Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 10:41:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472488.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_SRR3472488 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472488_1.fastq.gz SRR3472488_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 10:41:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472488.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	34,314,096
Mapped reads	33,900,725 / 98.8%
Unmapped reads	413,371 / 1.2%
Mapped paired reads	33,900,725 / 98.8%
Mapped reads, first in pair	16,998,754 / 49.54%
Mapped reads, second in pair	16,901,971 / 49.26%
Mapped reads, both in pair	33,694,570 / 98.19%
Mapped reads, singletons	206,155 / 0.6%
Secondary alignments	0
Supplementary alignments	137,995 / 0.4%
Read min/max/mean length	30 / 100 / 100.16
Duplicated reads (estimated)	22,903,092 / 66.75%
Duplication rate	47.71%
Clipped reads	2,824,033 / 8.23%

2.2. ACGT Content

Number/percentage of A's	922,353,983 / 27.65%
Number/percentage of C's	749,276,464 / 22.46%
Number/percentage of T's	917,845,551 / 27.52%
Number/percentage of G's	745,611,962 / 22.35%
Number/percentage of N's	519,589 / 0.02%

GC Percentage	44.82%

2.3. Coverage

Mean	1.0776
Standard Deviation	30.1714

2.4. Mapping Quality

Mean Mapping Quality	55.06

2.5. Insert size

Mean	32,211.38
Standard Deviation	1,754,231.01
P25/Median/P75	169 / 235 / 317

2.6. Mismatches and indels

General error rate	0.6%
Mismatches	19,751,551
Insertions	183,455
Mapped reads with at least one insertion	0.54%
Deletions	174,668
Mapped reads with at least one deletion	0.51%
Homopolymer indels	44.96%

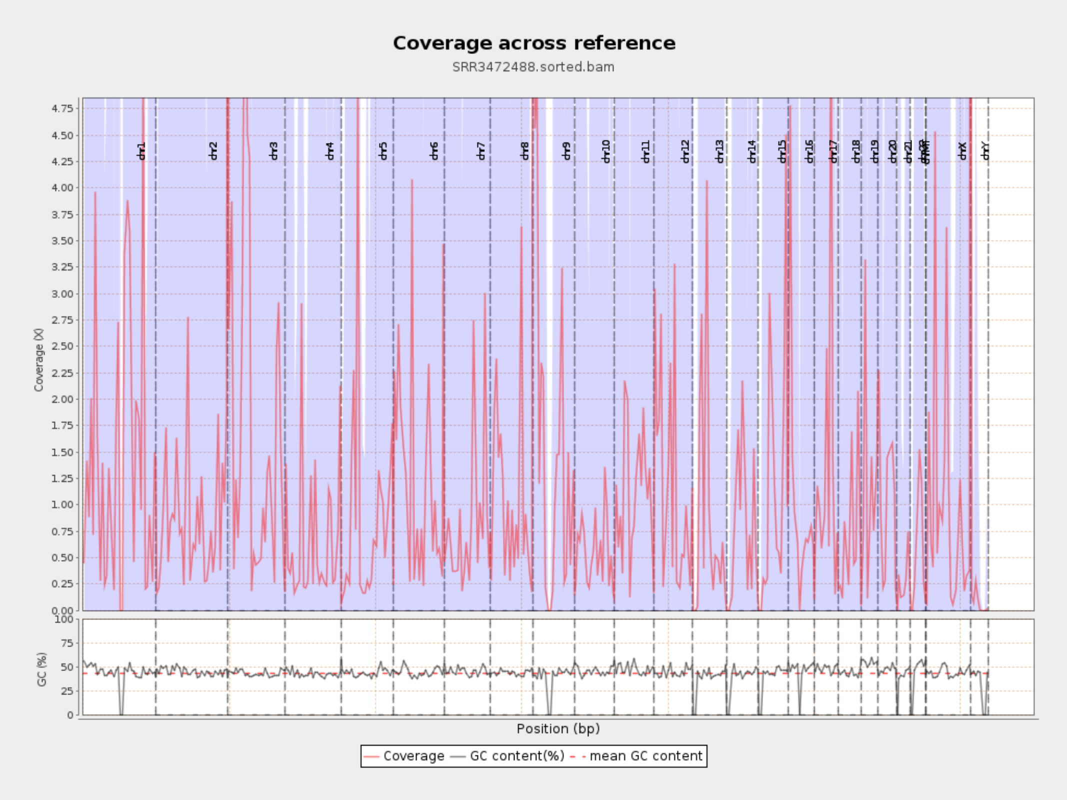
2.7. Chromosome stats

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

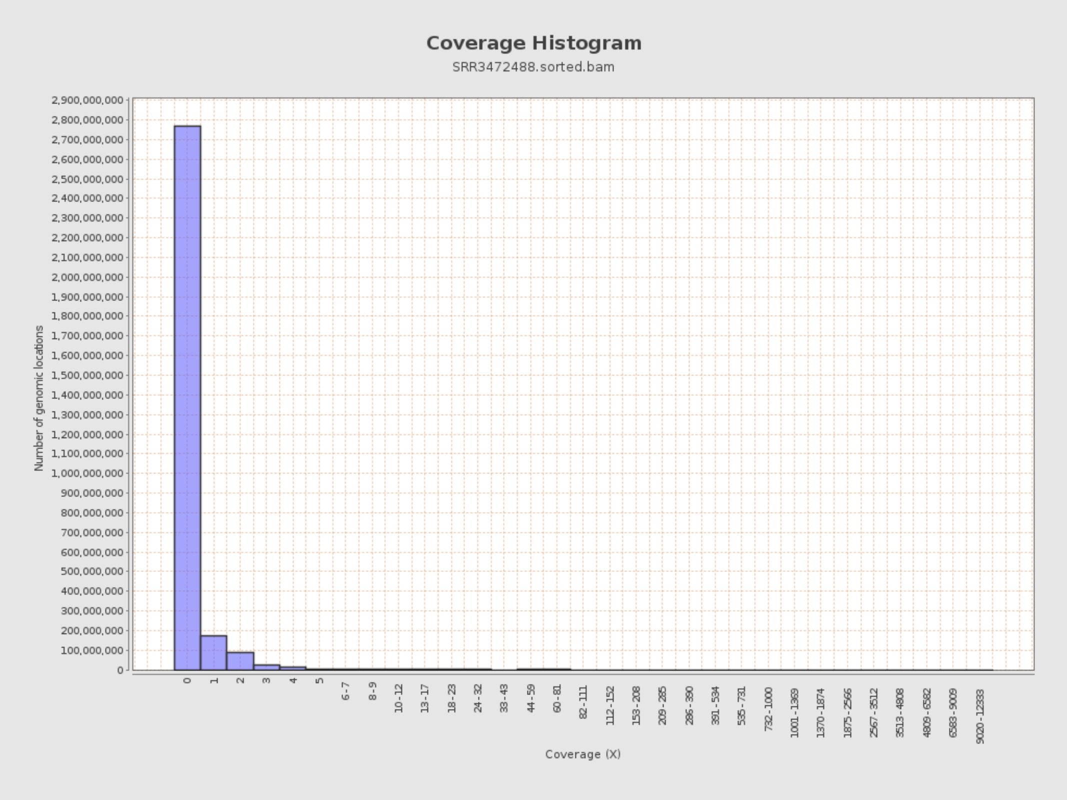
		bases	coverage	deviation
chr1	249250621	363726675	1.4593	42.5609
chr2	243199373	209882731	0.863	23.4466
chr3	198022430	369178701	1.8643	33.9248
chr4	191154276	129101919	0.6754	20.4717
chr5	180915260	163359883	0.903	25.2254
chr6	171115067	213434735	1.2473	28.3768
chr7	159138663	136694993	0.859	22.8698
chr8	146364022	151239115	1.0333	28.4229
chr9	141213431	217133119	1.5376	36.3308
chr10	135534747	78927465	0.5823	17.1422
chr11	135006516	148381573	1.0991	31.9233
chr12	133851895	165014468	1.2328	31.4023
chr13	115169878	101380923	0.8803	32.7586
chr14	107349540	87068876	0.8111	22.6877
chr15	102531392	119668601	1.1671	35.616
chr16	90354753	94479561	1.0457	21.9912
chr17	81195210	117865347	1.4516	33.1122
chr18	78077248	56304986	0.7211	20.3692
chr19	59128983	70199574	1.1872	30.2227
chr20	63025520	68076832	1.0801	28.01
chr21	48129895	13781608	0.2863	10.9301
chr22	51304566	32347408	0.6305	14.984
chrMT	16571	4448	0.2684	0.7594
chrX	155270560	224165069	1.4437	49.4119

chrY	59373566	4619897	0.0778	2.4998

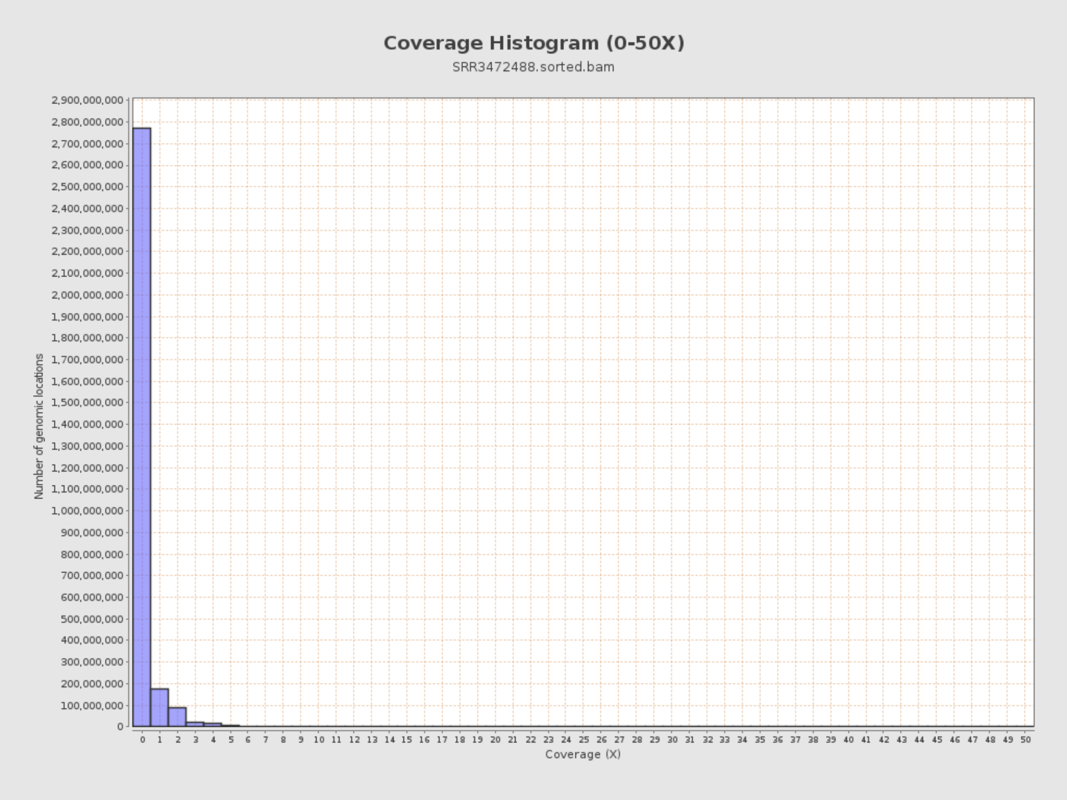
3. Results : Coverage across reference



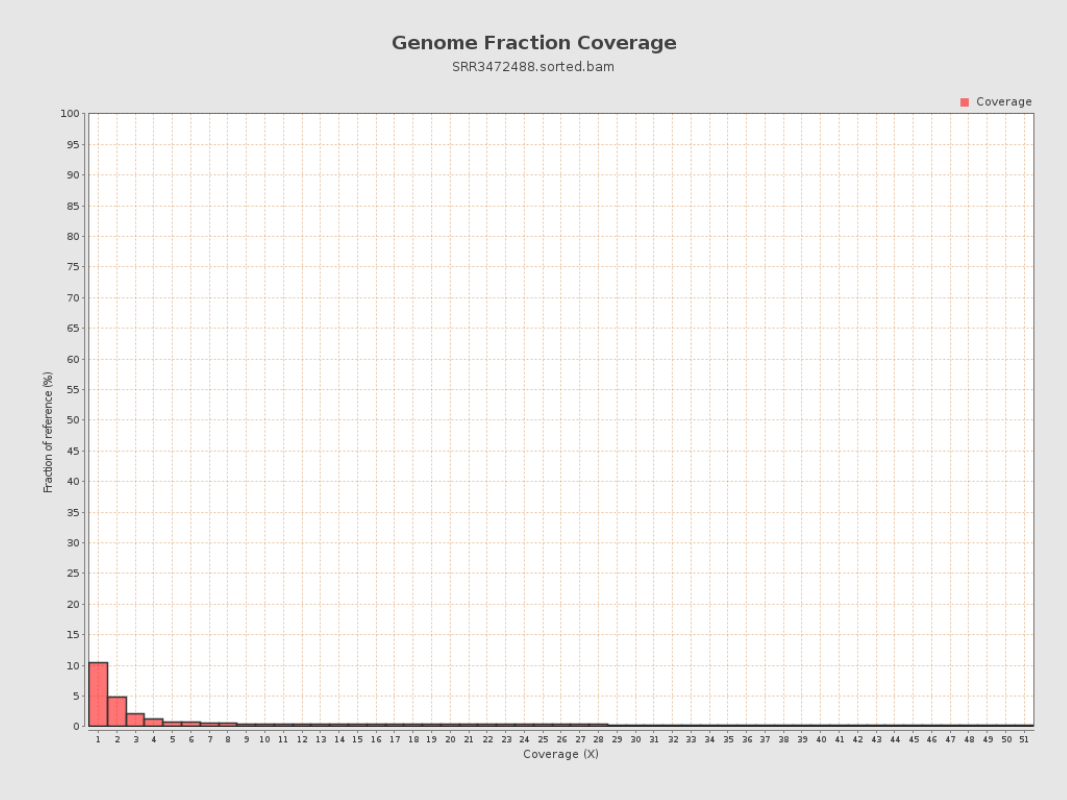
4. Results : Coverage Histogram



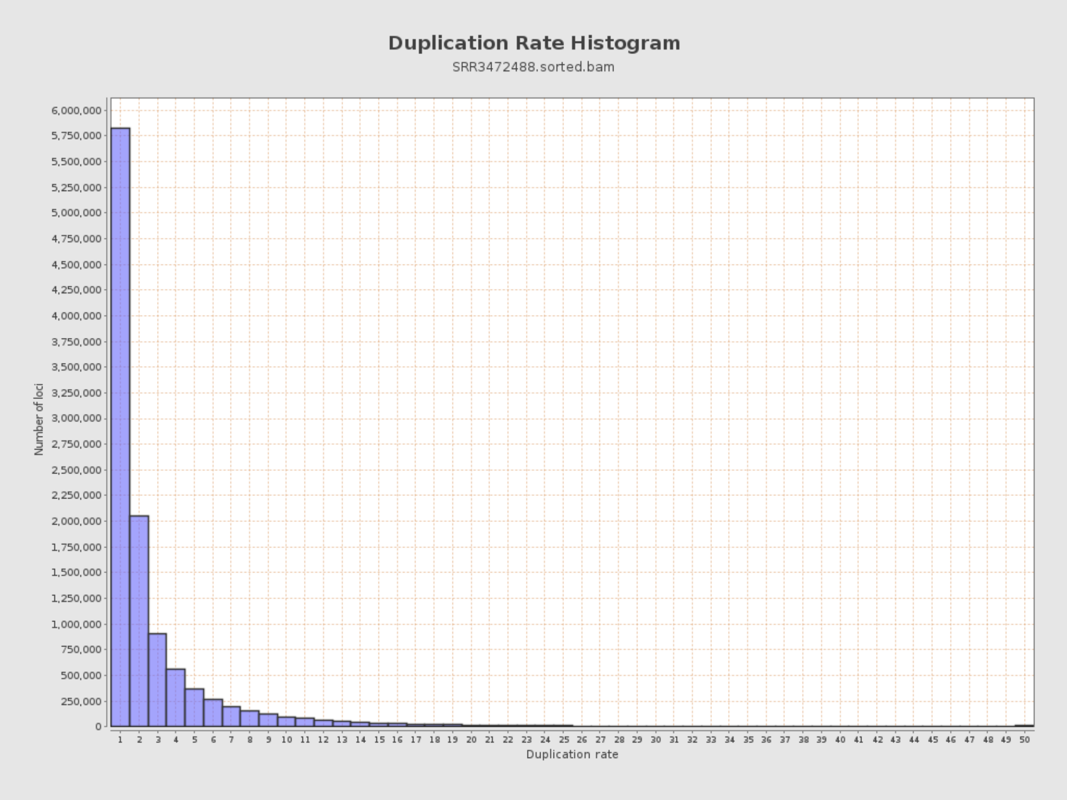
5. Results : Coverage Histogram (0-50X)



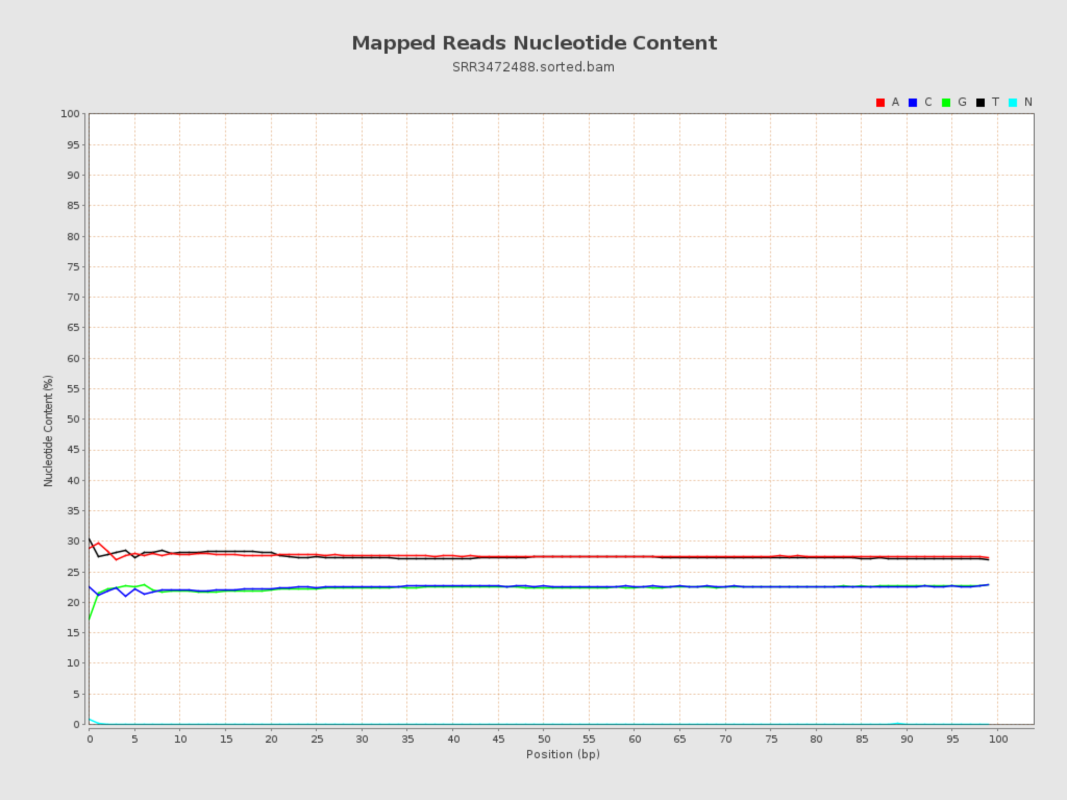
6. Results : Genome Fraction Coverage



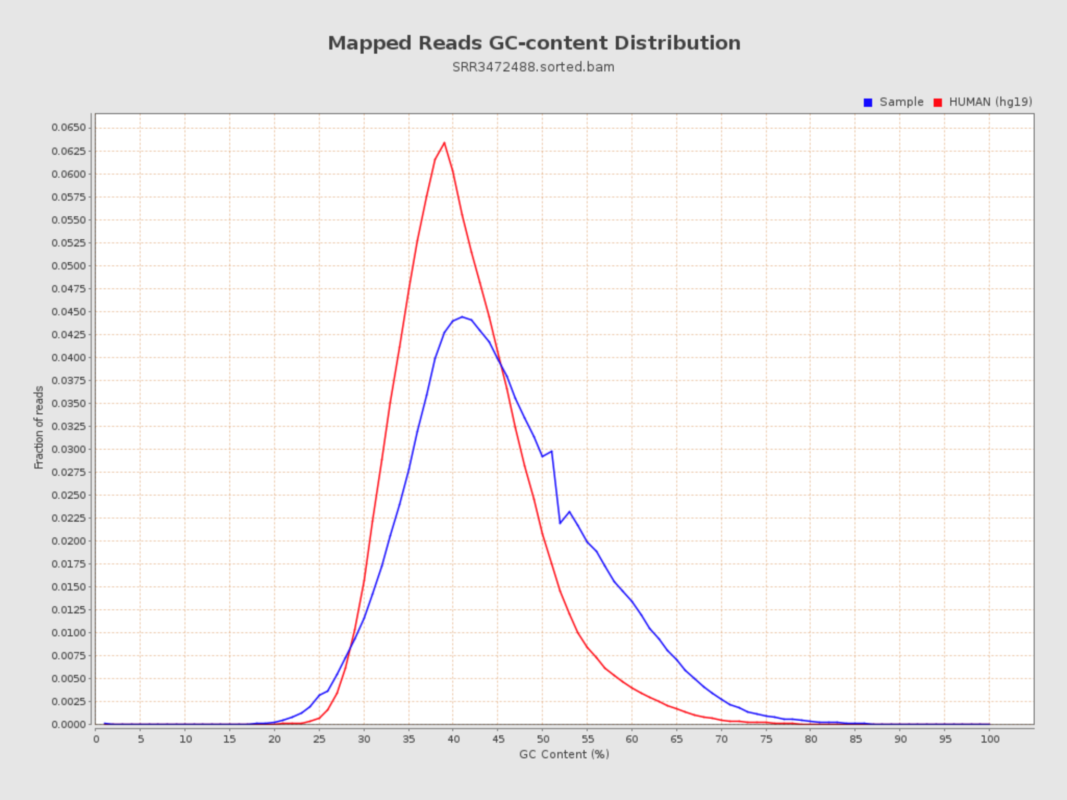
7. Results : Duplication Rate Histogram



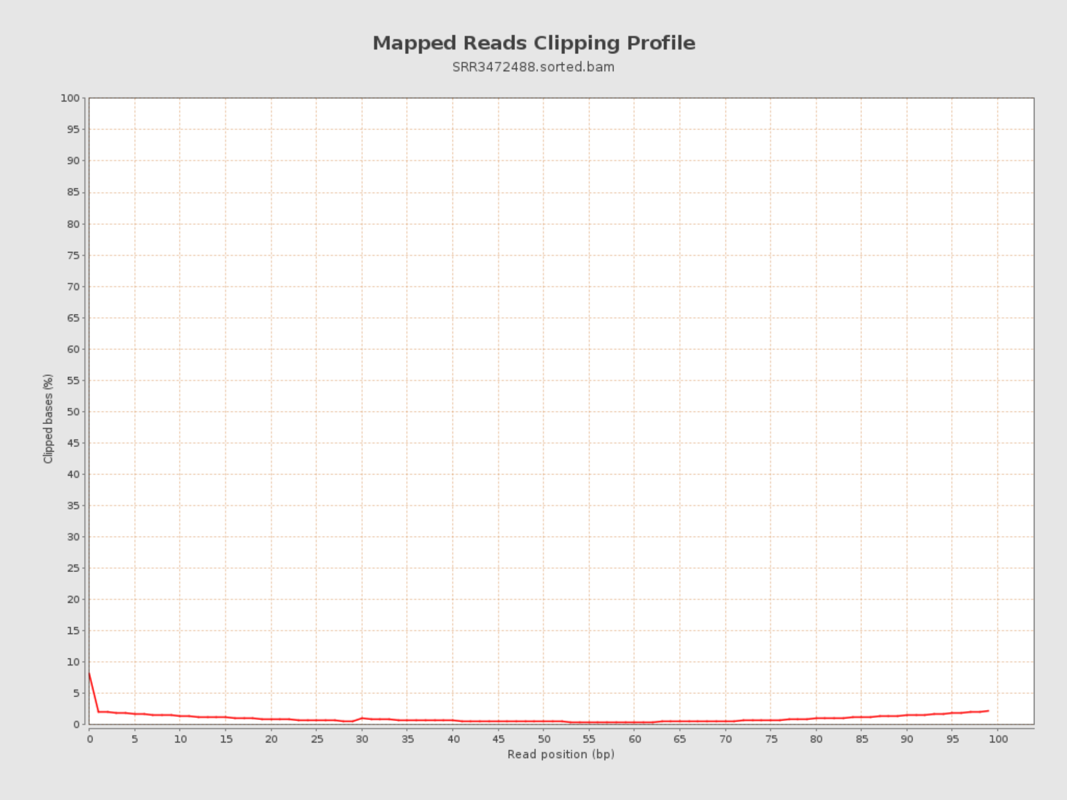
8. Results : Mapped Reads Nucleotide Content



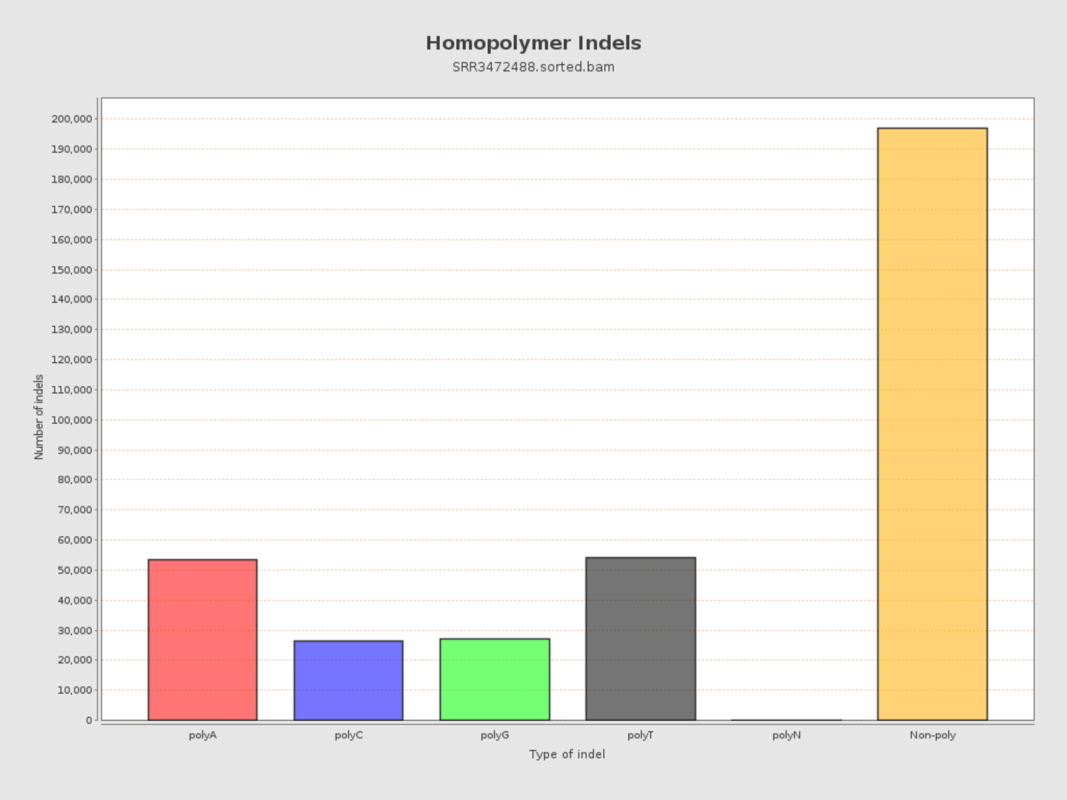
9. Results : Mapped Reads GC-content Distribution



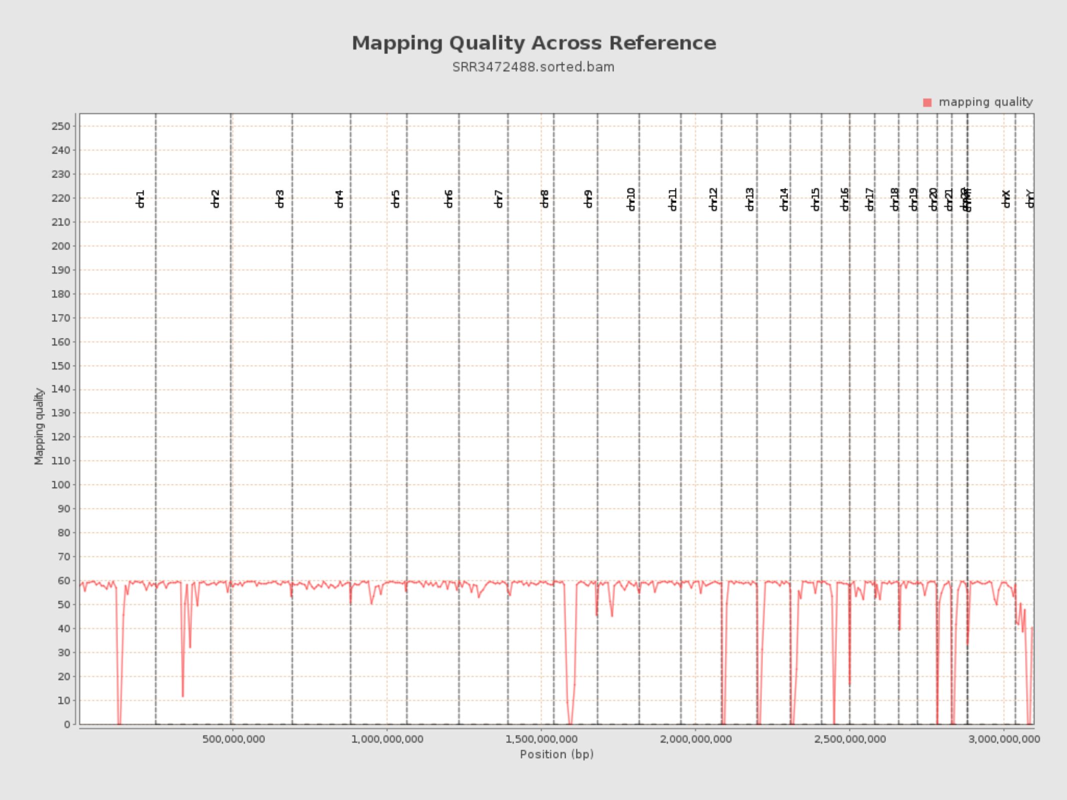
10. Results : Mapped Reads Clipping Profile



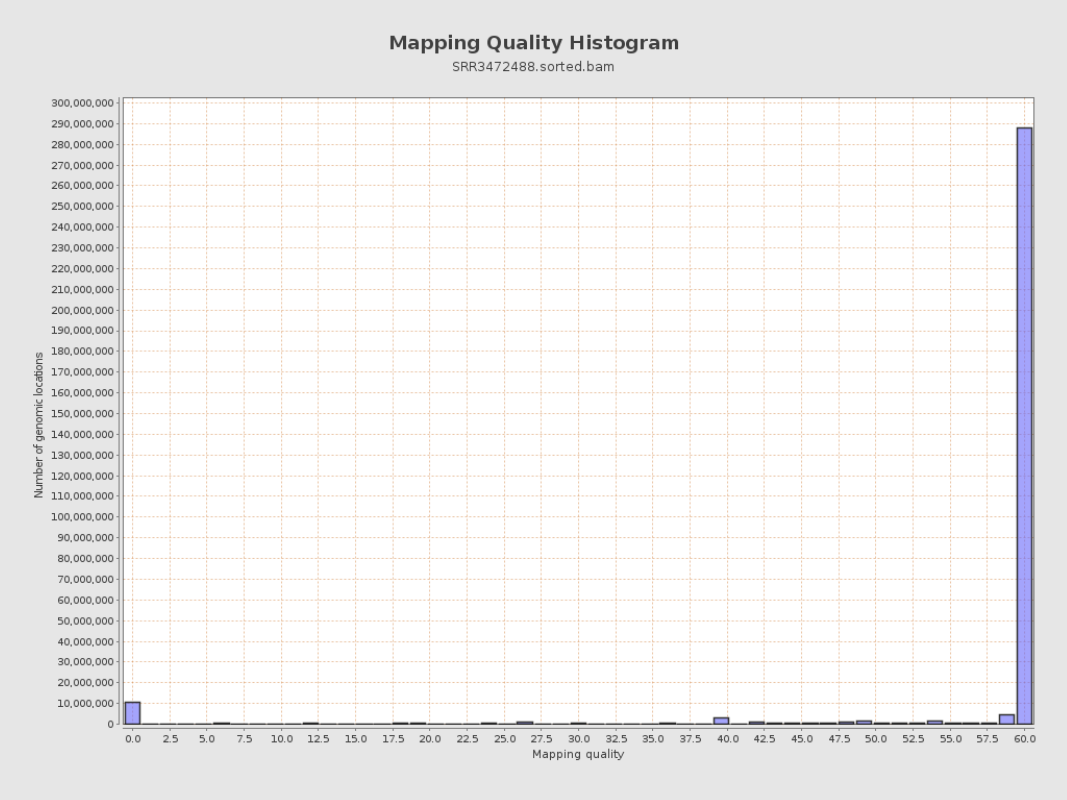
11. Results : Homopolymer Indels



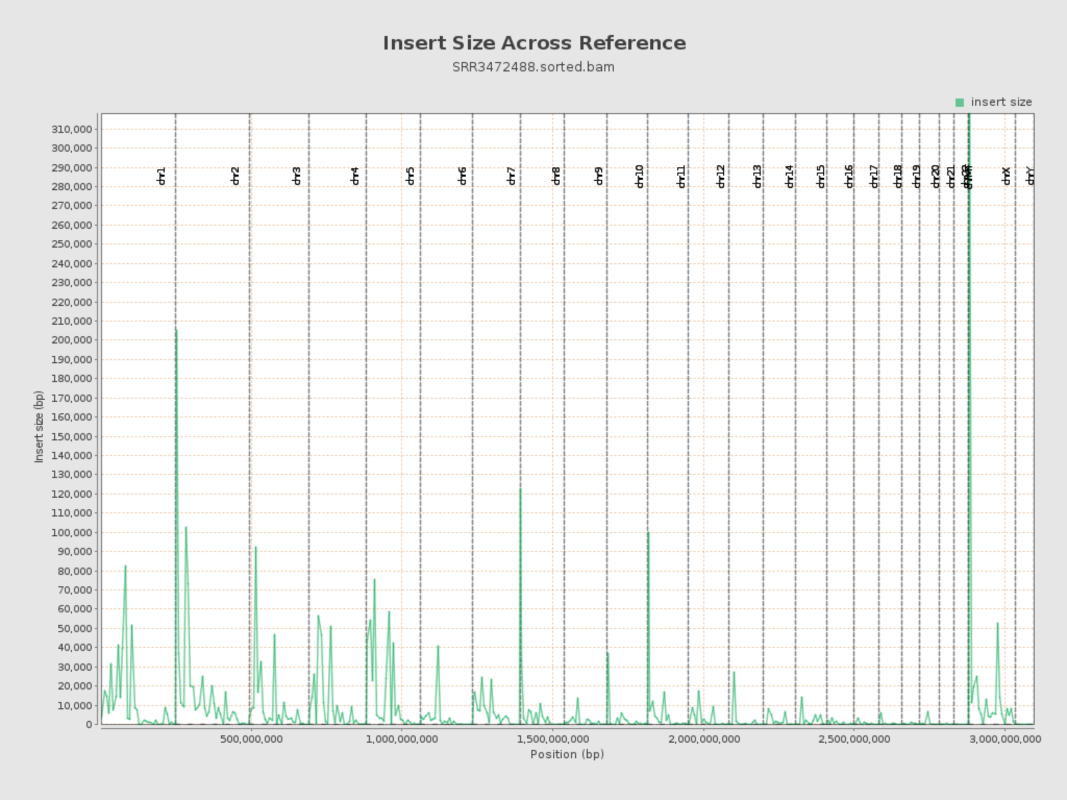
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram