Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/08 01:47:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617383.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_SRR617383 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617383_1.fastq.gz SRR617383_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 08 01:47:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617383.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	30,245,153 / 94.52%
Unmapped reads	1,754,847 / 5.48%
Mapped paired reads	30,245,153 / 94.52%
Mapped reads, first in pair	15,225,657 / 47.58%
Mapped reads, second in pair	15,019,496 / 46.94%
Mapped reads, both in pair	29,694,086 / 92.79%
Mapped reads, singletons	551,067 / 1.72%
Secondary alignments	0
Supplementary alignments	96,378 / 0.3%
Read min/max/mean length	30 / 100 / 100.12
Duplicated reads (estimated)	1,613,898 / 5.04%
Duplication rate	1.52%
Clipped reads	2,384,053 / 7.45%

2.2. ACGT Content

Number/percentage of A's	898,968,904 / 30.31%
Number/percentage of C's	588,370,277 / 19.84%
Number/percentage of T's	887,712,236 / 29.93%
Number/percentage of G's	590,369,491 / 19.9%
Number/percentage of N's	805,631 / 0.03%

GC Percentage	39.74%

2.3. Coverage

Mean	0.9585
Standard Deviation	9.8688

2.4. Mapping Quality

Mean Mapping Quality	53.42

2.5. Insert size

Mean	66,361.33
Standard Deviation	2,474,716.87
P25/Median/P75	172 / 213 / 276

2.6. Mismatches and indels

General error rate	1%
Mismatches	28,786,307
Insertions	301,623
Mapped reads with at least one insertion	0.97%
Deletions	363,011
Mapped reads with at least one deletion	1.16%
Homopolymer indels	41.28%

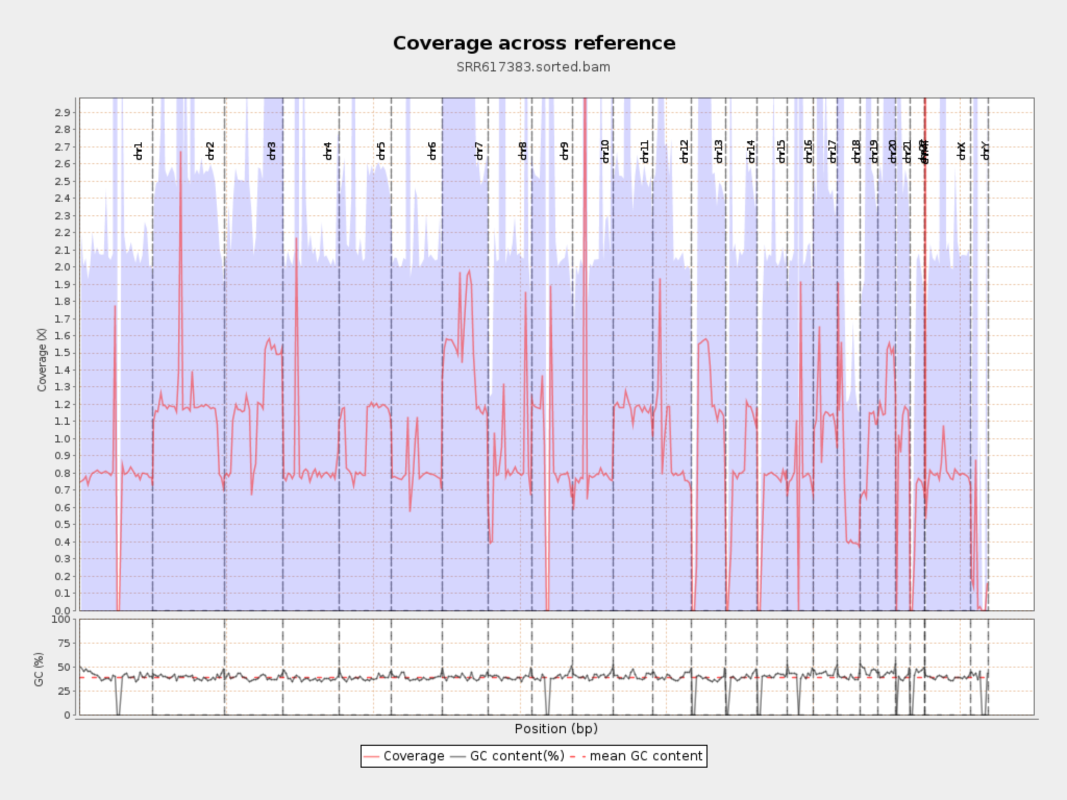
2.7. Chromosome stats

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

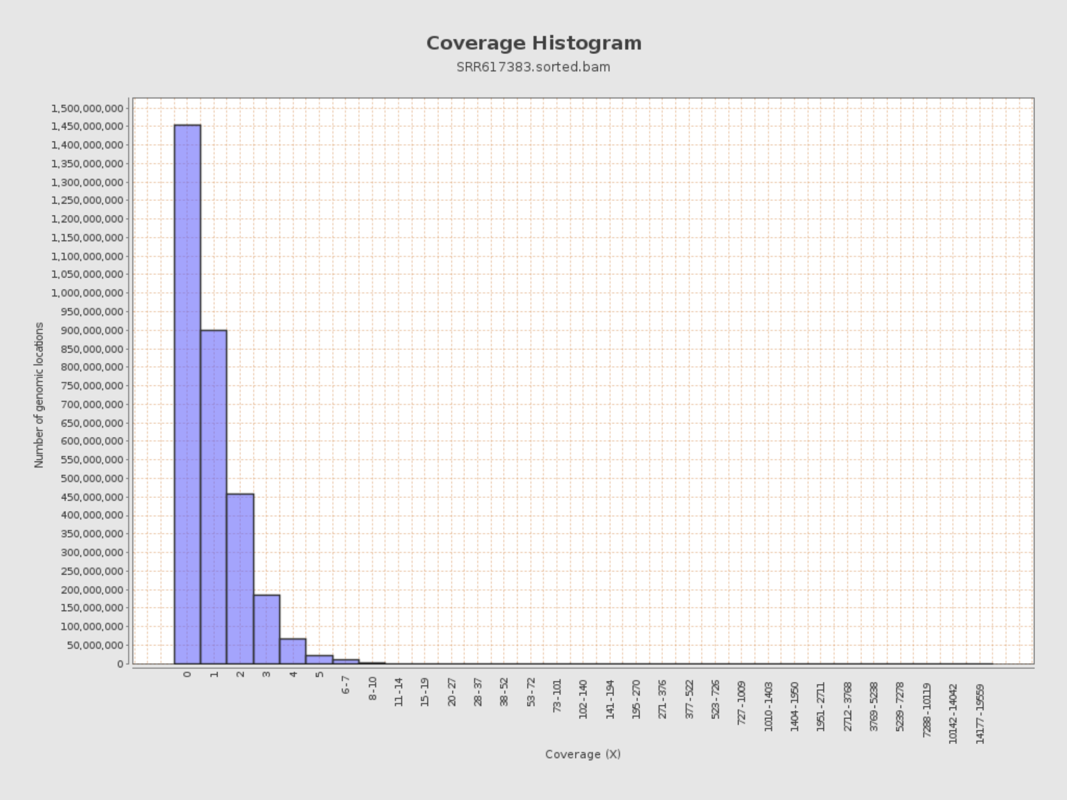
		bases	coverage	deviation
chr1	249250621	192869645	0.7738	20.0947
chr2	243199373	293032332	1.2049	8.9442
chr3	198022430	236127733	1.1924	1.4882
chr4	191154276	162581564	0.8505	9.4384
chr5	180915260	186111176	1.0287	1.4613
chr6	171115067	139053317	0.8126	3.6553
chr7	159138663	240639224	1.5121	10.8929
chr8	146364022	125005834	0.8541	7.661
chr9	141213431	125104506	0.8859	15.1176
chr10	135534747	124917084	0.9217	20.245
chr11	135006516	158997604	1.1777	5.6175
chr12	133851895	130954337	0.9784	1.3923
chr13	115169878	129098116	1.1209	1.3416
chr14	107349540	85941752	0.8006	1.376
chr15	102531392	66643412	0.65	1.1252
chr16	90354753	74657657	0.8263	7.9346
chr17	81195210	92419983	1.1382	7.2051
chr18	78077248	53807192	0.6892	15.4172
chr19	59128983	54985487	0.9299	9.5324
chr20	63025520	84876387	1.3467	2.4782
chr21	48129895	47244646	0.9816	3.229
chr22	51304566	26445900	0.5155	0.9357
chrMT	16571	2018861	121.831	20.2611
chrX	155270560	123361379	0.7945	3.0526

chrY	59373566	10210975	0.172	8.4652

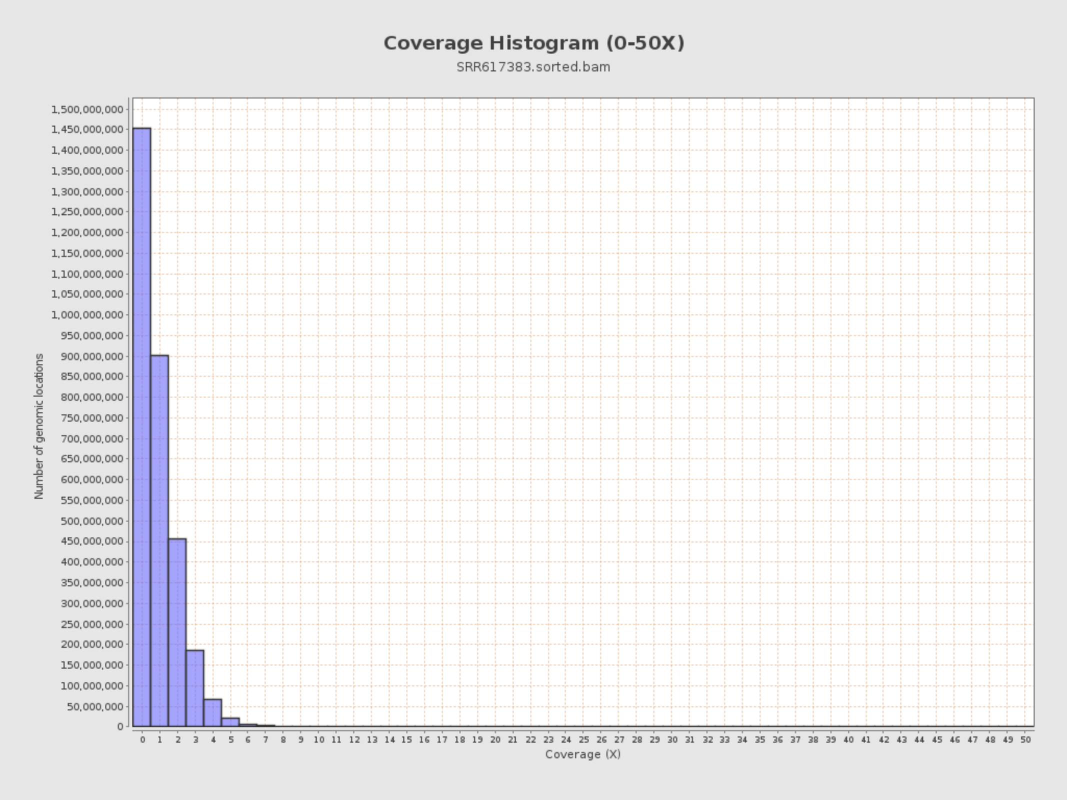
3. Results : Coverage across reference



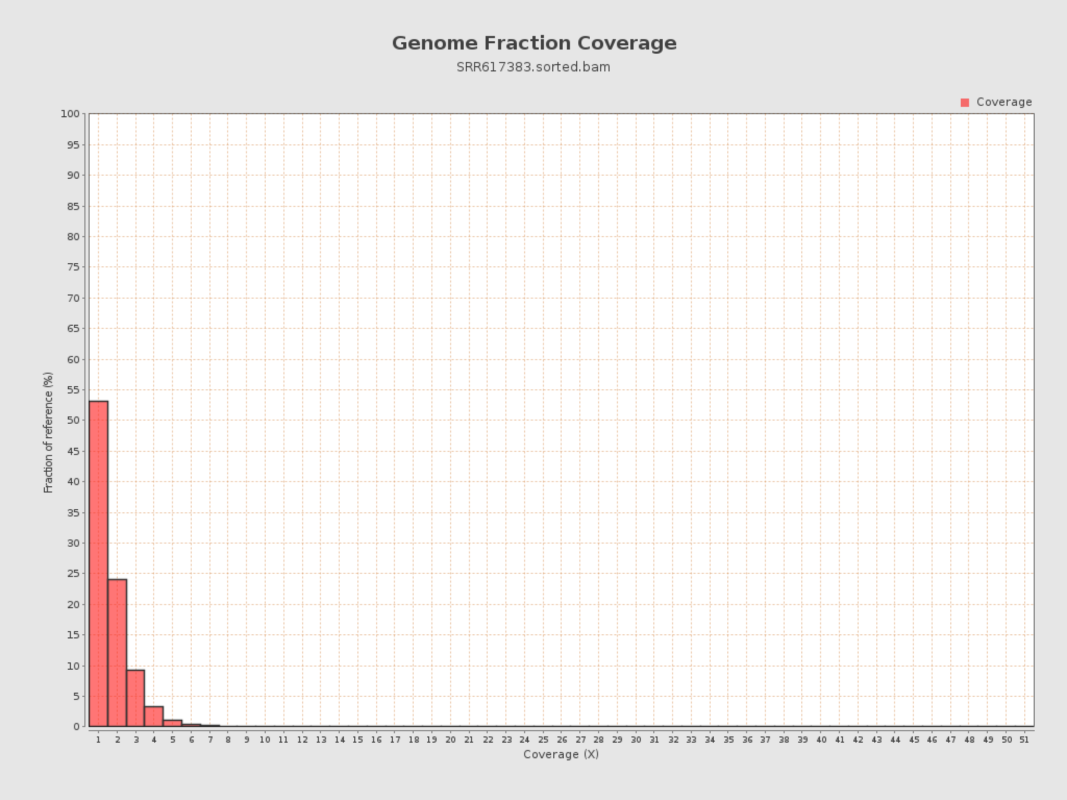
4. Results : Coverage Histogram



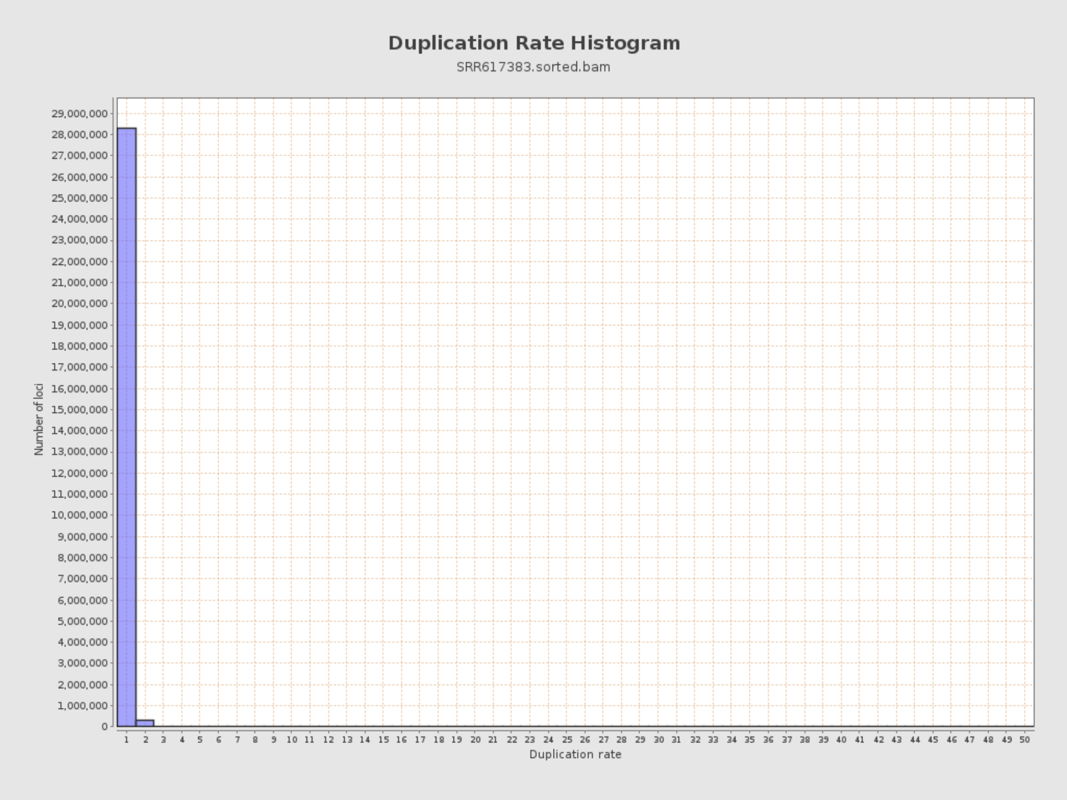
5. Results : Coverage Histogram (0-50X)



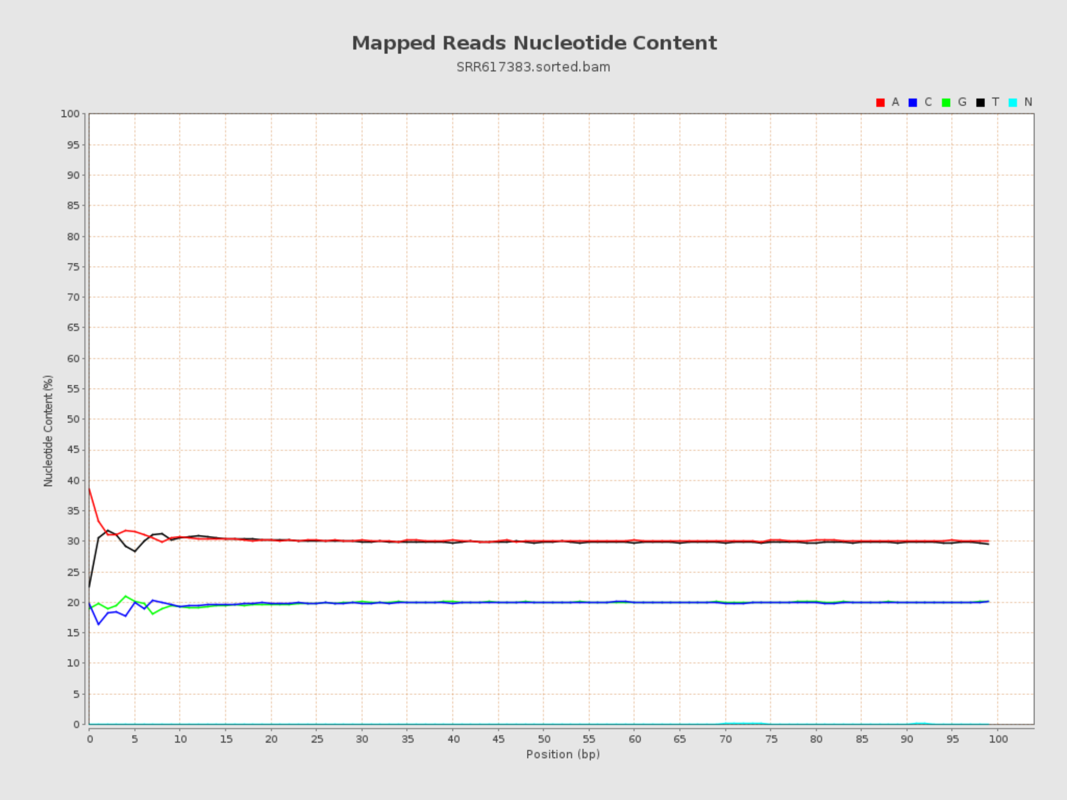
6. Results : Genome Fraction Coverage



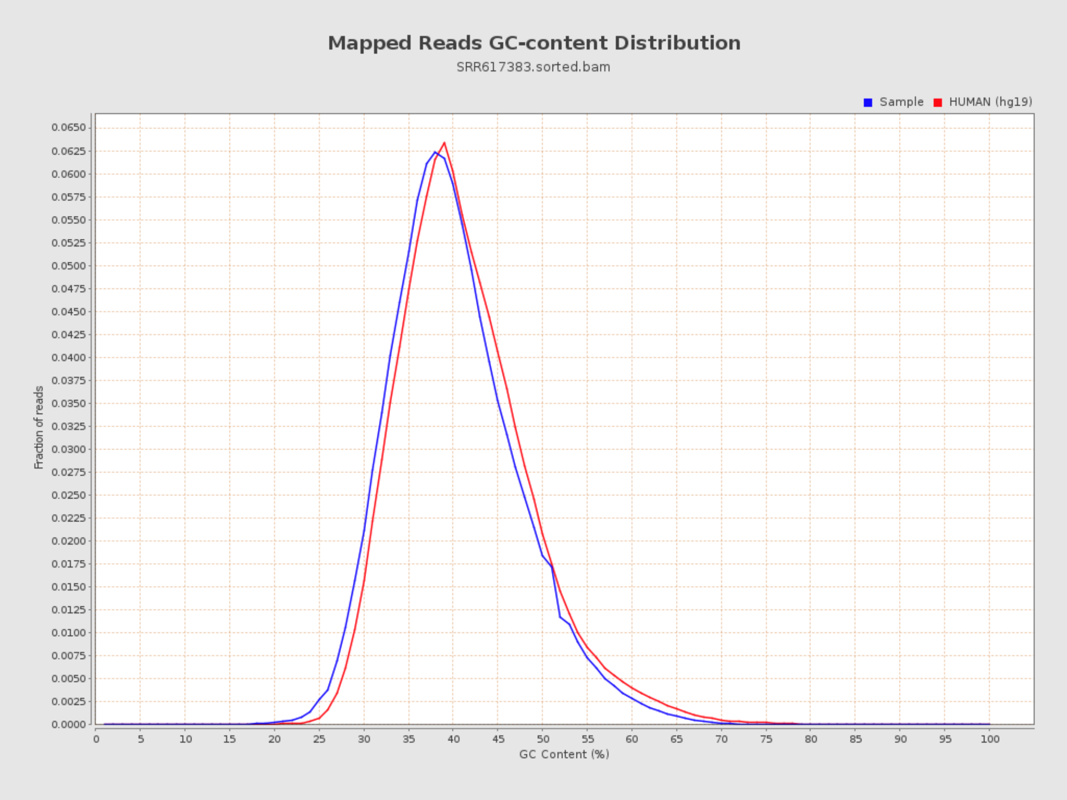
7. Results : Duplication Rate Histogram



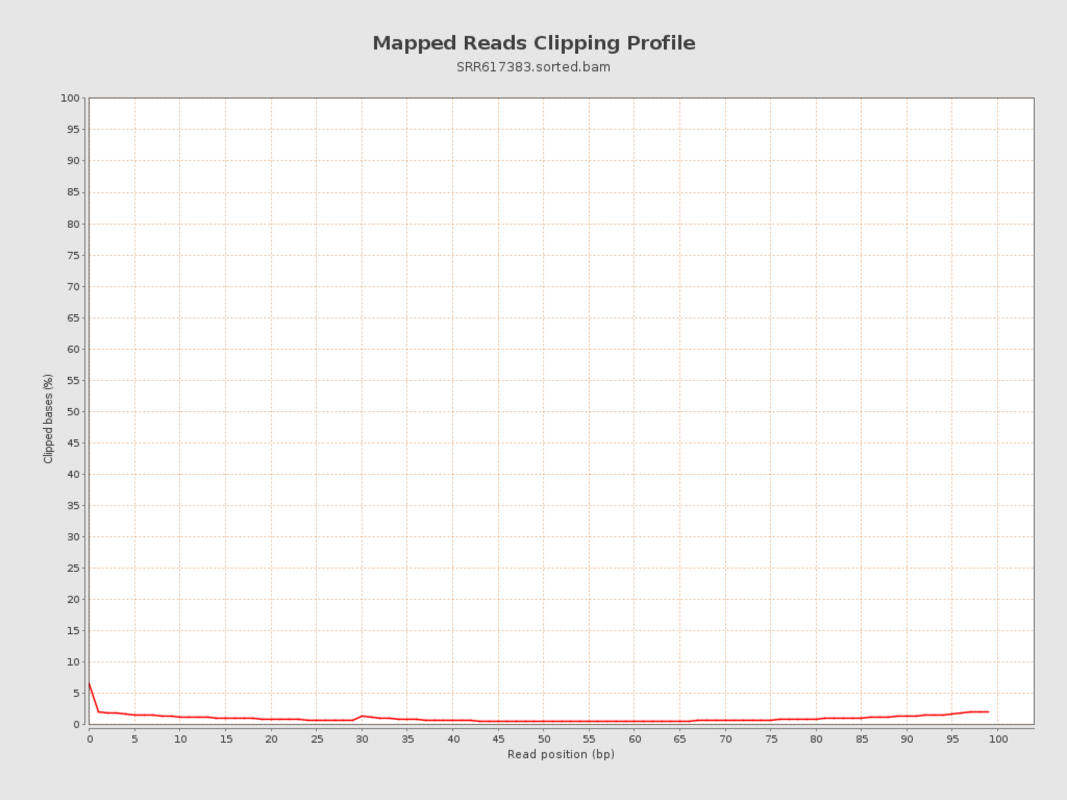
8. Results : Mapped Reads Nucleotide Content



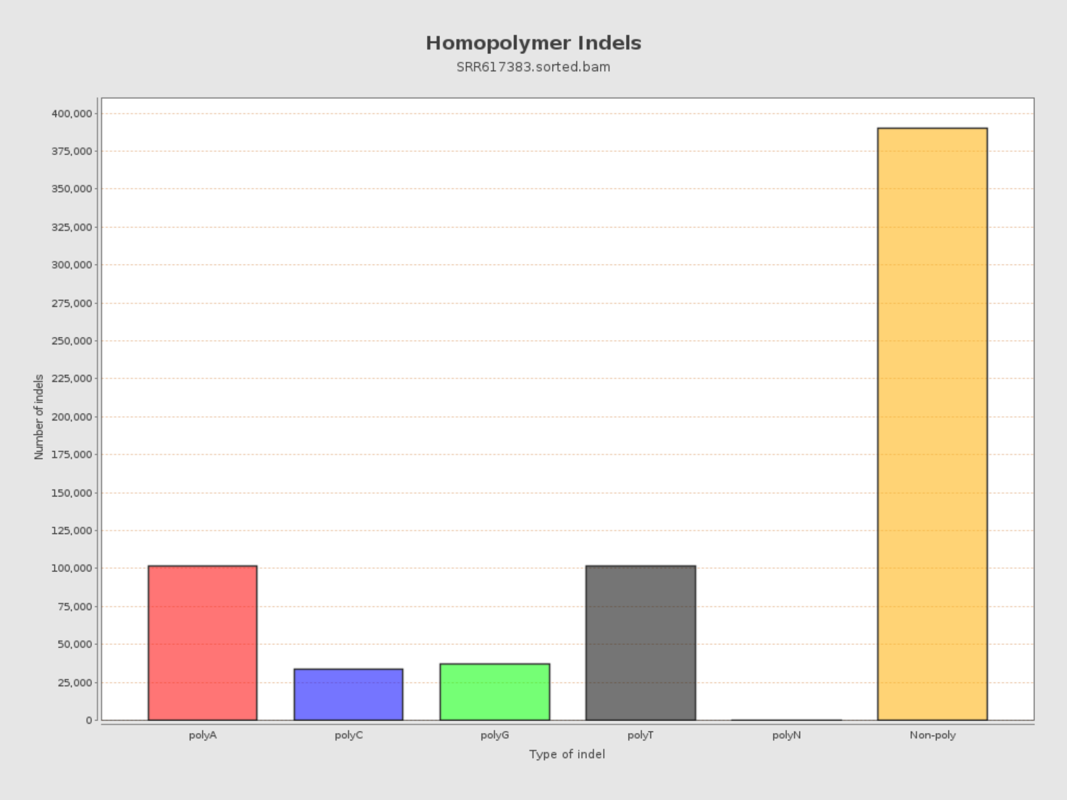
9. Results : Mapped Reads GC-content Distribution



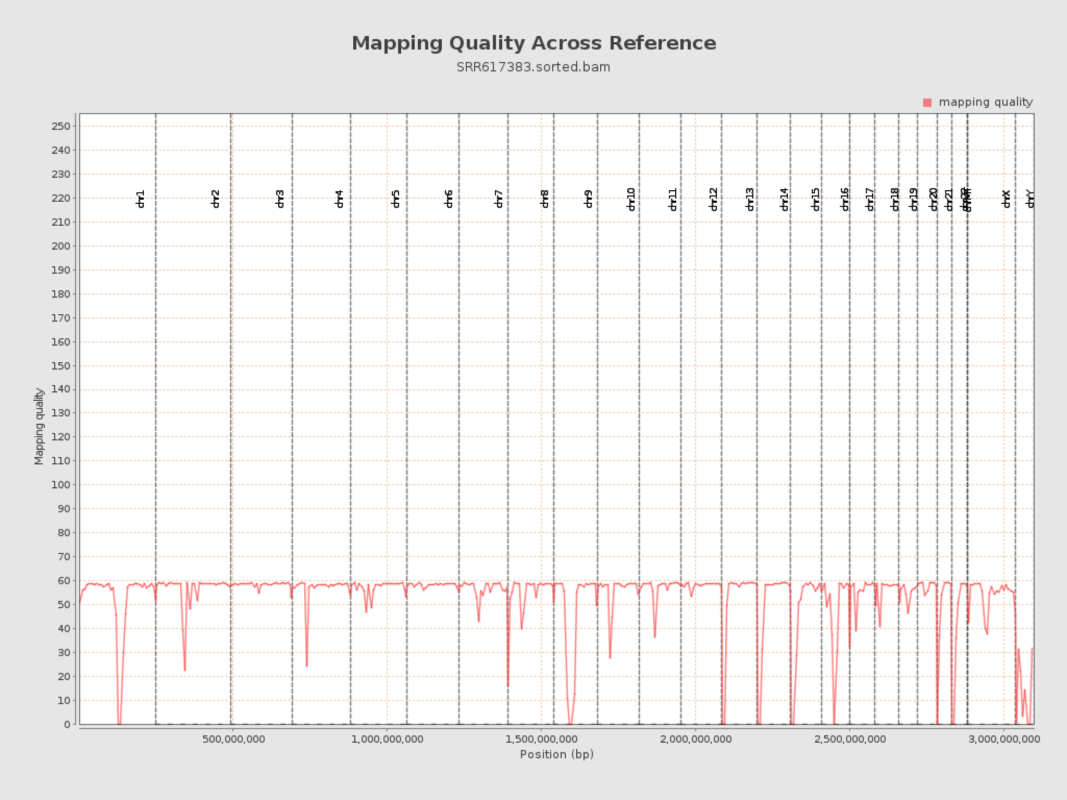
10. Results : Mapped Reads Clipping Profile



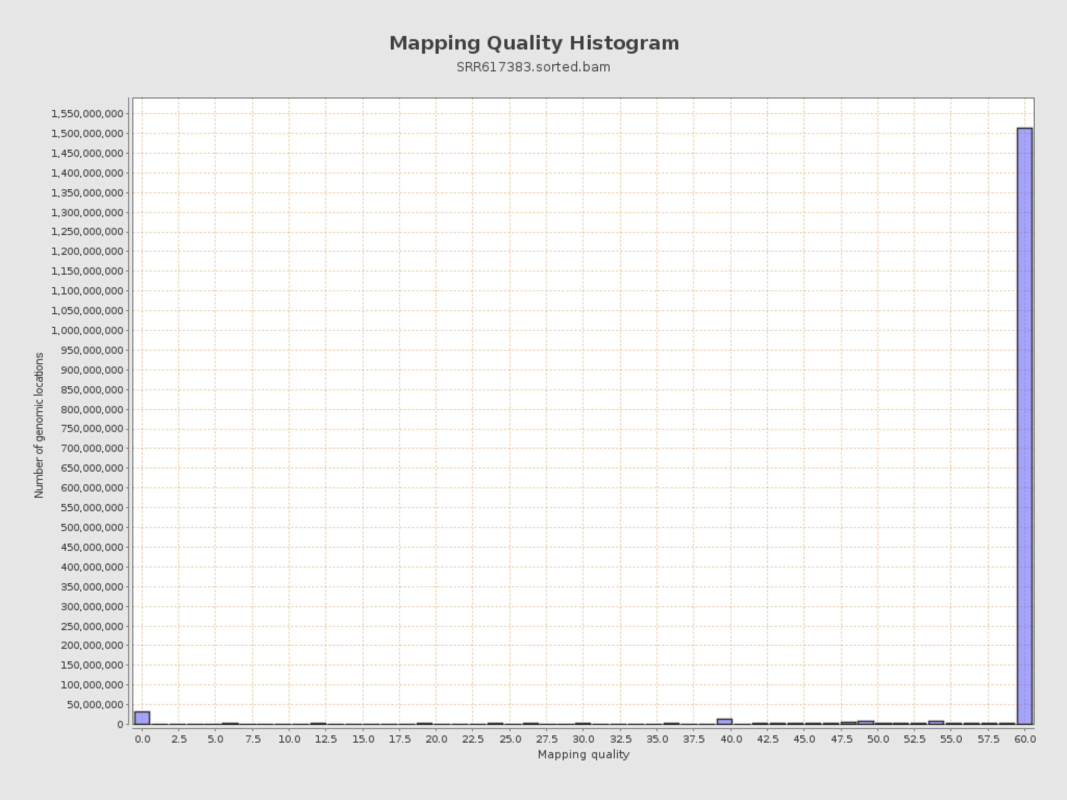
11. Results : Homopolymer Indels



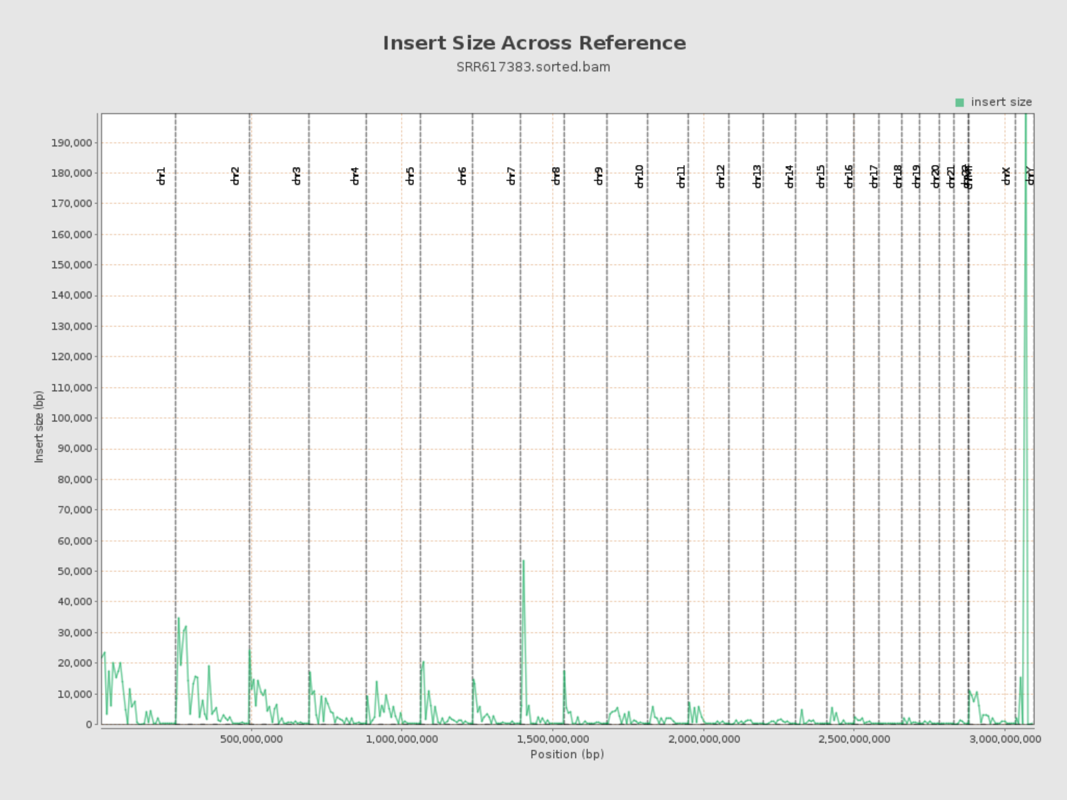
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram