Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/15 12:33:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038442.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_SRR5038442 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038442_1.fastq.gz SRR5038442_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 15 12:33:40 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038442.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	13,107,382
Mapped reads	12,439,134 / 94.9%
Unmapped reads	668,248 / 5.1%
Mapped paired reads	12,439,134 / 94.9%
Mapped reads, first in pair	6,291,199 / 48%
Mapped reads, second in pair	6,147,935 / 46.9%
Mapped reads, both in pair	12,274,938 / 93.65%
Mapped reads, singletons	164,196 / 1.25%
Secondary alignments	0
Supplementary alignments	215,005 / 1.64%
Read min/max/mean length	30 / 150 / 150.85
Duplicated reads (estimated)	1,727,770 / 13.18%
Duplication rate	7.86%
Clipped reads	2,742,374 / 20.92%

2.2. ACGT Content

Number/percentage of A's	520,938,929 / 29.21%
Number/percentage of C's	364,192,265 / 20.42%
Number/percentage of T's	522,684,200 / 29.31%
Number/percentage of G's	375,547,822 / 21.06%
Number/percentage of N's	37,515 / 0%

GC Percentage	41.48%

2.3. Coverage

Mean	0.5765
Standard Deviation	9.2235

2.4. Mapping Quality

Mean Mapping Quality	53.69

2.5. Insert size

Mean	96,993.26
Standard Deviation	2,932,558.98
P25/Median/P75	229 / 273 / 329

2.6. Mismatches and indels

General error rate	1.48%
Mismatches	25,525,081
Insertions	314,248
Mapped reads with at least one insertion	2.38%
Deletions	623,027
Mapped reads with at least one deletion	4.82%
Homopolymer indels	47.14%

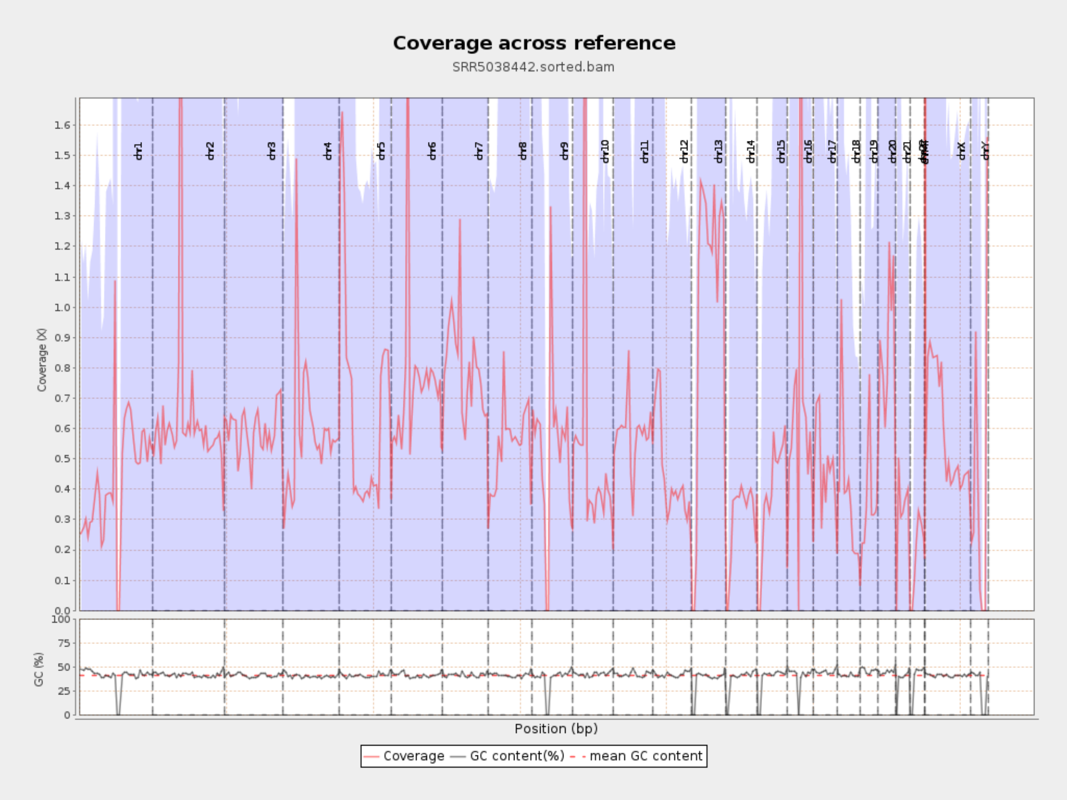
2.7. Chromosome stats

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

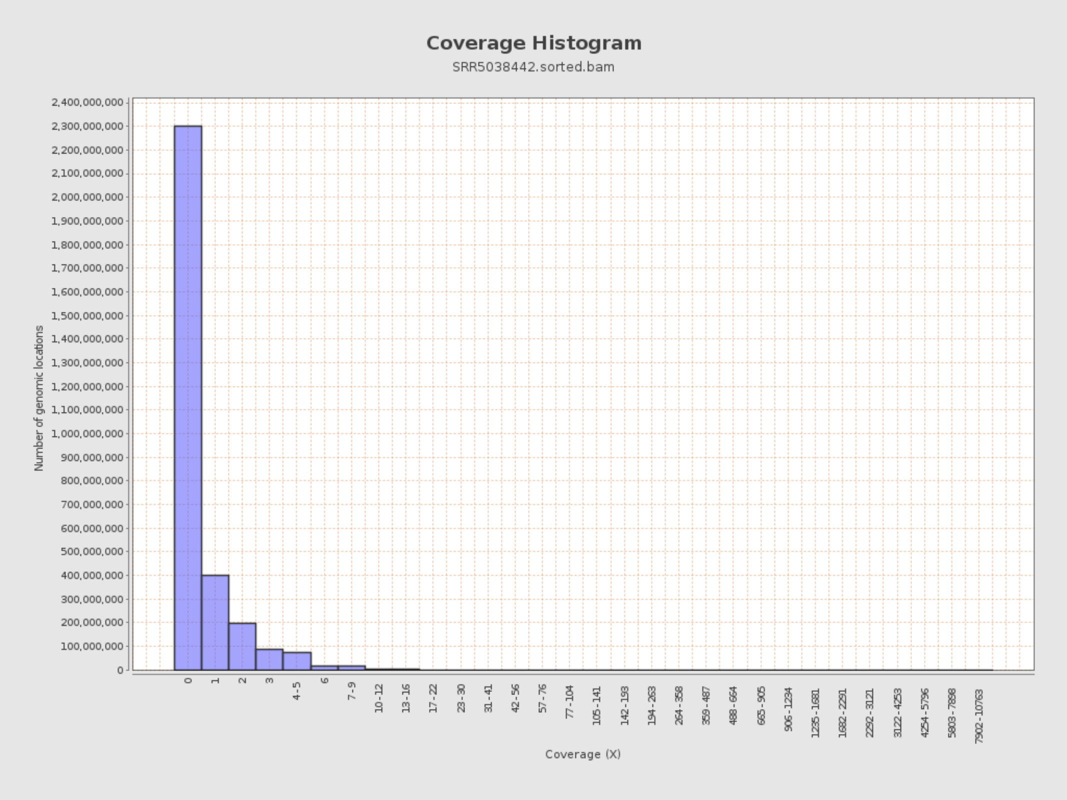
		bases	coverage	deviation
chr1	249250621	108221055	0.4342	11.2222
chr2	243199373	158982506	0.6537	11.8188
chr3	198022430	117701663	0.5944	1.3151
chr4	191154276	111711040	0.5844	7.3125
chr5	180915260	121711167	0.6728	1.5727
chr6	171115067	131348814	0.7676	15.5388
chr7	159138663	127452928	0.8009	10.6869
chr8	146364022	80203576	0.548	2.7194
chr9	141213431	73673233	0.5217	15.6319
chr10	135534747	74962277	0.5531	17.6954
chr11	135006516	77239958	0.5721	5.3126
chr12	133851895	60781997	0.4541	1.1702
chr13	115169878	120618475	1.0473	1.9419
chr14	107349540	32432936	0.3021	1.0592
chr15	102531392	39040567	0.3808	1.0006
chr16	90354753	63150598	0.6989	13.3509
chr17	81195210	37861470	0.4663	5.8886
chr18	78077248	29744553	0.381	12.7879
chr19	59128983	20430241	0.3455	6.4936
chr20	63025520	54300694	0.8616	2.6867
chr21	48129895	15618044	0.3245	3.5148
chr22	51304566	9437469	0.1839	0.7522
chrMT	16571	932102	56.249	33.0495
chrX	155270560	90826479	0.585	1.8647

chrY	59373566	26239509	0.4419	12.2123

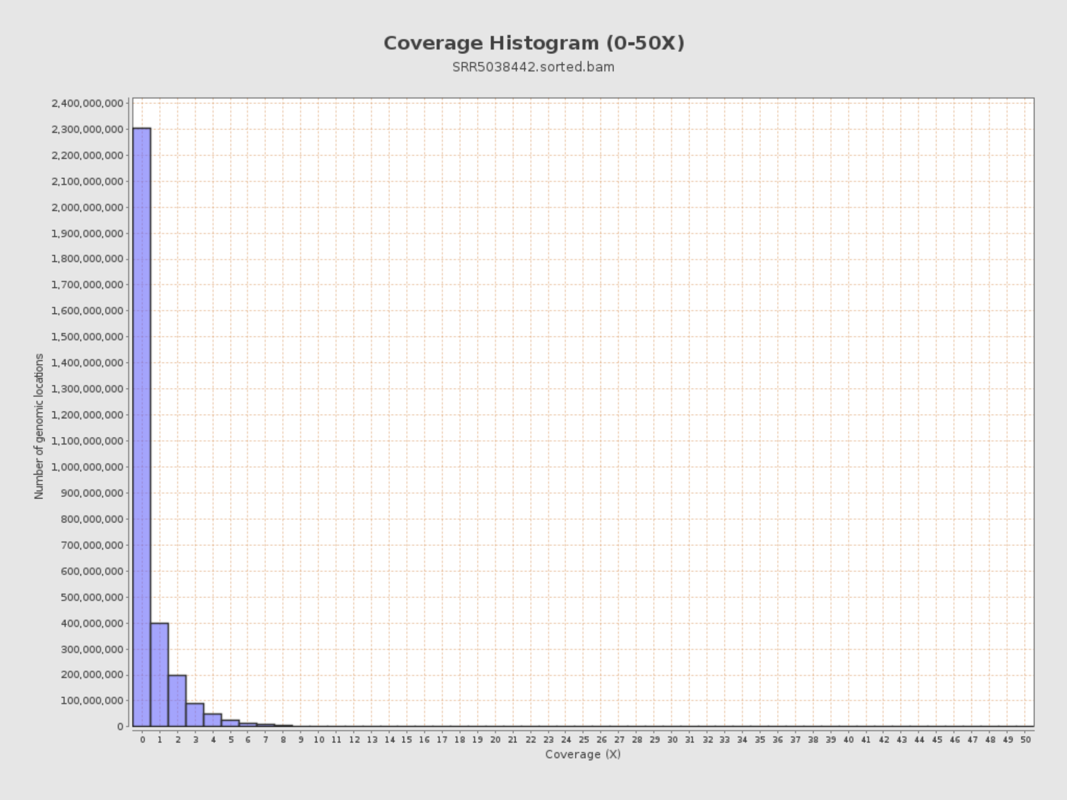
3. Results : Coverage across reference



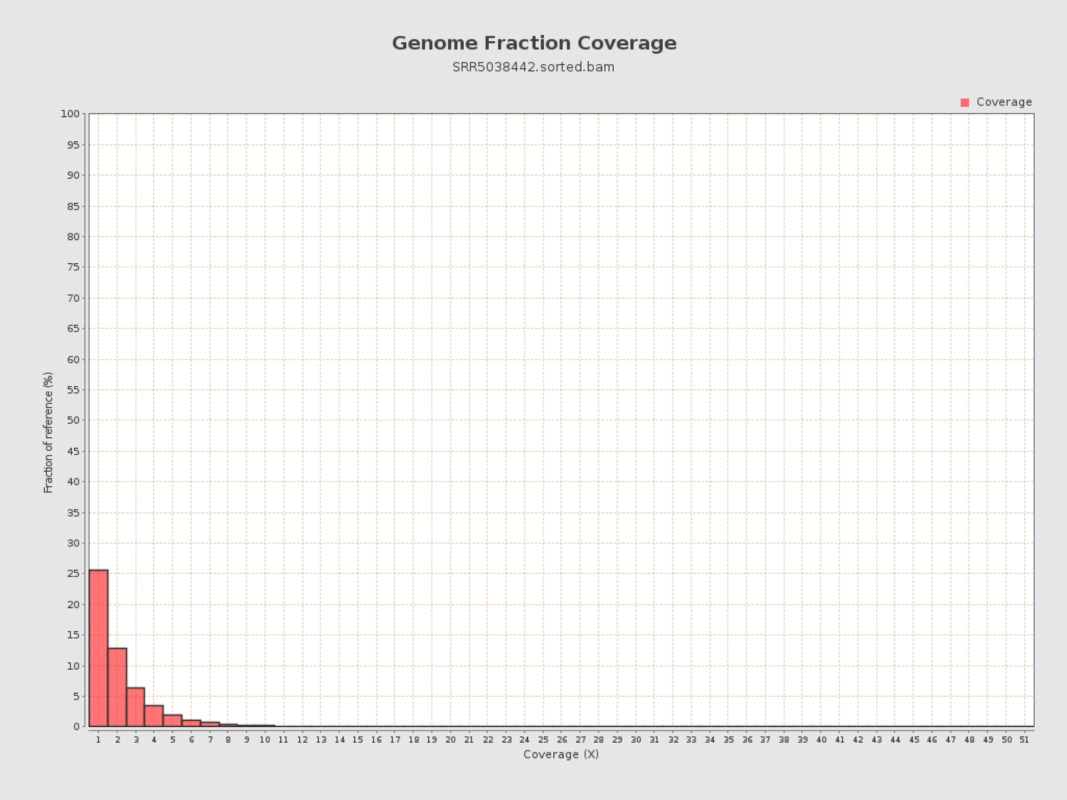
4. Results : Coverage Histogram



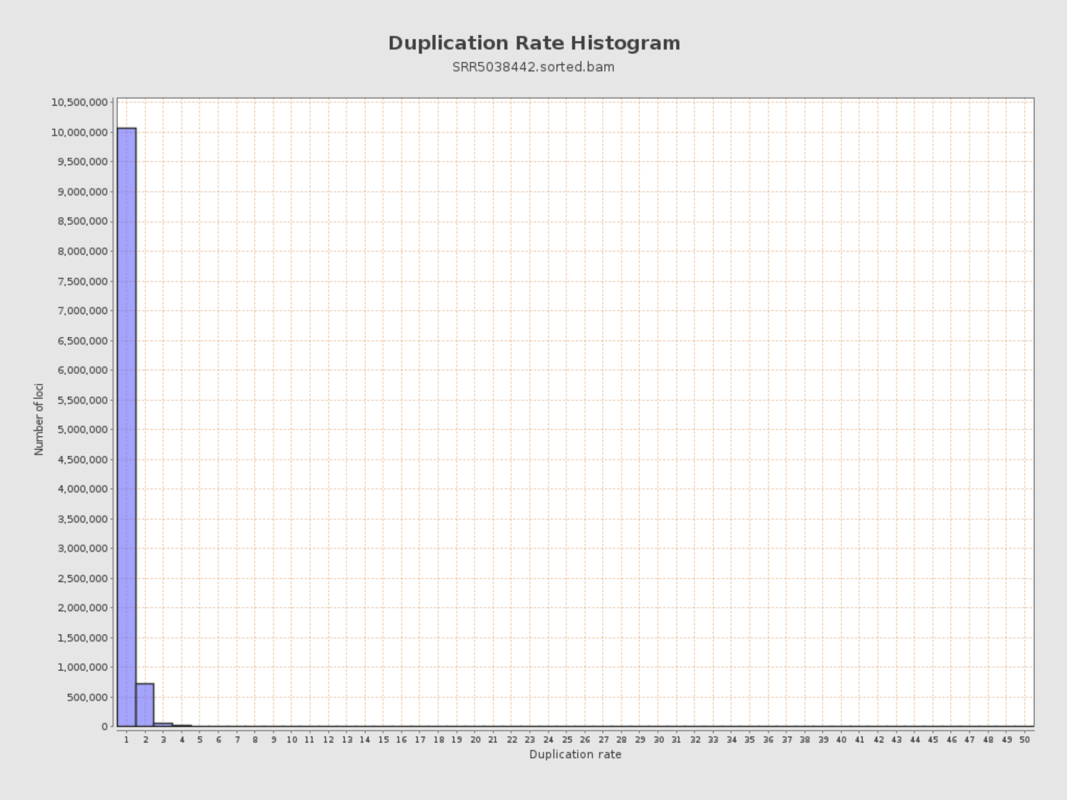
5. Results : Coverage Histogram (0-50X)



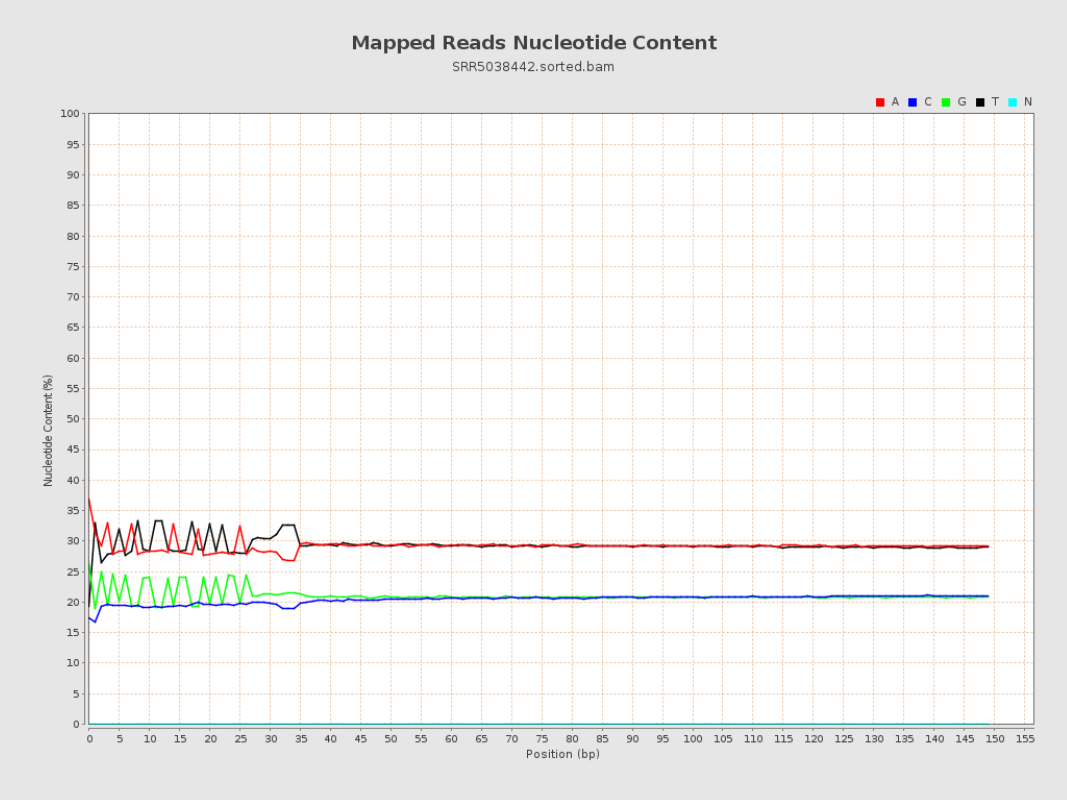
6. Results : Genome Fraction Coverage



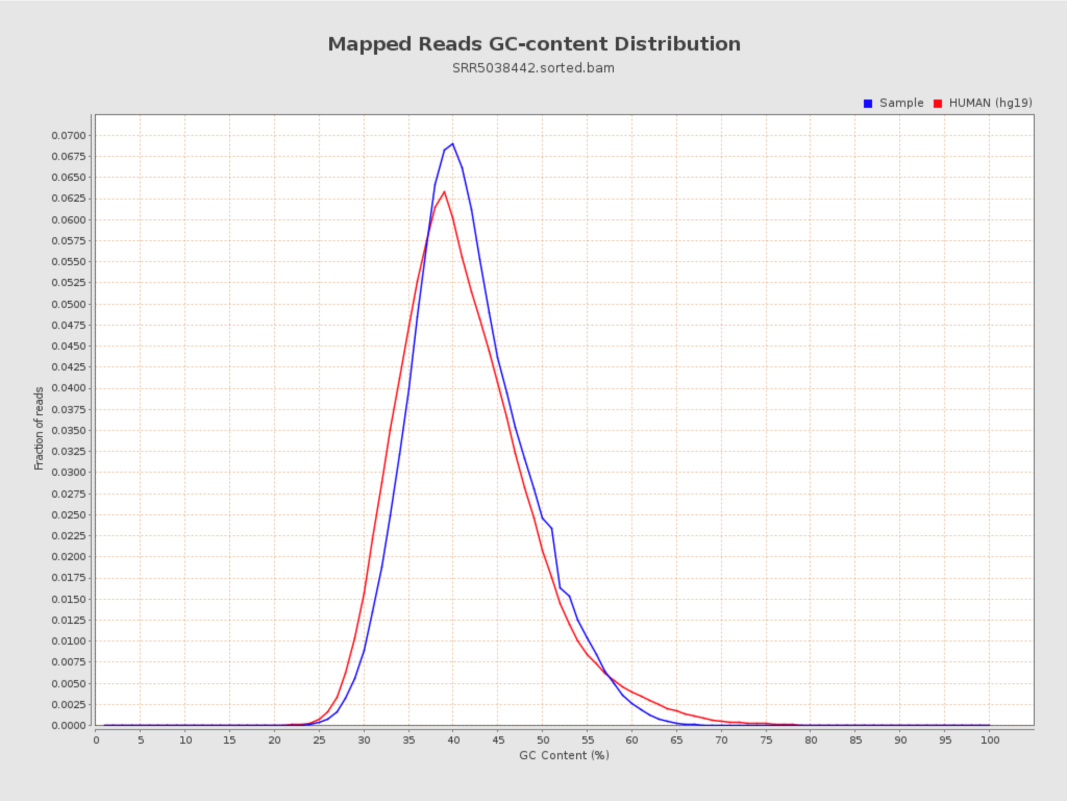
7. Results : Duplication Rate Histogram



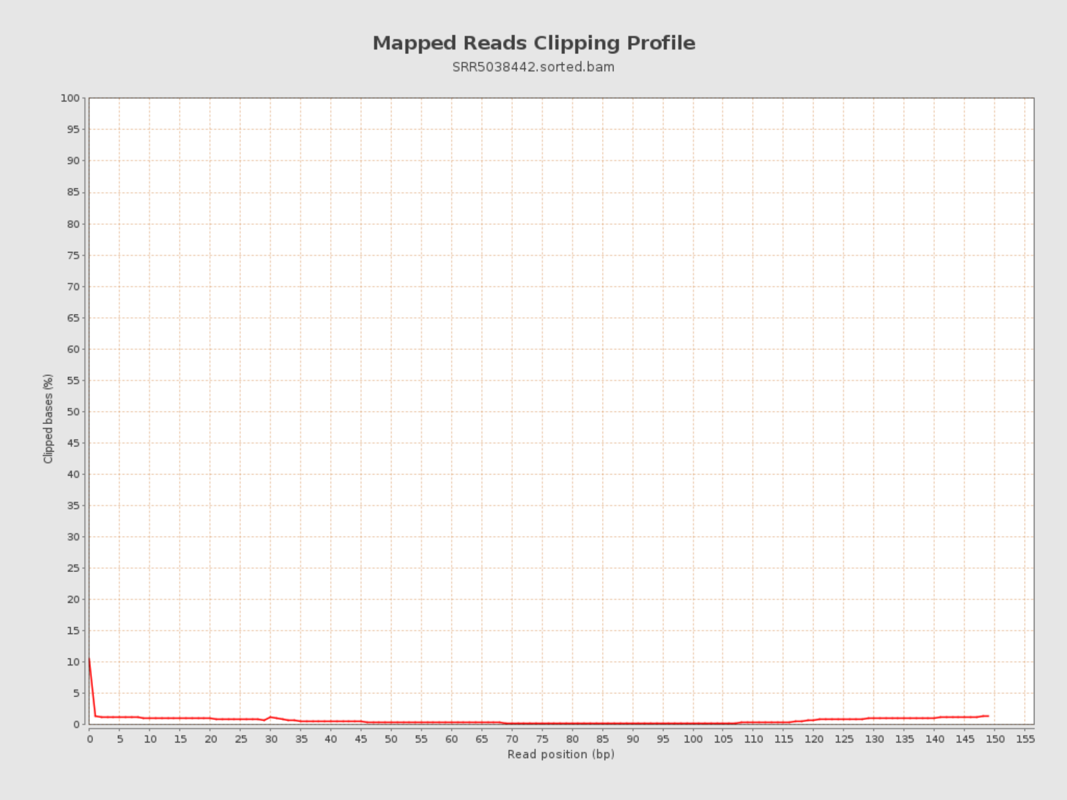
8. Results : Mapped Reads Nucleotide Content



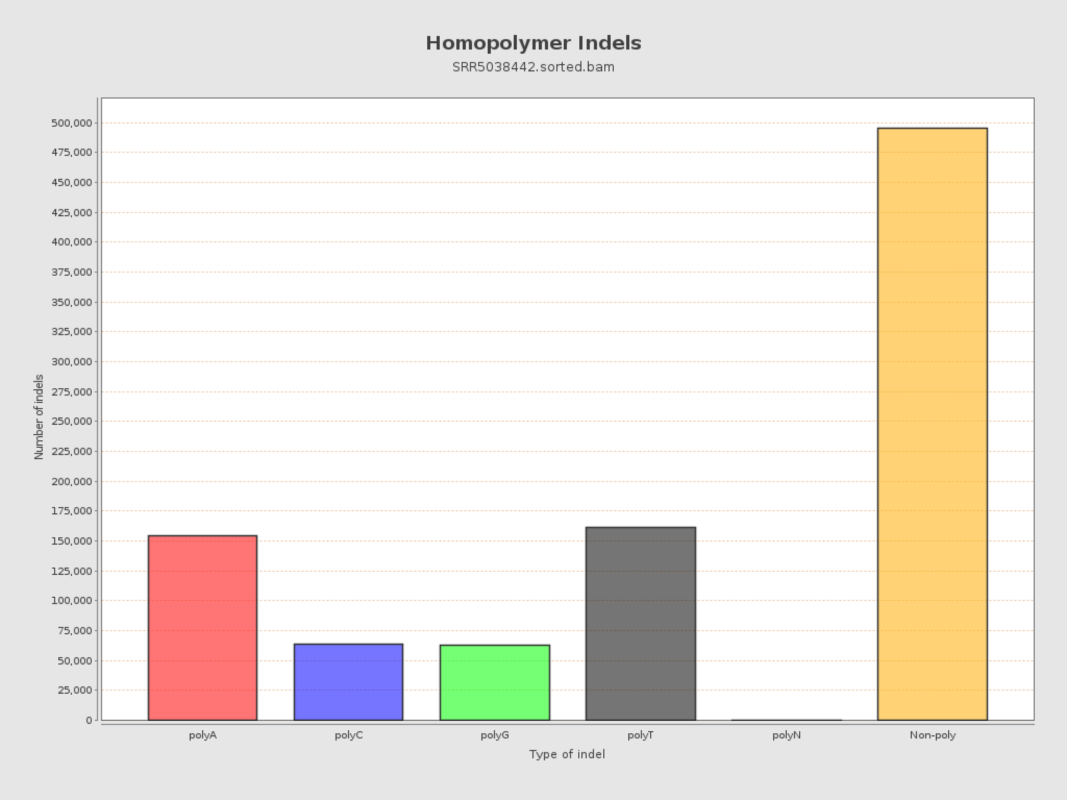
9. Results : Mapped Reads GC-content Distribution



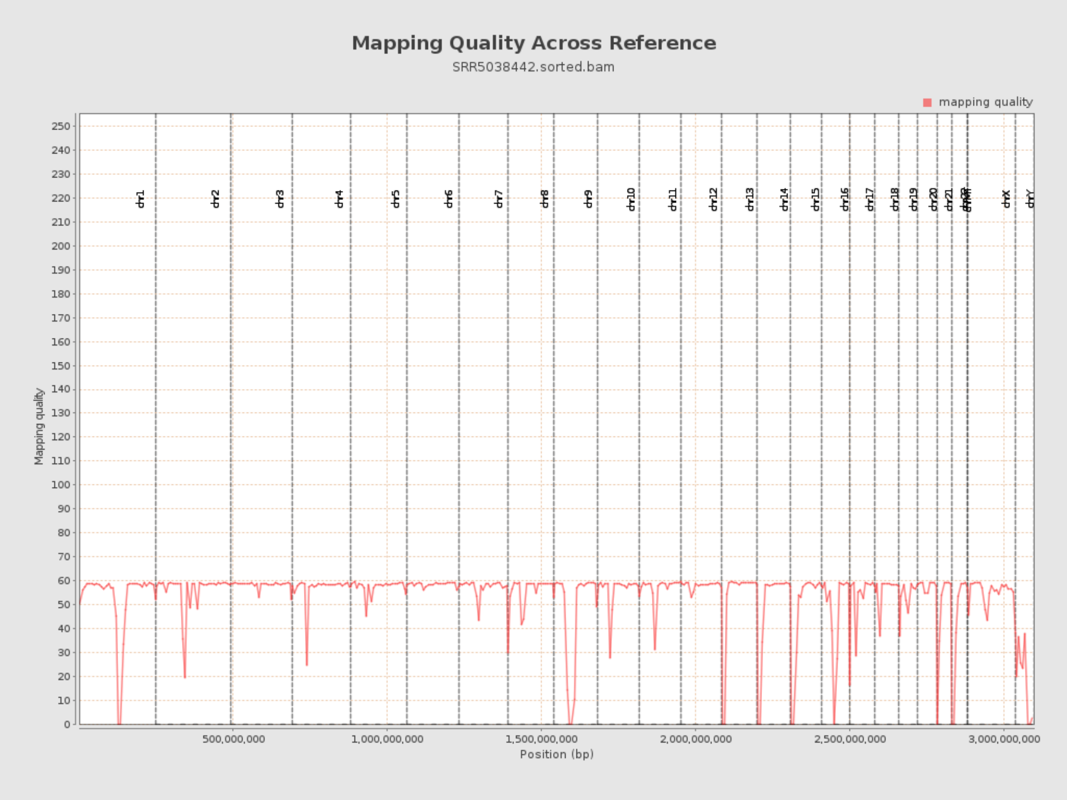
10. Results : Mapped Reads Clipping Profile



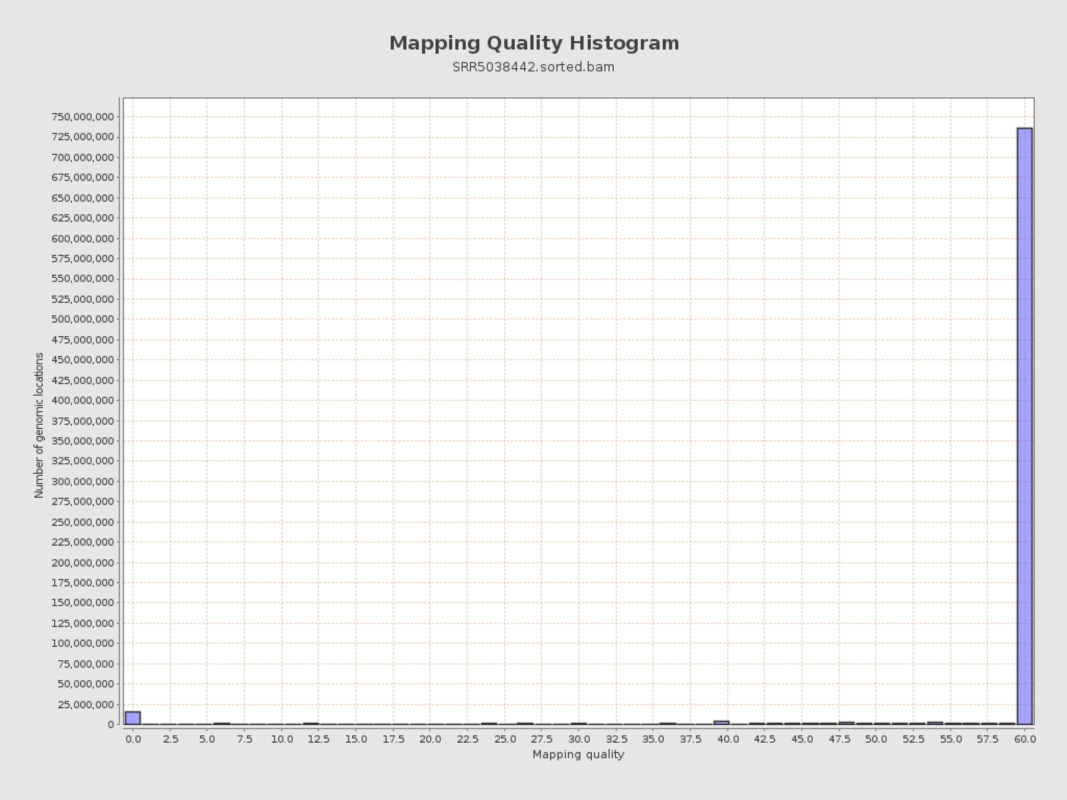
11. Results : Homopolymer Indels



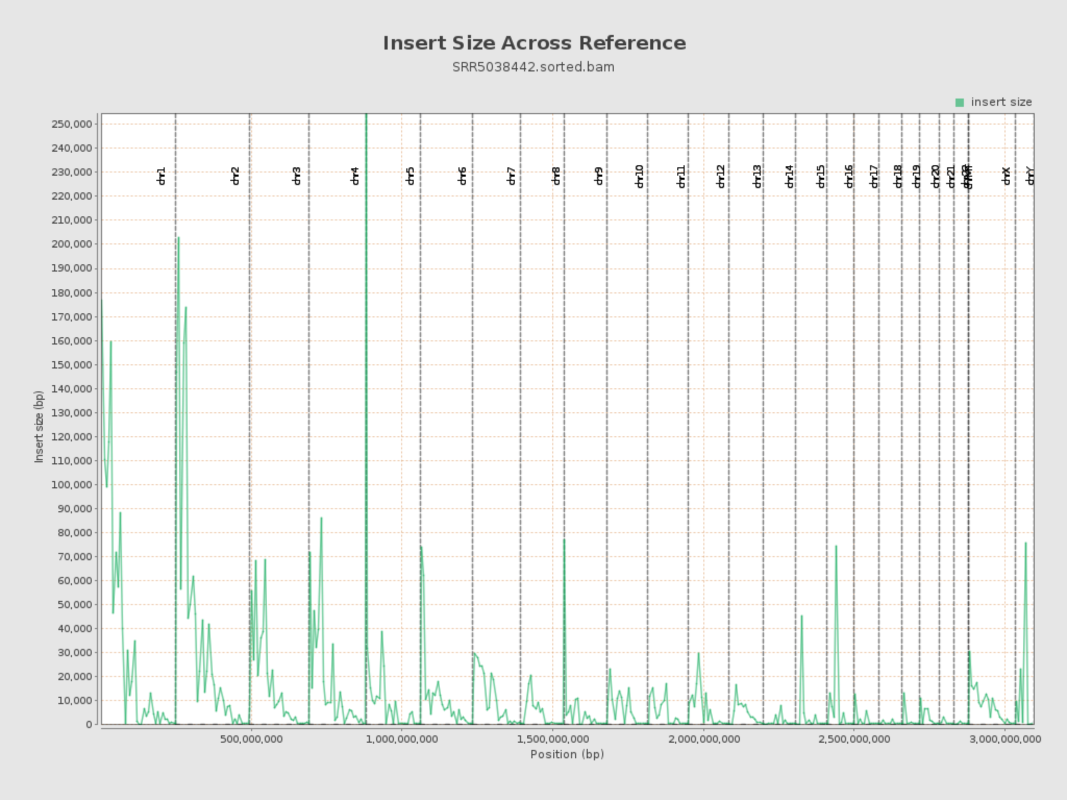
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram