Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/15 20:26:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038460.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_SRR5038460 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038460_1.fastq.gz SRR5038460_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 15 20:26:13 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038460.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	14,337,776
Mapped reads	13,459,441 / 93.87%
Unmapped reads	878,335 / 6.13%
Mapped paired reads	13,459,441 / 93.87%
Mapped reads, first in pair	6,856,035 / 47.82%
Mapped reads, second in pair	6,603,406 / 46.06%
Mapped reads, both in pair	13,116,064 / 91.48%
Mapped reads, singletons	343,377 / 2.39%
Secondary alignments	0
Supplementary alignments	233,010 / 1.63%
Read min/max/mean length	30 / 150 / 150.8
Duplicated reads (estimated)	3,454,422 / 24.09%
Duplication rate	18.22%
Clipped reads	7,879,289 / 54.95%

2.2. ACGT Content

Number/percentage of A's	509,404,196 / 28.93%
Number/percentage of C's	337,349,849 / 19.16%
Number/percentage of T's	523,282,625 / 29.72%
Number/percentage of G's	390,745,210 / 22.19%
Number/percentage of N's	129,665 / 0.01%

GC Percentage	41.35%

2.3. Coverage

Mean	0.5692
Standard Deviation	8.6622

2.4. Mapping Quality

Mean Mapping Quality	52.86

2.5. Insert size

Mean	75,356.94
Standard Deviation	2,645,985.9
P25/Median/P75	175 / 218 / 269

2.6. Mismatches and indels

General error rate	1.37%
Mismatches	23,288,242
Insertions	315,375
Mapped reads with at least one insertion	2.23%
Deletions	602,383
Mapped reads with at least one deletion	4.32%
Homopolymer indels	47.09%

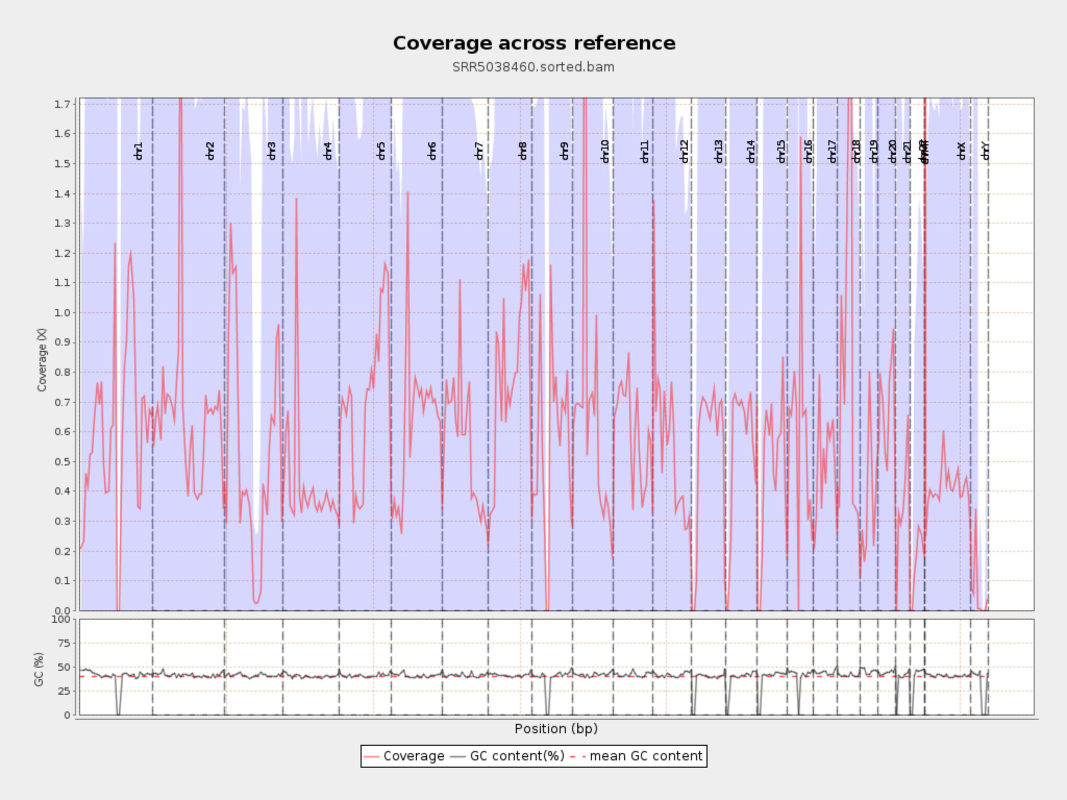
2.7. Chromosome stats

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

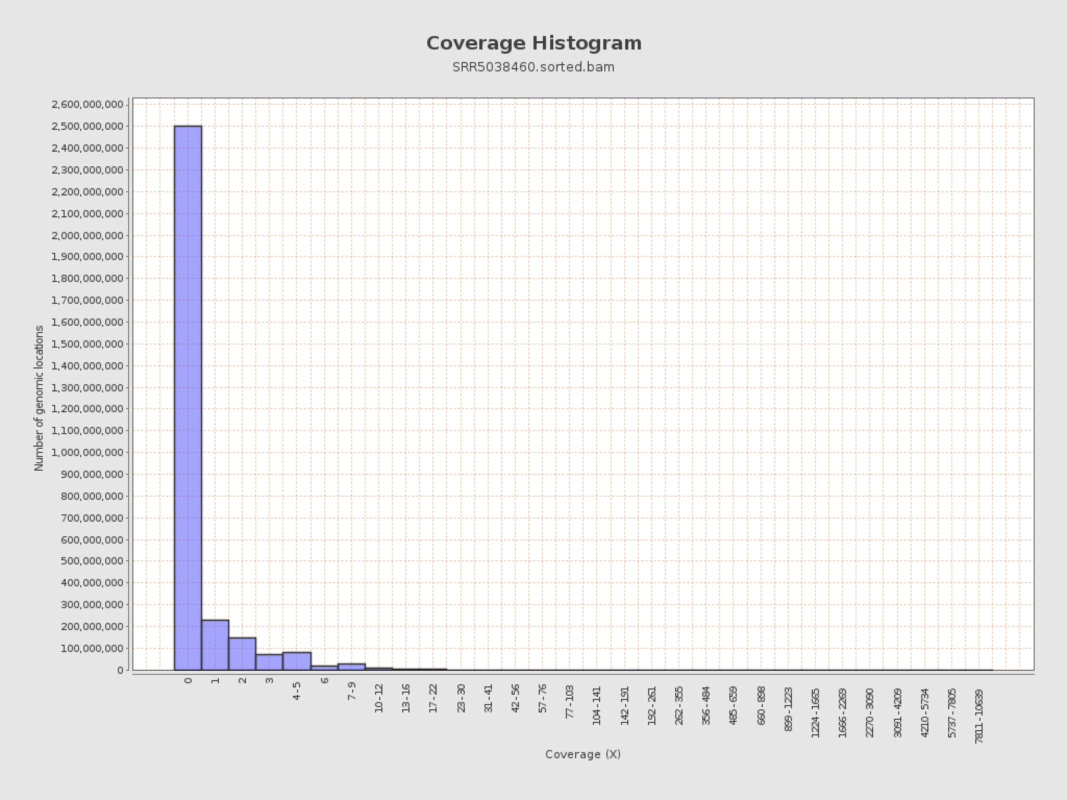
		bases	coverage	deviation
chr1	249250621	151556904	0.6081	10.6559
chr2	243199373	163475291	0.6722	11.5267
chr3	198022430	103834676	0.5244	1.687
chr4	191154276	81364049	0.4256	8.288
chr5	180915260	127724035	0.706	1.8974
chr6	171115067	109685192	0.641	8.0553
chr7	159138663	88434758	0.5557	9.5049
chr8	146364022	115019361	0.7858	4.3229
chr9	141213431	76812473	0.5439	13.9077
chr10	135534747	95242837	0.7027	21.3386
chr11	135006516	80529356	0.5965	6.2966
chr12	133851895	74164161	0.5541	1.736
chr13	115169878	63092892	0.5478	1.6725
chr14	107349540	58225775	0.5424	1.7378
chr15	102531392	47425986	0.4626	1.4768
chr16	90354753	52427104	0.5802	7.861
chr17	81195210	39166256	0.4824	9.0317
chr18	78077248	71023856	0.9097	11.7684
chr19	59128983	21400215	0.3619	5.3603
chr20	63025520	43246846	0.6862	3.2701
chr21	48129895	17398682	0.3615	3.9586
chr22	51304566	8354994	0.1629	1.0386
chrMT	16571	4770631	287.8904	242.9797
chrX	155270560	63902638	0.4116	2.03

chrY	59373566	3829931	0.0645	8.413

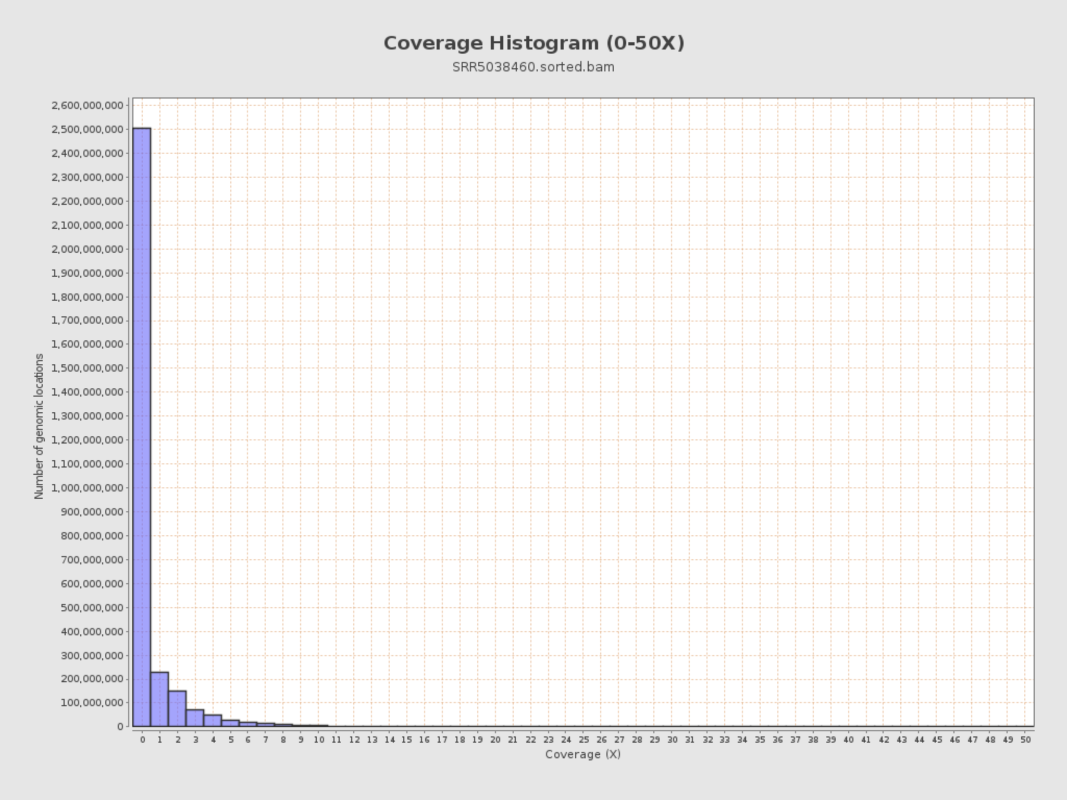
3. Results : Coverage across reference



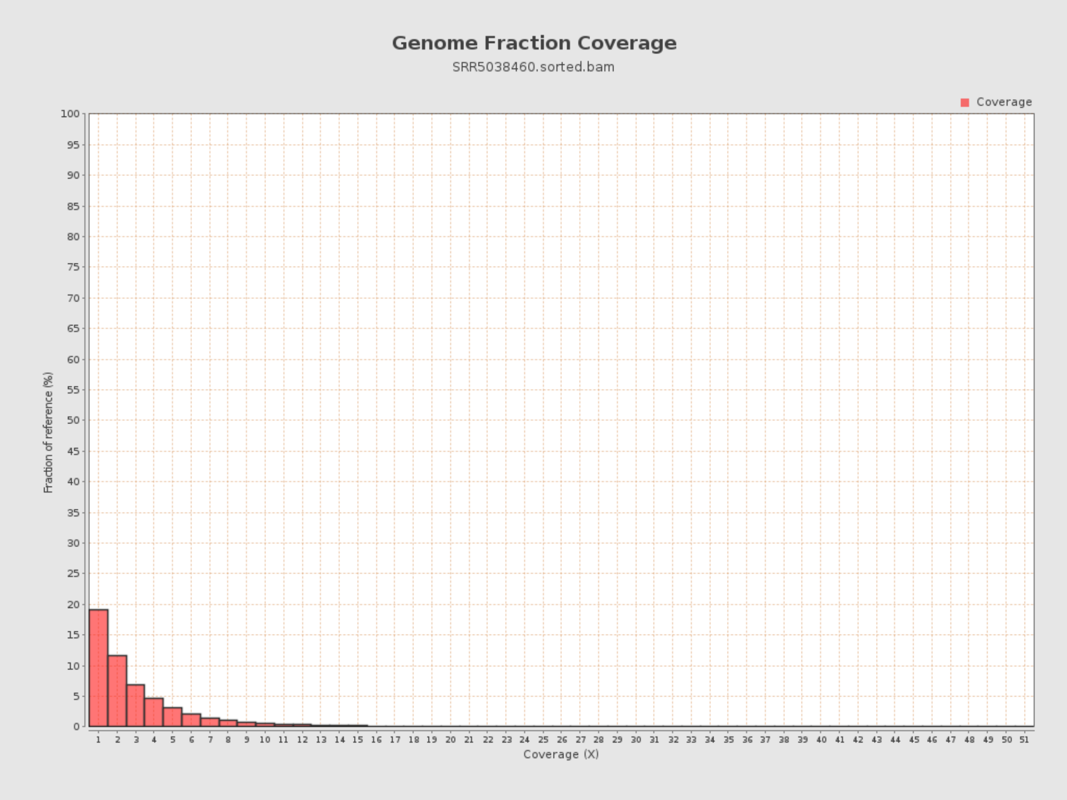
4. Results : Coverage Histogram



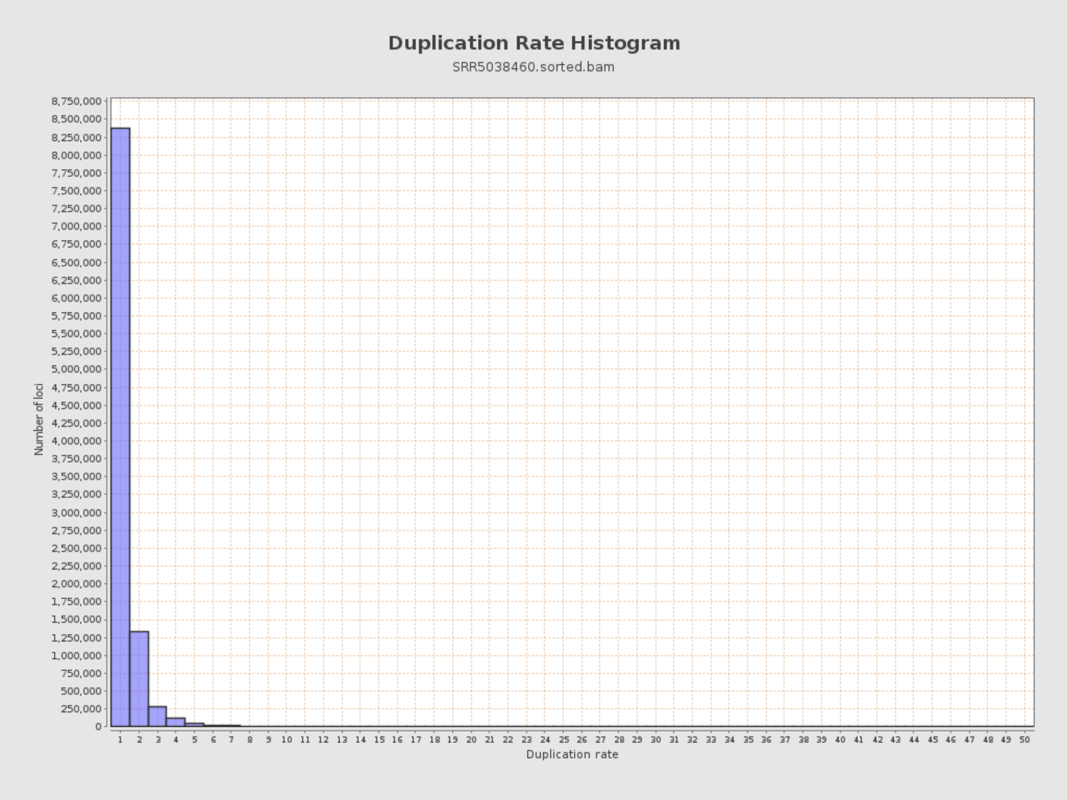
5. Results : Coverage Histogram (0-50X)



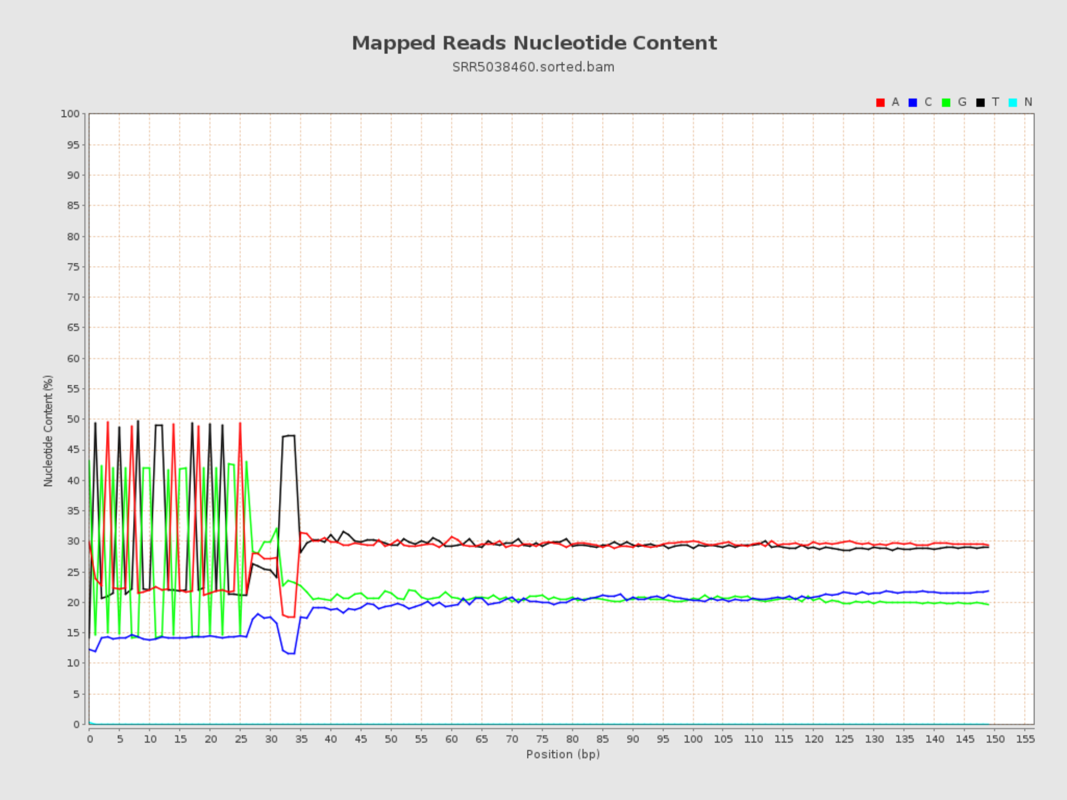
6. Results : Genome Fraction Coverage



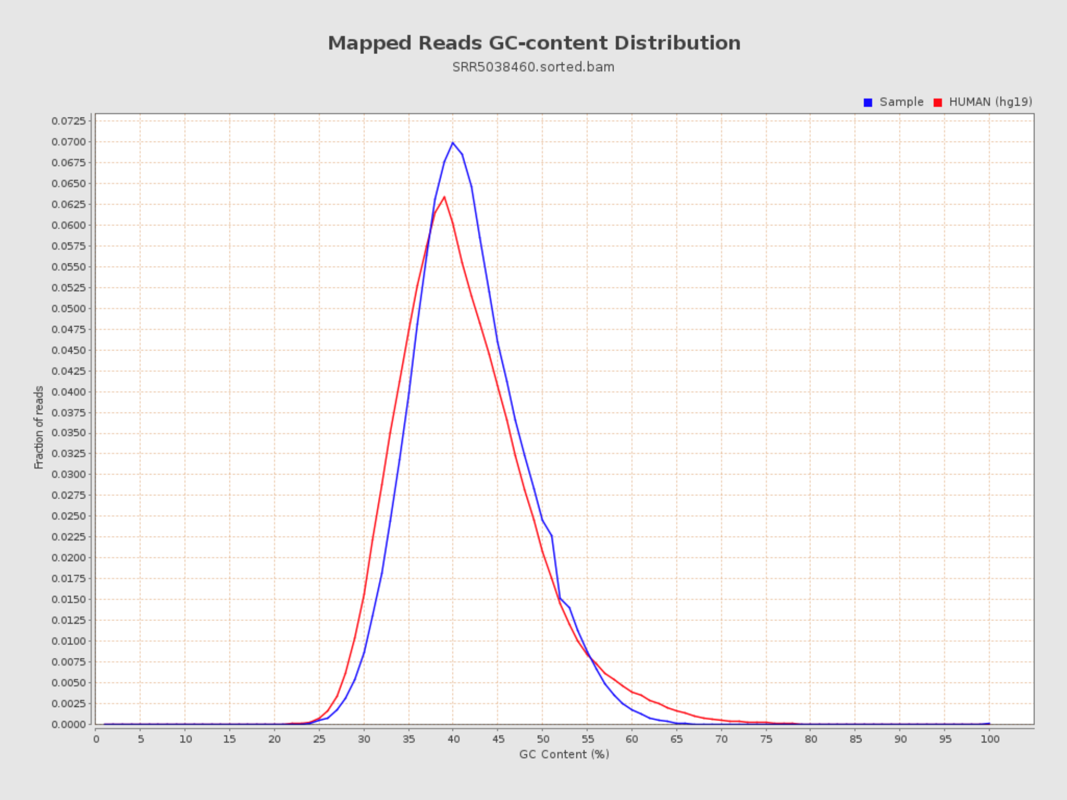
7. Results : Duplication Rate Histogram



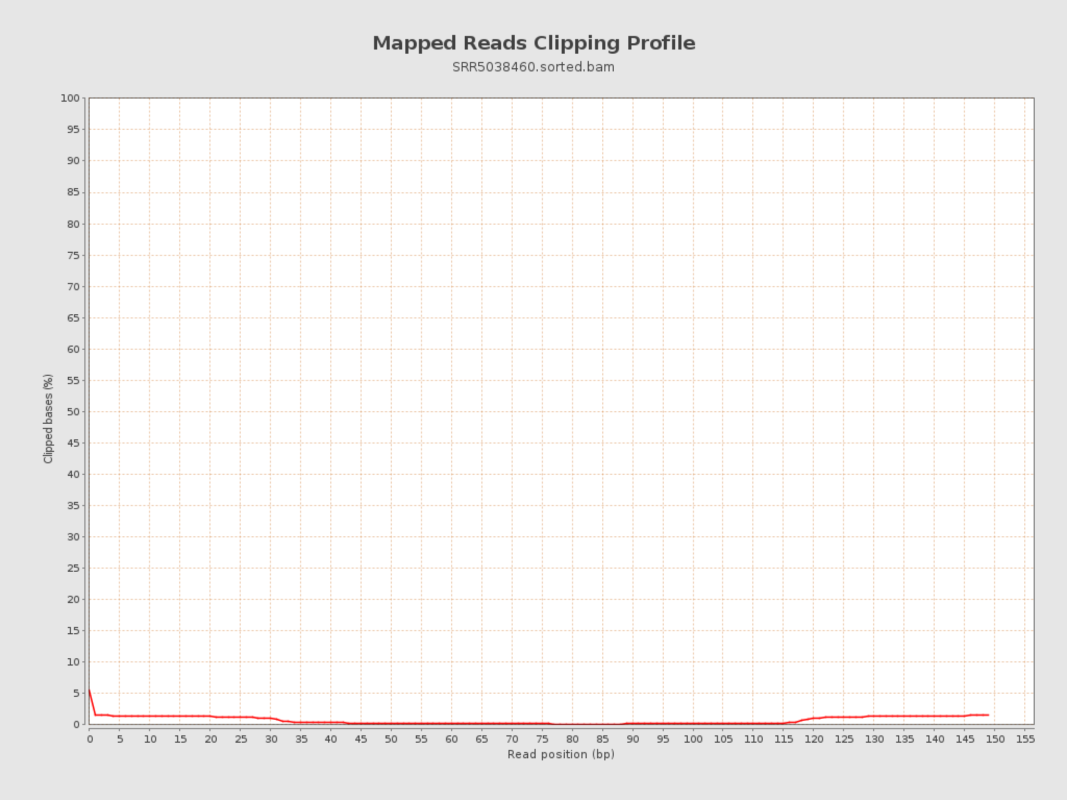
8. Results : Mapped Reads Nucleotide Content



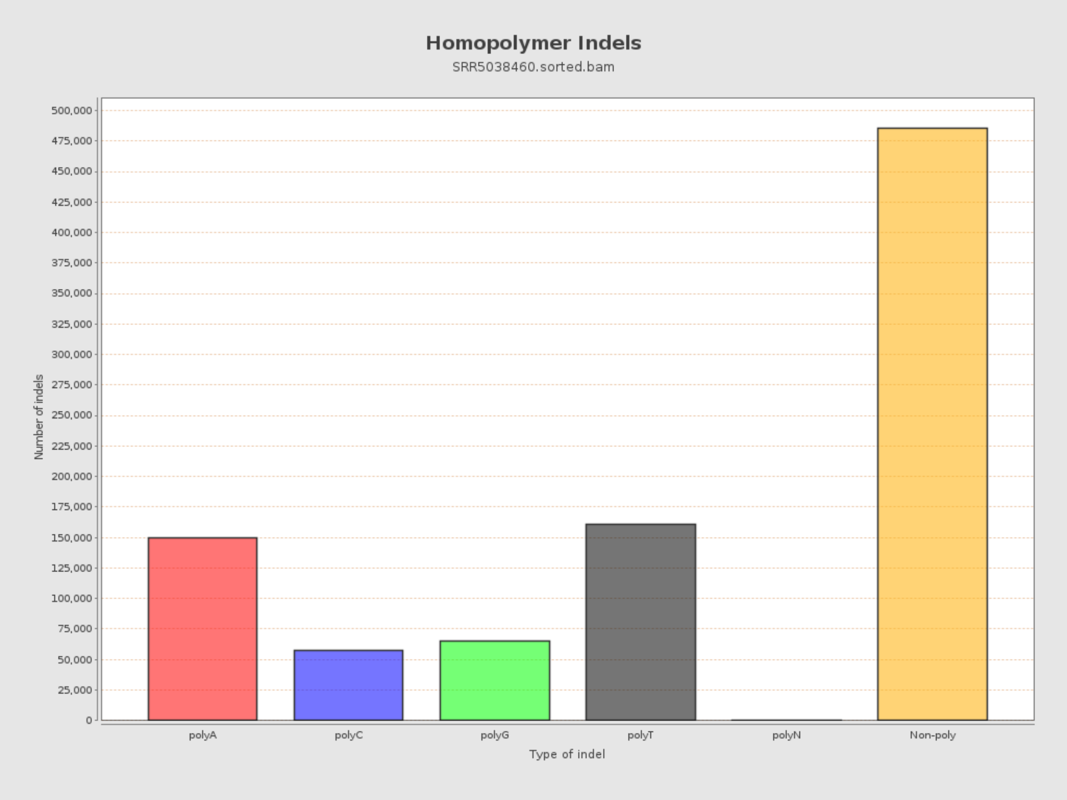
9. Results : Mapped Reads GC-content Distribution



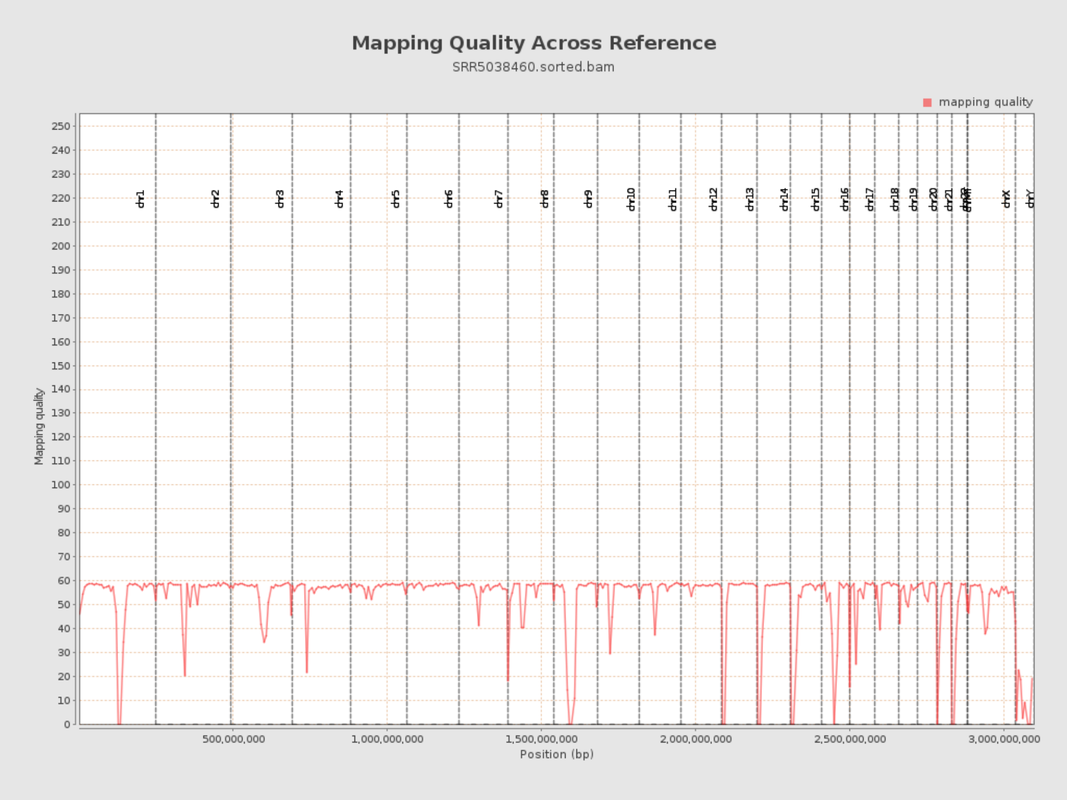
10. Results : Mapped Reads Clipping Profile



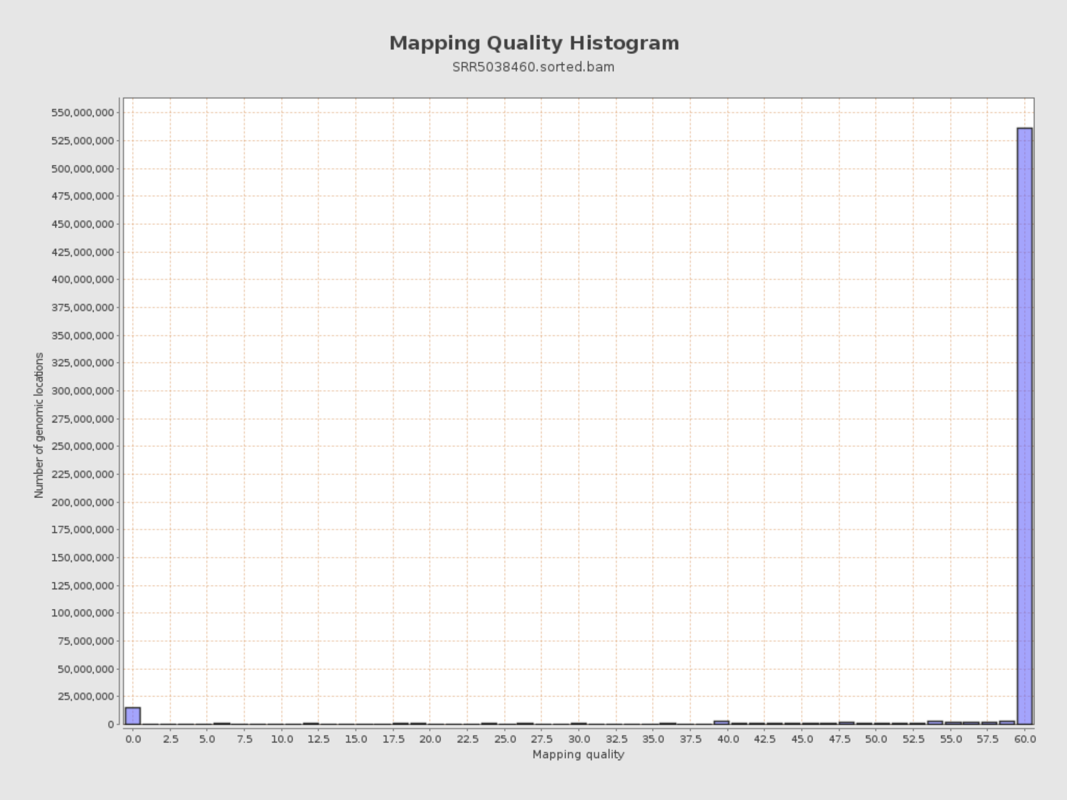
11. Results : Homopolymer Indels



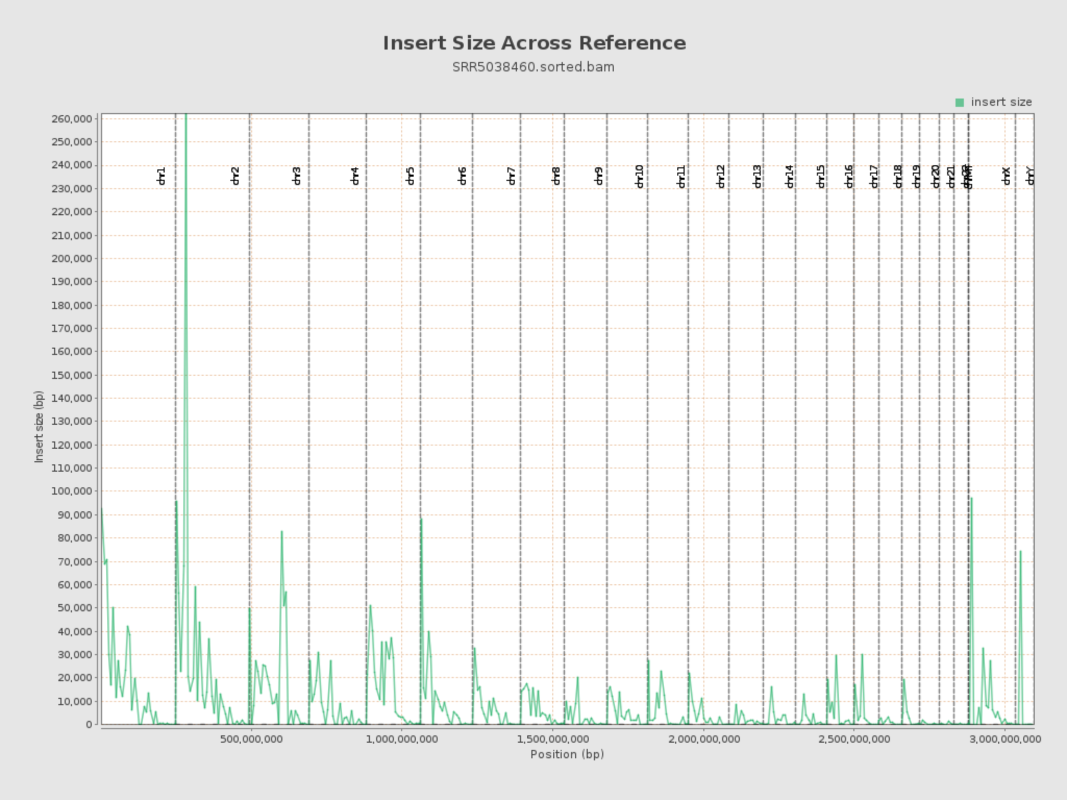
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram