Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/08 11:46:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779175.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_SRR1779175 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779175_1.fastq.gz SRR1779175_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 08 11:46:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779175.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	28,718,580
Mapped reads	27,561,614 / 95.97%
Unmapped reads	1,156,966 / 4.03%
Mapped paired reads	27,561,614 / 95.97%
Mapped reads, first in pair	13,852,695 / 48.24%
Mapped reads, second in pair	13,708,919 / 47.74%
Mapped reads, both in pair	27,290,856 / 95.03%
Mapped reads, singletons	270,758 / 0.94%
Secondary alignments	0
Supplementary alignments	176,455 / 0.61%
Read min/max/mean length	30 / 101 / 101.25
Duplicated reads (estimated)	984,992 / 3.43%
Duplication rate	3.23%
Clipped reads	2,126,672 / 7.41%

2.2. ACGT Content

Number/percentage of A's	836,850,523 / 30.45%
Number/percentage of C's	536,982,660 / 19.54%
Number/percentage of T's	826,209,415 / 30.07%
Number/percentage of G's	546,900,678 / 19.9%
Number/percentage of N's	1,114,615 / 0.04%

GC Percentage	39.44%

2.3. Coverage

Mean	0.8879
Standard Deviation	2.1818

2.4. Mapping Quality

Mean Mapping Quality	53.43

2.5. Insert size

Mean	86,979.98
Standard Deviation	2,781,662.56
P25/Median/P75	144 / 193 / 266

2.6. Mismatches and indels

General error rate	0.43%
Mismatches	11,266,248
Insertions	225,949
Mapped reads with at least one insertion	0.81%
Deletions	278,707
Mapped reads with at least one deletion	0.99%
Homopolymer indels	46.26%

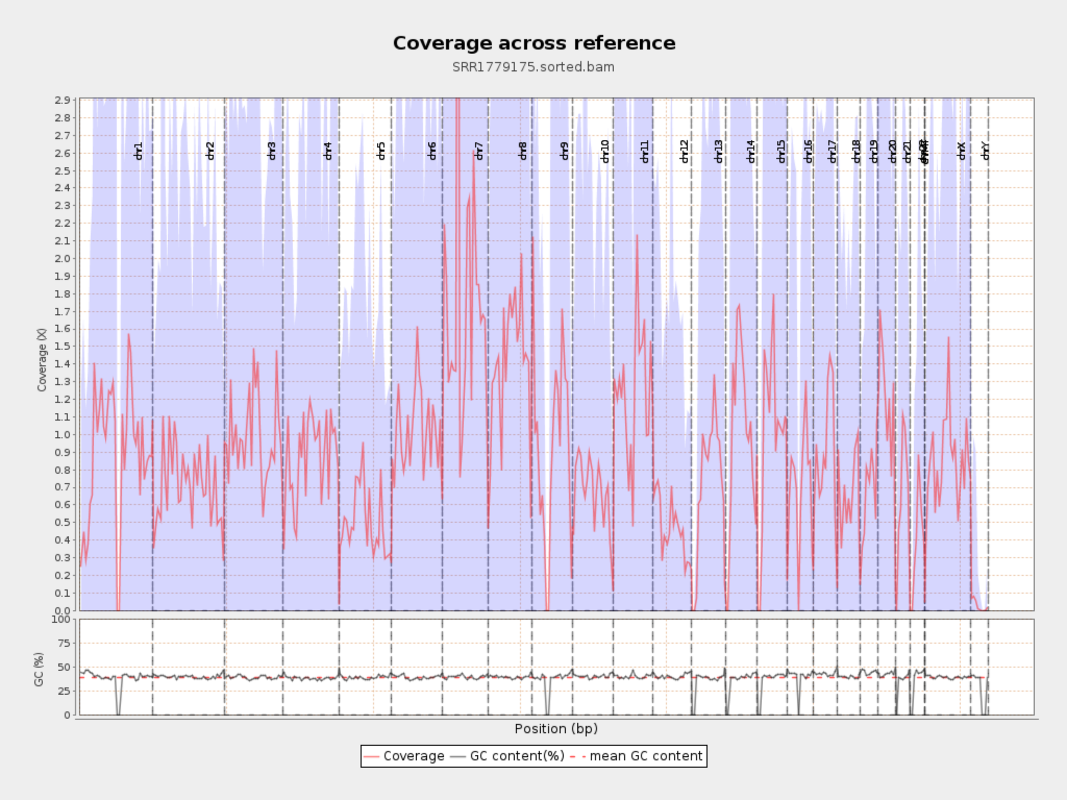
2.7. Chromosome stats

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

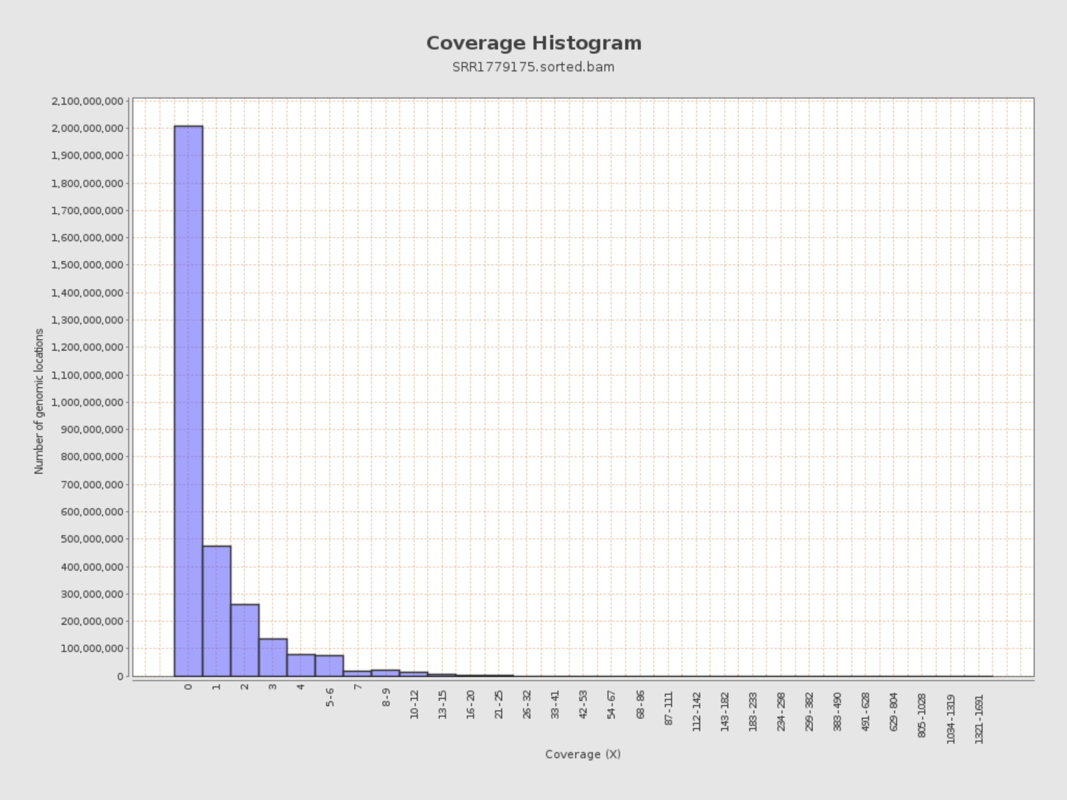
		bases	**coverage**	**deviation**
chr1	249250621	222232160	0.8916	2.321
chr2	243199373	173056607	0.7116	1.9911
chr3	198022430	195580969	0.9877	1.8998
chr4	191154276	168238842	0.8801	1.7599
chr5	180915260	90943393	0.5027	1.2497
chr6	171115067	178116712	1.0409	1.9673
chr7	159138663	284309515	1.7866	4.7224
chr8	146364022	208187051	1.4224	2.3335
chr9	141213431	129136610	0.9145	1.9912
chr10	135534747	91696136	0.6766	2.6587
chr11	135006516	167072180	1.2375	2.173
chr12	133851895	63487186	0.4743	1.3282
chr13	115169878	83365263	0.7238	1.6359
chr14	107349540	107622351	1.0025	1.9549
chr15	102531392	102893233	1.0035	2.1456
chr16	90354753	61481825	0.6804	1.487
chr17	81195210	71608674	0.8819	1.8943
chr18	78077248	52202358	0.6686	1.4825
chr19	59128983	38038429	0.6433	1.7078
chr20	63025520	74259544	1.1782	2.4123
chr21	48129895	32026613	0.6654	1.5377
chr22	51304566	19922867	0.3883	1.1206
chrMT	16571	749	0.0452	0.249
chrX	155270560	131510126	0.847	1.8265

chrY	59373566	1692042	0.0285	0.4754

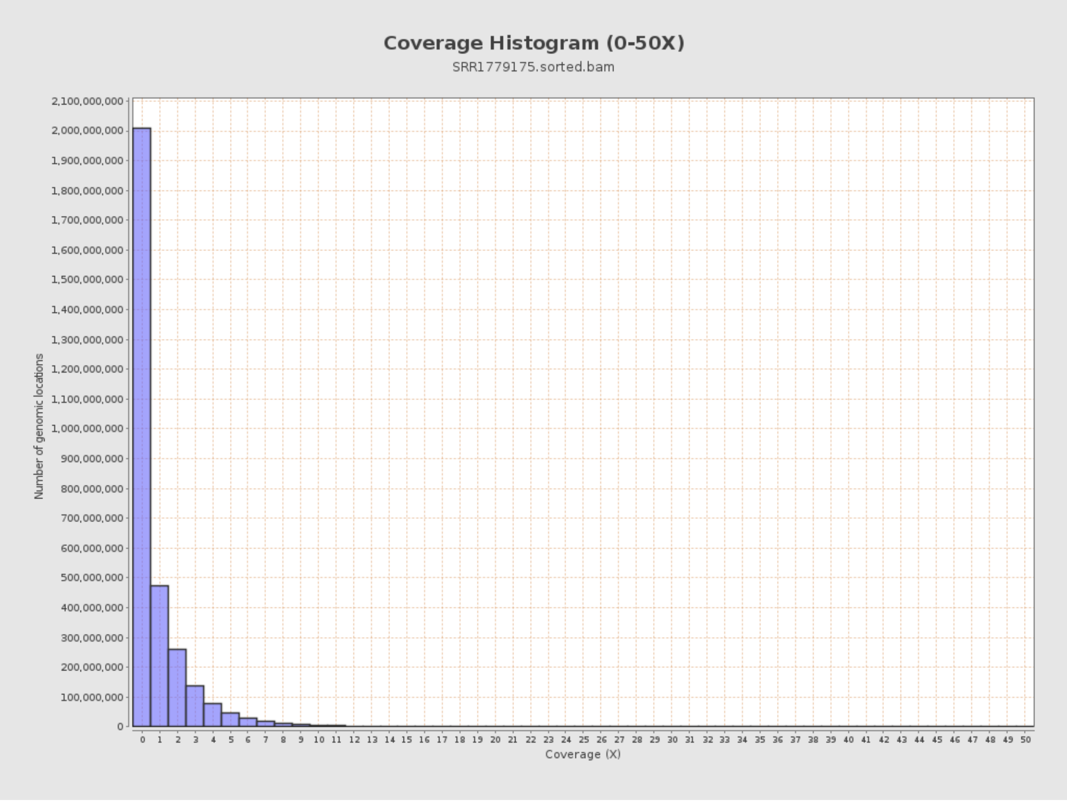
3. Results : Coverage across reference



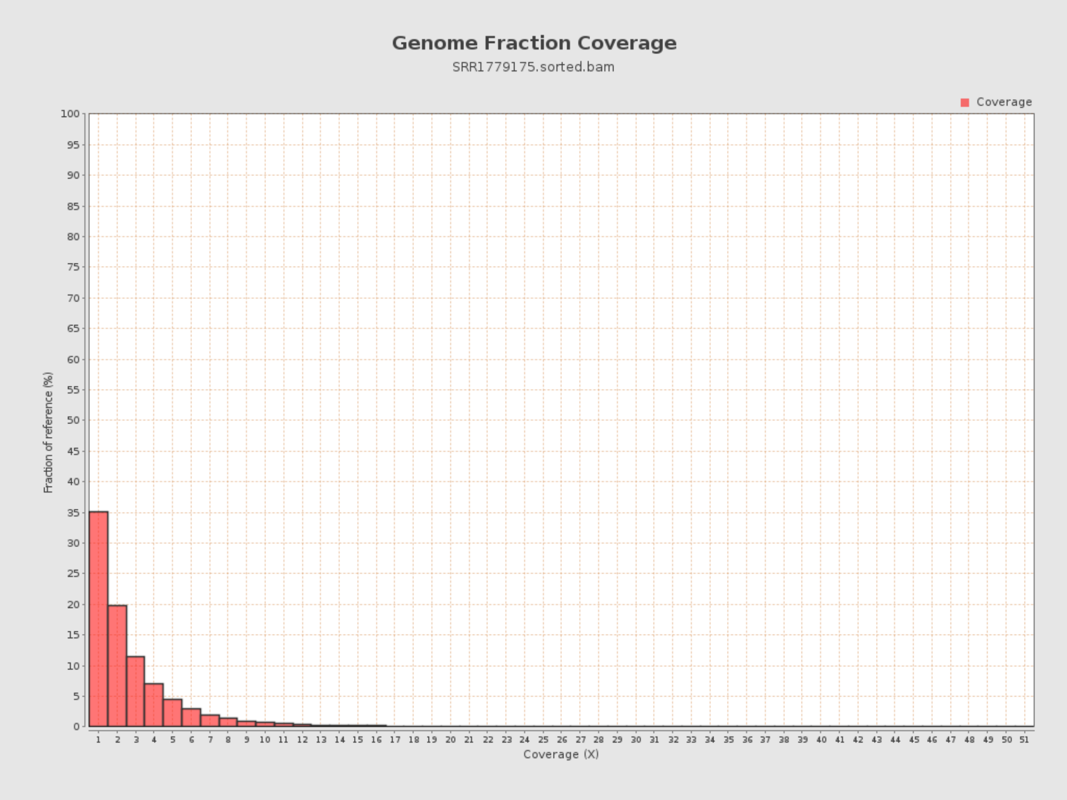
4. Results : Coverage Histogram



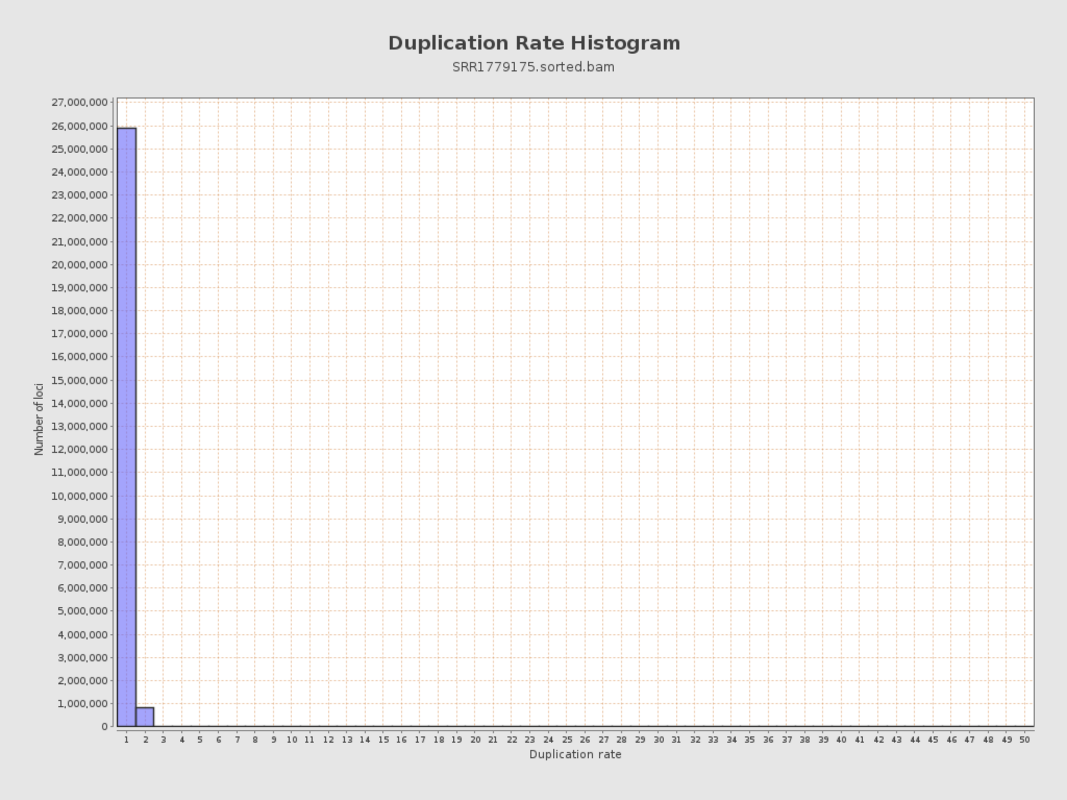
5. Results : Coverage Histogram (0-50X)



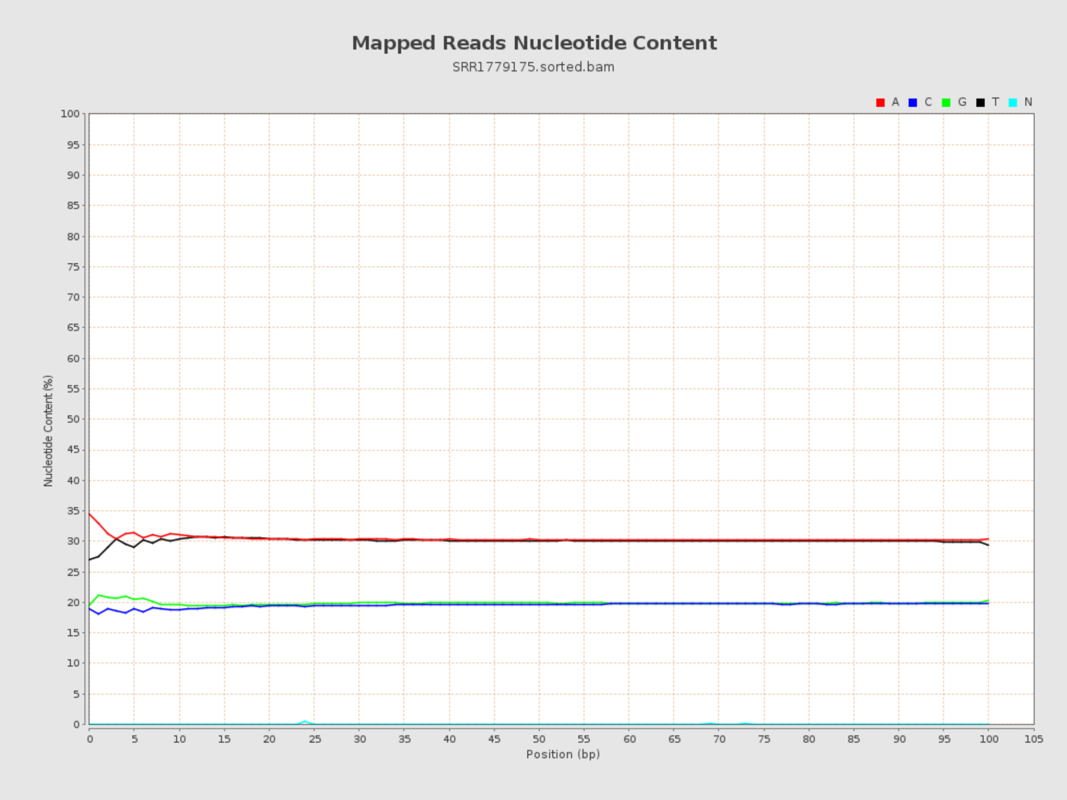
6. Results : Genome Fraction Coverage



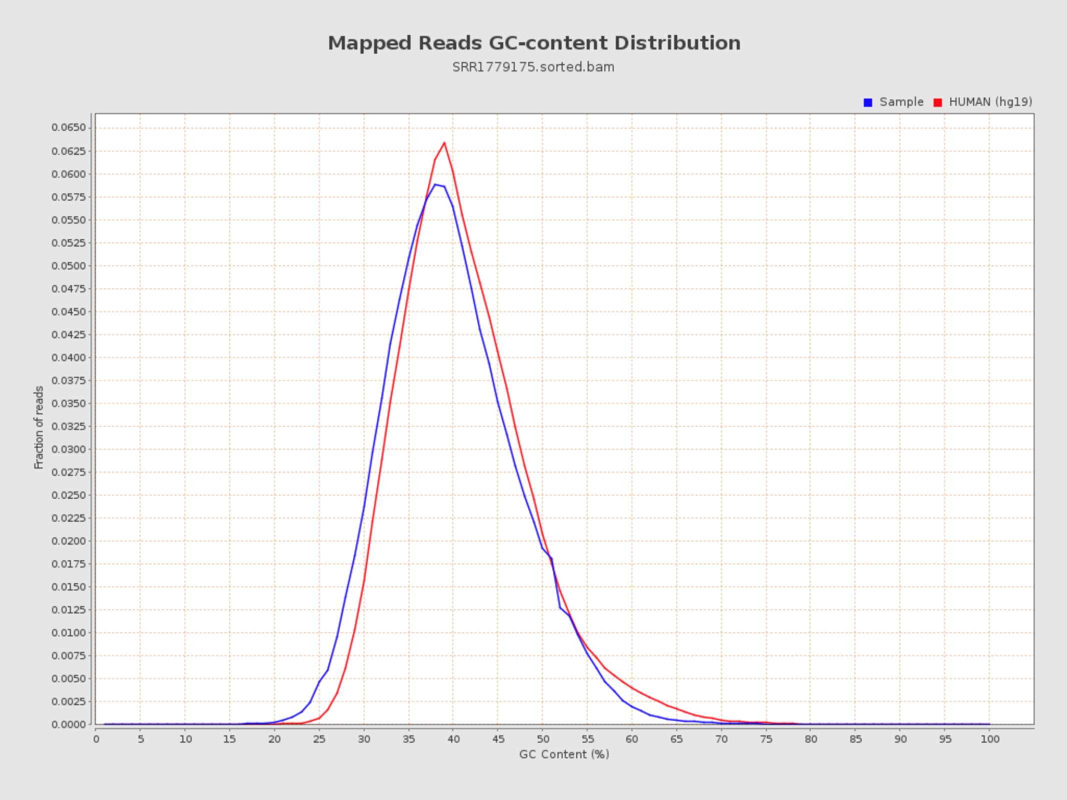
7. Results : Duplication Rate Histogram



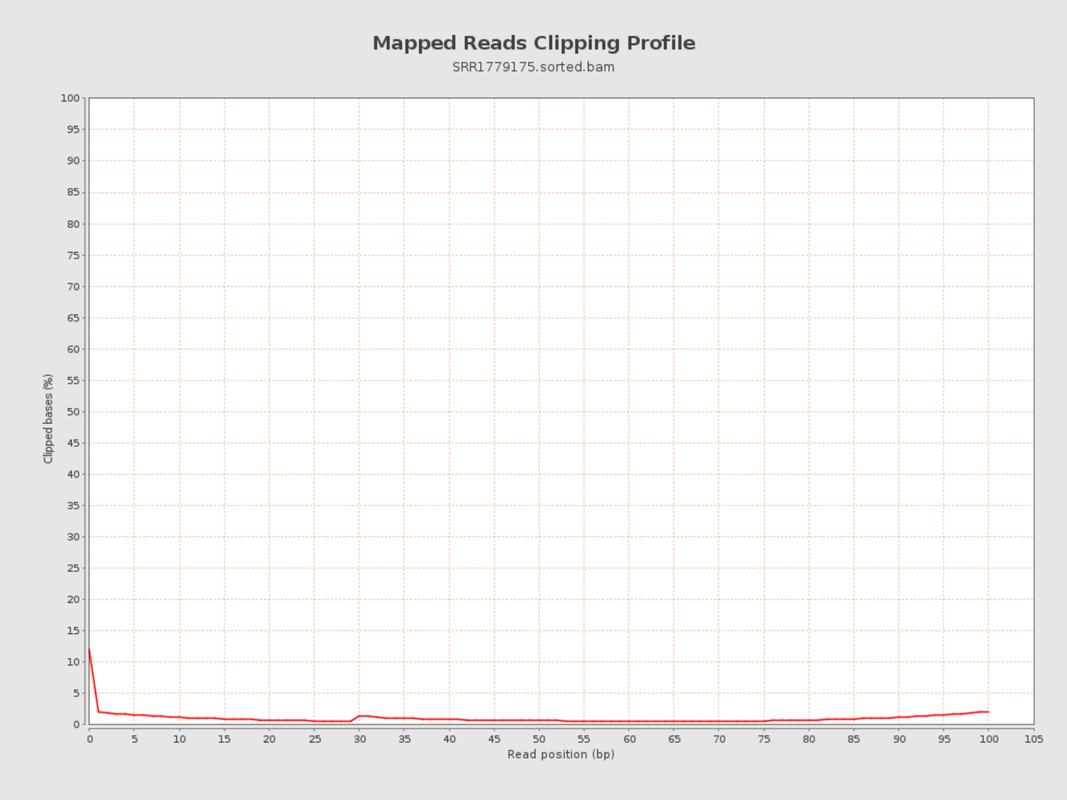
8. Results : Mapped Reads Nucleotide Content



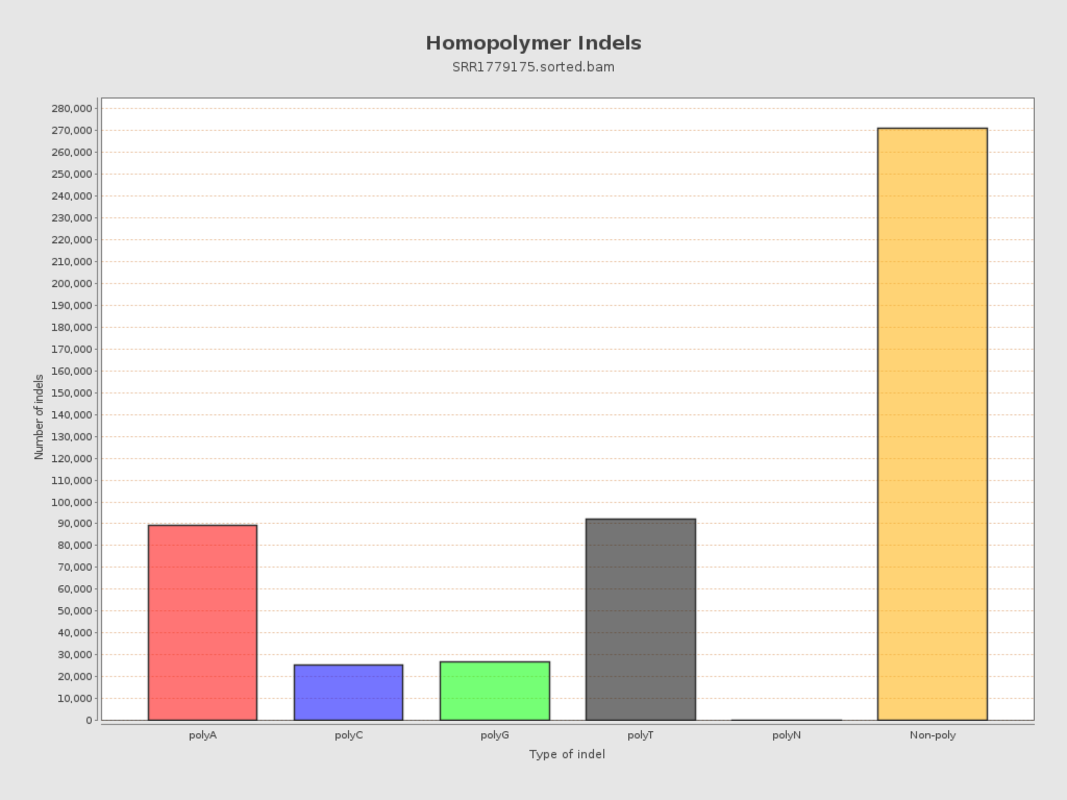
9. Results : Mapped Reads GC-content Distribution



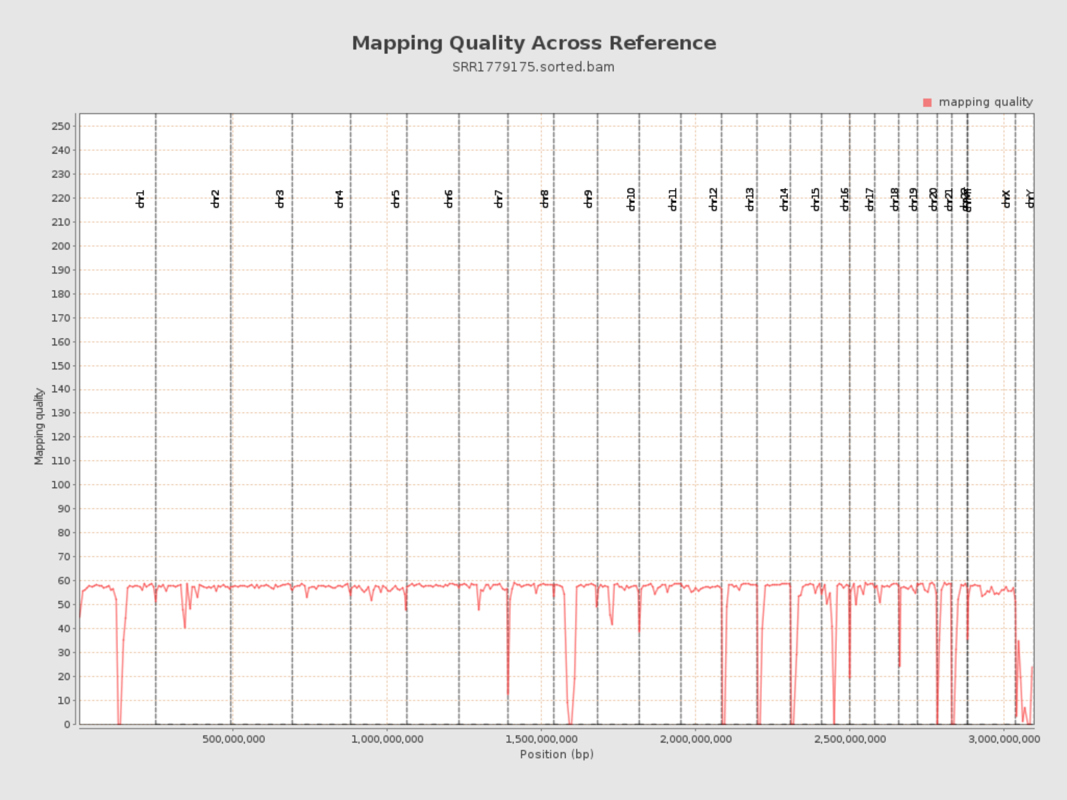
10. Results : Mapped Reads Clipping Profile



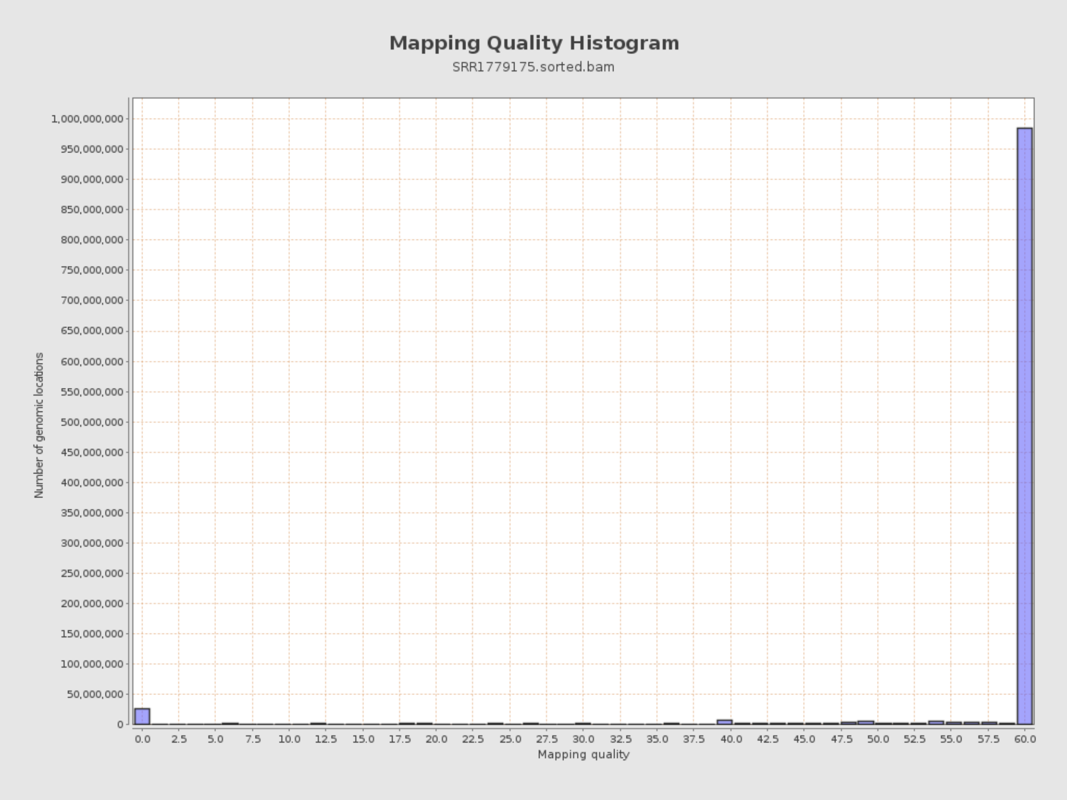
11. Results : Homopolymer Indels



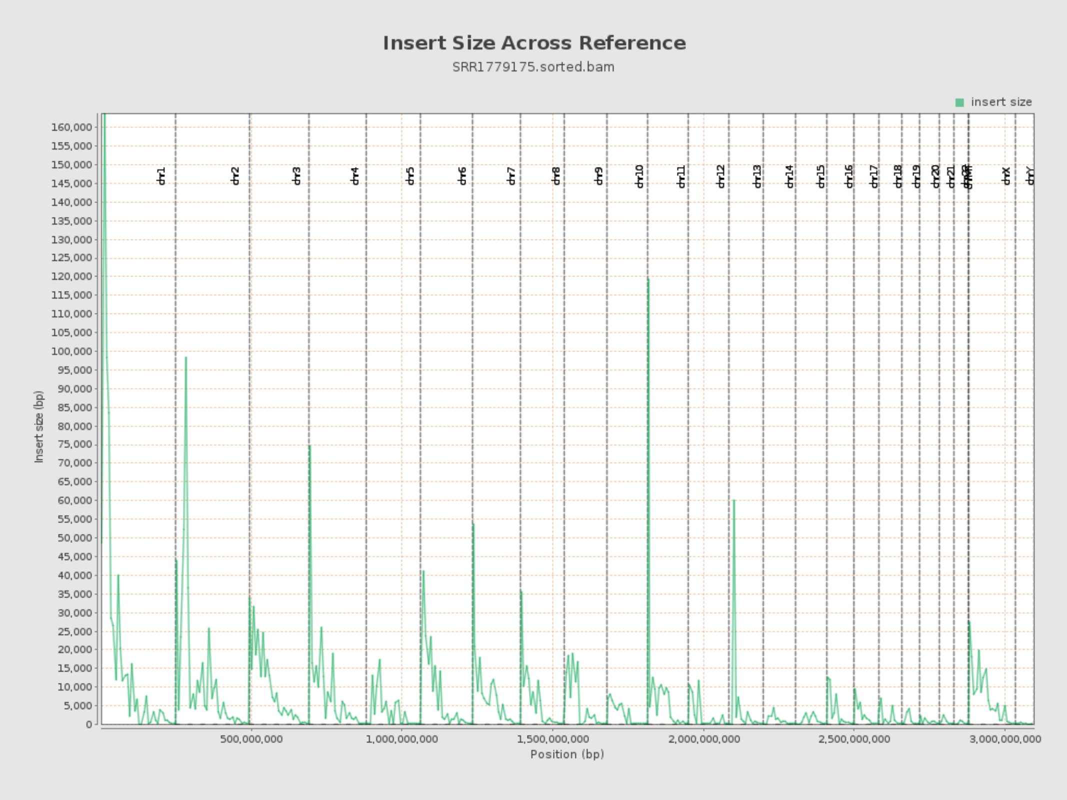
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram