Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/30 22:09:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2046545.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_SRR2046545 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2046545_1.fastq.gz SRR2046545_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Mar 30 22:09:13 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2046545.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,690,830
Mapped reads	7,546,991 / 98.13%
Unmapped reads	143,839 / 1.87%
Mapped paired reads	7,546,991 / 98.13%
Mapped reads, first in pair	3,831,558 / 49.82%
Mapped reads, second in pair	3,715,433 / 48.31%
Mapped reads, both in pair	7,419,162 / 96.47%
Mapped reads, singletons	127,829 / 1.66%
Secondary alignments	0
Supplementary alignments	33,184 / 0.43%
Read min/max/mean length	30 / 100 / 100.17
Duplicated reads (estimated)	5,063,375 / 65.84%
Duplication rate	42.56%
Clipped reads	2,402,312 / 31.24%

2.2. ACGT Content

Number/percentage of A's	206,826,484 / 29.38%
Number/percentage of C's	145,274,751 / 20.64%
Number/percentage of T's	204,504,744 / 29.05%
Number/percentage of G's	147,222,907 / 20.92%
Number/percentage of N's	63,479 / 0.01%

GC Percentage	41.55%

2.3. Coverage

Mean	0.2274
Standard Deviation	14.1067

2.4. Mapping Quality

Mean Mapping Quality	53.15

2.5. Insert size

Mean	27,017.88
Standard Deviation	1,667,916.12
P25/Median/P75	93 / 127 / 178

2.6. Mismatches and indels

General error rate	0.37%
Mismatches	2,486,690
Insertions	54,874
Mapped reads with at least one insertion	0.71%
Deletions	65,815
Mapped reads with at least one deletion	0.85%
Homopolymer indels	48.21%

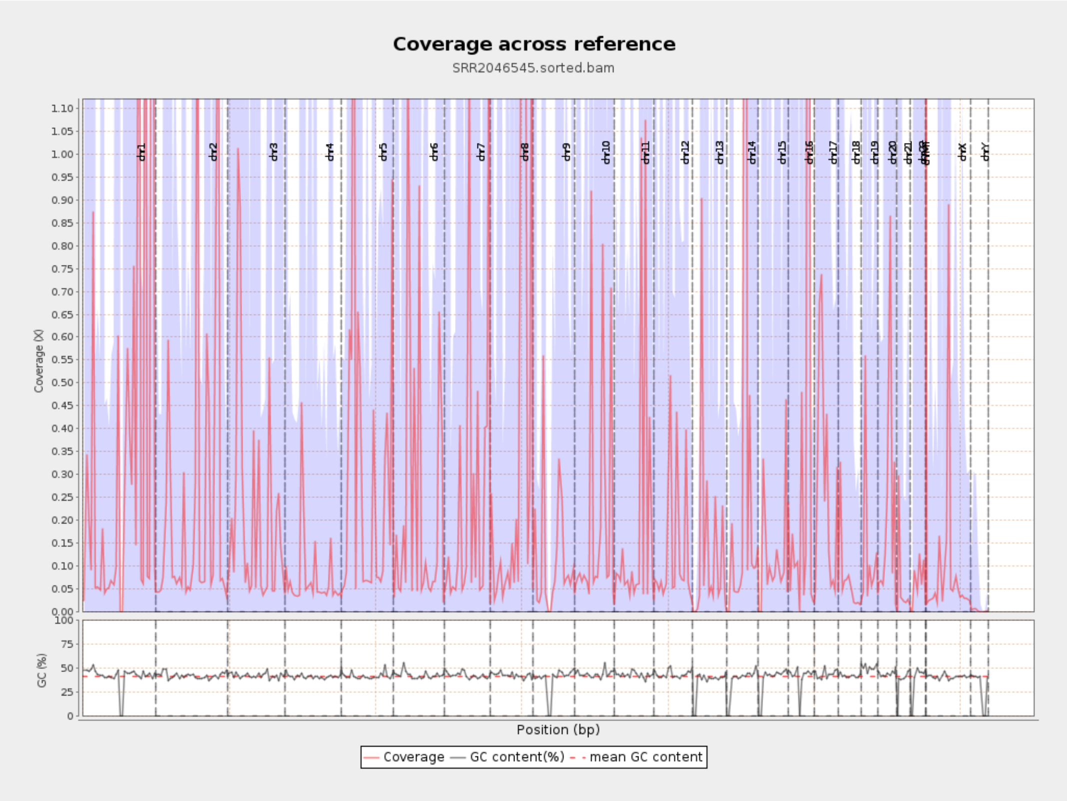
2.7. Chromosome stats

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

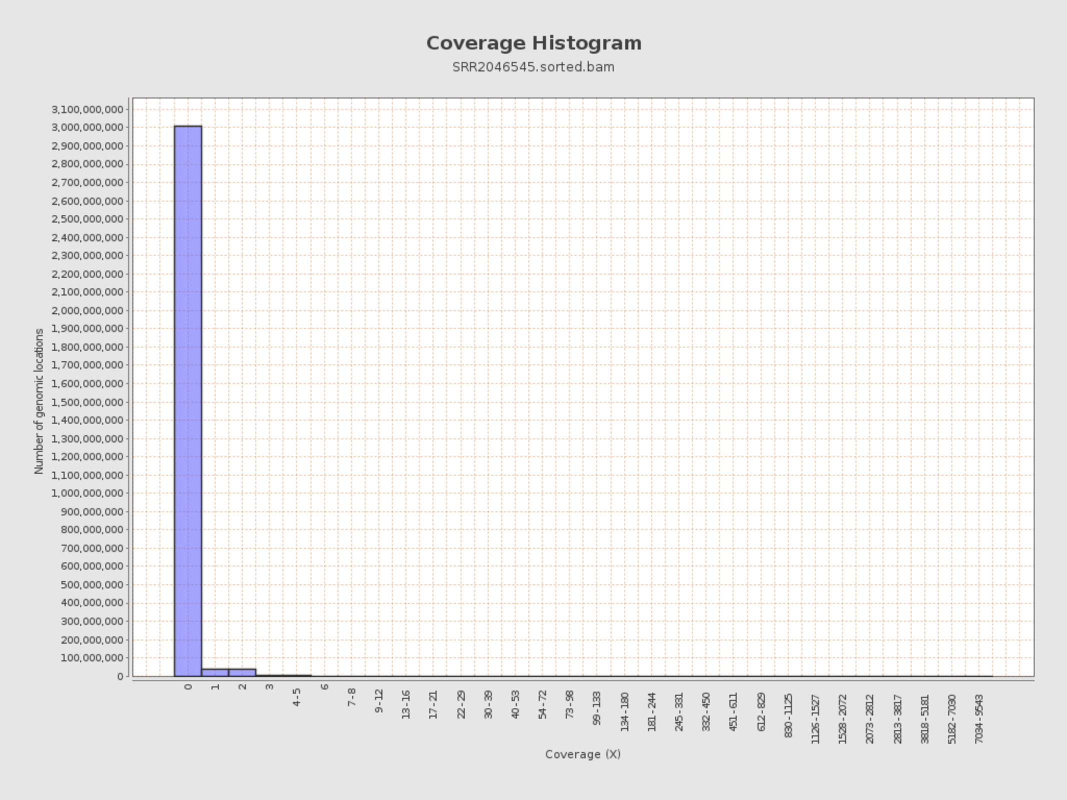
		bases	coverage	deviation
chr1	249250621	97844718	0.3926	18.5404
chr2	243199373	61570940	0.2532	12.8132
chr3	198022430	42653085	0.2154	11.9255
chr4	191154276	15085940	0.0789	3.8329
chr5	180915260	58734570	0.3247	20.7276
chr6	171115067	43433666	0.2538	11.3061
chr7	159138663	43144770	0.2711	14.6325
chr8	146364022	86160266	0.5887	31.601
chr9	141213431	16307765	0.1155	9.6944
chr10	135534747	29299720	0.2162	13.8095
chr11	135006516	26754657	0.1982	10.4476
chr12	133851895	18759964	0.1402	7.0542
chr13	115169878	15726335	0.1365	6.6413
chr14	107349540	33885517	0.3157	18.7939
chr15	102531392	13114389	0.1279	6.1267
chr16	90354753	30362087	0.336	21.1372
chr17	81195210	22465542	0.2767	11.0198
chr18	78077248	5619861	0.072	3.1693
chr19	59128983	7848493	0.1327	6.2682
chr20	63025520	14208775	0.2254	12.388
chr21	48129895	3137856	0.0652	5.4936
chr22	51304566	3389552	0.0661	2.4939
chrMT	16571	46193	2.7876	2.4293
chrX	155270560	14356600	0.0925	6.9189

chrY	59373566	157365	0.0027	0.1613

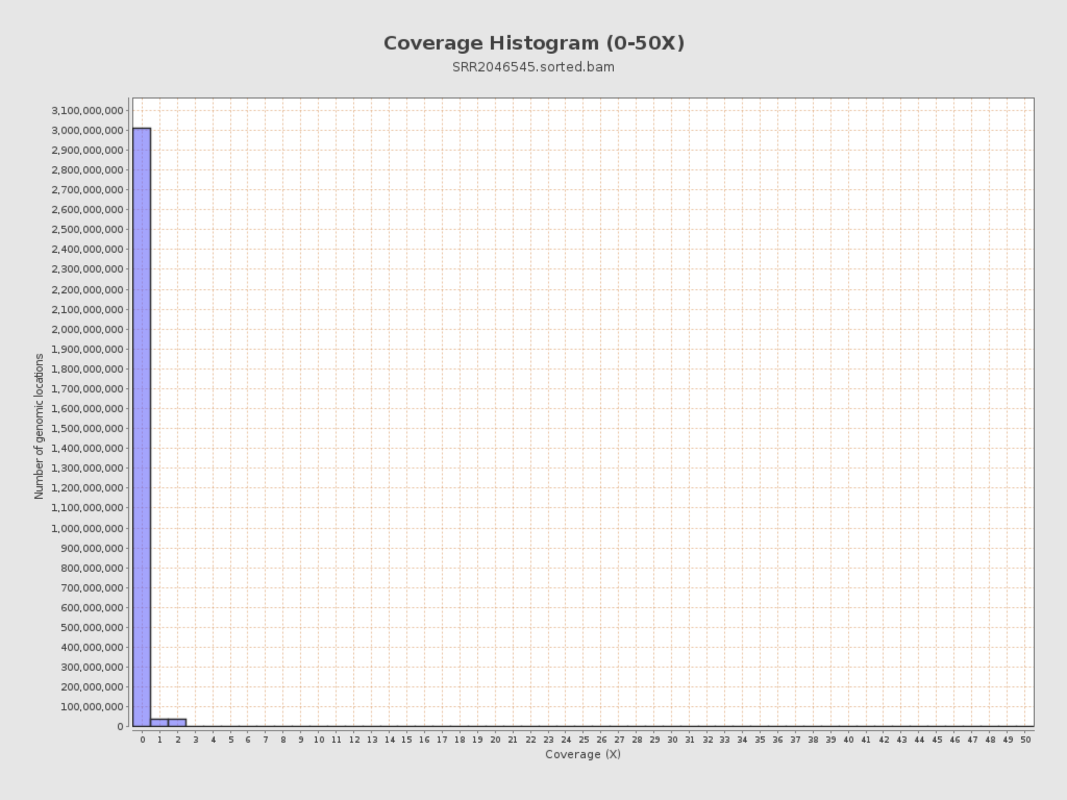
3. Results : Coverage across reference



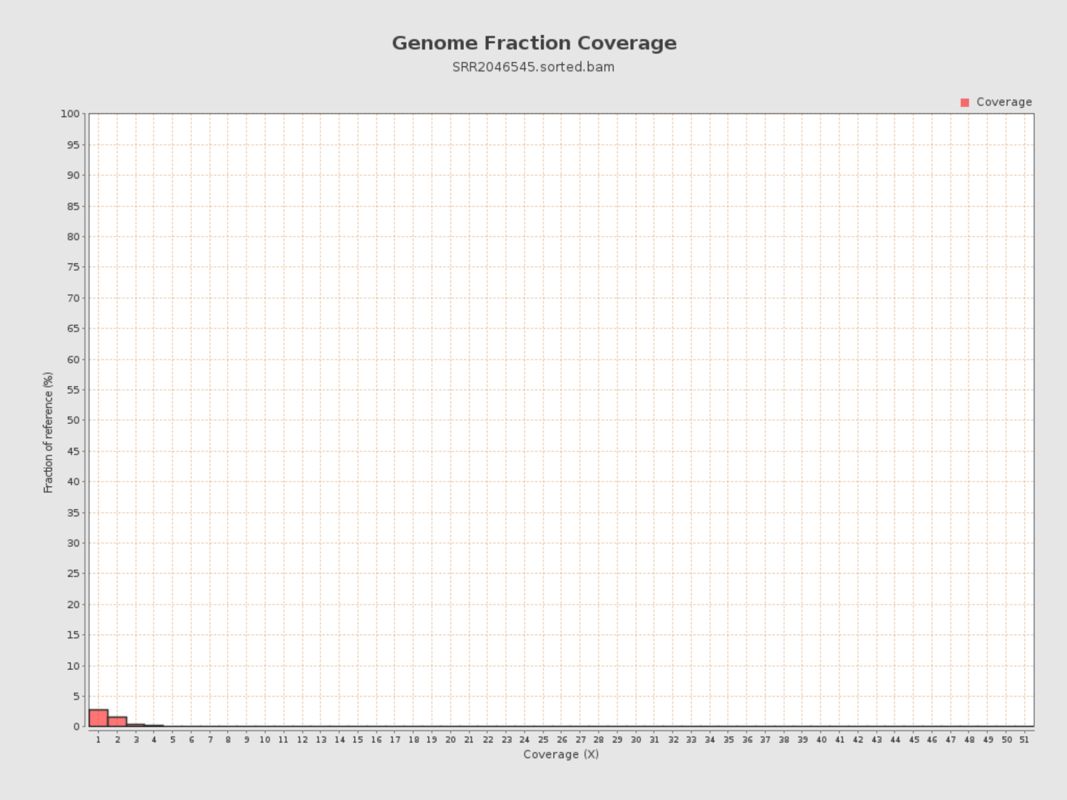
4. Results : Coverage Histogram



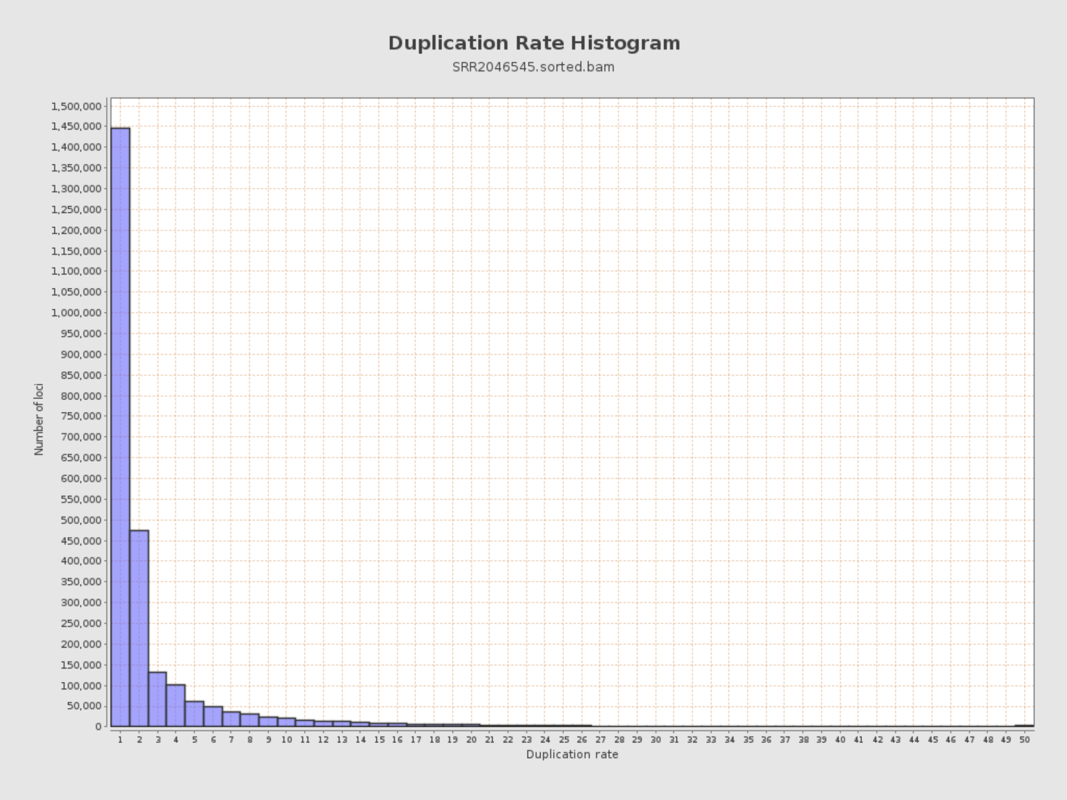
5. Results : Coverage Histogram (0-50X)



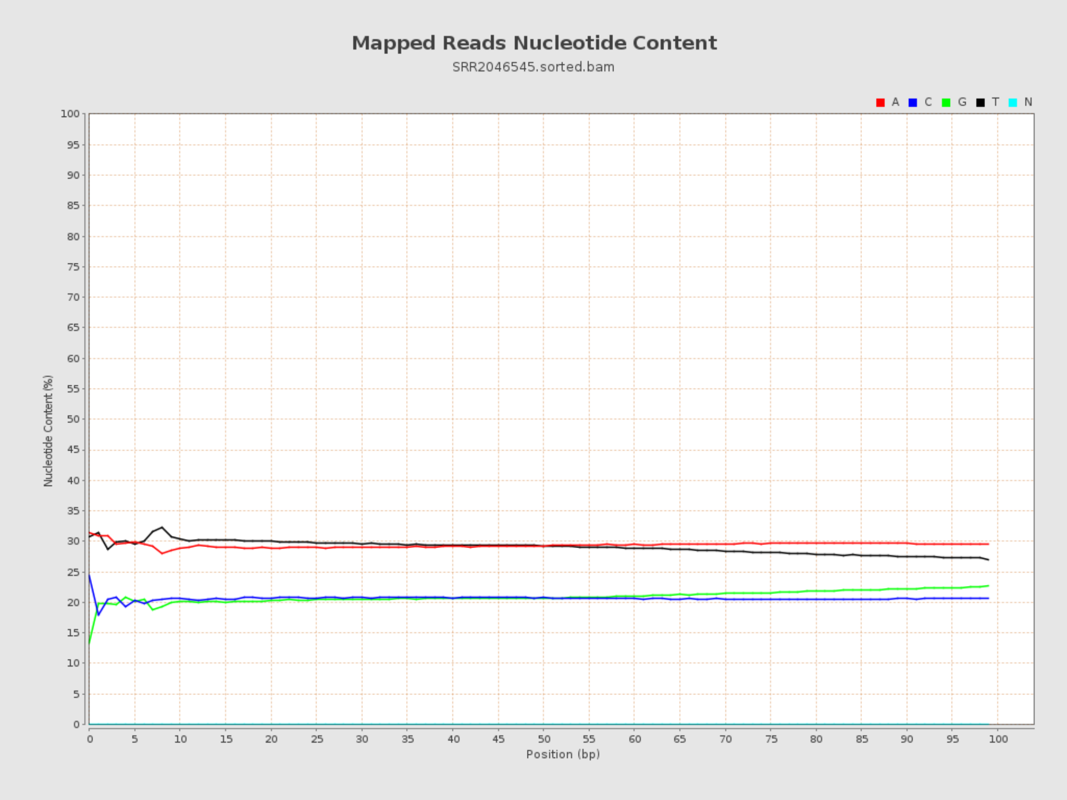
6. Results : Genome Fraction Coverage



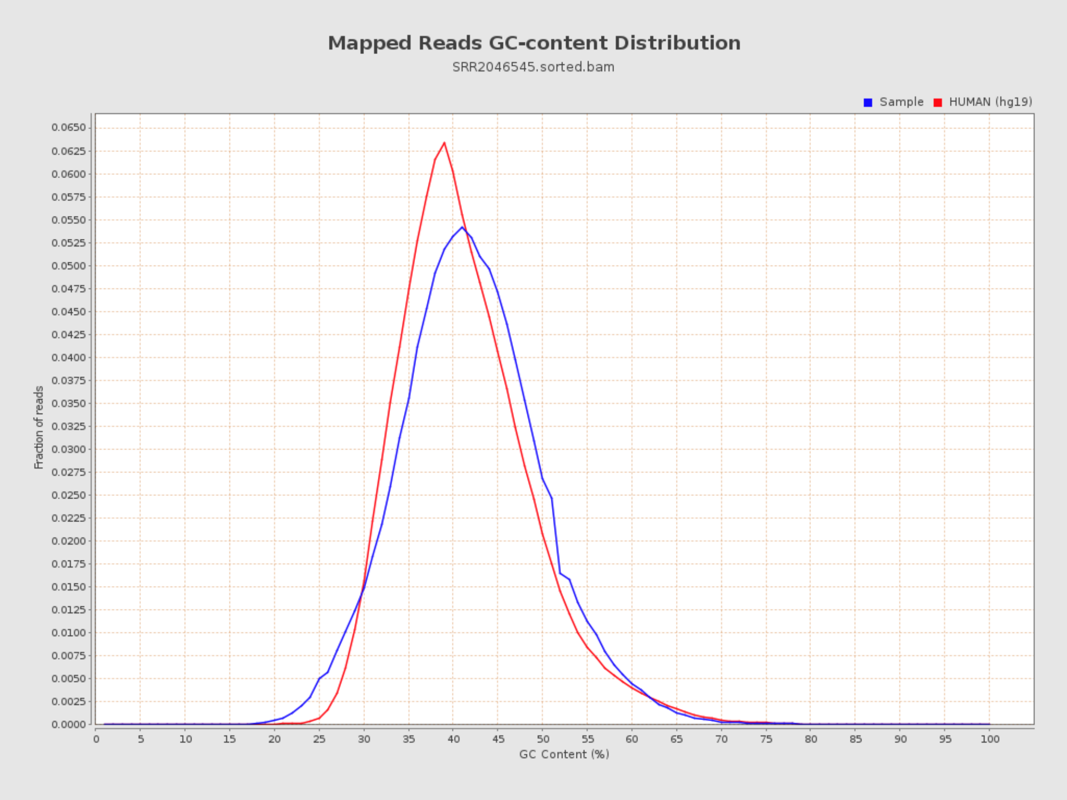
7. Results : Duplication Rate Histogram



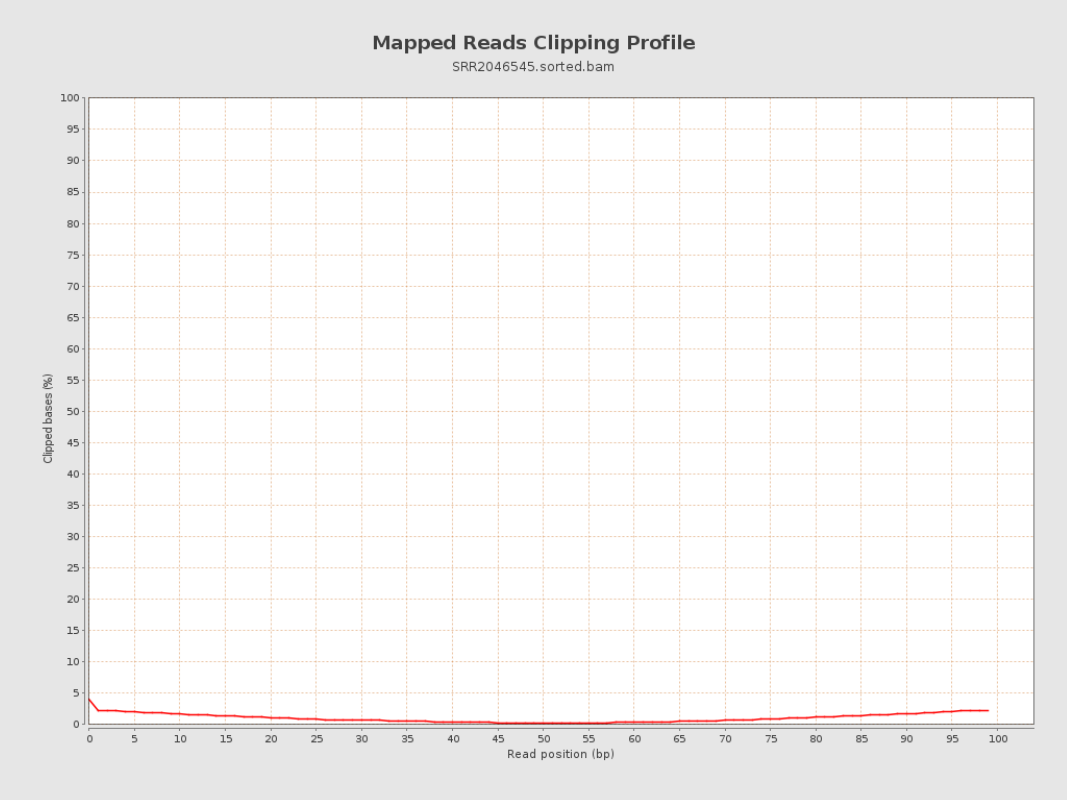
8. Results : Mapped Reads Nucleotide Content



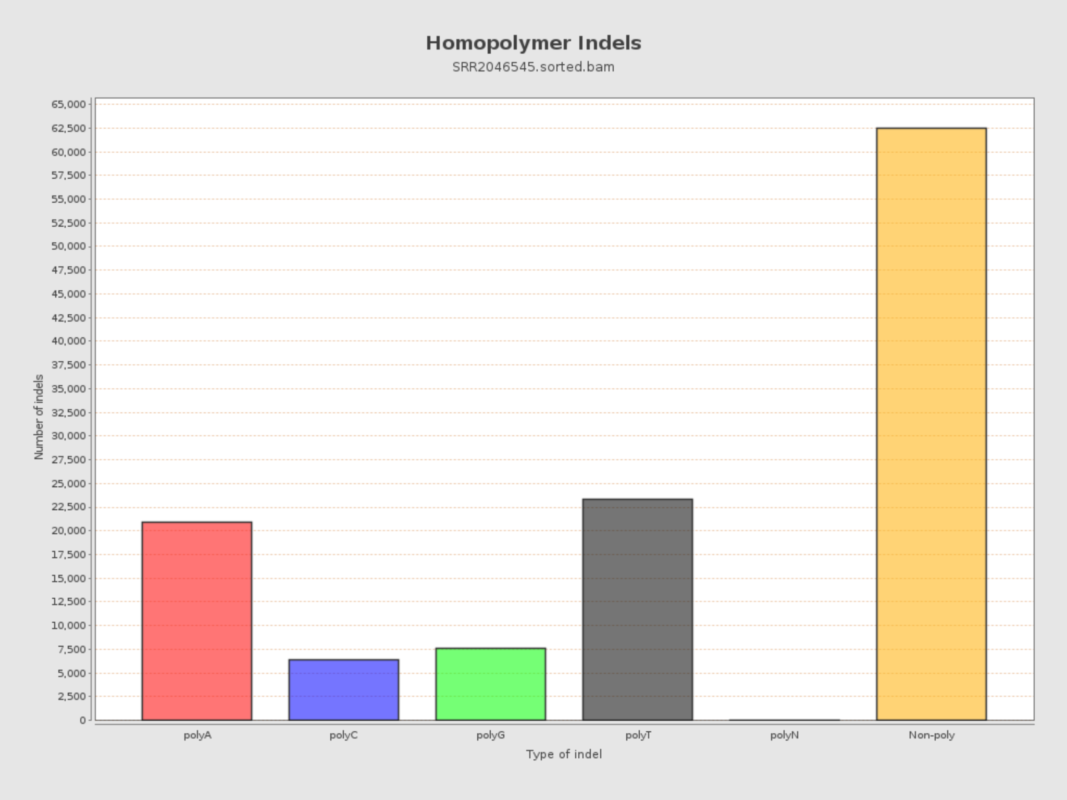
9. Results : Mapped Reads GC-content Distribution



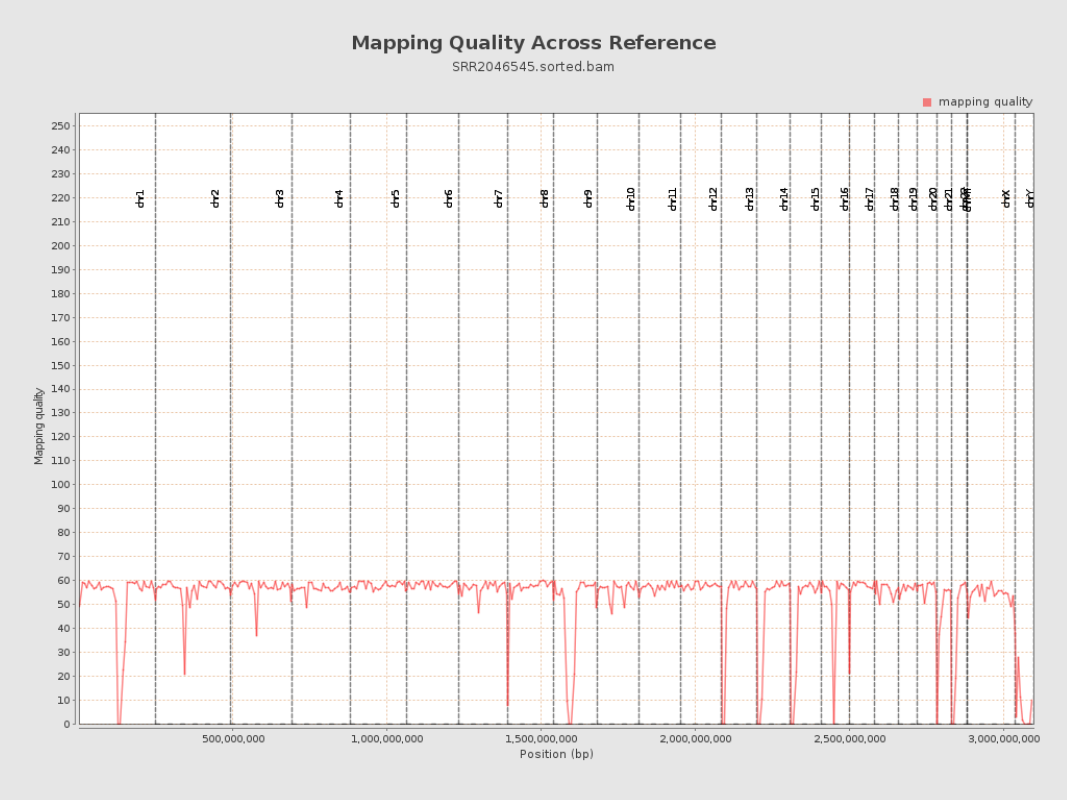
10. Results : Mapped Reads Clipping Profile



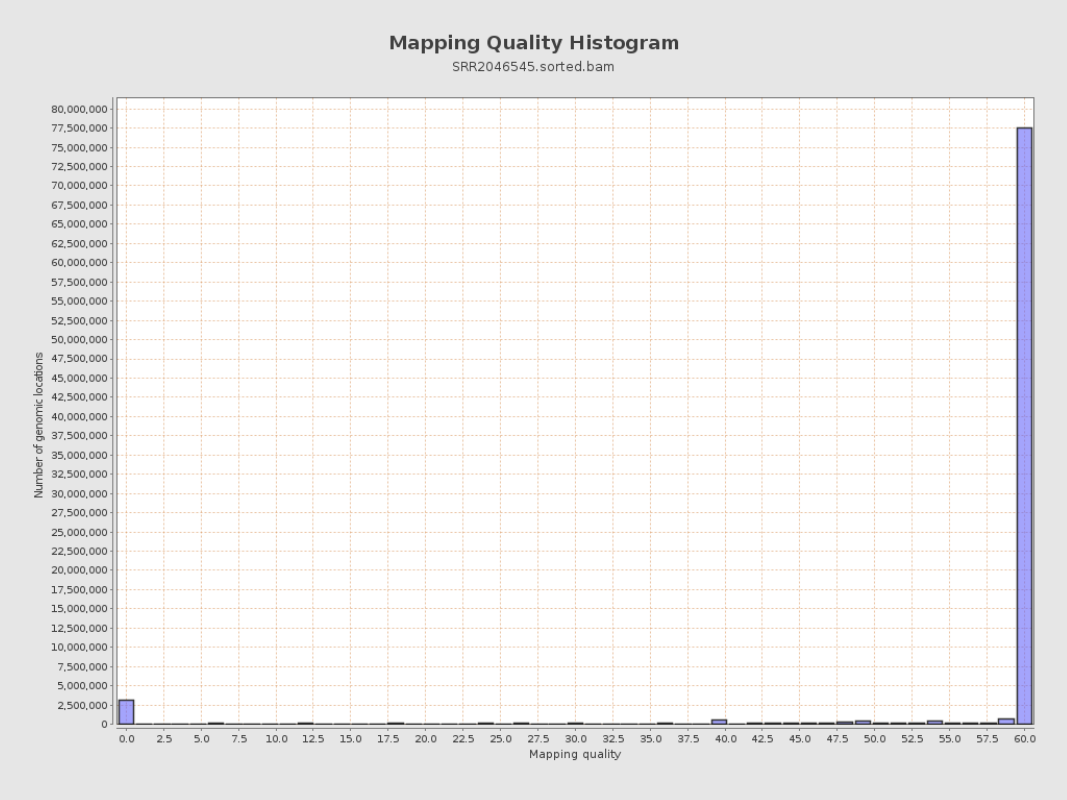
11. Results : Homopolymer Indels



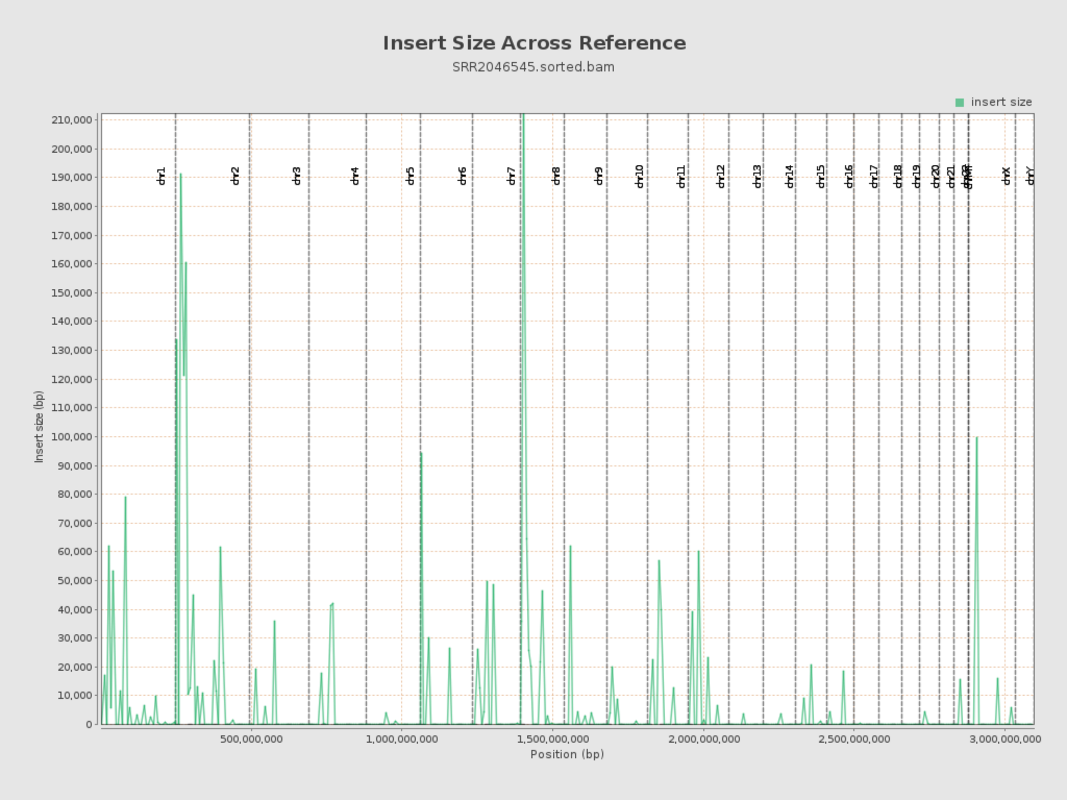
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram