Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/09 02:41:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617414.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_SRR617414 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617414_1.fastq.gz SRR617414_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 09 02:41:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617414.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	30,304,536 / 94.7%
Unmapped reads	1,695,464 / 5.3%
Mapped paired reads	30,304,536 / 94.7%
Mapped reads, first in pair	15,229,304 / 47.59%
Mapped reads, second in pair	15,075,232 / 47.11%
Mapped reads, both in pair	29,888,696 / 93.4%
Mapped reads, singletons	415,840 / 1.3%
Secondary alignments	0
Supplementary alignments	464,163 / 1.45%
Read min/max/mean length	30 / 100 / 100.6
Duplicated reads (estimated)	1,396,184 / 4.36%
Duplication rate	4.19%
Clipped reads	3,053,054 / 9.54%

2.2. ACGT Content

Number/percentage of A's	891,347,018 / 29.82%
Number/percentage of C's	601,005,041 / 20.1%
Number/percentage of T's	882,949,133 / 29.53%
Number/percentage of G's	613,029,631 / 20.51%
Number/percentage of N's	1,260,441 / 0.04%

GC Percentage	40.61%

2.3. Coverage

Mean	0.9659
Standard Deviation	2.9514

2.4. Mapping Quality

Mean Mapping Quality	53.96

2.5. Insert size

Mean	46,754.76
Standard Deviation	2,047,940.45
P25/Median/P75	172 / 211 / 274

2.6. Mismatches and indels

General error rate	1.01%
Mismatches	29,710,181
Insertions	242,893
Mapped reads with at least one insertion	0.79%
Deletions	291,265
Mapped reads with at least one deletion	0.94%
Homopolymer indels	44.81%

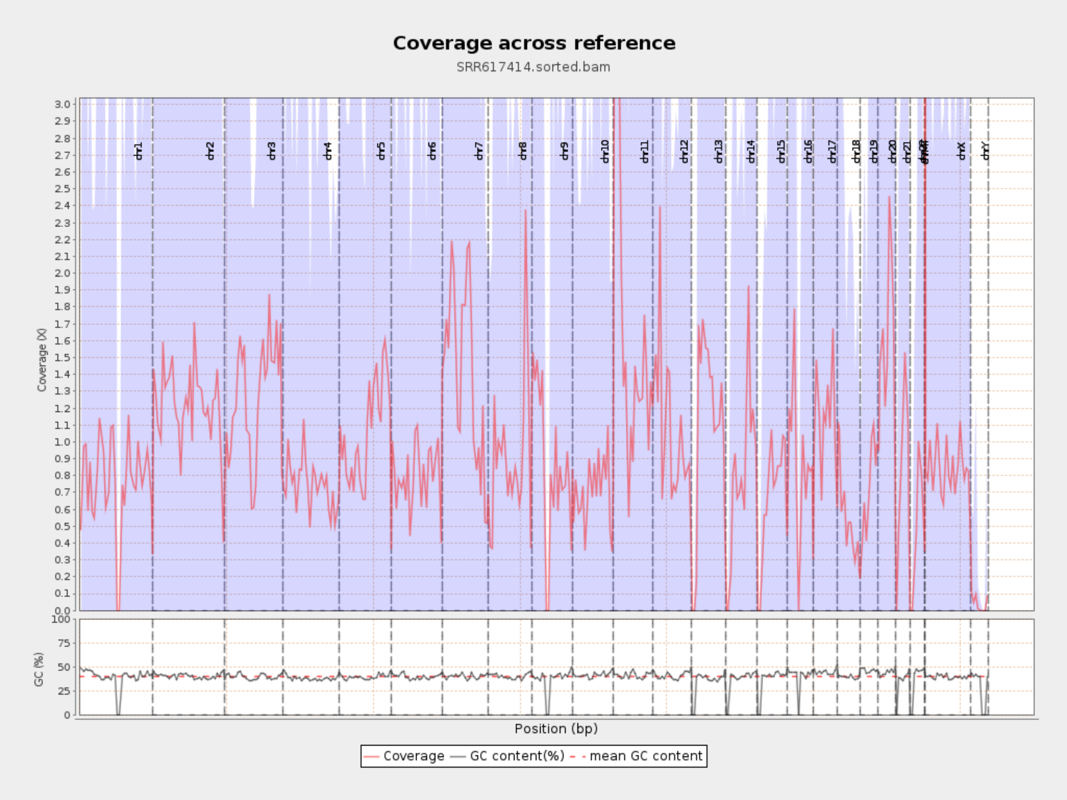
2.7. Chromosome stats

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

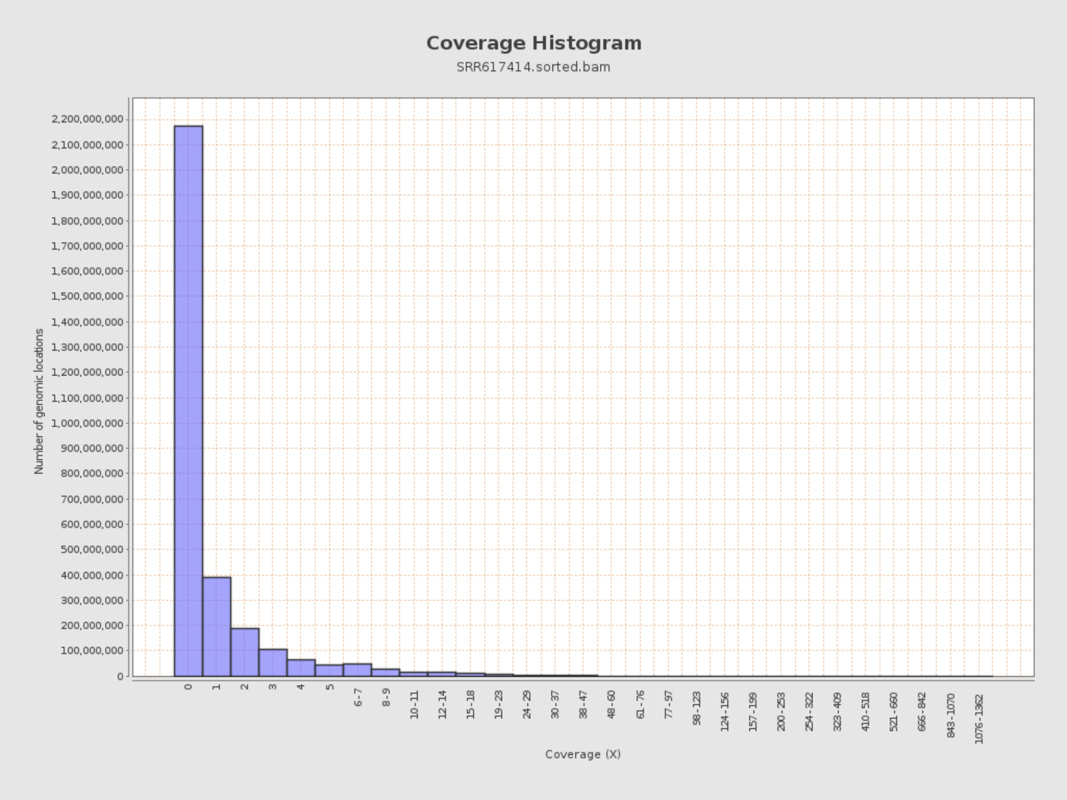
		bases	coverage	deviation
chr1	249250621	192426277	0.772	2.7713
chr2	243199373	298040623	1.2255	3.0889
chr3	198022430	252341672	1.2743	3.4459
chr4	191154276	143405757	0.7502	2.2932
chr5	180915260	191037811	1.056	2.8888
chr6	171115067	137061615	0.801	2.6234
chr7	159138663	224481550	1.4106	3.2707
chr8	146364022	132439089	0.9049	3.3064
chr9	141213431	119427193	0.8457	2.6373
chr10	135534747	95758579	0.7065	2.4362
chr11	135006516	222451321	1.6477	3.8824
chr12	133851895	142523893	1.0648	2.7984
chr13	115169878	129421415	1.1237	2.7803
chr14	107349540	86571870	0.8064	2.9082
chr15	102531392	68619954	0.6693	2.3655
chr16	90354753	75583320	0.8365	3.3626
chr17	81195210	92262158	1.1363	3.7418
chr18	78077248	42961464	0.5502	2.0206
chr19	59128983	42666872	0.7216	2.3613
chr20	63025520	101864114	1.6162	4.7767
chr21	48129895	40972643	0.8513	2.5603
chr22	51304566	24099051	0.4697	2.0918
chrMT	16571	189250	11.4206	5.5143
chrX	155270560	131253301	0.8453	2.5883

chrY	59373566	2383741	0.0401	0.5835

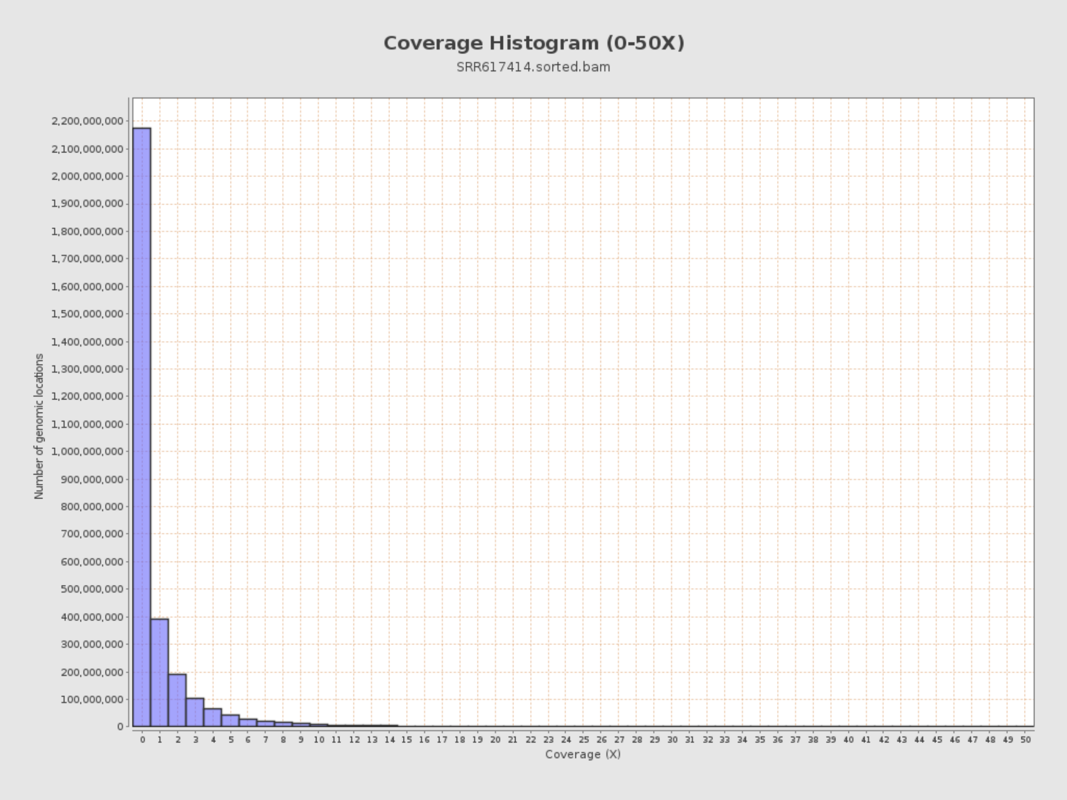
3. Results : Coverage across reference



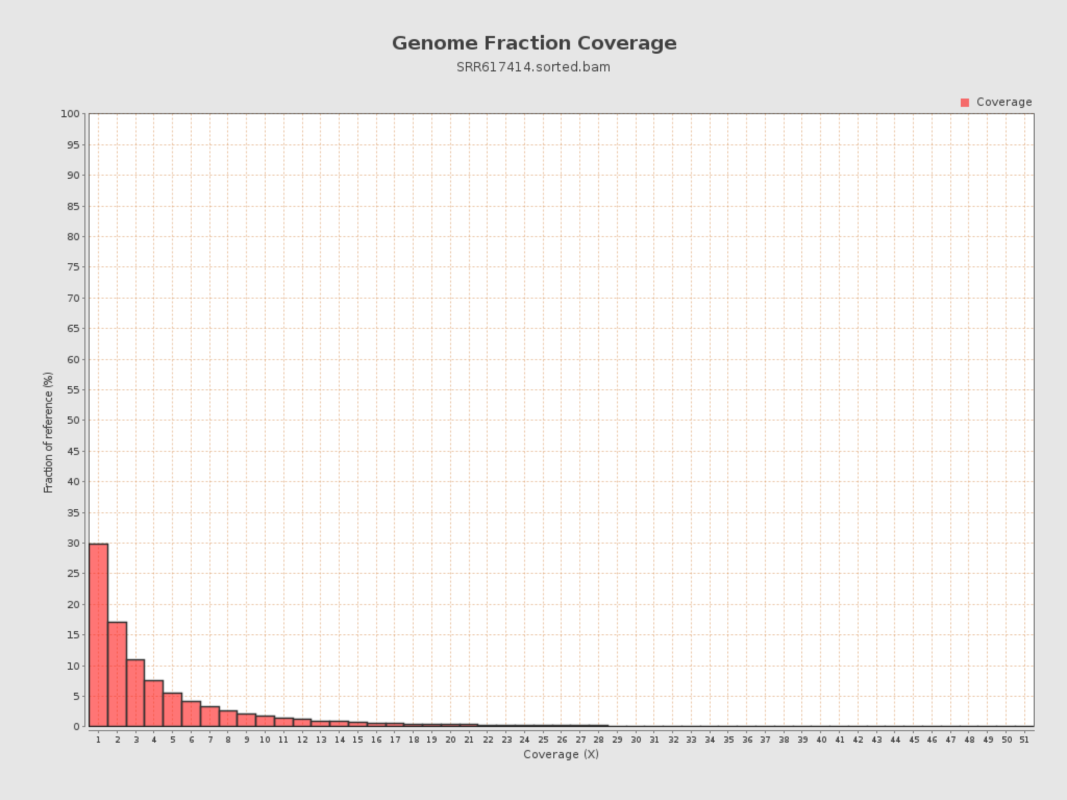
4. Results : Coverage Histogram



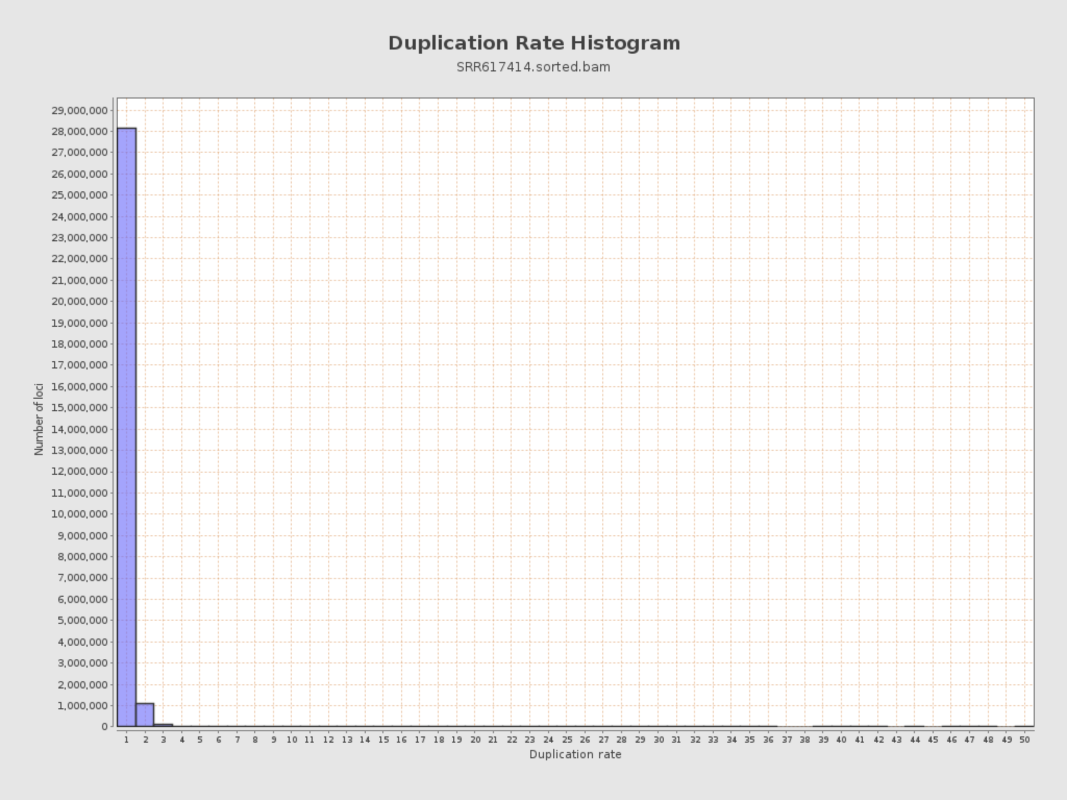
5. Results : Coverage Histogram (0-50X)



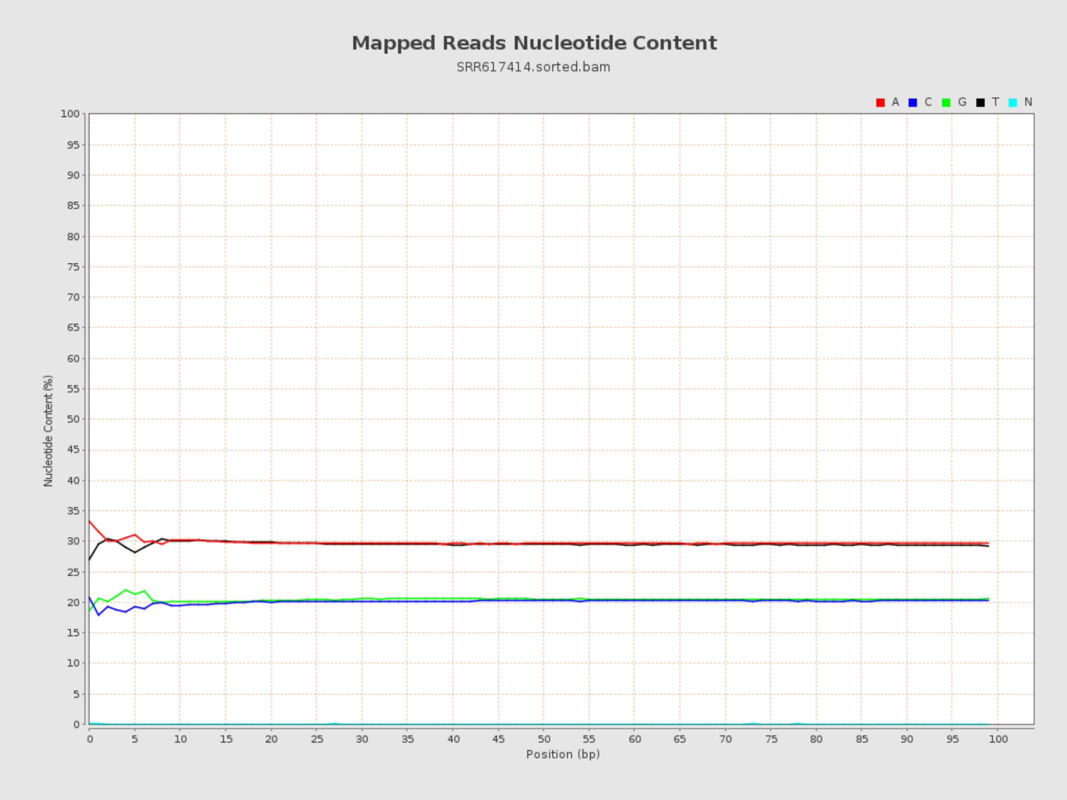
6. Results : Genome Fraction Coverage



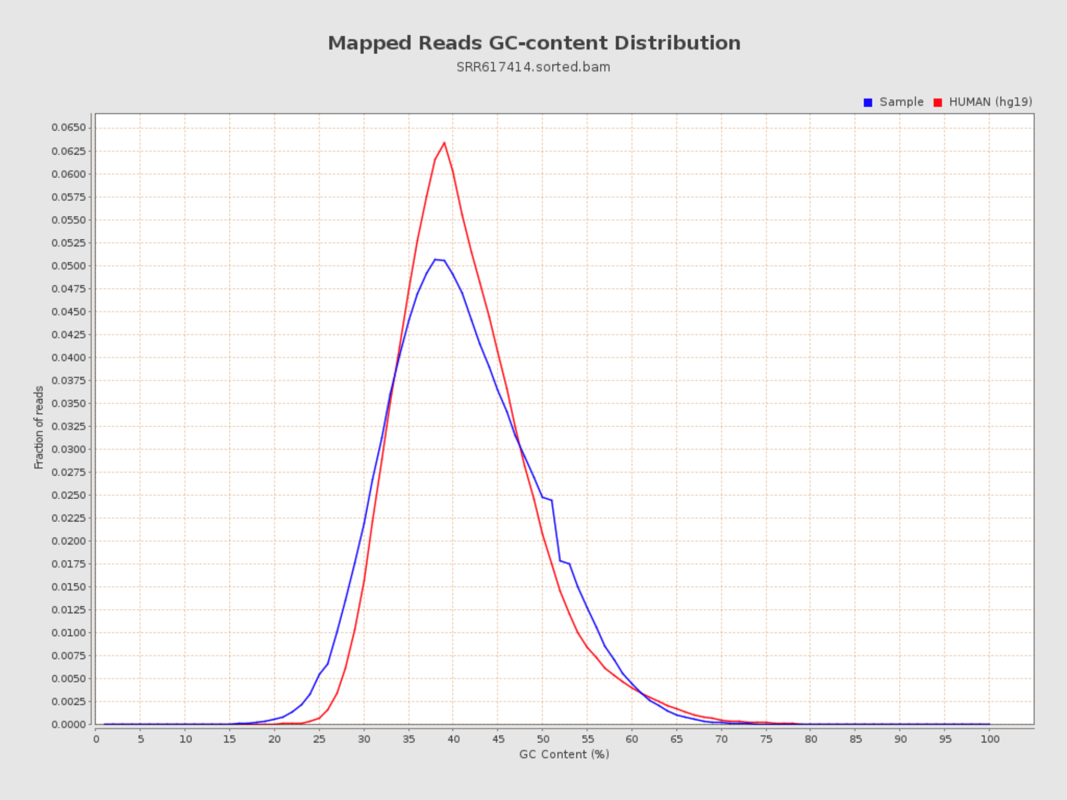
7. Results : Duplication Rate Histogram



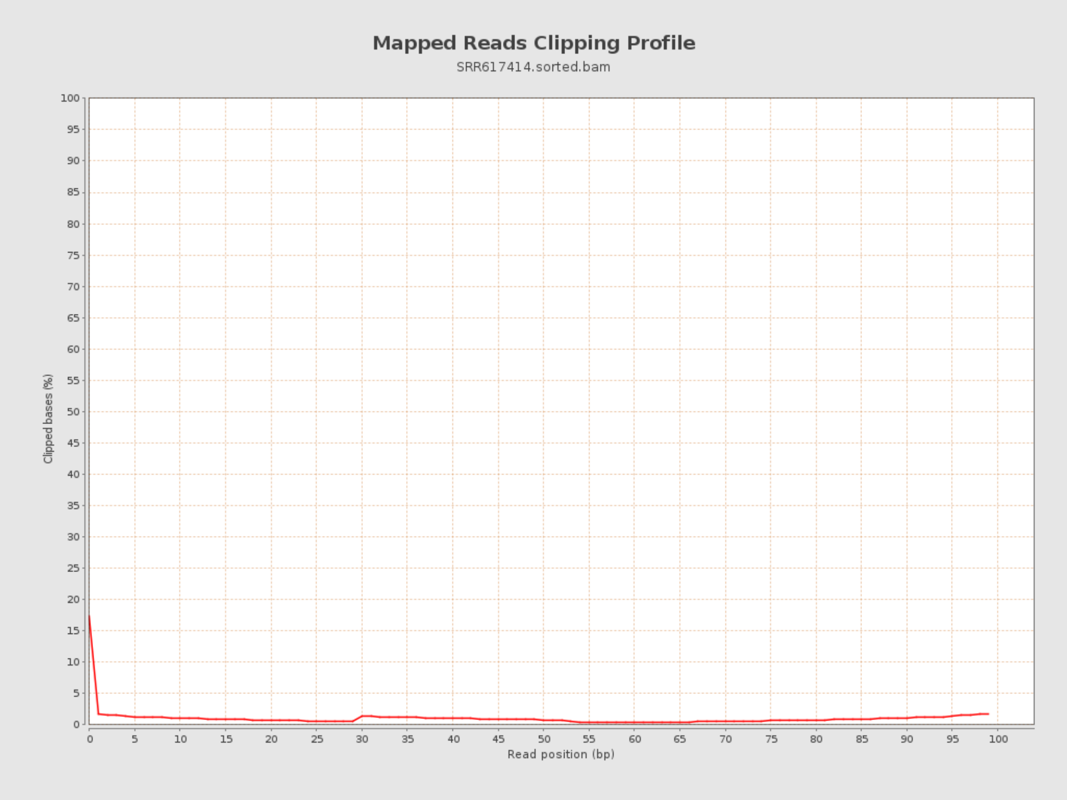
8. Results : Mapped Reads Nucleotide Content



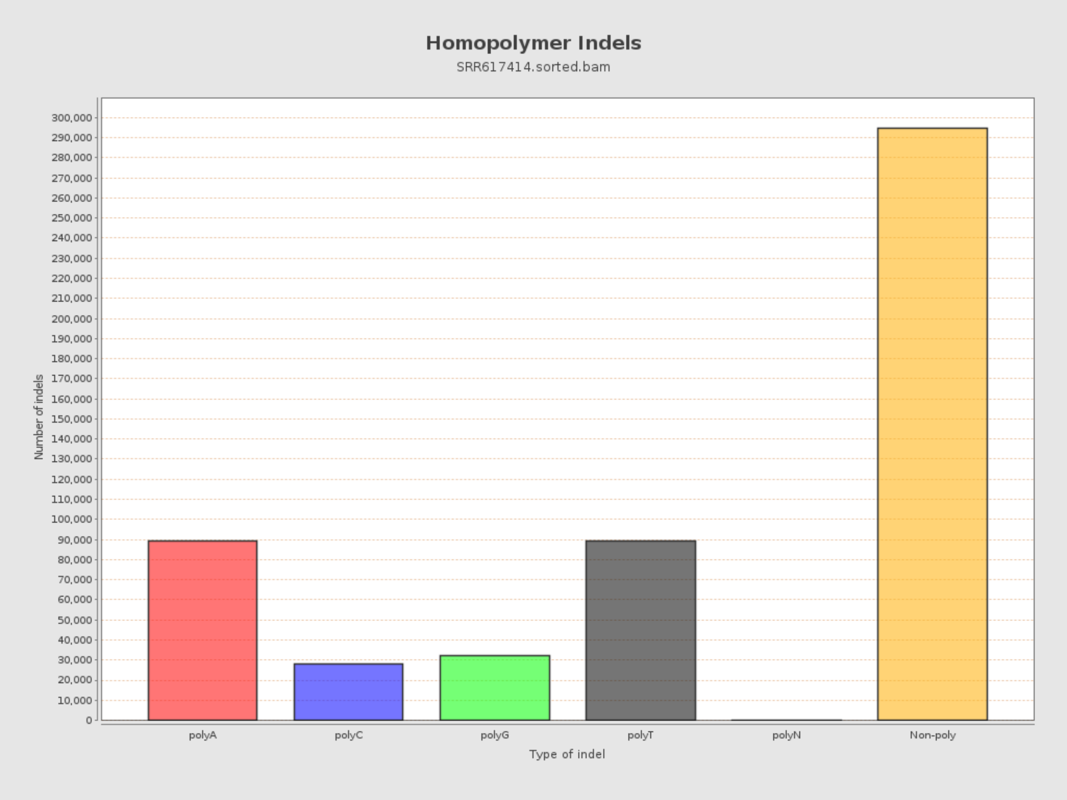
9. Results : Mapped Reads GC-content Distribution



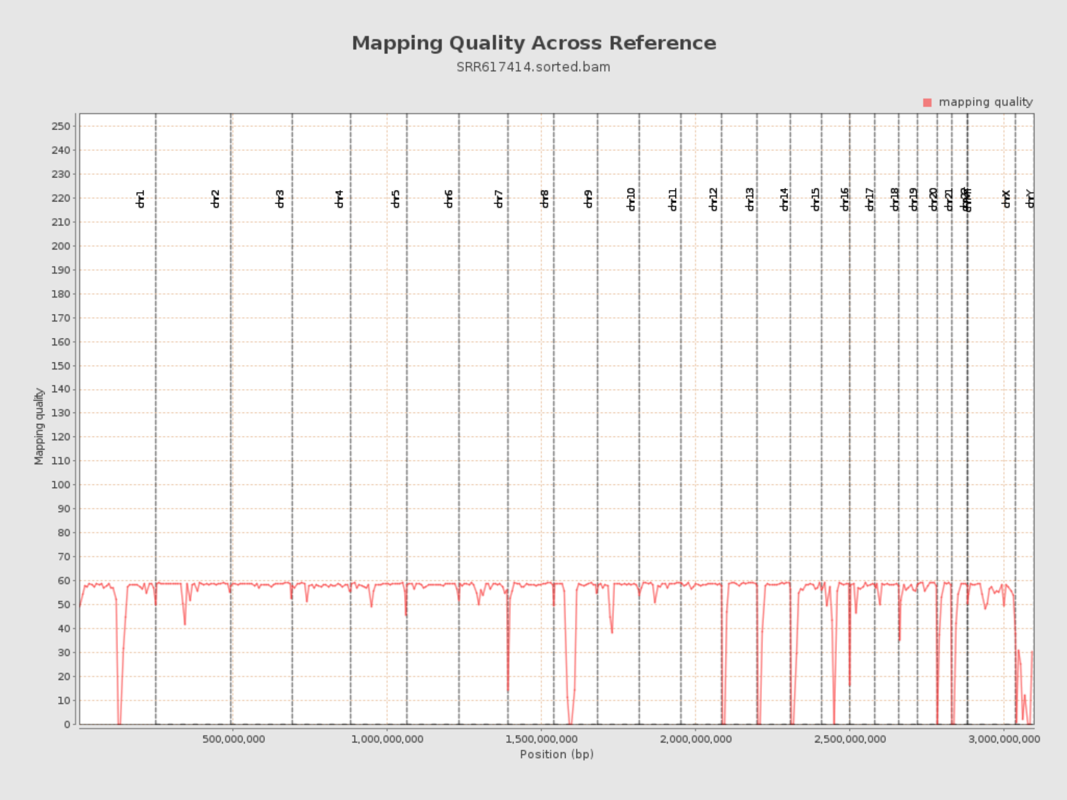
10. Results : Mapped Reads Clipping Profile



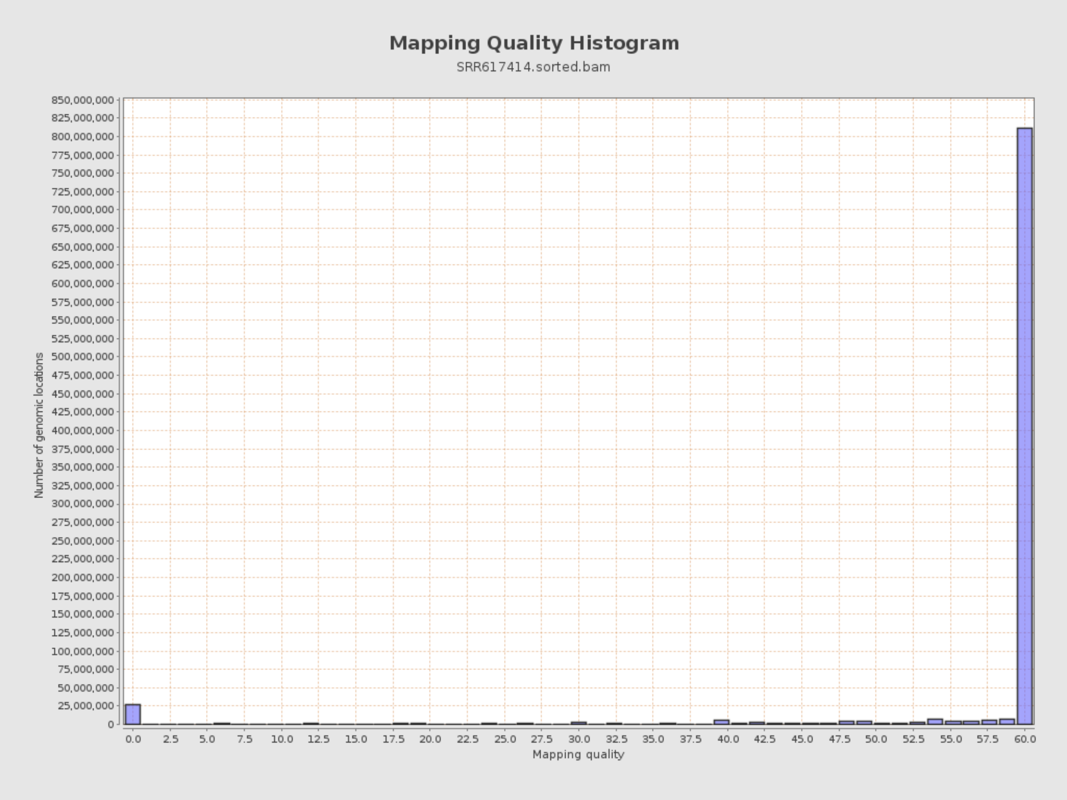
11. Results : Homopolymer Indels



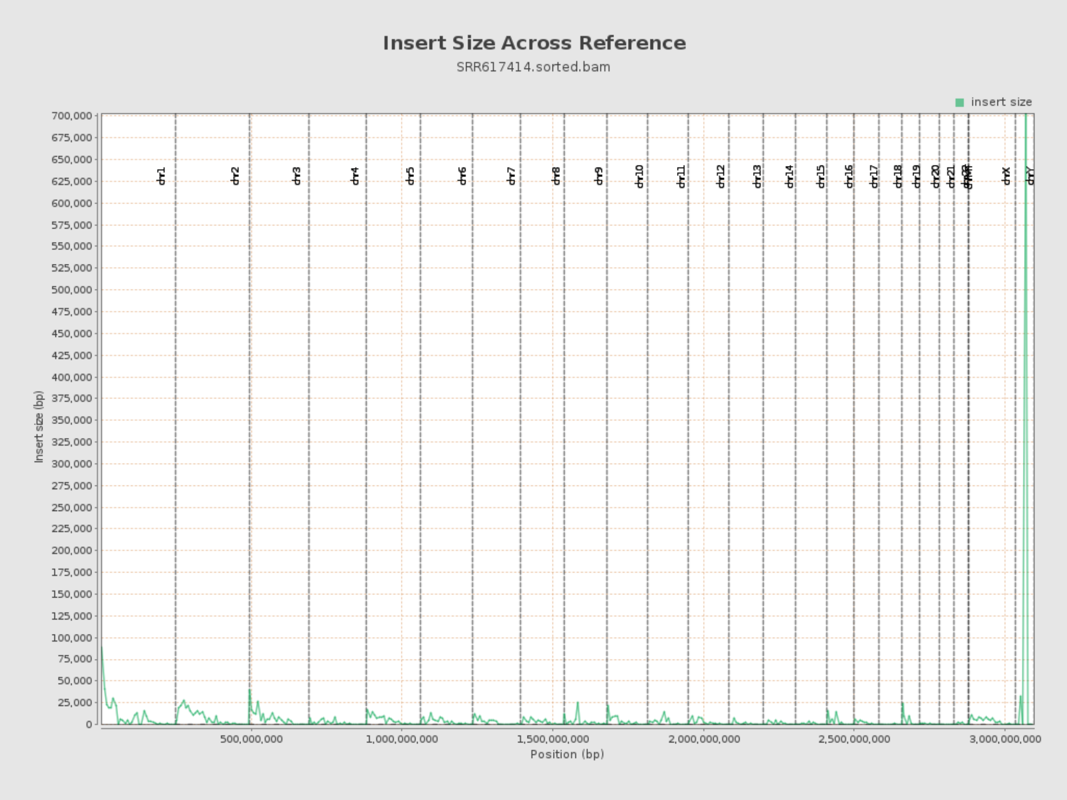
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram