Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 01:32:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124889.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_SRR3124889 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124889_1.fastq.gz SRR3124889_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 01:32:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124889.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,933,798
Mapped reads	5,749,767 / 96.9%
Unmapped reads	184,031 / 3.1%
Mapped paired reads	5,749,767 / 96.9%
Mapped reads, first in pair	2,906,379 / 48.98%
Mapped reads, second in pair	2,843,388 / 47.92%
Mapped reads, both in pair	5,653,098 / 95.27%
Mapped reads, singletons	96,669 / 1.63%
Secondary alignments	0
Supplementary alignments	6,335 / 0.11%
Read min/max/mean length	30 / 76 / 76.04
Duplicated reads (estimated)	312,245 / 5.26%
Duplication rate	3.74%
Clipped reads	2,189,617 / 36.9%

2.2. ACGT Content

Number/percentage of A's	104,741,738 / 28.16%
Number/percentage of C's	67,333,274 / 18.1%
Number/percentage of T's	111,601,535 / 30%
Number/percentage of G's	88,269,063 / 23.73%
Number/percentage of N's	3,286 / 0%

GC Percentage	41.83%

2.3. Coverage

Mean	0.1202
Standard Deviation	0.9401

2.4. Mapping Quality

Mean Mapping Quality	51.94

2.5. Insert size

Mean	39,921.99
Standard Deviation	1,915,492.46
P25/Median/P75	147 / 192 / 263

2.6. Mismatches and indels

General error rate	0.66%
Mismatches	2,406,665
Insertions	38,598
Mapped reads with at least one insertion	0.67%
Deletions	100,206
Mapped reads with at least one deletion	1.73%
Homopolymer indels	50.15%

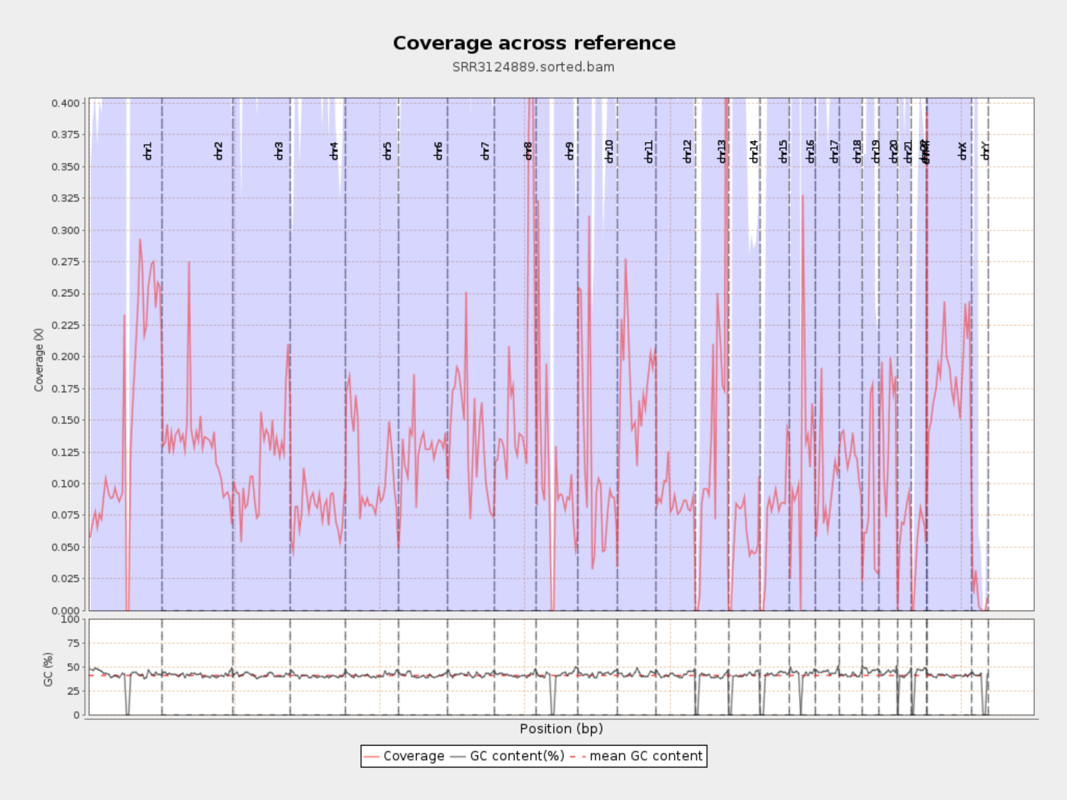
2.7. Chromosome stats

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

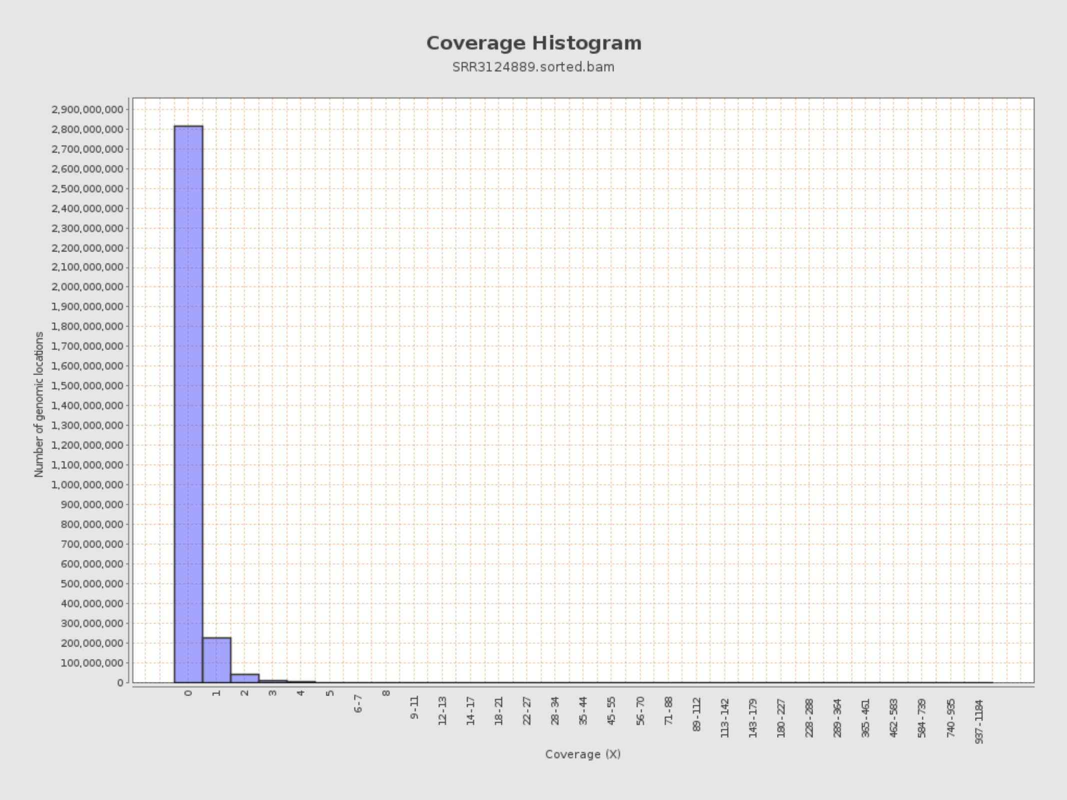
		bases	coverage	deviation
chr1	249250621	37422938	0.1501	1.2618
chr2	243199373	31843249	0.1309	1.002
chr3	198022430	23181908	0.1171	0.4169
chr4	191154276	15049761	0.0787	0.4062
chr5	180915260	20090915	0.1111	0.4004
chr6	171115067	21314133	0.1246	0.7637
chr7	159138663	22162159	0.1393	1.7264
chr8	146364022	27140996	0.1854	0.6652
chr9	141213431	14247157	0.1009	0.8776
chr10	135534747	15571080	0.1149	1.9642
chr11	135006516	23741917	0.1759	0.7514
chr12	133851895	11680572	0.0873	0.3569
chr13	115169878	17923548	0.1556	0.6325
chr14	107349540	5927289	0.0552	0.3257
chr15	102531392	7571986	0.0739	0.3308
chr16	90354753	10852551	0.1201	1.3874
chr17	81195210	7795542	0.096	1.071
chr18	78077248	9633749	0.1234	1.29
chr19	59128983	4823360	0.0816	0.8956
chr20	63025520	9234651	0.1465	0.4751
chr21	48129895	3109217	0.0646	0.3347
chr22	51304566	2466894	0.0481	0.2555
chrMT	16571	6522	0.3936	0.699
chrX	155270560	28672828	0.1847	0.7526

chrY	59373566	629532	0.0106	0.3564

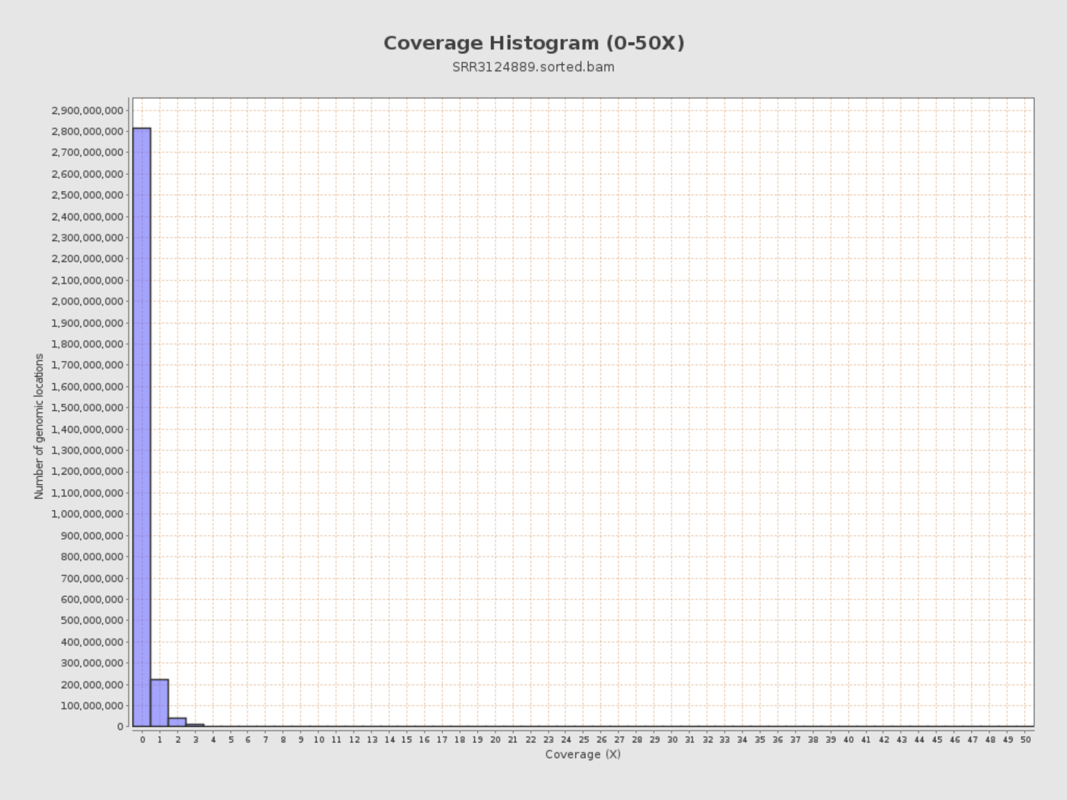
3. Results : Coverage across reference



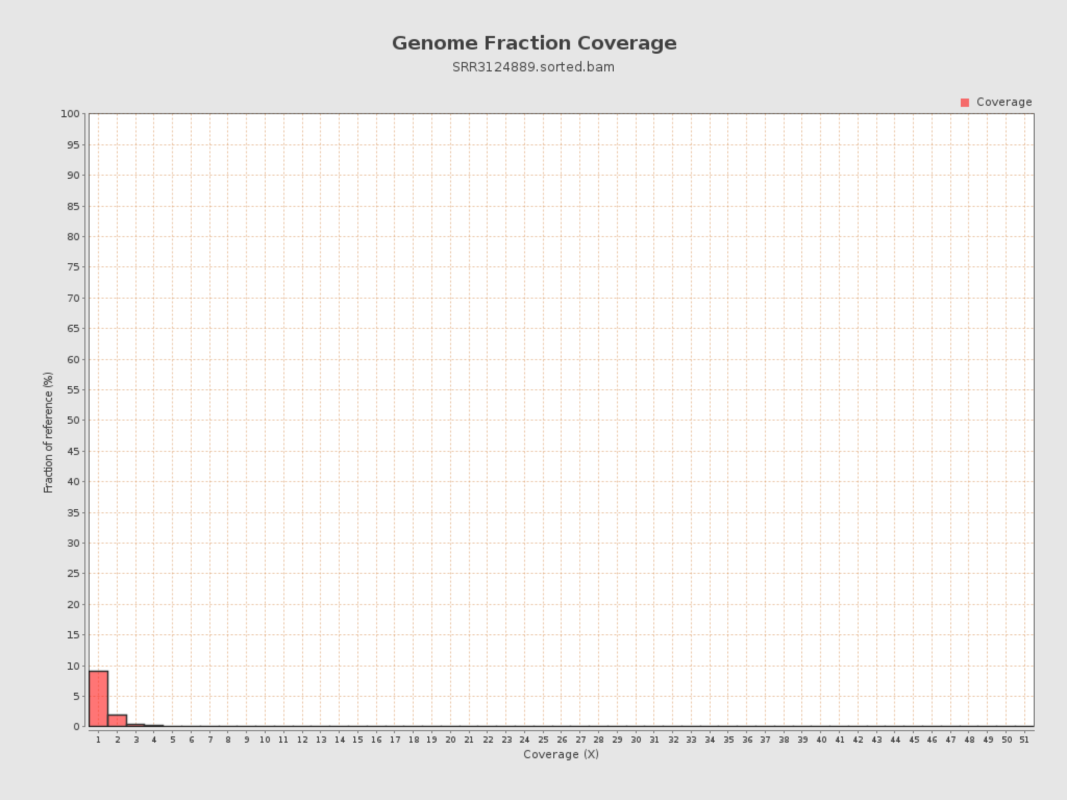
4. Results : Coverage Histogram



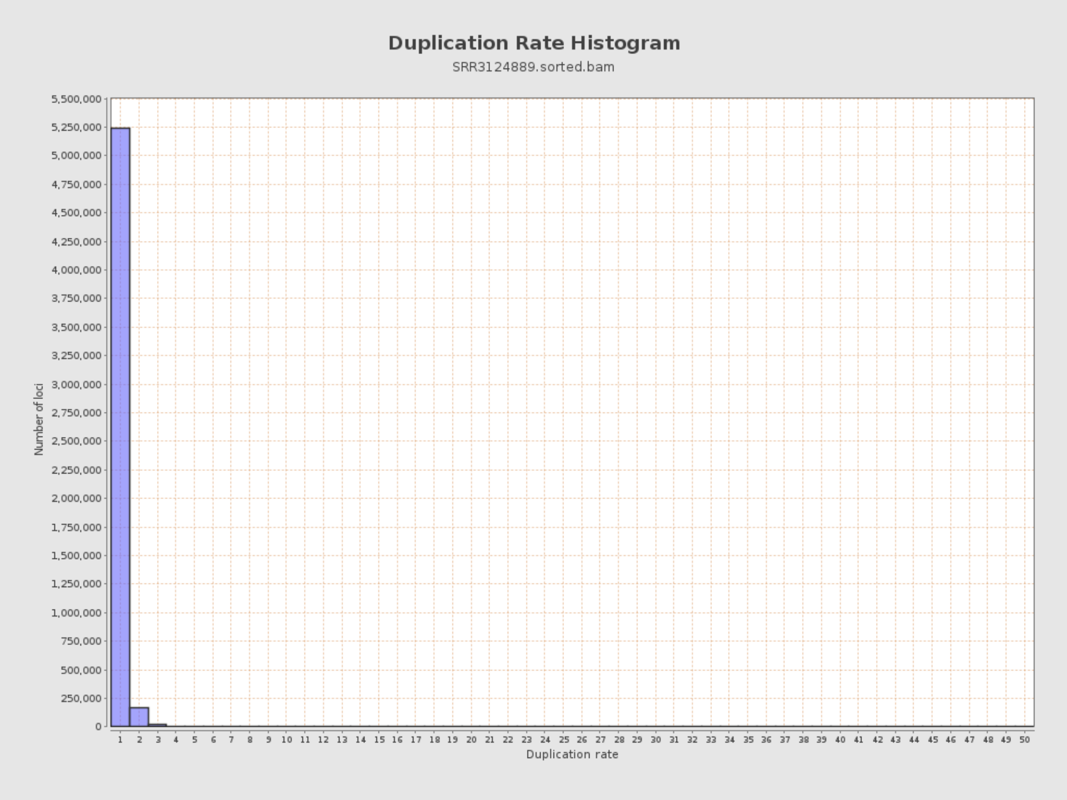
5. Results : Coverage Histogram (0-50X)



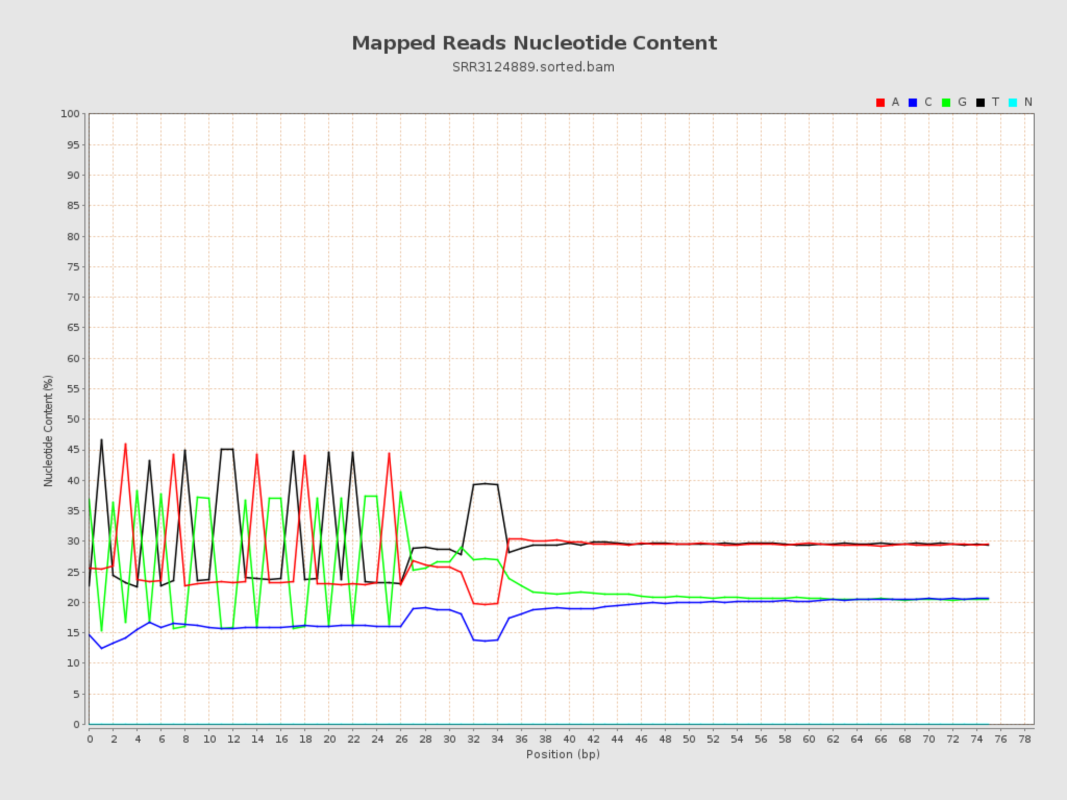
6. Results : Genome Fraction Coverage



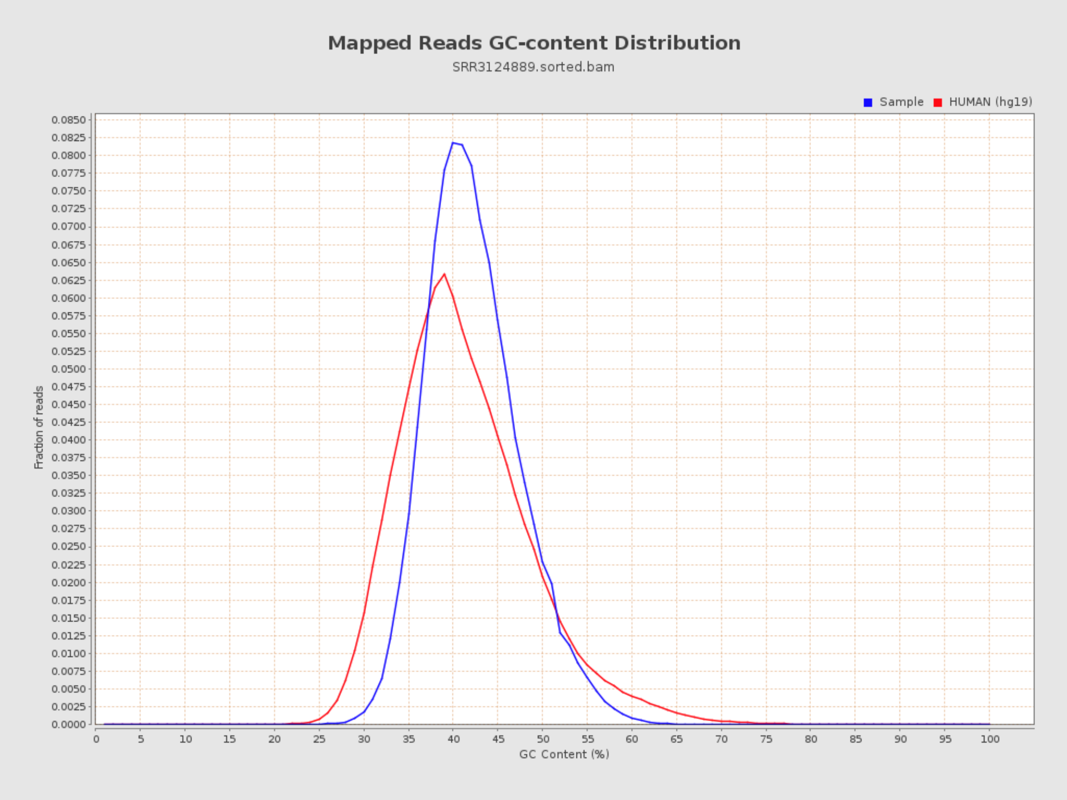
7. Results : Duplication Rate Histogram



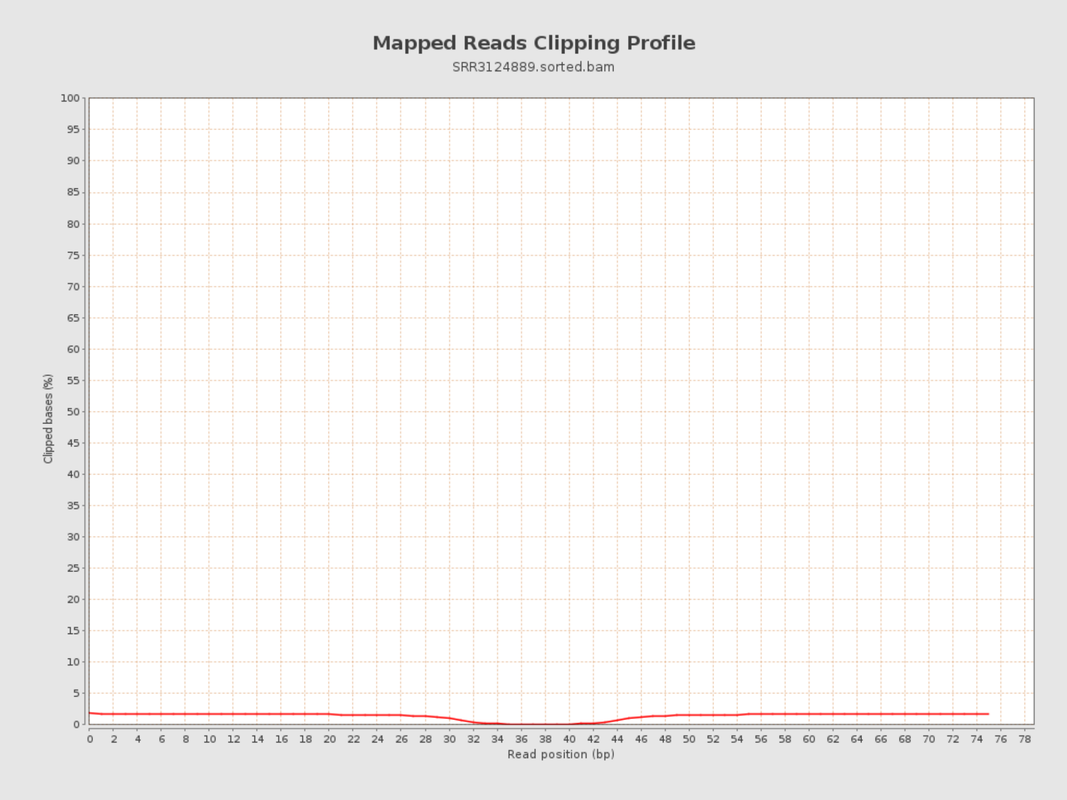
8. Results : Mapped Reads Nucleotide Content



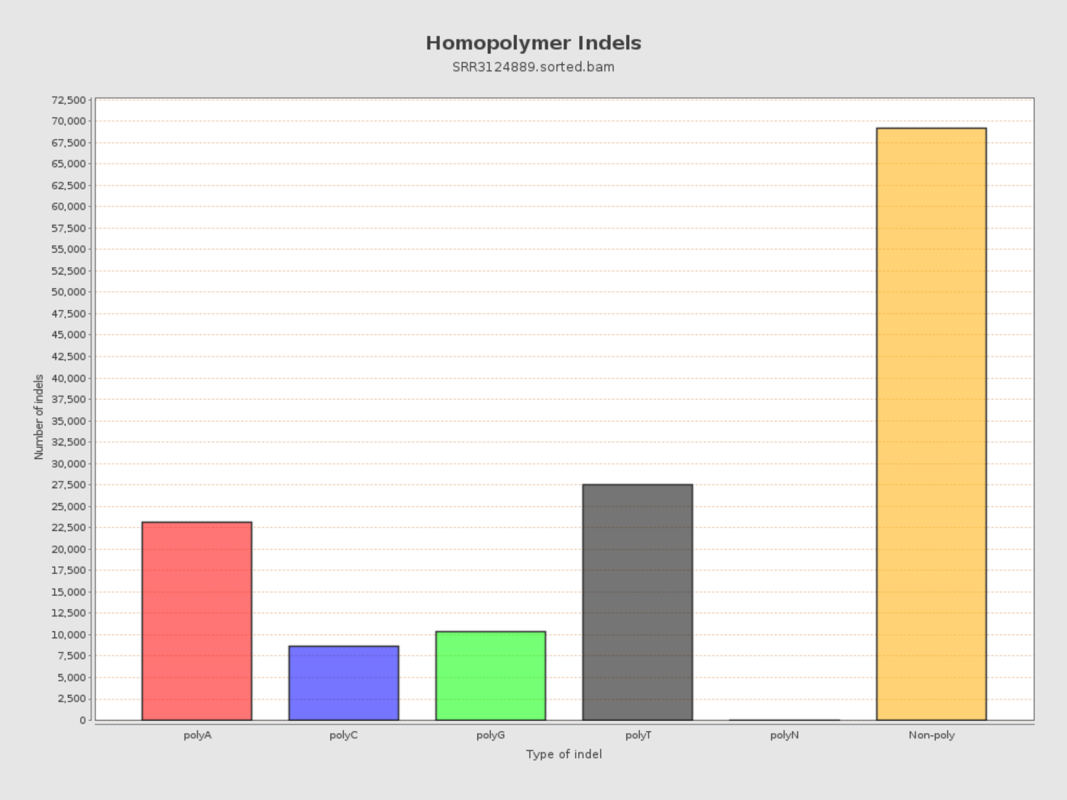
9. Results : Mapped Reads GC-content Distribution



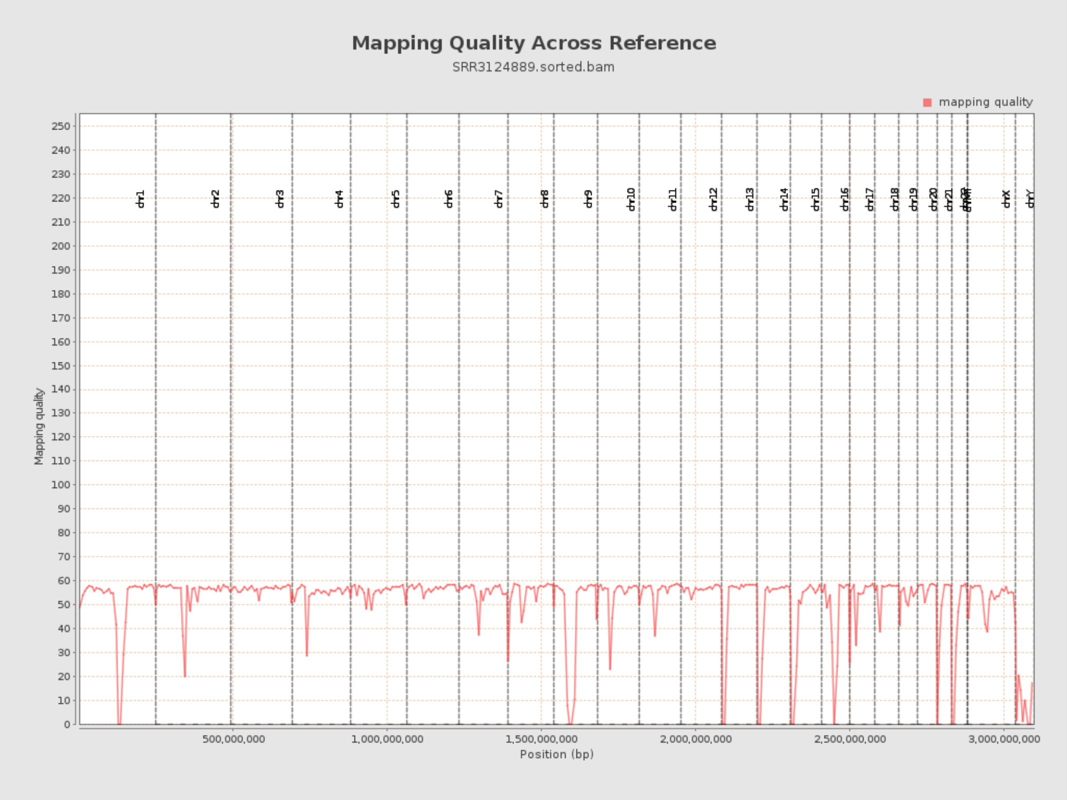
10. Results : Mapped Reads Clipping Profile



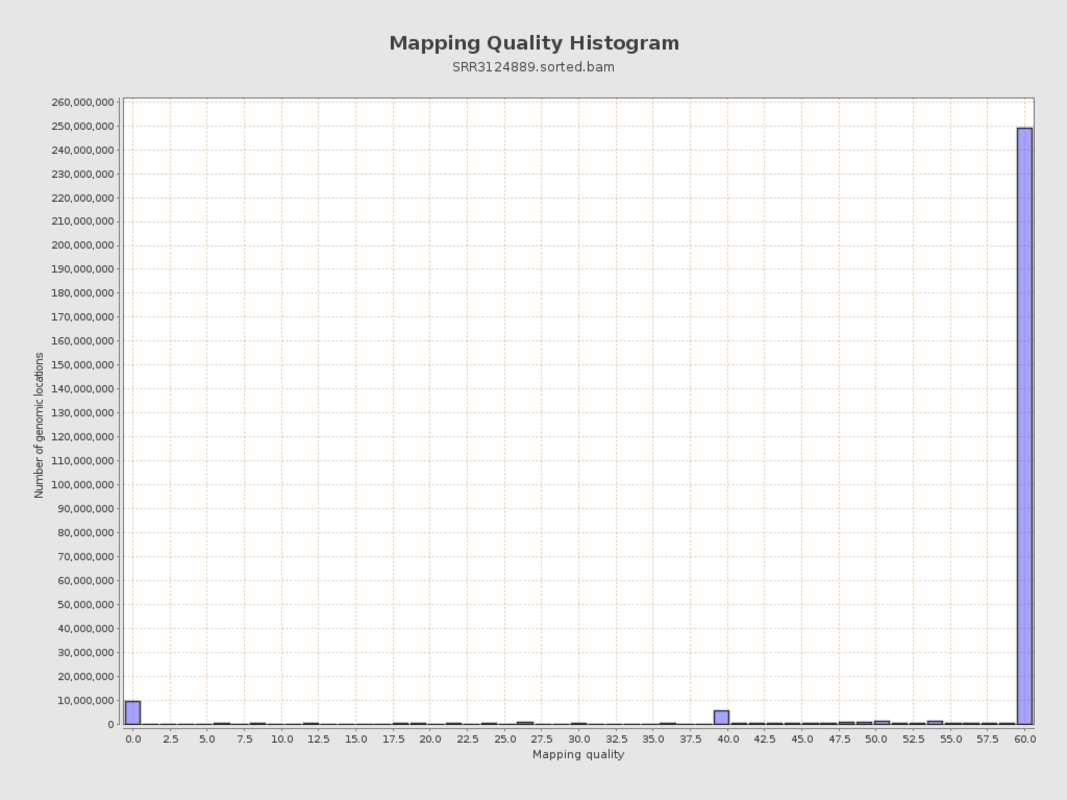
11. Results : Homopolymer Indels



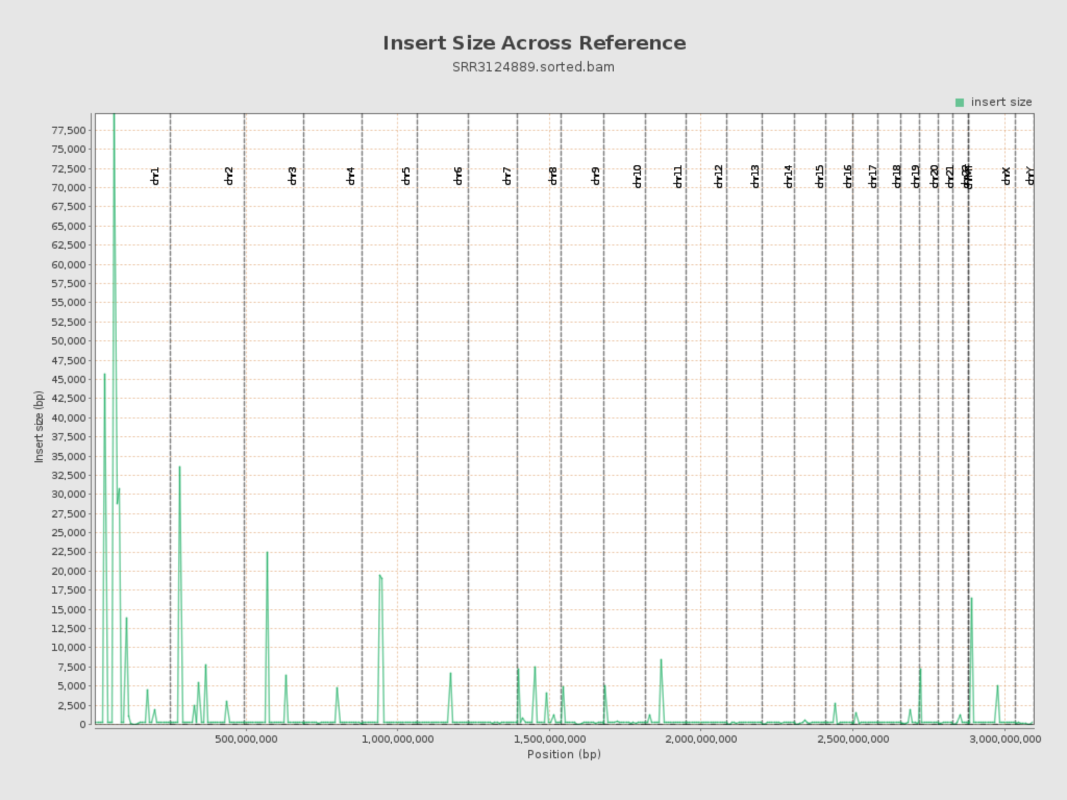
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram