Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/30 17:57:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2046486.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_SRR2046486 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2046486_1.fastq.gz SRR2046486_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Mar 30 17:57:23 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2046486.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	41,899,884
Mapped reads	41,743,436 / 99.63%
Unmapped reads	156,448 / 0.37%
Mapped paired reads	41,743,436 / 99.63%
Mapped reads, first in pair	20,910,330 / 49.91%
Mapped reads, second in pair	20,833,106 / 49.72%
Mapped reads, both in pair	41,632,246 / 99.36%
Mapped reads, singletons	111,190 / 0.27%
Secondary alignments	0
Supplementary alignments	179,518 / 0.43%
Read min/max/mean length	30 / 100 / 100.18
Duplicated reads (estimated)	36,703,513 / 87.6%
Duplication rate	22.18%
Clipped reads	4,338,812 / 10.36%

2.2. ACGT Content

Number/percentage of A's	1,130,608,620 / 27.54%
Number/percentage of C's	920,535,859 / 22.42%
Number/percentage of T's	1,136,417,216 / 27.68%
Number/percentage of G's	917,338,090 / 22.35%
Number/percentage of N's	391,714 / 0.01%

GC Percentage	44.77%

2.3. Coverage

Mean	1.3264
Standard Deviation	219.1273

2.4. Mapping Quality

Mean Mapping Quality	52.43

2.5. Insert size

Mean	15,163
Standard Deviation	1,222,407.53
P25/Median/P75	129 / 164 / 205

2.6. Mismatches and indels

General error rate	0.41%
Mismatches	16,197,173
Insertions	247,649
Mapped reads with at least one insertion	0.58%
Deletions	282,936
Mapped reads with at least one deletion	0.66%
Homopolymer indels	49.65%

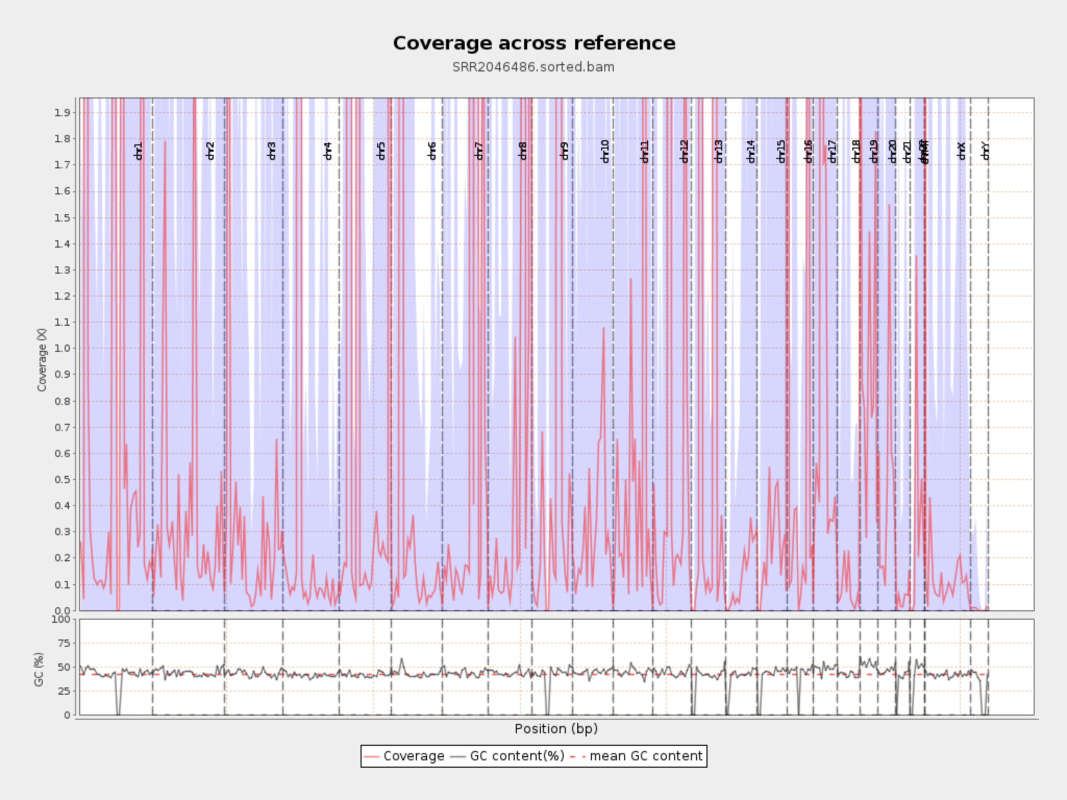
2.7. Chromosome stats

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

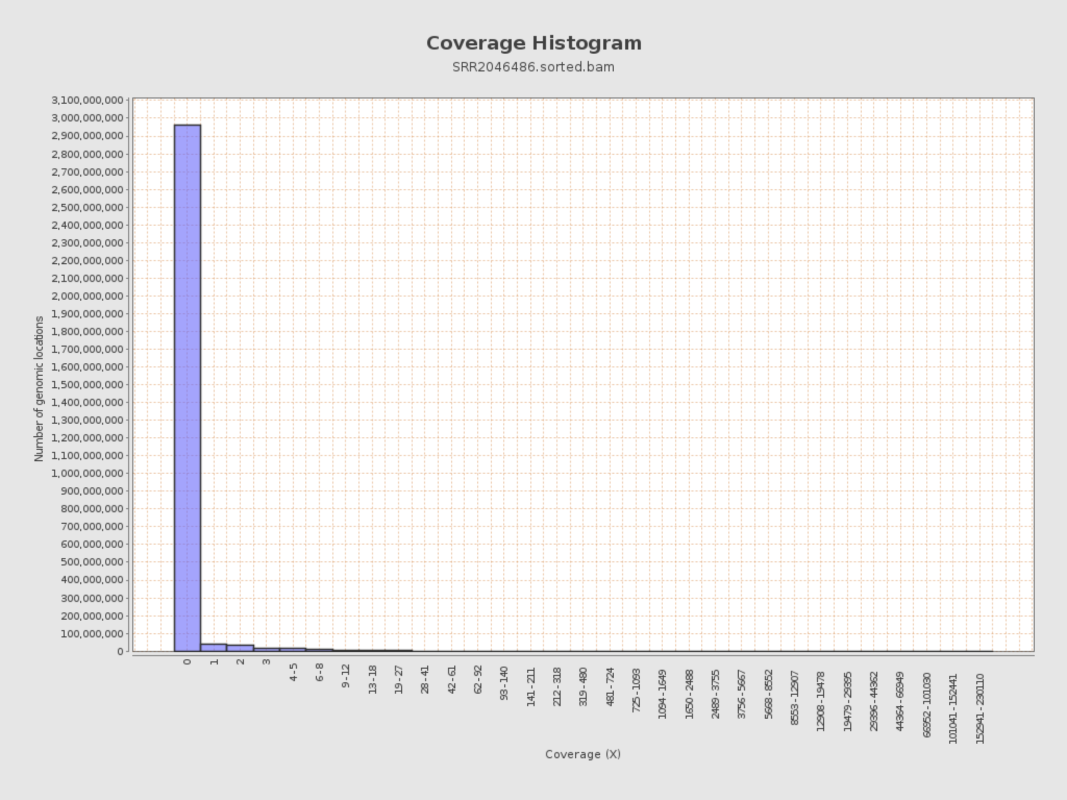
		bases	coverage	deviation
chr1	249250621	750485579	3.011	424.2333
chr2	243199373	94430338	0.3883	39.8827
chr3	198022430	73525844	0.3713	41.9269
chr4	191154276	310734848	1.6256	234.4949
chr5	180915260	618997142	3.4215	422.9599
chr6	171115067	109555847	0.6402	108.9212
chr7	159138663	504631414	3.171	359.3918
chr8	146364022	344430750	2.3532	293.3737
chr9	141213431	243063887	1.7213	231.1597
chr10	135534747	43396650	0.3202	17.6383
chr11	135006516	104089455	0.771	66.0825
chr12	133851895	261376219	1.9527	221.6745
chr13	115169878	228682552	1.9856	241.832
chr14	107349540	14367838	0.1338	3.5219
chr15	102531392	23871867	0.2328	7.0576
chr16	90354753	118932700	1.3163	126.8045
chr17	81195210	122418305	1.5077	145.593
chr18	78077248	6148657	0.0788	1.7561
chr19	59128983	61622883	1.0422	45.8024
chr20	63025520	31955100	0.507	39.2529
chr21	48129895	2381082	0.0495	1.2382
chr22	51304566	18438980	0.3594	40.8544
chrMT	16571	764567	46.1389	15.7395
chrX	155270560	17366233	0.1118	8.7449

chrY	59373566	415490	0.007	0.255

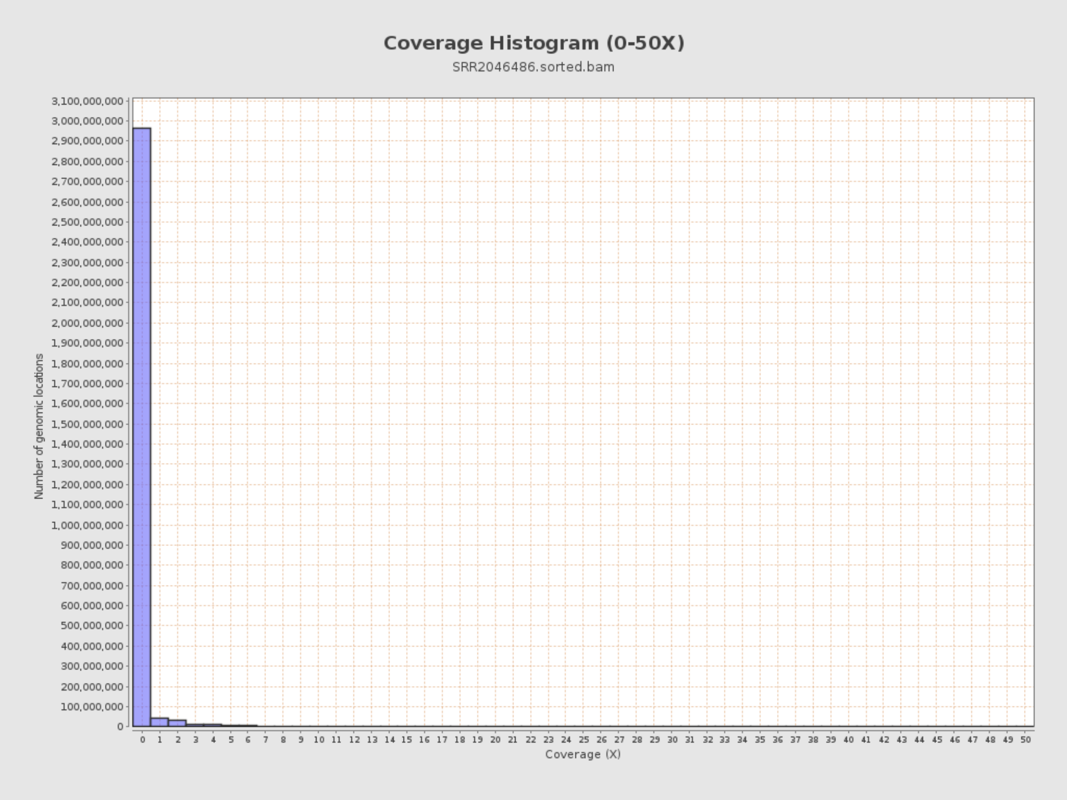
3. Results : Coverage across reference



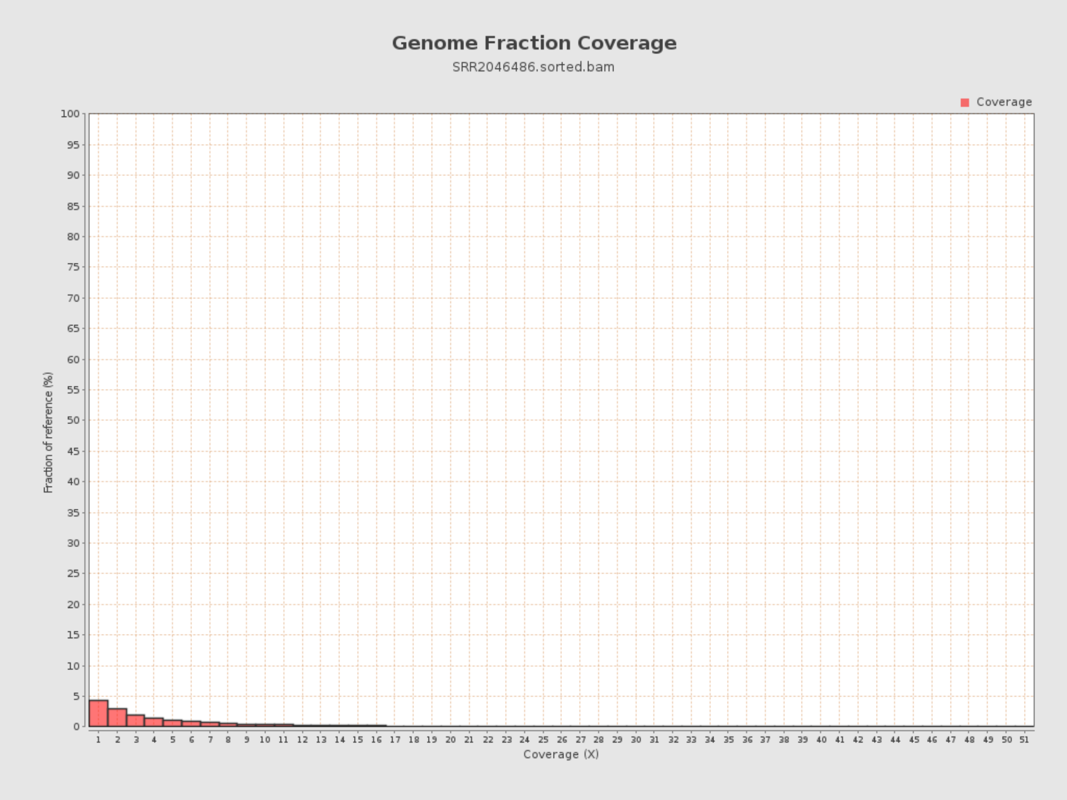
4. Results : Coverage Histogram



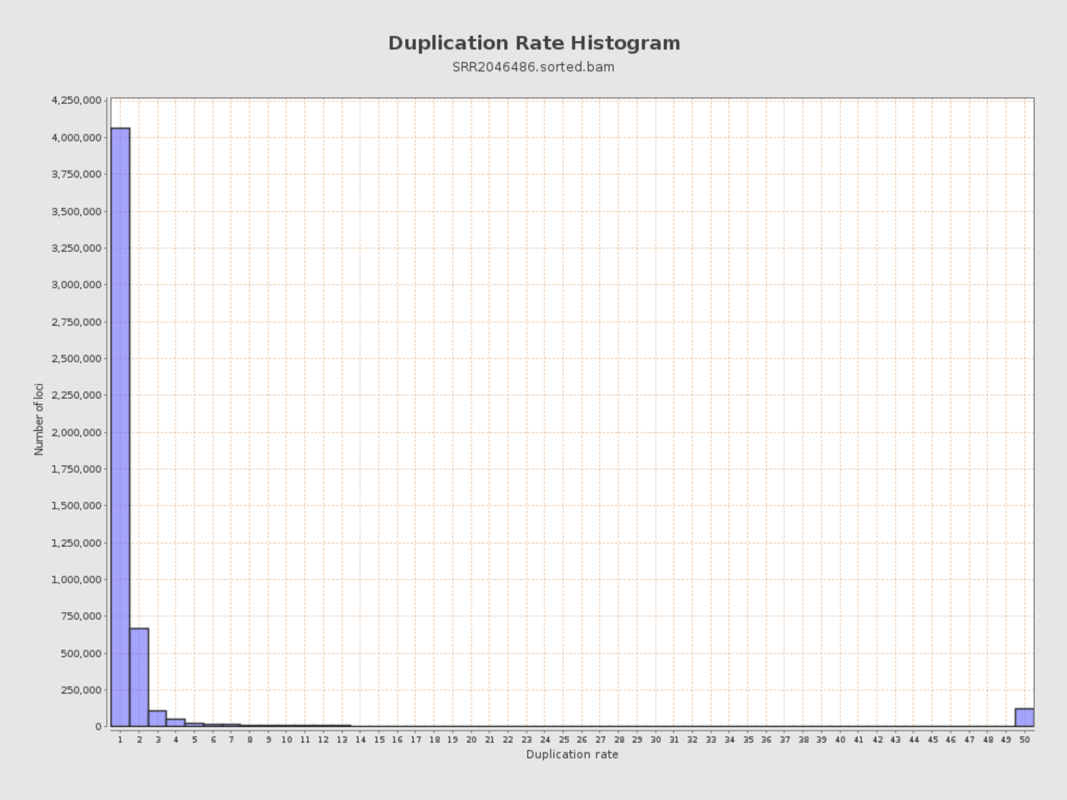
5. Results : Coverage Histogram (0-50X)



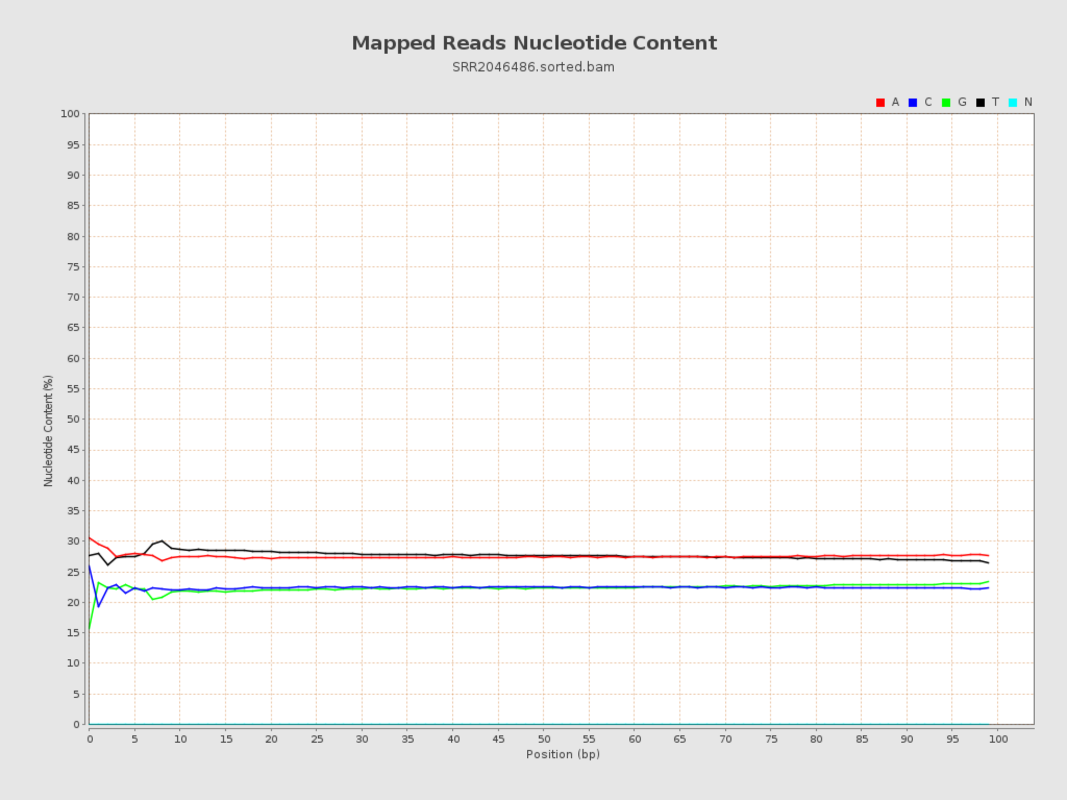
6. Results : Genome Fraction Coverage



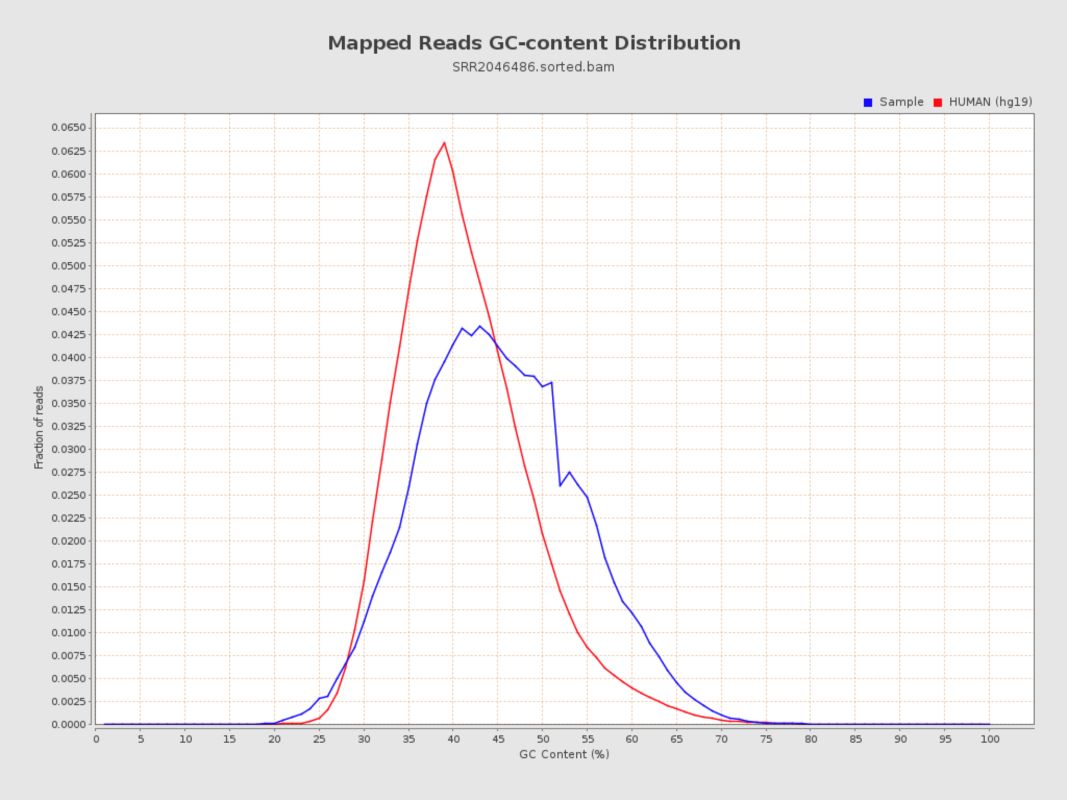
7. Results : Duplication Rate Histogram



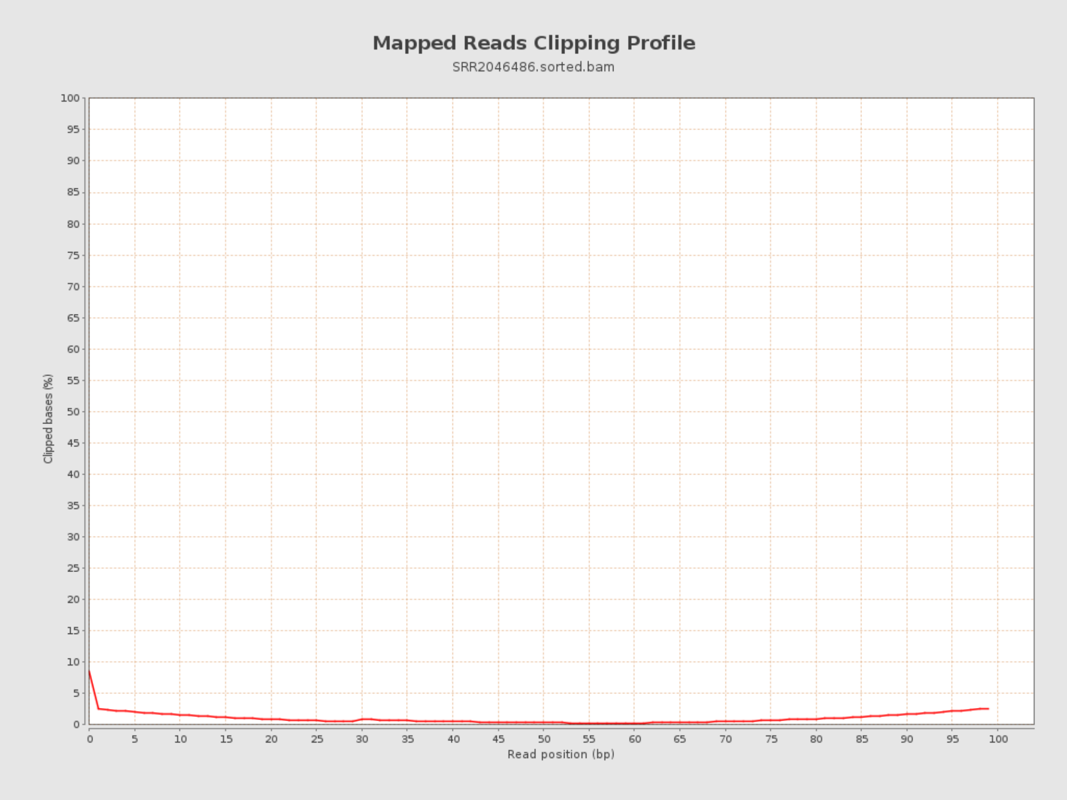
8. Results : Mapped Reads Nucleotide Content



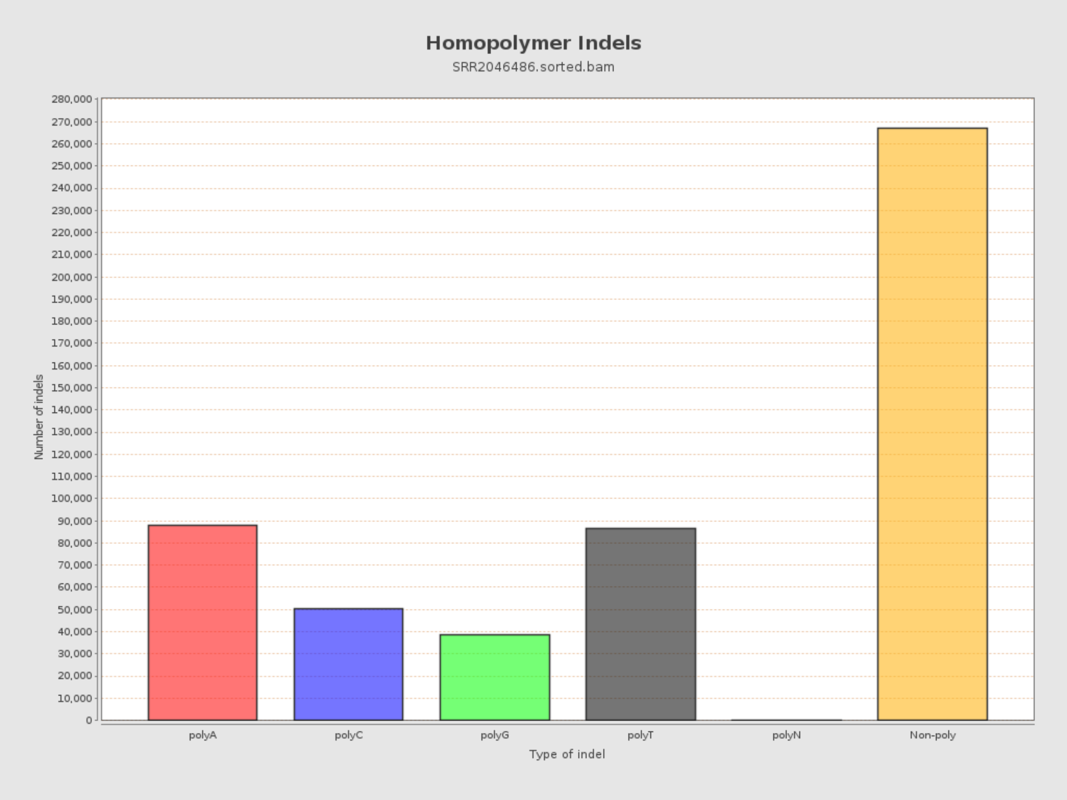
9. Results : Mapped Reads GC-content Distribution



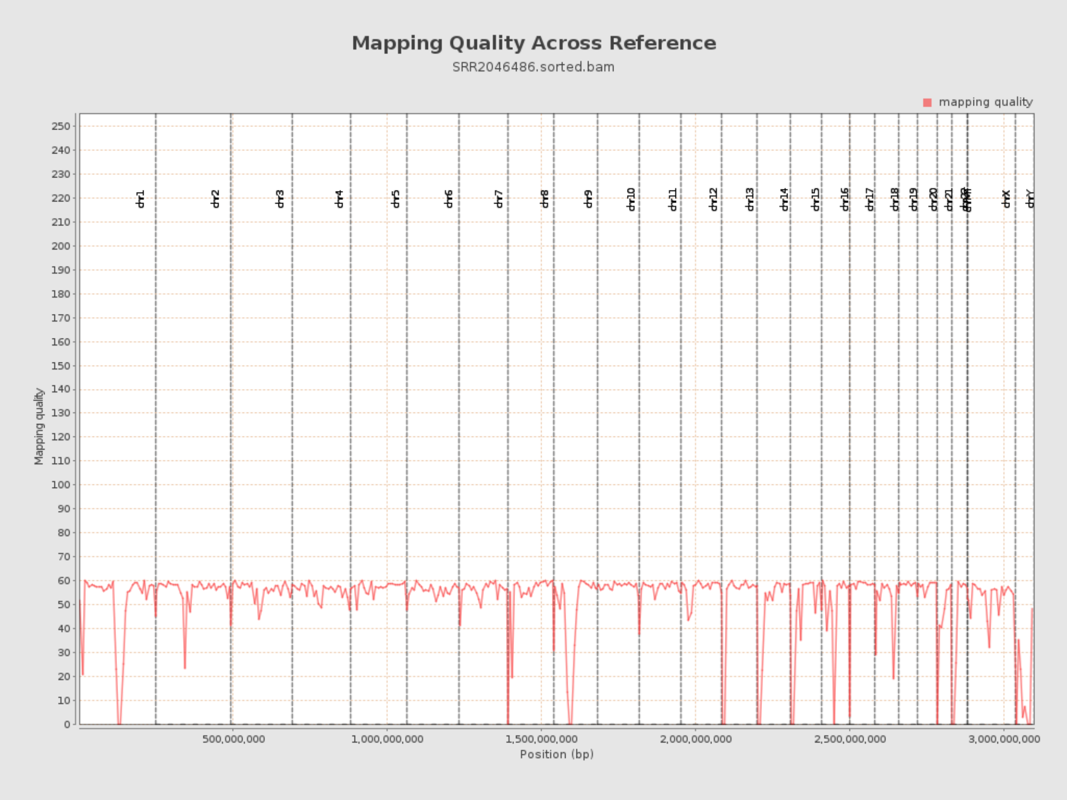
10. Results : Mapped Reads Clipping Profile



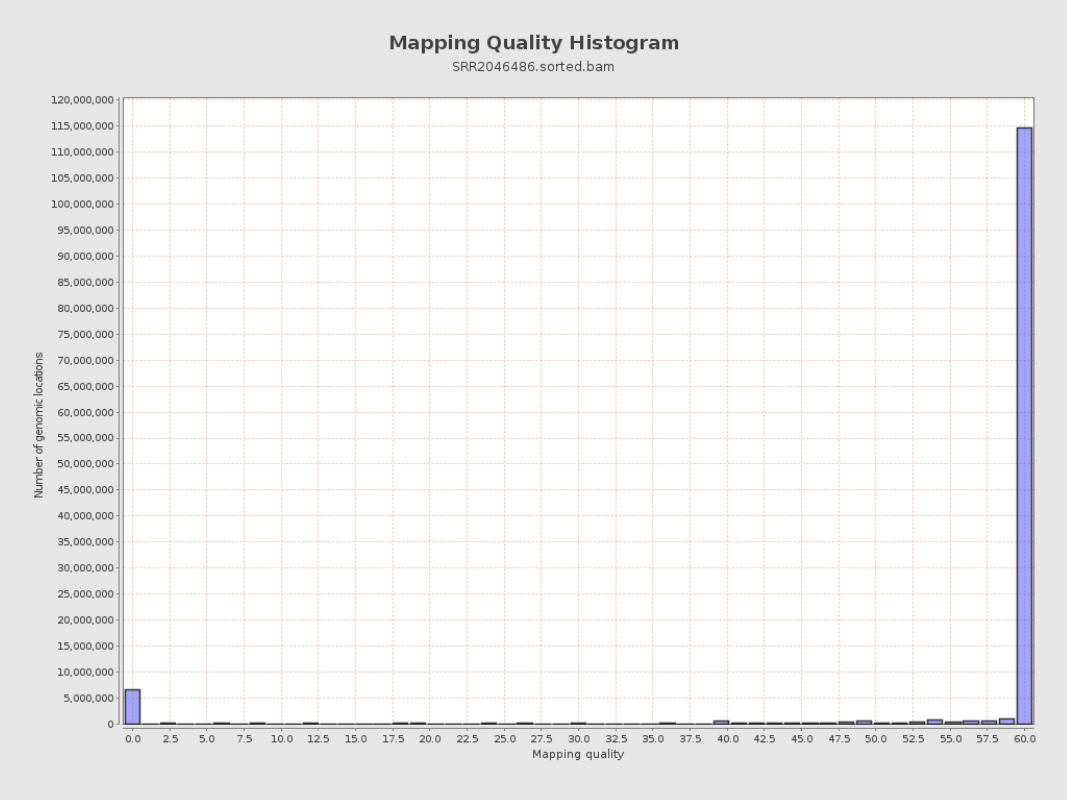
11. Results : Homopolymer Indels



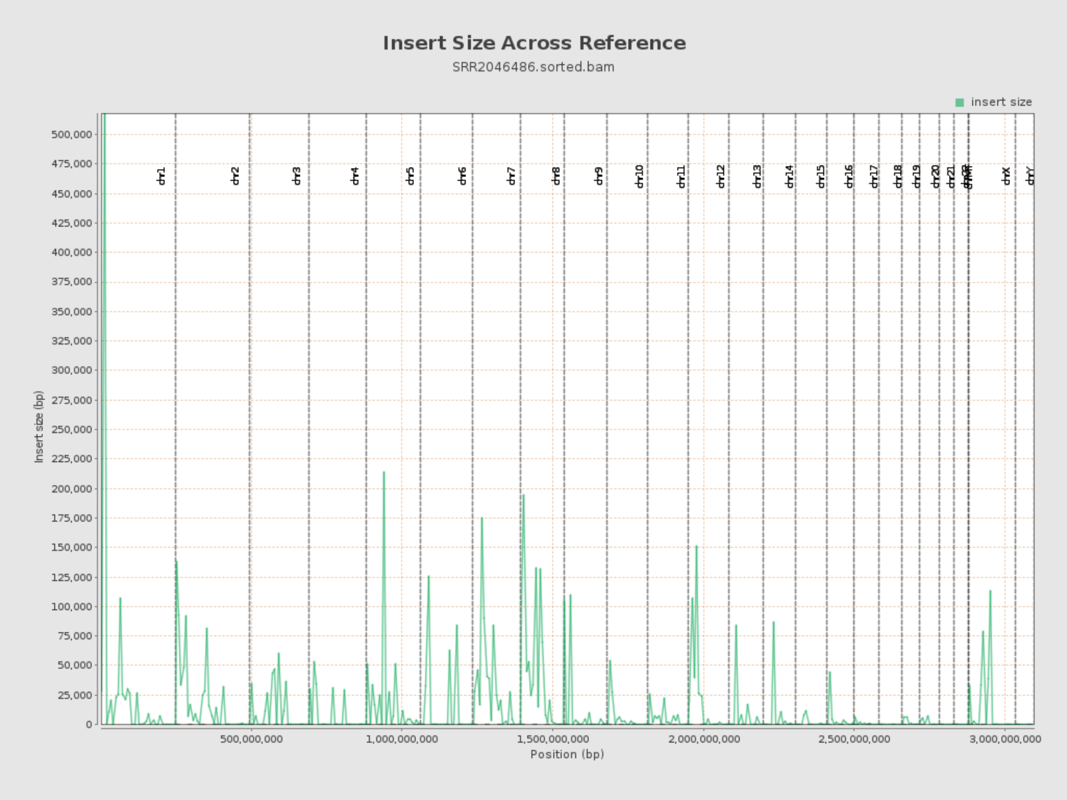
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram