Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/05 04:38:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124827.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_SRR3124827 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124827_1.fastq.gz SRR3124827_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Dec 05 04:38:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124827.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	27,380,426
Mapped reads	27,003,211 / 98.62%
Unmapped reads	377,215 / 1.38%
Mapped paired reads	27,003,211 / 98.62%
Mapped reads, first in pair	13,531,503 / 49.42%
Mapped reads, second in pair	13,471,708 / 49.2%
Mapped reads, both in pair	26,885,468 / 98.19%
Mapped reads, singletons	117,743 / 0.43%
Secondary alignments	0
Supplementary alignments	124,384 / 0.45%
Read min/max/mean length	30 / 101 / 101.18
Duplicated reads (estimated)	5,258,661 / 19.21%
Duplication rate	12.5%
Clipped reads	13,362,072 / 48.8%

2.2. ACGT Content

Number/percentage of A's	652,683,941 / 27.88%
Number/percentage of C's	440,033,312 / 18.8%
Number/percentage of T's	693,636,975 / 29.63%
Number/percentage of G's	554,342,482 / 23.68%
Number/percentage of N's	19,729 / 0%

GC Percentage	42.48%

2.3. Coverage

Mean	0.7566
Standard Deviation	5.9418

2.4. Mapping Quality

Mean Mapping Quality	52.72

2.5. Insert size

Mean	37,881.79
Standard Deviation	1,823,513.75
P25/Median/P75	149 / 203 / 284

2.6. Mismatches and indels

General error rate	0.78%
Mismatches	17,506,244
Insertions	323,250
Mapped reads with at least one insertion	1.16%
Deletions	814,203
Mapped reads with at least one deletion	2.95%
Homopolymer indels	46.03%

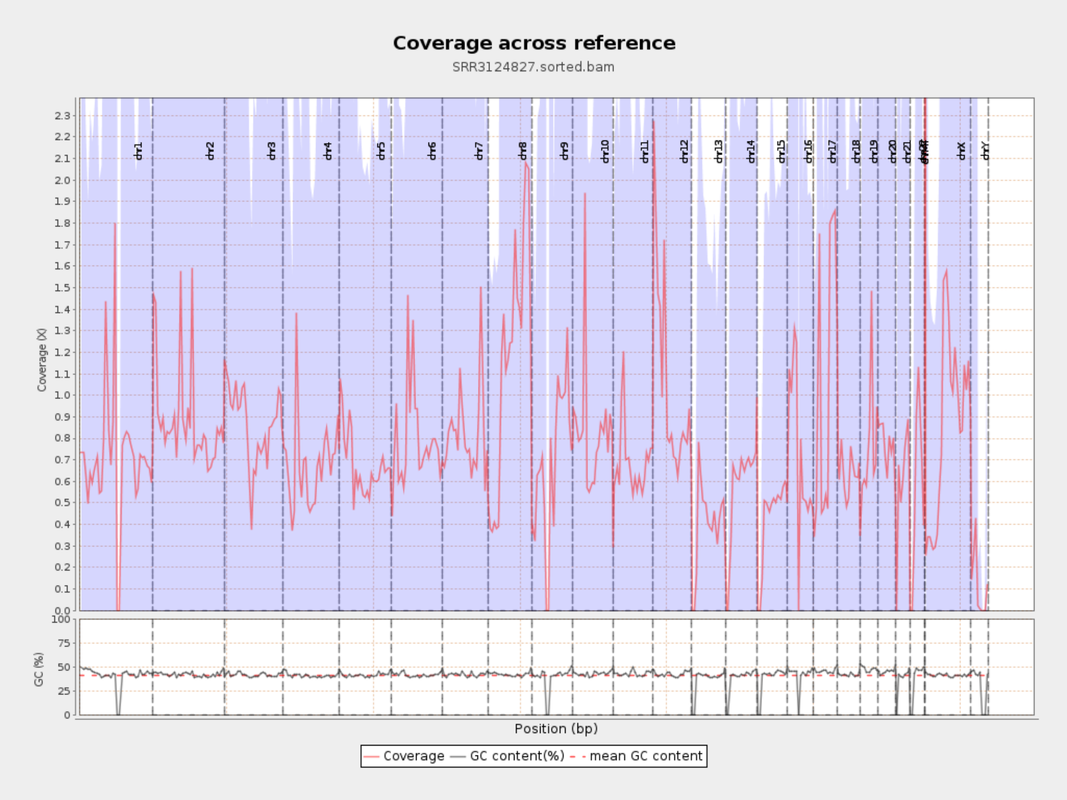
2.7. Chromosome stats

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

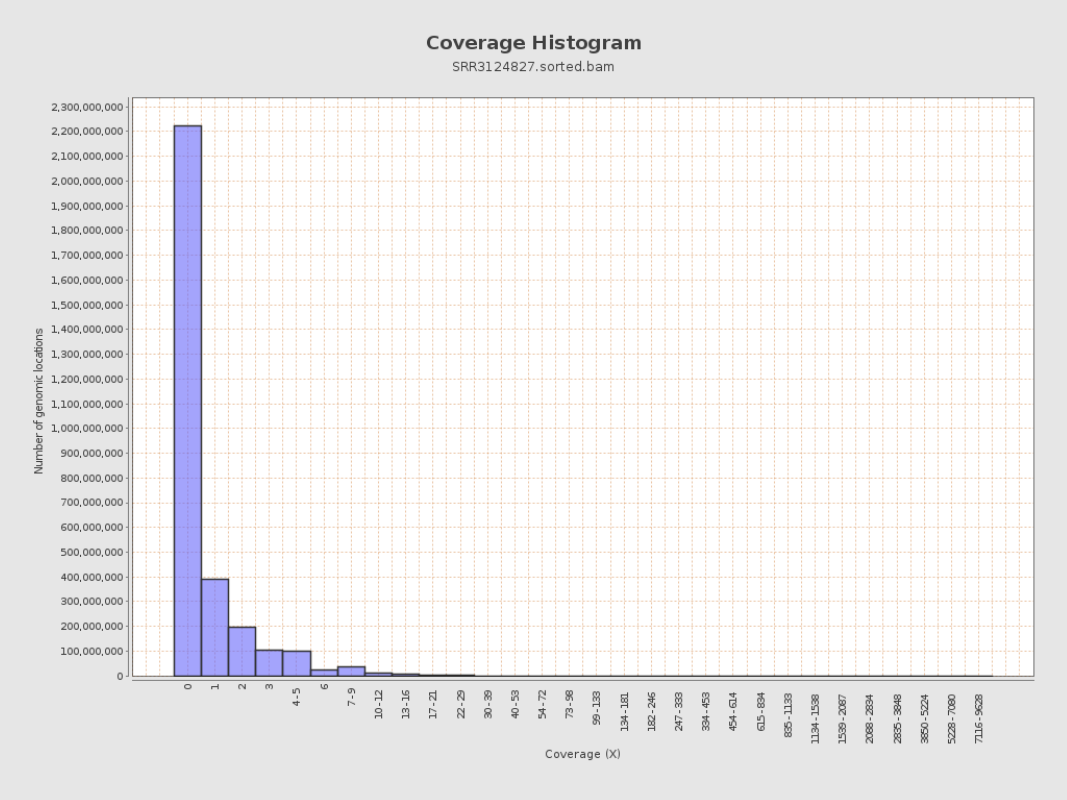
		bases	coverage	deviation
chr1	249250621	176064179	0.7064	6.5458
chr2	243199373	217171702	0.893	9.6349
chr3	198022430	171435026	0.8657	1.9528
chr4	191154276	127727495	0.6682	4.4135
chr5	180915260	122503452	0.6771	1.9269
chr6	171115067	136193784	0.7959	5.0047
chr7	159138663	131745788	0.8279	7.6572
chr8	146364022	171873459	1.1743	4.4963
chr9	141213431	95994790	0.6798	8.401
chr10	135534747	113880619	0.8402	10.0851
chr11	135006516	92144025	0.6825	5.2906
chr12	133851895	142119653	1.0618	2.4226
chr13	115169878	46949684	0.4077	1.2686
chr14	107349540	60567599	0.5642	1.9569
chr15	102531392	43256241	0.4219	1.323
chr16	90354753	64362945	0.7123	6.0924
chr17	81195210	82887948	1.0208	10.4196
chr18	78077248	49644502	0.6358	8.1086
chr19	59128983	44843529	0.7584	3.5065
chr20	63025520	48418985	0.7682	2.3928
chr21	48129895	29880056	0.6208	2.8032
chr22	51304566	28565121	0.5568	1.9452
chrMT	16571	3780941	228.1661	137.2809
chrX	155270560	132853537	0.8556	3.0642

chrY	59373566	7254444	0.1222	7.6925

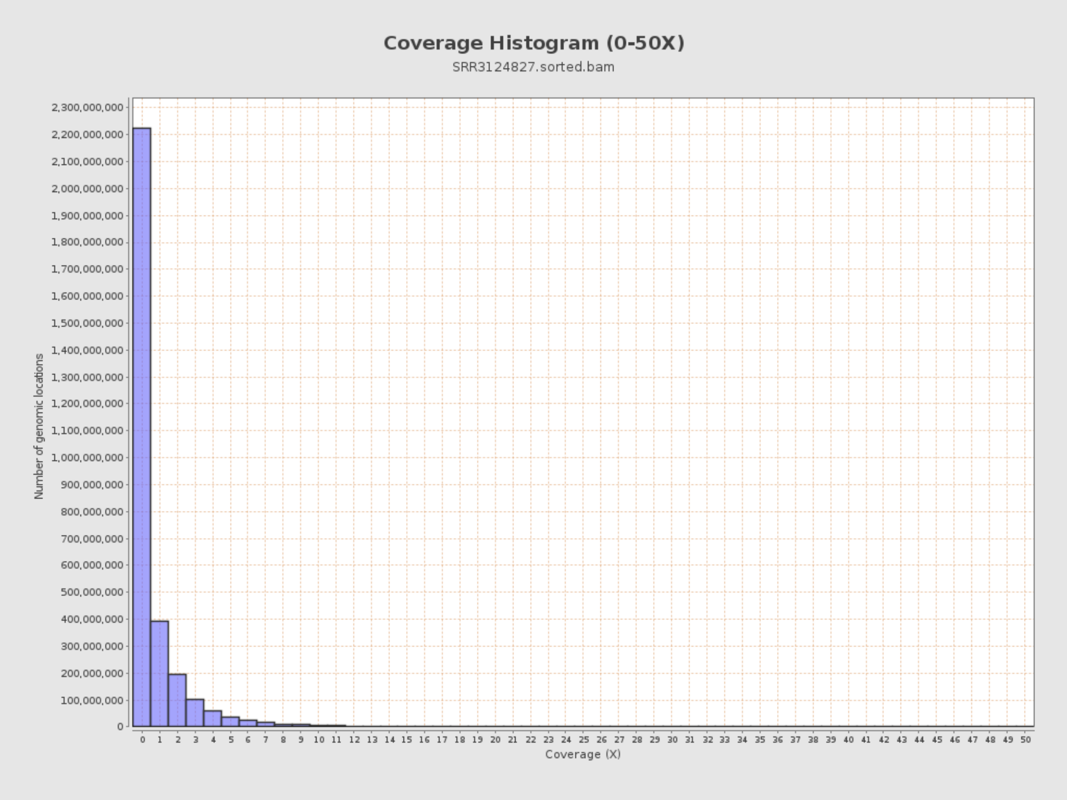
3. Results : Coverage across reference



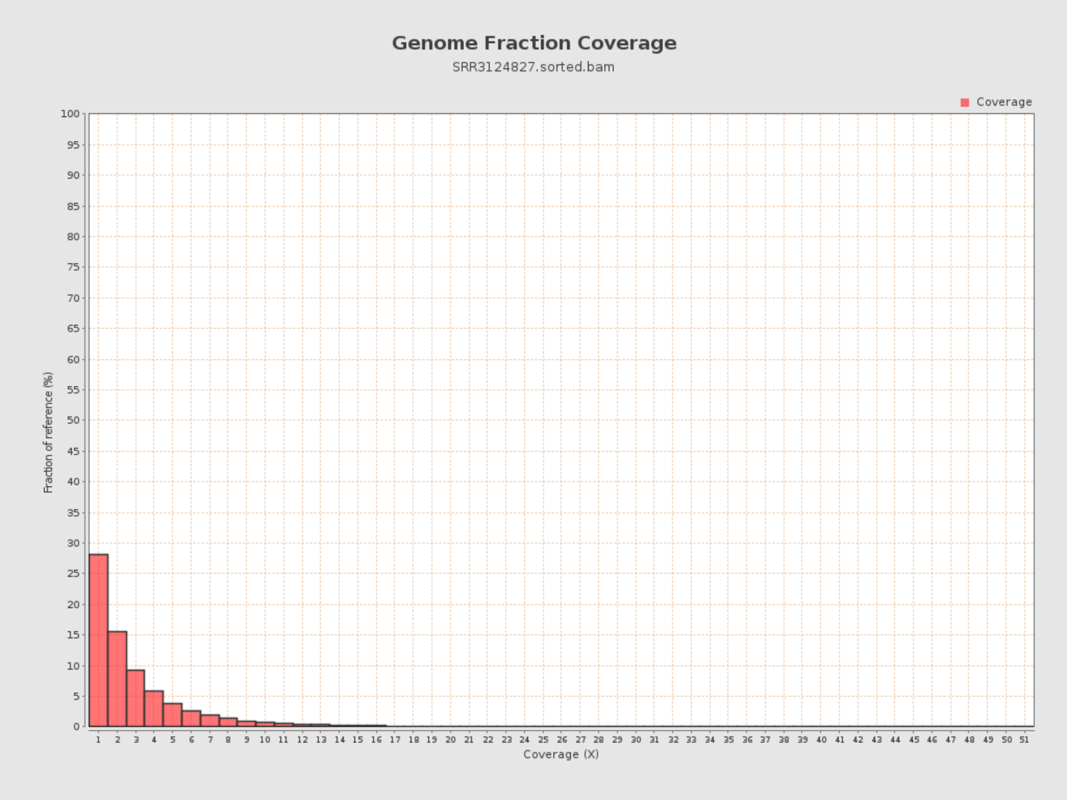
4. Results : Coverage Histogram



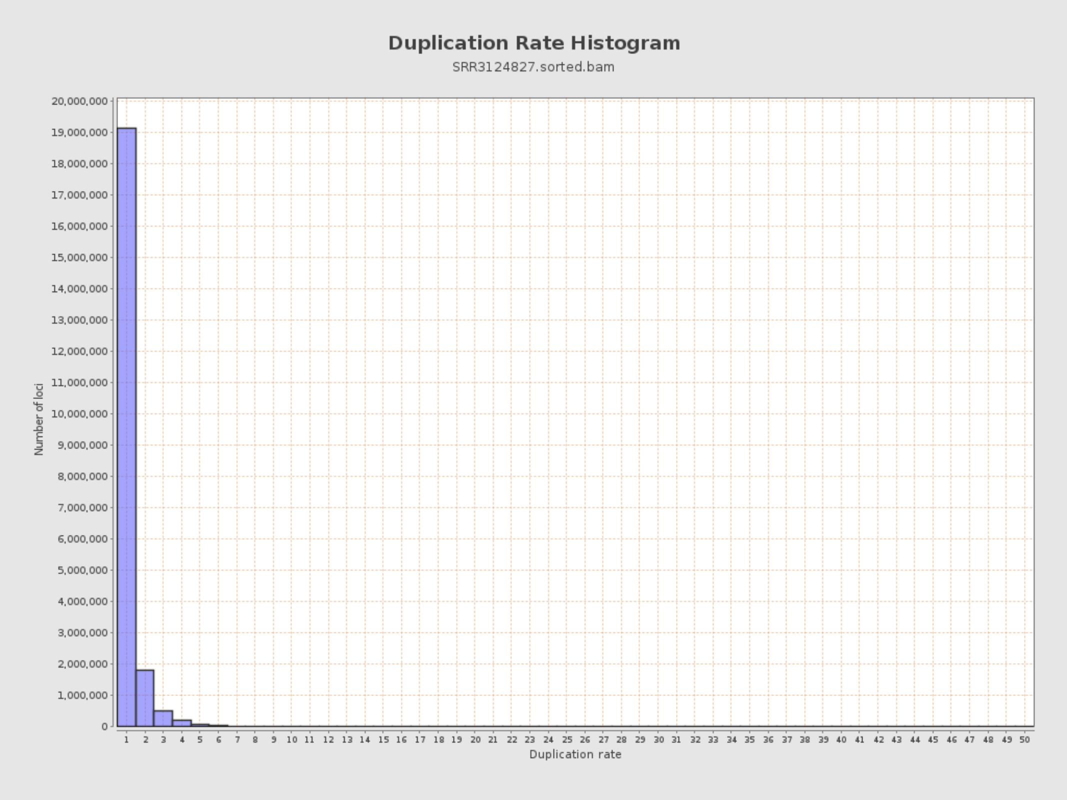
5. Results : Coverage Histogram (0-50X)



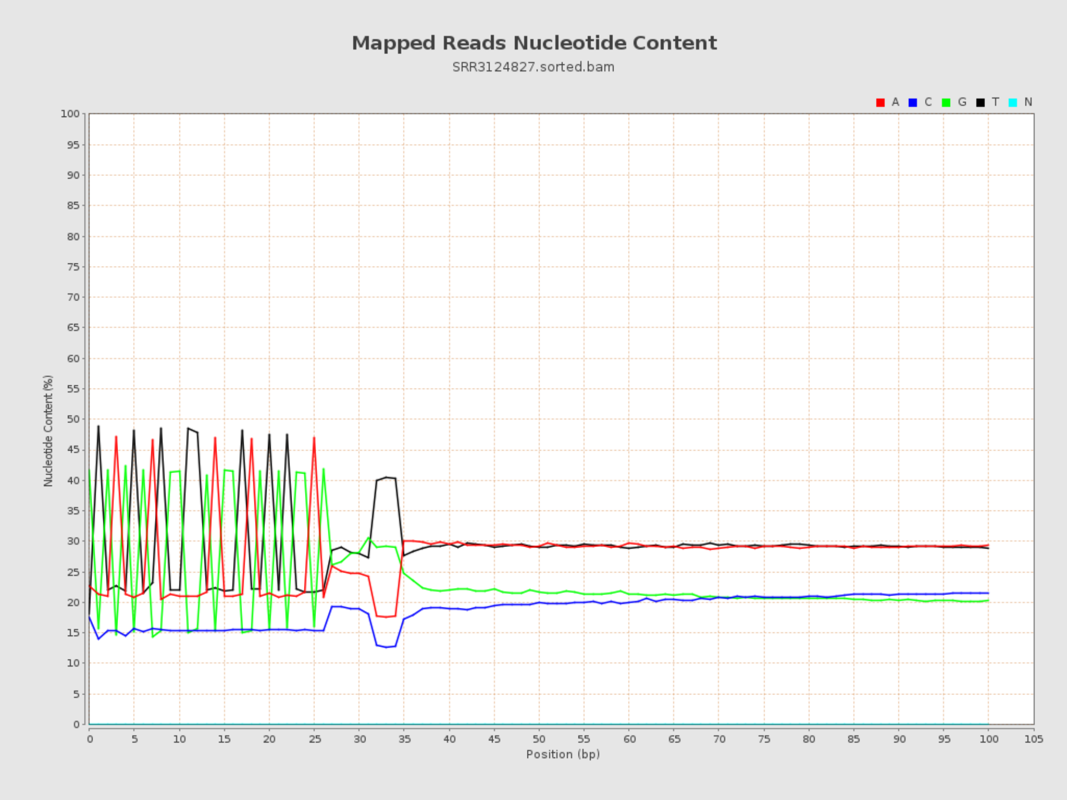
6. Results : Genome Fraction Coverage



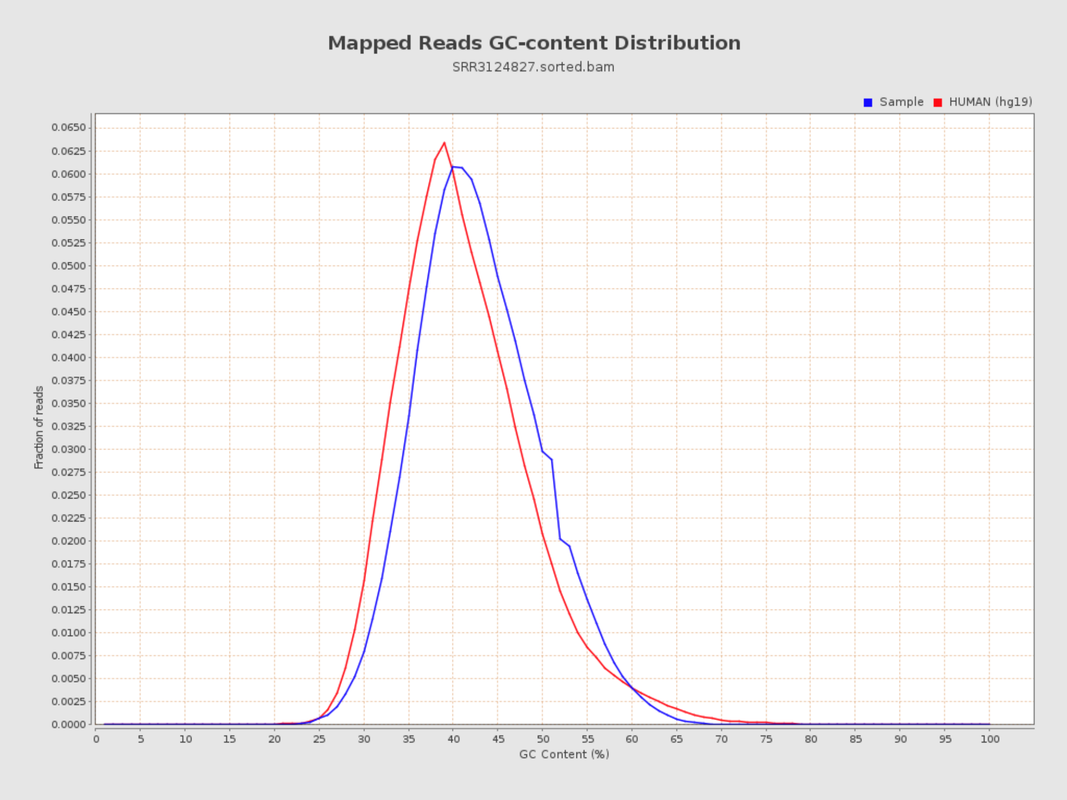
7. Results : Duplication Rate Histogram



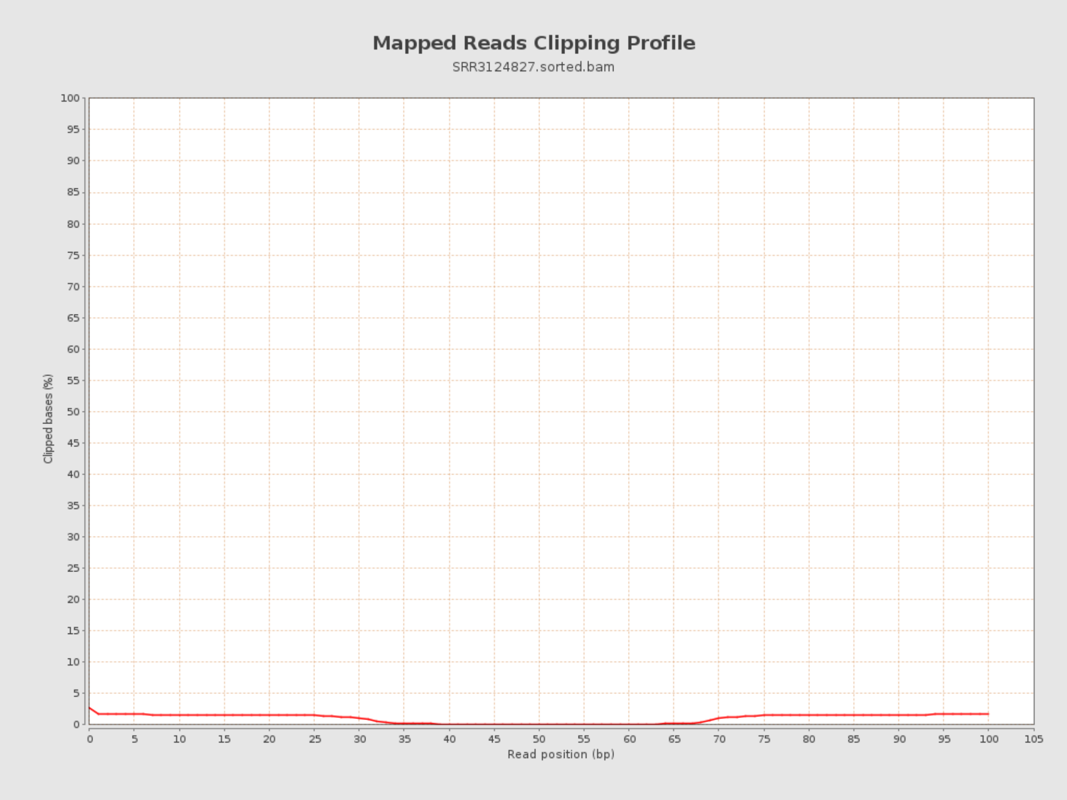
8. Results : Mapped Reads Nucleotide Content



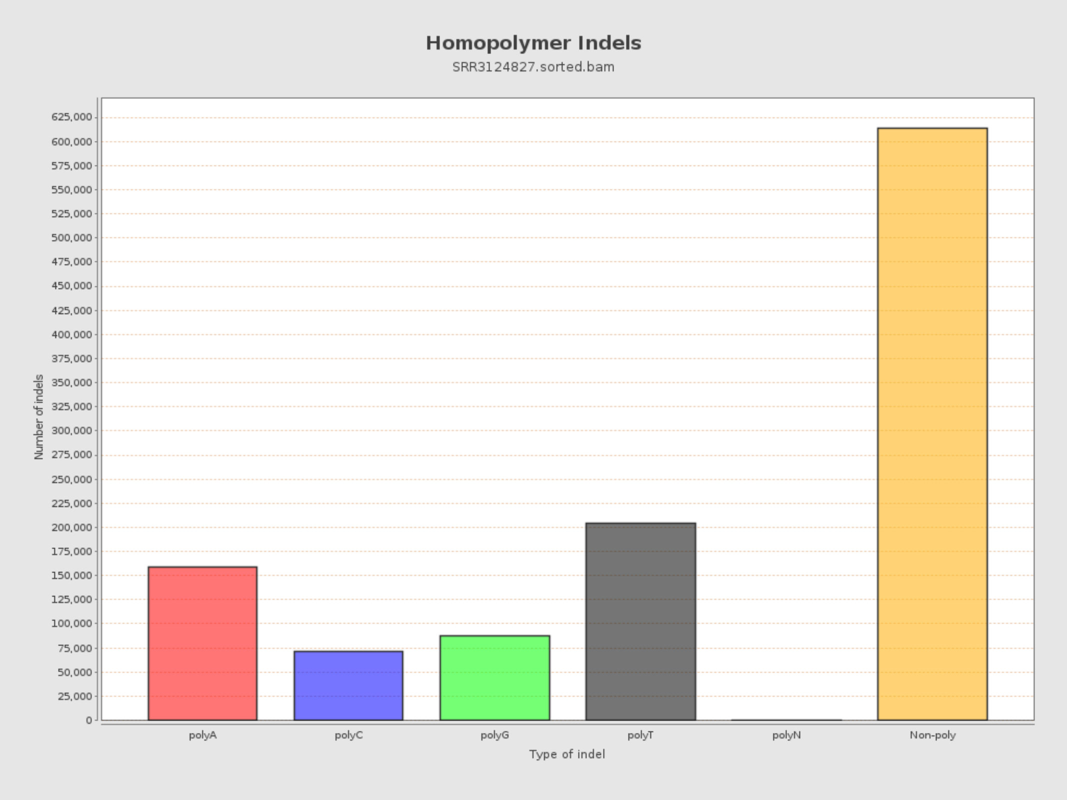
9. Results : Mapped Reads GC-content Distribution



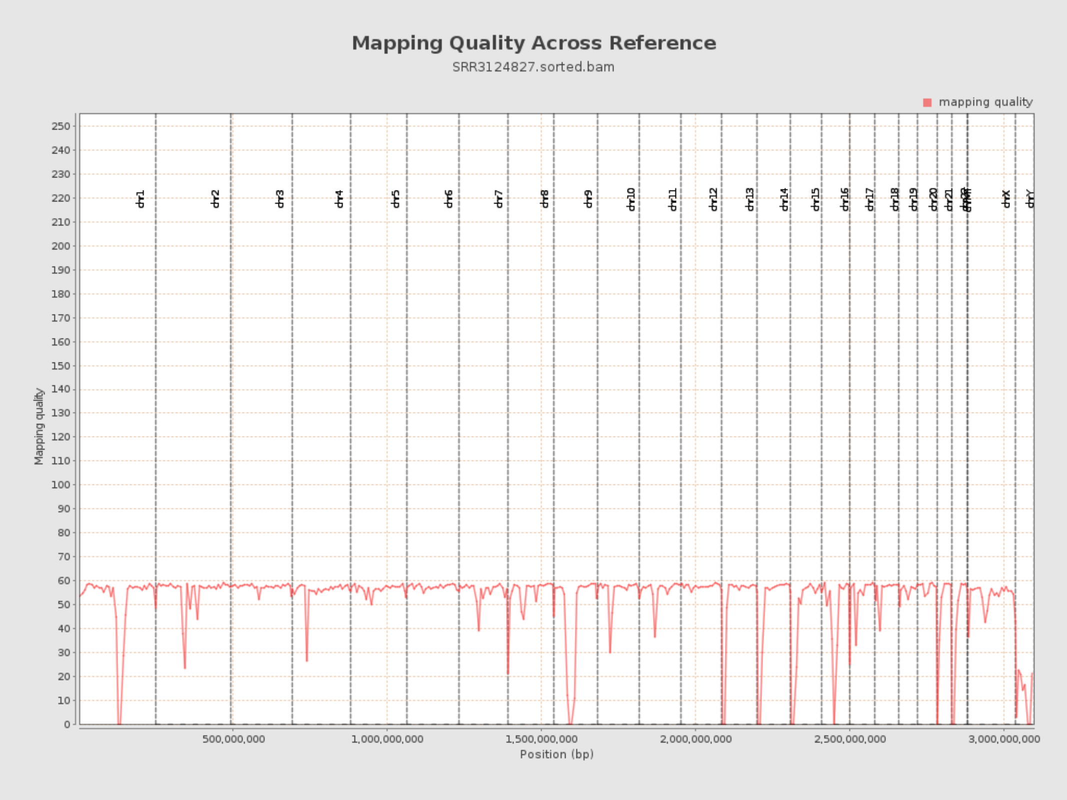
10. Results : Mapped Reads Clipping Profile



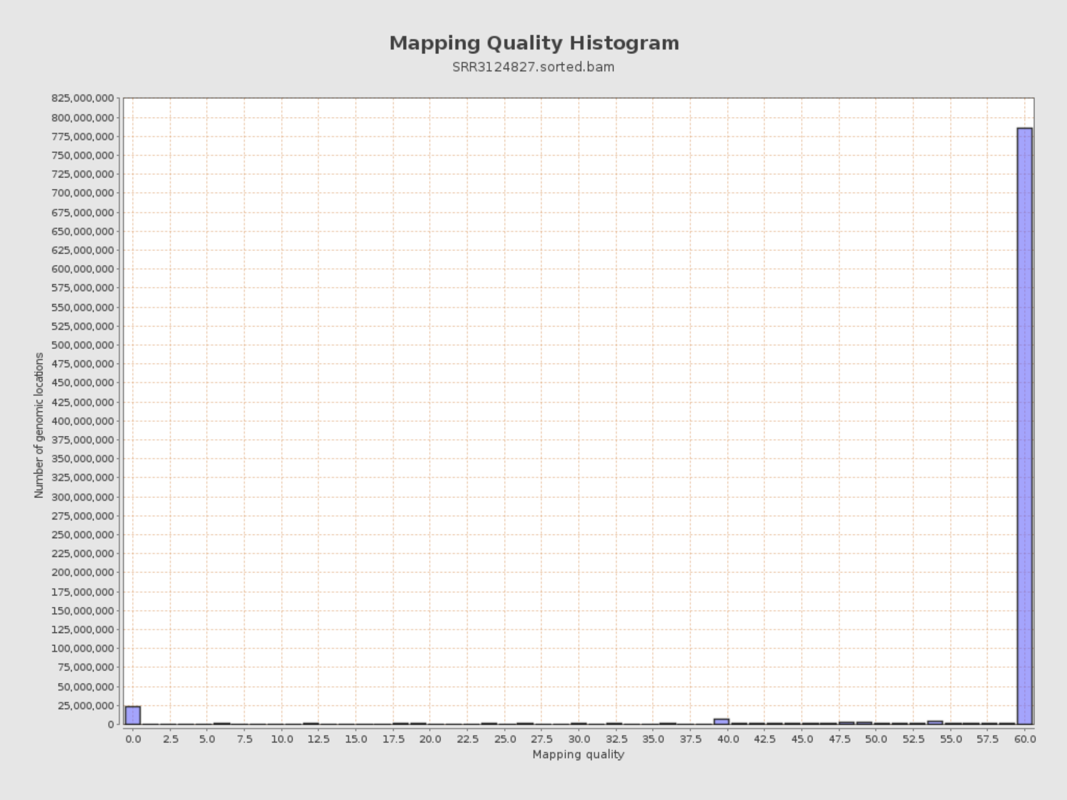
11. Results : Homopolymer Indels



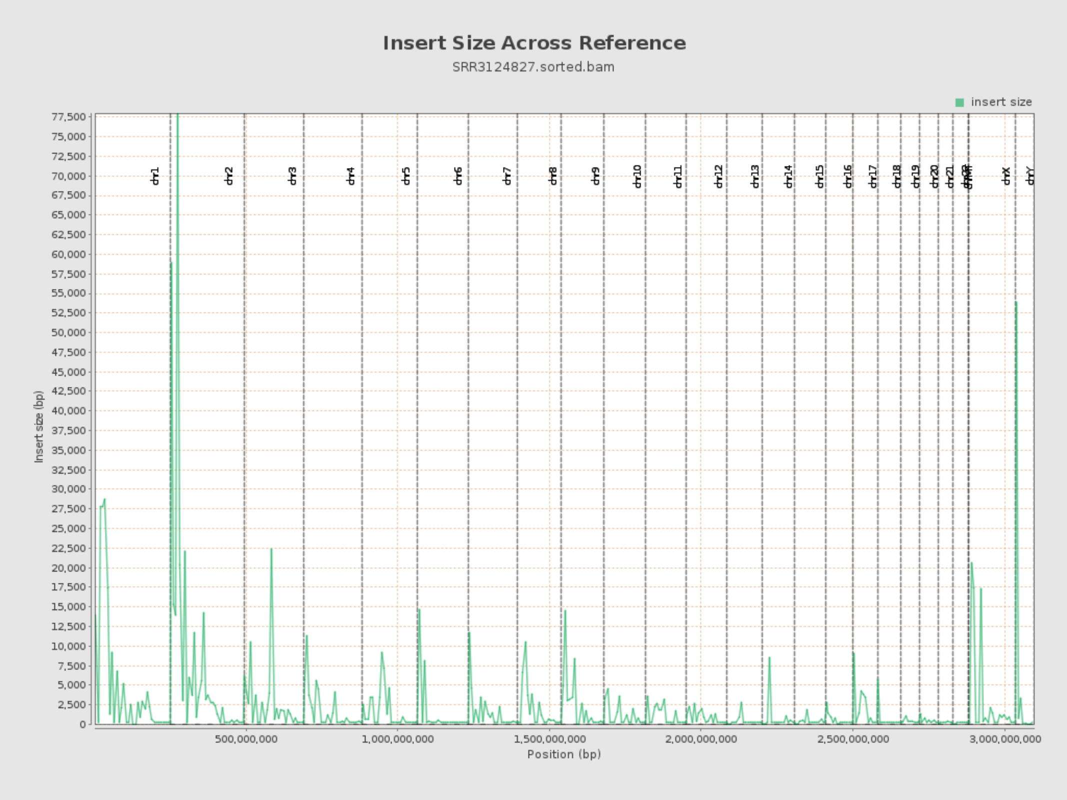
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram