Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/15 21:24:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038462.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_SRR5038462 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038462_1.fastq.gz SRR5038462_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 15 21:24:26 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038462.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	18,644,106
Mapped reads	17,149,743 / 91.98%
Unmapped reads	1,494,363 / 8.02%
Mapped paired reads	17,149,743 / 91.98%
Mapped reads, first in pair	8,696,718 / 46.65%
Mapped reads, second in pair	8,453,025 / 45.34%
Mapped reads, both in pair	16,849,168 / 90.37%
Mapped reads, singletons	300,575 / 1.61%
Secondary alignments	0
Supplementary alignments	251,503 / 1.35%
Read min/max/mean length	30 / 150 / 150.68
Duplicated reads (estimated)	3,490,111 / 18.72%
Duplication rate	14.53%
Clipped reads	8,066,751 / 43.27%

2.2. ACGT Content

Number/percentage of A's	658,760,144 / 28.52%
Number/percentage of C's	460,595,055 / 19.94%
Number/percentage of T's	669,131,685 / 28.97%
Number/percentage of G's	520,817,839 / 22.55%
Number/percentage of N's	184,213 / 0.01%

GC Percentage	42.49%

2.3. Coverage

Mean	0.7466
Standard Deviation	9.3029

2.4. Mapping Quality

Mean Mapping Quality	53.47

2.5. Insert size

Mean	81,852.08
Standard Deviation	2,781,182.02
P25/Median/P75	201 / 255 / 322

2.6. Mismatches and indels

General error rate	1.3%
Mismatches	28,936,861
Insertions	404,167
Mapped reads with at least one insertion	2.24%
Deletions	844,503
Mapped reads with at least one deletion	4.75%
Homopolymer indels	47.96%

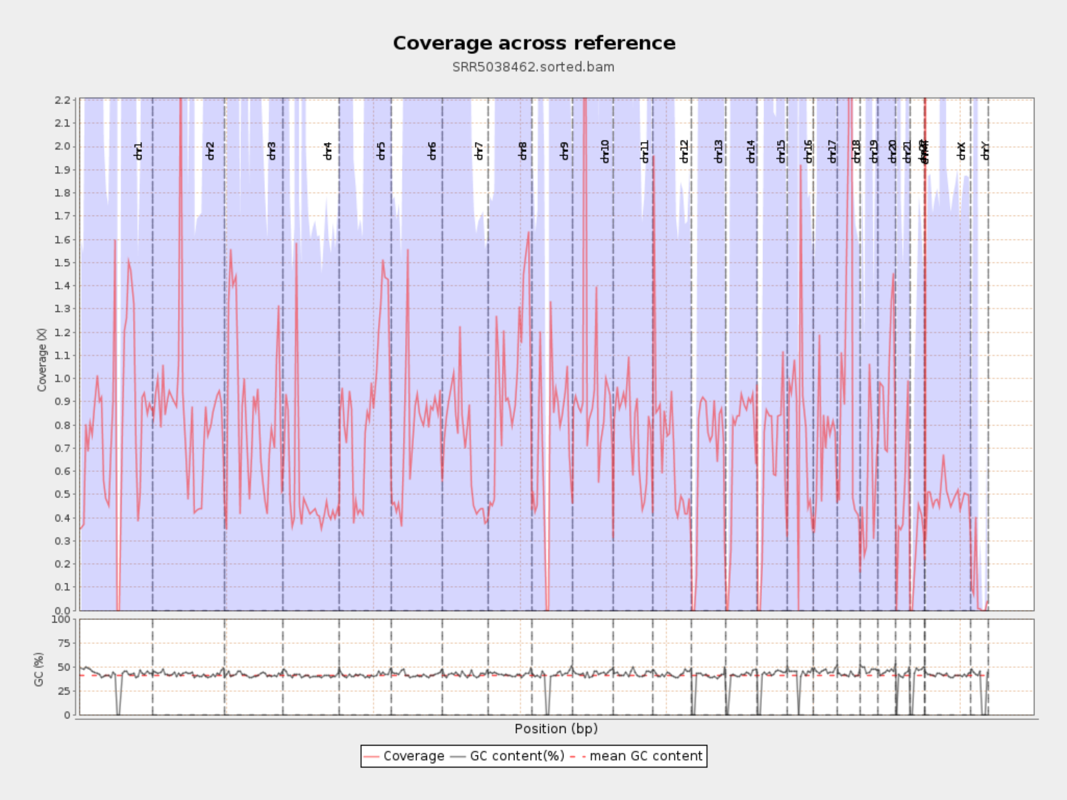
2.7. Chromosome stats

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

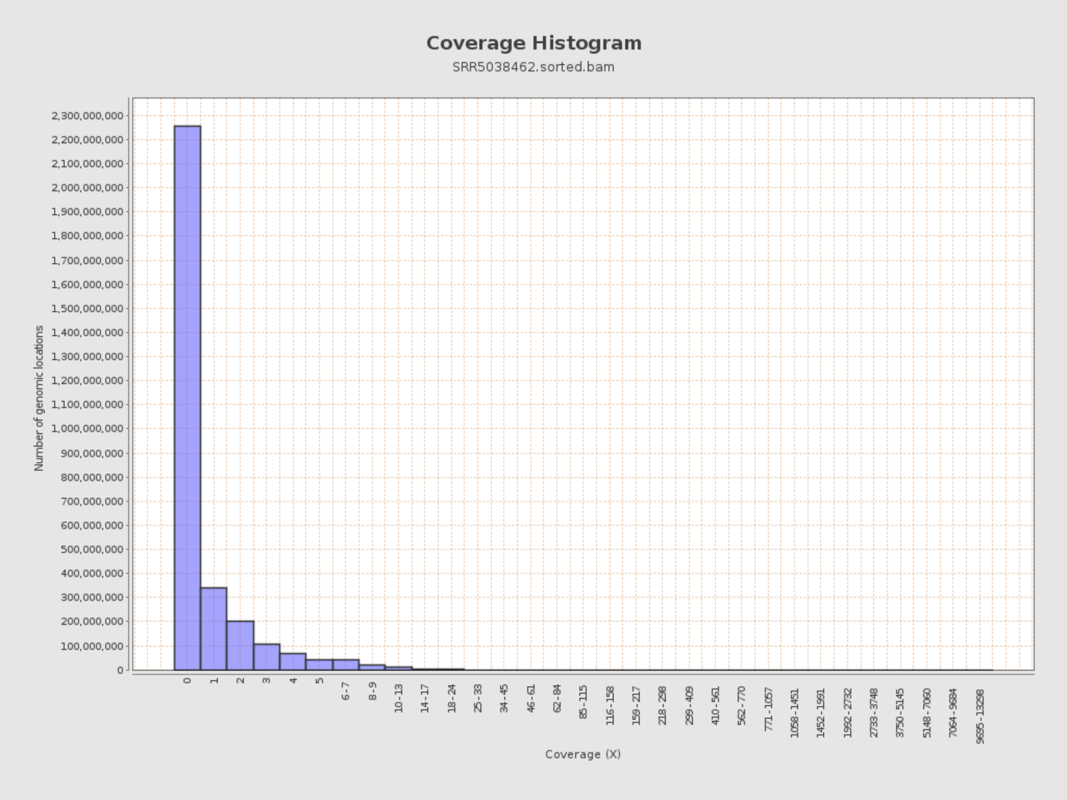
		bases	coverage	deviation
chr1	249250621	200897316	0.806	13.4192
chr2	243199373	207526254	0.8533	10.4435
chr3	198022430	168092481	0.8489	1.8925
chr4	191154276	98514116	0.5154	9.6406
chr5	180915260	159407708	0.8811	1.8719
chr6	171115067	133996696	0.7831	7.684
chr7	159138663	110775159	0.6961	9.2327
chr8	146364022	146703772	1.0023	3.8505
chr9	141213431	98084572	0.6946	16.1262
chr10	135534747	139623533	1.0302	22.2826
chr11	135006516	103764746	0.7686	7.5233
chr12	133851895	94944259	0.7093	1.827
chr13	115169878	77450702	0.6725	1.5835
chr14	107349540	75451868	0.7029	1.7233
chr15	102531392	63504629	0.6194	1.567
chr16	90354753	70020688	0.775	8.2707
chr17	81195210	57511542	0.7083	11.942
chr18	78077248	93214706	1.1939	10.9945
chr19	59128983	30444728	0.5149	5.8268
chr20	63025520	62038554	0.9843	3.5621
chr21	48129895	22673548	0.4711	4.7805
chr22	51304566	13240691	0.2581	0.9869
chrMT	16571	3016308	182.0233	107.8691
chrX	155270560	75625054	0.4871	2.119

chrY	59373566	4573669	0.077	9.9524

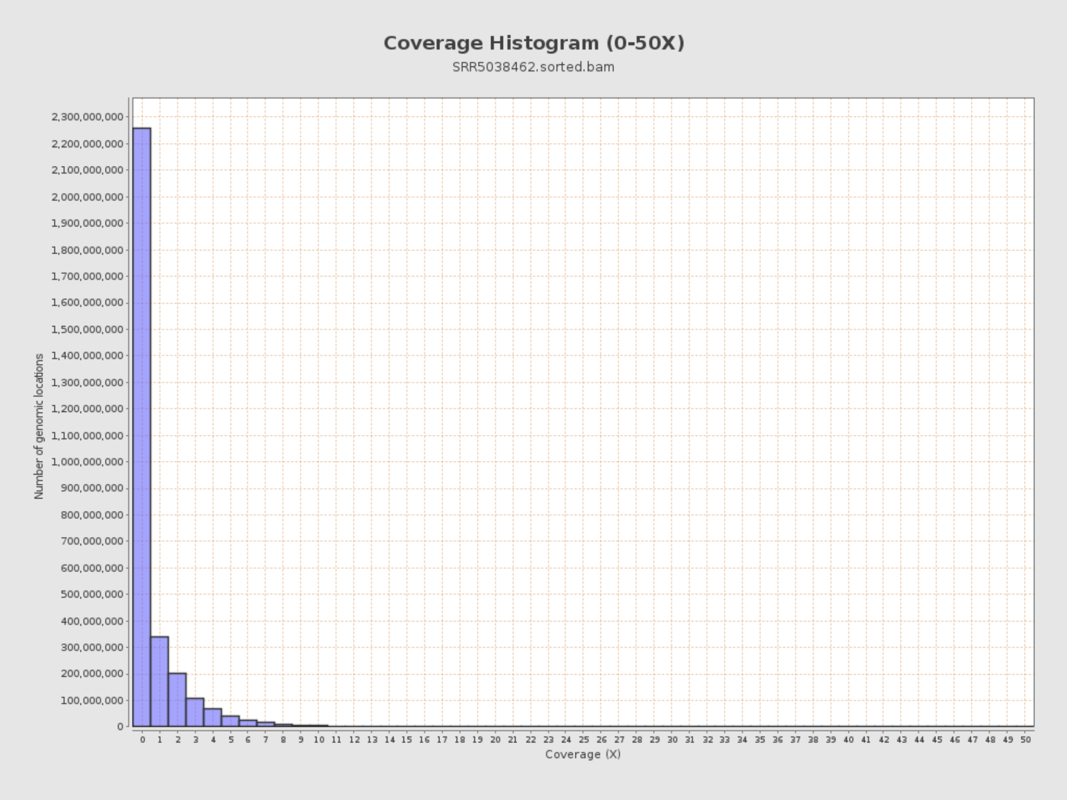
3. Results : Coverage across reference



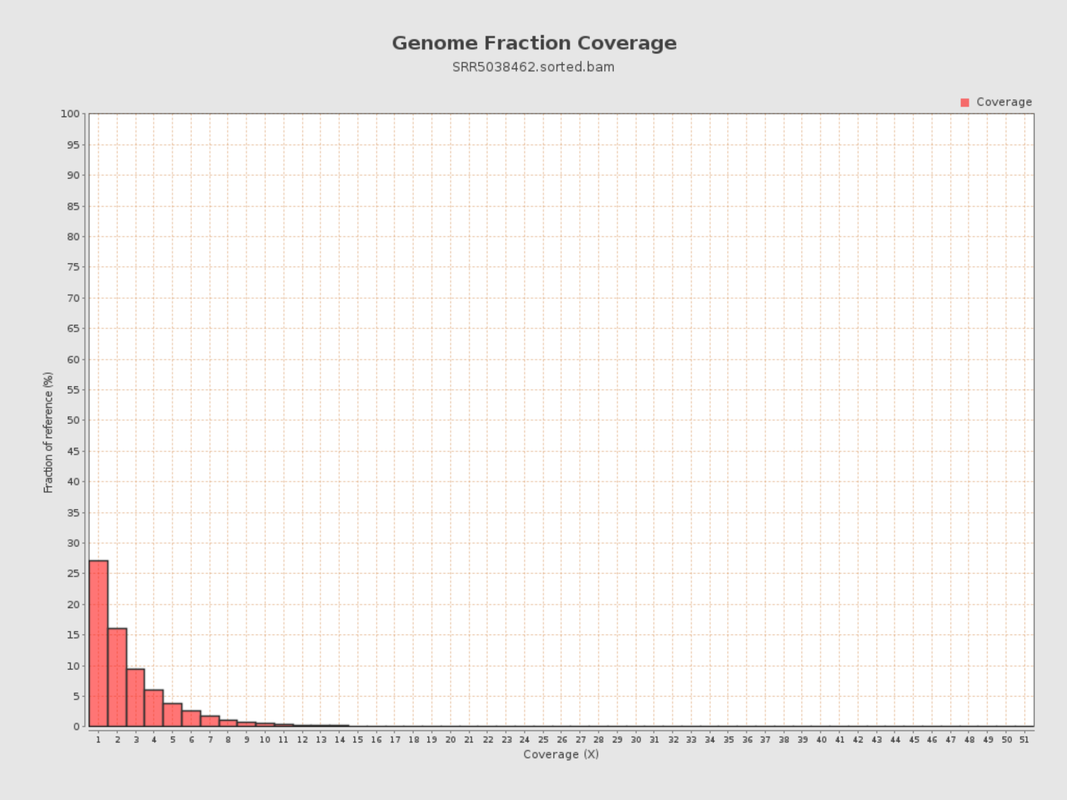
4. Results : Coverage Histogram



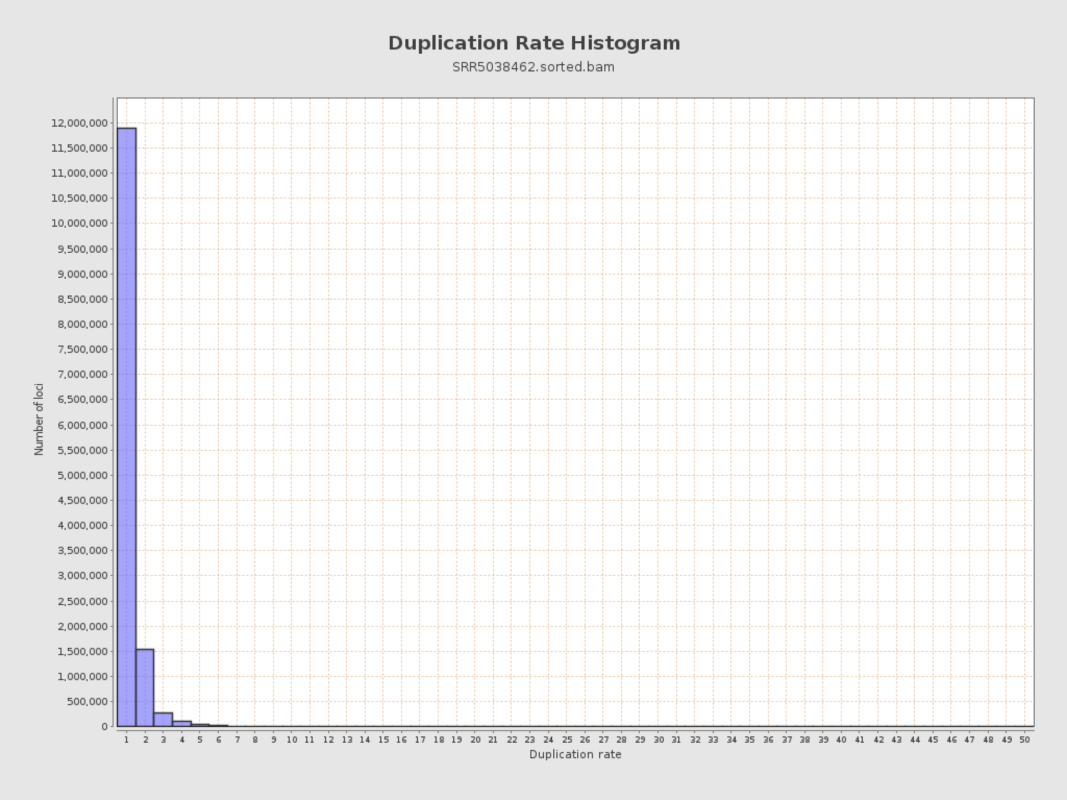
5. Results : Coverage Histogram (0-50X)



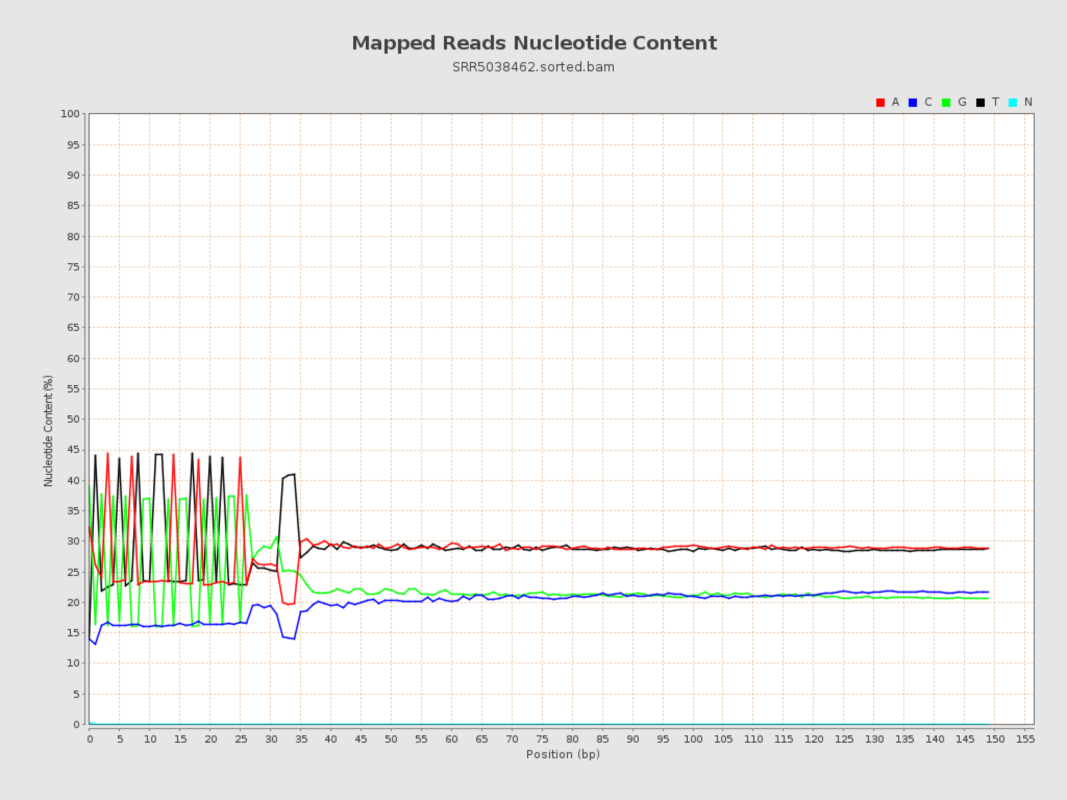
6. Results : Genome Fraction Coverage



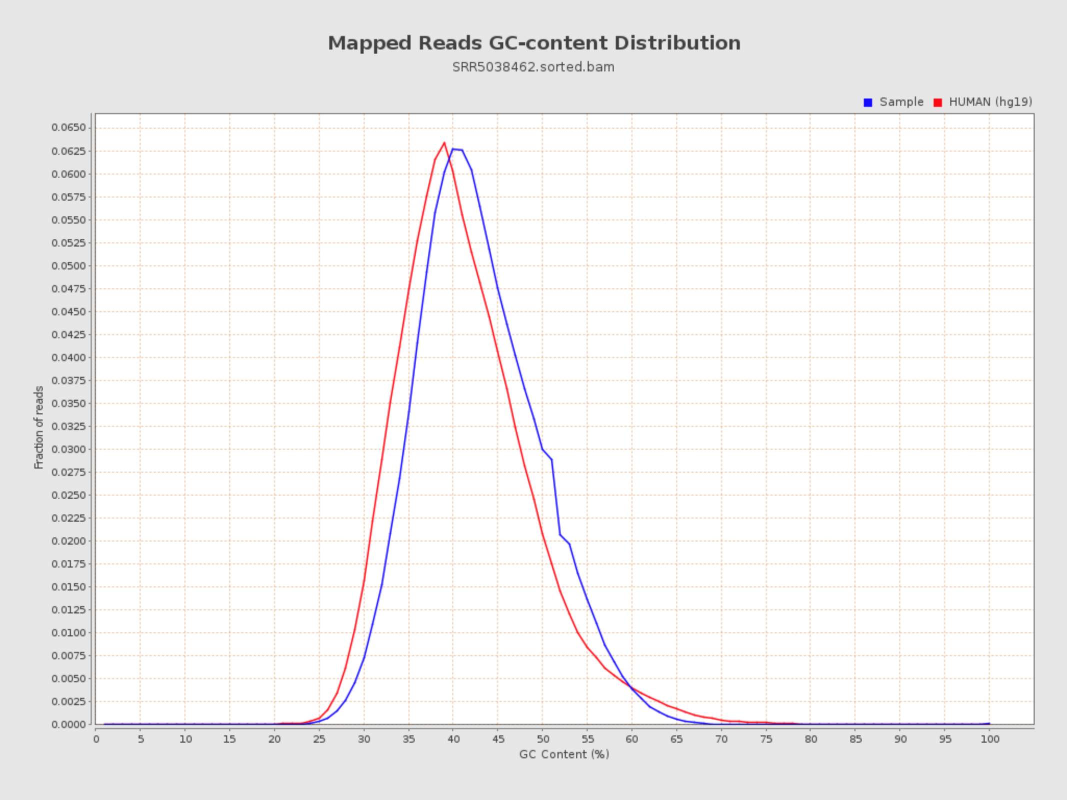
7. Results : Duplication Rate Histogram



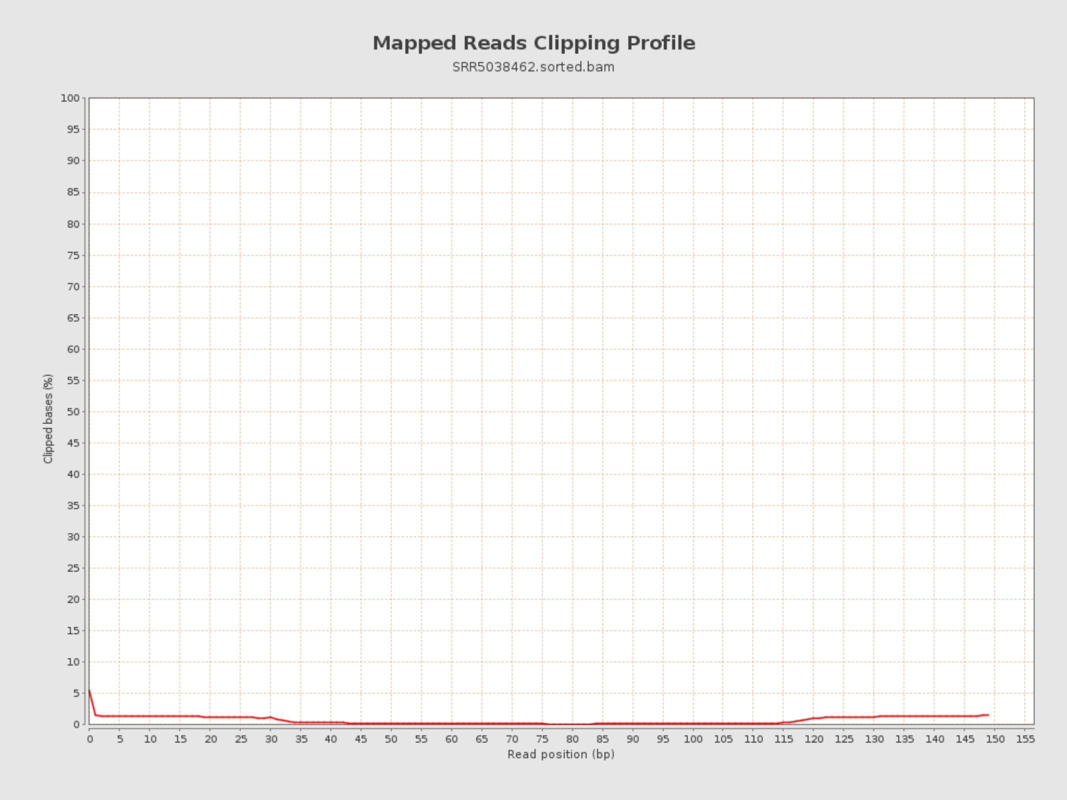
8. Results : Mapped Reads Nucleotide Content



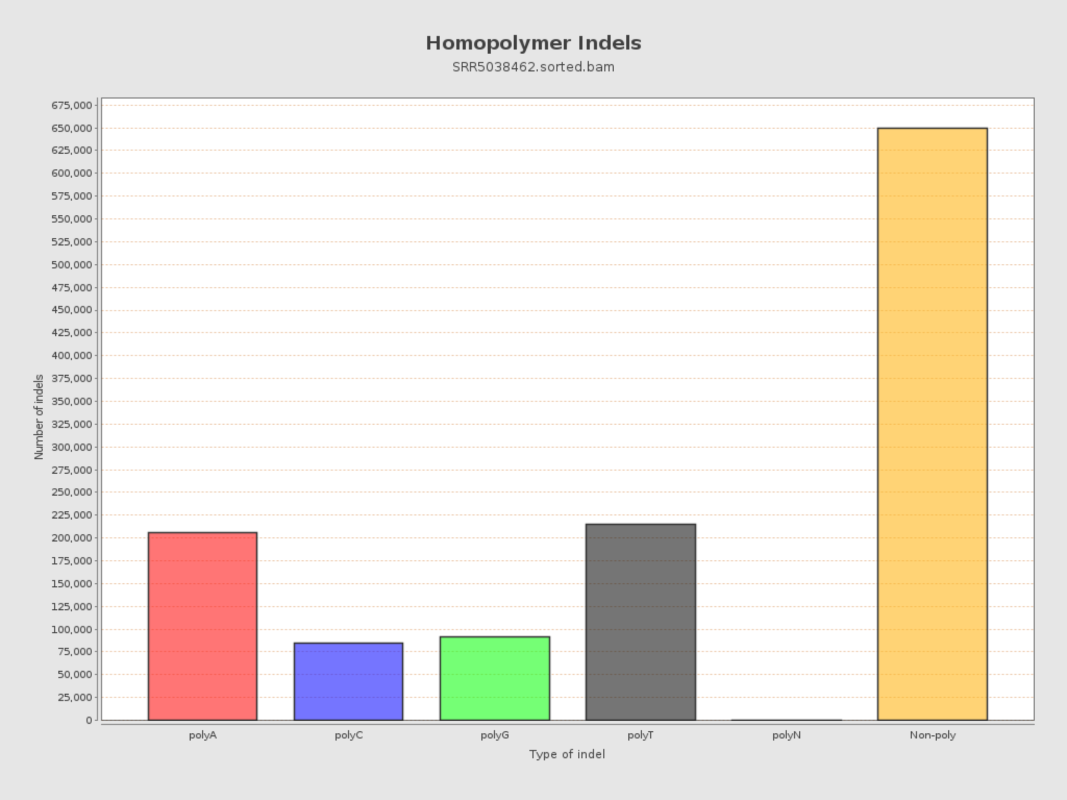
9. Results : Mapped Reads GC-content Distribution



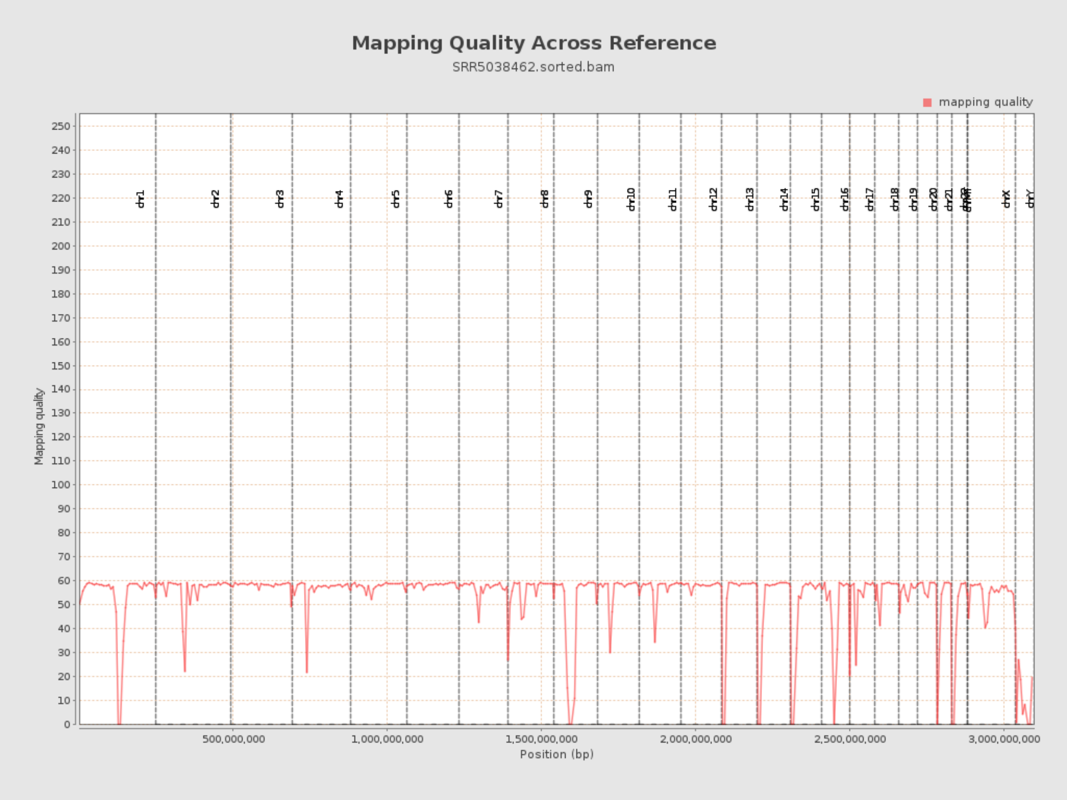
10. Results : Mapped Reads Clipping Profile



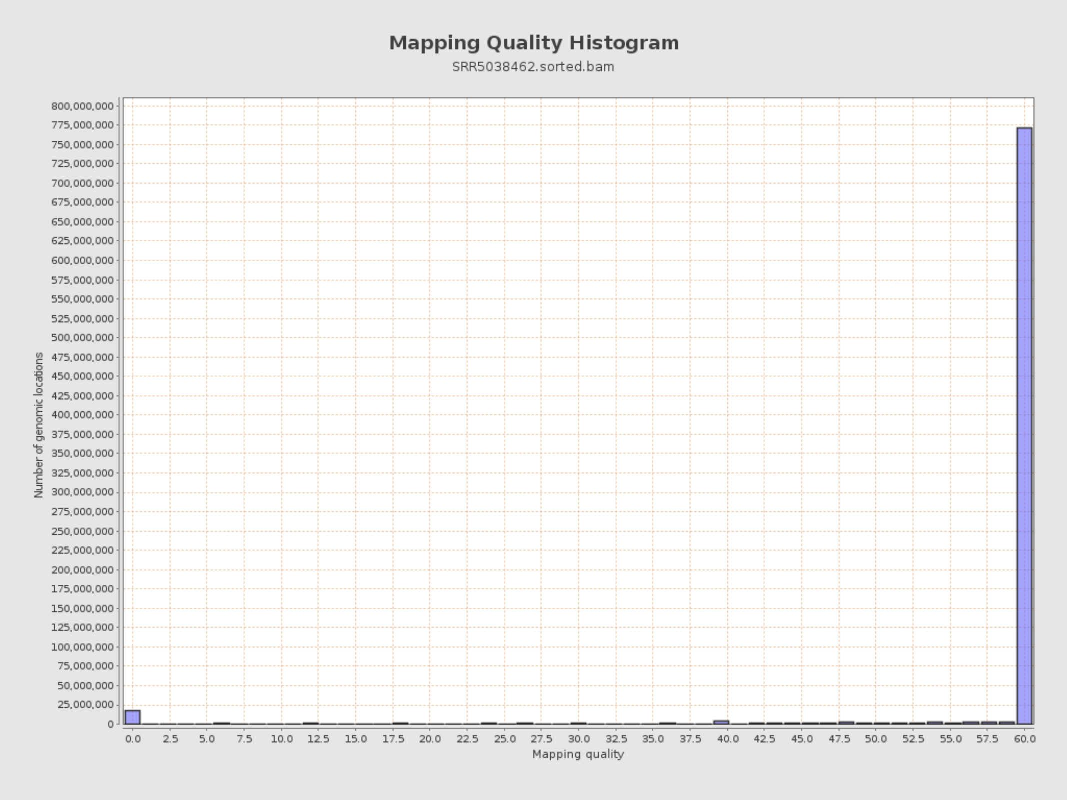
11. Results : Homopolymer Indels



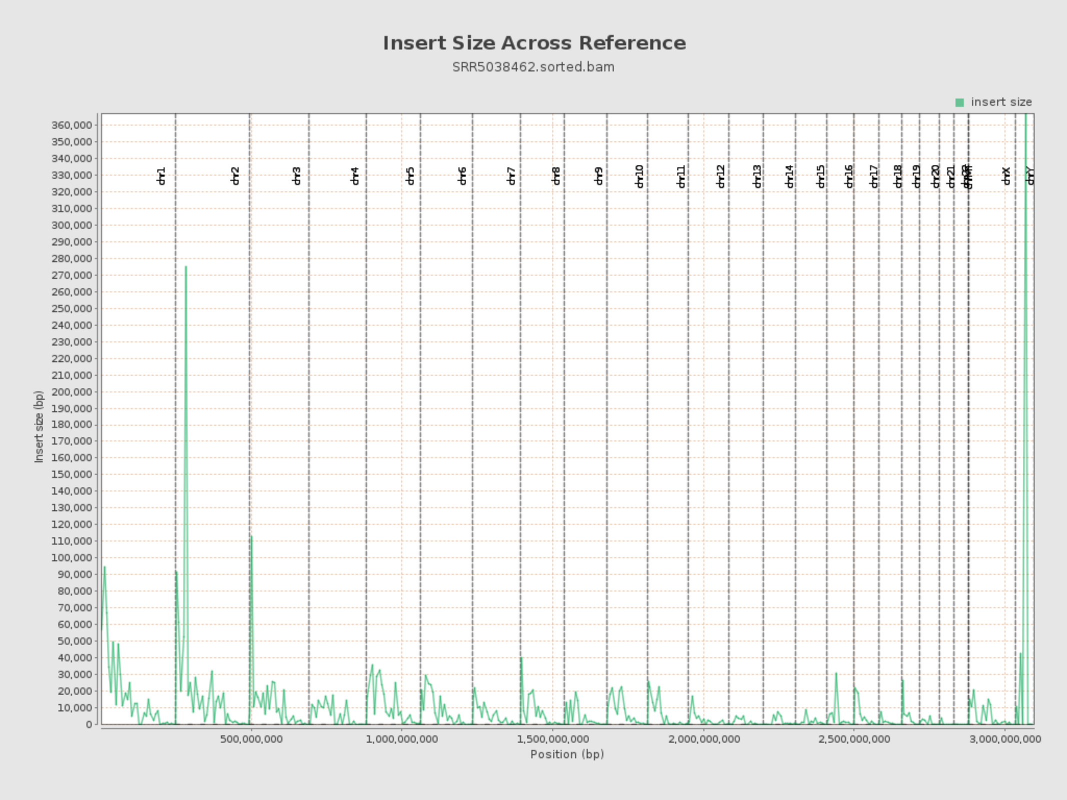
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram