

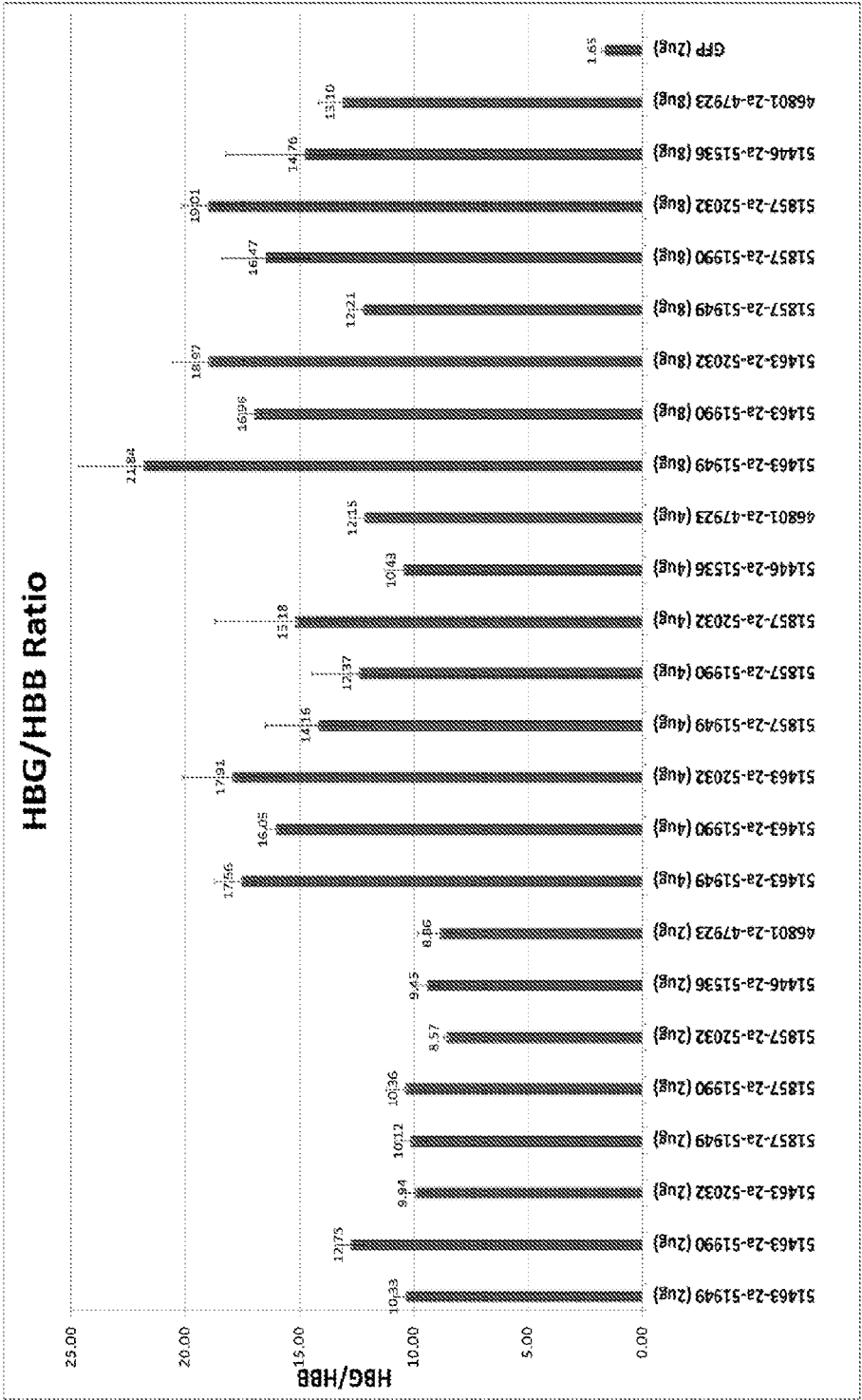
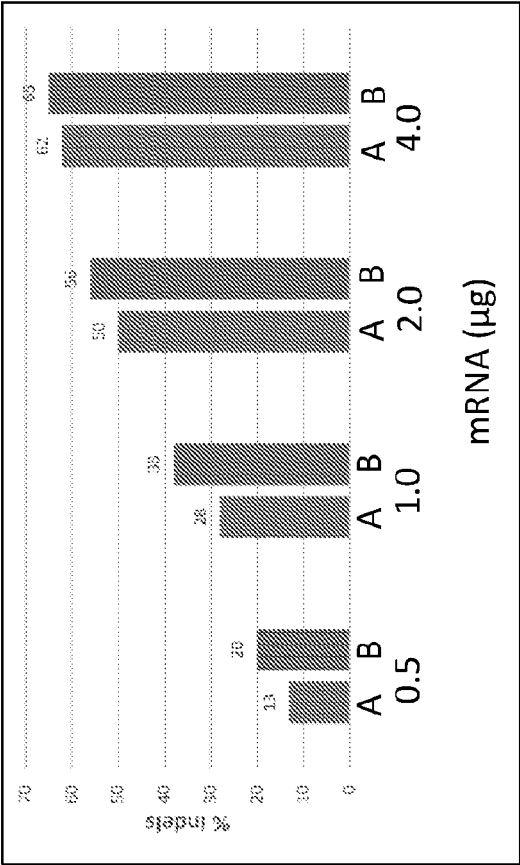


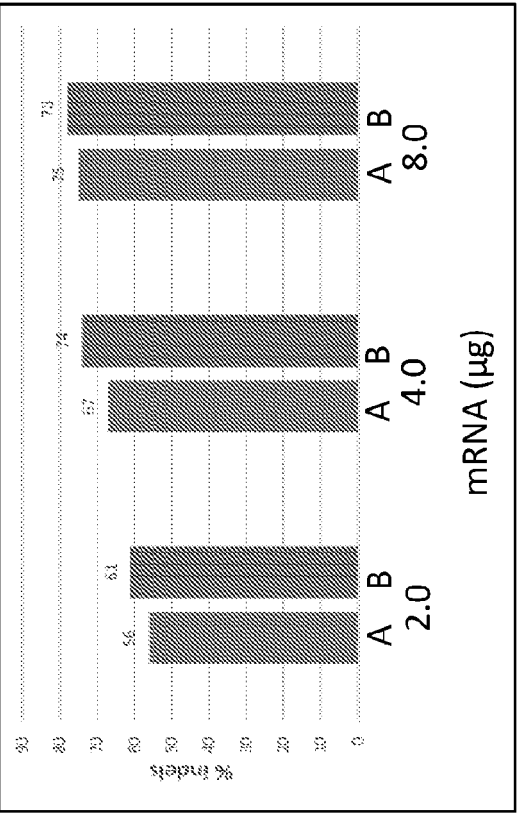
Figure 1

Figure 2A



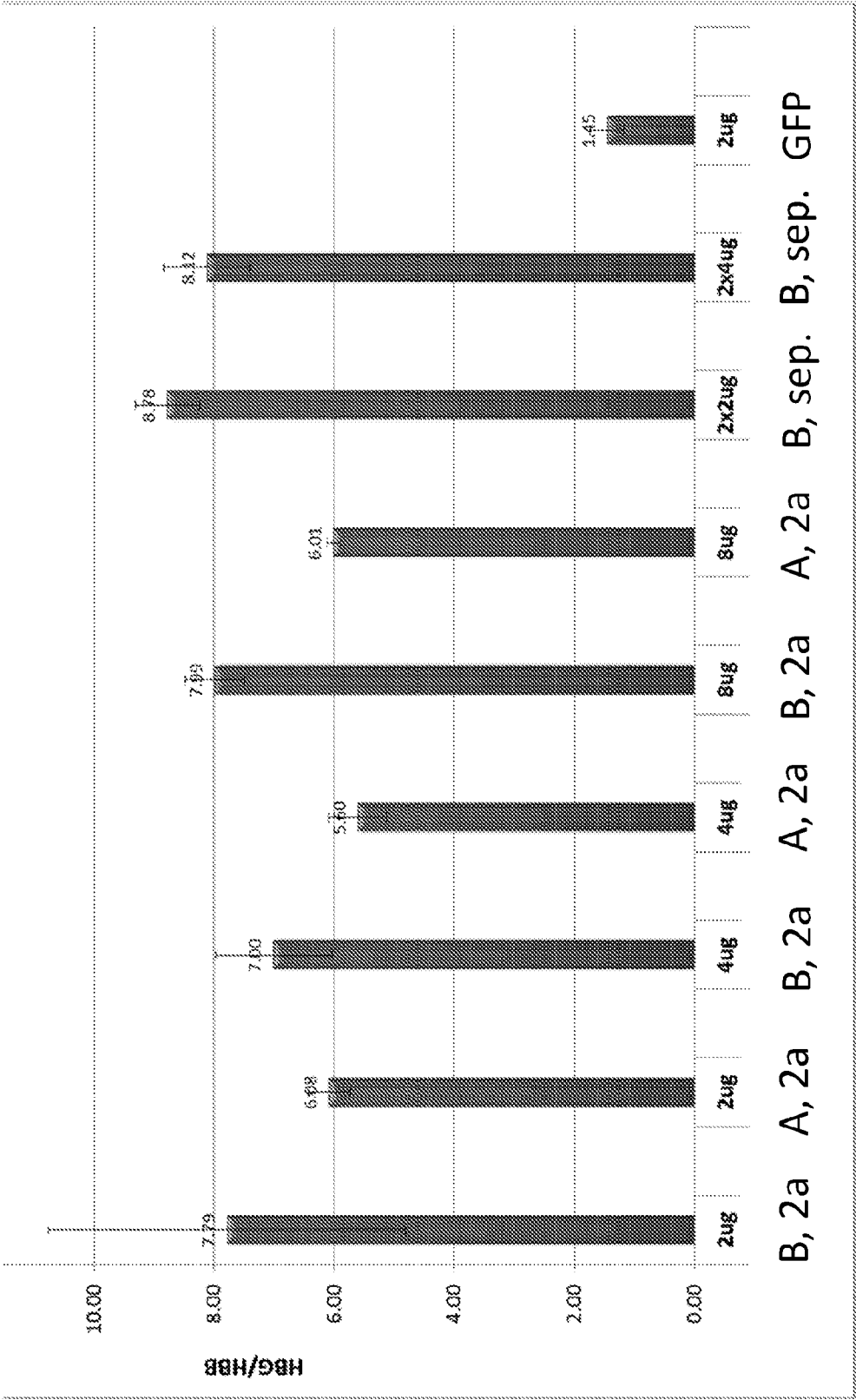
% Indels				
mRNA used/reaction	0.5	1.0	2.0	4.0
A: 51446_2a_51536	12.8	28.2	50.1	62.2
B: 51857_2a_51949	20.5	38.4	56.0	64.7

Figure 2B



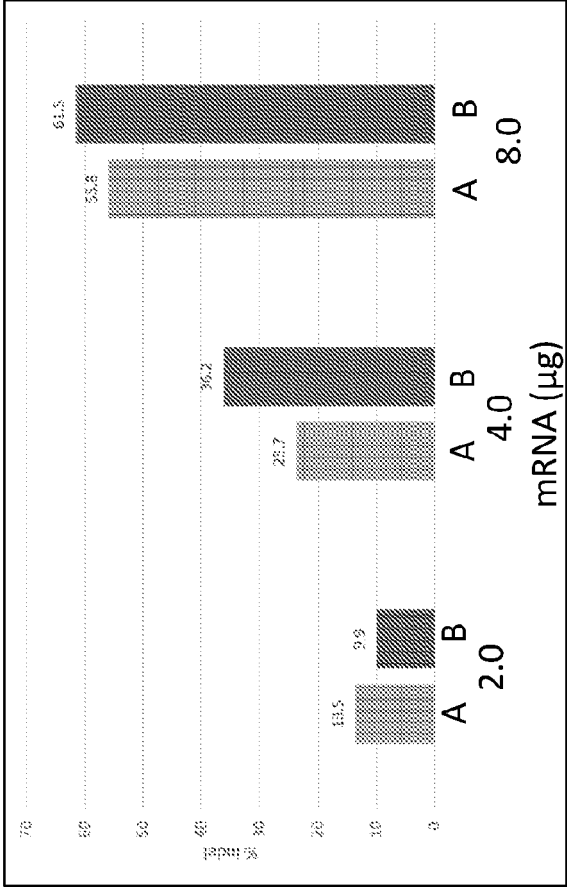
% Indels				
mRNA used/reaction	2.0	4.0	8.0	
A: 51446_2a_51536	56.4	66.7	74.9	
B: 51857_2a_51949	61.2	73.9	78.3	

Figure 3



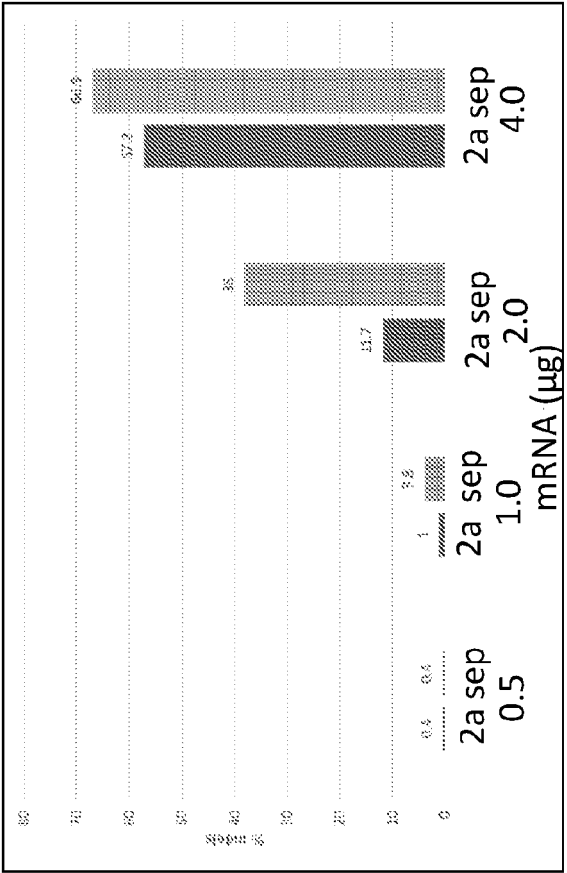
B, 2a A, 2a B, 2a A, 2a B, 2a A, 2a B, sep. B, sep. B, sep. GFP

Figure 4A



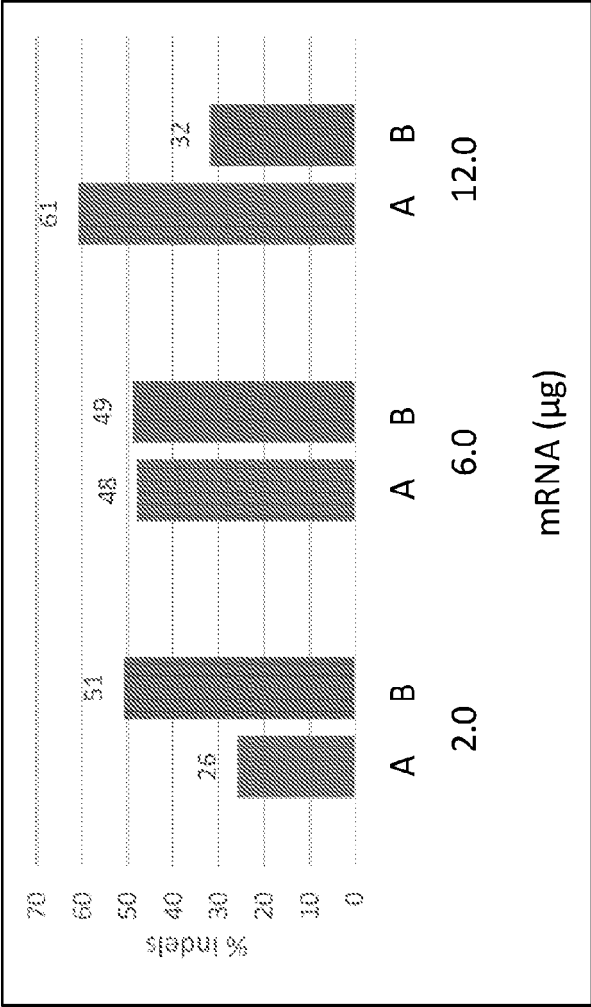
% Indels			
mRNA used/reaction	2.0	4.0	8.0
A: 51446_2a_51536	13.5	23.7	55.8
B: 51857_2a_51949	9.9	36.3	61.5

Figure 4B



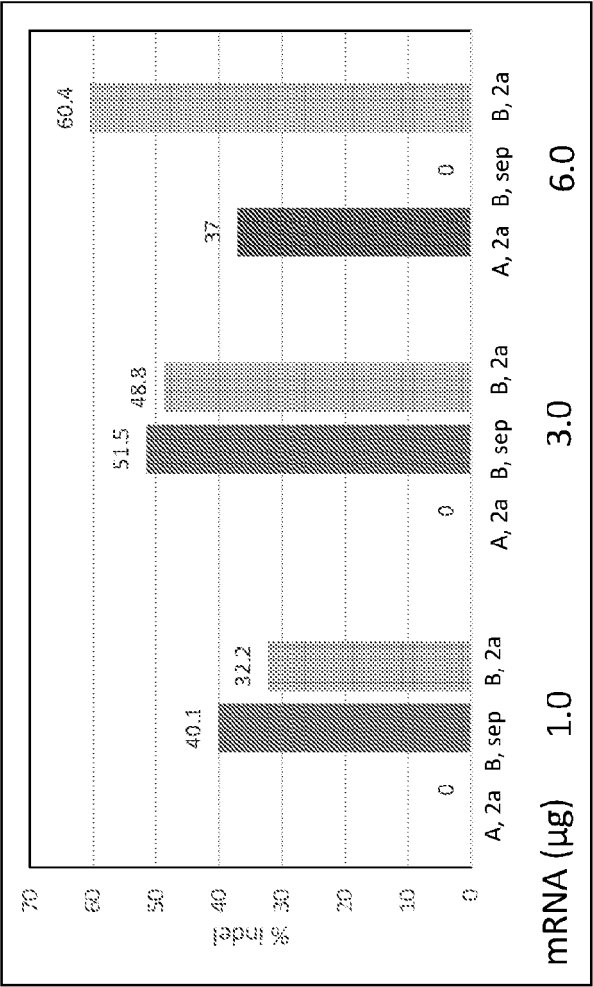
% Indels				
mRNA used/reaction	0.5	2.0	4.0	8.0
B: 51857_2a_51949	0.4	1.0	11.7	57.2
B: 51857: 51949 sep	0.4	3.8	38.0	66.9

Figure 5A



% Indels			
mRNA used/reaction	2.0	6.0	12.0
A: 51446_2a_51536	25.9	48.1	60.7
B: 51857_2a_51949	50.8	49.4	32.6

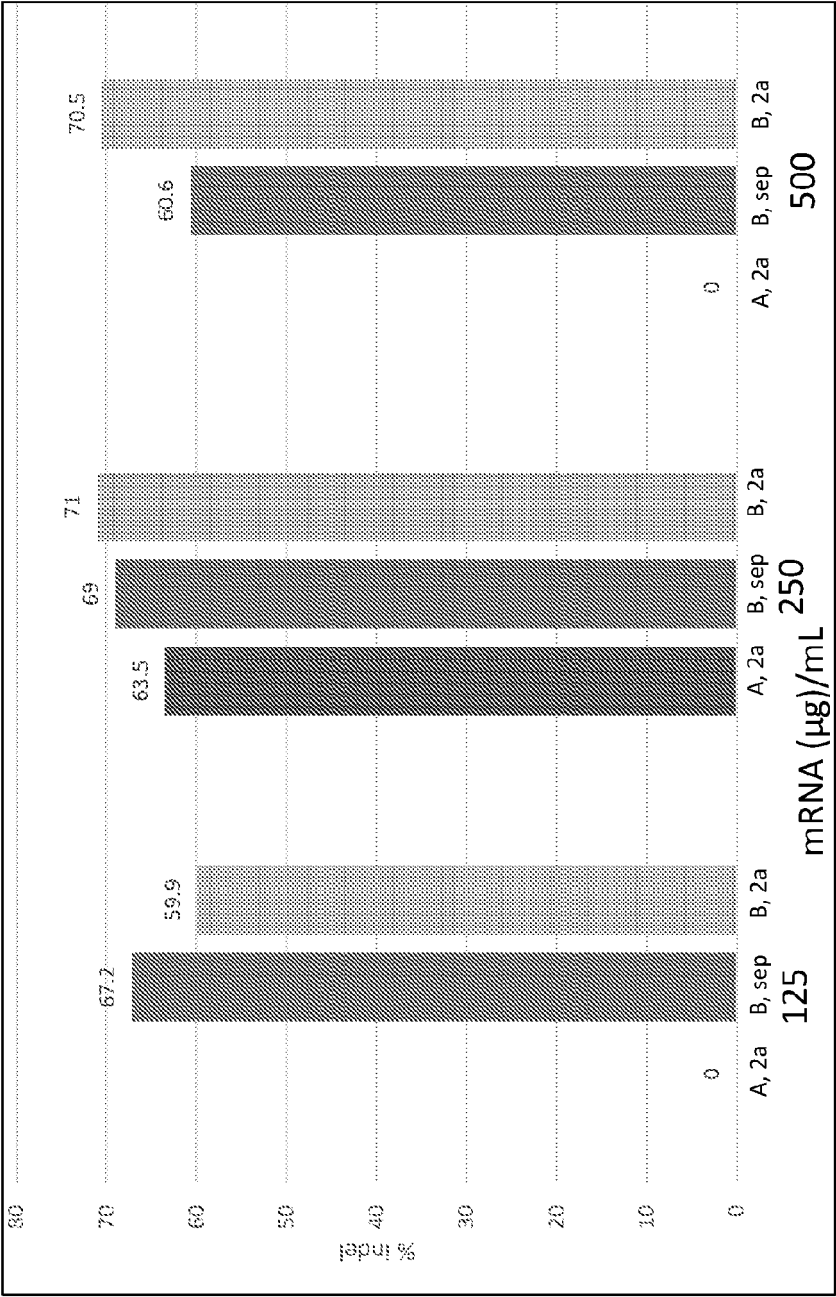
Figure 5B



% Indels			
mRNA used/reaction	1.0	3.0	6.0
A: 51446_2a_51536	nt	nt	37
B: 51857 + 51949, sep	40.1	51.5	nt
B: 51857_2a_51949	32.2	48.8	60.4

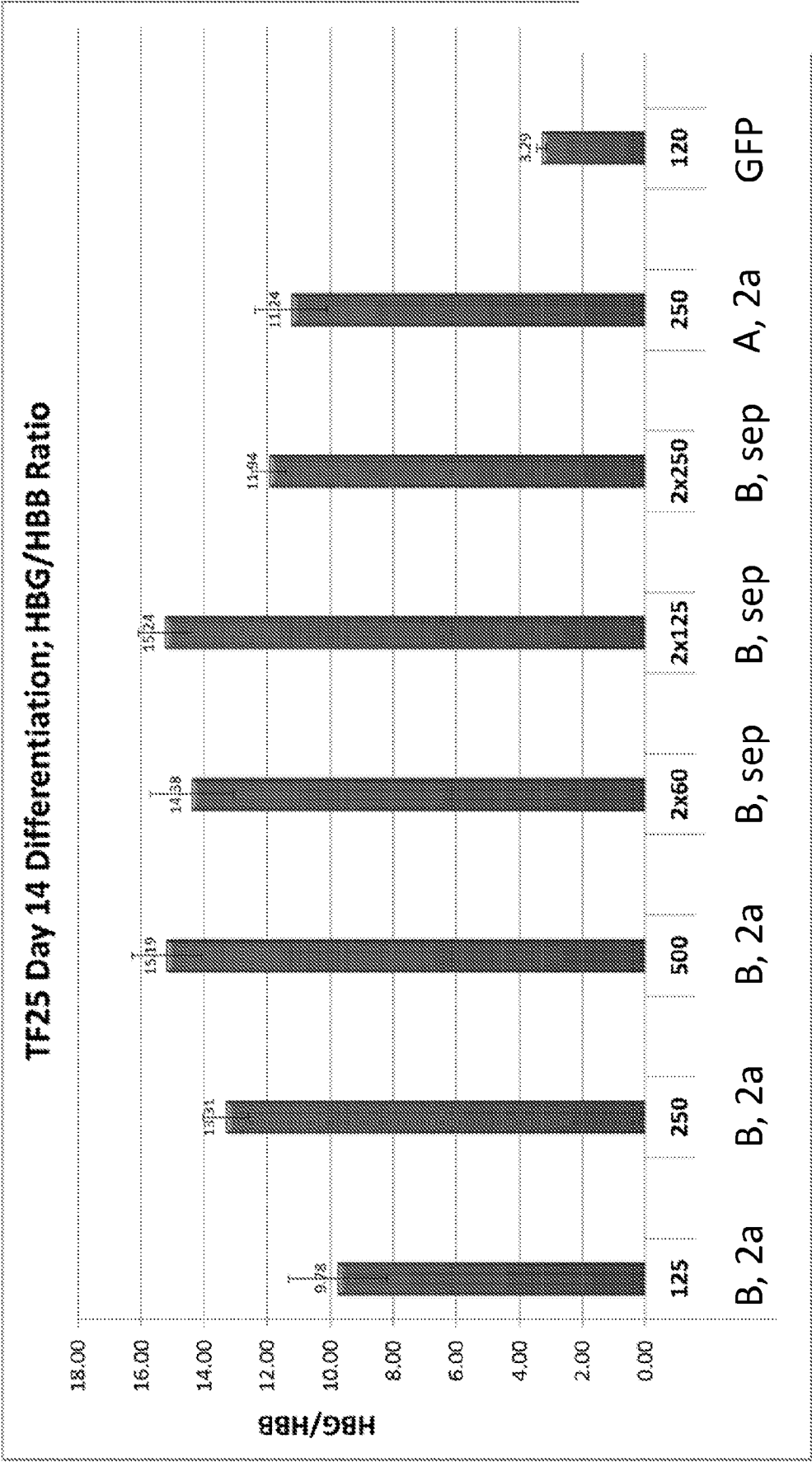
Nt- not tested

Figure 6



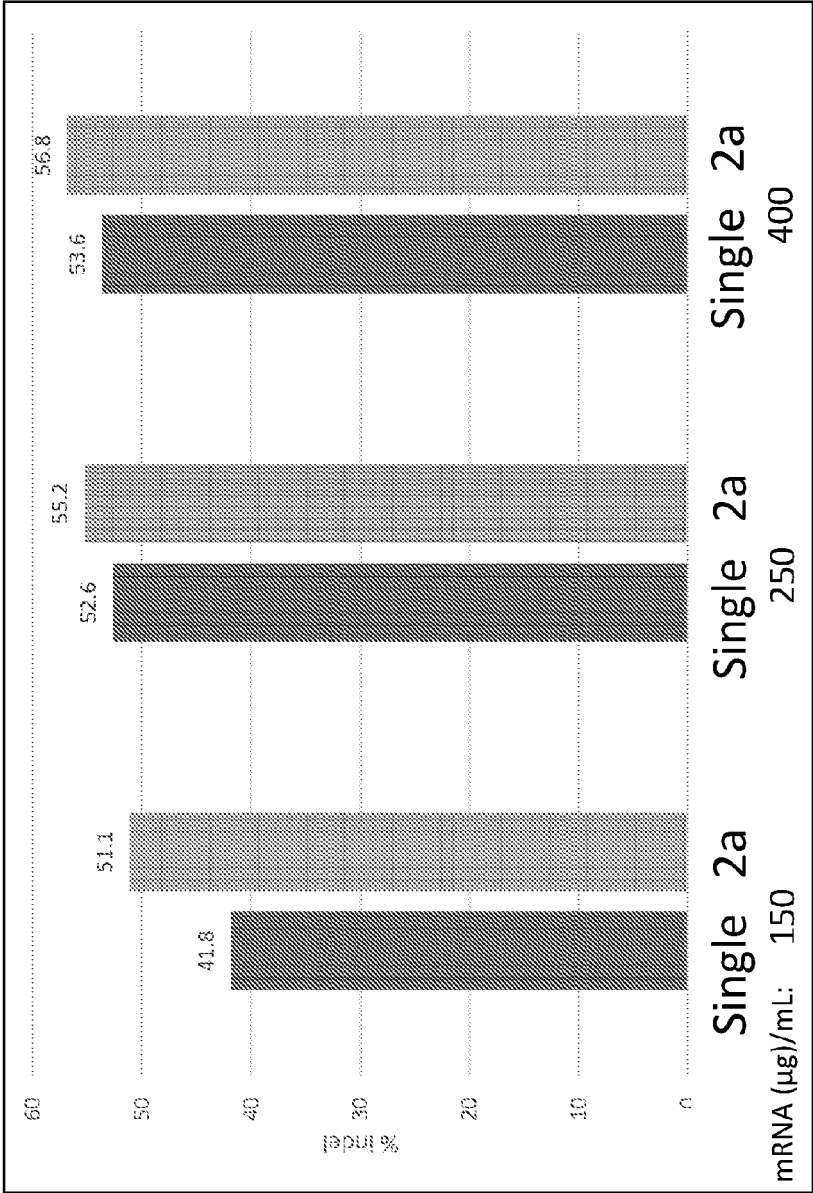
% Indels			
mRNA used/mL	125	250	500
A: 51446_2a_51536	nt	63.5	nt
B: 51857 + 51949, sep	67.2	69.0	60.6
B: 51857_2a_51949	59.9	71	70.5

Figure 7

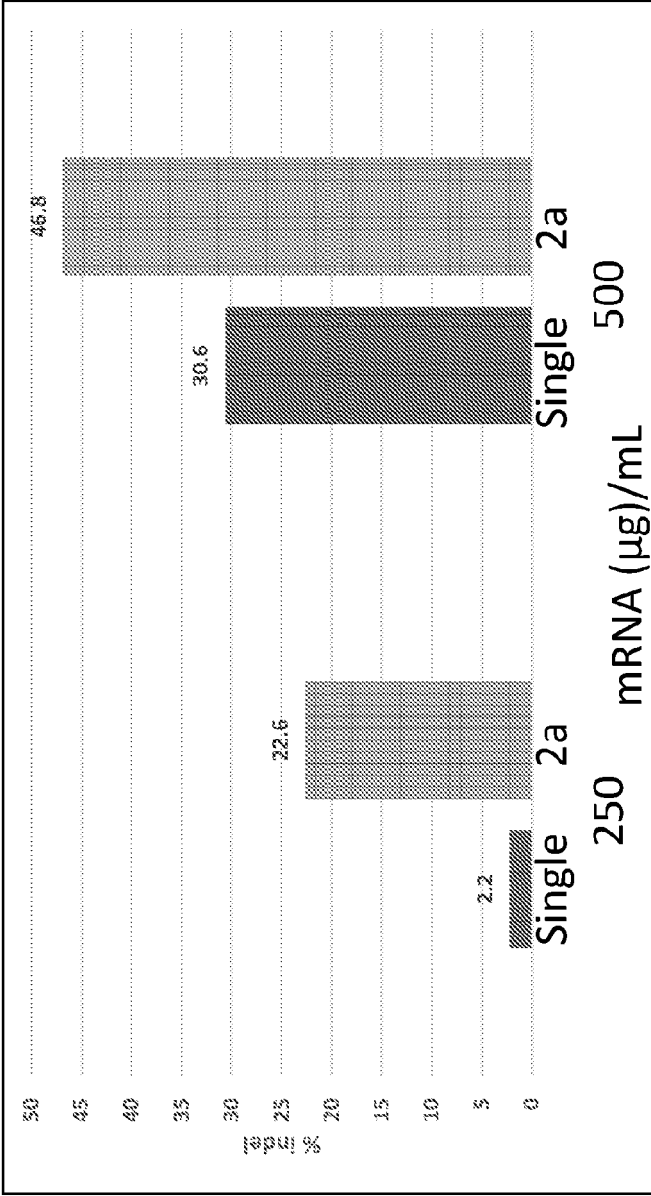


d0	59.92	71.00	70.49	67.15	69.04	60.62	63.50	0.58
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Figure 8

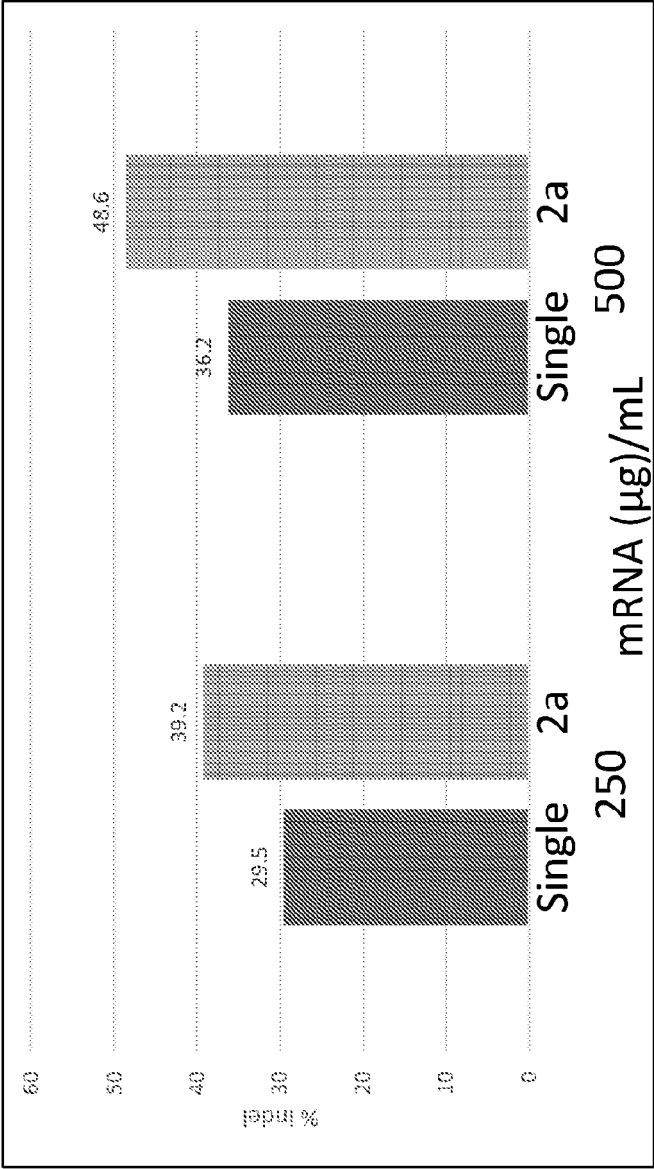


% Indels			
mRNA used/mL	150	250	400
B: 51857 + 51949, sep	41.8	52.6	53.6
B: 51857_2a_51949	51.0	55.2	56.8



% Indels		
mRNA used/mL	250	500
B: 51857 + 51949, sep	2.2	30.6
B: 51857_2a_51949	22.6	46.8

Figure 9A



% Indels		
mRNA used/mL	250	500
B: 51857 + 51949, sep	29.5	36.2
B: 51857_2a_51949	39.2	48.5

Figure 9B

Figure 10A

amplicon_location	treated_indel_freq	bonferroni_pva	lue	genic	coding	gene	location
chr2:60722338-60722476	63.261%	0.00000					
chr6:53670690-53670868	2.312%	0.00000	y	n		LRRC1	intron
chr17:35295932-35296095	1.184%	0.00000	y	n		LHX1	intron
chr8:140226152-140226311	0.711%	0.00000	n	n		n/a	intergenic
chr11:102556535-102556674	0.344%	0.00000	n	n		MMP27	upstream
chr13:76123418-76123581	0.674%	0.00000	y	n		COMMD6	exon 1
chr8:120868614-120868752	0.303%	0.00000	n	n		DSCC1	upstream
chr1:54972397-54972573	0.569%	0.00000	n	n		ACOT11	upstream
chr10:134468242-134468405	0.425%	0.00000	y	n		INPP5A	intron
chr3:178716601-178716740	0.117%	0.00029	n	n		ZMAT3	downstream
chr16:85350785-85350924	0.156%	0.00045	n	n		MIR5093	intergenic
chr17:35861457-35861634	0.221%	0.02113	y	n		DUSP14	intron
chr7:29662136-29662313	0.179%	0.08897	n	n		PRR15	intergenic
chr19:46189232-46189371	0.171%	0.09034	n	n		GIPR	intergenic
chr10:71330866-71331005	0.095%	0.24740	n	n		NEUROG3	downstream
chr2:62391864-62392042	0.147%	0.54640	n	n		COMMD1	intergenic
chr5:137673092-137673271	0.315%	1.00000	y	n		CDC25C	intron
chr2:23925597-23925776	0.132%	1.00000	y	n		KLHL29	intron
chr18:5447651-5447812	0.128%	1.00000	y	n		EPB41L3	intron
chr2:173883408-173883572	0.106%	1.00000	y	y		RAPGEF4	exon
chr19:3625953-3626129	0.094%	1.00000	y	n		CACTIN	intron
chr12:104442523-104442688	0.085%	1.00000	y	n		GLT8D2	intron

Figure 10B

amplicon_location	treated_indel_freq	bonferroni_p_value	genic_coding	gene	location
chr2:60722337-60722476	74.09%	0.00000			
chr8:120868614-120868752	10.36%	0.00000	n	DSCC1	upstream
chr2:62391864-62392042	1.13%	0.00000	n	COMMD1	intergenic
chr6:53670690-53670868	0.65%	0.00000	y	LRRC1	intron
chr2:23925597-23925775	0.58%	0.00000	y	KLHL29	intron
chr10:134468242-134468405	0.52%	0.00000	y	INPP5A	intron
chr1:54972398-54972568	0.51%	0.00000	n	ACOT11	upstream
chr10:71330866-71331005	0.49%	0.00000	n	NEUROG3	downstream
chr20:36335775-36335954	0.38%	0.11110	y	CTNBNB1	intron
chrX:134048679-134048858	0.35%	0.00000	y	MOSPD1	intron
chr14:67888671-67888848	0.30%	0.00000	n		intergenic
chr13:76123402-76123581	0.29%	0.00000	y	COMMD6	exon 1
chr11:102556535-102556674	0.27%	0.00000	n	MMP27	upstream
MULTIPLE_TIED_LOCI	0.26%	0.00000			
MULTIPLE_TIED_LOCI	0.22%	0.00000			
chr11:33915930-33916106	0.22%	0.00000	n	LMO2	upstream
chrX:30298492-30298671	0.20%	0.00372	n	MAGEB1	intergenic
chr17:27181433-27181606	0.18%	0.00206	n	ERAL1	upstream
chr1:29508603-29508766	0.16%	1.00000	n	SRSF4	upstream
chr12:10444253-104442688	0.11%	0.00077	y	GLT8D2	intron
chr19:45909865-45910028	0.11%	1.00000	y	CD3EAP	exon 1

Figure 11A

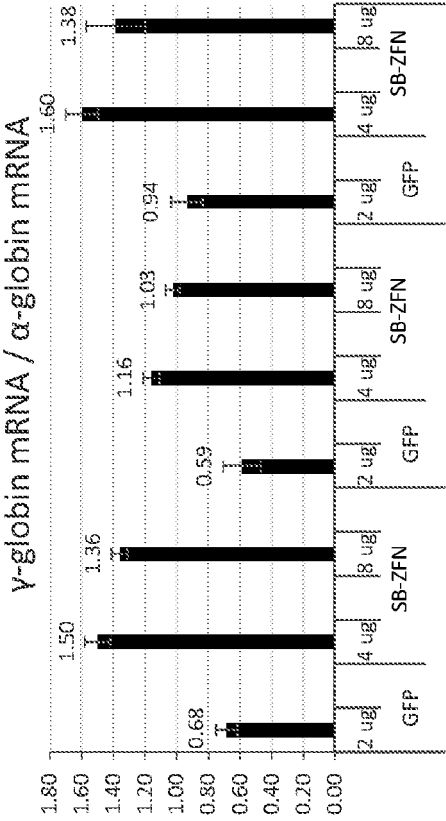
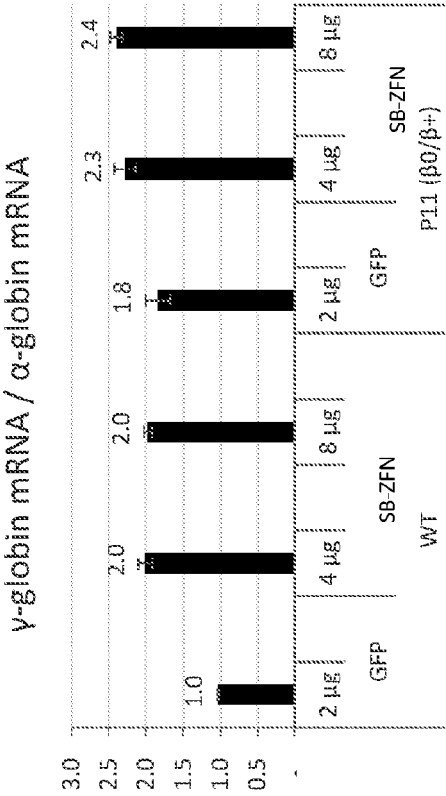


Figure 11B

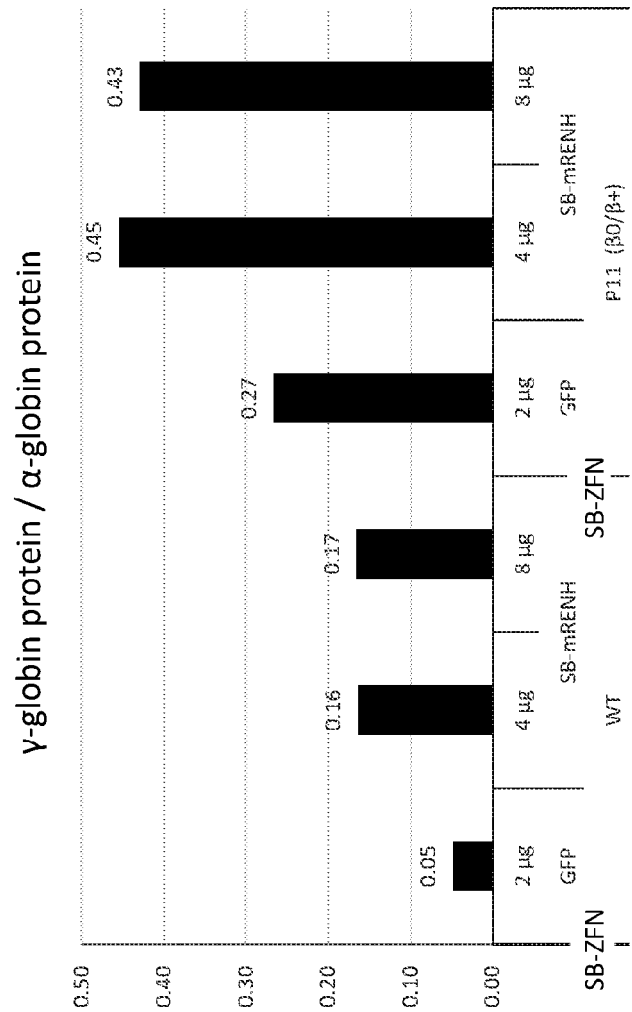


Figure 12A

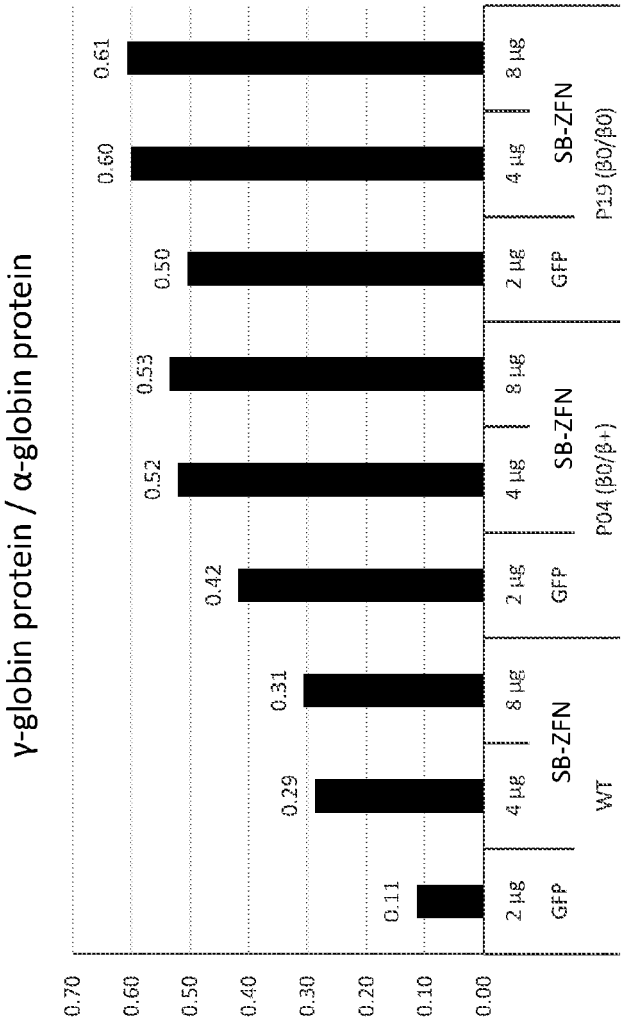


Figure 12B

Figure 13

