Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/24 06:04:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR927017.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_SRR927017 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR927017_1.fastq.gz SRR927017_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 24 06:04:01 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR927017.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	28,581,286
Mapped reads	28,110,623 / 98.35%
Unmapped reads	470,663 / 1.65%
Mapped paired reads	28,110,623 / 98.35%
Mapped reads, first in pair	14,092,908 / 49.31%
Mapped reads, second in pair	14,017,715 / 49.05%
Mapped reads, both in pair	27,881,736 / 97.55%
Mapped reads, singletons	228,887 / 0.8%
Secondary alignments	0
Supplementary alignments	248,483 / 0.87%
Read min/max/mean length	30 / 101 / 101.36
Duplicated reads (estimated)	1,854,613 / 6.49%
Duplication rate	4.94%
Clipped reads	6,963,048 / 24.36%

2.2. ACGT Content

Number/percentage of A's	764,083,651 / 28.75%
Number/percentage of C's	528,549,355 / 19.89%
Number/percentage of T's	772,796,800 / 29.08%
Number/percentage of G's	591,590,759 / 22.26%
Number/percentage of N's	573,893 / 0.02%

GC Percentage	42.15%

2.3. Coverage

Mean	0.8591
Standard Deviation	3.9452

2.4. Mapping Quality

Mean Mapping Quality	53.47

2.5. Insert size

Mean	99,441.34
Standard Deviation	3,099,138.34
P25/Median/P75	159 / 203 / 269

2.6. Mismatches and indels

General error rate	0.94%
Mismatches	24,206,058
Insertions	431,017
Mapped reads with at least one insertion	1.51%
Deletions	1,403,292
Mapped reads with at least one deletion	4.86%
Homopolymer indels	53.03%

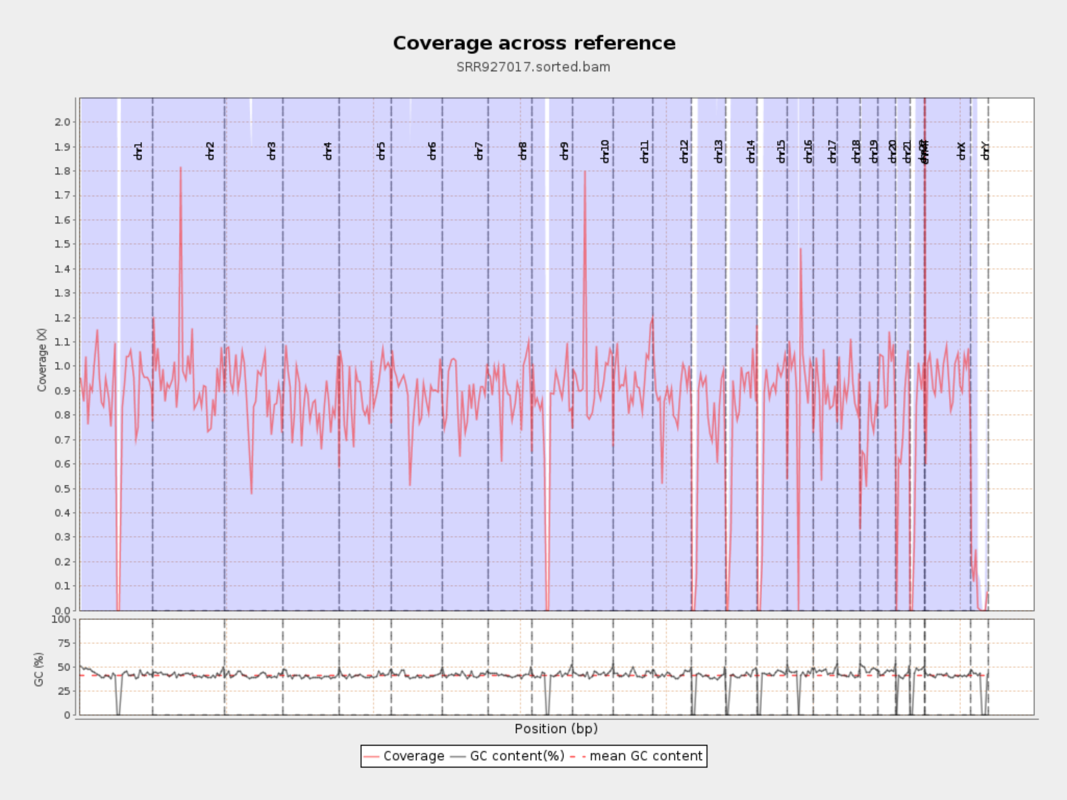
2.7. Chromosome stats

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

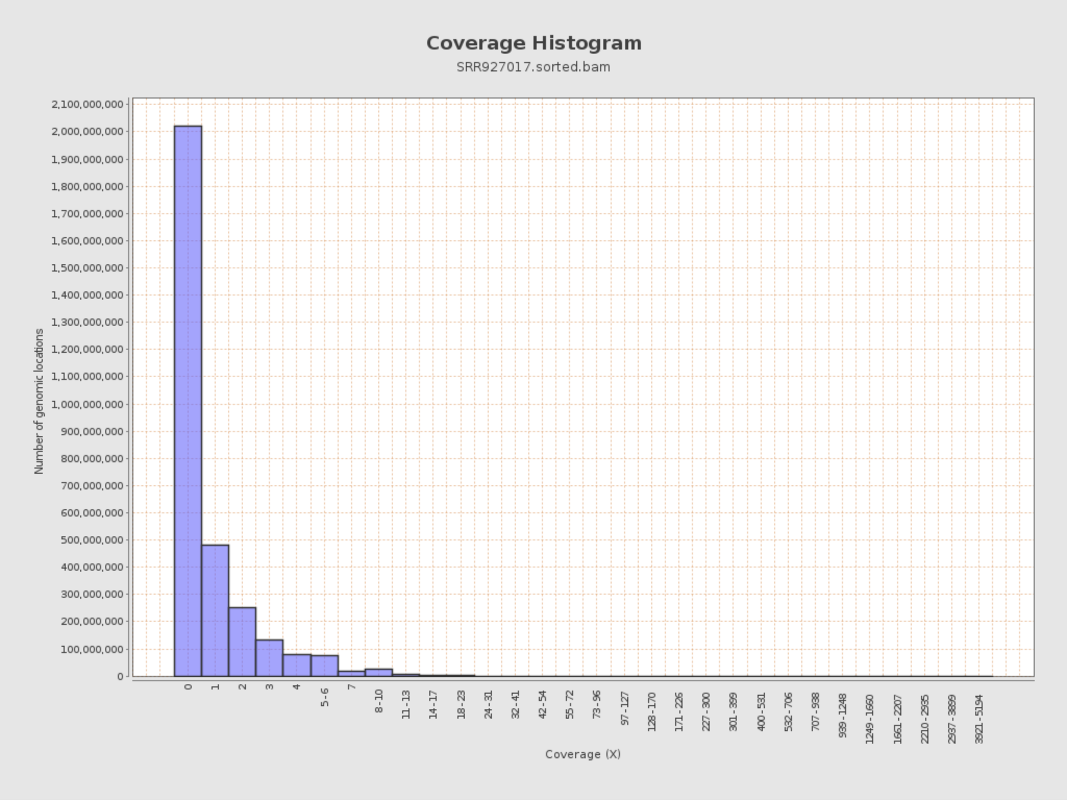
		bases	coverage	deviation
chr1	249250621	217576296	0.8729	5.6447
chr2	243199373	233809884	0.9614	6.1399
chr3	198022430	178562032	0.9017	1.7679
chr4	191154276	163259152	0.8541	2.6604
chr5	180915260	163273664	0.9025	1.736
chr6	171115067	151918486	0.8878	1.8073
chr7	159138663	138977052	0.8733	2.4423
chr8	146364022	133431517	0.9116	2.0714
chr9	141213431	111532461	0.7898	4.5063
chr10	135534747	132719375	0.9792	9.4269
chr11	135006516	127479620	0.9442	4.7785
chr12	133851895	117123992	0.875	1.7417
chr13	115169878	81405706	0.7068	1.5371
chr14	107349540	81391198	0.7582	1.6513
chr15	102531392	78065622	0.7614	1.6494
chr16	90354753	83226844	0.9211	5.3402
chr17	81195210	69972707	0.8618	2.3324
chr18	78077248	71792654	0.9195	4.708
chr19	59128983	42001409	0.7103	3.1346
chr20	63025520	62049923	0.9845	2.0371
chr21	48129895	34573136	0.7183	2.2211
chr22	51304566	32824452	0.6398	1.6043
chrMT	16571	37772	2.2794	2.714
chrX	155270560	148019865	0.9533	2.3292

chrY	59373566	4572351	0.077	2.3086

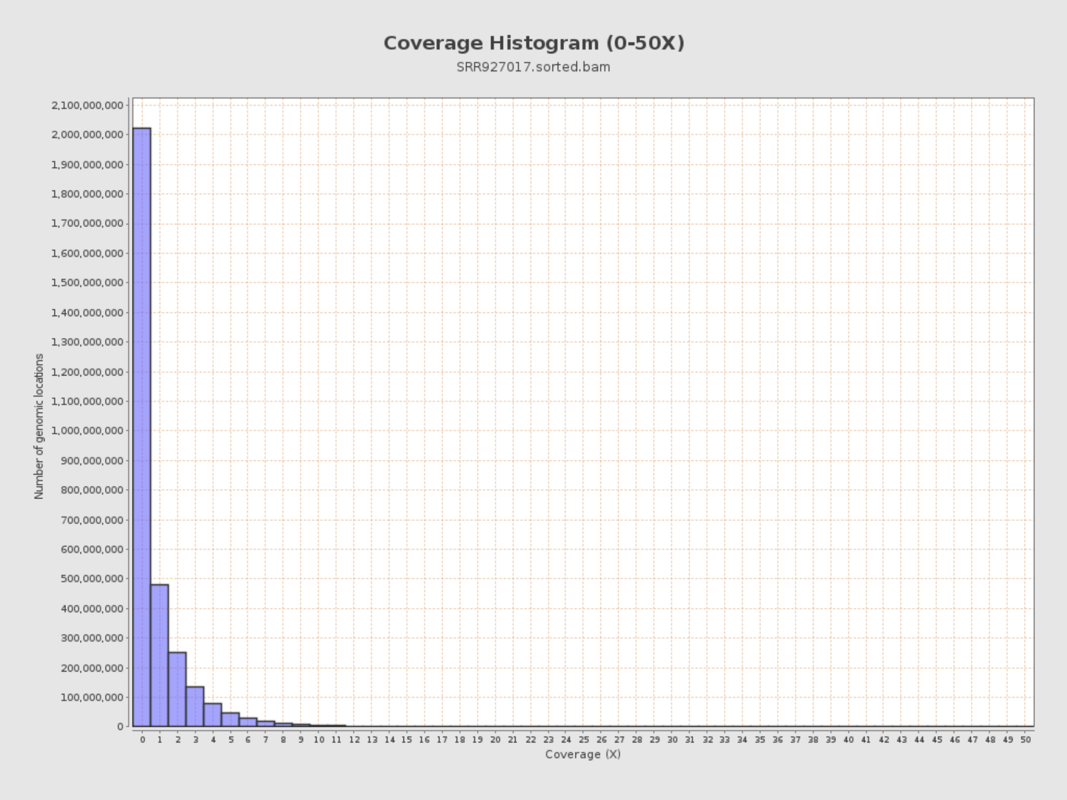
3. Results : Coverage across reference



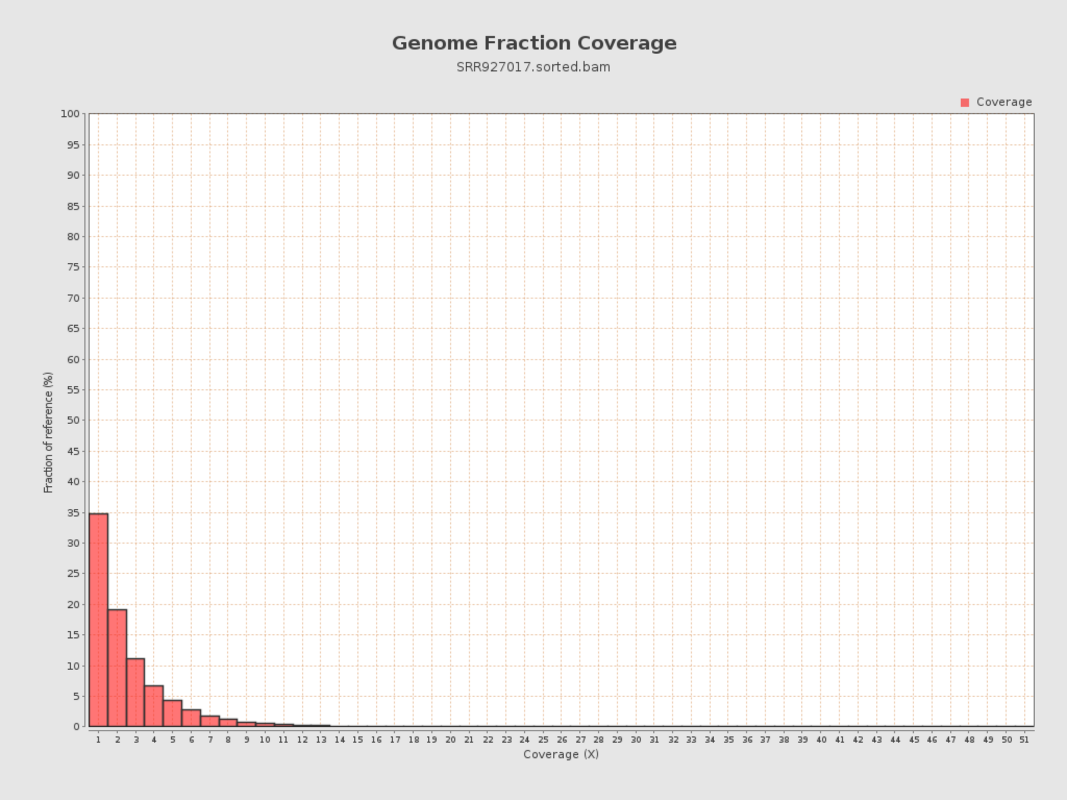
4. Results : Coverage Histogram



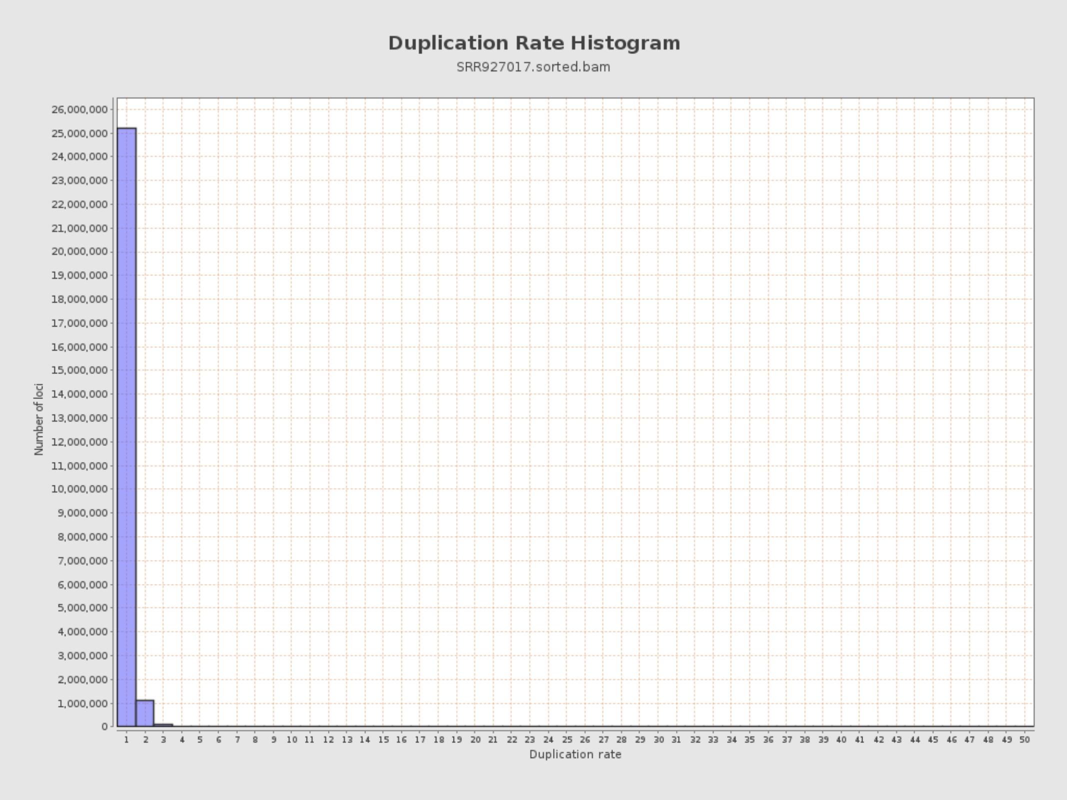
5. Results : Coverage Histogram (0-50X)



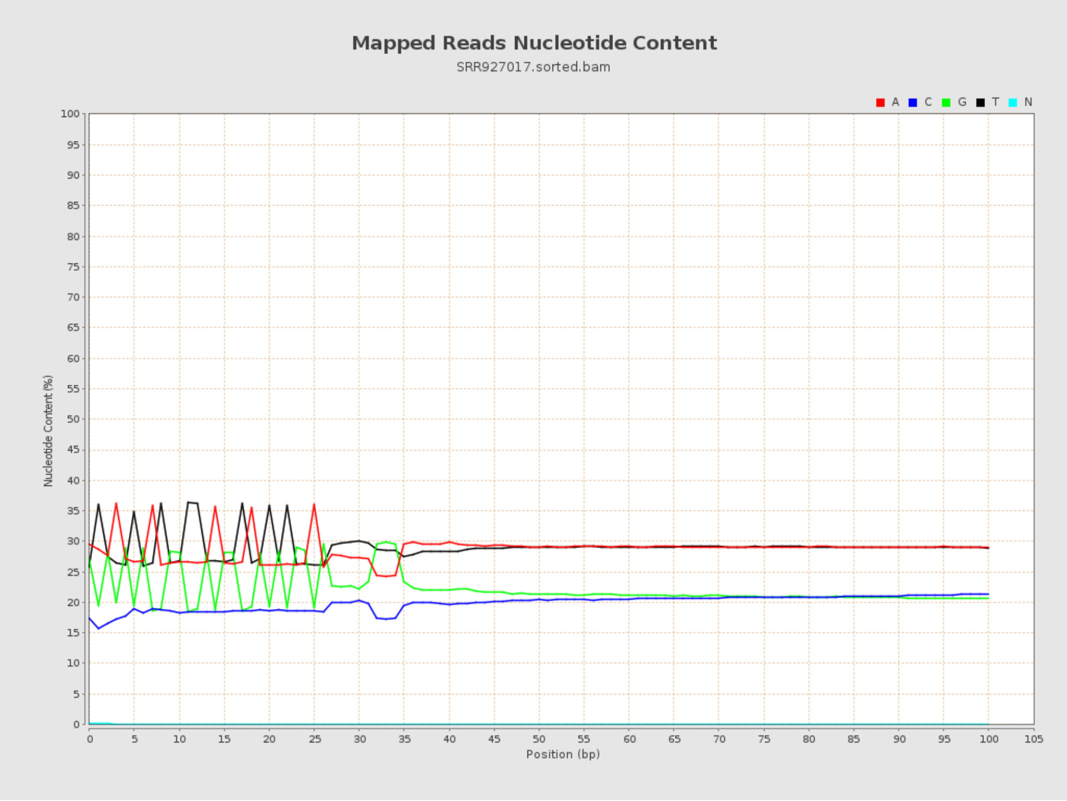
6. Results : Genome Fraction Coverage



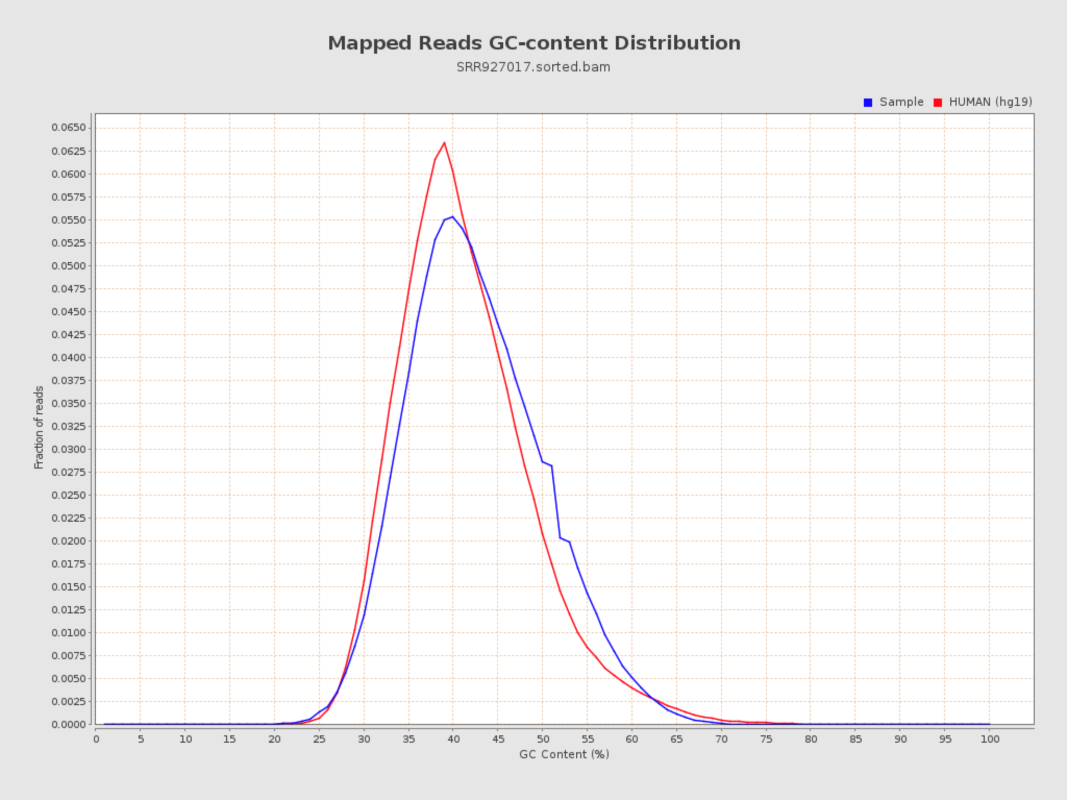
7. Results : Duplication Rate Histogram



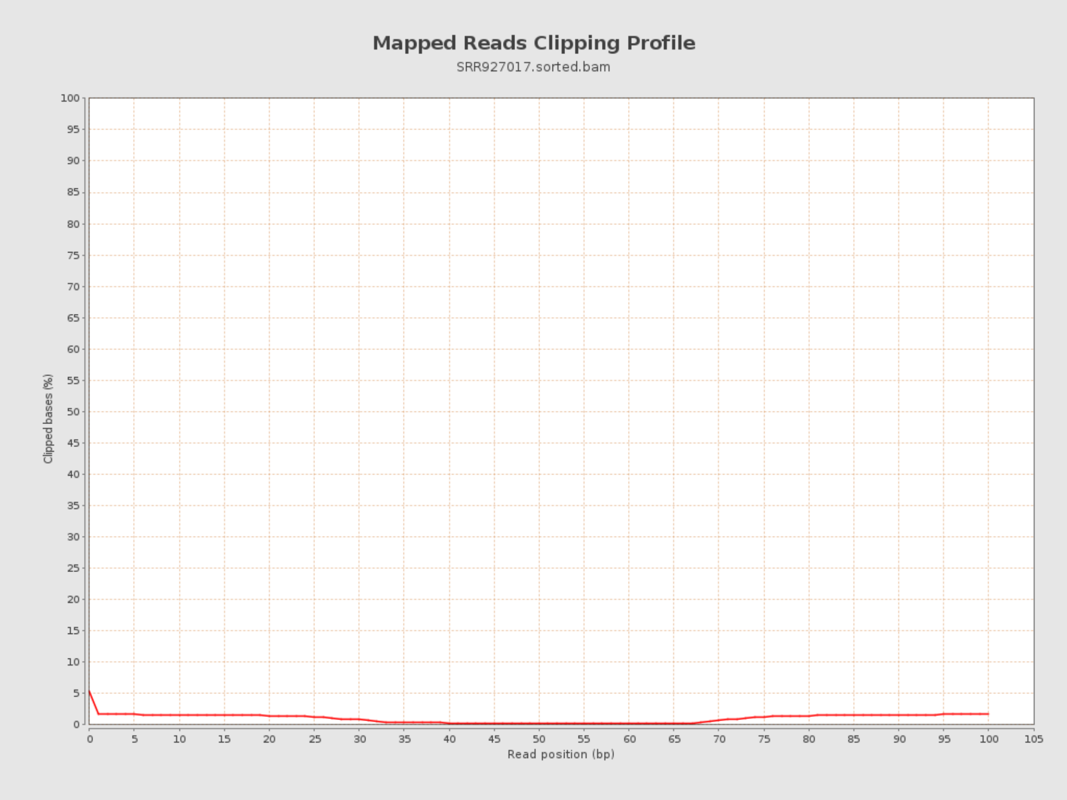
8. Results : Mapped Reads Nucleotide Content



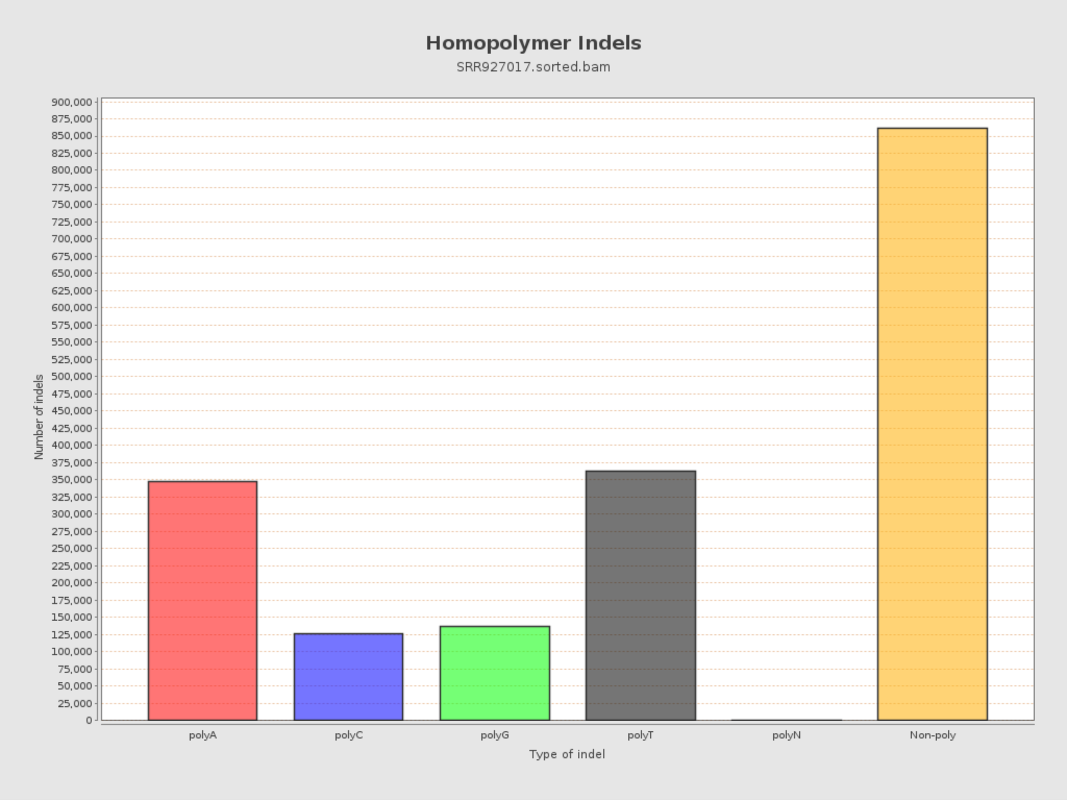
9. Results : Mapped Reads GC-content Distribution



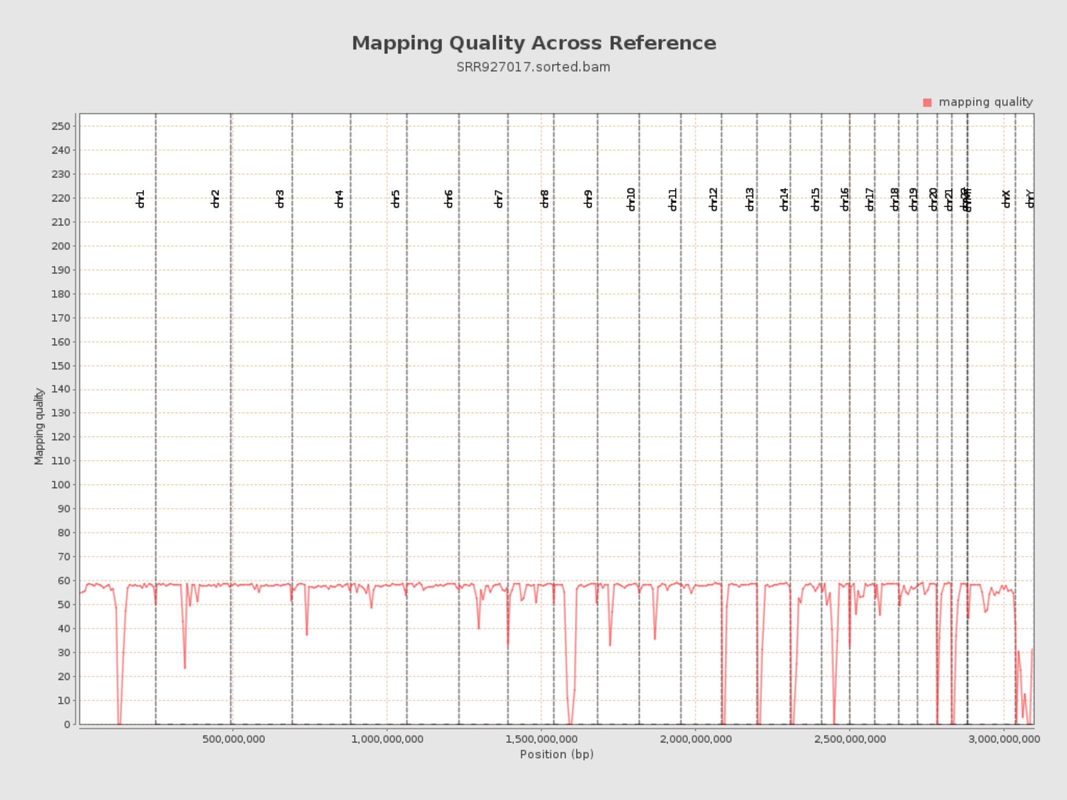
10. Results : Mapped Reads Clipping Profile



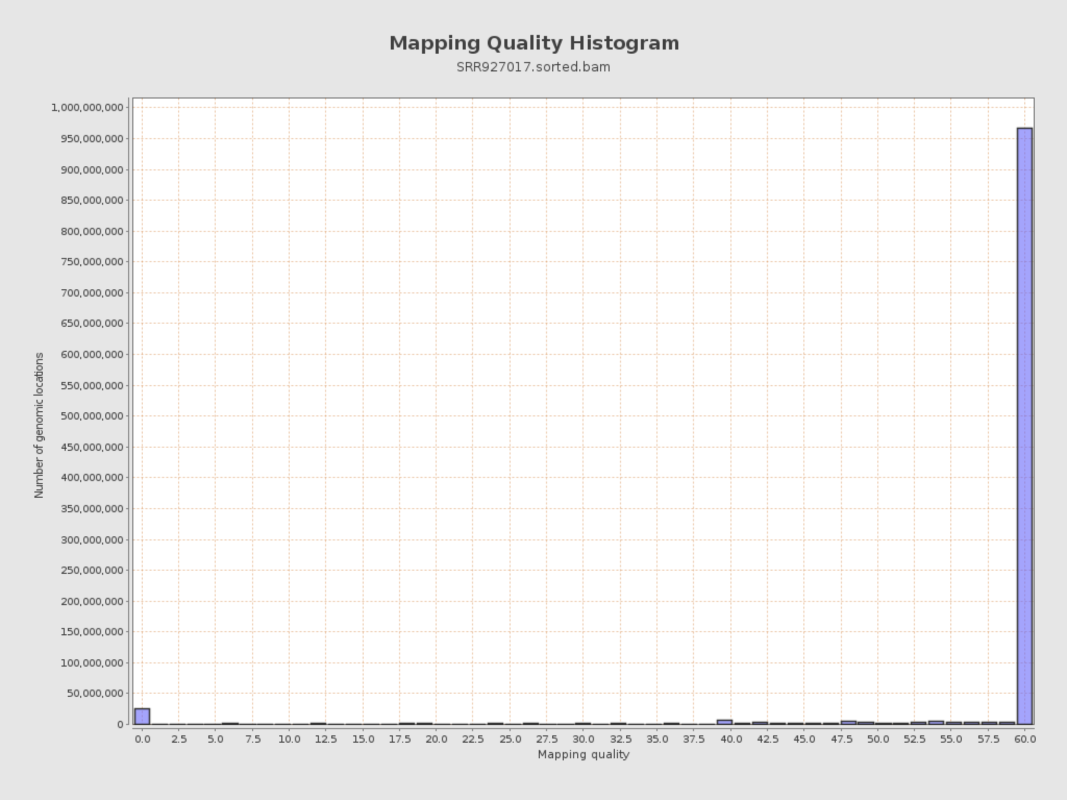
11. Results : Homopolymer Indels



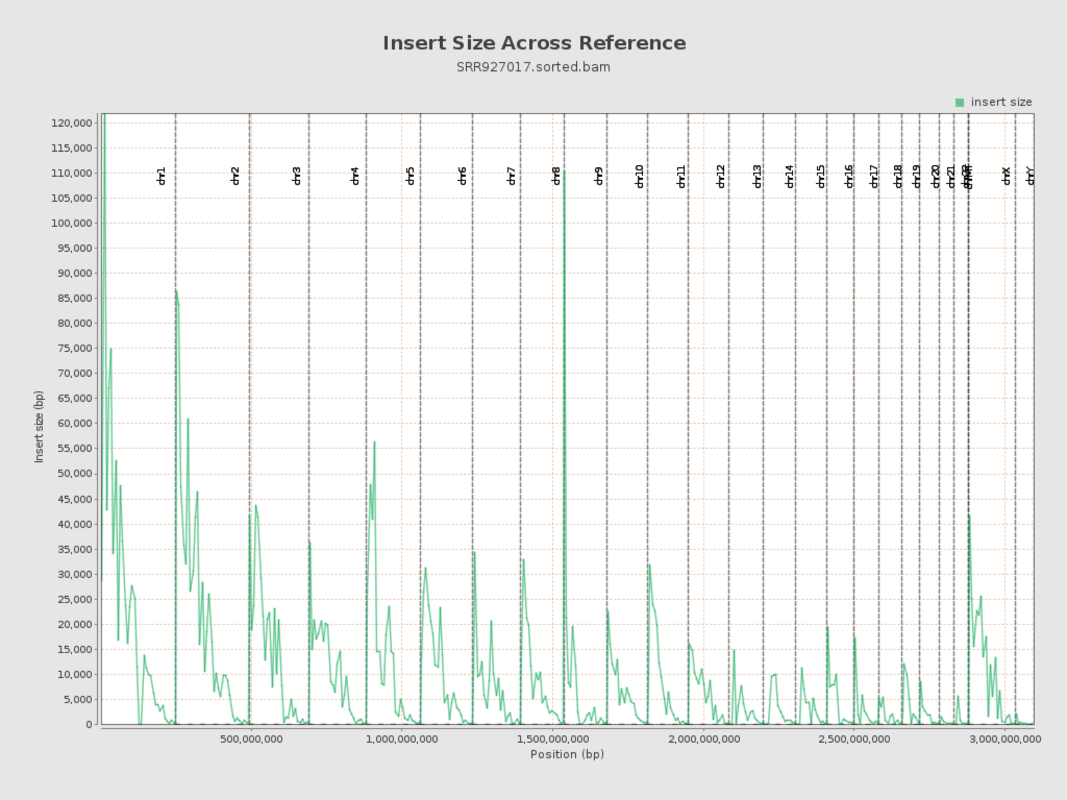
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram