Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/09 00:08:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779292.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_SRR1779292 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779292_1.fastq.gz SRR1779292_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 09 00:08:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779292.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	15,586,128
Mapped reads	15,253,233 / 97.86%
Unmapped reads	332,895 / 2.14%
Mapped paired reads	15,253,233 / 97.86%
Mapped reads, first in pair	7,670,639 / 49.21%
Mapped reads, second in pair	7,582,594 / 48.65%
Mapped reads, both in pair	15,147,412 / 97.19%
Mapped reads, singletons	105,821 / 0.68%
Secondary alignments	0
Supplementary alignments	39,840 / 0.26%
Read min/max/mean length	30 / 80 / 80.09
Duplicated reads (estimated)	294,928 / 1.89%
Duplication rate	1.72%
Clipped reads	496,589 / 3.19%

2.2. ACGT Content

Number/percentage of A's	370,870,490 / 30.55%
Number/percentage of C's	235,543,891 / 19.4%
Number/percentage of T's	367,223,068 / 30.25%
Number/percentage of G's	240,147,884 / 19.78%
Number/percentage of N's	233,546 / 0.02%

GC Percentage	39.18%

2.3. Coverage

Mean	0.3922
Standard Deviation	1.2283

2.4. Mapping Quality

Mean Mapping Quality	52.96

2.5. Insert size

Mean	55,464.87
Standard Deviation	2,237,525.38
P25/Median/P75	148 / 193 / 260

2.6. Mismatches and indels

General error rate	0.38%
Mismatches	4,435,993
Insertions	87,098
Mapped reads with at least one insertion	0.57%
Deletions	108,248
Mapped reads with at least one deletion	0.7%
Homopolymer indels	46.54%

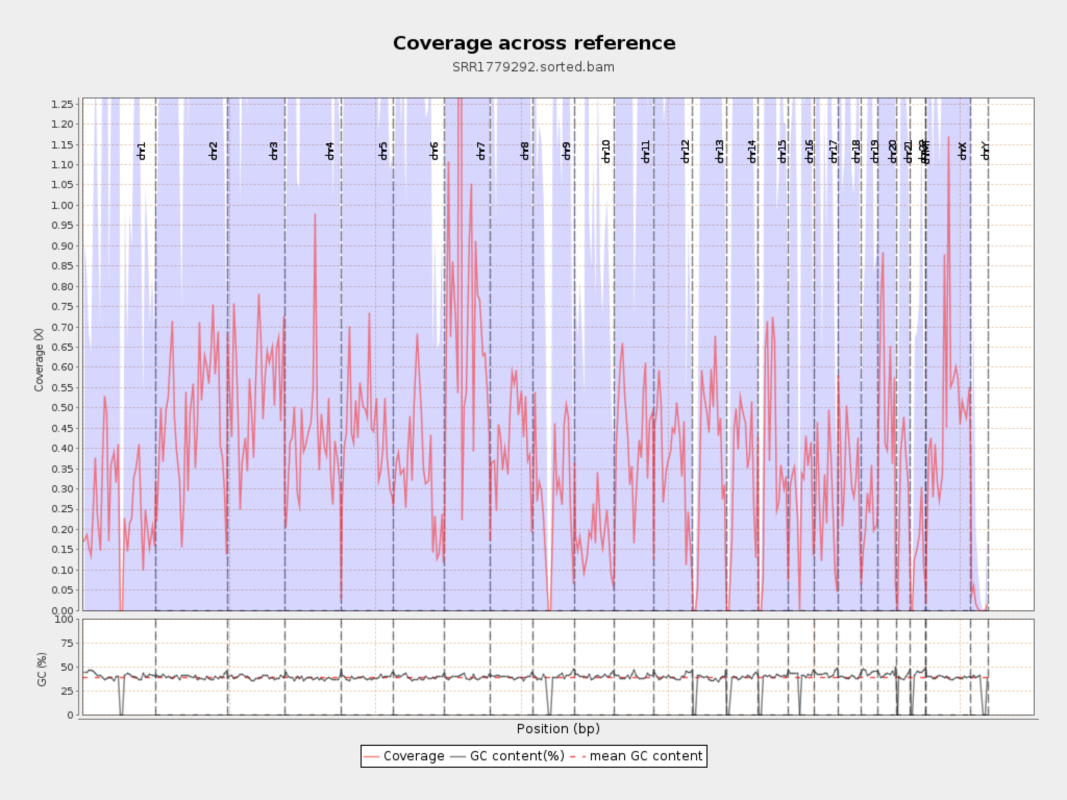
2.7. Chromosome stats

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

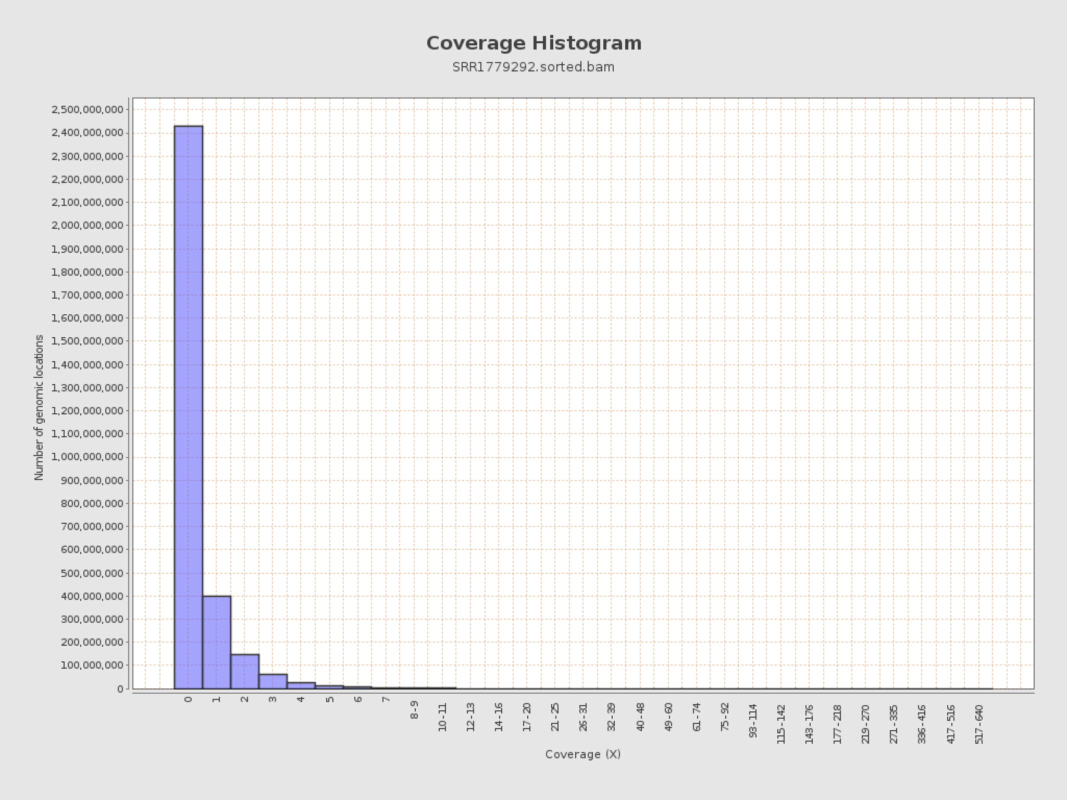
		bases	coverage	deviation
chr1	249250621	61715261	0.2476	0.943
chr2	243199373	115541063	0.4751	1.068
chr3	198022430	108662203	0.5487	1.148
chr4	191154276	80131027	0.4192	1.0089
chr5	180915260	80671117	0.4459	1.0131
chr6	171115067	59724999	0.349	0.9234
chr7	159138663	132004677	0.8295	3.3186
chr8	146364022	62643056	0.428	0.9926
chr9	141213431	40168479	0.2845	0.8262
chr10	135534747	24044989	0.1774	1.1778
chr11	135006516	58553429	0.4337	1.0206
chr12	133851895	50841788	0.3798	0.9407
chr13	115169878	44283833	0.3845	0.9596
chr14	107349540	36327711	0.3384	0.9582
chr15	102531392	36992951	0.3608	0.9629
chr16	90354753	25463914	0.2818	0.7856
chr17	81195210	22115344	0.2724	0.802
chr18	78077248	27711702	0.3549	0.8873
chr19	59128983	13444161	0.2274	0.8186
chr20	63025520	34255312	0.5435	1.1867
chr21	48129895	13760050	0.2859	0.7708
chr22	51304566	6978519	0.136	0.5295
chrMT	16571	240	0.0145	0.1442
chrX	155270560	77249608	0.4975	1.2103

chrY	59373566	959098	0.0162	0.2774

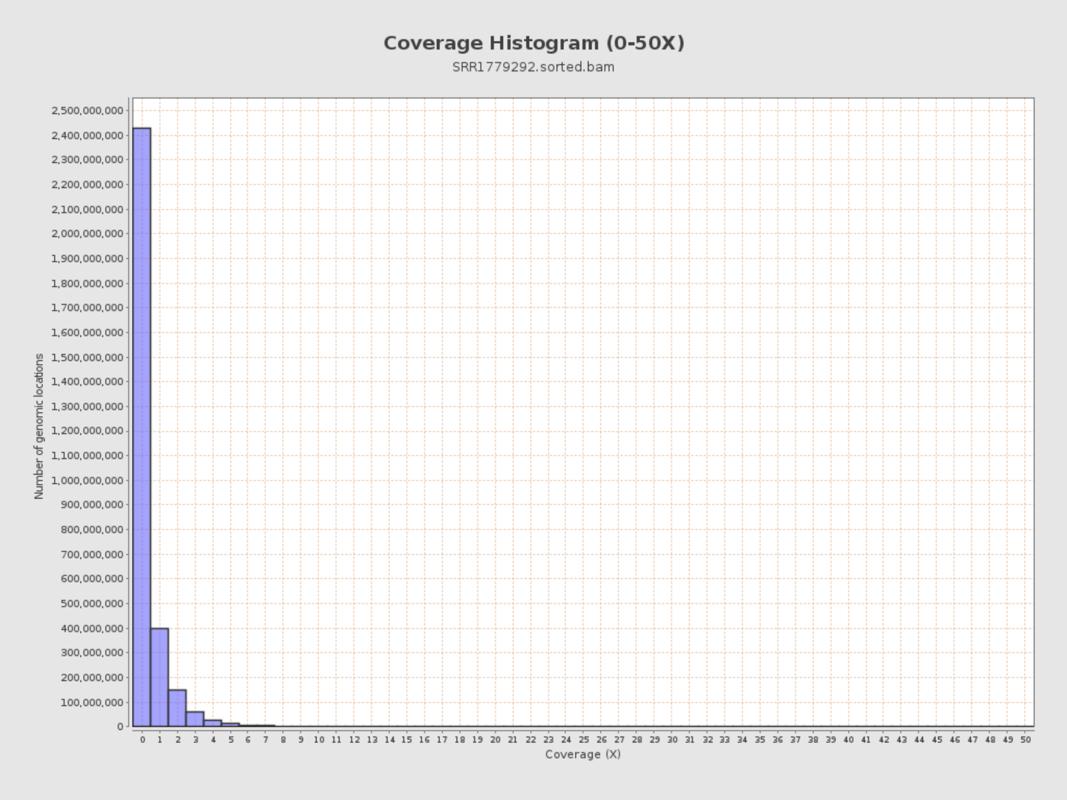
3. Results : Coverage across reference



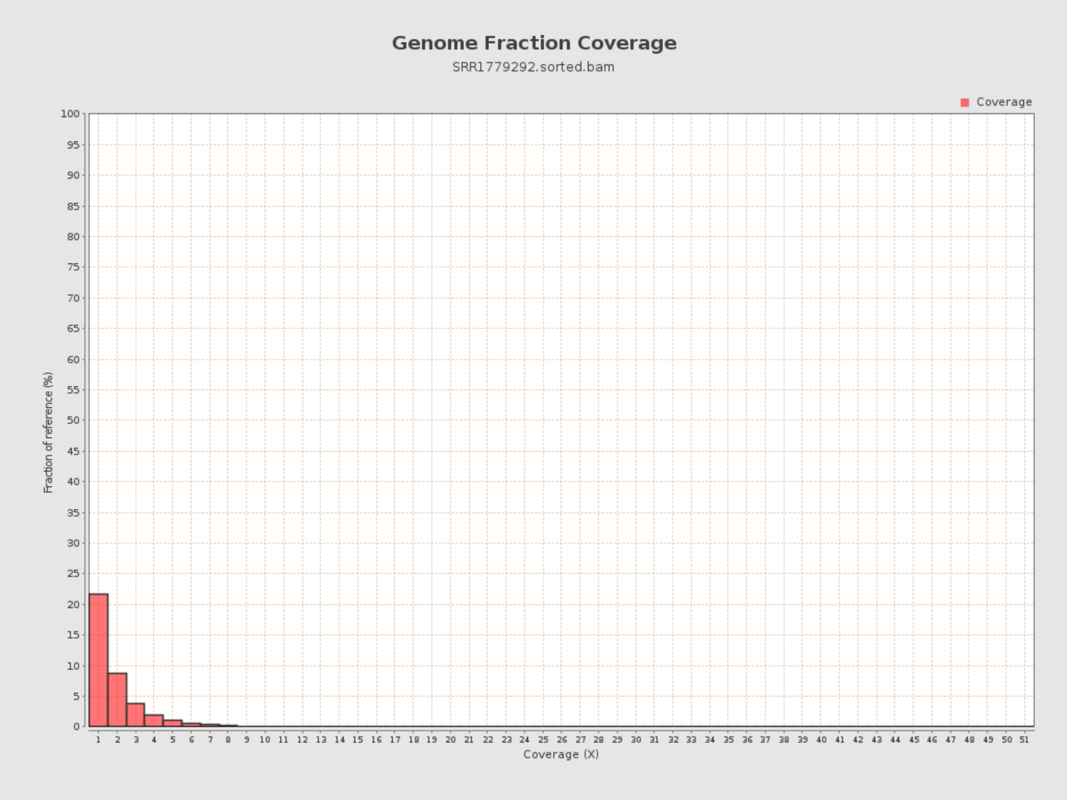
4. Results : Coverage Histogram



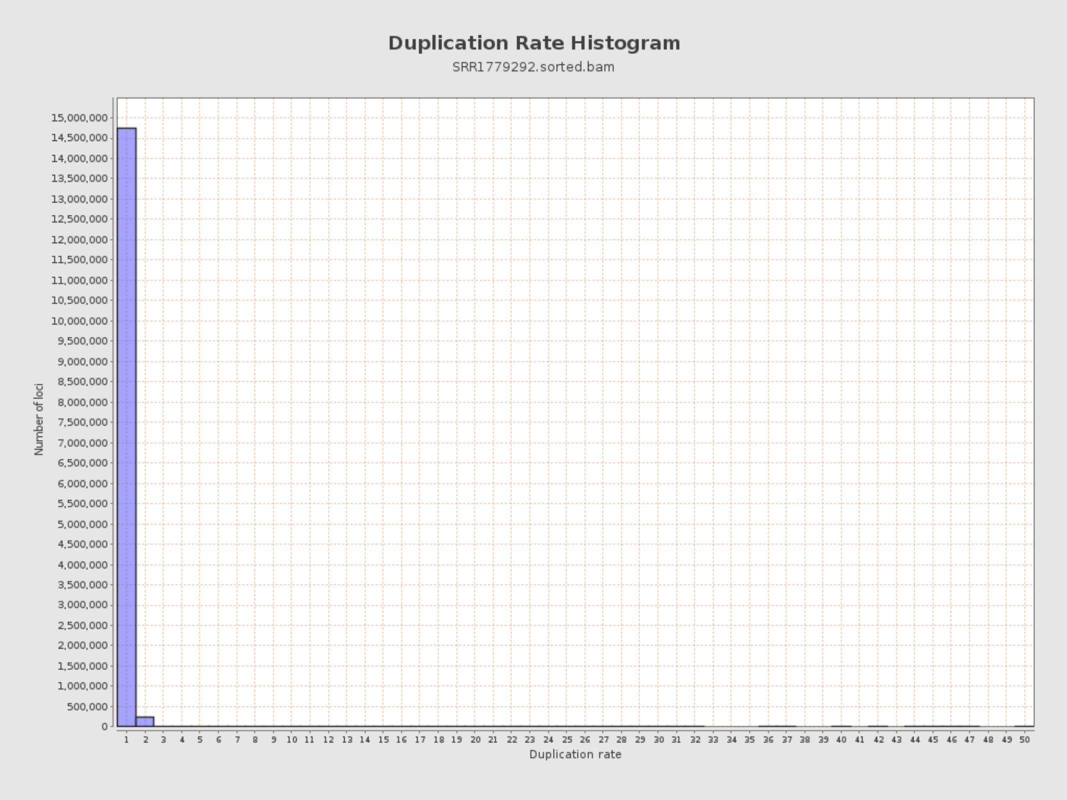
5. Results : Coverage Histogram (0-50X)



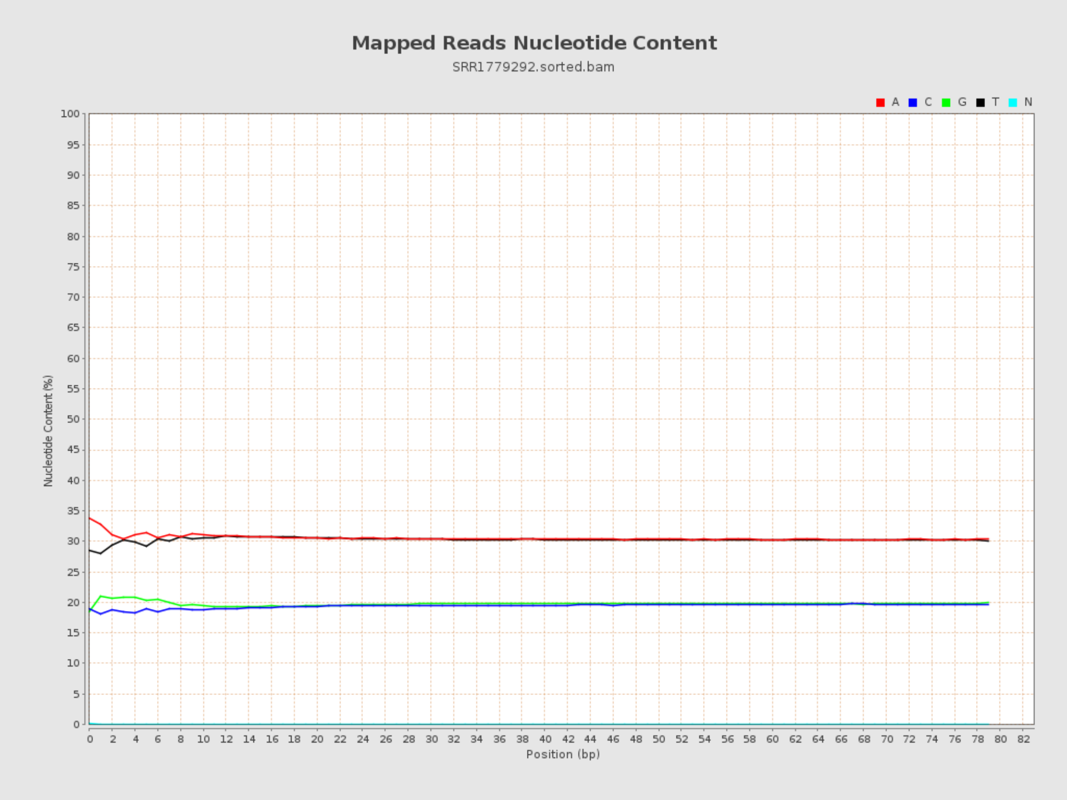
6. Results : Genome Fraction Coverage



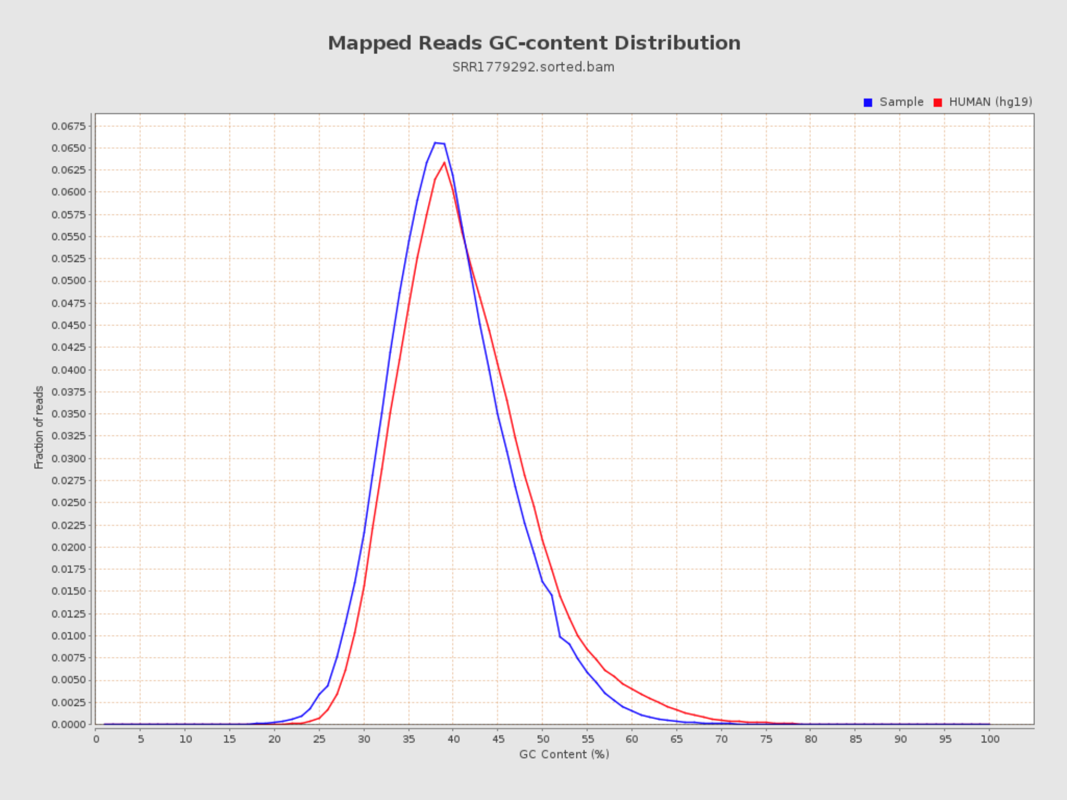
7. Results : Duplication Rate Histogram



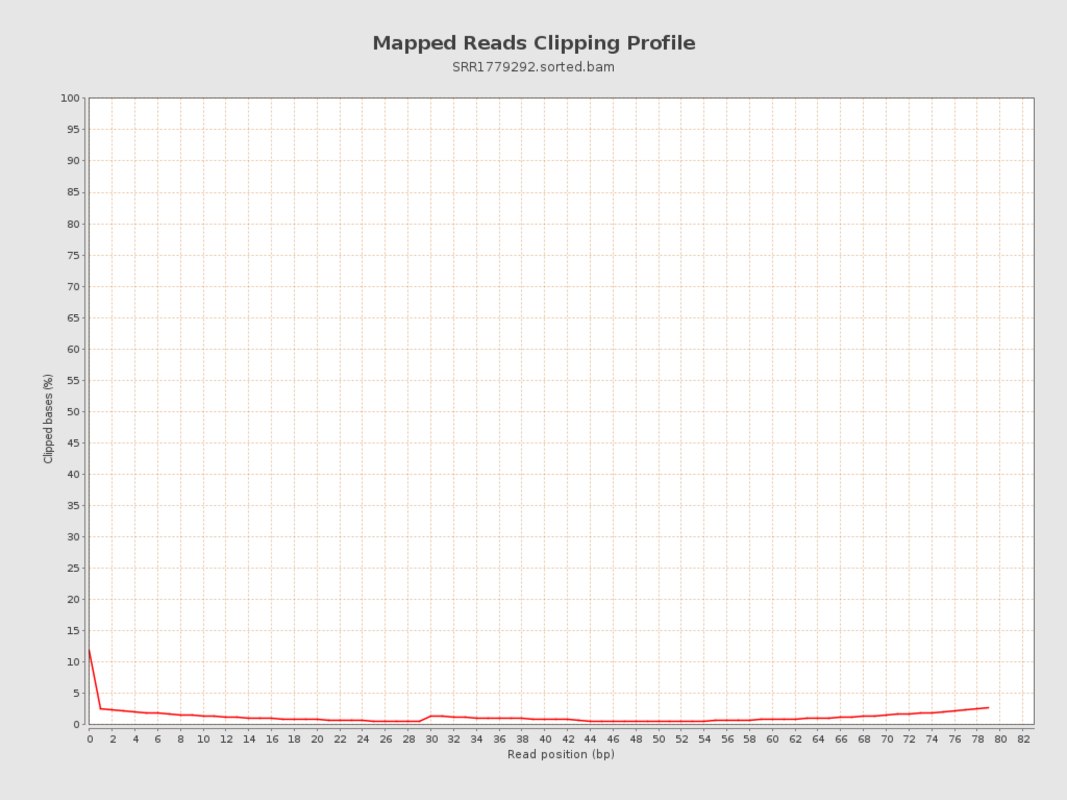
8. Results : Mapped Reads Nucleotide Content



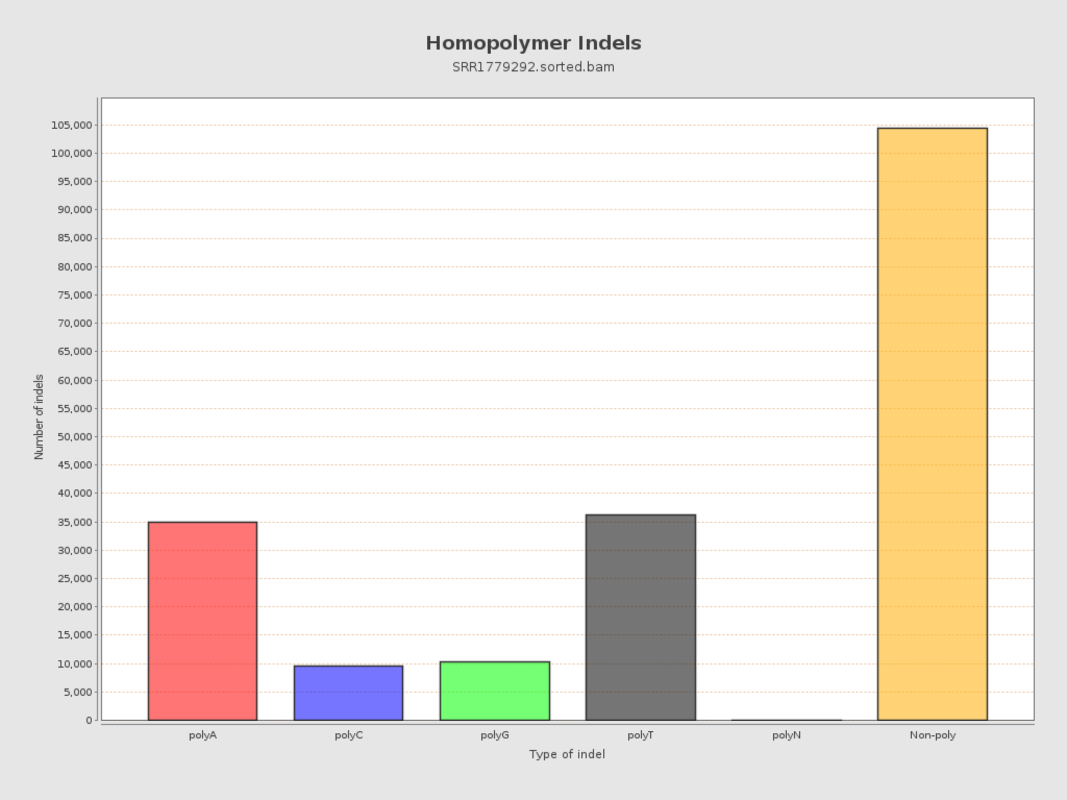
9. Results : Mapped Reads GC-content Distribution



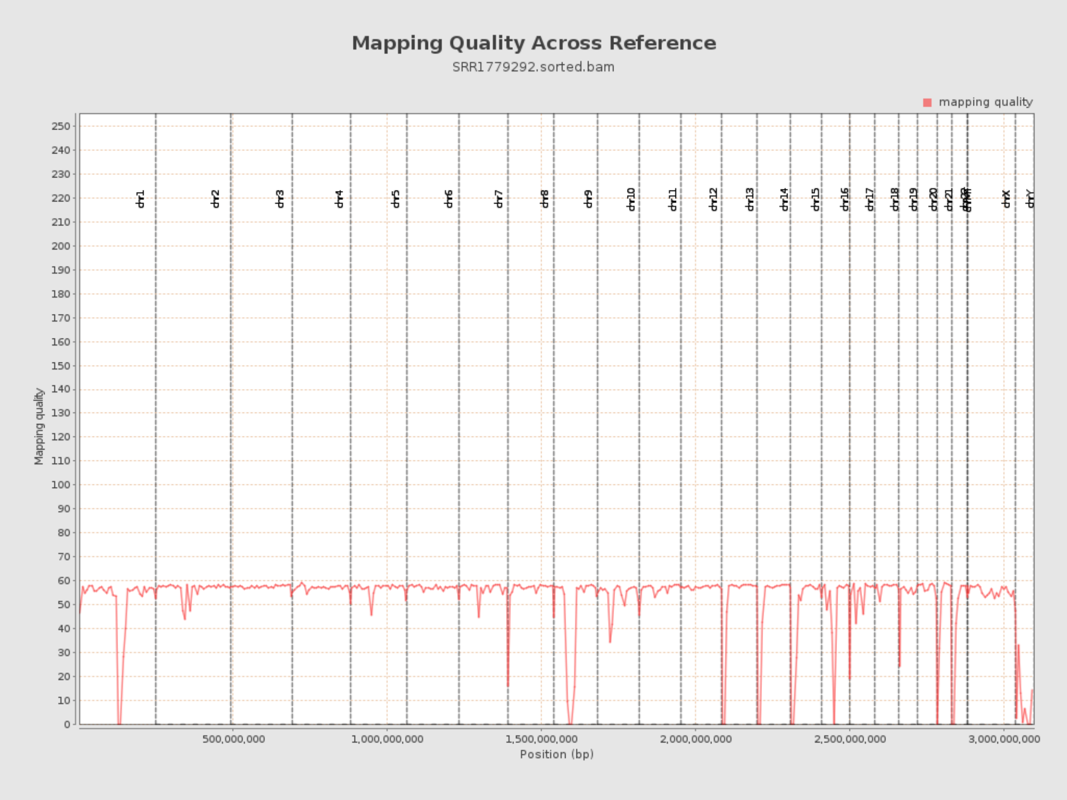
10. Results : Mapped Reads Clipping Profile



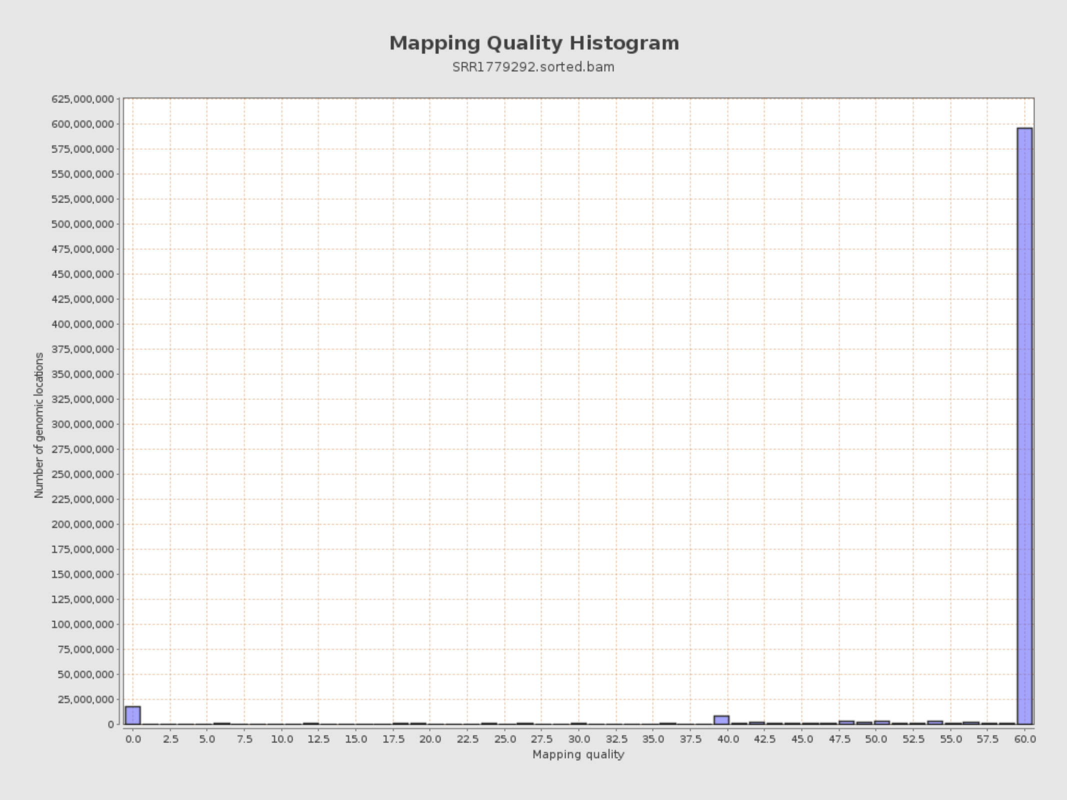
11. Results : Homopolymer Indels



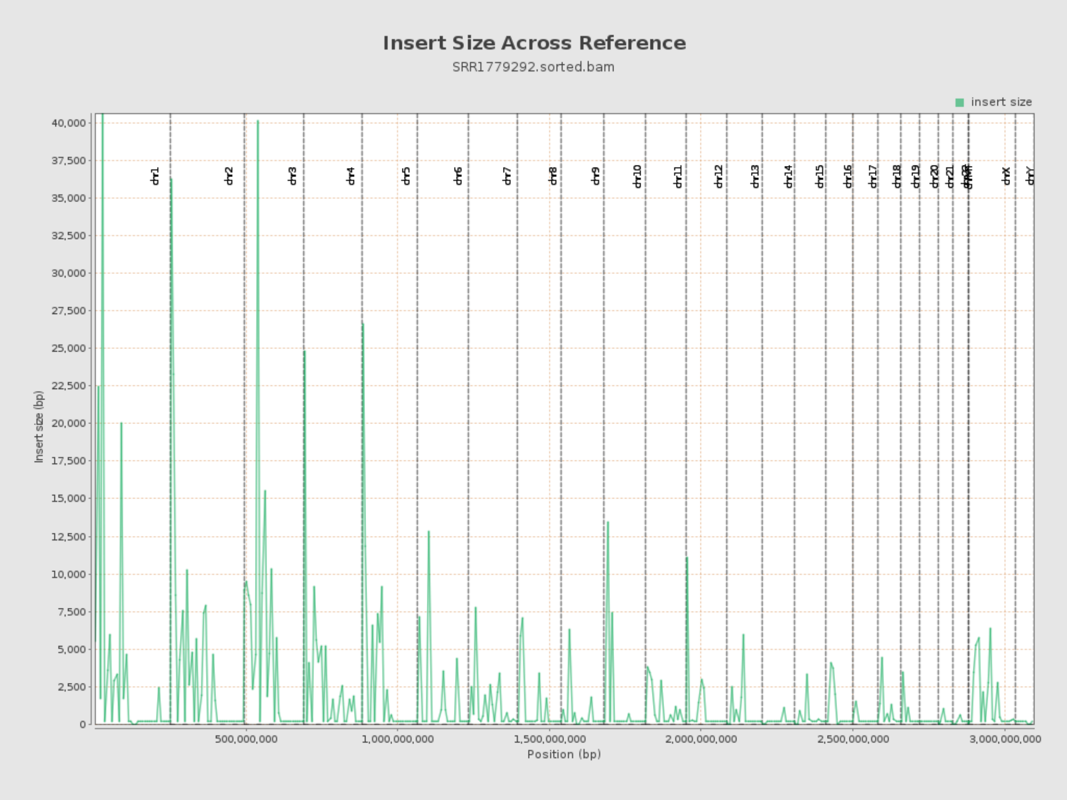
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram