

**Supplementary Table S3. Activity of Sp and Nm CRISPR-Cas9 at predicted off-target loci**

Sp Cas9	Sequence	Location hg38	Gene	Feature	Mock			Treated	
					Indel Reads	Total Reads	% Indels	Indel Reads	Total Reads
DHFR_ON	TTTTATAGGTAAACAGAATCTGG	chr5:80649480-80649502	DHFR	Exon	19	38816	0.05	24362	67623
SD_OT1	TTTTATAGGTAAACAGAATCAAG	chr20:61340824-61340846	CDH4	Intron	5	17474	0.03	96	38182
SD_OT2	AATTATGGTAAACAGAATCCAG	chr3:150716100-150716122	ERICH6-AS1	Intron	3	23246	0.01	5	50066
SD_OT3	AATTTTAGCTAAACAGAATCTGG	chr13:55202642-55202664	MIR5007	Intergenic	11	40058	0.03	16	65291
SD_OT4	CTTTTGAGATAAACAGAATCTGG	chr5:163324724-163324746	CCNG1	Intergenic	21	32157	0.07	17	40211
SD_OT5	CAATTTAGGTAAACAGAATCAAG	chr13:37451359-37451381	LINC01048	Intergenic	6	26412	0.02	8	43450
SD_OT6	AAATACAGGTAAACAGAATCCAG	chr9:89910167-89910189	LOC101927847	Intergenic	114	23182	0.49	158	56377
SD_OT7	AAATATGGTAAACAGAATCCAG	chr9:70312811-70312833	SMC5	Intron	4	31811	0.01	2	45981
SD_OT8	ATTTAGAATAAACAGAATCCGG	chr11:16695687-16695709	SOX6	Intron	4	23562	0.02	7	62543
SD_OT9	CTTTCTAGATAAACAGAATCAAG	chr11:104455058-104455080	LOC102723895	Intergenic	11	19886	0.06	15	45570
SD_OT10	AATTACTGGTAAACAGAATCCAG	chr11:63200259-63200281	SLC22A25 (10)	Intron	1	24995	0.00	4	28263
SD_OT11	GTTTTCAGGC AAACAGAATCTGG	chr15:63094584-63094606	TPM1	Intergenic	7	28389	0.02	12	38344
SD_OT12	ATTAATATGTAAACAGAATCAAG	chr7:51469279-51469301	COBL	Intergenic	9	22016	0.04	21	44310
SD_OT13	CCTAATAGTTAAACAGAATCCAG	chr1:105018549-105018571	LOC101928476	Intergenic	1	26125	0.00	4	30637
SD_OT14	ATCTGTAGCTAAACAGAATCTAG	chr1:81781462-81781484	LPHN2	Intron	15	26338	0.06	17	48806
SD_OT15	CTTTTAGGTAACAGAATCTAG	chr3:160203962-160203984	IL12A-AS1	Intron	2	43956	0.00	3	42969
SD_OT16	TTTAATAGTGAACAGAATCTGG	chr4:35028476-35028498	ARAP2	Intergenic	10	55621	0.02	10	75138
SD_OT17	CTTAAGAGTTAAACAGAATCCAG	chr20:24246166-24246188	FJL33581	Intergenic	2	42568	0.00	5	41383
SD_OT18	GTAGA-AGGTAAACAGAATCTGG	chr18:26171136-26171157	PSMA8 / DHFRP1	Intron	6	16293	0.04	9	40950
SD_OT19	GTAGA-AGGTAAACAGAATCTGG	chr6:31366749-31366770	DHFRP2	Intergenic	16	20928	0.08	12	31146
SD_OT20	ATTATAGGTCAACAGAATCTGG	chr15:48392787-48392809	FBN1	Intergenic	2	30373	0.01	3	35052

Nm Cas9	Sequence	Location	Gene	Feature	Mock			sgRNA Treated	
					Indel Reads	Total Reads	% Indels	Indel Reads	Total Reads
DHFR_ON	GTGATTTTTATAGGTAAACAGAATCTGGTGATT	chr5:80649475-80649506	DHFR	Exon	19	38816	0.05	6421	55610
ND_OT1	GAAATATTCAGGTAAACAGAATCTCTTGT	chr8:64850027-64850058	CYP7B1	Intergenic	2	51798	0.00	0	55302
ND_OT2	AAATATTAT-GGGAAACAGAATCTGCAGATT	chr4:148690476-148690506	NR3C2	Intergenic	11	54038	0.02	3	30395
ND_OT3	TTAATTTATAGGTAAAGAATCAAATGATT	chr9:20900423-20900454	FOCAD	Intron	43	57490	0.07	73	66537
ND_OT4	TTTCTGTTTAGG-AAACAGAATCTCTGCTT	chr7:12302402-12302432	VWDE	Intergenic	8	81574	0.01	3	63419
ND_OT5	TGTATTTTA-AGGGAACAGAATCTGCAGTTT	chr7:151403651-151403681	WDR86	Intron	8	80321	0.01	6	60575
ND_OT6	CTTGTTTTCTAGGTAA-CAGAATCTTATGTTT	chr1:219504572-219504602	LYPLAL1	Intergenic	2	31643	0.01	9	53989
ND_OT7	TTTCTTTTAT-GGTAAAAATAATCATAAGATT	chr17:51554583-51554613	CA10	Intergenic	45	62390	0.07	33	47487
ND_OT8	TTCTTTTTATAGGTTAA-AAATCTAAAGATT	chr10:27448879-27448909	PTCHD3	Intergenic	135	45931	0.29	204	68241
ND_OT9	AACTTTTTAAGGTAATA-AACTGGGGTTT	chr11:117048295-117048325	SIK3	Intron	23	40317	0.06	21	42971
ND_OT10	ATATTTTTATAGGAAA-AGTATCCTTAGTTT	chr1:39155639-39155669	MACF1	Intron	18	79849	0.02	13	51878
ND_OT11	CTCCTTTTGTAGG-AAACAGAAGCCTATGATT	chr10:25552204-25552234	GPR158	Intron	7	58567	0.01	11	58130
ND_OT12	GATATTTTGAAGGTAAACAGAATATAGTGATT	chr7:127127934-127127965	GRM8	Intron	3	31299	0.01	2	43458
ND_OT13	ATTGTTATACAGGTAAACAGAATCTGAGTTT	chr14:28701646-28701677	FOXG1-AS1	Intergenic	7	31059	0.02	12	50349
ND_OT14	GAAATTTAGAG-TAAACAGAATTTGAAGGATT	chr7:117455495-117455525	CFTR	Intergenic	66	136900	0.05	47	68285
ND_OT15	TTATTTTTATAGGCAAAACATTCAAAATGTTT	chr20:21946870-21946901	LINC01432	Intergenic	0	8682	0.00	7	46046
ND_OT16	ACATTTGTTAGAGGTAAACAGAAT-CCTTGTTT	chr3:86422139-86422169	CADM2	Intergenic	12	107018	0.01	20	116143
ND_OT17	TCTTTTTTATGGTAAA-AGAAATAGACAGATT	chr2:41797372-41797402	LOC388942	Intergenic	21	99208	0.02	19	81132
ND_OT18	AGAATTTTATAGGTAAATAGAATATTAGGATT	chr4:81123234-81123258	PRKG2	Intron	3	37590	0.01	5	62353
ND_OT19	TCATTTTTATAGTTAAAGAAT-GATTGCTT	chr10:56157234-56157256	ZWINT	Intergenic	37	44355	0.08	36	62022
ND_OT20	AAATTTTTATGGTAAACAGTAT-ATGTGTTT	chr7:112242118-112242148	ZNF277	Intron	13	52658	0.02	11	56758

Sp Cas9	Sequence	Location	Gene	Feature	Mock			Treated	
					Indel Reads	Total Reads	% Indels	Indel Reads	Total Reads
F8_ON	TCTAGTTGTGACAAGAAGACTGG	chrX:154931586-154931608	F8	Exon	13	34244	0.04	13012	23681

SF_OT1	TGAAGT <b>AGT</b> GACAAGAACACTAG	chr2:18300441-18300463	<i>RDH14</i>	Intergenic	9	27222	0.03	12	72012
SF_OT2	CCTC <b>TAT</b> TGTGACAAGAACAACAAG	chr17:3418064-3418086	<i>OR3A3</i>	Intergenic	9	34478	0.03	12	26961
SF_OT3	ACT <b>TTG</b> TGTGACAAGAACAACAAG	chr3:197606408-197606430	<i>LOC220729</i>	Intergenic	3	25034	0.01	11	55091
SF_OT4	C <b>TACT</b> TTTGTGACAAGAACAACAAG	chr18:65711730-65711752	<i>CDH7</i>	Intergenic	15	51199	0.03	9	54664
SF_OT5	CCTG <b>ATT</b> ATGACAAGAACAACAAG	chr3:119455673-119455695	<i>TMEM39A</i>	Intron	4	27641	0.01	4	42038
SF_OT6	GCT <b>ATTTATA</b> TACAAGAACAACAAG	chr1:53294379-53294401	<i>LRP8</i>	Intron	2	15765	0.01	12	28493
SF_OT7	GCTAG <b>CTGGT</b> ACAAGAACAACAAG	chr10:85183697-85183719	<i>LINC01519</i>	Intergenic	13	36896	0.04	160	25800
SF_OT8	T <b>TTA</b> ATTGTG <b>TA</b> AAGAACAACAAG	chr16:24493609-24493631	<i>RBBP6</i>	Intergenic	7	30507	0.02	1	15830
SF_OT9	GCTG <b>CT</b> TGTG <b>GA</b> AAGAACAACAAG	chr14:104429385-104429407	<i>C14orf180</i>	Intergenic	7	21857	0.03	8	64070
SF_OT10	ACTAG <b>ATG</b> CCAAGAACAACAAG	chr11:94895719-94895741	<i>AMOTL1</i>	Intergenic	6	34895	0.02	4	46116
SF_OT11	CCTAG <b>AGT</b> GAAGAACAACAAG	chr6:133740862-133740884	<i>TARID</i>	Intron	12	43313	0.03	2	35984
SF_OT12	CCTA <b>TTCT</b> GAAAGAACAACAAG	chr17:3212137-3212159	<i>OR1A1</i>	Intergenic	9	36370	0.02	7	43932
SF_OT13	C <b>TTAG</b> TTGT <b>CA</b> GAAGAACAACAAG	chr1:158161025-158161047	<i>CD1D</i>	Intergenic	3	50044	0.01	9	47983
SF_OT14	A <b>TTAG</b> CTGTG <b>ACC</b> AGAACAACAAG	chr12:40126208-40126230	<i>SLC2A13</i>	Intergenic	5	40849	0.01	12	46200
SF_OT15	A <b>AT</b> -GATGTGACAAGAACAACAAG	chr8:138011536-138011557	<i>LOC101927822</i>	Intergenic	15	38346	0.04	11	49675
SF_OT16	G <b>CT</b> -GATGTGACAAGAACAACAAG	chr3:18263971-18263992	<i>LOC339862</i>	Intron	6	30850	0.02	12	45603
SF_OT17	A <b>CC</b> TGT-GTGACAAGAACAACAAG	chr8:108019686-108019707	<i>RSPO2</i>	Intron	3	46437	0.01	9	54430
SF_OT18	AC-A <b>TTA</b> GTGACAAGAACAACAAG	chr15:50258679-50258700	<i>HDC</i>	Intron	14	29800	0.05	15	55272
SF_OT19	CCG <b>AG</b> TTG <b>AG</b> ACTAGAACAACAAG	chr12:52923288-52923310	<i>KRT8</i>	Intron	9	84604	0.01	9	50722
SF_OT20	CC <b>AG</b> TTGG <b>ACC</b> AGAACAACAAG	chr3:72124373-72124395	<i>LINC00877</i>	Intergenic	9	32763	0.03	10	38069

					Mock			sg RNA Treated	
<i>Nm</i> Cas9	Sequence	Location	Gene	Feature	Indel Reads	Total Reads	% Indels	Indel Reads	Total Reads
F8_ON	GGTTTCTAGTTGTGACAAGAACAACAAG	chrX:154931581-154931612	<i>F8</i>	Exon	13	34244	0.04	17208	58765
NF_OT1	GTTATCA <b>AGC</b> TGTG <b>AA</b> AAGAACAACAACAAG	chr11:81451988-81452019	<i>LOC101928989</i>	Intergenic	6	54770	0.01	1	74649
NF_OT2	CTC <b>ATCT</b> TGTTG <b>GG</b> AC-AGAACAACAACAACAAG	chr4:6449282-6449312	<i>PPP2R2C</i>	Intron	1	25192	0.00	1	115037
NF_OT3	TCTGTCT-GTTGT <b>CACT</b> AGAACAACAACAACAAG	chr14:103807364-103807394	<i>PPP1R13B</i>	Intron	7	28275	0.02	8	93749
NF_OT4	CCATTCTAG <b>ATGTCA</b> CTAAGAACAACAACAAG	chr11:17758431-17758463	<i>KCNC1</i>	Intron	4	27963	0.01	10	70226
NF_OT5	GACTTCTAG-TGTG <b>ATT</b> AGAACACCTCTGTTT	chr1:62221585-62221615	<i>L1TD1</i>	Intergenic	7	39236	0.02	14	58683
NF_OT6	TGACTC-AG <b>GT</b> GTGACA <b>CA</b> ACAACAACAACAACAAG	chr8:72549441-72549471	<i>KCNB2</i>	Intron	1	39232	0.00	6	101133
NF_OT7	GAGATC-AG <b>TGGT</b> GACA <b>TA</b> ACAACAACAACAACAAG	chr12:76595292-76595322	<i>OSBPL8</i>	Intergenic	10	30435	0.03	3	90764
NF_OT8	CAATTCTA <b>CTTGTGA</b> AAAAACAACAACAACAACAAG	chr4:103590707-103590738	<i>TACR3</i>	Intron	2	35073	0.01	7	103688
NF_OT9	TGCATT <b>AG</b> TTG-GAC <b>AAA</b> ACAACAACAACAACAAG	chr11:34919571-34919601	<i>PDHX</i>	Intron	29	30595	0.09	34	73117
NF_OT10	CTGCTCT-G <b>GT</b> GTGACA <b>AGC</b> CACACATGATT	chr17:14487388-14487418	<i>HS3ST3B1</i>	Intergenic	8	17438	0.05	6	25539
NF_OT11	AAGTCTCA <b>CTTGT</b> ACAAGAA-ACTATGGTTT	chr4:61801542-61801572	<i>LPHN3</i>	Intron	4	46087	0.01	7	112550
NF_OT12	TTATT <b>TA</b> -TTGTGACAAGAACA <b>CA</b> TTAAGTTT	chr13:47043063-47043093	<i>HTR2A</i>	Intergenic	2	40161	0.00	6	110758
NF_OT13	TCCATCTAG <b>TGGT</b> CACAAGAACA <b>CT</b> CCCAGATT	chr5:178551262-178551294	<i>COL23A1</i>	Intron	0	108	0.00	20	24377
NF_OT14	AACTTCTAGTTGTG <b>GCA</b> AGGA-ACACAGGTTT	chr19:4709257-4709287	<i>DPP9</i>	Intron	20	32561	0.06	8	71906
NF_OT15	ATGCTCTAGTT <b>CT</b> GACA-GAACA <b>G</b> TCCTGATT	chr3:174218934-174218964	<i>NLGN1</i>	Intron	2	20981	0.01	2	105950
NF_OT16	CCTGTCTA <b>CTT</b> GTGACA <b>AA</b> CA <b>AA</b> TAGGCTT	chr9:95685454-95685484	<i>LINC00476</i>	Intergenic	0	1082	0.00	10	87966
NF_OT17	GCTG <b>ACT</b> AGTTGTGACAAGAACA <b>TA</b> TATGGTTT	chr5:153668581-153668612	<i>GRIA1</i>	Intron	3	42277	0.01	5	83060

					Mock			Treated	
<i>Sp</i> Cas9	Sequence	Location	Gene	Feature	Indel Reads	Total Reads	% Indels	Indel Reads	Total Reads
HPSPON	TTATGCTGAGGATTTGGAAAGGG	chrX:134473412-134473434	<i>HPRT1</i>	Exon	39	90377	0.04	14199	18835
SH_OT1	AGATGCTGAGGATTTGGAAACAG	chr9:18850591-18850613	<i>ADAMTSL1</i>	Intron	16	88359	0.02	10565	76165
SH_OT2	A <b>AG</b> TGCTGAGGATTTGGAAAAAG	chr14:44234312-44234334	<i>FSCB</i>	Intergenic	9	43513	0.02	23	74296
SH_OT3	G <b>TTG</b> TGAGGATTTGGAAATAG	chr6:128025116-128025138	<i>PTPRK</i>	Intron	21	117152	0.02	14	106425
SH_OT4	T <b>GCT</b> GGT <b>GAG</b> GATTTGGAAAAAG	chr4:144173348-144173370	<i>GYPA</i>	Intergenic	128	104549	0.12	72	94169
SH_OT5	A <b>GAG</b> GGT <b>GAG</b> GATTTGGAAAGAG	chrX:49277223-49277245	<i>PPP1R3F</i>	Intron	24	106875	0.02	9	74314
SH_OT6	AT <b>CTG</b> CC <b>GAG</b> GATTTGGAAAAAG	chrX:114147063-114147085	<i>XACT</i>	Intergenic	36	63921	0.06	16	40354
SH_OT7	GTATT <b>GAG</b> GAGGATTTGGAAAGAG	chr9:97683356-97683378	<i>XPA</i>	Intron	10	46893	0.02	7	55163

SH_OT8	ATTGCTGAAGATTTGGAAATGG	chr12:12706721-12706743	<i>GPR19</i>	Intergenic	11	64173	0.02	13	81505
SH_OT9	ATAAGCTGAGGTTTTGGAAAGAG	chr11:69522853-69522875	<i>LINC01488</i>	Intergenic	21	82103	0.03	19	74913
SH_OT10	TTATCTGAGGCTTTGGAAAGAG	chr11:107227503-107227525	<i>CWF19L2</i>	Intergenic	7	60916	0.01	15	80116
SH_OT11	AAATGCTTAGAATTTGGAAAAAG	chr13:78935858-78935880	<i>LINC00331</i>	Intergenic	40	92095	0.04	35	92193
SH_OT12	CCAGGCTGAGCATTGGAAACAG	chr2:75542297-75542319	<i>EVA1A</i>	Intron	3	48516	0.01	5	27812
SH_OT13	TCAGCTCAGGGTTTGGAAAAAG	chr9:134602667-134602689	<i>COL5A1</i>	Intergenic	11	35396	0.03	14	43755
SH_OT14	AGATACTGAGTATTTGGAAAGAG	chr10:65363709-65363731	<i>LINC01515</i>	Intergenic	15	86246	0.02	18	74460
SH_OT15	CTCAGCTGAGGGTTTGGAAATGG	chr7:76409916-76409938	<i>ZP3</i>	Intron	7	38076	0.02	5	35833
SH_OT16	TTCTTCTGAGTATTTGGAAAGAG	chr11:5316658-5316680	<i>OR51B2</i>	Intergenic	23	100611	0.02	8	89315
SH_OT17	TTCTGCAGAGTATTTGGAAAAAG	chr7:157005061-157005083	<i>MXN1</i>	Intron	41	70839	0.06	27	73454
SH_OT18	TTCTGCTTTGGATTTGGAAAGGG	chr3:139123737-139123759	<i>BPESC1</i>	Intron	15	45460	0.03	26	83052
SH_OT19	TTTTGGTGAGGCTTTGGAAAGGG	chr9:8153172-8153194	<i>PTPRD</i>	Intergenic	29	97642	0.03	31	87184

Nm Cas9	Sequence	Location	Gene	Feature	Mock			sgRNA Treated	
					Indel Reads	Total Reads	% Indels	Indel Reads	Total Reads
HPNMON	ATCATTATGCTGAGGATTTGGAAAGGGTGTTT	chrX:134473408-134473439	<i>HPRT1</i>	Exon	39	90377	0.04	15192	63286
NH_OT1	CTTTTTGTGCTGTGGATTTGGAAACACTGTTT	chr5:22612338-22612369	<i>CDH12</i>	Intron	6	57354	0.01	14	83328
NH_OT2	AGTTTTATGATGATGATTTGGAAAGAATGTTT	chr3:108393632-108393663	<i>MYH15</i>	Intron	7	53151	0.01	9	65204
NH_OT3	TATCTTATGCAGAGGAATTGGAAATGTGCTT	chr11:101512872-101512903	<i>TRPC6</i>	Intron	8	54510	0.01	8	72406
NH_OT4	TACTTCTGCAAGGATTTGGAAAACTGATT	chr2:54332913-54332944	<i>C2orf73</i>	Intron	10	58491	0.02	14	65082
NH_OT5	CATATTTGCTGCTGATTTGGAAATGTGCTT	chr1:50151661-50151692	<i>ELAVL4</i>	Intron	17	71101	0.02	13	81849
NH_OT6	CCCTTAAAGCTGGCATTGGAAAGGGAGGTT	chr1:154465575-154465606	<i>IL6R</i>	Exon	12	47982	0.03	15	64389
NH_OT7	CAGCTTATGCTGAGGAAGTGGAAAGGTTGATT	chr4:37604445-37604476	<i>RELL1</i>	Intron	3	46231	0.01	8	74672
NH_OT8	CATTTTATACTGAGGATATGGAAAGTGTGTTT	chr6:125945042-125945073	<i>HINT3</i>	Intergenic	4	72007	0.01	10	84934
NH_OT9	CCACTATGCAGAGGATTAAGAAAGGCTGATT	chr13:96849496-96849527	<i>HS6ST3</i>	Intergenic	12	53749	0.02	18	75090
NH_OT10	TCATTTCTGCTGAGATTTTGAAGCACGTTT	chr18:29157955-29157986	<i>CDH2</i>	Intergenic	4	67570	0.01	18	77857
NH_OT11	TAAATTATTCTGAGTATTTGAAAATAGAGTTT	chr15:45569282-45569313	<i>HMG2P46</i>	Intergenic	5	57218	0.01	8	68424
NH_OT12	CAAGATATGCTAAGGATTGGGAAAAGTGGCTT	chr4:10405508-10405539	<i>ZNF518B</i>	Intergenic	10	55722	0.02	19	73819
NH_OT13	CAAGATATGCTAAGGATTGGGAAAAGTGGCTT	chr4:10406724-10406755	<i>ZNF518B</i>	Intergenic	20	54186	0.04	21	69081
NH_OT14	TGTCTTGTGCTGGGATTTGAAAAGTGGGGTT	chr7:31944144-31944175	<i>PDE1C</i>	Intron	7	52646	0.01	10	85332
NH_OT15	CATATTCTGCTGAGGATCTGAAAAGTCTGCTT	chr15:22949770-22949801	<i>CYFIP1</i>	Intron	0	967	0.00	3	7578
NH_OT16	TGTATTACCCTGAGGATTTGGTAAGAGTCTT	chr2:233774831-233774862	<i>MROH2A</i>	Intergenic	13	76697	0.02	16	89721
NH_OT17	TTAATTATGTTGAGGATCTGGAACTTTGATT	chr6:82606316-82606347	<i>TPBG</i>	Intergenic	9	61139	0.01	6	80382
NH_OT18	ATGTTTATTCTGAGGATTTGCGAATATTGTTT	chr6:147073097-147073128	<i>STXBP5-AS1</i>	Intron	1	71151	0.00	5	86746
NH_OT19	TTGACTATGCTGAGGATTTGCCAAATATGGTT	chr12:41575307-41575338	<i>PDZRN4</i>	Intergenic	7	54063	0.01	13	81396

% Indels	P Value			Forward Primer	Reverse Primer
36.03	0			CTCCACTATGAGACATGATTTTCTGTGGTGA	GTGGCCCTGGCCAGGAATT
0.25	8.9987E-11			GCAATCCTCCTGCTTAAGCCTC	GGATGTTGCTTTCTGTTGCTTGGC
0.01	1.0000			GAATCCACATTTTCAGCTGCAGG	GGGCTGTTGAATTTTGTGCAAGGC
0.02	1.0000			CTATGCATTTGTAGTCTTGTGATTTGGGGAG	CTGCAGATGTAATTGTAGGATTTGAGCTTC
0.04	0.1938			AGCTGACTTTTCTTACCCTCCTGG	TAGACTCGCATGGAGCCTTGTTC
0.02	1.0000			ACTGCTTCCATCACCATCCC	GCCTGGAAGTTGGACTTTCAGAC
0.28	1			TGAGGCCACATCATCTGA	CCAGTGGTTTTGACATTGGTTC
0.00	0.2344			GAAGGATGAAACACTTCCCAAGTCTTTTATG	GGATGTCAAGTTTTTTCAGATGGTTTCTGC
0.01	1.0000			ATTGCCTGATGGCAAGAGACAGAC	AGGCCTGGCTAATTGTGTGTGTG
0.03	1.0000			AAGTTGTTCAAACCTCACAGCAACCTTAGGG	CATCATGCCCTTCTAGGCGC
0.01	0.3797			CTCCCTAACTCATTCTATGAGGGC	GCCTTTTCTGTATCTCTTGAGACAACCATG
0.03	0.6519			CTTCTTTCAGGCAAATGGGCAACC	GTCTATGGTATGCAGCAGAGTGG
0.05	0.8470			GGCTGTGGTGAGTTGAGATTGC	GTGAGATGTCATCTTGAAGGGGC
0.01	0.3829			TCTTGGCCAAGGAGACCACAG	GAAGCCGATGGTCAGTACTCGT
0.03	1.0000			CCTCCCATCTGTAACCAACCTG	GTAGTGACAAGGGTGTAGCTGAAG
0.01	0.6840			CTGGTCAAGGCTAGCCTAGG	AAGGGAGGGGAGAGATGCTG
0.01	1.0000			GAGTCTTCGTTCTCATTTTCAAACCTTGAACGC	CTTCCCATAGGATTCATAGTTCTATGCTATCG
0.01	0.2824			CTCTTGACCAAGGGGACCTC	CCAGAGCCAGGTTGTGATTCCG
0.02	1.0000			TCGTGCTGTGTCCAGAAC	GCCACCAACTATCCAGACCATG
0.04	0.0821			GGCAAGAAAATGAGCTCGTTGTGG	GAGCTCACCGCTGCTGTCAT
0.01	1.0000			GTTTCTCTGGGTTCCAGGCTAAGG	AATGCCTGTCTAGATCCACAGGAG

		2-RNA Treated					
% Indels	P Value	Indel Reads	Total Reads	% Indels	P Value		
11.55	0	14139	71676	19.73	0	CTCCACTATGAGACATGATTTTCTGTGGTGA	GTGGCCCTGGCCAGGAATT
0.00	0.2339	0	77297	0.00	0.1610	GGGGAGAGATAGAAAGCCTGC	GTGGTGCCATTGTTGAAAACTAACCTCC
0.01	0.4041	1	21194	0.00	0.1986	GGACTAGAGCAGCTTAGTGCA	GCTTGGCTGTTGAGAACGTTCTTG
0.11	0.0502	55	79236	0.07	1.0000	GCCTCAGCATTAGGTAATGAGCTC	GCACAGATGCTAACATTATTCCTTGTACTTCATATCA
0.00	0.3676	5	52942	0.01	1.0000	ATCCATGTGGAGTCCAGGCATAG	GGCACCAGGTGCCACCAATT
0.01	1.0000	3	99273	0.00	0.0733	CGGATCTGTTCCAGGGAAAG	CGACCCCTGAGTTAAGTTCAGT
0.02	0.3485	16	95751	0.02	0.2739	GTTGCCTGAGCTTGGCACTCT	CCTCCTCTGGAATGGATAACTG
0.07	0.9094	59	85756	0.07	1.0000	CTCACTGCAACCTCCGCCTA	CCAGGAAGAAAAGTCAGTACTGGG
0.30	0.9117	202	81168	0.25	1.0000	CCCCATCTCAGCTTTTTCTCCC	GAGTCTACCACCTGCCATAAC
0.05	0.6525	21	63057	0.03	0.0881	CTCGGCTTCCAAAGTGTCTG	CTGCTAAGGAATAATGGTTCAGAATGACCATC
0.03	1.0000	16	85571	0.02	0.6106	GATTGCTTTCAGATCATGACACAGAAGAGG	TTGAAACCCGGAGGCGGAAG
0.02	0.3575	7	90979	0.01	1.0000	GTGAATGTGTTTACTCTCAAGATTCCTTCTTA	CCTTTTCTTTGGTGAGCACCAGC
0.00	0.6556	2	115561	0.00	0.0685	TAGATTGGAAGGCCATGAGAGTGC	AATCAATGCCTGGTCTCTCCTTCC
0.02	1.0000	11	99281	0.01	1.0000	GCTTCTTGCATTTTACTCGAAGAGCTAG	GTCAGAGCTGGAGTTGAGTCCAAT
0.07	1.0000	23	102194	0.02	0.0012	CATTCCATGCCTGTACCAAAA	TCCAACCATTTTGCCTTTTACC
0.02	0.6061	7	70917	0.01	1.0000	GCTGTTCCGCAAGAGGCATTTT	GGTAATGCCTTTAGAGTAGCCAG
0.02	0.2891	11	89621	0.01	1.0000	GGAGTTTAAAATGCGGAGTTATAATGATGGAG	CTGAAATGTCTTTCTTTAGGAAAGGTGGAAACTG
0.02	1.0000	18	109294	0.02	0.5219	GCACCATTTGCTGAAAGGACTATTCTTCTC	AAGTGCTCCAAGGAGCATTTTCTTTGAGCAT
0.01	1.0000	9	84593	0.01	1.0000	GATCTAAATGTTCTACCAGTTCCTGAGGAACATA	GCAACAGAGCAAGACTCTGTCTCA
0.06	0.1239	70	105286	0.07	1.0000	CAGTCAACCCAGGCTAG	GGAAGGCAGCAAATATTAATAGCATGGGAAC
0.02	0.6838	7	70776	0.01	0.0677	CATGTTTCTTCTAGTGTGTTGAGAGC	GTGTTTAAATAGCACAGCAGGTTGACTACAG

% Indels	P Value		
54.95	0		
		TTGCTTTTGCCTAGTGCTAGGGTG	TCTGGGAATGGGAGAGAACCTCTA

0.02	1.0000
0.04	0.2726
0.02	0.5701
0.02	0.2200
0.01	1.0000
0.04	0.1597
0.62	2.0876E-46
0.01	0.2785
0.01	1.0000
0.01	0.3448
0.01	0.0282
0.02	0.4547
0.02	0.0863
0.03	0.2234
0.02	0.1679
0.03	0.6361
0.02	0.1611
0.03	1.0000
0.02	0.3311
0.03	1.0000

CAATAGGCTTTTTCTGTTGTAAGAAGATCTTCTG	CTCTGCAAGTTAAGCTGCACTCTC
GGGTAGAGGAGAGAACTAGGAC	GTCTCTAGAAGCCGGTCTTCAG
TCCATGCTTACACCACTACAGGC	GCCCTGTGAGTTACCAAACGTAG
CCAATGTTAAGTGAGTGTGACAGACAAAGAGTG	CACTGAGCAAGTGCATTATTTTGTAAAGTCTTTTC
CTACTTGGGTTGACATTTCCCTGG	GGTCTGTCAACCACAGGCATC
CTCACAATGACCCTGTGTCTC	CGACATCATAATCTGGTGCCATGG
GAGAATGGCTGGTGAAGGC	GATCTACTACTGCCACAGACCC
CCAACCTCAGCCTCCAAAG	TCAGCAGGAATGTATTGGACACTT
GTTTCCTGAAACATGAGGAGGGTG	TTCCCCCGTTCTACGGGTG
AGACTAGGCAGCTGGGGGAA	GCATTATTGCTGAGGGACACTGAG
CGTCTGACTCTCAGTGTCAATTGTG	GCTTCTCCCTGAACTCTCC
CTGGGTATAAGGTCTTTATGCCCTTG	CACTGGAAAAAGGGTCTCTGGG
ATTGGAGGCTAGTTGTGTATAGTGTGAGG	AATCTATGAACTTGGGGCACCTGG
AGCACTTTGGGAGGCCAGA	GTGCTAGCAAGAGCAGAGATGCAA
GGATTTAGAAGGGTAGTCATTTCAACTGCTC	GAGCACATGTCTGGAGCCATAAAC
CTGAGTAACCAAGAGTGGATCAGG	CTGATTCCATCCCTGTGGTGC
GCTAGTAGCACTAAACCAGAGCAC	GGTCTGAGCCAATTCTCAGTCAC
CTGGGGACTAATGTGAATACCACC	GCACAGAGTTGGCACCAGGA
CTCCAAAGTGCTCTAGGATGTGTG	CAACACAGCGAGACTCCATCTCA
AGCCTGGTCCCTGAAGGCTTT	CCTGCAGGGAAAAACAAAGTCAAGC

% Indels	P Value	2-RNA Treated			P Value		
		Indel Reads	Match Reads	% Indels			
29.28	0	10187	36874	27.63	0	TTGCTTTTGCCTAGTGCTAGGGTG	TCTGGGAATGGGAGAGAACCCTCTA
0.00	0.0469	0	25242	0.00	0.1863	AAAGCCAGGCAGGCAGGTTTC	CCCTCCTTCTCTCTCTCTTTTC
0.00	1.0000	4	81116	0.00	1.0000	CCACTCGTGGGATTTACCTTCAG	CTGTGTTTTCACTCCTCTCCAGC
0.01	1.0000	10	89358	0.01	1.0000	GCTTTTCCTTAACCGAGAGTCTACC	CTGGGCAACAGCGTGATACTC
0.01	1.0000	10	48450	0.02	0.7824	TGCAGCAATTCAGTCACTCTTCA	GCCCATGGACCAAGGAGTCA
0.02	0.6580	12	61703	0.02	1.0000	CTGTCTCAACTGAGAGAGCTGG	AACCCAGGAGGTGGAGCTTG
0.01	0.6815	8	41434	0.02	0.0397	CCACTGAGAAGTTCCTGTTGAGC	GCCCCCTAACATCAAGGTGTC
0.00	0.000131235	13	70730	0.02	1.0000	GAAAACAACACTCACAGCCTTTGTGCCAATG	GCAGTCCATTTGGAGTTAGCACC
0.01	1.0000	0	65715	0.00	0.1211	TGCTTGTGGGGTGTGAGGAA	TCTGCTTCCAGATAAAAAACCTT
0.05	1.0000	40	35604	0.11	0.5464	GTGCTGGCAGCATTTTTATGAGCTATGAC	GTGCCTGGCACCTAATAGATGCT
0.02	0.2765	15	37405	0.04	1.0000	TGGTCTGCCCCAGACATGGA	CGTAAGTGCAACCGCCTGG
0.01	1.0000	7	67854	0.01	1.0000	AGAAGGAGCAATTGATGCCTTATACCACG	CTATTTGAGCTCCAGCACCTGATG
0.01	1.0000	11	68702	0.02	0.1513	GGTGGTTTCCAGGGGCTGT	TGTTTCAATAGCTTGAGCAAAAATG
0.08	1.0000	0	2	0.00	1.0000	GCTCTTGGTTTGAACTTTTGTGTGC	CCAATTTGTAAGACCCACTGATGA
0.01	1.40403E-05	21	71876	0.03	1.0000	GAAATTCTGACCTCGTGATCTGCC	CGCACGATTTTTCTCCTTCCCAC
0.00	1.0000	7	82561	0.01	1.0000	CCAGCTGACAGTAGCCCATTTTC	GCAGTAGCTGGTGTATTGACATC
0.01	1.0000	20	78180	0.03	1.0000	GGGCTTTACTGGTGAGTTCTTGC	GCTGGCTGGTTTCCCTGGTT
0.01	1.0000	16	64026	0.02	0.034980447	GCCCAAAAATTTGGGAAAGCCATGCTC	GCTAGGTTCTCTCCTTGACAC

% Indels	P Value				
13.87	0			CCAGAGGCTGACTGTAGAAGAG	GGTAGGTTGACTGGGCTAG
0.03	0.3621			CCATGACATTGGTCTGGGTGATGA	GCAGTGAACATGGGAGTGCAG
0.01	0.4012			GATCACACAGTACTAGTTTATTTTGCAGTACAACAAG	CAATCTGTCTGAGCCAGAGACTTC
0.08	0.0014			CTCATCAGACTAATCACCGATGAAATGC	CGACAAGAGCAAGACTCCATCTCA
0.01	0.1149			AATGGCAGTCTGTGACTGCTCTGA	GCTAGTGAGCACTAGTCAAGCTG
0.04	0.2580			GGAGTGAGATTGCTGGGTCACA	GGACAAGACACCTACCAAAGAGGA
0.01	0.3351			CCTGAATCACAAAGGTAAGGCACAC	GAGGTGATTTCAAGGTAGCTGAG

0.02	1.0000
0.03	1.0000
0.02	0.3898
0.04	0.5663
0.02	0.1501
0.03	1.0000
0.02	0.3850
0.01	0.7756
0.01	0.0191
0.04	0.0692
0.03	1.0000
0.04	0.5193

CAAGAGAGAAGTAGGGAGACCATG	CCATCTGCTTACTCGACATCTCC
GCAGACCTGATTAGCTTTGACTCC	GGCCTGACCTCCAGCATTGA
TTTTTCCTGCTGGTACTCGCAGGAC	GAACCATAAACAAGCACTTAAGACAAGCACTG
GGTAGGAAACGGTGGTTCCAG	CCAGGGCCACTGCTACTGAA
CCTTCTGCCATGATTGTGAGGCC	TGTTTTGCCTGATGTTGGGCTGTG
AGGAAGAATGTGGCTCGCC	TCCTTAGCTTGATGGCCCC
CAAGAGAGCTTATCAGTTATCAACTCTCTAAGG	GGGGAAAAATGATAGGGCATGTAGAAGAG
GTTCAGGTTTCAGGAAGGCCTGG	CCATTGCACTCCAGCAGCCT
GTAGAGGTGGCATTGGAGTATGCA	CCTGGCACTCACCTATGCTG
TGAGAAGAACCACCCACCC	GTGGGCGATGGGAGAAGCTA
AGCACATGTA CTGCCTTTCTCCAC	TCAATGGGCTTTTGGGTTAGGGAG
GTATTCTTTGAGCACGTACCCAG	CAGCCAACAAGCATTGAAAAAGATTCTCAGC

% Indels	P Value	2-RNA Treated			P Value		
		Indel Reads	Match Reads	% Indels			
24.01	0	21902	66258	33.06	0	GTTTGTATCCTGTAATGCTCTCATTGAAACAGCT	CTGATACTAAGTAATTAGTAAGGCCCTCCTC
0.02	0.3713	9	80008	0.01	1.0000	TTTAGAAAGATAGAGAATCATCCGTCATTGCCAC	CTGGTGAGCTCTTTTCTTCCTTC
0.01	1.0000	11	74978	0.01	1.0000	GCAGGAGTCTTCTTTTGTGGTTAAGCC	CAGCCAACCTGAGCTCAACATC
0.01	1.0000	15	82851	0.02	0.6768	GATTTCCCTAACTTCTGCACACATACTCC	GTCCTTGGGGATCTGAACCTGAG
0.02	0.6842	19	82174	0.02	0.5726	GGAGTTTACTCCAGCTTTGTTGAATACCC	TGTTGGGTGATAACTATGAGAAACAGGTGG
0.02	0.2776	16	74072	0.02	0.8623	CCCTCTTCCGAGTCAACAAATC	CCCAGCCTCATTTAGGCATATCC
0.02	1.0000	13	65847	0.02	1.0000	GCTTCTCACTGCCATGCCAGCT	TGCAGAGGTGTTGAGGGTG
0.01	0.5485	7	70060	0.01	0.7492	TCCCCAAGTGACCCCTTTCAAC	CCATCTGCATTCCATCTCTCCTTC
0.01	0.2839	10	87994	0.01	0.2860	GACATGTCAGAAGATATAGGGCATTTCATGCA	CTTCAGACAGTGGTGAAGAGCAAAAATTTATTGG
0.02	1.0000	13	75182	0.02	1.0000	CCCATGACGGTTGGCTAGGA	GTTGGGCACTGACTTGCCCTAC
0.02	0.0090	9	91650	0.01	0.5766	CAAACATACTTCTGAGTTCTTTCAGATTTCAAAGC	AAAGAGAAACCAACCTAACTTAAAGGCTTTCCATG
0.01	0.7825	13	78470	0.02	0.2426	CTGGGTTCCAGGAACACCAC	AGGGGGTACAGCTATCACATAGG
0.03	0.4539	13	68803	0.02	1.0000	GAATCTGGCAACACACAGTGTAGC	GTAAGAAGCCGGCCAAAACCC
0.03	1.0000	11	70220	0.02	0.0280	GCTGACAGTTCAGGCCAGAATG	GGGGCATATCTGAGTTCCTAG
0.01	1.0000	8	69836	0.01	1.0000	TATTAAGCTTGGCCCAGGTGAGTG	ATCCCAGTCTAACTGTAGGCAAGC
0.04	1.0000	0	1312	0.00	1	CTCCCAAGTAGCTGGGACTG	CTCTTCAAAGTGCTTGCGG
0.02	1.0000	18	105093	0.02	1.0000	CCCAGCTCCAATTTGAAGCTTAC	CCTGTCAGTTTGATAGGAGAAAAGCAGGA
0.01	0.2028	6	78900	0.01	0.2976	CTAGGCAGCCAGTAACTTTAGGAC	GCATAGAACAGGTGGCTTGTGCT
0.01	0.2324	4	72689	0.01	0.3751	AAGGCCTCGGACAAAACCTCTGG	TCTCTGAGGAACTCCAGGTGAGC
0.02	0.8203	11	84541	0.01	1.0000	GTCAAGGTCAAACACACTAGGGG	CTGGCCTTCACTTTGGAGGTATG

### Primers for Illumina Reaction 1

Forward TCTACAGTCCGACGATCA-gene specific sequence  
Reverse GACGTGTGCTCTTCCGATC-gene specific sequence

### Primers for Illumina Reaction 2

Forward Rxn2 AATGATACGGCGACCACCGAGAT**TCTACACGTTTCAGAGTTCTACAGTCCGACGATCA**

Kozich\_bar\_1 CAAGCAGAAGACGGCATAACGAGat**AAGTCGAGATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATC**  
Kozich\_bar\_2 CAAGCAGAAGACGGCATAACGAGat**ATACCTTCGATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATC**  
Kozich\_bar\_3 CAAGCAGAAGACGGCATAACGAGat**AGCTGCTAATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATC**  
Kozich\_bar\_4 CAAGCAGAAGACGGCATAACGAGat**CATAGAGAATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATC**  
Kozich\_bar\_5 CAAGCAGAAGACGGCATAACGAGat**CGTAGATCATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATC**  
Kozich\_bar\_6 CAAGCAGAAGACGGCATAACGAGat**CTCGTTACATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATC**  
Kozich\_bar\_7 CAAGCAGAAGACGGCATAACGAGat**GCGCACGTATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATC**  
Kozich\_bar\_8 CAAGCAGAAGACGGCATAACGAGat**GGTACTATATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATC**  
Kozich\_bar\_9 CAAGCAGAAGACGGCATAACGAGat**GTATACGCATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATC**  
Kozich\_bar\_10 CAAGCAGAAGACGGCATAACGAGat**TACGAGCAATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATC**  
Kozich\_bar\_11 CAAGCAGAAGACGGCATAACGAGat**TCAGCGTTATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATC**  
Kozich\_bar\_12 CAAGCAGAAGACGGCATAACGAGat**TCGCTACGATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATC**

### Custom Sequencing Primers

NewIndex\_Read **GATCGGAAGAGCACACGTCTGAACTCCAGTCACAT**  
NewRead\_1 **TCTACACGTTTCAGAGTTCTACAGTCCGACGATCA**  
NewRead\_2 **TGTGACTGGAGTTCAGACGTGTGCTCTTCCGATC**