Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/05 15:15:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1770534.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_SRR1770534 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1770534_1.fastq.gz SRR1770534_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Oct 05 15:15:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1770534.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	538,057,998
Mapped reads	519,143,331 / 96.48%
Unmapped reads	18,914,667 / 3.52%
Mapped paired reads	519,143,331 / 96.48%
Mapped reads, first in pair	262,273,987 / 48.74%
Mapped reads, second in pair	256,869,344 / 47.74%
Mapped reads, both in pair	510,916,896 / 94.96%
Mapped reads, singletons	8,226,435 / 1.53%
Secondary alignments	0
Supplementary alignments	1,598,342 / 0.3%
Read min/max/mean length	30 / 101 / 101.11
Duplicated reads (estimated)	73,773,479 / 13.71%
Duplication rate	9.89%
Clipped reads	37,106,159 / 6.9%

2.2. ACGT Content

Number/percentage of A's	15,235,844,631 / 29.53%
Number/percentage of C's	10,554,871,476 / 20.46%
Number/percentage of T's	15,222,601,104 / 29.5%
Number/percentage of G's	10,567,412,457 / 20.48%
Number/percentage of N's	16,415,640 / 0.03%

GC Percentage	40.94%

2.3. Coverage

Mean	16.6722
Standard Deviation	180.5209

2.4. Mapping Quality

Mean Mapping Quality	53.6

2.5. Insert size

Mean	42,186.3
Standard Deviation	1,960,183.09
P25/Median/P75	156 / 203 / 268

2.6. Mismatches and indels

General error rate	0.67%
Mismatches	331,051,318
Insertions	5,122,493
Mapped reads with at least one insertion	0.96%
Deletions	6,302,054
Mapped reads with at least one deletion	1.18%
Homopolymer indels	42.78%

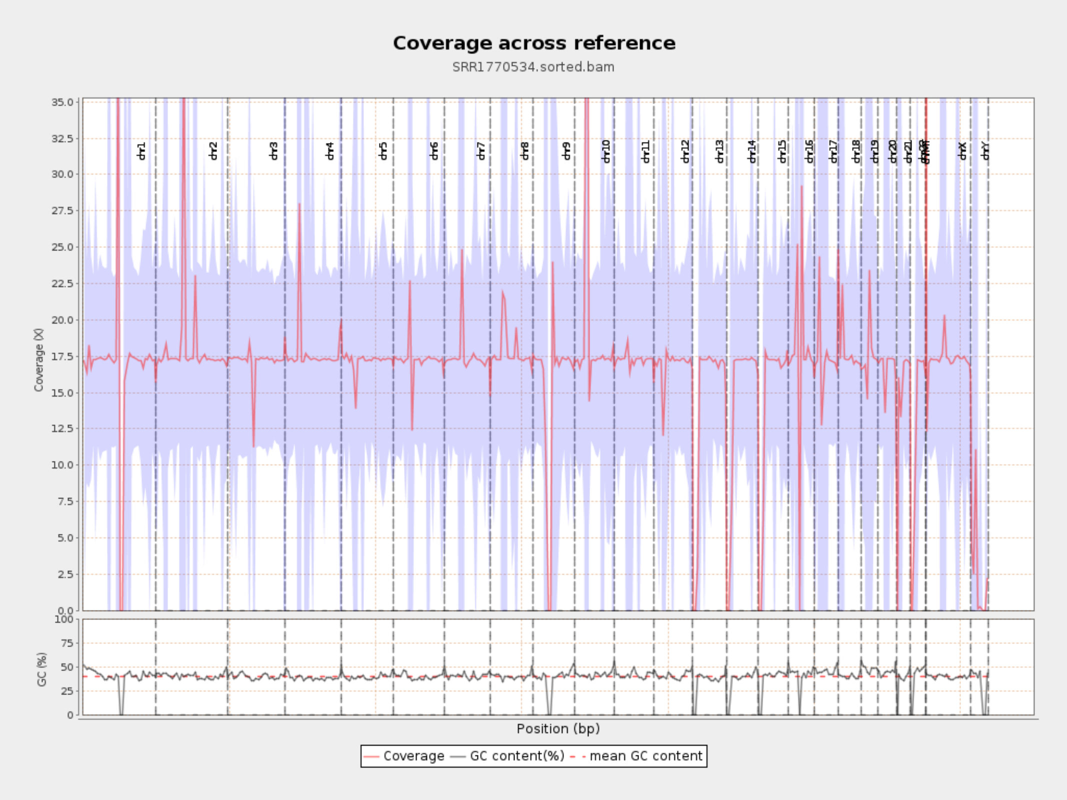
2.7. Chromosome stats

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

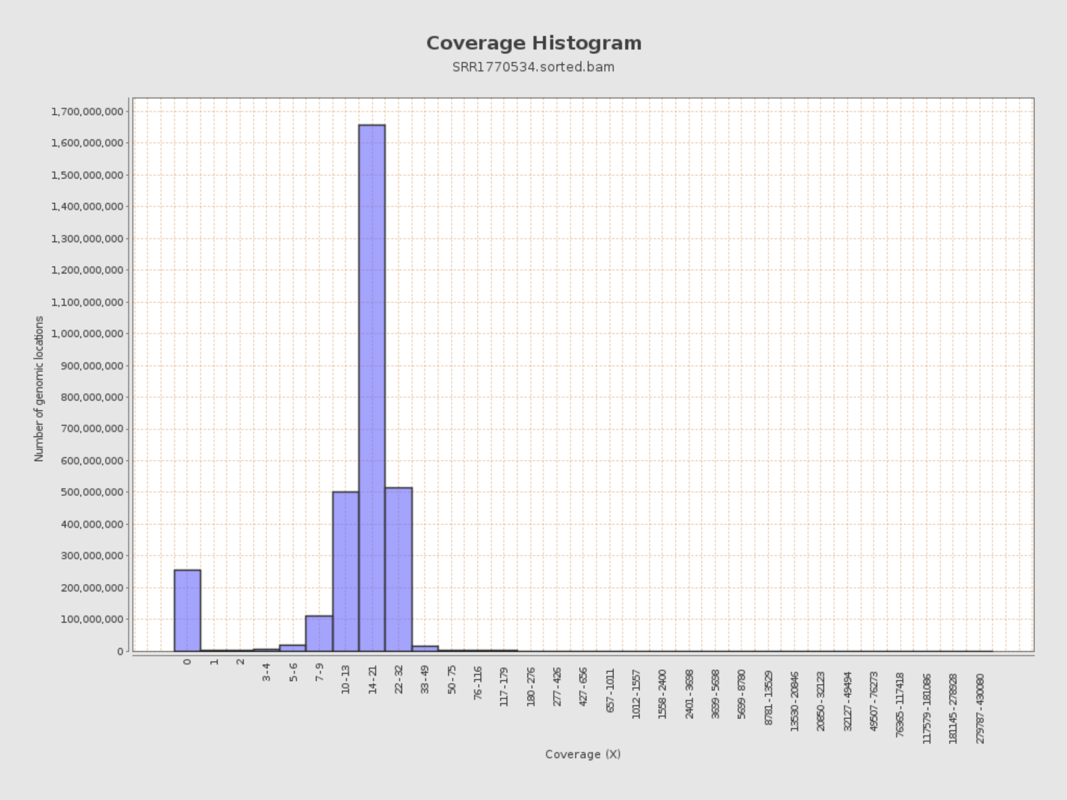
		bases	coverage	deviation
chr1	249250621	4198543535	16.8447	454.8705
chr2	243199373	4438225184	18.2493	140.7889
chr3	198022430	3388736525	17.1129	17.877
chr4	191154276	3403242885	17.8036	89.9838
chr5	180915260	3102146835	17.147	13.6278
chr6	171115067	2955663048	17.273	65.6579
chr7	159138663	2800138137	17.5956	149.6349
chr8	146364022	2613217535	17.8542	257.8316
chr9	141213431	2170800021	15.3725	184.5238
chr10	135534747	2626333755	19.3776	318.8609
chr11	135006516	2330748252	17.264	70.4335
chr12	133851895	2268776091	16.9499	16.1644
chr13	115169878	1651164229	14.3368	10.8775
chr14	107349540	1547041872	14.4113	20.1377
chr15	102531392	1434715960	13.9929	11.4334
chr16	90354753	1586483354	17.5584	106.8531
chr17	81195210	1414765749	17.4243	99.5023
chr18	78077248	1411816652	18.0823	201.1717
chr19	59128983	1045713964	17.6853	232.3742
chr20	63025520	1057459279	16.7783	30.0091
chr21	48129895	710002747	14.7518	52.759
chr22	51304566	610671342	11.9029	12.8245
chrMT	16571	21362316	1,289.1386	125.3272
chrX	155270560	2675663548	17.2323	46.4406

chrY	59373566	148592708	2.5027	107.2548

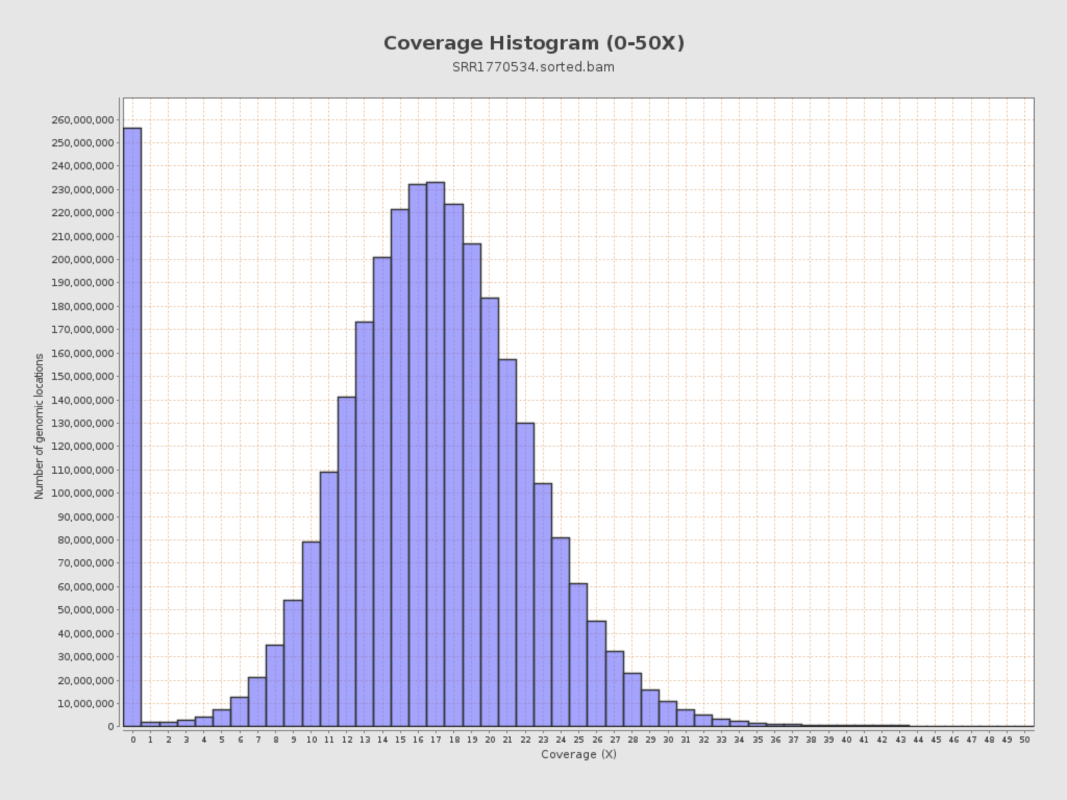
3. Results : Coverage across reference



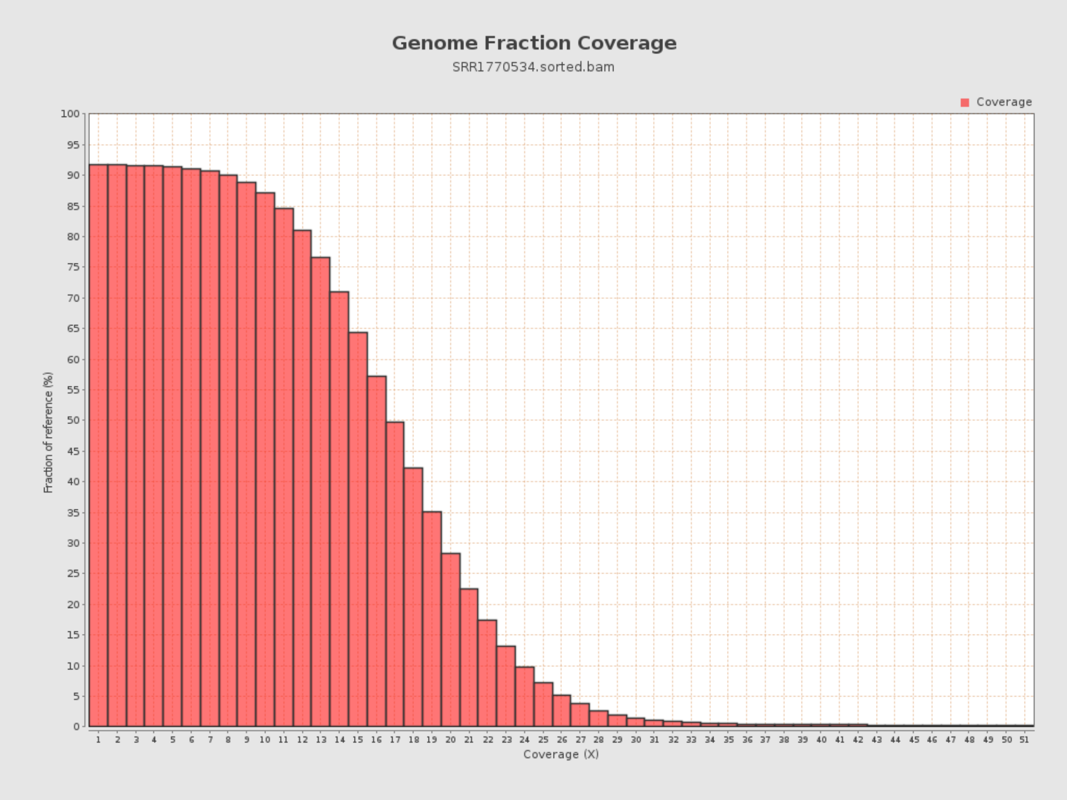
4. Results : Coverage Histogram



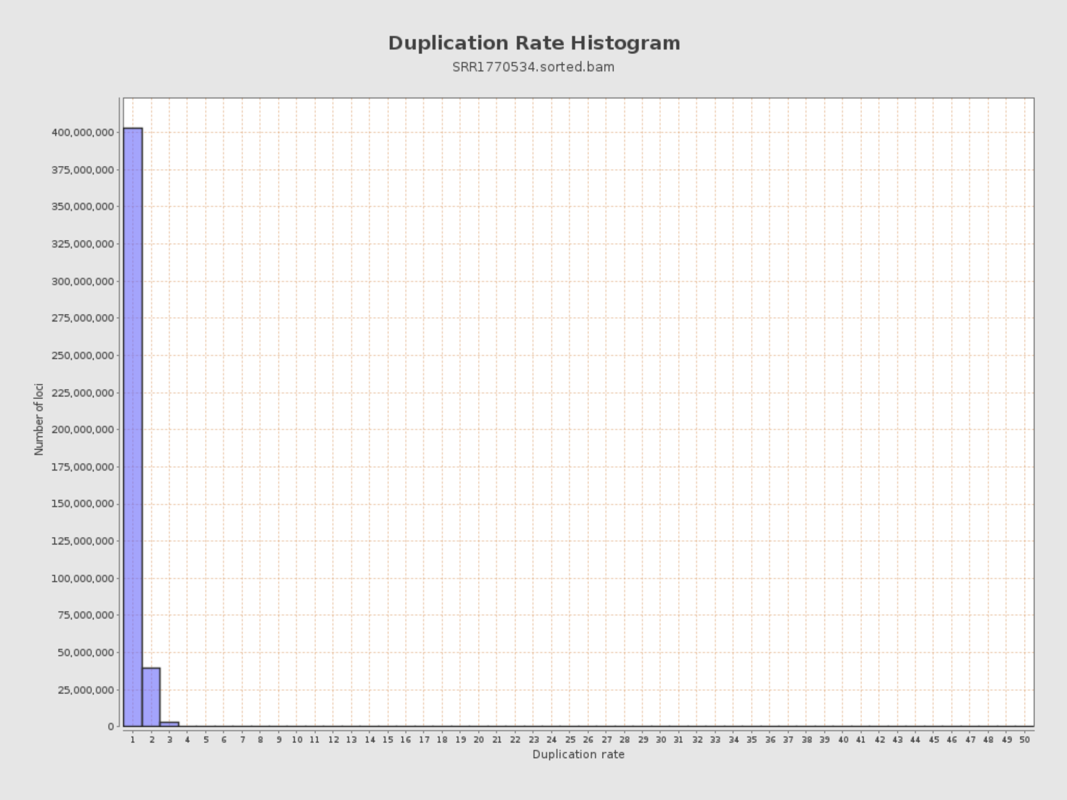
5. Results : Coverage Histogram (0-50X)



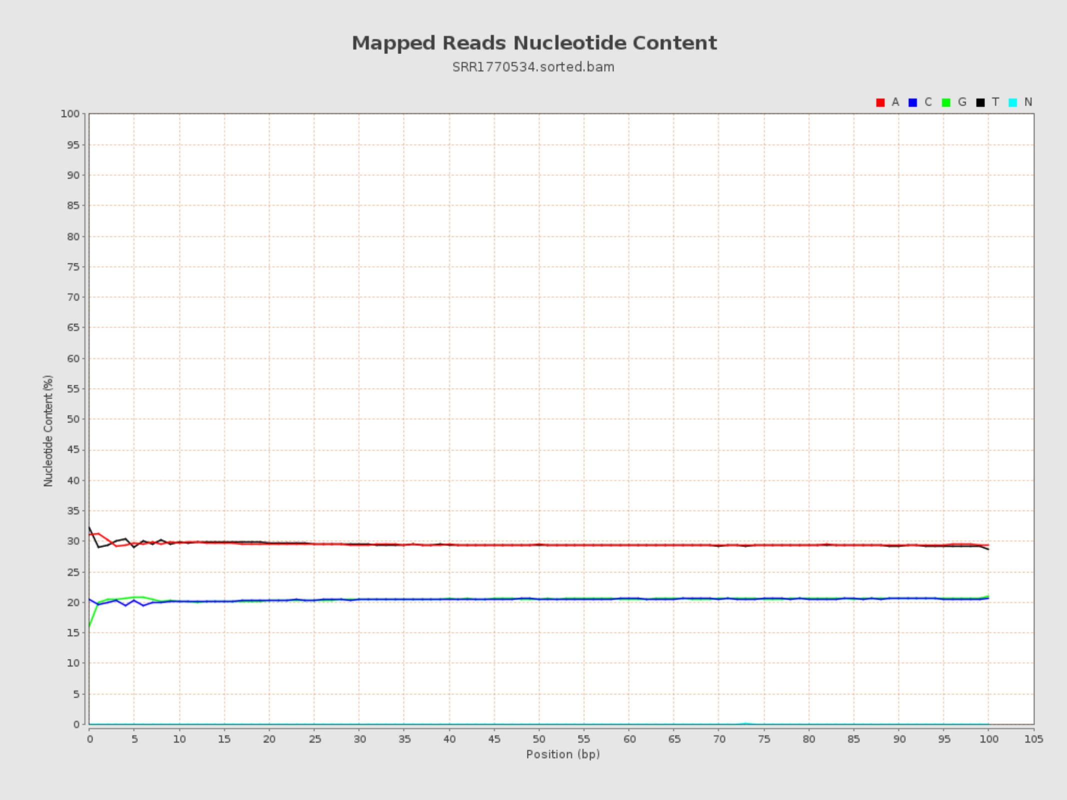
6. Results : Genome Fraction Coverage



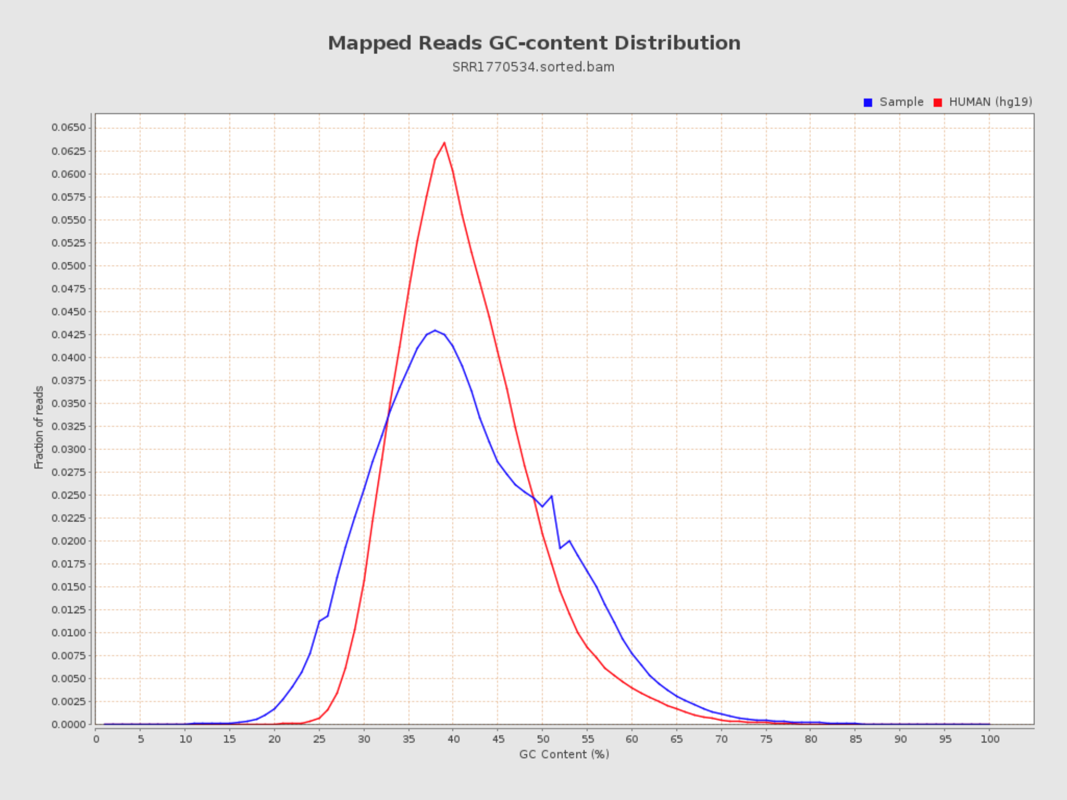
7. Results : Duplication Rate Histogram



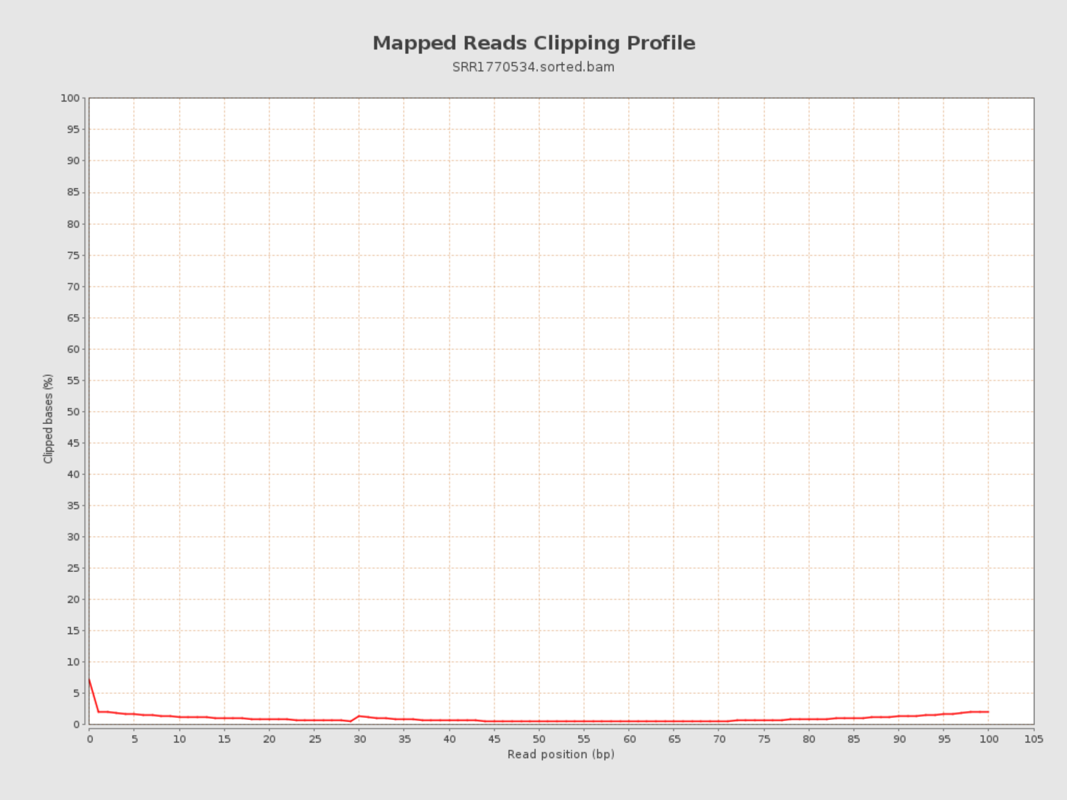
8. Results : Mapped Reads Nucleotide Content



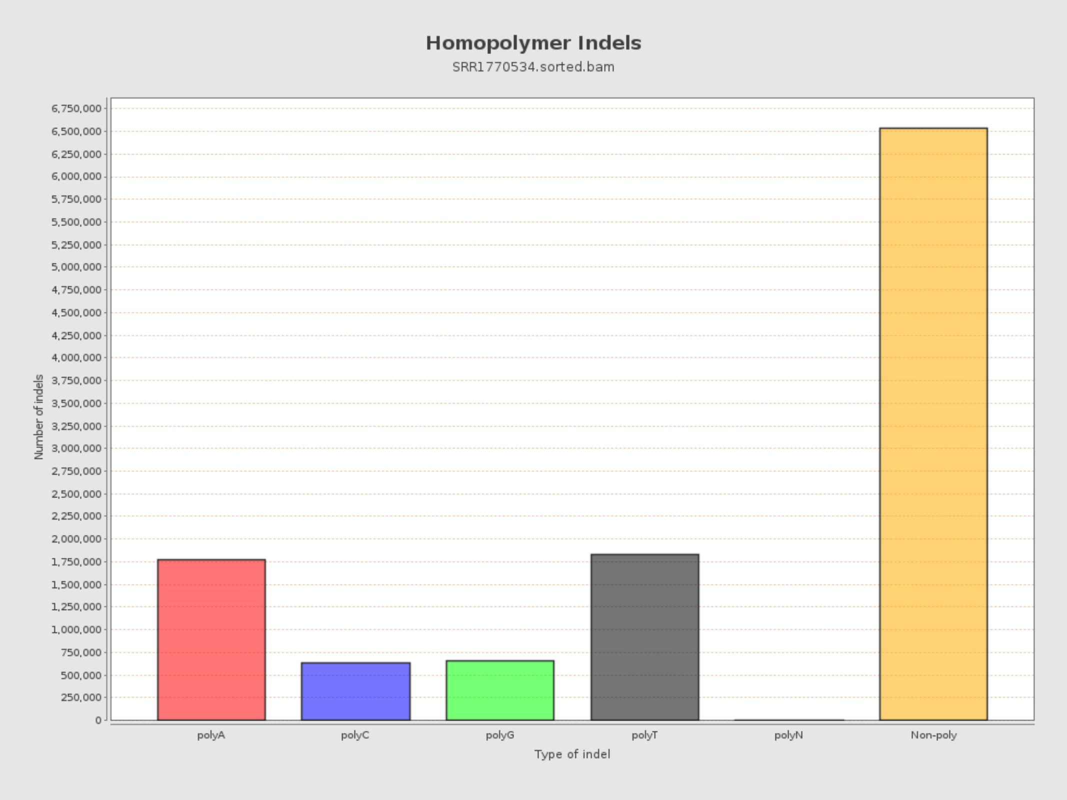
9. Results : Mapped Reads GC-content Distribution



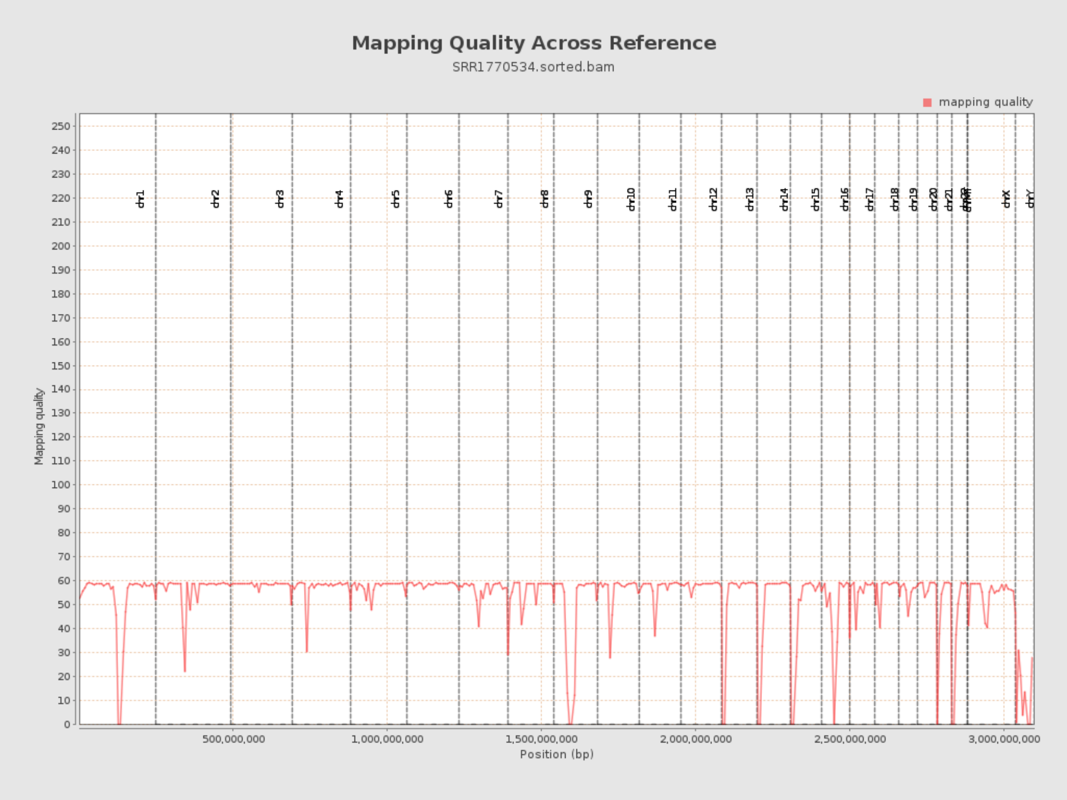
10. Results : Mapped Reads Clipping Profile



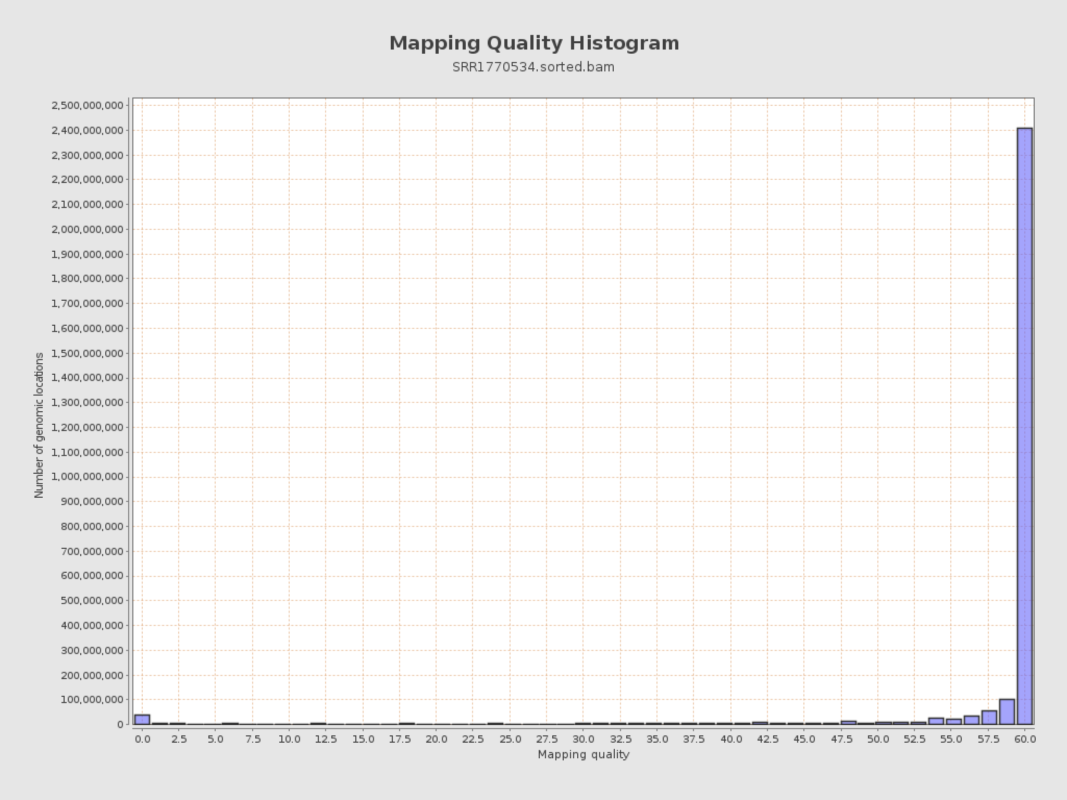
11. Results : Homopolymer Indels



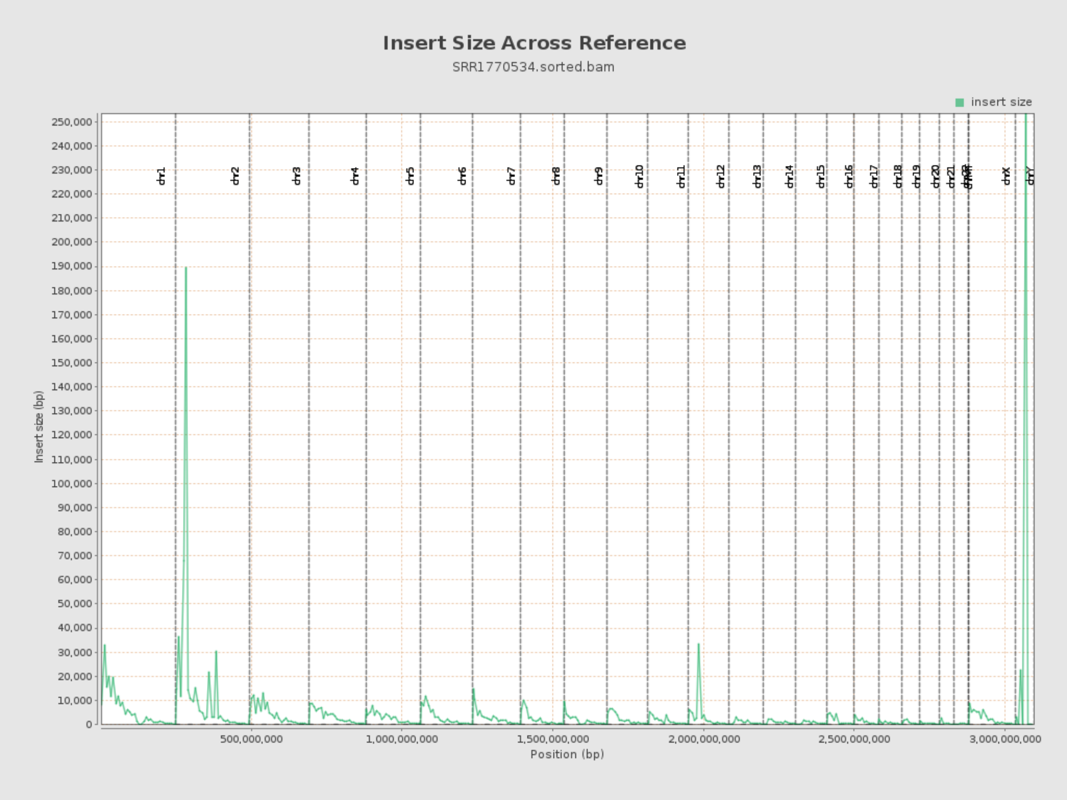
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram