Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/08 21:47:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779280.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_SRR1779280 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779280_1.fastq.gz SRR1779280_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 08 21:47:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779280.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	11,377,640
Mapped reads	10,935,893 / 96.12%
Unmapped reads	441,747 / 3.88%
Mapped paired reads	10,935,893 / 96.12%
Mapped reads, first in pair	5,506,544 / 48.4%
Mapped reads, second in pair	5,429,349 / 47.72%
Mapped reads, both in pair	10,841,660 / 95.29%
Mapped reads, singletons	94,233 / 0.83%
Secondary alignments	0
Supplementary alignments	25,870 / 0.23%
Read min/max/mean length	30 / 80 / 80.08
Duplicated reads (estimated)	149,043 / 1.31%
Duplication rate	1.2%
Clipped reads	376,547 / 3.31%

2.2. ACGT Content

Number/percentage of A's	266,425,455 / 30.62%
Number/percentage of C's	167,855,027 / 19.29%
Number/percentage of T's	264,425,259 / 30.39%
Number/percentage of G's	171,182,333 / 19.67%
Number/percentage of N's	165,262 / 0.02%

GC Percentage	38.97%

2.3. Coverage

Mean	0.2811
Standard Deviation	0.9048

2.4. Mapping Quality

Mean Mapping Quality	53.02

2.5. Insert size

Mean	57,391.44
Standard Deviation	2,255,045.25
P25/Median/P75	142 / 191 / 260

2.6. Mismatches and indels

General error rate	0.39%
Mismatches	3,304,669
Insertions	62,849
Mapped reads with at least one insertion	0.57%
Deletions	80,005
Mapped reads with at least one deletion	0.72%
Homopolymer indels	46.18%

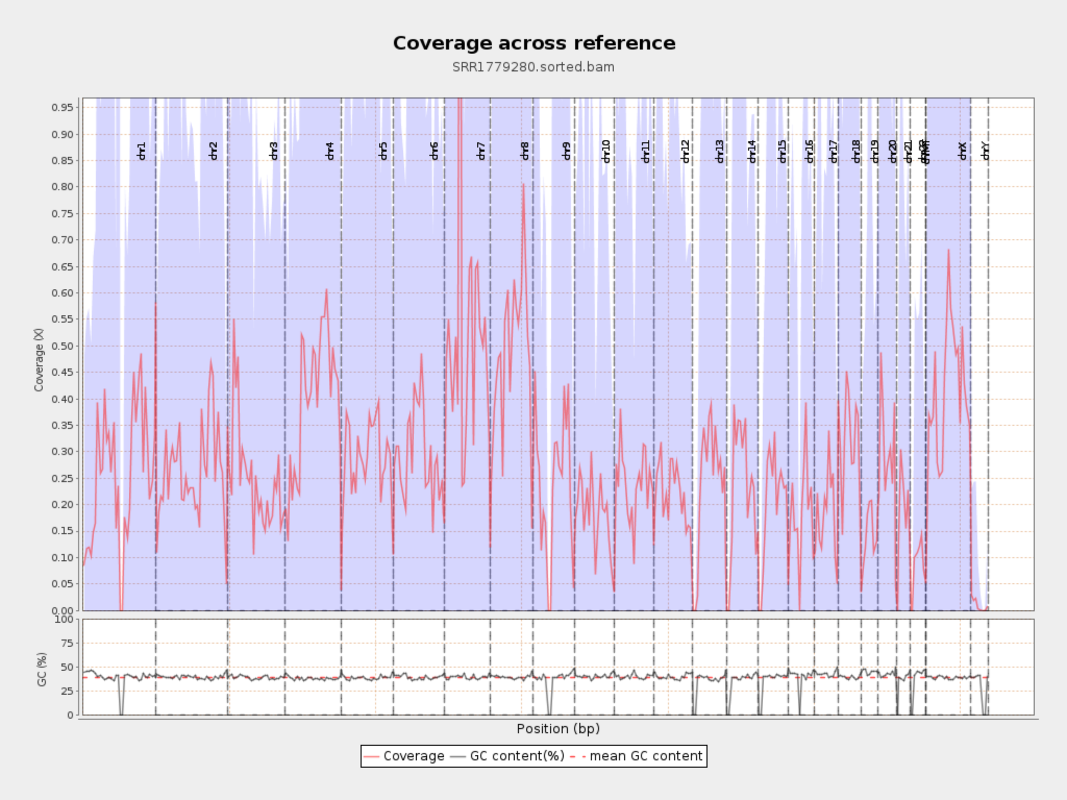
2.7. Chromosome stats

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

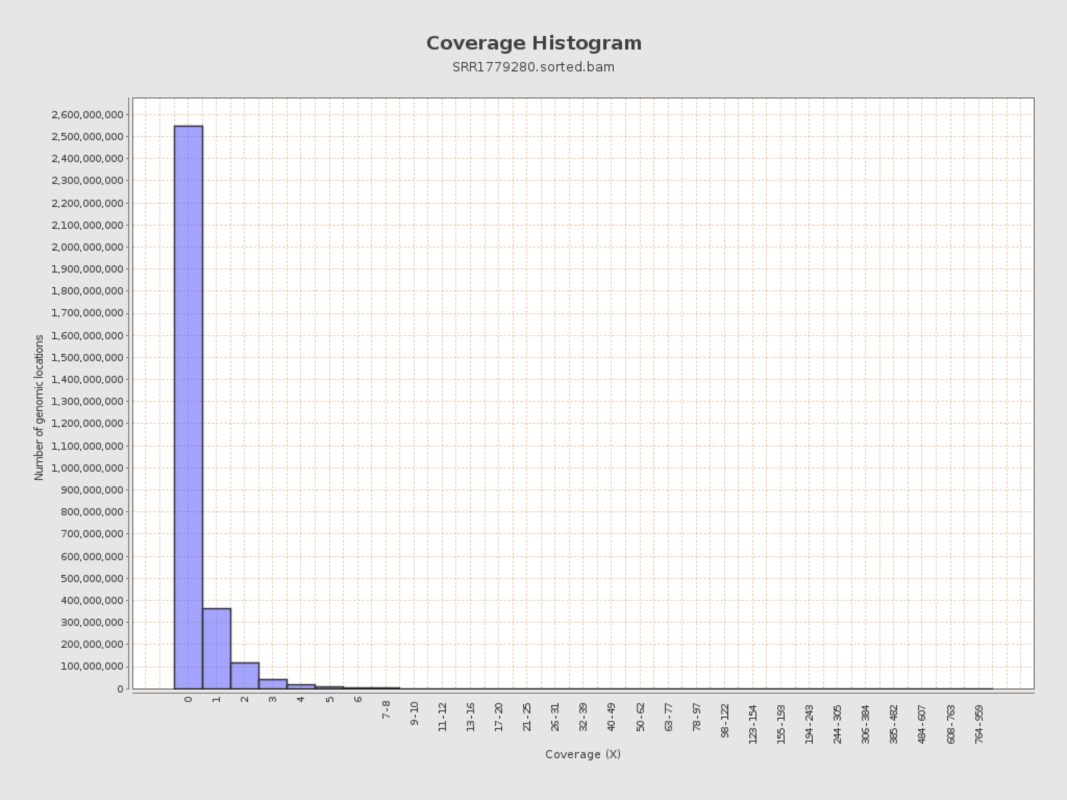
		bases	coverage	deviation
chr1	249250621	63917578	0.2564	1.1815
chr2	243199373	63927878	0.2629	0.7058
chr3	198022430	49839844	0.2517	0.6774
chr4	191154276	76669497	0.4011	0.8929
chr5	180915260	51514695	0.2847	0.7195
chr6	171115067	50925561	0.2976	0.7497
chr7	159138663	85546033	0.5376	1.8123
chr8	146364022	71914610	0.4913	0.9778
chr9	141213431	33850947	0.2397	0.7154
chr10	135534747	25022991	0.1846	1.3704
chr11	135006516	31882467	0.2362	0.6733
chr12	133851895	29496942	0.2204	0.624
chr13	115169878	27619491	0.2398	0.6574
chr14	107349540	24989954	0.2328	0.6684
chr15	102531392	20479424	0.1997	0.6243
chr16	90354753	16446158	0.182	0.5917
chr17	81195210	15090922	0.1859	0.6907
chr18	78077248	25138955	0.322	0.7931
chr19	59128983	8530519	0.1443	0.7489
chr20	63025520	19173090	0.3042	0.7848
chr21	48129895	8567608	0.178	0.5796
chr22	51304566	4361685	0.085	0.3935
chrMT	16571	868	0.0524	0.2606
chrX	155270560	64749058	0.417	0.9462

chrY	59373566	562653	0.0095	0.1385

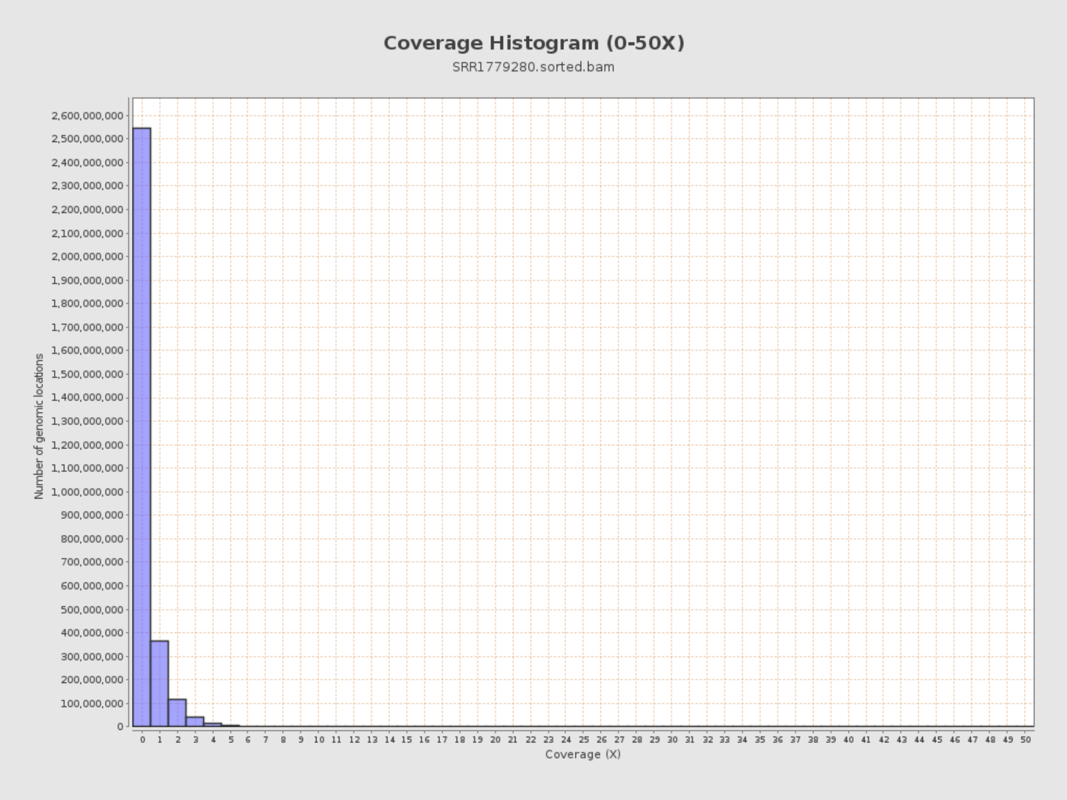
3. Results : Coverage across reference



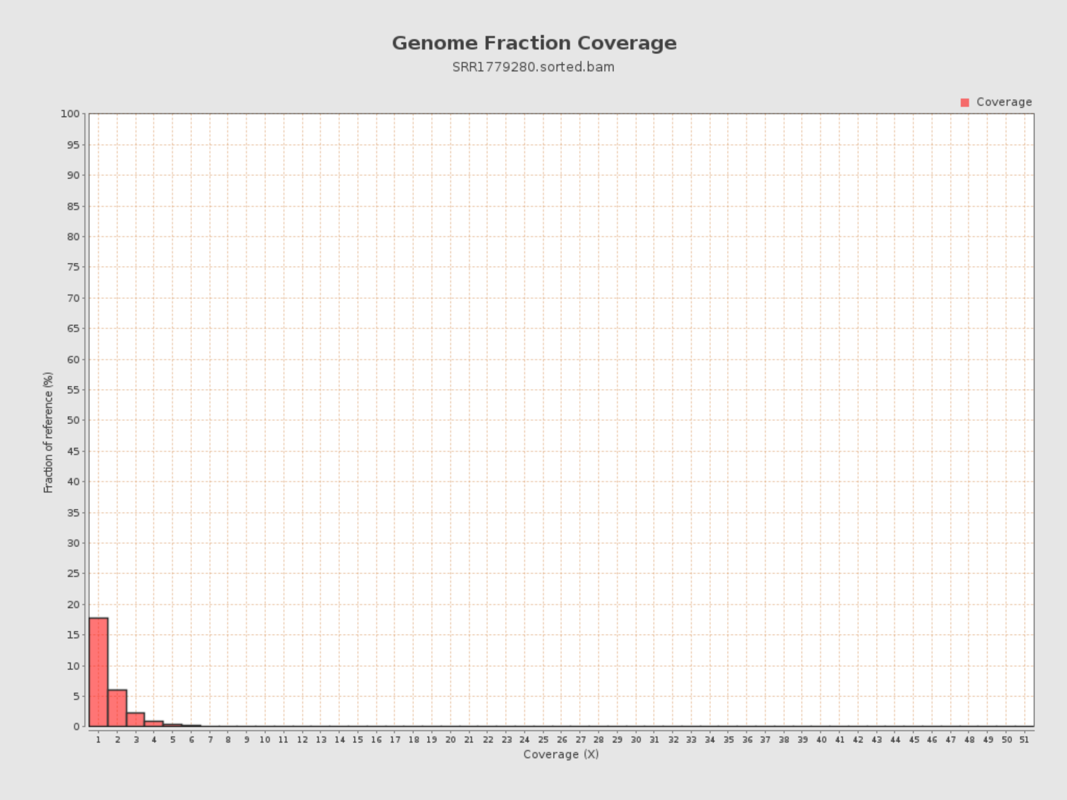
4. Results : Coverage Histogram



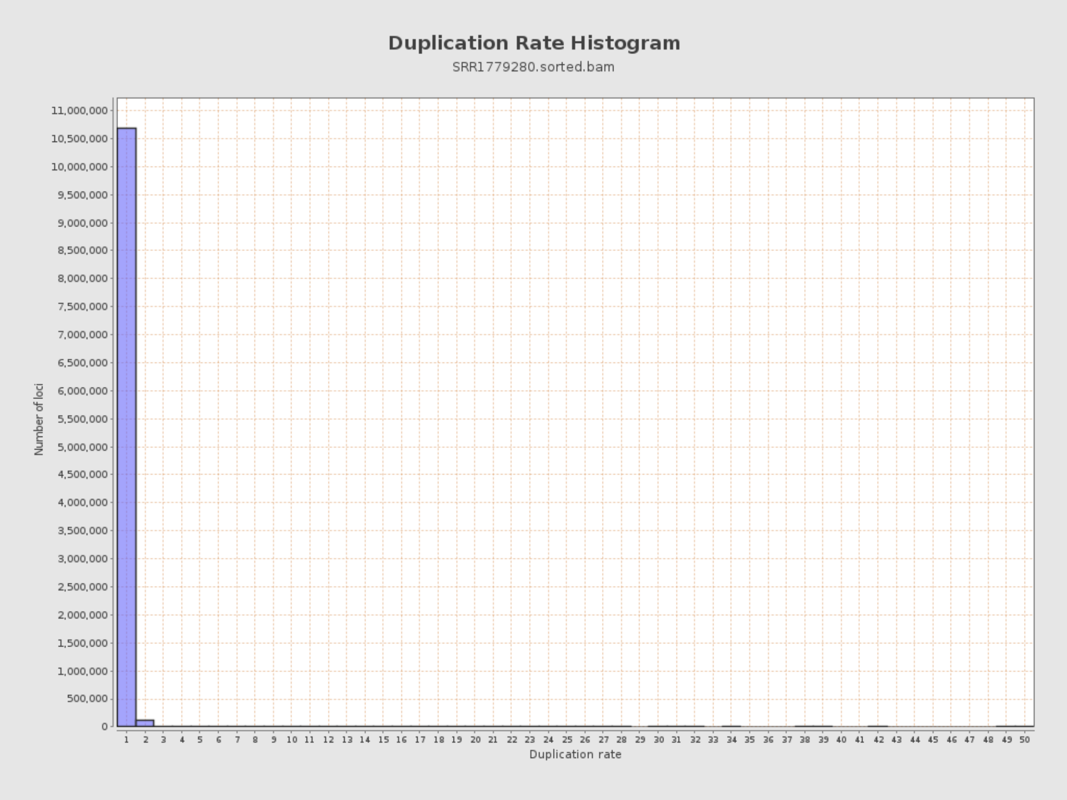
5. Results : Coverage Histogram (0-50X)



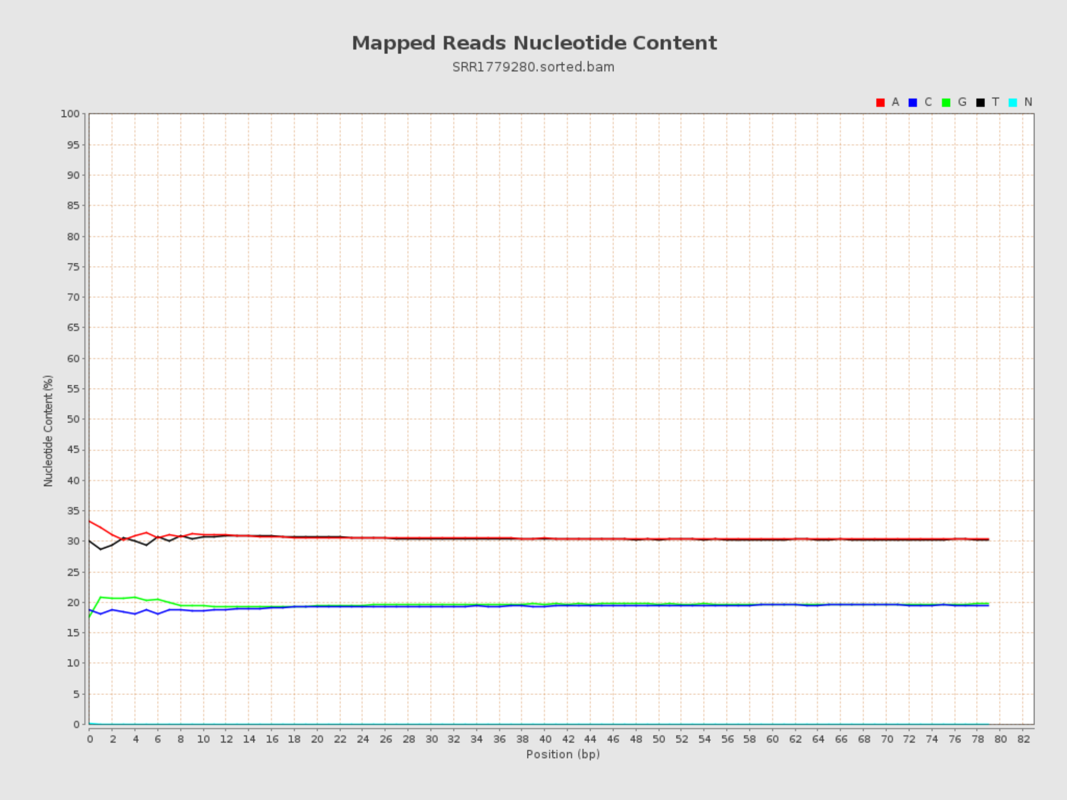
6. Results : Genome Fraction Coverage



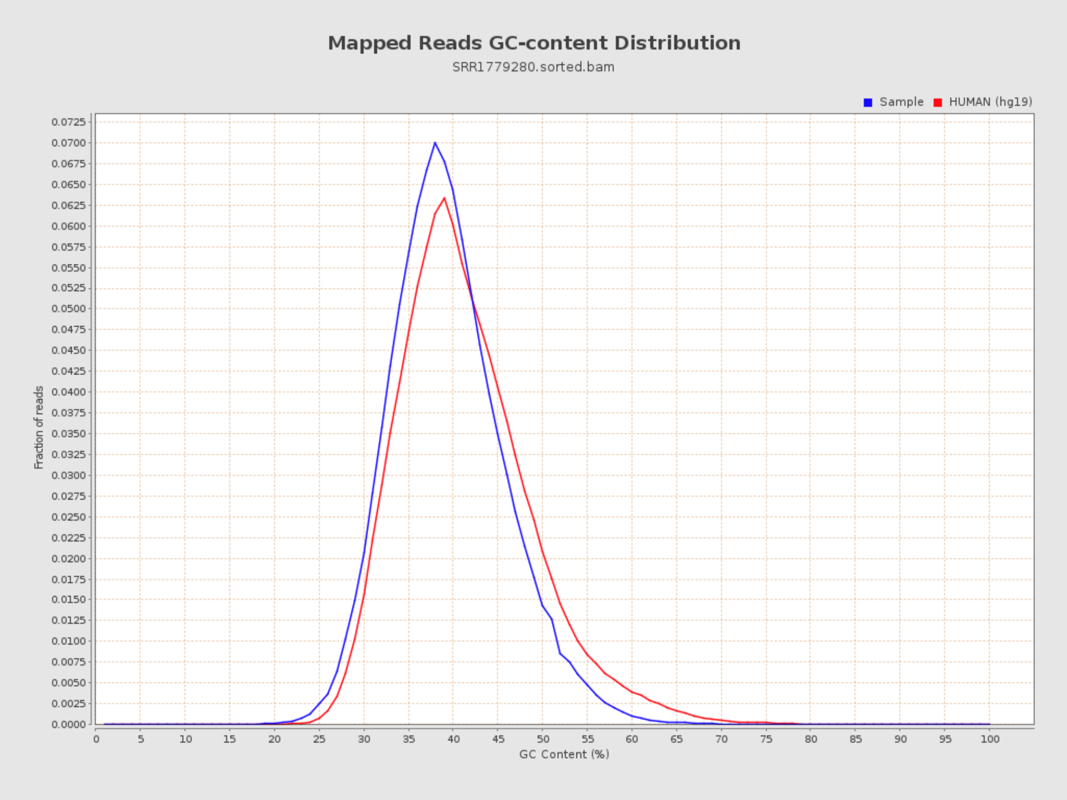
7. Results : Duplication Rate Histogram



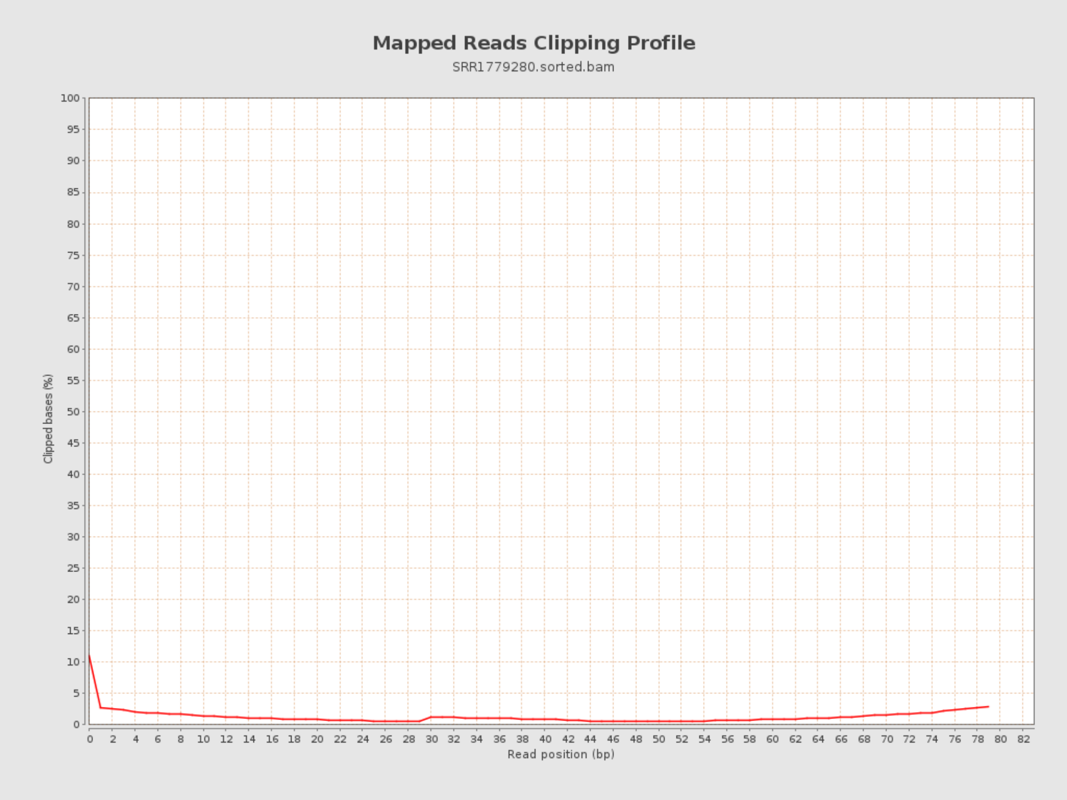
8. Results : Mapped Reads Nucleotide Content



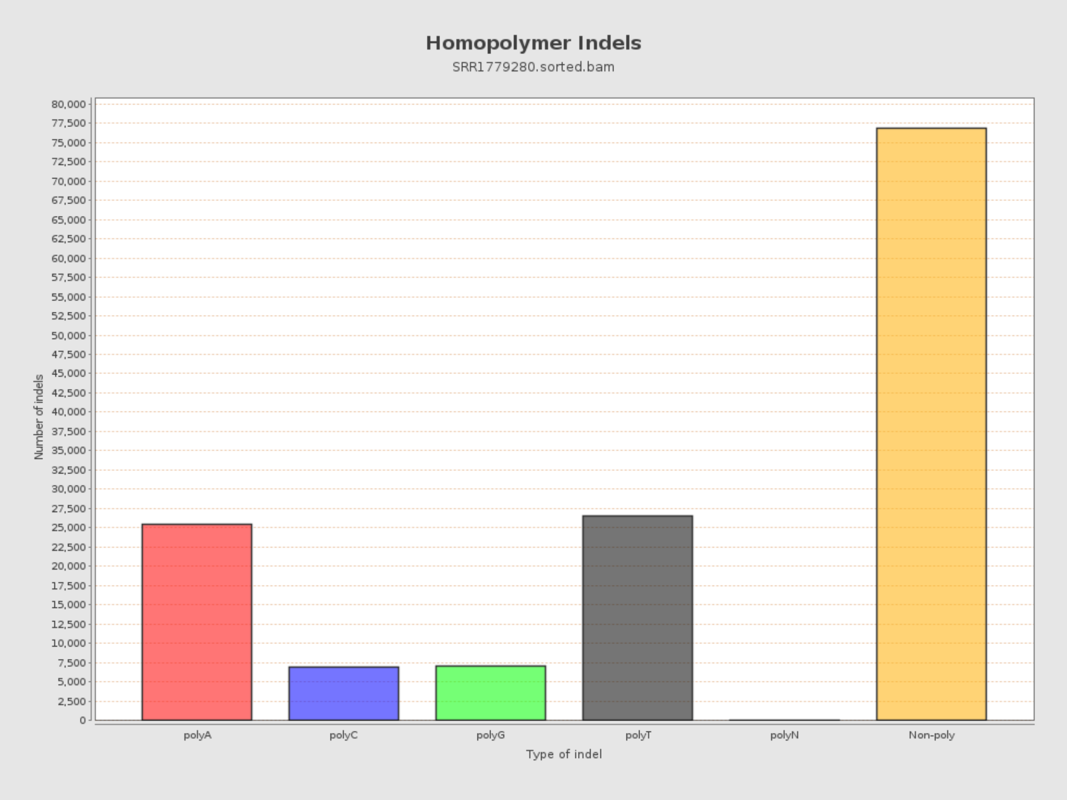
9. Results : Mapped Reads GC-content Distribution



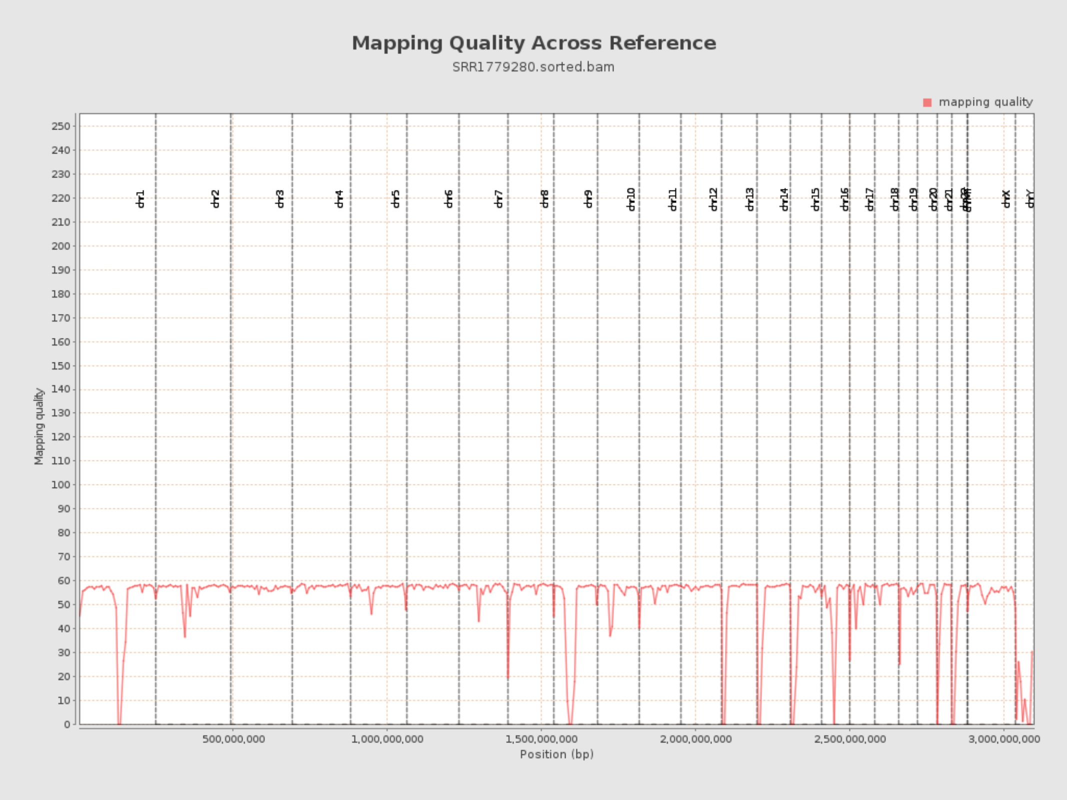
10. Results : Mapped Reads Clipping Profile



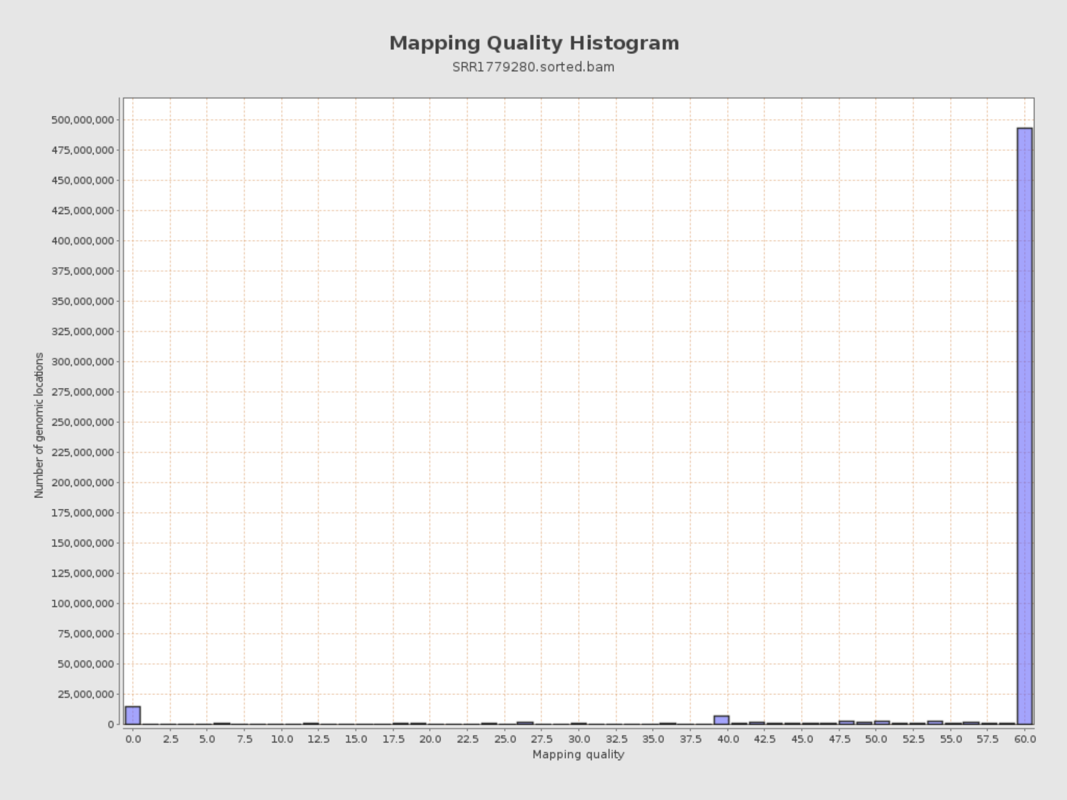
11. Results : Homopolymer Indels



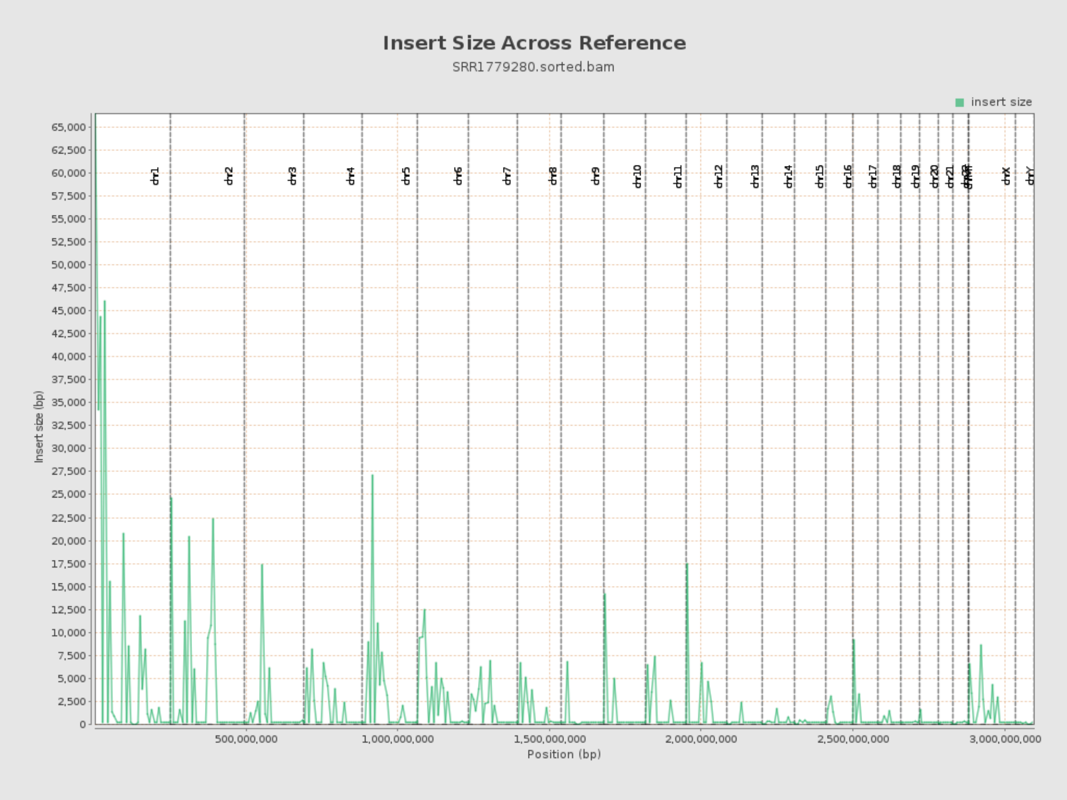
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram