

Figure S1. Performance comparison in terms of PCC of CrnnCrispr and four existing deep learning-based methods on nine datasets with various scales under a leave-one-cell-out procedure.

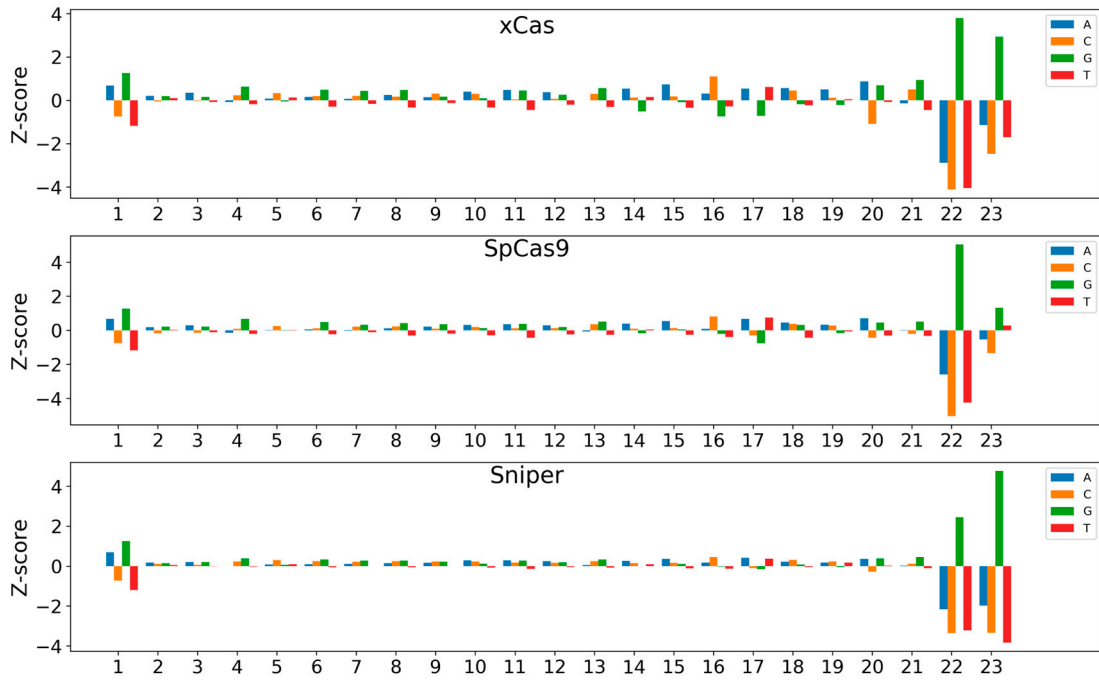


Figure S2. Impact of nucleotide composition of sgRNA activity on three medium-scale datasets. Bars show the Z-scores of nucleotide frequency for each position. The numbers below represent the positions of the sequence.

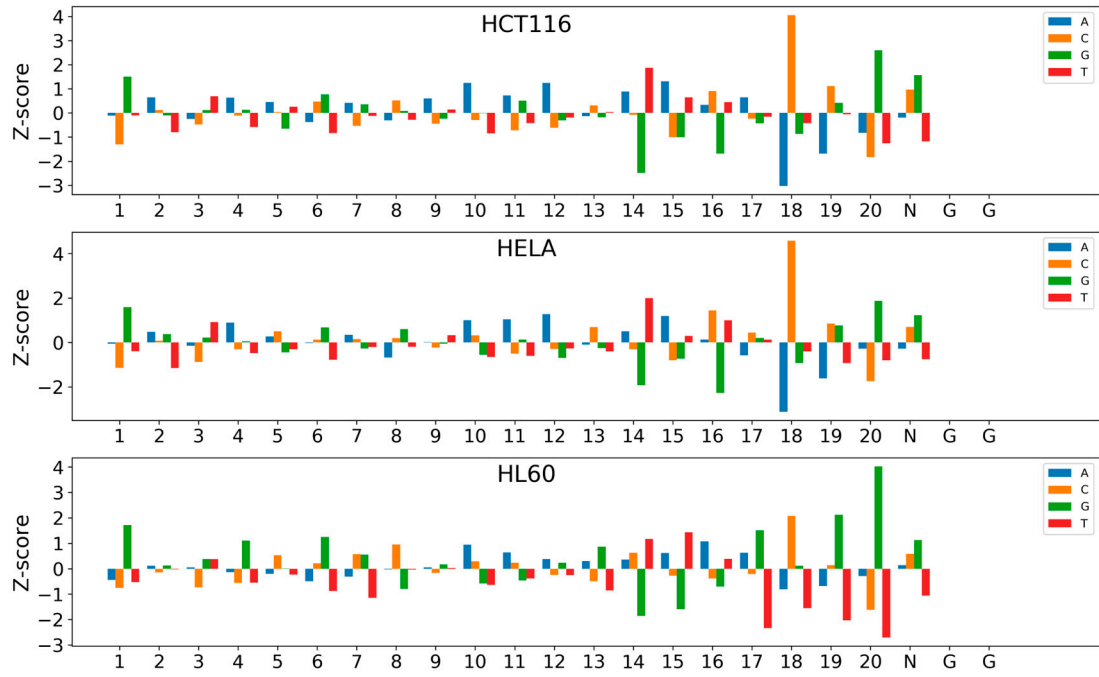


Figure S3. Impact of nucleotide composition of sgRNA activity on three small-scale datasets. Bars show the Z-scores of nucleotide frequency for each position. The numbers below represent the positions of the sequence.

	A	A	A	A	T	C	A	A	G	A	C	A	T	G	G	G	C	A	C	T	G	G	G
1	2	2	2	2	5	3	2	2	4	2	3	2	5	4	4	4	3	2	3	5	4	4	4
Label Encoding																							
A	1	1	1	1	0	0	1	1	0	1	0	1	0	0	0	0	0	1	0	0	0	0	0
C	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0
G	0	0	0	0	0	0	0	0	1	0	1	0	0	1	1	1	0	0	0	0	1	1	1
T	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23
One-hot Encoding																							

Figure S4. An example of the one-hot encoding and label encoding representation schema for sgRNA.