Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/17 13:43:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006018.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_SRR1006018 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006018_1.fastq.gz SRR1006018_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 17 13:43:02 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006018.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	11,735,334
Mapped reads	8,537,642 / 72.75%
Unmapped reads	3,197,692 / 27.25%
Mapped paired reads	8,537,642 / 72.75%
Mapped reads, first in pair	4,321,166 / 36.82%
Mapped reads, second in pair	4,216,476 / 35.93%
Mapped reads, both in pair	7,591,532 / 64.69%
Mapped reads, singletons	946,110 / 8.06%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	327,033 / 2.79%
Duplication rate	3.19%
Clipped reads	668,643 / 5.7%

2.2. ACGT Content

Number/percentage of A's	95,247,640 / 28.87%
Number/percentage of C's	69,313,960 / 21.01%
Number/percentage of T's	94,782,853 / 28.72%
Number/percentage of G's	70,371,932 / 21.33%
Number/percentage of N's	255,692 / 0.08%
GC Percentage	42.33%

2.3. Coverage

Mean	0.1066
Standard Deviation	0.6079

2.4. Mapping Quality

Mean Mapping Quality	47.44

2.5. Insert size

Mean	69,559.07
Standard Deviation	2,573,613.27
P25/Median/P75	76 / 111 / 165

2.6. Mismatches and indels

General error rate	0.67%
Mismatches	2,195,963
Insertions	9,053
Mapped reads with at least one insertion	0.11%
Deletions	28,071
Mapped reads with at least one deletion	0.33%
Homopolymer indels	43.76%

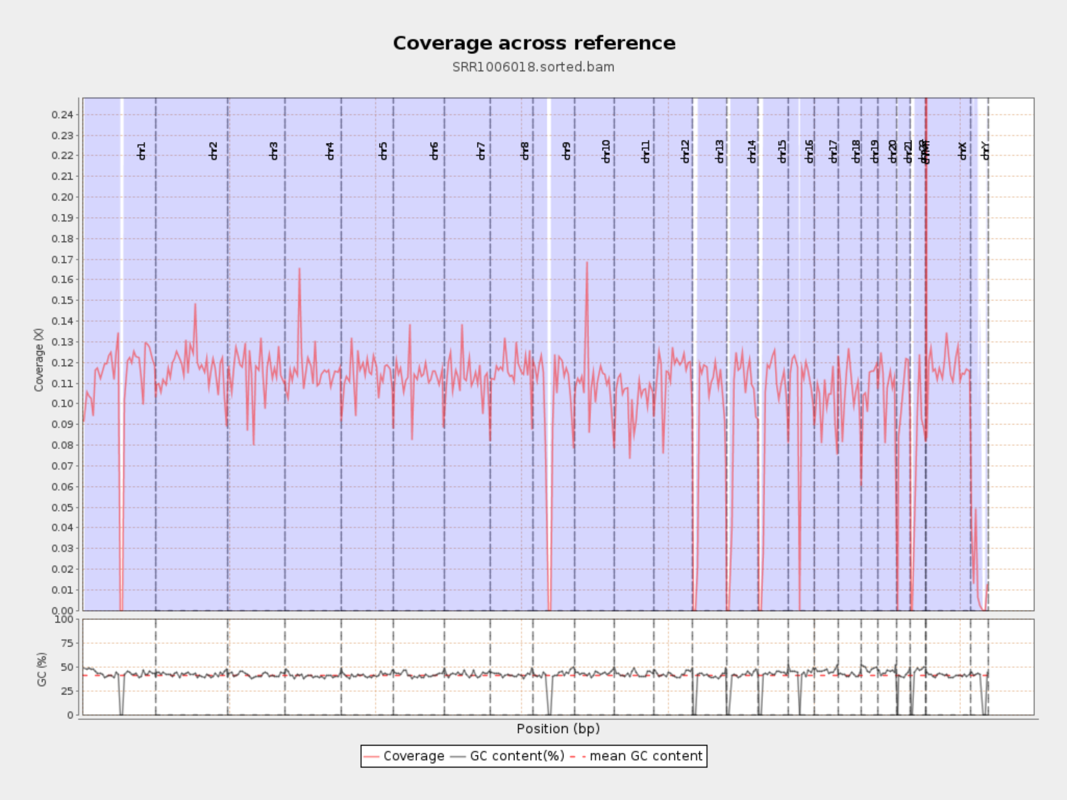
2.7. Chromosome stats

Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**

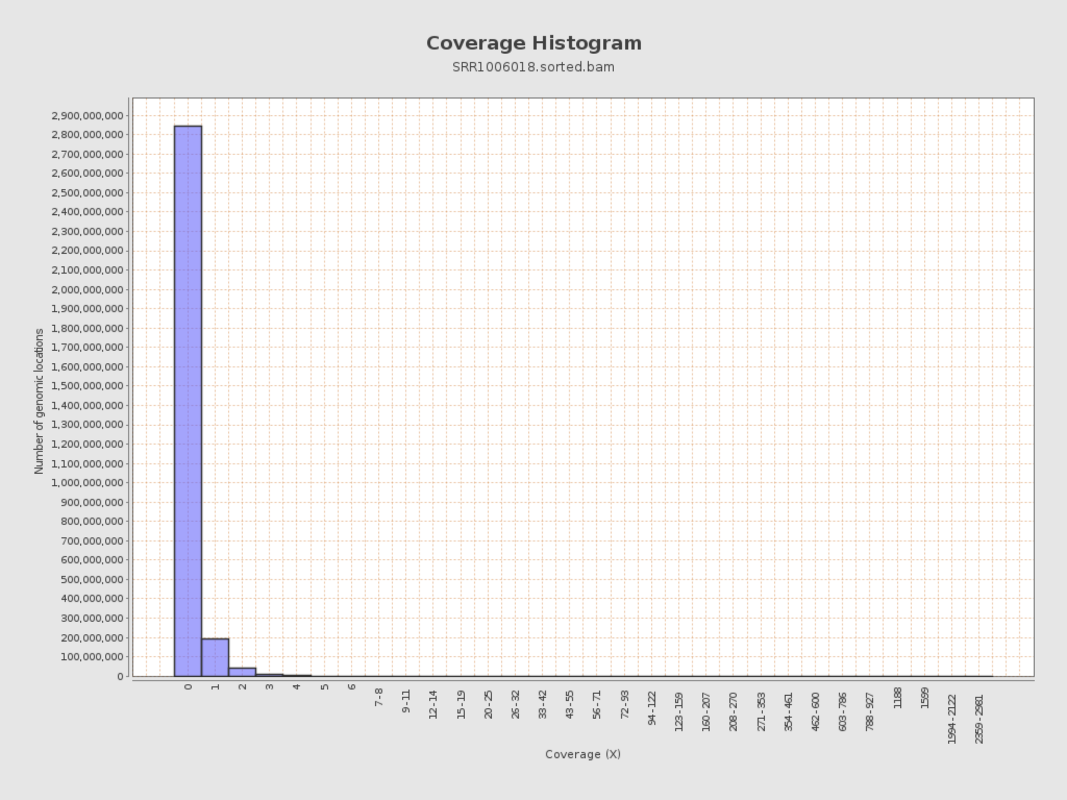
chr1	249250621	27194967	0.1091	0.8557
chr2	243199373	28525834	0.1173	0.5142
chr3	198022430	22805036	0.1152	0.4184
chr4	191154276	22279290	0.1166	0.4971
chr5	180915260	20583872	0.1138	0.4178
chr6	171115067	19357308	0.1131	0.5087
chr7	159138663	17946738	0.1128	0.6519
chr8	146364022	17030544	0.1164	1.507
chr9	141213431	13802837	0.0977	0.4411
chr10	135534747	15076088	0.1112	0.6396
chr11	135006516	13823433	0.1024	0.4334
chr12	133851895	15424745	0.1152	0.4264
chr13	115169878	10667793	0.0926	0.376
chr14	107349540	10062079	0.0937	0.3942
chr15	102531392	9247247	0.0902	0.3708
chr16	90354753	9337982	0.1033	0.4725
chr17	81195210	8165053	0.1006	0.4087
chr18	78077248	8337099	0.1068	0.6237
chr19	59128983	6377549	0.1079	0.714
chr20	63025520	6792090	0.1078	0.4298
chr21	48129895	4592090	0.0954	0.4268
chr22	51304566	3566351	0.0695	0.3455
chrMT	16571	53544	3.2312	2.6411
chrX	155270560	18104671	0.1166	0.4482

chrY	59373566	854279	0.0144	0.3324

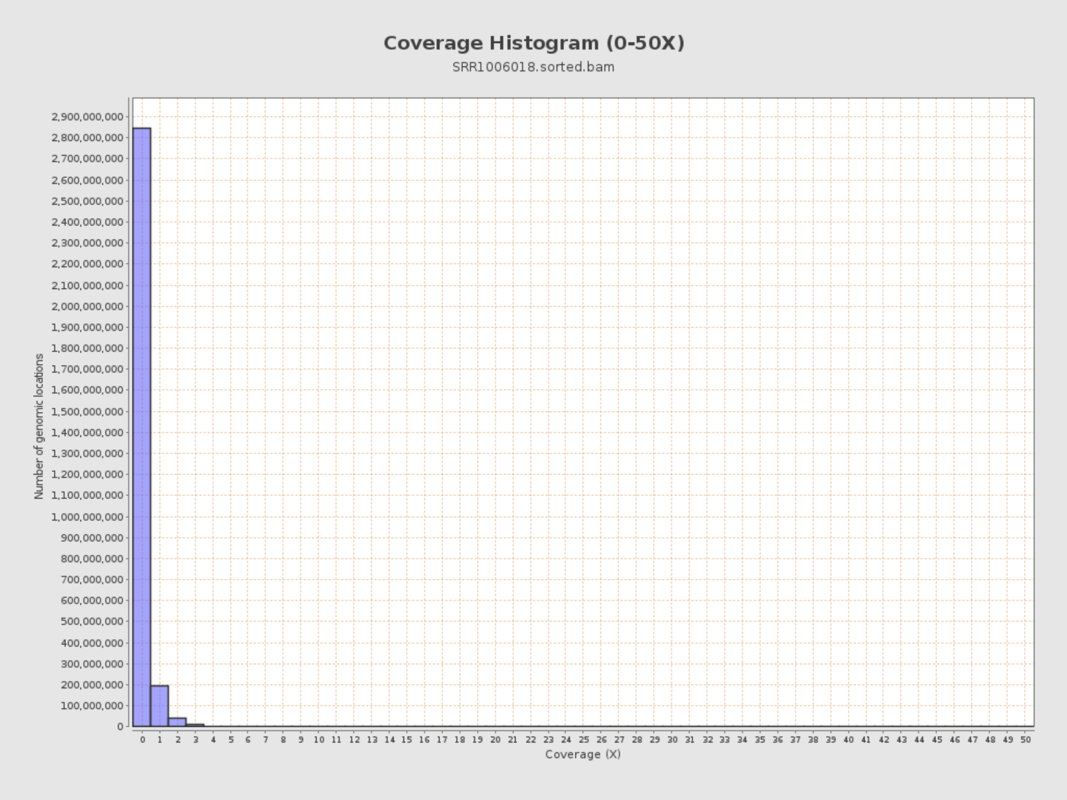
3. Results : Coverage across reference



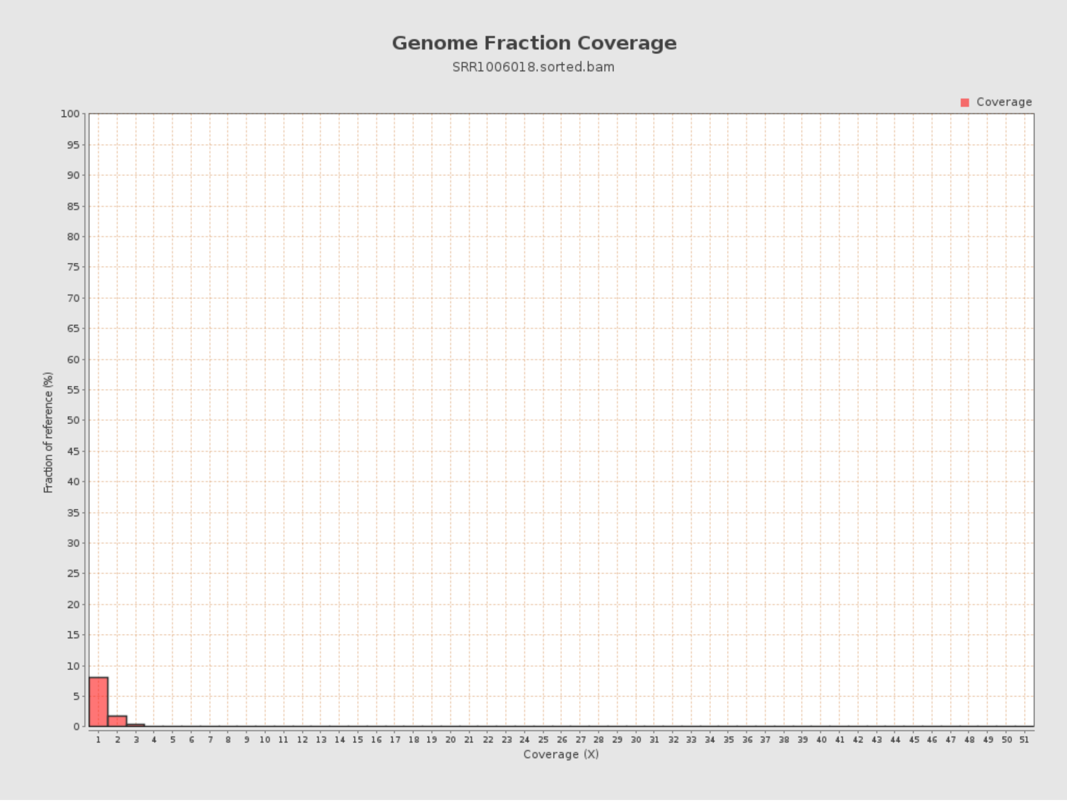
4. Results : Coverage Histogram



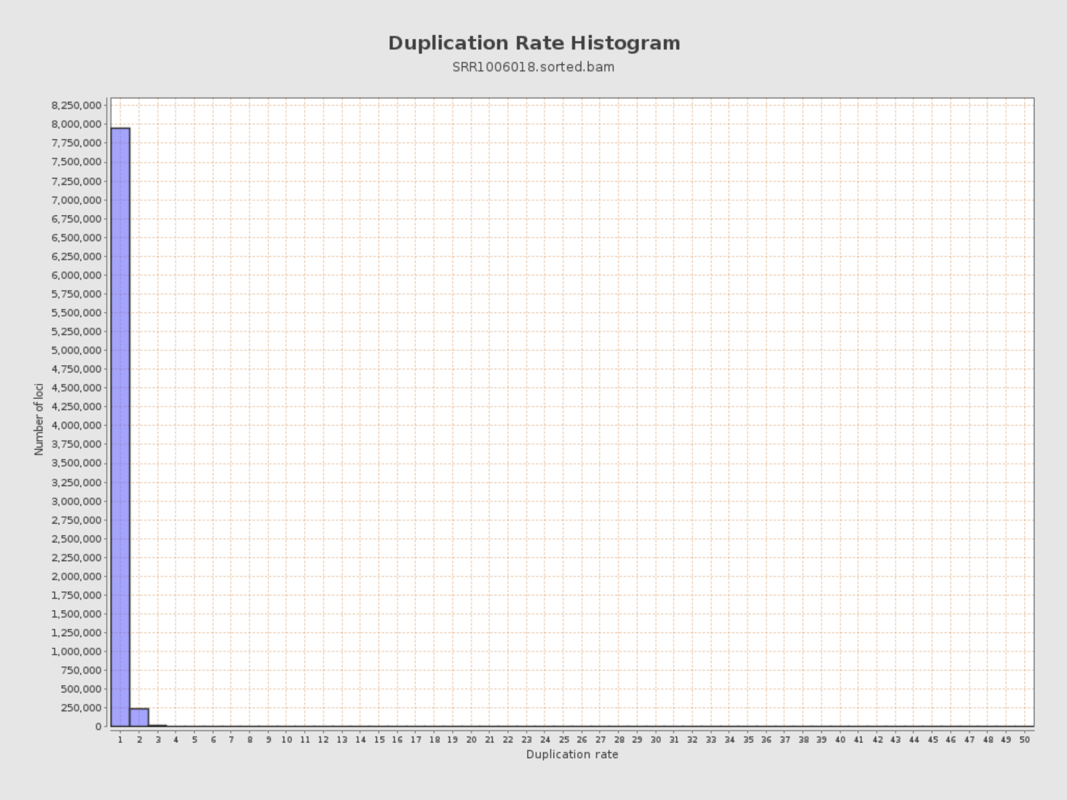
5. Results : Coverage Histogram (0-50X)



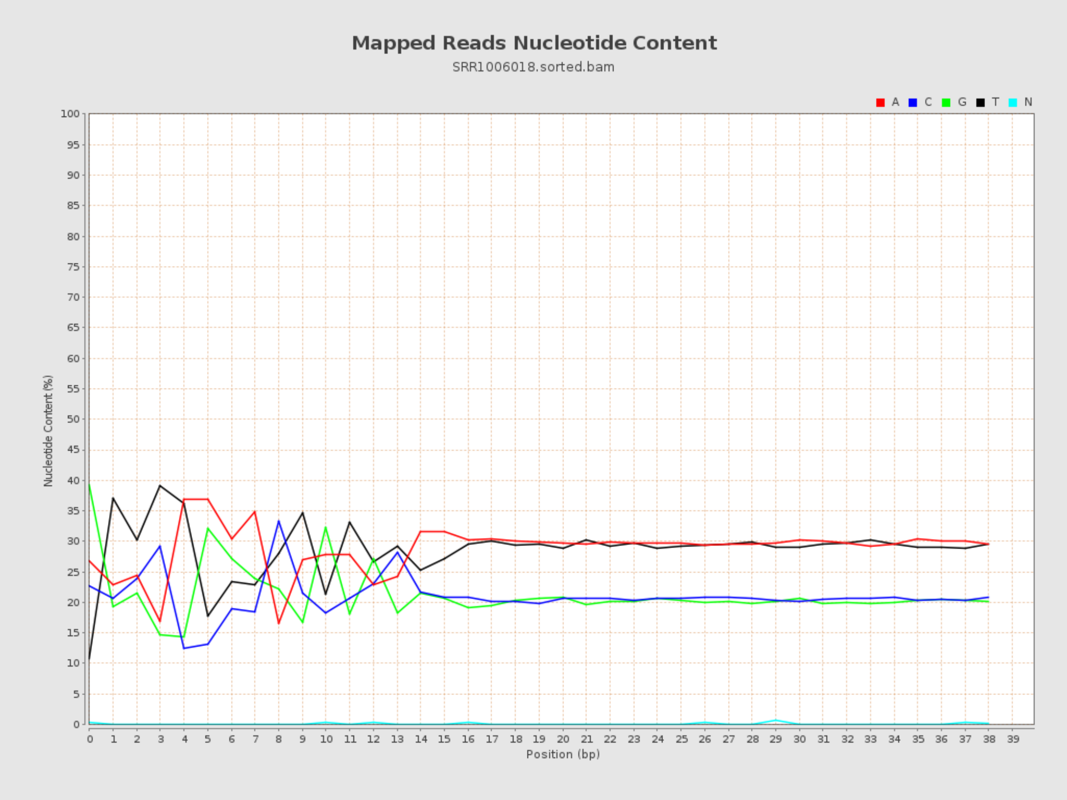
6. Results : Genome Fraction Coverage



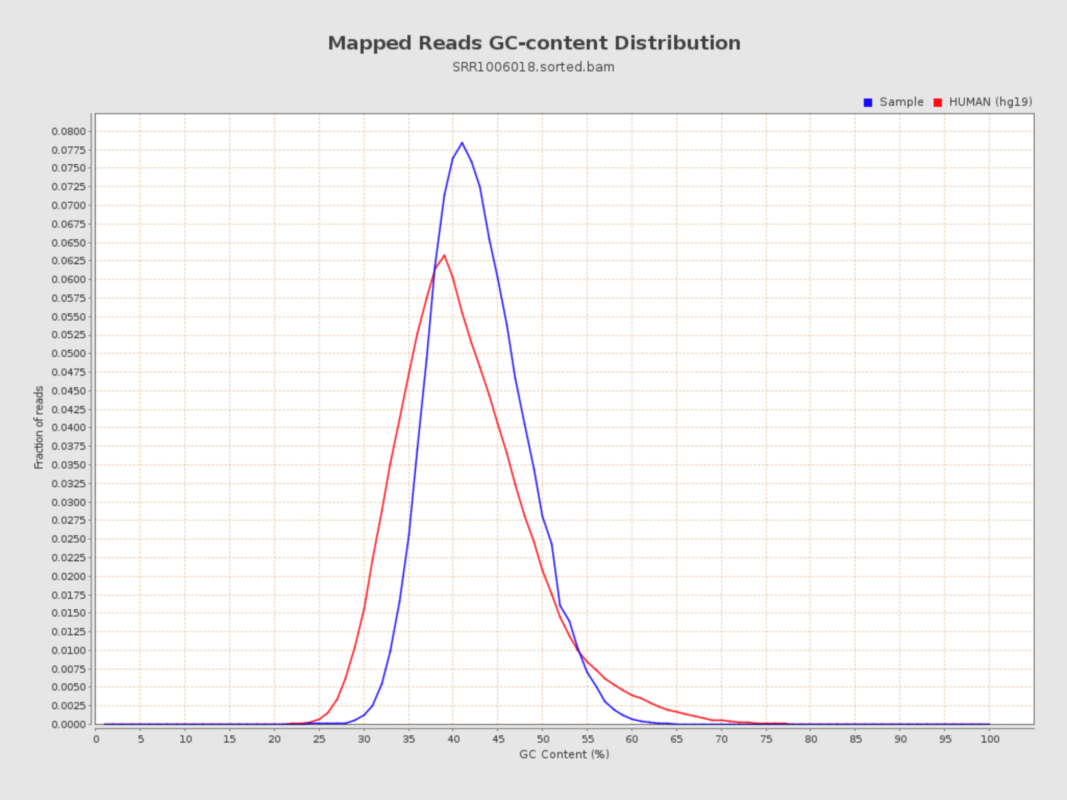
7. Results : Duplication Rate Histogram



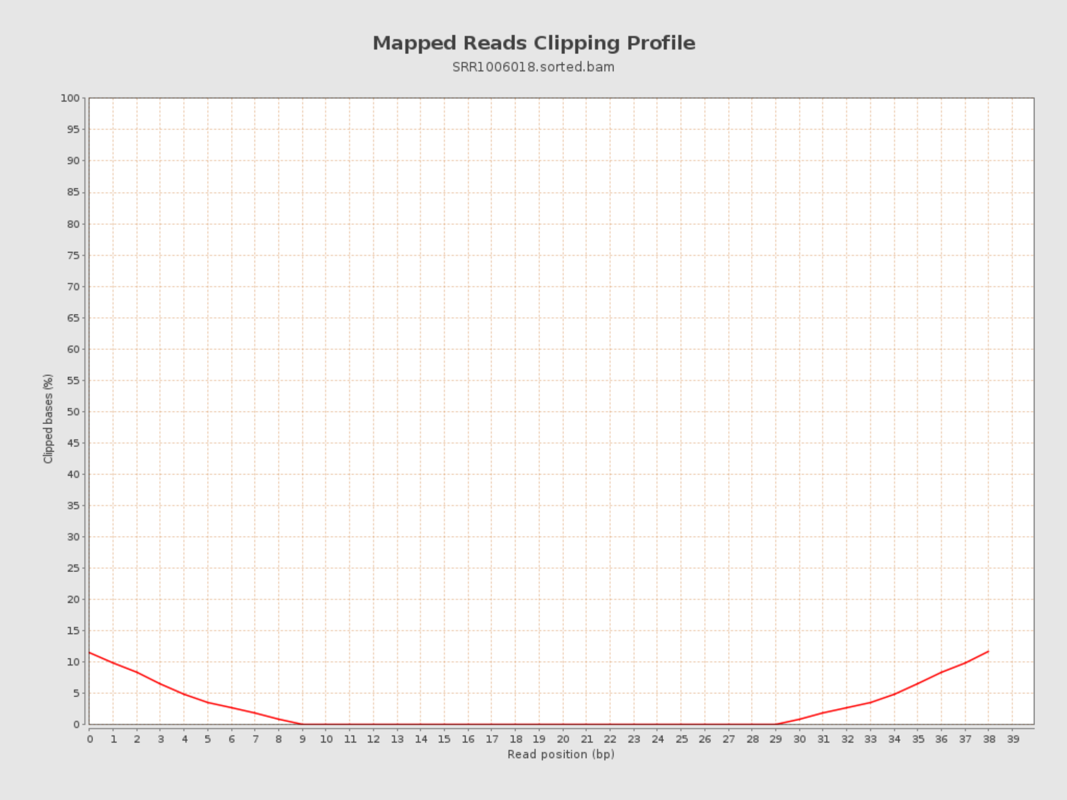
8. Results : Mapped Reads Nucleotide Content



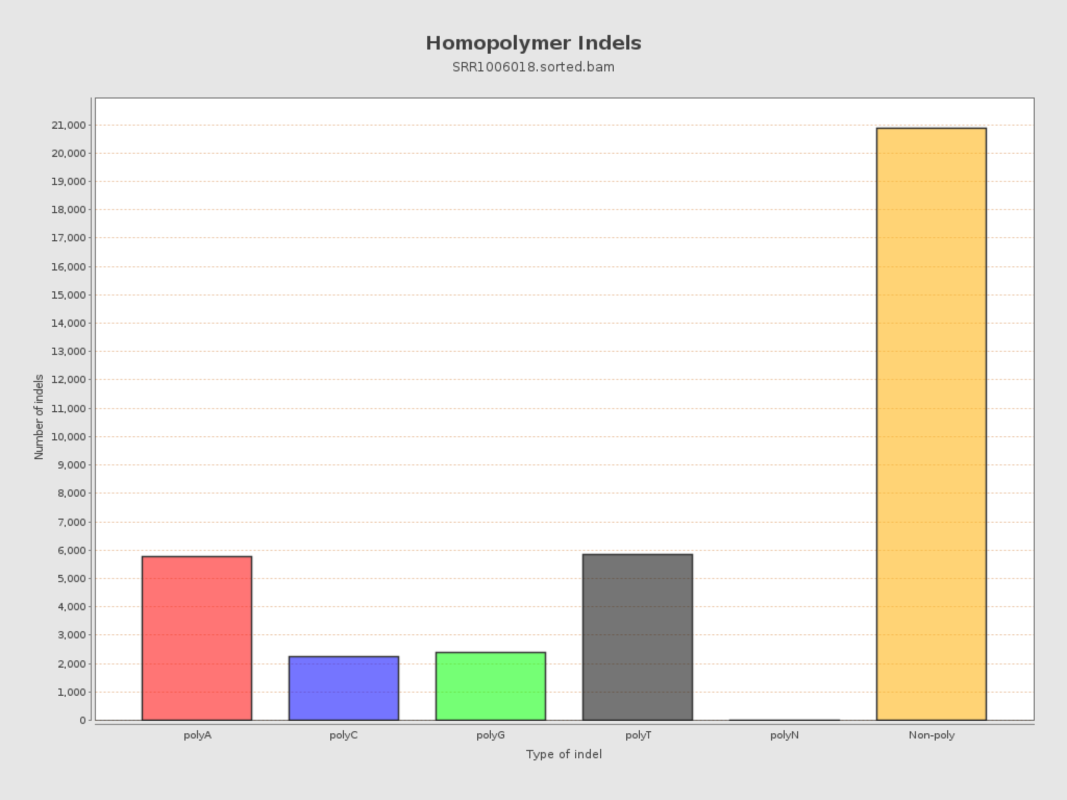
9. Results : Mapped Reads GC-content Distribution



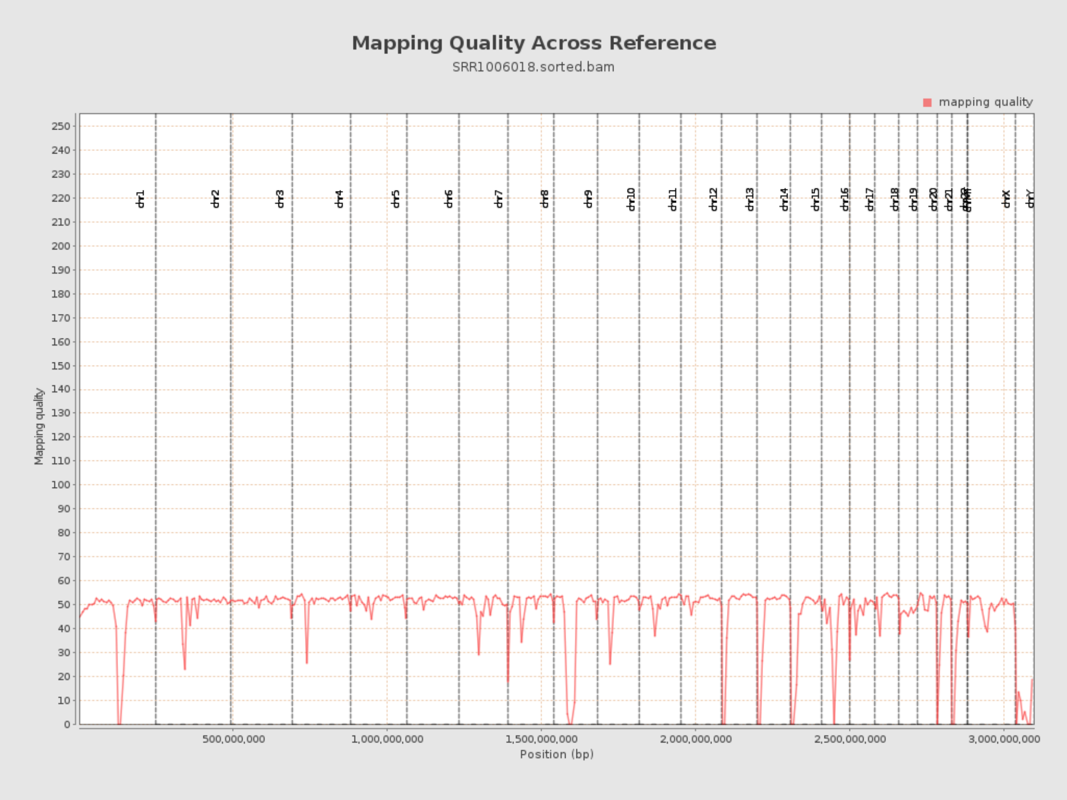
10. Results : Mapped Reads Clipping Profile



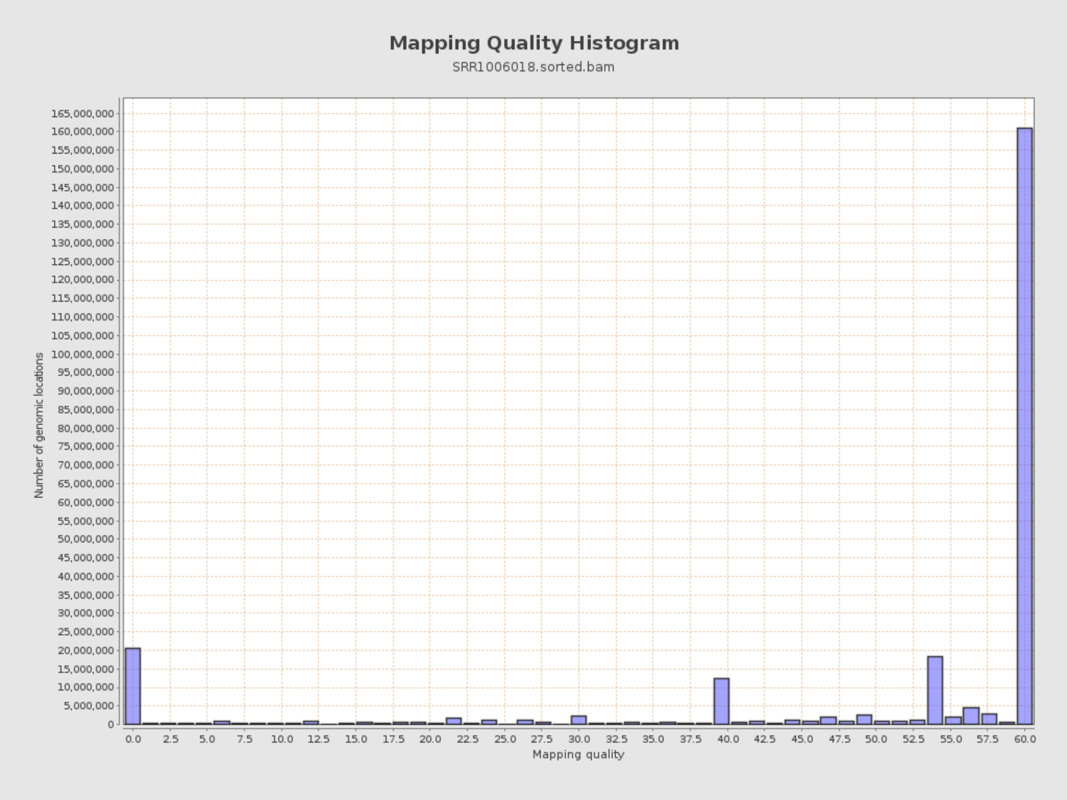
11. Results : Homopolymer Indels



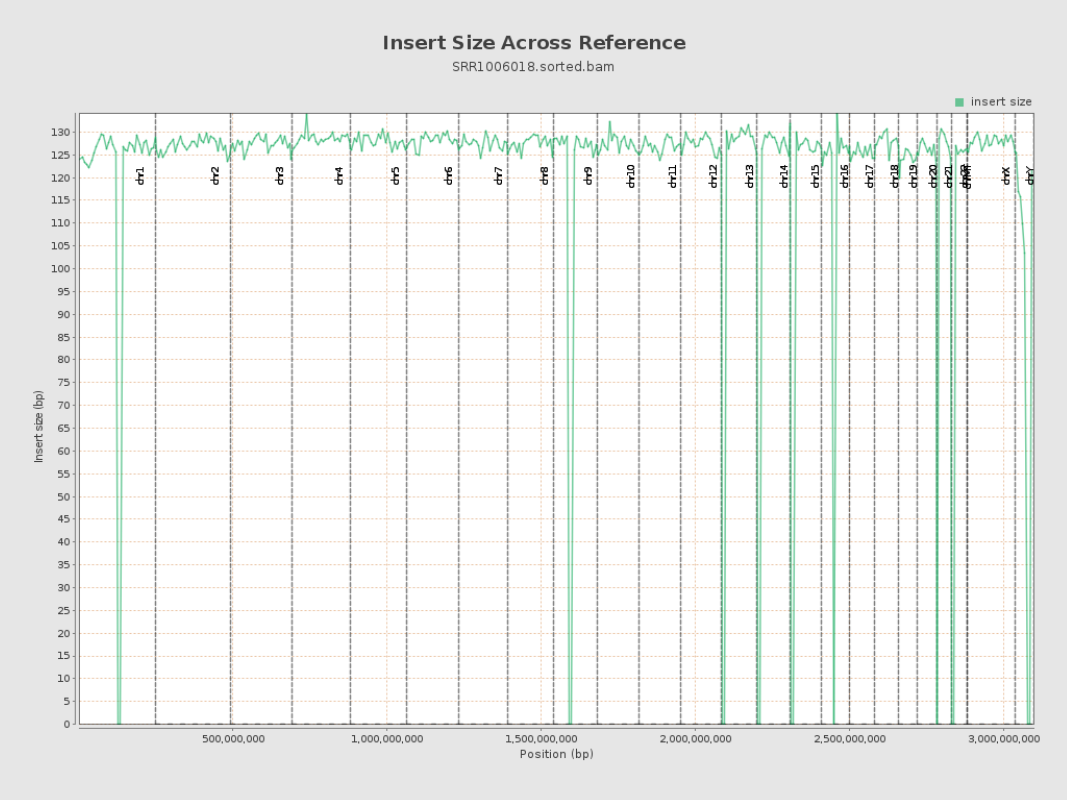
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram