Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/29 02:01:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472665.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_SRR3472665 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472665_1.fastq.gz SRR3472665_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 29 02:01:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472665.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	15,846,230
Mapped reads	15,731,706 / 99.28%
Unmapped reads	114,524 / 0.72%
Mapped paired reads	15,731,706 / 99.28%
Mapped reads, first in pair	7,886,326 / 49.77%
Mapped reads, second in pair	7,845,380 / 49.51%
Mapped reads, both in pair	15,653,224 / 98.78%
Mapped reads, singletons	78,482 / 0.5%
Secondary alignments	0
Supplementary alignments	94,092 / 0.59%
Read min/max/mean length	30 / 101 / 99.76
Duplicated reads (estimated)	10,793,206 / 68.11%
Duplication rate	49.23%
Clipped reads	1,155,518 / 7.29%

2.2. ACGT Content

Number/percentage of A's	419,129,437 / 27.08%
Number/percentage of C's	356,550,057 / 23.04%
Number/percentage of T's	420,652,318 / 27.18%
Number/percentage of G's	350,937,930 / 22.68%
Number/percentage of N's	285,961 / 0.02%

GC Percentage	45.72%

2.3. Coverage

Mean	0.5
Standard Deviation	22.5382

2.4. Mapping Quality

Mean Mapping Quality	54.54

2.5. Insert size

Mean	22,850.56
Standard Deviation	1,512,335.11
P25/Median/P75	152 / 209 / 282

2.6. Mismatches and indels

General error rate	0.61%
Mismatches	9,213,364
Insertions	96,801
Mapped reads with at least one insertion	0.61%
Deletions	78,298
Mapped reads with at least one deletion	0.49%
Homopolymer indels	45.81%

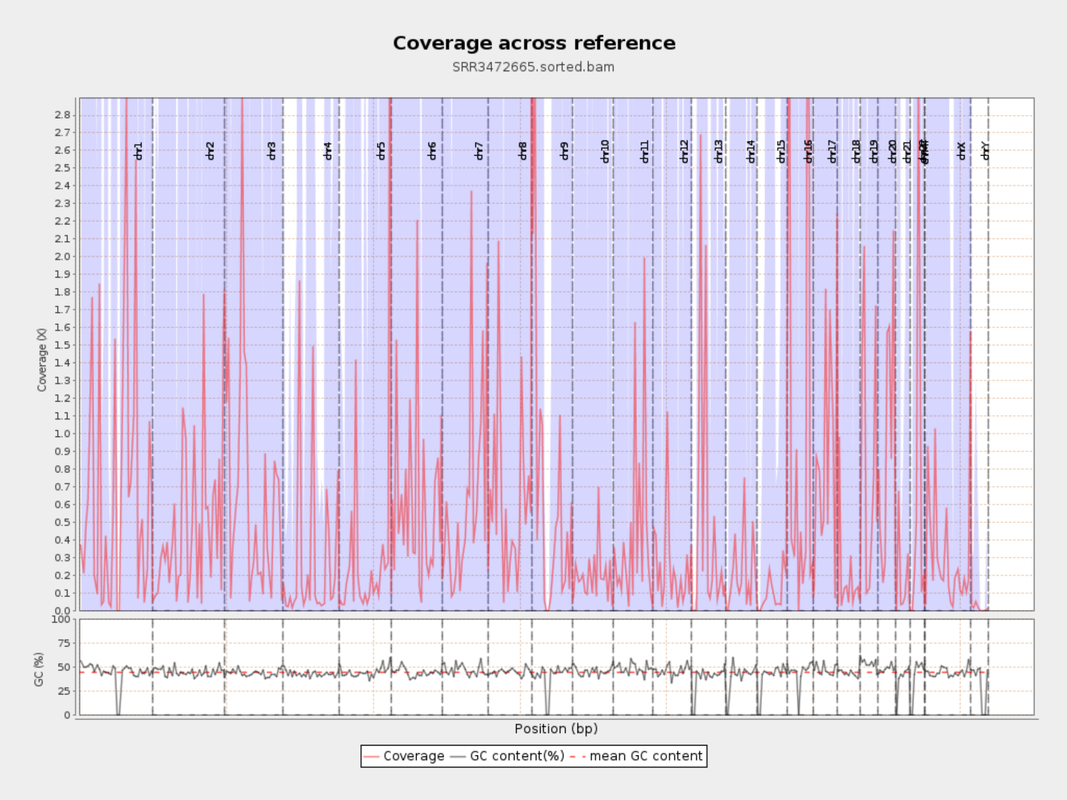
2.7. Chromosome stats

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

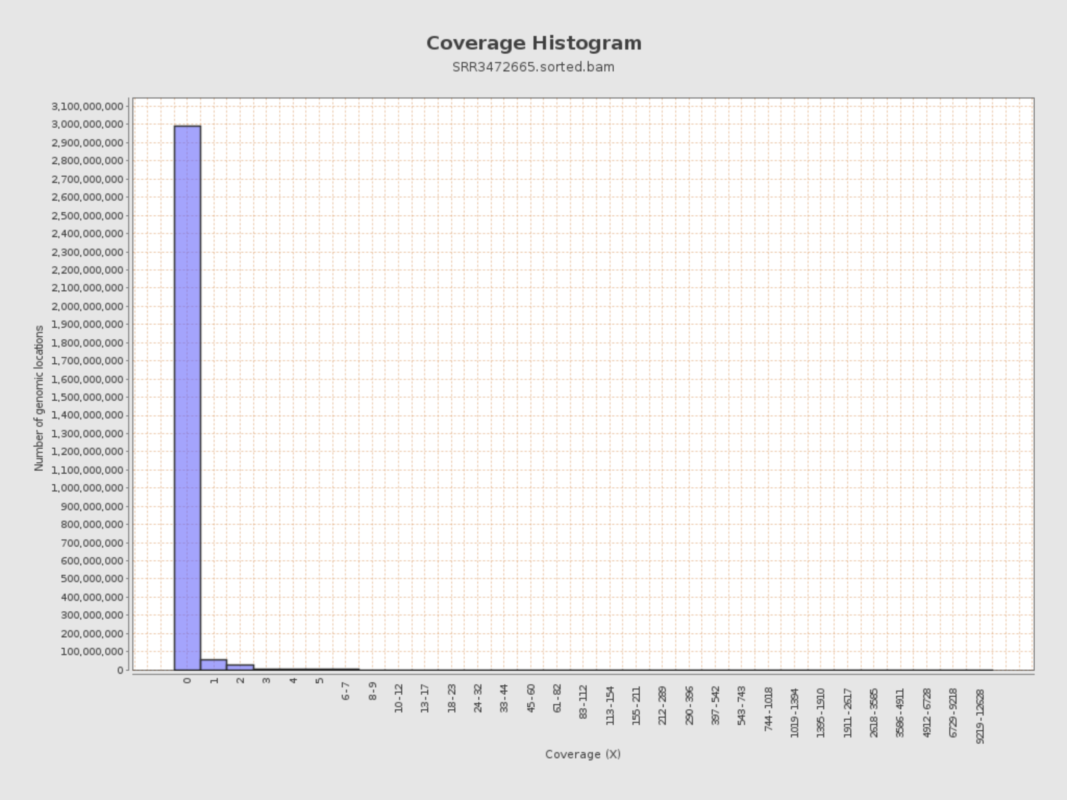
		bases	coverage	deviation
chr1	249250621	182017259	0.7303	28.9468
chr2	243199373	111874711	0.46	23.3744
chr3	198022430	139136933	0.7026	17.2416
chr4	191154276	51703818	0.2705	18.8763
chr5	180915260	72365525	0.4	32.5217
chr6	171115067	103880620	0.6071	19.5848
chr7	159138663	105198123	0.661	25.171
chr8	146364022	89735189	0.6131	24.881
chr9	141213431	96835597	0.6857	19.7952
chr10	135534747	27226867	0.2009	12.5924
chr11	135006516	59946113	0.444	23.7544
chr12	133851895	32627017	0.2438	11.9462
chr13	115169878	55910231	0.4855	22.088
chr14	107349540	21914050	0.2041	10.3294
chr15	102531392	10872107	0.106	4.341
chr16	90354753	100267191	1.1097	44.6938
chr17	81195210	70408760	0.8672	25.4873
chr18	78077248	15309506	0.1961	12.5345
chr19	59128983	52677025	0.8909	26.496
chr20	63025520	59758569	0.9482	26.9487
chr21	48129895	9239050	0.192	10.9545
chr22	51304566	31922344	0.6222	33.2533
chrMT	16571	3698	0.2232	0.6369
chrX	155270560	46017796	0.2964	10.8309

chrY	59373566	925232	0.0156	0.5521

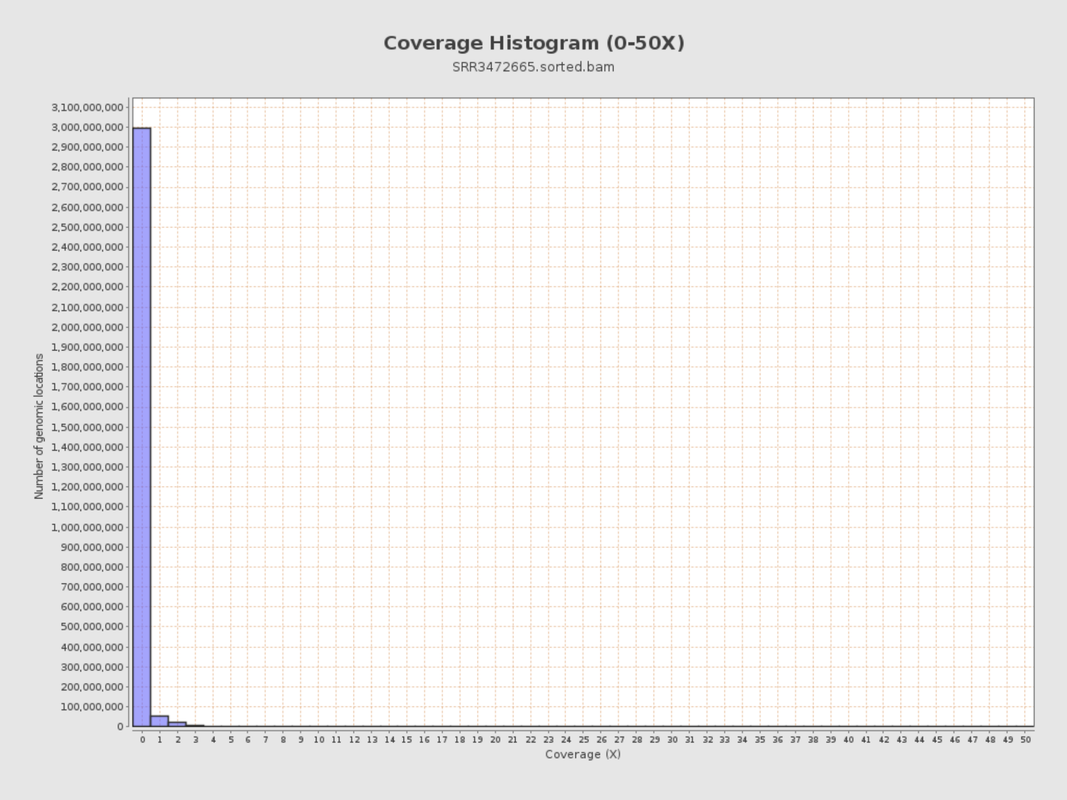
3. Results : Coverage across reference



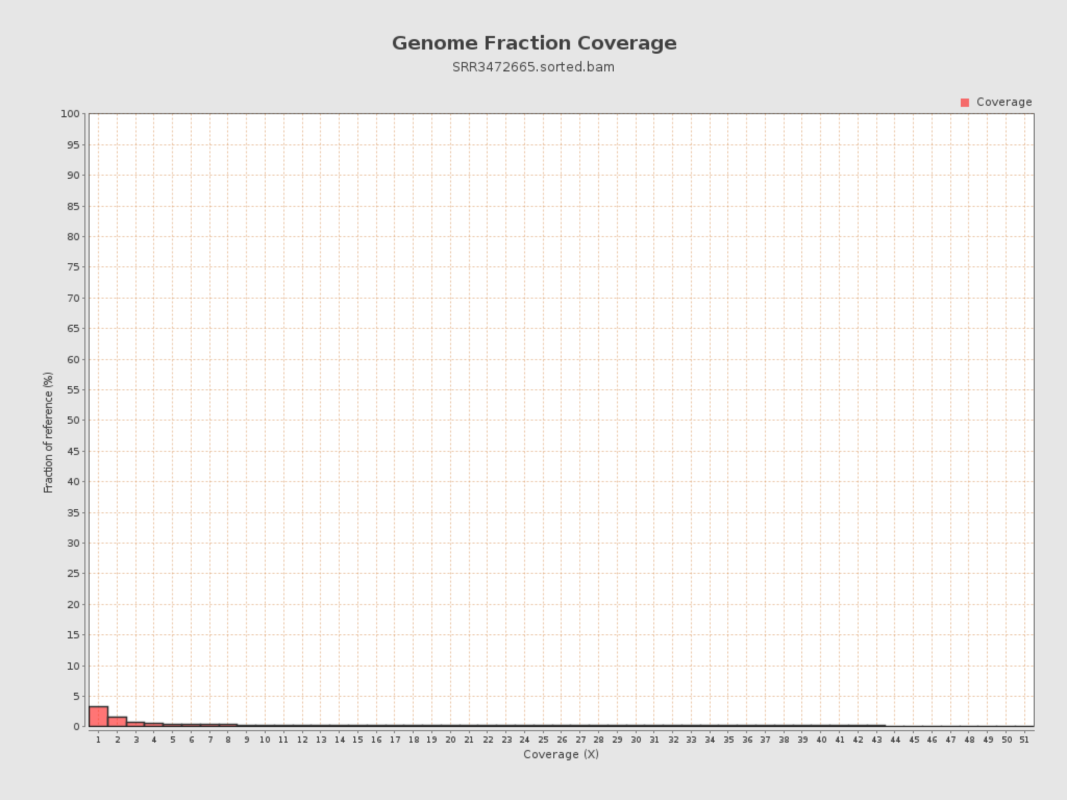
4. Results : Coverage Histogram



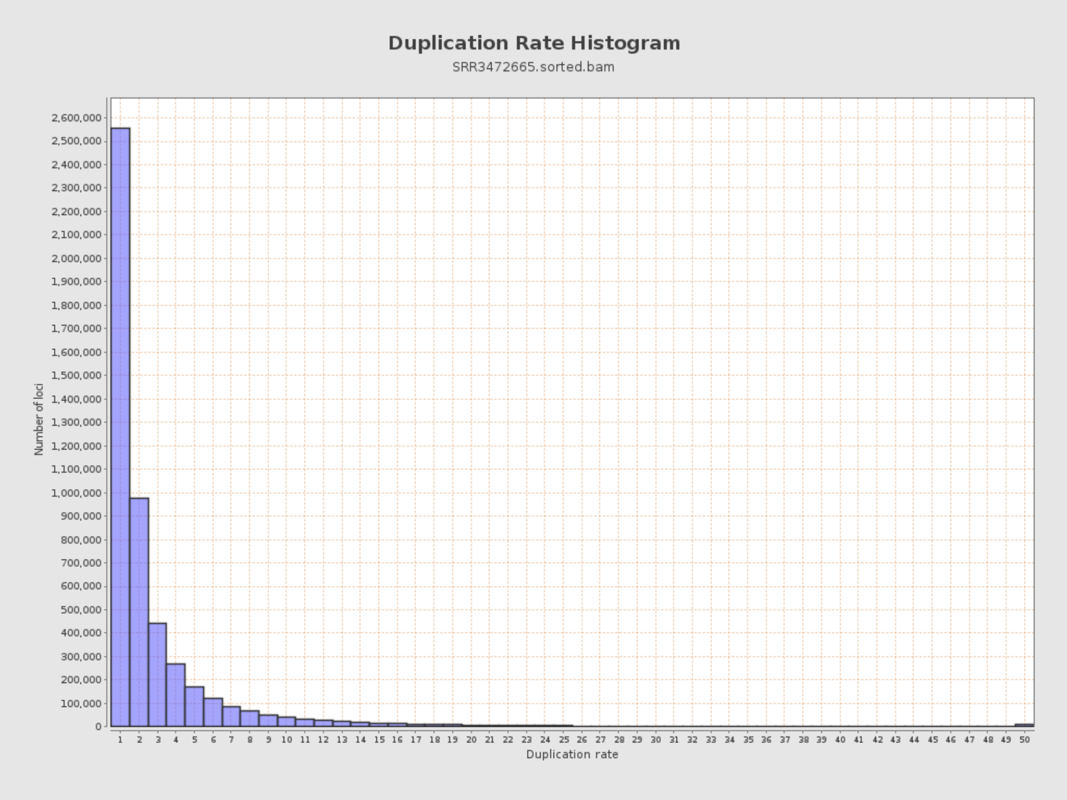
5. Results : Coverage Histogram (0-50X)



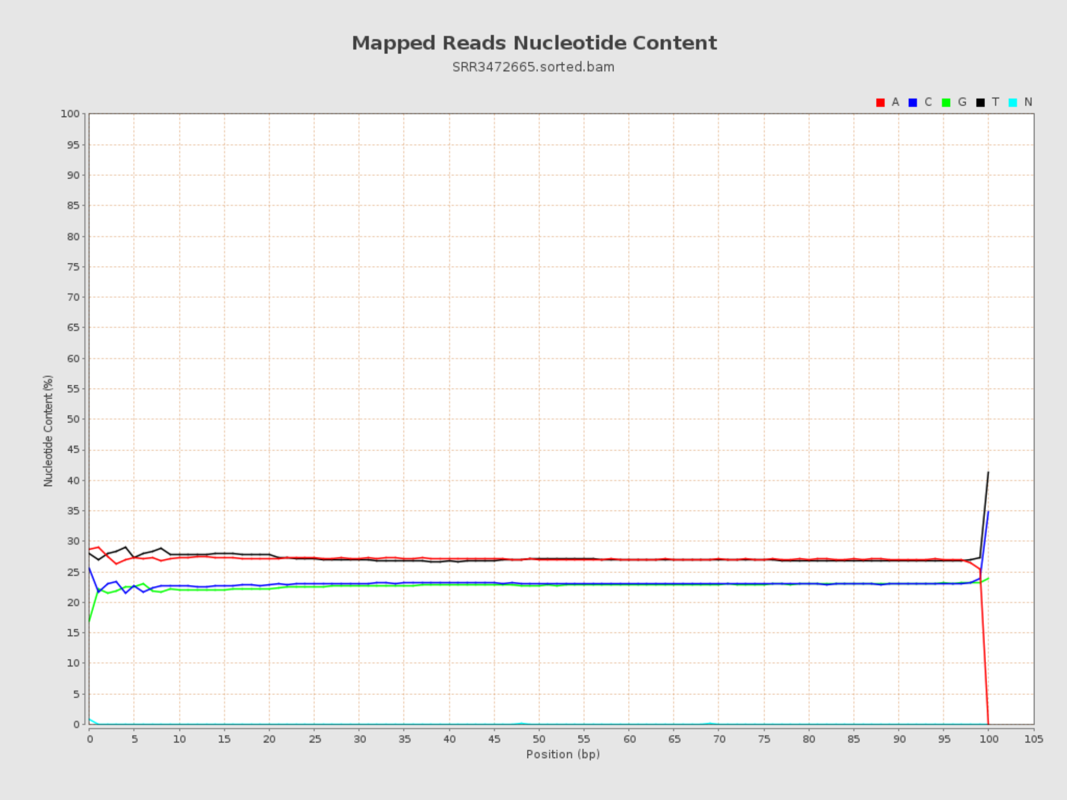
6. Results : Genome Fraction Coverage



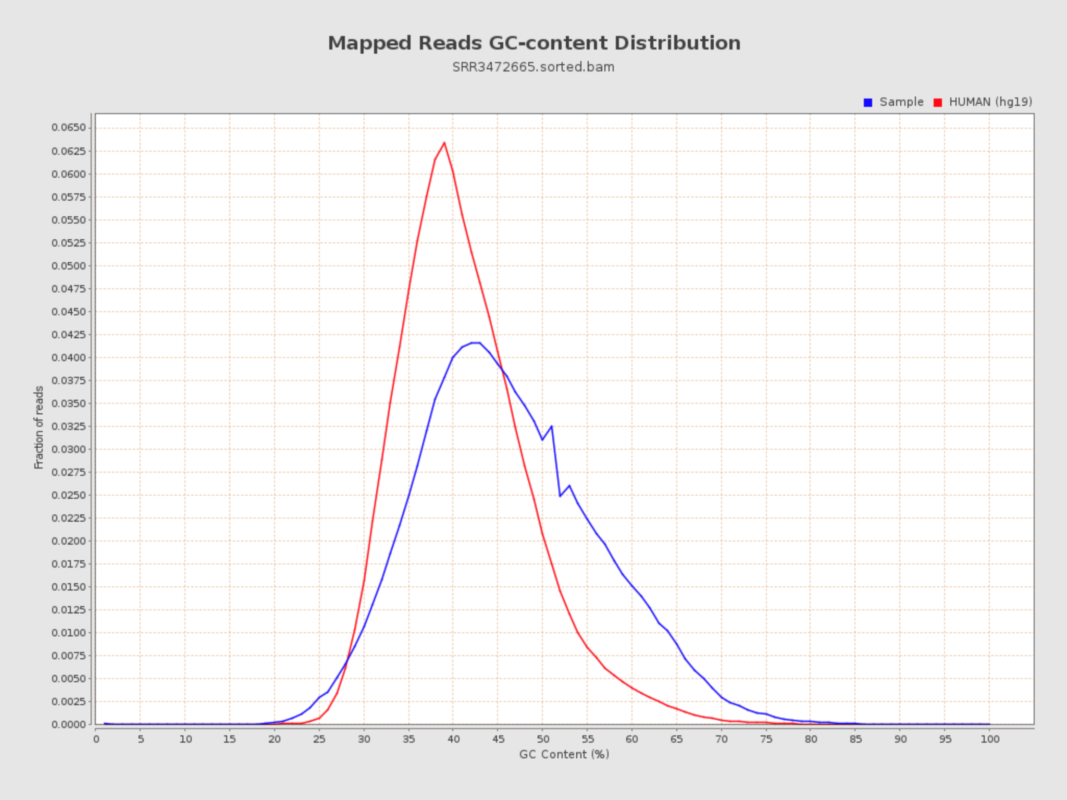
7. Results : Duplication Rate Histogram



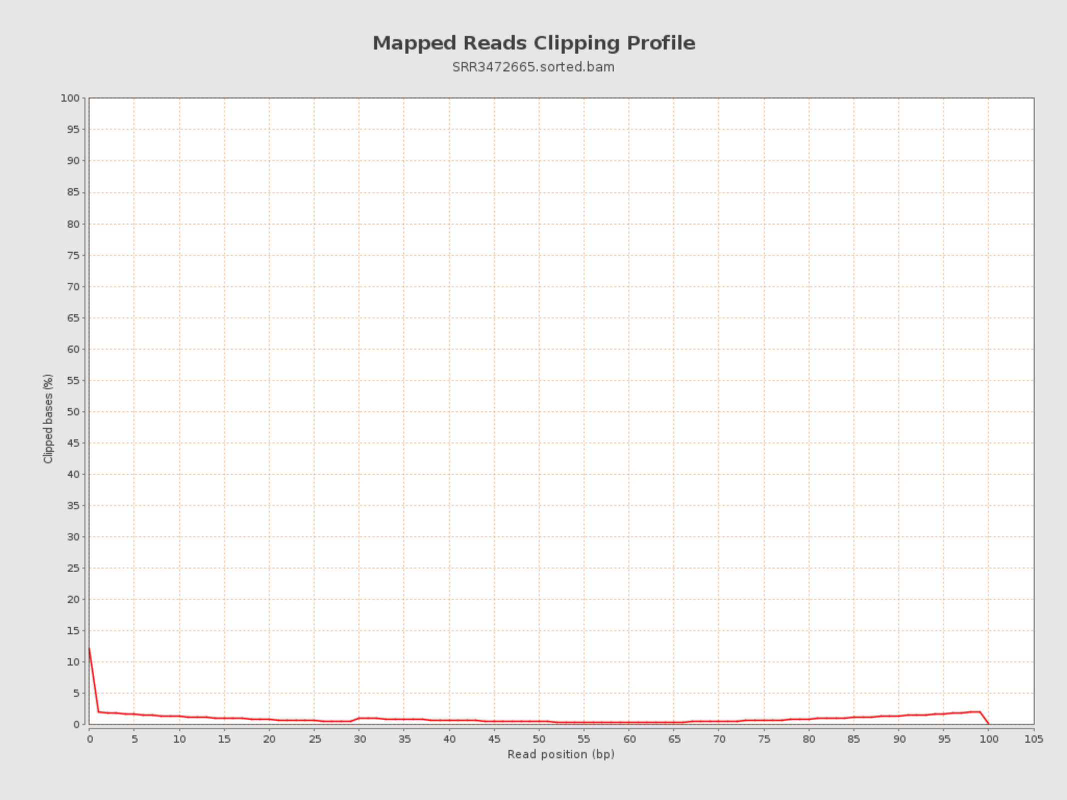
8. Results : Mapped Reads Nucleotide Content



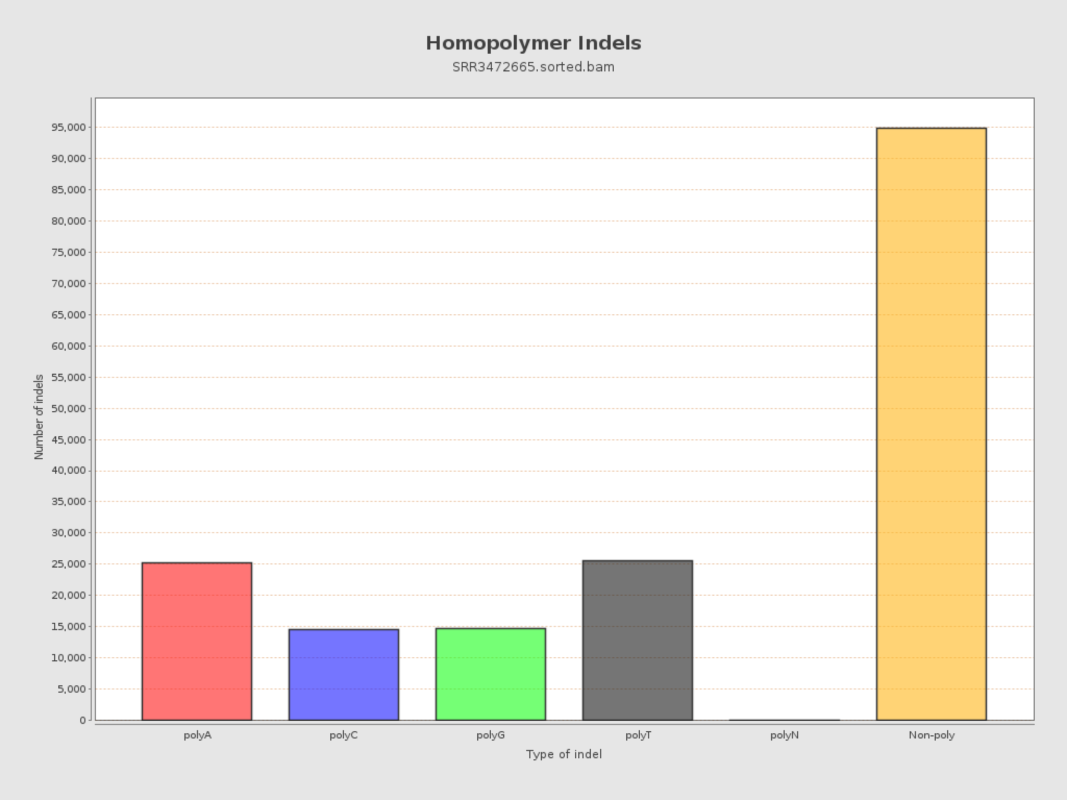
9. Results : Mapped Reads GC-content Distribution



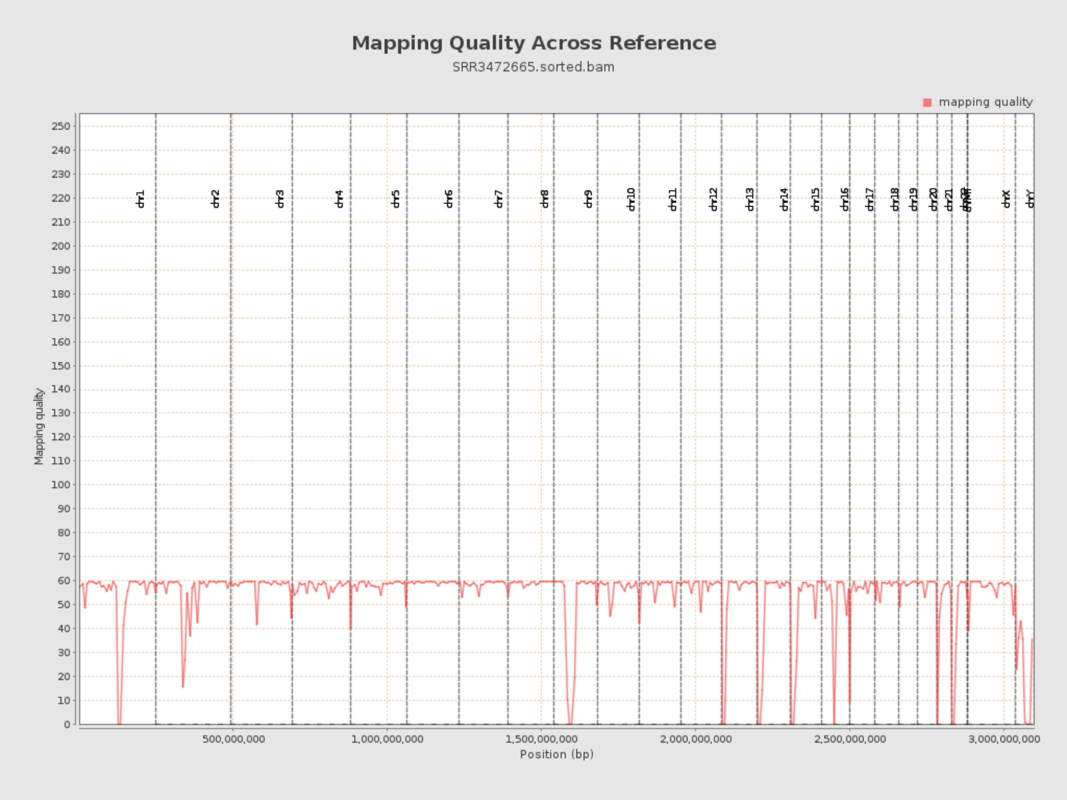
10. Results : Mapped Reads Clipping Profile



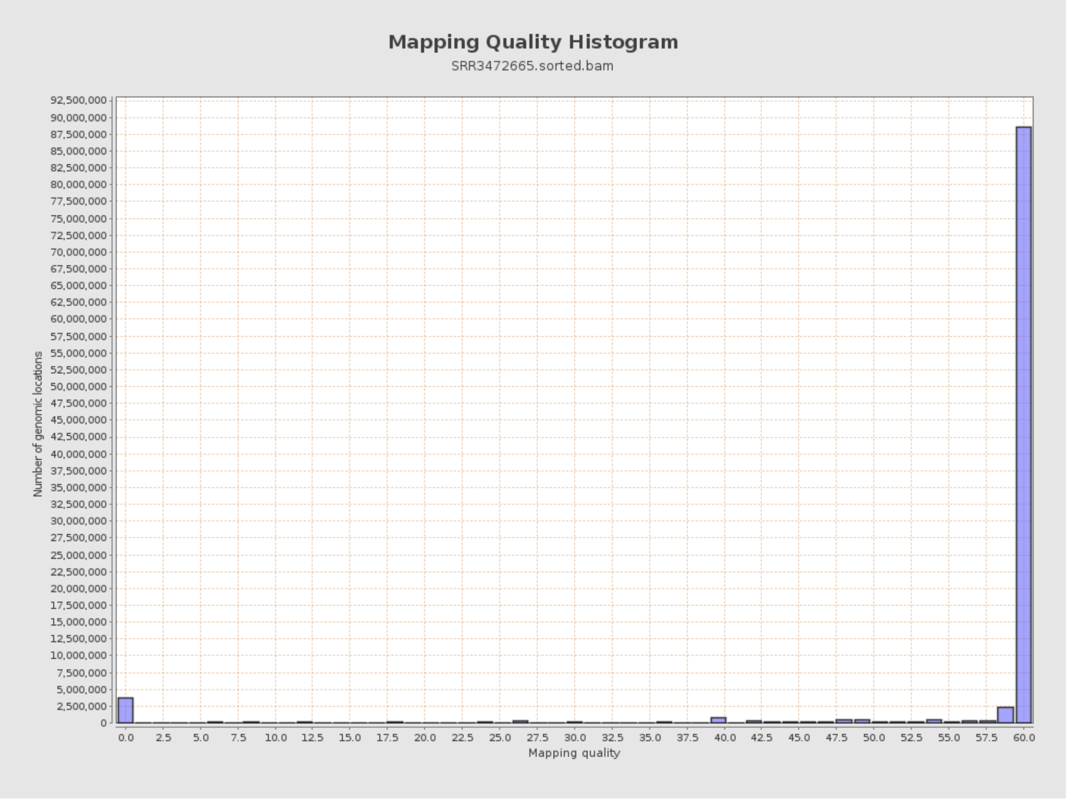
11. Results : Homopolymer Indels



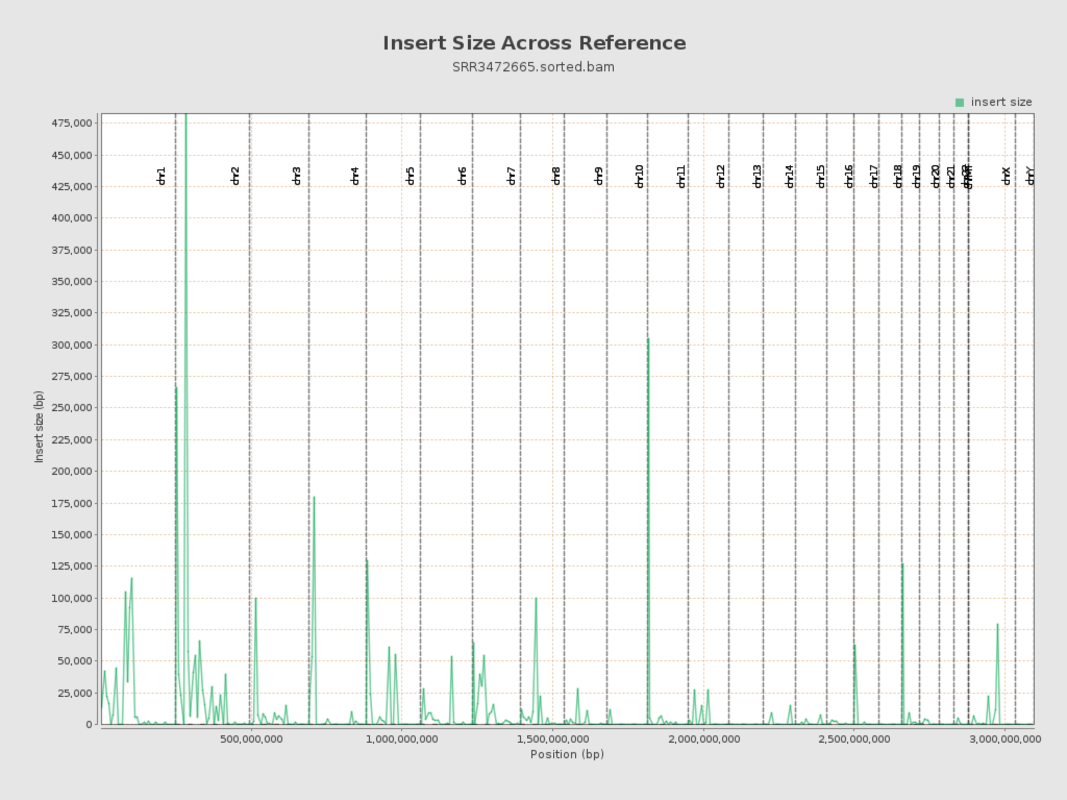
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram