Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/29 17:55:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472715.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_SRR3472715 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472715_1.fastq.gz SRR3472715_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 29 17:55:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472715.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	15,893,226
Mapped reads	15,749,524 / 99.1%
Unmapped reads	143,702 / 0.9%
Mapped paired reads	15,749,524 / 99.1%
Mapped reads, first in pair	7,902,587 / 49.72%
Mapped reads, second in pair	7,846,937 / 49.37%
Mapped reads, both in pair	15,661,186 / 98.54%
Mapped reads, singletons	88,338 / 0.56%
Secondary alignments	0
Supplementary alignments	53,594 / 0.34%
Read min/max/mean length	30 / 100 / 100.14
Duplicated reads (estimated)	9,634,896 / 60.62%
Duplication rate	46.64%
Clipped reads	1,256,357 / 7.9%

2.2. ACGT Content

Number/percentage of A's	433,570,813 / 27.95%
Number/percentage of C's	344,726,015 / 22.22%
Number/percentage of T's	429,903,043 / 27.71%
Number/percentage of G's	342,983,849 / 22.11%
Number/percentage of N's	297,260 / 0.02%

GC Percentage	44.33%

2.3. Coverage

Mean	0.5012
Standard Deviation	16.8907

2.4. Mapping Quality

Mean Mapping Quality	55.21

2.5. Insert size

Mean	24,948.7
Standard Deviation	1,552,321.98
P25/Median/P75	175 / 248 / 335

2.6. Mismatches and indels

General error rate	0.64%
Mismatches	9,694,778
Insertions	91,987
Mapped reads with at least one insertion	0.58%
Deletions	80,366
Mapped reads with at least one deletion	0.5%
Homopolymer indels	44.42%

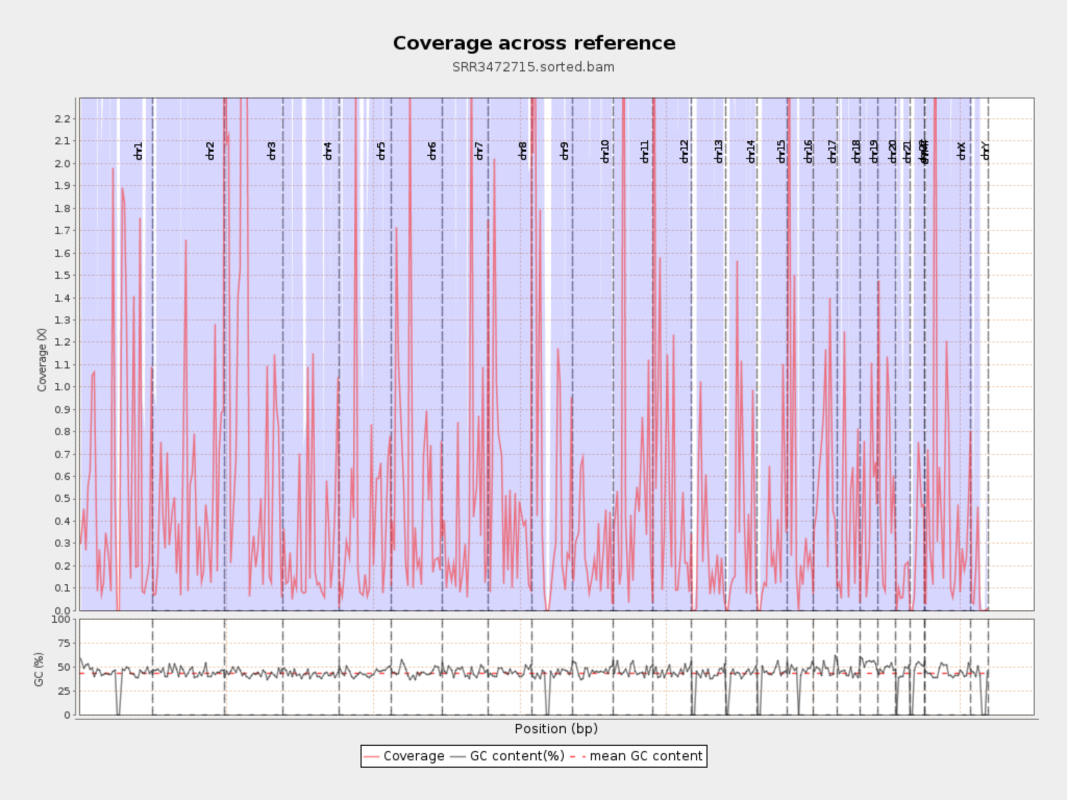
2.7. Chromosome stats

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

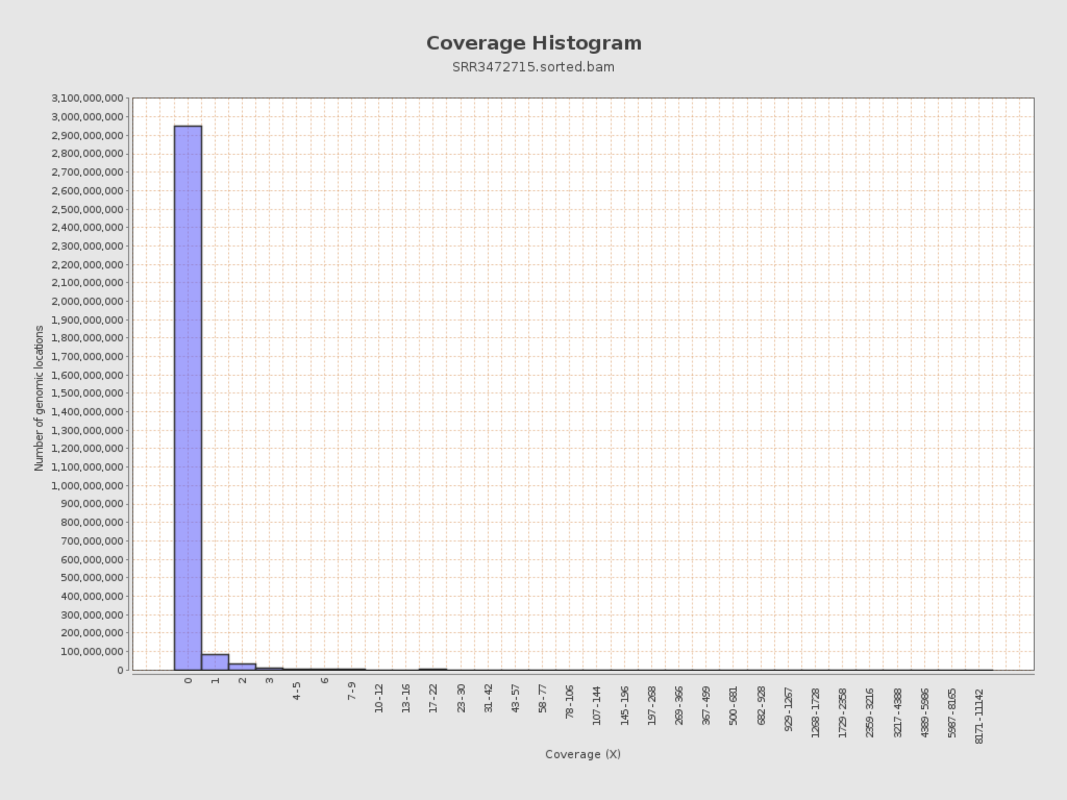
		bases	coverage	deviation
chr1	249250621	146419446	0.5874	20.4104
chr2	243199373	113006091	0.4647	14.1603
chr3	198022430	199145677	1.0057	25.8886
chr4	191154276	59438994	0.3109	11.5968
chr5	180915260	74420424	0.4114	13.5082
chr6	171115067	96258805	0.5625	15.1129
chr7	159138663	72597426	0.4562	15.3138
chr8	146364022	72077261	0.4925	17.3135
chr9	141213431	98041847	0.6943	16.7955
chr10	135534747	37796015	0.2789	10.0307
chr11	135006516	79645501	0.5899	27.9089
chr12	133851895	91673755	0.6849	21.0199
chr13	115169878	29473368	0.2559	9.6743
chr14	107349540	42547652	0.3963	13.4833
chr15	102531392	29743027	0.2901	8.4621
chr16	90354753	48234333	0.5338	23.3848
chr17	81195210	52035558	0.6409	14.6929
chr18	78077248	32322654	0.414	17.1009
chr19	59128983	30424192	0.5145	14.0573
chr20	63025520	38163703	0.6055	17.5811
chr21	48129895	5369024	0.1116	4.3552
chr22	51304566	16138657	0.3146	9.961
chrMT	16571	3532	0.2131	0.7172
chrX	155270560	81217471	0.5231	14.7899

chrY	59373566	5490356	0.0925	6.4261

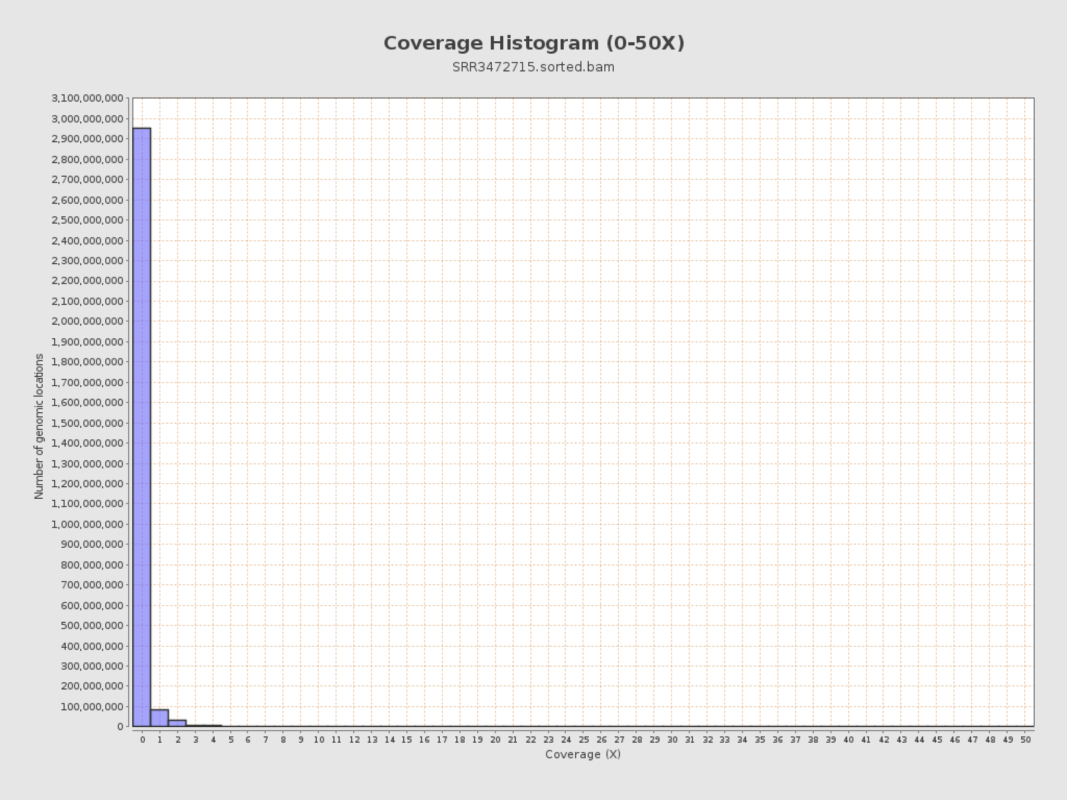
3. Results : Coverage across reference



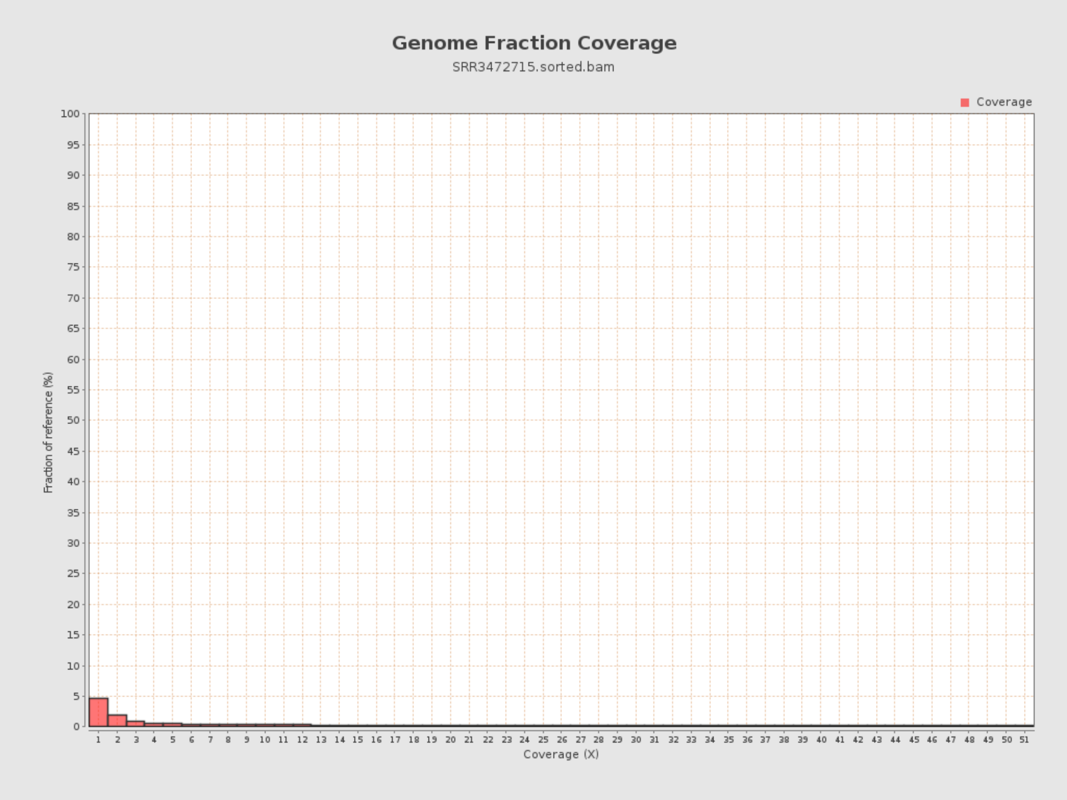
4. Results : Coverage Histogram



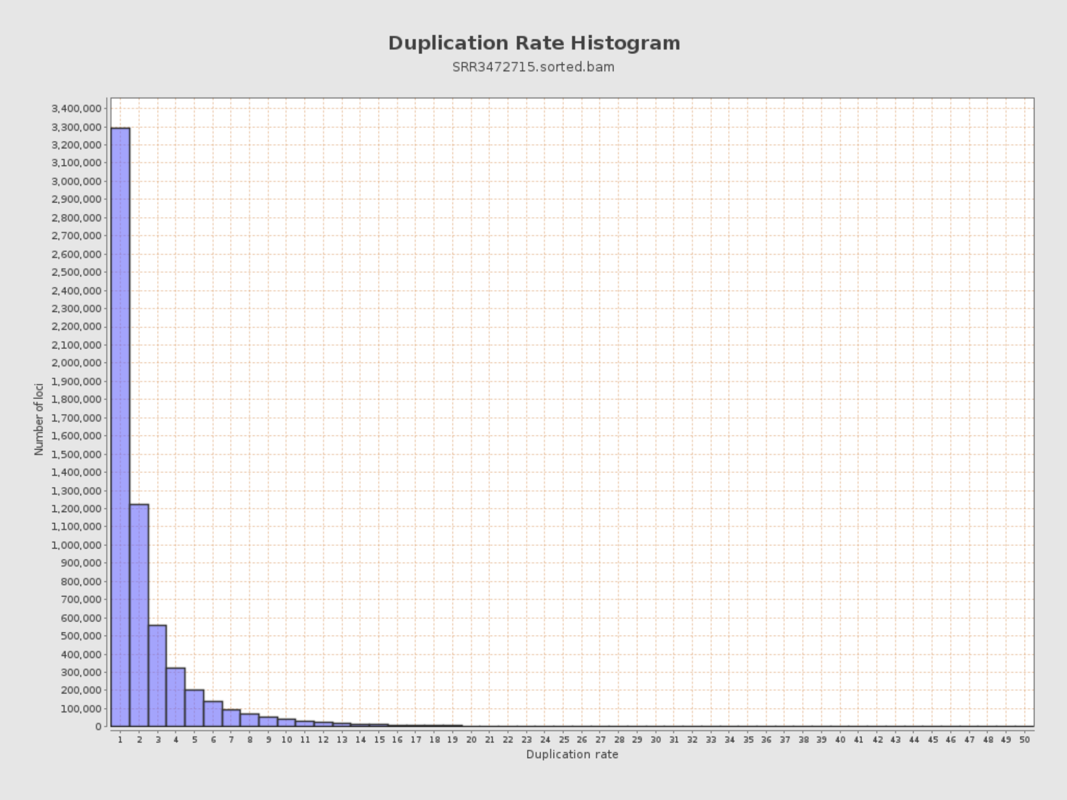
5. Results : Coverage Histogram (0-50X)



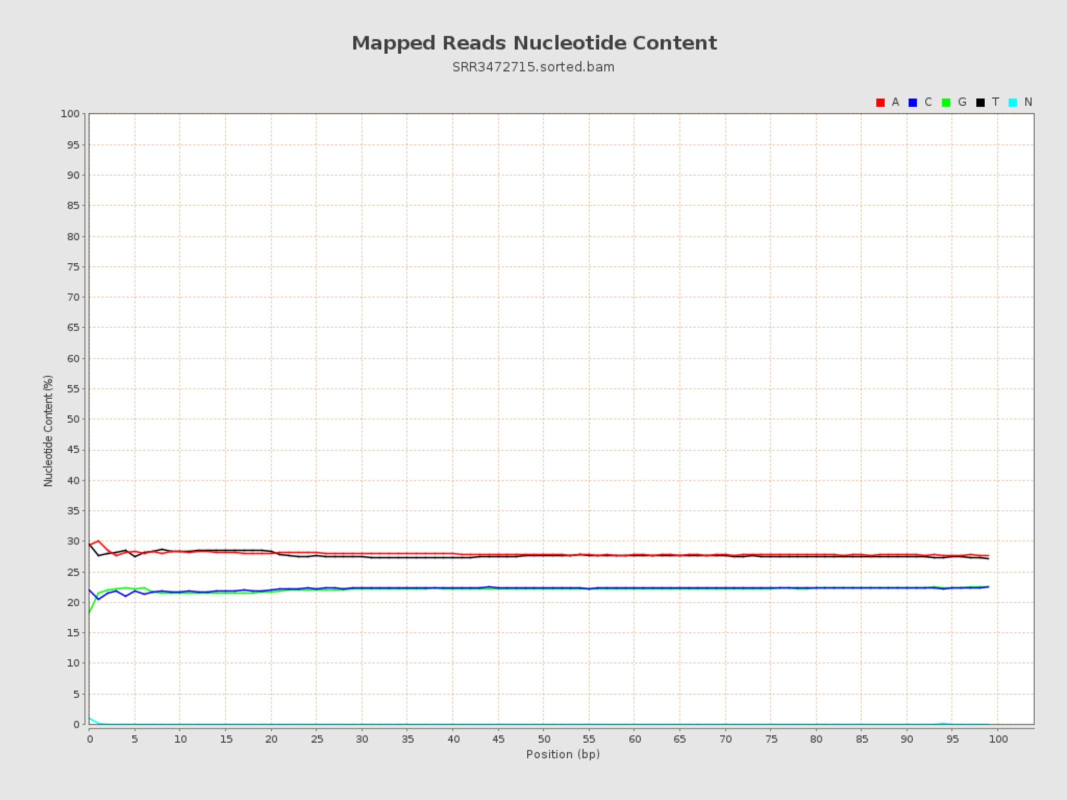
6. Results : Genome Fraction Coverage



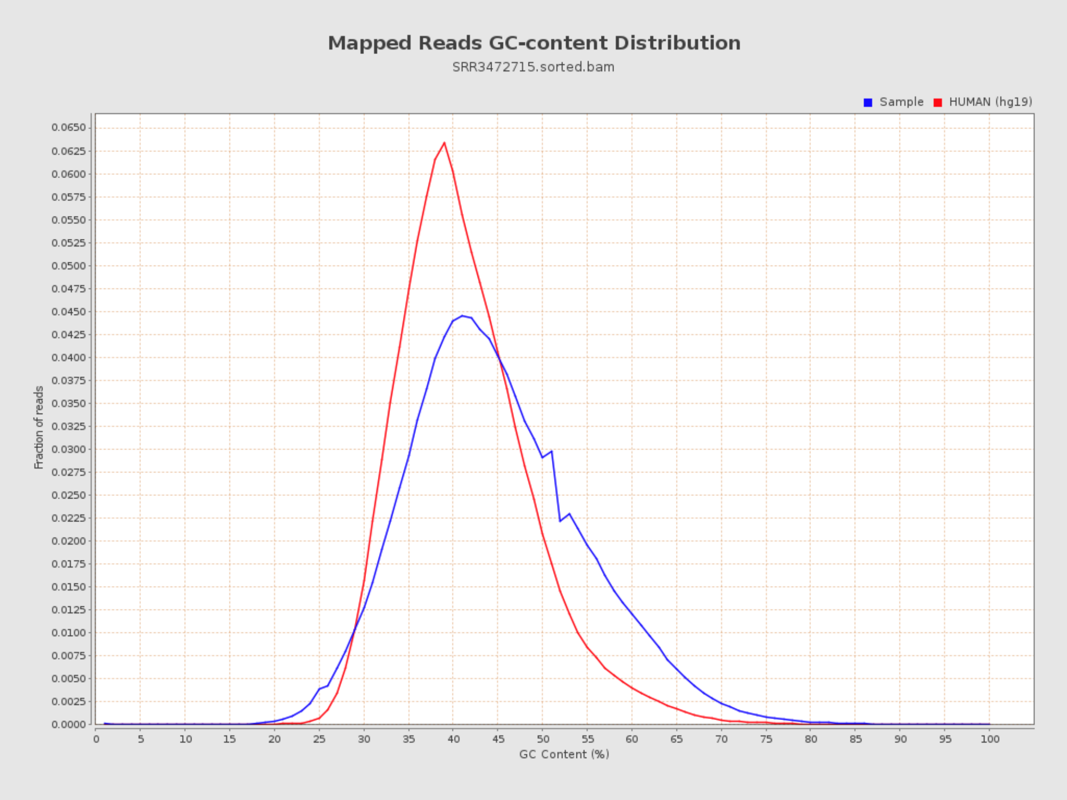
7. Results : Duplication Rate Histogram



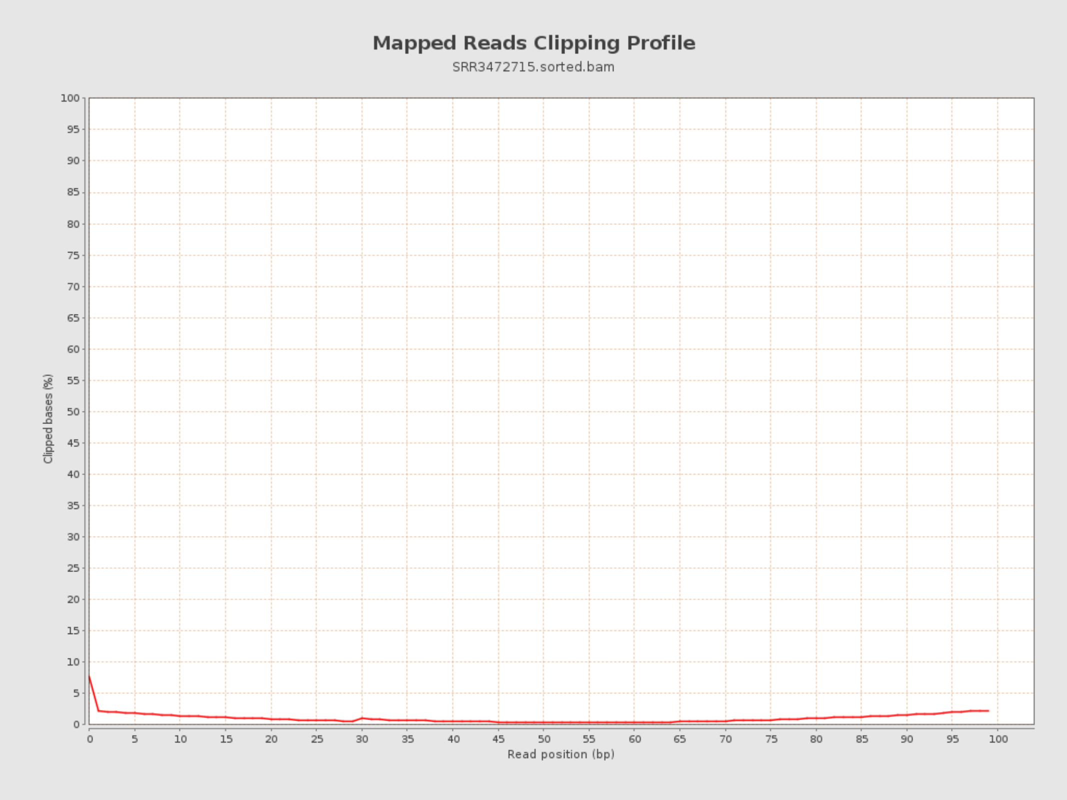
8. Results : Mapped Reads Nucleotide Content



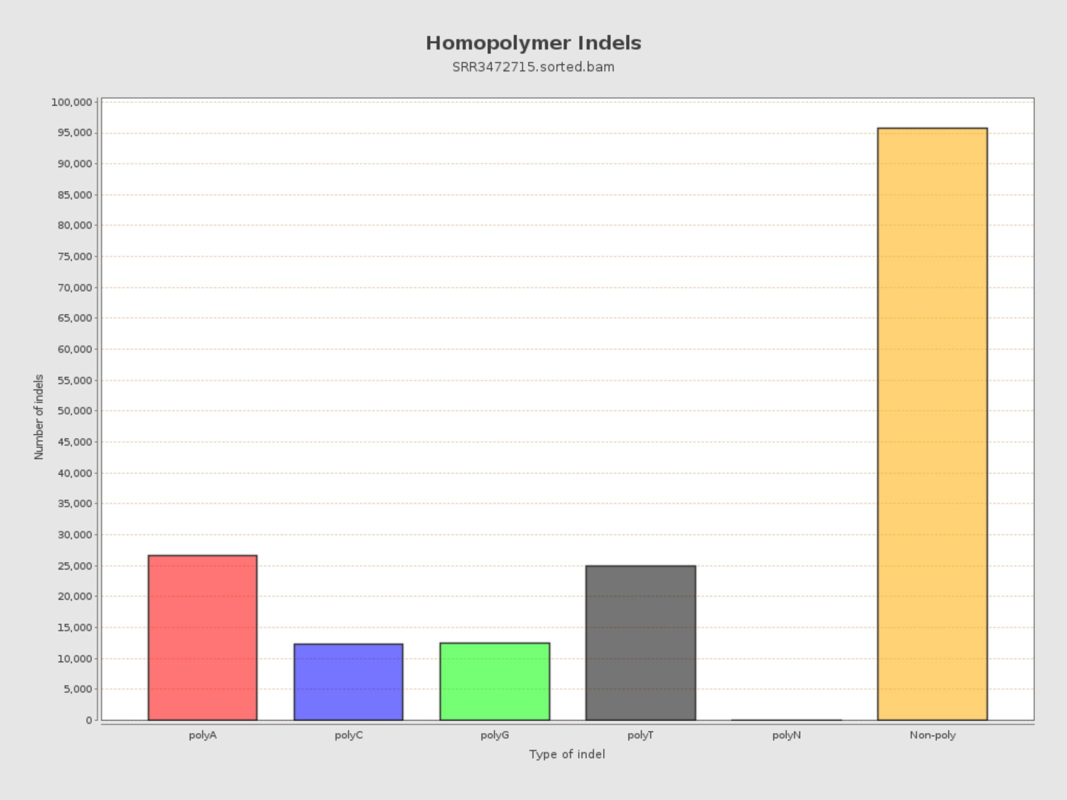
9. Results : Mapped Reads GC-content Distribution



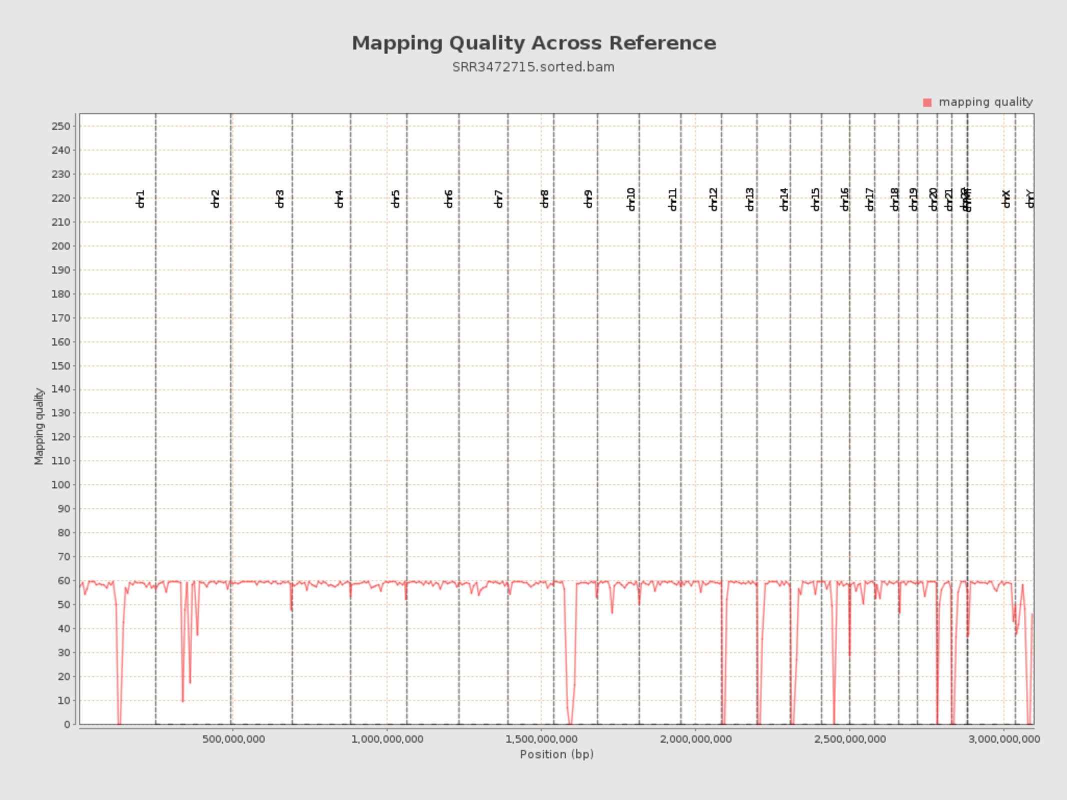
10. Results : Mapped Reads Clipping Profile



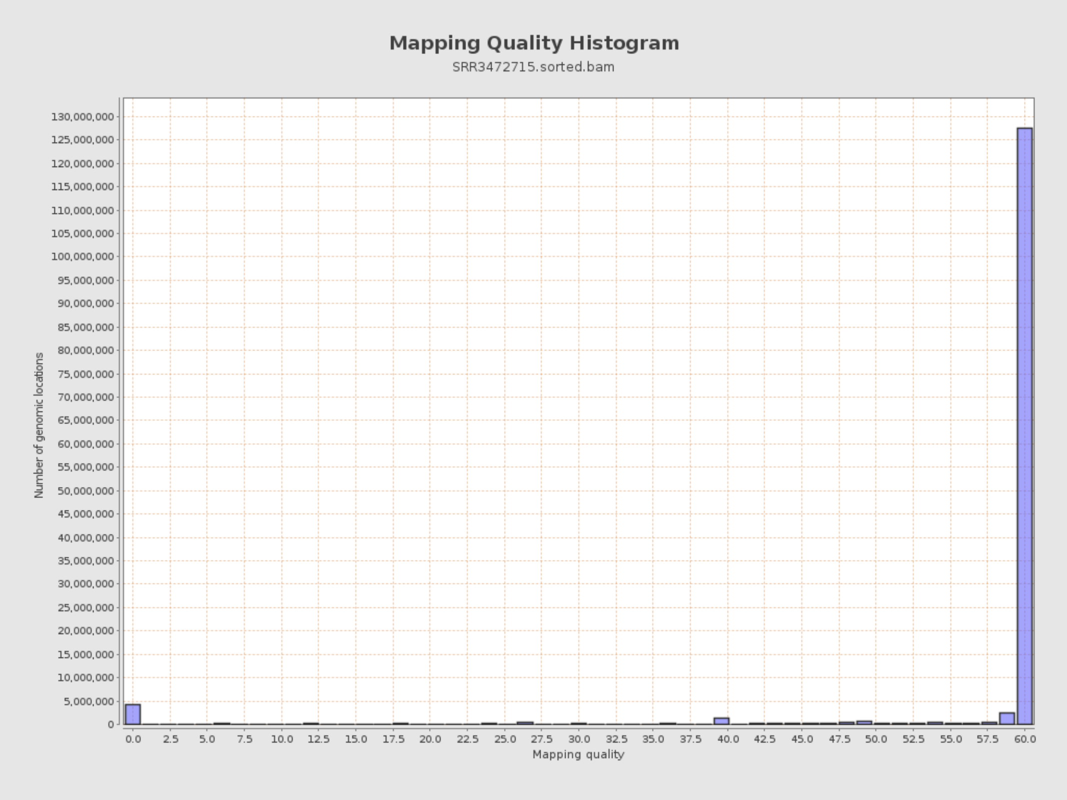
11. Results : Homopolymer Indels



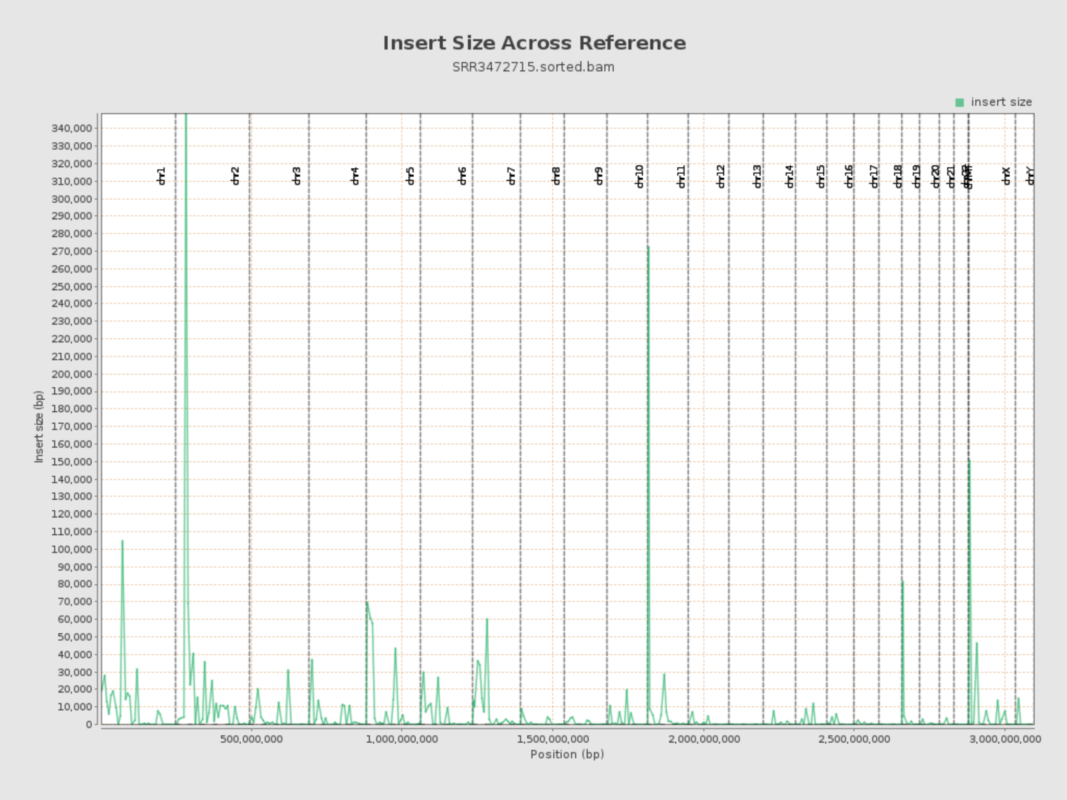
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram