Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/15 07:01:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038434.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_SRR5038434 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038434_1.fastq.gz SRR5038434_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 15 07:01:42 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038434.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	78,963,578
Mapped reads	78,598,645 / 99.54%
Unmapped reads	364,933 / 0.46%
Mapped paired reads	78,598,645 / 99.54%
Mapped reads, first in pair	39,418,584 / 49.92%
Mapped reads, second in pair	39,180,061 / 49.62%
Mapped reads, both in pair	78,323,716 / 99.19%
Mapped reads, singletons	274,929 / 0.35%
Secondary alignments	0
Supplementary alignments	106,508 / 0.13%
Read min/max/mean length	30 / 150 / 150.06
Duplicated reads (estimated)	30,374,351 / 38.47%
Duplication rate	36.62%
Clipped reads	5,049,355 / 6.39%

2.2. ACGT Content

Number/percentage of A's	2,951,596,002 / 25.27%
Number/percentage of C's	2,886,638,984 / 24.72%
Number/percentage of T's	2,972,664,134 / 25.45%
Number/percentage of G's	2,866,740,537 / 24.55%
Number/percentage of N's	1,186,385 / 0.01%

GC Percentage	49.26%

2.3. Coverage

Mean	3.7732
Standard Deviation	23.6034

2.4. Mapping Quality

Mean Mapping Quality	55.73

2.5. Insert size

Mean	20,743.68
Standard Deviation	1,510,183.78
P25/Median/P75	202 / 236 / 276

2.6. Mismatches and indels

General error rate	0.55%
Mismatches	62,270,970
Insertions	556,824
Mapped reads with at least one insertion	0.68%
Deletions	677,166
Mapped reads with at least one deletion	0.84%
Homopolymer indels	46.45%

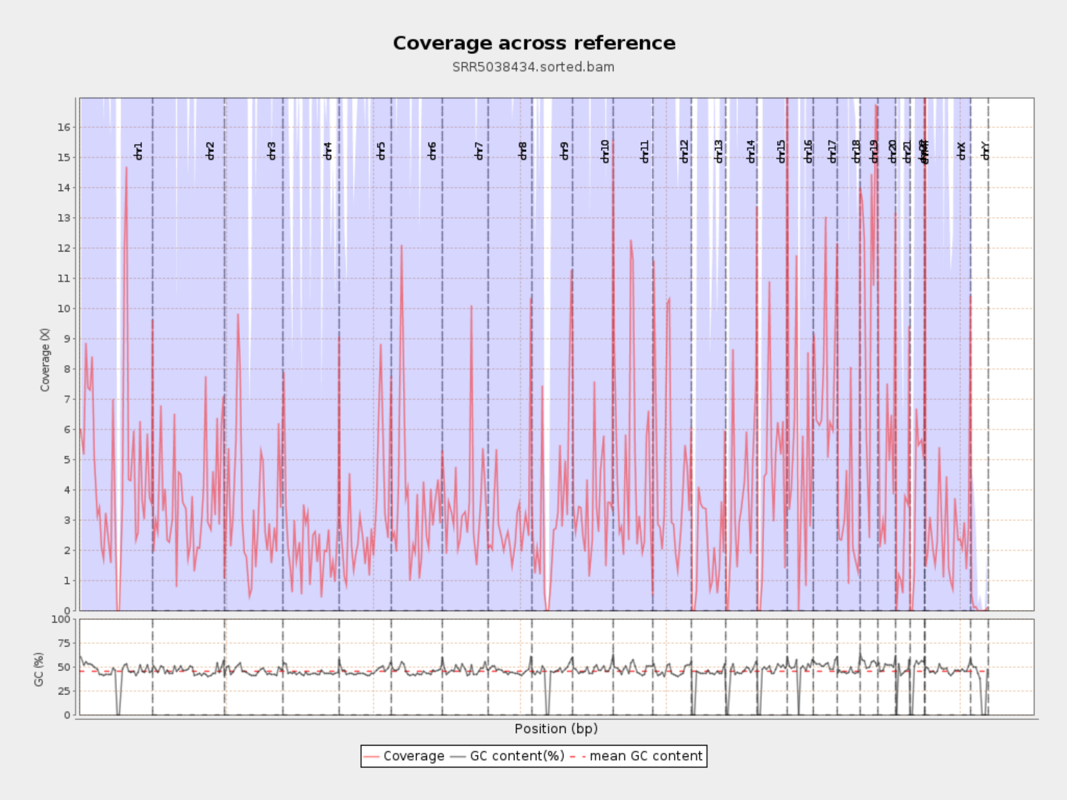
2.7. Chromosome stats

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

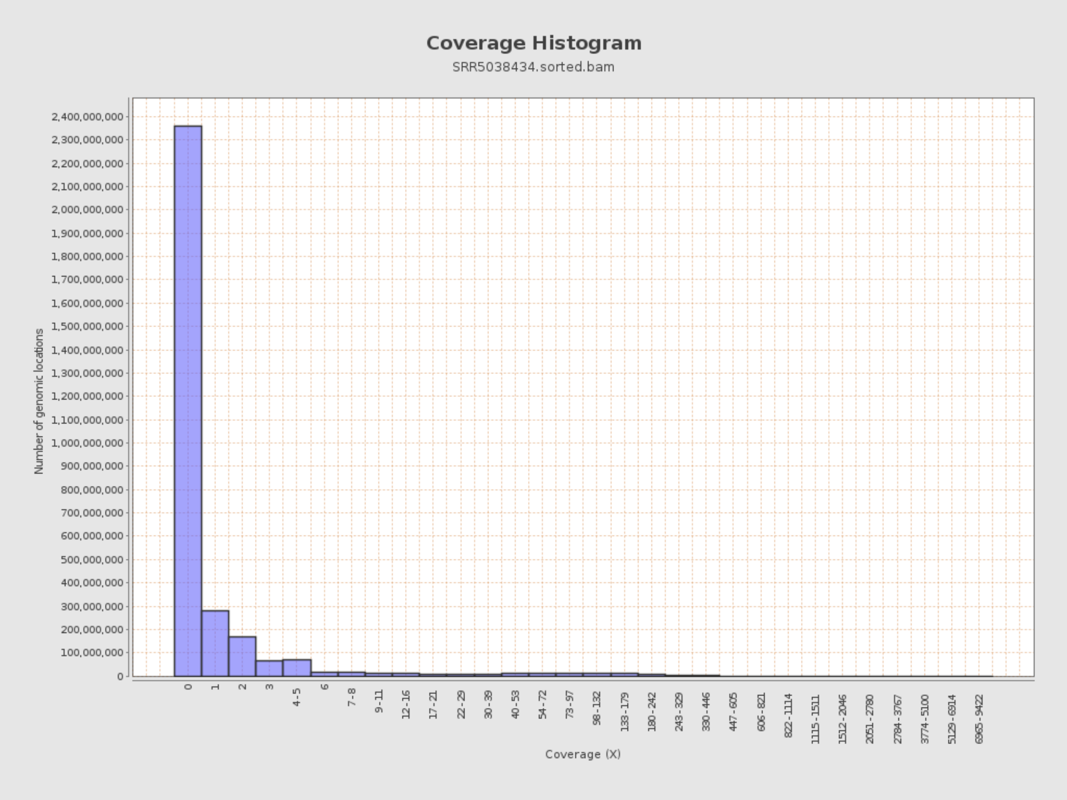
		bases	coverage	deviation
chr1	249250621	1188155715	4.7669	27.4978
chr2	243199373	876500994	3.604	23.9908
chr3	198022430	677221932	3.4199	21.9633
chr4	191154276	420369325	2.1991	16.4694
chr5	180915260	574421969	3.1751	21.9132
chr6	171115067	602238005	3.5195	22.7117
chr7	159138663	566388162	3.5591	22.7514
chr8	146364022	445650467	3.0448	21.092
chr9	141213431	477021334	3.378	21.9974
chr10	135534747	460273503	3.396	21.1048
chr11	135006516	680321082	5.0392	28.4095
chr12	133851895	620762641	4.6377	25.7491
chr13	115169878	229849109	1.9957	16.426
chr14	107349540	398152803	3.7089	23.4235
chr15	102531392	423346812	4.1289	23.9761
chr16	90354753	488222960	5.4034	28.3455
chr17	81195210	631095148	7.7726	33.0589
chr18	78077248	224480758	2.8751	23.3583
chr19	59128983	663016948	11.2131	40.2899
chr20	63025520	311274159	4.9389	27.7479
chr21	48129895	124339148	2.5834	22.0564
chr22	51304566	204951063	3.9948	20.9046
chrMT	16571	1041185	62.8318	22.8245
chrX	155270560	386390491	2.4885	17.6762

chrY	59373566	5218633	0.0879	2.2833

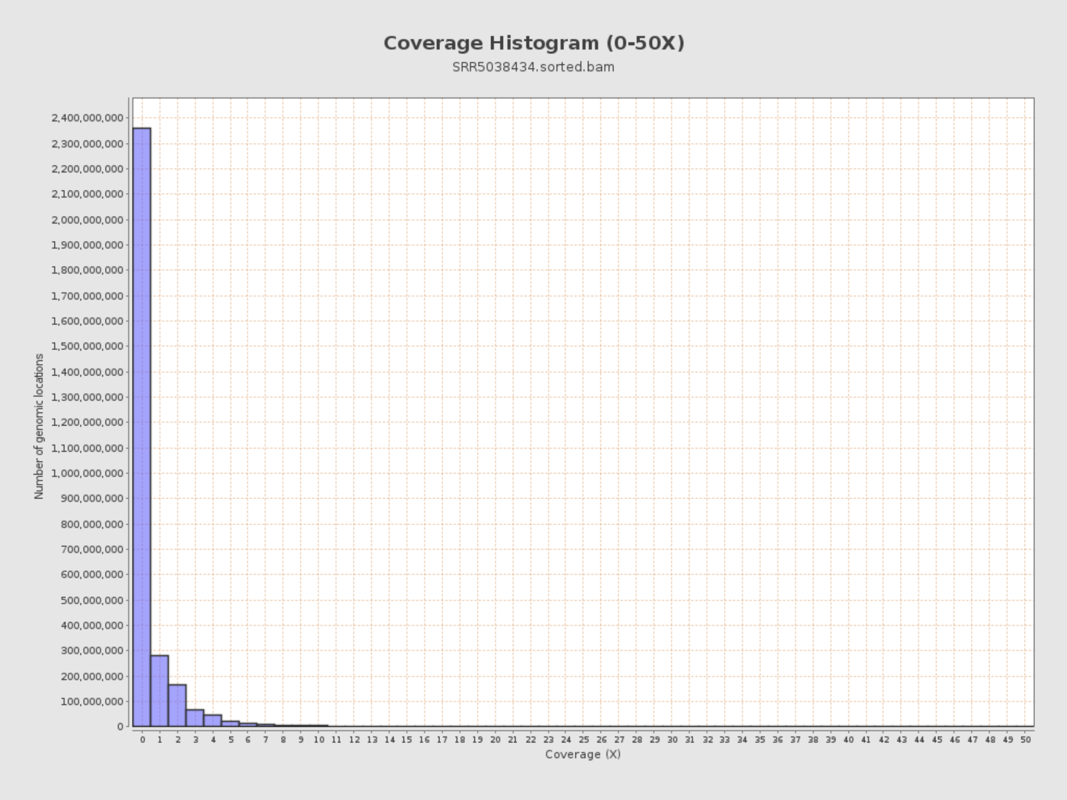
3. Results : Coverage across reference



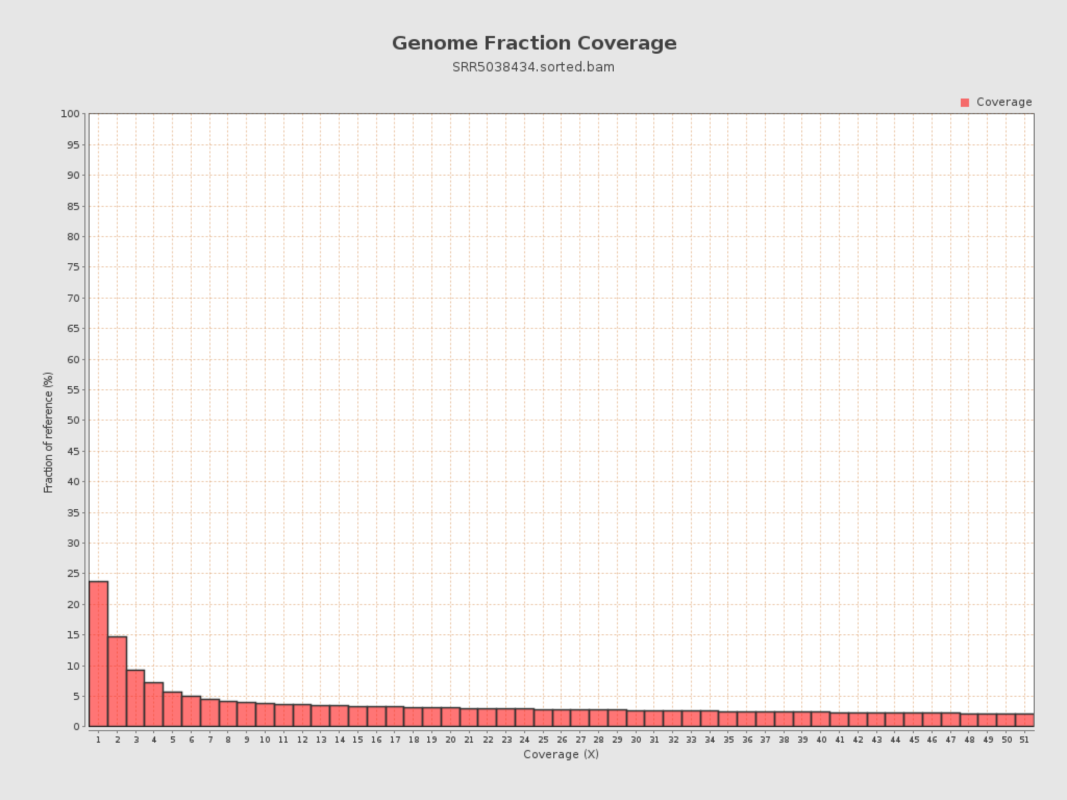
4. Results : Coverage Histogram



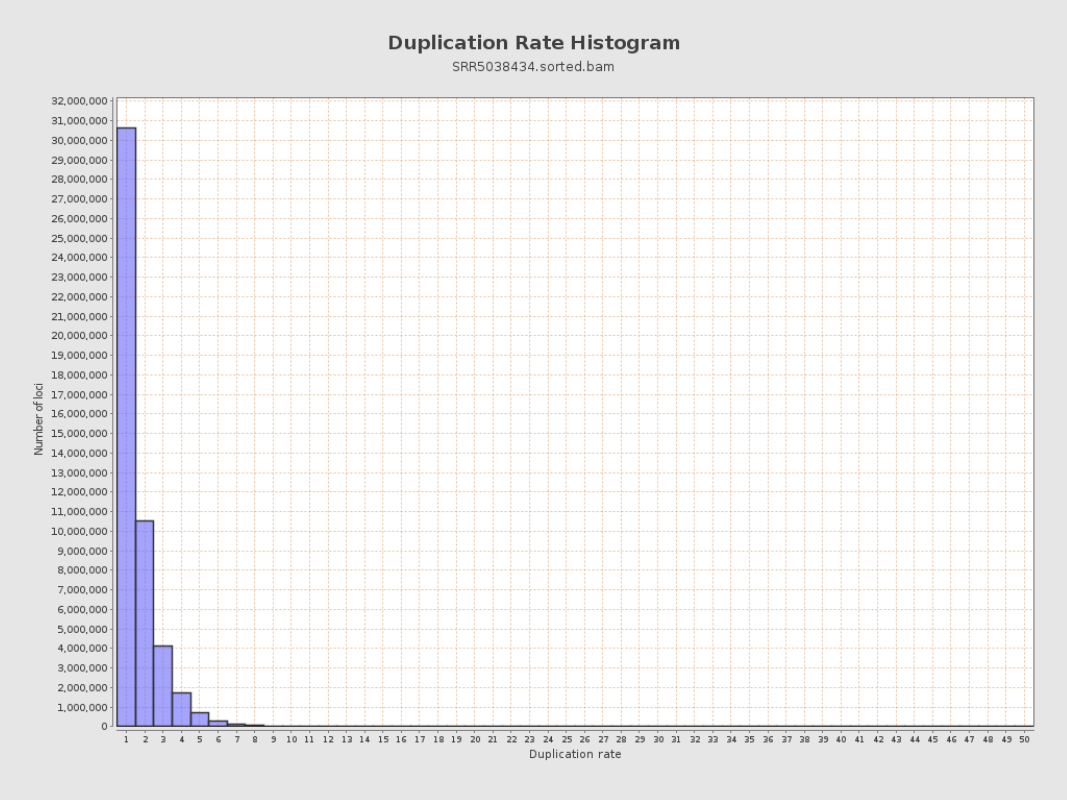
5. Results : Coverage Histogram (0-50X)



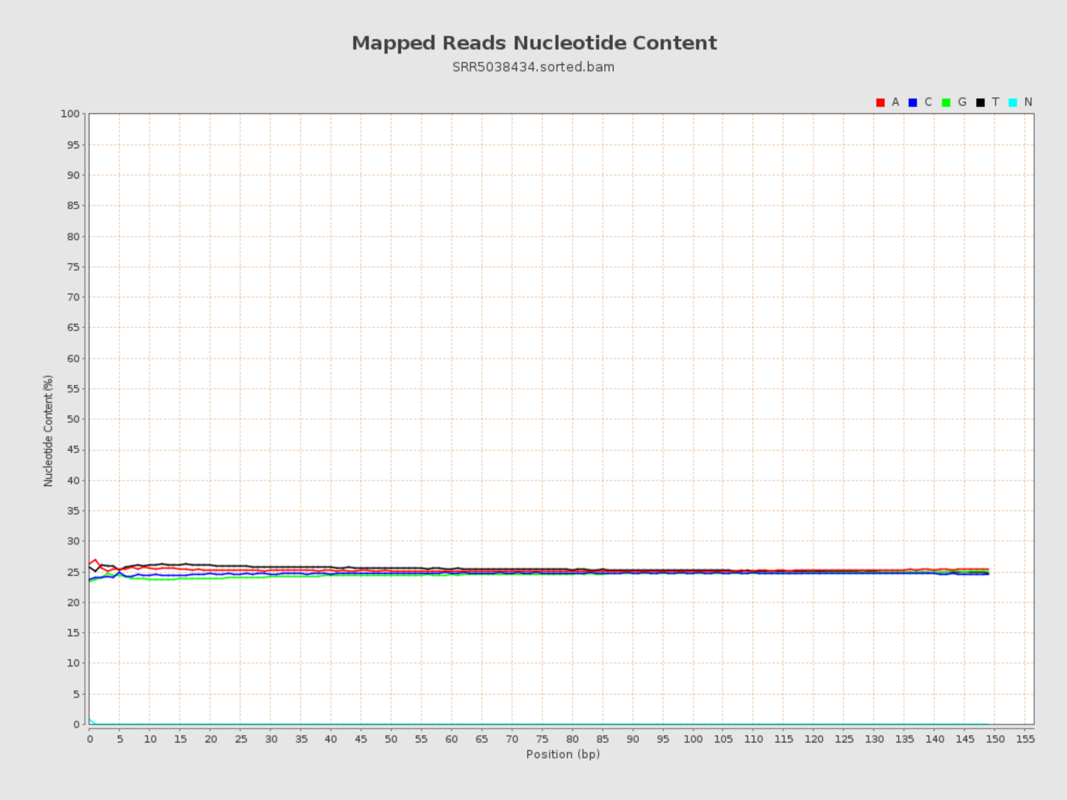
6. Results : Genome Fraction Coverage



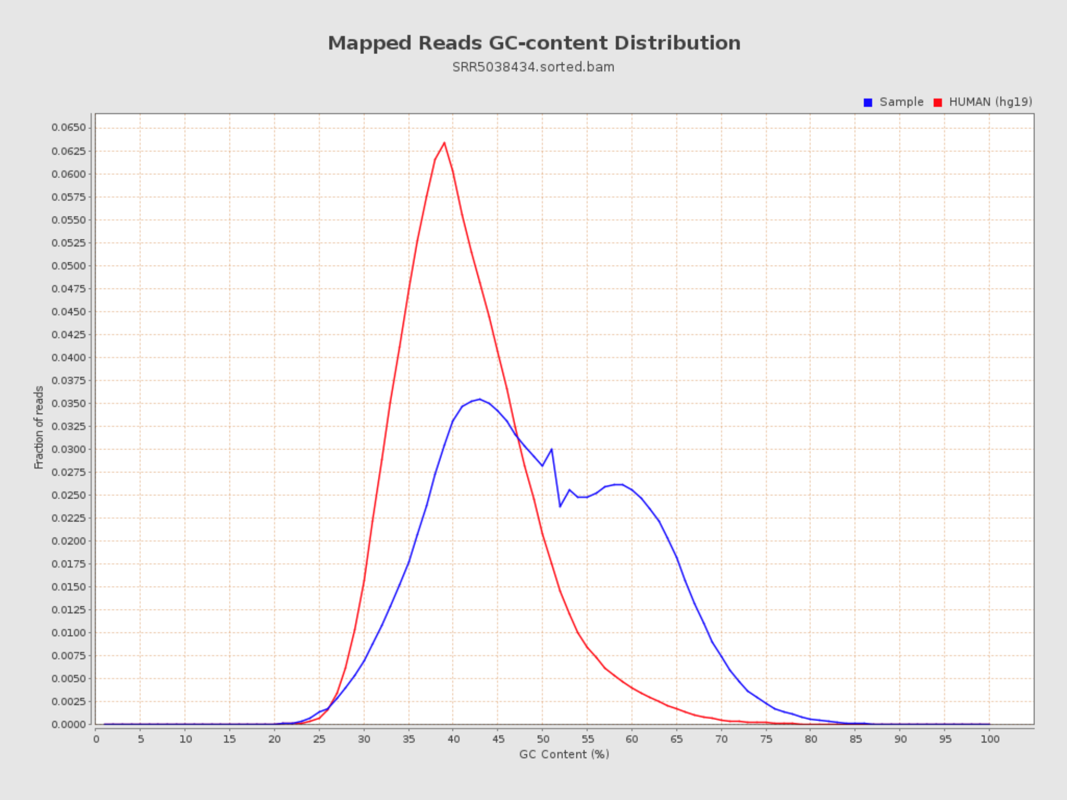
7. Results : Duplication Rate Histogram



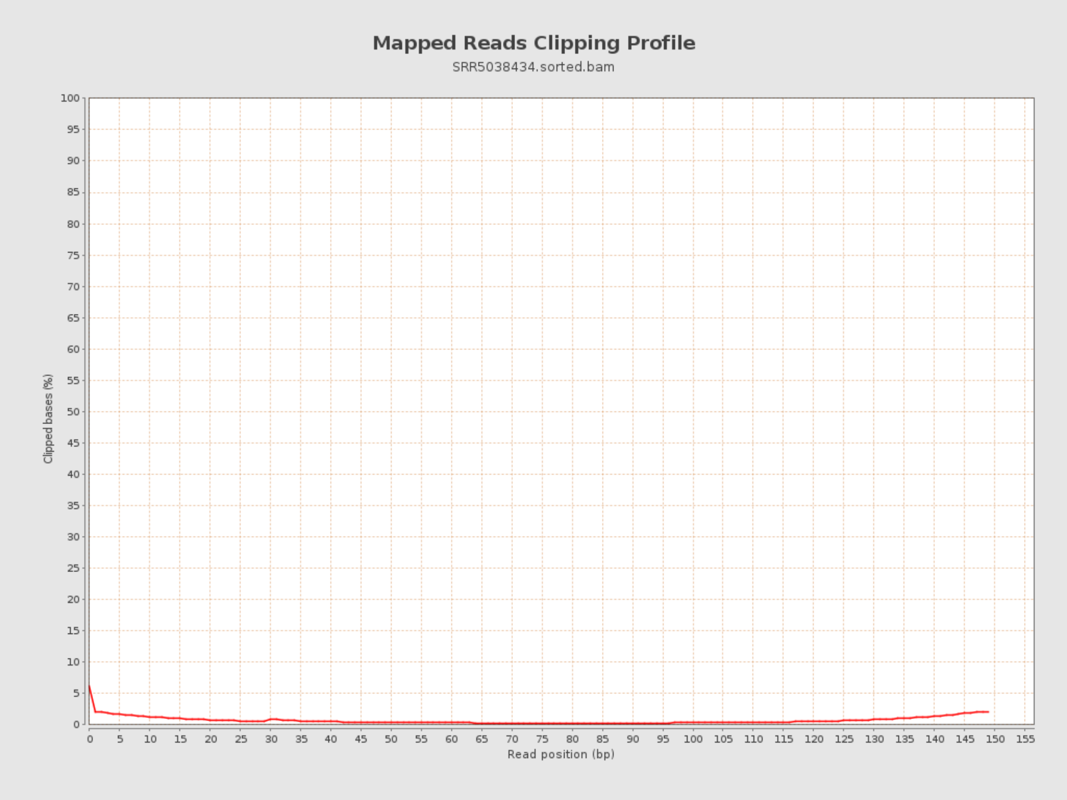
8. Results : Mapped Reads Nucleotide Content



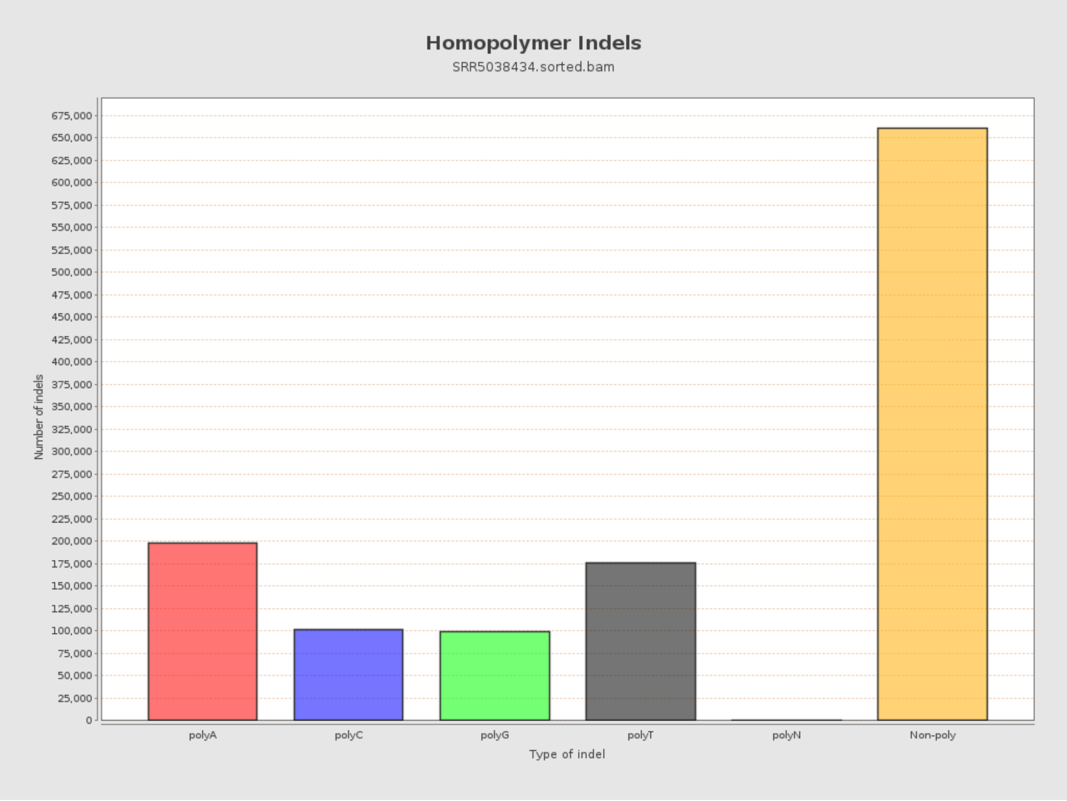
9. Results : Mapped Reads GC-content Distribution



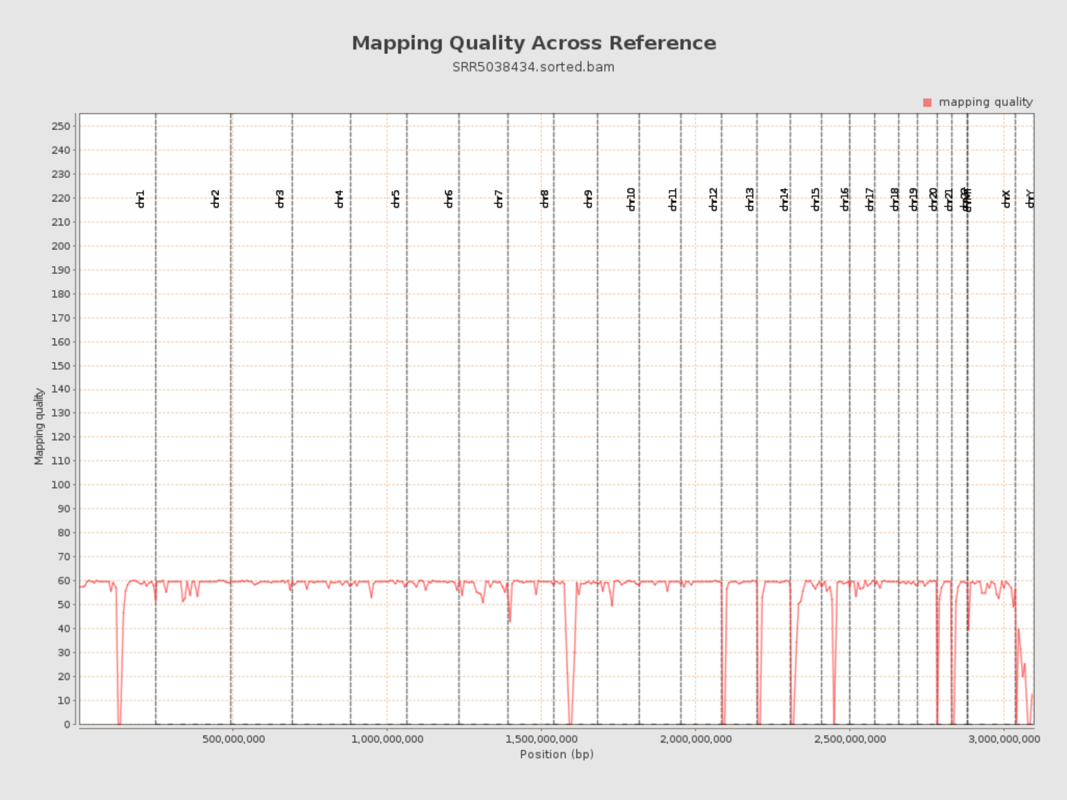
10. Results : Mapped Reads Clipping Profile



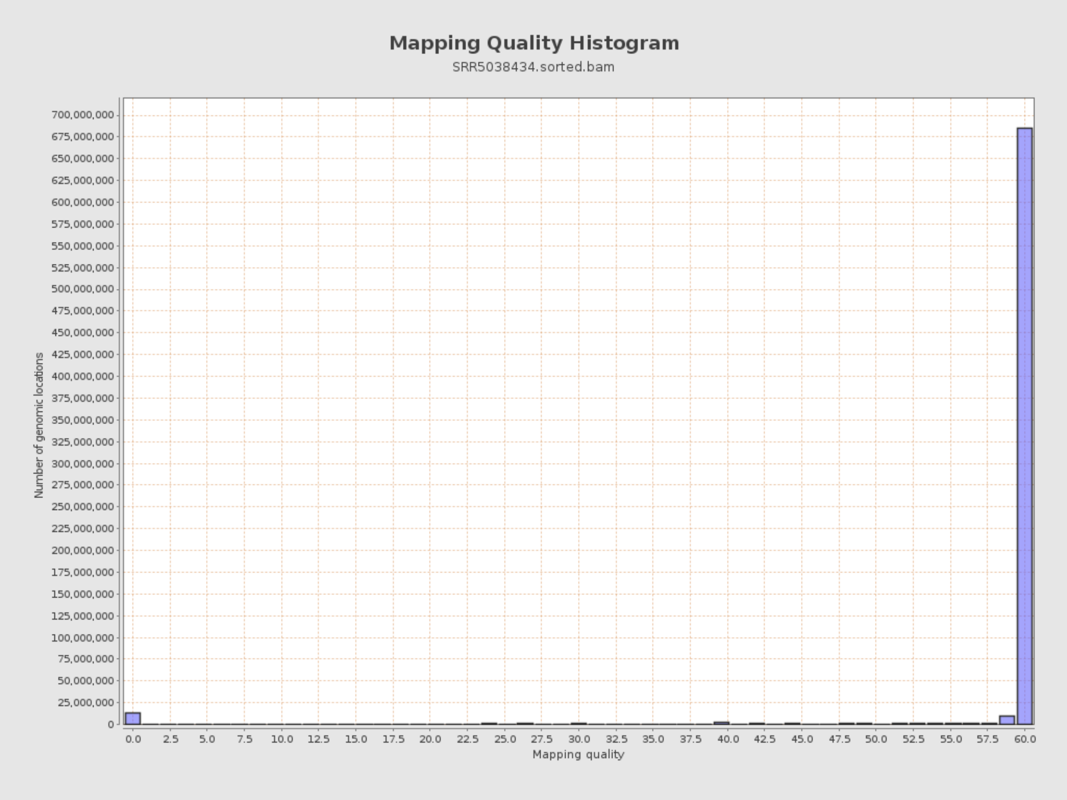
11. Results : Homopolymer Indels



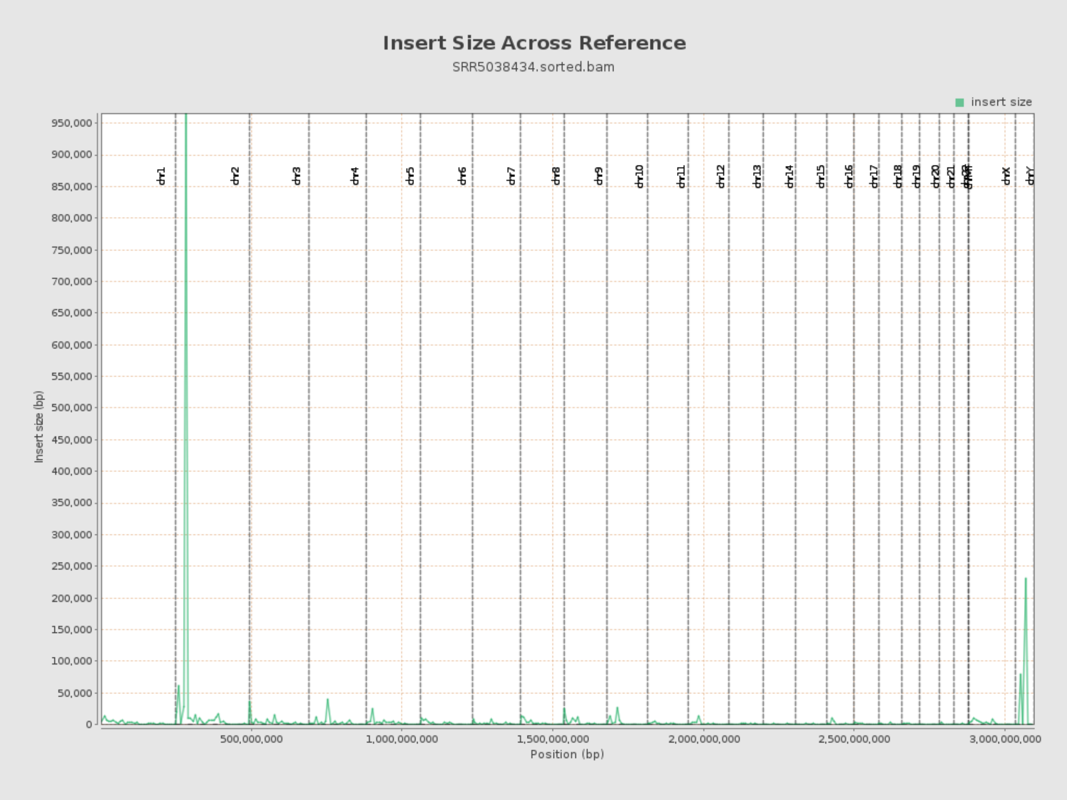
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram