Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/15 03:37:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038427.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_SRR5038427 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038427_1.fastq.gz SRR5038427_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 15 03:37:01 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038427.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	15,920,932
Mapped reads	14,975,180 / 94.06%
Unmapped reads	945,752 / 5.94%
Mapped paired reads	14,975,180 / 94.06%
Mapped reads, first in pair	7,573,222 / 47.57%
Mapped reads, second in pair	7,401,958 / 46.49%
Mapped reads, both in pair	14,779,184 / 92.83%
Mapped reads, singletons	195,996 / 1.23%
Secondary alignments	0
Supplementary alignments	219,319 / 1.38%
Read min/max/mean length	30 / 150 / 150.72
Duplicated reads (estimated)	2,389,605 / 15.01%
Duplication rate	9.74%
Clipped reads	3,031,951 / 19.04%

2.2. ACGT Content

Number/percentage of A's	633,833,546 / 29.37%
Number/percentage of C's	441,769,956 / 20.47%
Number/percentage of T's	631,727,600 / 29.27%
Number/percentage of G's	450,564,286 / 20.88%
Number/percentage of N's	47,043 / 0%

GC Percentage	41.35%

2.3. Coverage

Mean	0.6975
Standard Deviation	11.406

2.4. Mapping Quality

Mean Mapping Quality	53.78

2.5. Insert size

Mean	66,692.99
Standard Deviation	2,451,981.48
P25/Median/P75	203 / 247 / 302

2.6. Mismatches and indels

General error rate	1.48%
Mismatches	30,948,562
Insertions	369,938
Mapped reads with at least one insertion	2.33%
Deletions	733,564
Mapped reads with at least one deletion	4.72%
Homopolymer indels	47.03%

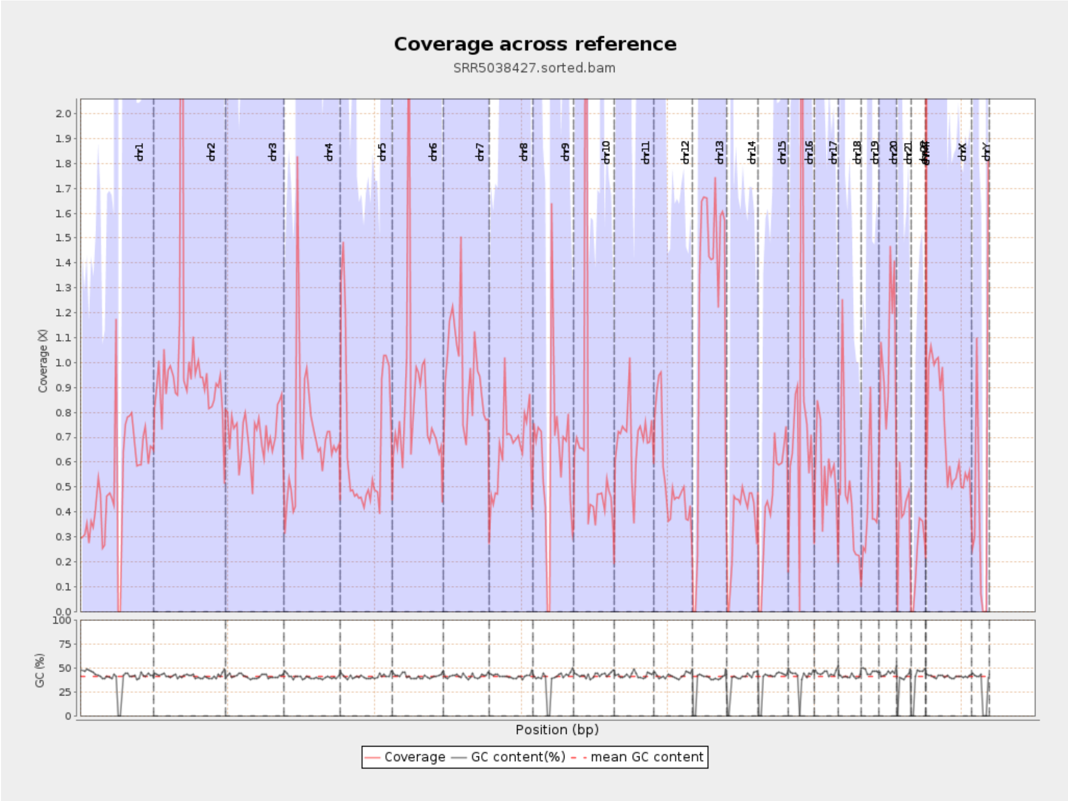
2.7. Chromosome stats

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

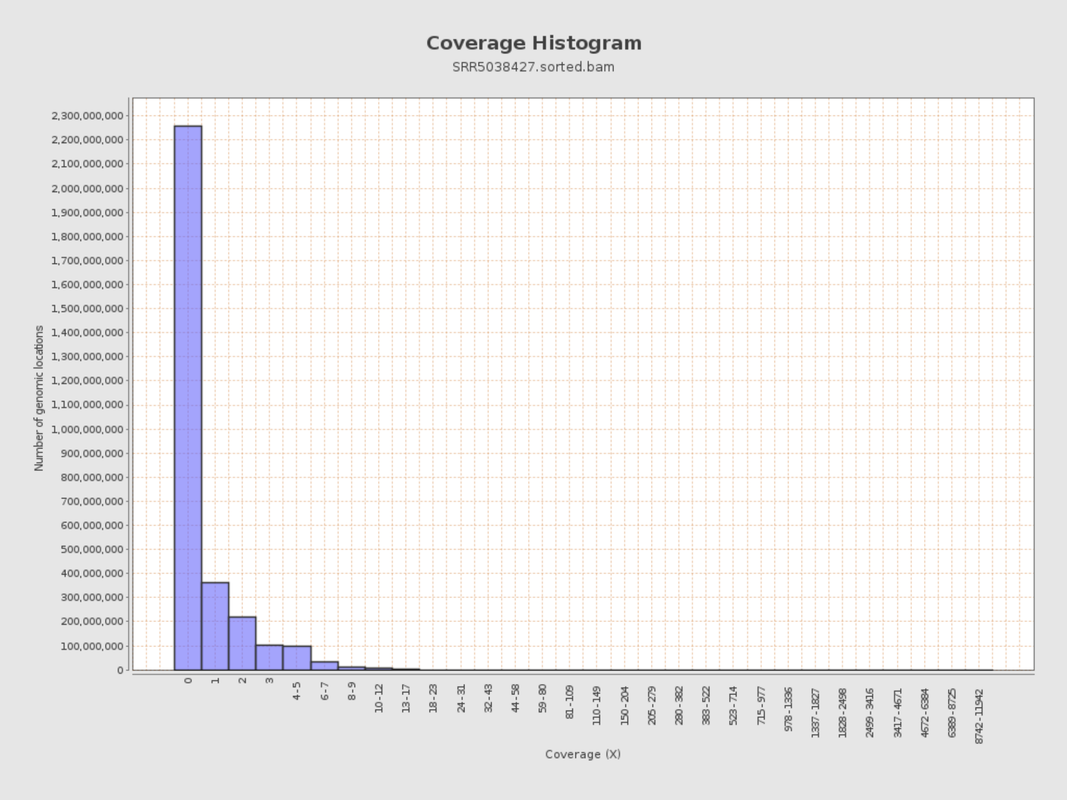
		bases	coverage	deviation
chr1	249250621	128137213	0.5141	11.6946
chr2	243199373	246859690	1.0151	17.1941
chr3	198022430	141180699	0.713	1.5839
chr4	191154276	133195102	0.6968	8.6667
chr5	180915260	124289132	0.687	1.6714
chr6	171115067	146522756	0.8563	18.4684
chr7	159138663	152455737	0.958	12.3629
chr8	146364022	96324598	0.6581	3.518
chr9	141213431	87068549	0.6166	19.7261
chr10	135534747	90643109	0.6688	22.5786
chr11	135006516	92295265	0.6836	6.4679
chr12	133851895	73079324	0.546	1.3947
chr13	115169878	144634068	1.2558	2.3588
chr14	107349540	39270972	0.3658	1.3208
chr15	102531392	46982420	0.4582	1.2004
chr16	90354753	75510693	0.8357	16.4701
chr17	81195210	44907582	0.5531	6.3699
chr18	78077248	35727809	0.4576	15.8235
chr19	59128983	23429386	0.3962	6.8366
chr20	63025520	65133145	1.0334	3.1997
chr21	48129895	18825865	0.3911	4.3616
chr22	51304566	11228405	0.2189	0.8753
chrMT	16571	1332940	80.4381	48.8164
chrX	155270560	109524047	0.7054	2.2785

chrY	59373566	30834502	0.5193	14.8857

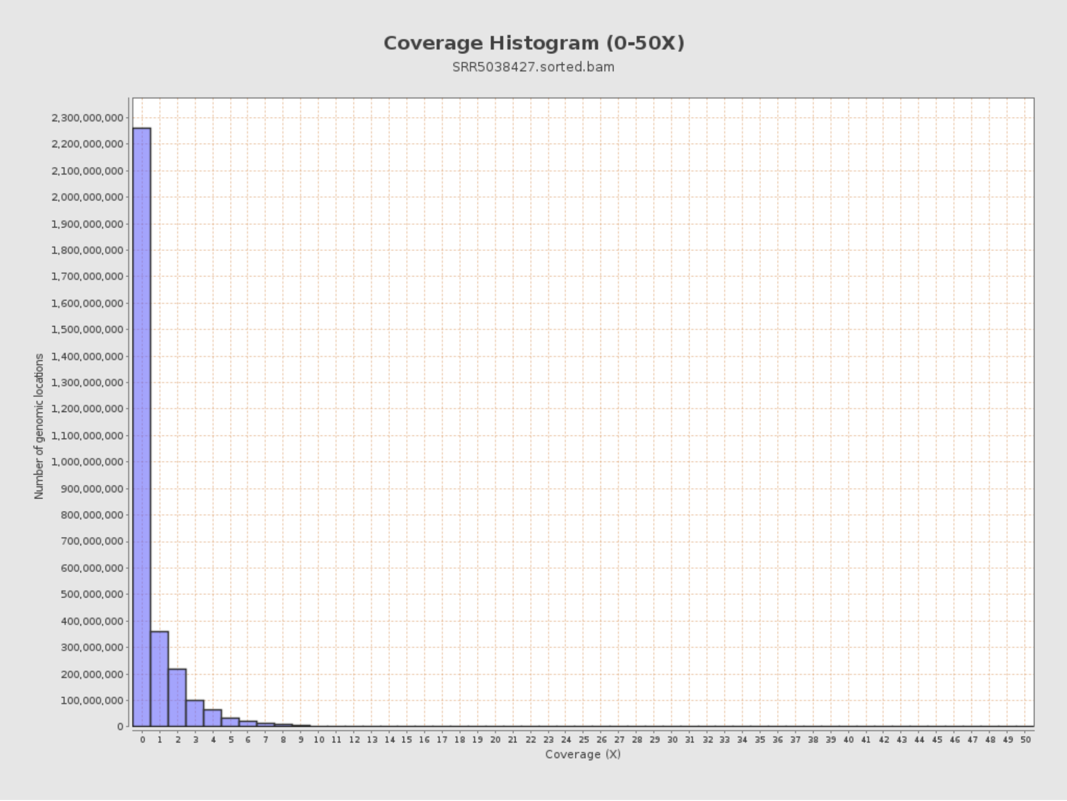
3. Results : Coverage across reference



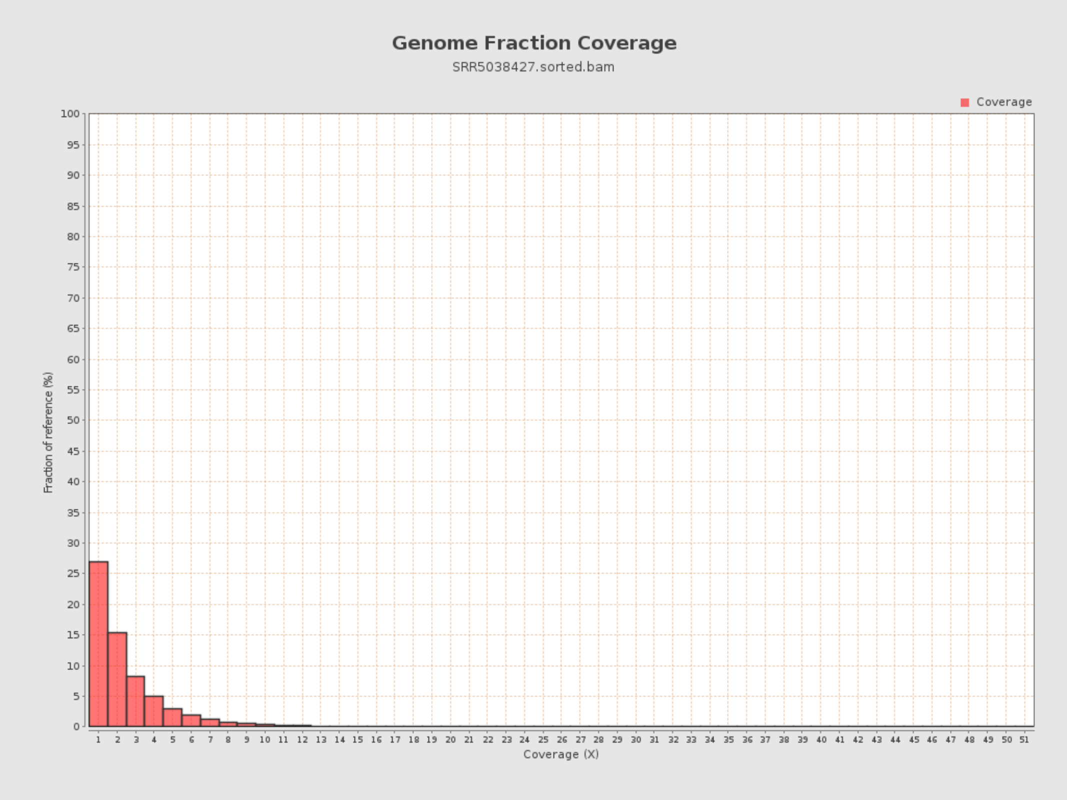
4. Results : Coverage Histogram



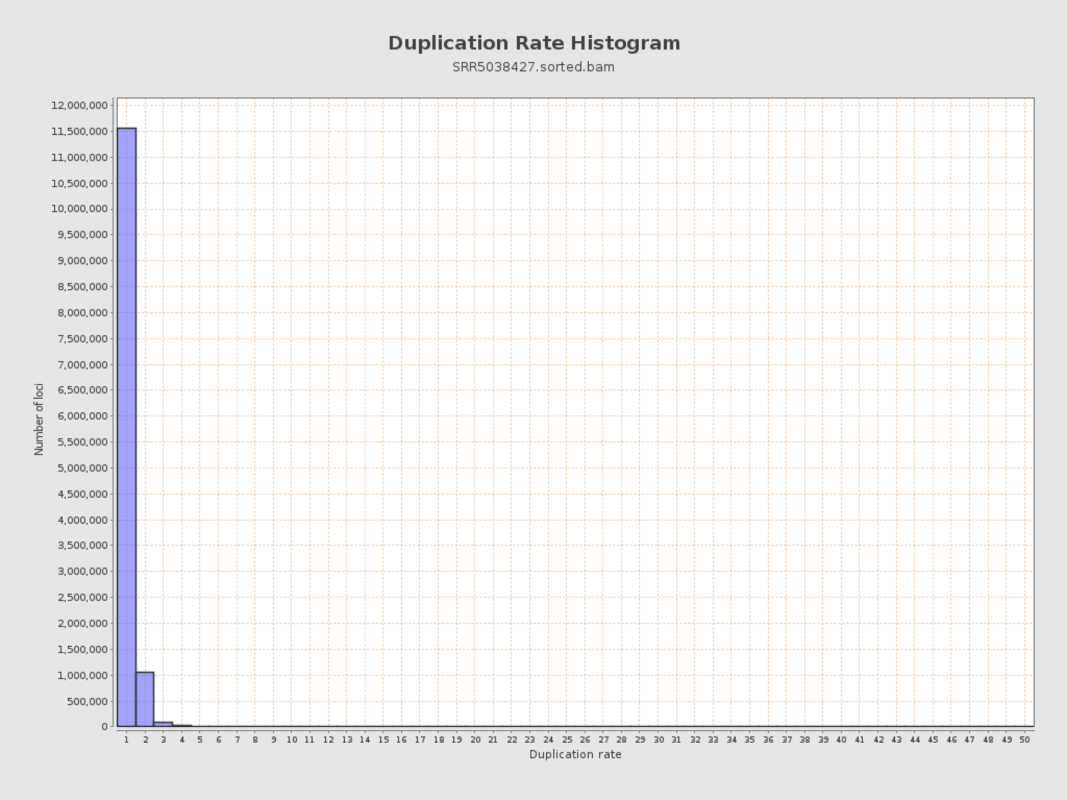
5. Results : Coverage Histogram (0-50X)



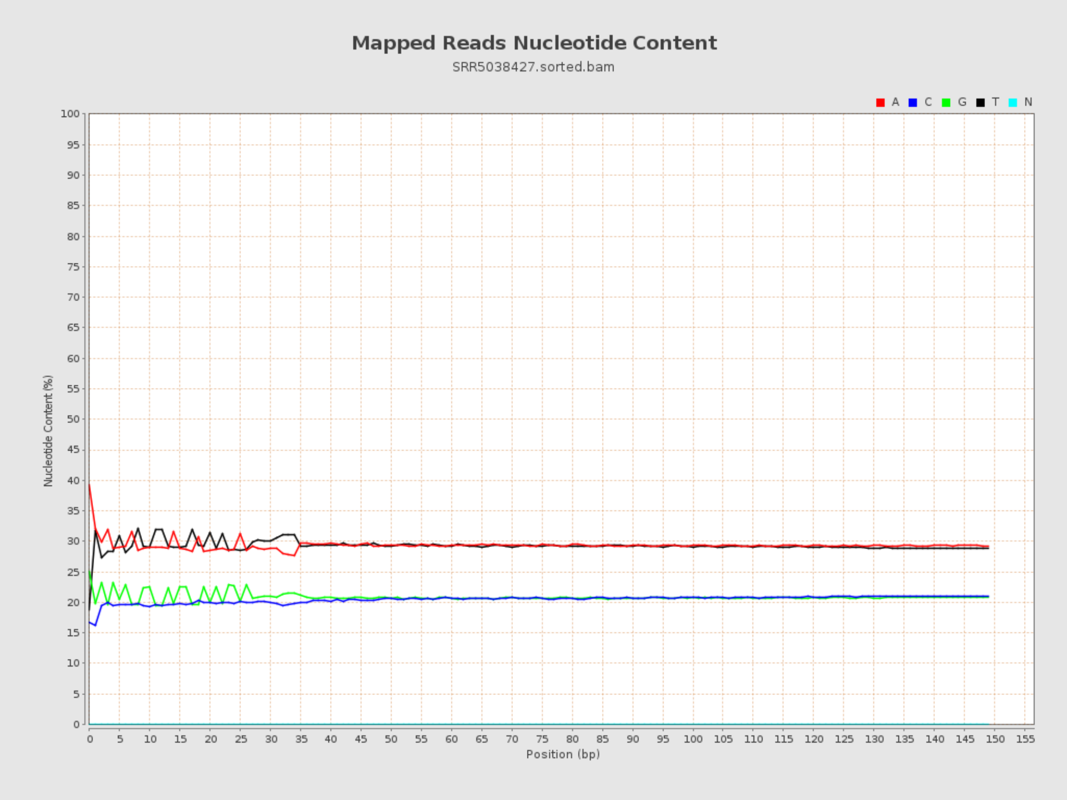
6. Results : Genome Fraction Coverage



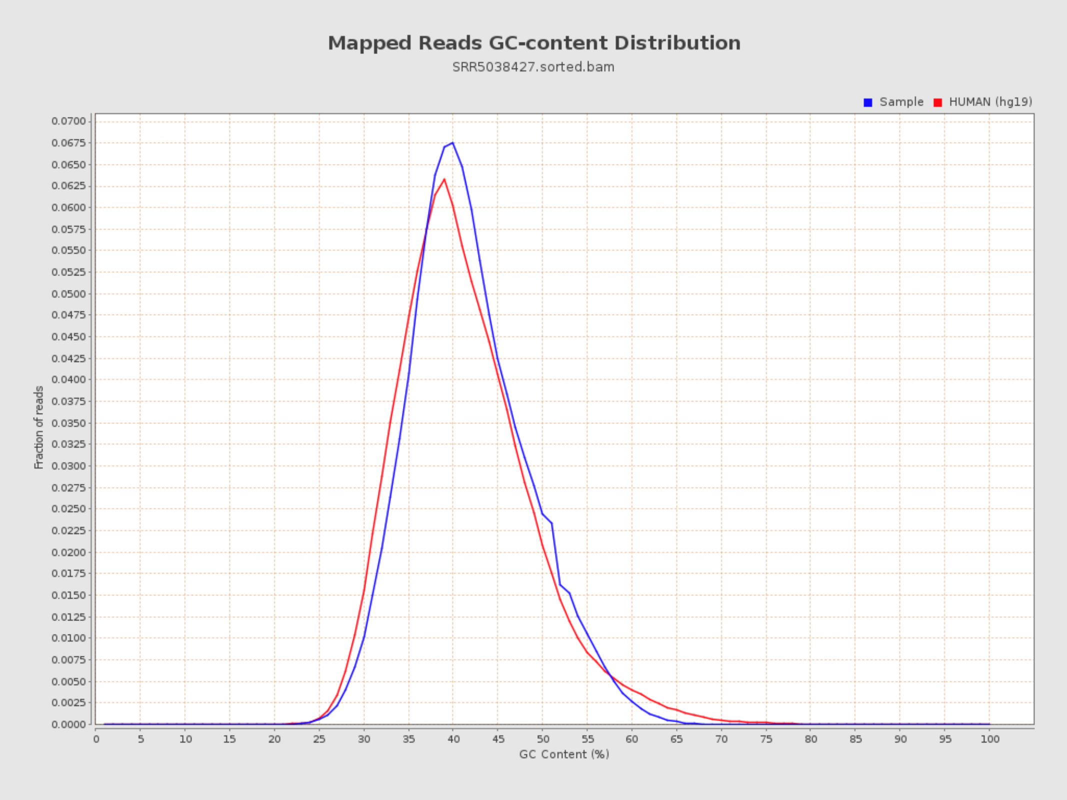
7. Results : Duplication Rate Histogram



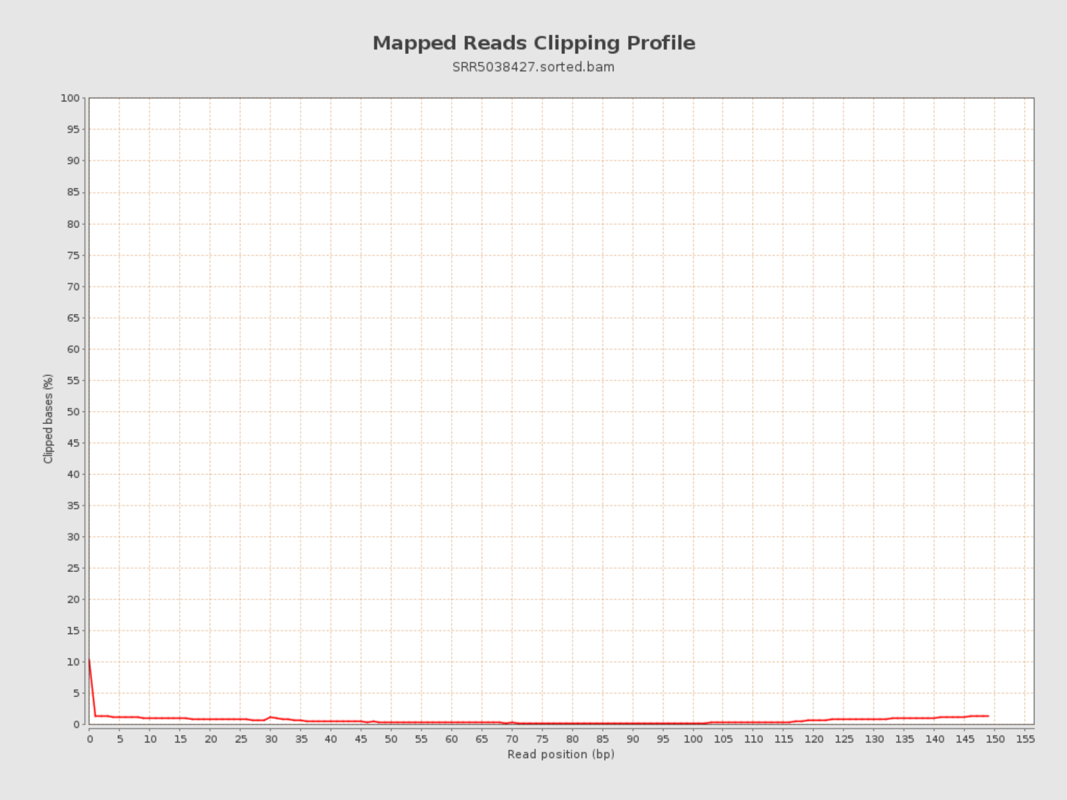
8. Results : Mapped Reads Nucleotide Content



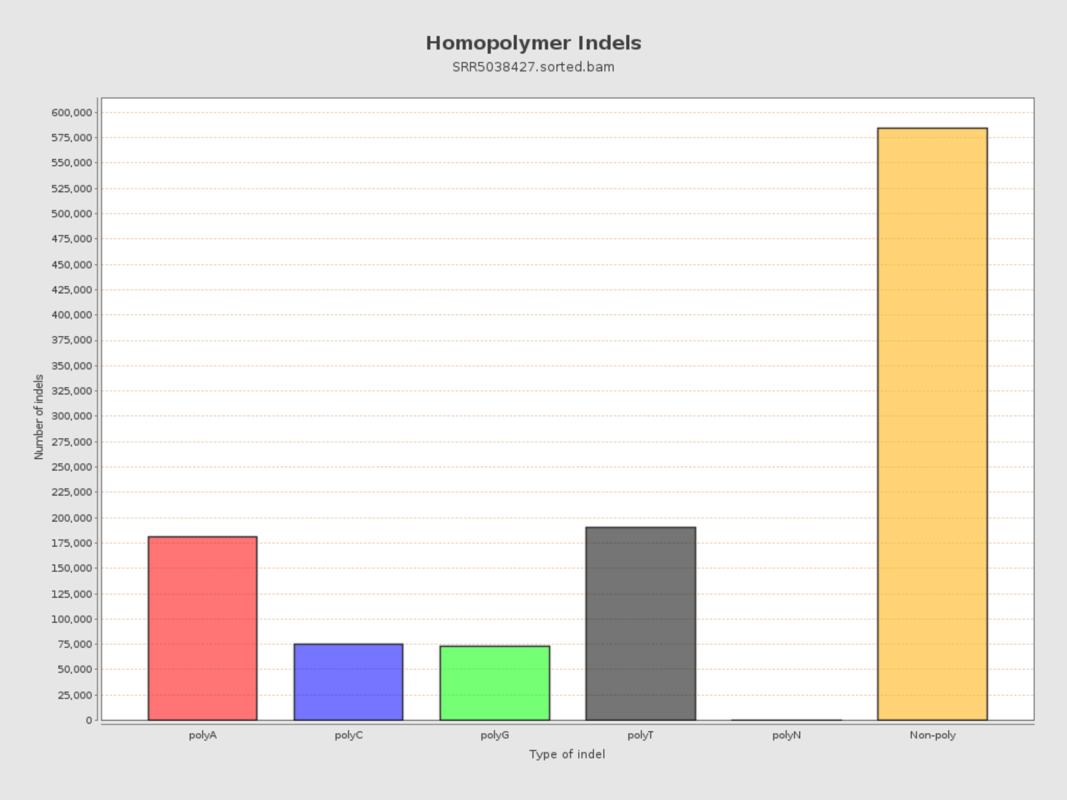
9. Results : Mapped Reads GC-content Distribution



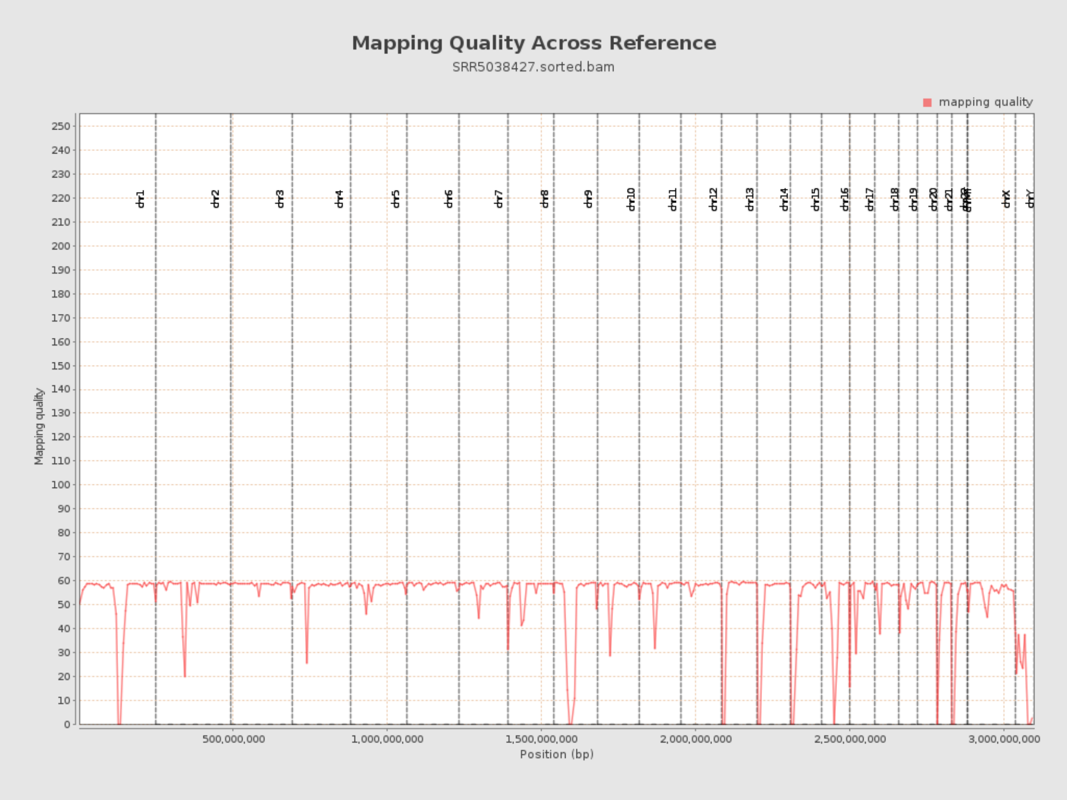
10. Results : Mapped Reads Clipping Profile



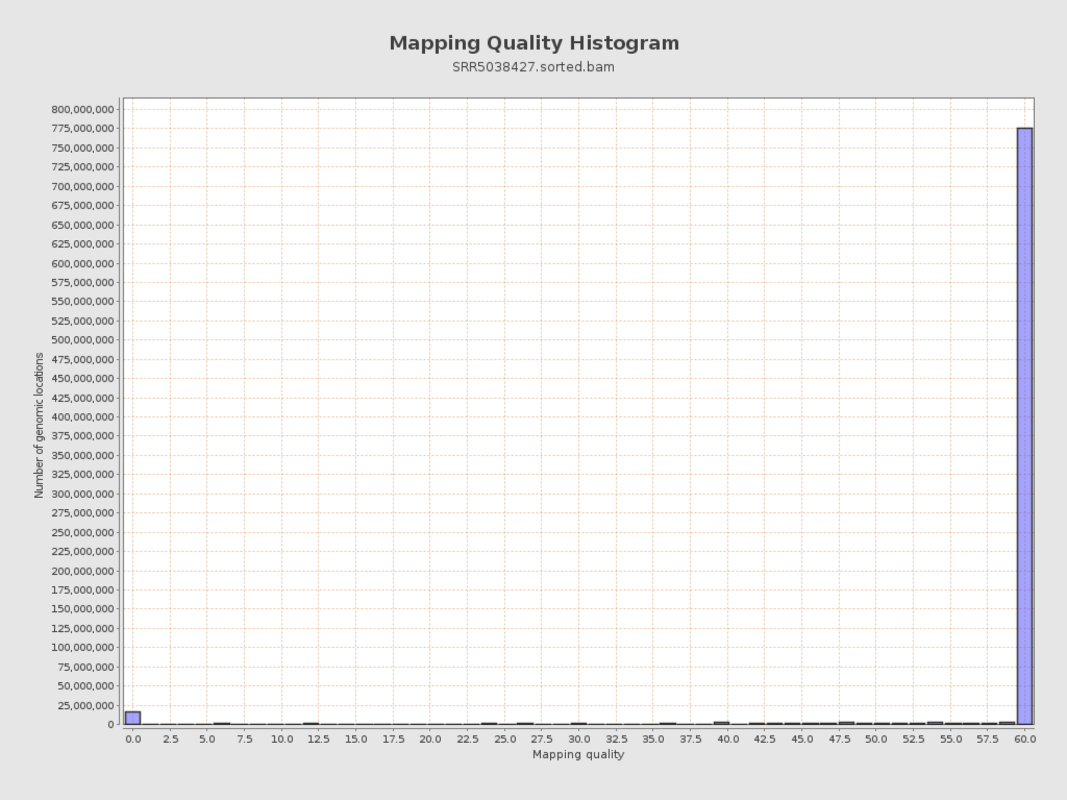
11. Results : Homopolymer Indels



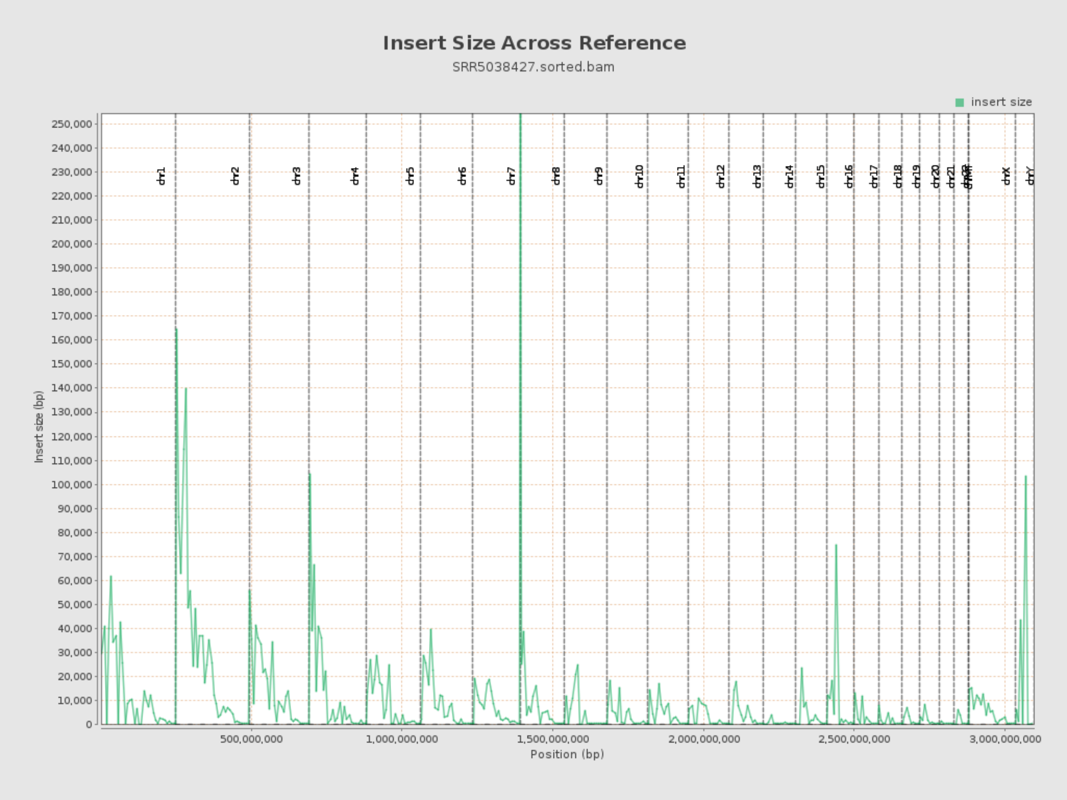
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram