Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/10 02:08:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617502.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_SRR617502 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617502_1.fastq.gz SRR617502_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 10 02:08:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617502.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	30,208,719 / 94.4%
Unmapped reads	1,791,281 / 5.6%
Mapped paired reads	30,208,719 / 94.4%
Mapped reads, first in pair	15,264,099 / 47.7%
Mapped reads, second in pair	14,944,620 / 46.7%
Mapped reads, both in pair	29,559,310 / 92.37%
Mapped reads, singletons	649,409 / 2.03%
Secondary alignments	0
Supplementary alignments	175,153 / 0.55%
Read min/max/mean length	30 / 100 / 100.21
Duplicated reads (estimated)	6,206,990 / 19.4%
Duplication rate	9.94%
Clipped reads	6,215,949 / 19.42%

2.2. ACGT Content

Number/percentage of A's	865,396,087 / 29.52%
Number/percentage of C's	591,540,326 / 20.18%
Number/percentage of T's	865,028,626 / 29.51%
Number/percentage of G's	606,639,546 / 20.69%
Number/percentage of N's	3,012,732 / 0.1%

GC Percentage	40.87%

2.3. Coverage

Mean	0.9476
Standard Deviation	9.5099

2.4. Mapping Quality

Mean Mapping Quality	52.62

2.5. Insert size

Mean	48,683.66
Standard Deviation	2,082,880.04
P25/Median/P75	174 / 220 / 292

2.6. Mismatches and indels

General error rate	1.26%
Mismatches	36,025,261
Insertions	439,623
Mapped reads with at least one insertion	1.43%
Deletions	1,020,321
Mapped reads with at least one deletion	3.31%
Homopolymer indels	47.36%

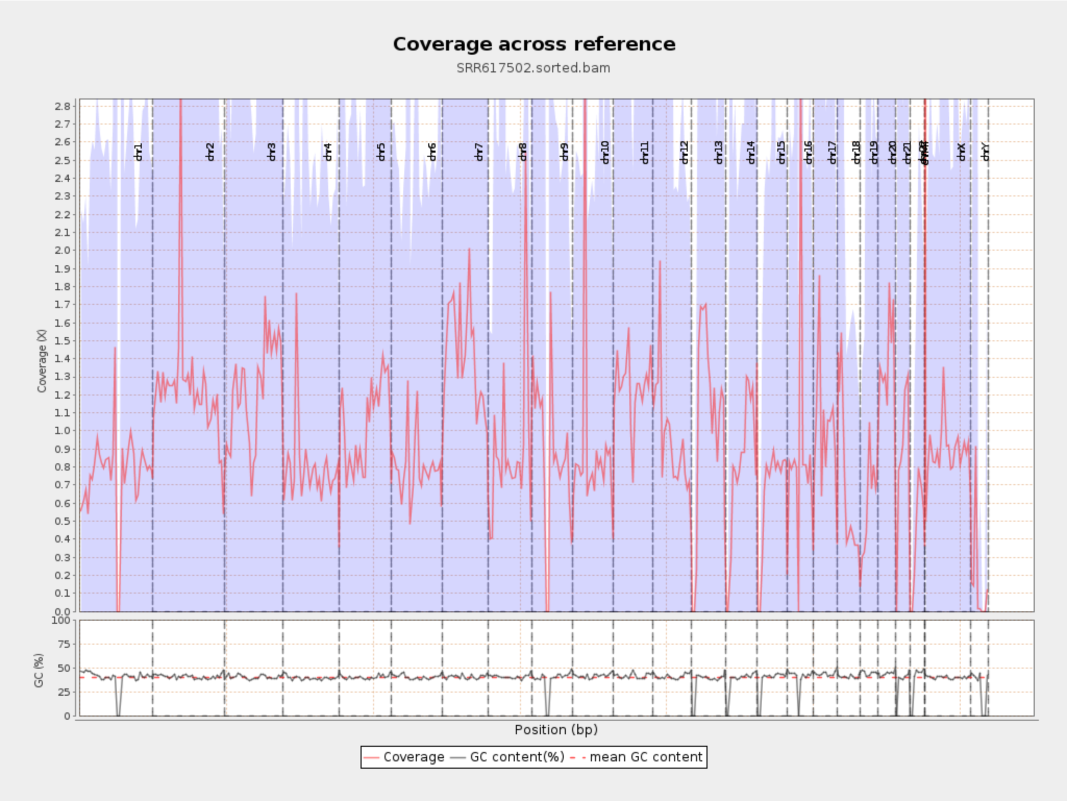
2.7. Chromosome stats

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

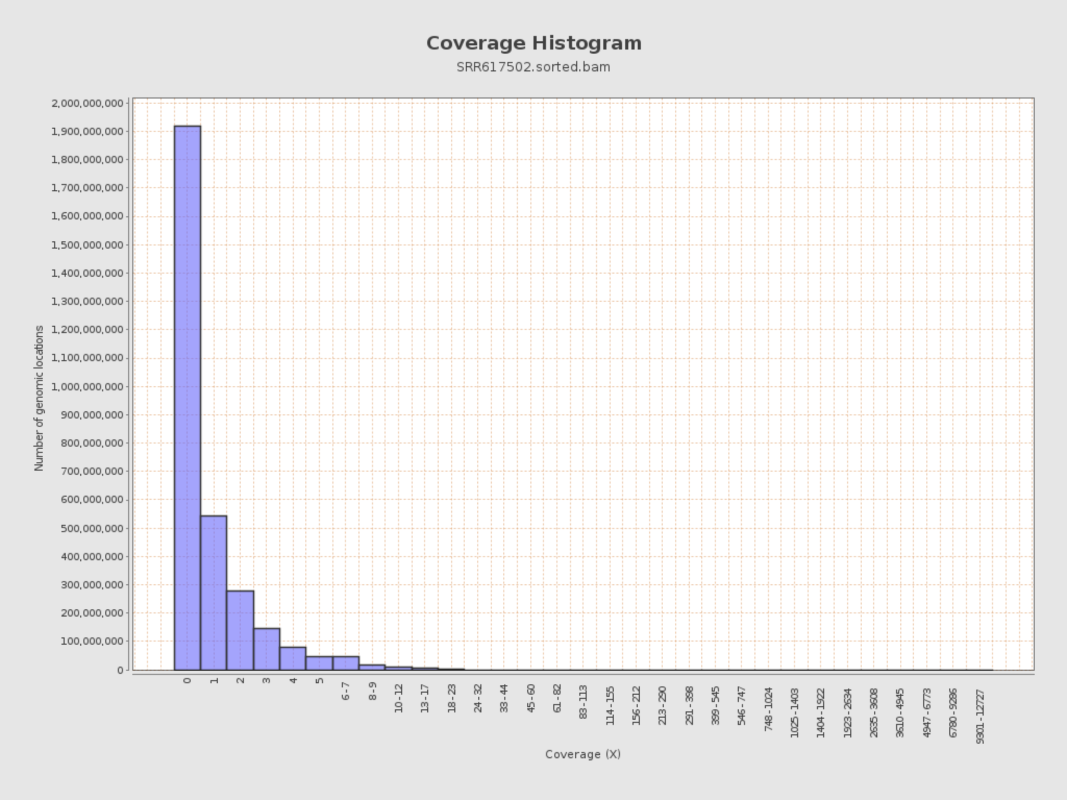
		bases	coverage	deviation
chr1	249250621	188972724	0.7582	9.2573
chr2	243199373	302944774	1.2457	11.2403
chr3	198022430	241951046	1.2218	2.2375
chr4	191154276	151662467	0.7934	5.9901
chr5	180915260	187815525	1.0381	2.0683
chr6	171115067	138226023	0.8078	5.2252
chr7	159138663	226072922	1.4206	12.999
chr8	146364022	130393753	0.8909	3.831
chr9	141213431	121400867	0.8597	17.9023
chr10	135534747	124544183	0.9189	18.4141
chr11	135006516	165286057	1.2243	12.3655
chr12	133851895	128418695	0.9594	2.086
chr13	115169878	124712669	1.0829	2.1626
chr14	107349540	85404861	0.7956	2.2055
chr15	102531392	66501624	0.6486	1.6456
chr16	90354753	79144638	0.8759	14.5983
chr17	81195210	81832604	1.0079	13.1858
chr18	78077248	52585399	0.6735	16.6181
chr19	59128983	35075908	0.5932	5.5509
chr20	63025520	86582268	1.3738	2.7674
chr21	48129895	42105618	0.8748	3.7184
chr22	51304566	21998899	0.4288	1.2519
chrMT	16571	2071193	124.989	91.382
chrX	155270560	137498483	0.8855	4.0415

chrY	59373566	10154927	0.171	13.4004

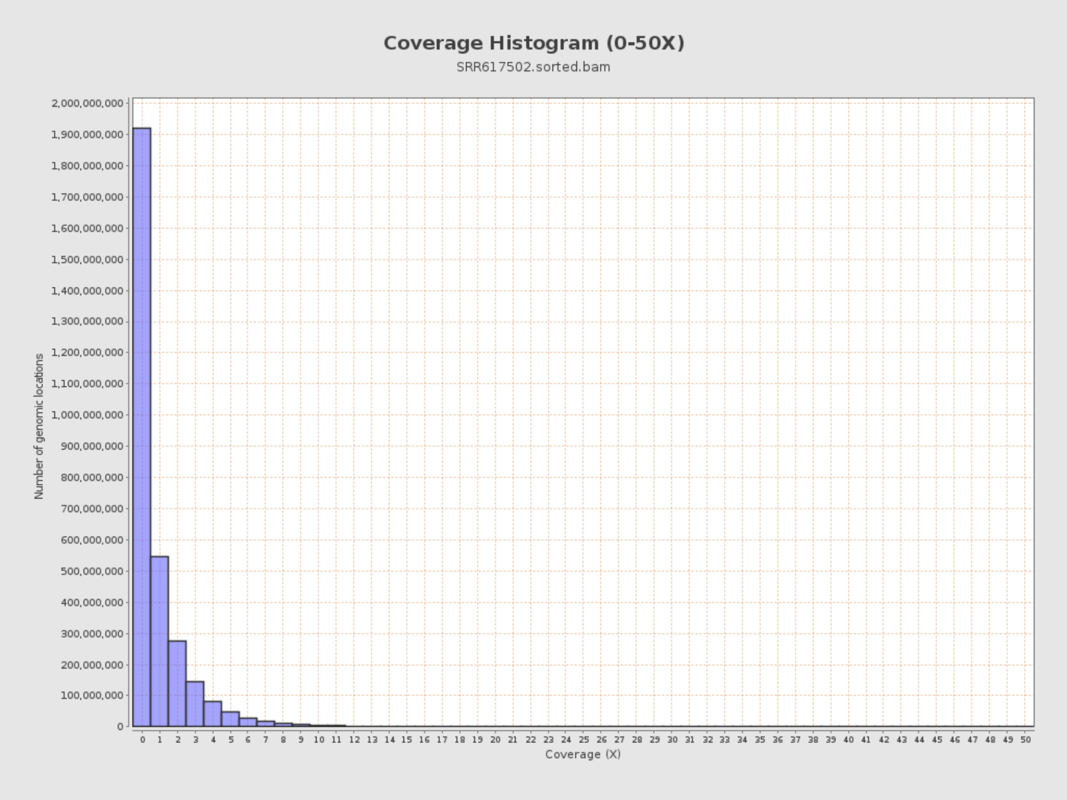
3. Results : Coverage across reference



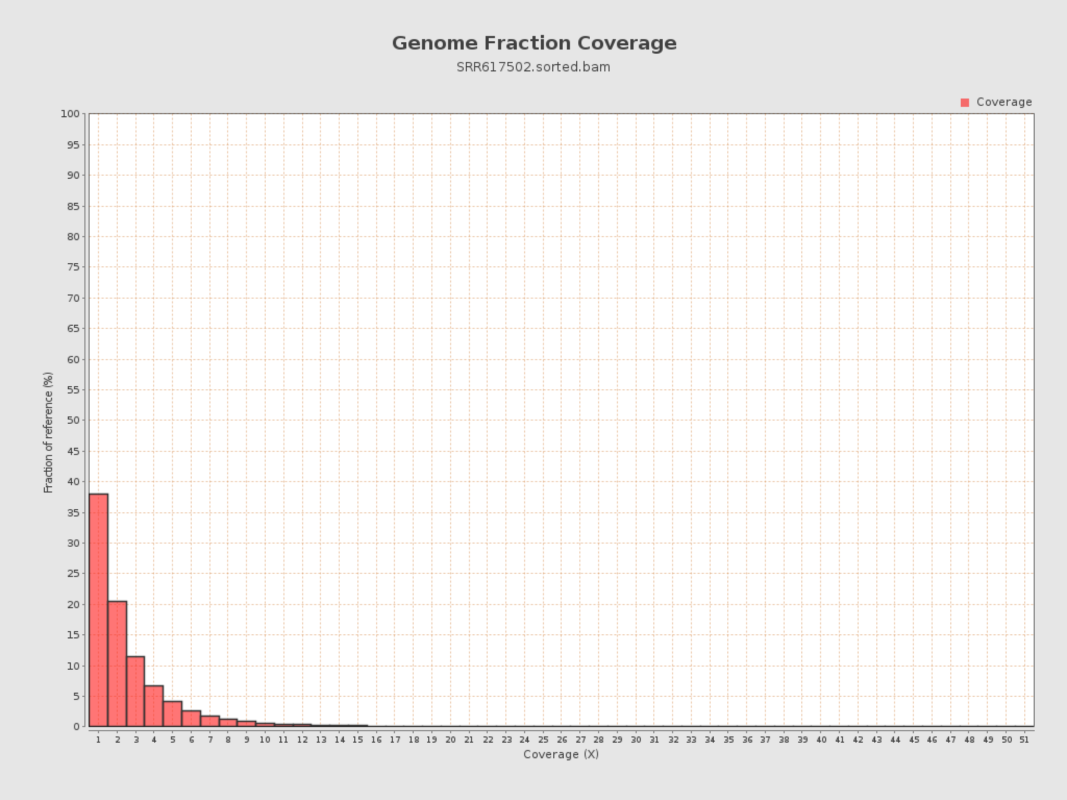
4. Results : Coverage Histogram



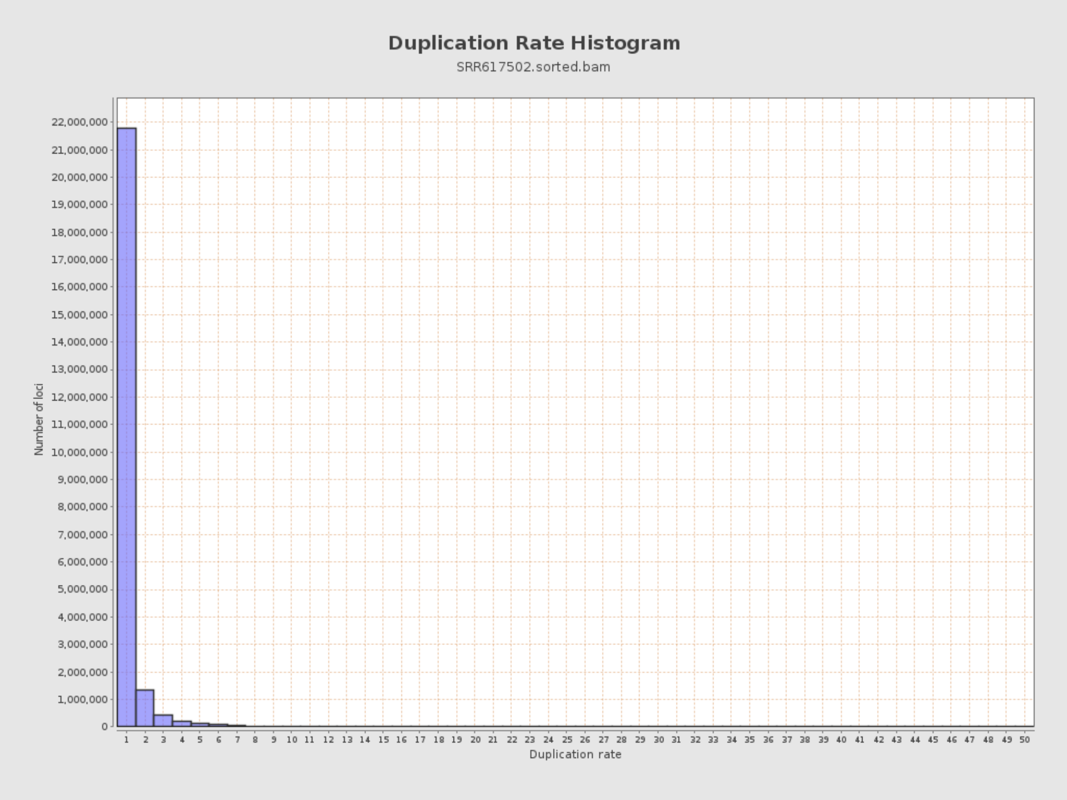
5. Results : Coverage Histogram (0-50X)



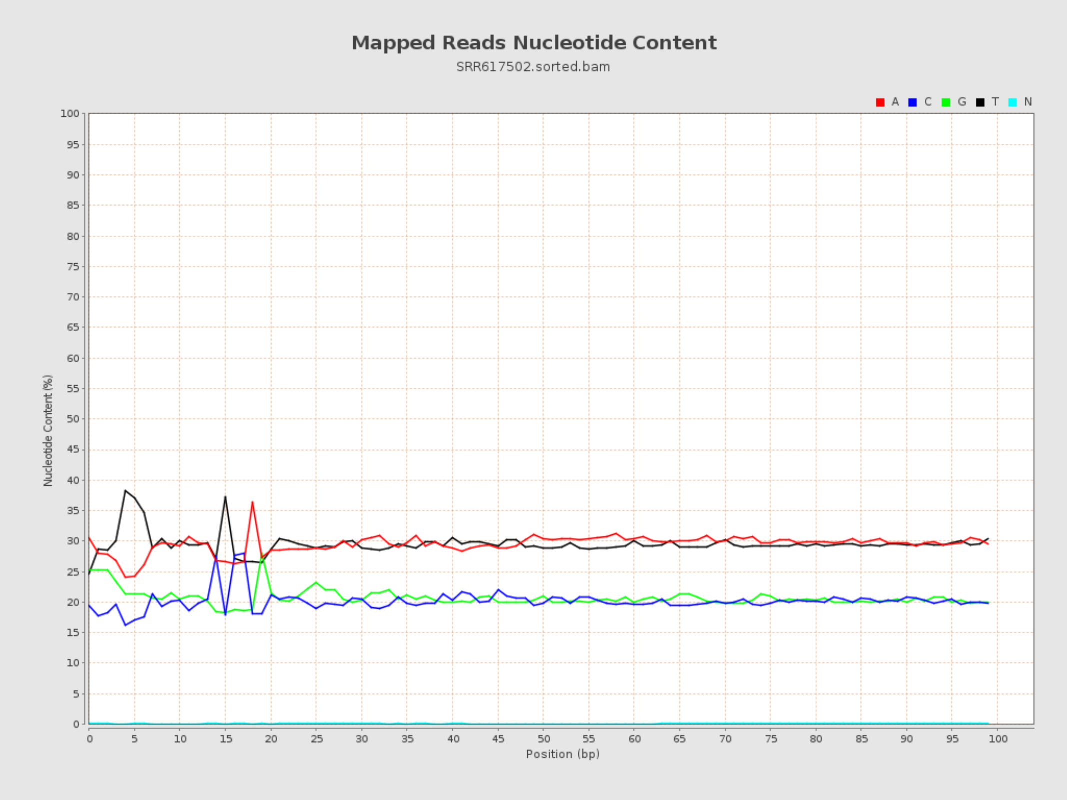
6. Results : Genome Fraction Coverage



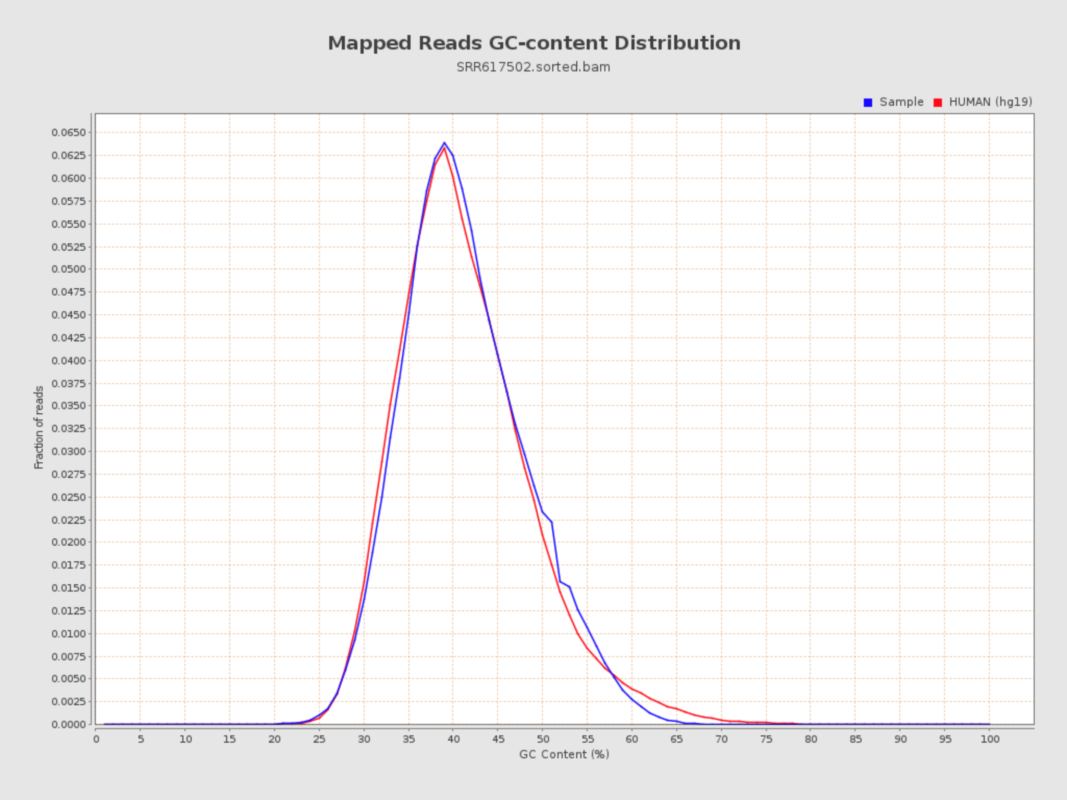
7. Results : Duplication Rate Histogram



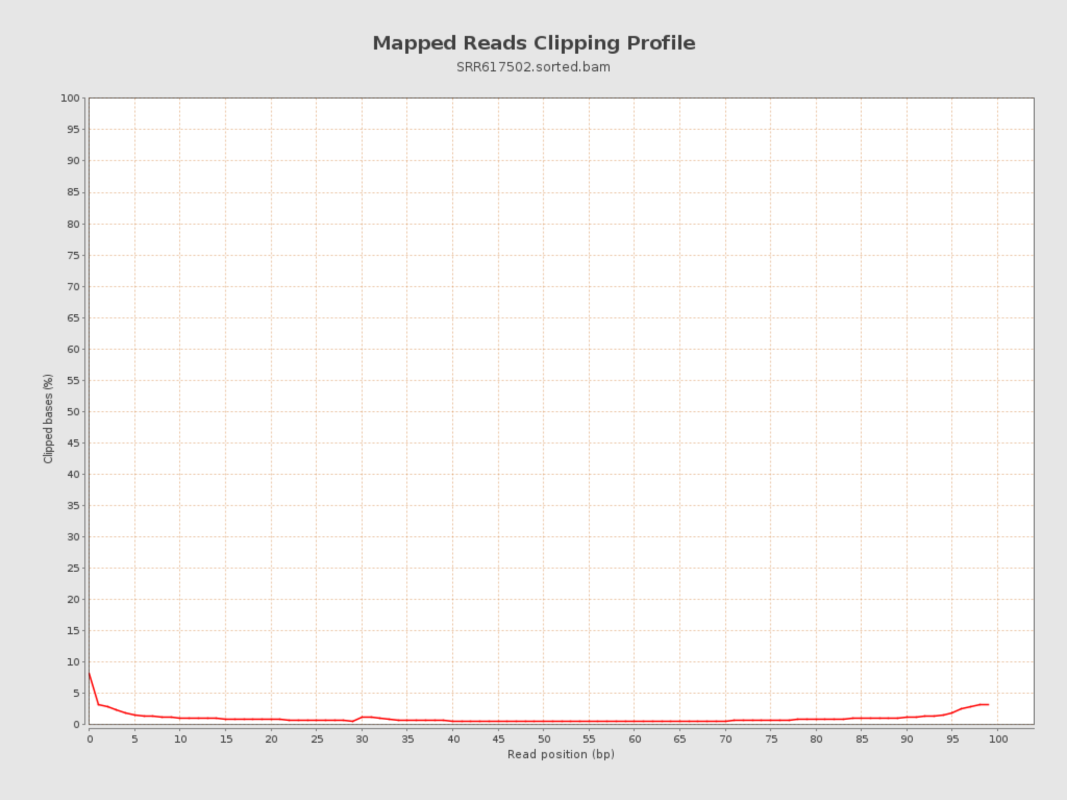
8. Results : Mapped Reads Nucleotide Content



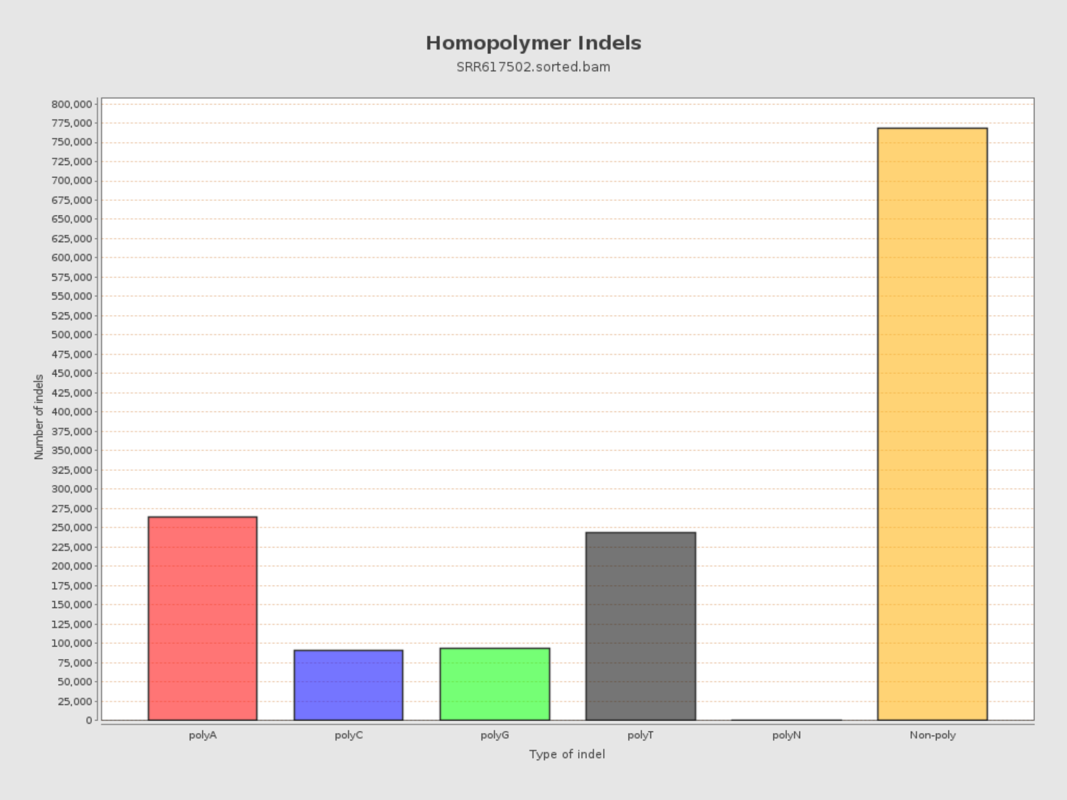
9. Results : Mapped Reads GC-content Distribution



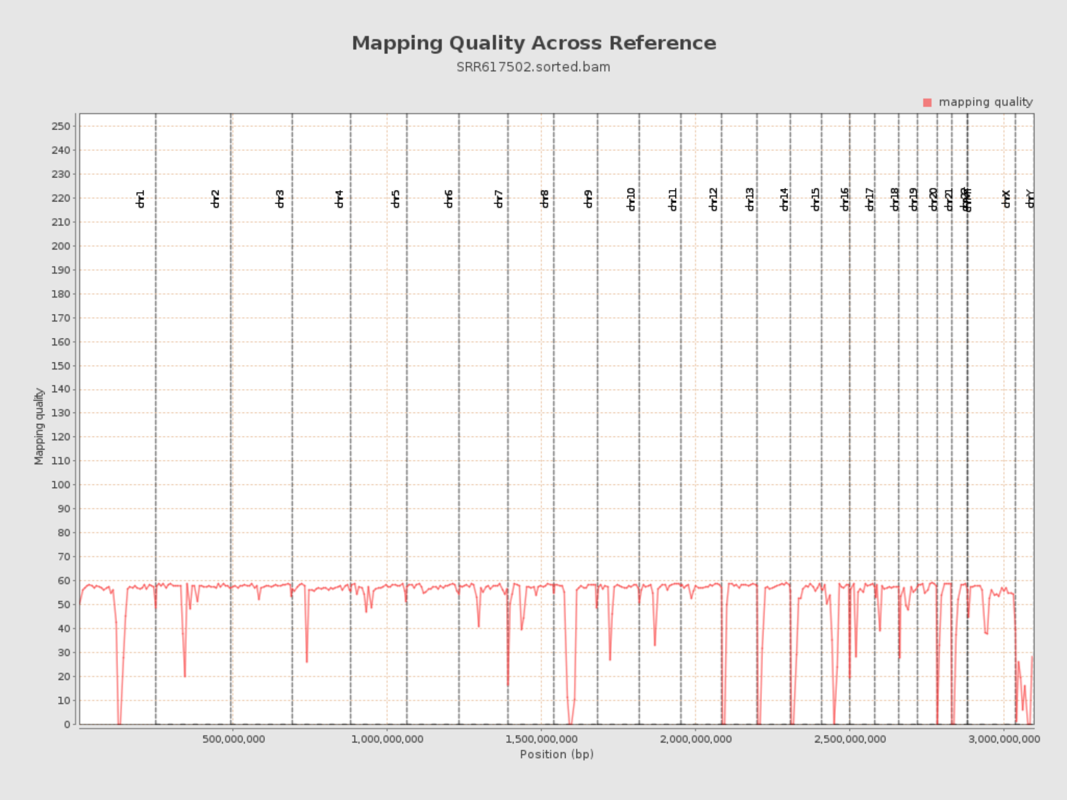
10. Results : Mapped Reads Clipping Profile



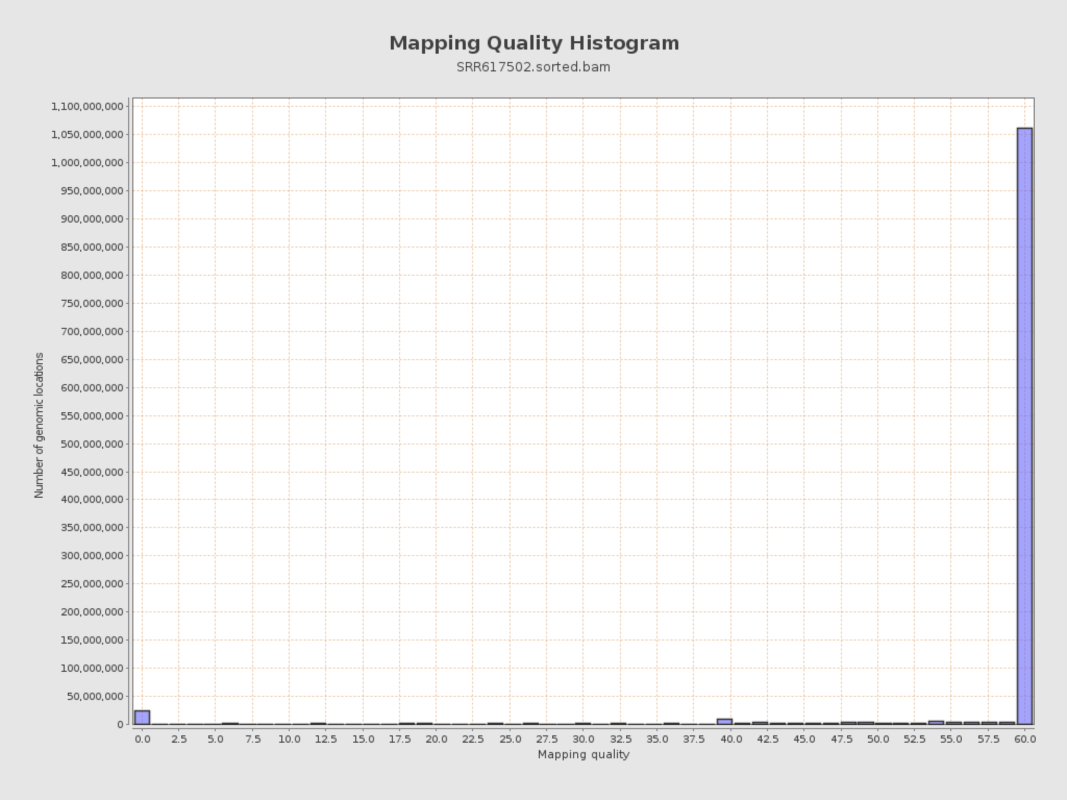
11. Results : Homopolymer Indels



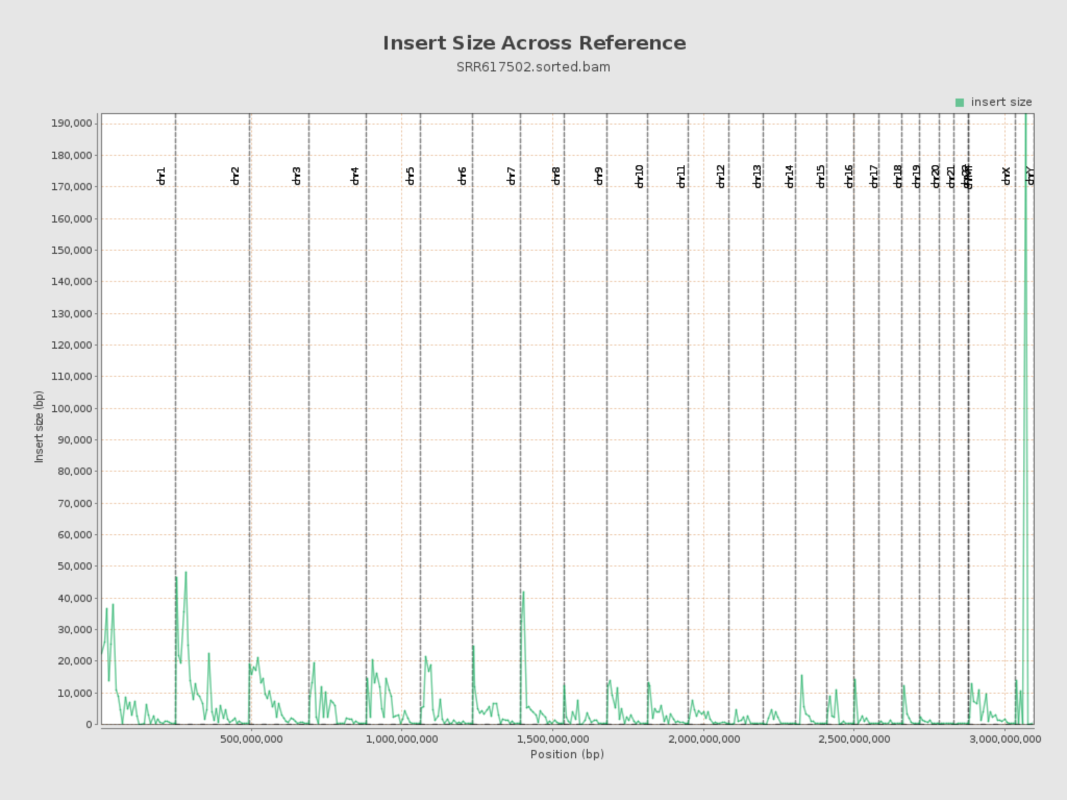
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram