Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/14 20:20:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038412.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_SRR5038412 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038412_1.fastq.gz SRR5038412_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Apr 14 20:20:17 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038412.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	12,247,794
Mapped reads	11,997,553 / 97.96%
Unmapped reads	250,241 / 2.04%
Mapped paired reads	11,997,553 / 97.96%
Mapped reads, first in pair	6,059,926 / 49.48%
Mapped reads, second in pair	5,937,627 / 48.48%
Mapped reads, both in pair	11,859,446 / 96.83%
Mapped reads, singletons	138,107 / 1.13%
Secondary alignments	0
Supplementary alignments	252,759 / 2.06%
Read min/max/mean length	30 / 150 / 151.07
Duplicated reads (estimated)	1,768,062 / 14.44%
Duplication rate	8.25%
Clipped reads	3,182,871 / 25.99%

2.2. ACGT Content

Number/percentage of A's	485,573,500 / 28.46%
Number/percentage of C's	360,304,531 / 21.12%
Number/percentage of T's	484,988,803 / 28.43%
Number/percentage of G's	375,291,887 / 22%
Number/percentage of N's	35,594 / 0%

GC Percentage	43.11%

2.3. Coverage

Mean	0.5516
Standard Deviation	9.4153

2.4. Mapping Quality

Mean Mapping Quality	53.55

2.5. Insert size

Mean	91,376.21
Standard Deviation	2,846,670.11
P25/Median/P75	215 / 254 / 302

2.6. Mismatches and indels

General error rate	1.51%
Mismatches	24,873,273
Insertions	322,567
Mapped reads with at least one insertion	2.5%
Deletions	583,256
Mapped reads with at least one deletion	4.65%
Homopolymer indels	45.85%

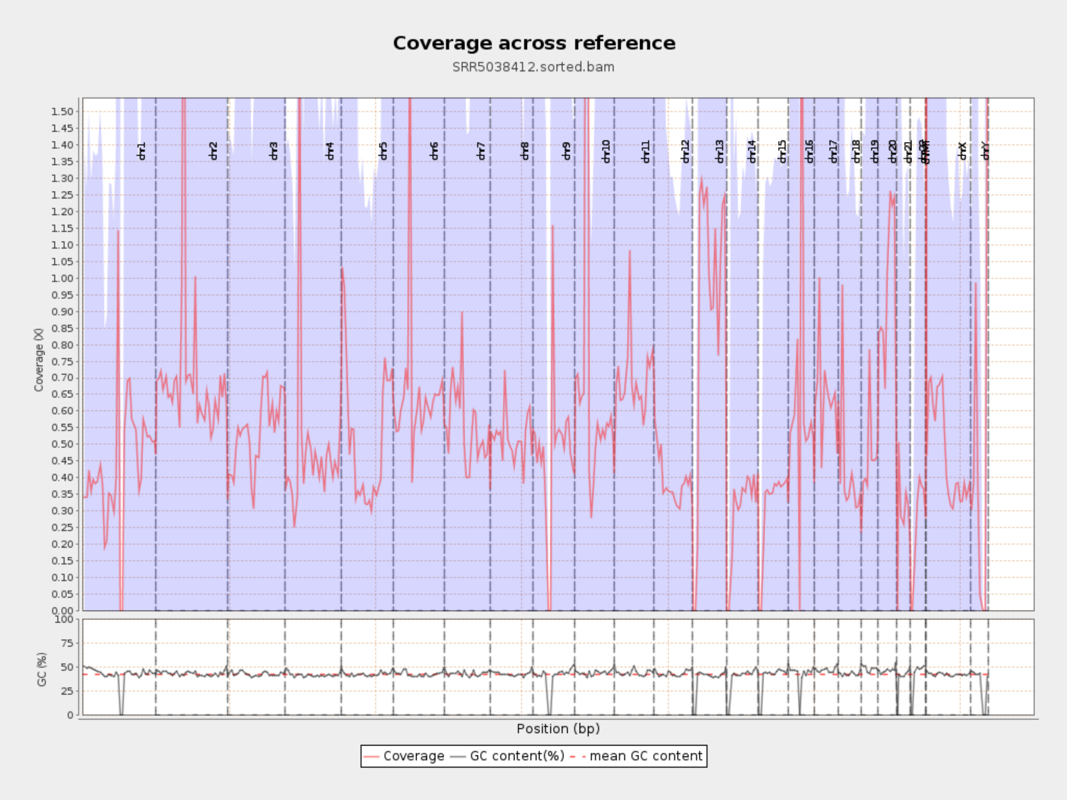
2.7. Chromosome stats

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

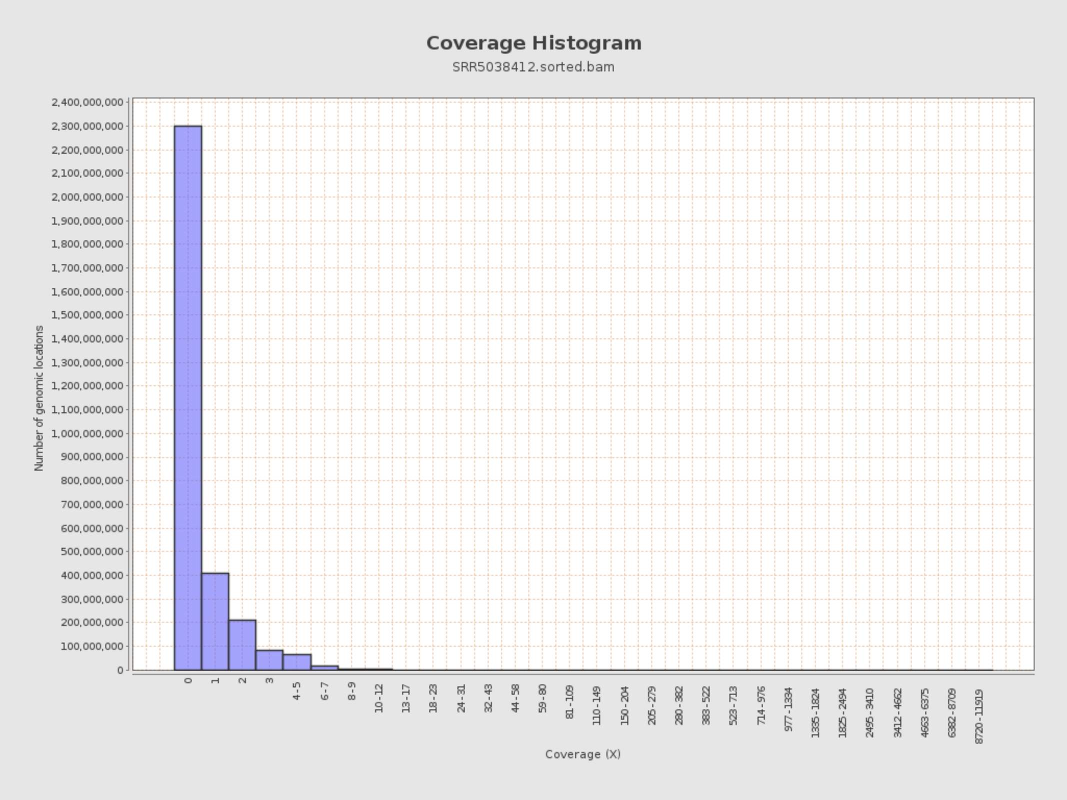
		bases	**coverage**	**deviation**
chr1	249250621	108684816	0.436	12.4522
chr2	243199373	176209414	0.7245	10.0801
chr3	198022430	106473826	0.5377	1.2524
chr4	191154276	92870827	0.4858	8.9903
chr5	180915260	95197954	0.5262	1.2481
chr6	171115067	113856063	0.6654	14.0541
chr7	159138663	88961831	0.559	6.3882
chr8	146364022	76017664	0.5194	2.1944
chr9	141213431	67104840	0.4752	12.826
chr10	135534747	96567754	0.7125	23.4023
chr11	135006516	93659361	0.6937	8.017
chr12	133851895	52774776	0.3943	1.022
chr13	115169878	106306292	0.923	1.7317
chr14	107349540	31863826	0.2968	1.0138
chr15	102531392	31189942	0.3042	0.8323
chr16	90354753	60024418	0.6643	11.5639
chr17	81195210	53421093	0.6579	9.5482
chr18	78077248	33312096	0.4267	11.9048
chr19	59128983	27368283	0.4629	7.3017
chr20	63025520	62290476	0.9883	3.1377
chr21	48129895	14372987	0.2986	3.7091
chr22	51304566	12876935	0.251	0.8656
chrMT	16571	4661796	281.3226	194.9838
chrX	155270560	73634019	0.4742	2.06

chrY	59373566	27779176	0.4679	12.6669

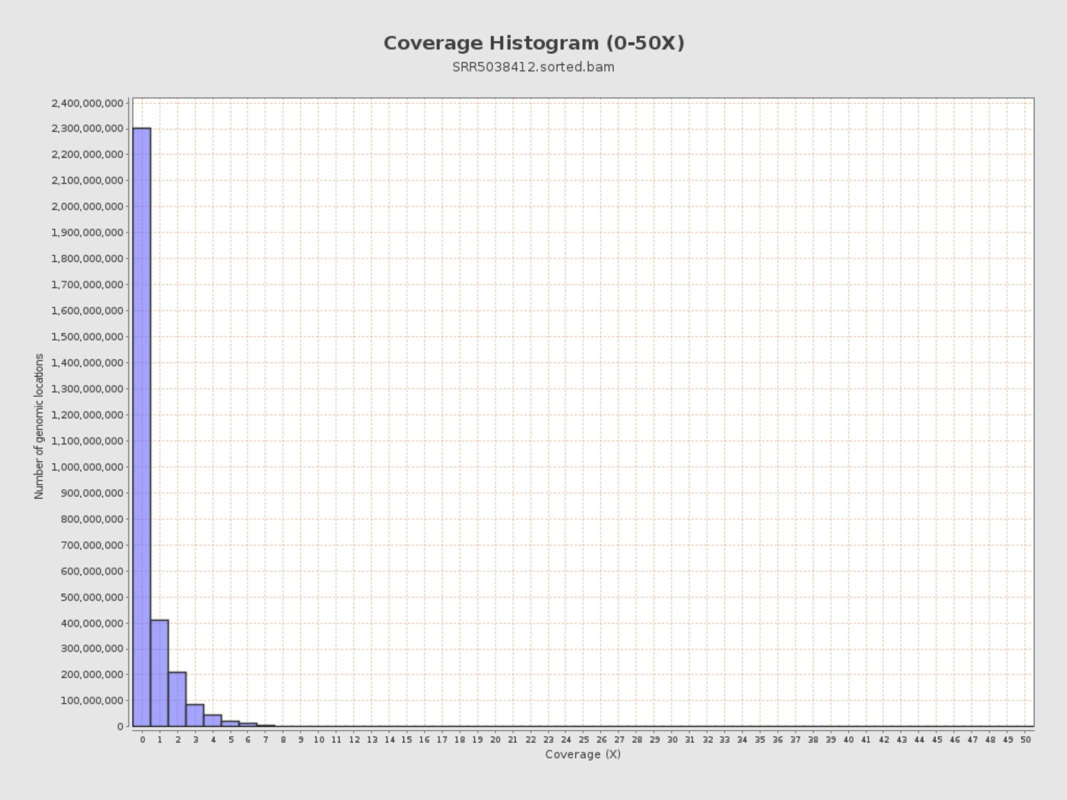
3. Results : Coverage across reference



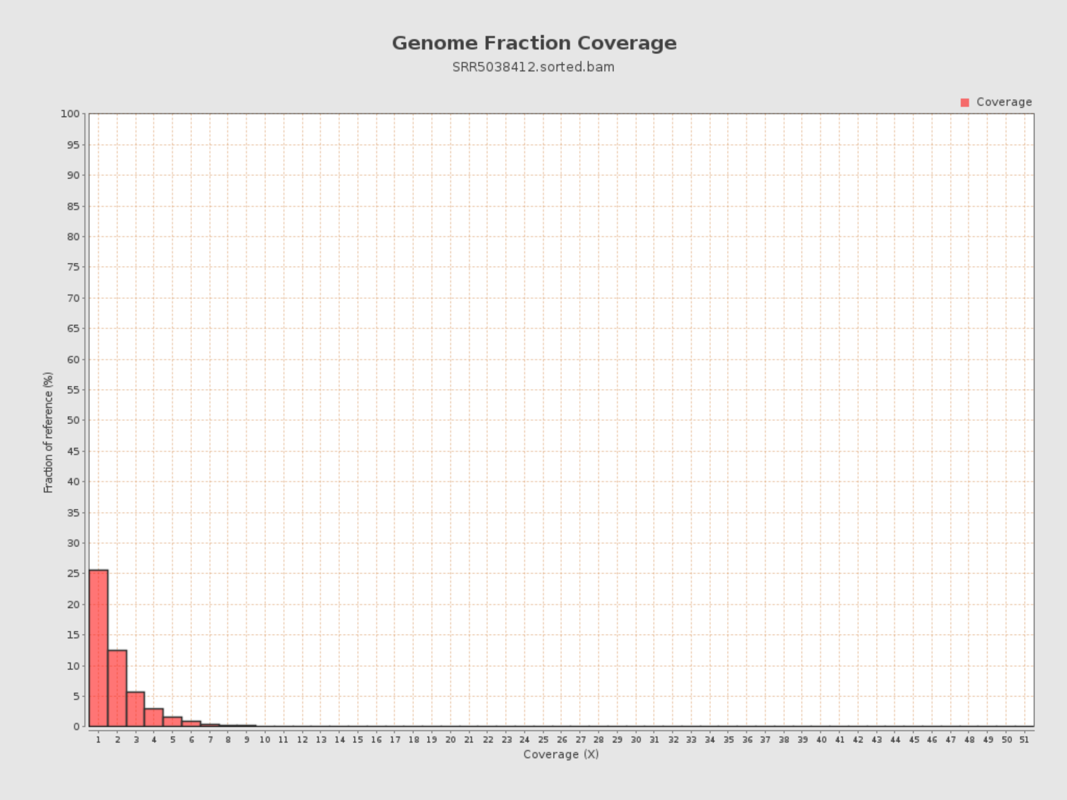
4. Results : Coverage Histogram



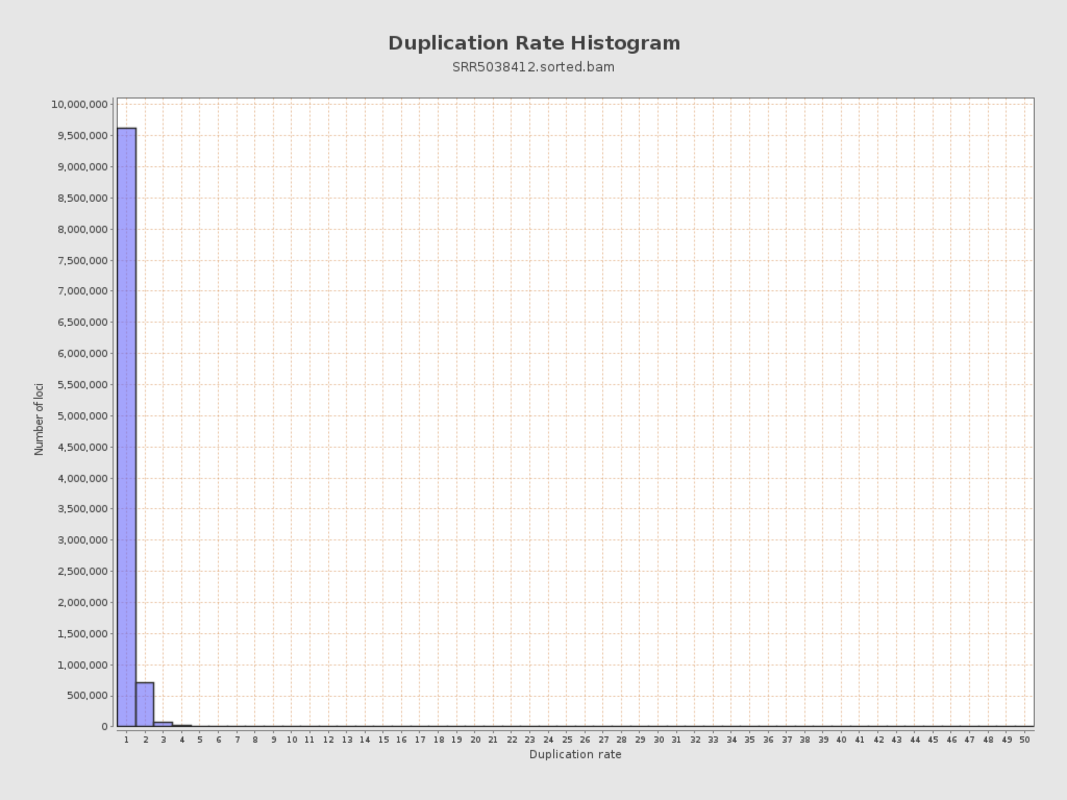
5. Results : Coverage Histogram (0-50X)



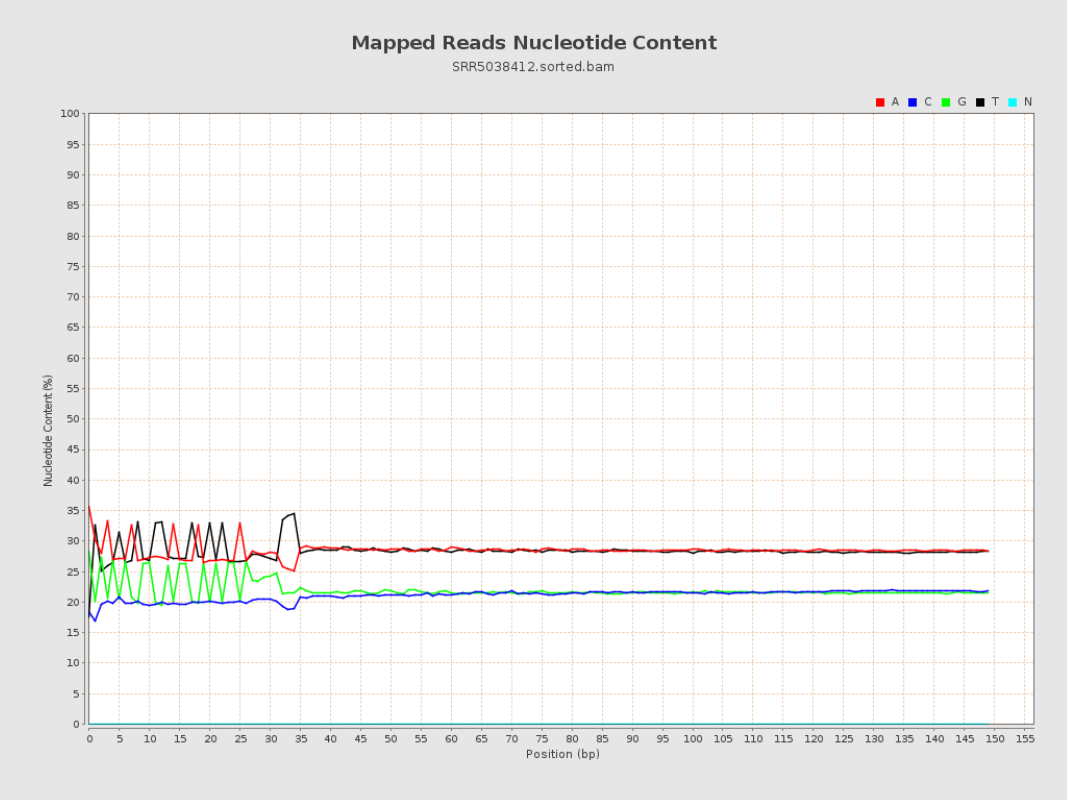
6. Results : Genome Fraction Coverage



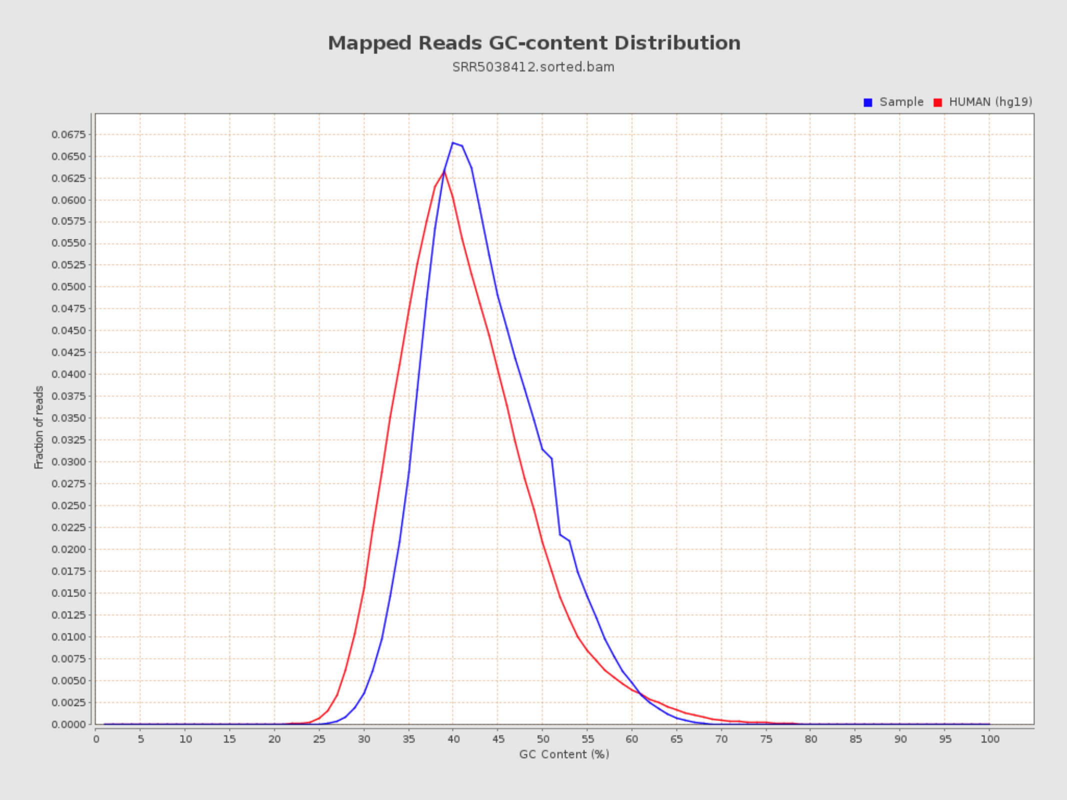
7. Results : Duplication Rate Histogram



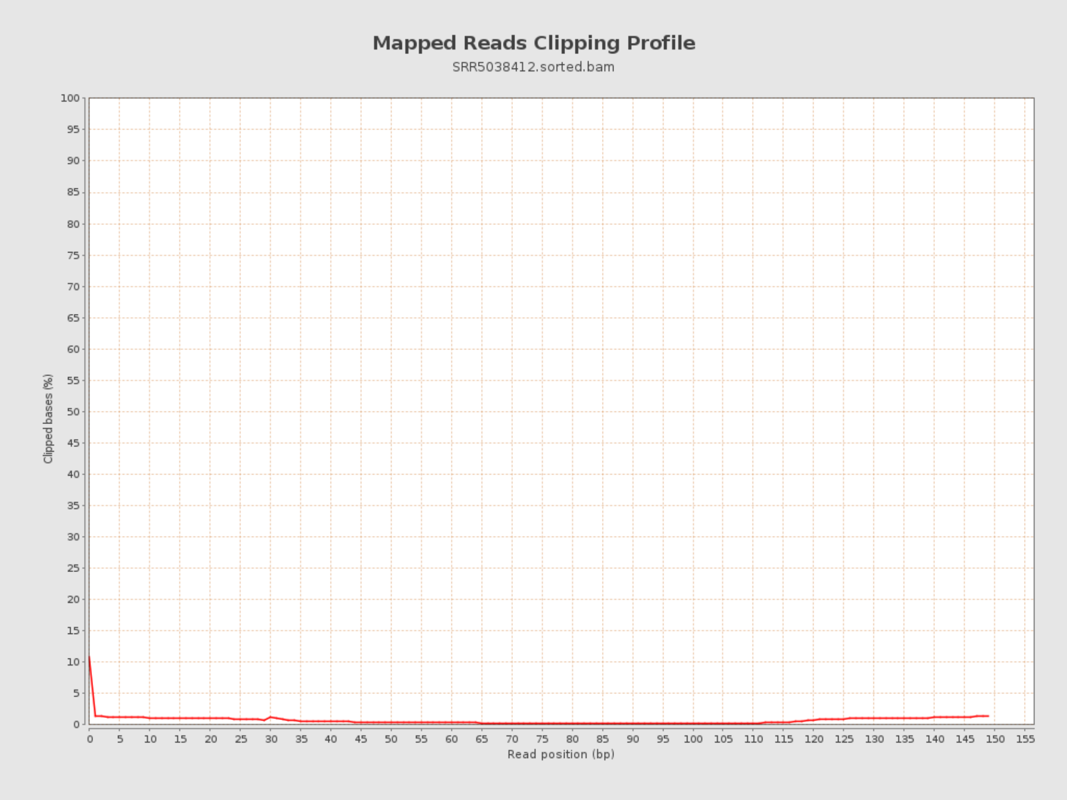
8. Results : Mapped Reads Nucleotide Content



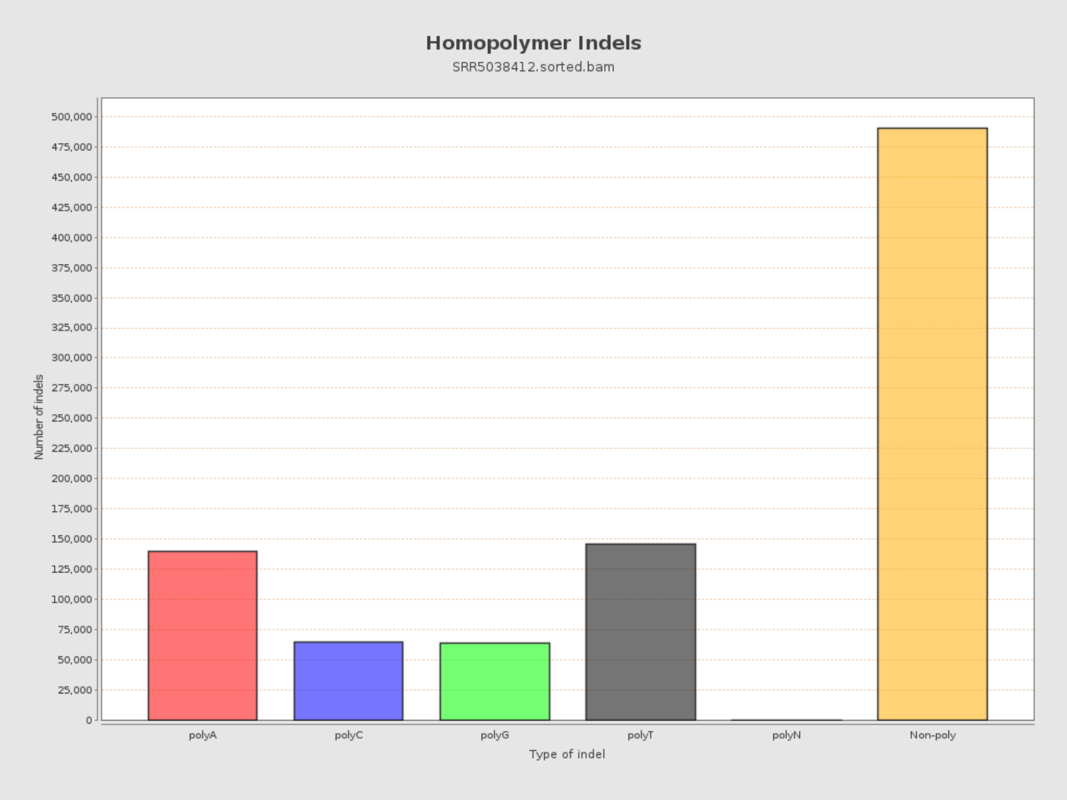
9. Results : Mapped Reads GC-content Distribution



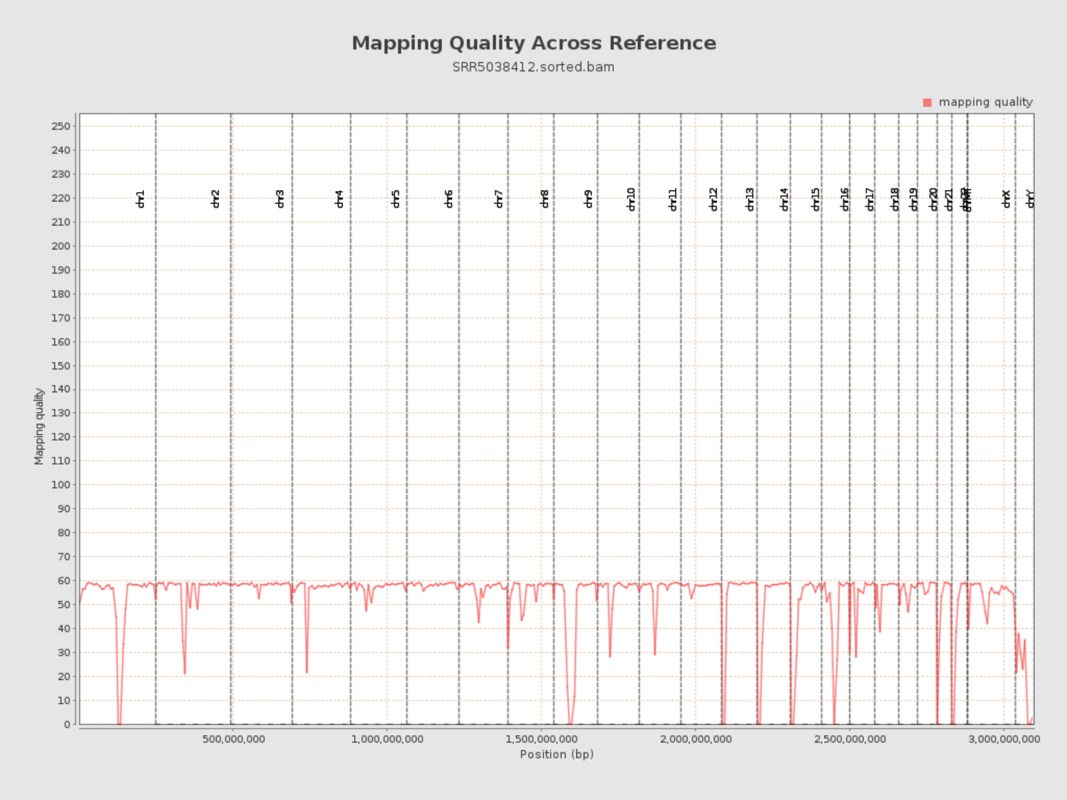
10. Results : Mapped Reads Clipping Profile



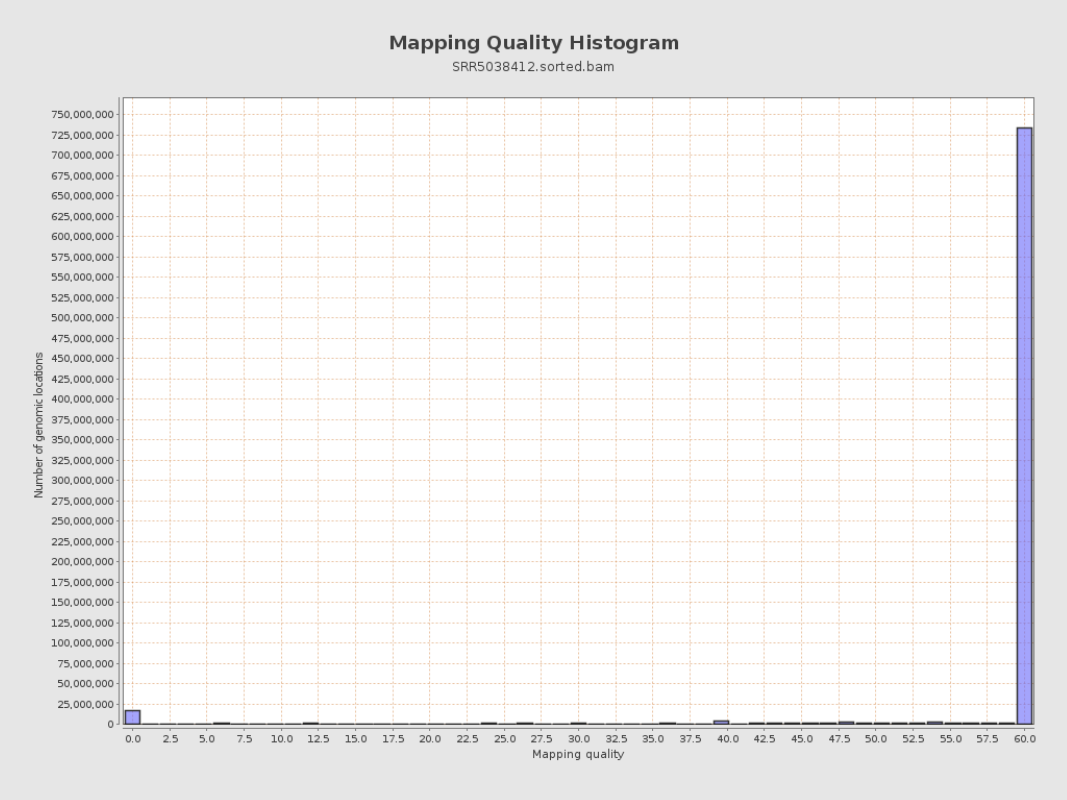
11. Results : Homopolymer Indels



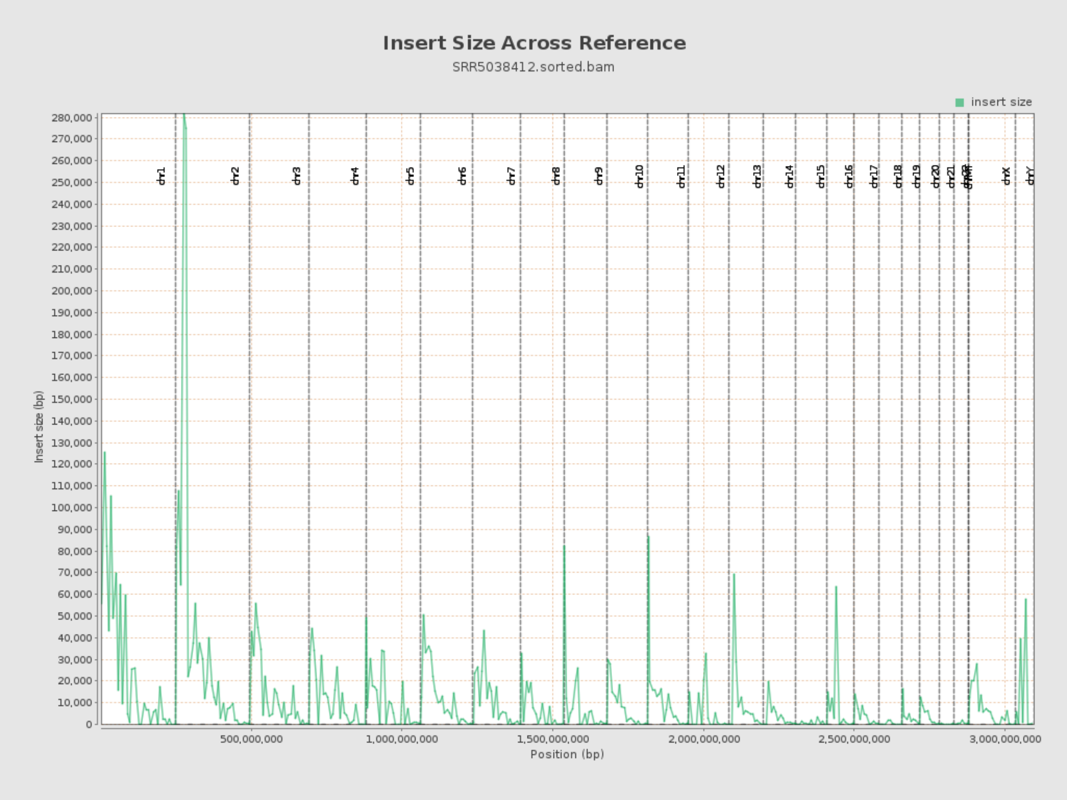
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram