Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/16 08:36:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038487.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_SRR5038487 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038487_1.fastq.gz SRR5038487_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Apr 16 08:36:03 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038487.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	16,292,648
Mapped reads	15,576,459 / 95.6%
Unmapped reads	716,189 / 4.4%
Mapped paired reads	15,576,459 / 95.6%
Mapped reads, first in pair	7,859,907 / 48.24%
Mapped reads, second in pair	7,716,552 / 47.36%
Mapped reads, both in pair	15,412,904 / 94.6%
Mapped reads, singletons	163,555 / 1%
Secondary alignments	0
Supplementary alignments	222,564 / 1.37%
Read min/max/mean length	30 / 150 / 150.71
Duplicated reads (estimated)	2,474,054 / 15.19%
Duplication rate	10.22%
Clipped reads	3,185,918 / 19.55%

2.2. ACGT Content

Number/percentage of A's	654,075,705 / 29.1%
Number/percentage of C's	466,719,719 / 20.77%
Number/percentage of T's	649,954,254 / 28.92%
Number/percentage of G's	476,777,210 / 21.21%
Number/percentage of N's	49,360 / 0%

GC Percentage	41.98%

2.3. Coverage

Mean	0.7265
Standard Deviation	11.53

2.4. Mapping Quality

Mean Mapping Quality	53.7

2.5. Insert size

Mean	62,844.85
Standard Deviation	2,372,818.87
P25/Median/P75	197 / 241 / 296

2.6. Mismatches and indels

General error rate	1.4%
Mismatches	30,552,283
Insertions	378,204
Mapped reads with at least one insertion	2.3%
Deletions	760,693
Mapped reads with at least one deletion	4.7%
Homopolymer indels	47.46%

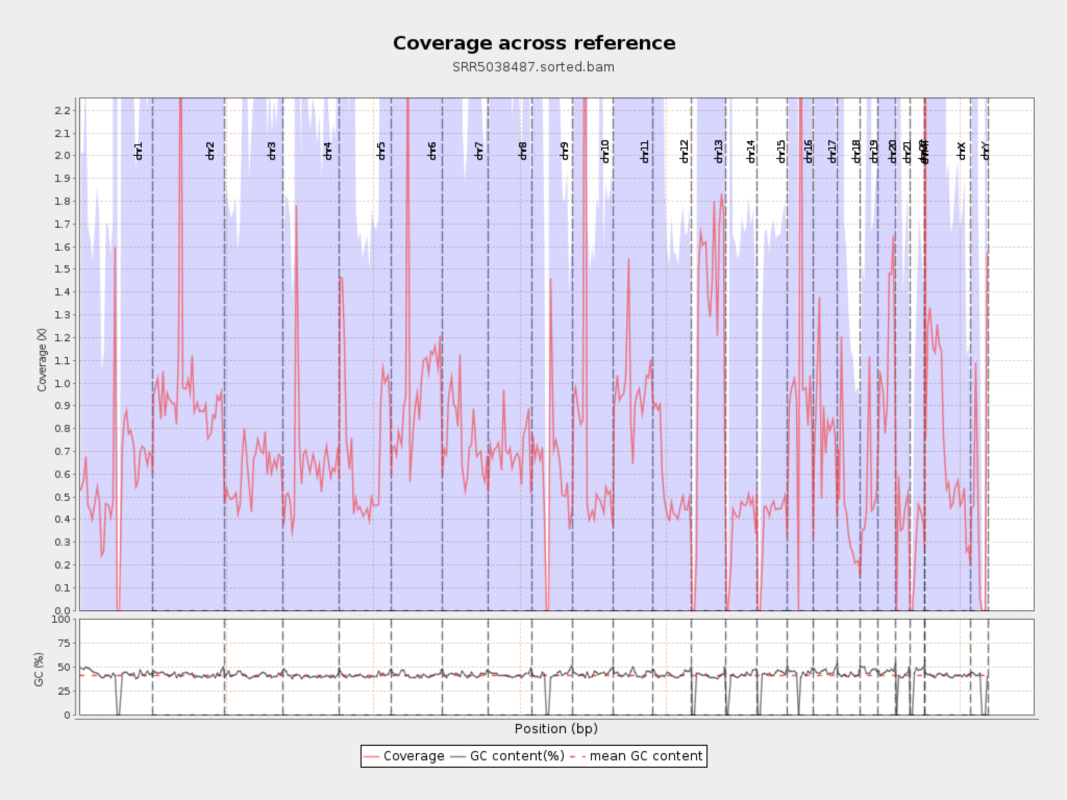
2.7. Chromosome stats

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

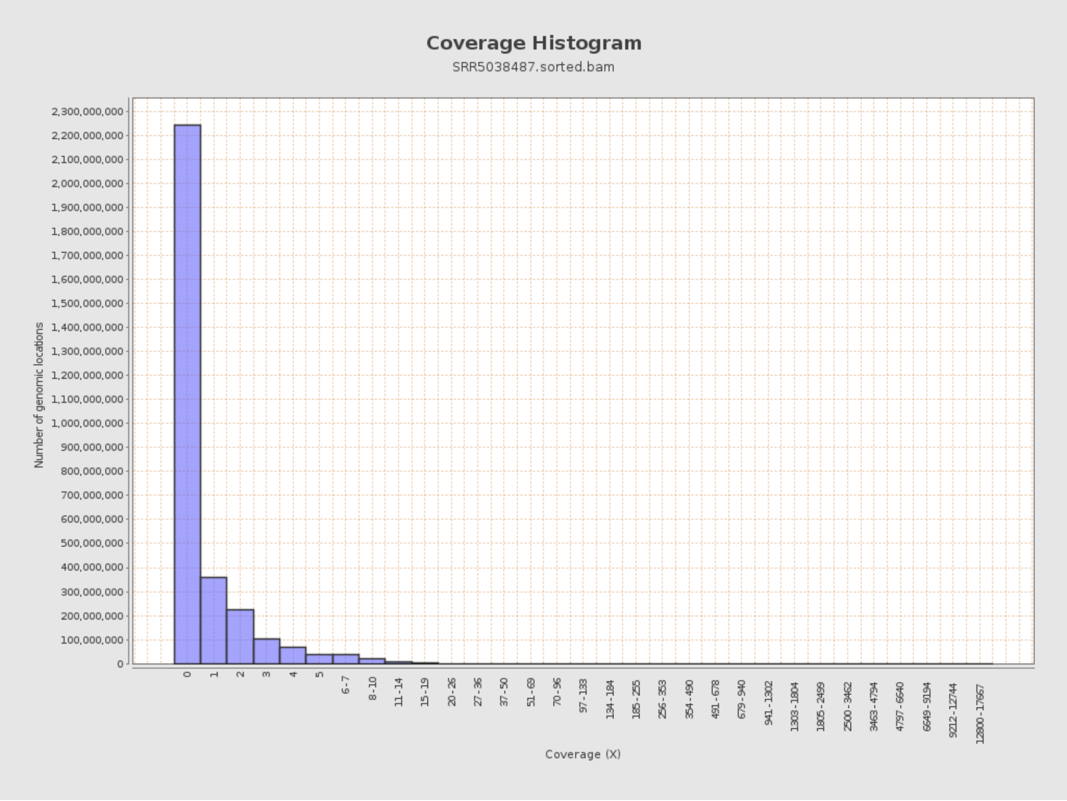
		bases	coverage	deviation
chr1	249250621	144099024	0.5781	18.0553
chr2	243199373	239988645	0.9868	11.9641
chr3	198022430	121689698	0.6145	1.4892
chr4	191154276	123012795	0.6435	8.1944
chr5	180915260	130100487	0.7191	1.6887
chr6	171115067	173014106	1.0111	19.7653
chr7	159138663	119224716	0.7492	8.5331
chr8	146364022	103805853	0.7092	2.939
chr9	141213431	82950392	0.5874	16.5047
chr10	135534747	103890451	0.7665	22.7587
chr11	135006516	129986854	0.9628	11.3401
chr12	133851895	74437889	0.5561	1.4
chr13	115169878	148927913	1.2931	2.4233
chr14	107349540	40013377	0.3727	1.3063
chr15	102531392	38461832	0.3751	1.0567
chr16	90354753	92049019	1.0188	15.4294
chr17	81195210	65668496	0.8088	14.3036
chr18	78077248	33538989	0.4296	15.0447
chr19	59128983	29633963	0.5012	10.6415
chr20	63025520	71498023	1.1344	3.2613
chr21	48129895	19015886	0.3951	3.9074
chr22	51304566	13970265	0.2723	0.93
chrMT	16571	3040721	183.4965	132.3209
chrX	155270560	116009860	0.7471	3.1613

chrY	59373566	31043542	0.5229	11.7647

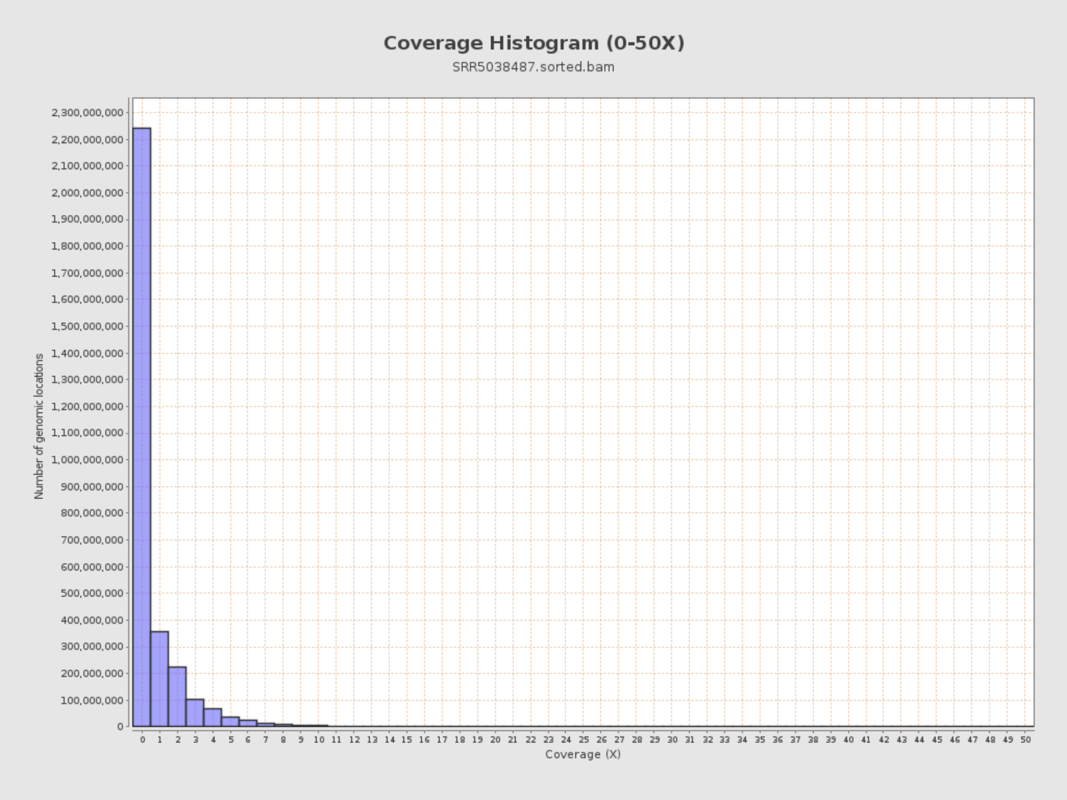
3. Results : Coverage across reference



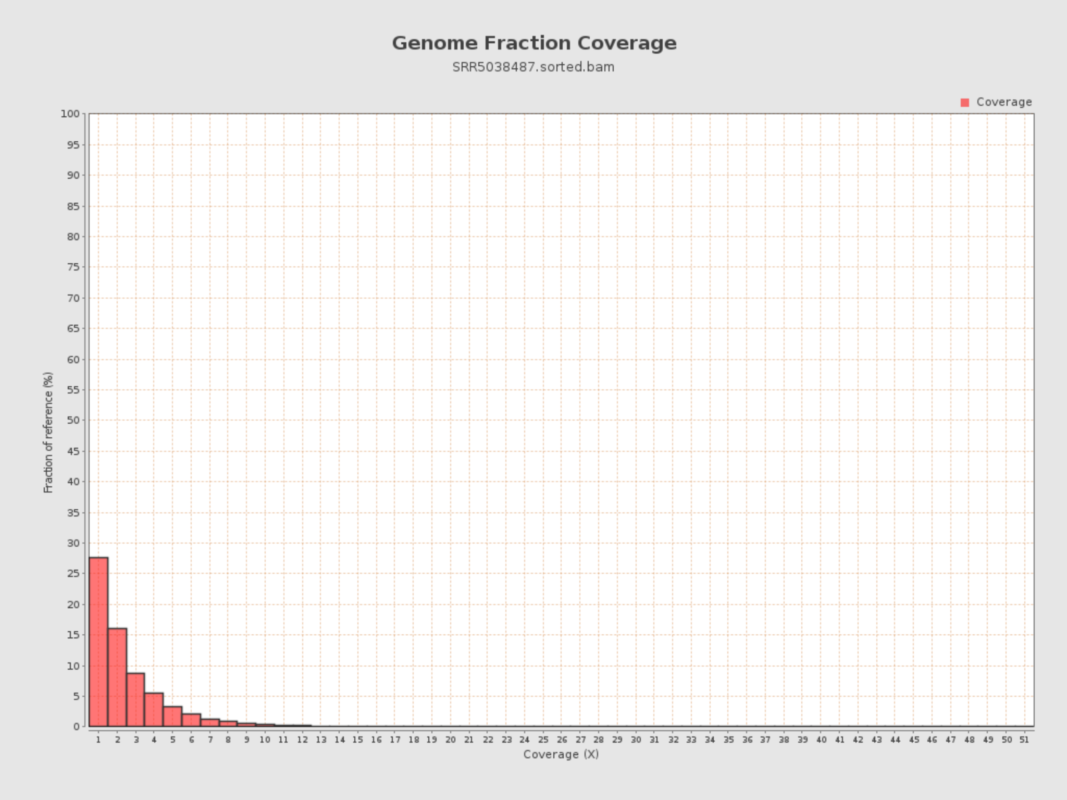
4. Results : Coverage Histogram



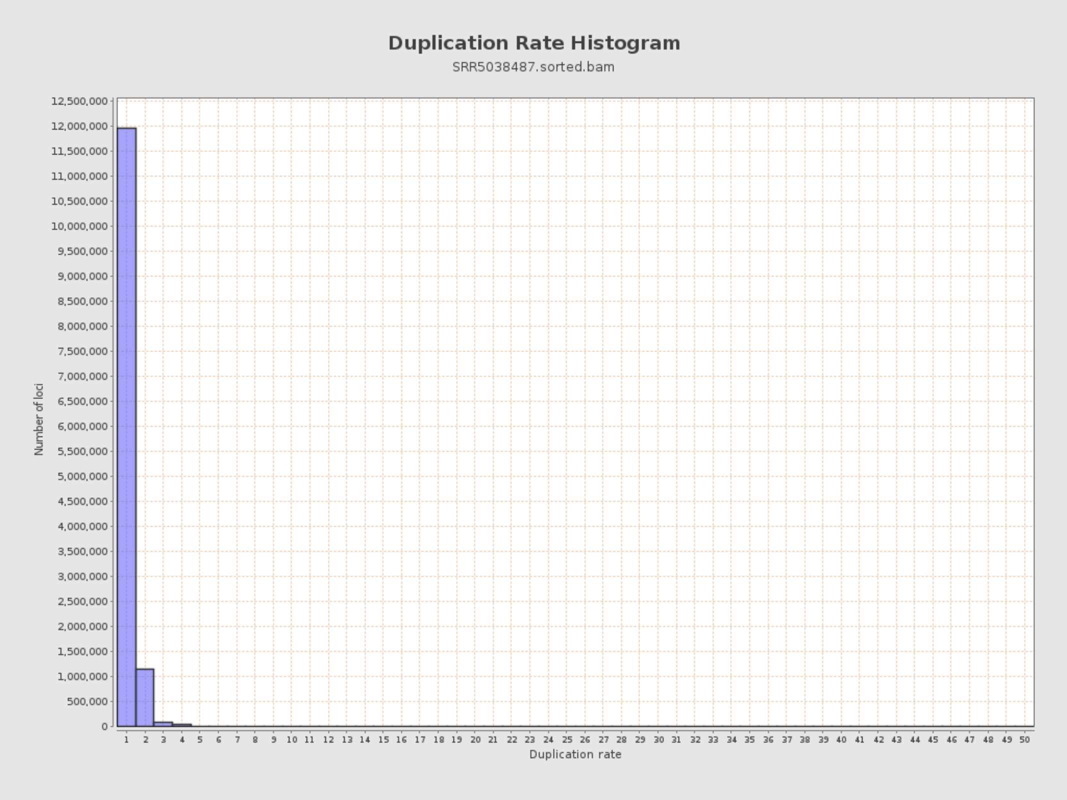
5. Results : Coverage Histogram (0-50X)



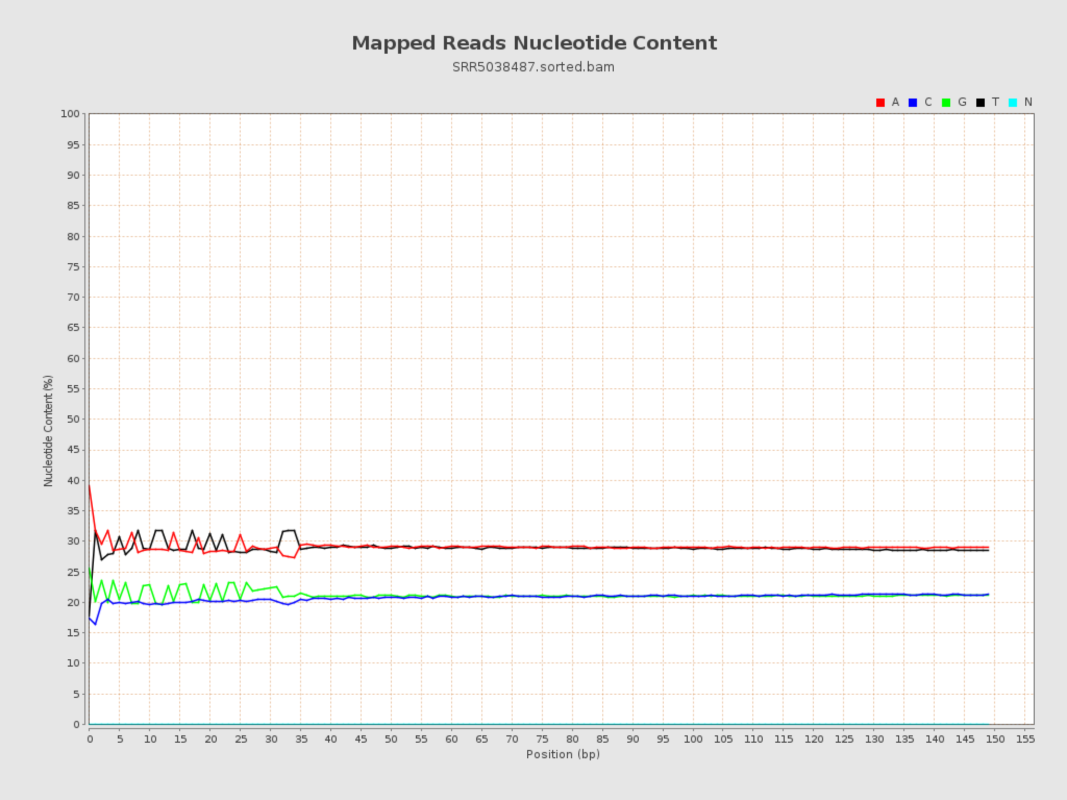
6. Results : Genome Fraction Coverage



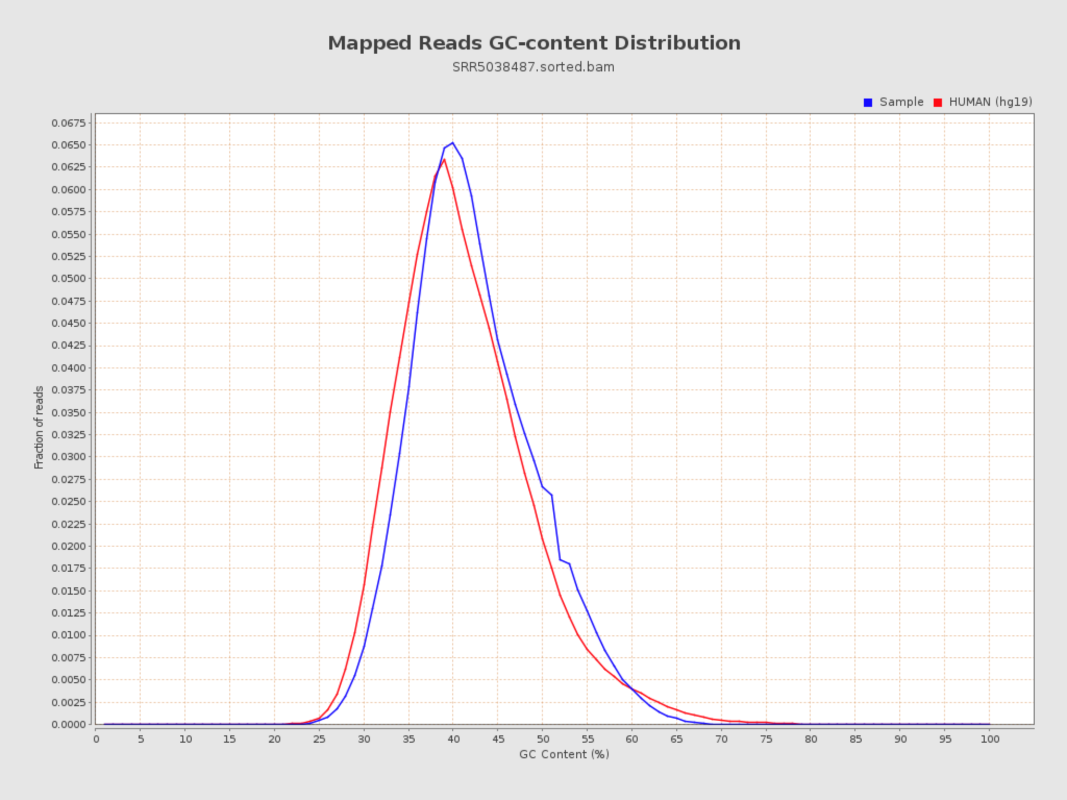
7. Results : Duplication Rate Histogram



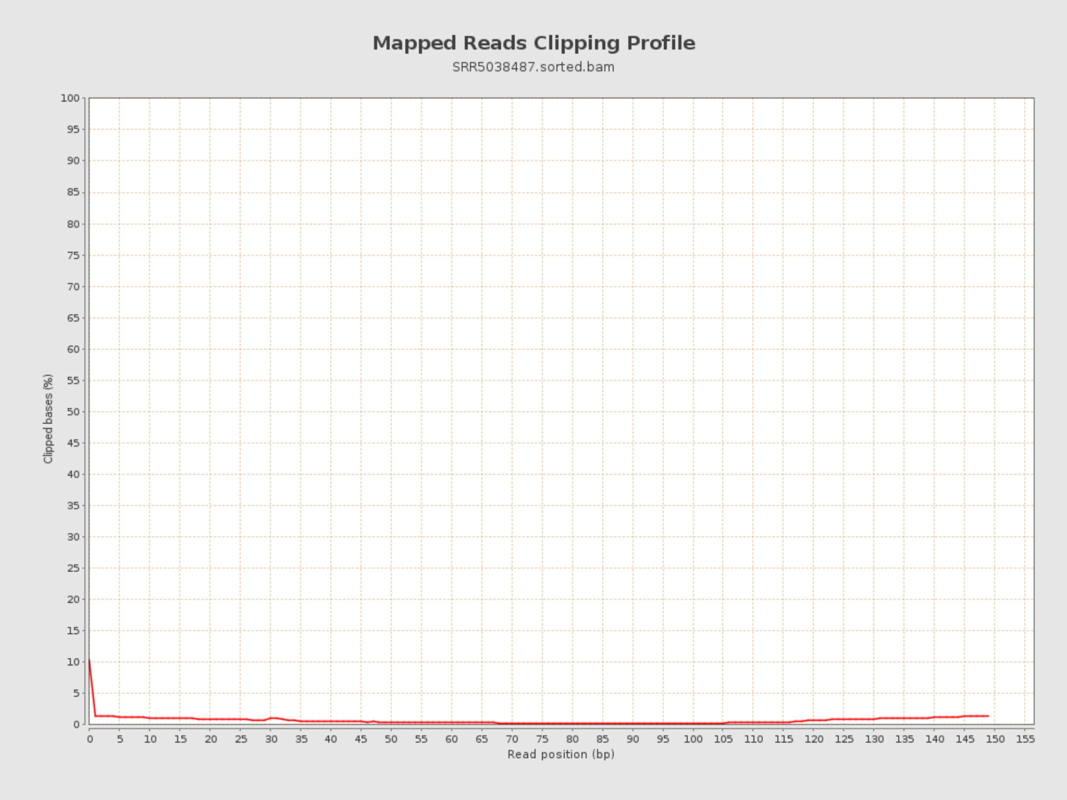
8. Results : Mapped Reads Nucleotide Content



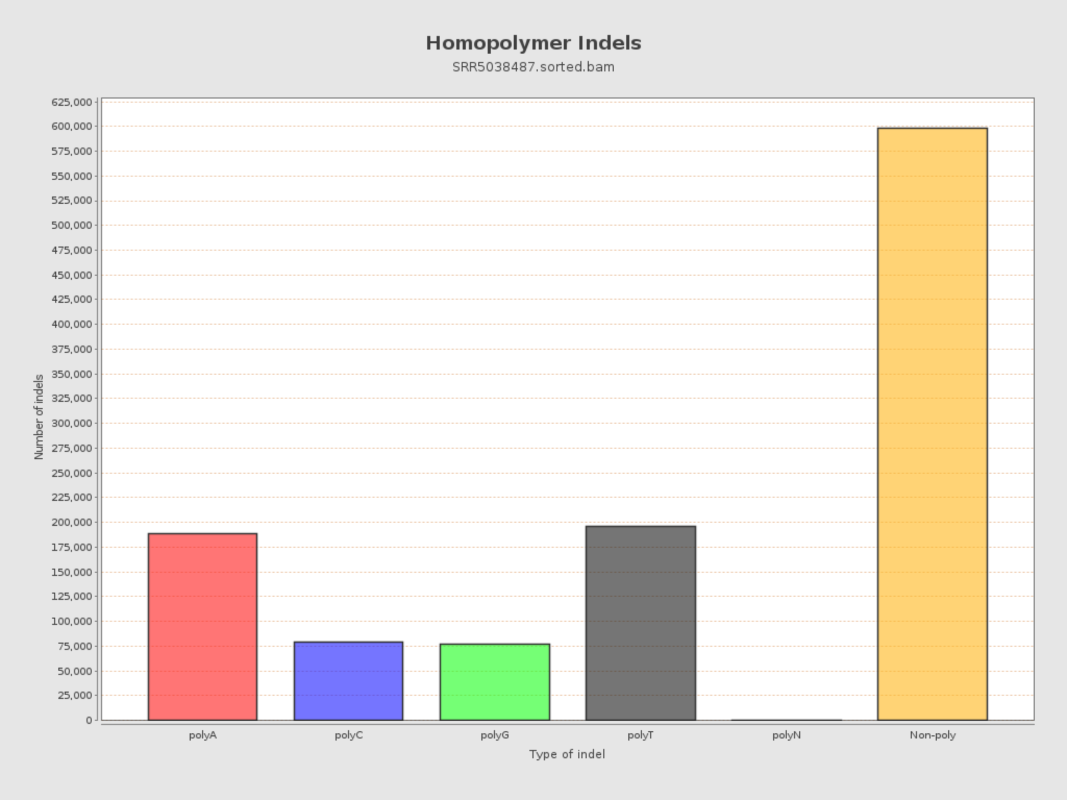
9. Results : Mapped Reads GC-content Distribution



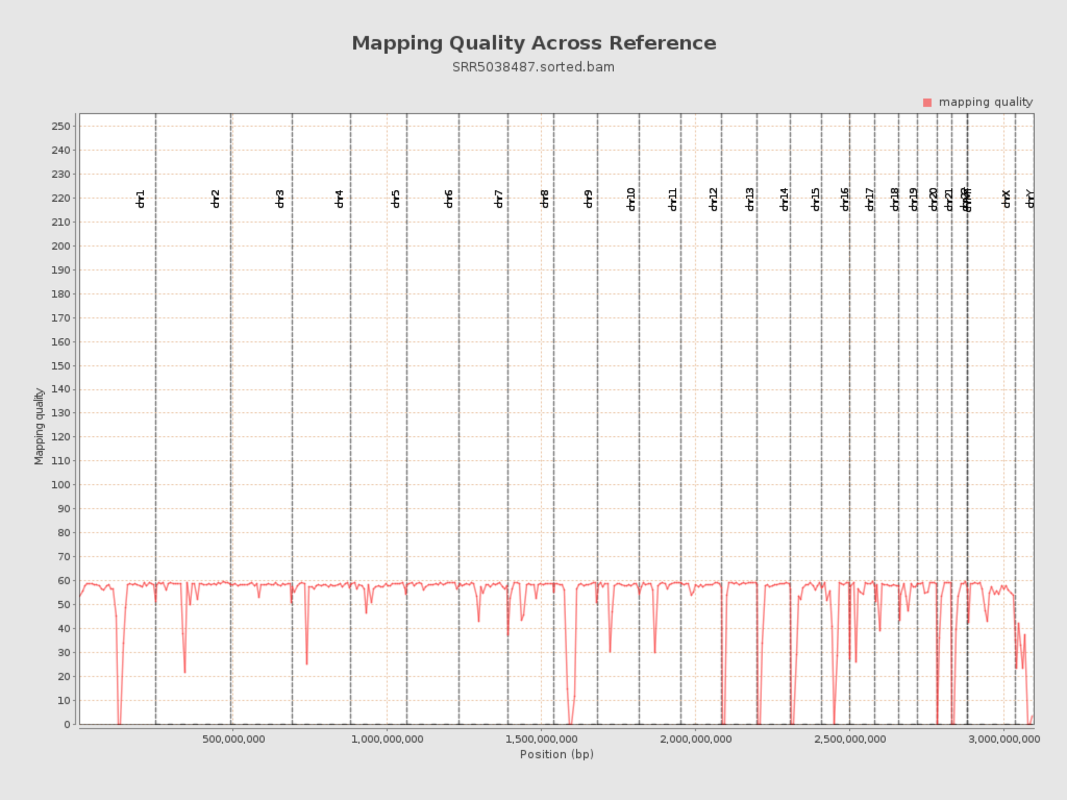
10. Results : Mapped Reads Clipping Profile



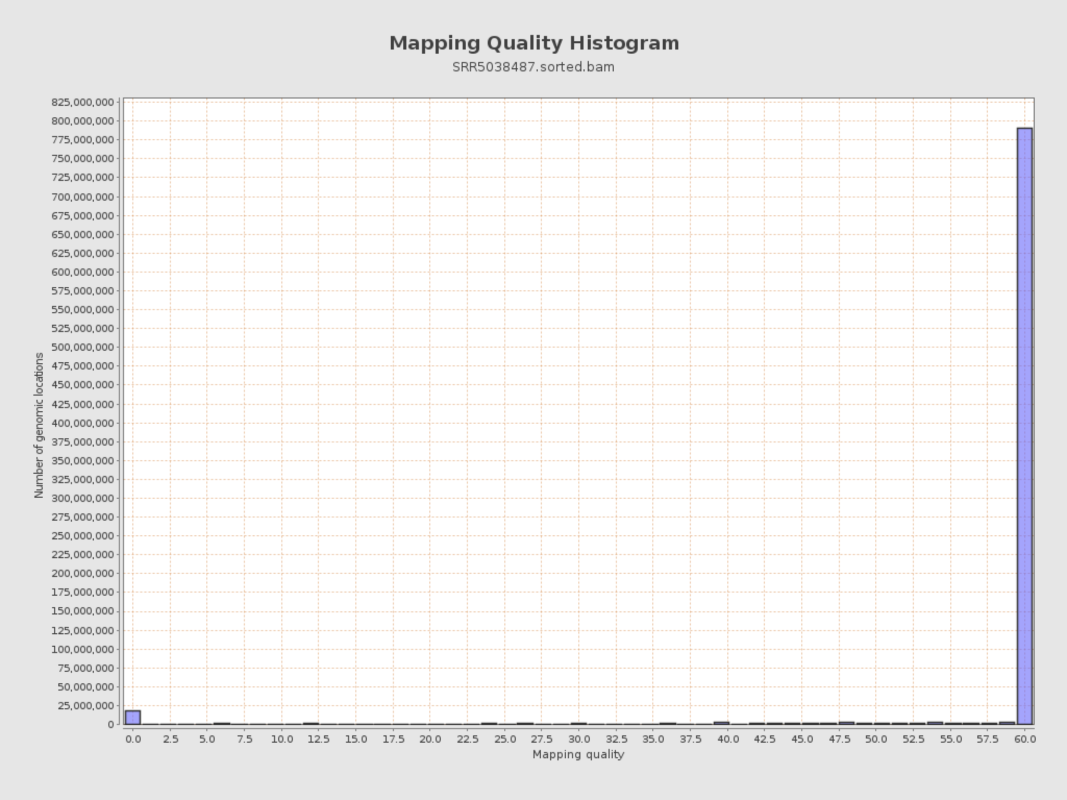
11. Results : Homopolymer Indels



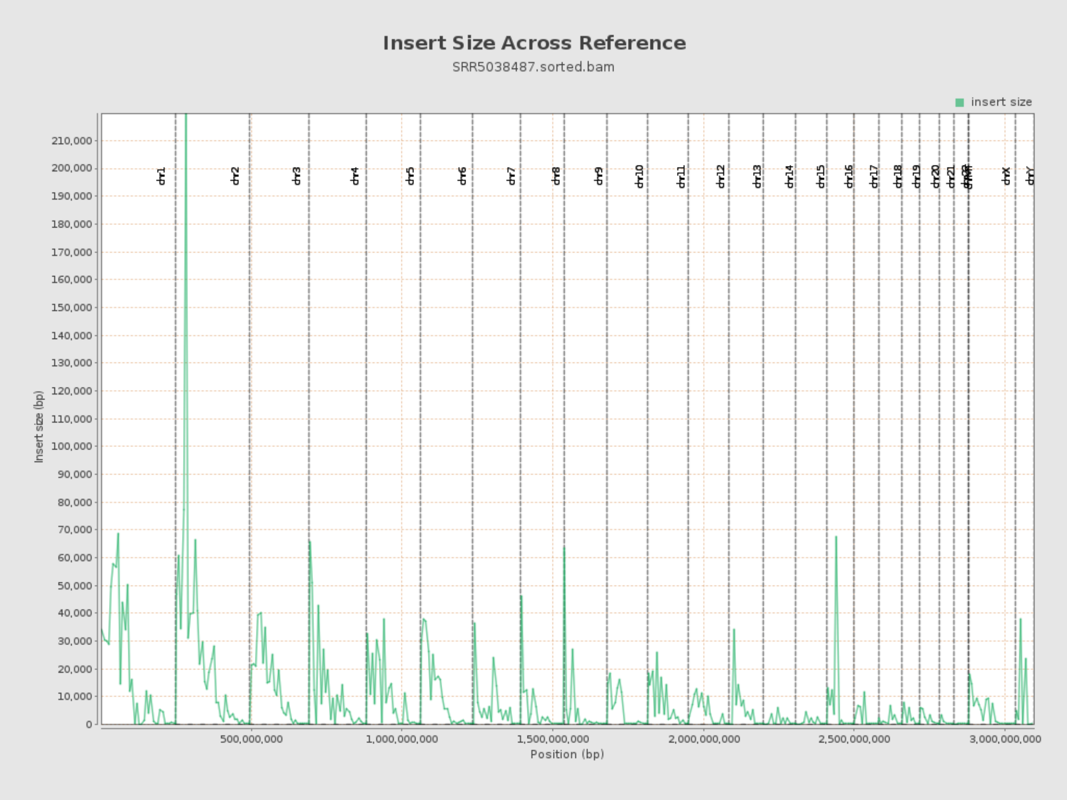
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram