Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/15 02:54:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038425.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_SRR5038425 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038425_1.fastq.gz SRR5038425_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 15 02:54:31 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038425.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	11,461,958
Mapped reads	10,787,050 / 94.11%
Unmapped reads	674,908 / 5.89%
Mapped paired reads	10,787,050 / 94.11%
Mapped reads, first in pair	5,453,063 / 47.58%
Mapped reads, second in pair	5,333,987 / 46.54%
Mapped reads, both in pair	10,648,970 / 92.91%
Mapped reads, singletons	138,080 / 1.2%
Secondary alignments	0
Supplementary alignments	229,628 / 2%
Read min/max/mean length	30 / 150 / 151.03
Duplicated reads (estimated)	1,594,901 / 13.91%
Duplication rate	8.7%
Clipped reads	3,303,611 / 28.82%

2.2. ACGT Content

Number/percentage of A's	441,499,435 / 29.11%
Number/percentage of C's	306,738,754 / 20.22%
Number/percentage of T's	443,286,354 / 29.23%
Number/percentage of G's	325,240,201 / 21.44%
Number/percentage of N's	33,063 / 0%

GC Percentage	41.67%

2.3. Coverage

Mean	0.4904
Standard Deviation	8.1299

2.4. Mapping Quality

Mean Mapping Quality	53.61

2.5. Insert size

Mean	92,434.96
Standard Deviation	2,883,570.76
P25/Median/P75	220 / 261 / 312

2.6. Mismatches and indels

General error rate	1.45%
Mismatches	21,078,608
Insertions	297,535
Mapped reads with at least one insertion	2.58%
Deletions	552,470
Mapped reads with at least one deletion	4.91%
Homopolymer indels	46.7%

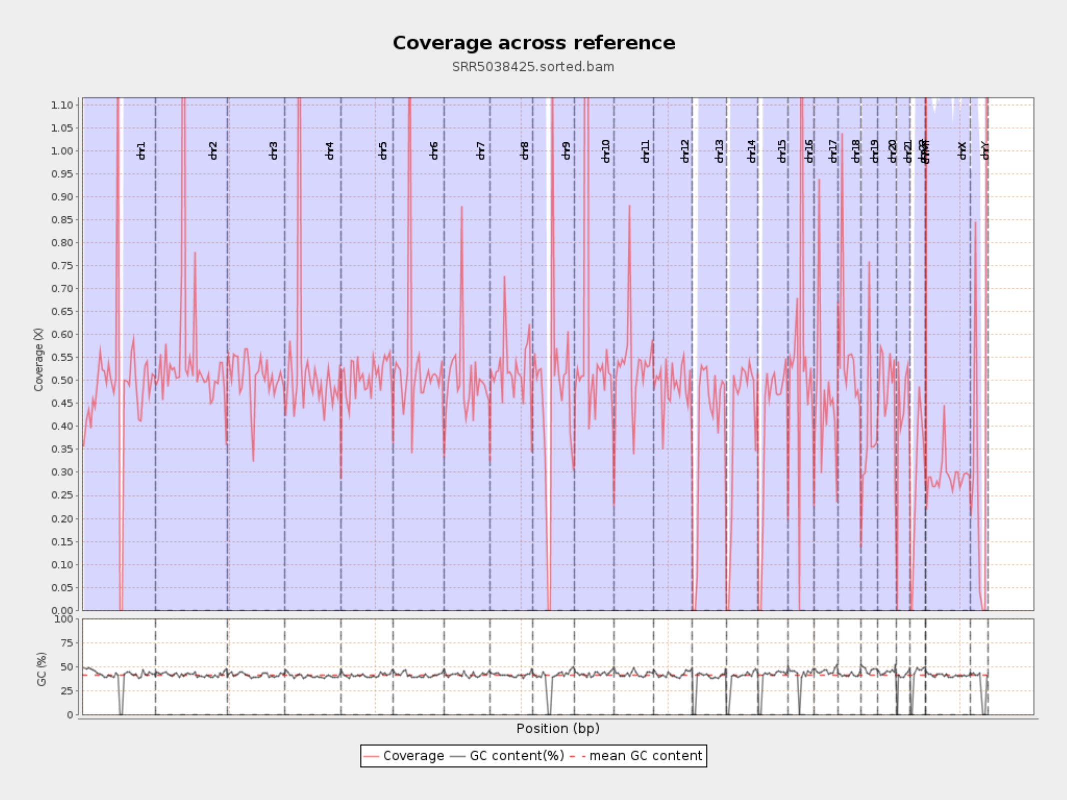
2.7. Chromosome stats

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

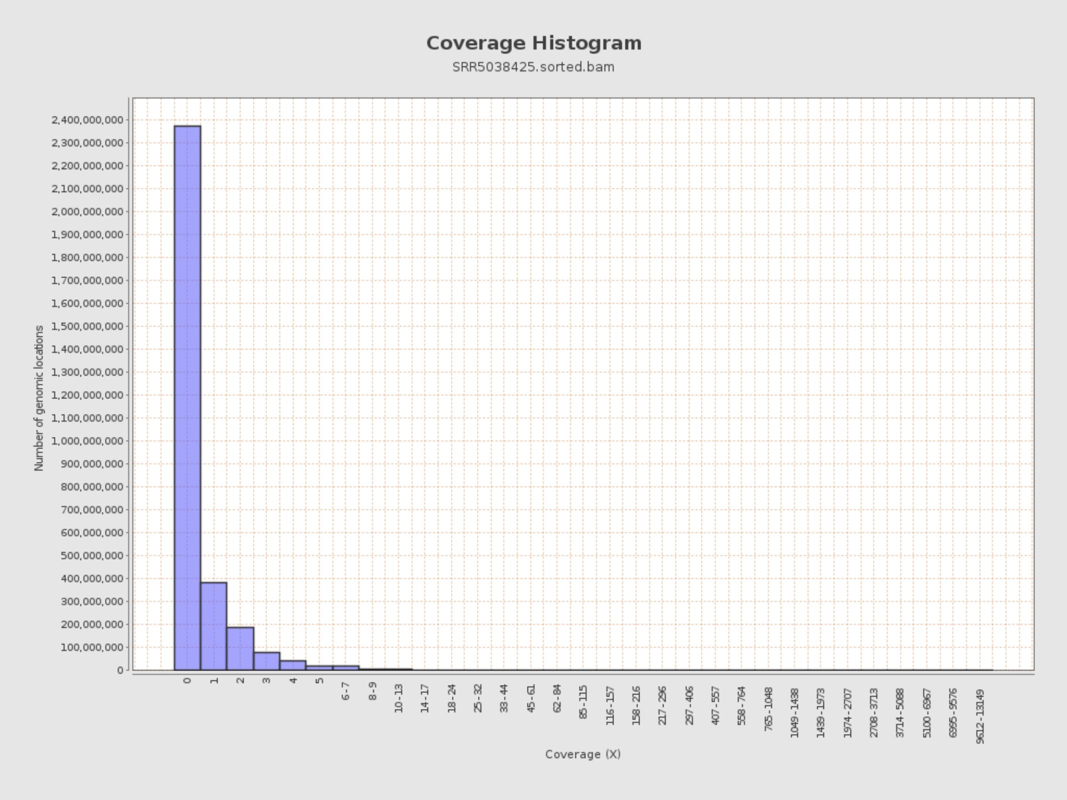
		bases	coverage	deviation
chr1	249250621	120209679	0.4823	13.6621
chr2	243199373	138193814	0.5682	8.2984
chr3	198022430	100485091	0.5074	1.1686
chr4	191154276	103677518	0.5424	8.3628
chr5	180915260	91629555	0.5065	1.245
chr6	171115067	92874266	0.5428	10.8486
chr7	159138663	79724314	0.501	6.4604
chr8	146364022	76609880	0.5234	2.0835
chr9	141213431	66419688	0.4703	14.5974
chr10	135534747	82850011	0.6113	14.338
chr11	135006516	72143627	0.5344	6.0389
chr12	133851895	65388320	0.4885	1.1632
chr13	115169878	45740649	0.3972	1
chr14	107349540	43867223	0.4086	1.1317
chr15	102531392	40937304	0.3993	1.0101
chr16	90354753	51701070	0.5722	8.512
chr17	81195210	38289462	0.4716	7.6965
chr18	78077248	44632083	0.5716	11.9557
chr19	59128983	22797079	0.3855	6.9178
chr20	63025520	31268069	0.4961	2.5031
chr21	48129895	20195968	0.4196	3.5377
chr22	51304566	14477679	0.2822	0.9156
chrMT	16571	5676394	342.5499	228.7765
chrX	155270560	45317479	0.2919	1.6406

chrY	59373566	22871409	0.3852	10.8293

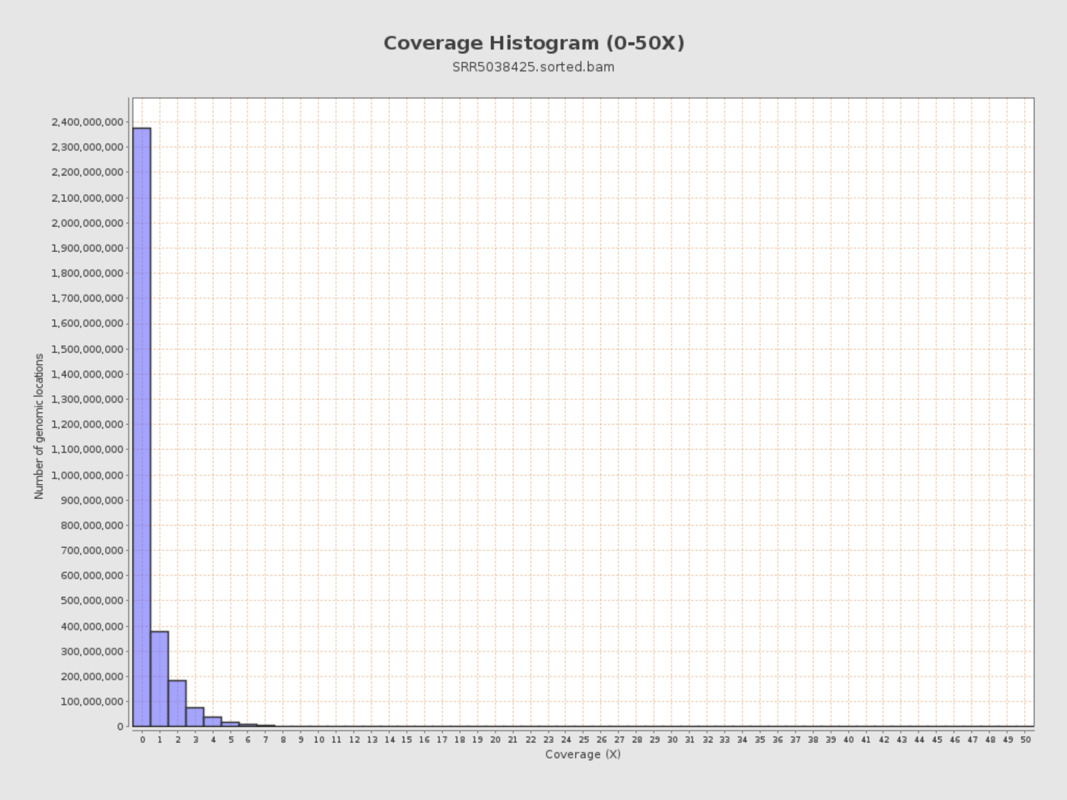
3. Results : Coverage across reference



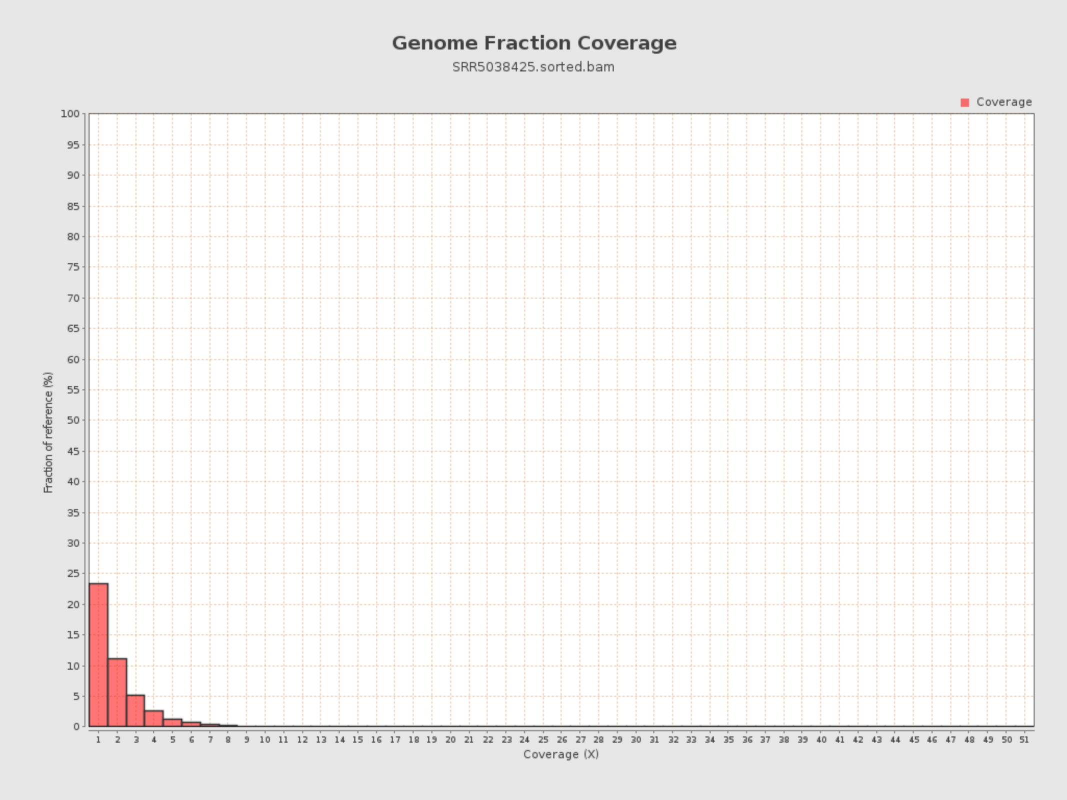
4. Results : Coverage Histogram



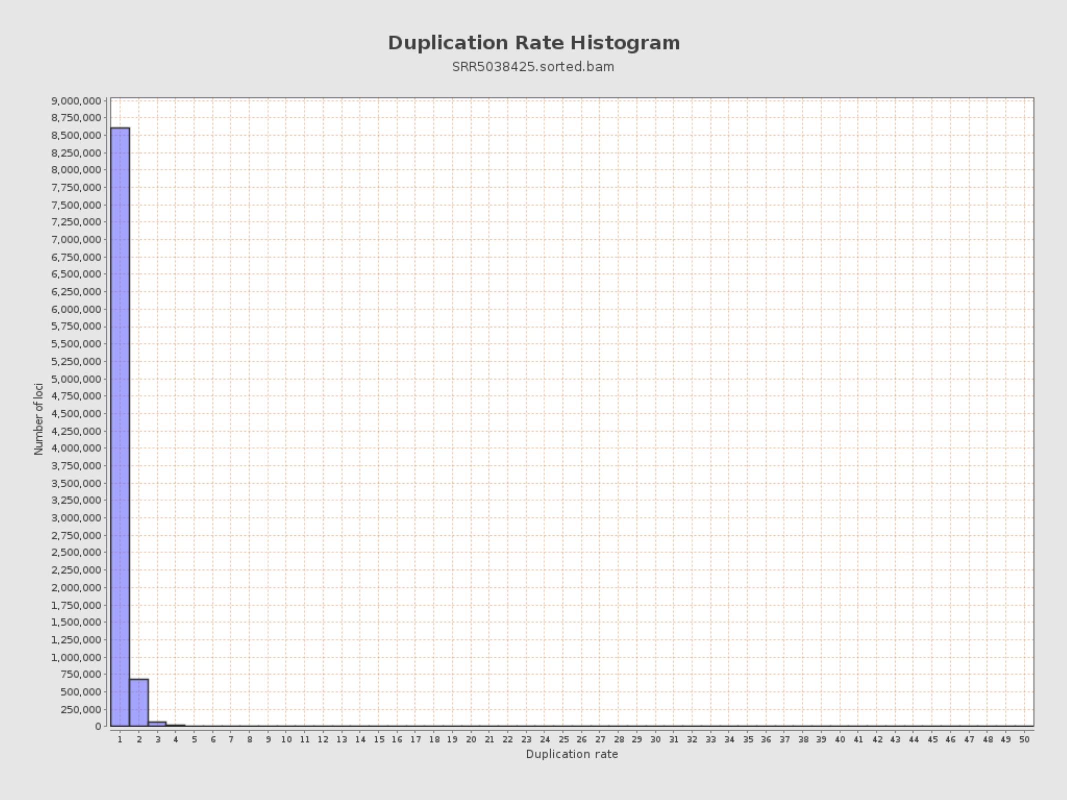
5. Results : Coverage Histogram (0-50X)



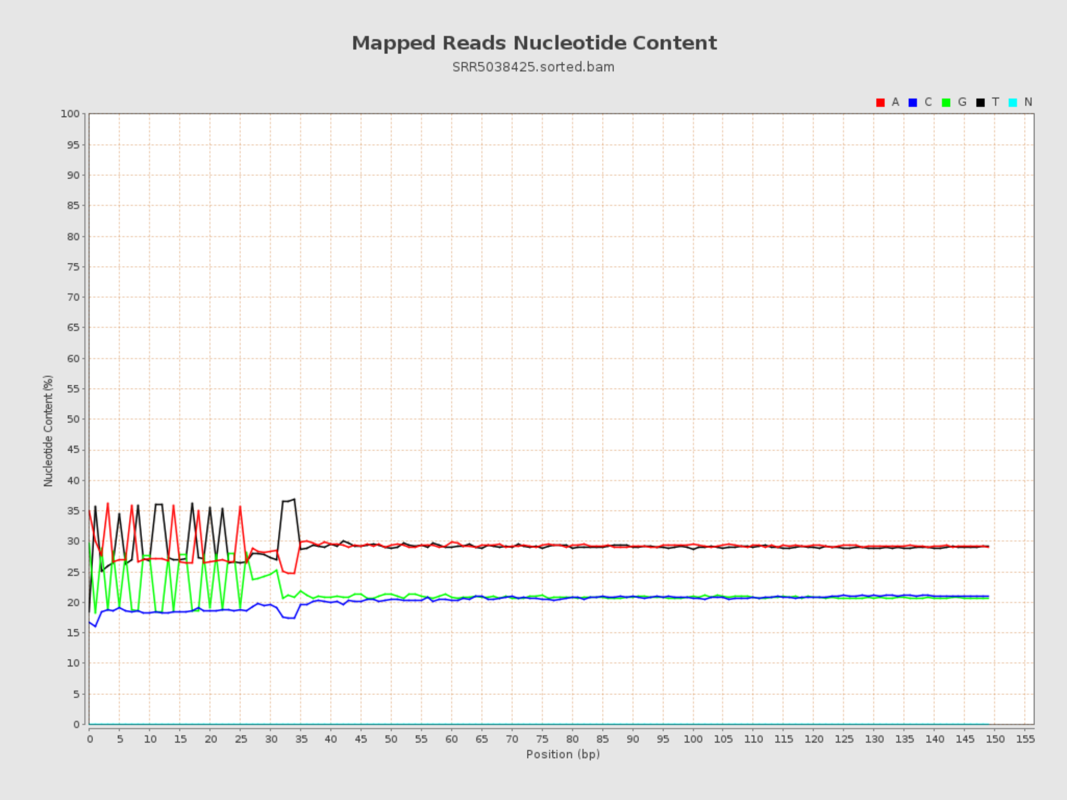
6. Results : Genome Fraction Coverage



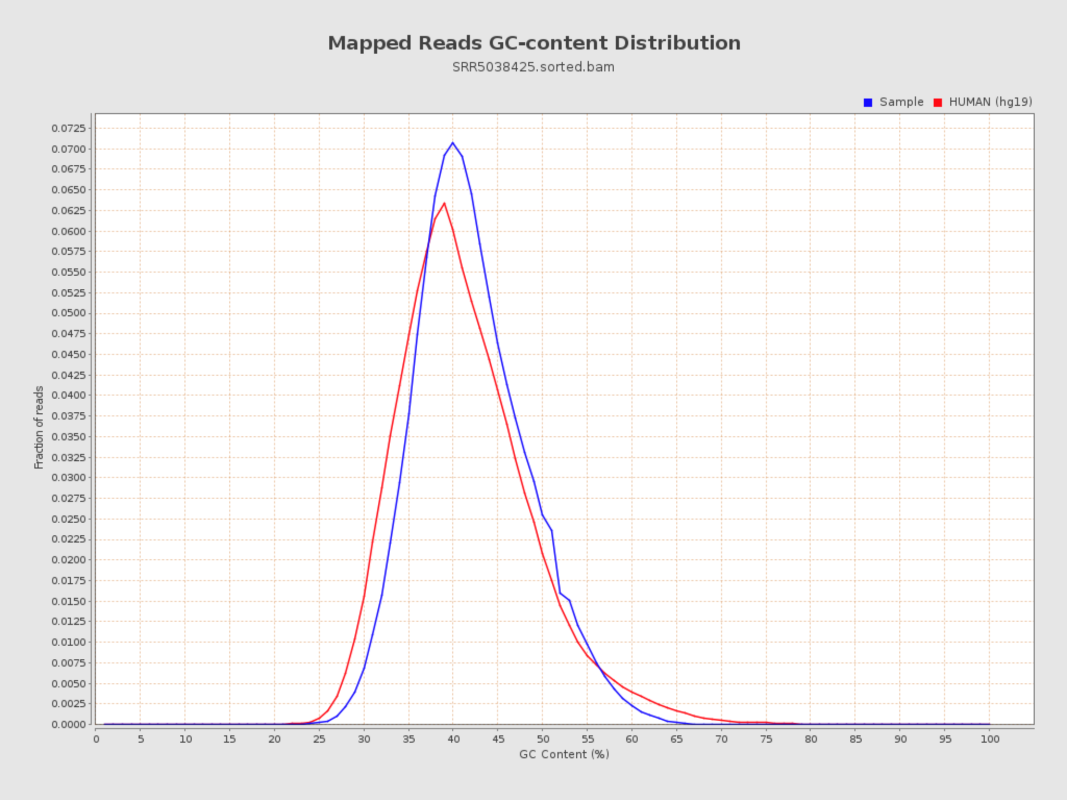
7. Results : Duplication Rate Histogram



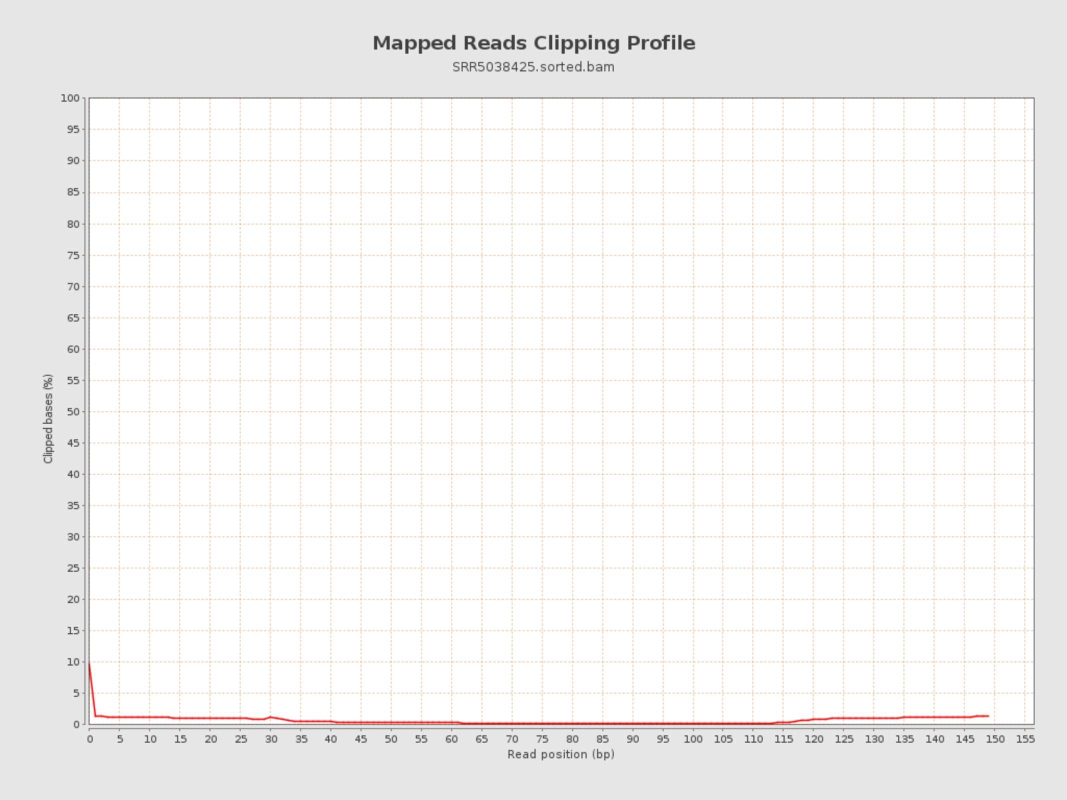
8. Results : Mapped Reads Nucleotide Content



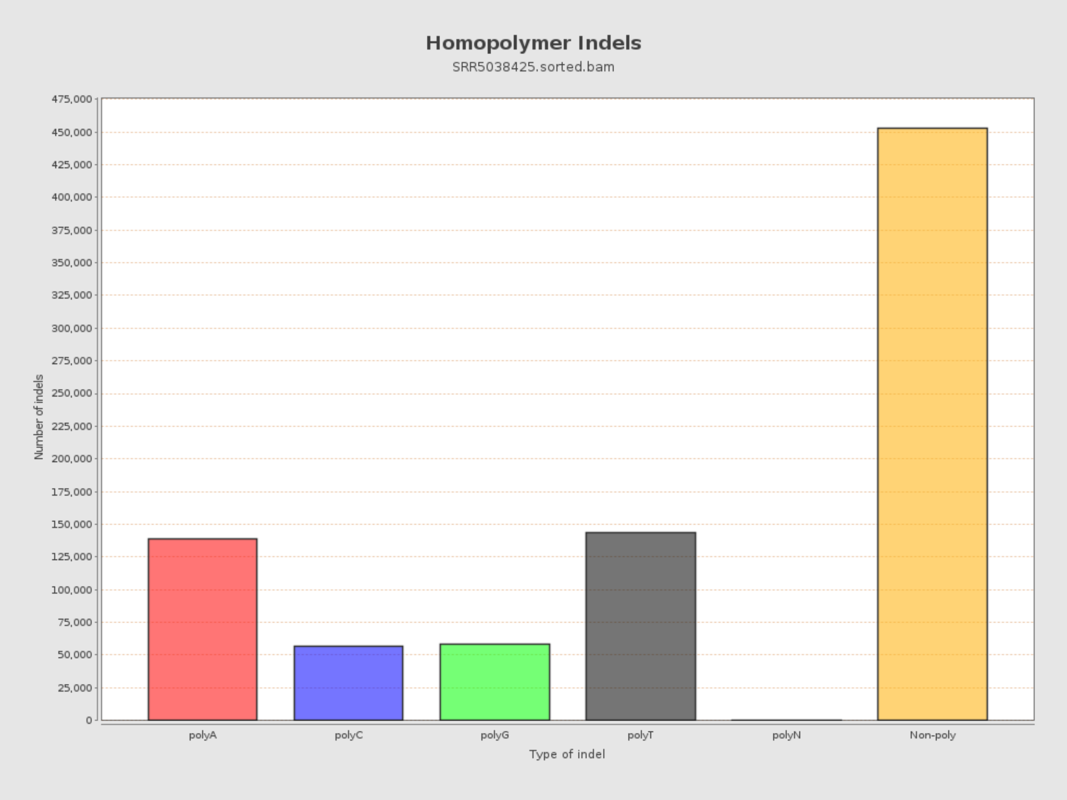
9. Results : Mapped Reads GC-content Distribution



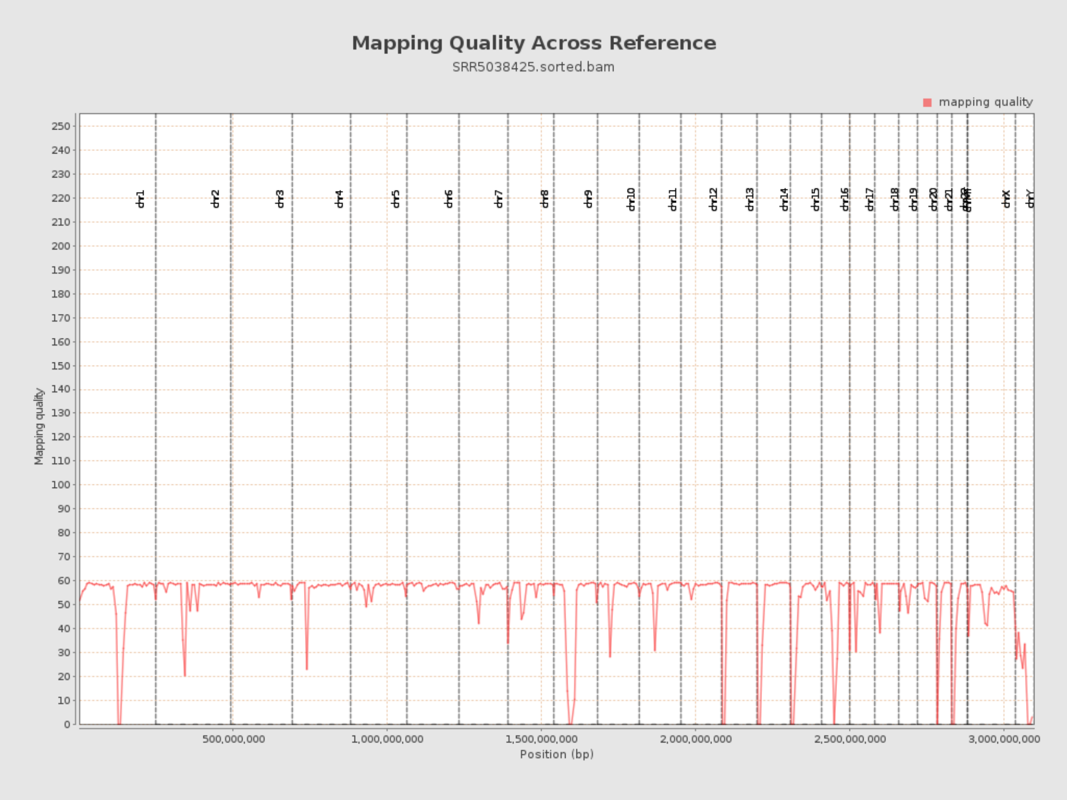
10. Results : Mapped Reads Clipping Profile



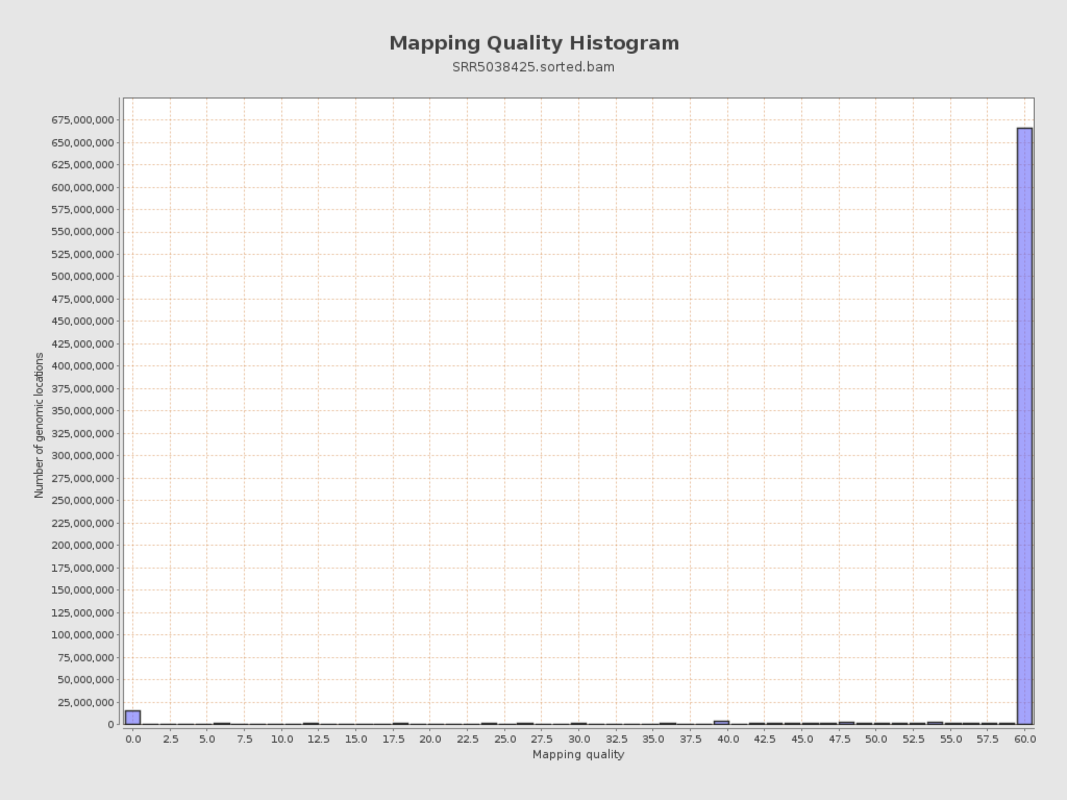
11. Results : Homopolymer Indels



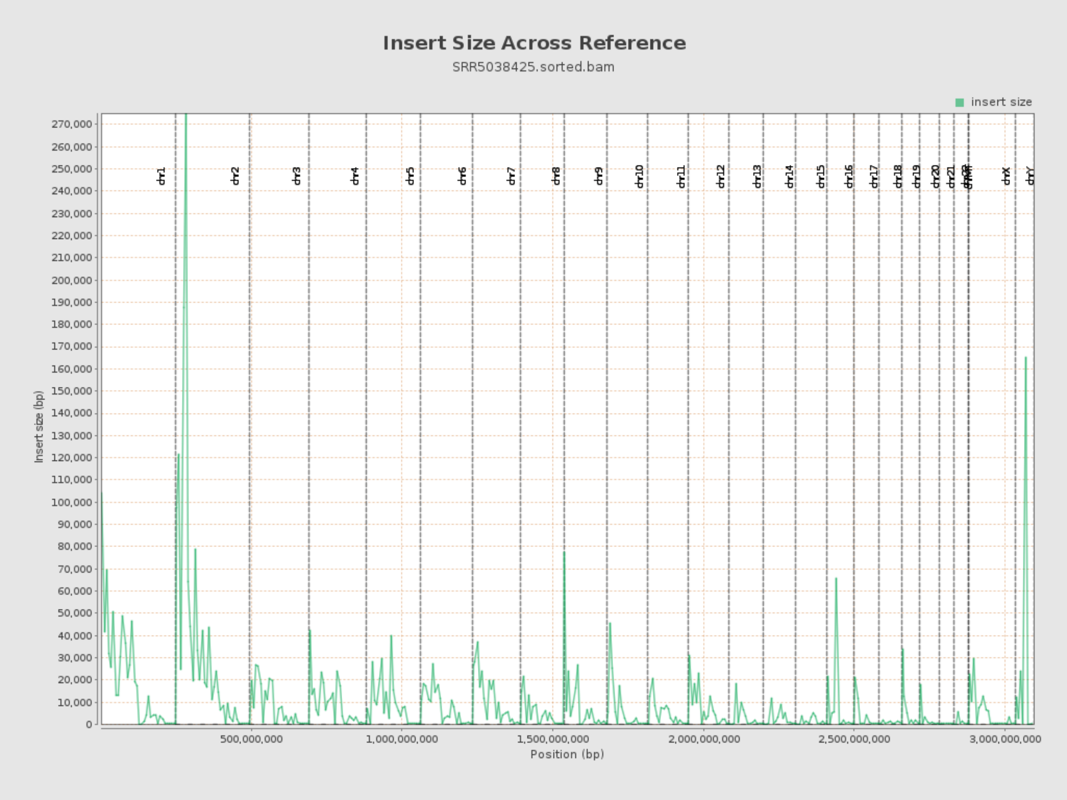
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram