Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/24 05:20:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR927015.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_SRR927015 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR927015_1.fastq.gz SRR927015_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 24 05:20:11 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR927015.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	28,344,068
Mapped reads	27,655,683 / 97.57%
Unmapped reads	688,385 / 2.43%
Mapped paired reads	27,655,683 / 97.57%
Mapped reads, first in pair	13,850,942 / 48.87%
Mapped reads, second in pair	13,804,741 / 48.7%
Mapped reads, both in pair	27,287,764 / 96.27%
Mapped reads, singletons	367,919 / 1.3%
Secondary alignments	0
Supplementary alignments	621,230 / 2.19%
Read min/max/mean length	30 / 101 / 101.91
Duplicated reads (estimated)	2,069,832 / 7.3%
Duplication rate	5.79%
Clipped reads	9,606,763 / 33.89%

2.2. ACGT Content

Number/percentage of A's	732,215,630 / 28.55%
Number/percentage of C's	507,569,657 / 19.79%
Number/percentage of T's	742,487,104 / 28.95%
Number/percentage of G's	582,664,371 / 22.72%
Number/percentage of N's	134,039 / 0.01%

GC Percentage	42.5%

2.3. Coverage

Mean	0.8292
Standard Deviation	3.4994

2.4. Mapping Quality

Mean Mapping Quality	52.74

2.5. Insert size

Mean	236,814.06
Standard Deviation	4,785,286.17
P25/Median/P75	149 / 192 / 256

2.6. Mismatches and indels

General error rate	0.94%
Mismatches	23,474,976
Insertions	427,406
Mapped reads with at least one insertion	1.52%
Deletions	1,309,607
Mapped reads with at least one deletion	4.62%
Homopolymer indels	52.54%

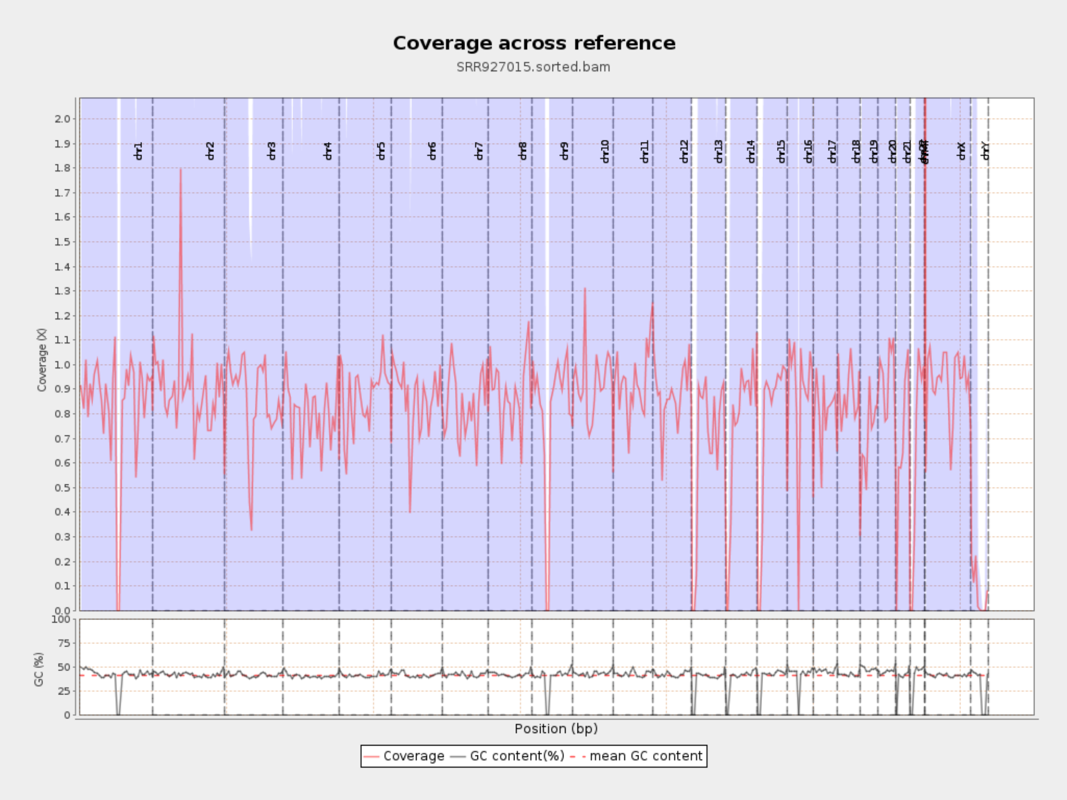
2.7. Chromosome stats

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

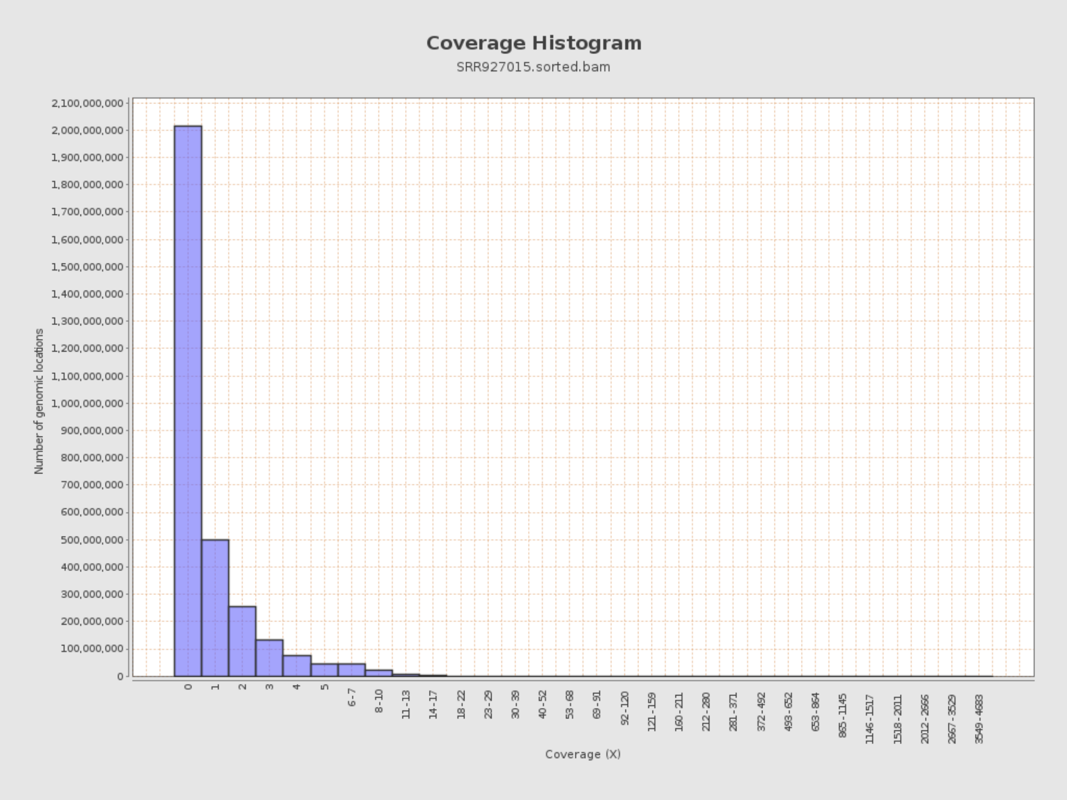
		bases	coverage	deviation
chr1	249250621	207887425	0.834	5.1778
chr2	243199373	222381788	0.9144	6.63
chr3	198022430	170222713	0.8596	1.6775
chr4	191154276	152966866	0.8002	2.0701
chr5	180915260	158325940	0.8751	1.6867
chr6	171115067	147807800	0.8638	2.0137
chr7	159138663	133742465	0.8404	2.759
chr8	146364022	128888110	0.8806	1.9934
chr9	141213431	113010824	0.8003	4.1973
chr10	135534747	126275910	0.9317	5.9307
chr11	135006516	124064078	0.9189	4.2173
chr12	133851895	118255916	0.8835	1.7515
chr13	115169878	77436643	0.6724	1.4655
chr14	107349540	78587059	0.7321	1.611
chr15	102531392	76685427	0.7479	1.6154
chr16	90354753	78292297	0.8665	3.5106
chr17	81195210	65439544	0.806	1.8875
chr18	78077248	69408308	0.889	4.5065
chr19	59128983	41623111	0.7039	2.9608
chr20	63025520	60119348	0.9539	1.8983
chr21	48129895	33425052	0.6945	2.5661
chr22	51304566	33220912	0.6475	1.583
chrMT	16571	1173758	70.8321	54.148
chrX	155270560	143240881	0.9225	2.154

chrY	59373566	4499986	0.0758	1.9131

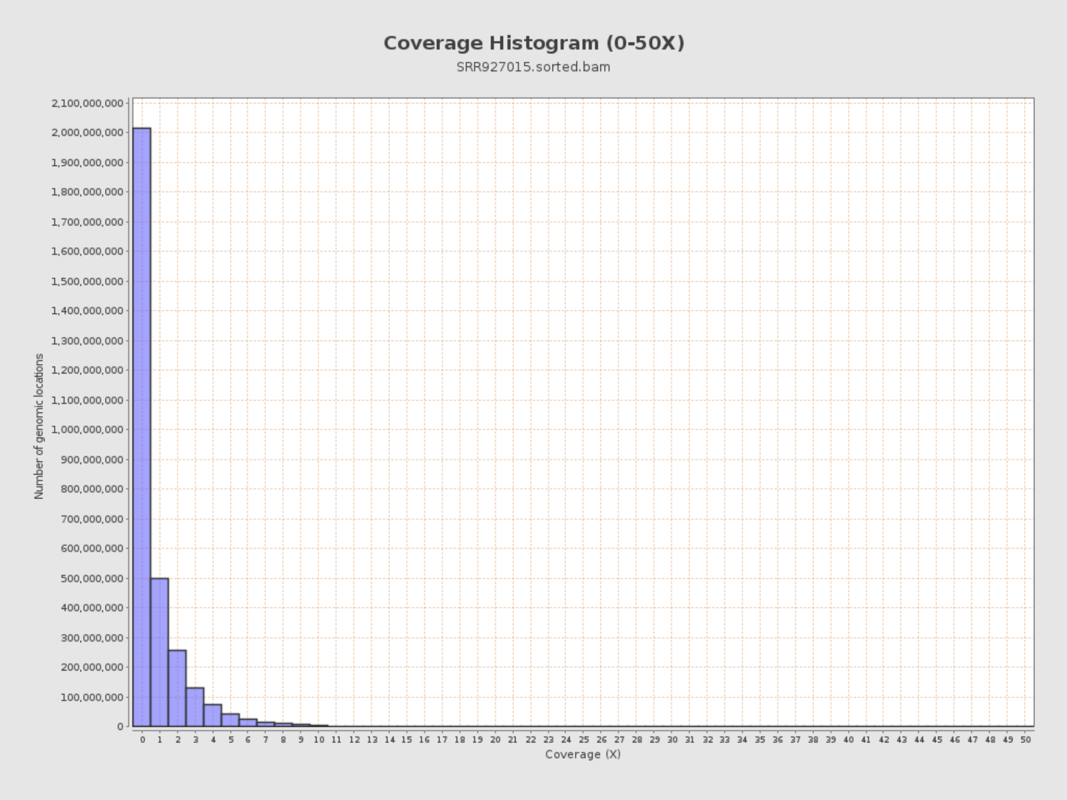
3. Results : Coverage across reference



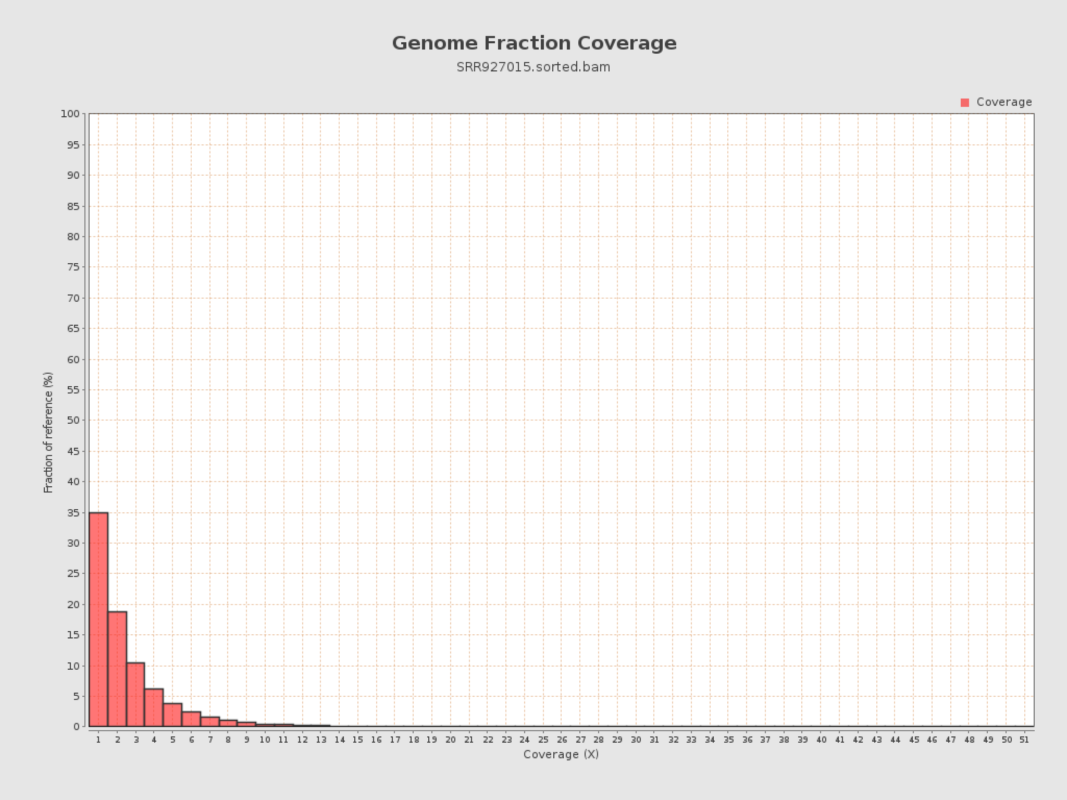
4. Results : Coverage Histogram



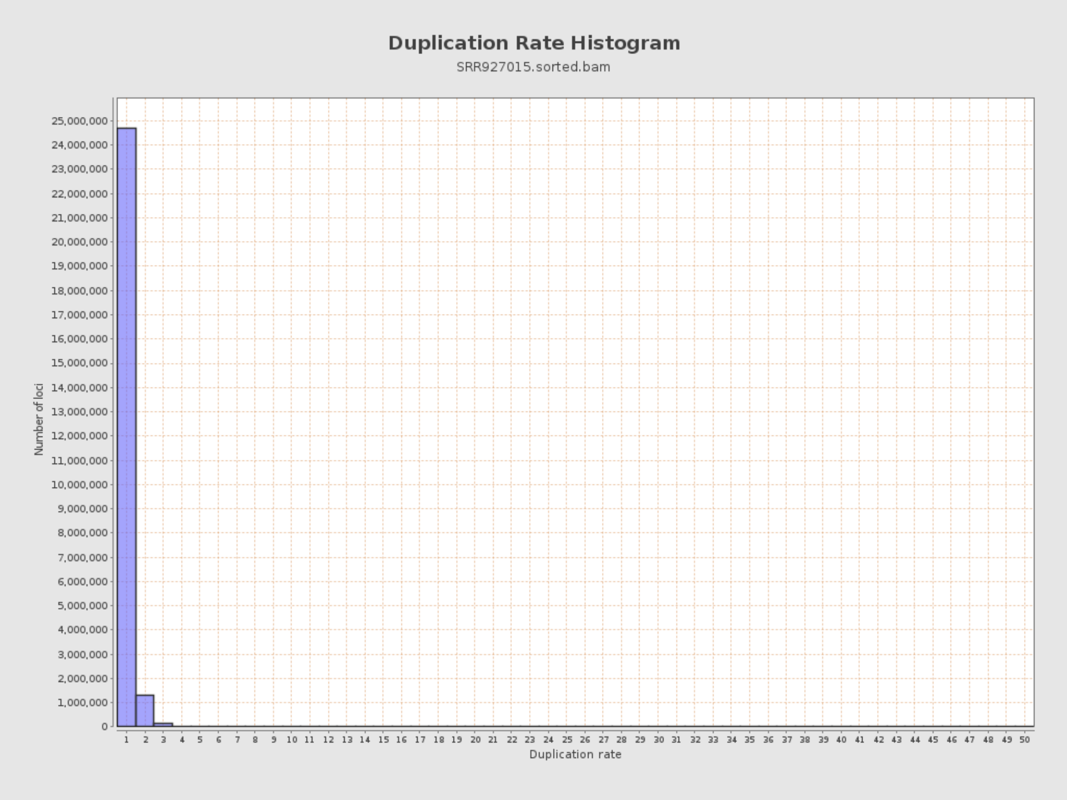
5. Results : Coverage Histogram (0-50X)



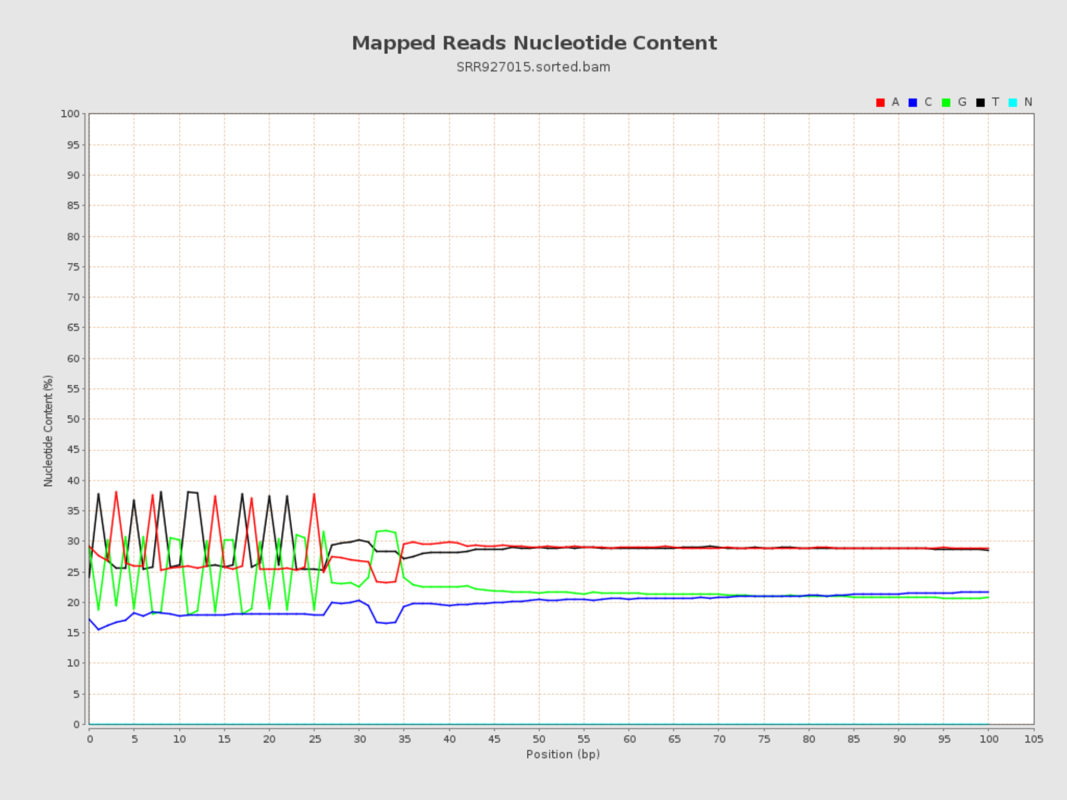
6. Results : Genome Fraction Coverage



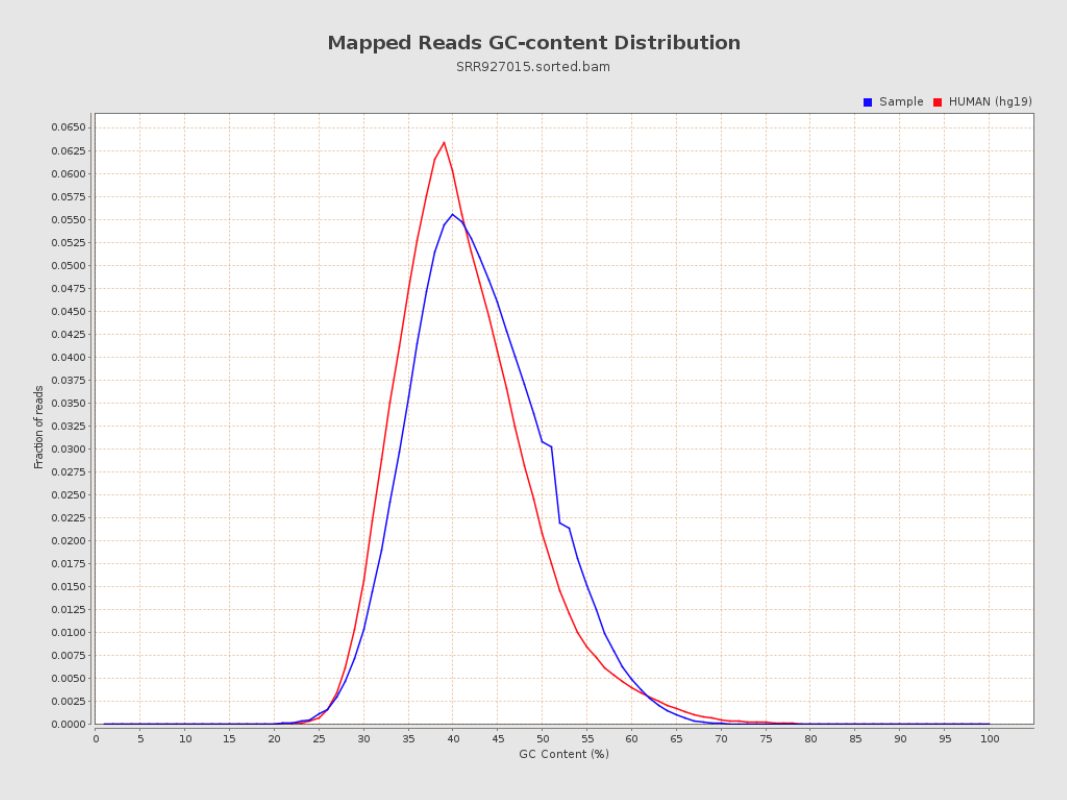
7. Results : Duplication Rate Histogram



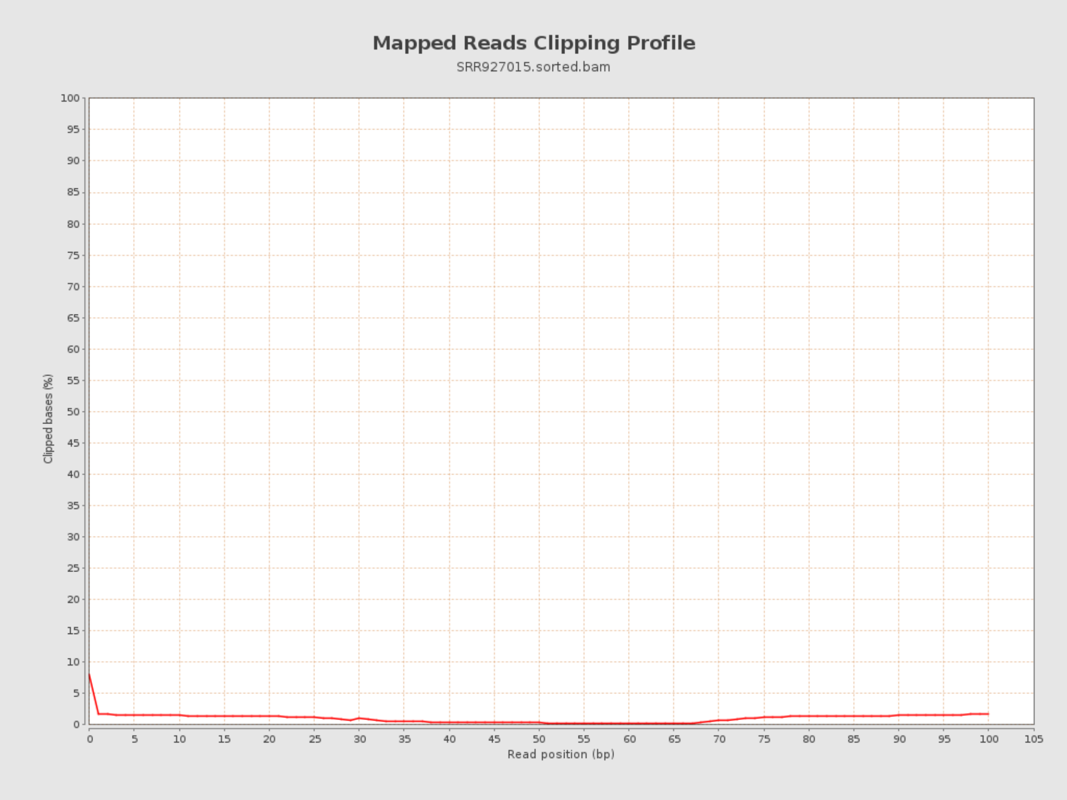
8. Results : Mapped Reads Nucleotide Content



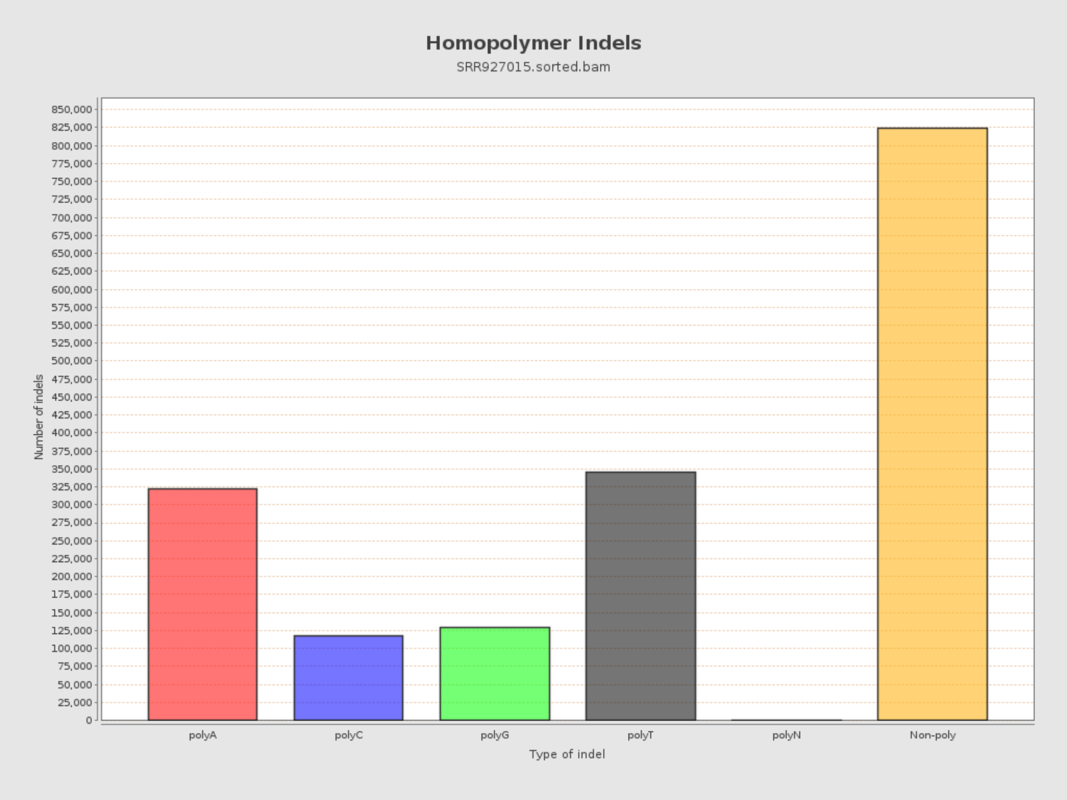
9. Results : Mapped Reads GC-content Distribution



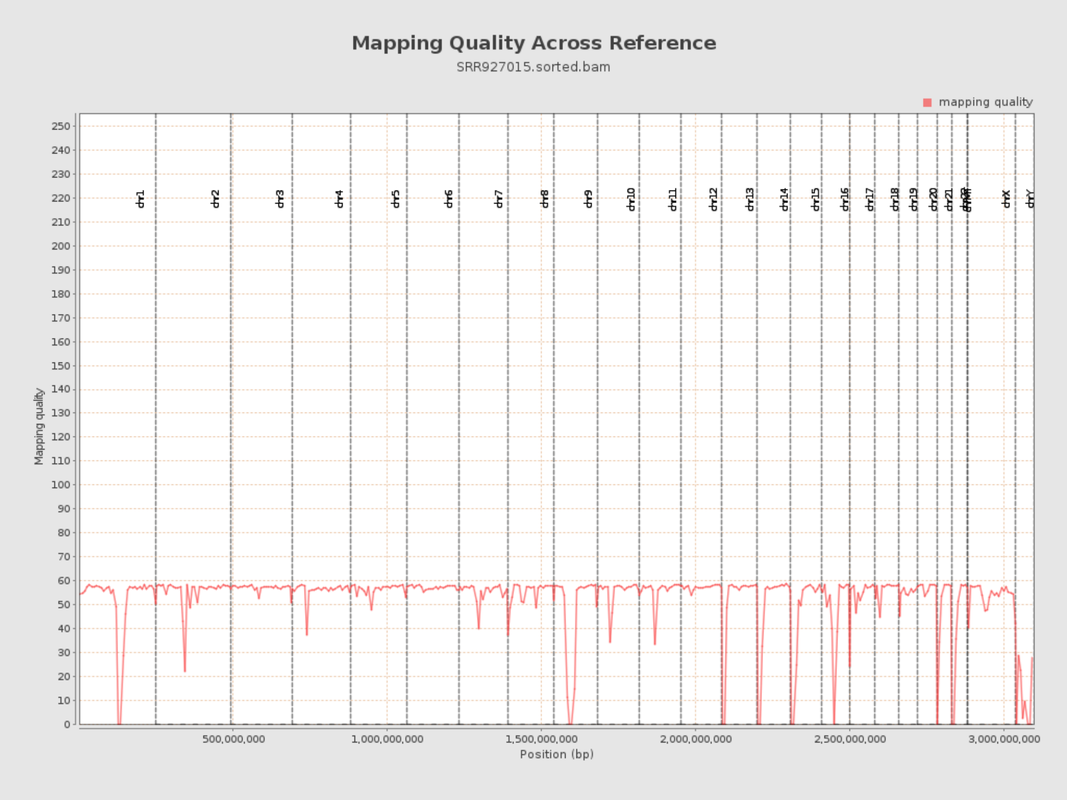
10. Results : Mapped Reads Clipping Profile



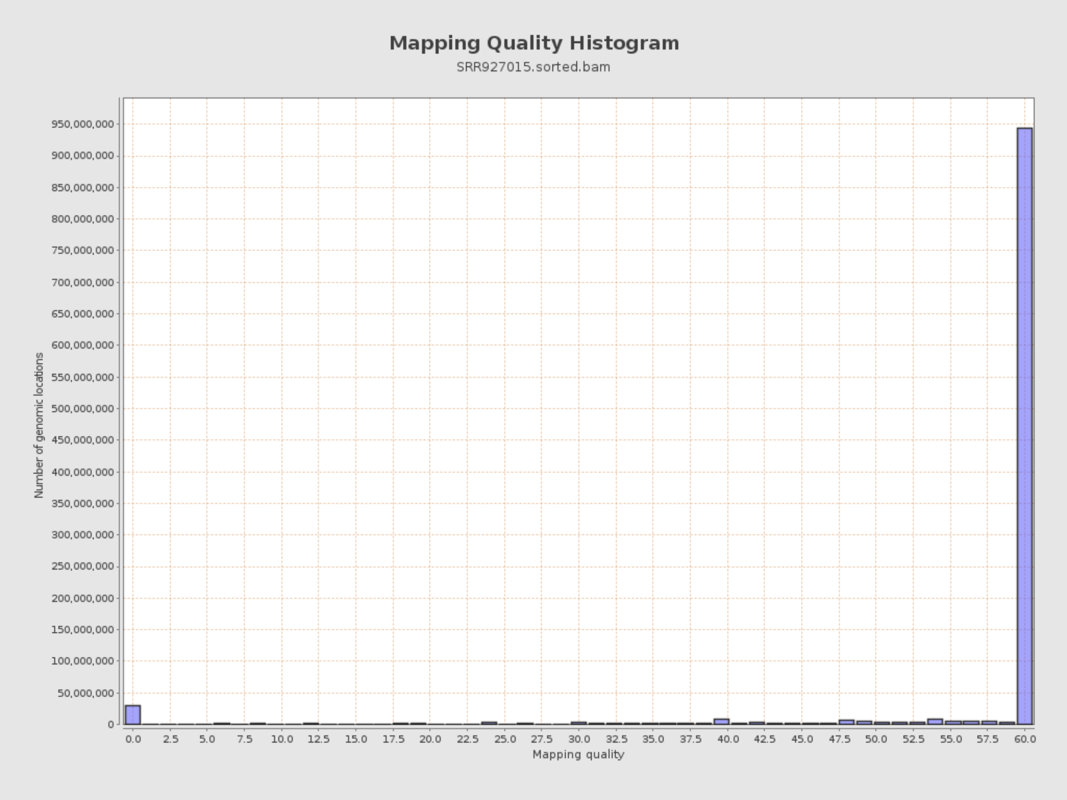
11. Results : Homopolymer Indels



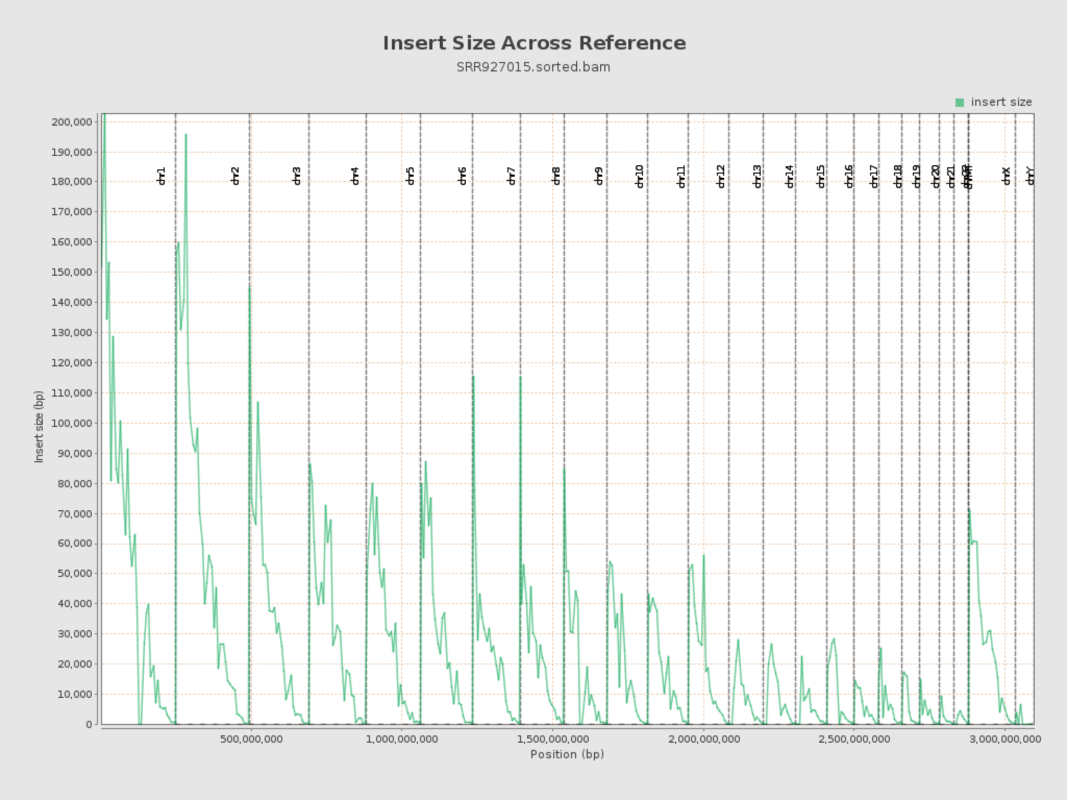
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram