Table S1: List of the 66 sequences containing a stop codon, with basal readthrough (B), gentamicin induced readthrough (G), increase factor between basal and induced readthrough (I) and the classified group in response-type.

Stop codon and its nucleotide context [a]: -6 -5 -4 3 -2 -1	Stop	+4 +5 +6 +7 +8 +9	Name [b]	B	G±	I	Response-Type
A G A A A C A C T T T T	T G A	C A T A G T G T G	p53 213	0.47%	2.79%	6,0	1
C G C T C T A T C G C G	T A A	C T A G G C A T A	CF 122	0.52%	1.71%	3.3	1
C T C A T C C A G C T T	T G A	C A T G G C A A T	APC 360	0.20%	1.58%	7.8	1
G C C A C A C T G A G T	T A G	C T G C A C T G T	beta 90	0.18%	1.43%	7.9	1
G C C A G A G A G A A A	T A G	C T A C A G A C A	DMD 931	0.36%	0.94%	2.6	1
A A A A A C A A A T T T	T G A	A C C A A A A G G	DMD 3381	0.11%	0.93%	8.3	1
T T C T G C A C G T G C	T G A	C C T G G A G C C	CMD 1549	0.11%	0.82%	7.5	1
T C A G A A A C A A A T	T G A	G T G G G T T C T	APC 1114	0.07%	0.73%	10.8	2
C T G G C C C C T C C T	T A G	C A T C T T A T C	p53 192	0.05%	0.66%	12.9	2
G A C C G A C A A G G G	T G A	T T T G A C A G A	DMD 2098	0.27%	0.65%	2.4	1
G T C A C C A C C A C T	T A G	C C A T C A C T A	DMD 673	0.11%	0.57%	5.2	1
T A T G A T A C G G G A	T G A	A C A G G G A G G	DMD 3190	0.18%	0.57%	3.2	1
G A G C C T C A C C A C	T A G	C T G C C C C C A	p53 298	0.07%	0.52%	7.6	2
A G C C C A T T T C C T	T G A	C A G C A T T T G	DMD 319	0.06%	0.53%	8.8	2
T T T G C T C A G T T T	T G A	A G A C T A A A C	DMD 1967	0.07%	0.40%	5.8	3
A C C T G C C C T G T G	T A G	C T G T G G G T T	p53 144	0.09%	0.39%	4.9	3
A G C T C C T C T C C C	T A G	C C A A A G A A G	p53 317	0.04%	0.37%	9.5	2
A C T T T G C A A C A G	T G A	A G G A A A G C C	CF 282	0.12%	0.35%	3.0	3
G T T A C T G C C C T G	T G A	G G C A A G G T G	beta 15 TGA	0.09%	0.34%	3.8	3
G A T G A T A A T A G G	T G A	G A C A A T T T T	APC 811	0.04%	0.34%	8.9	2
A T C C A A T C T G A T	T A G	A C A A G T C A T	DMD 1417	0.05%	0.33%	7.0	3
T T C G A G A T G T T C	T G A	G A G C T G A A T	p53 342	0.06%	0.32%	5.5	3
G C T C A A A C C A A G	T G A	G A A G T A C C T	APC 1450	0.04%	0.31%	8.0	2
C A G C A T C T T A T C	T G A	G T G G A A G G A	p53 196	0.04%	0.31%	6.9	3
C C T G T G C A G C T G	T G A	G T T G A T T C C	p53 146	0.06%	0.30%	4.8	3
G T G G T C T A C C C T	T G A	A C C C A G A G G	beta 37TGA	0.03%	0.30%	10.2	2
G A T A T G G A A A A A	T G A	G C A C A G C G A	APC 213	0.05%	0.28%	6.0	3
G T T A C T G C C C T G	T A G	G G C A A G G T G	beta 15 TAG	0.08%	0.27%	3.5	3
A A T A T A G T T C T T	T G A	G A A G G T G G A	CF 542	0.02%	0.26%	13.0	2
A G T A T T C C G T T C	T G A	G G T T G C A T C	CMD 3085	0.05%	0.25%	5.0	3
G A A G T T G G T G G T	T A G	G C C C T G G G C	beta 26	0.05%	0.24%	4.9	3
G G G A G C A C T A A G	T G A	G C A C T G C C C	p53 306	0.05%	0.24%	5.2	3
G A T A G C C C T G G A	T A A	A C C A T G C C A	APC 1429	0.08%	0.23%	2.8	3
A G G C C C T G G A A C	T G A	G G G G C G T T C	STOP LAM	0.05%	0.23%	5.0	3
G A T A T T G A A C A A	T A G	T T C A C T G A A	p53 53	0.04%	0.23%	5.3	3
C G A T C T G T G A G C	T G A	G T C T T T A A G	CF 1162	0.02%	0.22%	10.0	2
G G C T G T G T T C C C	T G A	A A C T G C A A T	CMD 967	0.04%	0.22%	5.8	3
T T G C C C C T G C G C	T A G	G G A A T T C T C	DMD 2264	0.05%	0.21%	4.3	3
C C T A G G C A C A G G	T G A	G T T A A C G G C	CMD 744	0.04%	0.20%	5.0	3
A A C G T G C T G G T C	T G A	G T G C T G G C C	beta 112	0.06%	0.20%	3.0	3
A G A A C T G T G A C C	T G A	G A A G A C T T C	CMD 1326	0.02%	0.18%	9.1	2
C A G T C T T T G T G T	T A A	G A A G A T G A C	APC 1131	0.01%	0.18%	16.3	2
C T G G A T G G A G A A	T A A	T T C A C C C T T	p53 327	0.03%	0.15%	5.9	3
G T G A A C G T G G A T	T A A	G T T G G T G G T	beta E22	0.03%	0.14%	4.6	3
C A G A G G T T C T T T	T A G	T C C T T T G G G	beta 43	0.01%	0.14%	10.9	2
A A A A G T G G T G C T	T A G	A C A C C C A A A	APC 1367	0.02%	0.13%	6.7	3
A A A C T T C C A G A A	T A A	T T T G A A G G A	CMD 1240	0.02%	0.12%	6.6	3
C A G G A T T T G G A A	T A G	A G G C G T C C C	DMD 2522	0.02%	0.12%	6.7	3
A T G G A T A T C C T G	T A G	A T T A T T A A T	DMD 3149	0.04%	0.12%	3.0	3
A A C C C T A A G G T G	T A G	G C T C A T G G C	beta 61	0.03%	0.12%	4.4	3
G A T A G A A G T T T G	T A G	A G A G A A C G C	APC 853	0.02%	0.12%	5.4	3
T A C C C T T G G A C C	T A G	A G G T T C T T T	beta 39	0.03%	0.11%	4.2	3
C A A T G T T G G T G C	T A A	C C T G G A G T C	CMD 988	0.02%	0.11%	6.6	3
A A G A A G A A G A A G	T A G	A A G C A A C C C	STOP PLATI	0.03%	0.10%	3.0	3
G C A G A A A T A A A A	T A A	A A G A T T G G A	APC 1309	0.02%	0.10%	5.2	3
G C T A C A G A T A T G	T A A	T T G A C A A A G	DMD 1593	0.03%	0.09%	3.2	3
G C C C T G T G G G G C	T A G	G T G A A C G T G	beta 17	0.03%	0.09%	2.9	3
C A T C G T A G T A A G	T A G	A G A C A C A A G	APC 789	0.03%	0.09%	3.4	3
C A C T T T G G C A A A	T A A	T T C A C C C C A	beta 121	0.03%	0.09%	3.4	3
G T G G T C T A C C C T	T A G	A C C C A G A G G	beta 37 TAG	0.02%	0.09%	5.6	3
C T G C T G C T G C T C	T A A	C C T T G G A C C	beta 35	0.02%	0.08%	5.5	3
G A T C A C A T G T G C	T A A	C A G G T C T A T	DMD 1143	0.01%	0.08%	10.7	2
T T G A A A G A G C A A	T A A	A A T G G C T T C	MDX	0.02%	0.06%	3.6	3
A C A G A A G C T G A A	T A G	T T T C T C A G A	DMD 2125	0.04%	0.06%	1.6	3
A C C C C A C C A G T G	T A G	G C T G C C T A T	beta 127	0.02%	0.05%	3.1	3
G A A A G G C T C C T A	T A A	G A C T C C A A G	DMD 2726	0.01%	0.04%	5.9	3

[a] These sequences were inserted into the dual reporter vector in order to determine readthrough level.

[b] Nonsense mutations are named by the gene or the disease related to and by their position (amino-acid). p53 mutations are involved in cancers; DMD and CMD mutations are involved in muscular dystrophies; CF mutations are involved in cystic fibrosis and beta mutations are involved in beta-thalassemia disease (see Materials et Methods for references).

[±] Nonsense mutations are classified according to their gentamicin induced readthrough level.