Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/17 17:24:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006063.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_SRR1006063 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006063_1.fastq.gz SRR1006063_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 17 17:24:13 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006063.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,994,212
Mapped reads	9,412,360 / 85.61%
Unmapped reads	1,581,852 / 14.39%
Mapped paired reads	9,412,360 / 85.61%
Mapped reads, first in pair	4,776,653 / 43.45%
Mapped reads, second in pair	4,635,707 / 42.16%
Mapped reads, both in pair	8,531,386 / 77.6%
Mapped reads, singletons	880,974 / 8.01%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	731,480 / 6.65%
Duplication rate	7.1%
Clipped reads	953,560 / 8.67%

2.2. ACGT Content

Number/percentage of A's	96,698,168 / 26.67%
Number/percentage of C's	80,456,669 / 22.19%
Number/percentage of T's	99,968,992 / 27.57%
Number/percentage of G's	85,459,230 / 23.57%
Number/percentage of N's	14,500 / 0%
GC Percentage	45.76%

2.3. Coverage

Mean	0.1171
Standard Deviation	0.638

2.4. Mapping Quality

Mean Mapping Quality	46.49

2.5. Insert size

Mean	70,993.59
Standard Deviation	2,625,170.5
P25/Median/P75	64 / 95 / 129

2.6. Mismatches and indels

General error rate	0.61%
Mismatches	2,196,031
Insertions	13,153
Mapped reads with at least one insertion	0.14%
Deletions	32,355
Mapped reads with at least one deletion	0.34%
Homopolymer indels	43.96%

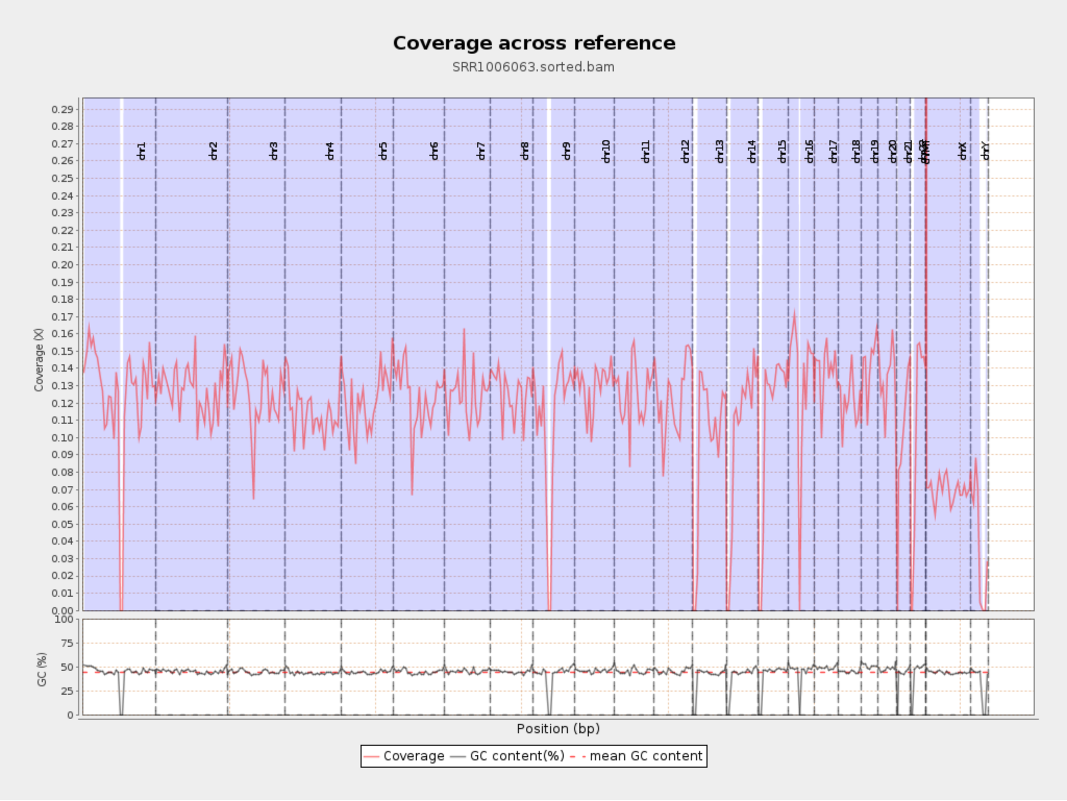
2.7. Chromosome stats

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

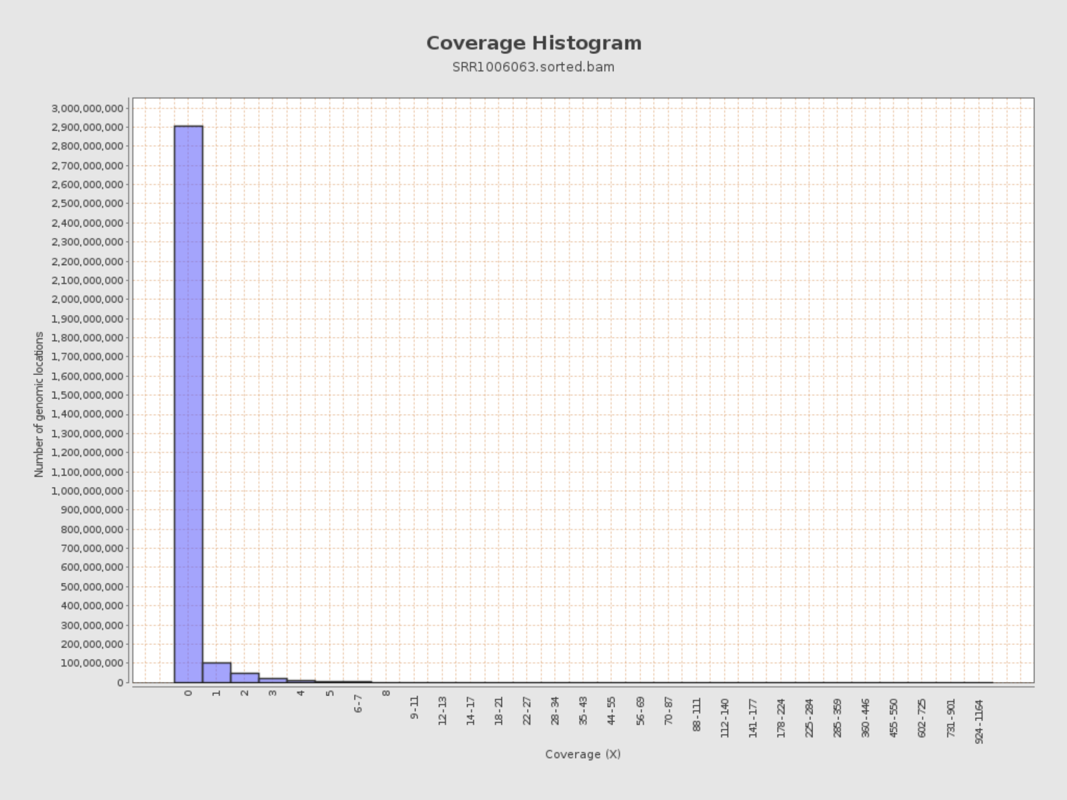
chr1	249250621	30888195	0.1239	0.6949
chr2	243199373	31040358	0.1276	0.6991
chr3	198022430	24698931	0.1247	0.5829
chr4	191154276	21862522	0.1144	0.5784
chr5	180915260	22047054	0.1219	0.5809
chr6	171115067	21009668	0.1228	0.664
chr7	159138663	19800208	0.1244	0.746
chr8	146364022	18324788	0.1252	0.7029
chr9	141213431	15438889	0.1093	0.5853
chr10	135534747	17599430	0.1299	0.6177
chr11	135006516	16923043	0.1253	0.8673
chr12	133851895	16638710	0.1243	0.5897
chr13	115169878	11239461	0.0976	0.5214
chr14	107349540	11068055	0.1031	0.5417
chr15	102531392	11173287	0.109	0.5581
chr16	90354753	11847621	0.1311	0.6499
chr17	81195210	11365908	0.14	0.6824
chr18	78077248	9407252	0.1205	0.684
chr19	59128983	8377666	0.1417	0.778
chr20	63025520	8510872	0.135	0.6269
chr21	48129895	4888017	0.1016	0.6075
chr22	51304566	5260686	0.1025	0.5951
chrMT	16571	70884	4.2776	5.3855
chrX	155270560	10843771	0.0698	0.4462

chrY	59373566	2312675	0.039	0.3561

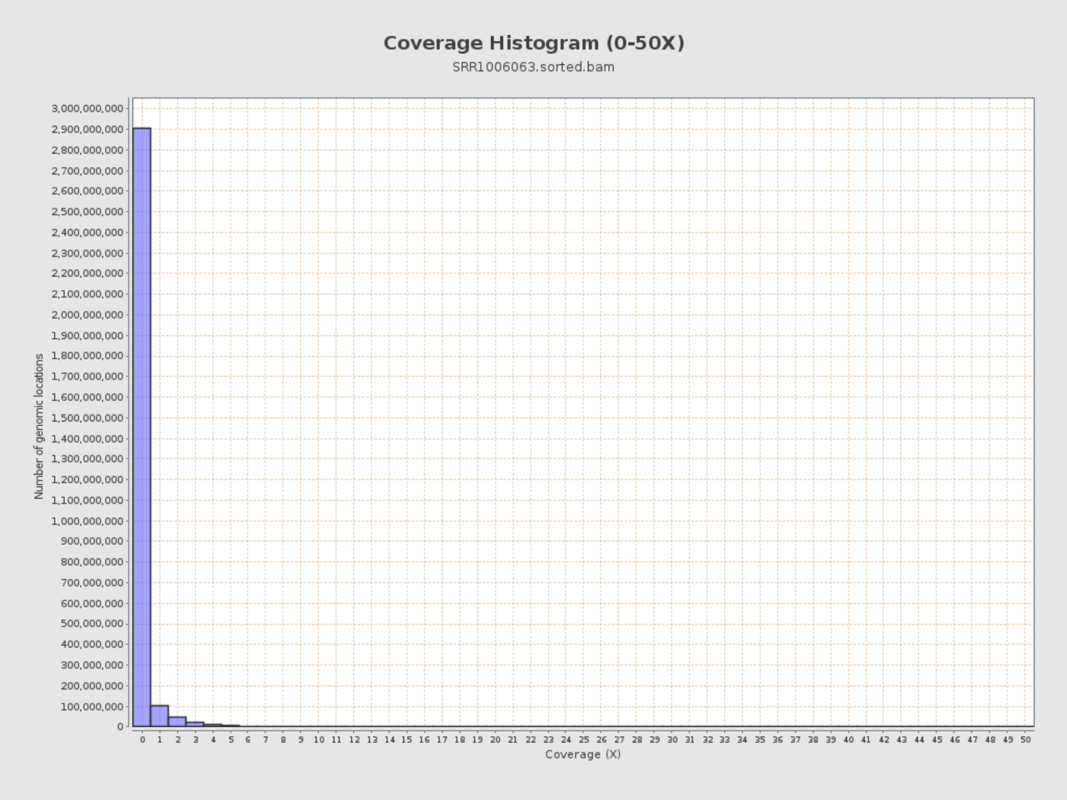
3. Results : Coverage across reference



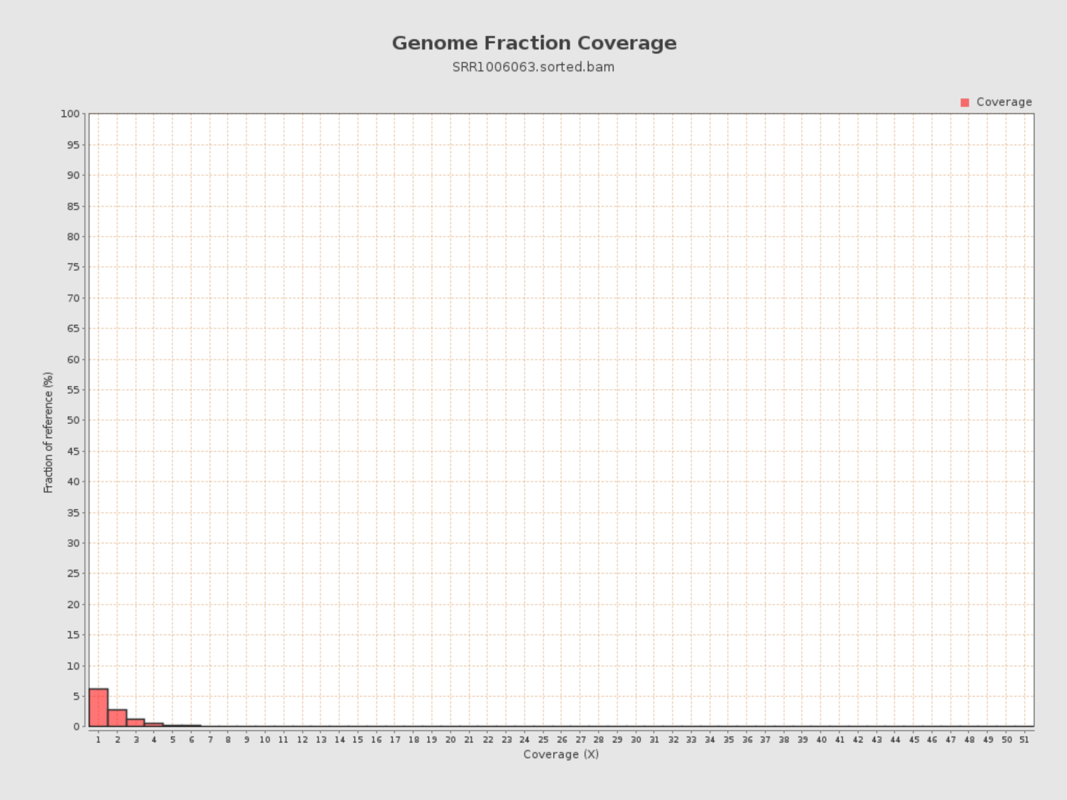
4. Results : Coverage Histogram



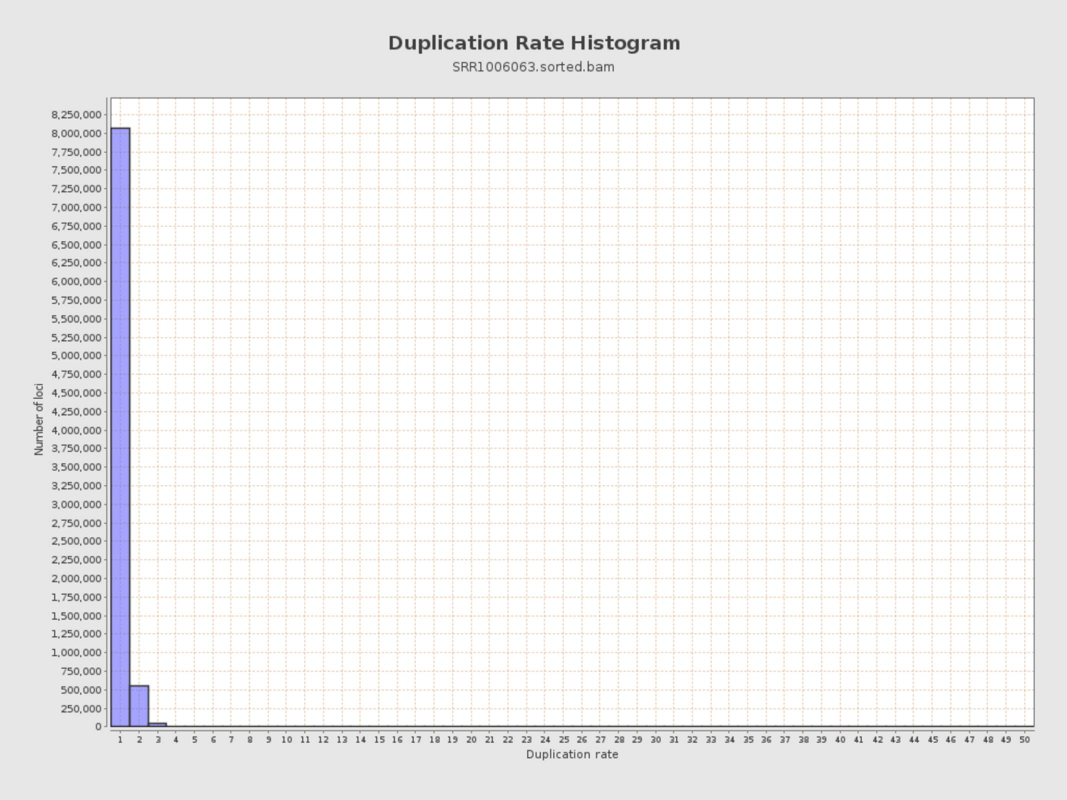
5. Results : Coverage Histogram (0-50X)



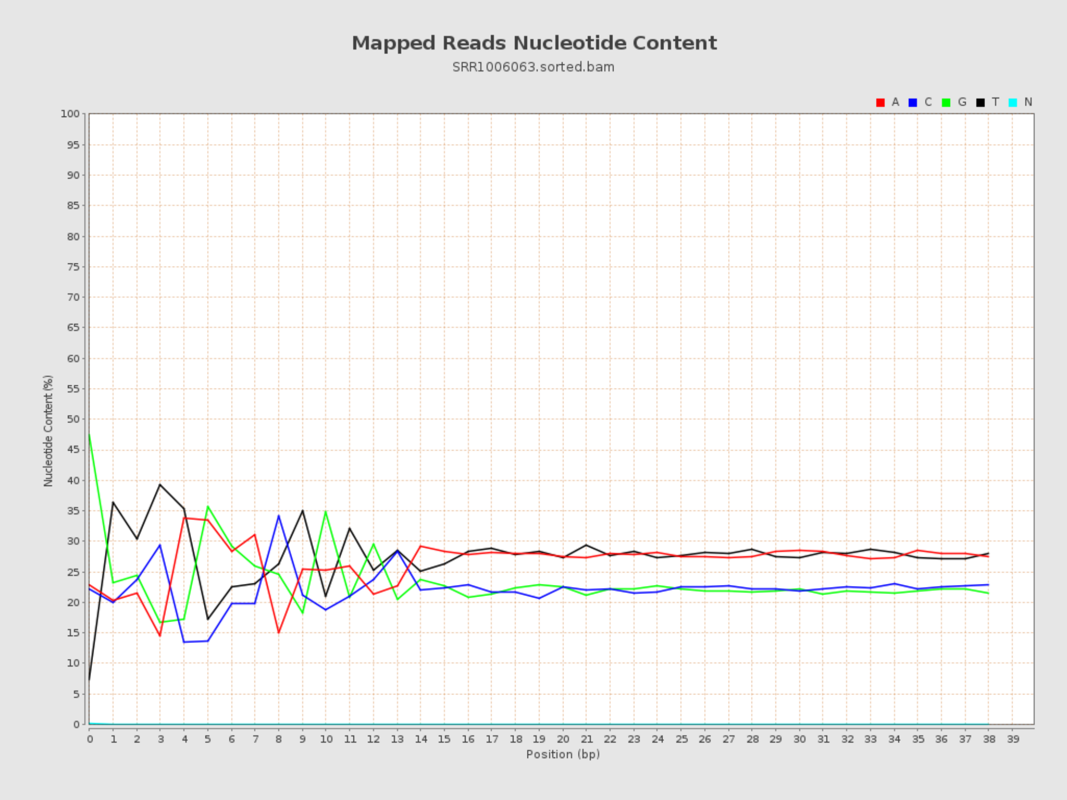
6. Results : Genome Fraction Coverage



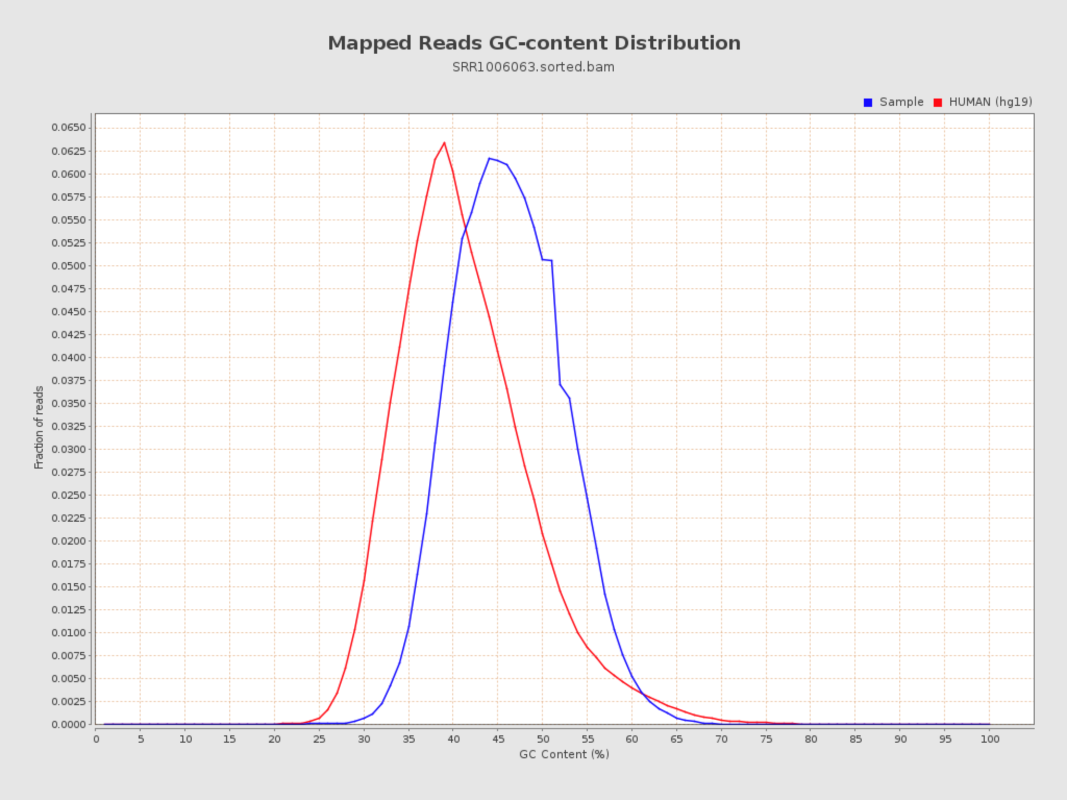
7. Results : Duplication Rate Histogram



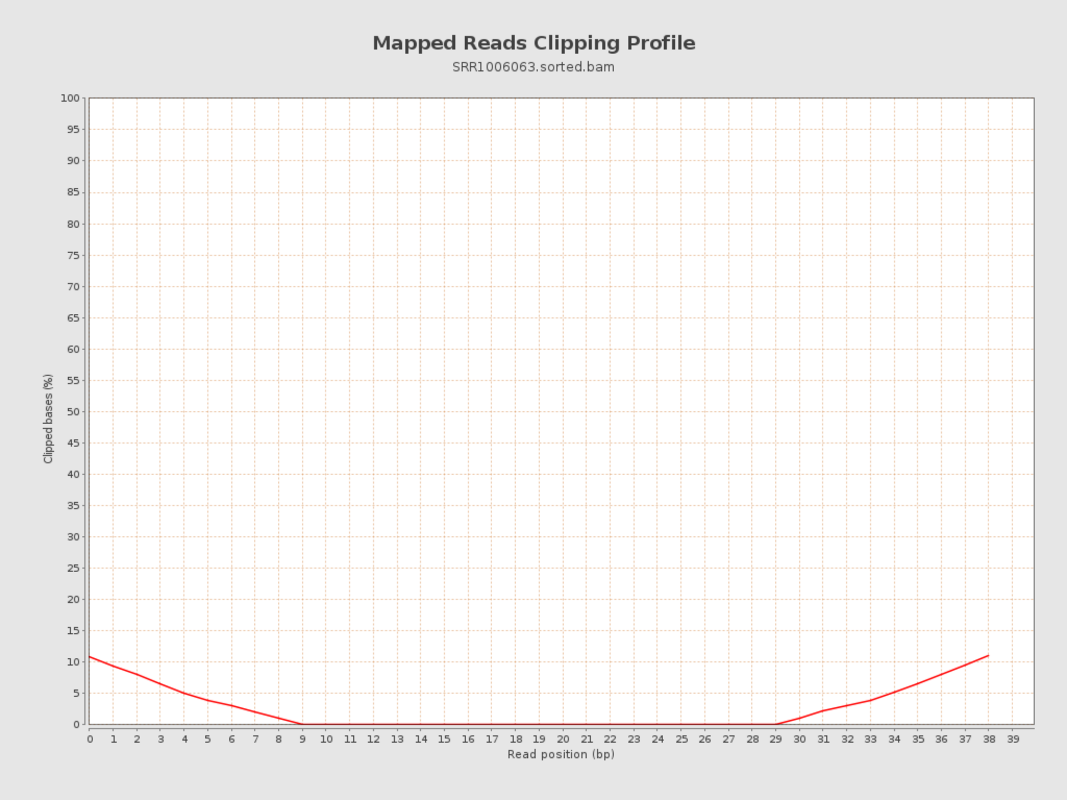
8. Results : Mapped Reads Nucleotide Content



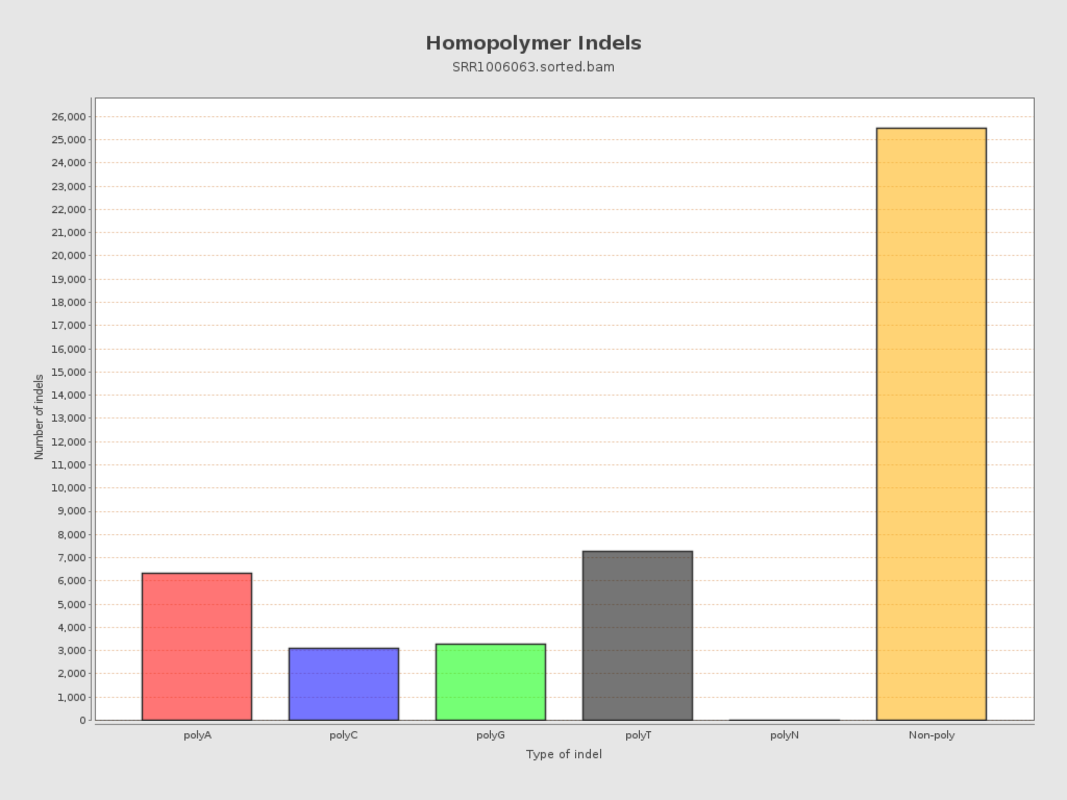
9. Results : Mapped Reads GC-content Distribution



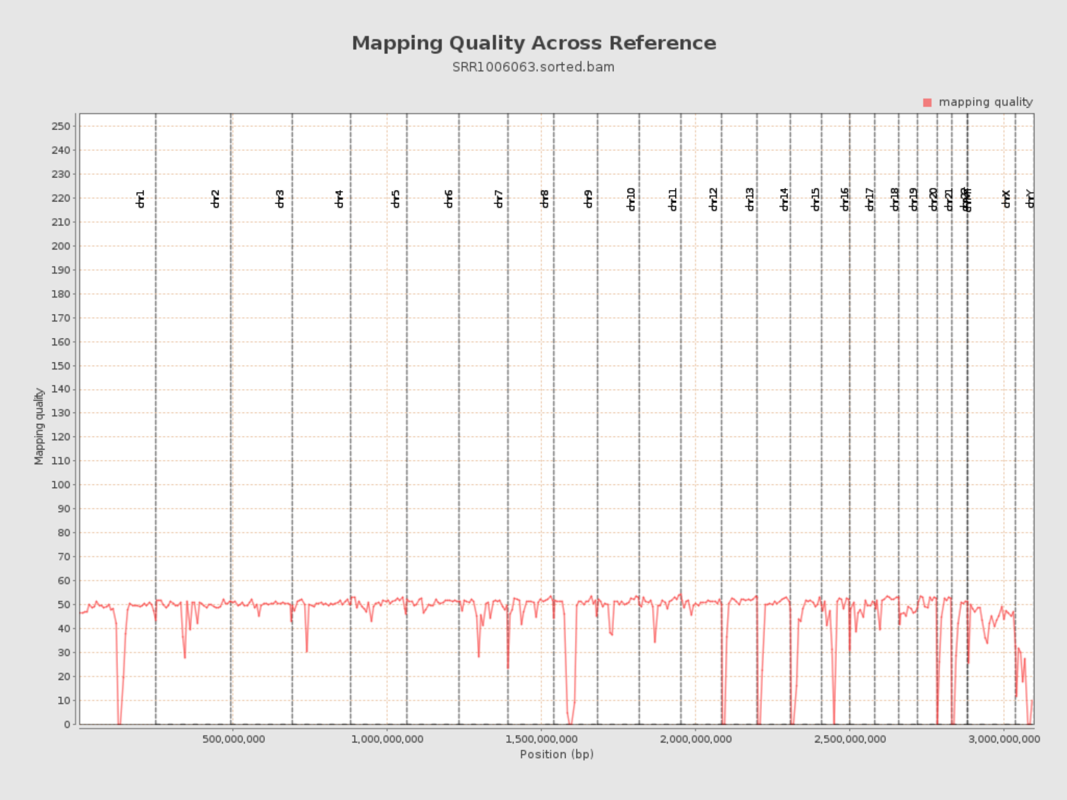
10. Results : Mapped Reads Clipping Profile



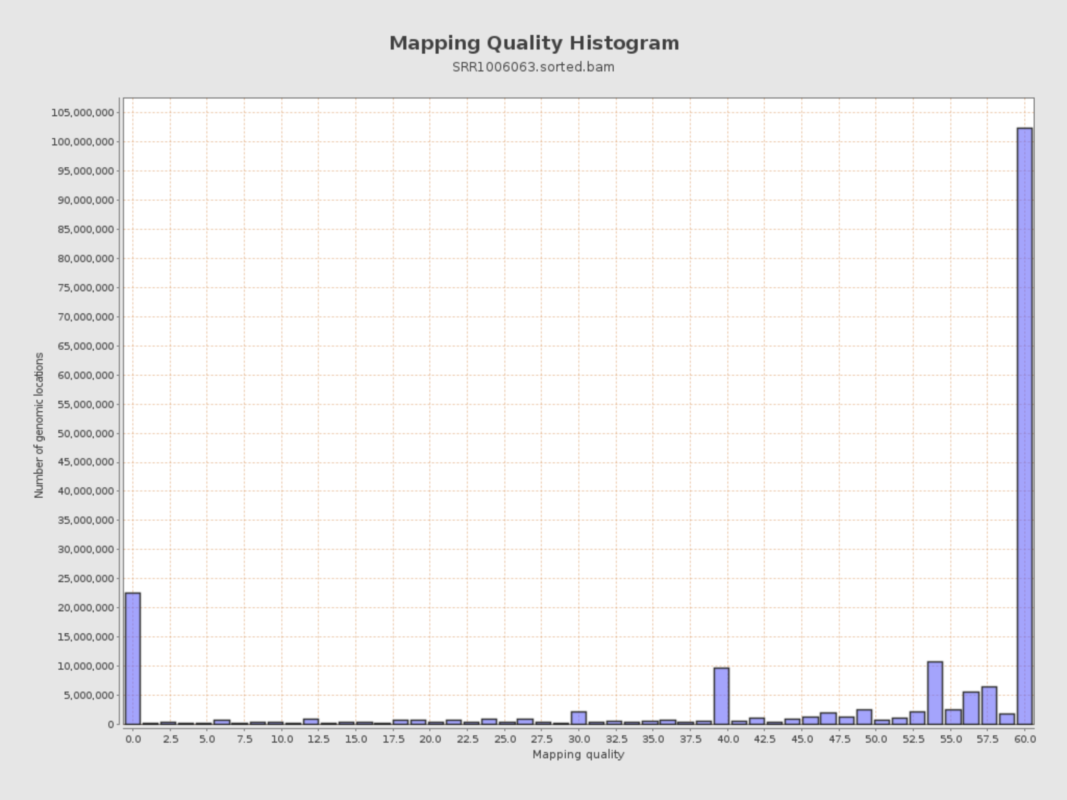
11. Results : Homopolymer Indels



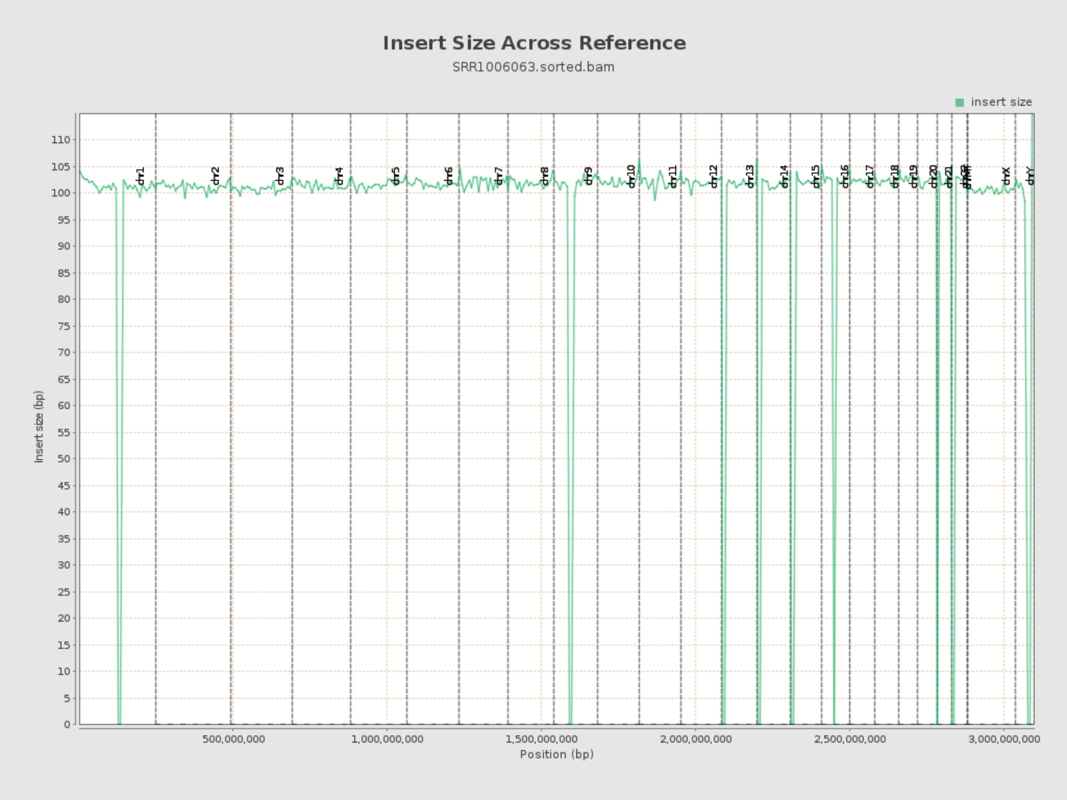
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram