Table S7. Matrix of specific substitution types in S-ExoN1 Sanger and deep genomes.

WT nt	Substitution[a]			
	A	C	G	T
A	–	0 (2.9)	16.1 (19.1)	7.1 (7.4)
C	0 (0)	–	0 (0)	12.1 (13.2)
G	13.1 (7.4)	0 (0)	–	1.0 (1.5)
T	7.1 (7.4)	42.4 (41.2)	1.0 (0)	–

[a] Percentages of total non-redundant substitutions in 10 combined S-ExoN1 P3 clones determined by Sanger sequencing are shown, and those in combined P1', P5', and P10' S-ExoN1 determined by deep sequencing are shown in parentheses. Blue, transitions; black, transversions.