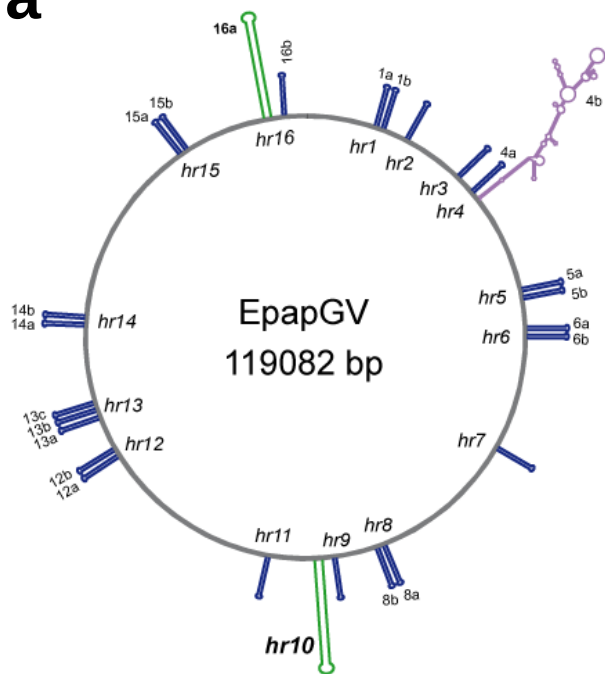
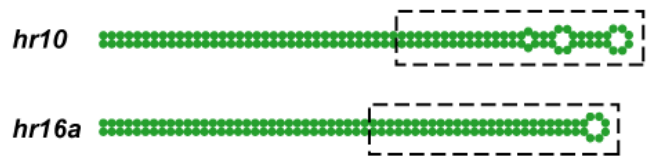


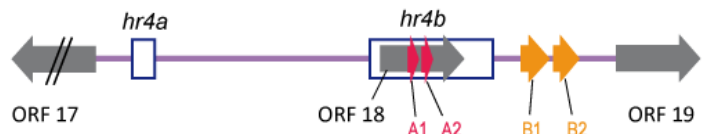
a



b



c



Direct repeats:

A1: TACGTGACAATAACAAAGTAATTAACCTTGA (31 bp)

A2: TACGTGACAATAACAAAGTAATTAACCTTGA (31 bp)

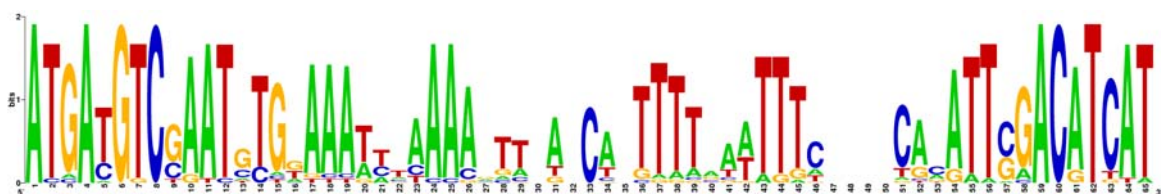
B1: CTTGTGTGACTGTTACAACCTGGTTCGATTCCACCAATCTTATGTAATTGGTATAACACGTGGTTCGATTCCACCGA (79 bp)

B2: CTTGTGTGACTGTTACAACCTGGTTCGA-----AATCTTATGTAATTGGTATAACACGTGGTTCGATTCCACCGA (72 bp)

d

		1	10	20	30	40	50	65	
hr10	58387	ATGATGTCGAATGTG	AAAAAT-CTAAAACCCA	--ACTTTT	TATTTTG---	CACATT	CGACATCAT	58444	
hr15a	107672	ATGATGTCGAATGTG	AAAAA-TCAAAACCCA	--ACTTTT	CAATTTT---	CACATT	CGACATCAT	107729	
hr12a	78898	ATGATGTCTAA-CTCGAAAT	-TCAAAAGTTAA--	ACTTTT	AAATTTTA---	CACATT	CGACGTCAT	78954	
hr1b	6508	ATGATGTCCAATCTG	CAAATCTAAAAAGTTA	--ACTTTT	CAATTTTC---	CACATT	CGACATCAT	6566	
hr6a	29006	ATGATGTCCAATACG	GAAATCGCAAAAATCA	--AATGTT	TGATTGC---	CACATT	CGACATCAA	29064	
hr14a	90521	ATGATGTCGAATGTG	GAAATTAAAAAGTAG	--AGTTT	-GATTTTC---	CACATT	CGACATCAT	90577	
hr7	29354	ATGATGTCGAATGTG	GAAATTTAAAAGTTG	--AGTTT	TGATTTTC---	CACATT	CGACATCAT	29411	
hr2	8837	ATGATGTCGAATGTG	TAAATCTAAAAGTTG	--AGTTT	TGAATTTA---	CACATT	CGACATCAT	8894	
hr16a	116146	ATGATGTCGAATGCG	GAAATTTAAAAGTTG	--GATTTT	TAAATTTT---	CGCATT	CGACATCAT	116203	
hr3	12548	ACAACGCGCGTTGTT	TAAAACAACA	CTGTGGCTACTT	AAAAATGTT---	TCGAAACA	AACATGTT	12608	
hr4a	14626	ATGACGTCGAACTCA	TTCCGC-AAAAAAATA	--AAGTTT	TATATTTT---	CACATT	CGACATCAT	14683	
hr15b	107842	ATGATGTCGAATTTG	GAAAT--AAAACTTTT	-AATTTT	TACAATTT---	CAAATT	TGGACATCAT	107898	
hr12b	79119	ATGACGTCTAATGTG	TAAATATAAACTTTGA	--TTTT	TGGCCATTTT---	CGTATT	CGACATCAT	79177	
hr5a	25628	ATGATGTCCAATGTG	GAAATATAAACTTT	-A--TTTTTT	TGATTTT---	CACATT	TGAACGTCAT	25685	
hr5b	25872	ATGATGTCCAATCTG	GAAATATAAACTTT	-A--CTTTTT	TCAATTTT---	CATGTT	CGACATCAT	25929	
hr8a	52795	ATGATGTCCAATCTG	GAAAT-TCAAACTATA	--ACTTTT	TAAAATTC---	CACATT	CGACATCAT	52852	
hr14b	90689	ATGATGTCGAATGTG	AAAATTATAAAAGTAA	--A-GTTT	TATATTTT---	CAGATT	TGGACATCAT	90746	
hr16b	116463	ATGATGTCCAATCTG	GAA-TTATAAAATCAA	--AAGTTT	TATATTTT---	CAGATT	TGGACATTAT	116520	
hr13a	82900	ATGACGTCCAATGTG	GAAATATCAAACTTG	--ACTTTT	TAAATTTT---	CAGATT	TACACATCAT	82957	
hr1a	6310	ATGACGTGCAATACGT	-----AAAAGTTT	-TATTTT	TAAATTTT---	CAAATT	TGAACAT---	6358	
hr13b	83069	ATGACGTGCAATGTG	TAAATCAAAAAGTTT	--ATTTT	TCTGTGAT---	CACATT	TGGACGTCAT	83126	
hr13c	83350	ATGATGTCGAATGTG	TAAATTTAAAAGTA	---ACTTTT	AAATTTTC---	CGAGTT	TGGACATCAT	83406	
hr6b	29354	ATGATGTCGAATGTG	TAAATTATAAAAGTATG	--ATTTT	TGATTTTC---	GTA-TT	TGGACATCAT	29411	
hr8b	53015	ATGATGTCGAATGTG	AAAACGAAAAGTTGA	--TTTT	TACGATTTTA---	TGAGAT	CGACATCAT	53073	
hr9	57008	ATGATGTCGAATGTG	TAAATGAAAAGTTAA	--CTTTT	TAGATTTGC---	AGA-TT	TGGACATCAT	57065	
hr11	61297	ATCAAGT-GGATCTG	AGTAGACAA	CGGTTCTACA	ATAAAGA	AATTGAATCGT	AAATTGGACAT	61360	
Consensus		ATGATGTCGAATGTG	AAAT AAAA TT A	A TTTT AATTTT		CACATT	CGACATCAT		

e



f

Consensus EpapGV **ATGATGTCGAATGTG--N (19-34) ---CACATTTCGACATCAT**

Consensus other GVs **ATGAGTCGAGT-T---N (39-296) ---A-ACTCGGACTCAT**

Consensus **ATGA CGA T T A A TCG TCAT**