Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/08 19:31:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779229.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_SRR1779229 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779229_1.fastq.gz SRR1779229_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 08 19:31:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779229.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	13,487,208
Mapped reads	13,215,151 / 97.98%
Unmapped reads	272,057 / 2.02%
Mapped paired reads	13,215,151 / 97.98%
Mapped reads, first in pair	6,637,071 / 49.21%
Mapped reads, second in pair	6,578,080 / 48.77%
Mapped reads, both in pair	13,139,662 / 97.42%
Mapped reads, singletons	75,489 / 0.56%
Secondary alignments	0
Supplementary alignments	34,410 / 0.26%
Read min/max/mean length	30 / 80 / 80.09
Duplicated reads (estimated)	160,716 / 1.19%
Duplication rate	1.15%
Clipped reads	433,603 / 3.21%

2.2. ACGT Content

Number/percentage of A's	321,828,783 / 30.6%
Number/percentage of C's	203,410,421 / 19.34%
Number/percentage of T's	318,988,801 / 30.33%
Number/percentage of G's	207,348,585 / 19.71%
Number/percentage of N's	199,240 / 0.02%

GC Percentage	39.05%

2.3. Coverage

Mean	0.3398
Standard Deviation	0.8801

2.4. Mapping Quality

Mean Mapping Quality	53.05

2.5. Insert size

Mean	55,321.56
Standard Deviation	2,195,818.25
P25/Median/P75	145 / 192 / 259

2.6. Mismatches and indels

General error rate	0.38%
Mismatches	3,868,194
Insertions	74,811
Mapped reads with at least one insertion	0.56%
Deletions	93,645
Mapped reads with at least one deletion	0.7%
Homopolymer indels	46.83%

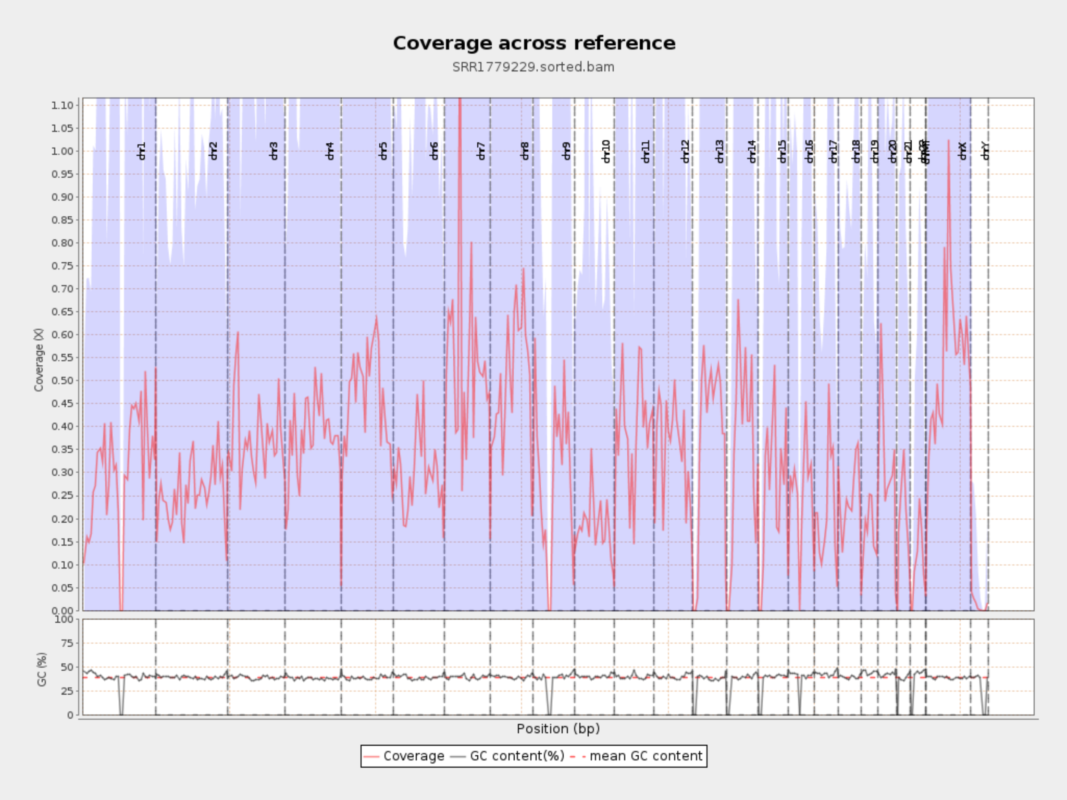
2.7. Chromosome stats

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

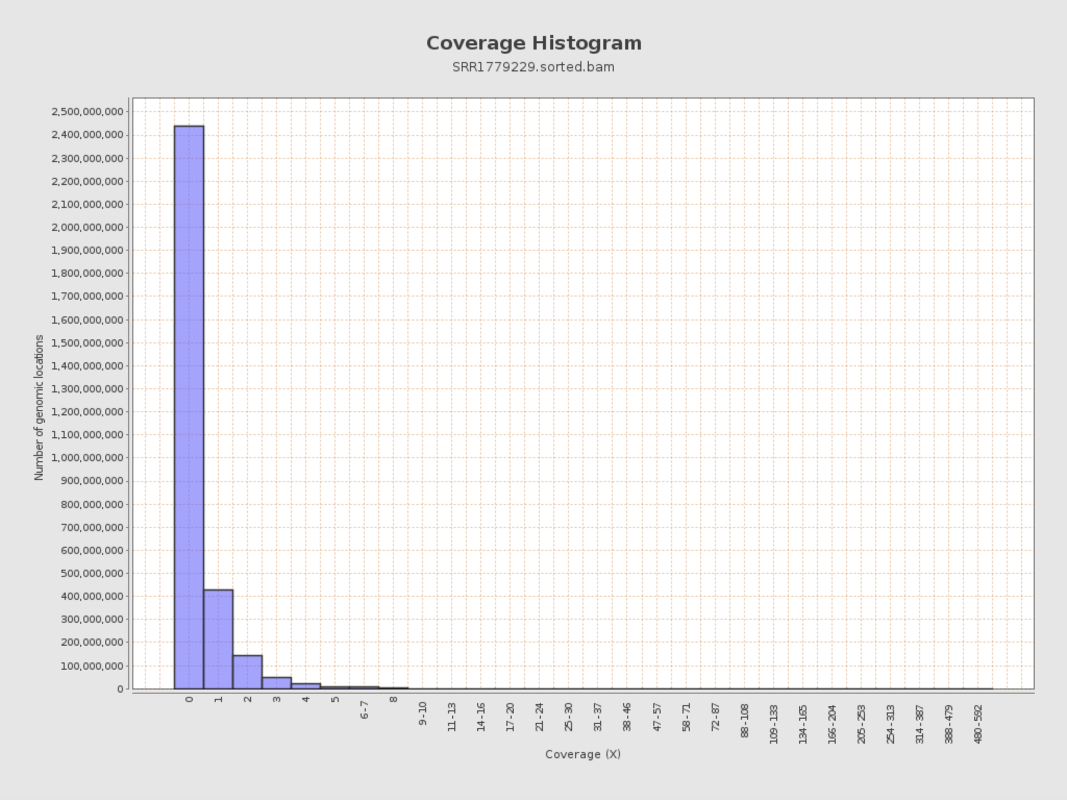
		bases	coverage	deviation
chr1	249250621	75046846	0.3011	0.9626
chr2	243199373	61986780	0.2549	0.6773
chr3	198022430	74522121	0.3763	0.8314
chr4	191154276	72833451	0.381	0.8359
chr5	180915260	83896025	0.4637	0.9254
chr6	171115067	51484776	0.3009	0.7462
chr7	159138663	88126909	0.5538	1.4116
chr8	146364022	74403978	0.5083	1.0206
chr9	141213431	41817188	0.2961	0.7734
chr10	135534747	25283798	0.1865	0.9828
chr11	135006516	53055855	0.393	0.8641
chr12	133851895	47375736	0.3539	0.8123
chr13	115169878	43918708	0.3813	0.8532
chr14	107349540	38140659	0.3553	0.8369
chr15	102531392	27395439	0.2672	0.717
chr16	90354753	22494100	0.249	0.6768
chr17	81195210	18138872	0.2234	0.6502
chr18	78077248	19436990	0.2489	0.6644
chr19	59128983	10309822	0.1744	0.6788
chr20	63025520	21570898	0.3423	0.832
chr21	48129895	9131488	0.1897	0.605
chr22	51304566	5630307	0.1097	0.4365
chrMT	16571	794	0.0479	0.2192
chrX	155270560	85269820	0.5492	1.1241

chrY	59373566	698211	0.0118	0.1532

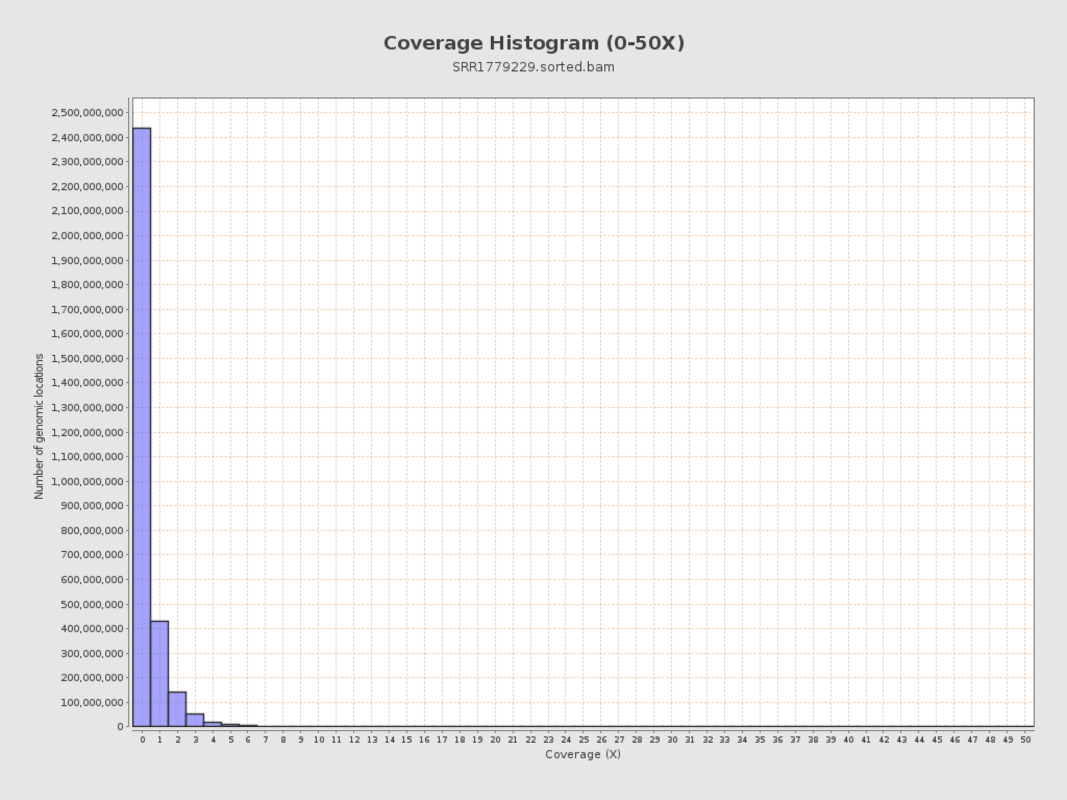
3. Results : Coverage across reference



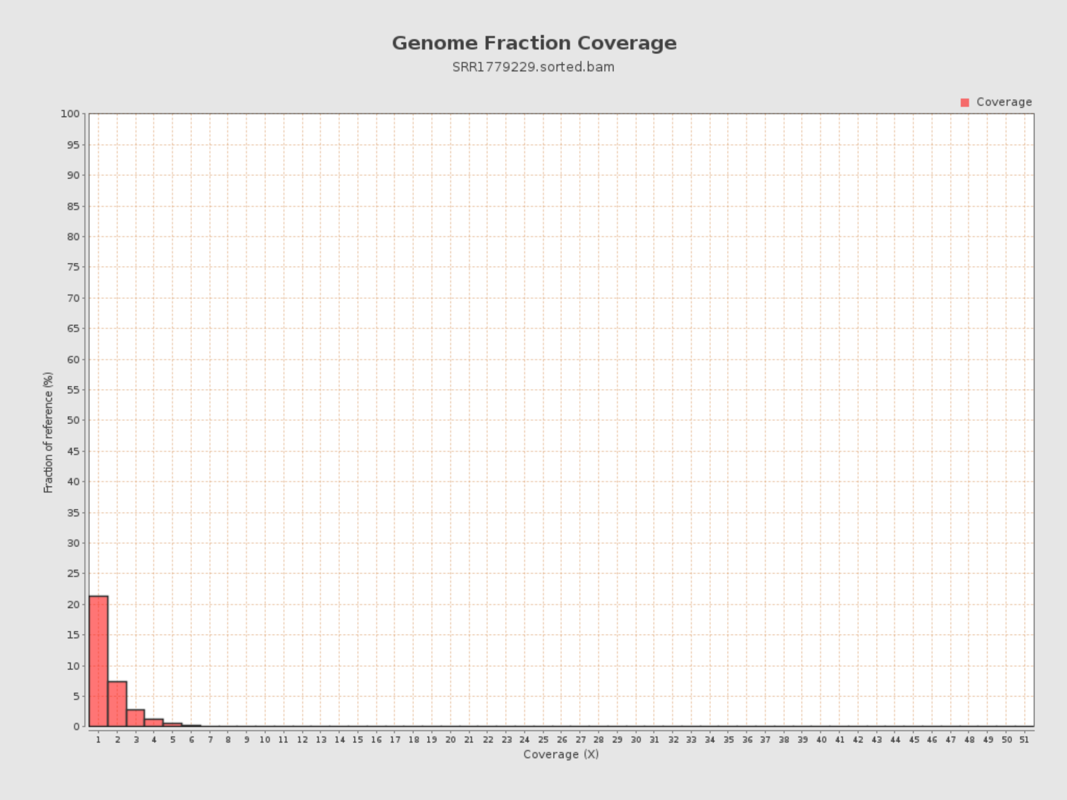
4. Results : Coverage Histogram



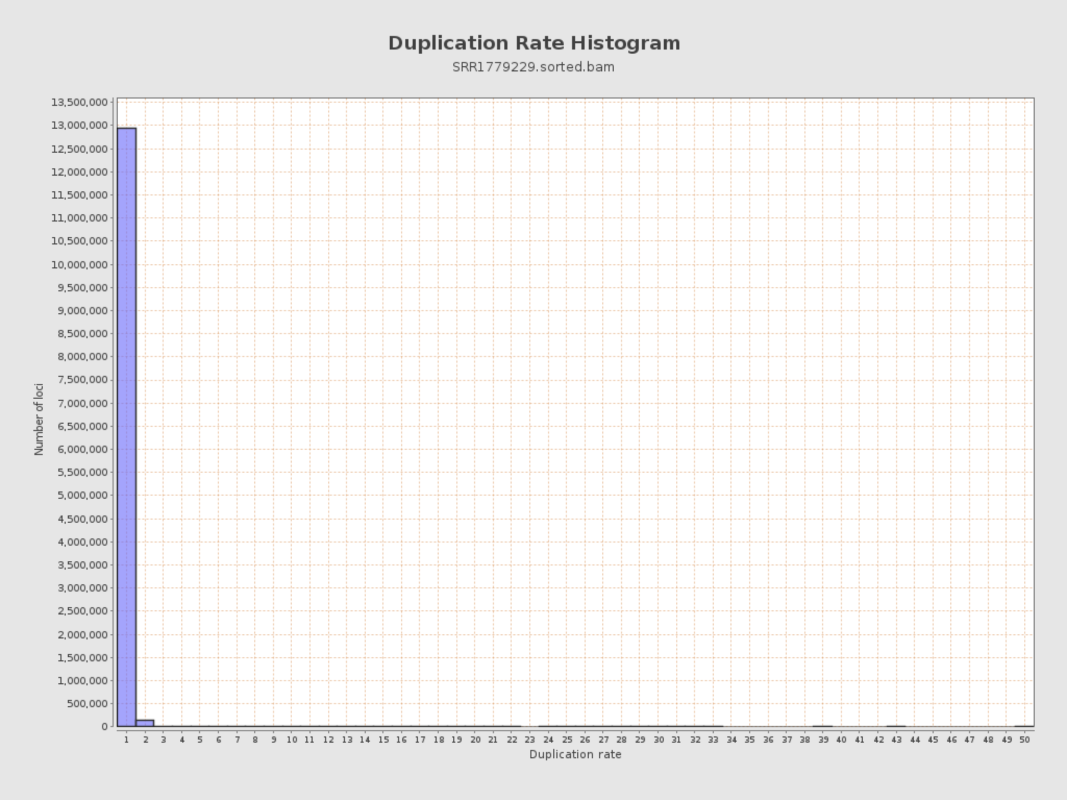
5. Results : Coverage Histogram (0-50X)



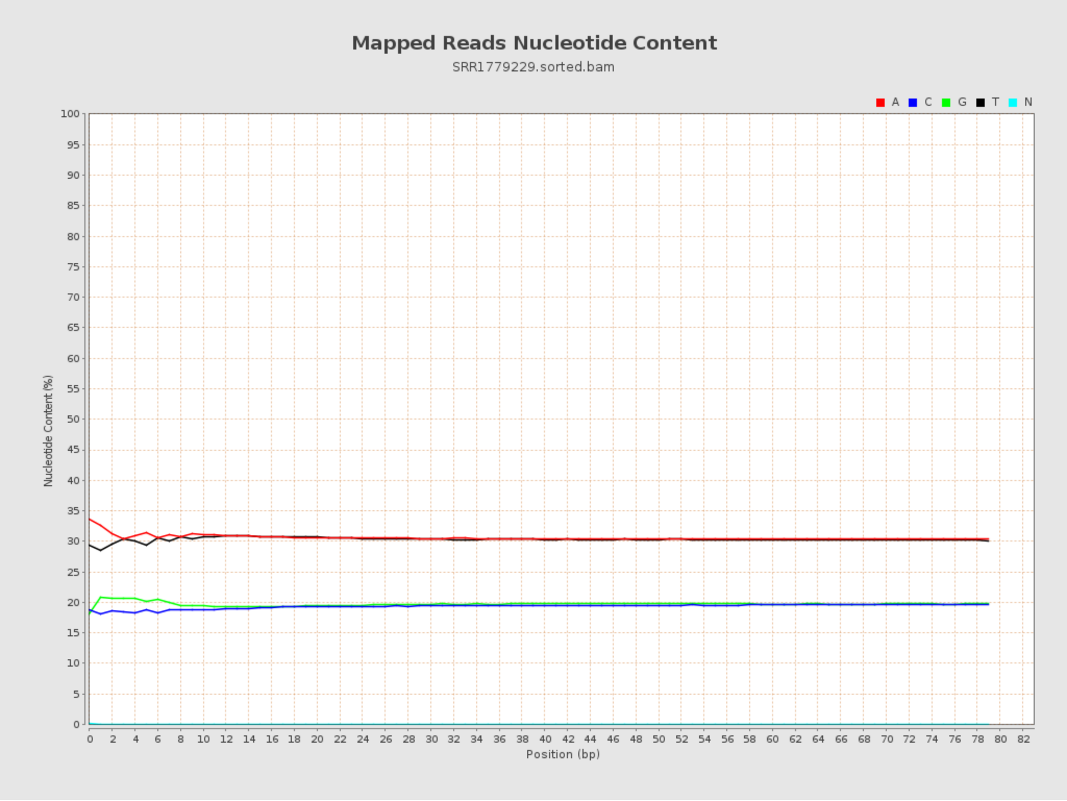
6. Results : Genome Fraction Coverage



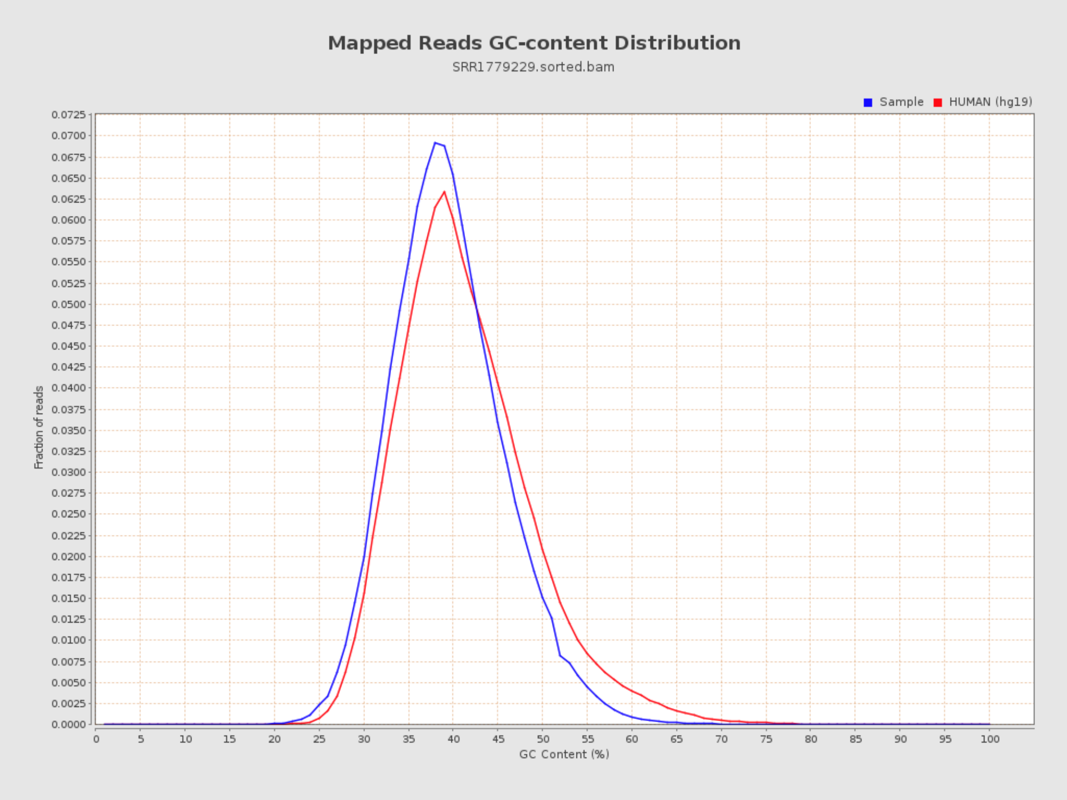
7. Results : Duplication Rate Histogram



8. Results : Mapped Reads Nucleotide Content



9. Results : Mapped Reads GC-content Distribution



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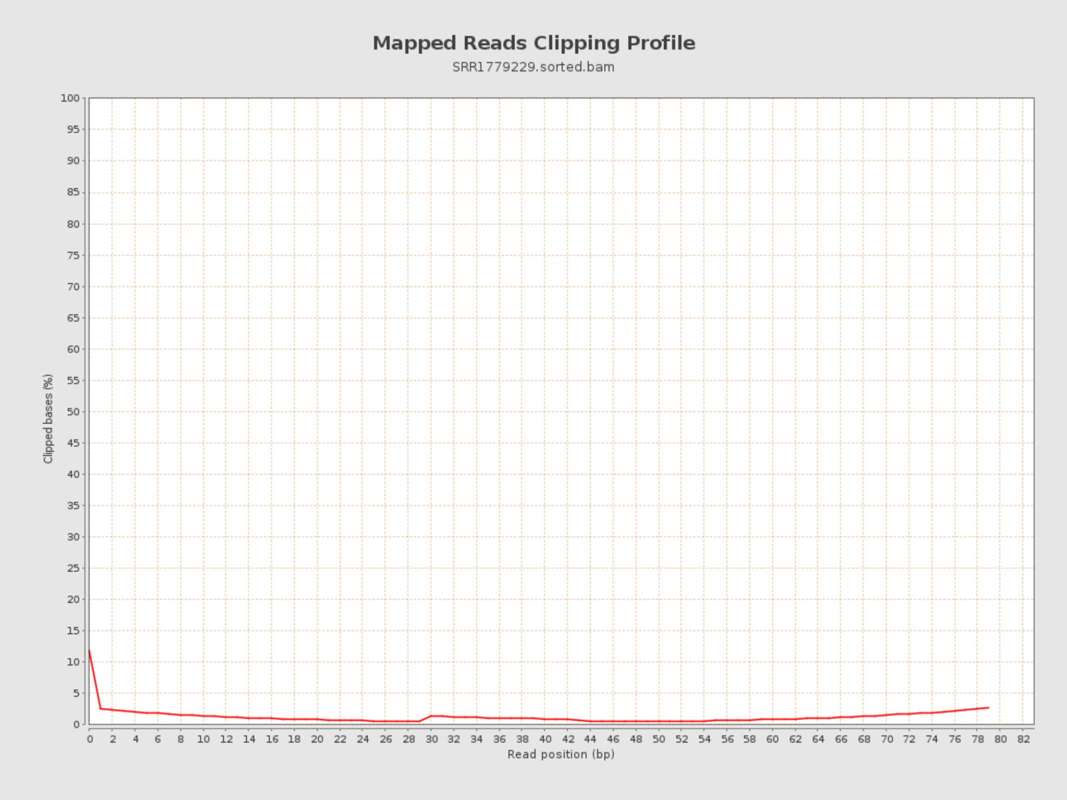
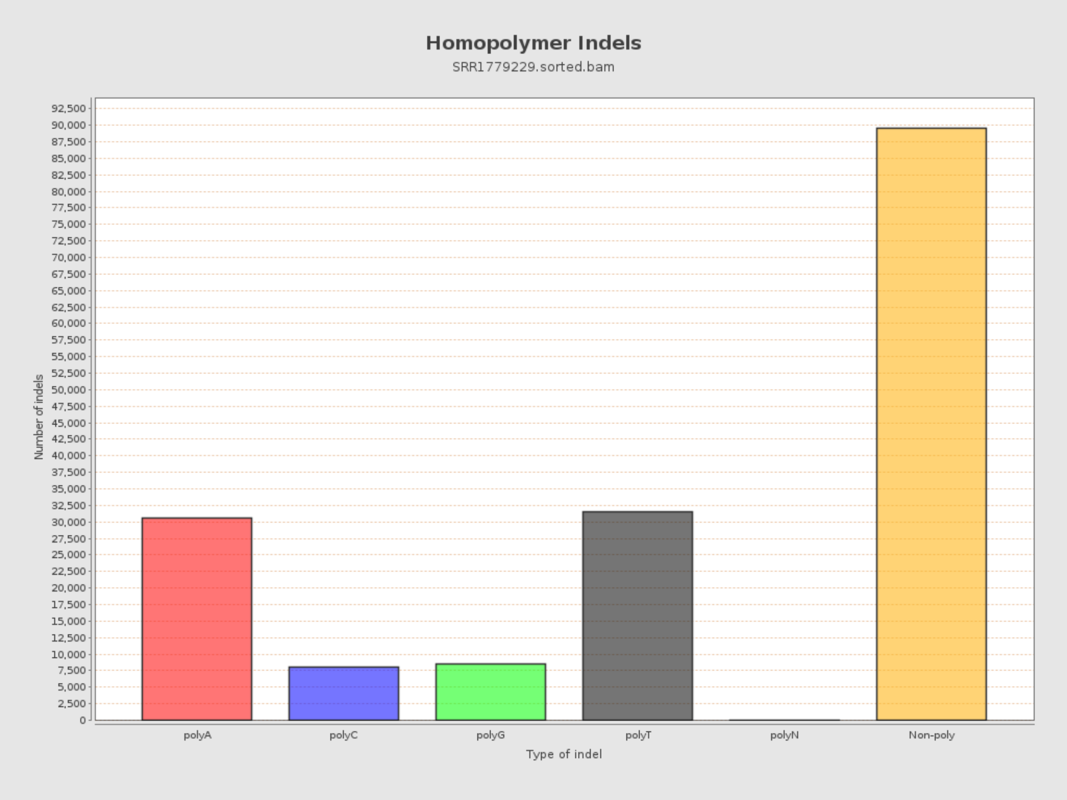
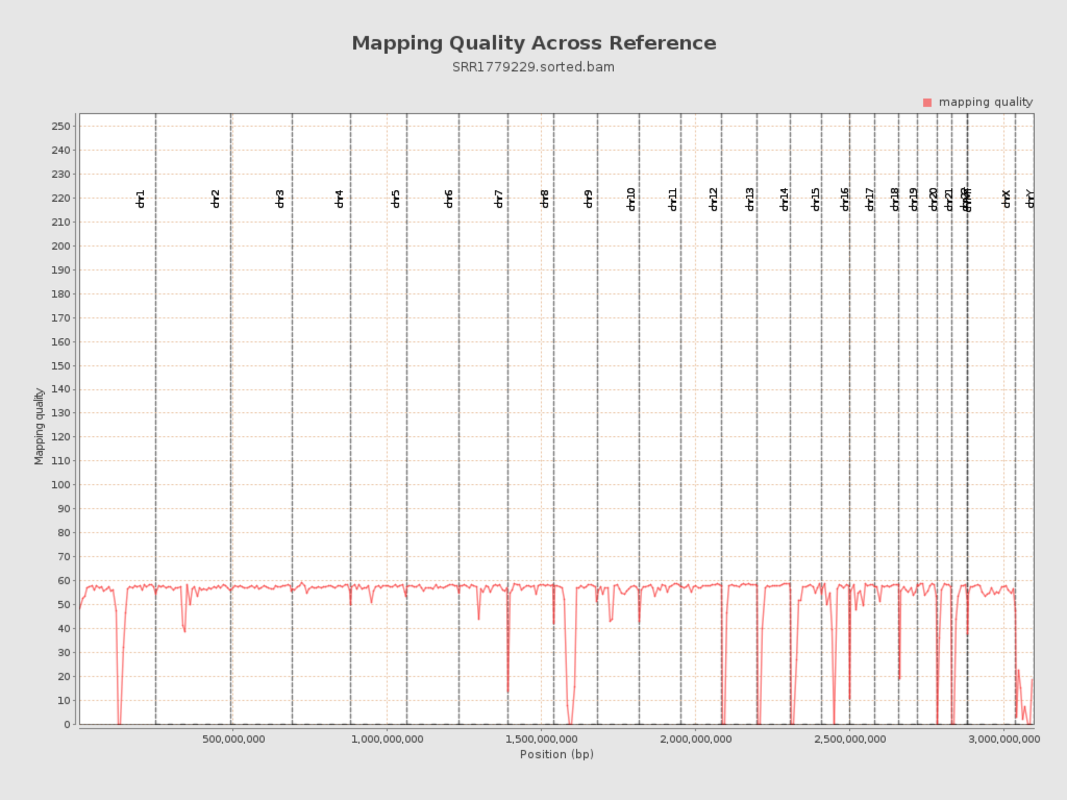
10. Results : Mapped Reads Clipping Profile



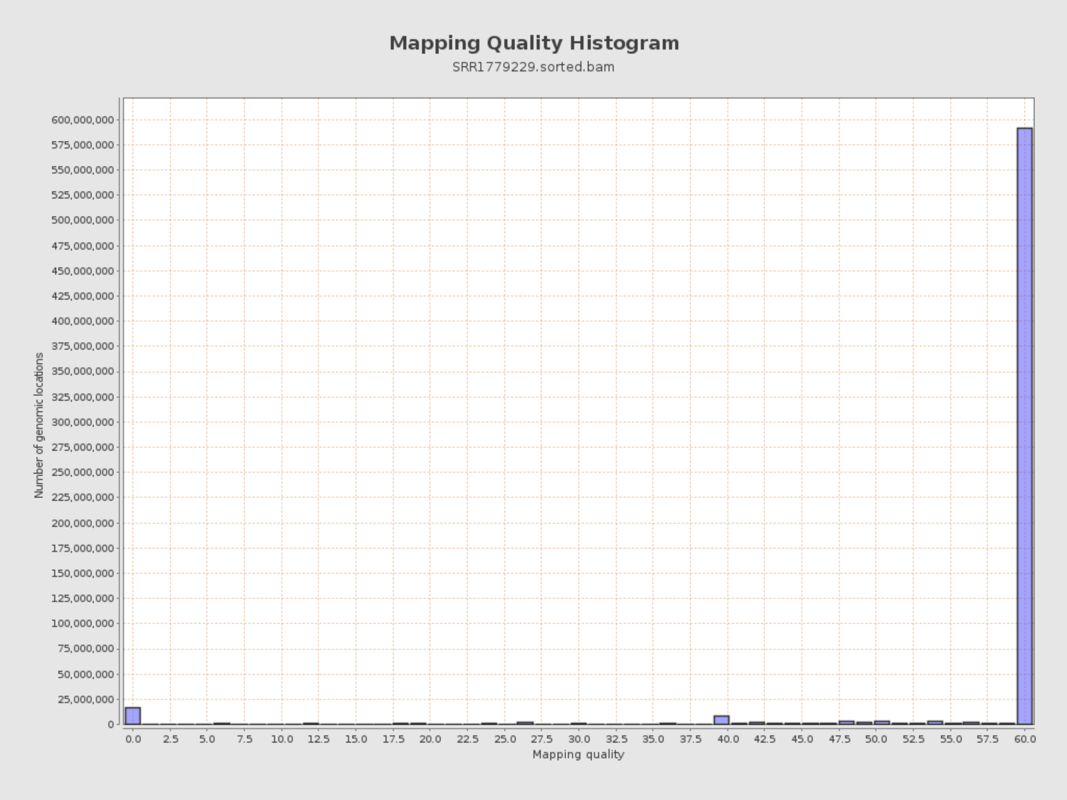
11. Results : Homopolymer Indels



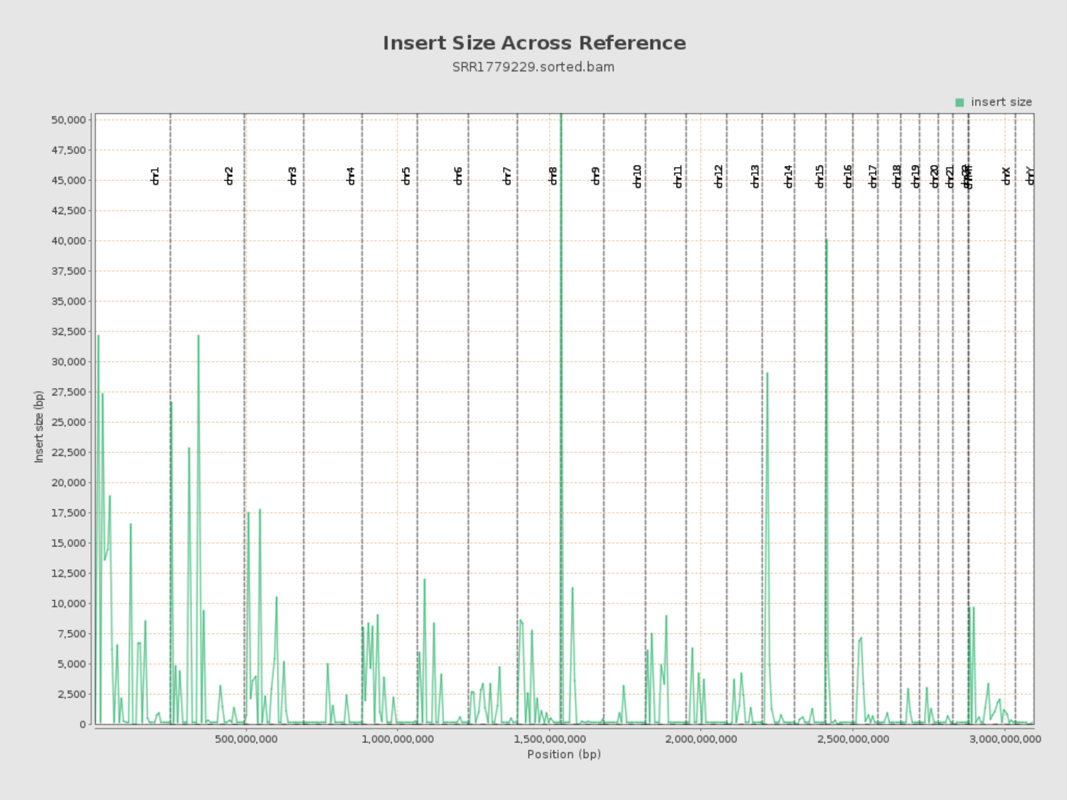
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram