Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/28 04:19:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472589.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_SRR3472589 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472589_1.fastq.gz SRR3472589_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 28 04:19:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472589.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,102,094
Mapped reads	9,255,481 / 91.62%
Unmapped reads	846,613 / 8.38%
Mapped paired reads	9,255,481 / 91.62%
Mapped reads, first in pair	4,670,702 / 46.23%
Mapped reads, second in pair	4,584,779 / 45.38%
Mapped reads, both in pair	9,043,652 / 89.52%
Mapped reads, singletons	211,829 / 2.1%
Secondary alignments	0
Supplementary alignments	279,558 / 2.77%
Read min/max/mean length	30 / 100 / 101.07
Duplicated reads (estimated)	1,514,126 / 14.99%
Duplication rate	14.29%
Clipped reads	7,031,183 / 69.6%

2.2. ACGT Content

Number/percentage of A's	194,560,947 / 25.89%
Number/percentage of C's	151,163,320 / 20.12%
Number/percentage of T's	222,559,116 / 29.62%
Number/percentage of G's	182,650,981 / 24.31%
Number/percentage of N's	477,423 / 0.06%

GC Percentage	44.42%

2.3. Coverage

Mean	0.2428
Standard Deviation	2.1847

2.4. Mapping Quality

Mean Mapping Quality	50.57

2.5. Insert size

Mean	217,136.94
Standard Deviation	4,453,904.19
P25/Median/P75	89 / 126 / 174

2.6. Mismatches and indels

General error rate	1.17%
Mismatches	8,649,920
Insertions	69,968
Mapped reads with at least one insertion	0.74%
Deletions	172,449
Mapped reads with at least one deletion	1.83%
Homopolymer indels	42.77%

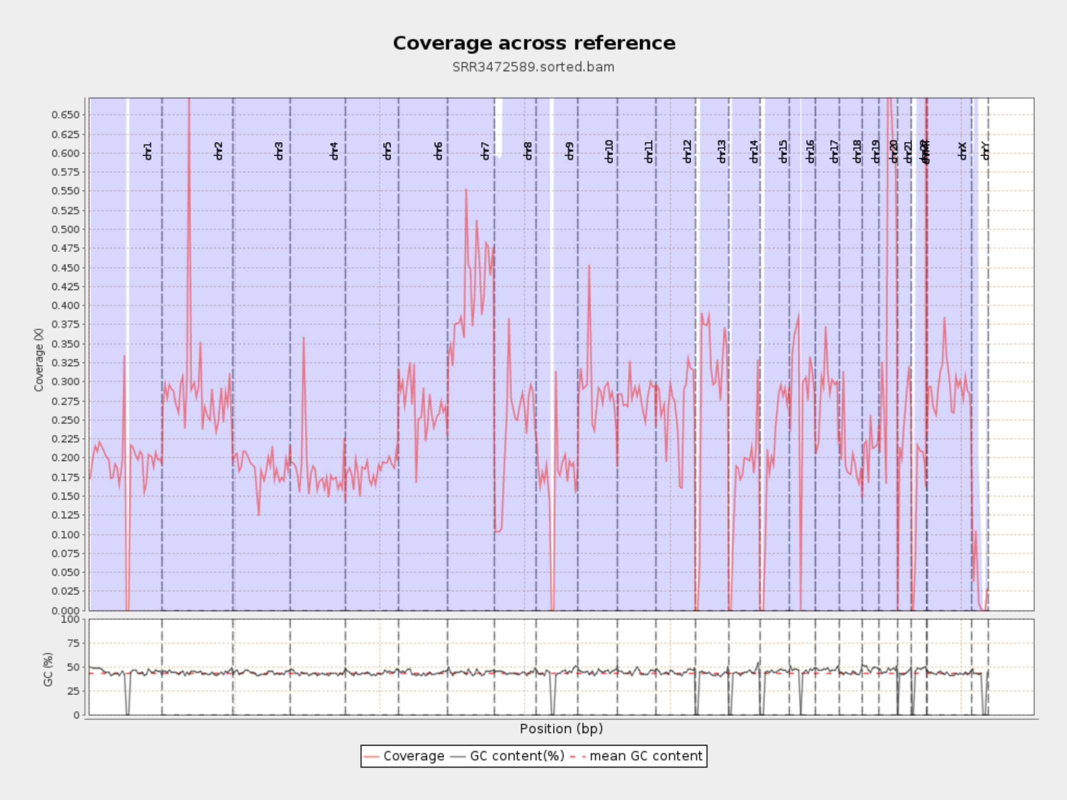
2.7. Chromosome stats

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

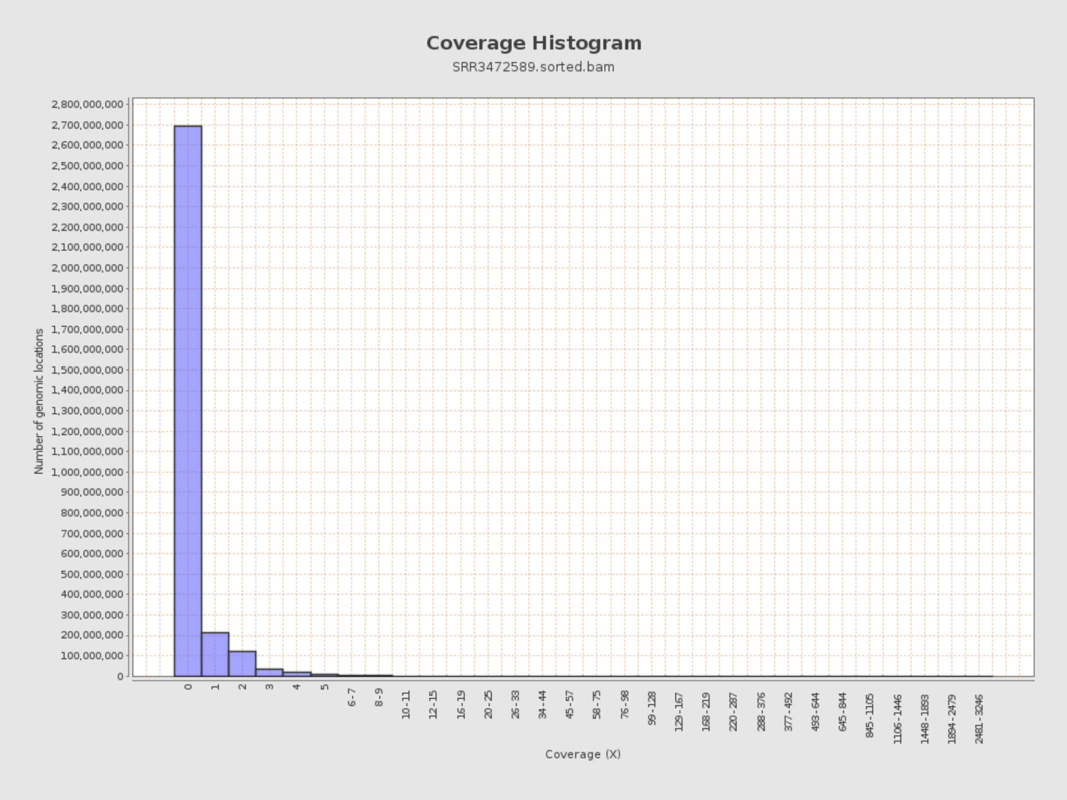
		bases	coverage	deviation
chr1	249250621	47051613	0.1888	2.6285
chr2	243199373	70646616	0.2905	3.1477
chr3	198022430	36935721	0.1865	0.6602
chr4	191154276	35040975	0.1833	1.1393
chr5	180915260	33283998	0.184	0.6819
chr6	171115067	45850578	0.268	1.2181
chr7	159138663	66591341	0.4184	3.8161
chr8	146364022	34138461	0.2332	1.7779
chr9	141213431	23717116	0.168	2.2409
chr10	135534747	39250216	0.2896	2.1125
chr11	135006516	37796181	0.28	2.0617
chr12	133851895	35689865	0.2666	0.827
chr13	115169878	32691167	0.2839	0.8536
chr14	107349540	18366748	0.1711	5.258
chr15	102531392	20504534	0.2	0.7046
chr16	90354753	26560947	0.294	1.2439
chr17	81195210	23292378	0.2869	1.6171
chr18	78077248	15694011	0.201	3.5477
chr19	59128983	12640156	0.2138	1.9025
chr20	63025520	29257980	0.4642	1.5171
chr21	48129895	11101898	0.2307	0.985
chr22	51304566	7237612	0.1411	0.5867
chrMT	16571	857069	51.721	29.1646
chrX	155270560	45623729	0.2938	1.1904

chrY	59373566	1914731	0.0322	0.968

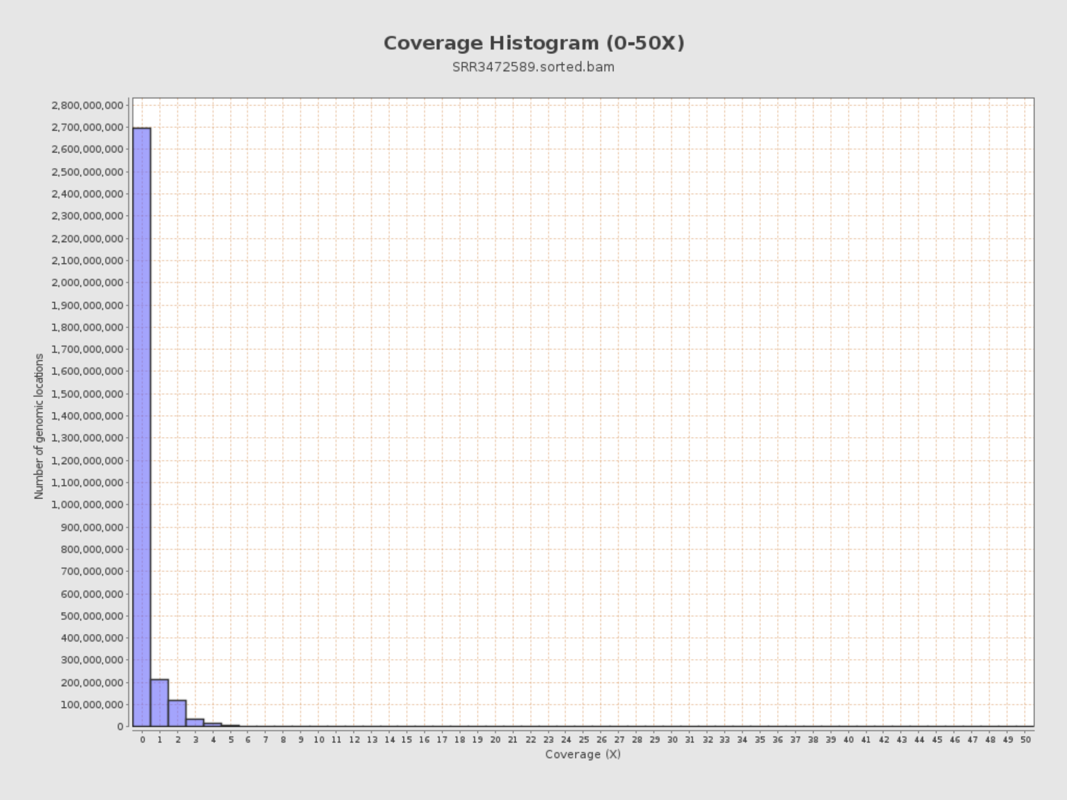
3. Results : Coverage across reference



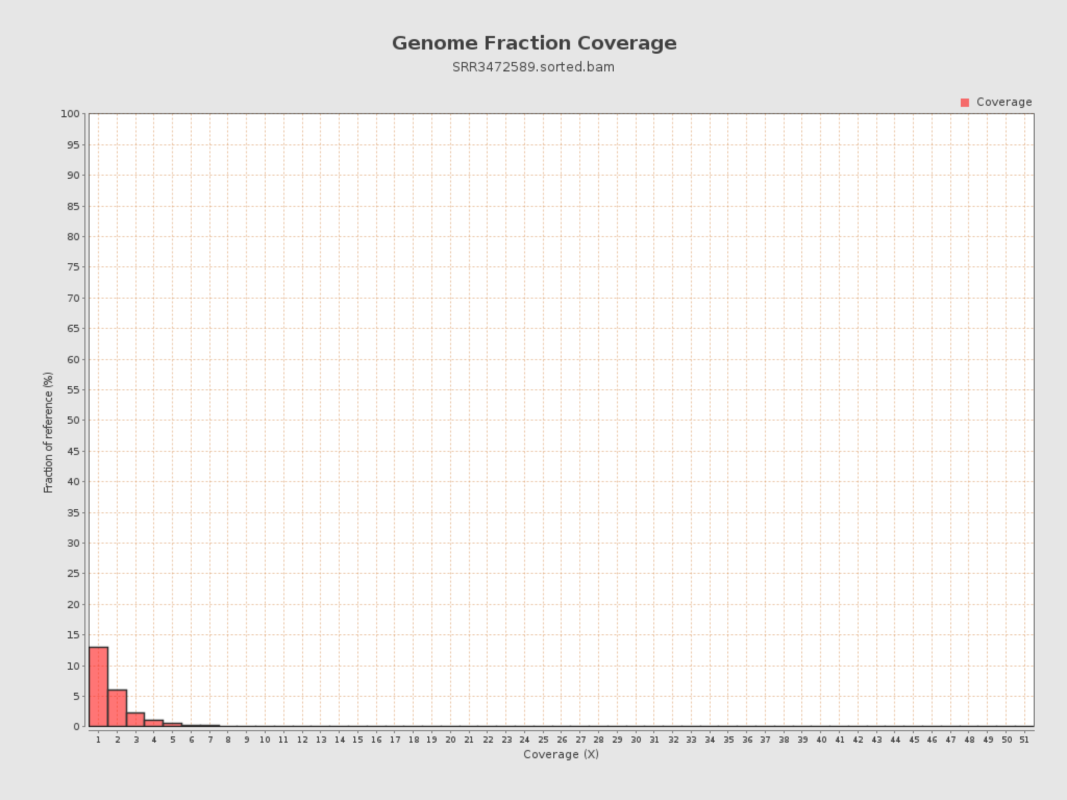
4. Results : Coverage Histogram



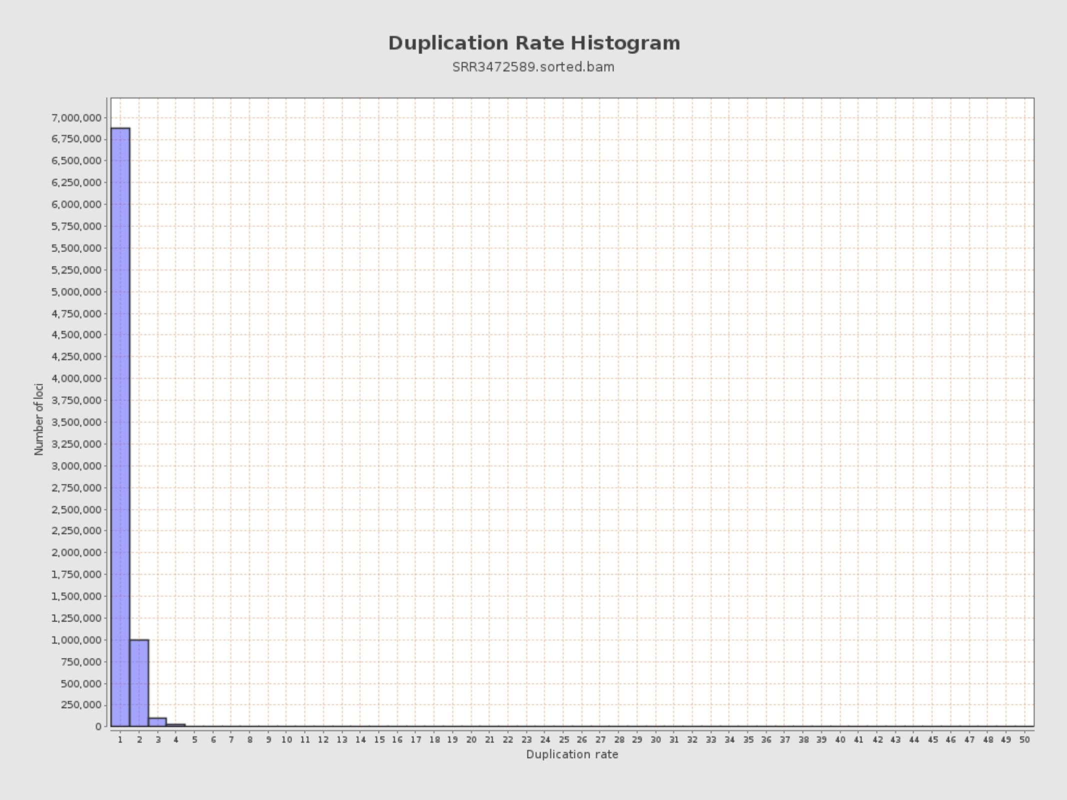
5. Results : Coverage Histogram (0-50X)



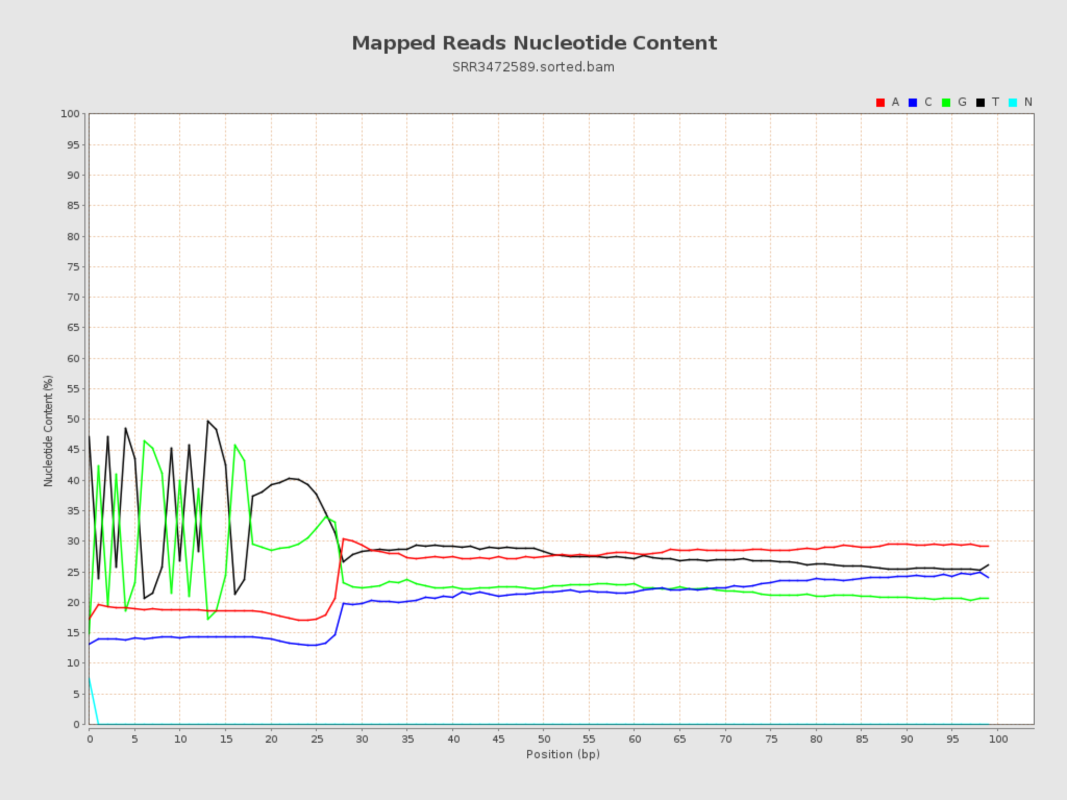
6. Results : Genome Fraction Coverage



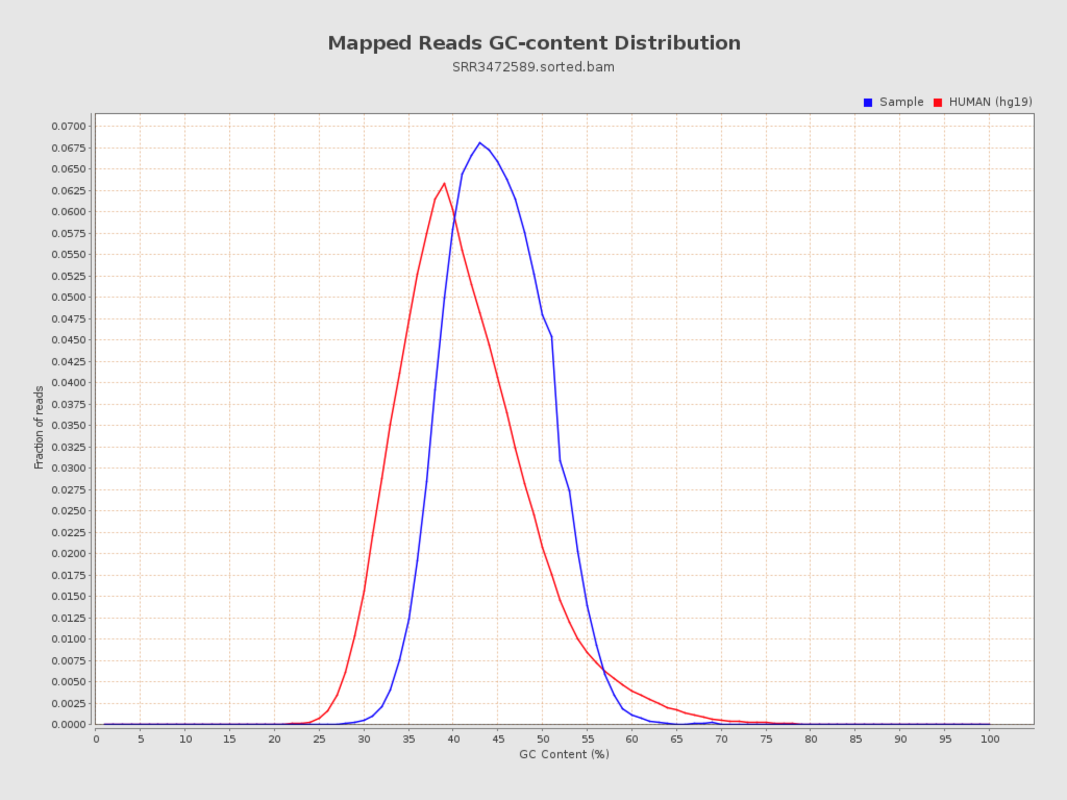
7. Results : Duplication Rate Histogram



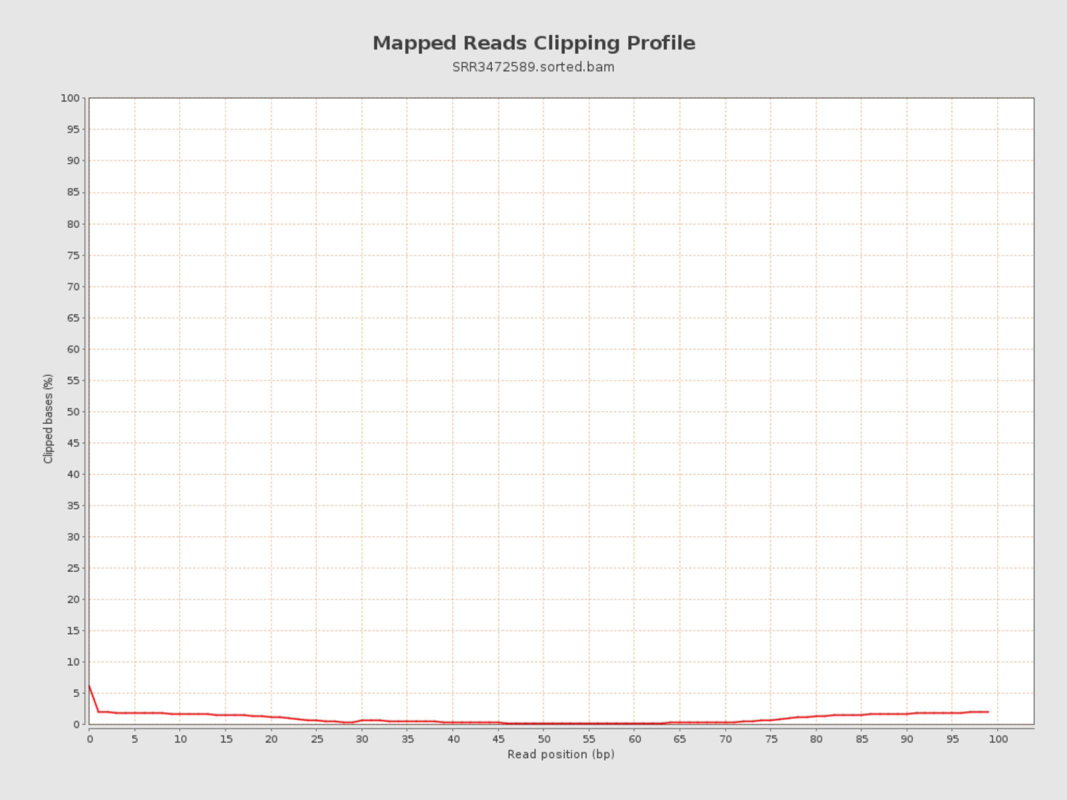
8. Results : Mapped Reads Nucleotide Content



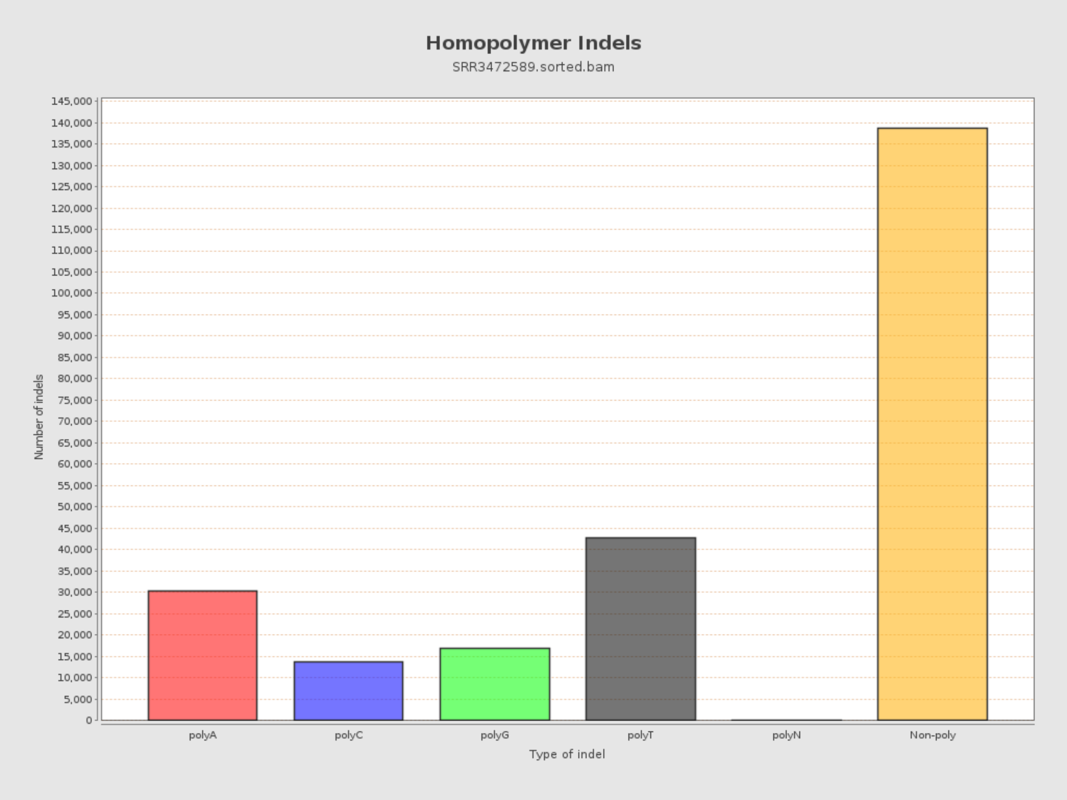
9. Results : Mapped Reads GC-content Distribution



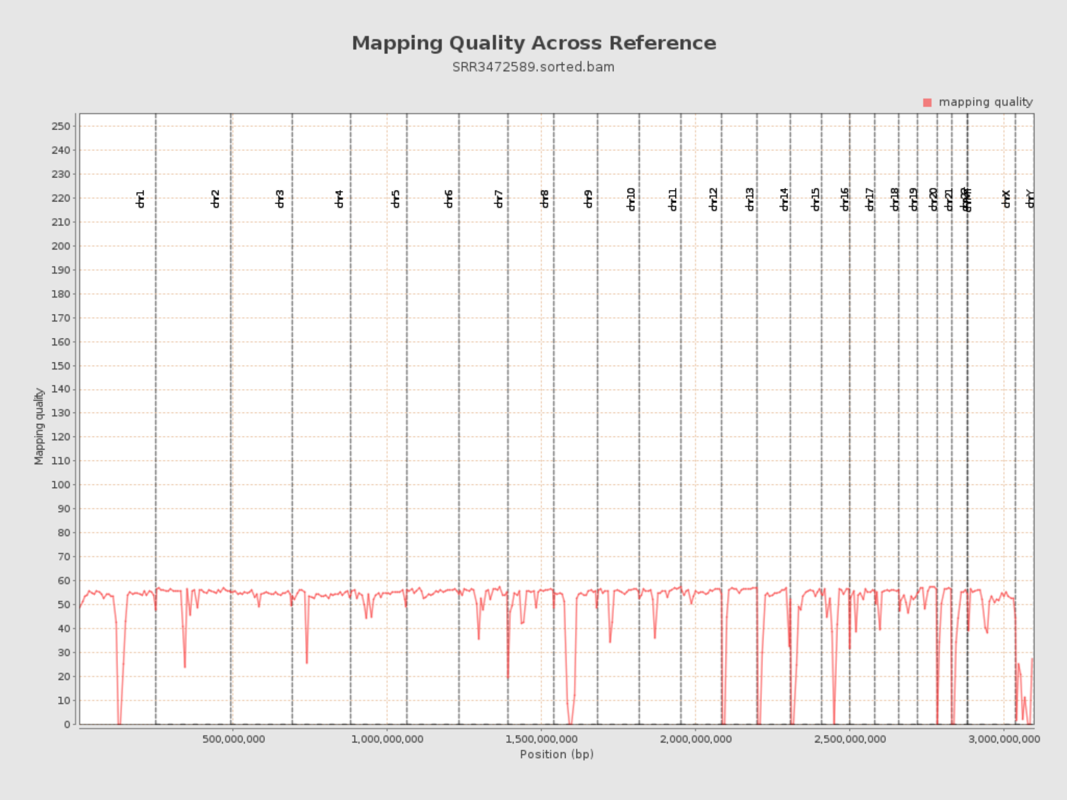
10. Results : Mapped Reads Clipping Profile



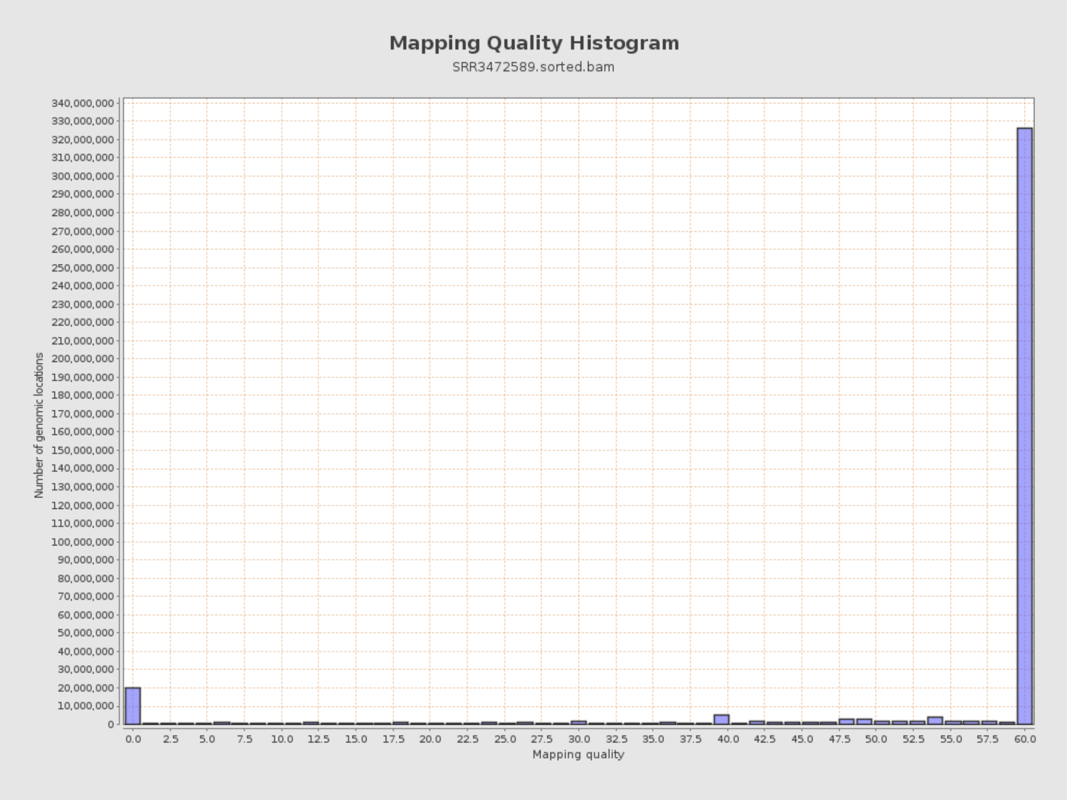
11. Results : Homopolymer Indels



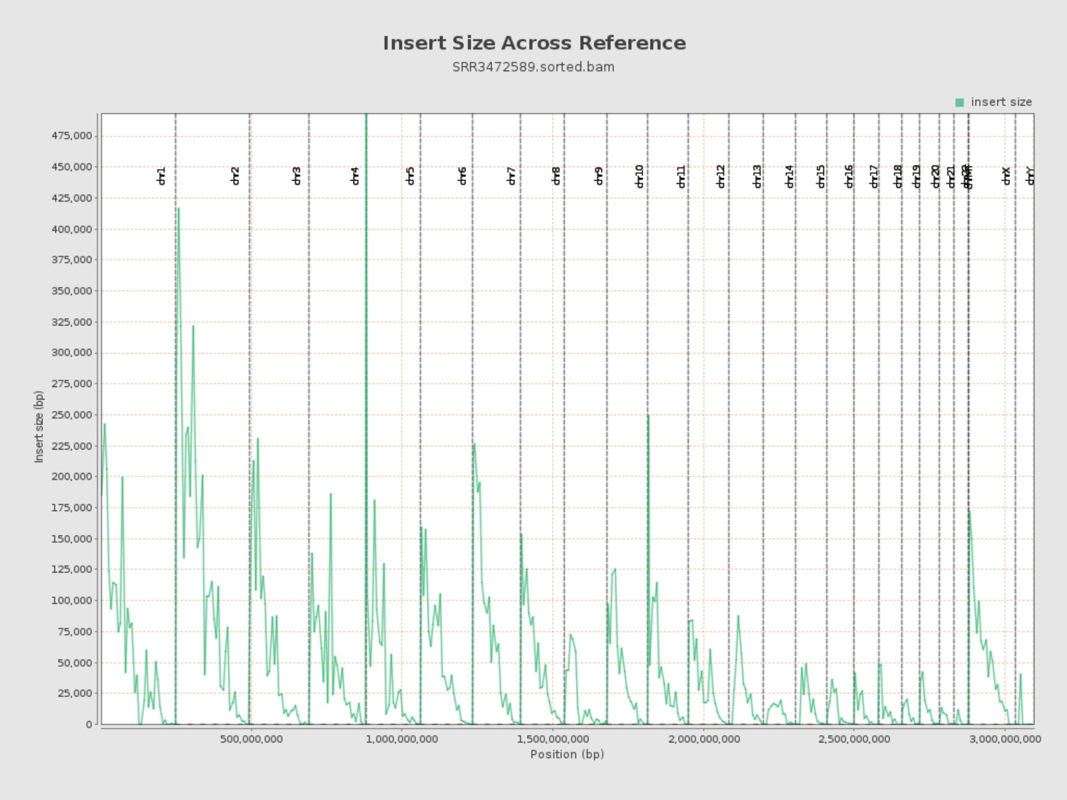
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram