Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/10 12:29:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779369.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_SRR1779369 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779369_1.fastq.gz SRR1779369_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 10 12:29:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779369.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	12,465,586
Mapped reads	11,944,353 / 95.82%
Unmapped reads	521,233 / 4.18%
Mapped paired reads	11,944,353 / 95.82%
Mapped reads, first in pair	6,012,449 / 48.23%
Mapped reads, second in pair	5,931,904 / 47.59%
Mapped reads, both in pair	11,838,722 / 94.97%
Mapped reads, singletons	105,631 / 0.85%
Secondary alignments	0
Supplementary alignments	62,569 / 0.5%
Read min/max/mean length	30 / 80 / 80.18
Duplicated reads (estimated)	913,890 / 7.33%
Duplication rate	7.23%
Clipped reads	1,318,309 / 10.58%

2.2. ACGT Content

Number/percentage of A's	278,137,519 / 29.57%
Number/percentage of C's	191,624,756 / 20.37%
Number/percentage of T's	276,030,590 / 29.34%
Number/percentage of G's	194,700,547 / 20.7%
Number/percentage of N's	201,020 / 0.02%

GC Percentage	41.07%

2.3. Coverage

Mean	0.3039
Standard Deviation	1.7422

2.4. Mapping Quality

Mean Mapping Quality	49.13

2.5. Insert size

Mean	59,216.77
Standard Deviation	2,358,989.76
P25/Median/P75	99 / 128 / 169

2.6. Mismatches and indels

General error rate	0.35%
Mismatches	3,087,619
Insertions	105,538
Mapped reads with at least one insertion	0.87%
Deletions	111,489
Mapped reads with at least one deletion	0.92%
Homopolymer indels	46.89%

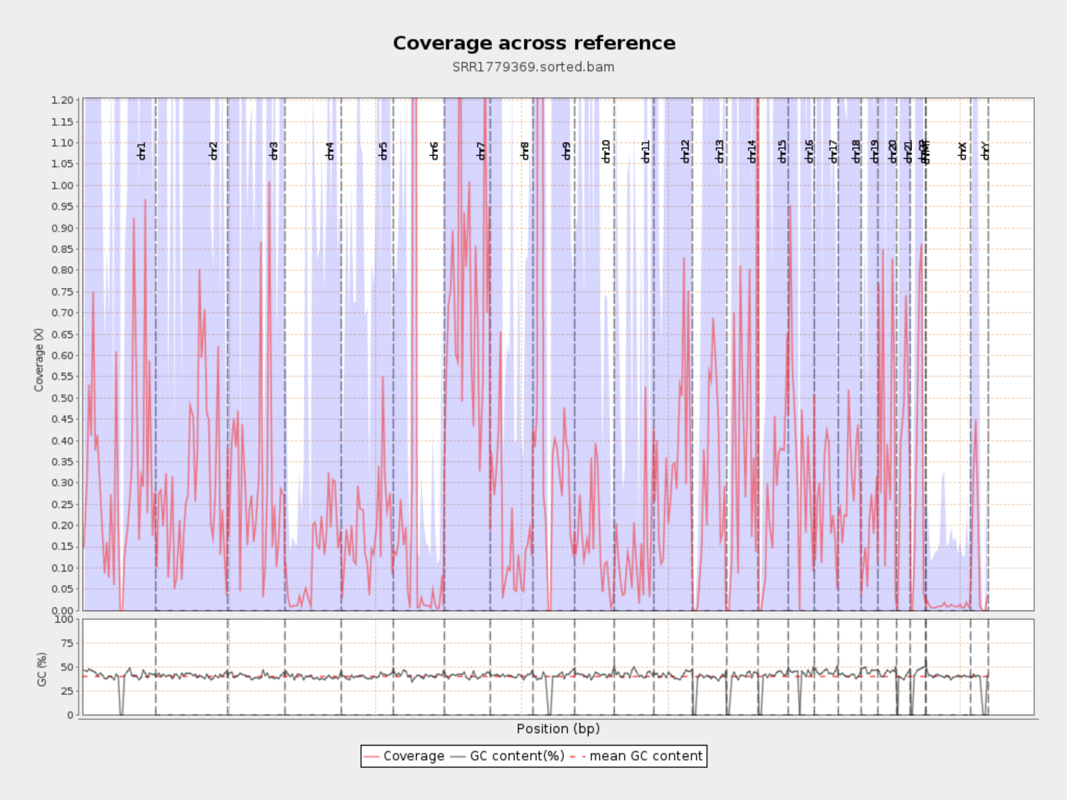
2.7. Chromosome stats

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

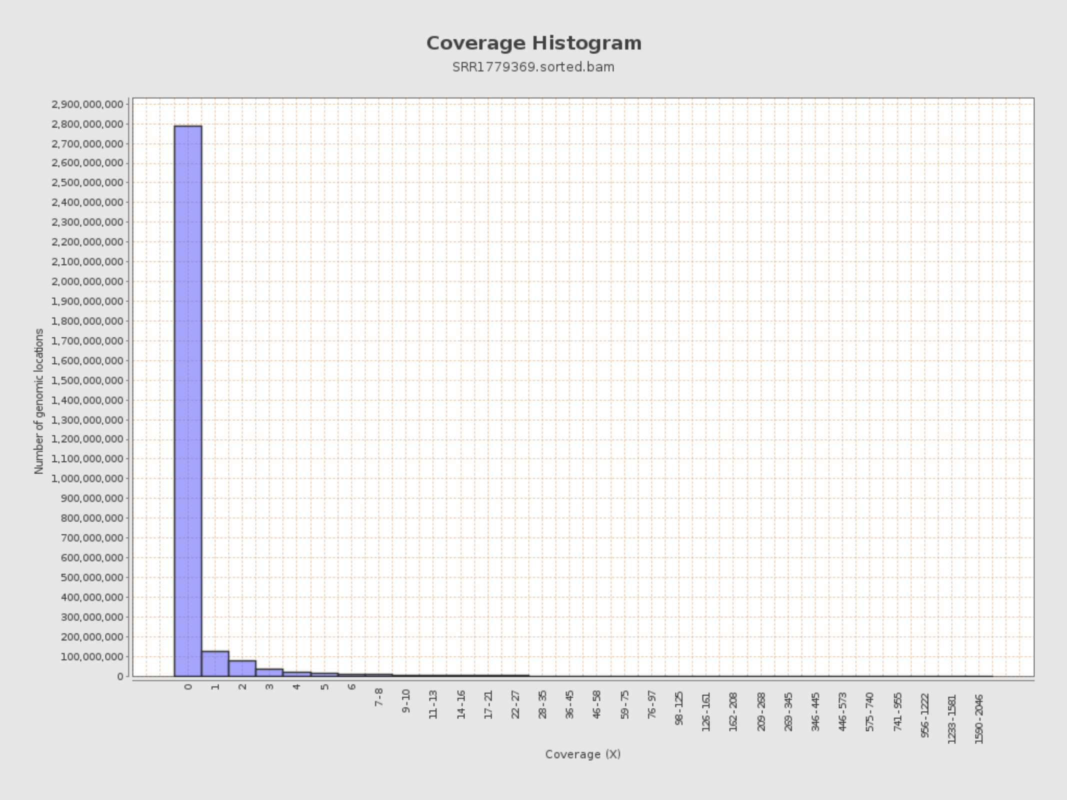
		bases	coverage	deviation
chr1	249250621	80255190	0.322	2.455
chr2	243199373	71342844	0.2934	1.2289
chr3	198022430	59332621	0.2996	1.2233
chr4	191154276	23334783	0.1221	0.6693
chr5	180915260	33881837	0.1873	0.8641
chr6	171115067	42424164	0.2479	2.2029
chr7	159138663	122492905	0.7697	2.4314
chr8	146364022	27259290	0.1862	0.8901
chr9	141213431	127648603	0.9039	4.4111
chr10	135534747	22230796	0.164	1.7151
chr11	135006516	18526026	0.1372	0.7748
chr12	133851895	47568872	0.3554	1.3523
chr13	115169878	33251527	0.2887	1.2444
chr14	107349540	40389506	0.3762	1.5744
chr15	102531392	26414499	0.2576	1.0456
chr16	90354753	33538573	0.3712	1.4271
chr17	81195210	20036036	0.2468	1.1542
chr18	78077248	23615620	0.3025	1.2722
chr19	59128983	10401108	0.1759	1.3559
chr20	63025520	29553156	0.4689	1.6604
chr21	48129895	18937542	0.3935	1.4325
chr22	51304566	17659472	0.3442	1.5901
chrMT	16571	80	0.0048	0.0693
chrX	155270560	1820460	0.0117	0.1795

chrY	59373566	9014227	0.1518	0.7874

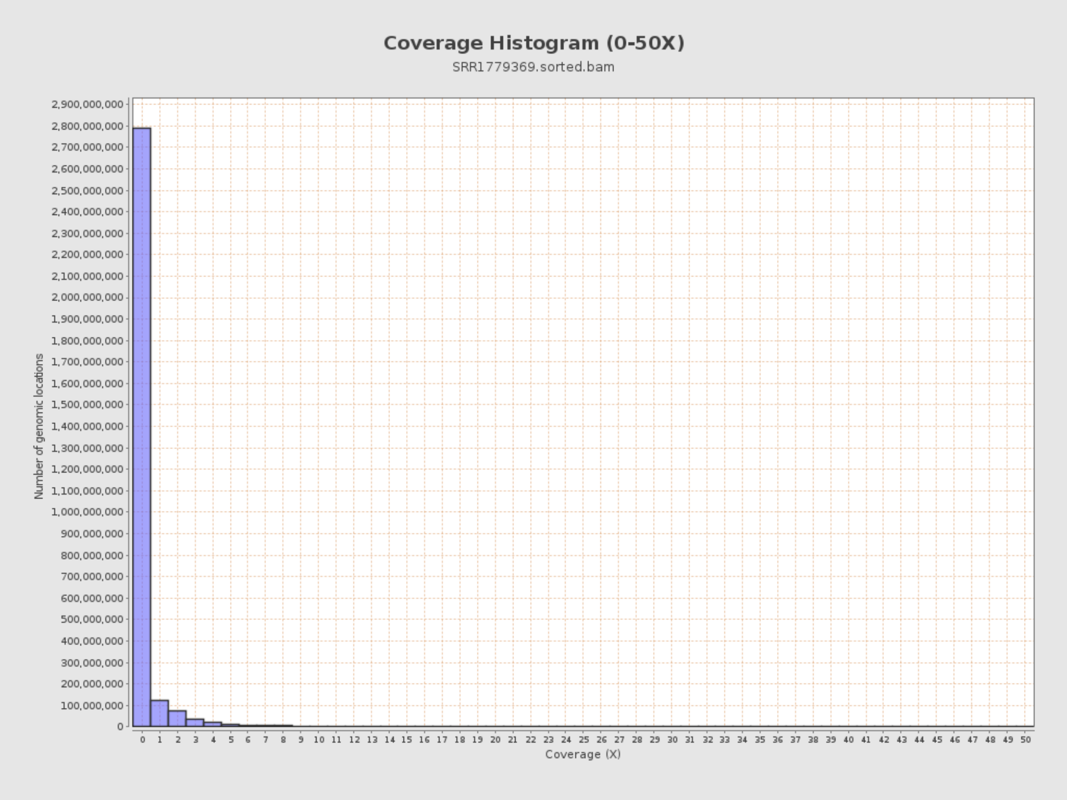
3. Results : Coverage across reference



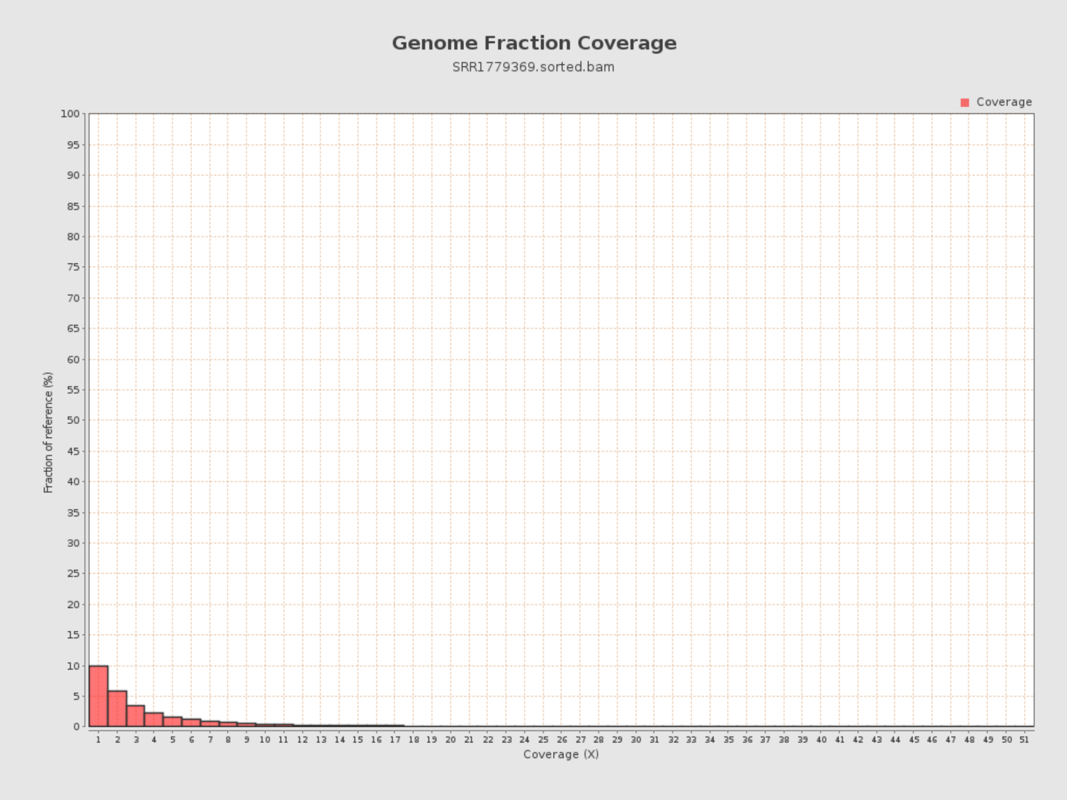
4. Results : Coverage Histogram



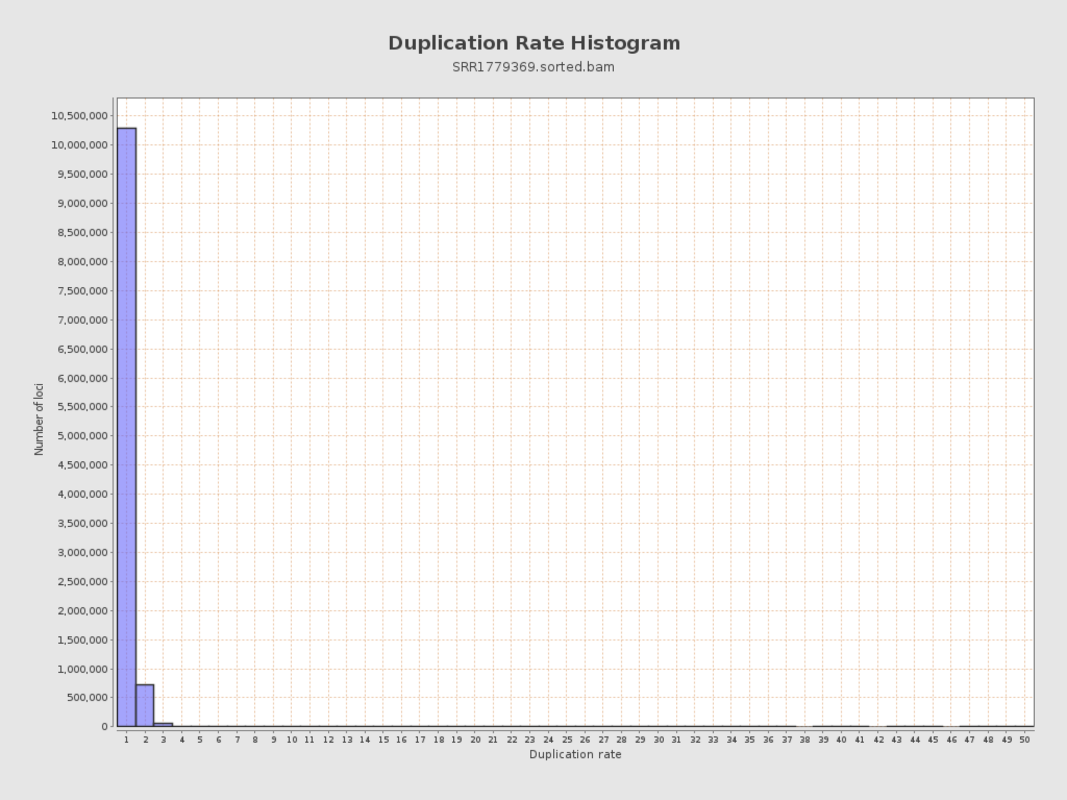
5. Results : Coverage Histogram (0-50X)



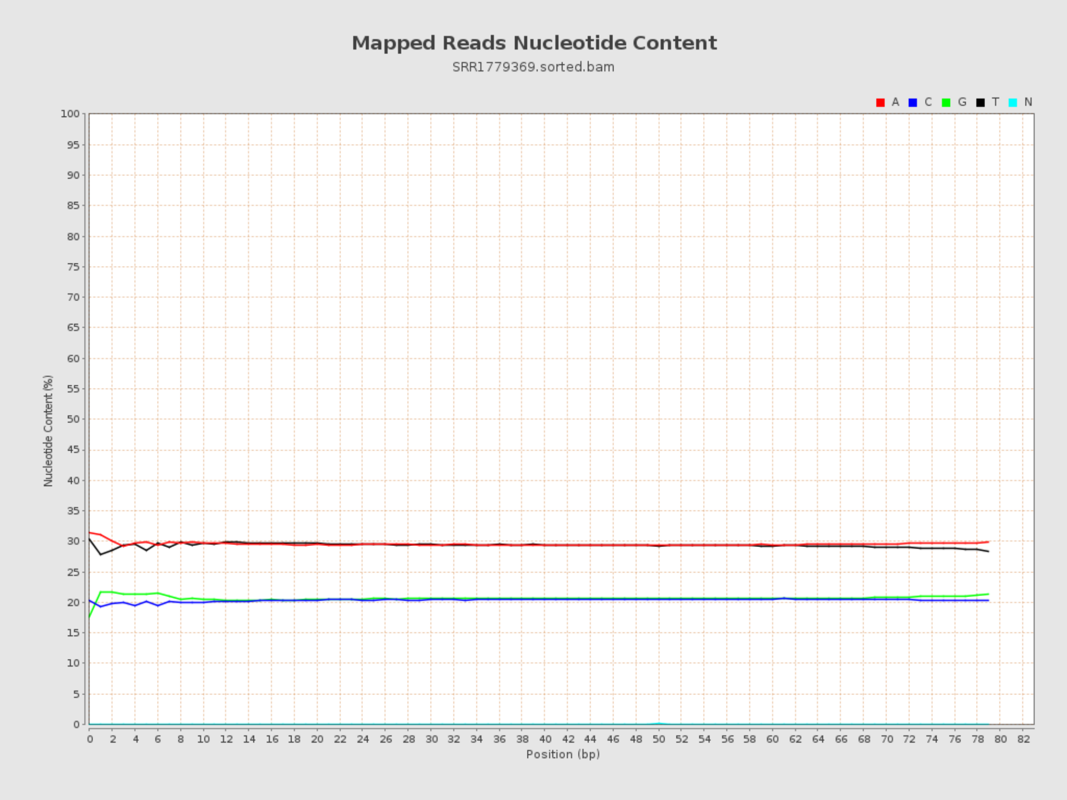
6. Results : Genome Fraction Coverage



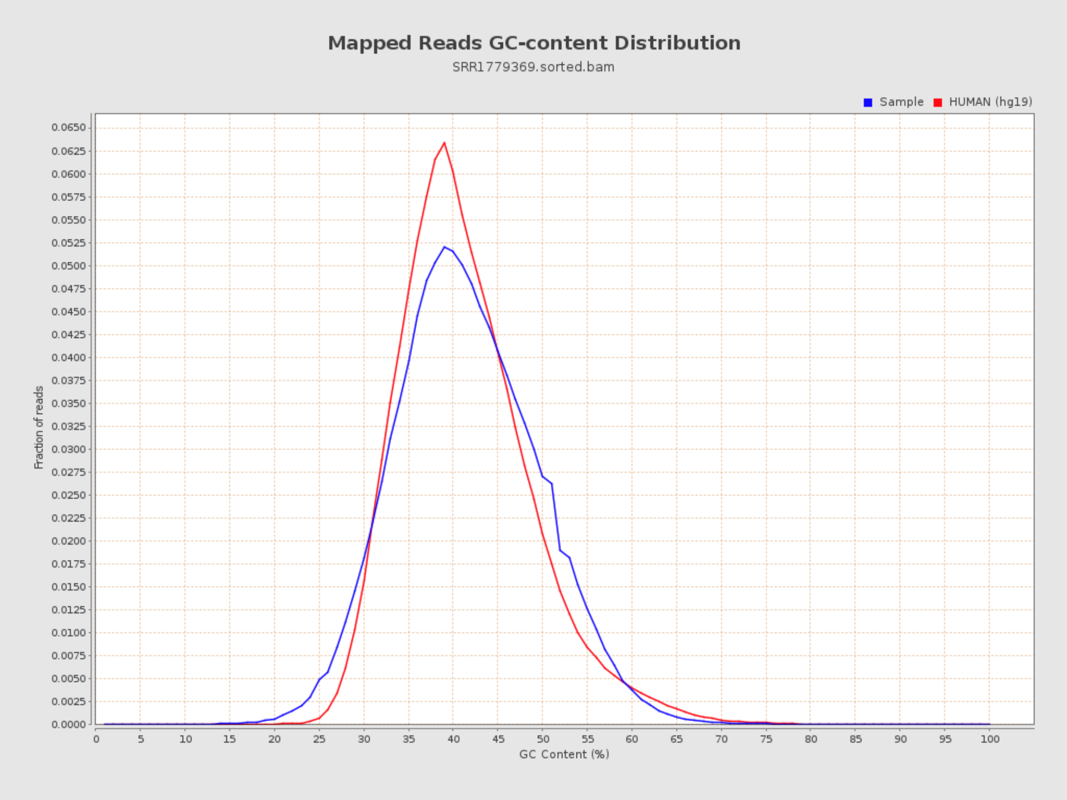
7. Results : Duplication Rate Histogram



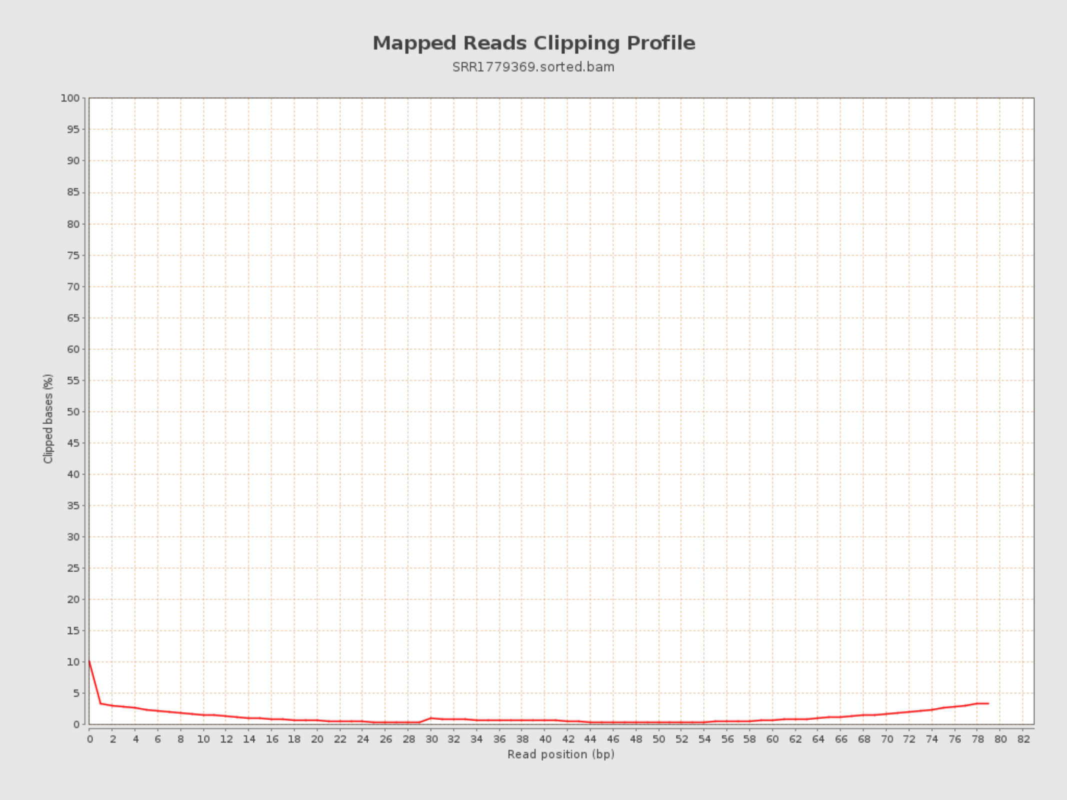
8. Results : Mapped Reads Nucleotide Content



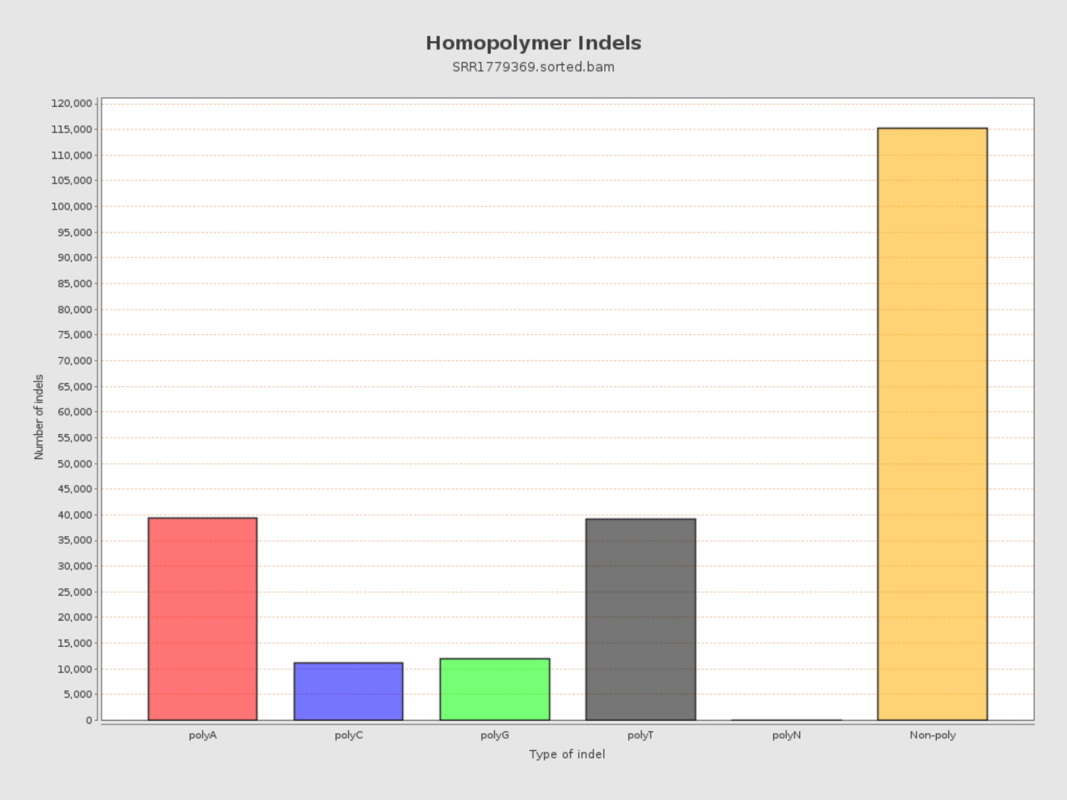
9. Results : Mapped Reads GC-content Distribution



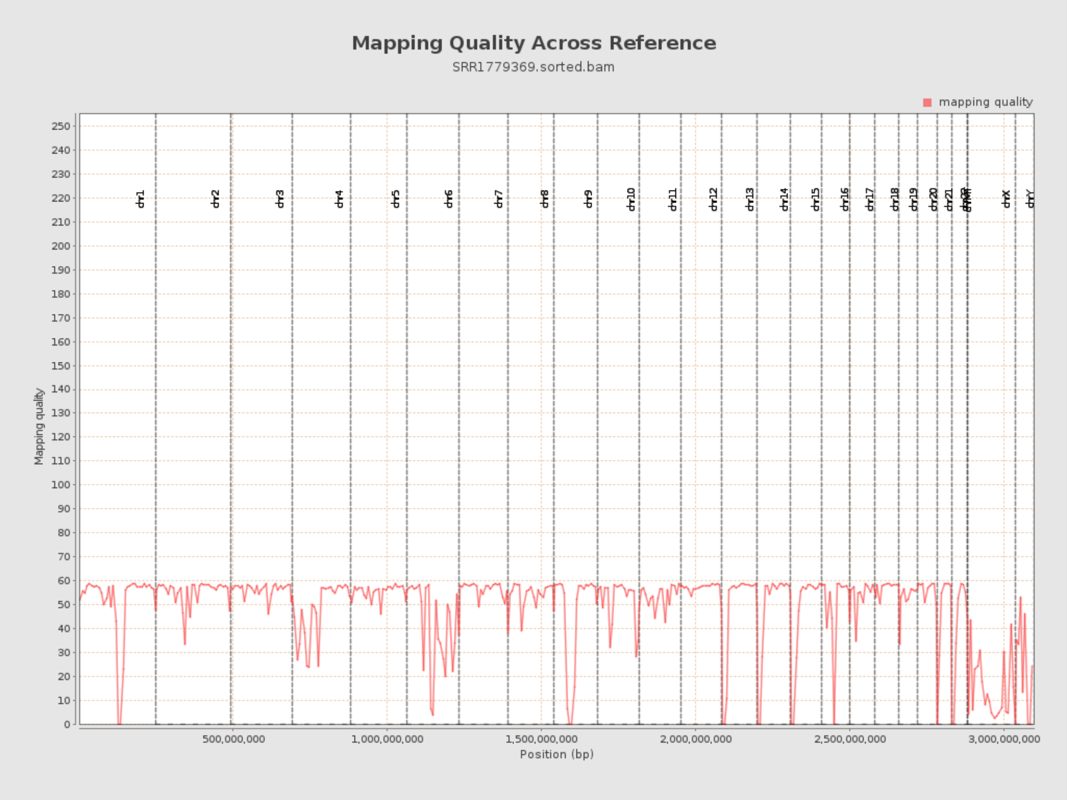
10. Results : Mapped Reads Clipping Profile



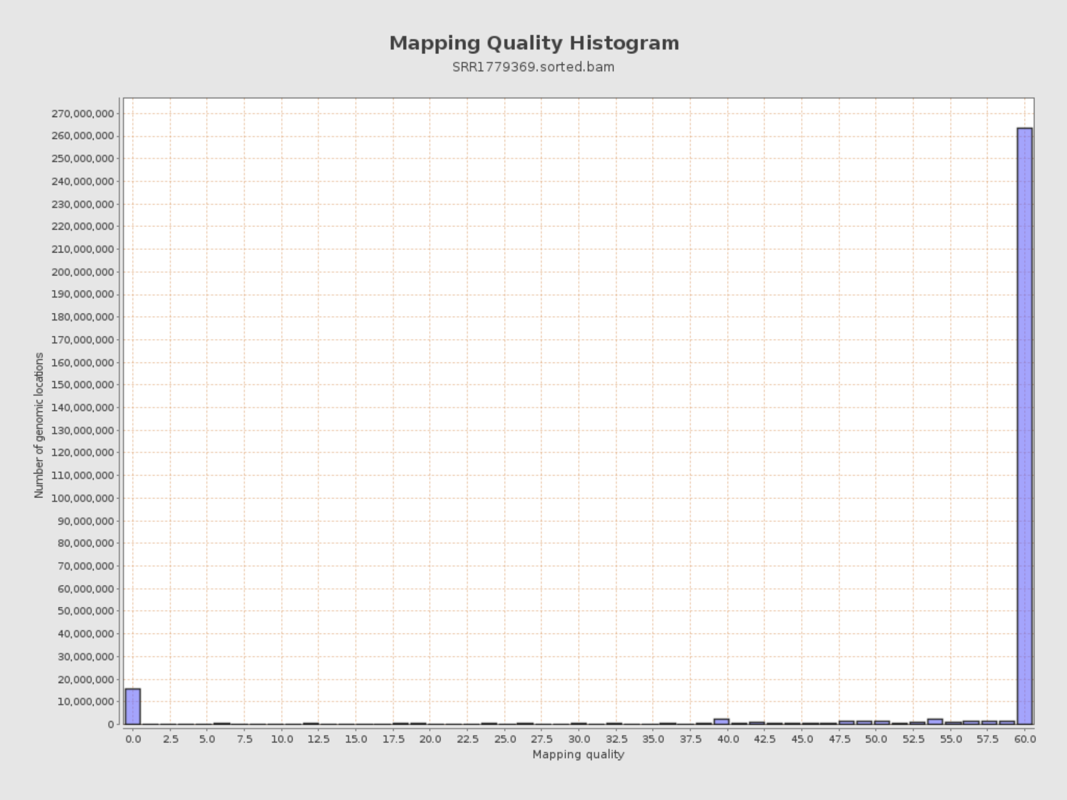
11. Results : Homopolymer Indels



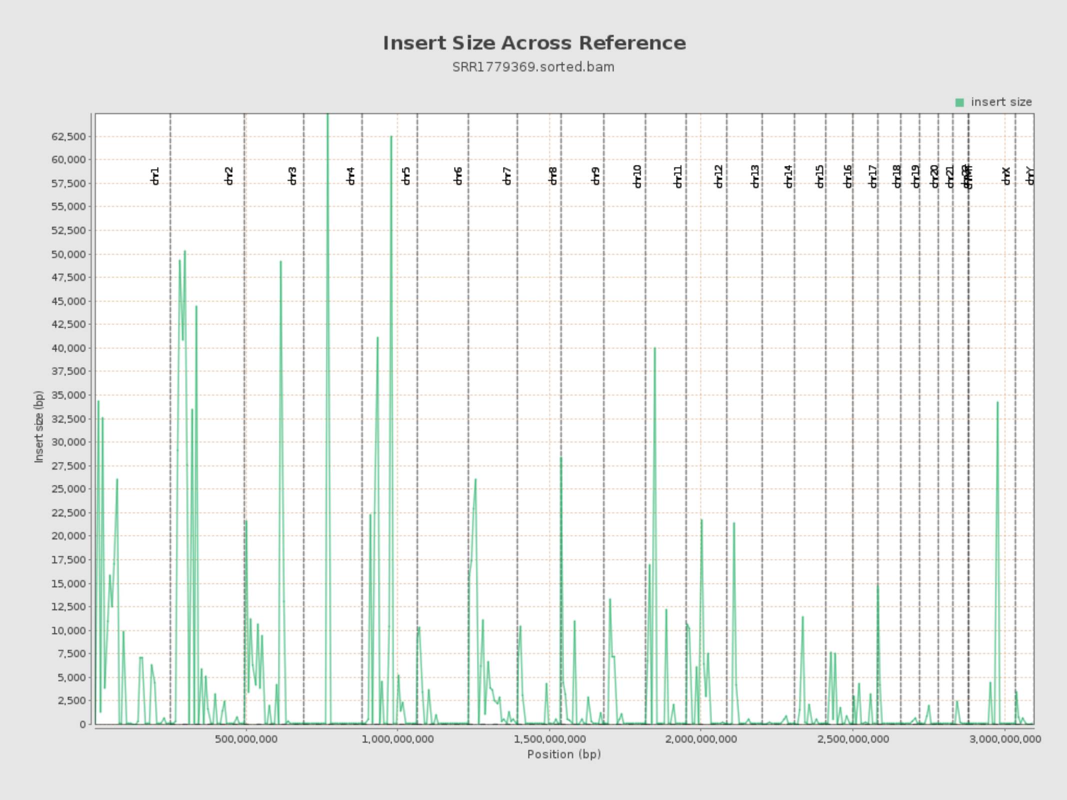
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram