Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/16 07:57:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038485.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_SRR5038485 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038485_1.fastq.gz SRR5038485_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Apr 16 07:57:00 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038485.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	17,263,240
Mapped reads	16,341,672 / 94.66%
Unmapped reads	921,568 / 5.34%
Mapped paired reads	16,341,672 / 94.66%
Mapped reads, first in pair	8,291,373 / 48.03%
Mapped reads, second in pair	8,050,299 / 46.63%
Mapped reads, both in pair	16,054,406 / 93%
Mapped reads, singletons	287,266 / 1.66%
Secondary alignments	0
Supplementary alignments	236,880 / 1.37%
Read min/max/mean length	30 / 150 / 150.68
Duplicated reads (estimated)	3,046,537 / 17.65%
Duplication rate	13.23%
Clipped reads	7,552,950 / 43.75%

2.2. ACGT Content

Number/percentage of A's	635,659,128 / 28.78%
Number/percentage of C's	432,761,413 / 19.6%
Number/percentage of T's	648,348,415 / 29.36%
Number/percentage of G's	491,402,245 / 22.25%
Number/percentage of N's	175,196 / 0.01%

GC Percentage	41.85%

2.3. Coverage

Mean	0.7138
Standard Deviation	8.7355

2.4. Mapping Quality

Mean Mapping Quality	53.49

2.5. Insert size

Mean	79,645.44
Standard Deviation	2,734,259.49
P25/Median/P75	211 / 264 / 330

2.6. Mismatches and indels

General error rate	1.3%
Mismatches	27,756,540
Insertions	386,487
Mapped reads with at least one insertion	2.26%
Deletions	771,333
Mapped reads with at least one deletion	4.56%
Homopolymer indels	48.34%

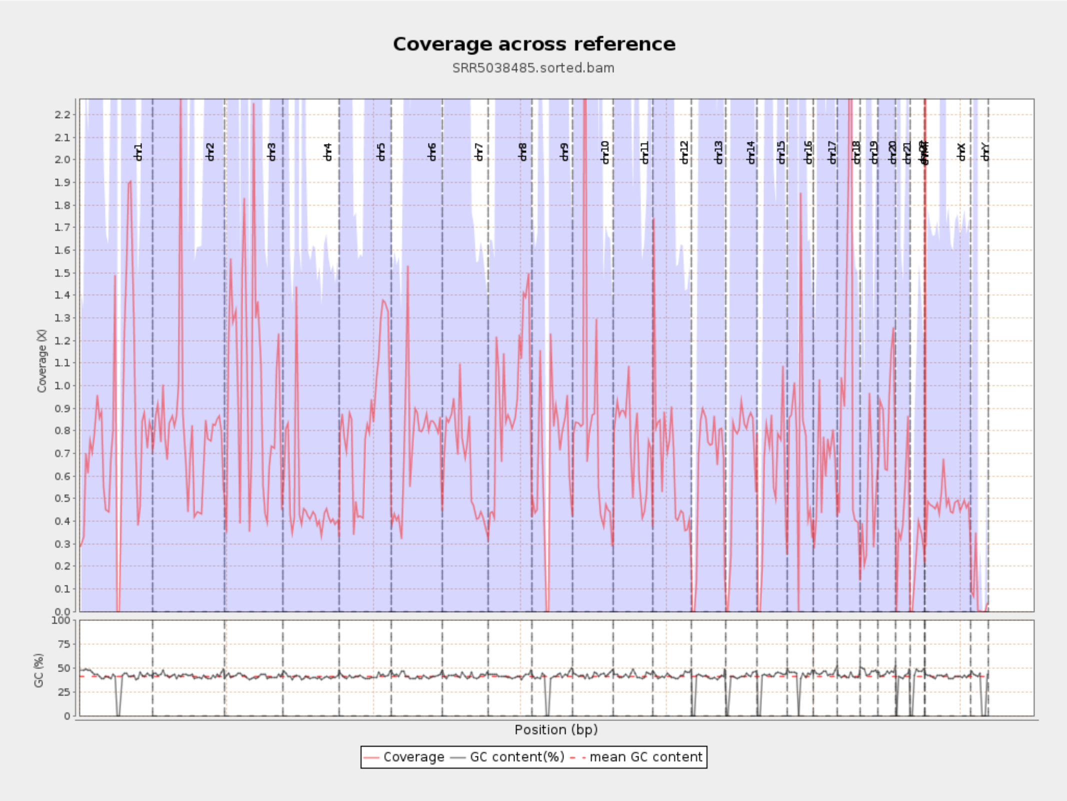
2.7. Chromosome stats

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

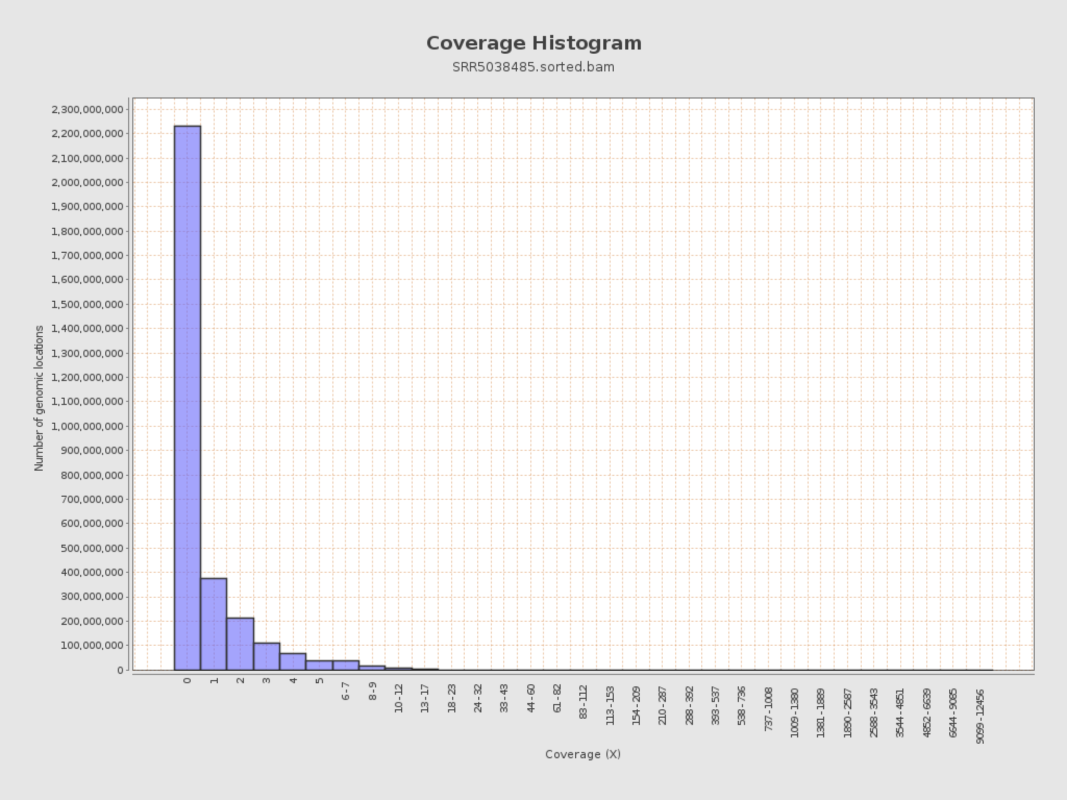
		bases	coverage	deviation
chr1	249250621	198894734	0.798	12.4796
chr2	243199373	193585044	0.796	9.6922
chr3	198022430	197796183	0.9989	2.0271
chr4	191154276	94086944	0.4922	8.6145
chr5	180915260	152272559	0.8417	1.715
chr6	171115067	128697833	0.7521	7.6026
chr7	159138663	104493430	0.6566	8.1346
chr8	146364022	138638398	0.9472	3.5351
chr9	141213431	92067959	0.652	15.1253
chr10	135534747	114701495	0.8463	21.5142
chr11	135006516	98876868	0.7324	7.2316
chr12	133851895	89050456	0.6653	1.6628
chr13	115169878	73629137	0.6393	1.4551
chr14	107349540	71768590	0.6686	1.5724
chr15	102531392	59053074	0.576	1.41
chr16	90354753	64883644	0.7181	8.0278
chr17	81195210	51747495	0.6373	10.0151
chr18	78077248	86381613	1.1064	10.1144
chr19	59128983	27169223	0.4595	5.4304
chr20	63025520	55502796	0.8806	3.1509
chr21	48129895	21361777	0.4438	4.0628
chr22	51304566	11379007	0.2218	0.828
chrMT	16571	6510403	392.8793	233.9643
chrX	155270560	73240806	0.4717	1.9641

chrY	59373566	4043045	0.0681	8.4927

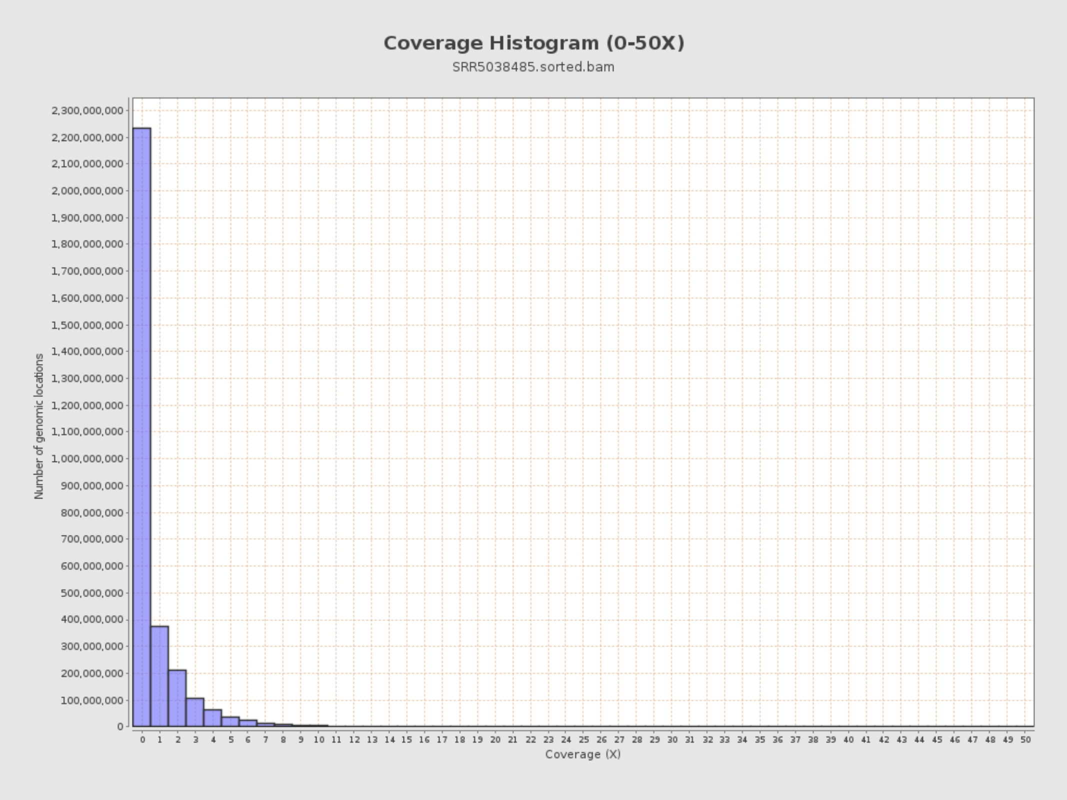
3. Results : Coverage across reference



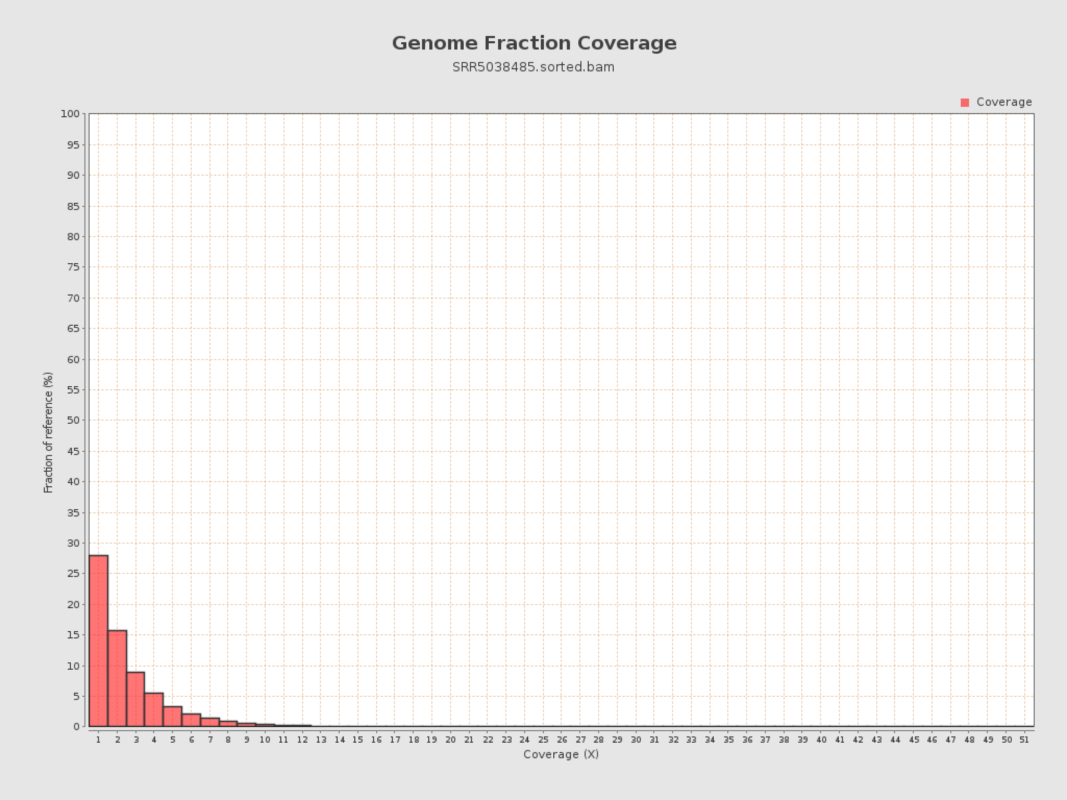
4. Results : Coverage Histogram



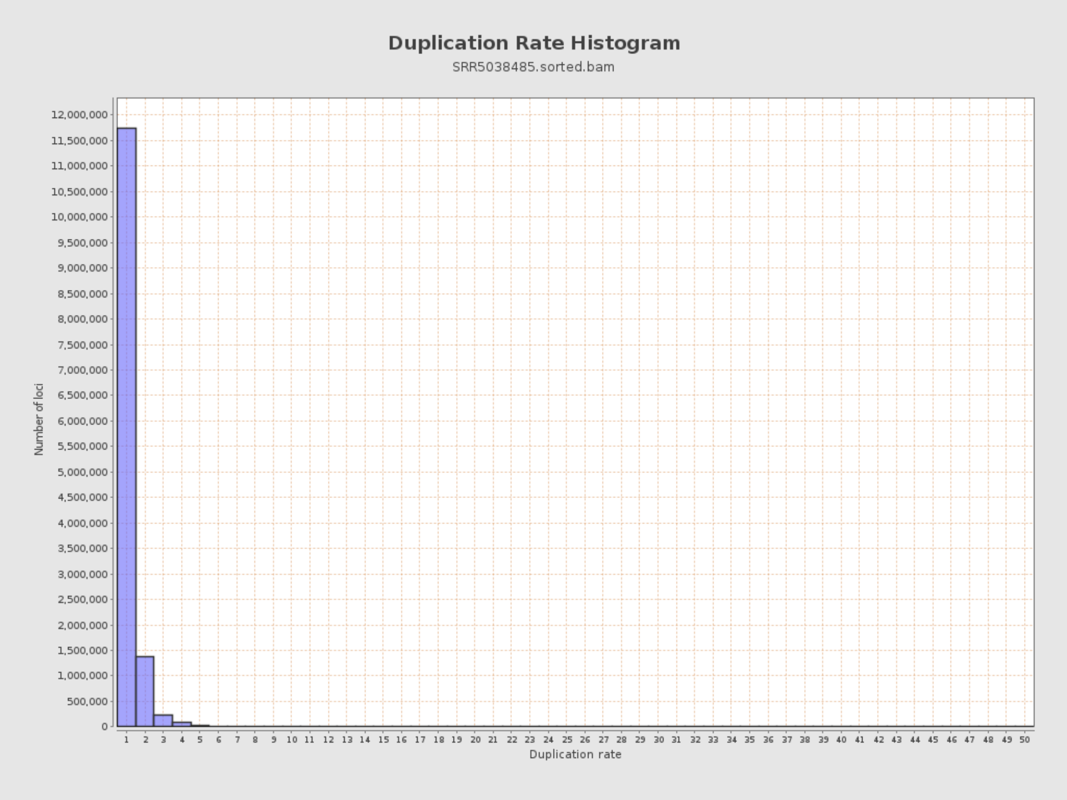
5. Results : Coverage Histogram (0-50X)



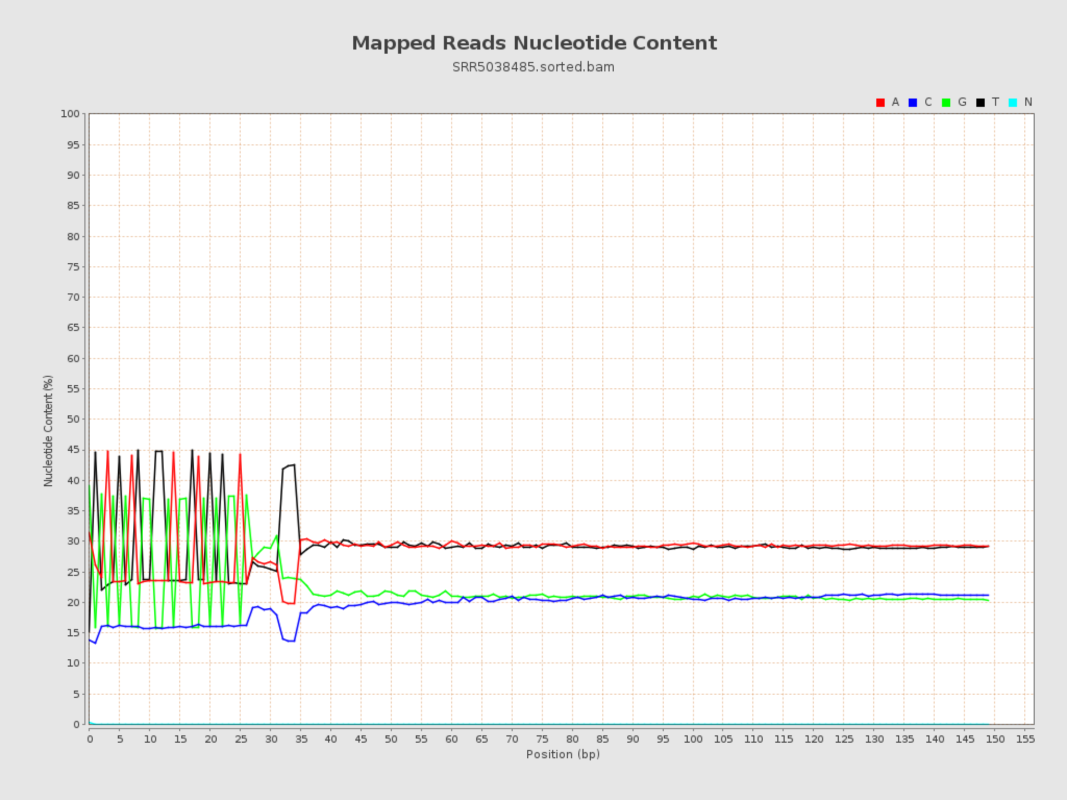
6. Results : Genome Fraction Coverage



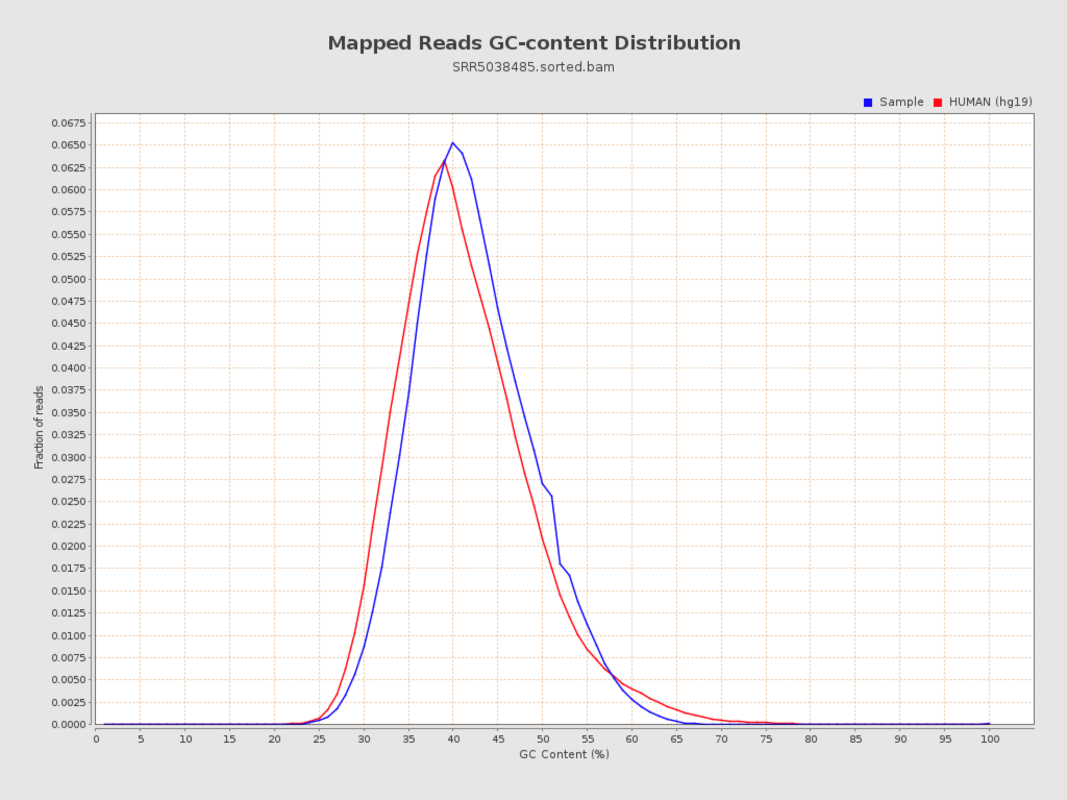
7. Results : Duplication Rate Histogram



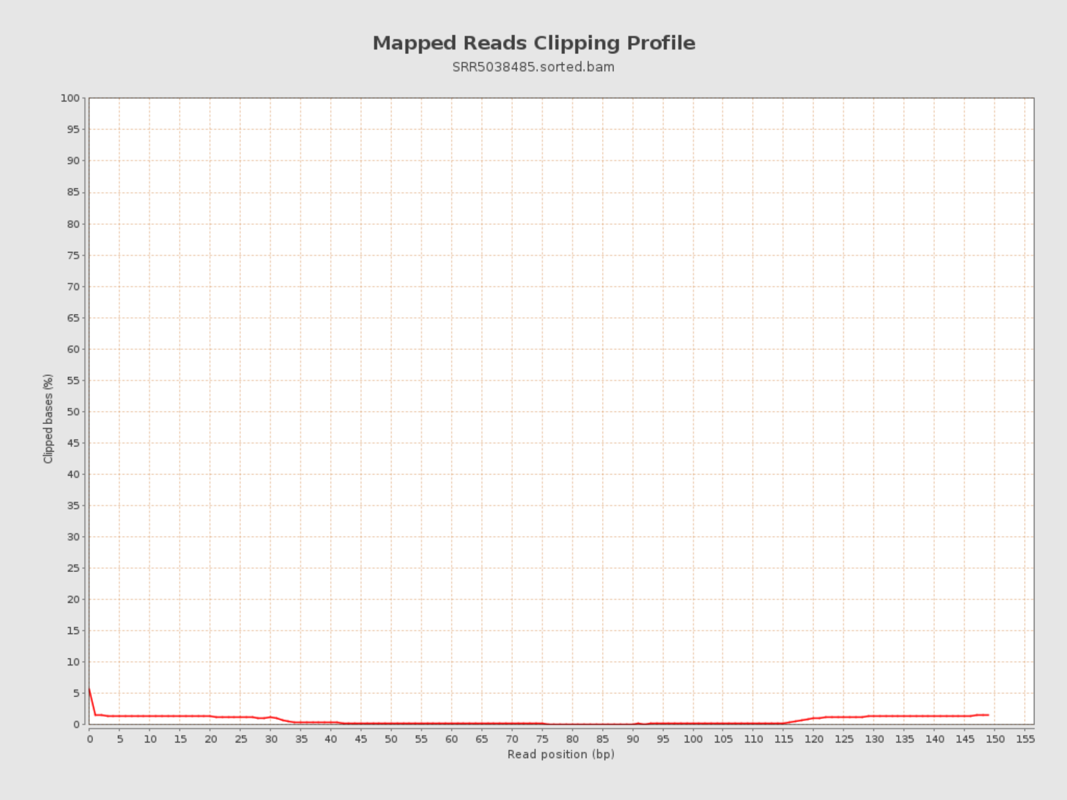
8. Results : Mapped Reads Nucleotide Content



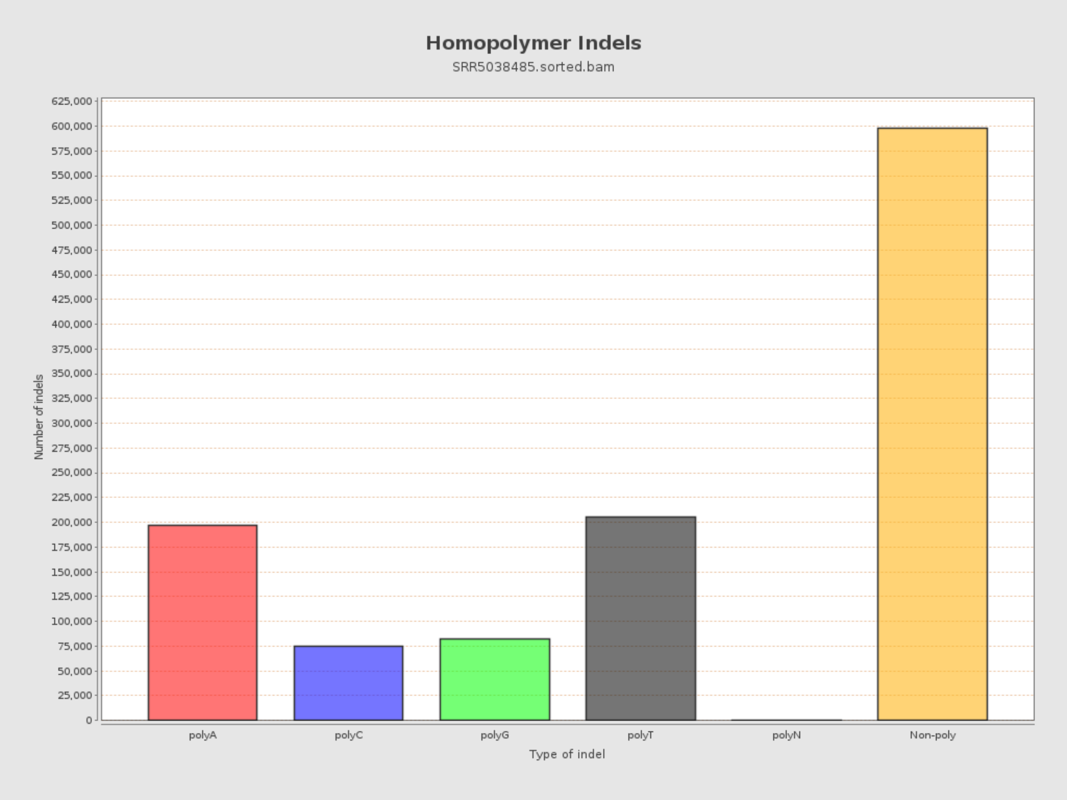
9. Results : Mapped Reads GC-content Distribution



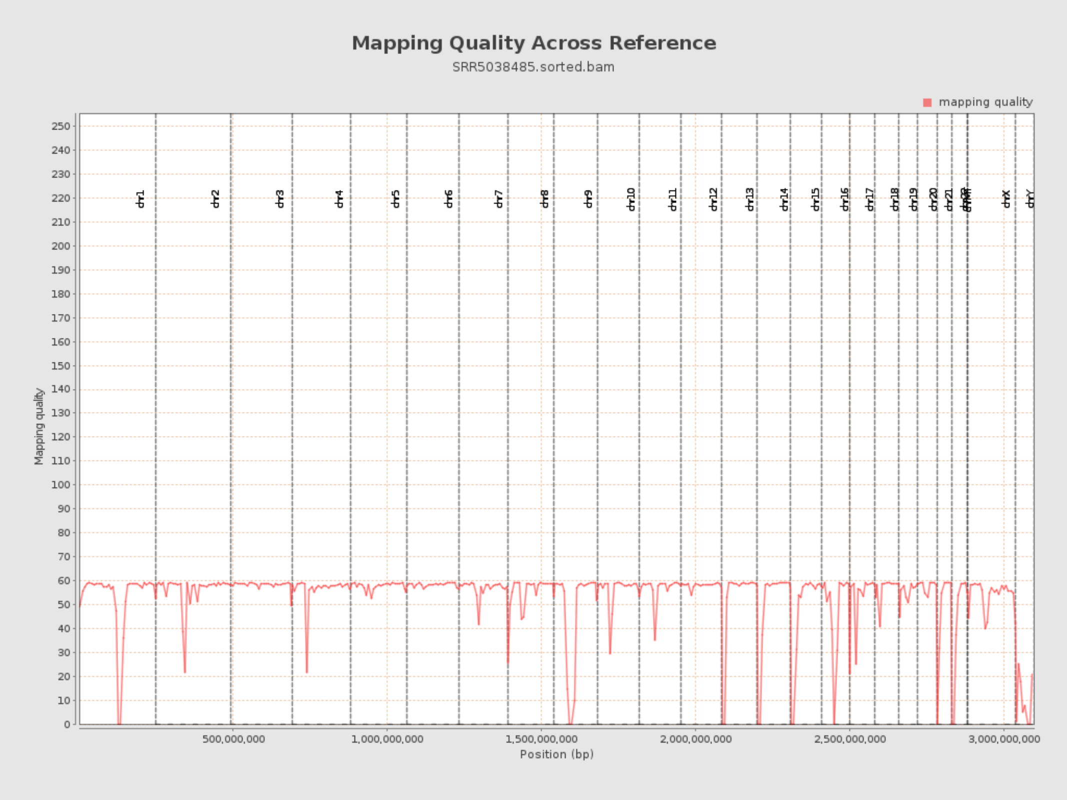
10. Results : Mapped Reads Clipping Profile



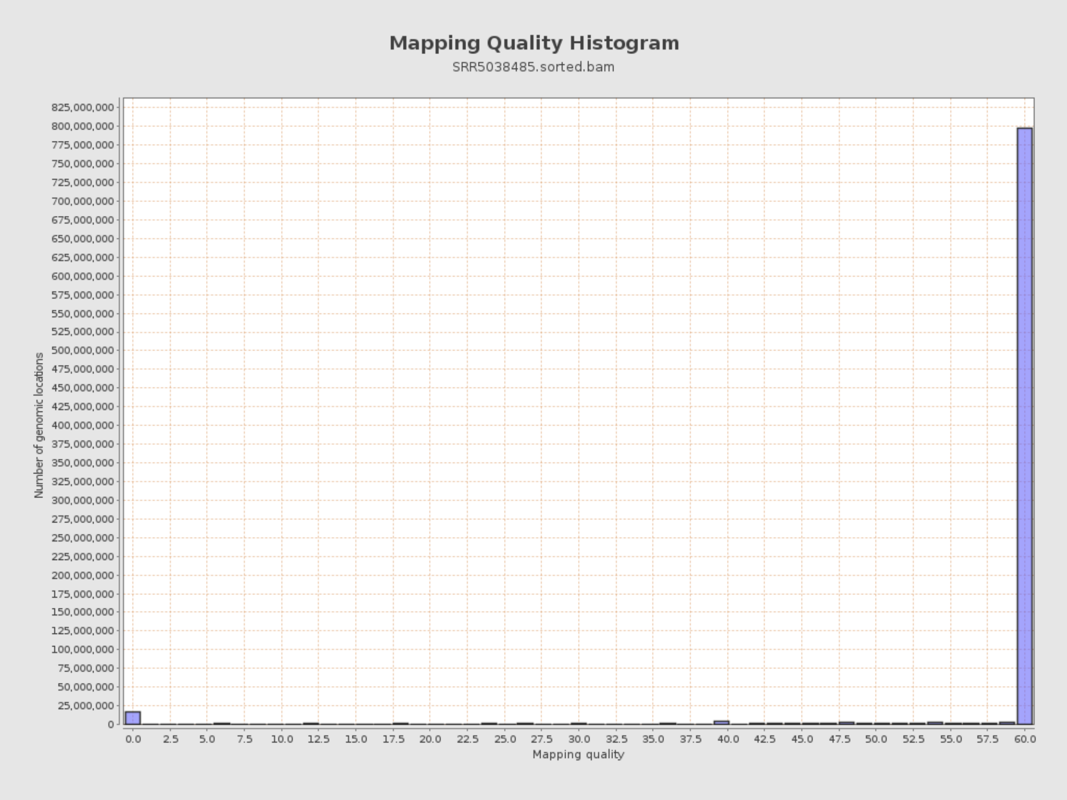
11. Results : Homopolymer Indels



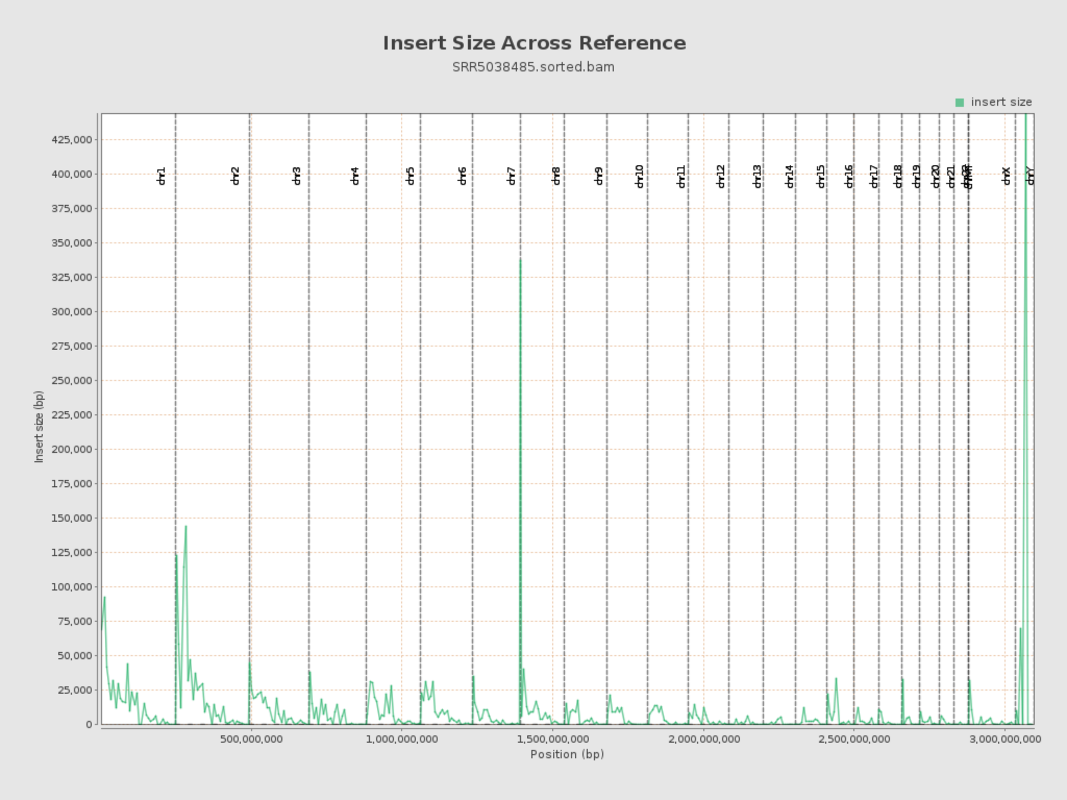
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram