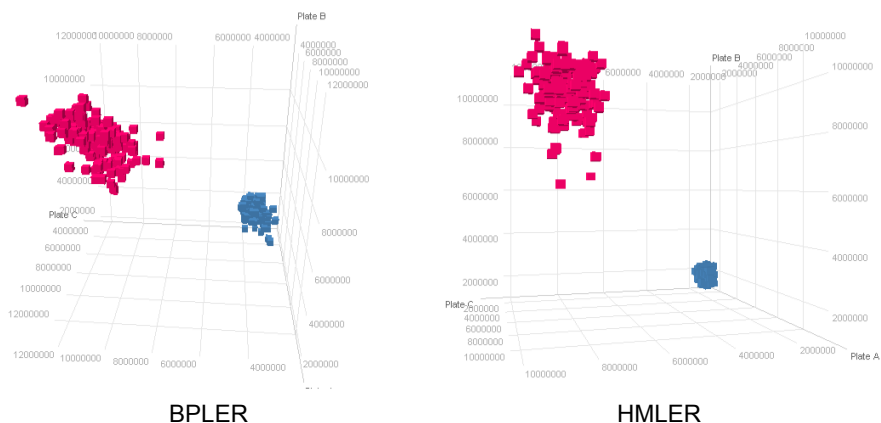
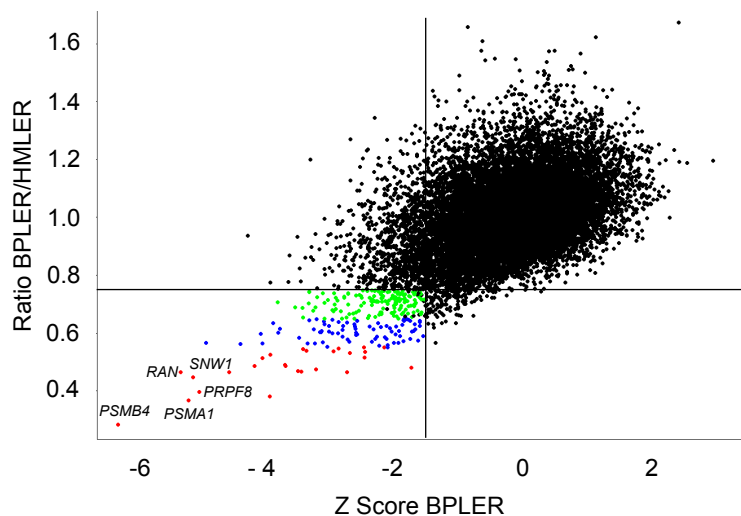


A

■ Non-targeting siRNA #4 ■ *PLK1* siRNA



B



C

Screening Hits	Ratio	Hits	Confirmed Hits	Validation rate
Highly Selective	$R \leq 0.55$	26	23	88%
Moderately Selective	$0.55 < R \leq 0.65$	76	57	75%
Poorly Selective	$0.65 < R \leq 0.75$	143	74	52%
Total		245	154	63%

D

Highly selective hits			
	Z score	Ratio	siRNAs scoring +
<i>PSMB4</i>	-6.73	0.28	4
<i>RAN</i>	-5.67	0.47	2
<i>PSMA1</i>	-5.53	0.37	4
<i>SNW1</i>	-5.45	0.45	3
<i>PRPF8</i>	-5.34	0.40	2
<i>DDX19B</i>	-4.84	0.46	3
<i>ZNF490</i>	-4.40	0.49	1
<i>DHX8</i>	-4.27	0.51	4
<i>PSMA2</i>	-4.14	0.38	2
<i>UBL5</i>	-4.14	0.53	2
<i>PSMD7</i>	-3.88	0.49	2
<i>DHRS13</i>	-3.66	0.47	1
<i>RACGAP1</i>	-3.61	0.47	4
<i>ZNF574</i>	-3.52	0.54	1
<i>ZNF643</i>	-3.05	0.54	1
<i>FIZ1</i>	-2.97	0.55	1
<i>RFT1</i>	-2.82	0.47	1
<i>PPP2CA</i>	-2.77	0.53	2
<i>HAUS3</i>	-2.52	0.52	3
<i>ETHE1</i>	-2.19	0.55	1
<i>PSMC3</i>	-1.77	0.49	4
<i>PSMA3</i>	-1.72	0.48	4
<i>PSMC1</i>	-1.50	0.52	2

■ Proteasome degradation  
 ■ RNA biogenesis  
 ■ Spindle checkpoint  
 ■ Transcription