Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/07 17:05:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617374.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_SRR617374 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617374_1.fastq.gz SRR617374_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Oct 07 17:05:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617374.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	30,580,675 / 95.56%
Unmapped reads	1,419,325 / 4.44%
Mapped paired reads	30,580,675 / 95.56%
Mapped reads, first in pair	15,354,621 / 47.98%
Mapped reads, second in pair	15,226,054 / 47.58%
Mapped reads, both in pair	30,141,338 / 94.19%
Mapped reads, singletons	439,337 / 1.37%
Secondary alignments	0
Supplementary alignments	67,394 / 0.21%
Read min/max/mean length	30 / 100 / 100.09
Duplicated reads (estimated)	1,582,180 / 4.94%
Duplication rate	1.48%
Clipped reads	2,309,750 / 7.22%

2.2. ACGT Content

Number/percentage of A's	908,772,036 / 30.24%
Number/percentage of C's	596,718,647 / 19.86%
Number/percentage of T's	897,329,222 / 29.86%
Number/percentage of G's	600,115,302 / 19.97%
Number/percentage of N's	2,180,860 / 0.07%

GC Percentage	39.83%

2.3. Coverage

Mean	0.971
Standard Deviation	9.8607

2.4. Mapping Quality

Mean Mapping Quality	53.51

2.5. Insert size

Mean	58,125.45
Standard Deviation	2,312,100.95
P25/Median/P75	174 / 216 / 282

2.6. Mismatches and indels

General error rate	1.02%
Mismatches	29,802,657
Insertions	304,024
Mapped reads with at least one insertion	0.96%
Deletions	369,223
Mapped reads with at least one deletion	1.17%
Homopolymer indels	41.23%

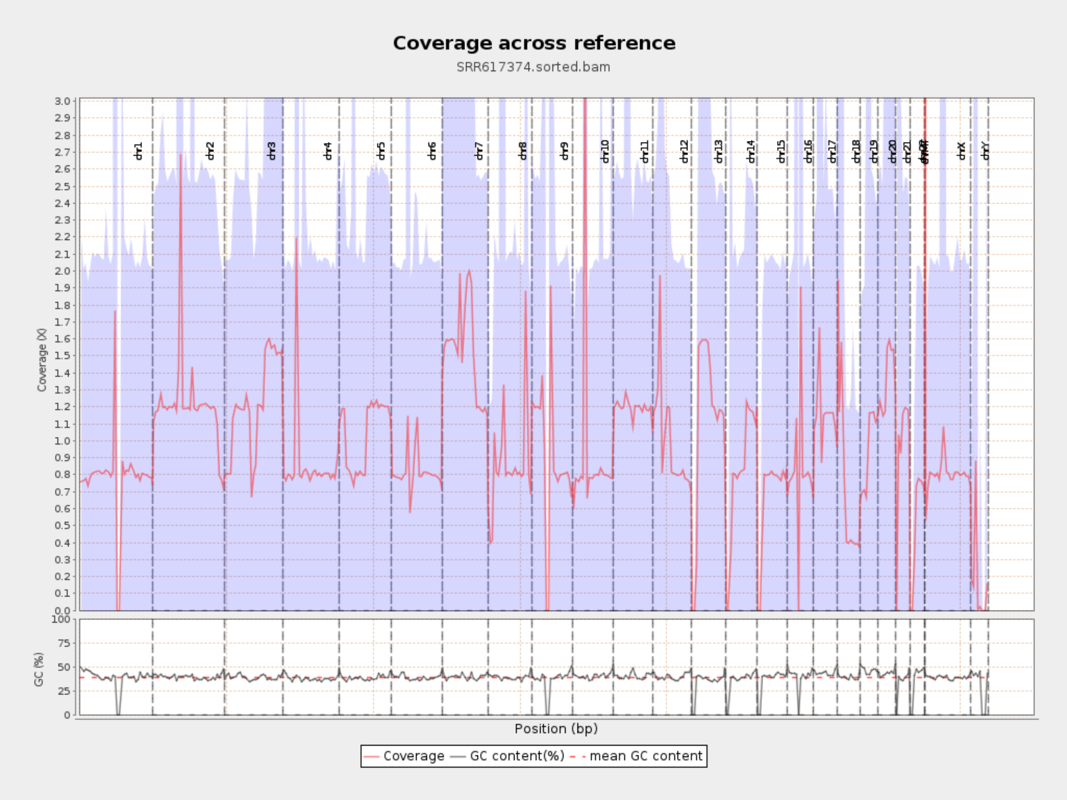
2.7. Chromosome stats

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

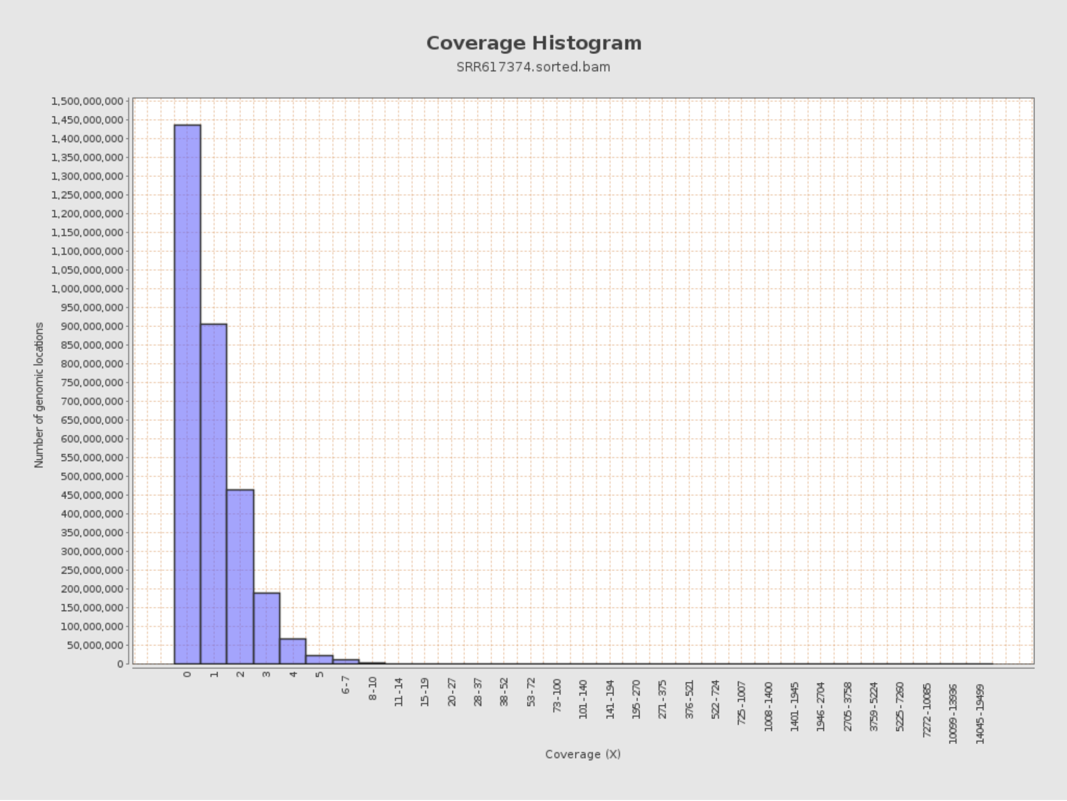
		bases	coverage	deviation
chr1	249250621	195244510	0.7833	19.9475
chr2	243199373	296593446	1.2195	8.943
chr3	198022430	239155277	1.2077	1.4669
chr4	191154276	164411098	0.8601	9.5704
chr5	180915260	188623603	1.0426	1.4658
chr6	171115067	141020031	0.8241	3.683
chr7	159138663	244297803	1.5351	11.1285
chr8	146364022	126558780	0.8647	7.8396
chr9	141213431	126711383	0.8973	15.0494
chr10	135534747	126345161	0.9322	20.0769
chr11	135006516	160964966	1.1923	5.5811
chr12	133851895	133118569	0.9945	1.3491
chr13	115169878	130799847	1.1357	1.2962
chr14	107349540	86931470	0.8098	1.3871
chr15	102531392	67505668	0.6584	0.9807
chr16	90354753	75465075	0.8352	7.9168
chr17	81195210	93749318	1.1546	7.1295
chr18	78077248	54518701	0.6983	15.6195
chr19	59128983	55962433	0.9464	9.6724
chr20	63025520	86381638	1.3706	2.5141
chr21	48129895	47836022	0.9939	3.3586
chr22	51304566	26821185	0.5228	0.9193
chrMT	16571	2063409	124.5193	20.9531
chrX	155270560	124665273	0.8029	2.9429

chrY	59373566	10265729	0.1729	8.5255

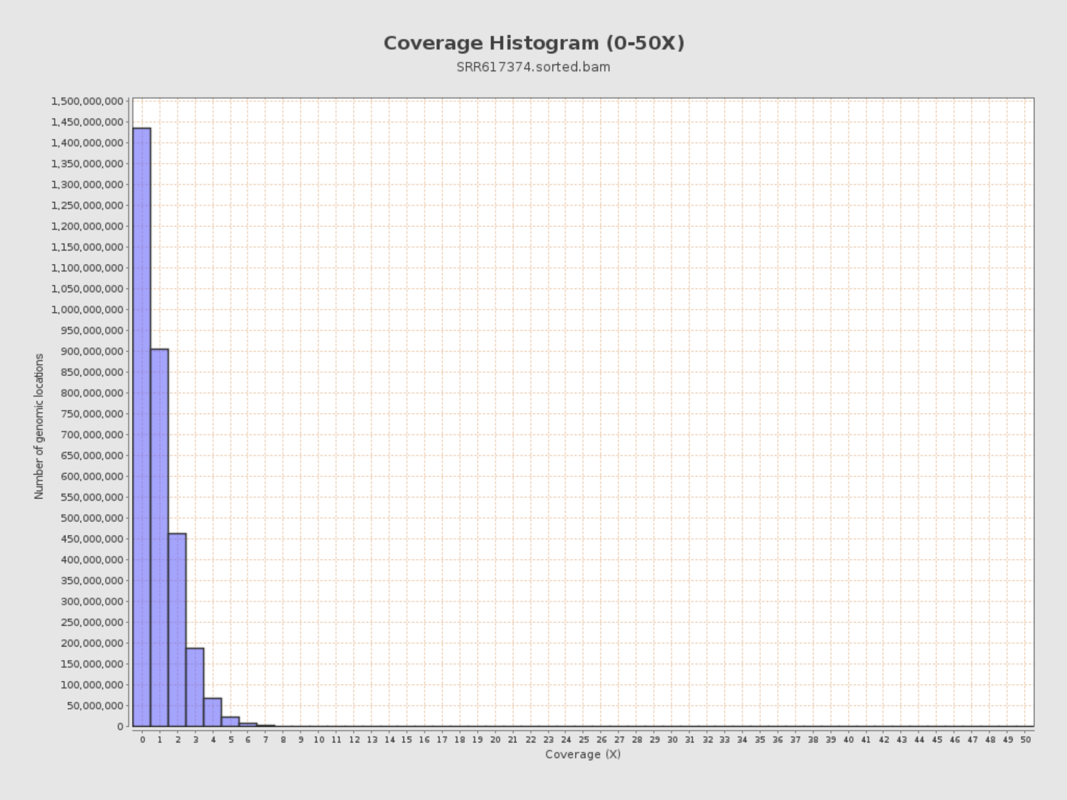
3. Results : Coverage across reference



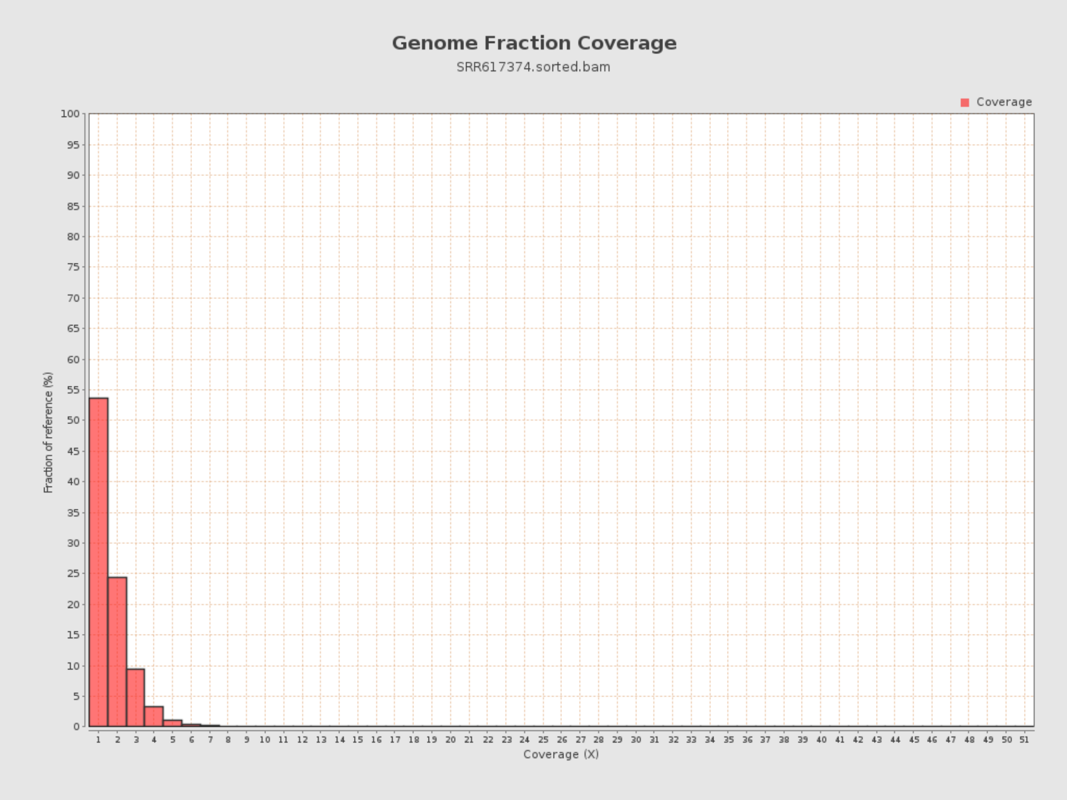
4. Results : Coverage Histogram



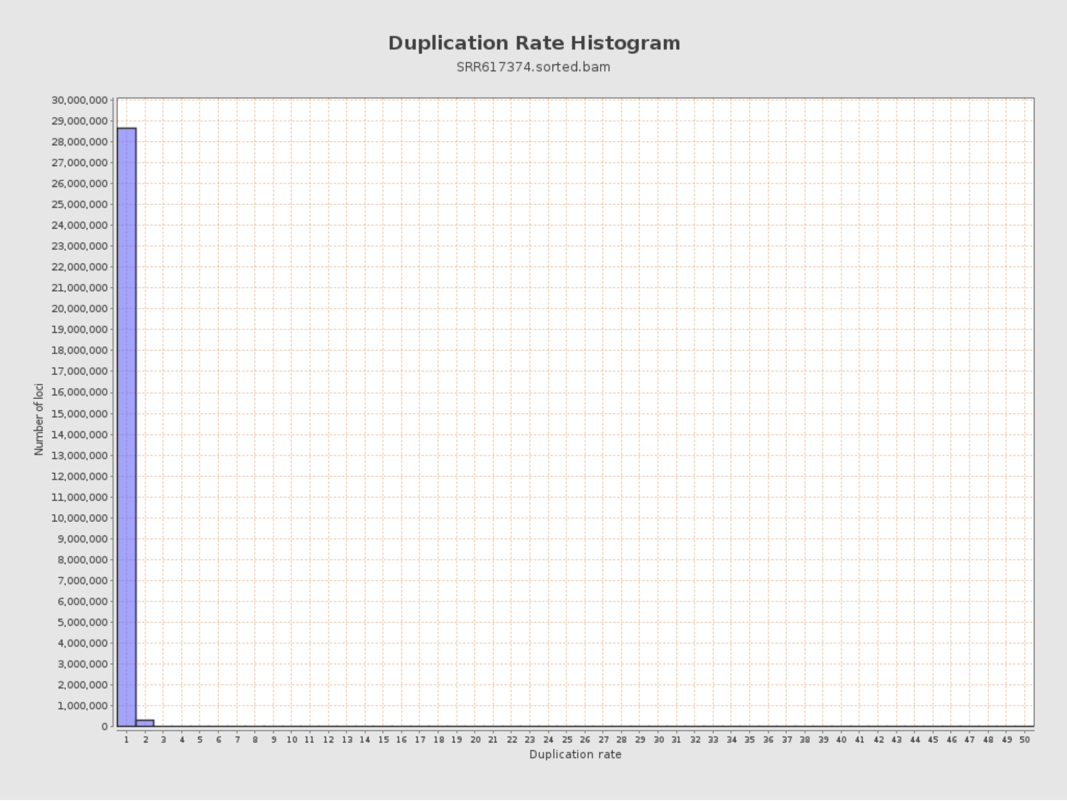
5. Results : Coverage Histogram (0-50X)



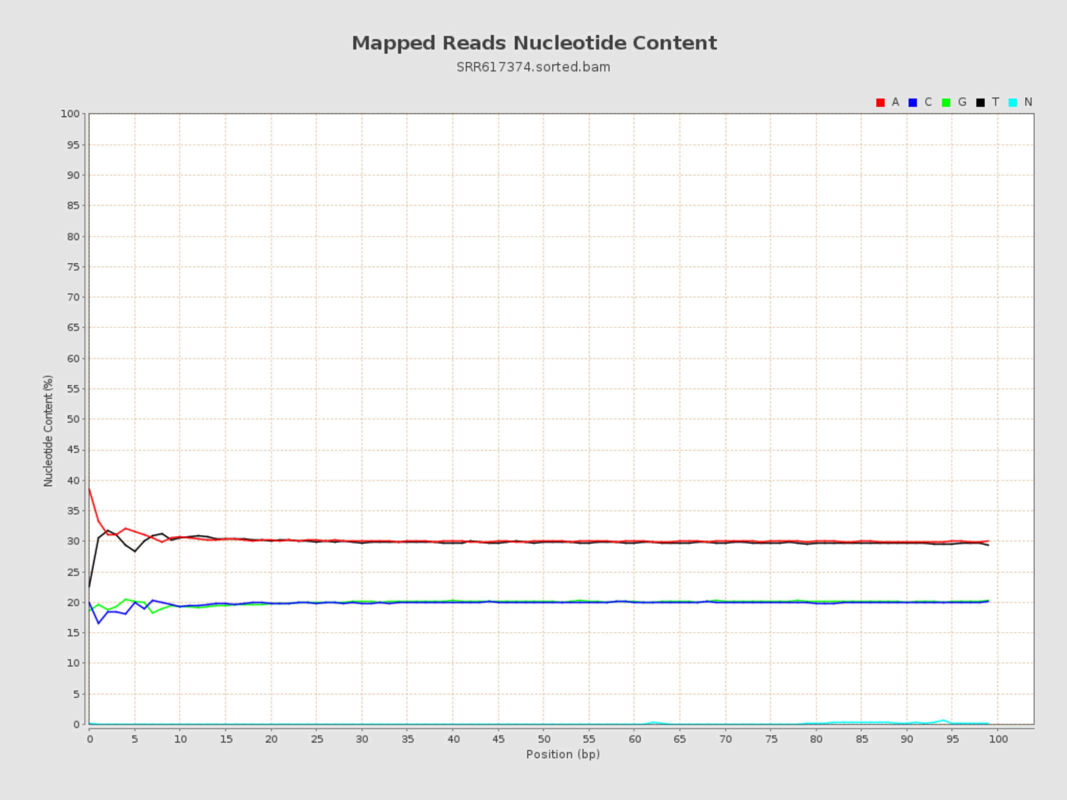
6. Results : Genome Fraction Coverage



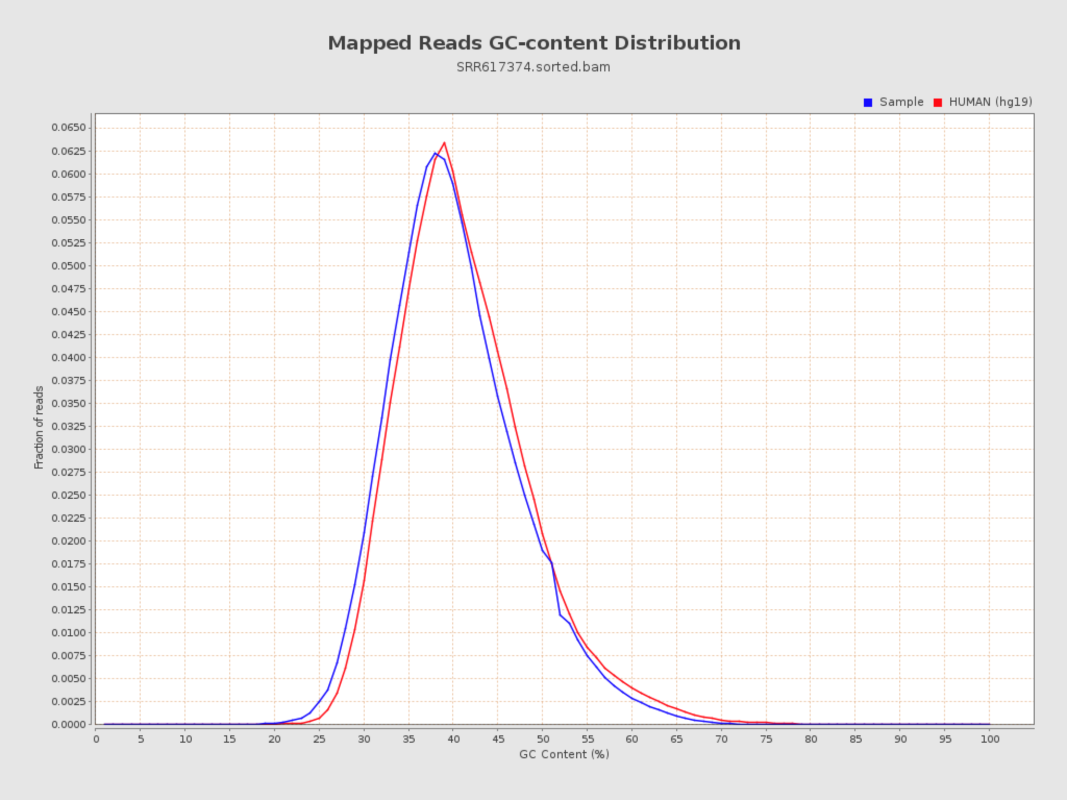
7. Results : Duplication Rate Histogram



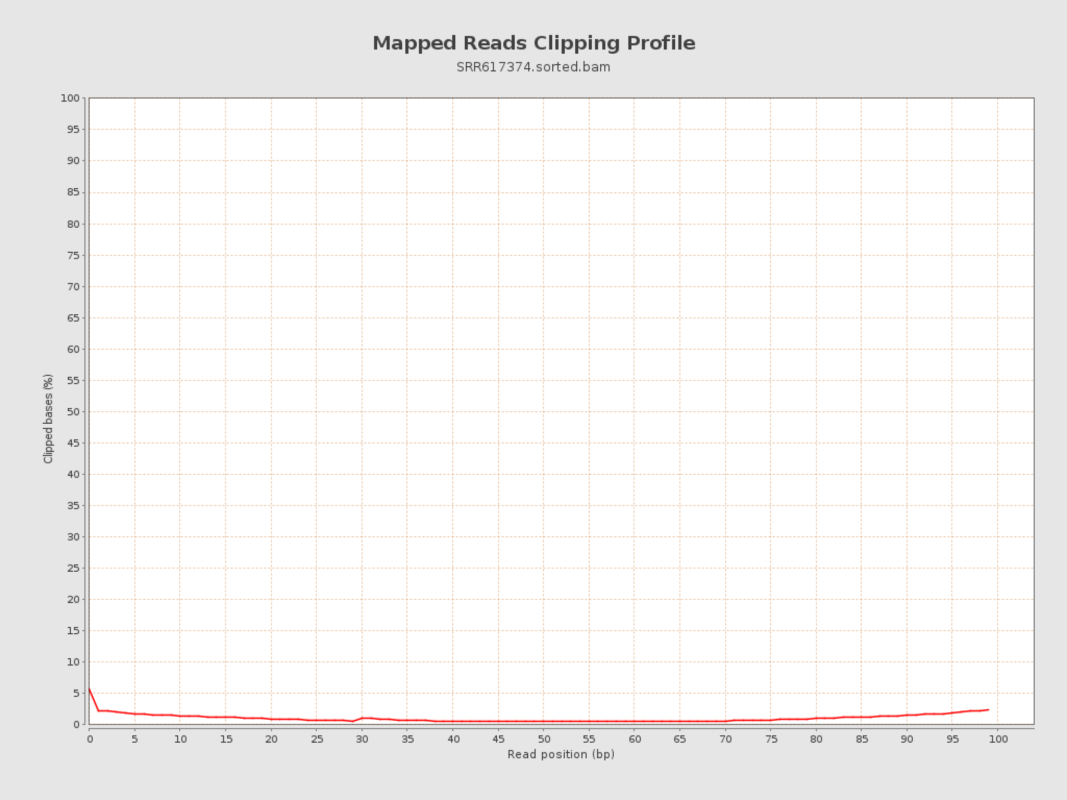
8. Results : Mapped Reads Nucleotide Content



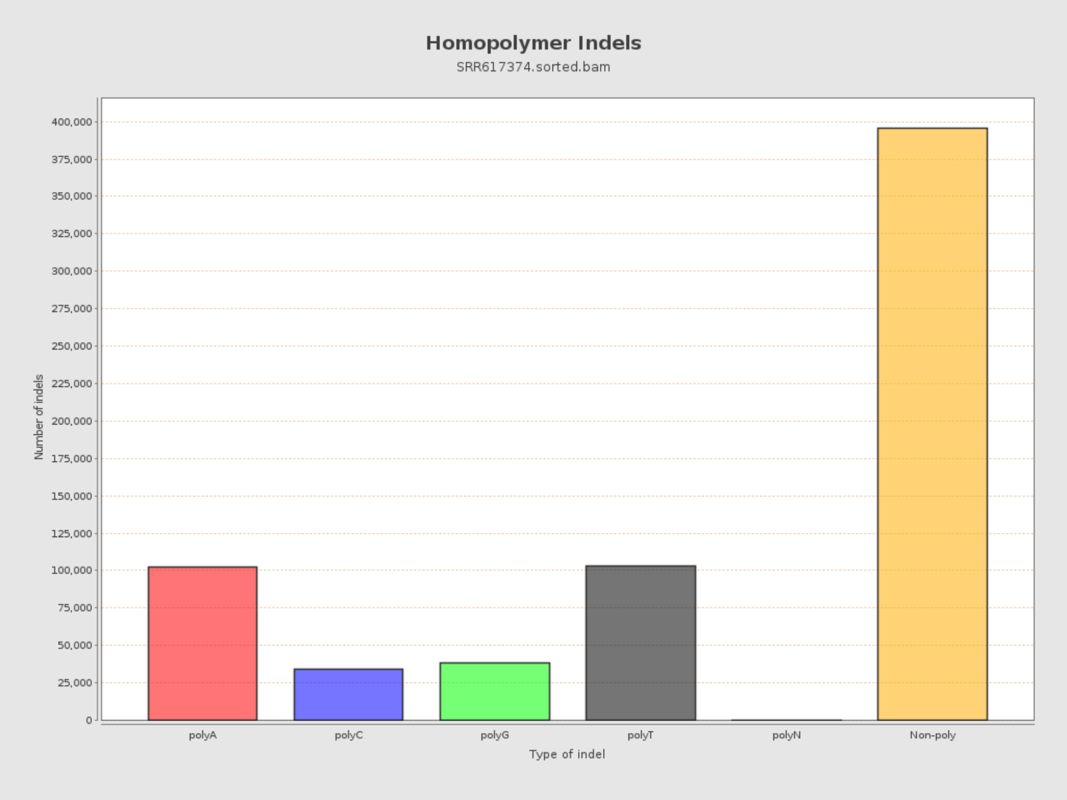
9. Results : Mapped Reads GC-content Distribution



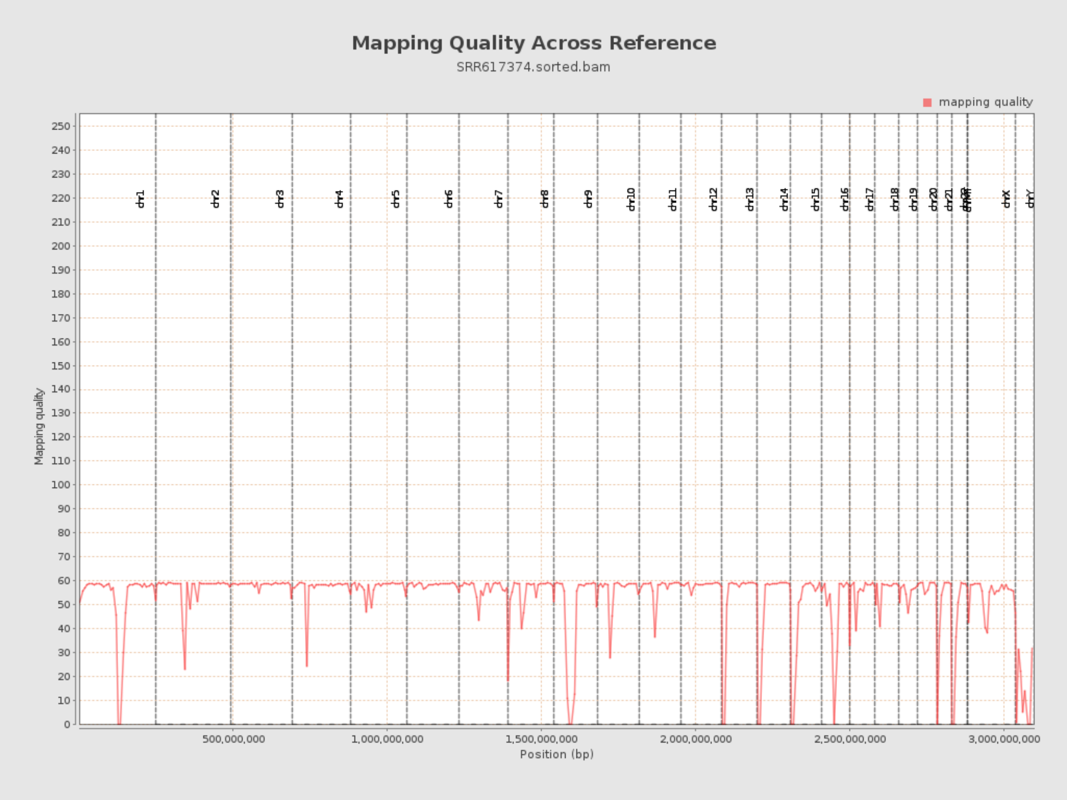
10. Results : Mapped Reads Clipping Profile



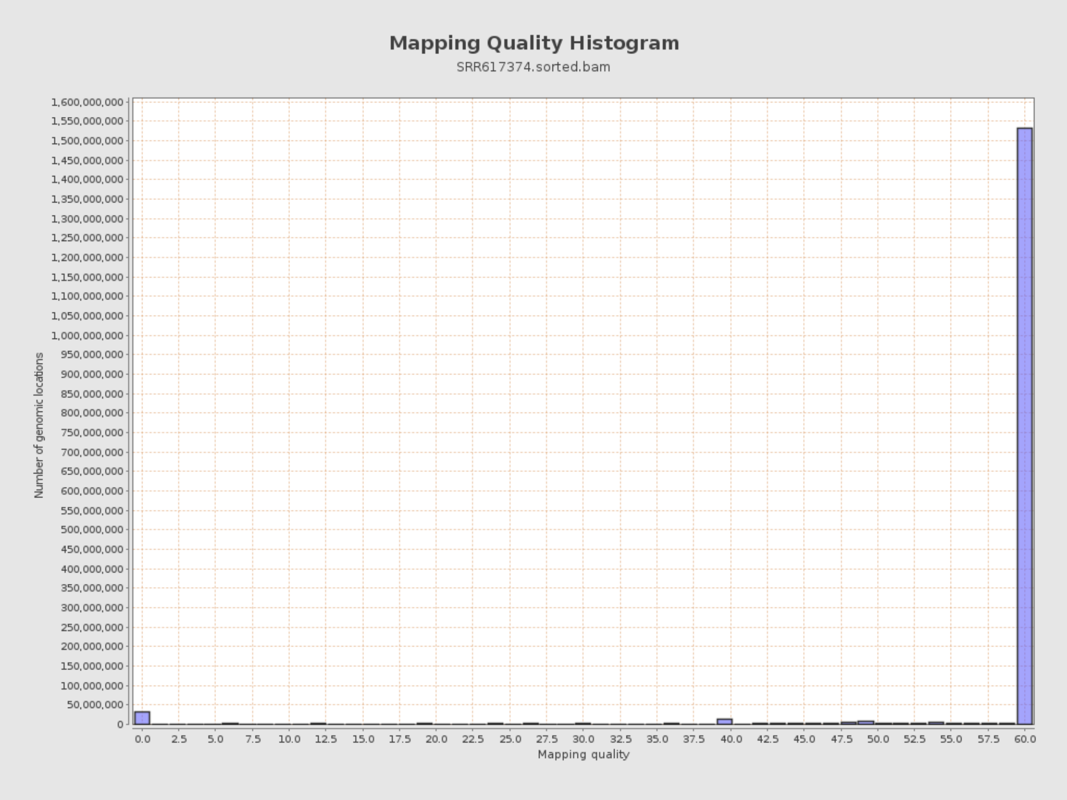
11. Results : Homopolymer Indels



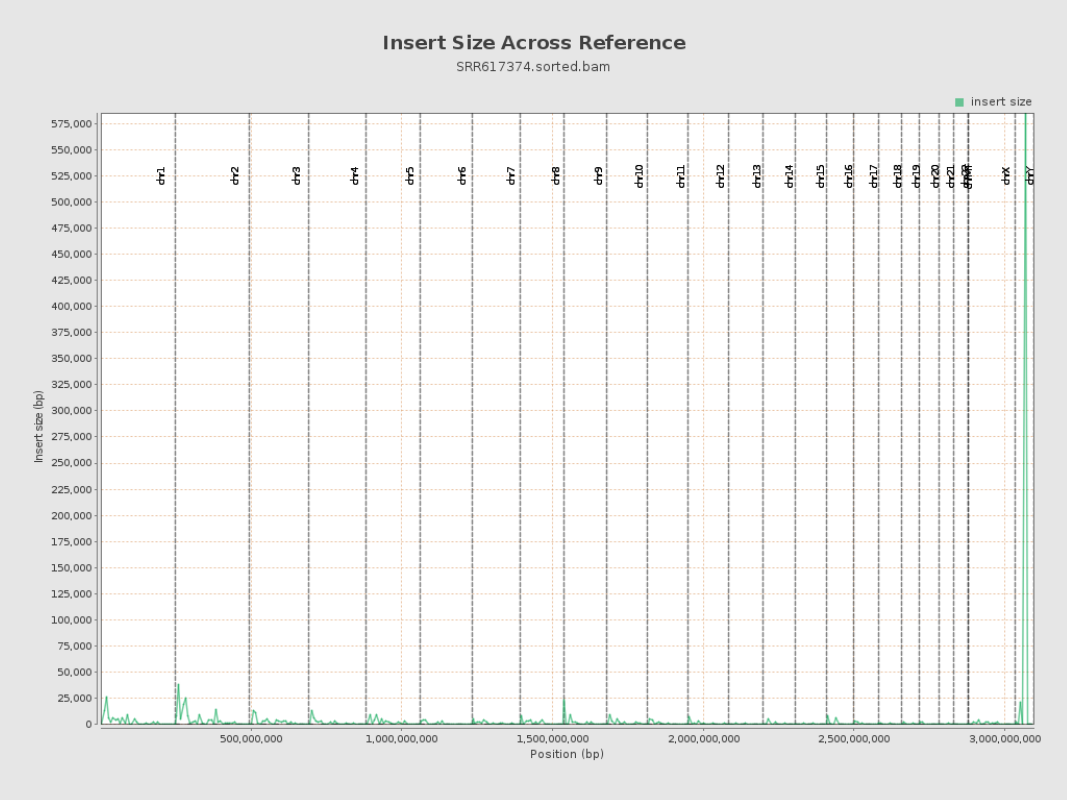
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram