

SUPPLEMENTARY TABLES

Table 1. crRNA sequences for *TP53* CRISPR/Cas9 digestion

Table 2. *TP53* hybridization capture probes

Table 3. CRISPR-DS sequencing results for 15 samples processed with 250ng input DNA

Supplementary Table 1. crRNA sequences for TP53 CRISPR/Cas9 digestion

Target description:	Name:	Sequence plus pam site:	Position start:	Position end:	Zhang score
TP53 - upstream of exon 11	TP53e11_US	GTGGGCCCCTACCTAGAATGTGG	7572606	7572628	79
TP53 - downstream of exon 11	TP53e11_DS	ATTCCCGTTGTCCCAGCCTTAGG	7573118	7573096	70
TP53 - upstream of exon 10	TP53e10_US	TGGTTATAGGATTCAACCGGAGG	7573754	7573776	91
TP53 - downstream of exon 10	TP53e10_DS	CTGATTGCAATCTCCGCCTCTGG	7574261	7574283	86
TP53 - upstream of exons 9-8	TP53e9-8_DS	CGGCATTTTGAGTGTTAGACTGG	7576792	7576814	80
TP53 - downstream of exons 9-8	TP53e9-8_US	CTTTGGGACCTCTTAACCTGTGG	7577324	7577302	80
TP53 - downstream of exon 7	TP53e7_DS.v2	CAGGTCTCCCCAAGGCGCACTGG	7577660	7577638	81
TP53 - upstream of exons 6-5	TP53e6-5_US	GCACATCTCATGGGGTTATAGGG	7578050	7578072	84
TP53 - downstream of exons 6-5	TP53e6-5_DS	CAGGGGAGTACTGTAGGAAGAGG	7578545	7578567	61
TP53 - upstream of exons 4-3	TP53e4-3_US.v2	TGCACGGTCAGTTGCCCTGAGGG	7579317	7579295	81
TP53 - downstream of exons 4-3	TP53e4-3_DS	ATGGAATTTTCGCTTCCCACAGG	7579751	7579773	79
TP53 - downstream of exon 2	TP53e2_DS	TGGGAATAGGGTGCACATTTAGG	7580242	7580220	66

Supplementary Table 2. TP53 hybridization capture probes

Targeted		
exon:	IDT probe name:	IDT probe sequence:
Exon11	TP53_e11.A.2	CCCCGGGACAAAGCAAATGGAAGTCCTGGGTGCTTCTGACGCACACCTATTGCAAGCAAGGGTTCAAAGACCCAAACCCAAAATGGCAGGGGAGGGAGAGATGGGGGTGGGAGGCTGTC
Exon11	TP53_e11.A.1	AGTGGGGAAACAAGAGTGGAGAATGTCAGTCTGAGTCAGGCGCCTTCTGTCTTGAACATGAGTTTTTATGGCGGGAGGTAGACTGACCCTTTTTGGACTTCAGTGGCTGTAGGAGACAG
Exon10	TP53_e10.1	ACTCACCTGGAGTGAGCCCTGCTCCCCCTGGCTCCTTCCCGCCTGGGCATCCTTGAGTTCGAAGGCCTCATTGAGCTCTCGGAACATCTCGAAGCGCTCACGCCCACGGATCTGCAGC
Exon10	TP53_e10.1_1	AATCCTATGGCTTTCCAACCTAGGAAGCCAGGGGAGTAGGGCCAGGAAGGGGTGAGGTCACCTACCTGGAGTGAGCCCTGCTCCCCCTGGCTCCTTCCCAGCCTGGGCATCCTTGAGT
Exon10	TP53_e10.1_2	TCCAAGGCCTCATTGAGCTCTCGGAACATCTCGAAGCGCTCACGCCCCACGGATCTGCAGCAACAGAGGAGGGGGAGAAGTAAGTATATACACAGTACCTGAGTAAAAAGATGGTTCAAGT
Exon9-8	TP53_e8.1	AAGAGGTCCCAAGACTTAGTACCTGAAGGGTGAAATATTCTCCATCCAGTGGTTTTCTTTGGCTGGGGAGAGGAGCTGGTGTGTTGGGCAGTGTAGGAAAGAGGCAAGGAAAGGTG
Exon9-8	TP53_e7.2	GCATAACTGCACCCTTGGTCTCCTCCACCGCTTCTTGCTGCTTGCTTACCTCGCTTAGTGCTCCTGGGGGCAGCTCGTGGTGAGGCTCCCTTTCTTGCAGATTCTCTTCTCTG
Exon9-8	TP53_e7.1	TGCGCCGGTCTCTCCAGGACAGGCACAAACACGCACCTCAAAGCTGTTCCGTCCAGTAGATTACCACTACTCAGGATAGGAAAAGAGAAGCAAGAGGCAGTAAGGAAATCAGGTCCTA
Exon7	TP53_e6.1	TGACCTGGAGTCTTCCAGTGTGATGATGGTGAGGATGGGCCTCCGGTTTCATGCCGCCATGCAGGAAGTGTACACATGTAGTTGTAGTGGATGGGTACAGTCAGAGCCAACCTAGGA
Exon7	TP53_e6.2	ATGTGATGAGAGGTGGATGGGTAGTAGTATGGAAGAAATCGGTAAAGAGGTGGGCCAGGGTGCAGAGGCAAGCAGAGGCTGGGGCACAGCAGGCCAGTGTGCAGGGTGGCAAGTGGCTCC
Exon6-5	TP53_e5.1	GACCTCAGGCGGCTCATAGGGCACCAACACACTATGTGCAAAAGTGTTCGTGCATCCAAATACTCCACACGCAAAATTCCTTCCACTCGGATAAGATGCTGAGGAGGGGCCAGACCTAA
Exon6-5	TP53_e5.1_1	CTGGAGGGCCACTGACAACCAACCTTAACCCCTCCTCCAGAGACCCCAAGTTCGCAACCAAGACCTCAGGCGGCTCATAGGGCACCACCACTATGTCGAAAAGTGTTCGTGATCCAA
Exon6-5	TP53_e4.3	CACCTCAGGCGGCTCATAGGGCACCAACACACTATGTGCAAAAGTGTTCGTGCATCCAAATACTCCACACGCAAAATTCCTTCCACTCGGATAAGATGCTGAGGAGGGGCCAGACCTAA
Exon6-5	TP53_e4.3_1	GAATCAGAGGCGCTGGGGACCTGGGCAACCAACCCCTGTCGTCTCTCAGAGCCCAAGTGTGCATCACCATCGCTATCTGAGAGCGCTCATGGTGGGGGCAGCGCTCACAACCTCCGTCA
Exon6-5	TP53_e4.2	CAACCCACAGCTGCACAGGCGAGGCTTGGCCAGTTGGCAAAACATCTTGTGAGGGCAGGGGAGTACTGTAGGAAGAGGAAGGAGACAGAGTTGAAAGTCAGGGCACAAGTGAACAGAT
Exon4-3	TP53_e3.3	ATTGAAGTCTCATGGAAGCCAGCCCTCAGGGCAACTGACCGTGCAAGTCACAGACTTGGCTGTCCAGAAATGCAGAAGCCAGACGCAAAACCTAGCTGCCCTGGTAGGTTTTCTGGG
Exon4-3	TP53_e3.2	AAGGACAGACAAGATGACAGGGGGCAGGAGGGGGCTGGTGAGGGGCCCGGGTGTAGGAGCTGCTGGTGACAGGGGCCACGGGGGAGCAGCCTCTGGCATTCTGGGAGCTTCATCTGGAC
Exon4-3	TP53_e3.1	CTGGGTCTTCAGTGAACCATTTGTTCAATATGCTCGGGGGACAGCATCAATCATCATTTGCTTGGGACGGCAAGGGGGAAGTGTAGATGGGTGAAAAGAGCAGTCAGAGGACCAGGTCCTC
Exon4-3	TP53_e2.3	GCCCCCAGCCCTCCAGGTCCCAGCCCTCCAGGTCGCCAGCCCAACCCCTGTGCTTACCAGAACGTGTGTTTTCAGGAAGTCTGAAAAGACAAGAGCAGAAAGTCAGTCCCATGGAAATTTT
Exon2	TP53_e2.2	CGCTTCCCACAGGTCTCTGCTAGGGGGCTGGGGTTGGGGTGGGGGTGGTGGGCTGCCCTTCCAATGGATCCACTCACAGTTTTCCATAGGTCGAAAATGTTTTCTGACTCAGAGGGGGC
Exon2	TP53_e2.1	TCGACGCTAGGATCTGACTGCGGCTCCTCCATGCGAGTGACCCGGAAGGCAGTCTGGCTGCTGCAAGAGGAAAAGTGGGGATCCAGCATGAGACACTTCCAACCTGGGTACCTGGGCG

Supplementary Table 3. CRISPR-DS sequencing results for 13 samples processed with 250ng input DNA

Sample ID	DIN	DNA input		# Raw reads	% of Raw Reads on target	# DCS reads	% of DCS Reads on target		Recovery rate
		(ng)					DCS depth		
B1		6.8	250	7751046	44.0%	68906	100.0%	6143.2	7.4%
B2a		6.9	250	4575484	43.0%	37984	99.1%	3386.4	4.1%
B2b		6.9	250	4855458	47.5%	42815	99.1%	3817.1	4.6%
B3		8.2	250	4214290	85.8%	30847	98.8%	2750.1	3.3%
B4a		8.8	250	4200814	84.4%	85822	99.0%	7651.3	9.3%
B4b		8.8	250	4581646	86.6%	84051	99.1%	7493.4	9.1%
B5		8.5	250	3938328	98.4%	101201	98.7%	9022.4	10.9%
B6		8.7	250	4640288	78.0%	69002	98.8%	6151.7	7.5%
B7		7.6	250	4230402	91.2%	60950	98.8%	5433.9	6.6%
B8		7.0	250	3869654	93.6%	38586	98.9%	3440.1	4.2%
B9		8.9	250	4594068	96.6%	75089	99.2%	6694.4	8.1%
B10		8.6	250	5764098	79.0%	61303	99.1%	5465.3	6.6%
B11		8.5	250	5764650	80.9%	71381	99.3%	6363.8	7.7%
B12		7.9	250	5234650	85.9%	40092	99.4%	3574.3	4.3%
B13		7.0	250	3737110	74.0%	71138	99.1%	6284.8	7.6%