Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/24 05:41:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR927016.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_SRR927016 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR927016_1.fastq.gz SRR927016_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 24 05:41:22 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR927016.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,528,924
Mapped reads	10,308,180 / 97.9%
Unmapped reads	220,744 / 2.1%
Mapped paired reads	10,308,180 / 97.9%
Mapped reads, first in pair	5,172,656 / 49.13%
Mapped reads, second in pair	5,135,524 / 48.78%
Mapped reads, both in pair	10,163,092 / 96.53%
Mapped reads, singletons	145,088 / 1.38%
Secondary alignments	0
Supplementary alignments	288,535 / 2.74%
Read min/max/mean length	30 / 101 / 102.14
Duplicated reads (estimated)	573,851 / 5.45%
Duplication rate	4.29%
Clipped reads	4,395,836 / 41.75%

2.2. ACGT Content

Number/percentage of A's	266,334,448 / 28.44%
Number/percentage of C's	182,253,062 / 19.46%
Number/percentage of T's	271,694,566 / 29.01%
Number/percentage of G's	216,179,011 / 23.08%
Number/percentage of N's	173,007 / 0.02%

GC Percentage	42.54%

2.3. Coverage

Mean	0.3028
Standard Deviation	1.5837

2.4. Mapping Quality

Mean Mapping Quality	52.43

2.5. Insert size

Mean	324,976.15
Standard Deviation	5,612,209.24
P25/Median/P75	144 / 187 / 252

2.6. Mismatches and indels

General error rate	0.98%
Mismatches	8,850,866
Insertions	161,656
Mapped reads with at least one insertion	1.54%
Deletions	482,876
Mapped reads with at least one deletion	4.57%
Homopolymer indels	51.8%

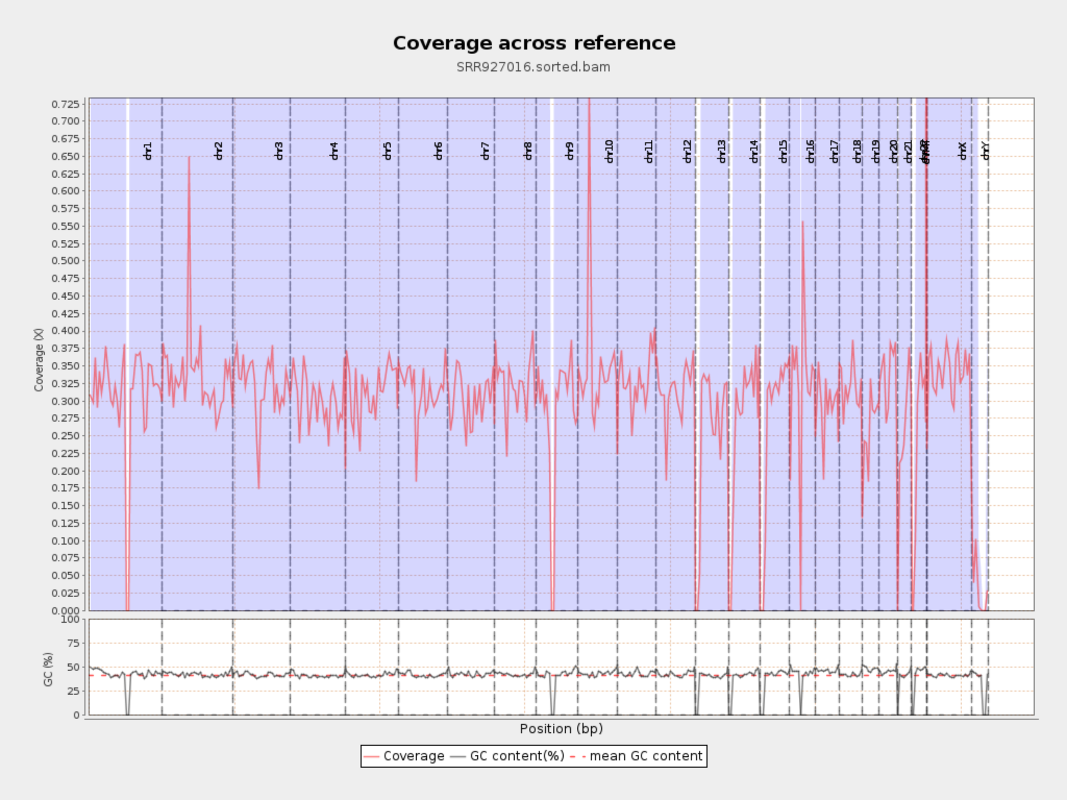
2.7. Chromosome stats

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

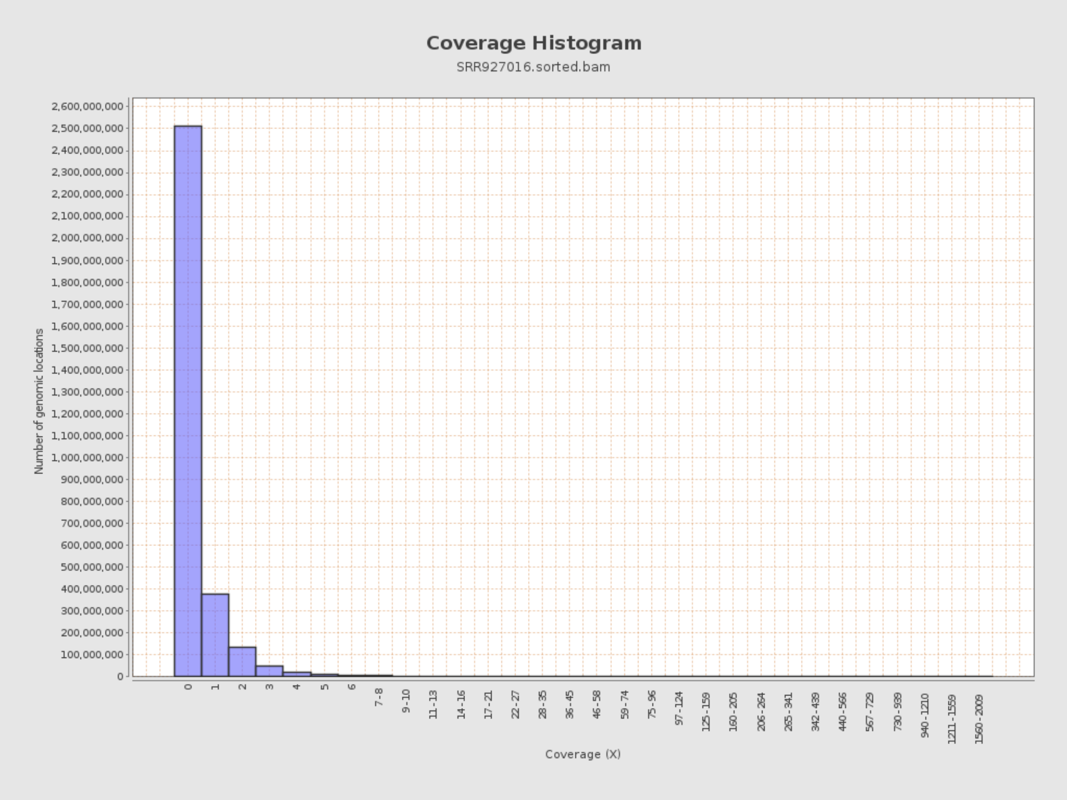
		bases	coverage	deviation
chr1	249250621	75928637	0.3046	1.925
chr2	243199373	82280303	0.3383	2.2642
chr3	198022430	63773184	0.3221	0.8219
chr4	191154276	57534252	0.301	1.0658
chr5	180915260	57065089	0.3154	0.7783
chr6	171115067	54060952	0.3159	0.8721
chr7	159138663	48225082	0.303	1.1018
chr8	146364022	47818332	0.3267	0.9062
chr9	141213431	39639954	0.2807	1.7259
chr10	135534747	47560907	0.3509	4.3676
chr11	135006516	44467944	0.3294	1.5369
chr12	133851895	42017764	0.3139	0.7878
chr13	115169878	28581786	0.2482	0.6895
chr14	107349540	28327147	0.2639	0.7372
chr15	102531392	27112367	0.2644	0.7244
chr16	90354753	29180202	0.323	2.1203
chr17	81195210	23739750	0.2924	0.8572
chr18	78077248	25115972	0.3217	1.719
chr19	59128983	15405909	0.2605	1.312
chr20	63025520	21319436	0.3383	0.8486
chr21	48129895	12062768	0.2506	1.0714
chr22	51304566	11539476	0.2249	0.6941
chrMT	16571	63056	3.8052	3.5713
chrX	155270560	52730797	0.3396	0.9078

chrY	59373566	1792745	0.0302	0.9662

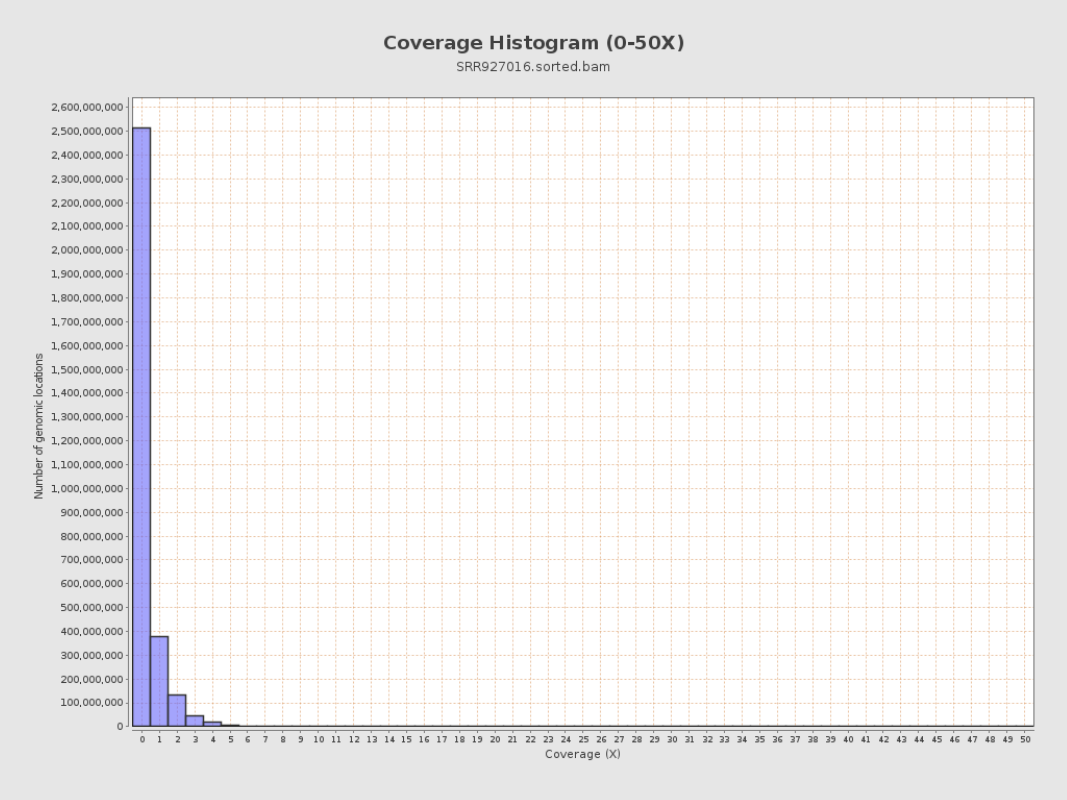
3. Results : Coverage across reference



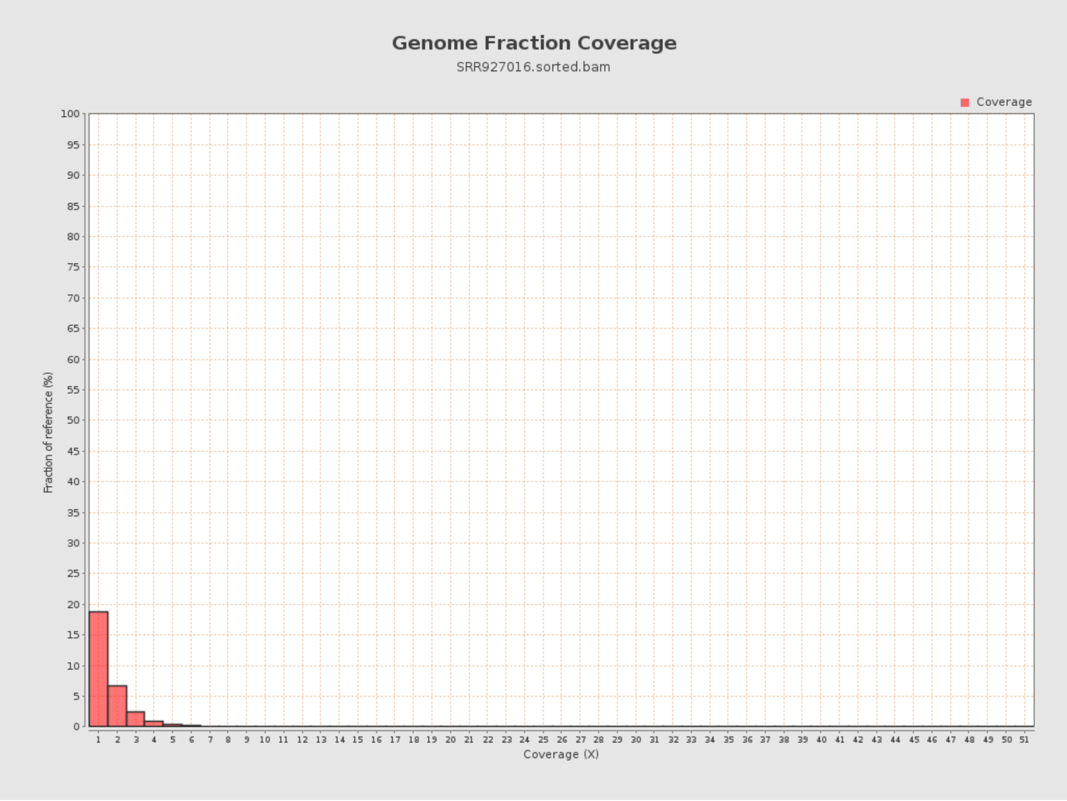
4. Results : Coverage Histogram



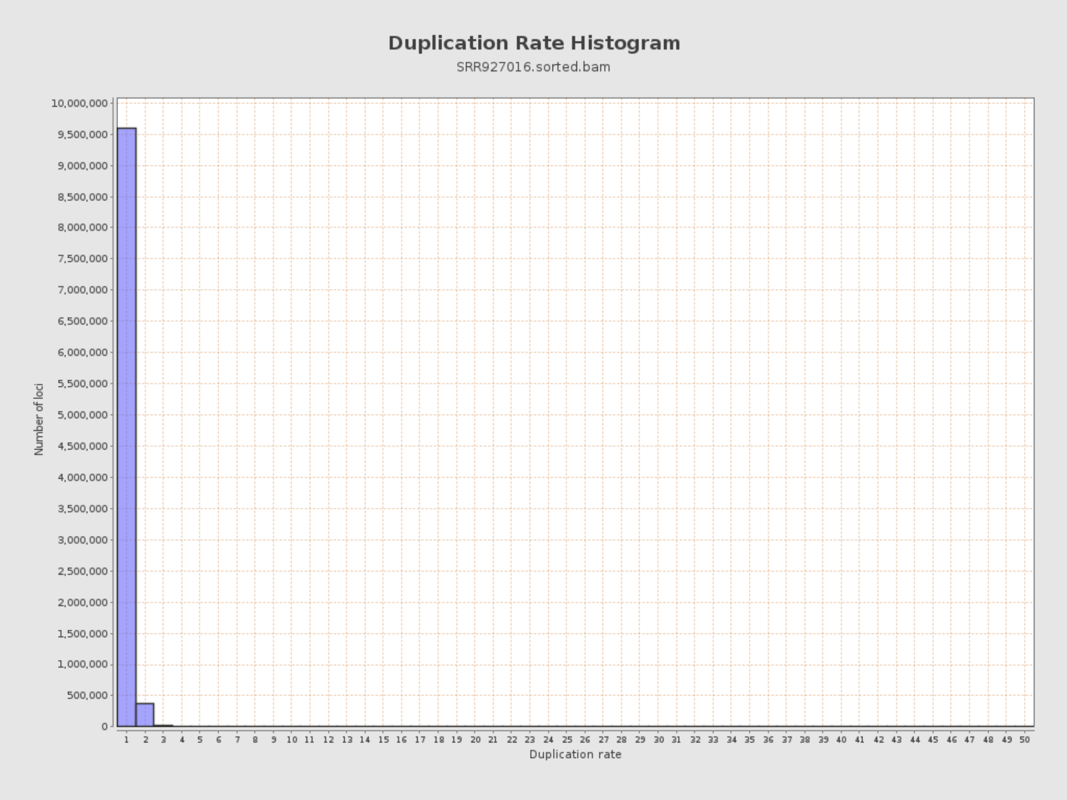
5. Results : Coverage Histogram (0-50X)



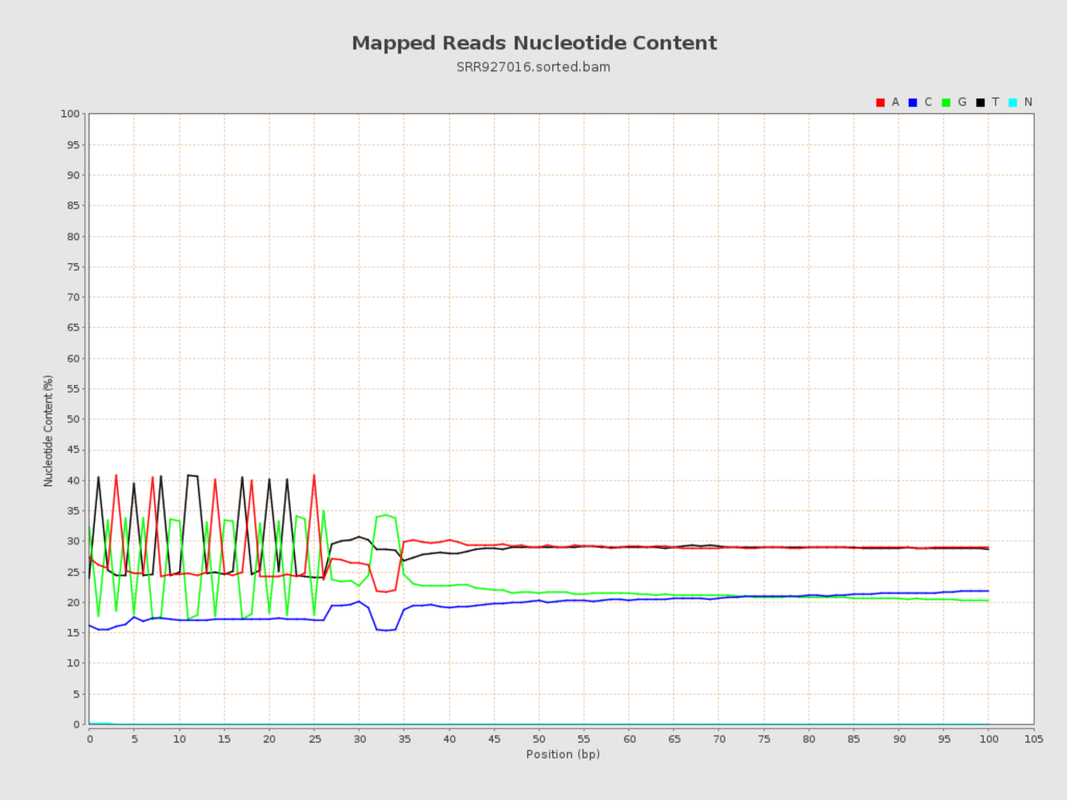
6. Results : Genome Fraction Coverage



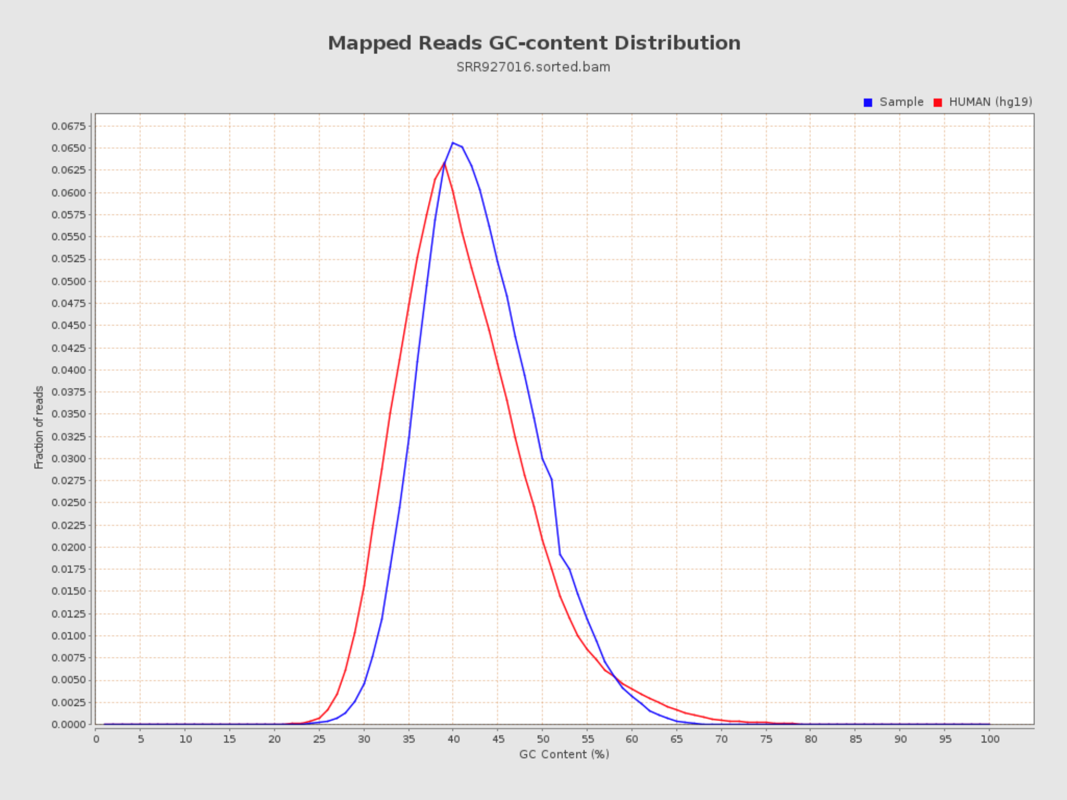
7. Results : Duplication Rate Histogram



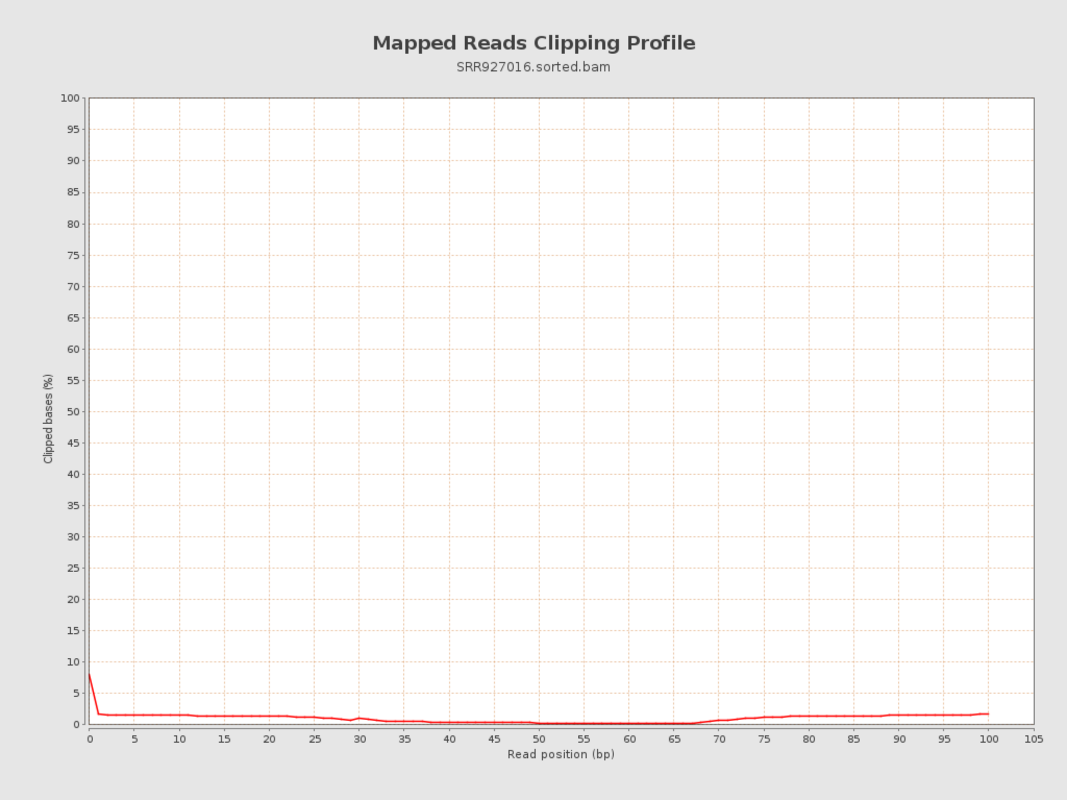
8. Results : Mapped Reads Nucleotide Content



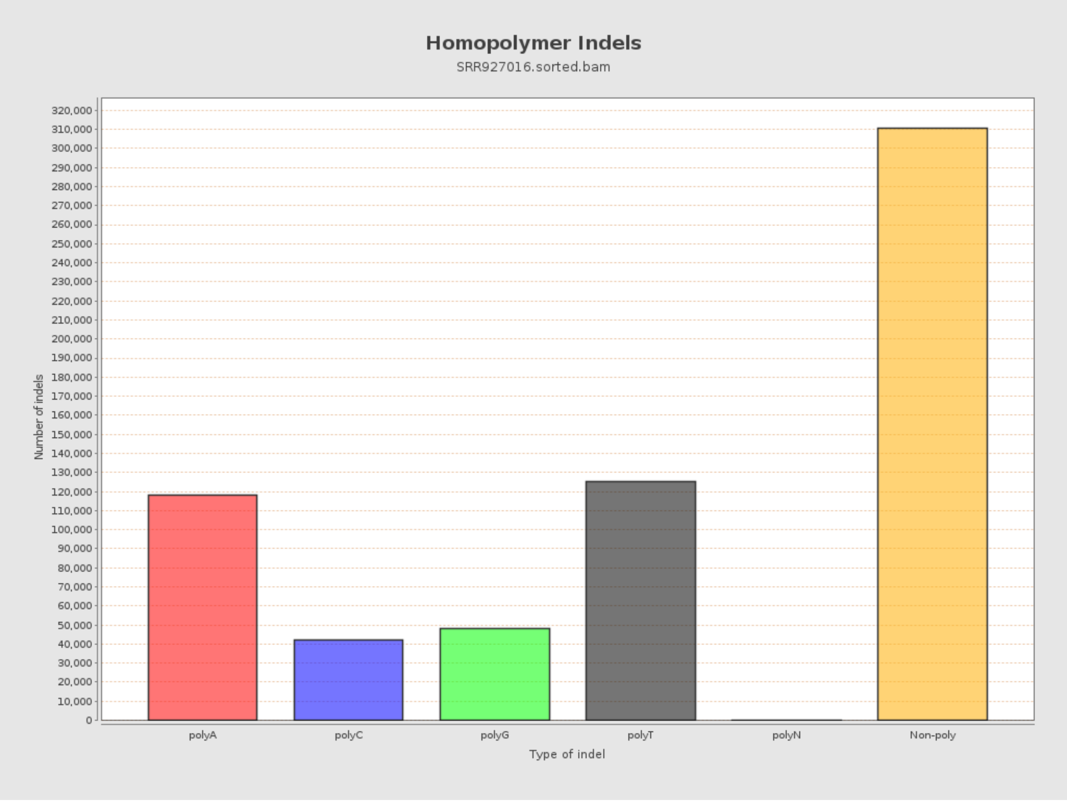
9. Results : Mapped Reads GC-content Distribution



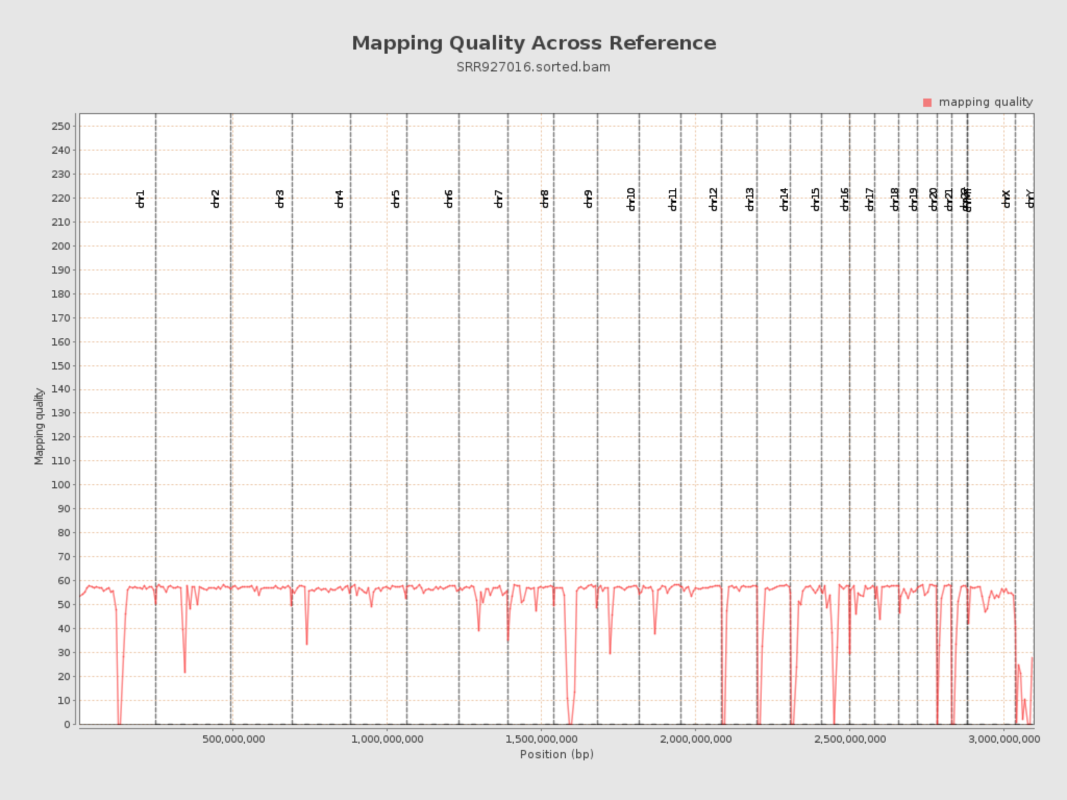
10. Results : Mapped Reads Clipping Profile



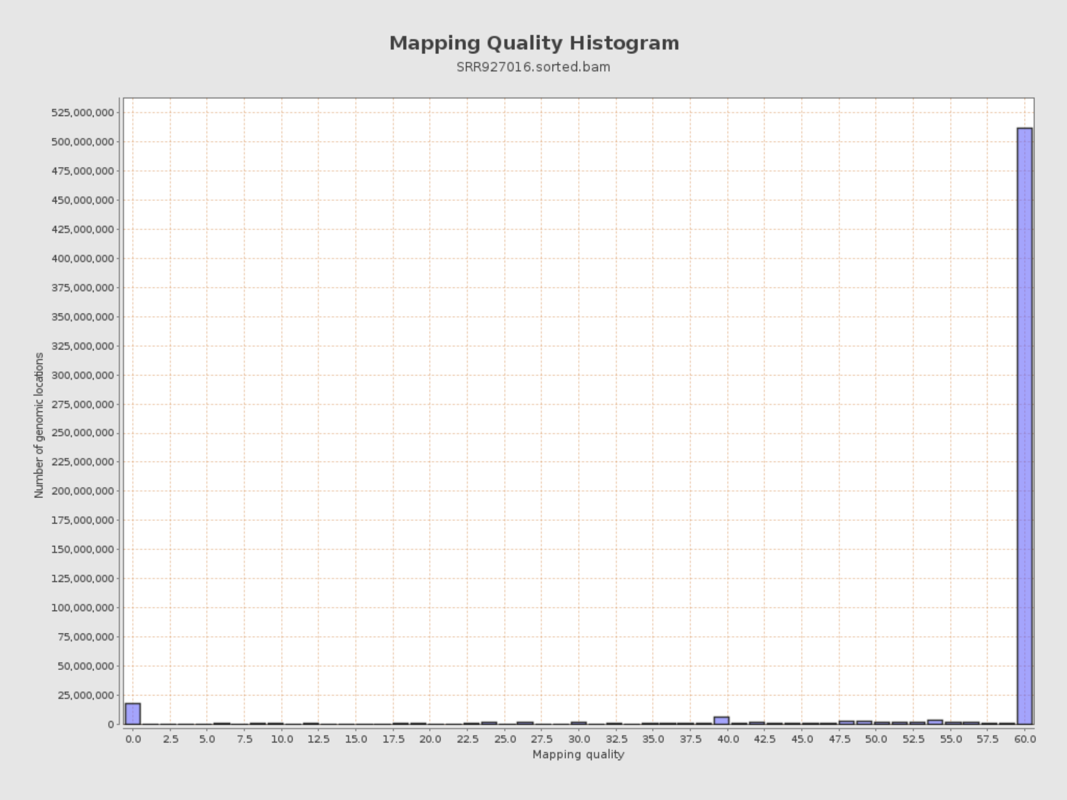
11. Results : Homopolymer Indels



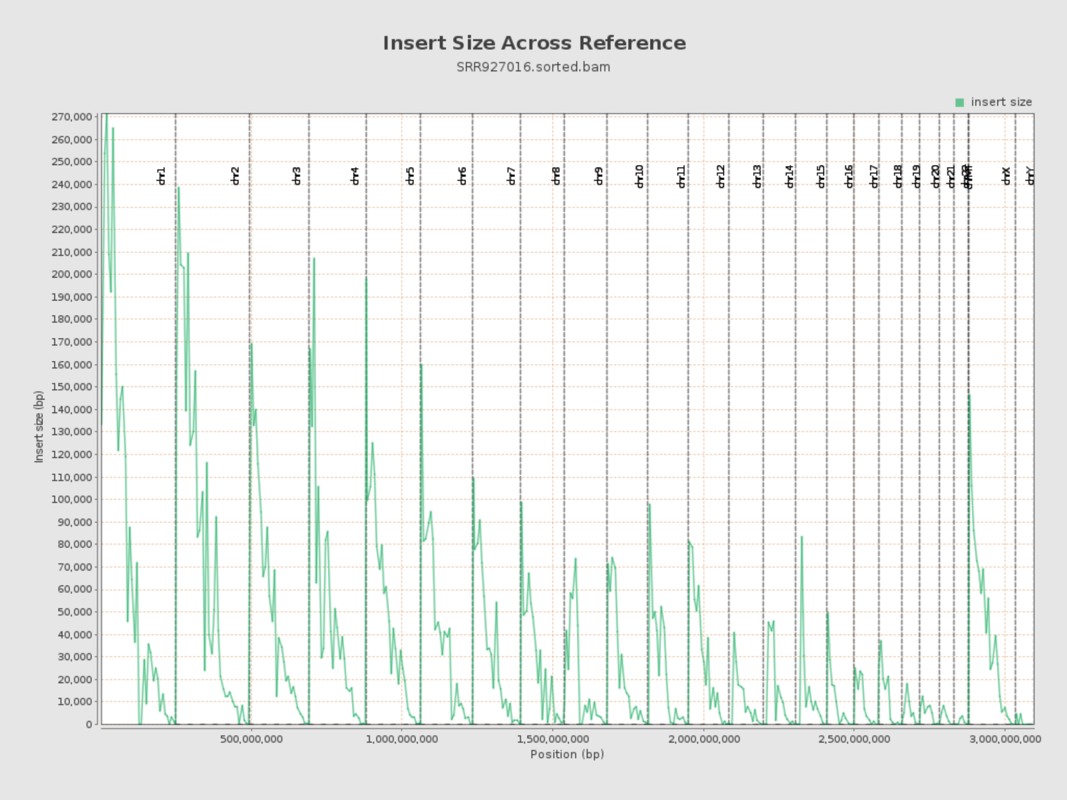
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram