Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/22 21:56:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926933.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_SRR926933 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926933_1.fastq.gz SRR926933_2.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 22 21:56:17 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926933.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,330,990
Mapped reads	8,062,629 / 96.78%
Unmapped reads	268,361 / 3.22%
Mapped paired reads	8,062,629 / 96.78%
Mapped reads, first in pair	4,042,321 / 48.52%
Mapped reads, second in pair	4,020,308 / 48.26%
Mapped reads, both in pair	7,941,456 / 95.32%
Mapped reads, singletons	121,173 / 1.45%
Secondary alignments	0
Supplementary alignments	305,638 / 3.67%
Read min/max/mean length	30 / 101 / 102.52
Duplicated reads (estimated)	449,215 / 5.39%
Duplication rate	4.63%
Clipped reads	3,685,642 / 44.24%

2.2. ACGT Content

Number/percentage of A's	208,976,998 / 28.57%
Number/percentage of C's	142,319,926 / 19.46%
Number/percentage of T's	212,768,791 / 29.09%
Number/percentage of G's	167,217,093 / 22.86%
Number/percentage of N's	136,547 / 0.02%

GC Percentage	42.32%

2.3. Coverage

Mean	0.2365
Standard Deviation	1.0404

2.4. Mapping Quality

Mean Mapping Quality	52.36

2.5. Insert size

Mean	375,739.52
Standard Deviation	5,977,625.51
P25/Median/P75	134 / 174 / 234

2.6. Mismatches and indels

General error rate	0.99%
Mismatches	6,984,564
Insertions	128,676
Mapped reads with at least one insertion	1.57%
Deletions	389,446
Mapped reads with at least one deletion	4.7%
Homopolymer indels	51.68%

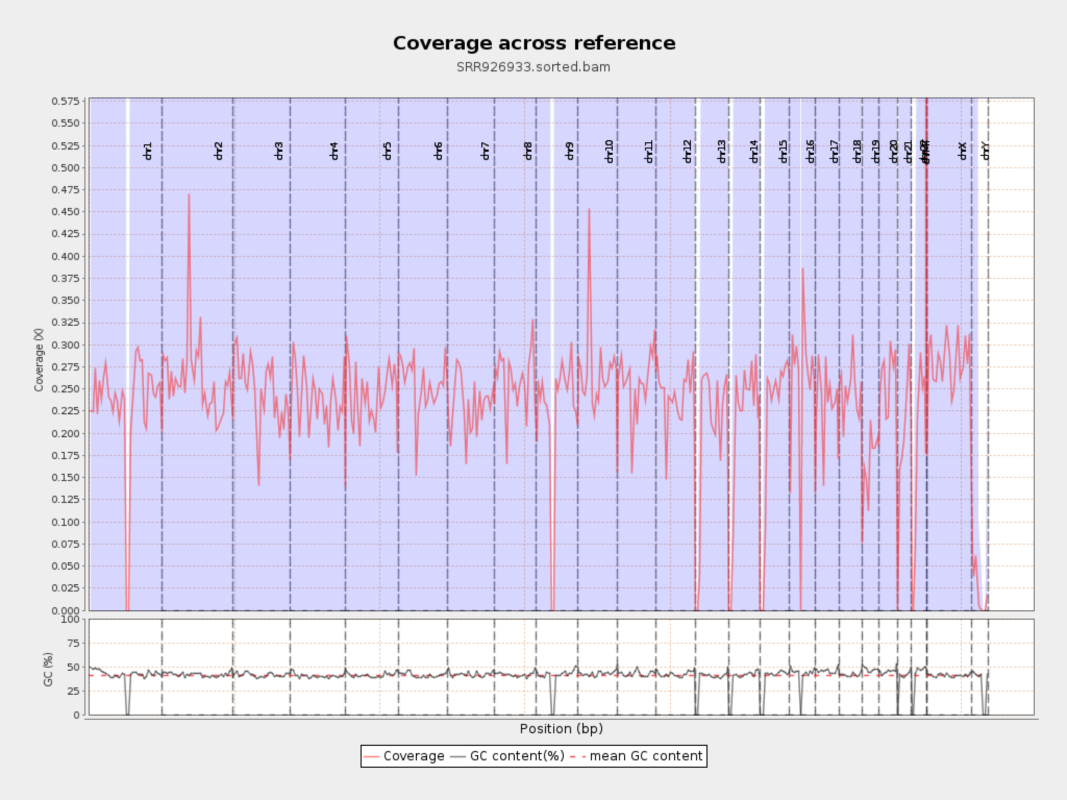
2.7. Chromosome stats

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

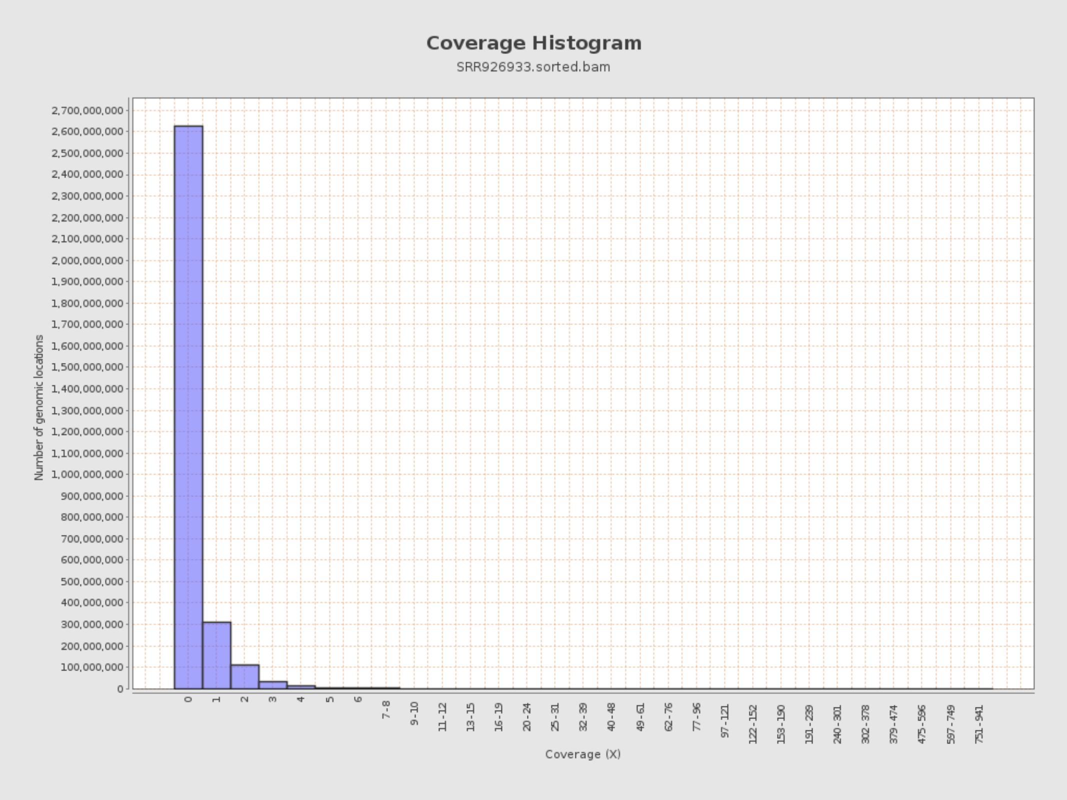
		bases	coverage	deviation
chr1	249250621	57706415	0.2315	0.9601
chr2	243199373	63868849	0.2626	1.6956
chr3	198022430	49022921	0.2476	0.6868
chr4	191154276	45833968	0.2398	0.9588
chr5	180915260	44093960	0.2437	0.6707
chr6	171115067	43824979	0.2561	0.9355
chr7	159138663	36889501	0.2318	0.7741
chr8	146364022	38323253	0.2618	0.7542
chr9	141213431	31545778	0.2234	1.1279
chr10	135534747	36780030	0.2714	2.2192
chr11	135006516	34572449	0.2561	0.8479
chr12	133851895	32565541	0.2433	0.6955
chr13	115169878	22711800	0.1972	0.6046
chr14	107349540	22053699	0.2054	0.6329
chr15	102531392	21571365	0.2104	0.6385
chr16	90354753	23145555	0.2562	1.4982
chr17	81195210	19050328	0.2346	0.7754
chr18	78077248	19380709	0.2482	1.2029
chr19	59128983	9895873	0.1674	0.7468
chr20	63025520	16378448	0.2599	0.7289
chr21	48129895	9395016	0.1952	0.7779
chr22	51304566	8824523	0.172	0.5996
chrMT	16571	48773	2.9433	2.8081
chrX	155270560	43209921	0.2783	0.7598

chrY	59373566	1299778	0.0219	0.7586

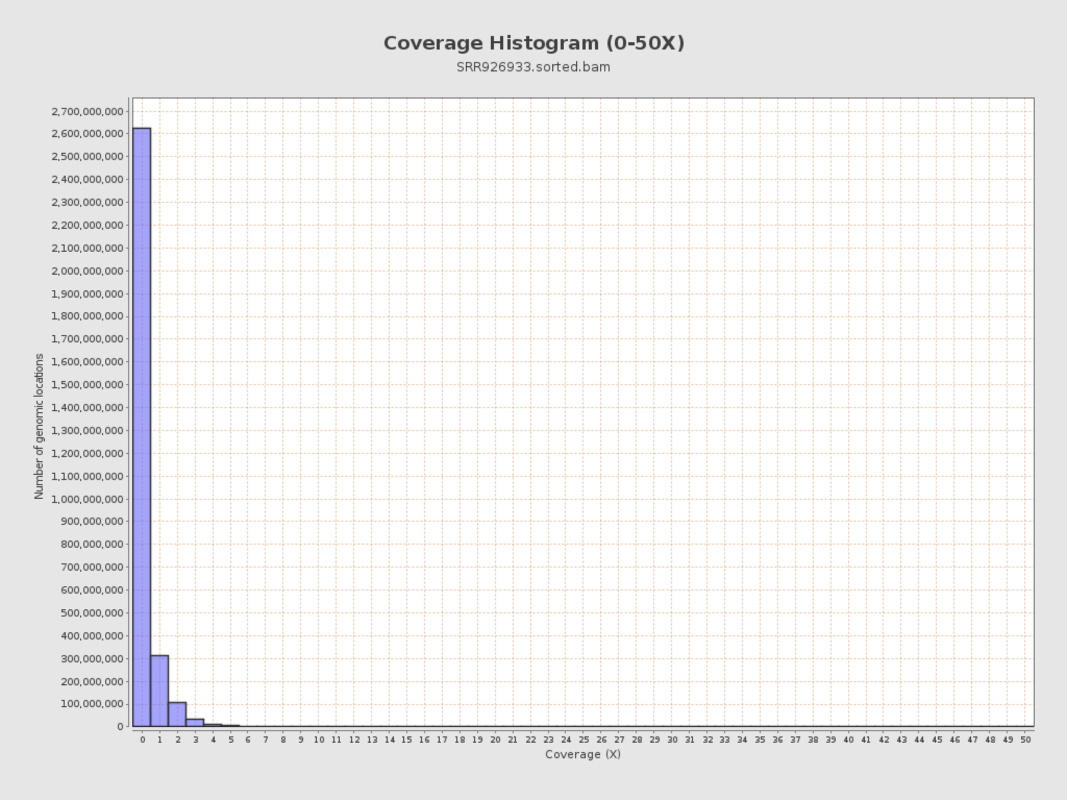
3. Results : Coverage across reference



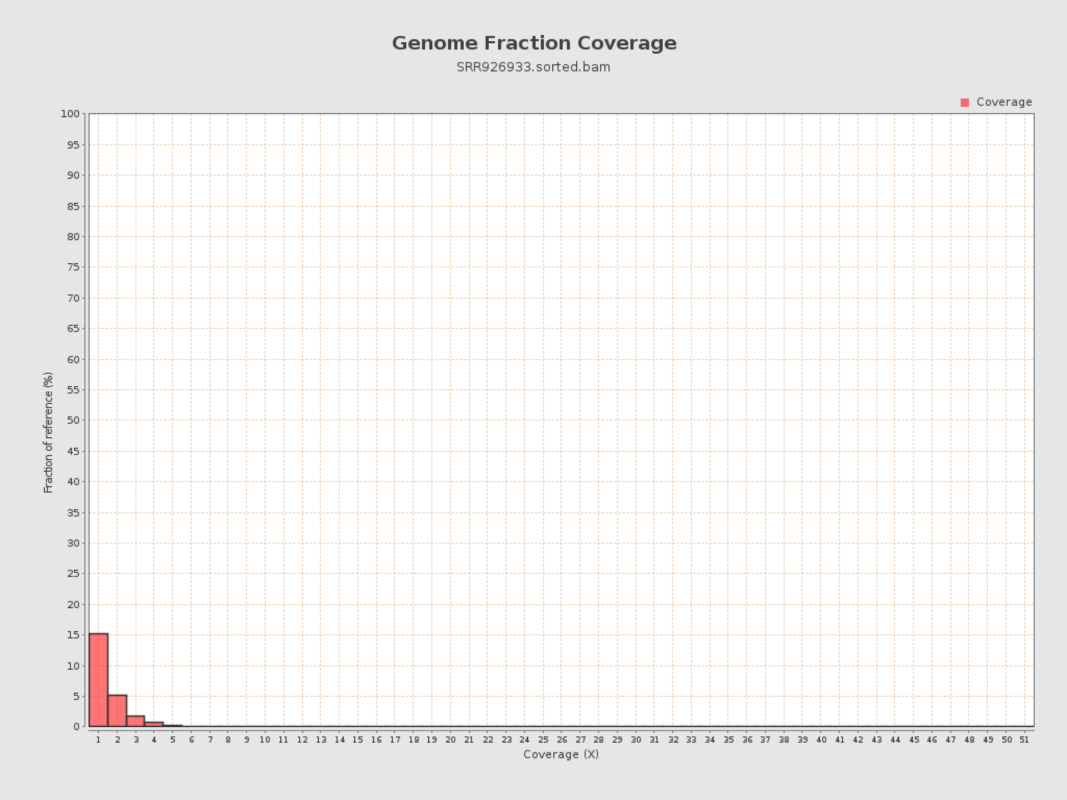
4. Results : Coverage Histogram



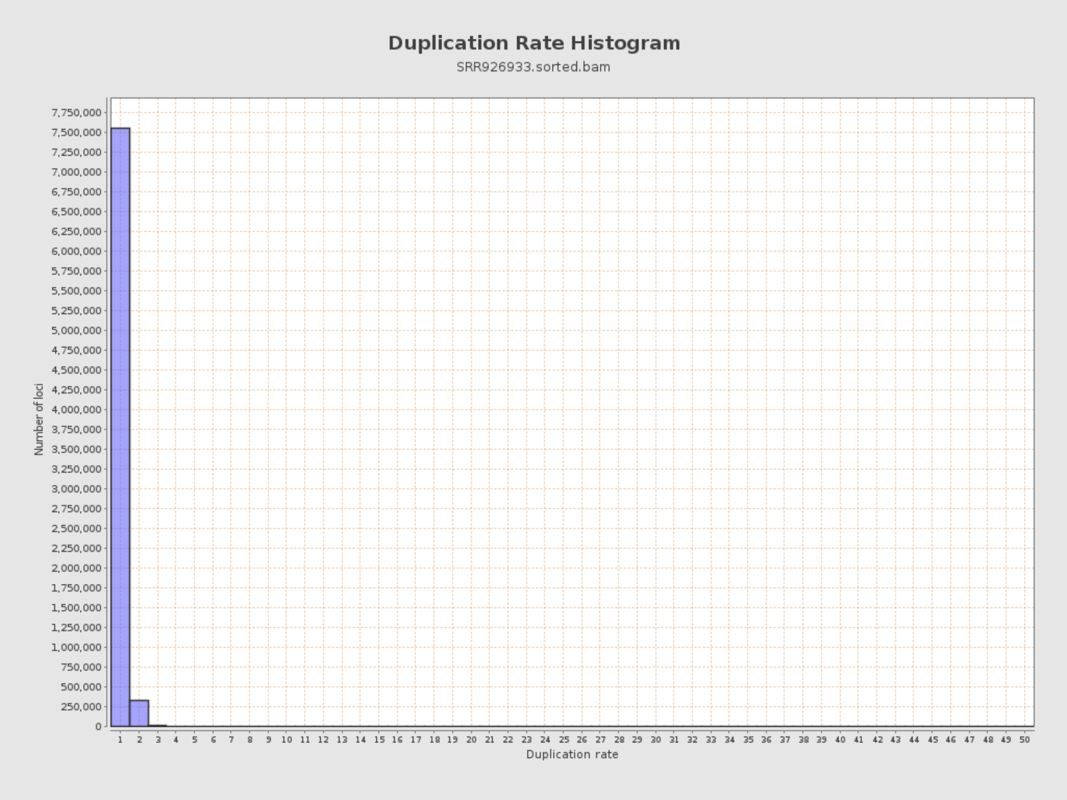
5. Results : Coverage Histogram (0-50X)



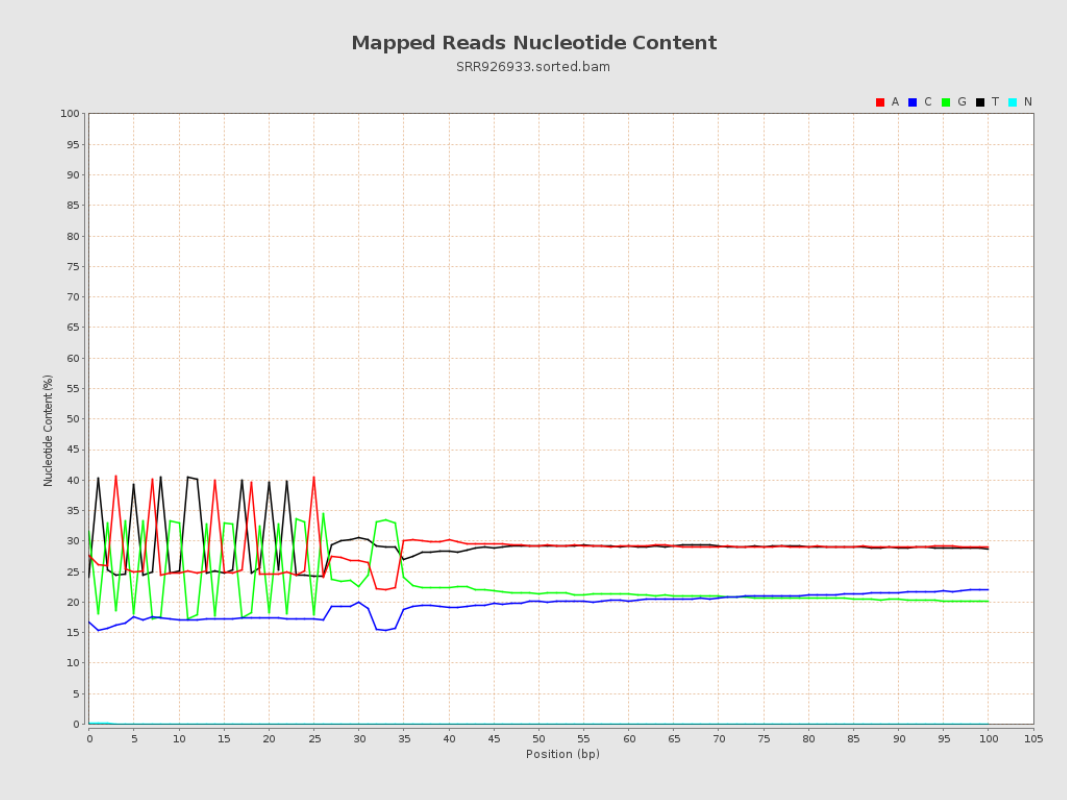
6. Results : Genome Fraction Coverage



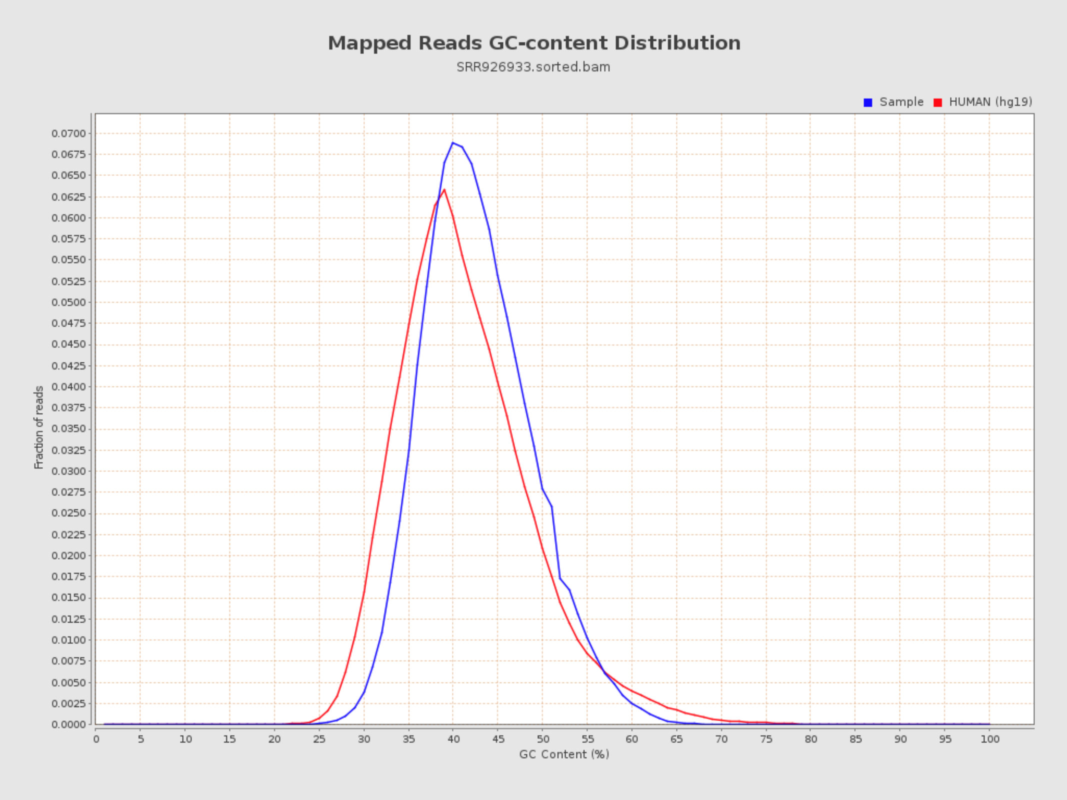
7. Results : Duplication Rate Histogram



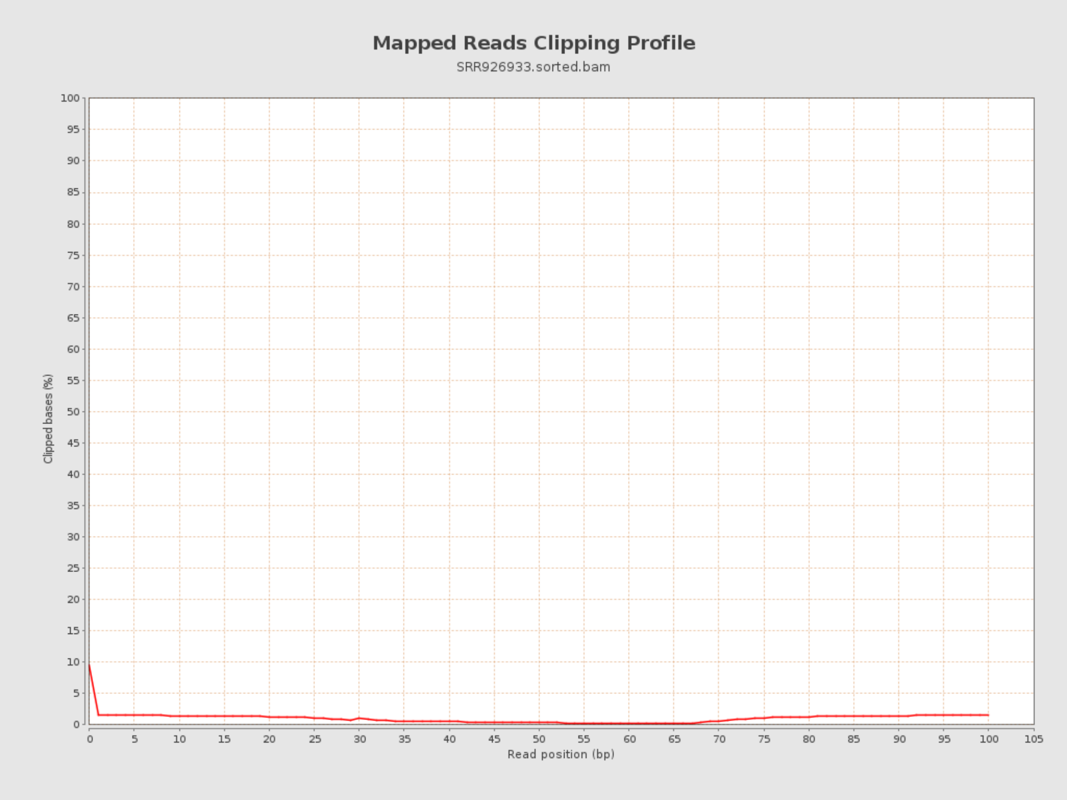
8. Results : Mapped Reads Nucleotide Content



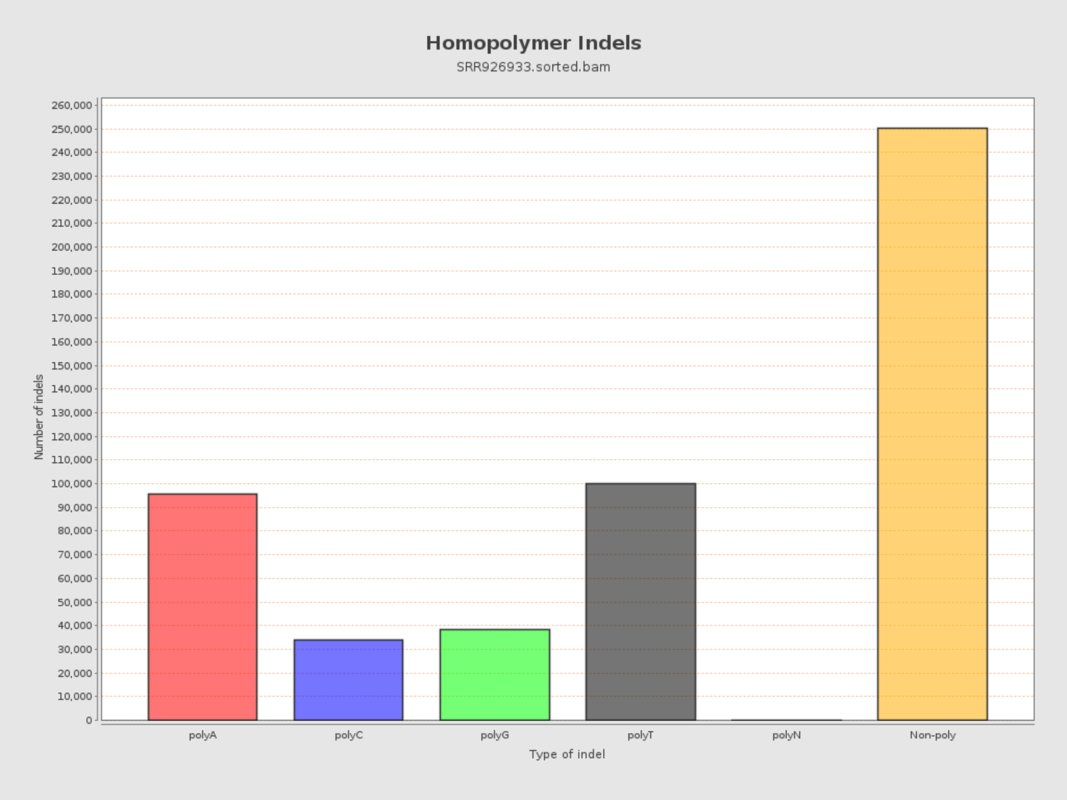
9. Results : Mapped Reads GC-content Distribution



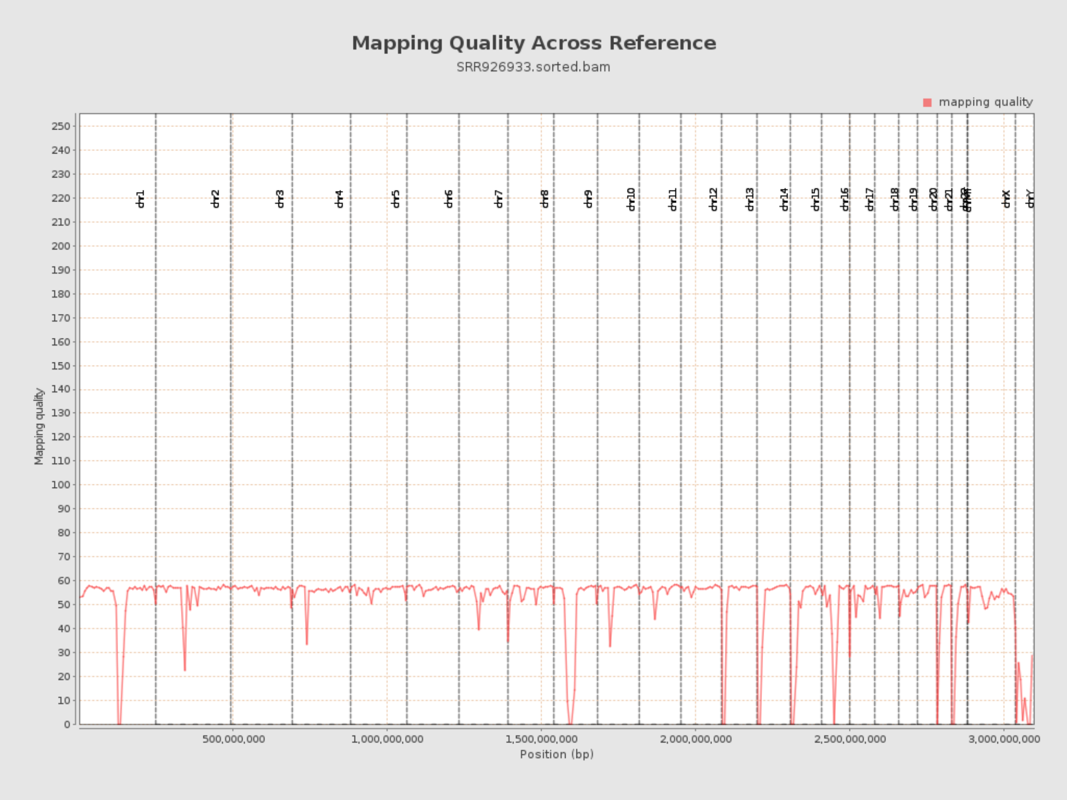
10. Results : Mapped Reads Clipping Profile



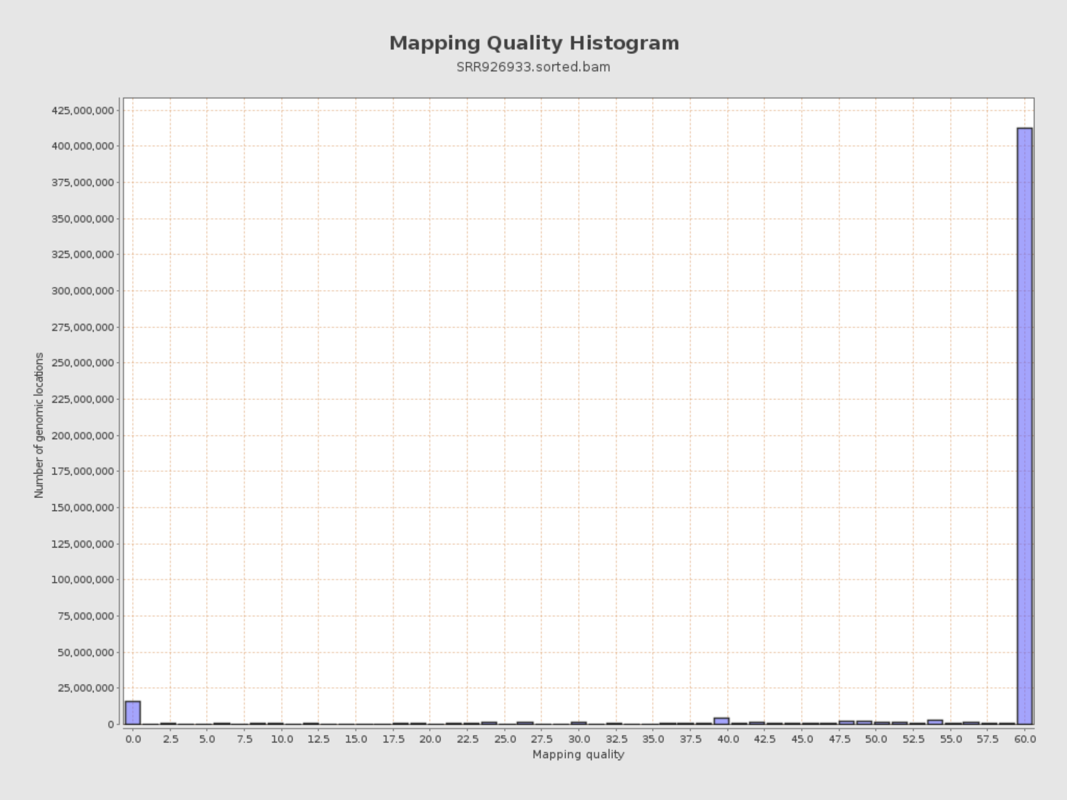
11. Results : Homopolymer Indels



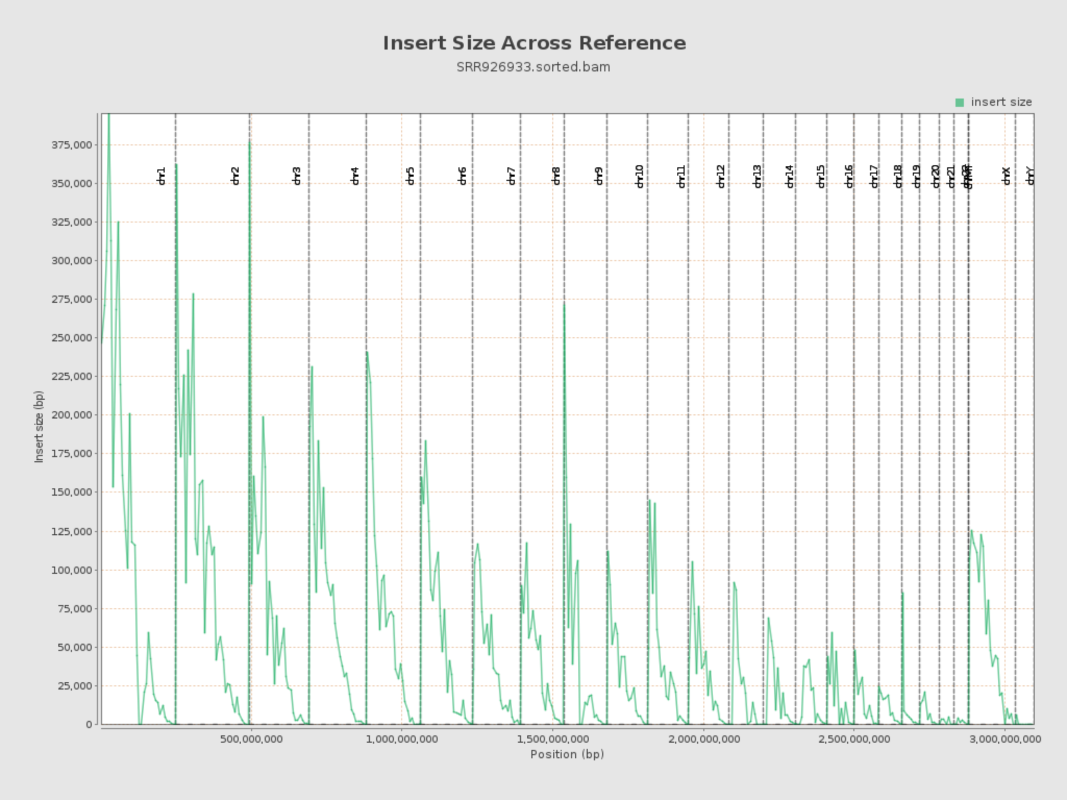
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram