Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/15 08:56:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR630500.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR630500_1.fastq.gz SRR630500_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Mar 15 08:56:50 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR630500.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	102,227,202
Mapped reads	101,897,372 / 99.68%
Unmapped reads	329,830 / 0.32%
Mapped paired reads	101,897,372 / 99.68%
Mapped reads, first in pair	51,053,582 / 49.94%
Mapped reads, second in pair	50,843,790 / 49.74%
Mapped reads, both in pair	101,661,542 / 99.45%
Mapped reads, singletons	235,830 / 0.23%
Secondary alignments	0
Supplementary alignments	614,736 / 0.6%
Read min/max/mean length	30 / 101 / 101.25
Duplicated reads (estimated)	19,784,281 / 19.35%
Duplication rate	16.4%
Clipped reads	7,272,095 / 7.11%

2.2. ACGT Content

Number/percentage of A's	3,183,571,835 / 31.32%
Number/percentage of C's	1,897,892,336 / 18.67%
Number/percentage of T's	3,173,517,543 / 31.22%
Number/percentage of G's	1,909,598,919 / 18.79%
Number/percentage of N's	861,367 / 0.01%

GC Percentage	37.46%

2.3. Coverage

Mean	3.2844
Standard Deviation	13.0868

2.4. Mapping Quality

Mean Mapping Quality	53.8

2.5. Insert size

Mean	47,904.05
Standard Deviation	2,050,338.91
P25/Median/P75	247 / 307 / 373

2.6. Mismatches and indels

General error rate	0.79%
Mismatches	78,839,893
Insertions	868,570
Mapped reads with at least one insertion	0.84%
Deletions	943,394
Mapped reads with at least one deletion	0.9%
Homopolymer indels	44.94%

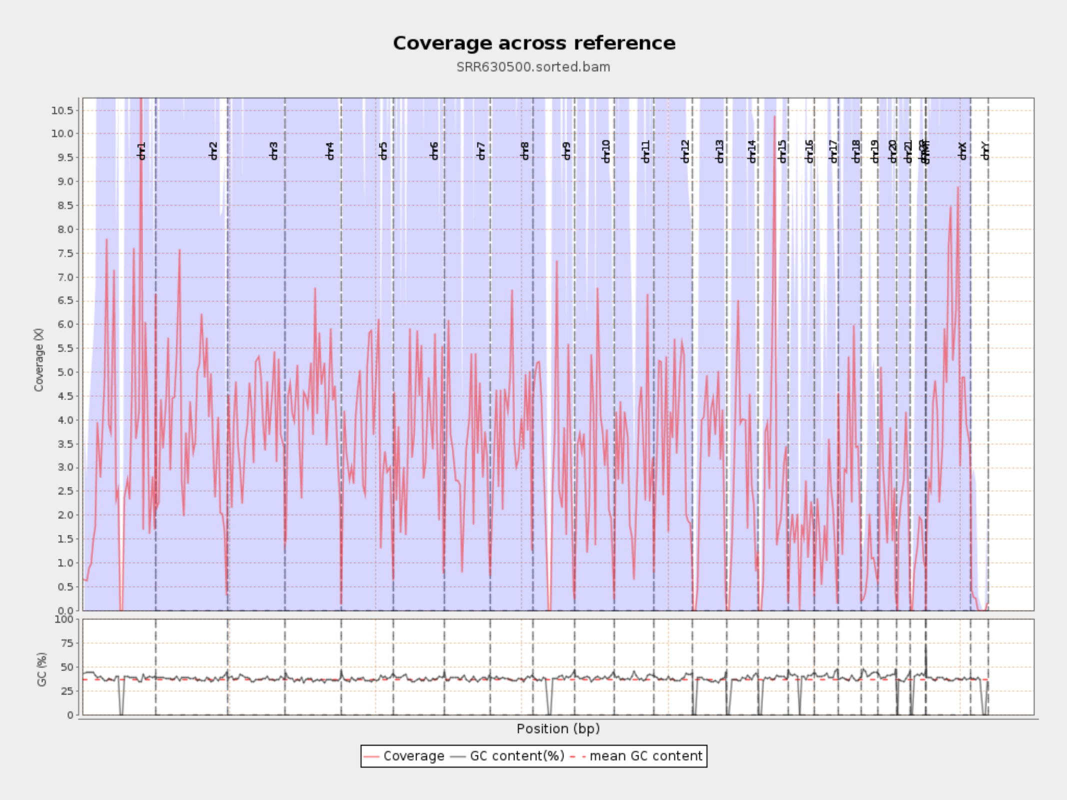
2.7. Chromosome stats

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

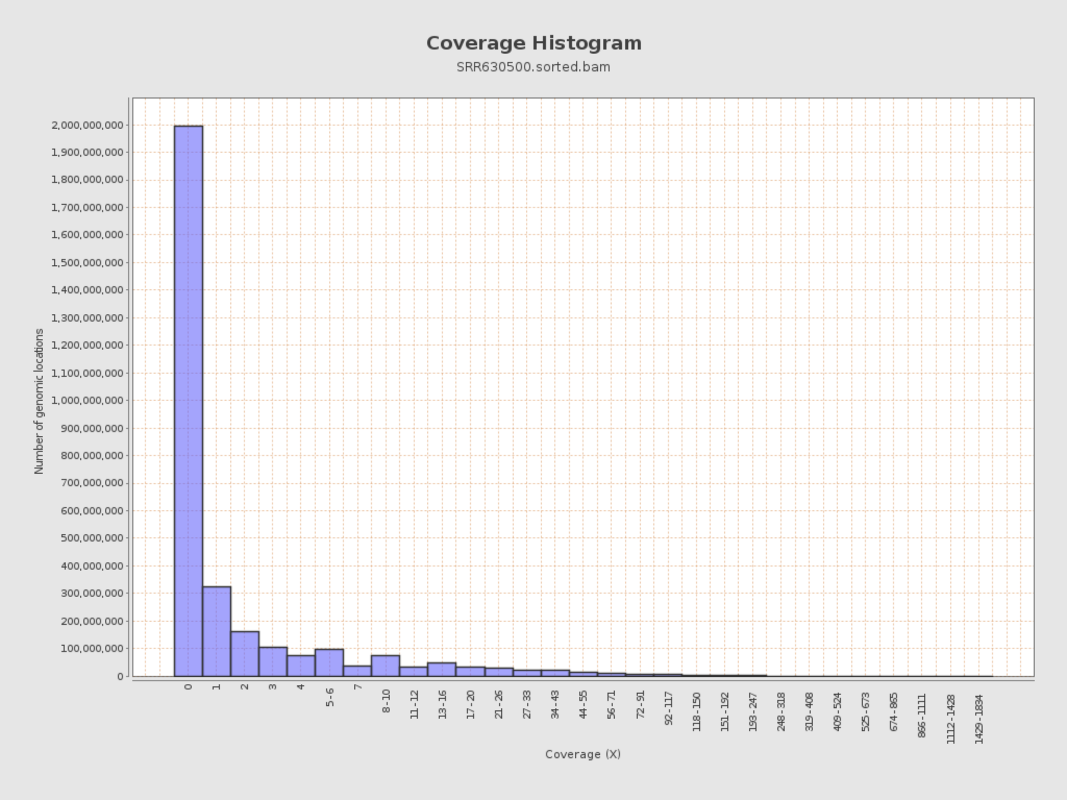
		bases	coverage	deviation
chr1	249250621	834693214	3.3488	18.1611
chr2	243199373	936934251	3.8525	14.1463
chr3	198022430	791341907	3.9962	13.5766
chr4	191154276	824346384	4.3125	14.7975
chr5	180915260	641959979	3.5484	12.2706
chr6	171115067	642631385	3.7556	13.2805
chr7	159138663	522936616	3.286	12.616
chr8	146364022	552704344	3.7762	13.6228
chr9	141213431	457750158	3.2415	12.9418
chr10	135534747	432900022	3.194	12.1146
chr11	135006516	424513984	3.1444	12.4211
chr12	133851895	492783332	3.6816	12.7171
chr13	115169878	351483224	3.0519	10.6512
chr14	107349540	307729699	2.8666	10.2973
chr15	102531392	305062479	2.9753	15.2007
chr16	90354753	142549960	1.5777	6.2139
chr17	81195210	139509959	1.7182	6.5185
chr18	78077248	258392751	3.3095	11.5818
chr19	59128983	50345160	0.8514	3.6142
chr20	63025520	159505140	2.5308	10.5796
chr21	48129895	105558057	2.1932	9.7326
chr22	51304566	56385607	1.099	6.7075
chrMT	16571	80	0.0048	0.0693
chrX	155270560	727945918	4.6882	16.4524

chrY	59373566	7602500	0.128	1.6862

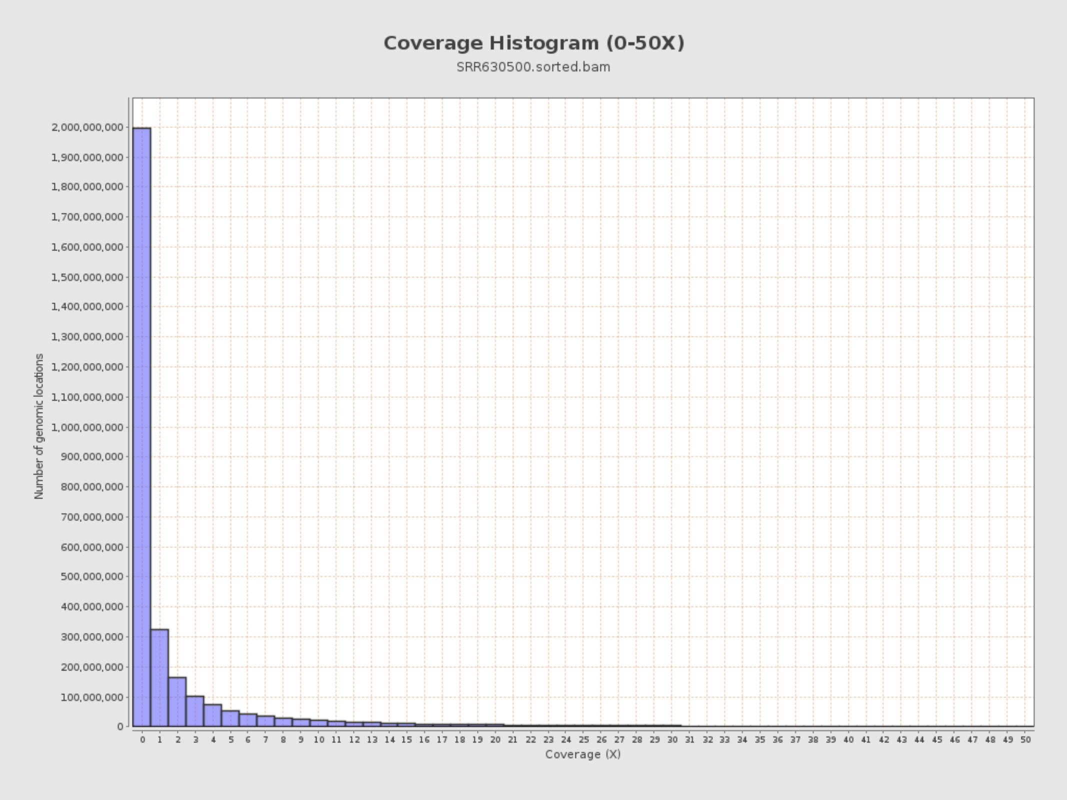
3. Results : Coverage across reference



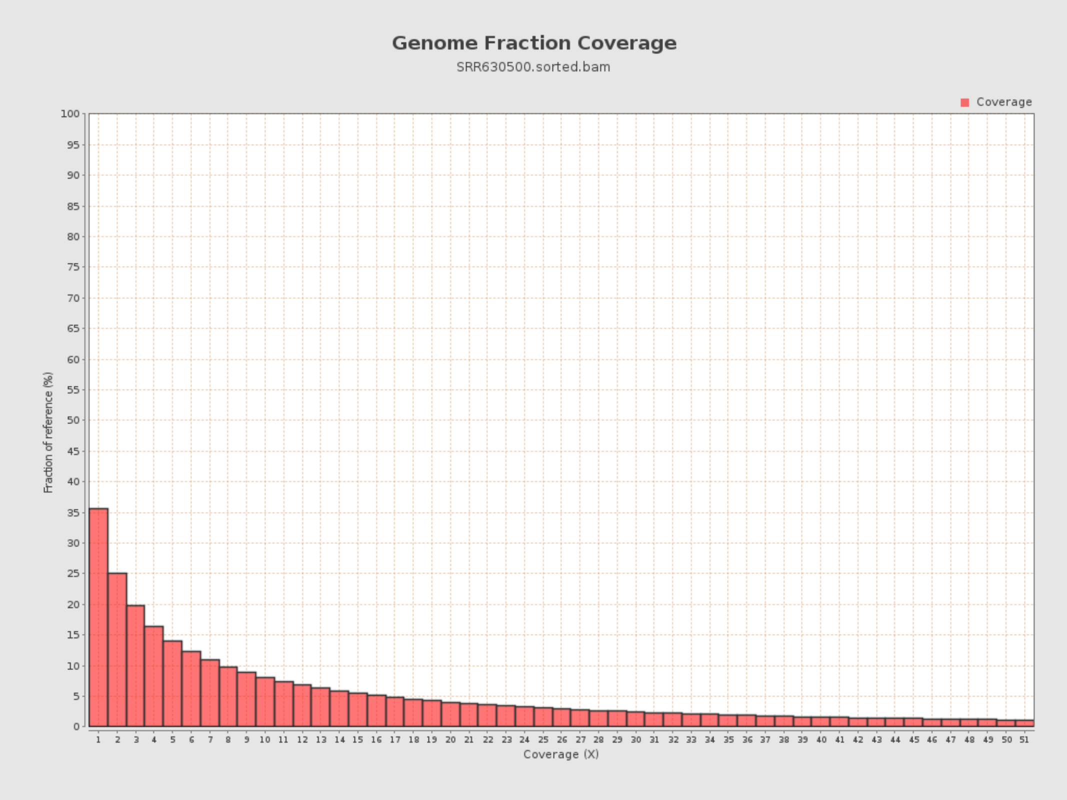
4. Results : Coverage Histogram



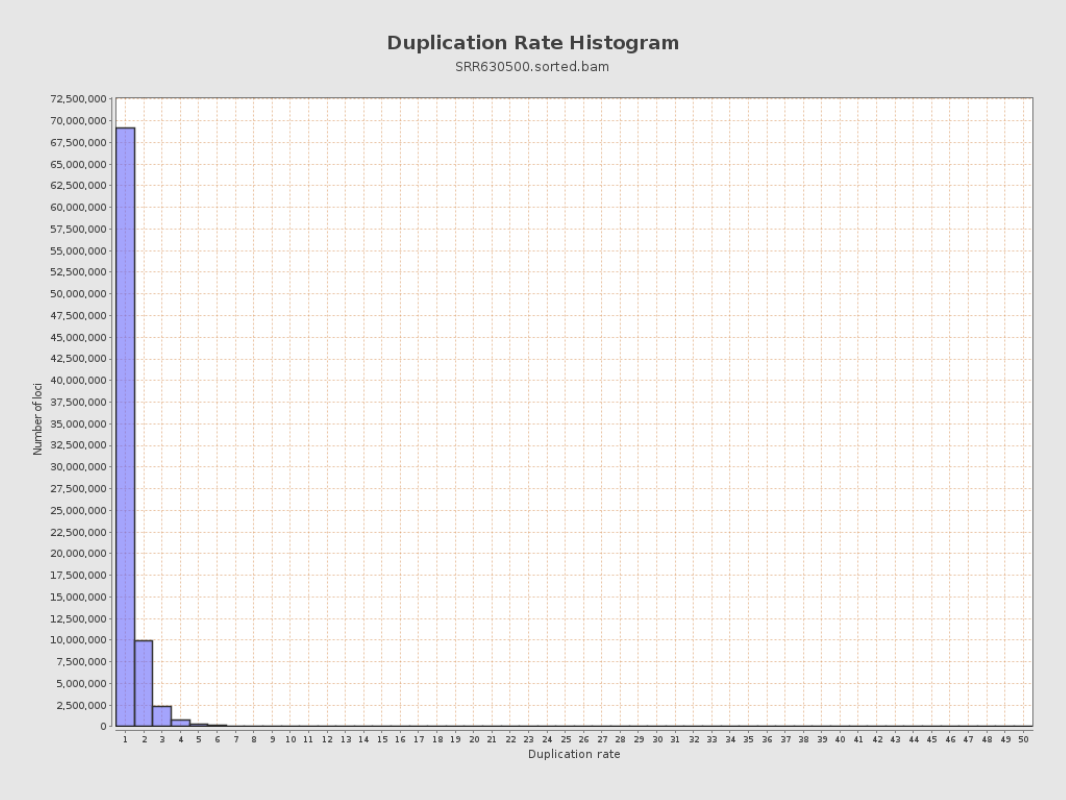
5. Results : Coverage Histogram (0-50X)



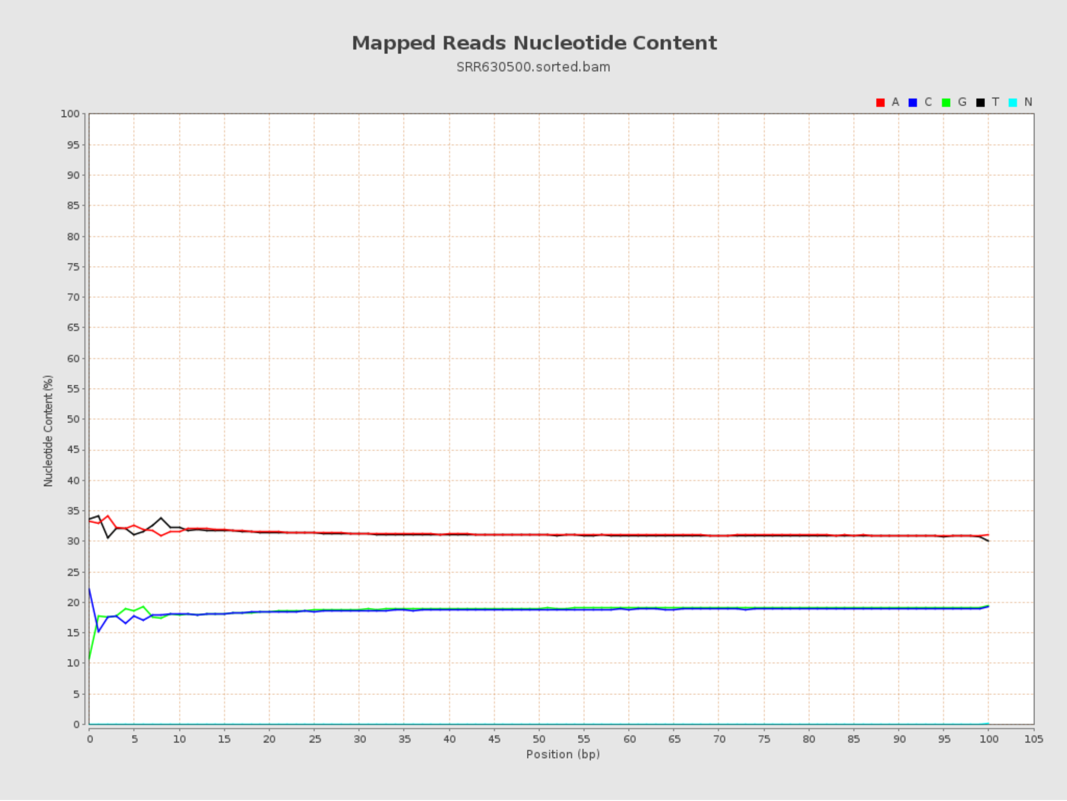
6. Results : Genome Fraction Coverage



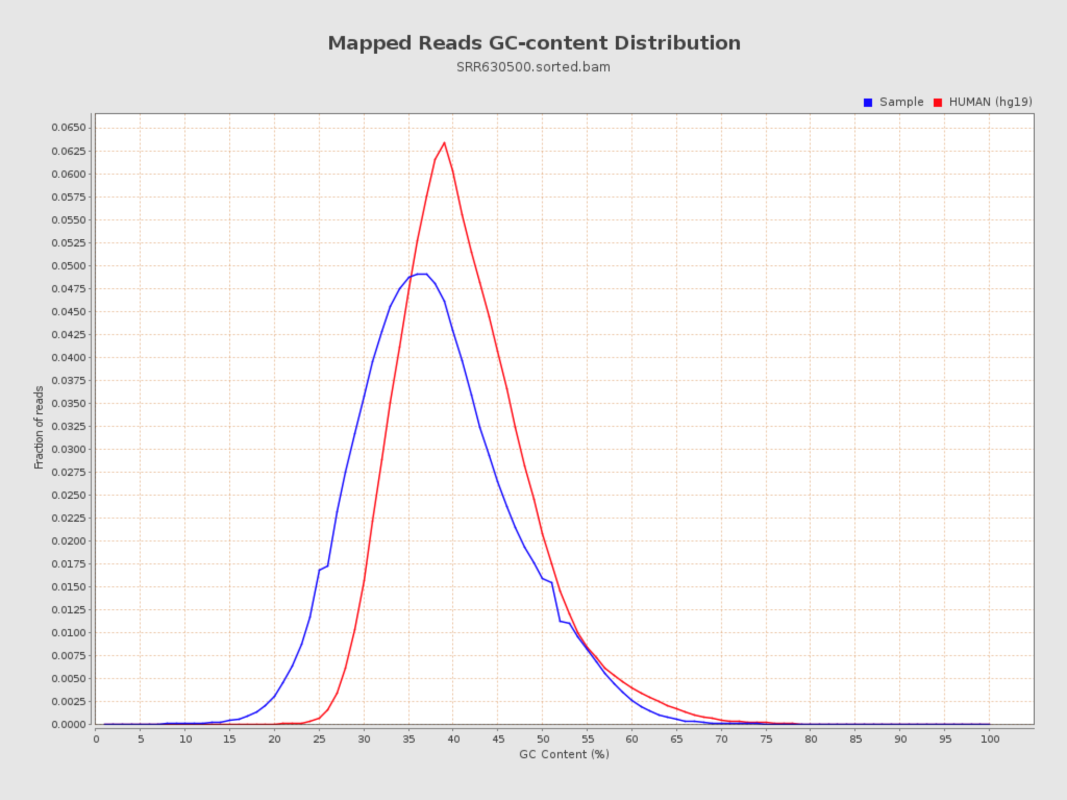
7. Results : Duplication Rate Histogram



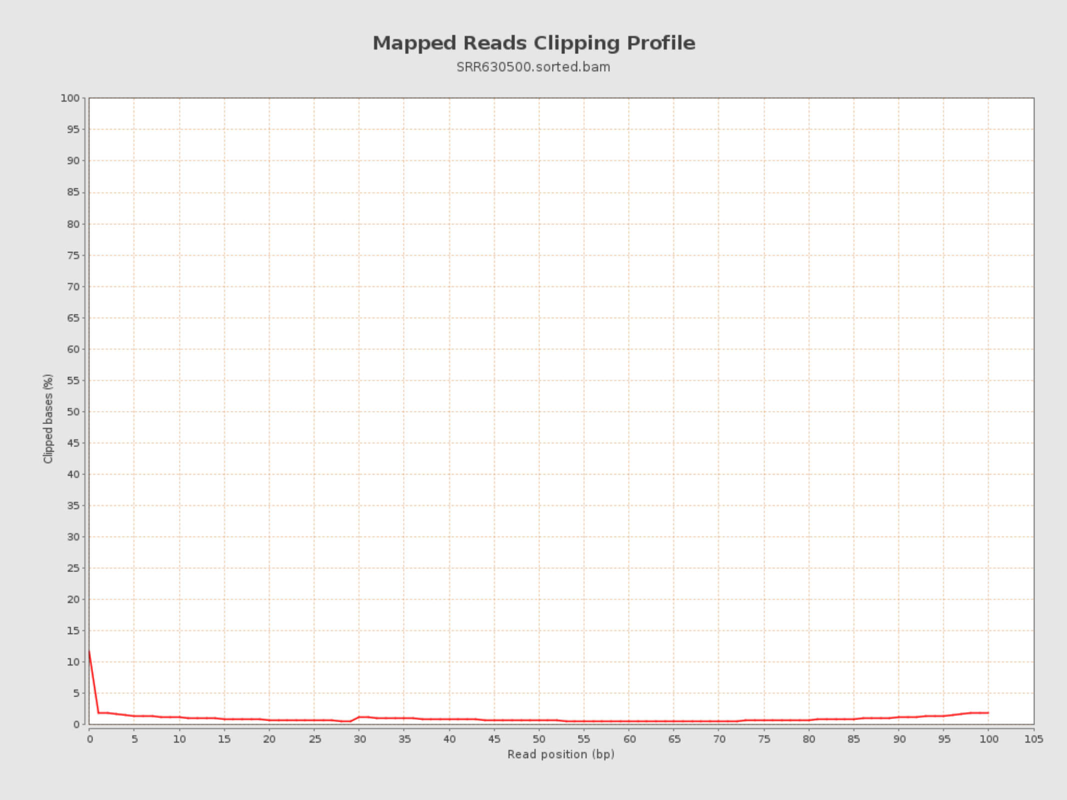
8. Results : Mapped Reads Nucleotide Content



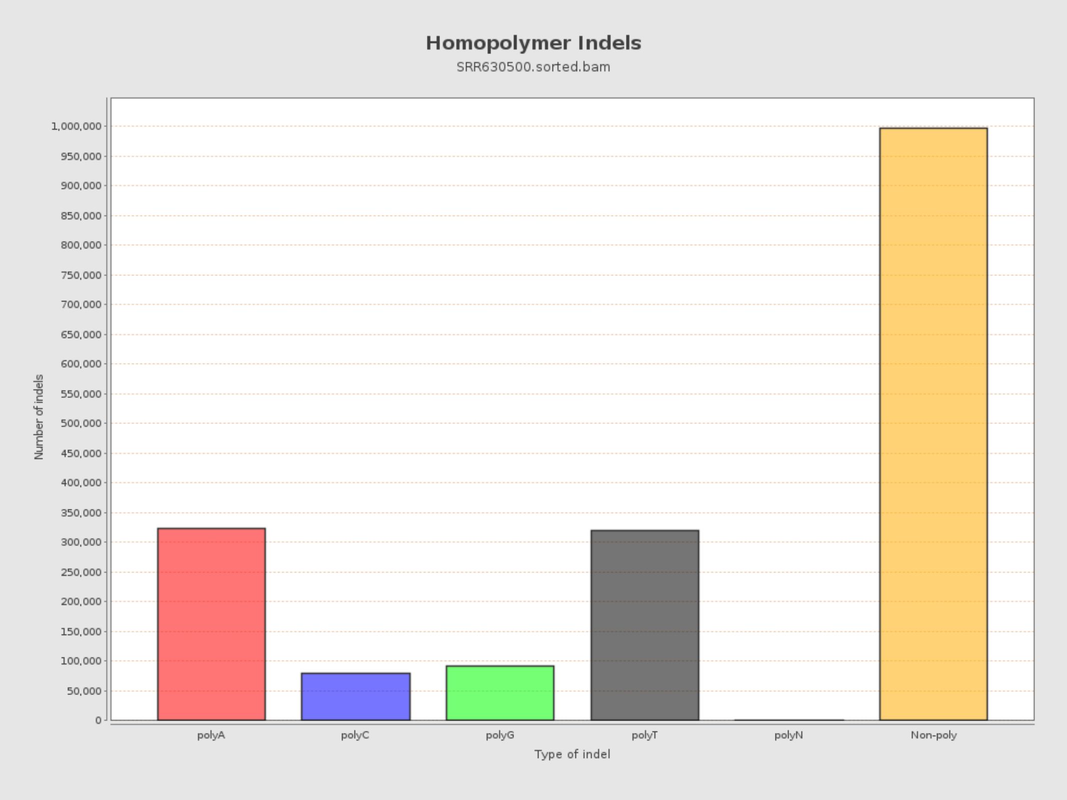
9. Results : Mapped Reads GC-content Distribution



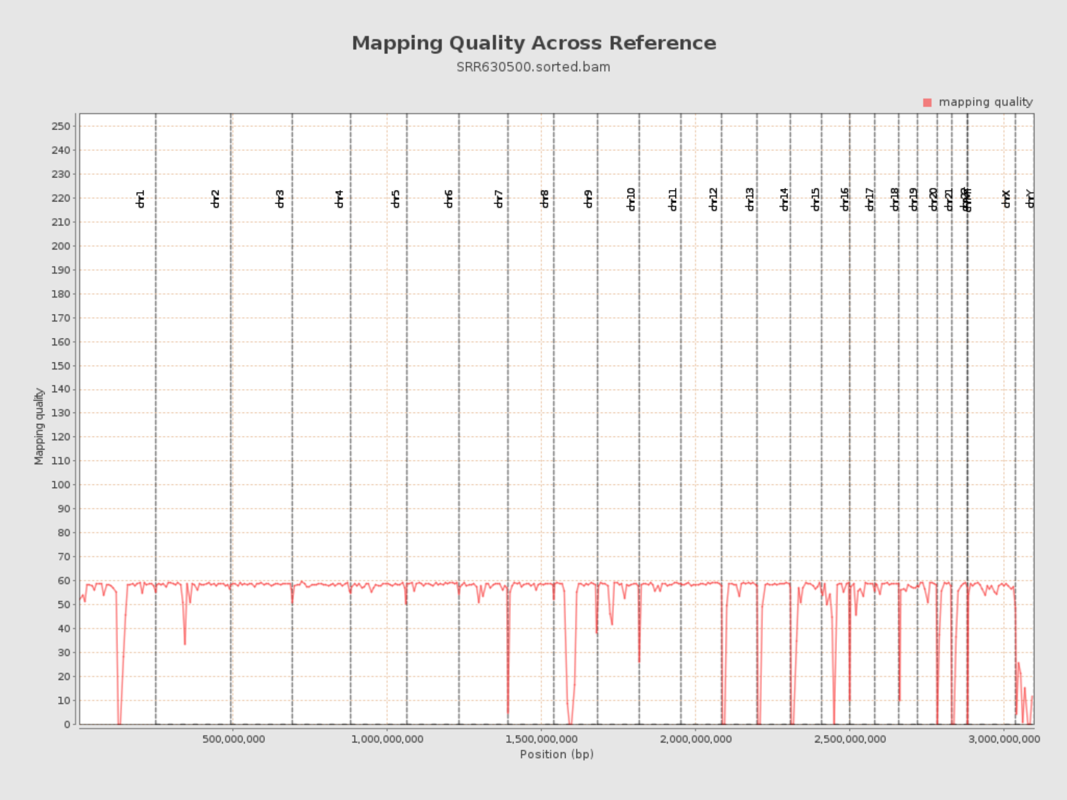
10. Results : Mapped Reads Clipping Profile



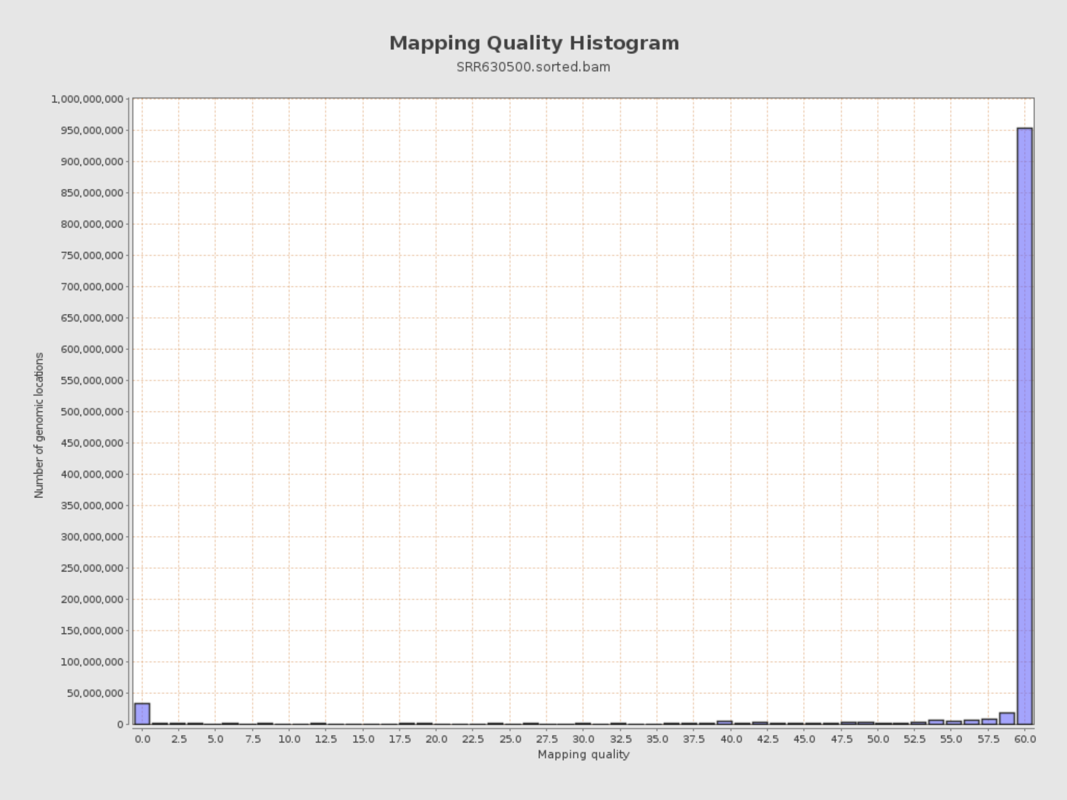
11. Results : Homopolymer Indels



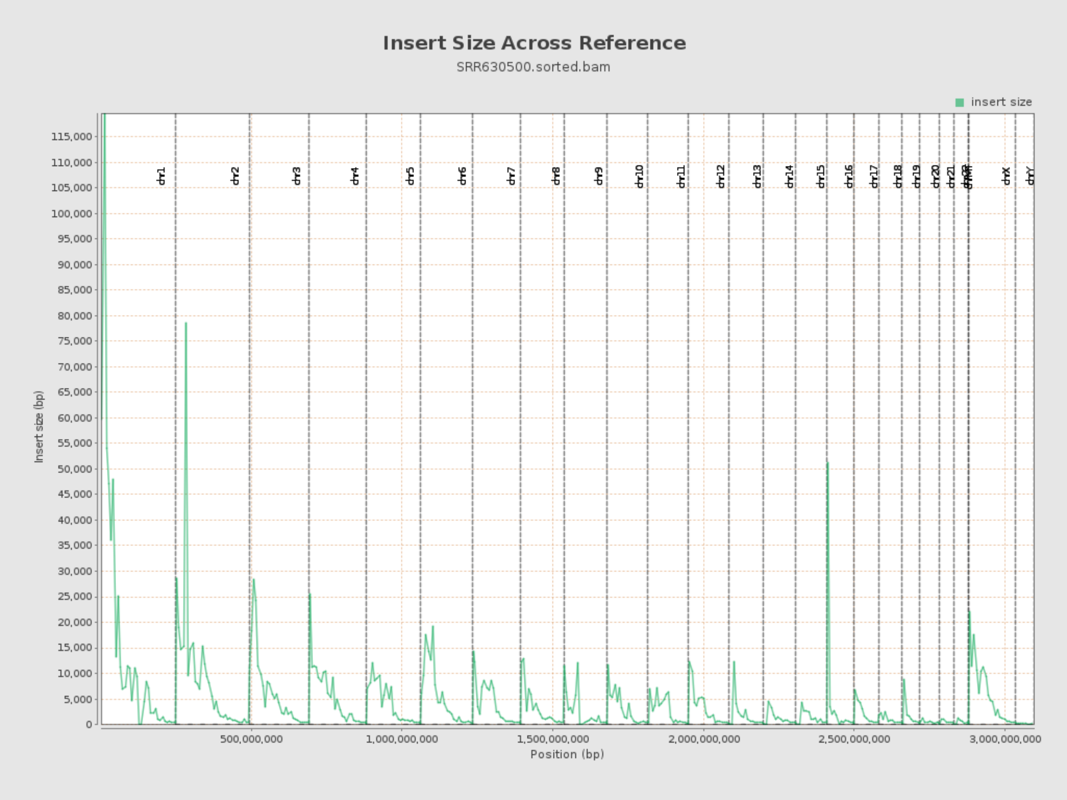
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram