Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/17 22:03:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006160.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_SRR1006160 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006160_1.fastq.gz SRR1006160_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 17 22:03:01 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006160.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,061,324
Mapped reads	8,707,180 / 86.54%
Unmapped reads	1,354,144 / 13.46%
Mapped paired reads	8,707,180 / 86.54%
Mapped reads, first in pair	4,374,401 / 43.48%
Mapped reads, second in pair	4,332,779 / 43.06%
Mapped reads, both in pair	8,151,938 / 81.02%
Mapped reads, singletons	555,242 / 5.52%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	563,684 / 5.6%
Duplication rate	5.76%
Clipped reads	691,467 / 6.87%

2.2. ACGT Content

Number/percentage of A's	89,400,822 / 26.59%
Number/percentage of C's	77,092,431 / 22.93%
Number/percentage of T's	90,836,826 / 27.02%
Number/percentage of G's	78,796,524 / 23.44%
Number/percentage of N's	45,222 / 0.01%
GC Percentage	46.37%

2.3. Coverage

Mean	0.1086
Standard Deviation	0.6448

2.4. Mapping Quality

Mean Mapping Quality	46.77

2.5. Insert size

Mean	54,254.4
Standard Deviation	2,281,652.58
P25/Median/P75	53 / 74 / 108

2.6. Mismatches and indels

General error rate	0.38%
Mismatches	1,260,297
Insertions	11,252
Mapped reads with at least one insertion	0.13%
Deletions	30,104
Mapped reads with at least one deletion	0.35%
Homopolymer indels	39.03%

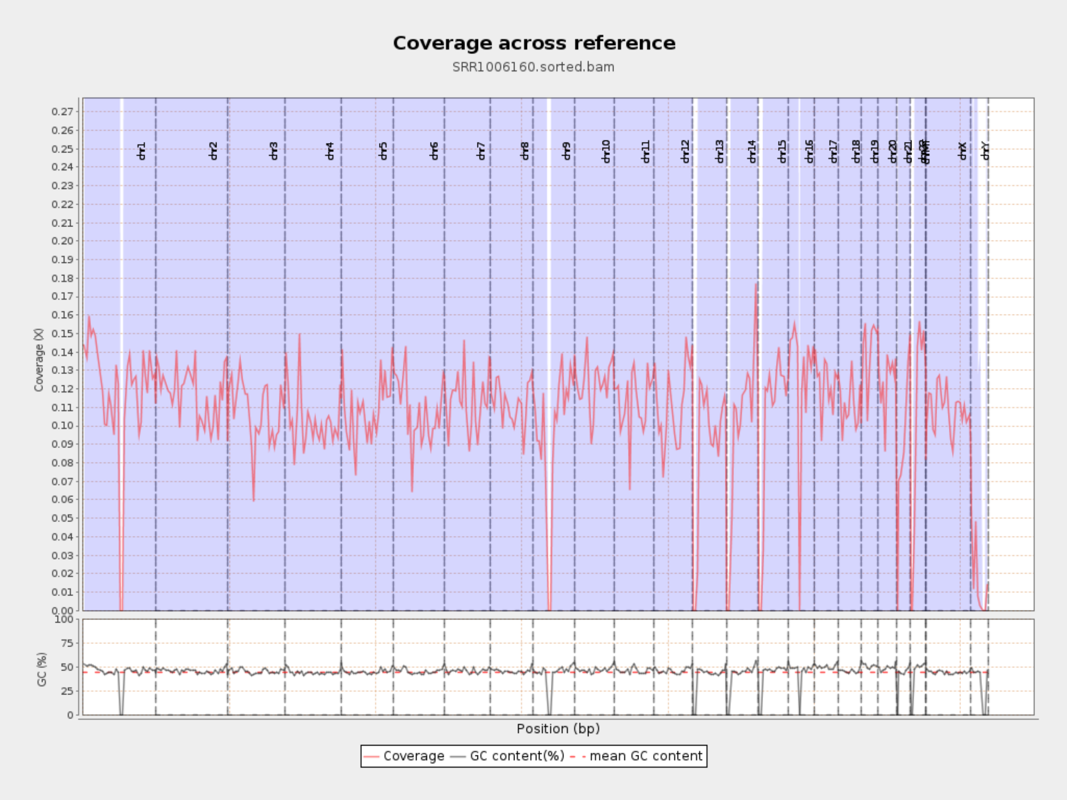
2.7. Chromosome stats

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

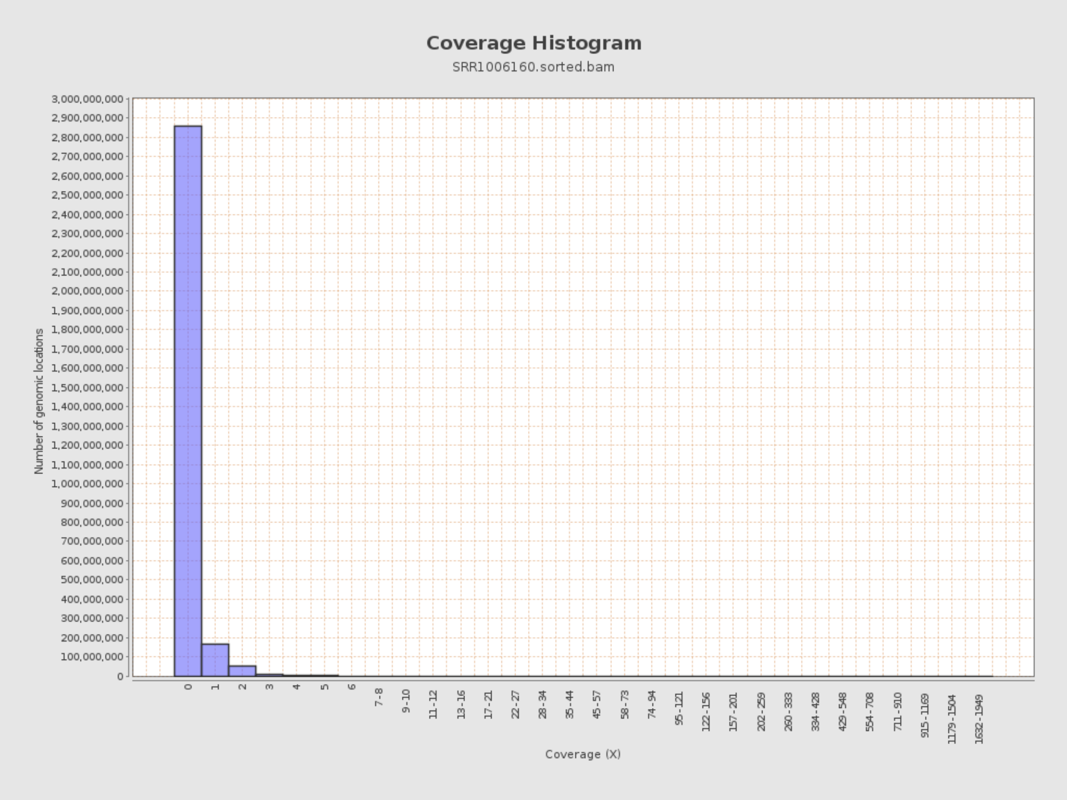
chr1	249250621	29476082	0.1183	0.701
chr2	243199373	28545988	0.1174	0.5498
chr3	198022430	21283723	0.1075	0.4315
chr4	191154276	19730949	0.1032	0.4877
chr5	180915260	19742618	0.1091	0.4397
chr6	171115067	18330924	0.1071	0.4779
chr7	159138663	18024084	0.1133	0.6256
chr8	146364022	16410088	0.1121	1.0533
chr9	141213431	13514110	0.0957	0.4709
chr10	135534747	16576596	0.1223	0.6275
chr11	135006516	15184324	0.1125	0.5182
chr12	133851895	14960789	0.1118	0.4545
chr13	115169878	10208482	0.0886	0.4009
chr14	107349540	10748119	0.1001	1.7228
chr15	102531392	10172466	0.0992	0.4206
chr16	90354753	11290650	0.125	0.5292
chr17	81195210	9971255	0.1228	0.4994
chr18	78077248	8640438	0.1107	0.6695
chr19	59128983	8267937	0.1398	0.6758
chr20	63025520	7756153	0.1231	0.5068
chr21	48129895	4392698	0.0913	0.5012
chr22	51304566	5172810	0.1008	0.7535
chrMT	16571	1357	0.0819	0.5703
chrX	155270560	16902140	0.1089	0.4596

chrY	59373566	906954	0.0153	0.3557

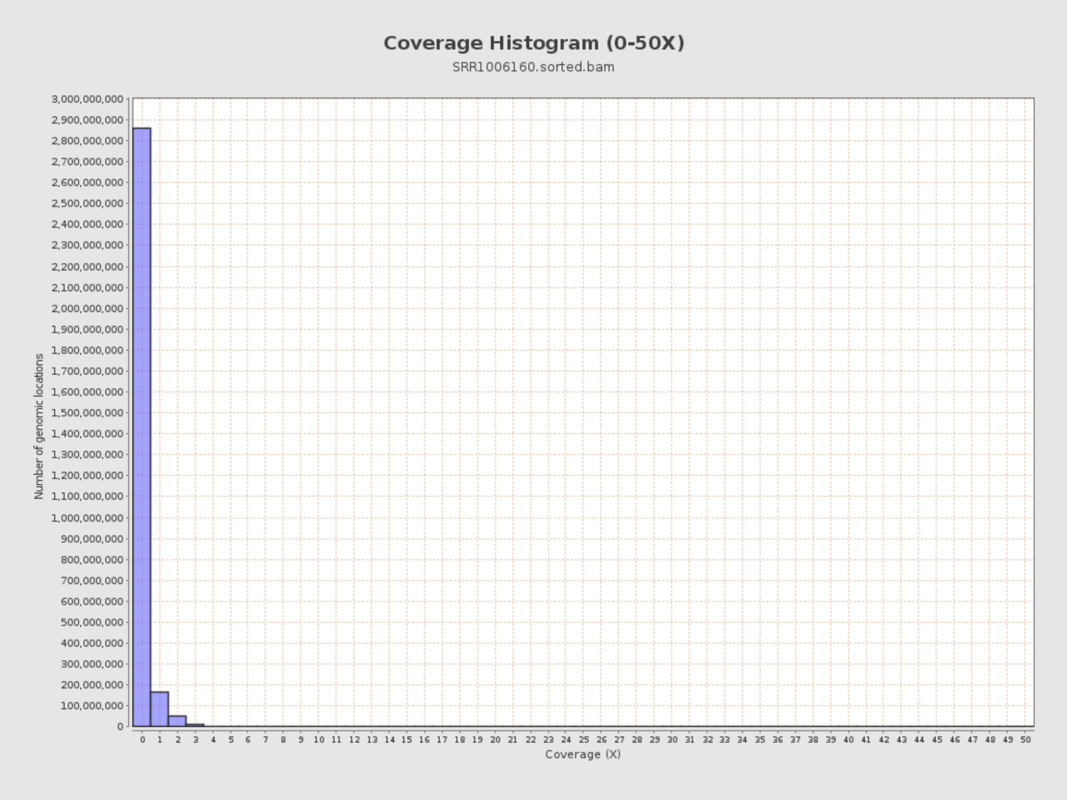
3. Results : Coverage across reference



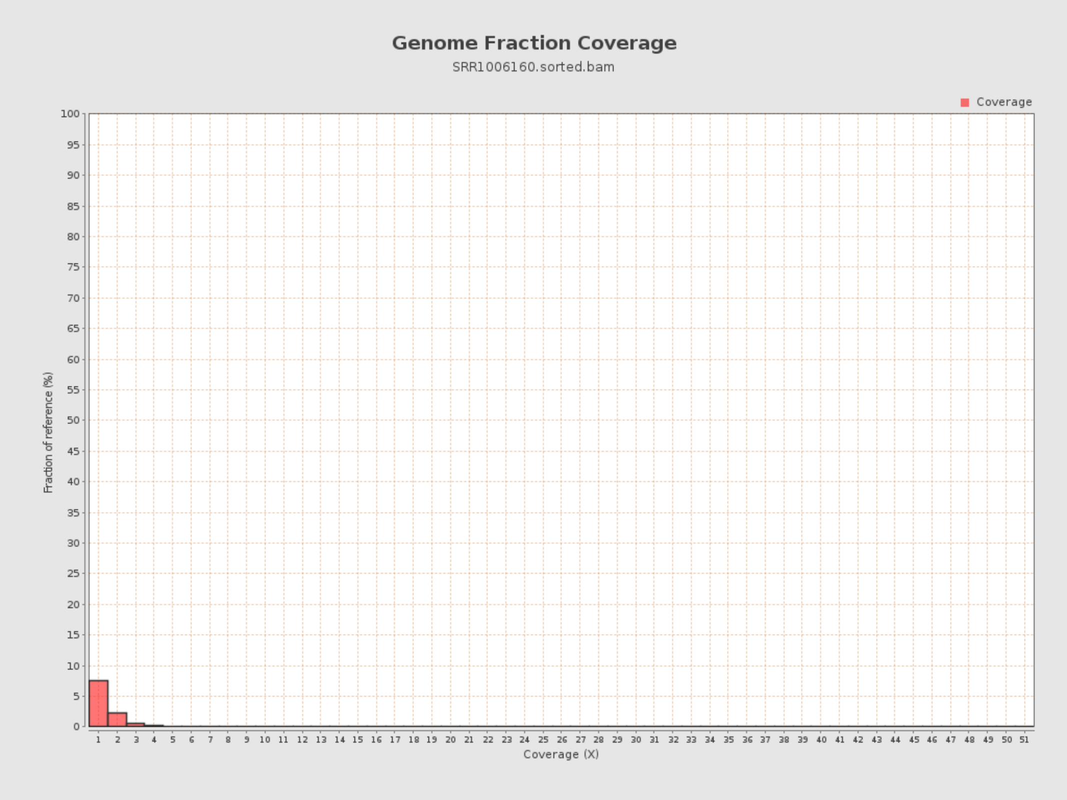
4. Results : Coverage Histogram



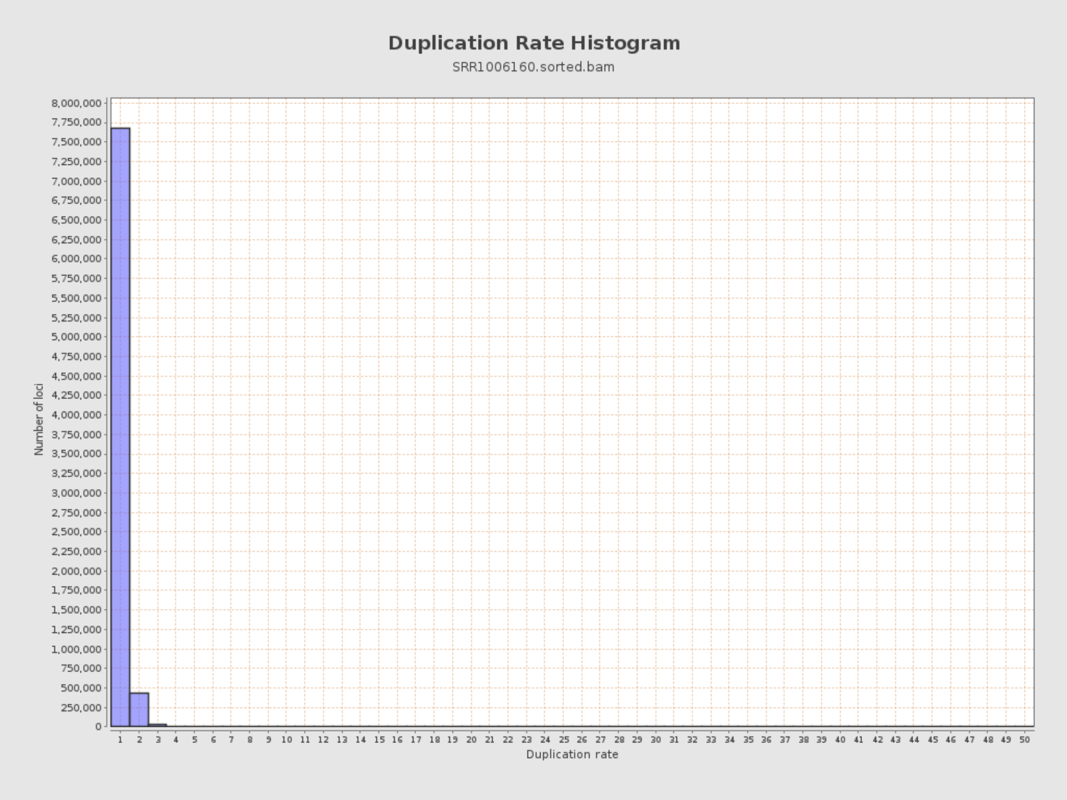
5. Results : Coverage Histogram (0-50X)



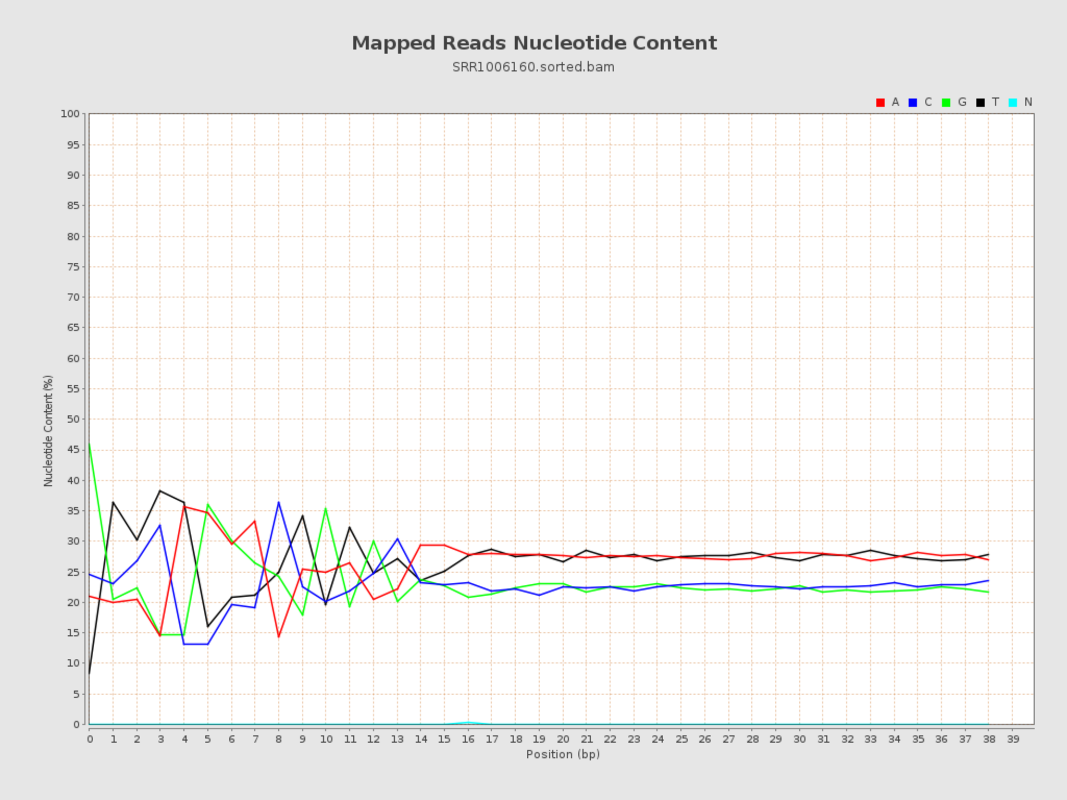
6. Results : Genome Fraction Coverage



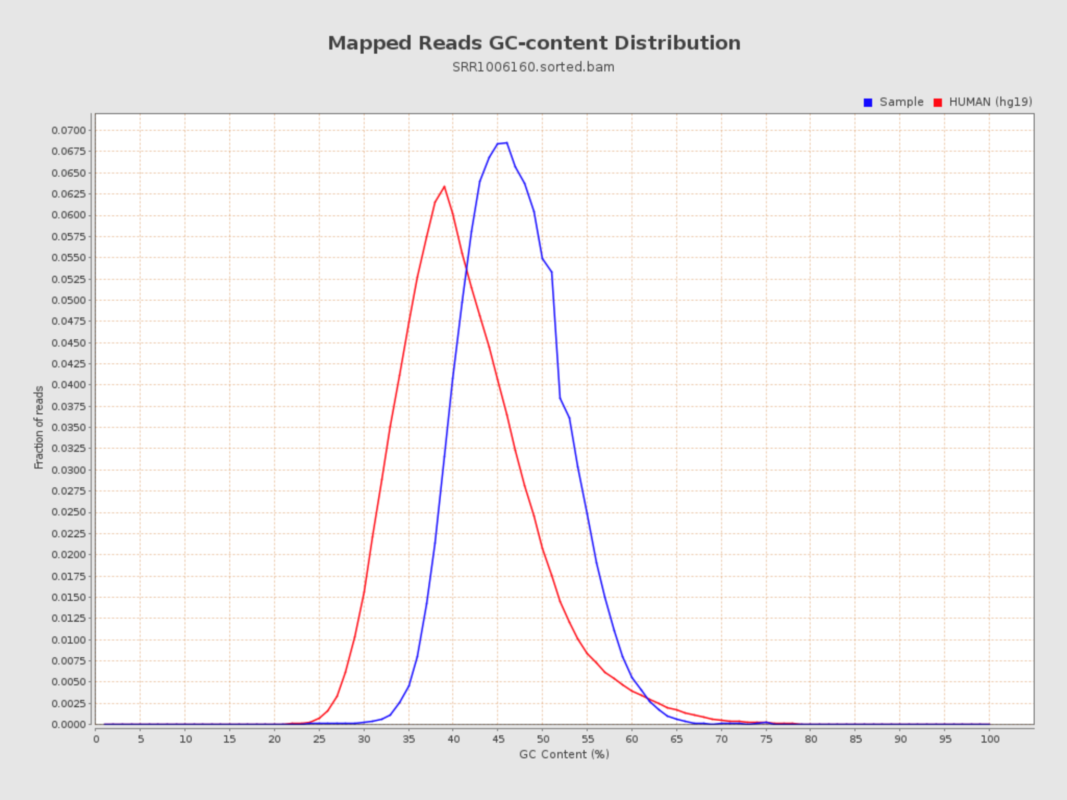
7. Results : Duplication Rate Histogram



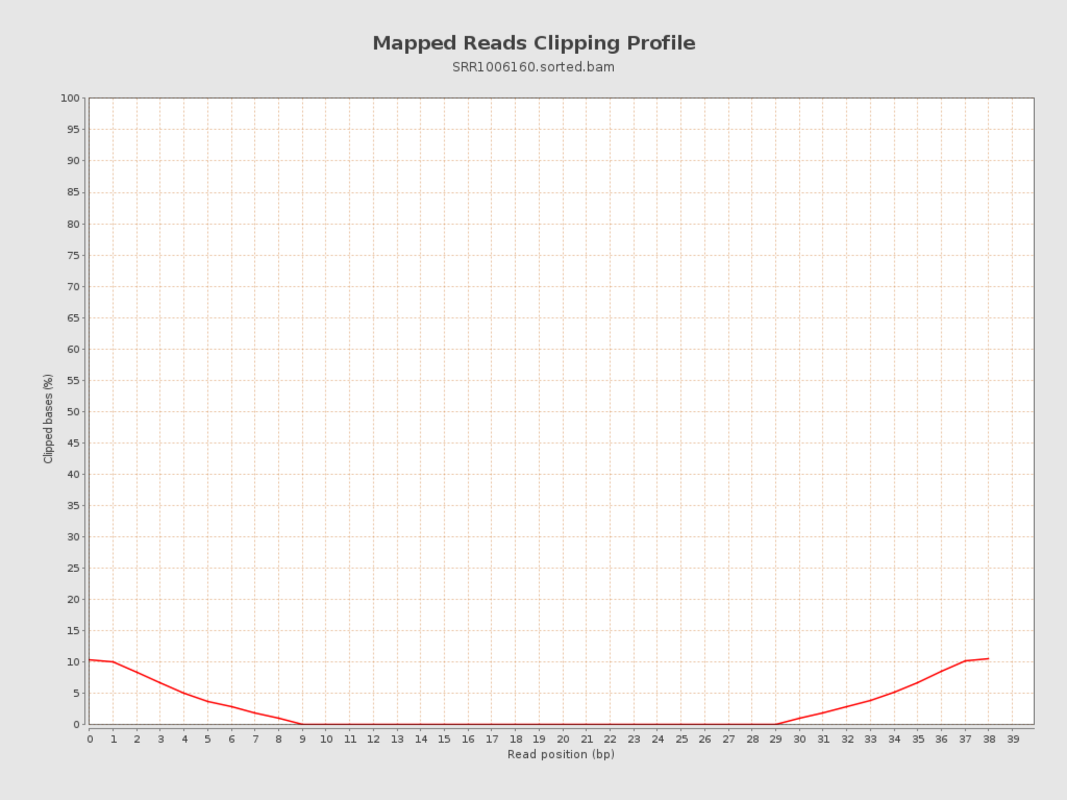
8. Results : Mapped Reads Nucleotide Content



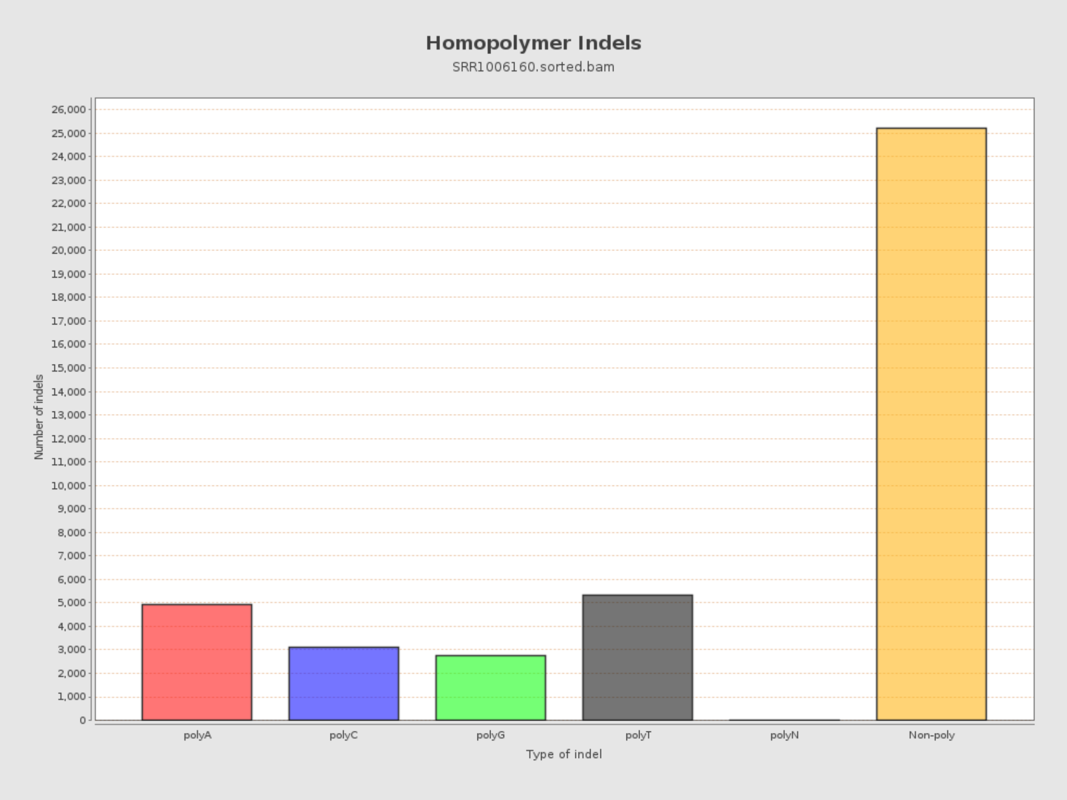
9. Results : Mapped Reads GC-content Distribution



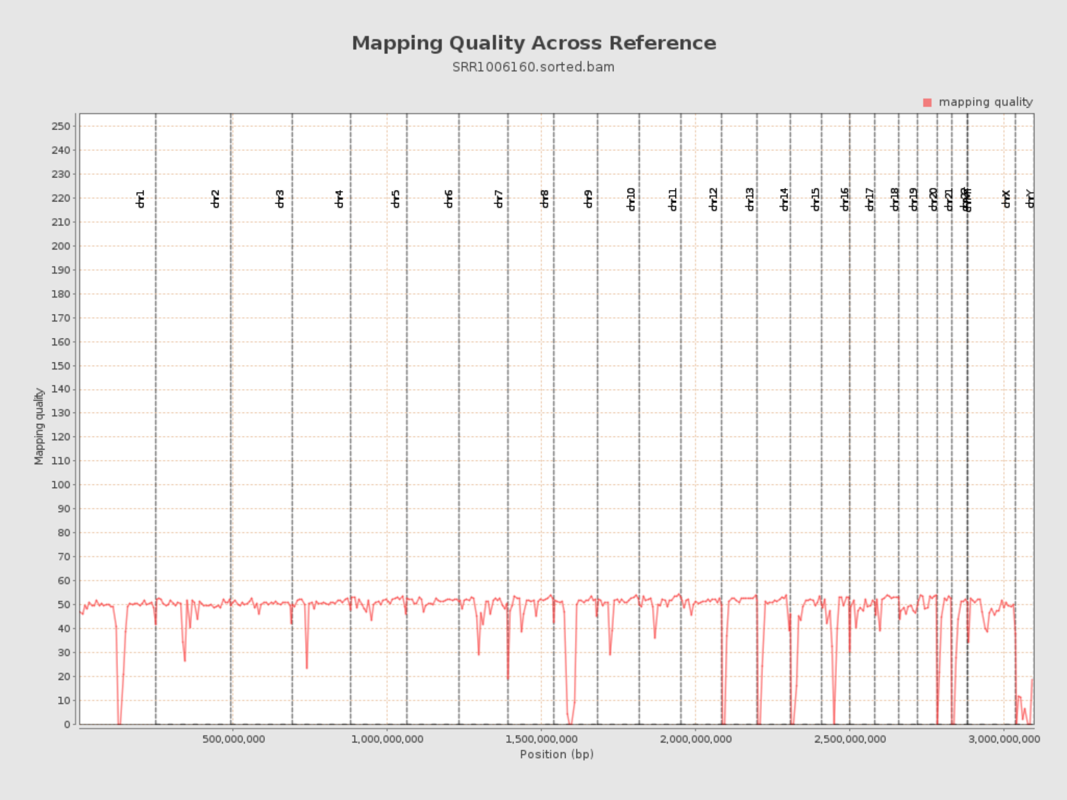
10. Results : Mapped Reads Clipping Profile



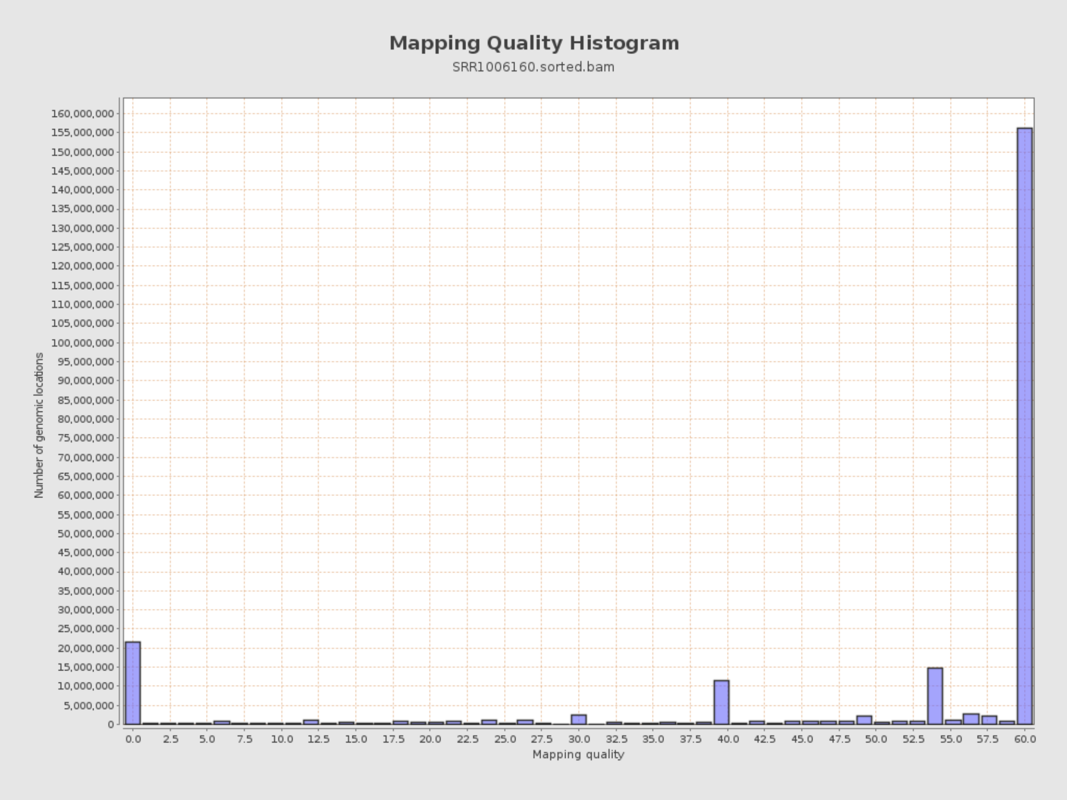
11. Results : Homopolymer Indels



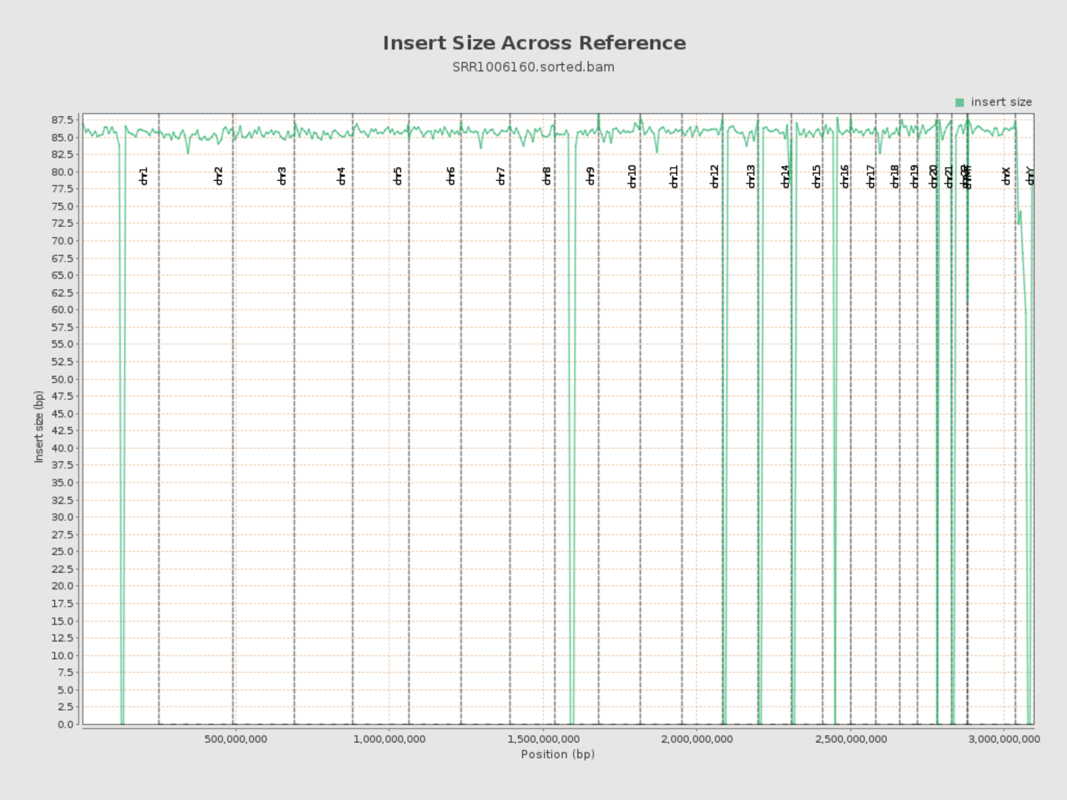
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram