

ChIP peak name	ChIP peak height	Number of mismatches	sgRNA matched sequences at dCas9 binding sites															PAM				
			1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	1	2	3
<i>SHB</i> on-target	7067	0	T	G	T	G	C	T	A	A	A	C	C	T	C	C	C	G	T	T	G	G
Off-Target #1	124	3	G	G	T	G	C	C	C	A	A	C	C	T	C	C	C	G	T	T	G	G
Off-Target #2	142	5	G	C	A	C	T	T	A	A	A	C	C	T	C	C	C	G	T	T	G	G
Off-Target #3	160	6	G	C	C	C	G	G	A	A	A	C	C	T	C	C	C	G	T	G	G	G
Off-Target #4	171	4	T	C	T	C	T	G	A	A	A	C	C	T	C	C	C	G	T	T	G	G
Off-Target #5	262	5	A	A	T	C	A	C	A	A	A	C	C	T	C	C	C	G	T	C	G	G
Off-Target #6	293	5	A	G	C	T	G	T	T	A	A	C	C	T	C	C	C	G	T	C	G	G
Off-Target #7	296	6	G	C	C	T	A	C	A	A	A	C	C	T	C	C	C	G	T	A	G	G
Off-Target #8	336	5	A	C	T	A	A	G	A	A	A	C	C	T	C	C	C	G	T	G	G	G
Off-Target #9	489	6	C	T	C	T	G	C	A	A	A	C	C	T	C	C	C	G	T	G	G	G
Off-Target #10	2860	2	T	G	G	A	C	T	A	A	A	C	C	T	C	C	C	G	T	A	G	G
Off-Target #11	202	5	C	C	T	A	G	G	A	A	A	C	C	T	C	C	C	G	T	C	G	G
Off-Target #12	129	6	A	A	T	T	A	C	A	A	A	C	C	T	C	C	C	A	T	G	G	G

Supplemental Figure S8: dC9Sun-D3A off-target peak analysis of predicted SHB sgRNA homology to the genomic DNA
dCas9 off-target ChIP-seq peak analysis for the *SHB* sgRNA sequence homology, with the *SHB* sgRNA sequence reference highlighted in orange. Matching bases in blue, mismatches in white, matched PAM site (NGG) in light green for 'N' and in gray for 'GG' leaway