Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/28 04:03:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472588.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_SRR3472588 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472588_1.fastq.gz SRR3472588_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 28 04:03:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472588.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,652,308
Mapped reads	7,988,281 / 92.33%
Unmapped reads	664,027 / 7.67%
Mapped paired reads	7,988,281 / 92.33%
Mapped reads, first in pair	4,037,039 / 46.66%
Mapped reads, second in pair	3,951,242 / 45.67%
Mapped reads, both in pair	7,792,958 / 90.07%
Mapped reads, singletons	195,323 / 2.26%
Secondary alignments	0
Supplementary alignments	200,409 / 2.32%
Read min/max/mean length	30 / 100 / 100.9
Duplicated reads (estimated)	1,241,487 / 14.35%
Duplication rate	12.7%
Clipped reads	5,989,006 / 69.22%

2.2. ACGT Content

Number/percentage of A's	168,678,965 / 25.71%
Number/percentage of C's	126,605,879 / 19.3%
Number/percentage of T's	201,008,743 / 30.64%
Number/percentage of G's	159,359,875 / 24.29%
Number/percentage of N's	434,164 / 0.07%

GC Percentage	43.59%

2.3. Coverage

Mean	0.212
Standard Deviation	2.1808

2.4. Mapping Quality

Mean Mapping Quality	51.21

2.5. Insert size

Mean	179,530.55
Standard Deviation	4,157,132.18
P25/Median/P75	104 / 143 / 195

2.6. Mismatches and indels

General error rate	1.23%
Mismatches	7,978,711
Insertions	57,741
Mapped reads with at least one insertion	0.71%
Deletions	143,650
Mapped reads with at least one deletion	1.76%
Homopolymer indels	43.66%

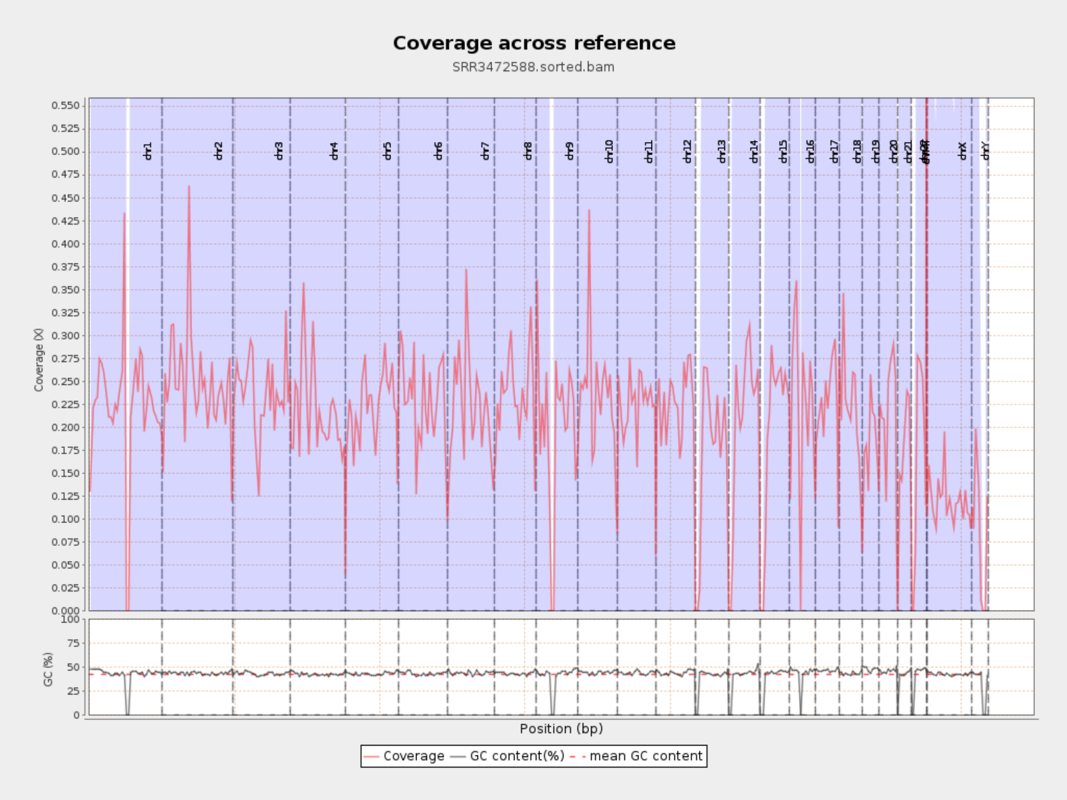
2.7. Chromosome stats

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

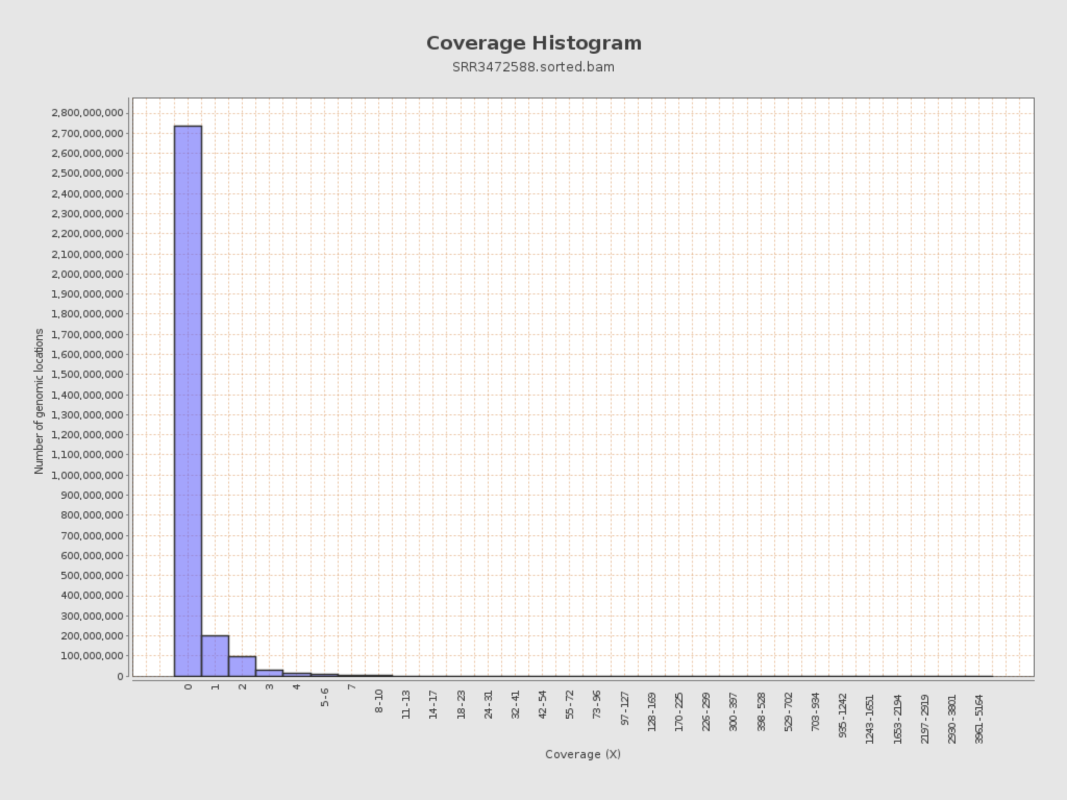
		bases	coverage	deviation
chr1	249250621	55328275	0.222	4.3981
chr2	243199373	60709850	0.2496	1.9113
chr3	198022430	46489102	0.2348	0.7584
chr4	191154276	41533652	0.2173	1.195
chr5	180915260	40274884	0.2226	0.7744
chr6	171115067	39591013	0.2314	1.1666
chr7	159138663	35845934	0.2252	3.0022
chr8	146364022	34523504	0.2359	1.6673
chr9	141213431	27612082	0.1955	2.5124
chr10	135534747	32032326	0.2363	2.4799
chr11	135006516	30106023	0.223	1.8039
chr12	133851895	30185750	0.2255	0.7638
chr13	115169878	19548452	0.1697	0.6429
chr14	107349540	22033092	0.2052	4.094
chr15	102531392	20178117	0.1968	0.7102
chr16	90354753	20153966	0.2231	1.1454
chr17	81195210	18218403	0.2244	1.3598
chr18	78077248	17663073	0.2262	4.1242
chr19	59128983	10704264	0.181	2.4844
chr20	63025520	13917768	0.2208	0.9601
chr21	48129895	7867750	0.1635	0.854
chr22	51304566	8317571	0.1621	0.9876
chrMT	16571	22422	1.3531	1.8627
chrX	155270560	18625594	0.12	0.8719

chrY	59373566	4875162	0.0821	1.1291

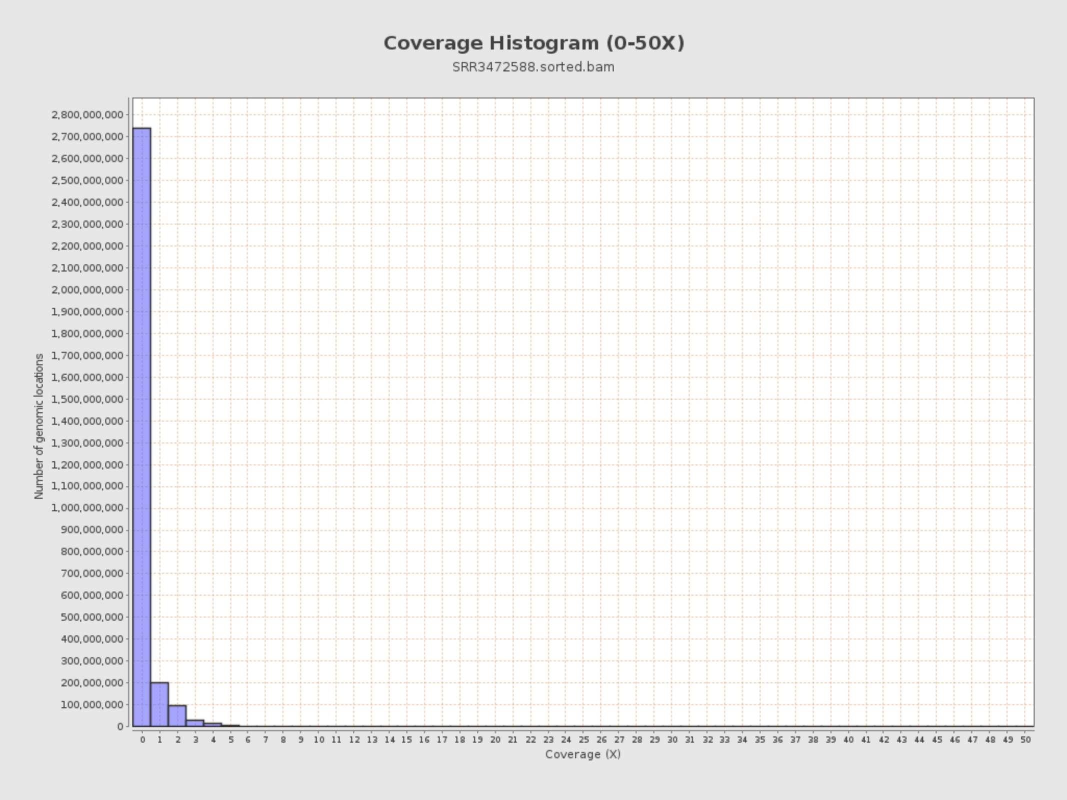
3. Results : Coverage across reference



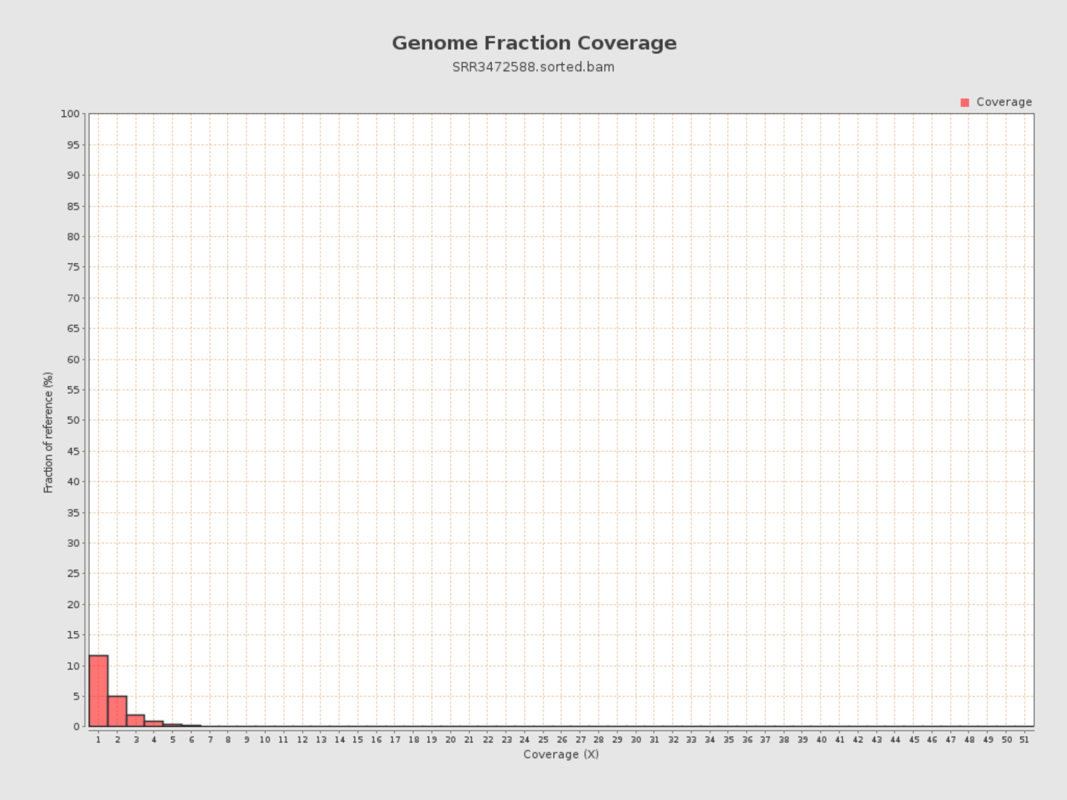
4. Results : Coverage Histogram



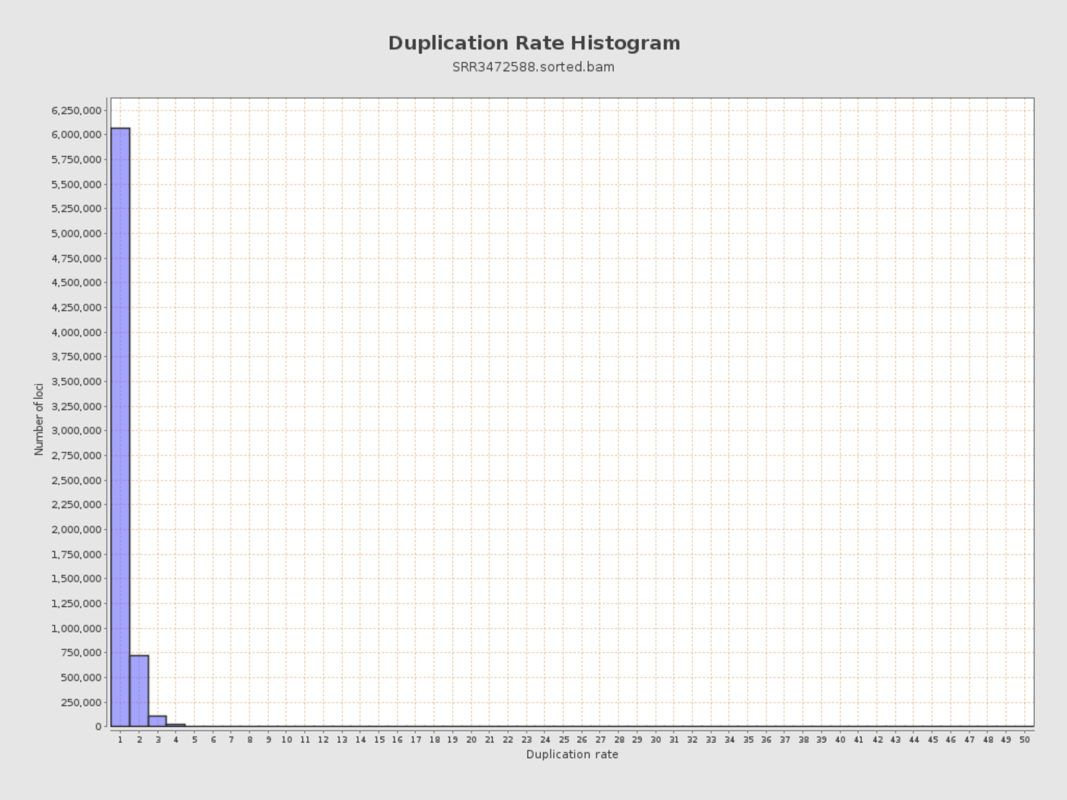
5. Results : Coverage Histogram (0-50X)



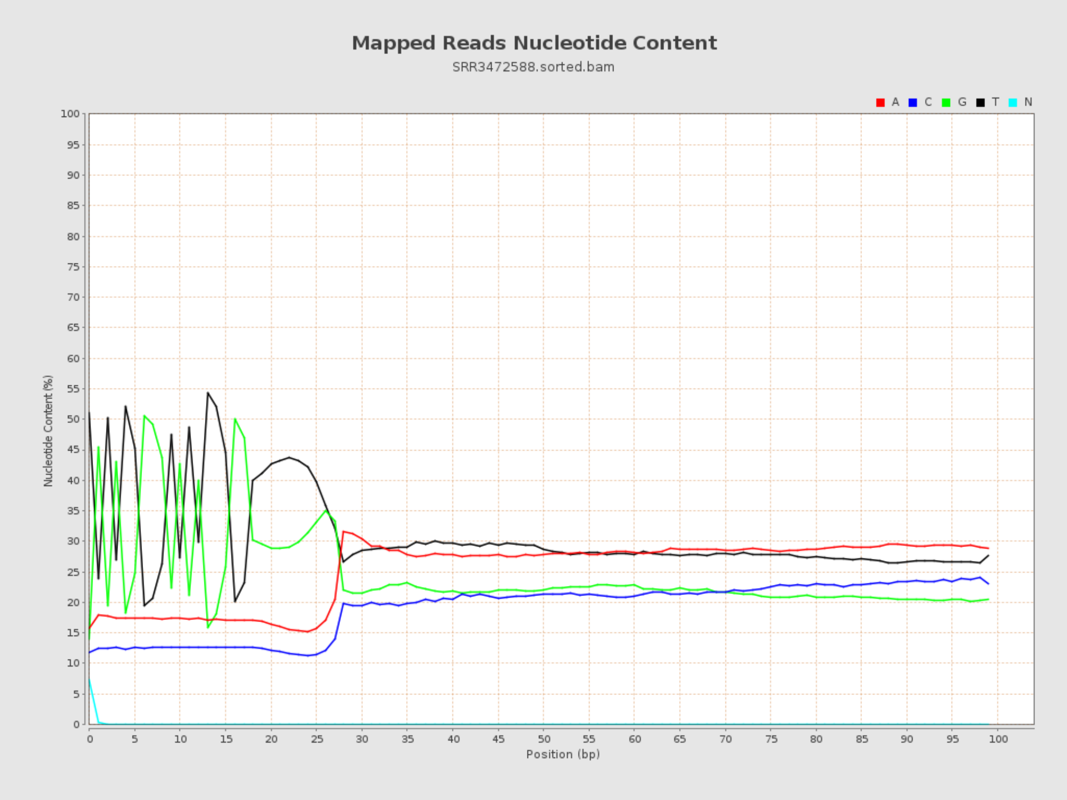
6. Results : Genome Fraction Coverage



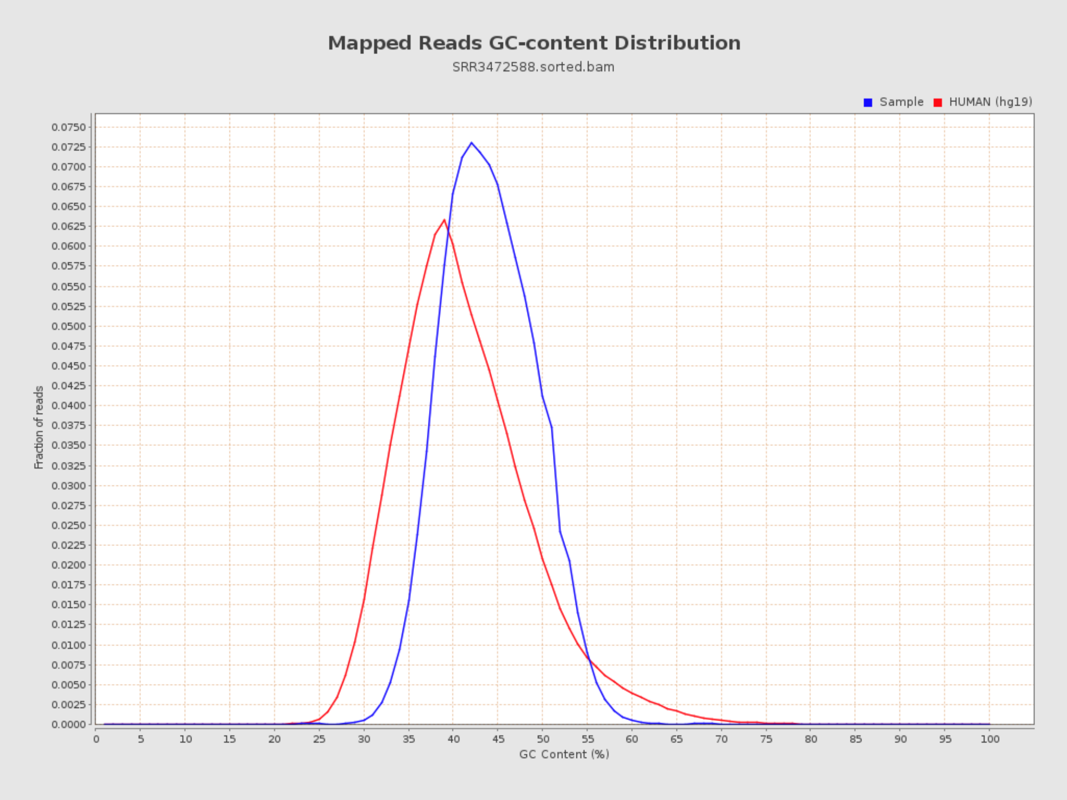
7. Results : Duplication Rate Histogram



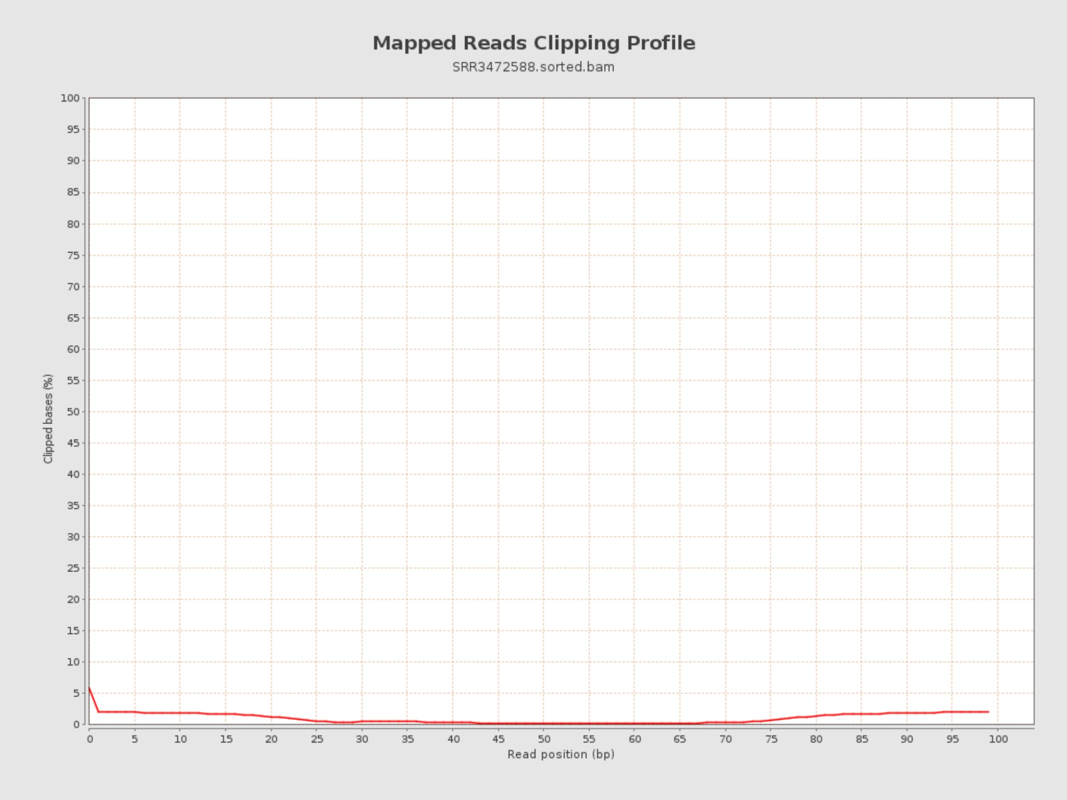
8. Results : Mapped Reads Nucleotide Content



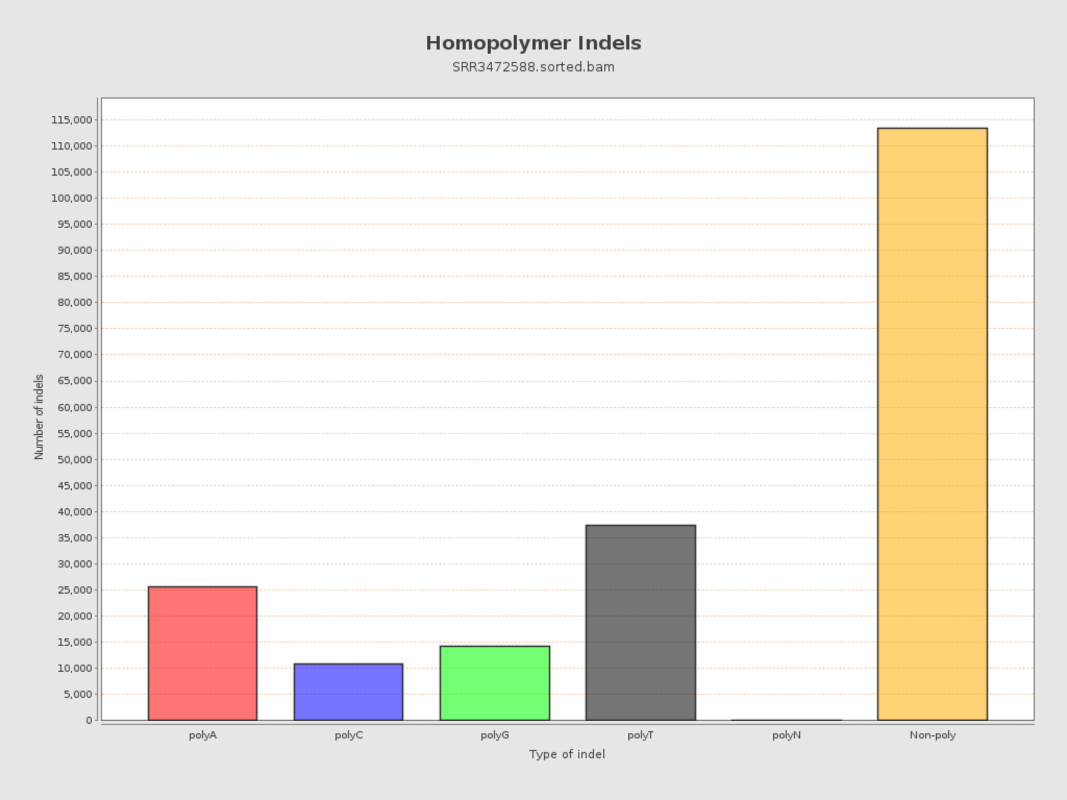
9. Results : Mapped Reads GC-content Distribution



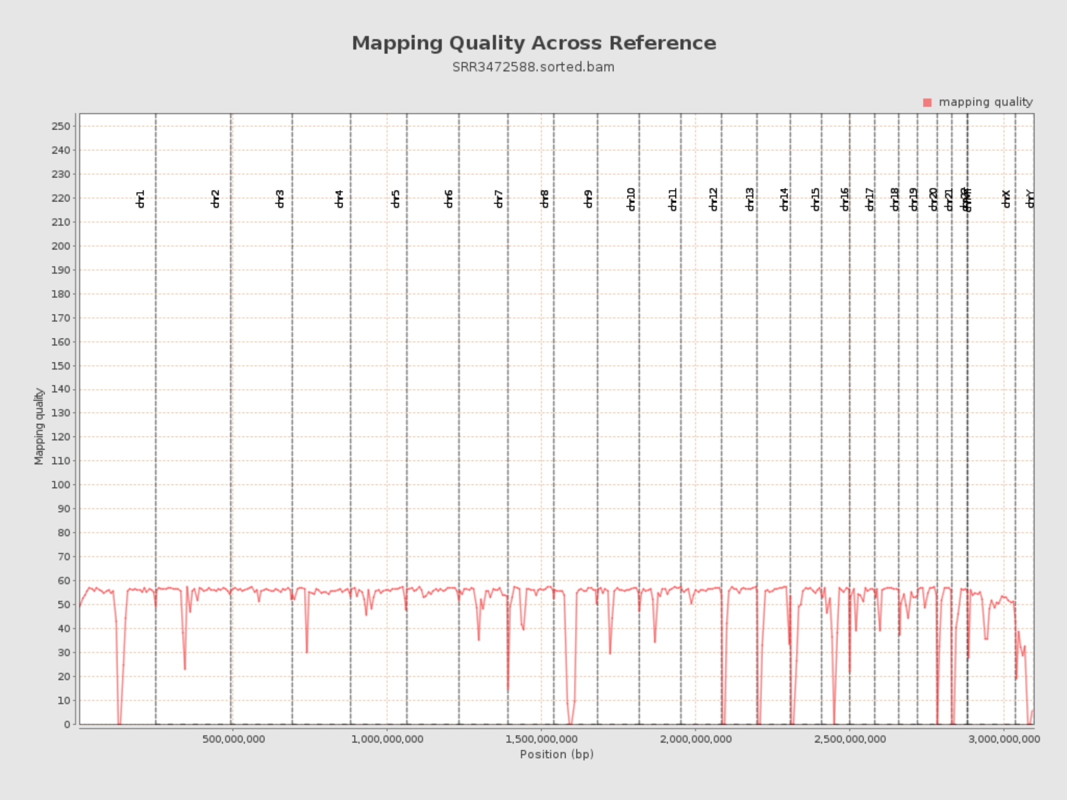
10. Results : Mapped Reads Clipping Profile



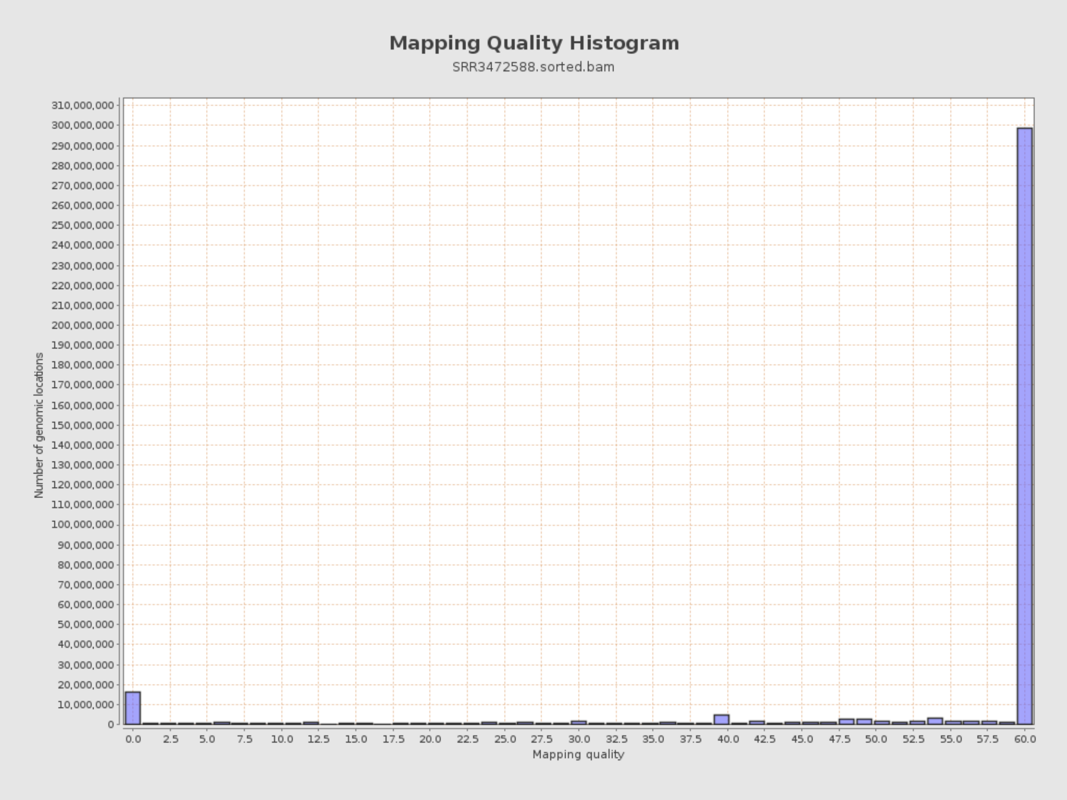
11. Results : Homopolymer Indels



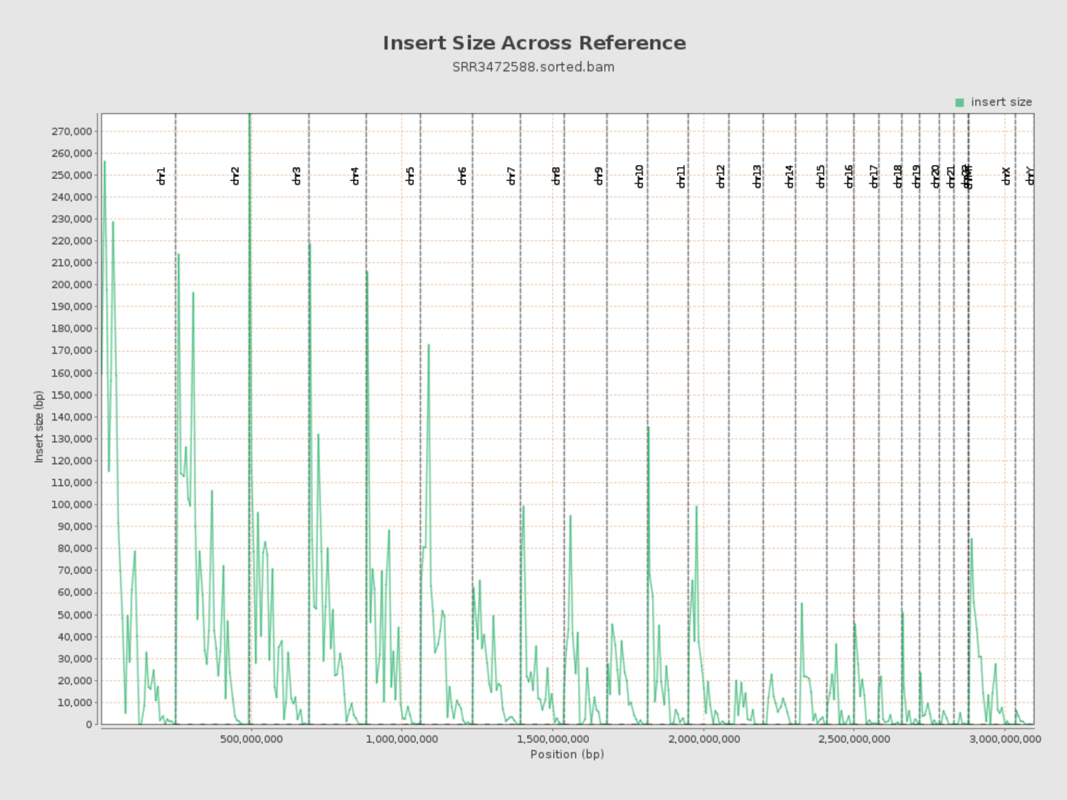
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram