Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/10 02:50:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617503.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_SRR617503 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617503_1.fastq.gz SRR617503_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 10 02:50:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617503.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	30,539,059 / 95.43%
Unmapped reads	1,460,941 / 4.57%
Mapped paired reads	30,539,059 / 95.43%
Mapped reads, first in pair	15,400,475 / 48.13%
Mapped reads, second in pair	15,138,584 / 47.31%
Mapped reads, both in pair	30,004,622 / 93.76%
Mapped reads, singletons	534,437 / 1.67%
Secondary alignments	0
Supplementary alignments	160,113 / 0.5%
Read min/max/mean length	30 / 100 / 100.2
Duplicated reads (estimated)	6,306,445 / 19.71%
Duplication rate	9.99%
Clipped reads	5,985,832 / 18.71%

2.2. ACGT Content

Number/percentage of A's	876,313,564 / 29.48%
Number/percentage of C's	600,620,989 / 20.21%
Number/percentage of T's	876,839,728 / 29.5%
Number/percentage of G's	615,782,260 / 20.72%
Number/percentage of N's	2,948,189 / 0.1%

GC Percentage	40.92%

2.3. Coverage

Mean	0.9608
Standard Deviation	9.6995

2.4. Mapping Quality

Mean Mapping Quality	52.72

2.5. Insert size

Mean	38,390.07
Standard Deviation	1,829,960.46
P25/Median/P75	174 / 219 / 291

2.6. Mismatches and indels

General error rate	1.2%
Mismatches	34,685,899
Insertions	444,808
Mapped reads with at least one insertion	1.43%
Deletions	1,037,188
Mapped reads with at least one deletion	3.32%
Homopolymer indels	47.47%

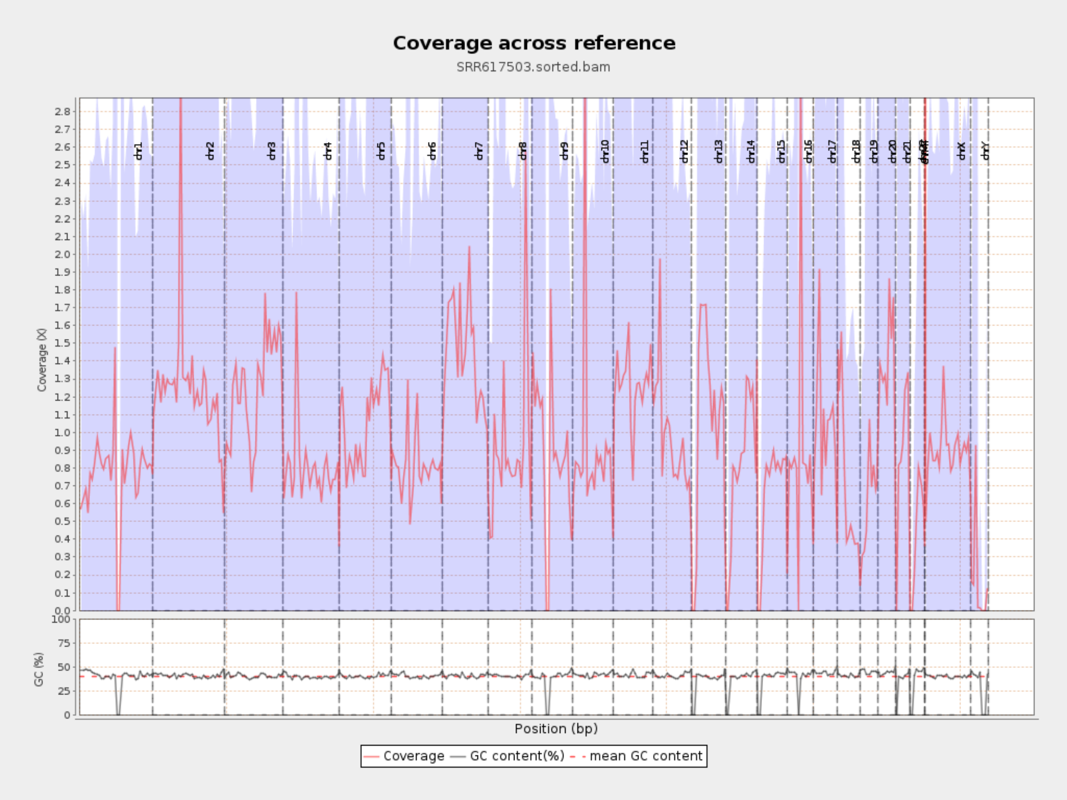
2.7. Chromosome stats

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

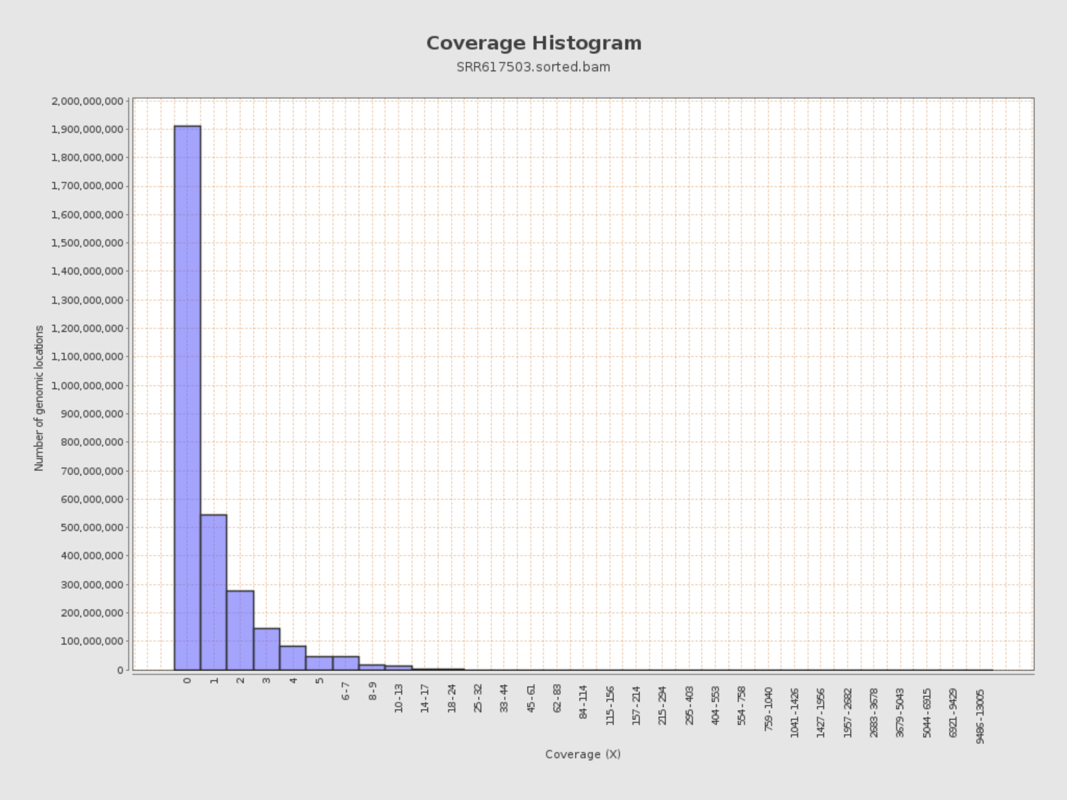
		bases	coverage	deviation
chr1	249250621	191305236	0.7675	9.3662
chr2	243199373	307197841	1.2632	11.4655
chr3	198022430	245985349	1.2422	2.2489
chr4	191154276	153566105	0.8034	6.163
chr5	180915260	190136180	1.051	2.0808
chr6	171115067	140208586	0.8194	5.3662
chr7	159138663	229298483	1.4409	13.0066
chr8	146364022	132196486	0.9032	3.8627
chr9	141213431	123461565	0.8743	18.4007
chr10	135534747	125934546	0.9292	18.5964
chr11	135006516	167760800	1.2426	12.8382
chr12	133851895	130233018	0.973	2.0101
chr13	115169878	125935228	1.0935	2.132
chr14	107349540	86512515	0.8059	2.2218
chr15	102531392	67317596	0.6566	1.4967
chr16	90354753	79966938	0.885	14.8566
chr17	81195210	83288197	1.0258	13.7074
chr18	78077248	53272723	0.6823	17.1125
chr19	59128983	35552639	0.6013	5.7384
chr20	63025520	88075323	1.3975	2.798
chr21	48129895	42860335	0.8905	3.7843
chr22	51304566	22345982	0.4356	1.2553
chrMT	16571	2081051	125.5839	93.4616
chrX	155270560	139503890	0.8985	4.1183

chrY	59373566	10280726	0.1732	13.6486

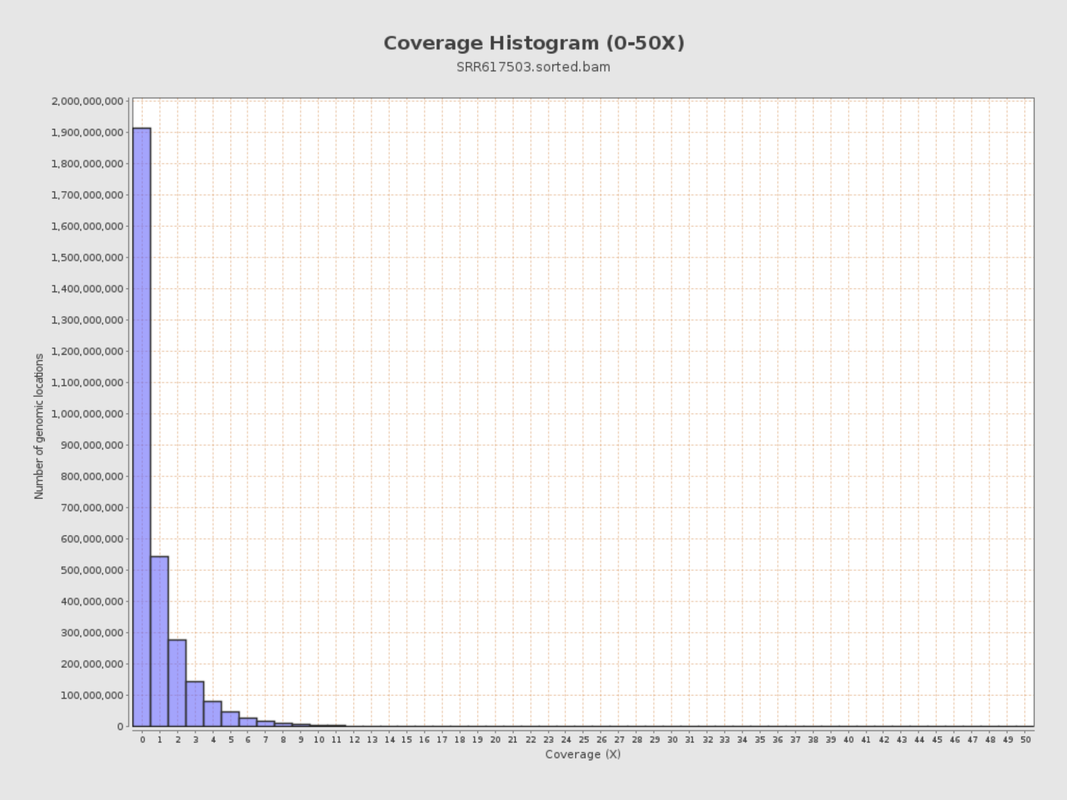
3. Results : Coverage across reference



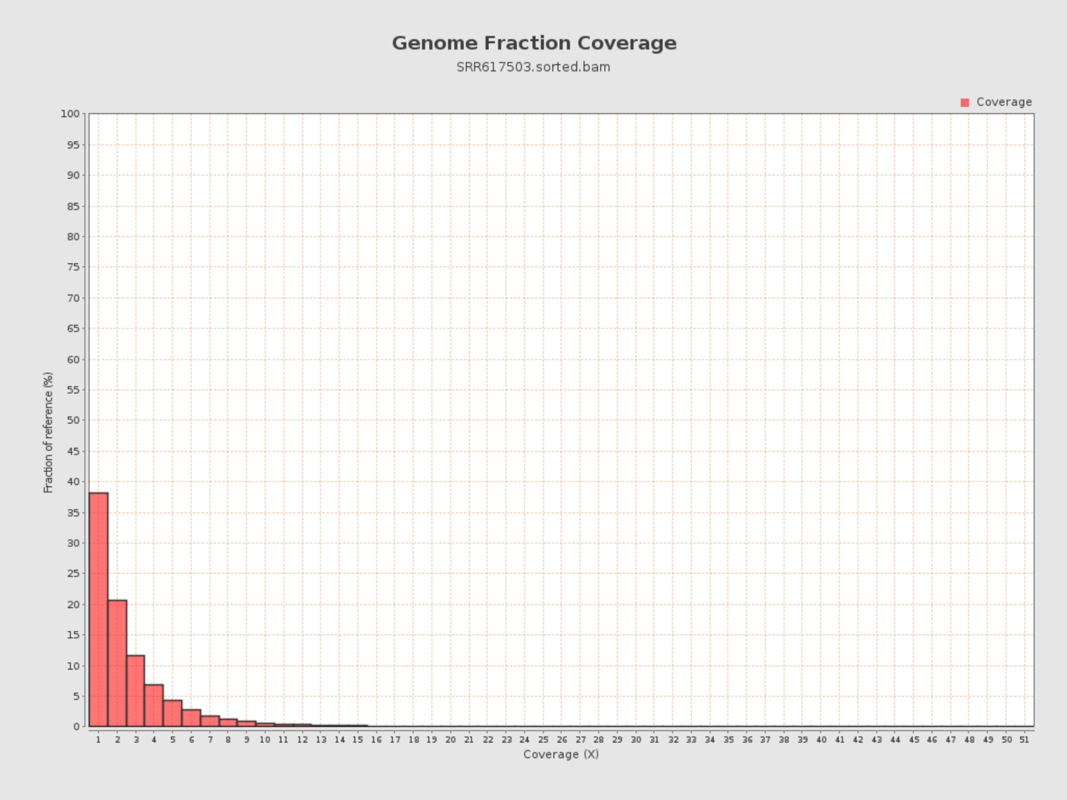
4. Results : Coverage Histogram



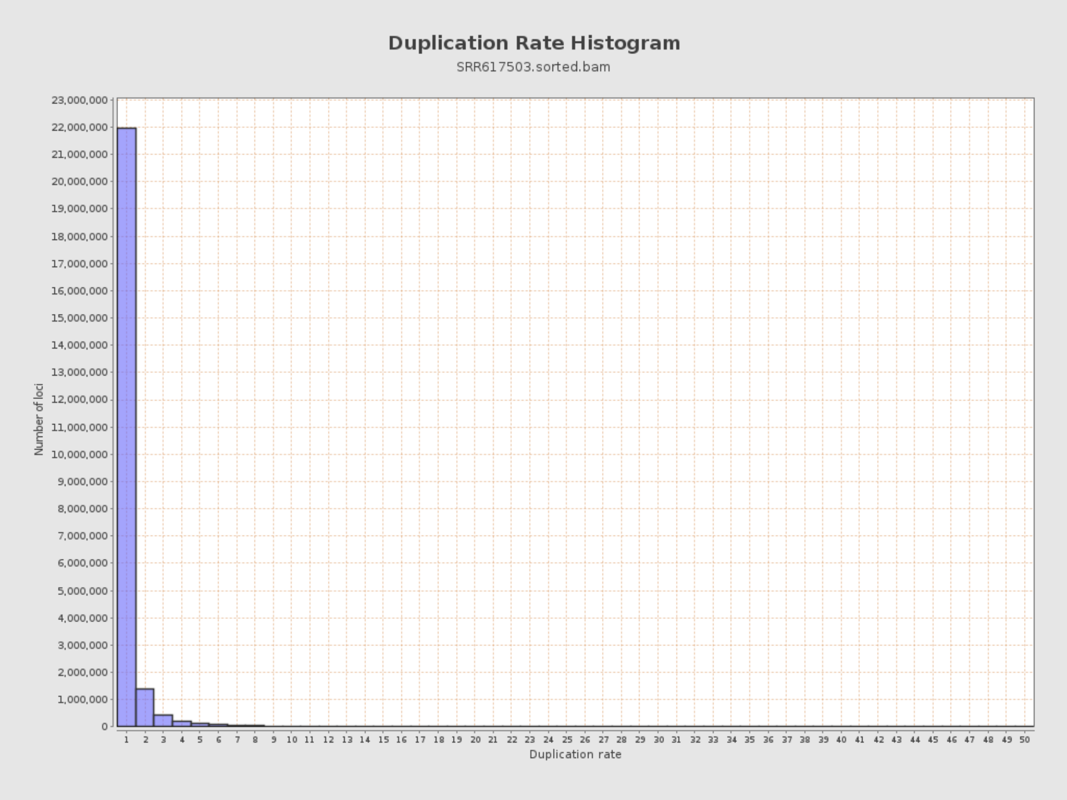
5. Results : Coverage Histogram (0-50X)



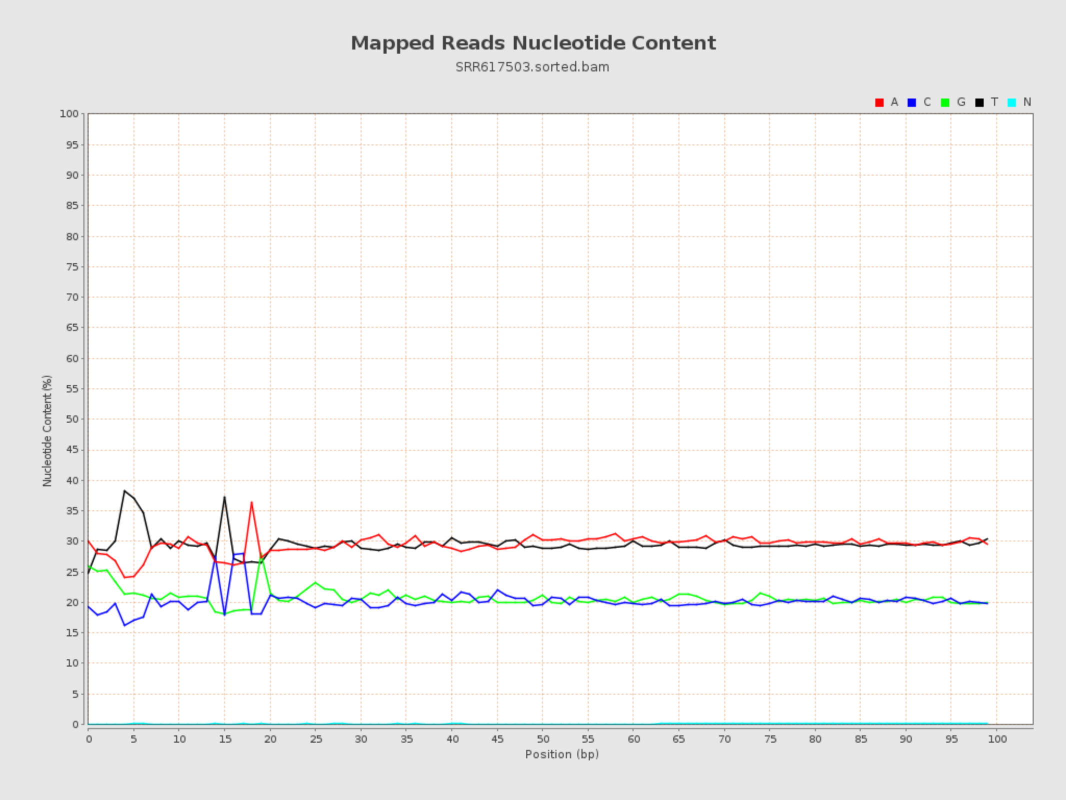
6. Results : Genome Fraction Coverage



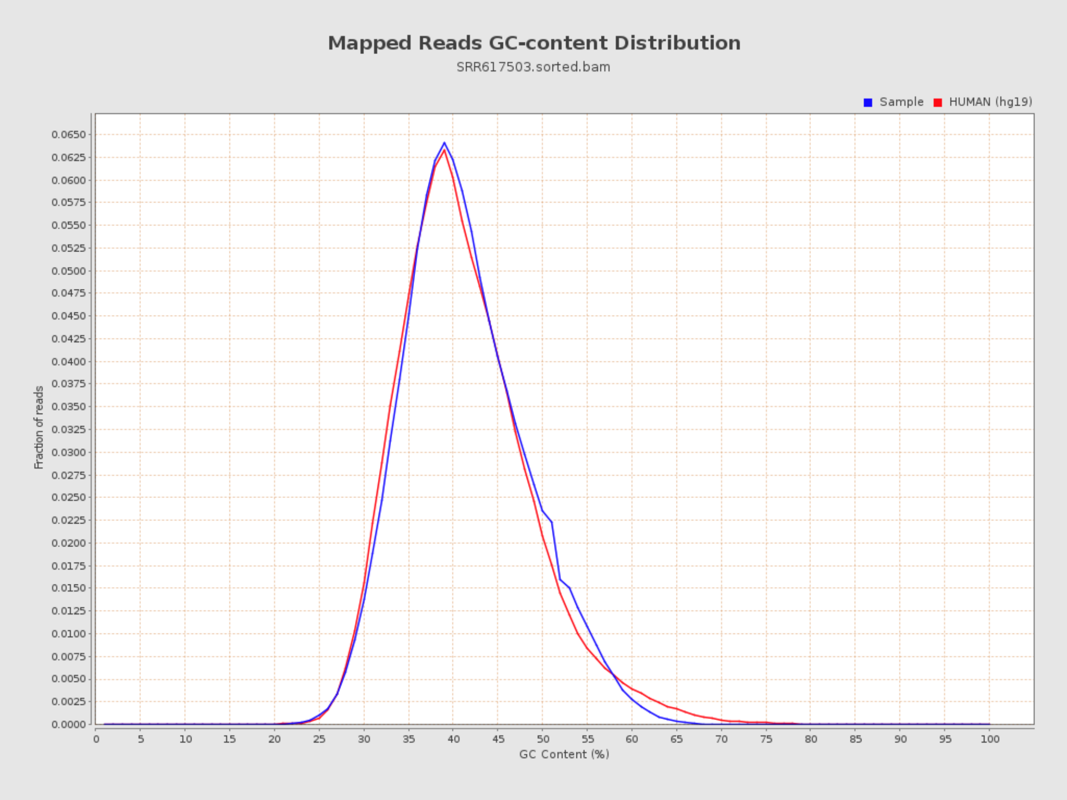
7. Results : Duplication Rate Histogram



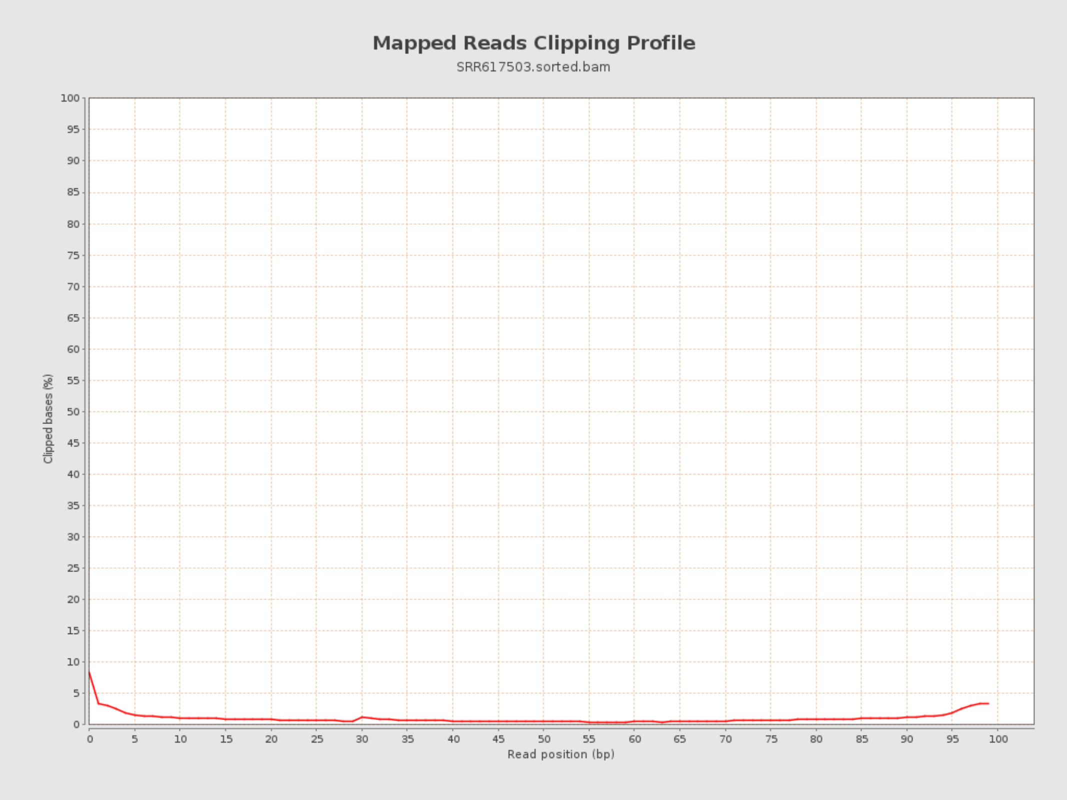
8. Results : Mapped Reads Nucleotide Content



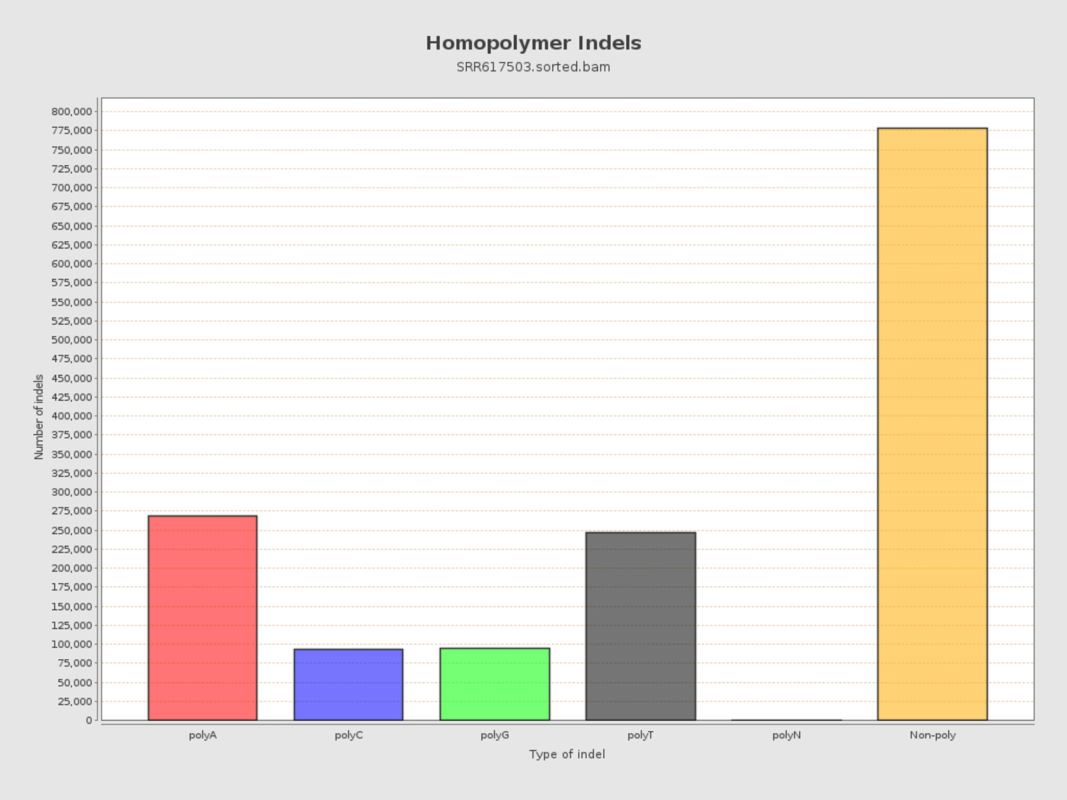
9. Results : Mapped Reads GC-content Distribution



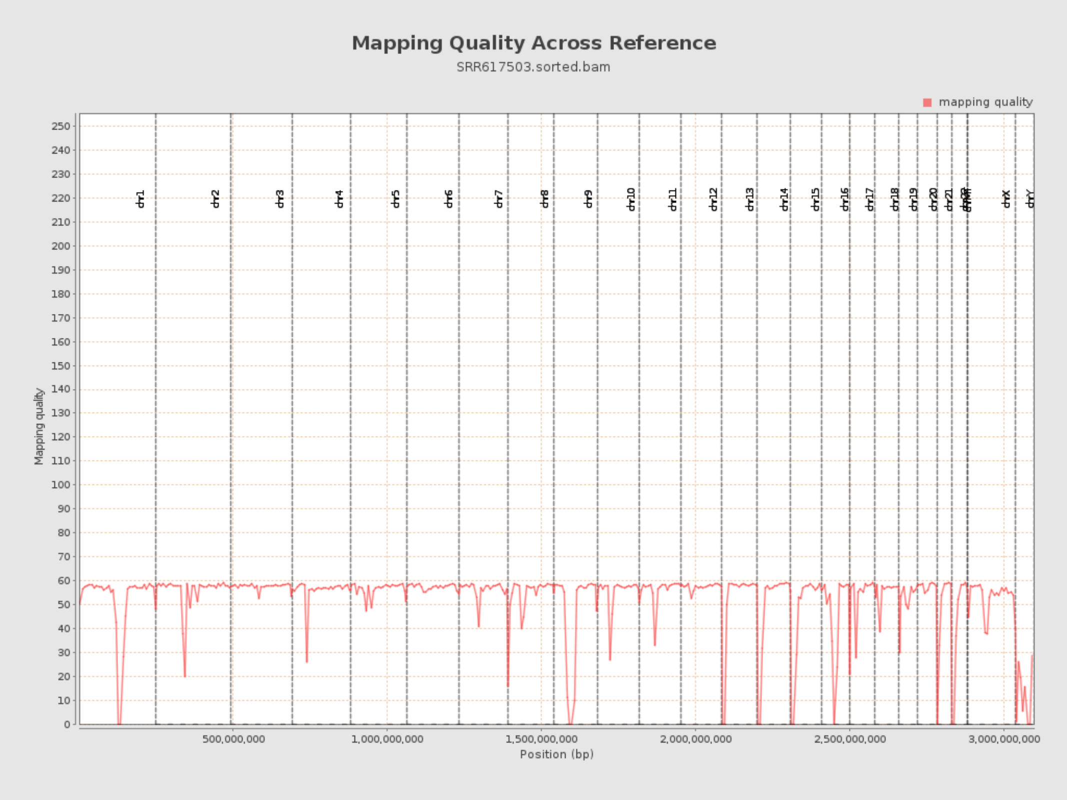
10. Results : Mapped Reads Clipping Profile



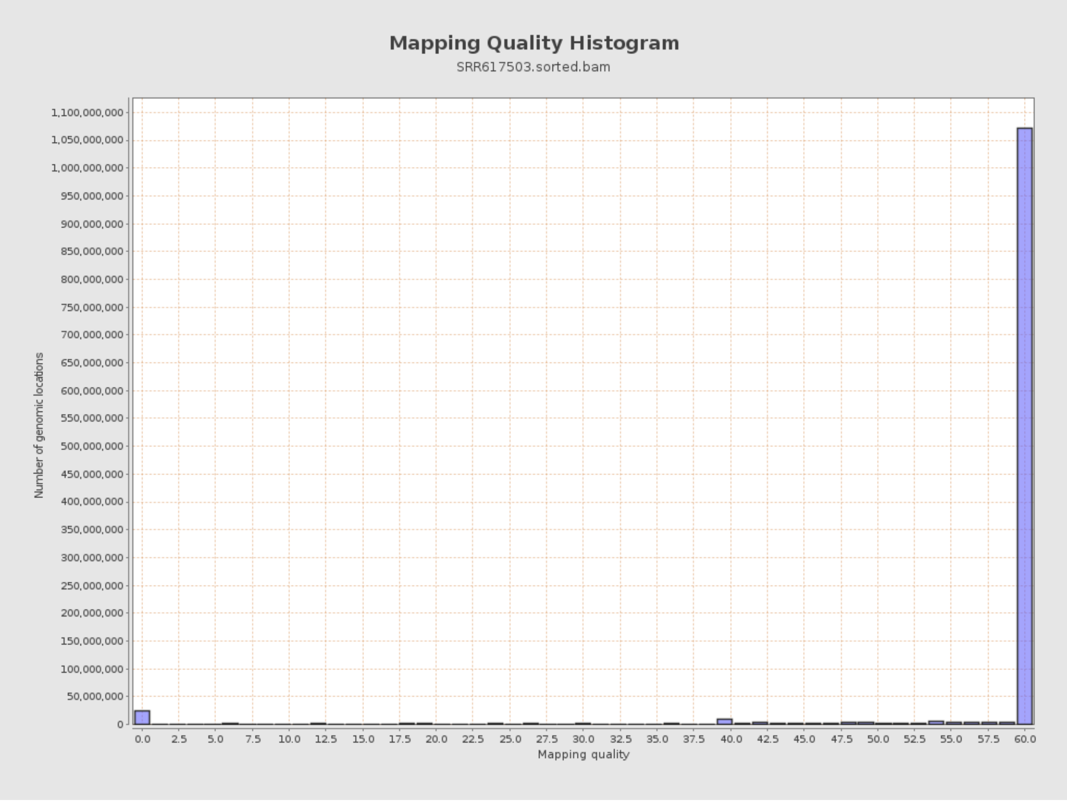
11. Results : Homopolymer Indels



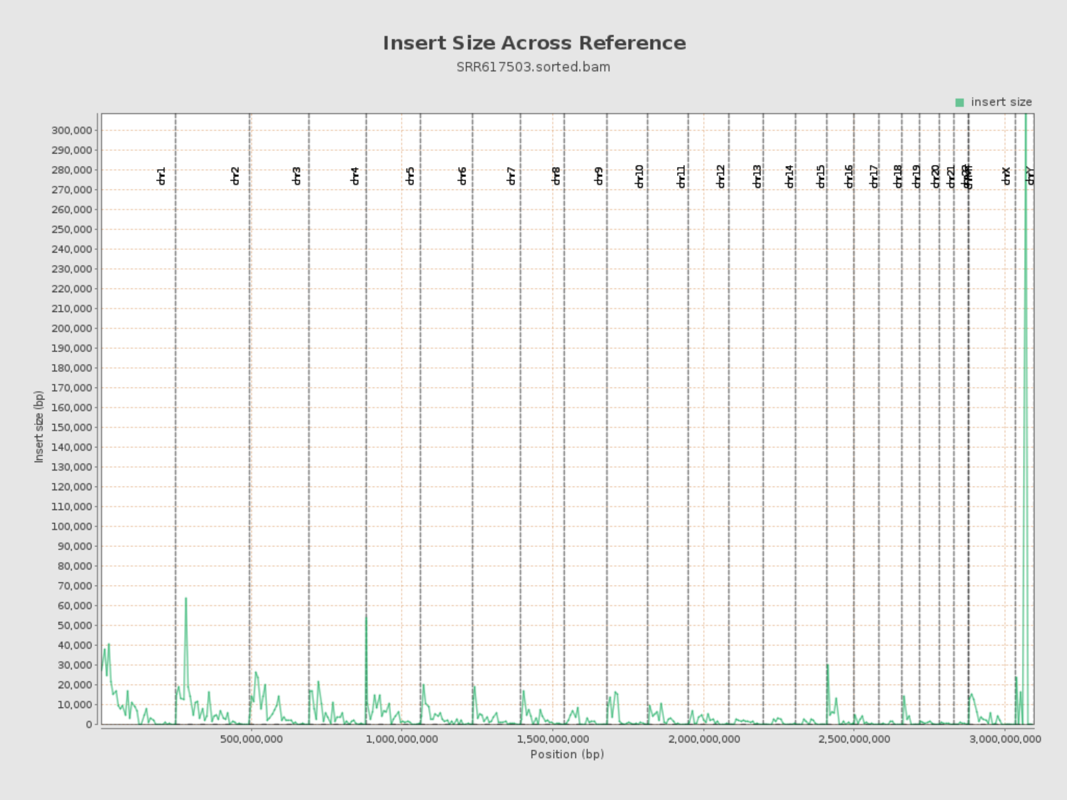
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram