### **Supplementary Data**

# A high-throughput radioactivity-based assay for screening SARS-CoV-2 nsp10-nsp16 complex

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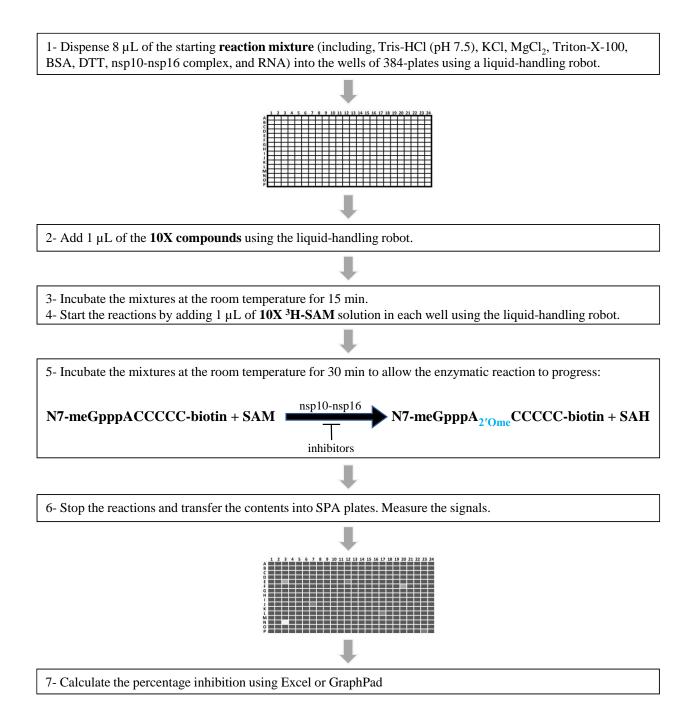
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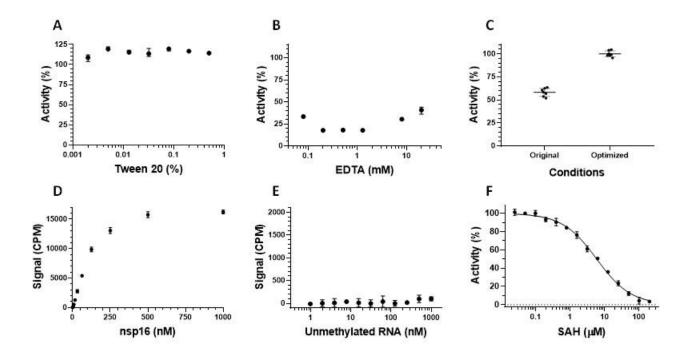
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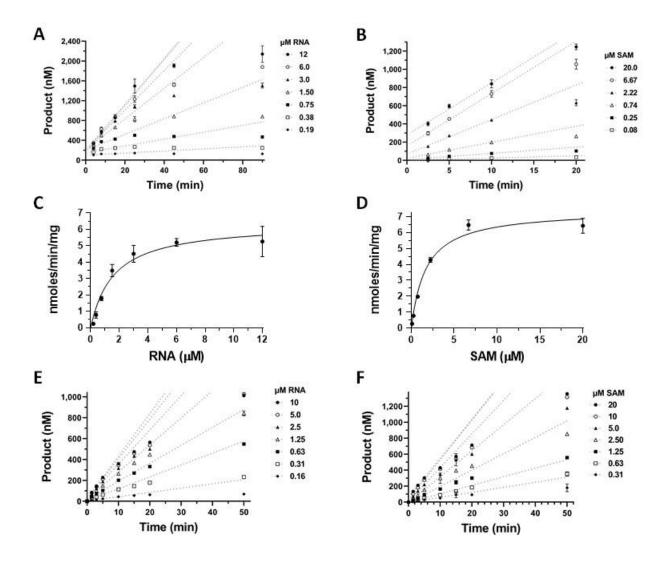
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#### Supplementary Scheme 1. Assay workflow.

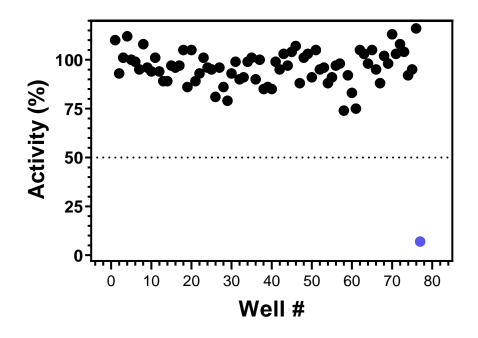




**Supplementary Figure 1.** Assay optimization. (A) Effect of Tween-20 on activity of nsp10nsp16 complex. (B) The inhibitory effect of EDTA on nsp10-nsp16 at various concentrations. (C) Comparison of nsp10-nsp16 MTase activity in the original buffer (50 mM Tris pH 8.0, 1 mM MgCl<sub>2</sub>, and 5 mM DTT) versus the optimized buffer condition (50 mM Tris pH 7.5, 100 mM KCl, 1.5 mM MgCl<sub>2</sub>, 5 mM DTT, 0.01% BSA, 0.01% Triton X-100), in the presence of 2  $\mu$ M RNA substrate, 5  $\mu$ M SAM (16% <sup>3</sup>H-SAM), and 250 nM nsp16. (D) MTase activity at various concentrations of nsp10-nsp16 complex using N7-meGpppACCCCC RNA (Cap-0). (E) The N7unmethylated RNA is not a substrate for nsp10-nsp16 complex; here reactions were performed in the presence of 125 nM nsp10-nsp16, 5  $\mu$ M SAM and varying concentrations of N7-unmethylated RNA substrate (0.97 nM to 1  $\mu$ M) for 30 minutes. (F) SAH inhibited nsp10-nsp16 with an IC<sub>50</sub> value of 5.9  $\pm$  0.6  $\mu$ M (Hill Slope: -0.9). The values in panel C are from seven independent experiments (n=7). All other experiments were performed in triplicate (n=3).



Supplementary Figure 2. Linearity of initial velocities at 125 and 250 nM of nsp10-nsp16 complex. The initial velocities were determined at 250 nM of nsp10-nsp16 complex using (A) various concentrations of RNA (as indicated on the plot) and fixed SAM concentration (6  $\mu$ M), and (B) varying concentrations of SAM and fixed RNA concentration of 5.6  $\mu$ M under the optimized condition. The first 10 minutes linear initial velocities from A and B were used to calculate the  $K_m$  values for (C) RNA substrate and (D) SAM. The linearity of the initial velocities was also assessed at 125 nM of nsp10-nsp16 complex (E and F). The velocities at various concentrations of (E) RNA and (F) SAM are shown up to 50 minutes. The linear portion of the initial velocities from E and F are re-plotted and shown in Figure 2A and 2B, respectively. All experiments were performed in triplicate (n=3)



Supplementary Figure 3. Screening of 76 chemical probes against nsp10-nsp16 complex. A collection of 76 chemical probes for epigenetic targets including 20 methyltransferase inhibitors were screened at 50  $\mu$ M against nsp10-nsp16 under the optimized screening assay conditions (i.e., 0.8  $\mu$ M RNA, 1.7  $\mu$ M SAM, and 125 nM nsp16 enzyme). The corresponding percentage activity data for each probe is shown on the graph with a black dot. SAH was used at the same concentration as a control (blue dot). Please note that the dotted line marks the 50% activity threshold.

Supplementary Table 1. 76 chemical probes were screened against nsp10-nsp16 complex. 76 chemical probes including 20 methyltransferase inhibitors were screened against SARS-CoV-2 nsp10-nsp16 using the optimized HTS assay. The observed percentage of activity of nsp10-nsp16 in the presence of each of these compounds (at 50  $\mu$ M) is presented. The list of compounds (available at <u>https://www.thesgc.org/chemical-probes</u>), and their specific protein targets are provided. Negative control analogues of the chemical probes are specified with "Negative Ctrl" under the "Specific Targets" column.

Compound	Specific Targets	<u>% activity</u>
		<u>@ 50 µМ</u>
UNC1215	L3MBTL3	103
BSP UNC0638	pan-Bromodomain	105
01100038	EHMT2 (G9a), EHTM1 (GLP) EHMT2 (G9a), EHTM1 (GLP)	102
UNC0737	(Negative Ctrl)	113
A-395	EED	100
A-395N	EED (Negative Ctrl)	99
TP-064	CARM1 (PRMT4)	98
TP-064N	CARM1 (PRMT4) (Negative Ctrl)	105
MS023	Type I PRMTs (PRMT1,3,4,6,8)	99
MS094	Type I PRMTs (PRMT1,3,4,6,8) (Negative Ctrl)	103
UNC1999	EZH2	108
UNC2400	EZH2 (Negative Ctrl)	104
PFI-2	SETD7	105
(S)-PFI-2	SETD7 (Negative Ctrl)	110
SGC-CBP30	CREBBP, EP300	103
A-366	EHMT2 (G9a), EHMT1 (GLP)	112
OICR-9429	WDR5	103
OICR-0547	WDR5 (Negative Ctrl)	101
NVS-PAK1-1	PAK1	107
GSK864	Mutant isocitrate dehydrogenase 1	81
BI-9321	NSD3	97
BI-9466	NSD3 (Negative Ctrl)	105
SGC707	PRMT3	105
XY1	PRMT3 (Negative Ctrl)	116
PFI-3	SMARCA2, SMARCA4, PBRM1 (PB1)	95
GSK-J1	KDM6B (JMJD3), KDM6A (UTX), KDM5B (JARID1B)	96
A-485	p300, CBP	95
A-486	p300, CBP (Negative Ctrl)	108
SGC0946	DOT1L	97
SGC0649	DOT1L (Negative Ctrl)	91
UNC0642	EHMT2 (G9a), EHTM1 (GLP)	98
GSK343	EZH2	93
L-Moses	KAT2B (PCAF), KAT2A (GCN5)	100
GSK484	PAD-4	101
BAY-876	GLUT1	97
BAY-588	GLUT1 (Negative Ctrl)	94
PFI-5	SMYD2	88
NVS-CECR2-1	CECR2	104
OF-1	BRPF1, BRD1 (BRPF2), BRPF3	88

Compound	Specific Targets	<u>% activity</u> @ 50 µM
IOX1	pan-2-OG	<u>99</u>
I-BRD9	BRD9	79
LP99	BRD9, BRD7	85
NI-57	BRPF1, BRD1 (BRPF2), BRPF3	97
I-CBP112	CREBBP, EP300	93
GSK-LSD1	KDM1A (LSD1)	86
GSK 2801	BAZ2A, BAZ2B	89
BAZ2-ICR	BAZ2A, BAZ2B	96
PFI-4	BRPF1B	96
A-196	SUV420H1/H2	93
A-197, SGC2043	SUV420H1/H2 (Negative Ctrl)	101
GSK591	PRMT5	96
SGC2096	PRMT5 (Negative Ctrl)	98
IOX2	pan-2-OG	90
PFI-1	BRD2, BRD3, BRD4, BRDT (BET)	91
JQ1	BRD2, BRD3, BRD4, BRDT (BET)	91
<b>TP-472</b>	BRD9, BRD7	88
MS049	PRMT4 (CARM1), PRMT6	95
BAY-299	BRD1, TAF1	96
TP-238	CECR2, BPTF (FALZ)	95
LLY-507	SMYD2	90
BAY-598	SMYD2	89
BAY-369	SMYD2 (Negative Ctrl)	94
BI-9564	BRD9, BRD7	86
GSK6853	BRPF1	95
SGC6870	PRMT6	83
SGC6870N	PRMT6 (Negative Ctrl)	75
MRK-740	PRDM9	86
MRK-740-NC	PRDM9 (Negative Ctrl)	85
SGC3027	PRMT7	74
SGC3027N	PRMT7 (Negative Ctrl)	92
UNC6934	NSD2-PWWP1	92
UNC7145	NSD2-PWWP1 (Negative Ctrl)	95
LLY-283	PRMT5	99
LLY-284	PRMT5 (Negative Ctrl)	101
BAY-6035	SMYD3	89
BAY-444	SMYD3 (Negative Ctrl)	101
SAH (Control)	_	7