

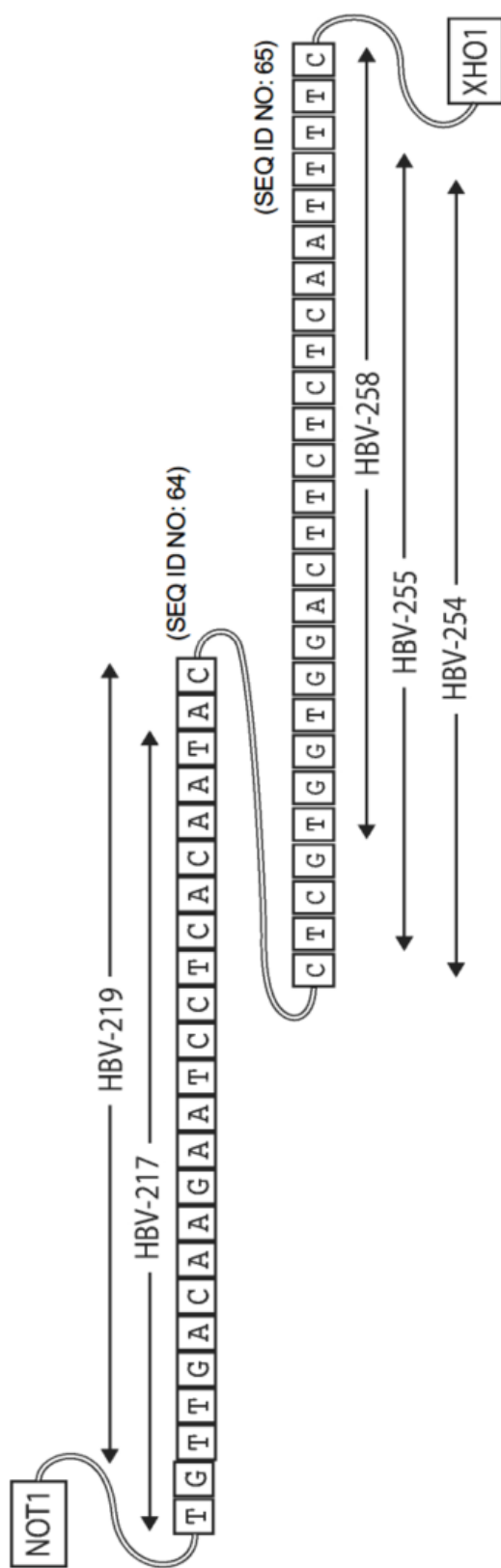


FIG. 6

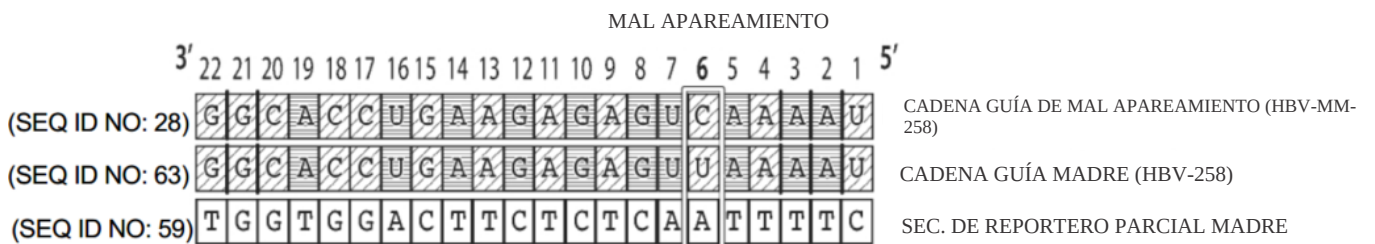
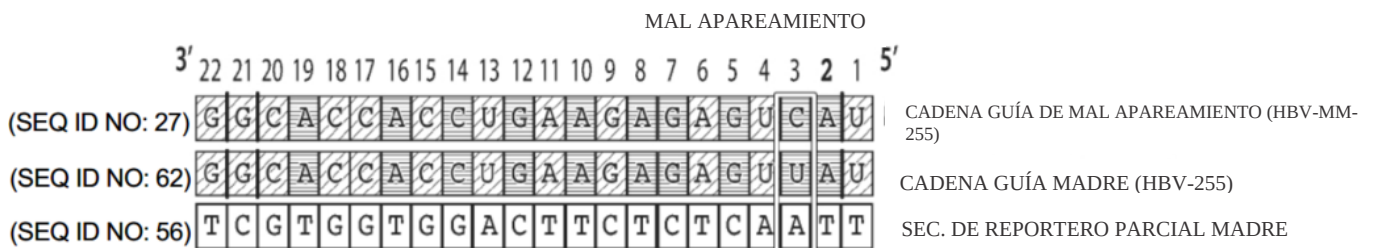
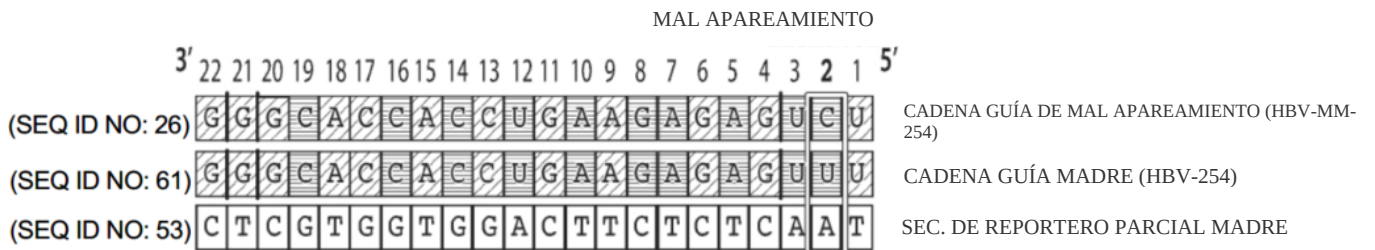
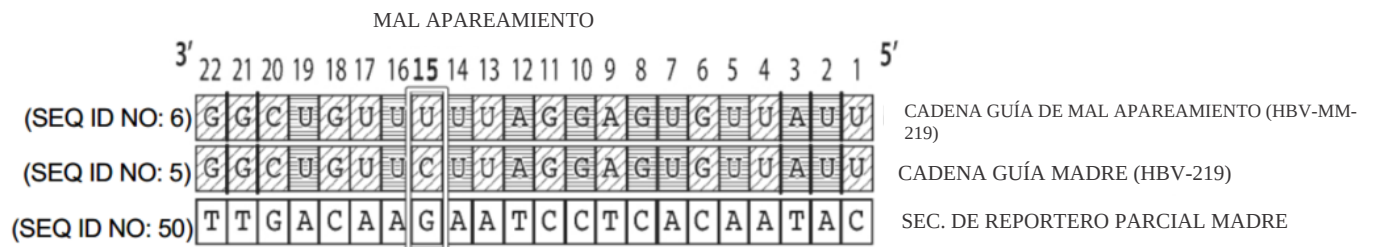
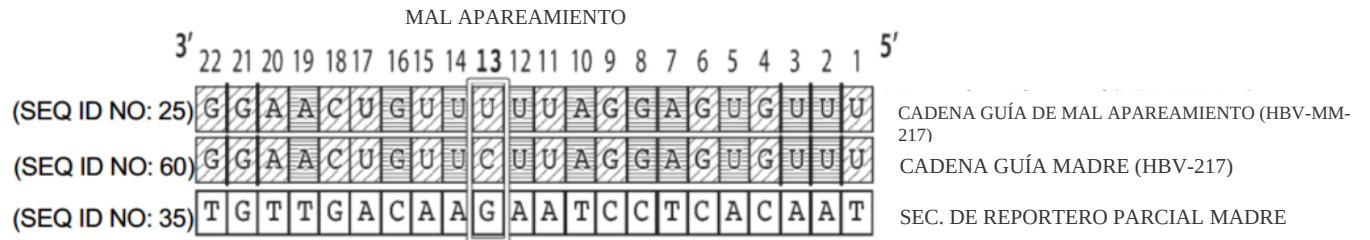


FIG. 7

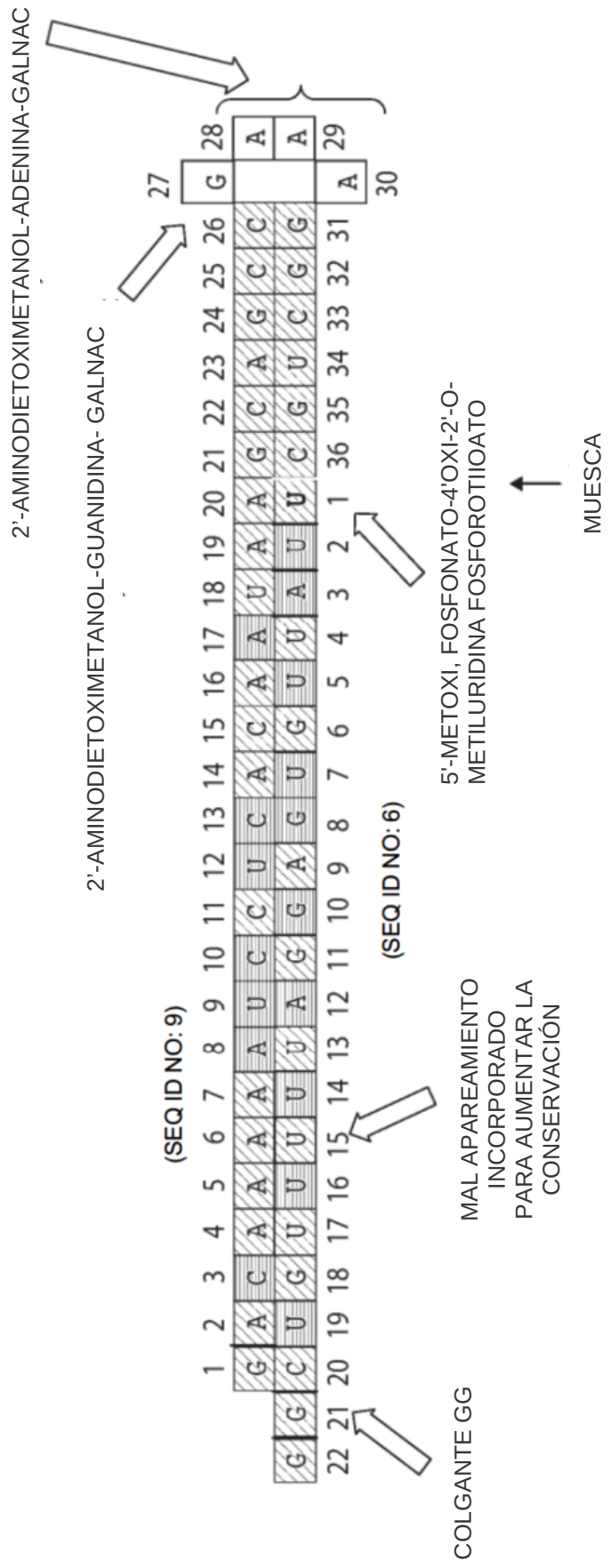


FIG. 10

	HBV-219	HBV-254	HBV-258
ORF Objetivo	S	S	S
Sentido 19-mer	GACAAGAATCCTCACAATA A (SEQ ID: NO:29)	CGTGGTGGACTTCTCTCAA A (SEQ ID: NO:30)	GTGGACTTCTCTCAATTTT A (SEQ ID: NO:31)
Sentido 19-mer c/Base ambigua	GACAANAATCCTCACAAT A (SEQ ID: NO:32)	CGTGGTGGACTTCTCTCAN A (SEQ ID: NO:33)	GTGGACTTCTCTCANTTTT A (SEQ ID: NO:34)
Posición de la Guía de Mal apareamiento	15	2	6
de Conservación genotipo*	Genotipo A	97/99 [3278]	94/97 [4002]
	Genotipo B	03/95 [2563]	81/97 [2700]
	Genotipo C	92/97 [4783]	95/97 [4938]
	Genotipo D	95/97 [4311]	96/99 [4395]
	Genotipo E	01/98 [1039]	93/95 [1234]
	Genotipo F	01/90 [425]	94/96 [501]
	Genotipo G	92/99 [83]	98/98 [85]
	Genotipo H	03/92 [71]	86/97 [78]
	Genotipo I	00/100 [18]	95/100 [22]
TOTAL (Análisis enfocado)	72/97 [17021]	93/97 [17995]	93/98 [17959]
TOTAL (Análisis inicial)	66/96 [5628]	94/98 [5628]	94/98 [5628]

*Por ciento de conservación reportado como (*perfectolMM*), con valores <90% mostrados en letras negritas; [Total N#]

FIG. 20