Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/25 05:04:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR927062.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_SRR927062 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR927062_1.fastq.gz SRR927062_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 25 05:04:18 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR927062.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	31,243,586
Mapped reads	30,423,938 / 97.38%
Unmapped reads	819,648 / 2.62%
Mapped paired reads	30,423,938 / 97.38%
Mapped reads, first in pair	15,270,343 / 48.88%
Mapped reads, second in pair	15,153,595 / 48.5%
Mapped reads, both in pair	29,993,038 / 96%
Mapped reads, singletons	430,900 / 1.38%
Secondary alignments	0
Supplementary alignments	1,024,273 / 3.28%
Read min/max/mean length	30 / 101 / 102.35
Duplicated reads (estimated)	2,827,214 / 9.05%
Duplication rate	7.48%
Clipped reads	12,232,348 / 39.15%

2.2. ACGT Content

Number/percentage of A's	790,667,297 / 28.26%
Number/percentage of C's	562,134,520 / 20.09%
Number/percentage of T's	799,923,309 / 28.59%
Number/percentage of G's	645,372,022 / 23.06%
Number/percentage of N's	191,003 / 0.01%

GC Percentage	43.15%

2.3. Coverage

Mean	0.9046
Standard Deviation	2.9705

2.4. Mapping Quality

Mean Mapping Quality	52.82

2.5. Insert size

Mean	334,969.38
Standard Deviation	5,717,020.02
P25/Median/P75	134 / 176 / 240

2.6. Mismatches and indels

General error rate	0.97%
Mismatches	26,272,111
Insertions	477,103
Mapped reads with at least one insertion	1.54%
Deletions	1,426,974
Mapped reads with at least one deletion	4.57%
Homopolymer indels	51.84%

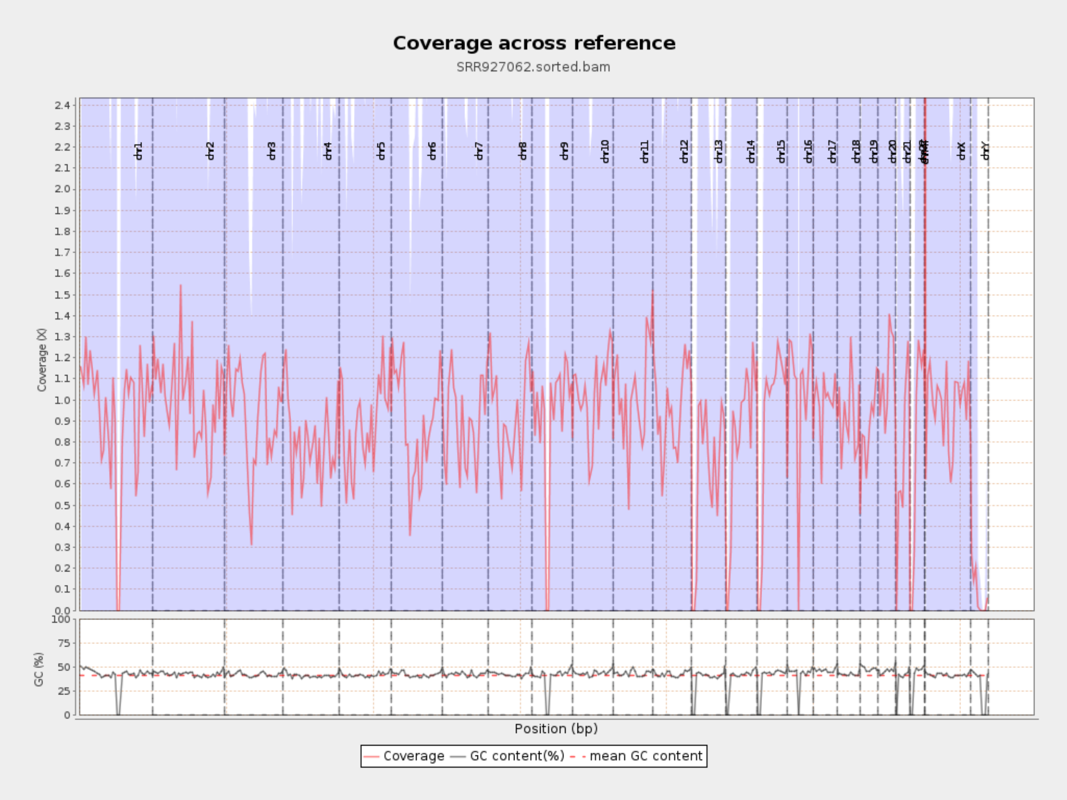
2.7. Chromosome stats

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

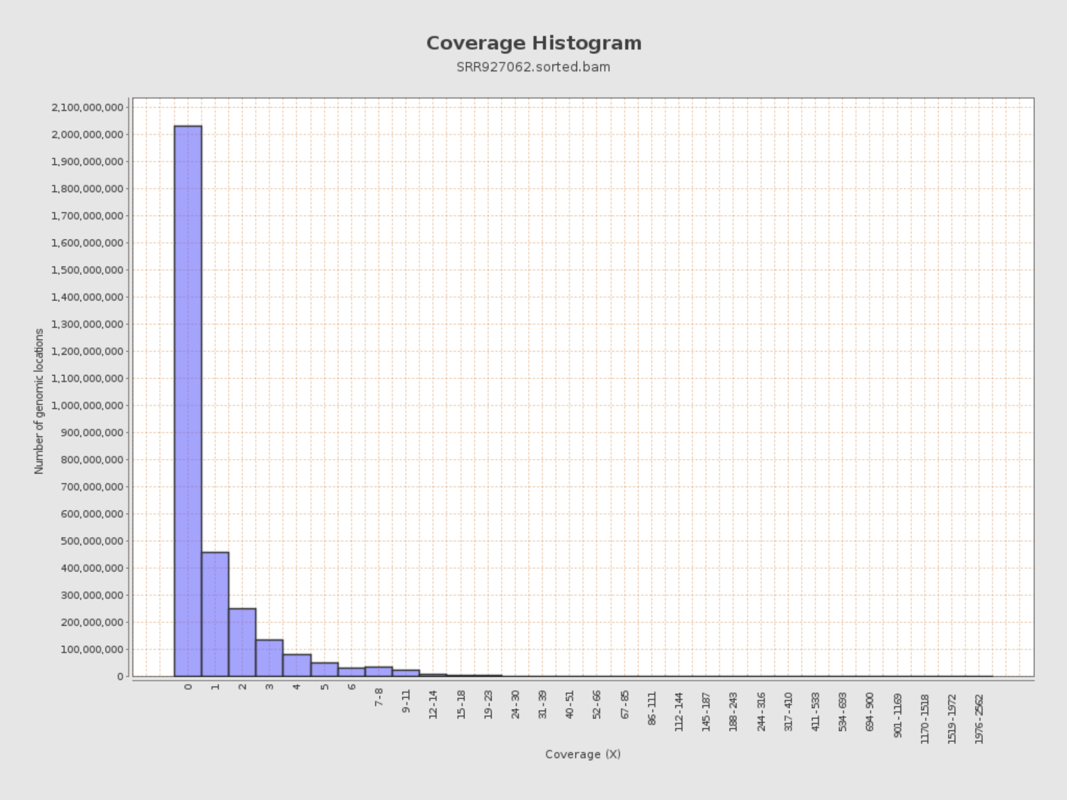
		bases	coverage	deviation
chr1	249250621	232131064	0.9313	2.8812
chr2	243199373	245752171	1.0105	5.3246
chr3	198022430	183966018	0.929	1.8993
chr4	191154276	153864613	0.8049	2.2292
chr5	180915260	161770808	0.8942	1.8605
chr6	171115067	153600191	0.8976	1.885
chr7	159138663	141987336	0.8922	2.1387
chr8	146364022	134355015	0.918	2.0227
chr9	141213431	129099045	0.9142	3.0711
chr10	135534747	140358989	1.0356	3.9729
chr11	135006516	136837974	1.0136	2.4229
chr12	133851895	128343176	0.9588	2.1479
chr13	115169878	76541643	0.6646	1.6291
chr14	107349540	85910505	0.8003	1.8579
chr15	102531392	90716634	0.8848	1.958
chr16	90354753	93116399	1.0306	3.8942
chr17	81195210	80225701	0.9881	2.1683
chr18	78077248	72776622	0.9321	3.0257
chr19	59128983	51330489	0.8681	2.2625
chr20	63025520	70428013	1.1175	2.2596
chr21	48129895	35701051	0.7418	2.569
chr22	51304566	40633039	0.792	2.0068
chrMT	16571	5984184	361.1239	273.9846
chrX	155270560	150272883	0.9678	2.0315

chrY	59373566	4691571	0.079	2.7882

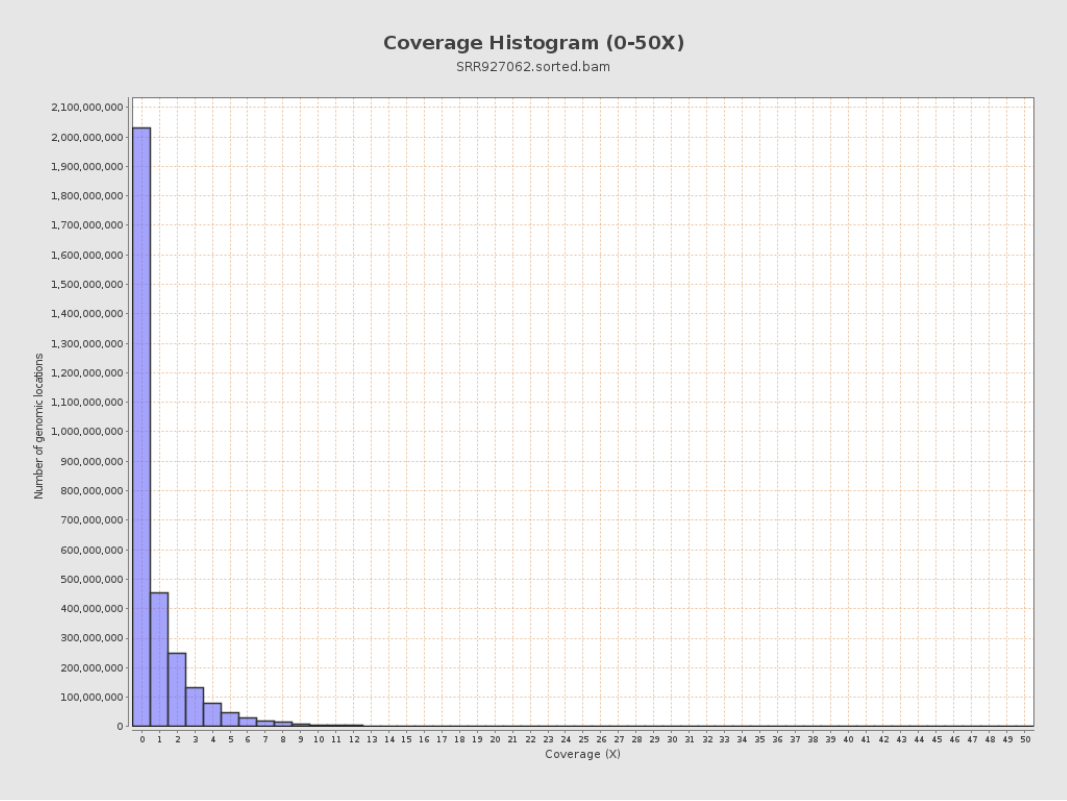
3. Results : Coverage across reference



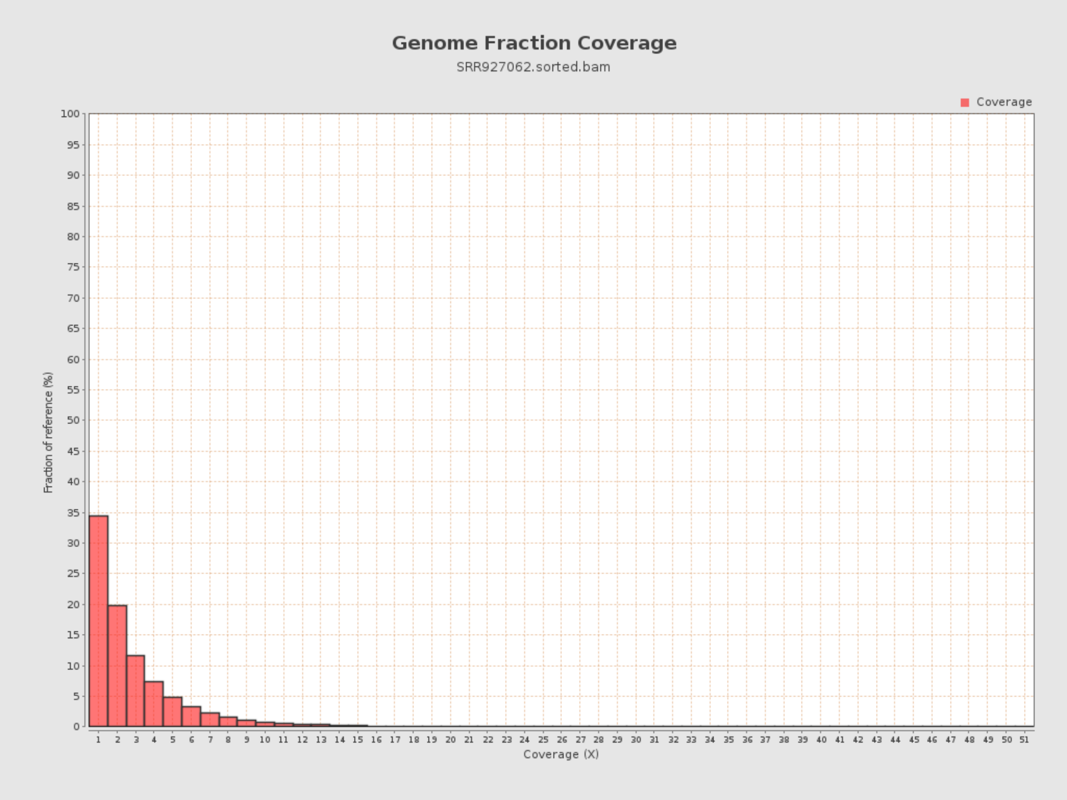
4. Results : Coverage Histogram



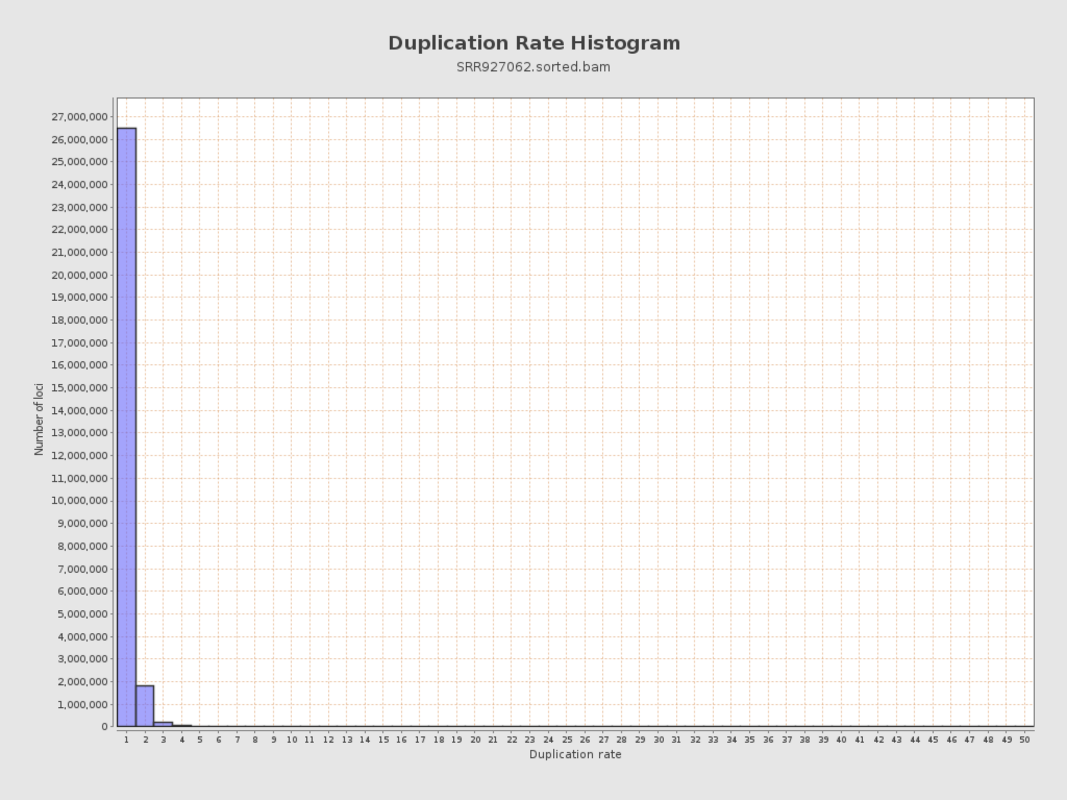
5. Results : Coverage Histogram (0-50X)



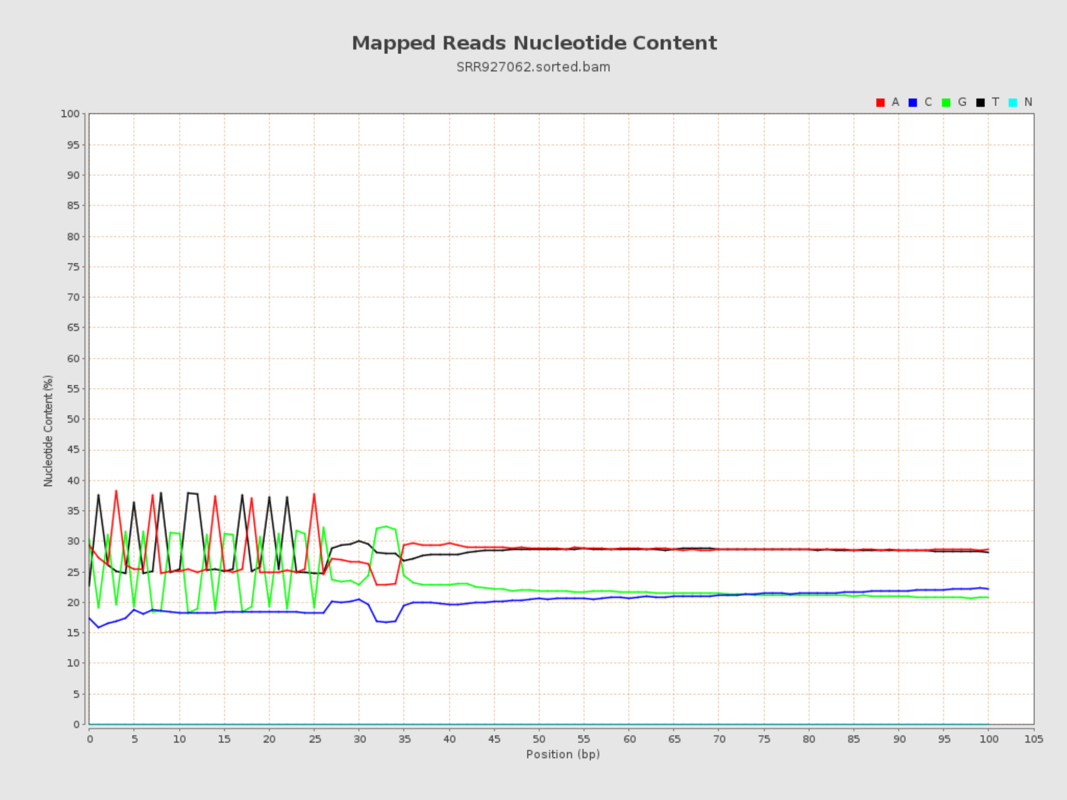
6. Results : Genome Fraction Coverage



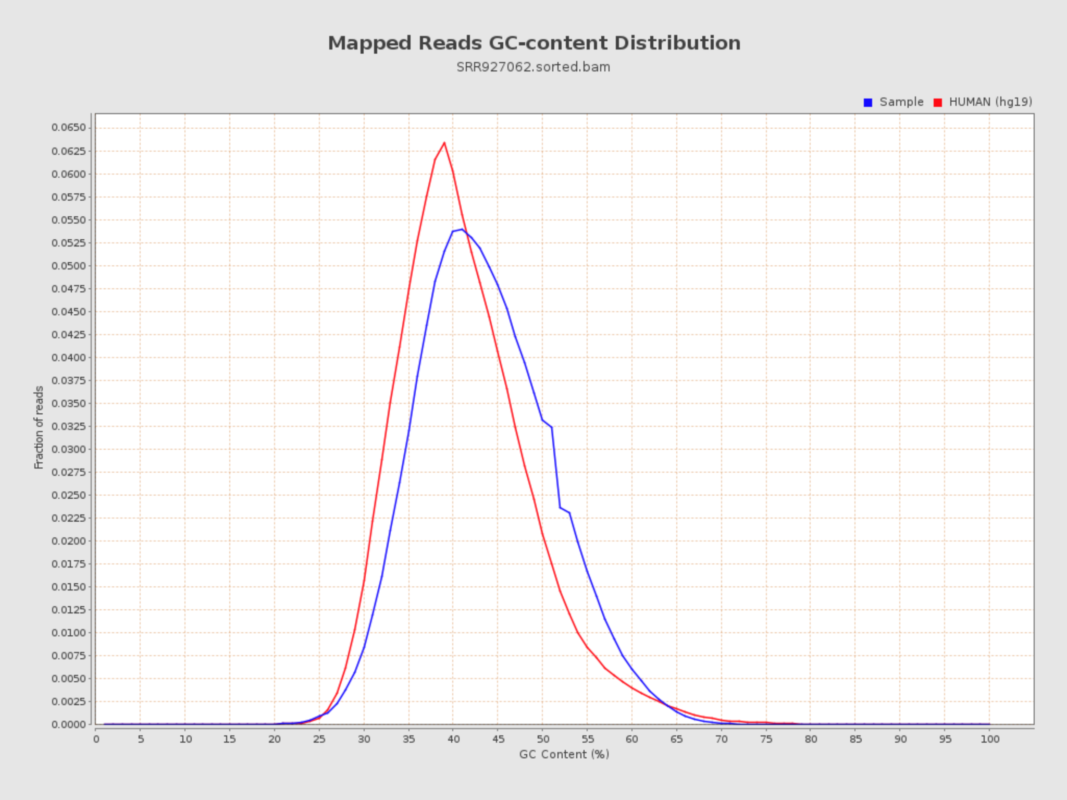
7. Results : Duplication Rate Histogram



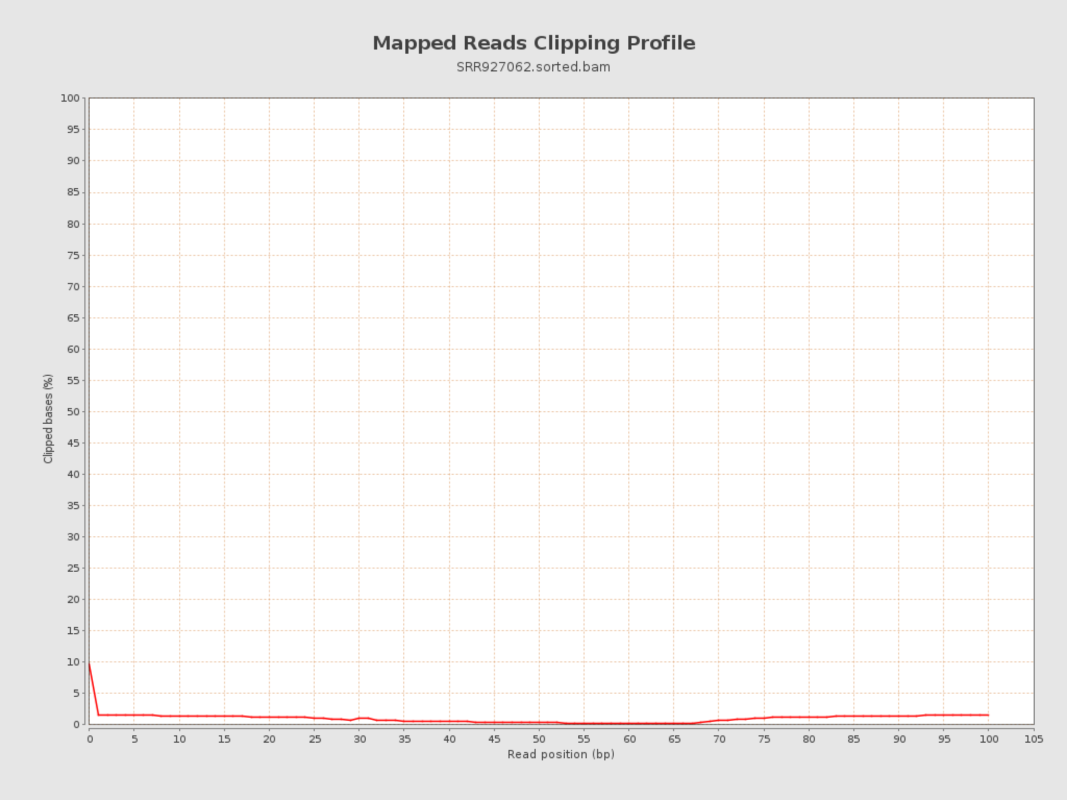
8. Results : Mapped Reads Nucleotide Content



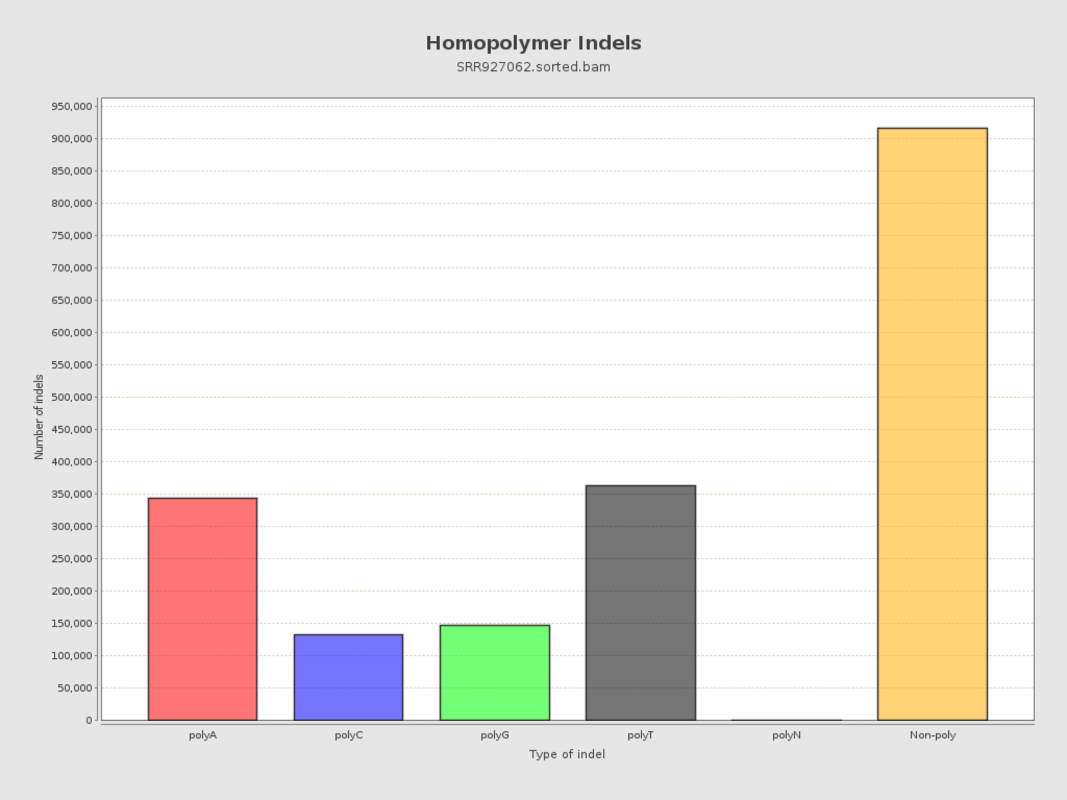
9. Results : Mapped Reads GC-content Distribution



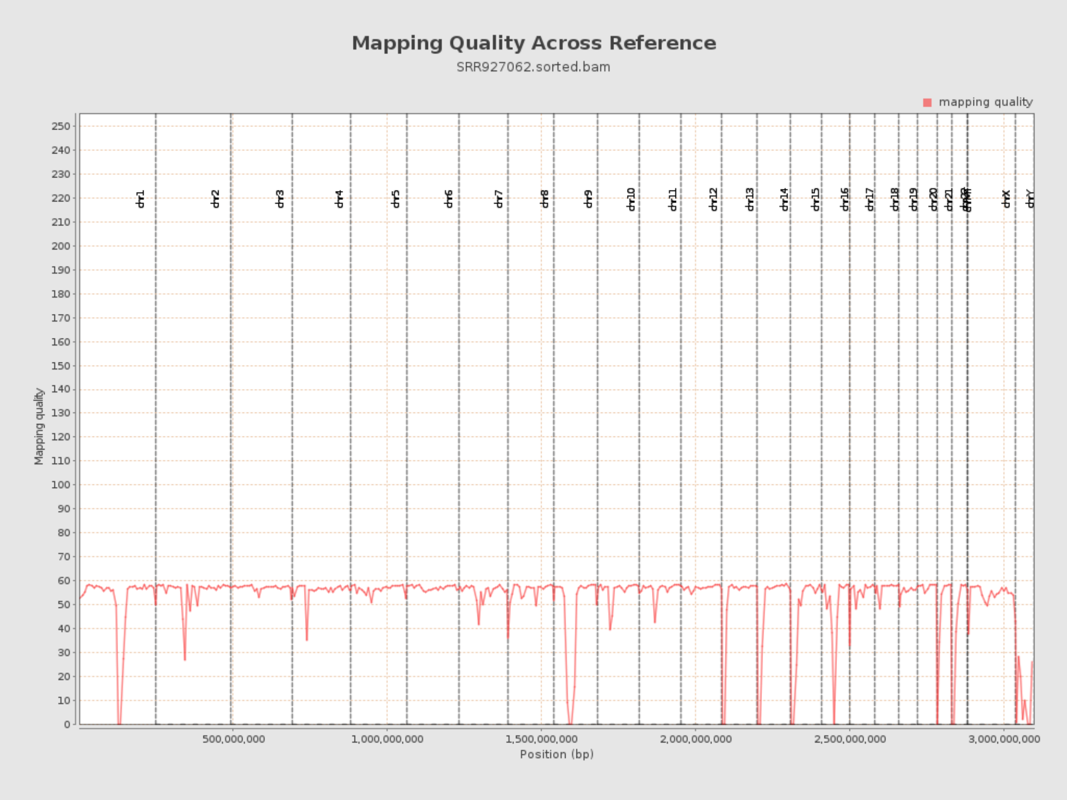
10. Results : Mapped Reads Clipping Profile



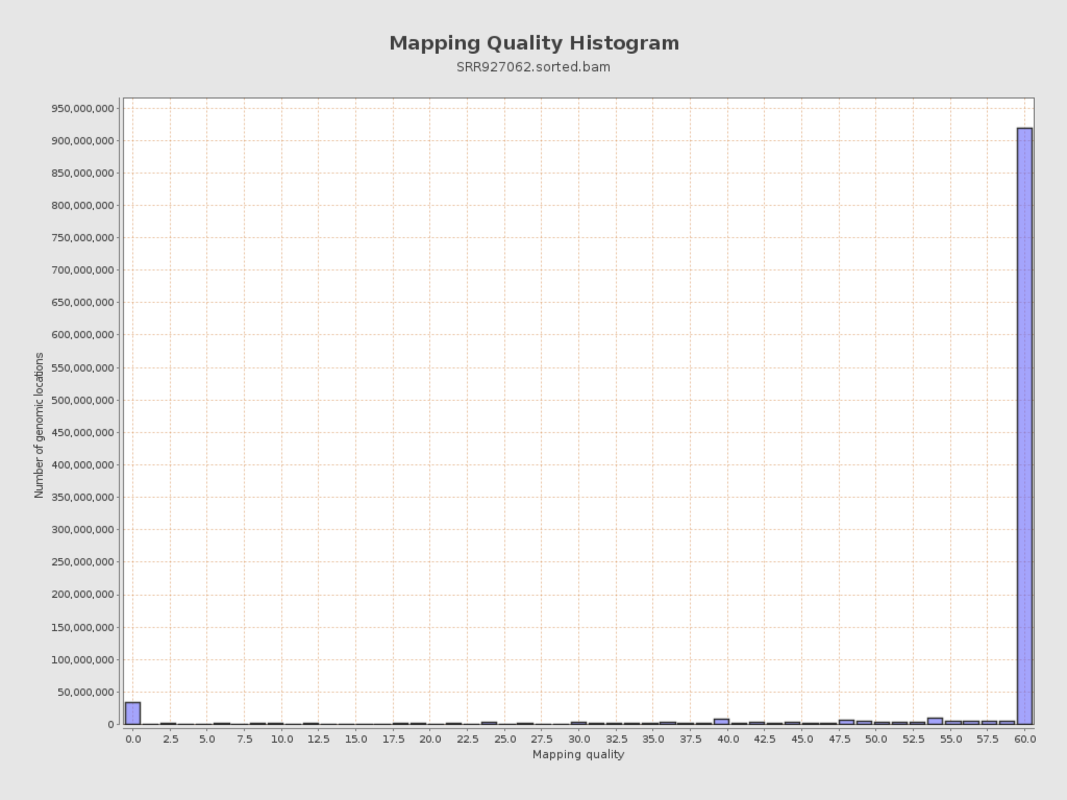
11. Results : Homopolymer Indels



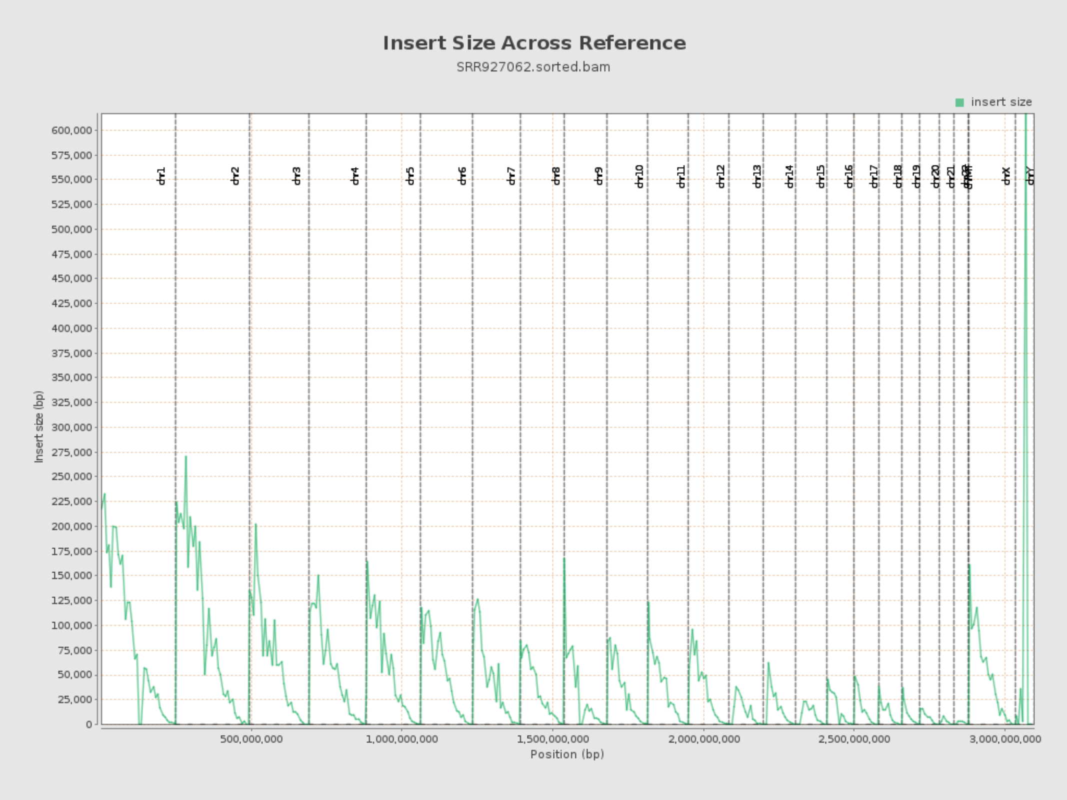
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram