Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/17 12:49:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006006.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_SRR1006006 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006006_1.fastq.gz SRR1006006_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 17 12:49:46 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006006.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	33,655,654
Mapped reads	27,123,330 / 80.59%
Unmapped reads	6,532,324 / 19.41%
Mapped paired reads	27,123,330 / 80.59%
Mapped reads, first in pair	13,737,821 / 40.82%
Mapped reads, second in pair	13,385,509 / 39.77%
Mapped reads, both in pair	24,309,766 / 72.23%
Mapped reads, singletons	2,813,564 / 8.36%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	2,120,843 / 6.3%
Duplication rate	6.56%
Clipped reads	1,794,221 / 5.33%

2.2. ACGT Content

Number/percentage of A's	297,038,329 / 28.32%
Number/percentage of C's	224,598,061 / 21.41%
Number/percentage of T's	298,695,335 / 28.48%
Number/percentage of G's	228,233,262 / 21.76%
Number/percentage of N's	323,627 / 0.03%
GC Percentage	43.17%

2.3. Coverage

Mean	0.3389
Standard Deviation	1.8684

2.4. Mapping Quality

Mean Mapping Quality	47.1

2.5. Insert size

Mean	79,793.68
Standard Deviation	2,726,920.36
P25/Median/P75	77 / 109 / 159

2.6. Mismatches and indels

General error rate	0.5%
Mismatches	5,251,737
Insertions	29,801
Mapped reads with at least one insertion	0.11%
Deletions	94,827
Mapped reads with at least one deletion	0.35%
Homopolymer indels	44.61%

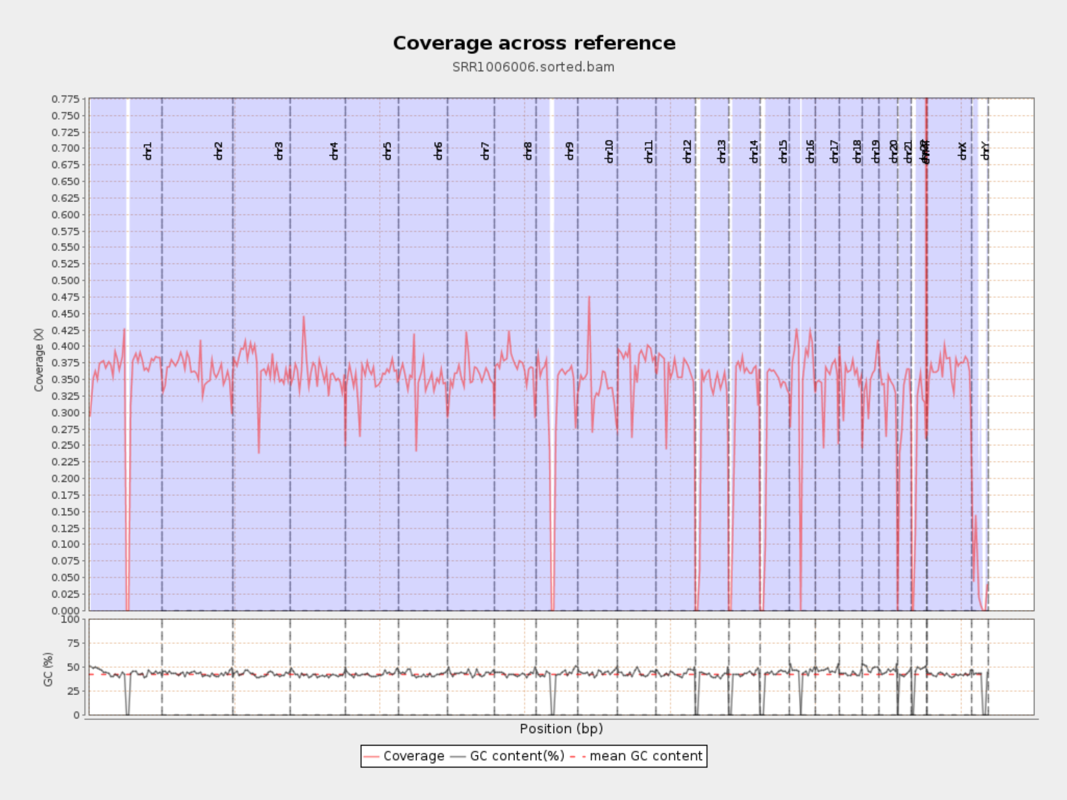
2.7. Chromosome stats

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

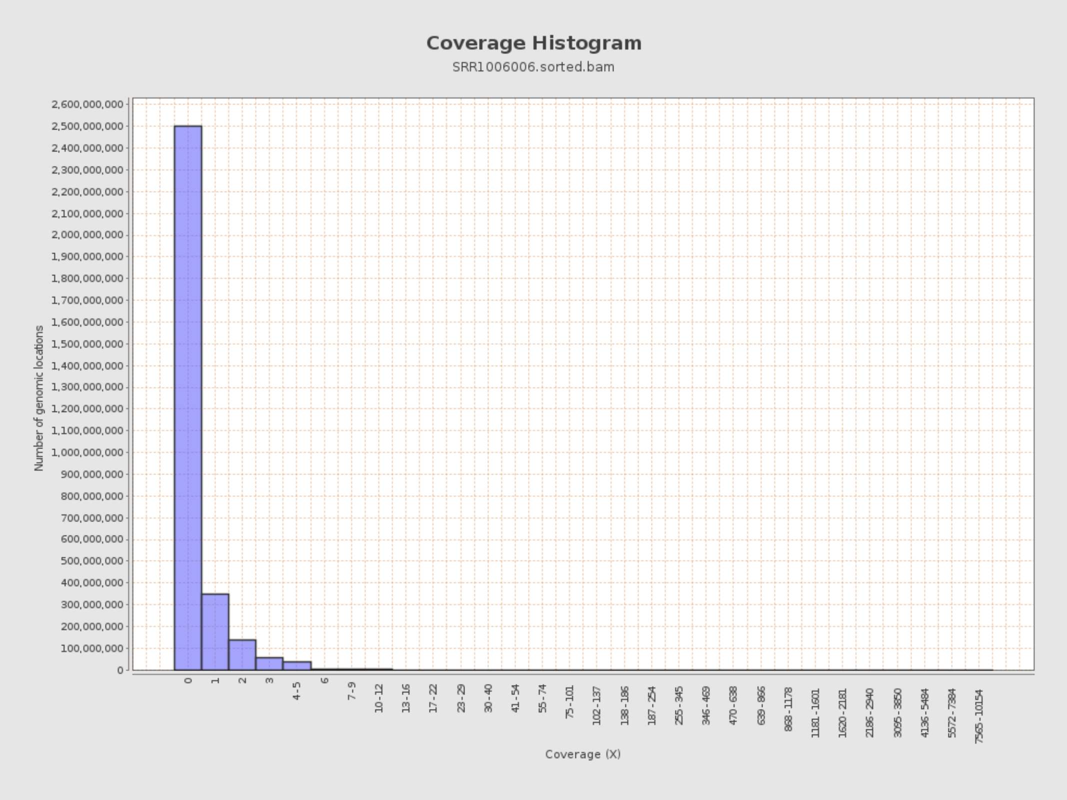
chr1	249250621	86809836	0.3483	2.609
chr2	243199373	88111308	0.3623	1.3268
chr3	198022430	72948203	0.3684	0.9343
chr4	191154276	68583014	0.3588	1.1001
chr5	180915260	63899474	0.3532	0.9205
chr6	171115067	59759598	0.3492	1.2678
chr7	159138663	57047774	0.3585	1.9665
chr8	146364022	54354722	0.3714	5.0301
chr9	141213431	43575385	0.3086	1.0894
chr10	135534747	46487667	0.343	1.6487
chr11	135006516	50827425	0.3765	1.1702
chr12	133851895	48064519	0.3591	0.9421
chr13	115169878	33423796	0.2902	0.8231
chr14	107349540	32345068	0.3013	0.9288
chr15	102531392	29014945	0.283	0.8188
chr16	90354753	31696892	0.3508	1.2283
chr17	81195210	27880738	0.3434	0.9852
chr18	78077248	27838150	0.3565	1.8091
chr19	59128983	20522323	0.3471	5.198
chr20	63025520	20818690	0.3303	0.9658
chr21	48129895	13753251	0.2858	0.9909
chr22	51304566	11635063	0.2268	0.7703
chrMT	16571	322423	19.4571	11.8217
chrX	155270560	56661316	0.3649	1.0711

chrY	59373566	2631524	0.0443	0.9443

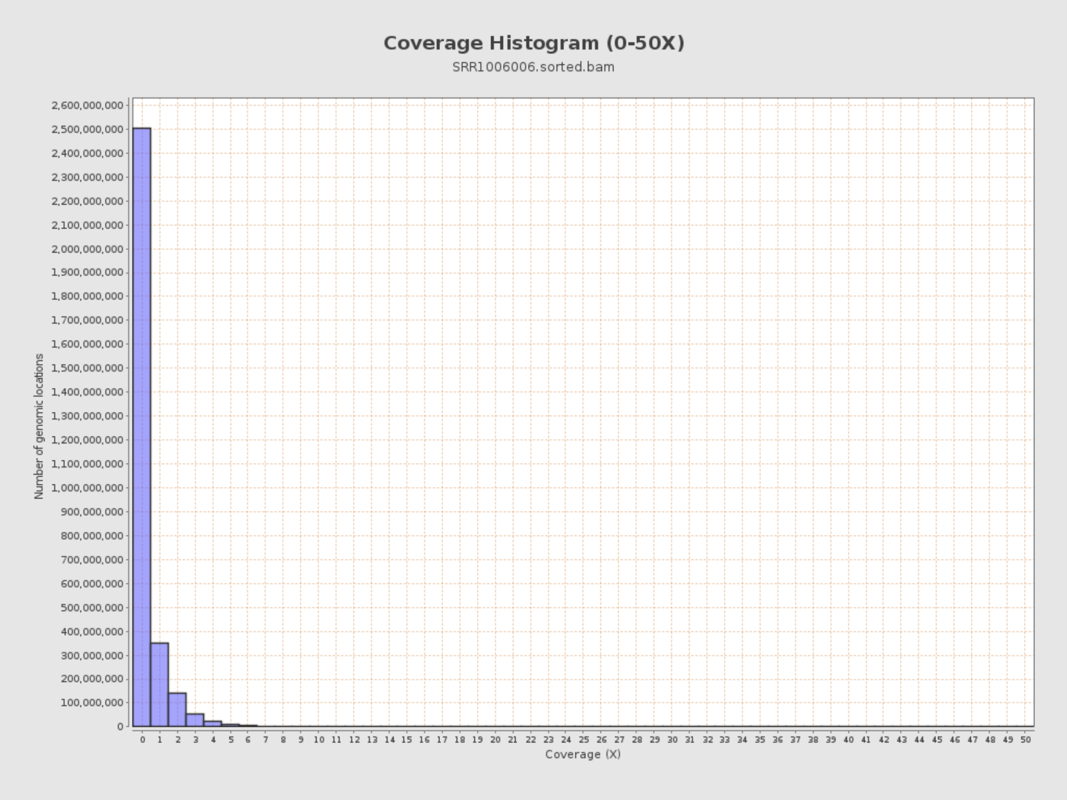
3. Results : Coverage across reference



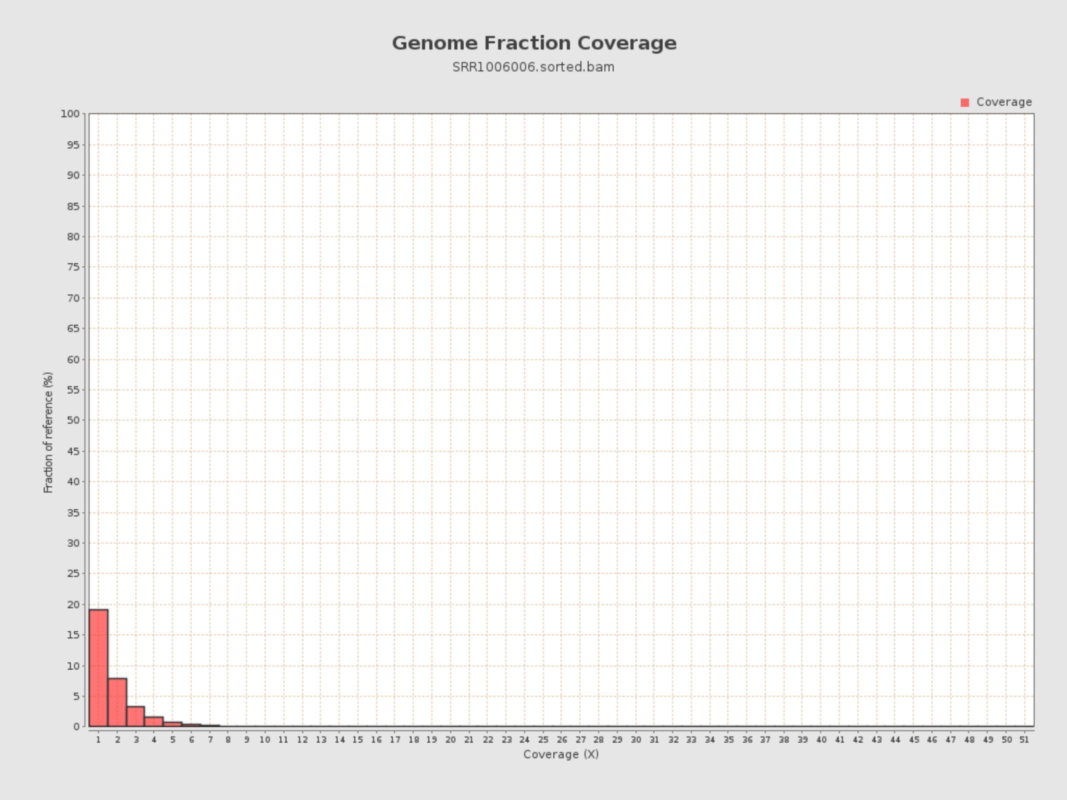
4. Results : Coverage Histogram



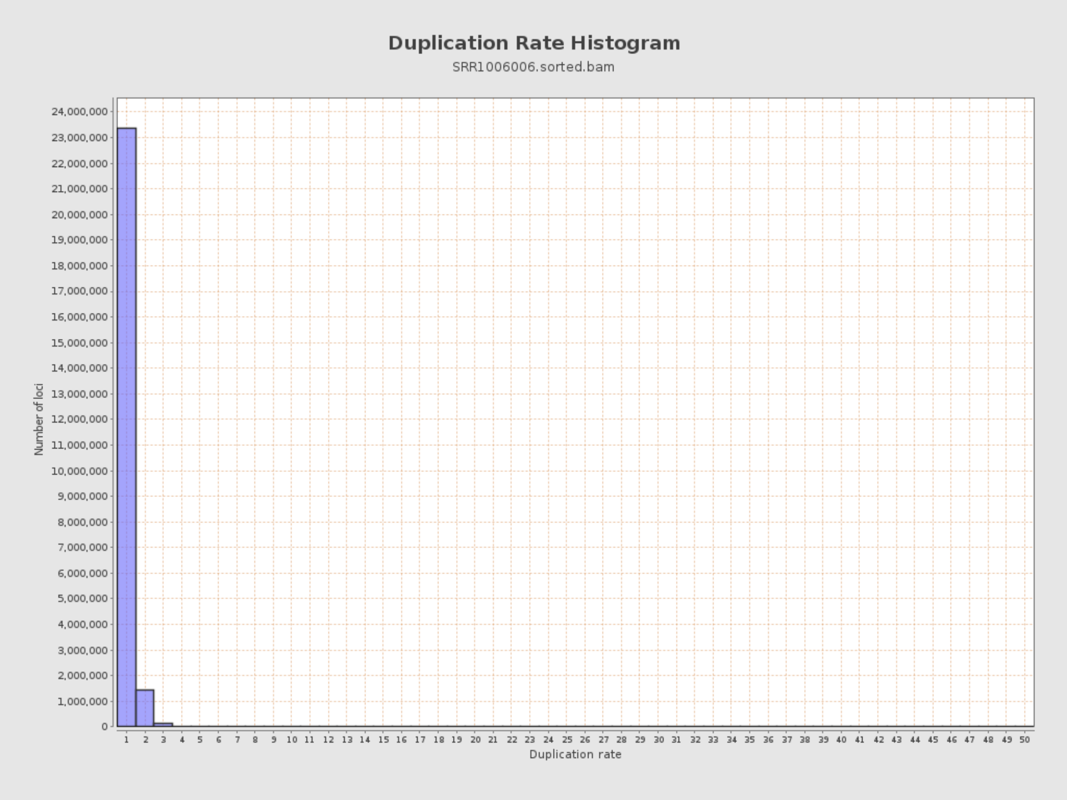
5. Results : Coverage Histogram (0-50X)



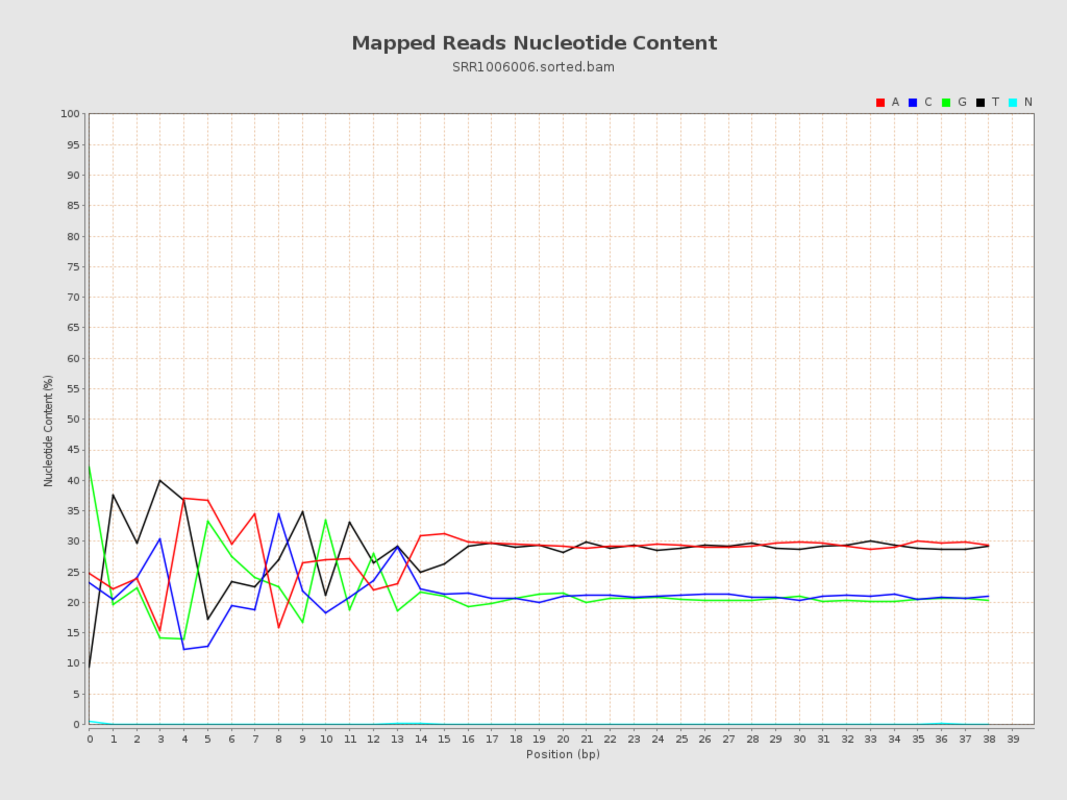
6. Results : Genome Fraction Coverage



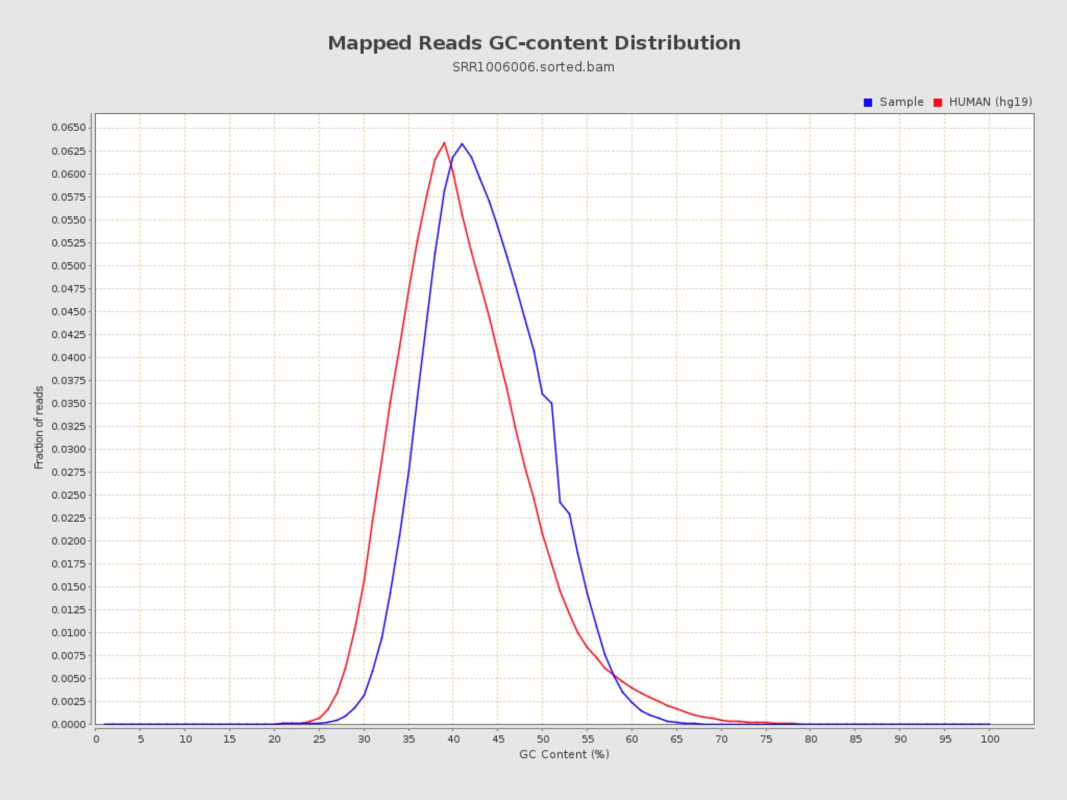
7. Results : Duplication Rate Histogram



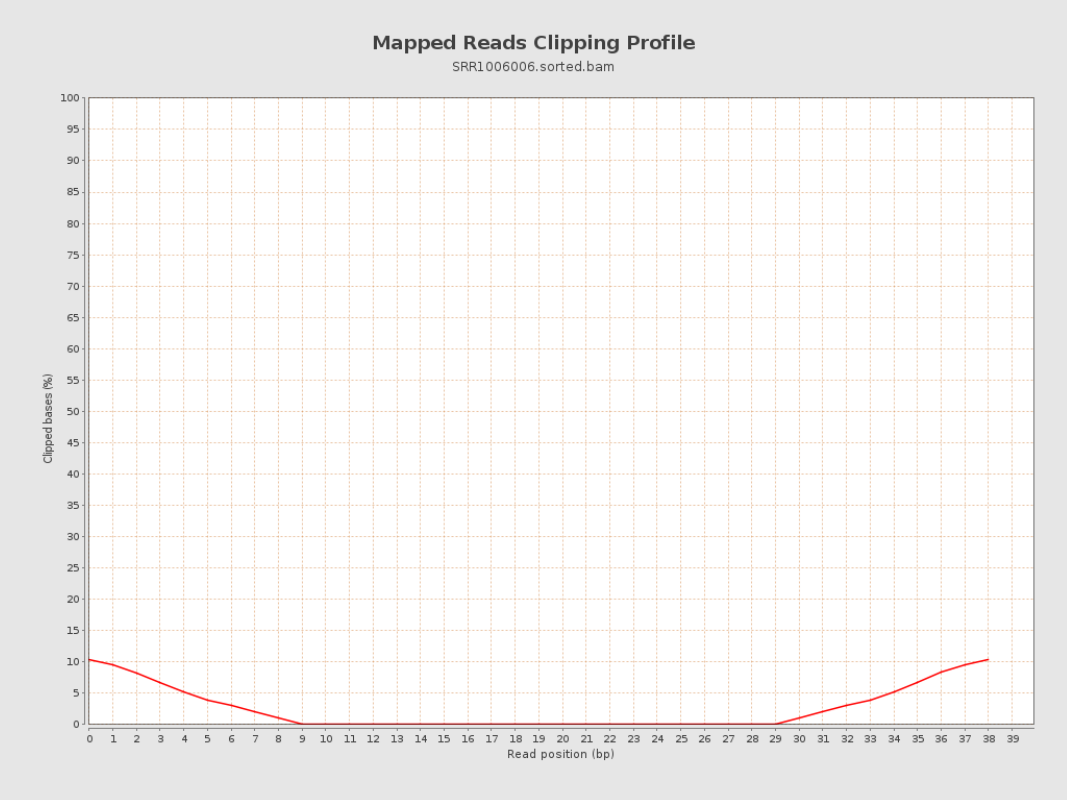
8. Results : Mapped Reads Nucleotide Content



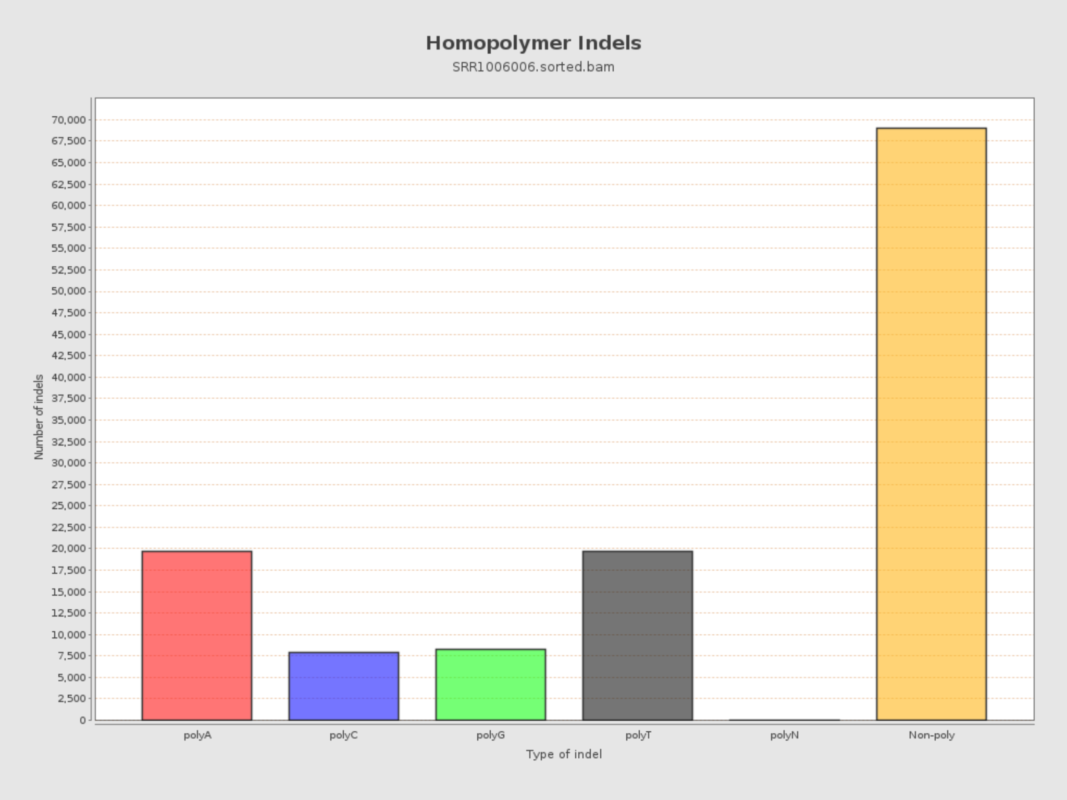
9. Results : Mapped Reads GC-content Distribution



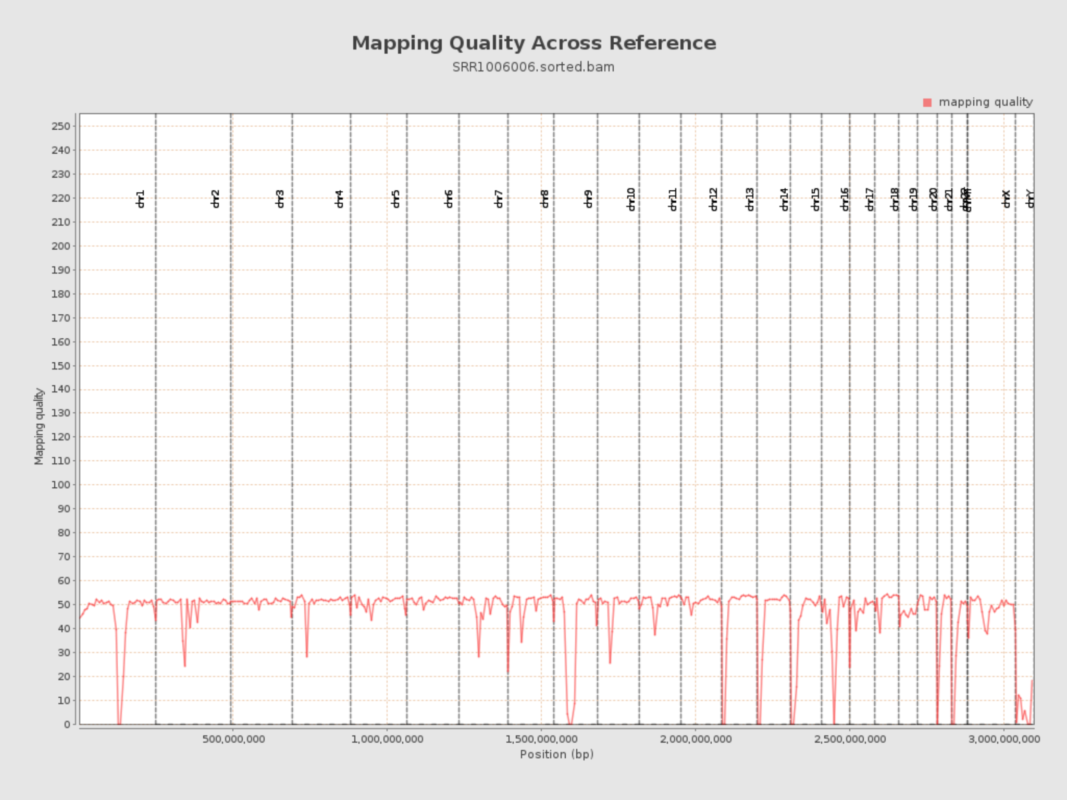
10. Results : Mapped Reads Clipping Profile



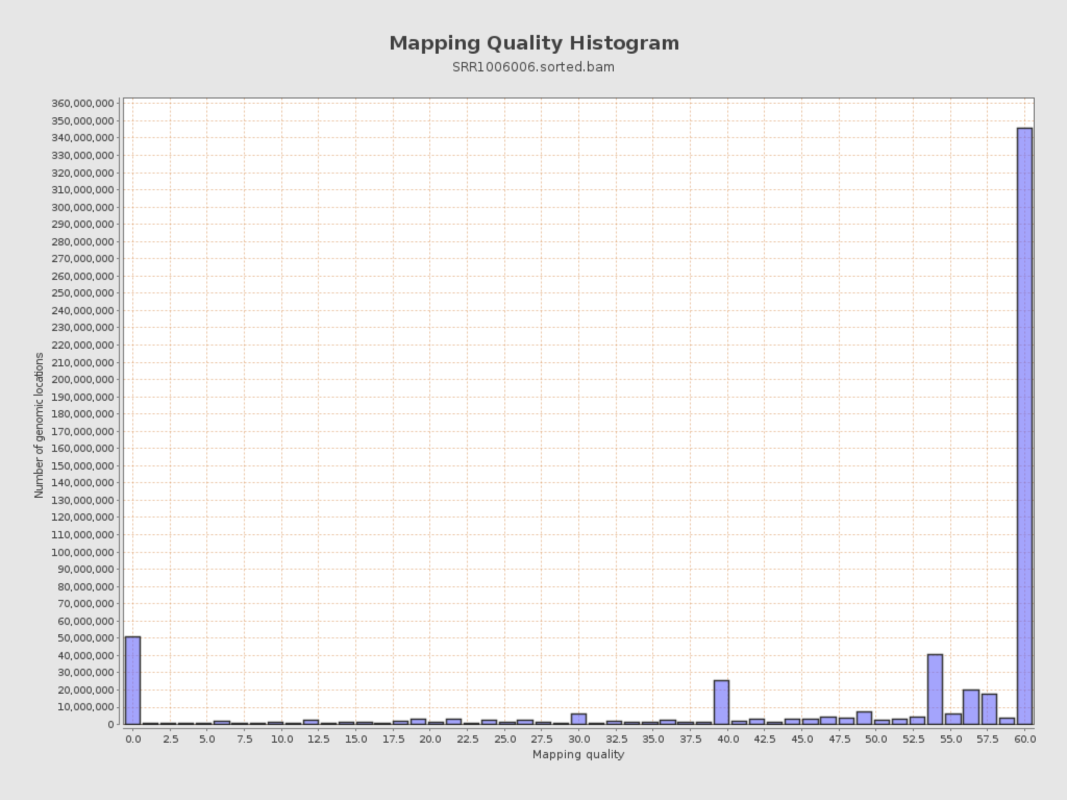
11. Results : Homopolymer Indels



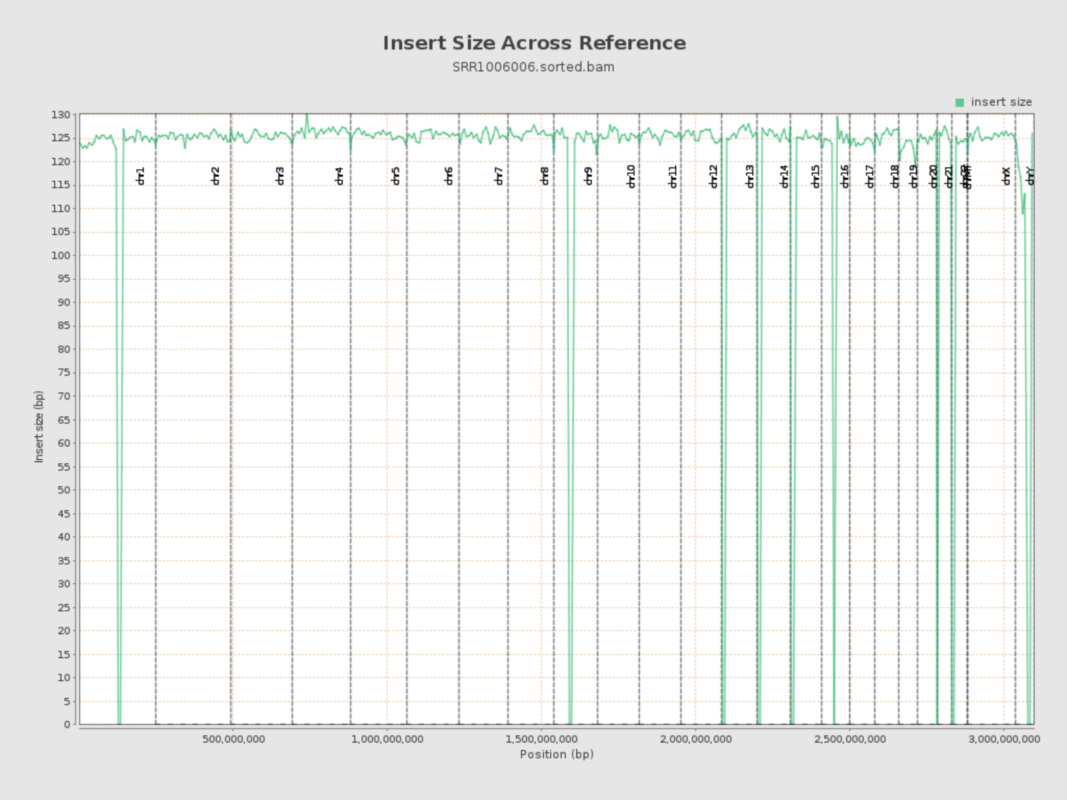
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram