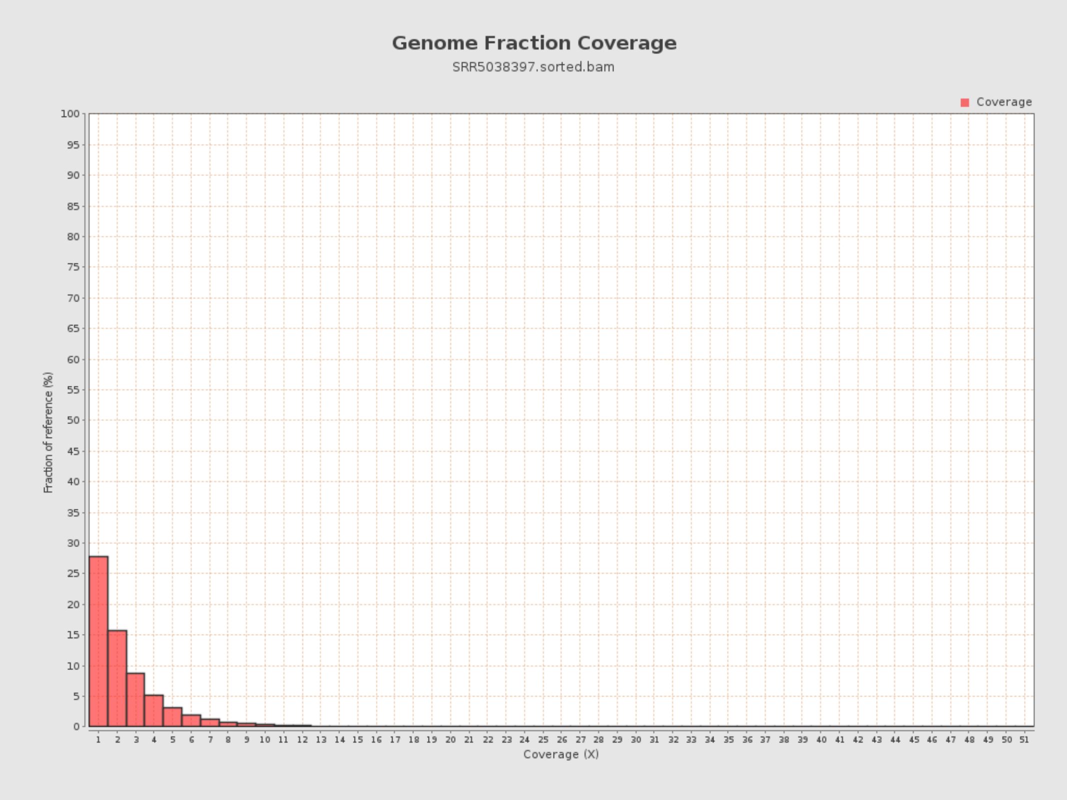
4. Results : Coverage Histogram



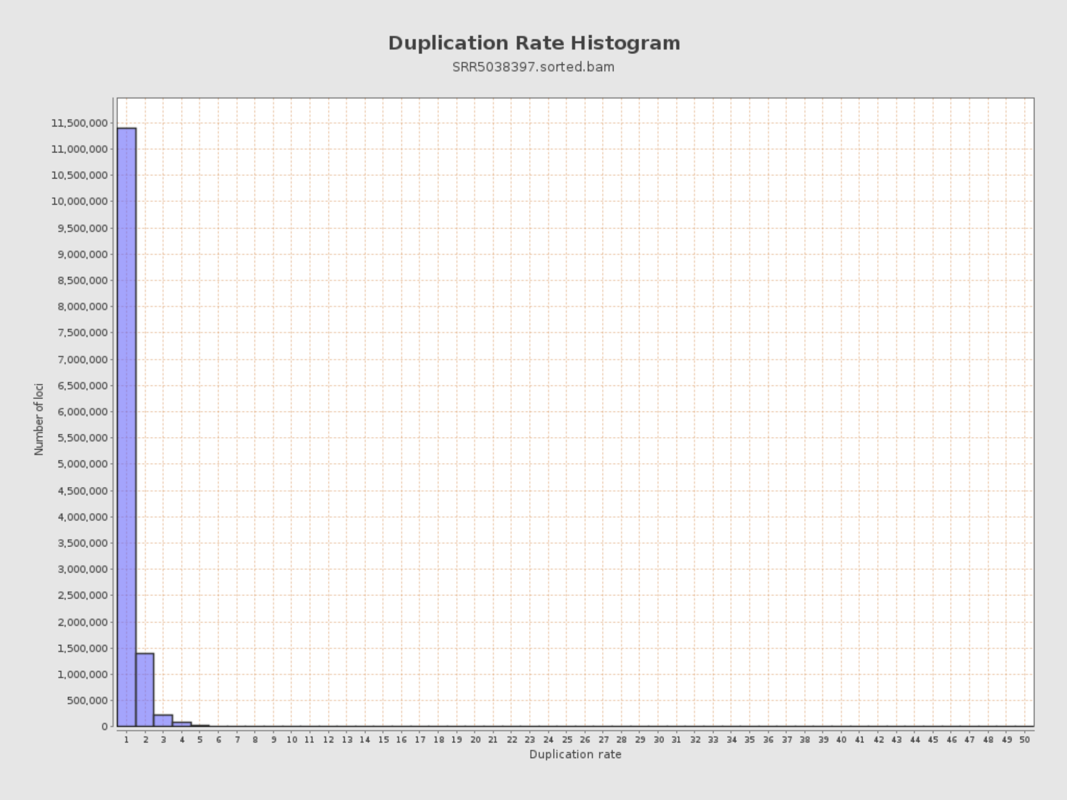
5. Results : Coverage Histogram (0-50X)



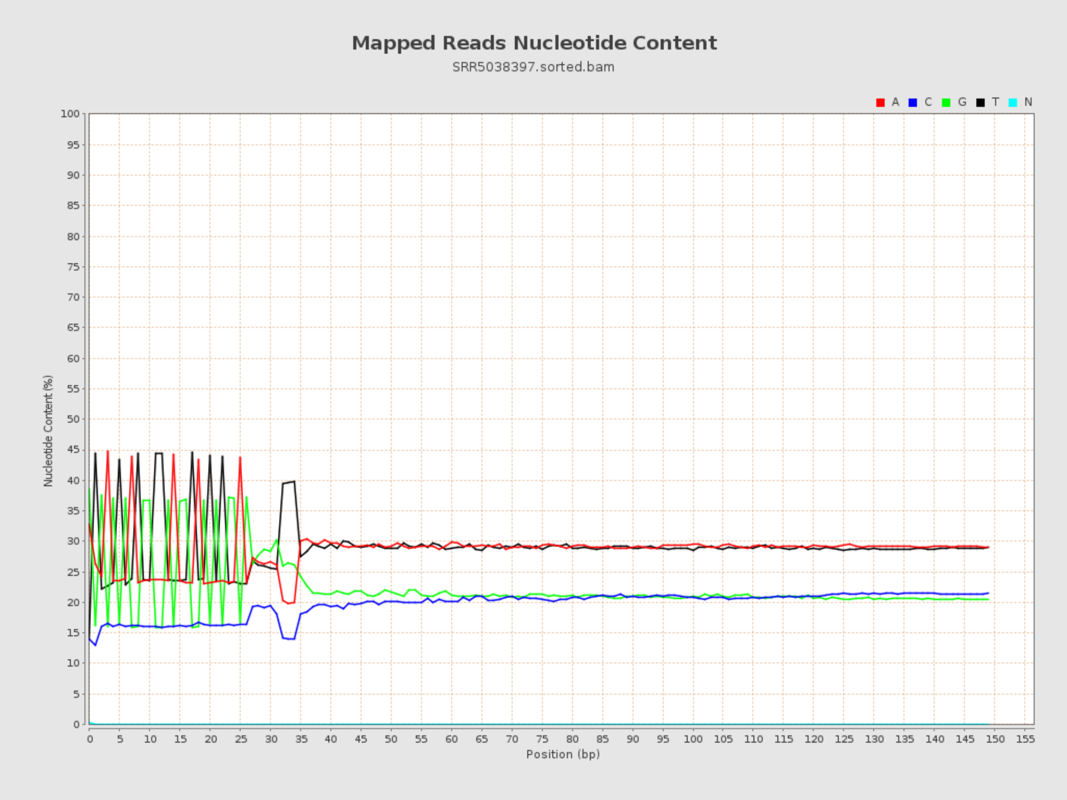
6. Results : Genome Fraction Coverage



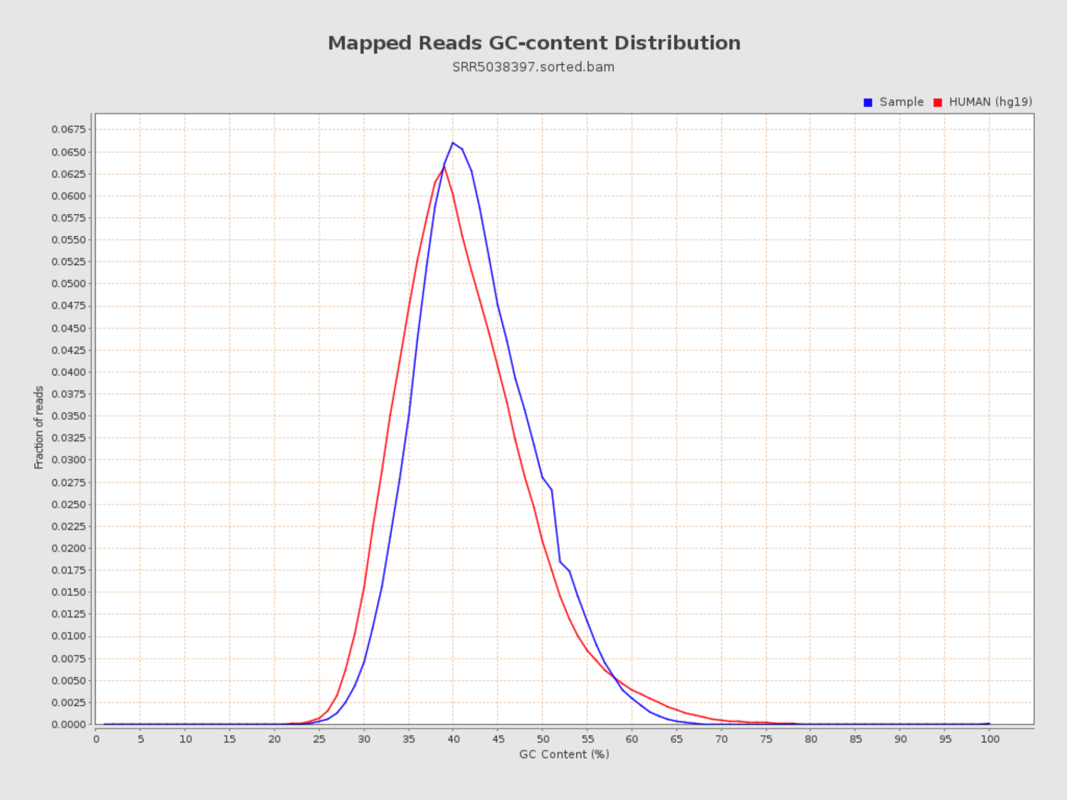
7. Results : Duplication Rate Histogram



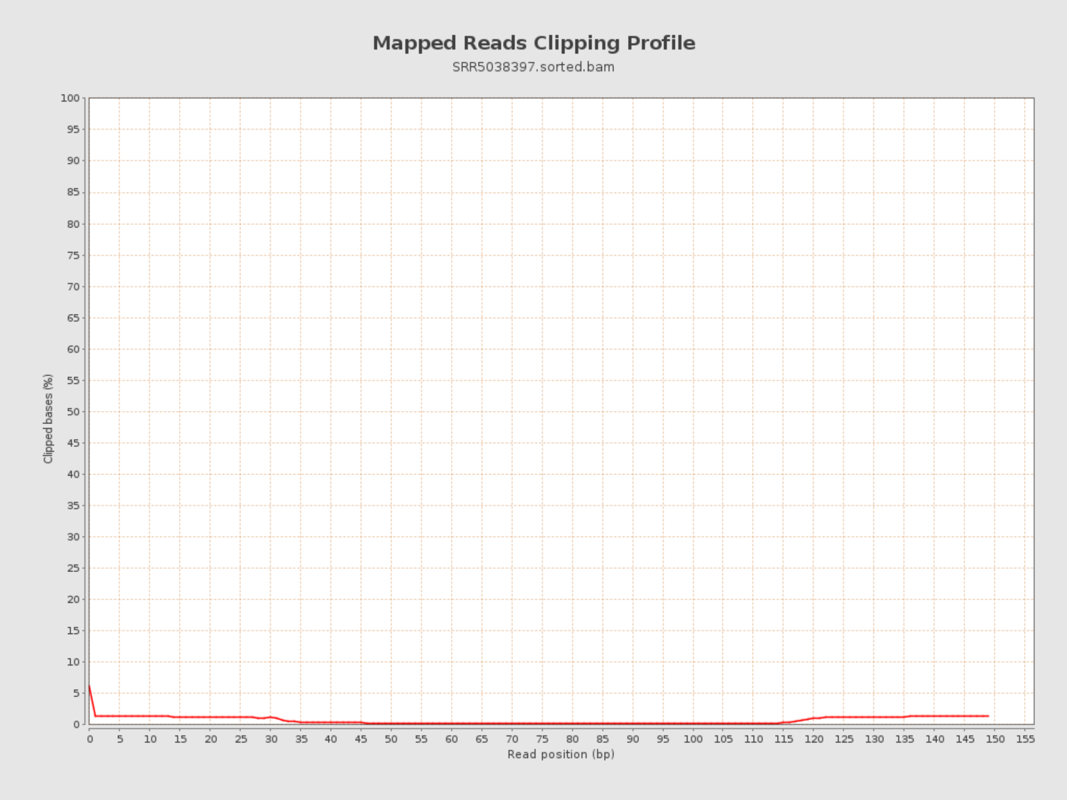
8. Results : Mapped Reads Nucleotide Content



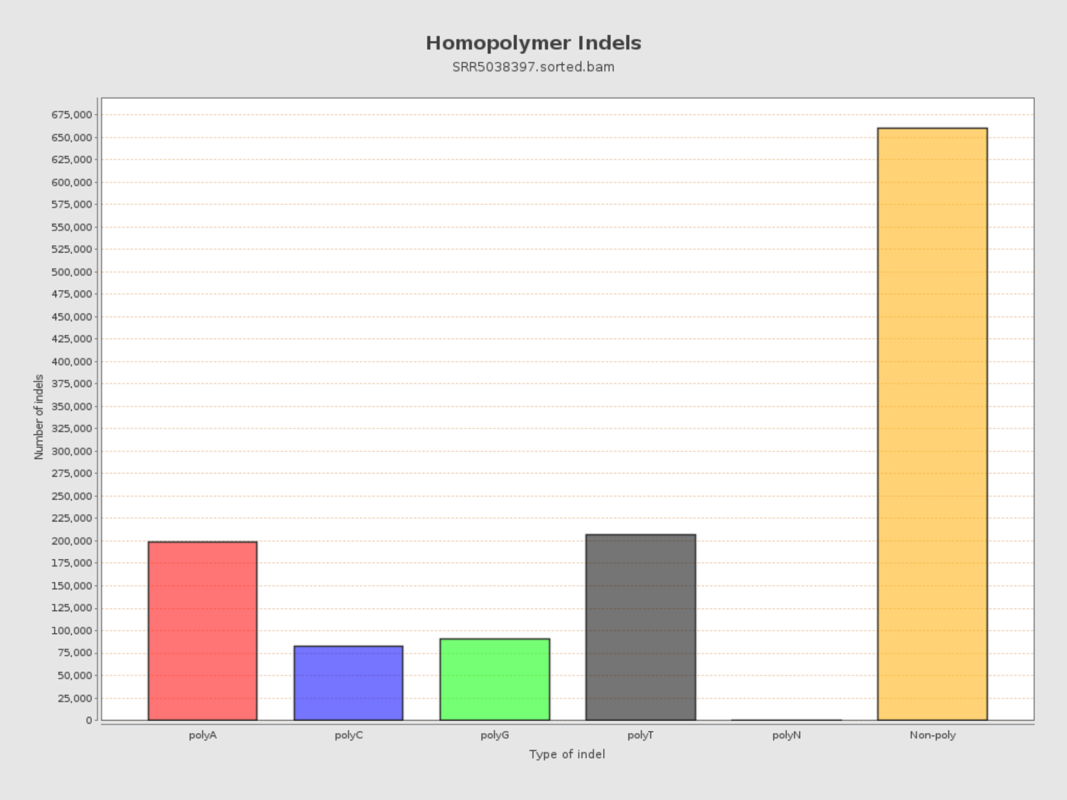
9. Results : Mapped Reads GC-content Distribution



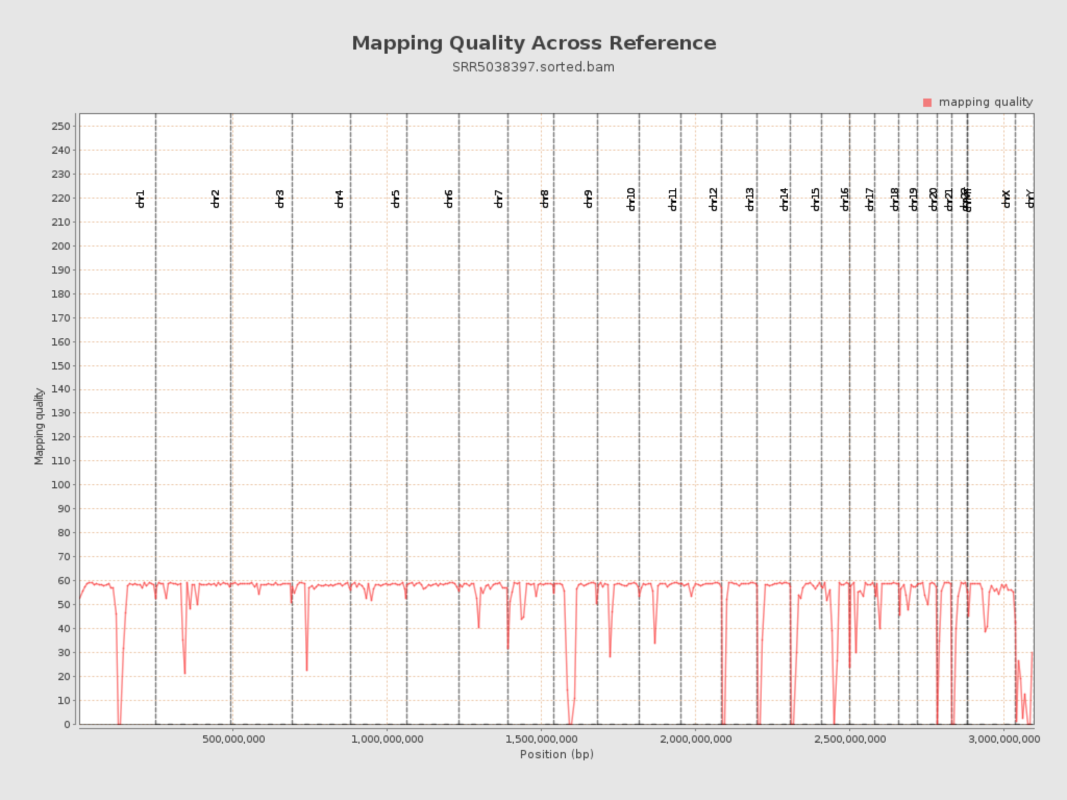
10. Results : Mapped Reads Clipping Profile



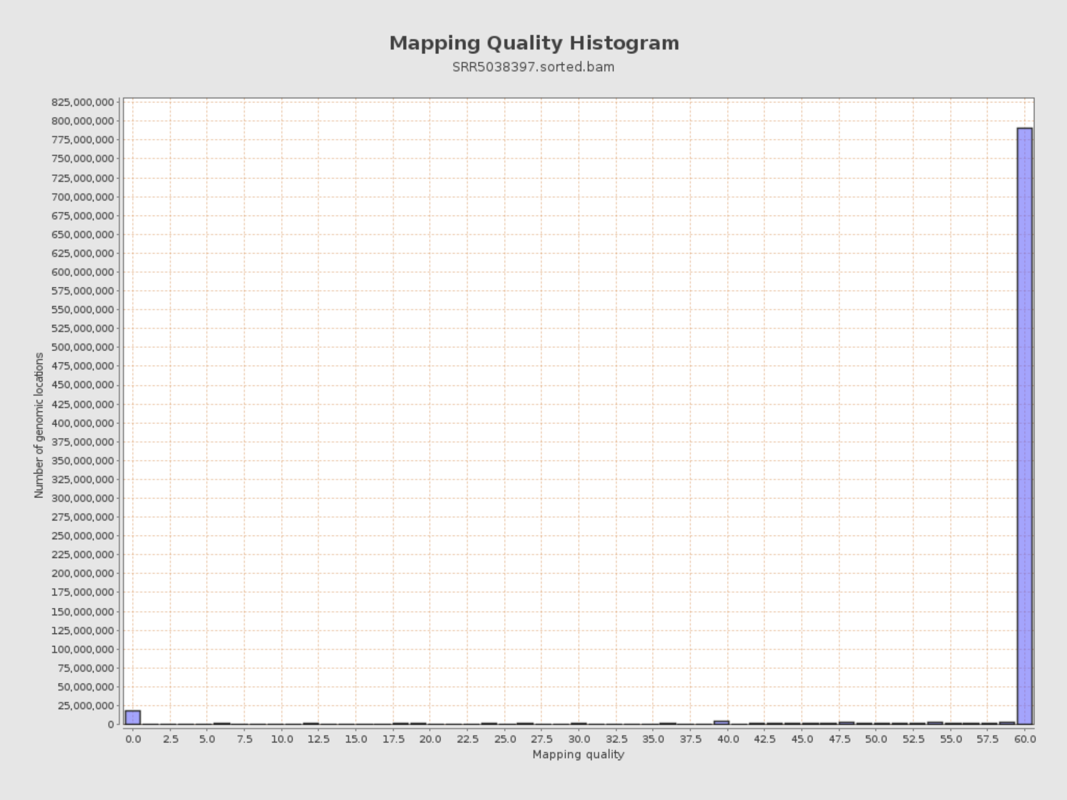
11. Results : Homopolymer Indels



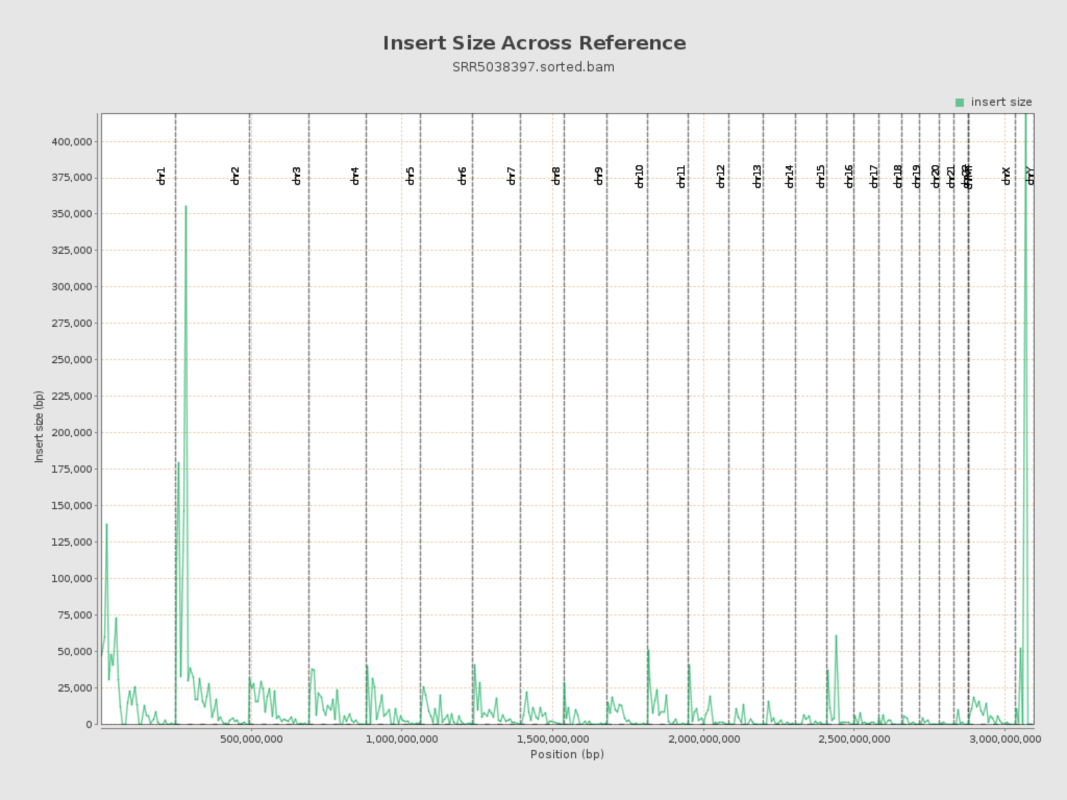
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram