Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/07 19:44:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617377.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_SRR617377 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617377_1.fastq.gz SRR617377_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Oct 07 19:44:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617377.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	30,478,284 / 95.24%
Unmapped reads	1,521,716 / 4.76%
Mapped paired reads	30,478,284 / 95.24%
Mapped reads, first in pair	15,300,521 / 47.81%
Mapped reads, second in pair	15,177,763 / 47.43%
Mapped reads, both in pair	30,045,148 / 93.89%
Mapped reads, singletons	433,136 / 1.35%
Secondary alignments	0
Supplementary alignments	67,099 / 0.21%
Read min/max/mean length	30 / 100 / 100.08
Duplicated reads (estimated)	1,578,545 / 4.93%
Duplication rate	1.48%
Clipped reads	2,337,745 / 7.31%

2.2. ACGT Content

Number/percentage of A's	906,401,540 / 30.27%
Number/percentage of C's	594,366,732 / 19.85%
Number/percentage of T's	894,663,979 / 29.88%
Number/percentage of G's	597,624,509 / 19.96%
Number/percentage of N's	1,491,265 / 0.05%

GC Percentage	39.81%

2.3. Coverage

Mean	0.9676
Standard Deviation	9.8549

2.4. Mapping Quality

Mean Mapping Quality	53.5

2.5. Insert size

Mean	54,303.5
Standard Deviation	2,218,935.35
P25/Median/P75	173 / 214 / 279

2.6. Mismatches and indels

General error rate	1.06%
Mismatches	30,998,173
Insertions	300,461
Mapped reads with at least one insertion	0.96%
Deletions	365,056
Mapped reads with at least one deletion	1.16%
Homopolymer indels	41.26%

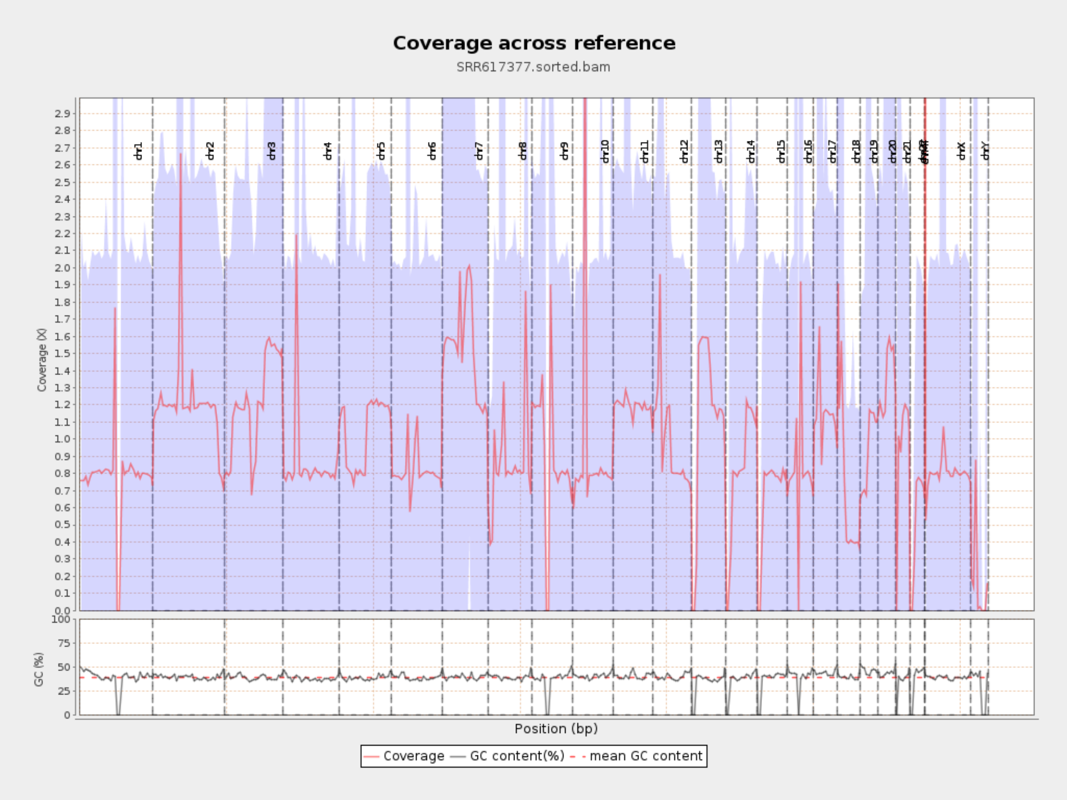
2.7. Chromosome stats

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

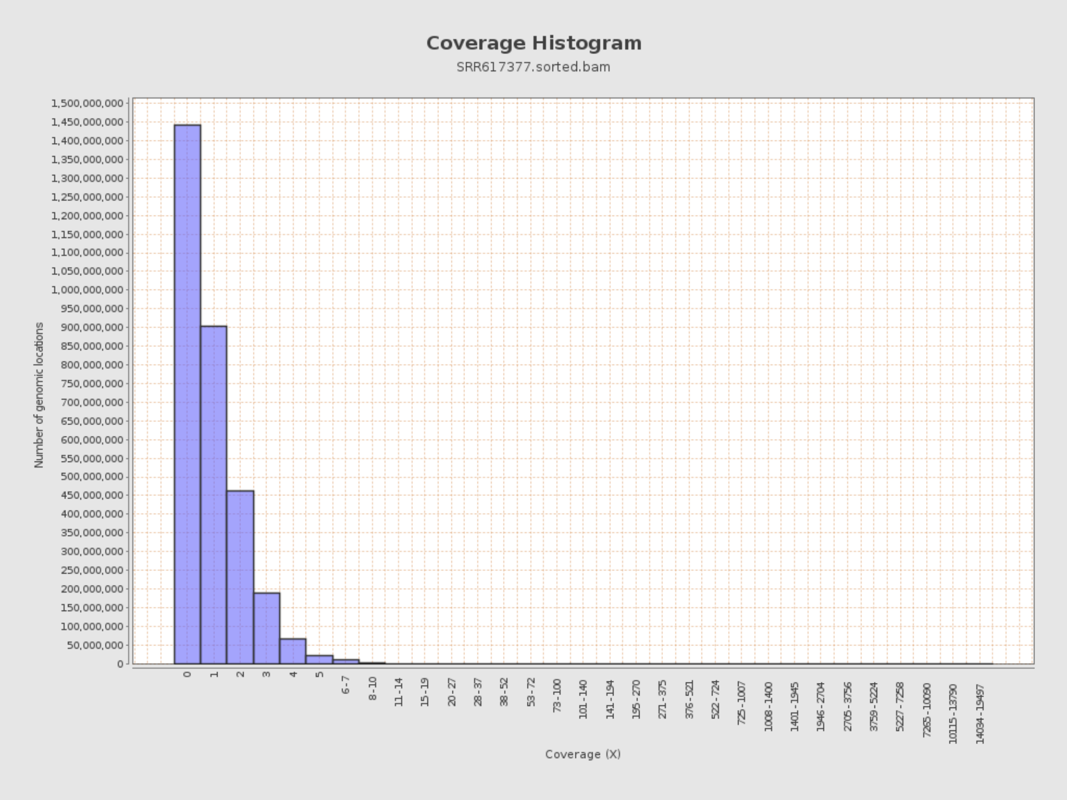
		bases	coverage	deviation
chr1	249250621	194607934	0.7808	19.9431
chr2	243199373	295456655	1.2149	8.8989
chr3	198022430	238431472	1.2041	1.4677
chr4	191154276	164019211	0.858	9.5232
chr5	180915260	188188568	1.0402	1.4705
chr6	171115067	140387859	0.8204	3.7564
chr7	159138663	243542121	1.5304	10.9919
chr8	146364022	126265283	0.8627	7.77
chr9	141213431	126201317	0.8937	15.0571
chr10	135534747	126065192	0.9301	20.2815
chr11	135006516	160972576	1.1923	5.5633
chr12	133851895	132160208	0.9874	1.3478
chr13	115169878	130449455	1.1327	1.2998
chr14	107349540	86629439	0.807	1.3903
chr15	102531392	67210979	0.6555	0.9785
chr16	90354753	75307547	0.8335	7.9702
chr17	81195210	93083460	1.1464	7.1667
chr18	78077248	54244605	0.6948	15.4814
chr19	59128983	55561552	0.9397	9.4311
chr20	63025520	85720397	1.3601	2.4677
chr21	48129895	47449023	0.9859	3.264
chr22	51304566	26683612	0.5201	0.9274
chrMT	16571	2034403	122.7689	18.8161
chrX	155270560	124507035	0.8019	3.0024

chrY	59373566	10250697	0.1726	8.4823

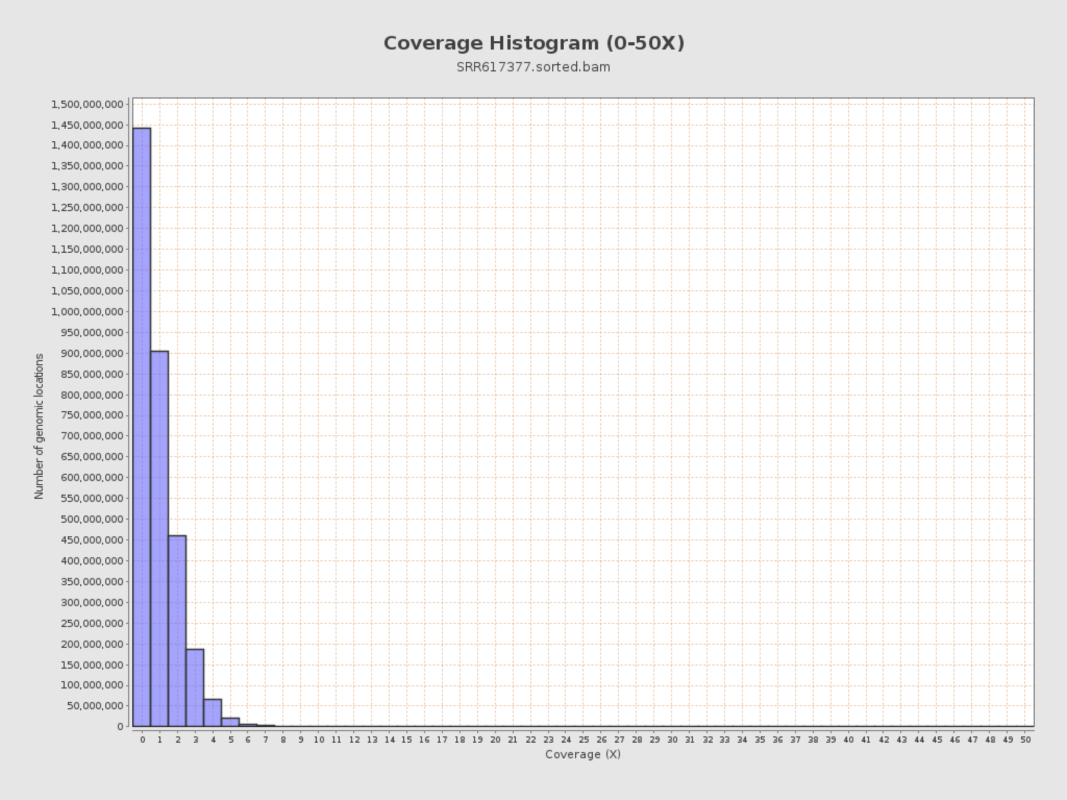
3. Results : Coverage across reference



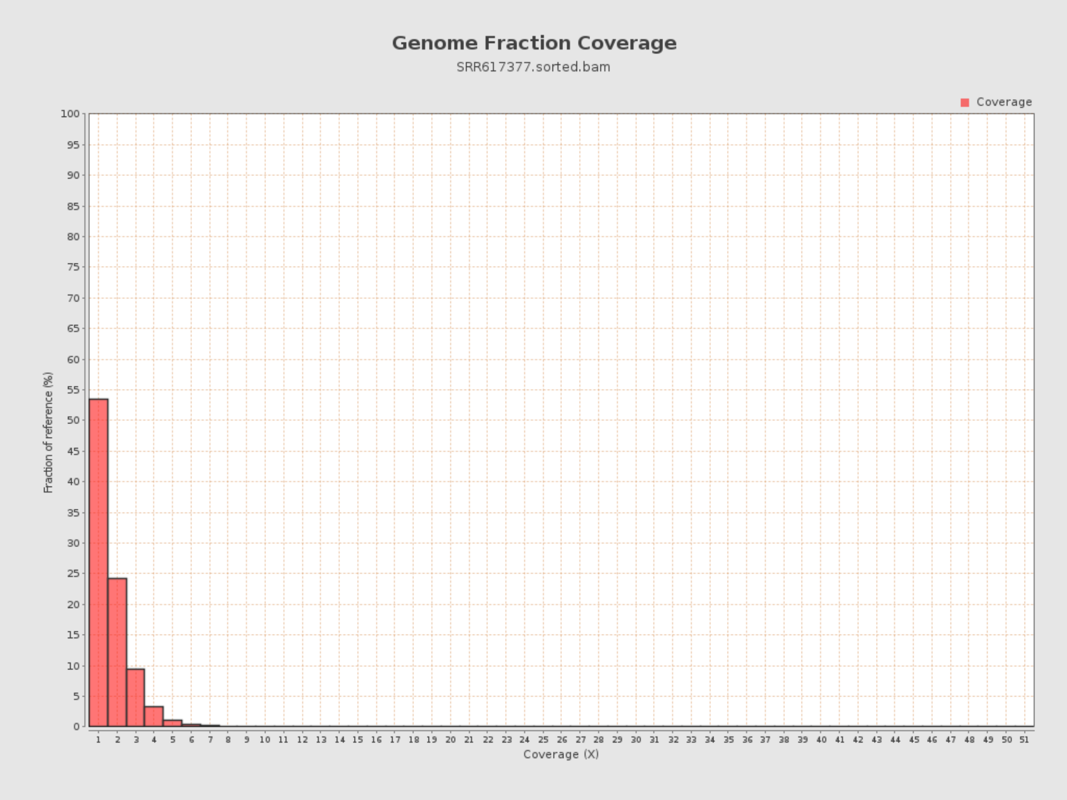
4. Results : Coverage Histogram



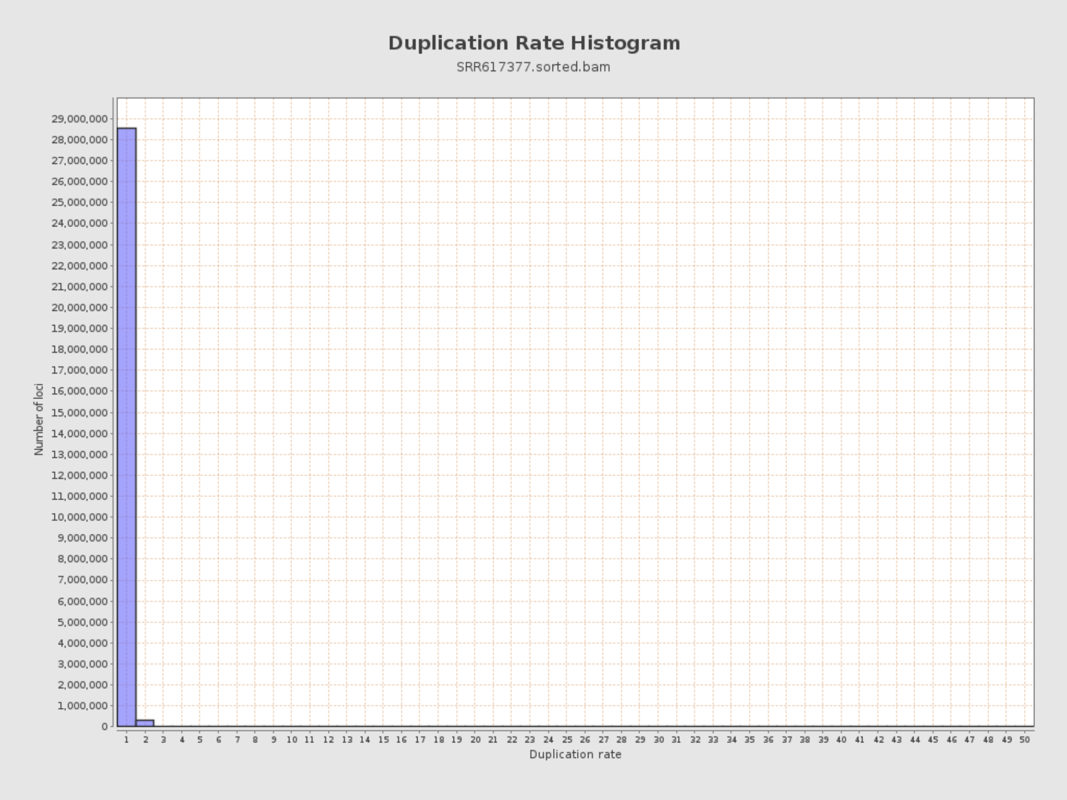
5. Results : Coverage Histogram (0-50X)



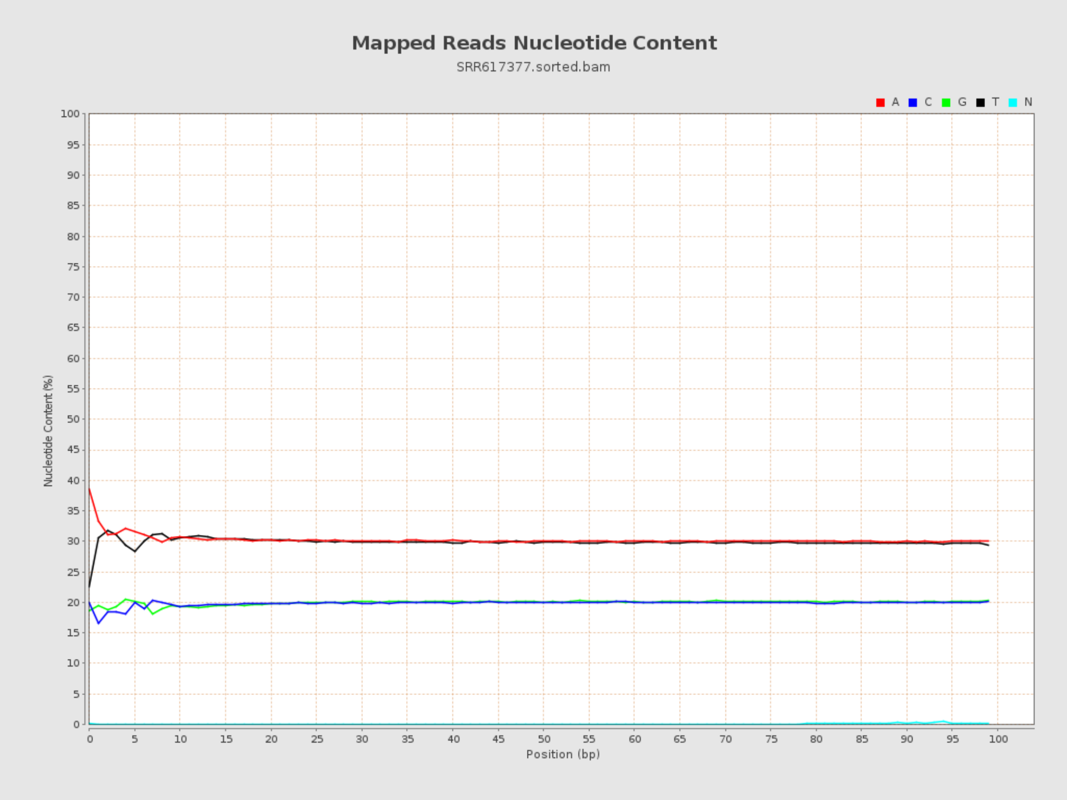
6. Results : Genome Fraction Coverage



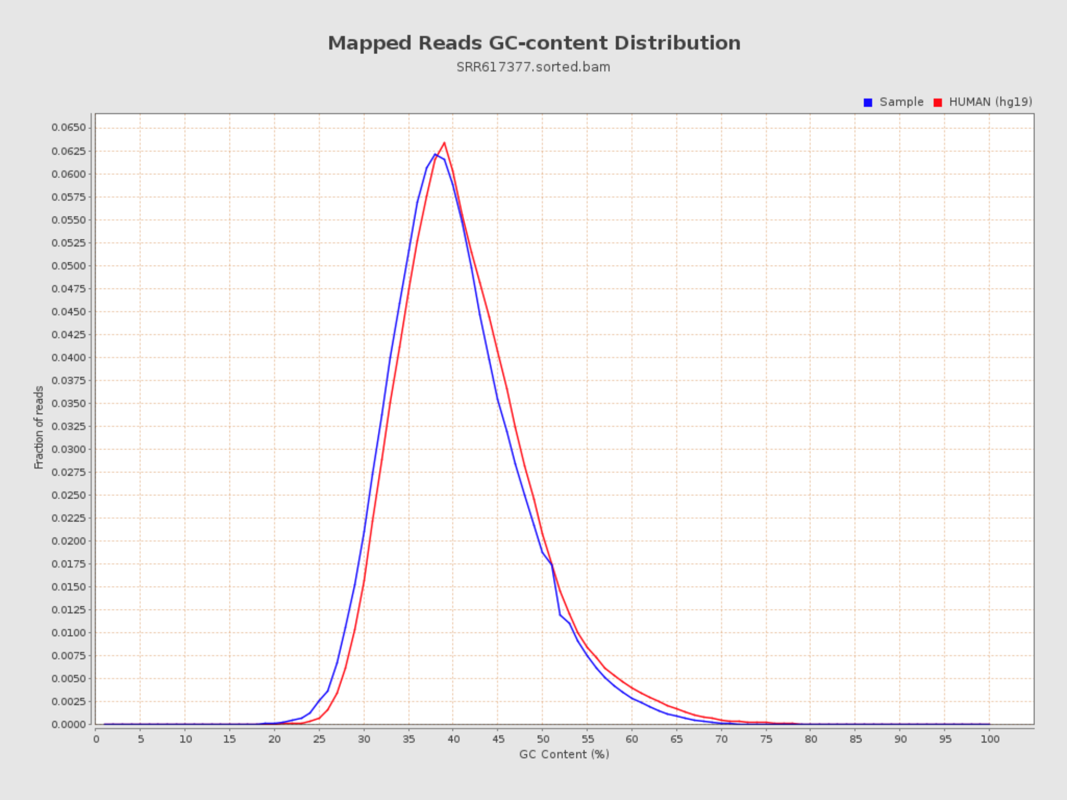
7. Results : Duplication Rate Histogram



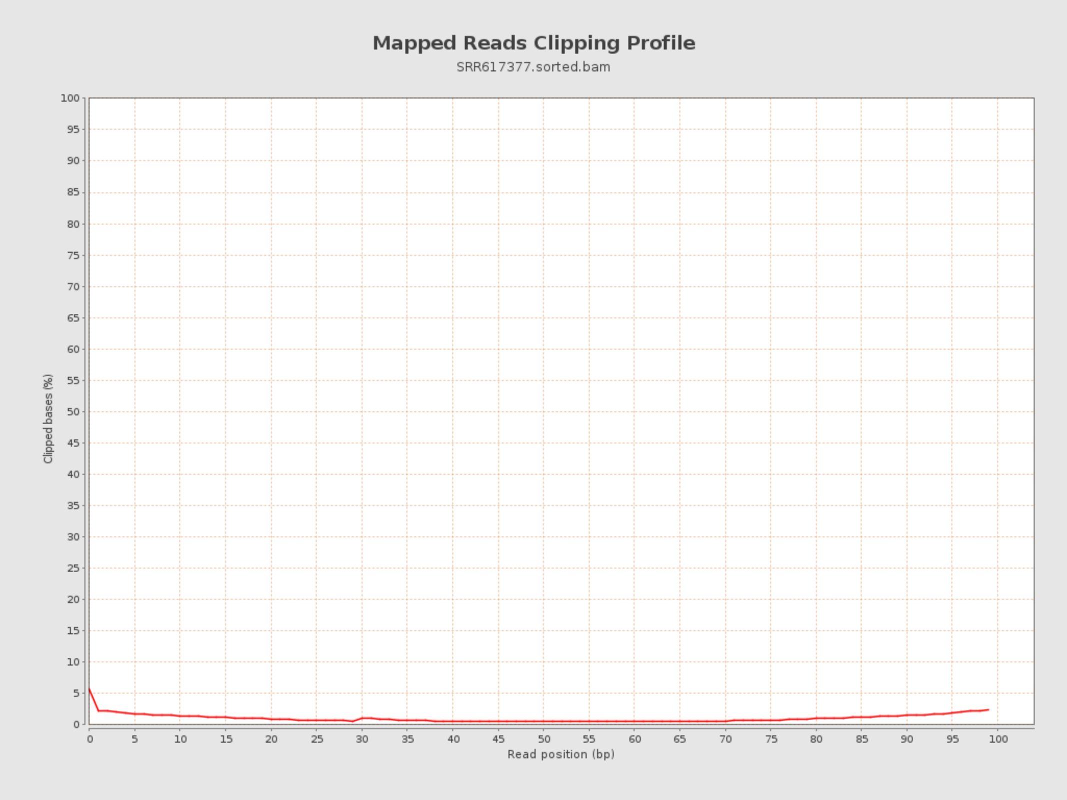
8. Results : Mapped Reads Nucleotide Content



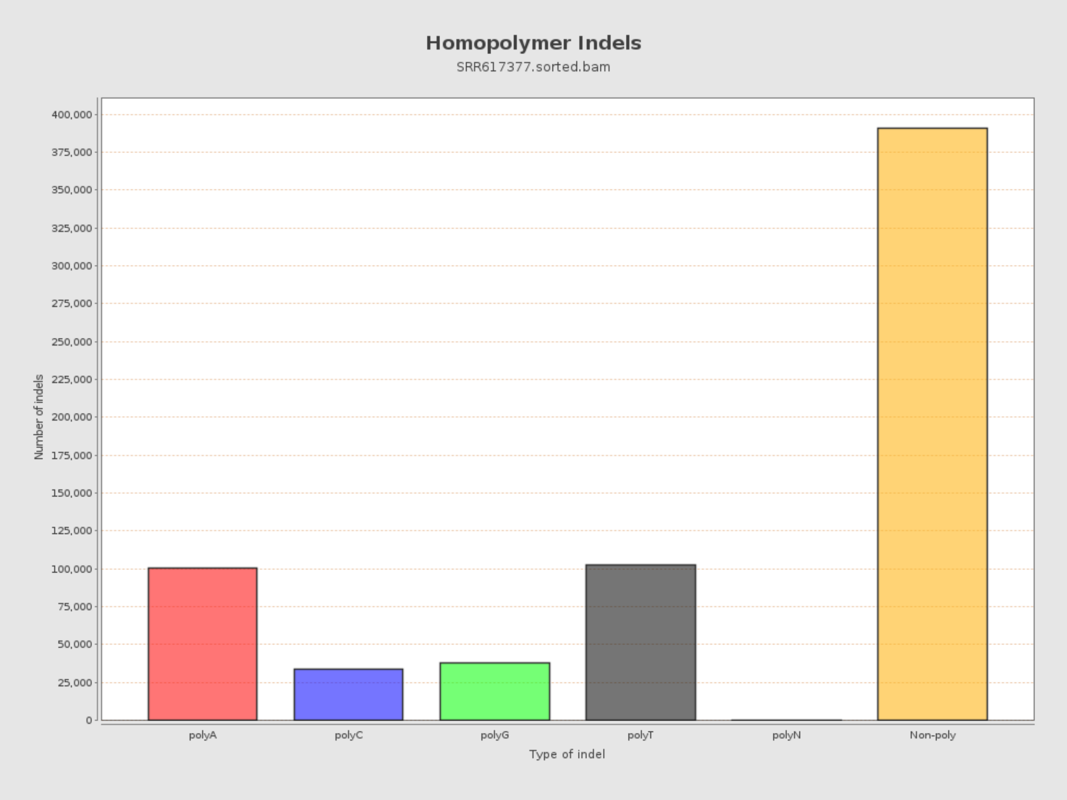
9. Results : Mapped Reads GC-content Distribution



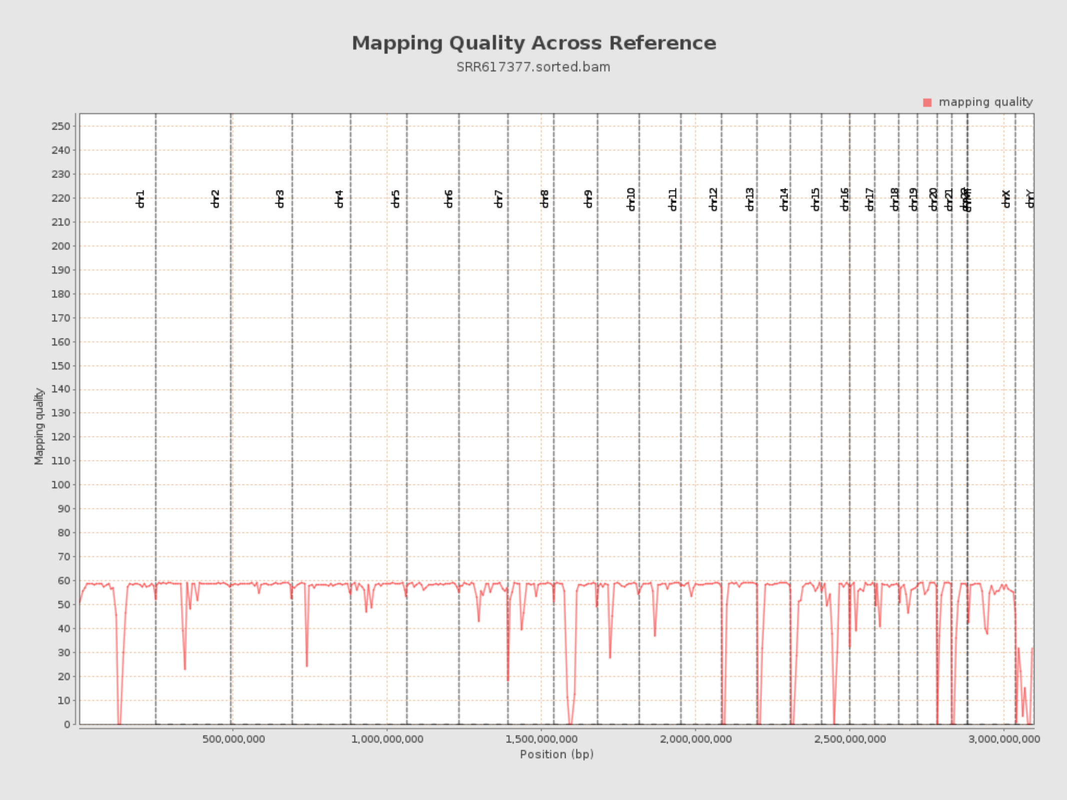
10. Results : Mapped Reads Clipping Profile



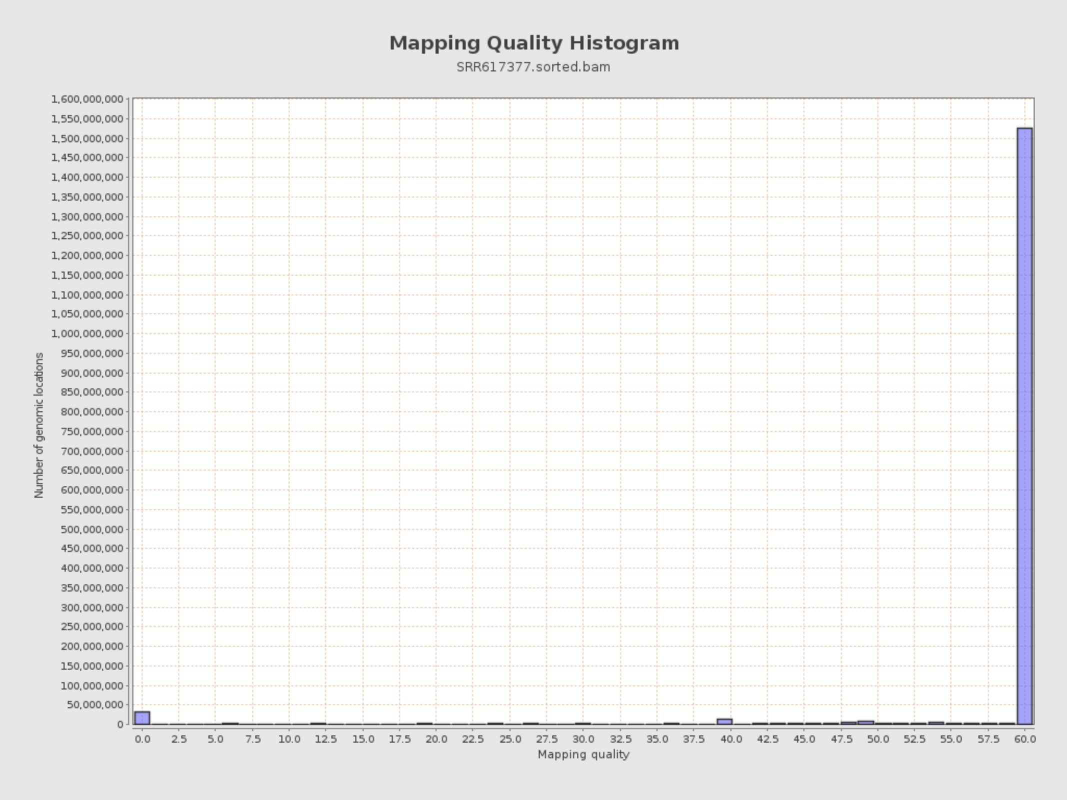
11. Results : Homopolymer Indels



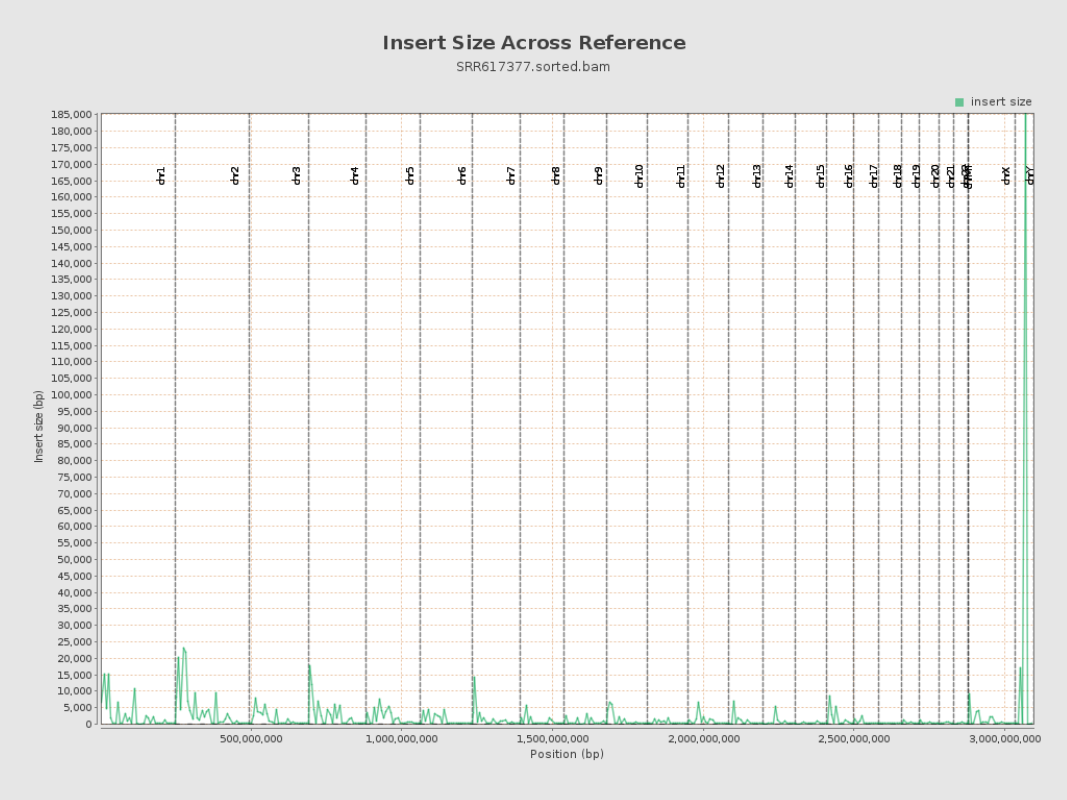
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram