Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/23 02:21:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926952.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_SRR926952 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926952_1.fastq.gz SRR926952_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Apr 23 02:21:26 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926952.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,611,404
Mapped reads	10,196,657 / 96.09%
Unmapped reads	414,747 / 3.91%
Mapped paired reads	10,196,657 / 96.09%
Mapped reads, first in pair	5,103,045 / 48.09%
Mapped reads, second in pair	5,093,612 / 48%
Mapped reads, both in pair	9,992,314 / 94.17%
Mapped reads, singletons	204,343 / 1.93%
Secondary alignments	0
Supplementary alignments	313,072 / 2.95%
Read min/max/mean length	30 / 101 / 102.22
Duplicated reads (estimated)	691,571 / 6.52%
Duplication rate	5.66%
Clipped reads	4,261,090 / 40.16%

2.2. ACGT Content

Number/percentage of A's	263,710,859 / 28.35%
Number/percentage of C's	183,832,346 / 19.76%
Number/percentage of T's	265,998,375 / 28.6%
Number/percentage of G's	216,601,961 / 23.29%
Number/percentage of N's	51,545 / 0.01%

GC Percentage	43.05%

2.3. Coverage

Mean	0.3007
Standard Deviation	1.2829

2.4. Mapping Quality

Mean Mapping Quality	52.78

2.5. Insert size

Mean	303,750.14
Standard Deviation	5,413,097.21
P25/Median/P75	146 / 194 / 264

2.6. Mismatches and indels

General error rate	1.03%
Mismatches	9,315,982
Insertions	157,774
Mapped reads with at least one insertion	1.52%
Deletions	486,376
Mapped reads with at least one deletion	4.65%
Homopolymer indels	52.51%

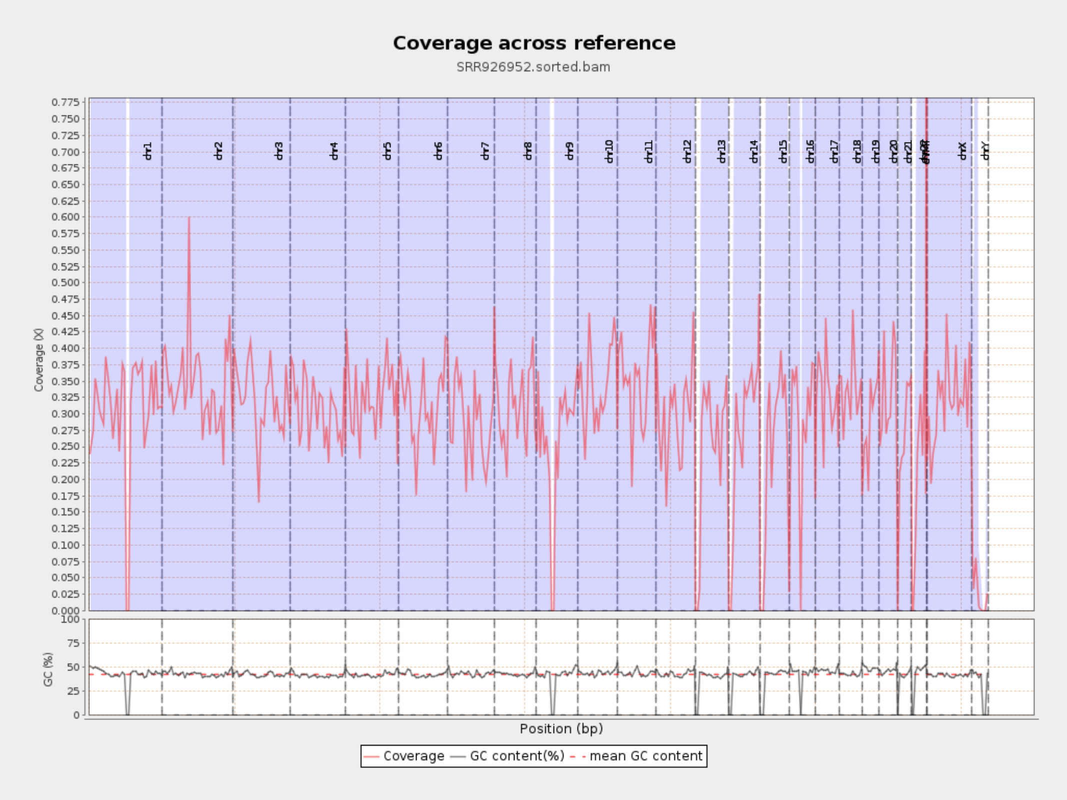
2.7. Chromosome stats

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

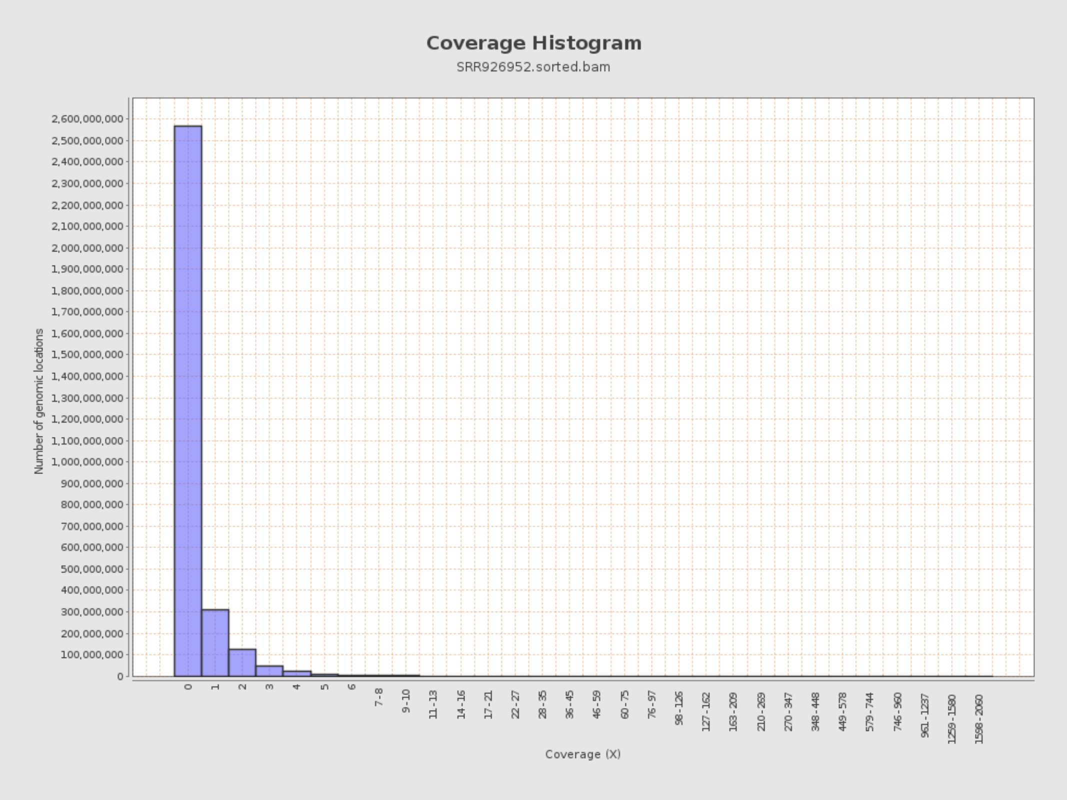
		bases	coverage	deviation
chr1	249250621	75443014	0.3027	1.5525
chr2	243199373	84429545	0.3472	2.3939
chr3	198022430	63916294	0.3228	0.861
chr4	191154276	58603844	0.3066	1.3036
chr5	180915260	59201771	0.3272	0.8623
chr6	171115067	54335811	0.3175	0.8955
chr7	159138663	45403188	0.2853	0.886
chr8	146364022	46155779	0.3153	0.9074
chr9	141213431	36021944	0.2551	1.137
chr10	135534747	46417518	0.3425	2.2458
chr11	135006516	47634709	0.3528	1.1014
chr12	133851895	39956434	0.2985	1.1823
chr13	115169878	28098606	0.244	0.7458
chr14	107349540	28366763	0.2642	0.7976
chr15	102531392	24768677	0.2416	0.7686
chr16	90354753	26591099	0.2943	0.9135
chr17	81195210	26889552	0.3312	0.9271
chr18	78077248	26555866	0.3401	1.3487
chr19	59128983	17169433	0.2904	1.1332
chr20	63025520	20895500	0.3315	0.9369
chr21	48129895	12378482	0.2572	1.2611
chr22	51304566	10419834	0.2031	0.7094
chrMT	16571	59907	3.6152	4.7534
chrX	155270560	49679969	0.32	0.8856

chrY	59373566	1509739	0.0254	0.9232

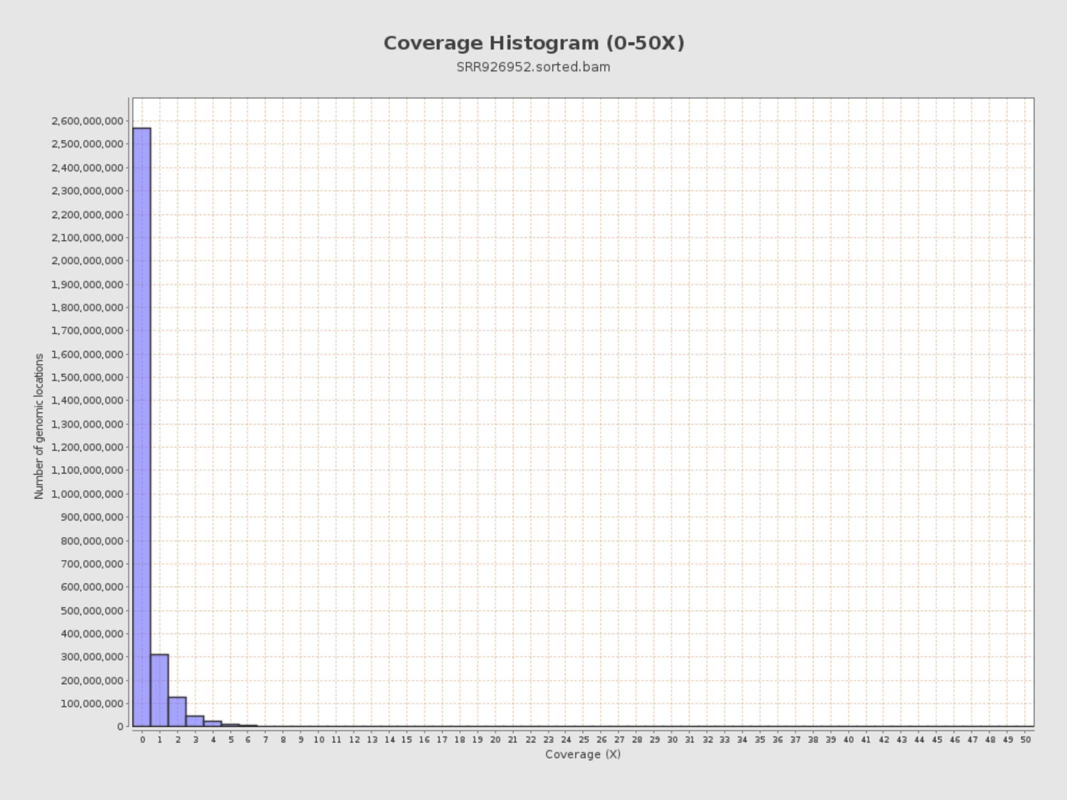
3. Results : Coverage across reference



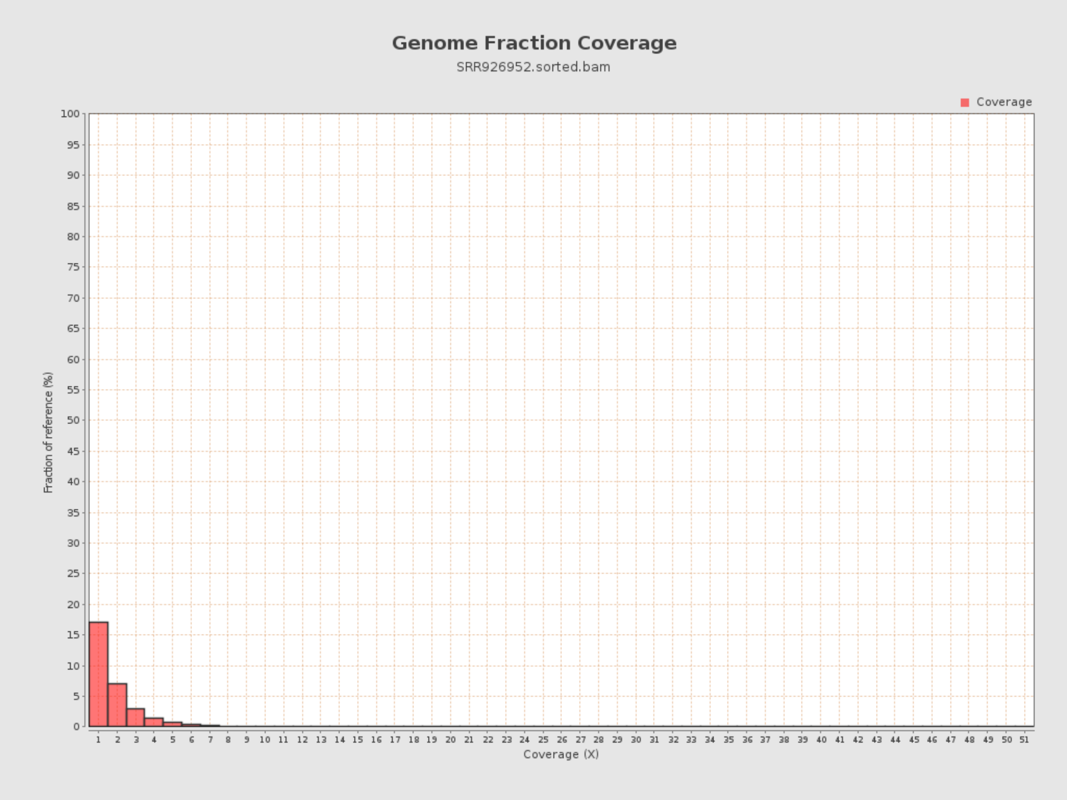
4. Results : Coverage Histogram



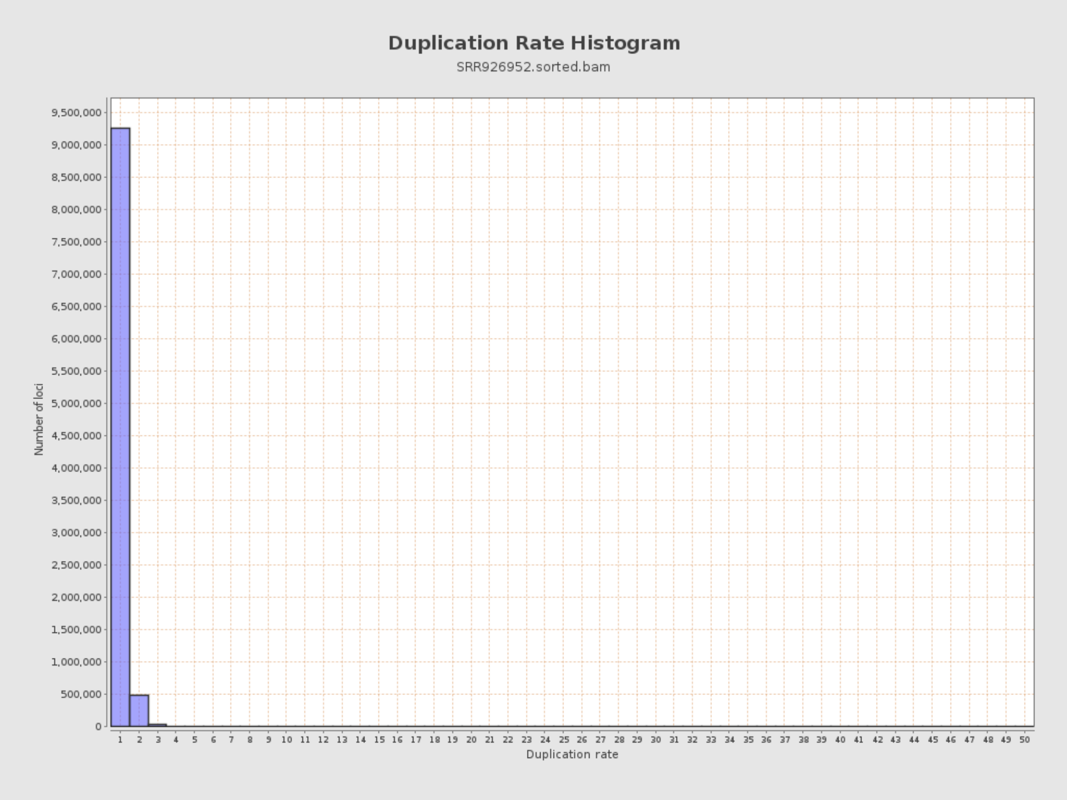
5. Results : Coverage Histogram (0-50X)



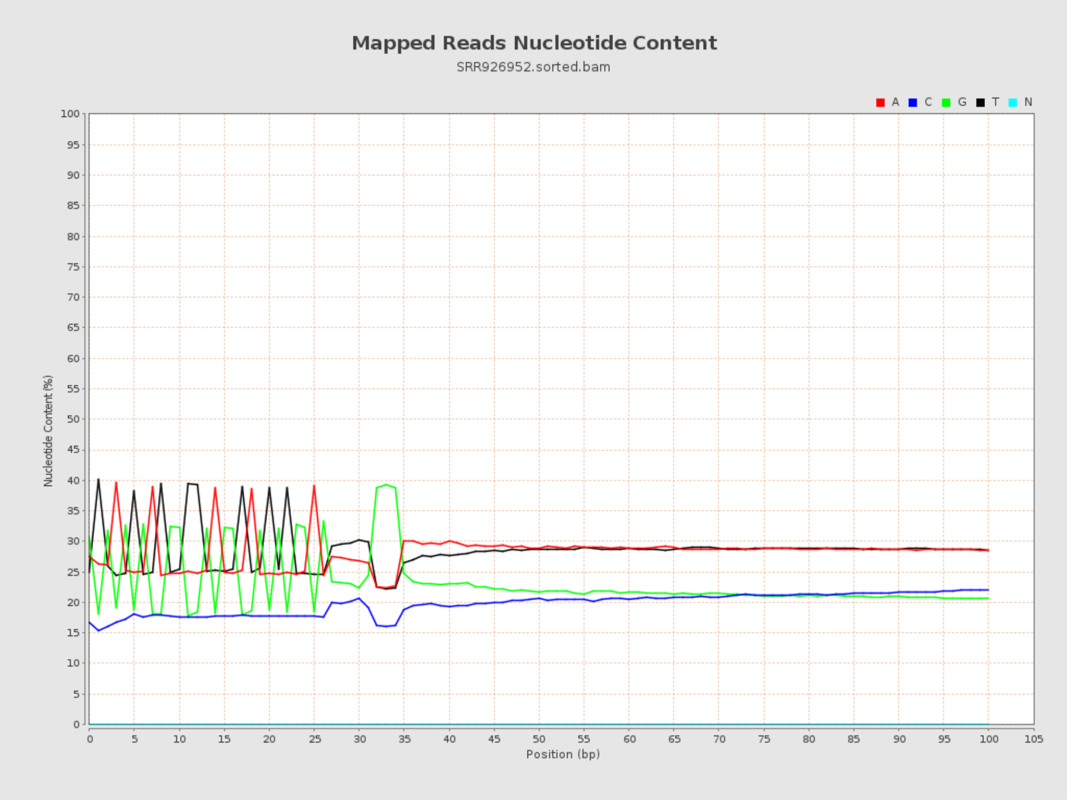
6. Results : Genome Fraction Coverage



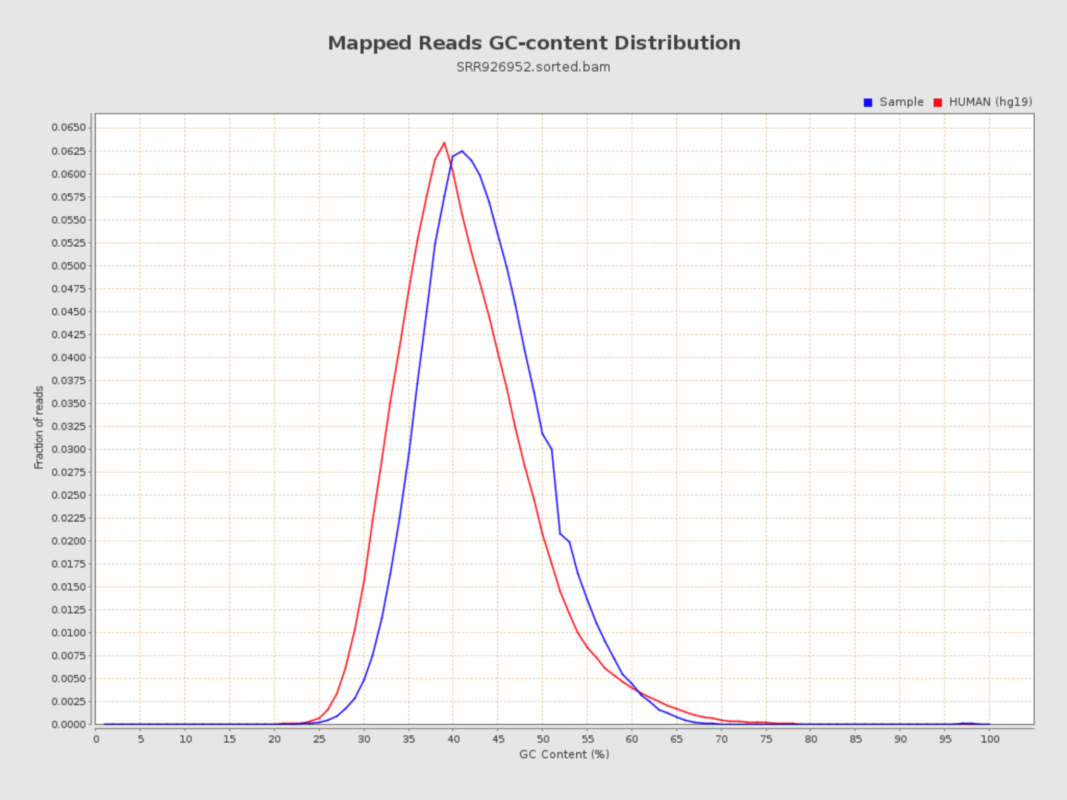
7. Results : Duplication Rate Histogram



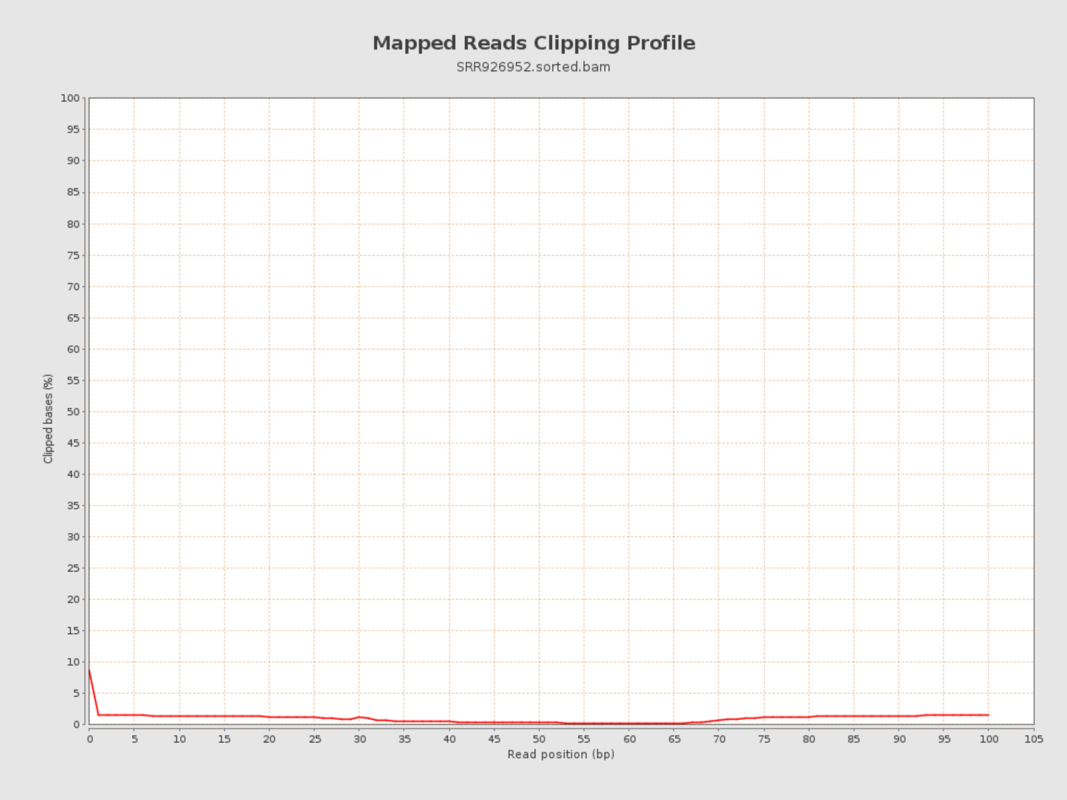
8. Results : Mapped Reads Nucleotide Content



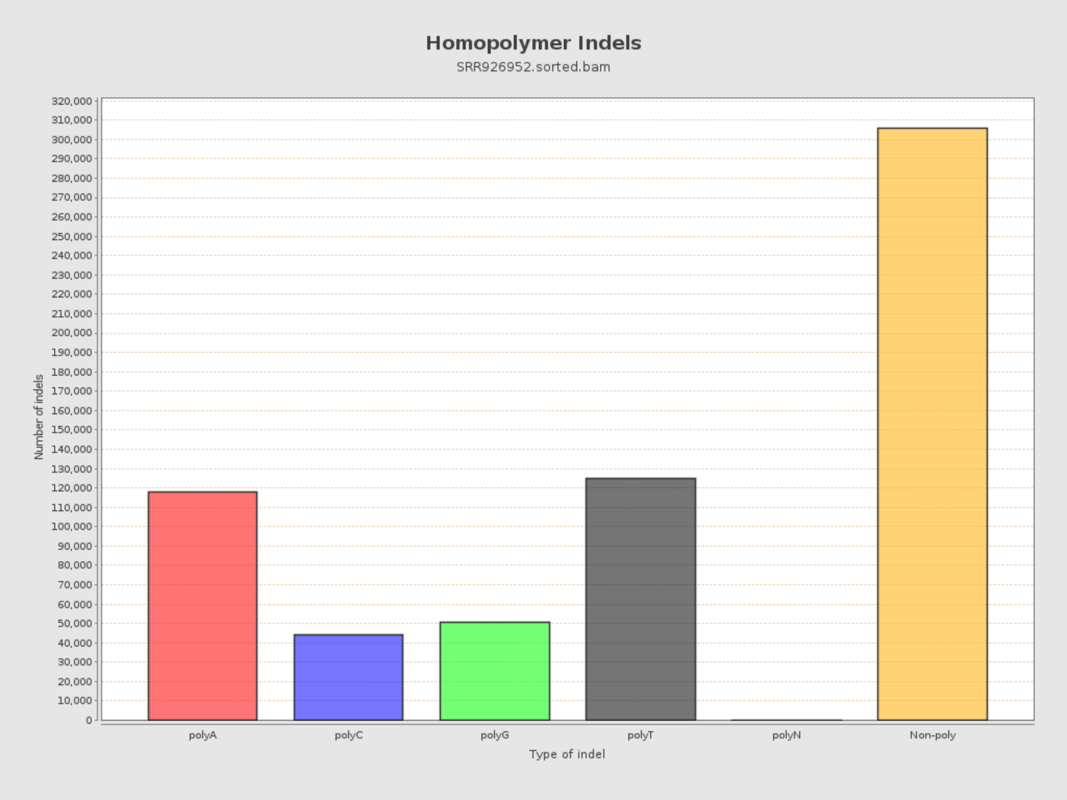
9. Results : Mapped Reads GC-content Distribution



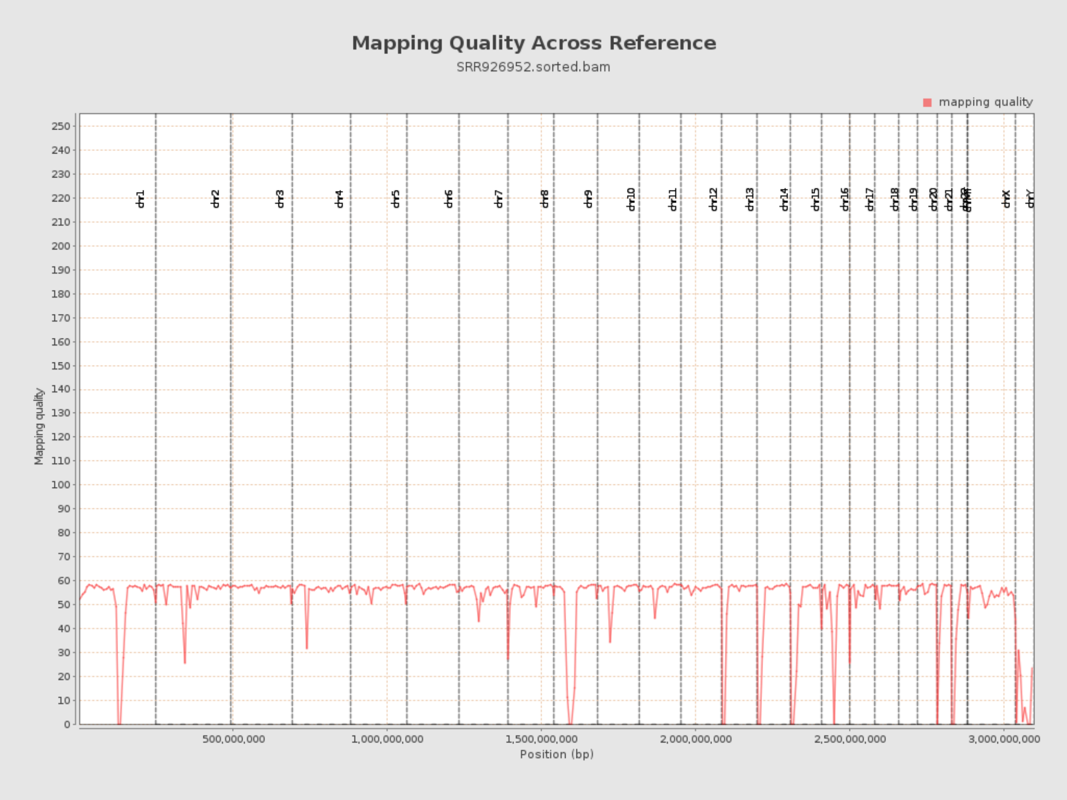
10. Results : Mapped Reads Clipping Profile



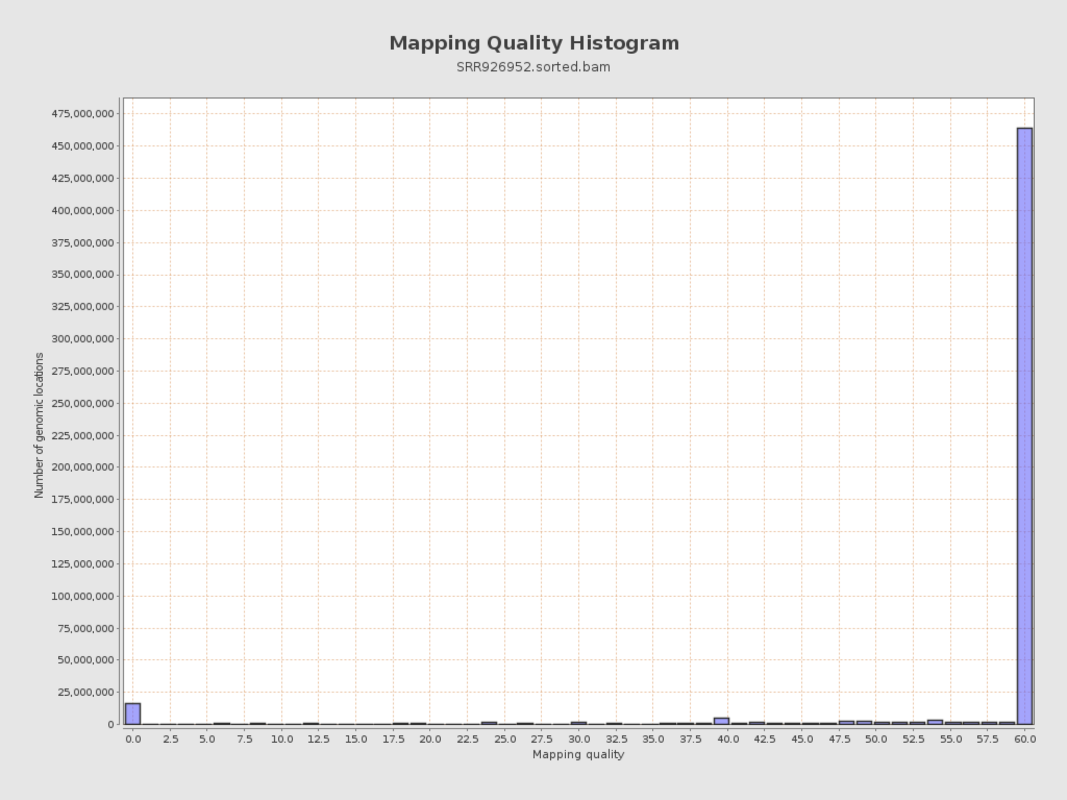
11. Results : Homopolymer Indels



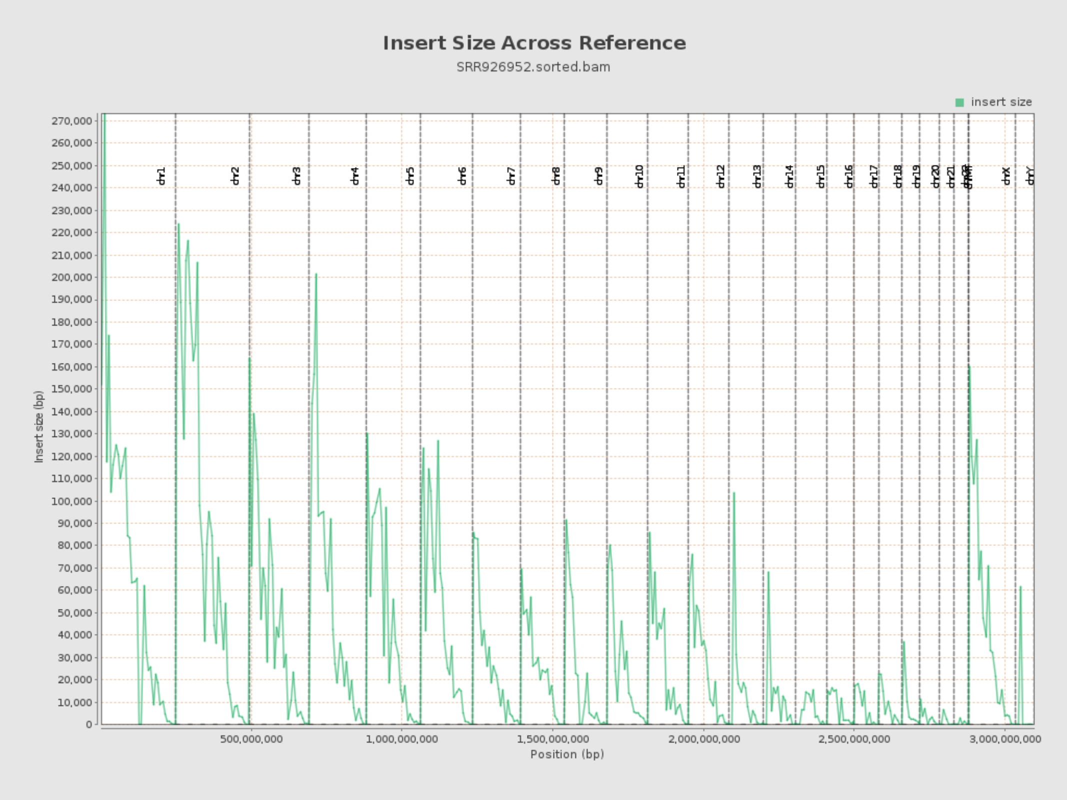
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram