

Supplemental Material : Figure and Table Legends

Supplemental Table 1 Organization of cloning trialanine mutants into nine chunks.

The L1 coding sequence was divided into nine chunks. Mutants contained in each chunk are shown.

Supplemental Figure 1 Detailed high-throughput cloning procedure used to create library. The detailed steps for building and validating the library in a high-throughput manner are depicted. The inset shows an agar plate after overnight growth of eight *E. coli* transformations of putative trialanine clones after using the “drop method”.

Supplemental Figure 2 Restriction digest used to validate final constructs in library. *Pst*I digestion was used to validate the final integrity of the backbone and the presence of the trialanine mutation for each clone. On top, a schematic of where *Pst*I cuts in the plasmid is shown. The trialanine DNA sequence was designed to contain a *Pst*I site, thus the predicted band sizes for each construct are unique. An agarose DNA gel shows diagnostic digests of each final correct clone in chunk 3, Mutants 110-160 (“WT” is the pEA0264 parent backbone and “L” is the 2-log ladder). Sanger sequencing (not shown) also confirmed the correct sequence for each mutant insert by spanning the Gibson homology arm boundaries for each clone.

Supplemental Table 2 Raw retrotransposition efficiency data for full library. For ORF1p and ORF2p, this table shows the IDs and raw retrotransposition data for each

mutant. The column *Trialanine construct ID* describes each mutant using the following format (with the information, separated by underscores): the pEA construct number, the first residue mutated, the last residue mutated, and the three WT amino acids (single letter code) mutated to alanine. The second column shows the raw data that corresponds to Figure 2: *retroT average*. The third and fourth columns show the *standard deviation* and *number of measurements*, respectively, for the measurements made for each mutant.

Supplemental Figure 3 High-throughput microscopy-based measurement of retrotransposition. (A) The protocol for the six-day 96-well, microscopy-based assay for plasmid transfection and measurement of the retrotransposition activity in human HeLa cells. Puromycin selection of the cells containing plasmid for five days was followed by dox-induced expression of L1 for four days. (B) Representative pictures of transfected WT constructs. This photo represents one quarter of one well in a 96-well plate. This shows two channels (DAPI and GFP) and the overlay. Blue (DAPI, alive) and green (GFP, retrotransposition-positive) cells were quantified. Raw wild-type retrotransposition values were reproducible and robust, usually showing ~13% GFP+ of live cells. (C) Because DNA was purified for 538 constructs in different batches, we wanted to be sure that there was no effect of the batch in which DNA was prepared on the retrotransposition efficiency. We measured retrotransposition for WT and two independent preparations of 5 different (color coded) mutants (chosen at random). (D) Comparison of transfecting different amounts of DNA. The fact that the retrotransposition frequency is independent of DNA concentrations within the range of

concentrations used here shows that small fluctuations DNA stock concentration will not affect comparisons among mutants. Cells died when transfected with too much DNA and gave reproducible results over a concentration range of 7- 68 ng (60 ng was used for experiments unless indicated otherwise).

Supplemental Figure 4 Retrotransposition levels mapped onto EN 3D structure. The crystal structure of the WT EN domain of ORF2 (PDB 1VYB) is shown and is color-coded to display retrotransposition efficiency of each trialanine mutant. Red: strong impact on retrotransposition in red, Gray: mild impact, Cyan: no impact. (Note that this color scheme is not identical in all the figures).

Supplemental Table 3 Raw protein expression data. Each mutant was measured for protein expression twice and the average value (after endogenous HeLa ORF1p subtraction) is shown. Gray indicates the mutants that were not measurable with this approach because the epitope was mutated. The other values are shown in blue (high ORF1p) or red (low ORF1p) and coincide with the representation in Figure 3B.

Supplemental Table 4 Categories of ORF1p mutants based on activity and protein abundance. The percentages of ORF1p mutants that show a strong, mild, or no effect on retrotransposition efficiency combined with whether or not they impact ORF1 protein abundance are represented in 4 categories (that correspond to Figure 4) for ORF1p. The values for the full-length protein and then for each domain are shown.

Supplemental Table 5 Composition of mutant pools for RNP studies. The composition of each of the pools (Pool 1- Pool 8), each mutant is listed using the pEA clone number as the ID. This experiment was done fully for the complete series of mutants of ORF1p, in which we measured levels of total DNA and RNA in the cell lysate.

Supplemental Table 6 An analysis of ORF1p mutants that localize to the nucleolus. Comparison of nucleolar localization phenotype in immunocytochemistry of ORF1p mutants. 40 of the 113 ORF1p mutants in the mutant library were evaluated for nucleolar ORF1p localization by immunofluorescence staining followed by blinded counting. Two mutants were considered positive for the nucleolar phenotype, with a nucleolar phenotype rate of greater than one standard deviation above the mean nucleolar phenotype rate across all tested mutants. A minimum of 20 cells were counted for each mutant. The ORF1p domain column refers to the region of the protein in which the mutation occurs for a given mutant; NTR: N-terminal region, CC: coiled coil, RRM: RNA recognition motif, CTD: C-terminal domain. Retrotransposition rates are separated into 3 categories: high (++ , > 80% of wild-type), reduced (+, between 25 and 80% of wild-type), and poor (–, < 25% of wild-type). All mutants tested produced more than 35% of wild-type ORF1p protein levels as measured by Western blot. The number of measurements indicates the number of separate experiments that include independent transfections of the given mutant.

Supplemental Table 7 The IDs of the fifty-five LINE-1 ORF2p sequences used for phylogenetic conservation analysis. We used the human ORF2p from L1-rp (accession

number AF148856). For the remainder, the DNA sequences were provided by Stephane Boissinot (Boissinot and Sookdeo 2016) and were then prepared for protein multiple sequence alignment by Oliver Weichenrieder. These were carefully curated as the most reliable mammalian and non-mammalian vertebrate ORF2p consensus sequences. (Note that these were used as the basis for analyses presented in Supplemental Table 8 and Figure 7.)

Supplemental Figure 5 Alignment of a subset of the ORF2p sequences presented in Supplemental Table 7. This shows a multiple sequence alignment produced by Geneious for human L1-rp and 25 other L1 (13 mammalian and 12 non-mammalian vertebrate) ORF2p sequences. The identities of the organisms are along the far left (highlighted in purple). The domains of ORF2p are indicated in tracks above the alignment, which is numerated every 10 amino acids for the reference human ORF2p sequence. This used a Blosum62 Score Matrix and the individual residues are color coded as follows: 100% similar (green), 80-100% similar (greenish-yellow), 60-80% similar (yellow), <60% similar (white). Listed here are how we refer to the IDs (Supplemental Table 7) in the alignment (shown in parentheses) : HUMAN L1-rp (HUMAN) , RABBIT (RABBIT) , PIG (PIG) , COW (COW) , DOG (DOG) , PANDA (PANDA) , HORSE (HORSE) , LEMUR (LEMUR) , ELEPHANT (ELEPHANT) , HYRAX (HYRAX) , ARMADILLO (ARMADILLO) , MOUSE (MOUSE) , RAT (RAT) , OPOSSUM (OPOSSUM) , FROG_L1-6 (FROG_6) , FROG_L1-32 (FROG_32) , FROG_L1-15 (FROG_15) , FROG_L1-29 (FROG_29) , ZEBRAFISH_L1-1 (FISH_1) , ZEBRAFISH_L1-7B (FISH_7B) , ZEBRAFISH_L1-13A (FISH_13A) , ZEBRAFISH_L1-

17B (FISH_17B) , LIZARD_L1_AC1 (LIZ_AC1) , LIZARD_L1_AC14 (LIZ_AC14) ,
LIZARD_L1_AC15 (LIZ_AC15) , LIZARD_L1_AC17 (LIZ_AC17).

Supplemental Table 8 Phylogenetic conservation values of ORF2p mutants used for sensitivity analysis. The sequences shown in Supplemental Table 7 were aligned using the Geneious multiple protein sequence alignment tool and identity calculation tools. Column one indicates the ORF2p trialanine mutant. Columns two and three show the conservation results for mammals only and then for mammals and other vertebrates. Since each mutant spans three amino acid residues, the value shown is that of the residue with the highest identity score. The fourth column shows the average retrotransposition of the given mutant. The last column indicates the domain of ORF2p in which the mutant lies. For all columns, low is indicated in red and high is indicated in green. The last two columns show the retrotransposition efficiency (green : >80% of WT, gray : 25-80% of WT, and red : <25% of WT) and domain within which each mutant is located.

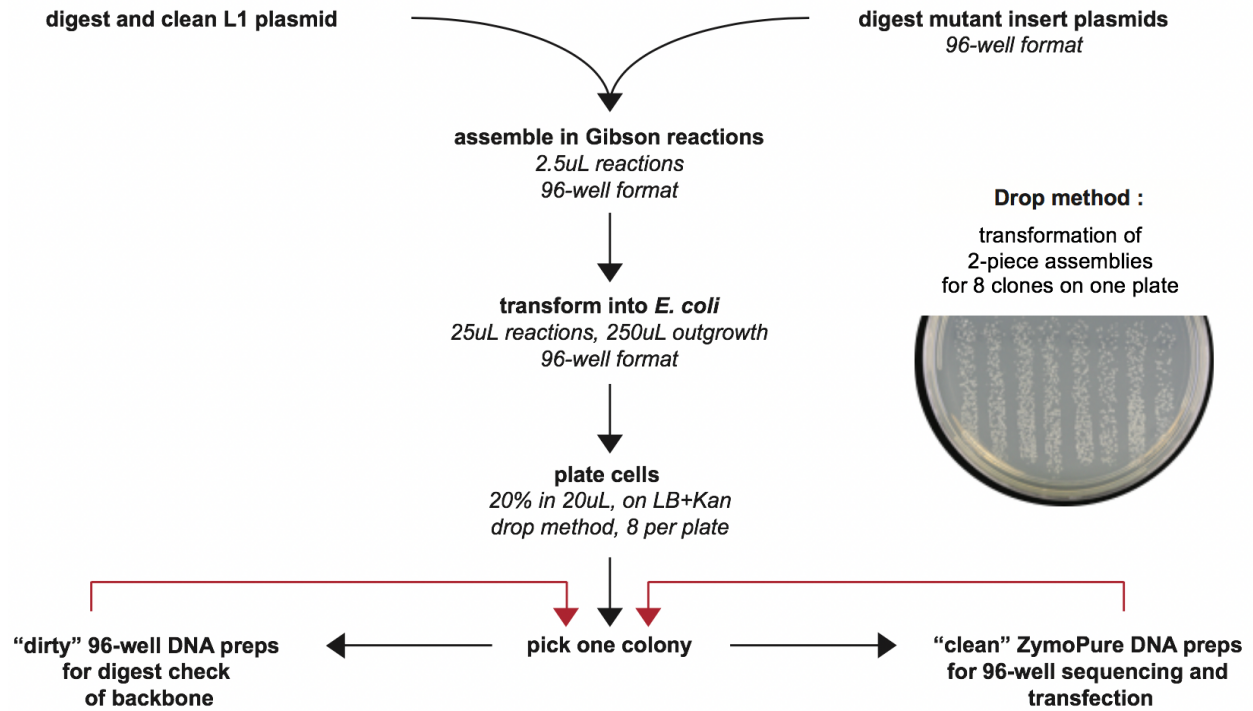
Supplemental Material : Figures and Tables

Supplemental Table 1

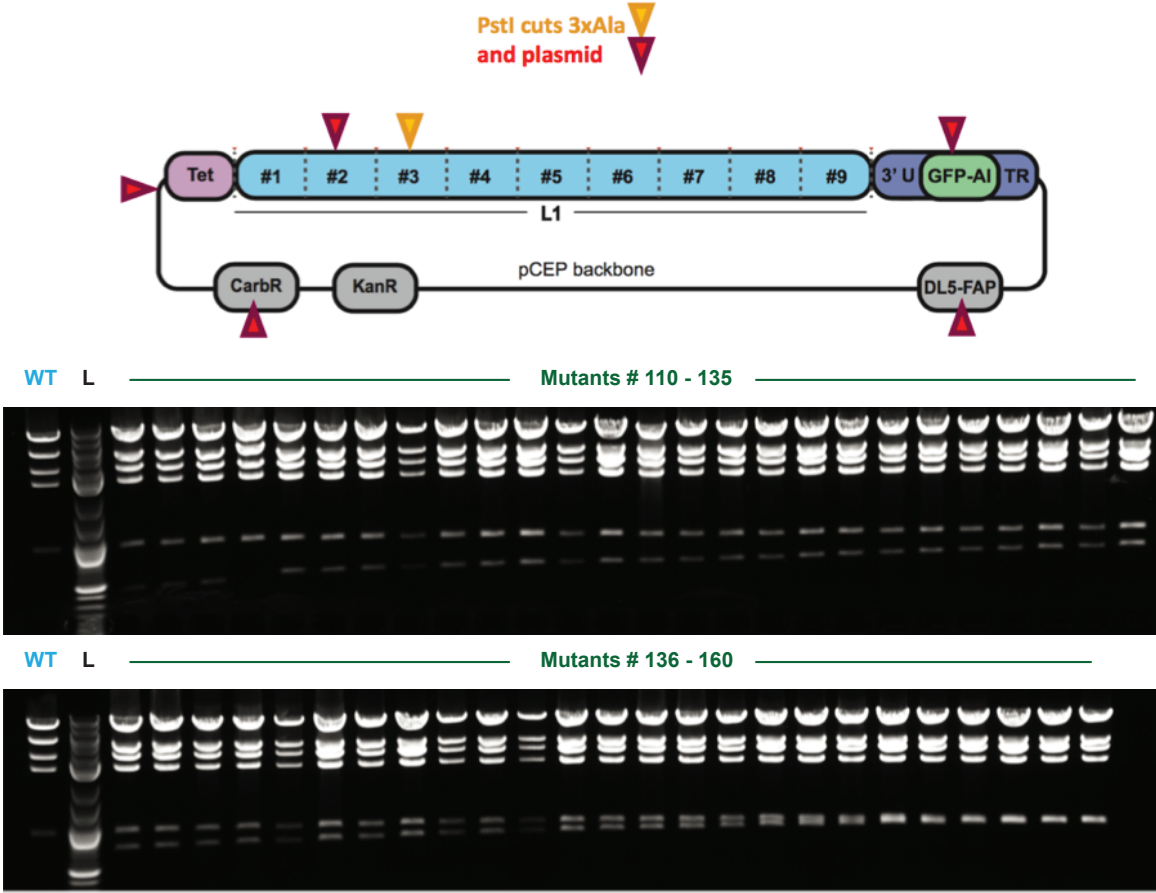
chunk #	range of mutated residues		total # residues	total # 3xAla mutants	unique flanking restriction sites	
	ORF1	ORF2				
1	2 - 175		174	58	<i>NotI</i>	<i>SbfI</i>
2	176 - 328		153	51	<i>SbfI</i>	<i>AgeI</i>
3	329 - 338	2 - 144	153	52*	<i>AgeI</i>	<i>VspI</i>
4		145 - 315	171	57	<i>VspI</i>	<i>Clal</i>
5		316 - 504	189	63	<i>Clal</i>	<i>BamHI</i>
6		505 - 717	213	71	<i>BamHI</i>	<i>AflII</i>
7		718 - 903	186	62	<i>AflII</i>	<i>BsWI</i>
8		904 - 1083	180	60	<i>BsWI</i>	<i>BstBI</i>
9		1084 - 1275	192	64	<i>BstBI</i>	<i>SphI</i>

* The final mutant for ORF1 mutates residue 338 (1xAla).
The first mutant for ORF2 mutates residues 2-3 (2xAla).

Supplemental Figure 1



Supplemental Figure 2



Supplemental Table 2

ORF1							
Mutant ID	retroT average	standard deviation	number of measurements	Mutant ID	retroT average	standard deviation	number of measurements
pEA807_2_4_GKK	4.8	3.8	4	pEA863_170_172_NGT	74.5	11.8	4
pEA808_5_7_QNR	76.2	3.4	4	pEA864_173_175_KLE	20.3	2.8	2
pEA809_8_10_KTG	111.0	7.1	4	pEA865_176_178_NTL	4.0	2.6	4
pEA810_11_13_NSK	95.5	27.3	2	pEA866_179_181_QDI	1.6	1.9	4
pEA811_14_16_TQS	85.9	14.0	4	pEA867_182_184_IQE	6.6	9.8	4
pEA812_17_19_ASP	82.0	29.4	4	pEA868_185_187_NFP	5.8	9.1	4
pEA813_20_22_PPK	83.2	16.2	4	pEA869_188_190_NLA	51.7	12.3	2
pEA814_23_25_ERS	70.2	17.8	4	pEA870_191_193_RQA	101.2	22.8	4
pEA815_26_28_SSP	73.1	13.3	4	pEA871_194_196_NVQ	92.7	9.9	4
pEA816_29_31_ATE	100.4	24.6	4	pEA872_197_199_IQE	30.0	5.4	2
pEA817_32_34_QSW	81.4	17.3	4	pEA873_200_202_IQR	2.5	3.3	4
pEA818_35_37_MEN	93.1	14.3	6	pEA874_203_205_TPQ	5.6	1.8	4
pEA819_38_40_DFD	95.9	14.3	6	pEA875_206_208_RYS	6.9	6.0	4
pEA820_41_43_ELR	97.3	13.3	6	pEA876_209_211_SRR	9.2	4.3	4
pEA821_44_46_EEG	58.5	18.6	4	pEA877_212_214_ATP	10.9	4.9	4
pEA822_47_49_FRR	76.1	4.5	2	pEA878_215_217_RHI	2.7	3.5	4
pEA823_50_52_SNY	53.8	19.4	2	pEA879_218_220_IVR	5.3	1.2	2
pEA824_53_55_SEL	9.0	10.3	4	pEA880_221_223_FTK	11.5	2.8	2
pEA825_56_58_RED	72.5	8.0	2	pEA881_224_226_VEM	53.4	17.6	4
pEA826_59_61_IQT	10.2	4.9	4	pEA882_227_229_KEK	49.5	14.6	2
pEA827_62_64_KGK	78.0	9.3	2	pEA883_230_232_MLR	4.3	6.2	4
pEA828_65_67_EVE	8.4	4.5	4	pEA884_233_235_AAR	36.6	13.4	4
pEA829_68_70_NFE	12.9	10.9	4	pEA885_236_238_EKG	76.8	8.4	4
pEA830_71_73_KNL	25.1	9.9	4	pEA886_239_241_RVT	4.1	2.8	4
pEA831_74_76_EEC	68.9	11.3	4	pEA887_242_244_LKG	4.2	4.4	4
pEA832_77_79_ITR	8.8	4.7	2	pEA888_245_247_KPI	3.9	3.5	4
pEA833_80_82_ITN	42.2	13.1	3	pEA889_248_250_RLT	5.2	8.0	4
pEA834_83_85_TEK	8.3	7.2	3	pEA890_251_253_ADL	3.4	3.4	4
pEA835_86_88_CLK	9.8	6.0	4	pEA891_254_256_SAE	68.8	11.0	4
pEA836_89_91_ELM	4.2	1.3	4	pEA892_257_259_TLQ	5.6	3.1	4
pEA837_92_94_ELK	0.7	1.0	2	pEA893_260_262_ARR	3.2	3.0	4
pEA838_95_97_TKA	103.1	10.5	4	pEA894_263_265_EWG	4.0	1.6	4
pEA839_98_100_REL	5.8	3.0	4	pEA895_266_268_PIF	2.5	2.5	4
pEA840_101_103_REE	33.0	7.7	4	pEA896_269_271_NIL	2.5	1.9	4
pEA841_104_106_CRS	7.7	0.5	4	pEA897_272_274_KEK	57.6	11.2	4
pEA842_107_109_LRS	9.4	4.6	4	pEA898_275_277_NFQ	13.2	1.3	4
pEA843_110_112_RCD	10.1	5.1	4	pEA899_278_280_PRI	3.4	3.5	4
pEA844_113_115_QLE	2.9	2.1	4	pEA900_281_283_SYP	5.9	3.9	4
pEA845_116_118_ERV	13.1	11.2	4	pEA901_284_286_AKL	2.8	2.6	4
pEA846_119_121_SAM	36.4	2.8	4	pEA902_287_289_SFI	4.0	5.3	4
pEA847_122_124_EDE	4.0	1.8	4	pEA903_290_292_SEG	3.0	2.8	4
pEA848_125_127_MNE	60.0	3.1	4	pEA904_293_295_EIK	63.0	20.9	4
pEA849_128_130_MKR	34.8	6.4	4	pEA905_296_298_YFI	2.0	1.7	4
pEA850_131_133_EGK	91.4	16.4	4	pEA906_299_301_DKQ	1.9	1.9	4
pEA851_134_136_FRE	86.5	10.5	4	pEA907_302_304_MLR	24.5	8.4	4
pEA852_137_139_KRI	50.8	5.2	4	pEA908_305_307_DFV	4.7	1.1	2
pEA853_140_142_KRN	35.5	7.8	4	pEA909_308_310_TTR	60.6	13.2	4
pEA854_143_145_EQS	63.2	11.4	4	pEA910_311_313_PAL	2.4	2.8	4
pEA855_146_148_LQE	13.9	5.4	3	pEA911_314_316_KEL	79.3	17.4	2
pEA856_149_151_IWD	5.0	6.2	4	pEA912_317_319_LKE	13.4	3.1	4
pEA857_152_154_YVK	3.9	2.2	4	pEA913_320_322_ALN	33.5	15.0	4
pEA858_155_157_RPN	7.1	5.9	4	pEA914_323_325_MER	37.9	9.6	4
pEA859_158_160_LRL	5.9	4.9	4	pEA915_326_328_NNR	76.5	22.1	4
pEA860_161_163_IGV	11.0	9.6	3	pEA916_329_331_YQP	107.3	14.5	6
pEA861_164_166_PES	11.4	1.3	2	pEA917_332_334_LQN	84.6	20.1	4
pEA862_167_169_DVE	45.8	0.3	2	pEA918_335_337_HAK	85.1	17.0	4
				pEA1361_338_M	77.4	12.2	4

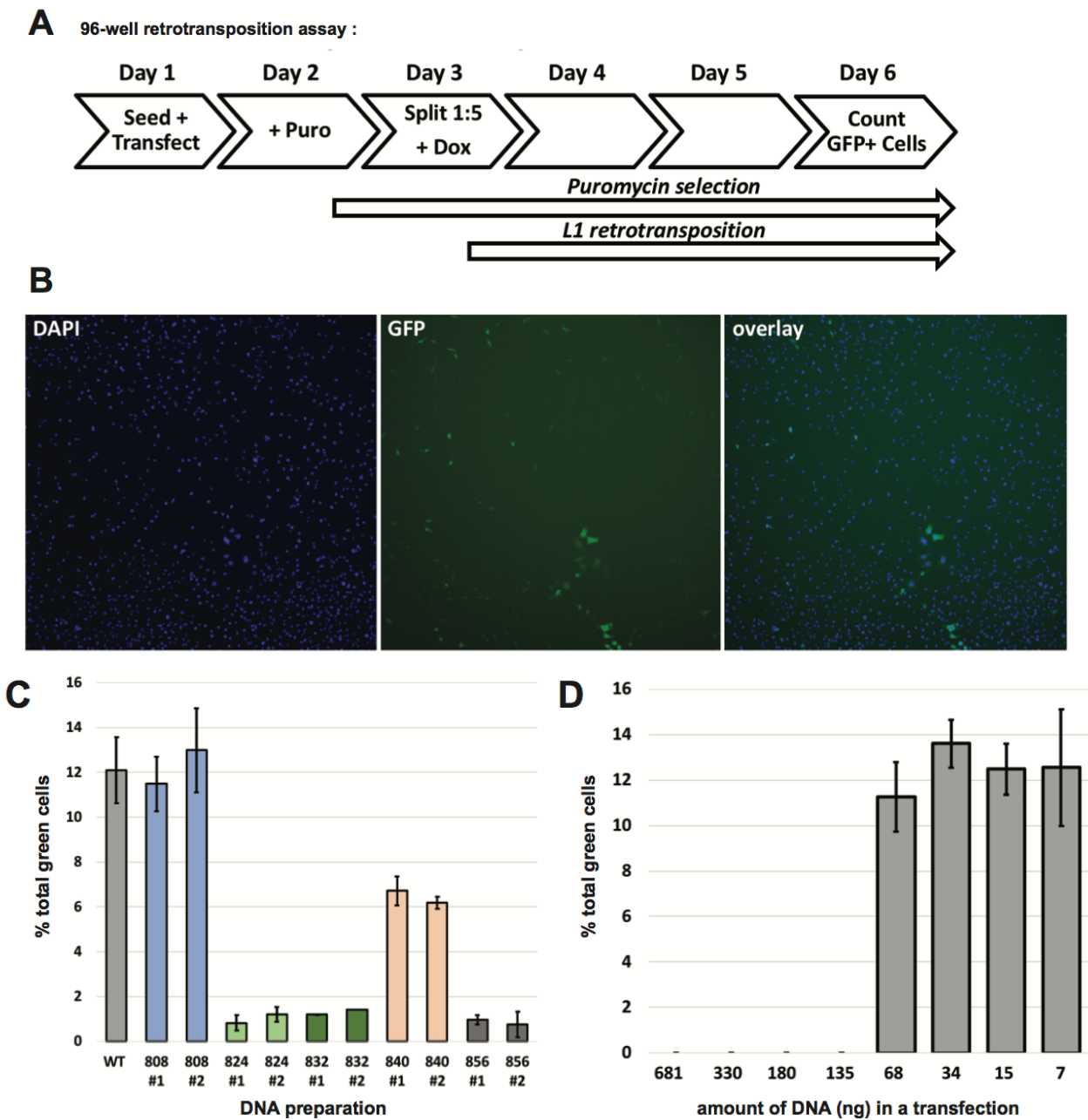
ORF2							
Mutant ID	retroT average	standard deviation	number of measurements	Mutant ID	retroT average	standard deviation	number of measurements
pEA1362_2_3_TG	24.8	1.5	4	pEA981_187_189_KST	87.9	11.6	4
pEA920_4_6_STS	72.0	5.5	2	pEA982_190_192_EYT	3.9	2.8	4
pEA921_7_9_HIT	17.6	20.4	4	pEA983_193_195_FFS	2.4	2.2	4
pEA922_10_12_ILT	4.3	5.0	4	pEA984_196_198_APH	10.3	5.2	4
pEA923_13_15_LNI	6.3	4.3	4	pEA985_199_201_HTY	6.0	1.1	2
pEA924_16_18_NGL	4.8	3.0	4	pEA986_202_204_SKI	7.5	5.1	4
pEA925_19_21_NSA	8.6	3.4	4	pEA987_205_207_DHI	1.9	1.8	4
pEA926_22_24_IKR	10.7	12.9	4	pEA988_208_210_VGS	6.6	5.1	4
pEA927_25_27_HRL	36.5	8.7	3	pEA989_211_213_KAL	6.0	3.4	4
pEA928_28_30_ASW	18.3	2.6	4	pEA990_214_216_LSK	61.5	23.9	4
pEA929_31_33_IKS	10.0	11.6	4	pEA991_217_219_CKR	91.6	29.0	4
pEA930_34_36_QDP	42.7	6.0	2	pEA992_220_222_TEI	45.9	8.8	4
pEA931_37_39_SVC	0.0	0.0	2	pEA993_223_225_ITN	33.4	8.6	4
pEA932_40_42_CIQ	2.3	2.5	4	pEA994_226_228_YLS	16.8	5.1	2
pEA933_43_45_ETH	1.7	2.1	4	pEA995_229_231_DHS	2.9	3.0	4
pEA934_46_48_LTC	5.8	3.9	4	pEA996_232_234_AIK	13.7	7.7	4
pEA935_49_51_RDT	81.1	3.7	4	pEA997_235_237_LEL	7.3	1.8	2
pEA936_52_54_HRL	4.2	5.0	4	pEA998_238_240_RIK	91.3	28.2	4
pEA937_55_57_KIK	15.0	7.0	4	pEA999_241_243_NLT	103.9	28.5	6
pEA938_58_60_GWR	3.9	0.8	2	pEA1000_244_246_QSR	60.4	13.1	2
pEA939_61_63_KIY	0.0	0.0	2	pEA1001_247_249_STT	87.9	26.3	4
pEA940_64_66_QAN	83.8	20.3	4	pEA1002_250_252_WKL	4.5	4.8	4
pEA941_67_69_GKQ	52.0	11.5	4	pEA1003_253_255_NNL	41.7	9.8	4
pEA942_70_72_KKA	7.2	4.6	4	pEA1004_256_258_LLN	9.6	2.0	4
pEA943_73_75_GVA	3.5	3.5	4	pEA1005_259_261_DYW	29.4	15.9	4
pEA944_76_78_ILV	1.6	1.8	4	pEA1006_262_264_VHN	106.1	12.5	2
pEA945_79_81_SDK	2.2	1.3	4	pEA1007_265_267_EMK	21.5	7.7	4
pEA946_82_84_TDF	6.3	0.1	2	pEA1008_268_270_AEI	13.0	9.9	3
pEA947_85_87_KPT	17.8	20.7	4	pEA1009_271_273_KMF	7.3	6.3	4
pEA948_88_90_KIK	10.0	2.3	4	pEA1010_274_276_FET	16.2	2.7	2
pEA949_91_93_RDK	10.0	7.6	2	pEA1011_277_279_NEN	12.2	6.9	4
pEA950_94_96_EGH	3.1	2.0	4	pEA1012_280_282_KDT	27.6	6.4	4
pEA951_97_99_YIM	2.3	2.5	4	pEA1013_283_285_TYQ	18.6	11.7	4
pEA952_100_102_VKG	3.4	1.8	4	pEA1014_286_288_NLW	2.6	2.7	4
pEA953_103_105_SIQ	27.8	8.3	4	pEA1015_289_291_DAF	3.2	2.2	4
pEA954_106_108_QEE	32.9	0.6	2	pEA1016_292_294_KAV	2.5	2.8	4
pEA955_109_111_LTI	5.3	4.6	3	pEA1017_295_297_CRG	4.8	4.2	4
pEA956_112_114_LNI	2.5	2.9	4	pEA1018_298_300_KFI	3.0	3.2	4
pEA957_115_117_YAP	2.2	1.5	4	pEA1019_301_303_ALN	103.0	25.1	4
pEA958_118_120_NTG	24.1	7.9	4	pEA1020_304_306_AYK	73.5	18.6	4
pEA959_121_123_APR	65.5	4.5	2	pEA1021_307_309_RKQ	62.5	4.2	2
pEA960_124_126_FIK	4.8	3.6	4	pEA1022_310_312_ERS	64.3	16.7	4
pEA961_127_129_QVL	2.1	2.1	4	pEA1023_313_315_KID	62.2	20.1	4
pEA962_130_132 SDL	39.8	3.6	2	pEA1024_316_318_TLT	59.4	5.4	4
pEA963_133_135_QRD	23.4	27.0	4	pEA1025_319_321_SQL	72.9	13.9	3
pEA964_136_138_LDS	7.2	0.1	2	pEA1026_322_324_KEL	68.7	14.0	4
pEA965_139_141_HTL	2.7	3.1	4	pEA1027_325_327_EKQ	86.9	7.9	4
pEA966_142_144_IMG	2.4	2.4	4	pEA1028_328_330_EQT	76.7	18.9	4
pEA967_145_147_DFN	4.0	4.6	4	pEA1029_331_333_HSK	82.8	20.4	4
pEA968_148_150_TPL	6.2	3.5	4	pEA1030_334_336_ASR	93.7	23.7	4
pEA969_151_153_STL	63.8	21.4	4	pEA1031_337_339_RQE	19.6	9.4	4
pEA970_154_156_DRS	2.5	2.9	4	pEA1032_340_342_ITK	31.1	3.5	4
pEA971_157_159_TRQ	51.5	15.9	4	pEA1033_343_345_IRA	29.6	8.2	4
pEA972_160_162_KVN	48.1	16.4	4	pEA1034_346_348_ELK	14.2	9.9	4
pEA973_163_165_KDT	96.8	11.9	4	pEA1035_349_351_EIE	59.0	8.5	2
pEA974_166_168_QEL	19.1	3.1	4	pEA1036_352_354_TQK	53.5	8.1	4
pEA975_169_171_NSA	79.4	21.8	4	pEA1037_355_357_TLQ	30.7	2.8	4
pEA976_172_174_LHQ	25.0	14.2	4	pEA1038_358_360_KIN	56.8	31.2	4
pEA977_175_177_ADL	8.4	0.7	2	pEA1039_361_363_ESR	31.5	15.2	3
pEA978_178_180_IDI	2.8	3.2	4	pEA1040_364_366_SWF	11.7	1.9	3
pEA979_181_183_YRT	2.9	2.1	4	pEA1041_367_369_FER	23.6	1.3	2
pEA980_184_186_LHP	4.9	0.7	2	pEA1042_370_372_INK	17.3	7.1	4

ORF2							
Mutant ID	retroT average	standard deviation	number of measurements	Mutant ID	retroT average	standard deviation	number of measurements
pEA1043_373_375_IDR	61.2	11.0	4	pEA1101_547_549_LAN	53.5	3.8	4
pEA1044_376_378_PLA	41.7	13.5	4	pEA1102_550_552_RIQ	8.1	2.3	4
pEA1045_379_381_RLI	65.1	8.6	4	pEA1103_553_555_QHI	88.6	17.3	4
pEA1046_382_384_KKK	56.9	0.4	2	pEA1104_556_558_KKL	43.4	4.8	4
pEA1047_385_387_REK	58.6	1.3	2	pEA1105_559_561_IHH	16.3	11.5	4
pEA1048_388_390_NQI	59.8	20.4	4	pEA1106_562_564_DQV	6.2	3.5	4
pEA1049_391_393_DTI	60.3	12.5	6	pEA1107_565_567_GFI	20.4	7.8	4
pEA1050_394_396_KND	76.5	33.4	4	pEA1108_568_570_PGM	53.3	9.2	4
pEA1051_397_399_KGD	55.1	24.2	4	pEA1109_571_573_QGW	15.8	3.1	4
pEA1052_400_402_ITT	22.5	7.0	4	pEA1110_574_576_FNI	36.0	12.5	4
pEA1053_403_405_DPT	45.1	7.8	4	pEA1111_577_579_RKS	4.7	1.1	4
pEA1054_406_408_EIQ	14.4	5.0	4	pEA1112_580_582_INV	30.0	8.2	4
pEA1055_409_411_TTI	27.7	1.0	2	pEA1113_583_585_IQH	61.4	4.7	4
pEA1056_412_414_REY	27.9	3.8	3	pEA1114_586_588_INR	57.4	17.8	4
pEA1057_415_417_YKH	33.2	6.6	4	pEA1115_589_591_AKD	78.6	11.3	4
pEA1058_418_420_LYA	30.7	6.0	4	pEA1116_592_594_KNH	53.5	8.9	4
pEA1059_421_423_NKL	65.6	10.7	4	pEA1117_595_597_MII	6.3	2.0	4
pEA1060_424_426_ENL	49.6	7.7	4	pEA1118_598_600_SID	5.3	1.3	4
pEA1061_427_429_EEM	38.0	9.4	4	pEA1119_601_603_AEK	62.1	9.5	4
pEA1062_430_432_DTF	20.1	20.2	4	pEA1120_604_606_AFD	3.8	1.5	4
pEA1063_433_435_LDT	5.5	4.4	4	pEA1121_607_609_KIQ	38.7	6.4	4
pEA1064_436_438_YTL	18.5	14.5	4	pEA1122_610_612_QPF	5.1	0.6	2
pEA1065_439_441_PRL	22.6	34.5	4	pEA1123_613_615_MLK	6.4	1.9	4
pEA1066_442_444_NQE	73.3	11.8	4	pEA1124_616_618_TLN	35.5	3.2	4
pEA1067_445_447_EVE	42.9	16.2	4	pEA1125_619_621_KLG	13.0	2.1	3
pEA1068_448_450_SLN	30.3	12.9	3	pEA1126_622_624_IDG	7.9	4.3	4
pEA1069_451_453_RPI	30.8	33.2	4	pEA1127_625_627_TYF	18.8	7.9	4
pEA1070_454_456_TGS	87.5	18.3	4	pEA1128_628_630_KII	4.3	1.4	4
pEA1071_457_459_EIV	3.4	2.5	4	pEA1129_631_633_RAI	25.4	6.2	4
pEA1072_460_462_AII	16.3	4.1	3	pEA1130_634_636_YDK	13.6	1.0	4
pEA1073_463_465_NSL	12.6	12.9	3	pEA1131_637_639_PTA	62.5	12.6	4
pEA1074_466_468_PTK	40.0	4.9	2	pEA1132_640_642_NII	4.1	0.8	4
pEA1075_469_471_KSP	61.9	13.8	2	pEA1133_643_645_LNG	13.0	2.3	4
pEA1076_472_474_GPD	3.5	2.2	4	pEA1134_646_648_QKL	44.5	4.6	4
pEA1077_475_477_GFT	7.4	6.9	4	pEA1135_649_651_EAF	6.2	3.5	4
pEA1078_478_480_AEF	18.5	10.6	4	pEA1136_652_654_PLK	35.3	5.1	4
pEA1079_481_483_YQR	14.4	13.8	4	pEA1137_655_657_TGT	10.7	1.1	4
pEA1080_484_486_YKE	8.0	2.4	2	pEA1138_658_660_RQG	8.7	5.6	4
pEA1081_487_489_ELV	9.7	6.4	4	pEA1139_661_663_CPL	5.6	1.5	4
pEA1082_490_492_PFL	8.1	7.5	4	pEA1140_664_666_SPL	4.8	1.3	4
pEA1083_493_495_LKL	6.2	2.0	4	pEA1141_667_669_LFN	11.6	3.0	4
pEA1084_496_498_FQS	28.1	8.4	4	pEA1142_670_672_IVL	13.9	5.4	4
pEA1085_499_501_IEK	79.3	27.2	4	pEA1143_673_675_EVL	4.9	1.2	4
pEA1086_502_504_EGI	38.1	9.5	4	pEA1144_676_678_ARA	123.2	15.7	4
pEA1087_505_507_LPN	8.2	1.6	4	pEA1145_679_681_IRQ	5.9	1.0	4
pEA1088_508_510_SFY	8.9	2.4	4	pEA1146_682_684_EKE	29.2	5.8	4
pEA1089_511_513_EAS	41.1	6.5	4	pEA1147_685_687_IKG	4.4	1.4	4
pEA1090_514_516_IIL	5.9	2.3	4	pEA1148_688_690_IQL	9.1	1.9	4
pEA1091_517_519_IPK	8.2	0.9	3	pEA1149_691_693_GKE	51.7	12.3	4
pEA1092_520_522_PGR	9.9	6.1	4	pEA1150_694_696_EVK	3.4	1.1	4
pEA1093_523_525_DTT	80.1	24.7	4	pEA1151_697_699_LSL	36.9	4.3	4
pEA1094_526_528_KKE	82.6	6.7	4	pEA1152_700_702_FAD	9.4	6.3	4
pEA1095_529_531_NFR	5.6	0.7	4	pEA1153_703_705_DMI	4.0	1.3	4
pEA1096_532_534_PIS	5.7	2.6	4	pEA1154_706_708_VYL	7.3	3.0	3
pEA1097_535_537_LMN	9.7	5.4	2	pEA1155_709_711_ENP	15.8	7.2	3
pEA1098_538_540_IDA	8.0	6.7	4	pEA1156_712_714_IVS	34.3	4.1	4
pEA1099_541_543_KIL	4.5	1.5	4	pEA1157_715_717_AQN	88.0	12.9	3
pEA1100_544_546_NKI	58.1	7.5	4	pEA1158_718_720_LLK	7.3	4.0	4

ORF2							
Mutant ID	retroT average	standard deviation	number of measurements	Mutant ID	retroT average	standard deviation	number of measurements
pEA1159_721_723_LIS	6.0	3.1	4	pEA1221_907_909_IMP	112.1	4.0	4
pEA1160_724_726_NFS	5.4	1.1	4	pEA1222_910_912_HIY	88.5	4.0	4
pEA1161_727_729_KVS	20.1	7.2	4	pEA1223_913_915_NYL	105.1	4.0	4
pEA1162_730_732_GYK	5.6	2.6	4	pEA1224_916_918_IFD	7.3	4.0	4
pEA1163_733_735_INV	11.4	3.2	4	pEA1225_919_921_KPE	95.3	4.0	4
pEA1164_736_738_QKS	5.3	1.9	4	pEA1226_922_924_KNK	79.0	4.0	4
pEA1165_739_741_QAF	8.5	2.9	4	pEA1227_925_927_QWG	112.0	4.0	4
pEA1166_742_744_LYT	6.4	2.2	4	pEA1228_928_930_KDS	73.2	4.0	4
pEA1167_745_747_NNR	59.7	10.0	4	pEA1229_931_933_LFN	48.9	4.0	4
pEA1168_748_750_QTE	92.1	7.4	4	pEA1230_934_936_KWC	75.3	4.0	4
pEA1169_751_753_SQI	119.7	4.0	4	pEA1231_937_939_WEN	64.5	4.0	4
pEA1170_754_756_MGE	115.8	11.8	6	pEA1232_940_942_WLA	18.7	4.0	4
pEA1171_757_759_LPF	22.2	0.9	4	pEA1233_943_945_ICR	96.0	4.0	4
pEA1172_760_762_TIA	92.5	27.1	4	pEA1234_946_948_KLK	97.5	4.0	4
pEA1173_763_765_SKR	66.0	14.7	4	pEA1235_949_951_LDP	70.9	4.0	4
pEA1174_766_768_IKY	10.2	3.2	4	pEA1236_952_954_FLT	16.2	4.0	4
pEA1175_769_771_LGI	4.3	2.4	4	pEA1237_955_957_PYT	3.8	4.0	4
pEA1176_772_774_QLT	20.0	3.0	4	pEA1238_958_960_KIN	7.9	4.0	4
pEA1177_775_777_RDV	78.3	17.3	4	pEA1239_961_963_SRW	9.7	4.0	4
pEA1178_778_780_KDL	44.3	11.3	4	pEA1240_964_966_IKD	42.0	4.0	4
pEA1179_781_783_FKE	82.7	8.9	4	pEA1241_967_969_LNV	7.6	4.0	4
pEA1180_784_786_NYK	14.2	2.7	4	pEA1242_970_972_KPK	64.2	4.0	4
pEA1181_787_789_PLL	42.3	2.2	4	pEA1243_973_975_TIK	13.8	2.0	2
pEA1182_790_792_KEI	53.8	5.4	4	pEA1244_976_978_TLE	27.6	4.0	4
pEA1183_793_795_KEE	75.4	12.4	4	pEA1245_979_981_ENL	63.0	4.0	4
pEA1184_796_798_TNK	104.1	15.3	4	pEA1246_982_984_GIT	25.0	3.0	3
pEA1185_799_801_WKN	62.1	6.6	4	pEA1247_985_987_IQD	50.7	4.0	4
pEA1186_802_804_IPC	79.9	9.3	4	pEA1248_988_990_IGV	10.2	4.0	4
pEA1187_805_807_SWV	24.5	9.2	4	pEA1249_991_993_GKD	97.4	4.0	4
pEA1188_808_810_GRI	34.3	4.9	4	pEA1250_994_996_FMS	8.0	4.0	4
pEA1189_811_813_NIV	41.4	7.7	4	pEA1251_997_999_KTP	93.4	4.0	4
pEA1190_814_816_KMA	35.3	15.8	4	pEA1252_1000_1002_KAM	103.2	4.0	4
pEA1191_817_819_ILP	10.7	3.3	4	pEA1253_1003_1005_ATK	108.8	4.0	4
pEA1192_820_822_KVI	19.4	3.8	4	pEA1254_1006_1008_DKI	77.3	4.0	4
pEA1193_823_825_YRF	100.1	26.0	4	pEA1255_1009_1011_DKW	11.0	4.0	4
pEA1194_826_828_NAI	55.8	3.9	4	pEA1256_1012_1014_DLI	10.6	4.0	4
pEA1195_829_831_PIK	5.2	0.4	4	pEA1257_1015_1017_KLK	10.7	4.0	4
pEA1196_832_834_LPM	66.1	21.2	4	pEA1258_1018_1020_SFC	6.4	4.0	4
pEA1197_835_837_TFF	34.8	17.9	4	pEA1259_1021_1023_TAK	92.8	4.0	4
pEA1198_838_840_TEL	67.4	13.5	4	pEA1260_1024_1026_ETT	91.0	4.0	4
pEA1199_841_843_EKT	82.5	6.4	4	pEA1261_1027_1029_IRV	109.8	4.0	4
pEA1200_844_846_TLK	97.6	18.3	2	pEA1262_1030_1032_NRQ	71.9	3.0	3
pEA1201_847_849_FIW	8.2	2.4	4	pEA1263_1033_1035_PTT	125.7	4.0	4
pEA1202_850_852_NQK	83.3	14.9	4	pEA1264_1036_1038_WEK	28.5	4.0	4
pEA1203_853_855_RAR	18.9	4.0	4	pEA1265_1039_1041_IFA	7.8	4.0	4
pEA1204_856_858_IAK	52.0	4.0	4	pEA1266_1042_1044_TYS	106.5	4.0	4
pEA1205_859_861_SIL	56.0	4.0	4	pEA1267_1045_1047_SDK	40.6	4.0	4
pEA1206_862_864_SQK	72.9	4.0	4	pEA1268_1048_1050_GLI	14.6	4.0	4
pEA1207_865_867_NKA	122.1	4.0	4	pEA1269_1051_1053_SRI	55.3	2.0	2
pEA1208_868_870_GGI	60.4	4.0	4	pEA1270_1054_1056_YNE	66.0	4.0	4
pEA1209_871_873_TLP	69.2	4.0	4	pEA1271_1057_1059_LKQ	82.3	4.0	4
pEA1210_874_876_DFK	6.7	4.0	4	pEA1272_1060_1062_IYK	66.5	2.0	2
pEA1211_877_879_LYY	5.6	4.0	4	pEA1273_1063_1065_KKT	107.5	4.0	4
pEA1212_880_882_VAT	59.9	4.0	4	pEA1274_1066_1068_NNP	56.6	4.0	4
pEA1213_883_885_VTK	62.3	4.0	4	pEA1275_1069_1071_IKK	42.6	2.0	2
pEA1214_886_888_TAW	36.4	4.0	4	pEA1276_1072_1074_WAK	17.6	4.0	4
pEA1215_889_891_YWY	3.9	4.0	4	pEA1277_1075_1077_DMN	5.4	4.0	4
pEA1216_892_894_QNR	37.8	4.0	4	pEA1278_1078_1080_RHF	14.2	4.0	4
pEA1217_895_897_DID	54.9	4.0	4	pEA1279_1081_1083_SKE	93.5	4.0	4
pEA1218_898_900_QWN	59.9	4.0	4	pEA1280_1084_1086_DIY	65.1	4.0	4
pEA1219_901_903_RTE	68.9	4.0	4	pEA1281_1087_1089_AAK	64.0	4.0	4
pEA1220_904_906_PSE	119.5	4.0	4	pEA1282_1090_1092_KHM	14.9	4.0	4

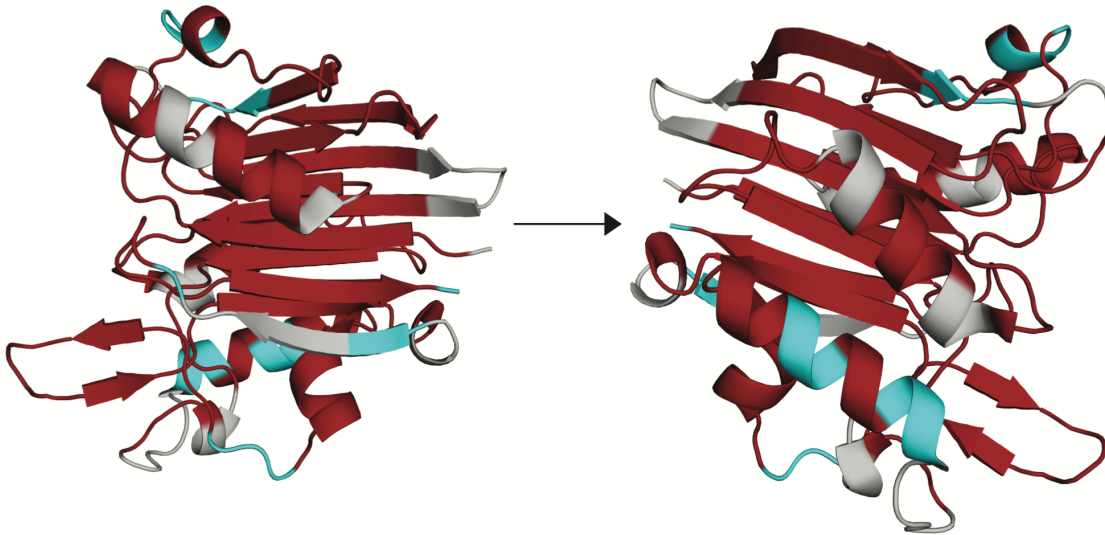
ORF2							
Mutant ID	retroT average	standard deviation	number of measurements	Mutant ID	retroT average	standard deviation	number of measurements
pEA1283_1093_1095_KKC	65.4	4.0	4	pEA1314_1186_1188_SCC	97.2	5.0	5
pEA1284_1096_1098_SSS	43.6	4.0	4	pEA1315_1189_1191_YKD	94.0	4.0	4
pEA1285_1099_1101_LAI	50.2	4.0	4	pEA1316_1192_1194_TCT	63.9	4.0	4
pEA1286_1102_1104_REM	24.2	4.0	4	pEA1317_1195_1197_RMF	19.2	4.0	4
pEA1287_1105_1107_QIK	27.9	4.0	4	pEA1318_1198_1200_IAA	102.4	6.0	6
pEA1288_1108_1110_TTM	43.7	4.0	4	pEA1319_1201_1203_LFT	82.2	4.0	4
pEA1289_1111_1113_RYH	5.3	2.0	2	pEA1320_1204_1206_IAC	68.5	2.0	2
pEA1290_1114_1116_LTP	21.1	2.0	2	pEA1321_1207_1209_TWN	13.1	2.0	2
pEA1291_1117_1119_VRM	70.3	4.0	4	pEA1322_1210_1212_QPK	85.6	2.0	2
pEA1292_1120_1122_AII	116.5	6.0	6	pEA1323_1213_1215_CPT	63.0	2.0	2
pEA1293_1123_1125_KKS	92.7	4.0	4	pEA1324_1216_1218_MID	91.0	4.0	4
pEA1294_1126_1128_GNN	97.2	4.0	4	pEA1325_1219_1221_WIK	24.9	4.0	4
pEA1295_1129_1131_RCW	7.9	4.0	4	pEA1326_1222_1224_KMW	7.8	4.0	4
pEA1296_1132_1134_RGC	6.3	4.0	4	pEA1327_1225_1227_HIY	24.1	4.0	4
pEA1297_1135_1137_GEI	126.9	4.0	4	pEA1328_1228_1230_TME	4.6	4.0	4
pEA1298_1138_1140_GTL	82.0	4.0	4	pEA1329_1231_1233_YYA	23.3	2.0	2
pEA1299_1141_1143_LHC	5.2	4.0	4	pEA1330_1234_1236_AIK	50.8	2.0	2
pEA1300_1144_1146_WWD	18.7	4.0	4	pEA1331_1237_1239_NDE	61.1	3.0	3
pEA1301_1147_1149_CKL	11.3	4.0	4	pEA1332_1240_1242_FIS	59.6	4.0	4
pEA1302_1150_1152_VQP	46.3	4.0	4	pEA1333_1243_1245_FVG	28.4	3.0	3
pEA1303_1153_1155_LWK	10.9	4.0	4	pEA1334_1246_1248_TWM	16.3	4.0	4
pEA1304_1156_1158_SVW	23.6	4.0	4	pEA1335_1249_1251_KLE	20.6	2.0	2
pEA1305_1159_1161_RFL	87.2	4.0	4	pEA1336_1252_1254_TII	8.8	4.0	4
pEA1306_1162_1164_RDL	100.4	4.0	4	pEA1337_1255_1257_LSK	56.4	4.0	4
pEA1307_1165_1167_ELE	79.5	4.0	4	pEA1338_1258_1260_LSQ	82.5	3.0	3
pEA1308_1168_1170_IPF	49.7	4.0	4	pEA1339_1261_1263_EQK	104.1	6.0	6
pEA1309_1171_1173_DPA	69.7	4.0	4	pEA1340_1264_1266_TKH	101.8	8.0	8
pEA1310_1174_1176_IPL	21.3	4.0	4	pEA1341_1267_1269_RIF	48.8	4.0	4
pEA1311_1177_1179_LGI	4.5	4.0	4	pEA1342_1270_1272_SLI	80.8	4.0	4
pEA1312_1180_1182_YPN	86.7	4.0	4	pEA1343_1273_1275_GGN	58.4	8.0	8
pEA1313_1183_1185_EYK	109.3	4.0	4				

Supplemental Figure 3



Supplemental Figure 4

Effect of mutations on retroT mapped onto EN crytsal structure :



Supplemental Table 3

ORF1			
Mutant ID		average	
pEA807_2_4_GKK	131.9	pEA864_173_175_KLE	49.6
pEA808_5_7_QNR	138.3	pEA865_176_178_NTL	22.2
pEA809_8_10_KTG	78.5	pEA866_179_181_QDI	3.2
pEA810_11_13_NSK	168.9	pEA867_182_184_IQE	8.7
pEA811_14_16_TQS	201.1	pEA868_185_187_NFP	11.5
pEA812_17_19_ASP	94.0	pEA869_188_190_NLA	133.5
pEA813_20_22_PPK	122.0	pEA870_191_193_RQA	120.4
pEA814_23_25_ERS	88.5	pEA871_194_196_NVQ	101.3
pEA815_26_28_SSP	94.9	pEA872_197_199_IQE	109.7
pEA816_29_31_ATE	93.3	pEA873_200_202_IQR	12.7
pEA817_32_34_QSW	151.2	pEA874_203_205_TPQ	90.0
pEA818_35_37_MEN	<i>mutates epitope</i>	pEA875_206_208_RYS	129.5
pEA819_38_40_DFD	<i>mutates epitope</i>	pEA876_209_211_SRR	108.2
pEA820_41_43_ELR	<i>mutates epitope</i>	pEA877_212_214_ATP	72.4
pEA821_44_46_EEG	<i>mutates epitope</i>	pEA878_215_217_RHI	24.1
pEA822_47_49_FRR	111.0	pEA879_218_220_IVR	4.9
pEA823_50_52_SNY	148.1	pEA880_221_223_FTK	46.7
pEA824_53_55_SEL	109.4	pEA881_224_226_VEM	106.4
pEA825_56_58_RED	102.9	pEA882_227_229_KEK	99.5
pEA826_59_61_IQT	110.6	pEA883_230_232_MLR	22.3
pEA827_62_64_KGK	153.9	pEA884_233_235_AAR	104.1
pEA828_65_67_EVE	104.4	pEA885_236_238_EKG	81.7
pEA829_68_70_NFE	139.7	pEA886_239_241_RVT	63.2
pEA830_71_73_KNL	161.1	pEA887_242_244_LKG	46.2
pEA831_74_76_EEC	93.5	pEA888_245_247_KPI	5.8
pEA832_77_79_ITR	196.1	pEA889_248_250_RLT	68.5
pEA833_80_82_ITN	160.9	pEA890_251_253_ADL	7.9
pEA834_83_85_TEK	106.3	pEA891_254_256_SAE	53.9
pEA835_86_88_CLK	187.7	pEA892_257_259_TLQ	109.0
pEA836_89_91_ELM	82.6	pEA893_260_262_ARR	81.2
pEA837_92_94_ELK	99.6	pEA894_263_265_EWG	10.6
pEA838_95_97_TKA	136.8	pEA895_266_268_PIF	13.4
pEA839_98_100_REL	119.7	pEA896_269_271_NIL	14.7
pEA840_101_103_REE	140.5	pEA897_272_274_KEK	118.9
pEA841_104_106_CRS	146.7	pEA898_275_277_NFQ	74.0
pEA842_107_109_LRS	175.6	pEA899_278_280_PRI	21.1
pEA843_110_112_RCD	188.7	pEA900_281_283_SYP	68.4
pEA844_113_115_QLE	147.2	pEA901_284_286_AKL	22.9
pEA845_116_118_ERV	90.0	pEA902_287_289_SFI	10.4
pEA846_119_121_SAM	87.4	pEA903_290_292_SEG	46.4
pEA847_122_124_EDE	169.1	pEA904_293_295_EIK	82.7
pEA848_125_127_MNE	134.7	pEA905_296_298_YFI	86.9
pEA849_128_130_MKR	175.3	pEA906_299_301_DKQ	19.4
pEA850_131_133_EGK	157.3	pEA907_302_304_MLR	89.1
pEA851_134_136_FRE	157.2	pEA908_305_307_DFV	47.8
pEA852_137_139_KRI	121.6	pEA909_308_310_TTR	126.1
pEA853_140_142_KRN	116.5	pEA910_311_313_PAL	42.4
pEA854_143_145_EQS	98.3	pEA911_314_316_KEL	89.8
pEA855_146_148_LQE	120.5	pEA912_317_319_LKE	39.6
pEA856_149_151_IWD	65.5	pEA913_320_322_ALN	119.0
pEA857_152_154_YVK	102.9	pEA914_323_325_MER	99.6
pEA858_155_157_RPN	93.2	pEA915_326_328_NNR	106.3
pEA859_158_160_LRL	11.4	pEA916_329_331_YQP	110.5
pEA860_161_163_IGV	12.6	pEA917_332_334_LQN	154.9
pEA861_164_166_PES	37.6	pEA918_335_337_HAK	91.9
pEA862_167_169_DVE	66.0	pEA1361_338_M	94.7
pEA863_170_172_NGT	104.0		

Supplemental Table 4

% of 3xala mutations that landed in each final functional category:				
ORF1p				
	WT retroT high ORF1p	reduced retroT high ORF1p	no retroT high ORF1p	no retroT low ORF1p
Full Length Protein	16	31	29	24
NTR	9	4	0	0
Coiled coil	3	11	16	0
RRM	0	7	6	14
CTD	2	6	5	10

Supplemental Table 5

Mutants in each pool (1348 is WT)																
Pool 1	807	815	823	831	839	847	855	863	869	877	885	893	901	909	917	1348
Pool 2	808	816	824	832	840	848	856	864	870	878	886	894	902	910	918	1348
Pool 3	809	817	825	833	841	849	857	871	879	887	895	903	911	1361		1348
Pool 4	810	818	826	834	842	850	858	865	873	881	889	897	905	913		1348
Pool 5	811	819	827	835	843	851	859	866	874	882	890	898	906	914		1348
Pool 6	812	820	828	836	844	852	860	867	875	883	891	899	907	915		1348
Pool 7	813	821	829	837	845	853	861	868	876	884	892	900	908	916		1348
Pool 8	814	822	830	838	846	854	862	872	880	888	896	904	912			1348

Supplemental Table 6

	ORF1p domain	retroT category	# of measurements	nucleolar phenotype (>5% positive)	aggregate blinded counting data	
					% nucleolar ORF1 positive cells	# of cells counted
WT			4	-	0.82	122
pEA807_2_4_GKK	NTR	-	2	-	0	41
pEA812_17_19_ASP		++	2	-	0	31
pEA814_23_25_ERS		+	2	-	0	57
pEA816_29_31_ATE		++	2	-	0	58
pEA824_53_55_SEL	CC	-	2	-	0	49
pEA826_59_61_IQT		-	2	-	0	51
pEA828_65_67_EVE		-	1	-	0	27
pEA829_68_70_NFE		-	1	-	2.7	37
pEA832_77_79_ITR		-	1	-	0	24
pEA833_80_82_ITN		+	1	-	0	32
pEA834_83_85_TEK		-	1	-	3.6	28
pEA835_86_88_CLK		-	2	+	7.5	67
pEA836_89_91_ELM		-	3	-	2.3	86
pEA837_92_94_ELK		-	3	-	0	72
pEA838_95_97_TKA		++	1	-	3.2	31
pEA839_98_100_REL		-	1	-	0	30
pEA841_104_106_CRS		-	1	-	0	21
pEA842_107_109_LRS		-	1	+	24.1	29
pEA843_110_112_RCD		-	1	-	0	21
pEA847_122_124_EDE		-	1	-	0	39
pEA850_131_133_EGK		++	1	-	0	22
pEA855_146_148_LQE		-	1	-	0	27
pEA858_155_157_RPN		-	1	-	0	37
pEA861_164_166_PES	RRM	-	1	-	3.6	28
pEA866_179_181_QDI		-	2	-	3.4	59
pEA870_191_193_RQA		++	1	-	0	21
pEA874_203_205_TPQ		-	1	-	0	33
pEA877_212_214_ATP		-	1	-	0	30
pEA880_221_223_FTK		-	2	-	0	45
pEA886_239_241_RVT		-	2	-	0	59
pEA887_242_244_LKG		-	1	-	0	37
pEA889_248_250_RLT		-	1	-	0	48
pEA893_260_262_ARR	CTD	-	1	-	0	33
pEA898_275_277_NFQ		-	1	-	0	37
pEA900_281_283_SYP		-	2	-	3.8	52
pEA903_290_292_SEG		-	1	-	0	43
pEA908_305_307_DfV		-	1	-	0	40
pEA910_311_313_PAL		-	2	-	2.7	73
pEA911_314_316_KEL		+	1	-	0	34
pEA914_323_325_MER		+	1	-	0	26

Supplemental Table 7

MAMMALIAN	NON-MAMMALIAN VERTEBRATE		
HUMAN L1 - RP	LIZARD L1_AC1	FROG L1-15	ZEBRAFISH L1-7B
ARMADILLO	LIZARD L1_AC3B	FROG L1-17	ZEBRAFISH L1-7C
COW	LIZARD L1_AC7	FROG L1-18	ZEBRAFISH L1-8
DOG	LIZARD L1_AC8	FROG L1-29	ZEBRAFISH L1-10B
PIG	LIZARD L1_AC9	FROG L1-32	ZEBRAFISH L1-11A
ELEPHANT	LIZARD L1_AC11	FROG L1-35	ZEBRAFISH L1-12A
HYRAX	LIZARD L1_AC12	FROG L1-38	ZEBRAFISH L1-12B
LEMUR	LIZARD L1_AC14	FROG L1-39	ZEBRAFISH L1-13A
OPOSSUM	LIZARD L1_AC15	FROG L1-46	ZEBRAFISH L1-13B
PANDA	LIZARD L1_AC17	FROG L1-47	ZEBRAFISH L1-13C
RABBIT	LIZARD L1_AC18	ZEBRAFISH L1-1	ZEBRAFISH L1-13D
RAT	LIZARD L1_AC20	ZEBRAFISH L1-1B	ZEBRAFISH L1-16B
HORSE	FROG L1-6	ZEBRAFISH L1-1D	ZEBRAFISH L1-17B
MOUSE	FROG L1-11	ZEBRAFISH L1-6	

Supplemental Figure 5



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RT (498-783)														D2 (774-1275)																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																														
	770	780	790	800	810	820	830	840	850	860	870	880																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																
HUMAN	VY	EN	PI	VS	AO	NL	LK	LL	SN	EF	KV	GY	KI	NO	QA	LF	YT	NN	RO	TS	OI	MG	EL	PF	TH	AS	KR	IK	YLG	TR	VD	KD	LE	KE	YK	PL	KE	IK	ED	TK	KN	KN	IP	CS	WG	RI	NI	VA	VI	AI	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA	IR	NA

	D2 (774-1275)																													
	1,150	1,160	1,170	1,180	1,190	1,200	1,210	1,220	1,230	1,240	1,250	1,260	1,270																	
HUMAN	KKKTN	--NP	IKKAKDMNRHFS	ED	IYAARKHMK	KCS	SLAIREMOIK	TM	YHLTP	VR	IA	IKKSGNN	--RWRGG	GE	IGTLL	HCW	EKL	VQPL	IKS	WRF	LRD	EE	LE	IP	DA	IP	GL	LYP		
RABBIT	KNKTN	--NP	IKKAKDMNRHFS	EE	QMANRHMK	KCS	SLAIREMOIK	TM	FHLTP	VR	IA	IKKSGNN	--RWRGG	GE	IGTLL	HCW	EKL	VQPL	IKS	WRF	LRN	EE	LE	IP	DA	IP	GL	LYP		
PIG	SKKTN	--OS	MEKAKDMNRHFS	ED	QMANRHMK	KCS	SLAIREMOIK	TM	FHLTP	VR	IA	IKKSGNN	--RWRGG	GE	IGTLL	HCW	EKL	VQPL	IKS	WRF	LRN	EE	LE	IP	DA	IP	GL	LYP		
COW	SRKIN	--DP	IKKAKDMNRHFS	KD	QMANRHMK	KCS	SLAIREMOIK	TM	FHLTP	VR	IA	IKKSGNN	--RWRGG	GE	IGTLL	HCW	EKL	VQPL	IKS	WRF	LRN	EE	LE	IP	DA	IP	GL	LYP		
DOG	TKETN	--NP	IKKAKDMNRNLTE	ED	QMANRHMK	KCS	SLAIREMOIK	TM	FHLTP	VR	IA	IKKSGNN	--RWRGG	GE	IGTLL	HCW	EKL	VQPL	IKS	WRF	LRN	EE	LE	IP	DA	IP	GL	LYP		
PANDA	TRETN	--KO	IKKAKDMNRHFS	ED	QMANRHMK	KCS	SLAIREMOIK	TM	FHLTP	VR	IA	IKKSGNN	--RWRGG	GE	IGTLL	HCW	EKL	VQPL	IKS	WRF	LRN	EE	LE	IP	DA	IP	GL	LYP		
HORSE	NKKTN	--NP	IKKAKDMNRHFS	ED	QMANRHMK	KCS	SLAIREMOIK	TM	FHLTP	VR	IA	IKKSGNN	--RWRGG	GE	IGTLL	HCW	EKL	VQPL	IKS	WRF	LRN	EE	LE	IP	DA	IP	GL	LYP		
LEMUR	KKKSN	--NP	IKKAKDMNRHFS	ED	QMANRHMK	KCS	SLAIREMOIK	TM	FHLTP	VR	IA	IKKSGNN	--RWRGG	GE	IGTLL	HCW	EKL	VQPL	IKS	WRF	LRN	EE	LE	IP	DA	IP	GL	LYP		
ELEPHANT	NKKTN	--NP	IKKAKDMNRHFS	ED	QANRHMK	KCS	SLAIREMOIK	TM	FHLTP	VR	IA	IKKSGNN	--RWRGG	GE	IGTLL	HCW	EKL	VQPL	IKS	WRF	LRN	EE	LE	IP	DA	IP	GL	LYP		
HYRAX	KKKIN	--HP	IKKAKDMNRHFS	EE	OAAKHMR	KCS	SLAIREMOIK	TM	FHLTP	VR	IA	IKKSGNN	--RWRGG	GE	IGTLL	HCW	EKL	VQPL	IKS	WRF	LRN	EE	LE	IP	DA	IP	GL	LYP		
ARMADILLO	NKKIN	--NP	IKKAKDMNRHFS	EE	OAAKHMR	KCS	SLAIREMOIK	TM	FHLTP	VR	IA	IKKSGNN	--RWRGG	EE	MGTL	HCW	EKL	VQPL	IKS	WRF	LRN	EE	LE	IP	DA	IP	GL	LYP		
MOUSE	FRKSN	--NP	IKKAGSEINK	FS	EEVRMAEK	HUK	KCS	SLAIREMOIK	TM	FHLTP	VR	IA	IKKSGNN	--RWRGG	GE	IGTLL	HCW	EKL	VQPL	IKS	WRF	LRN	EE	LE	IP	DA	IP	GL	LYP	
RAT	RRETN	--NP	IKKAGSEINK	FT	EECRMAEK	HUK	KCS	SLAIREMOIK	TM	FHLTP	VR	IA	IKKSGNN	--RWRGG	GE	IGTLL	HCW	EKL	VQPL	IKS	WRF	LRN	EE	LE	IP	DA	IP	GL	LYP	
OPOSSUM	KKSSH	--SP	IKKAKDMNRD	FS	KE	KTINK	HMK	KCS	SLAIREMOIK	TM	FHLTP	VR	IA	IKKSGNN	--RWRGG	GK	VGTL	HCW	EKL	VQPL	IKS	WRF	LRN	EE	LE	IP	DA	IP	GL	LYP
FROG_6	PPPFN	--RAROL	IKKAKDMNRHFS	ED	QMANRHMK	KCS	SLAIREMOIK	TM	FHLTP	VR	IA	IKKSGNN	--RWRGG	GE	IGTLL	HCW	EKL	VQPL	IKS	WRF	LRN	EE	LE	IP	DA	IP	GL	LYP		
FROG_32	OAPFH	--RTYL	IKKAKDMNRHFS	ED	QMANRHMK	KCS	SLAIREMOIK	TM	FHLTP	VR	IA	IKKSGNN	--RWRGG	GE	IGTLL	HCW	EKL	VQPL	IKS	WRF	LRN	EE	LE	IP	DA	IP	GL	LYP		
FROG_15	YSDTE	--PAKAR	IKKAKDMNRHFS	ED	QMANRHMK	KCS	SLAIREMOIK	TM	FHLTP	VR	IA	IKKSGNN	--RWRGG	GE	IGTLL	HCW	EKL	VQPL	IKS	WRF	LRN	EE	LE	IP	DA	IP	GL	LYP		
FROG_29	NKPLE	--TLRD	IKKAKDMNRHFS	ED	QMANRHMK	KCS	SLAIREMOIK	TM	FHLTP	VR	IA	IKKSGNN	--RWRGG	GE	IGTLL	HCW	EKL	VQPL	IKS	WRF	LRN	EE	LE	IP	DA	IP	GL	LYP		
FISH_1	LEPLV	--KLKR	IKKAKDMNRHFS	ED	QMANRHMK	KCS	SLAIREMOIK	TM	FHLTP	VR	IA	IKKSGNN	--RWRGG	GE	IGTLL	HCW	EKL	VQPL	IKS	WRF	LRN	EE	LE	IP	DA	IP	GL	LYP		
FISH_7B	SFPDG	--SLRTS	IKKAKDMNRHFS	ED	QMANRHMK	KCS	SLAIREMOIK	TM	FHLTP	VR	IA	IKKSGNN	--RWRGG	GE	IGTLL	HCW	EKL	VQPL	IKS	WRF	LRN	EE	LE	IP	DA	IP	GL	LYP		
FISH_13A	NTTLE	--KIKTE	IKKAKDMNRHFS	ED	QMANRHMK	KCS	SLAIREMOIK	TM	FHLTP	VR	IA	IKKSGNN	--RWRGG	GE	IGTLL	HCW	EKL	VQPL	IKS	WRF	LRN	EE	LE	IP	DA	IP	GL	LYP		
FISH_17B	YLPPL	--SLDSS	IKKAKDMNRHFS	ED	QMANRHMK	KCS	SLAIREMOIK	TM	FHLTP	VR	IA	IKKSGNN	--RWRGG	GE	IGTLL	HCW	EKL	VQPL	IKS	WRF	LRN	EE	LE	IP	DA	IP	GL	LYP		
LIZ_AC1	TESSR	--TKATT	IKKAKDMNRHFS	ED	QMANRHMK	KCS	SLAIREMOIK	TM	FHLTP	VR	IA	IKKSGNN	--RWRGG	GE	IGTLL	HCW	EKL	VQPL	IKS	WRF	LRN	EE	LE	IP	DA	IP	GL	LYP		
LIZ_AC14	TETEI	--KENMT	IKKAKDMNRHFS	ED	QMANRHMK	KCS	SLAIREMOIK	TM	FHLTP	VR	IA	IKKSGNN	--RWRGG	GE	IGTLL	HCW	EKL	VQPL	IKS	WRF	LRN	EE	LE	IP	DA	IP	GL	LYP		
LIZ_AC15	MEDNT	--KTVMI	IKKAKDMNRHFS	ED	QMANRHMK	KCS	SLAIREMOIK	TM	FHLTP	VR	IA	IKKSGNN	--RWRGG	GE	IGTLL	HCW	EKL	VQPL	IKS	WRF	LRN	EE	LE	IP	DA	IP	GL	LYP		
LIZ_AC17	EEIVE	--EIFOT	IKKAKDMNRHFS	ED	QMANRHMK	KCS	SLAIREMOIK	TM	FHLTP	VR	IA	IKKSGNN	--RWRGG	GE	IGTLL	HCW	EKL	VQPL	IKS	WRF	LRN	EE	LE	IP	DA	IP	GL	LYP		

	D2 (774-1275)																																																																																									
	1,280	1,290	1,300	1,310	1,320	1,330	1,340	1,350	1,360	1,370	1,378																																																																															
HUMAN	--NEYKSCCY	KDTC	TRMF	IAAL	FTIA	AKTN	OPK	CPTM	DI	IKMWH	IT	MEYYAA	IKND	----	E	F	IS	EVGT	IMK	LET	I	IL	SKLSO	EQKT	KHR	IF	SL	IGN																																																														
RABBIT	--K	EFLK	LANK	KAV	CTLM	IAAL	FTIA	AKTN	OPK	CPTM	DI	IKMWH	IT	MEYYAA	IKND	----	E	F	IS	EVGT	IMK	LET	I	IL	SKLSO	EQKT	KHR	IF	SL	IGN																																																												
PIG	--DK	--ALL	KRDTC	TRMF	IAAL	FTIA	AKTN	OPK	CPTM	DI	IKMWH	IT	MEYYAA	IKND	----	D	IMPE	AAT	ME	LEN	L	IL	SEM	SOK	DK	KY	H	M	L	IT	IGN																																																											
COW	--EE	--	TRRER	DTC	TRMF	IAAL	FTIA	AKTN	OPK	CPTM	DI	IKMWH	IT	MEYYAA	IKND	----	T	FES	VLM	R	M	K	E	P	I	IO	SE	V	S	O	K	E	K	H	Y	S	IL	TH	IT	IGN																																																		
DOG	--K	DTNAM	KRRDTC	TRMF	IAAL	FTIA	AKTN	OPK	CPTM	DI	IKMWH	IT	MEYYAA	IKND	----	K	YPP	FA	ST	ME	LEN	L	IL	SEM	SOK	DK	KY	H	M	L	IT	IGN																																																										
PANDA	--K	DTNAM	KRRDTC	TRMF	IAAL	FTIA	AKTN	OPK	CPTM	DI	IKMWH	IT	MEYYAA	IKND	----	E	FST	FA	ST	ME	LEN	L	IL	SEM	SOK	DK	KY	H	M	L	IT	IGN																																																										
HORSE	--K	DTNAM	KRRDTC	TRMF	IAAL	FTIA	AKTN	OPK	CPTM	DI	IKMWH	IT	MEYYAA	IKND	----	E	IGP	FT	ME	LEN	L	IL	SEM	SOK	DK	KY	H	M	L	IT	IGN																																																											
LEMUR	--K	DTNAM	KRRDTC	TRMF	IAAL	FTIA	AKTN	OPK	CPTM	DI	IKMWH	IT	MEYYAA	IKND	----	GD	I	AHL	IF	S	IL	E	P	I	IO	SE	V	S	O	K	E	K	H	Y	S	IL	TH	IT	IGN																																																			
ELEPHANT	--R	DTAF	I	OTD	I	CTMF	IAAL	FTIA	AKTN	OPK	CPTM	DI	IKMWH	IT	MEYYAA	IKND	----	DE	S	KHF	I	T	R	N	E	L	IL	SEM	SOK	DK	KY	H	M	L	IT	IGN																																																						
HYRAX	--D	SRFP	T	PTD	T	CTMF	IAAL	FTIA	AKTN	OPK	CPTM	DI	IKMWH	IT	MEYYAA	IKND	----	DD	S	RK	HL	T	F	O	E	D	I	IL	SEM	SOK	DK	KY	H	M	L	IT	IGN																																																					
ARMADILLO	--A	E	L	K	T	R	T	O	D	I	CTMF	IAAL	FTIA	AKTN	OPK	CPTM	DI	IKMWH	IT	MEYYAA	IKND	----	T	L	O	TH	I	T	R	N	E	L	IL	SEM	SOK	DK	KY	H	M	L	IT	IGN																																																
MOUSE	--E	DAPT	G	K	R	D	T	CTMF	IAAL	FTIA	AKTN	OPK	CPTM	DI	IKMWH	IT	MEYYAA	IKND	----	E	F	M	K	L	A	M	D	E	L	IL	SEM	SOK	DK	KY	H	M	L	IT	IGN																																																			
RAT	--K	DAST	Y	K	R	D	T	CTMF	IAAL	FTIA	AKTN	OPK	CPTM	DI	IKMWH	IT	MEYYAA	IKND	----	E	F	M	K	E	V	G	K	L	E	IL	SEM	SOK	DK	KY	H	M	L	IT	IGN																																																			
OPOSSUM	--K	DE	--	I	MD	K	R	D	T	CTMF	IAAL	FTIA	AKTN	OPK	CPTM	DI	IKMWH	IT	MEYYAA	IKND	----	K	V	DE	H	V	N	E	L	IL	SEM	SOK	DK	KY	H	M	L	IT	IGN																																																			
FROG_6	--D	IL	T	N	A	A	R	I	F	R	T	D	MEFY	IKKAKDMNRHFS	ED	QMANRHMK	KCS	SLAIREMOIK	TM	FHLTP	VR	IA	IKKSGNN	--RWRGG	GE	IGTLL	HCW	EKL	VQPL	IKS	WRF	LRN	EE	LE	IP	DA	IP	GL	LYP																																																			
FROG_32	--DOVG	STASR	L	FARS	L	YVRR	CK	I	LH	IGK	P	R	K	K	O	TK	L	NGAL	P	S	I	K	L	Y	ARG	----	C	PAK	FDK	I	OPWL	DEERDP	IP	RTV	SDPPH																																																							
FROG_15	--NTSL	DLHT	K	TF	I	KAL	F	OKR	I	UTL	R	K	DT	E	P	SMR	E	K	A	M	D	A	S	E	R	T	I	D	R	K	G	----	O	MLK	E	L	O	I	R	H	W	V	D	S	V																																													
FROG_29	--C	ET	ST	RYO	S	A	F	I	N	E	A	L	F	I	K	K	L	U	T	R	K	K	O	A	T	S	P	S	L	A	C	H	V	E	K	R	S	N	E	N	L	I	Y	C	K	R	G	----	S	P	K	K	Y	H	K	I	D	K	W	L	D	W	T																											
FISH_1	O	S	L	C	F	N	K	S	K	I	N	V	I	A	F	A	T	L	I	R	R	L	L	K	K	E	K	I	P	P	T	F	K	O	N	V	E	L	H	L	T	E	K	I	R	Y	T	L	G	G	----	C	T	D	M	E	F	L	T	O	P	V	L	D	H	V	K	K	M	D	P	S	V	I	L	E														
FISH_7B	D	N	Y	A	L	P	T	Y	L	N	F	V	A	F	T	L	I	R	R	V	L	L	Y	K	N	P	O	P	P	S	H	V	R	V	K	D	L	Y	F	V	K	L	E	K	I	R	Y	S	L	O	R	----	P	N	R	T	E	A	K	I	D	A	S	L	Y	V	K	T	L	O	L	D	L																	
FISH_13A	E	D	I	H	L	A	K	E	I	N	A	F	A	F	T	L	I	R	R	L	L	M	E	K	S	P	M	P	K	L	S	L	Y	S	D	M	L	F	K	T	E	K	I	K	Y	F	L	R	G	----	S	T	K	K	E	F	K	T	O	P	I	I	H	E	T	N	L	L	O	P	----	A	R	E	D	T	I	R	L	A	O	T	L	H	R	K	D	L	L	T
FISH_17B	C	D	K	I	D	P	N	T	D																																																																																	

Supplemental Table 8

Mutant ID	Conservation (residue with highest identity value as representative for 3xala mutant)		Avg retroT	Domain
	Mammals	Mammals + Verts		
pEA1362_2_3_TG	14	4	25	EN
pEA920_4_6_STS	20	6	72	EN
pEA921_7_9_HIT	62	29	18	EN
pEA922_10_12_ILT	56	52	4	EN
pEA923_13_15_LNI	100	100	6	EN
pEA924_16_18_NGL	100	96	5	EN
pEA925_19_21_NSA	100	67	9	EN
pEA926_22_24_IKR	100	96	11	EN
pEA927_25_27_HRL	86	27	36	EN
pEA928_28_30_ASW	100	14	18	EN
pEA929_31_33_IKS	73	42	10	EN
pEA930_34_36_QDP	100	20	43	EN
pEA931_37_39_SVC	100	66	0	EN
pEA932_40_42_CIQ	100	93	2	EN
pEA933_43_45_ETH	100	100	2	EN
pEA934_46_48_LTC	62	45	6	EN
pEA935_49_51_RDT	100	31	81	EN
pEA936_52_54_HRL	86	68	4	EN
pEA937_55_57_KIK	73	27	15	EN
pEA938_58_60_GWR	100	24	4	EN
pEA939_61_63_KIY	62	37	0	EN
pEA940_64_66_QAN	86	46	84	EN
pEA941_67_69_GKQ	41	13	52	EN
pEA942_70_72_KKA	86	50	7	EN
pEA943_73_75_GVA	100	100	4	EN
pEA944_76_78_ILV	86	60	2	EN
pEA945_79_81_SDK	100	28	2	EN
pEA946_82_84_TDF	86	51	6	EN
pEA947_85_87_KPT	42	14	18	EN
pEA948_88_90_KIK	39	18	10	EN
pEA949_91_93_RDK	100	100	10	EN
pEA950_94_96_EGH	100	100	3	EN
pEA951_97_99_YIM	74	36	2	EN
pEA952_100_102_VKG	100	42	3	EN
pEA953_103_105_SIQ	52	37	28	EN
pEA954_106_108_QEE	60	16	33	EN
pEA955_109_111_LTI	74	38	5	EN
pEA956_112_114_LNI	100	70	2	EN
pEA957_115_117_YAP	100	100	2	EN
pEA958_118_120_NTG	100	70	24	EN
pEA959_121_123_APR	100	15	65	EN
pEA960_124_126_FIK	51	37	5	EN
pEA961_127_129_QVL	100	26	2	EN
pEA962_130_132_SDL	51	38	40	EN
pEA963_133_135_QRD	62	12	23	EN
pEA964_136_138_LDS	56	9	7	EN
pEA965_139_141_HTL	86	64	3	EN
pEA966_142_144_IMG	100	96	2	EN
pEA967_145_147_DFN	100	100	4	EN
pEA968_148_150_TPL	100	39	6	EN
pEA969_151_153_STL	56	24	64	EN
pEA970_154_156_DRS	100	93	2	EN
pEA971_157_159_TRQ	56	17	52	EN
pEA972_160_162_KVN	60	11	48	EN
pEA973_163_165_KDT	62	22	97	EN
pEA974_166_168_QEL	86	31	19	EN
pEA975_169_171_NSA	41	13	79	EN
pEA976_172_174_LHQ	52	17	25	EN
pEA977_175_177_ADL	86	54	8	EN
pEA978_178_180_IDI	100	96	3	EN

Mutant ID	Conservation (residue with highest identity value as representative for 3xala mutant)		Avg retroT	Domain
	Mammals	Mammals + Verts		
pEA979_181_183_YRT	100	86	3	EN
pEA980_184_186_LHP	86	73	5	EN
pEA981_187_189_KST	25	33	88	EN
pEA982_190_192_EYT	86	54	4	EN
pEA983_193_195_FFS	100	93	2	EN
pEA984_196_198_APH	100	76	10	EN
pEA985_199_201_HTY	86	33	6	EN
pEA986_202_204_SKI	100	96	7	EN
pEA987_205_207_DHI	100	100	2	EN
pEA988_208_210_VGS	100	36	7	EN
pEA989_211_213_KAL	73	23	6	EN
pEA990_214_216_LSK	73	21	61	EN
pEA991_217_219_CKR	28	19	92	EN
pEA992_220_222_TEI	86	42	46	EN
pEA993_223_225_ITN	52	31	33	EN
pEA994_226_228_YLS	100	86	17	EN
pEA995_229_231_DHS	100	100	3	EN
pEA996_232_234_AIK	74	43	14	EN
pEA997_235_237_LEL	73	36	7	EN
pEA998_238_240_RIK	51	17	91	EN (1-239)
pEA999_241_243_NLT	15	8	104	DESERT 1 (240-379)
pEA1000_244_246_QSR	21	11	60	DESERT 1
pEA1001_247_249_STT	32	11	88	DESERT 1
pEA1002_250_252_WKL	100	96	5	DESERT 1
pEA1003_253_255_NNL	74	49	42	DESERT 1
pEA1004_256_258_LLW	100	67	10	DESERT 1
pEA1005_259_261_DYW	26	21	29	DESERT 1
pEA1006_262_264_VHN	64	20	106	DESERT 1
pEA1007_265_267_EMK	86	32	22	DESERT 1
pEA1008_268_270_AEI	74	53	13	DESERT 1
pEA1009_271_273_KMF	62	47	7	DESERT 1
pEA1010_274_276_FET	86	23	16	DESERT 1
pEA1011_277_279_NEN	100	96	12	DESERT 1
pEA1012_280_282_KDT	100	28	28	DESERT 1
pEA1013_283_285_TYQ	73	28	19	DESERT 1
pEA1014_286_288_NLW	100	100	3	DESERT 1
pEA1015_289_291_DAF	100	51	3	DESERT 1
pEA1016_292_294_KAV	100	100	3	DESERT 1
pEA1017_295_297_CRG	100	100	5	DESERT 1
pEA1018_298_300_KFI	100	73	3	DESERT 1
pEA1019_301_303_ALN	56	29	103	DESERT 1
pEA1020_304_306_AYK	86	29	73	DESERT 1
pEA1021_307_309_RKQ	86	58	62	DESERT 1
pEA1022_310_312_ERS	73	14	64	DESERT 1
pEA1023_313_315_KID	42	18	62	DESERT 1
pEA1024_316_318_TLT	100	57	59	DESERT 1
pEA1025_319_321_SQL	74	36	73	DESERT 1
pEA1026_322_324_KEL	73	38	69	DESERT 1
pEA1027_325_327_EKQ	100	52	87	DESERT 1
pEA1028_328_330_EQT	46	17	77	DESERT 1
pEA1029_331_333_HSK	86	56	83	DESERT 1
pEA1030_334_336_ASR	74	15	94	DESERT 1
pEA1031_337_339_RQE	86	32	20	DESERT 1
pEA1032_340_342_ITK	100	31	31	DESERT 1
pEA1033_343_345_IRA	74	24	30	DESERT 1
pEA1034_346_348_ELK	100	31	14	DESERT 1
pEA1035_349_351_EIE	100	23	59	DESERT 1
pEA1036_352_354_TQK	39	17	54	DESERT 1
pEA1037_355_357_TLQ	74	25	31	DESERT 1
pEA1038_358_360_KIN	100	28	57	DESERT 1

Mutant ID	Conservation (residue with highest identity value as representative for 3xala mutant)		Avg retroT	Domain
	Mammals	Mammals + Verts		
pEA1039_361_363_ESR	73	40	31	DESERT 1
pEA1040_364_366_SWF	100	25	12	DESERT 1
pEA1041_367_369_FER	100	56	24	DESERT 1
pEA1042_370_372_INK	100	86	17	DESERT 1
pEA1043_373_375_IDR	100	48	61	DESERT 1
pEA1044_376_378_PLA	100	90	42	DESERT 1
pEA1045_379_381_RLI	100	27	65	DESERT 1 (240-379)
pEA1046_382_384_KKK	73	46	57	Z (380-480)
pEA1047_385_387_REK	86	22	59	Z
pEA1048_388_390_NQI	100	80	60	Z
pEA1049_391_393_DTI	100	74	60	Z
pEA1050_394_396_KND	62	22	77	Z
pEA1051_397_399_KGD	86	56	55	Z
pEA1052_400_402_ITT	100	26	22	Z
pEA1053_403_405_DPT	51	27	45	Z
pEA1054_406_408_EIQ	100	96	14	Z
pEA1055_409_411_TTI	86	50	28	Z
pEA1056_412_414_REY	74	50	28	Z
pEA1057_415_417_YKH	74	86	33	Z
pEA1058_418_420_LYA	100	100	31	Z
pEA1059_421_423_NKL	100	21	66	Z
pEA1060_424_426_ENL	100	25	50	Z
pEA1061_427_429_EEM	100	24	38	Z
pEA1062_430_432_DTF	86	51	20	Z
pEA1063_433_435_LDT	86	55	6	Z
pEA1064_436_438_YTL	51	47	18	Z
pEA1065_439_441_PRL	100	54	23	Z
pEA1066_442_444_NQE	60	26	73	Z
pEA1067_445_447_EVE	62	23	43	Z
pEA1068_448_450_SLN	100	80	30	Z
pEA1069_451_453_RPI	100	74	31	Z
pEA1070_454_456_TGS	53	43	88	Z
pEA1071_457_459_EIV	100	96	3	Z
pEA1072_460_462_AII	100	76	16	Z
pEA1073_463_465_NSL	100	53	13	Z
pEA1074_466_468_PTK	100	28	40	Z
pEA1075_469_471_KSP	100	100	62	Z
pEA1076_472_474_GPD	100	100	4	Z
pEA1077_475_477_GFT	100	100	7	Z
pEA1078_478_480_AEF	100	54	18	Z (380-480)
pEA1079_481_483_YQR	100	90	14	
pEA1080_484_486_YKE	86	44	8	
pEA1081_487_489_ELV	74	56	10	
pEA1082_490_492_PFL	100	83	8	
pEA1083_493_495_LKL	86	26	6	
pEA1084_496_498_FQS	100	44	28	RT (498-773)
pEA1085_499_501_IEK	86	24	79	RT
pEA1086_502_504_EGI	100	35	38	RT
pEA1087_505_507_LPN	100	83	8	RT
pEA1088_508_510_SFY	100	41	9	RT
pEA1089_511_513_EAS	86	74	41	RT
pEA1090_514_516_IIL	100	96	6	RT
pEA1091_517_519_IPK	100	100	8	RT
pEA1092_520_522_PGR	100	54	10	RT
pEA1093_523_525_DTT	86	76	80	RT
pEA1094_526_528_KKE	100	27	83	RT
pEA1095_529_531_NFR	100	100	6	RT
pEA1096_532_534_PIS	100	100	6	RT
pEA1097_535_537_LMN	100	89	10	RT
pEA1098_538_540_IDA	100	96	8	RT

Mutant ID	Conservation (residue with highest identity value as representative for 3xala mutant)		Avg retroT	Domain
	Mammals	Mammals + Verts		
pEA1099_541_543_KIL	100	96	4	RT
pEA1100_544_546_NKI	100	67	58	RT
pEA1101_547_549_LAN	100	89	53	RT
pEA1102_550_552_RIQ	100	100	8	RT
pEA1103_553_555_QHI	86	38	89	RT
pEA1104_556_558_KKL	74	34	43	RT
pEA1105_559_561_IHH	100	67	16	RT
pEA1106_562_564_DQV	100	100	6	RT
pEA1107_565_567_GFI	100	100	20	RT
pEA1108_568_570_PGM	100	49	53	RT
pEA1109_571_573_QGW	100	22	16	RT
pEA1110_574_576_FNI	100	90	36	RT
pEA1111_577_579_RKS	100	93	5	RT
pEA1112_580_582_INV	100	30	30	RT
pEA1113_583_585_IQH	100	42	61	RT
pEA1114_586_588_INR	100	14	57	RT
pEA1115_589_591_AKD	60	17	79	RT
pEA1116_592_594_KNH	100	16	54	RT
pEA1117_595_597_MII	100	32	6	RT
pEA1118_598_600_SID	100	100	5	RT
pEA1119_601_603_AEK	100	100	62	RT
pEA1120_604_606_AFD	100	100	4	RT
pEA1121_607_609_KIQ	100	40	39	RT
pEA1122_610_612_QPF	100	53	5	RT
pEA1123_613_615_MLK	86	46	6	RT
pEA1124_616_618_TLN	100	56	35	RT
pEA1125_619_621_KLG	100	46	13	RT
pEA1126_622_624_IDG	100	38	8	RT
pEA1127_625_627_TYF	86	62	19	RT
pEA1128_628_630_KII	73	46	4	RT
pEA1129_631_633_RAI	100	46	25	RT
pEA1130_634_636_YDK	100	96	14	RT
pEA1131_637_639_PTA	100	96	63	RT
pEA1132_640_642_NII	100	48	4	RT
pEA1133_643_645_LNG	100	86	13	RT
pEA1134_646_648_QKL	100	37	45	RT
pEA1135_649_651_EAF	64	55	6	RT
pEA1136_652_654_PLK	86	44	35	RT
pEA1137_655_657_TGT	100	96	11	RT
pEA1138_658_660_RQG	100	100	9	RT
pEA1139_661_663_CPL	100	100	6	RT
pEA1140_664_666_SPL	100	100	5	RT
pEA1141_667_669_LFN	100	93	12	RT
pEA1142_670_672_IVL	100	39	14	RT
pEA1143_673_675_EVL	100	100	5	RT
pEA1144_676_678_ARA	100	53	123	RT
pEA1145_679_681_IRQ	100	77	6	RT
pEA1146_682_684_EKE	60	16	29	RT
pEA1147_685_687_IKG	100	93	4	RT
pEA1148_688_690_IQL	100	39	9	RT
pEA1149_691_693_GKE	100	25	52	RT
pEA1150_694_696_EVK	100	74	3	RT
pEA1151_697_699_LSL	100	58	37	RT
pEA1152_700_702_FAD	100	100	9	RT
pEA1153_703_705_DMI	100	100	4	RT
pEA1154_706_708_VYL	100	39	7	RT
pEA1155_709_711_ENP	100	80	16	RT
pEA1156_712_714_IVS	100	46	34	RT
pEA1157_715_717_AQN	60	25	88	RT
pEA1158_718_720_LLK	100	34	7	RT

Mutant ID	Conservation (residue with highest identity value as representative for 3xala mutant)		Avg retroT	Domain
	Mammals	Mammals + Verts		
pEA1159_721_723_LIS	100	51	6	RT
pEA1160_724_726_NFS	74	56	5	RT
pEA1161_727_729_KVS	100	57	20	RT
pEA1162_730_732_GYK	100	93	6	RT
pEA1163_733_735_INV	100	96	11	RT
pEA1164_736_738_QKS	100	100	5	RT
pEA1165_739_741_QAF	100	33	8	RT
pEA1166_742_744_LYT	100	33	6	RT
pEA1167_745_747_NNR	73	12	60	RT
pEA1168_748_750_QTE	62	12	92	RT
pEA1169_751_753_SQI	62	21	120	RT
pEA1170_754_756_MGE	31	9	116	RT
pEA1171_757_759_LPF	100	34	22	RT
pEA1172_760_762_TIA	86	23	92	RT
pEA1173_763_765_SKR	41	22	66	RT
pEA1174_766_768_IKY	100	100	10	RT
pEA1175_769_771_LGI	100	100	4	RT
pEA1176_772_774_QLT	100	36	20	RT (498-773)
pEA1177_775_777_RDV	64	16	78	DESERT 2 (774-1275)
pEA1178_778_780_KDL	100	52	44	DESERT 2
pEA1179_781_783_FKE	86	19	83	DESERT 2
pEA1180_784_786_NYK	100	100	14	DESERT 2
pEA1181_787_789_PLL	86	30	42	DESERT 2
pEA1182_790_792_KEI	73	37	54	DESERT 2
pEA1183_793_795_KEE	100	35	75	DESERT 2
pEA1184_796_798_TNK	40	32	104	DESERT 2
pEA1185_799_801_WKN	100	100	62	DESERT 2
pEA1186_802_804_IPC	100	47	80	DESERT 2
pEA1187_805_807_SWV	100	65	25	DESERT 2
pEA1188_808_810_GRI	100	77	34	DESERT 2
pEA1189_811_813_NIV	100	35	41	DESERT 2
pEA1190_814_816_KMA	100	100	35	DESERT 2
pEA1191_817_819_ILP	100	96	11	DESERT 2
pEA1192_820_822_KVI	100	64	19	DESERT 2
pEA1193_823_825_YRF	100	80	100	DESERT 2
pEA1194_826_828_NAI	100	35	56	DESERT 2
pEA1195_829_831_PIK	100	96	5	DESERT 2
pEA1196_832_834_LPM	86	42	66	DESERT 2
pEA1197_835_837_TFF	100	73	35	DESERT 2
pEA1198_838_840_TEL	53	29	67	DESERT 2
pEA1199_841_843_EKT	86	23	82	DESERT 2
pEA1200_844_846_TLK	52	31	98	DESERT 2
pEA1201_847_849_FIW	100	89	8	DESERT 2
pEA1202_850_852_NQK	86	70	83	DESERT 2
pEA1203_853_855_RAR	100	86	19	DESERT 2
pEA1204_856_858_IAK	100	60	52	DESERT 2
pEA1205_859_861_SIL	86	68	56	DESERT 2
pEA1206_862_864_SQK	86	19	73	DESERT 2
pEA1207_865_867_NKA	42	24	122	DESERT 2
pEA1208_868_870_GGI	100	100	60	DESERT 2
pEA1209_871_873_TLP	100	100	69	DESERT 2
pEA1210_874_876_DFK	86	38	7	DESERT 2
pEA1211_877_879_LYY	100	100	6	DESERT 2
pEA1212_880_882_KAT	100	83	60	DESERT 2
pEA1213_883_885_VTK	100	34	62	DESERT 2
pEA1214_886_888_TAW	100	20	36	DESERT 2
pEA1215_889_891_YWY	100	70	4	DESERT 2
pEA1216_892_894_QNR	100	13	38	DESERT 2
pEA1217_895_897_DID	100	12	55	DESERT 2
pEA1218_898_900_QWN	100	49	60	DESERT 2

Mutant ID	Conservation (residue with highest identity value as representative for 3xala mutant)		Avg retroT	Domain
	Mammals	Mammals + Verts		
pEA1219_901_903_RTE	86	83	69	DESERT 2
pEA1220_904_906_PSE	64	13	120	DESERT 2
pEA1221_907_909_IMP	86	19	112	DESERT 2
pEA1222_910_912_HIY	73	19	88	DESERT 2
pEA1223_913_915_NYL	74	26	105	DESERT 2
pEA1224_916_918_IFD	100	34	7	DESERT 2
pEA1225_919_921_KPE	86	19	95	DESERT 2
pEA1226_922_924_KNK	60	20	79	DESERT 2
pEA1227_925_927_QWG	86	9	112	DESERT 2
pEA1228_928_930_KDS	86	18	73	DESERT 2
pEA1229_931_933_LFN	100	22	49	DESERT 2
pEA1230_934_936_KWC	100	27	75	DESERT 2
pEA1231_937_939_WEN	86	19	64	DESERT 2
pEA1232_940_942_WLA	100	79	19	DESERT 2
pEA1233_943_945_ICR	86	16	96	DESERT 2
pEA1234_946_948_KLK	51	21	97	DESERT 2
pEA1235_949_951_LDP	86	14	71	DESERT 2
pEA1236_952_954_FLT	86	23	16	DESERT 2
pEA1237_955_957_PYT	100	40	4	DESERT 2
pEA1238_958_960_KIN	100	46	8	DESERT 2
pEA1239_961_963_SRW	100	30	10	DESERT 2
pEA1240_964_966_IKD	86	22	42	DESERT 2
pEA1241_967_969_LNV	100	16	8	DESERT 2
pEA1242_970_972_KPK	47	13	64	DESERT 2
pEA1243_973_975_TIK	74	16	14	DESERT 2
pEA1244_976_978_TLE	60	47	28	DESERT 2
pEA1245_979_981_ENL	62	22	63	DESERT 2
pEA1246_982_984_GIT	86	22	25	DESERT 2
pEA1247_985_987_IQD	51	34	51	DESERT 2
pEA1248_988_990_IGV	35	29	10	DESERT 2
pEA1249_991_993_GKD	34	14	97	DESERT 2
pEA1250_994_996_FMS	53	30	8	DESERT 2
pEA1251_997_999_KTP	31	27	93	DESERT 2
pEA1252_1000_1002_KAM	40	21	103	DESERT 2
pEA1253_1003_1005_ATK	28	15	109	DESERT 2
pEA1254_1006_1008_DKI	53	20	77	DESERT 2
pEA1255_1009_1011_DKW	86	23	11	DESERT 2
pEA1256_1012_1014_DLI	74	45	11	DESERT 2
pEA1257_1015_1017_KLK	53	48	11	DESERT 2
pEA1258_1018_1020_SFC	86	21	6	DESERT 2
pEA1259_1021_1023_TAK	86	17	93	DESERT 2
pEA1260_1024_1026_ETT	42	9	91	DESERT 2
pEA1261_1027_1029_IRV	42	8	110	DESERT 2
pEA1262_1030_1032_NRQ	86	14	72	DESERT 2
pEA1263_1033_1035_PTT	86	24	126	DESERT 2
pEA1264_1036_1038_WEK	100	42	29	DESERT 2
pEA1265_1039_1041_IFA	100	34	8	DESERT 2
pEA1266_1042_1044_TYS	26	10	106	DESERT 2
pEA1267_1045_1047_SDK	100	42	41	DESERT 2
pEA1268_1048_1050_GLI	100	44	15	DESERT 2
pEA1269_1051_1053_SRI	100	60	55	DESERT 2
pEA1270_1054_1056_YNE	100	96	66	DESERT 2
pEA1271_1057_1059_LKQ	86	44	82	DESERT 2
pEA1272_1060_1062_IYK	53	12	67	DESERT 2
pEA1273_1063_1065_KKT	53	12	108	DESERT 2
pEA1274_1066_1068_NNP	86	14	57	DESERT 2
pEA1275_1069_1071_IKK	74	29	43	DESERT 2
pEA1276_1072_1074_WAK	100	100	18	DESERT 2
pEA1277_1075_1077_DMN	74	35	5	DESERT 2
pEA1278_1078_1080_RHF	86	27	14	DESERT 2
pEA1279_1081_1083_SKE	74	35	94	DESERT 2
pEA1280_1084_1086_DIY	50	51	65	DESERT 2

Mutant ID	Conservation (residue with highest identity value as representative for 3xala mutant)		Avg retroT	Domain
	Mammals	Mammals + Verts		
pEA1281_1087_1089_AAK	86	21	64	DESERT 2
pEA1282_1090_1092_KHM	86	14	15	DESERT 2
pEA1283_1093_1095_KKC	100	24	65	DESERT 2
pEA1284_1096_1098_SSS	100	33	44	DESERT 2
pEA1285_1099_1101_LAI	100	20	50	DESERT 2
pEA1286_1102_1104_REM	100	41	24	DESERT 2
pEA1287_1105_1107_QIK	100	89	28	DESERT 2
pEA1288_1108_1110_TTM	100	24	44	DESERT 2
pEA1289_1111_1113_RYH	100	70	5	DESERT 2
pEA1290_1114_1116_LTP	100	69	21	DESERT 2
pEA1291_1117_1119_VRM	100	55	70	DESERT 2
pEA1292_1120_1122_AII	86	33	117	DESERT 2
pEA1293_1123_1125_KKS	62	27	93	DESERT 2
pEA1294_1126_1128_GNN	51	17	97	DESERT 2
pEA1295_1129_1131_RCW	100	100	8	DESERT 2
pEA1296_1132_1134_RGC	100	100	6	DESERT 2
pEA1297_1135_1137_GEI	86	19	127	DESERT 2
pEA1298_1138_1140_GTL	100	49	82	DESERT 2
pEA1299_1141_1143_LHC	100	100	5	DESERT 2
pEA1300_1144_1146_WWD	100	89	19	DESERT 2
pEA1301_1147_1149_CKL	100	100	11	DESERT 2
pEA1302_1150_1152_VQP	100	26	46	DESERT 2
pEA1303_1153_1155_LWK	100	100	11	DESERT 2
pEA1304_1156_1158_SVW	100	44	24	DESERT 2
pEA1305_1159_1161_RFL	86	29	87	DESERT 2
pEA1306_1162_1164_RDL	62	45	100	DESERT 2
pEA1307_1165_1167_ELE	60	16	79	DESERT 2
pEA1308_1168_1170_IPF	100	27	50	DESERT 2
pEA1309_1171_1173_DPA	100	67	70	DESERT 2
pEA1310_1174_1176_IPL	100	61	21	DESERT 2
pEA1311_1177_1179_LGI	100	71	4	DESERT 2
pEA1312_1180_1182_YPN	86	17	87	DESERT 2
pEA1313_1183_1185_EYK	34	10	109	DESERT 2
pEA1314_1186_1188_SCC	15	11	97	DESERT 2
pEA1315_1189_1191_YKD	51	13	94	DESERT 2
pEA1316_1192_1194_TCT	100	18	64	DESERT 2
pEA1317_1195_1197_RMF	100	18	19	DESERT 2
pEA1318_1198_1200_IAA	100	86	102	DESERT 2
pEA1319_1201_1203_LFT	62	26	82	DESERT 2
pEA1320_1204_1206_IAK	100	52	68	DESERT 2
pEA1321_1207_1209_TWN	100	100	13	DESERT 2
pEA1322_1210_1212_QPK	86	20	86	DESERT 2
pEA1323_1213_1215_CPT	100	73	63	DESERT 2
pEA1324_1216_1218_MID	51	16	91	DESERT 2
pEA1325_1219_1221_WIK	100	89	25	DESERT 2
pEA1326_1222_1224_KMW	100	21	8	DESERT 2
pEA1327_1225_1227_HIY	62	22	24	DESERT 2
pEA1328_1228_1230_TME	100	51	5	DESERT 2
pEA1329_1231_1233_YYA	100	23	23	DESERT 2
pEA1330_1234_1236_AIK	73	22	51	DESERT 2
pEA1331_1237_1239_NDE	46	17	61	DESERT 2
pEA1332_1240_1242_FIS	19	15	60	DESERT 2
pEA1333_1243_1245_FVG	43	37	28	DESERT 2
pEA1334_1246_1248_TWM	100	100	16	DESERT 2
pEA1335_1249_1251_KLE	100	22	21	DESERT 2
pEA1336_1252_1254_TII	62	19	9	DESERT 2
pEA1337_1255_1257_LSK	100	14	56	DESERT 2
pEA1338_1258_1260_LSQ	73	12	82	DESERT 2
pEA1339_1261_1263_EQK	64	15	104	DESERT 2
pEA1340_1264_1266_TKH	42	20	102	DESERT 2
pEA1341_1267_1269_RIF	46	20	49	DESERT 2
pEA1342_1270_1272_SLI	51	35	81	DESERT 2
pEA1343_1273_1275_GGN	51	40	58	DESERT 2