

Supplementary Table S1: Anoted SNPs from BRA1. Genome position number is given as BRA1 consensus reference.

Genome position	Change	Coverage	Variant Frequency	Variant P-Value	Amino Acid Change	Codon Change	Protein Effect	CDS
327	T -> A	201	25.90%	1.00E-123				LTR
502	A -> G	162	28.40%	8.40E-112	K -> R	AAG -> AGG	Substitution	Gag
1,067	G -> A	123	29.30%	3.80E-90		AAG -> AAA	None	Gag
1,799	G -> A	241	37.30%	2.50E-239		GAG -> GAA	None	Gag
1,830	A -> G	263	34.20%	1.10E-216	N -> D	AAC -> GAC	Substitution	Gag
2,024	T -> C	471	37.80%	0.00E+00		TTA -> CTA	None	Pol
2,046	A -> G	387	45.00%	0.00E+00	K -> R	AAG -> AGG	Substitution	Pol
2,155	G -> T	347	39.80%	0.00E+00	L -> F	TTG -> TTT	Substitution	Pol
2,157	A -> G	329	48.60%	0.00E+00	K -> R	AAG -> AGG	Substitution	Pol
2,308	T -> C	125	27.20%	3.40E-86		ATT -> ATC	None	Pol
2,364	G -> A	191	34.60%	6.80E-173	R -> K	AGA -> AAA	Substitution	Pol
2,462	A -> T	649	36.70%	0.00E+00	I -> L	ATA -> TTA	Substitution	Pol
2,478	C -> T	423	33.60%	0.00E+00	A -> V	GCT -> GTT	Substitution	Pol
2,539	A -> G	433	46.70%	0.00E+00		GGA -> GGG	None	Pol
2,952	A -> G	465	40.90%	0.00E+00	N -> S	AAT -> AGT	Substitution	Pol
3,144	A -> G	399	46.60%	0.00E+00	K -> R	AAA -> AGA	Substitution	Pol
3,184	G -> A	463	25.10%	1.90E-251		CAG -> CAA	None	Pol
3,482	A -> G	1,307	48.90%	0.00E+00	I -> V	ATA -> GTA	Substitution	Pol
3,699	G -> A	1,149	28.00%	0.00E+00	R -> K	AGG -> AAG	Substitution	Pol
3,727	C -> T	1,131	34.80%	0.00E+00		GAC -> GAT	None	Pol
3,985	C -> T	1,226	50.70%	0.00E+00		TAC -> TAT	None	Pol
4,099	A -> G	1,753	47.70%	0.00E+00		GGA -> GGG	None	Pol
4,249	G -> A	1,709	26.90%	0.00E+00		CAG -> CAA	None	Pol
4,273	T -> C	1,589	35.40%	0.00E+00		TCT -> TCC	None	Pol
4,381	A -> G	871	48.90%	0.00E+00		GCA -> GCG	None	Pol
4,693	A -> G	2,881	50.20%	0.00E+00		CAA -> CAG	None	Pol
5,881	G -> A	2,164	32.20%	0.00E+00	R -> K	AGA -> AAA	Substitution	Env
5,885	C -> G	2,104	32.70%	0.00E+00	N -> K	AAC -> AAG	Substitution	Env
5,912	A -> T	1,847	32.00%	0.00E+00	K -> N	AAA -> AAT	Substitution	Env
5,929	C -> A	2,105	97.10%	0.00E+00	T -> N	ACC -> AAC	Substitution	Env
5,941	A -> C	2,259	98.80%	0.00E+00	H -> P	CAT -> CCT	Substitution	Env
5,943	C -> T	2,283	99.20%	0.00E+00	H -> Y	CAT -> TAT	Substitution	Env
7,480	A -> G	16,497	54.30%	0.00E+00	N -> S	AAT -> AGT	Substitution	Env/Rev

Supplementary Figure S1: Alignment of env clone sequences of BRA1 and BRA2. The BRA1 sequence was used as reference to the alignment. Inclusions and deletions are marked in yellow. Hypervariable region V3 is highlighted in green and V4 in pink.

	1	10	20	30	40	50	60
BRA1	ATGGTCAGCATCGCGTTCTATGGGGGAATCCCAGGGGAATCTCGACCCCTATTATTCAA						
BRA1 Sequence 3	ATGGTCAGCATCGCGTTCTATGGGGGAATCCCAGGGGAATCTCGACCCCTATTATTCAA						
BRA2 sequence 4.1	-----						
BRA1 Sequence 1	-----						
BRA2 sequence 5.1	-----						
BRA1 Sequence 2	-----						
BRA2 sequence 2.1	-----						
BRA2 sequence 2.2	-----						
BRA2 sequence 4.2	-----						
BRA2 sequence 5.2	-----						
BRA2 sequence 3.2	-----						
BRA2 sequence 6.2	-----						
BRA1 Sequence 1	-----						
BRA2 sequence 1.1	-----						
BRA1 Sequence 4	-----						
BRA2 sequence 3.1	-----						
BRA1 Sequence 2	-----						
BRA1	TCTTCAGAAGAAGCTAGTCACACCAAGGGGATACAATATTTAAACCCCTATTGTTCTGAT						
BRA1 Sequence 3	TCTTCAGAAGAAGCTAGTCACACCAAGGGGATACAATATTTAAACCCCTATTGTTCTGAT						
BRA2 sequence 4.1	-----						
BRA1 Sequence 1	-----						
BRA2 sequence 5.1	-----						
BRA1 Sequence 2	-----						
BRA2 sequence 2.1	-----						
BRA2 sequence 2.2	-----						
BRA2 sequence 4.2	-----						
BRA2 sequence 5.2	-----						
BRA2 sequence 3.2	-----						
BRA2 sequence 6.2	-----						
BRA1 Sequence 1	-----						
BRA2 sequence 1.1	-----						
BRA1 Sequence 4	-----						
BRA2 sequence 3.1	-----						
BRA1 Sequence 2	-----						
BRA1	GAAAAAAGTAACAGGAATAAAACAATGGCGGAAGAAAGAGATTCAAGAGAACGAAGAGAA						
BRA1 Sequence 3	GAAAAAAGTAACAGGAATAAAACAATGGCGGAAGAAAGAGATTCAAGAGAACGAAGAGAA						
BRA2 sequence 4.1	-----						
BRA1 Sequence 1	-----						
BRA2 sequence 5.1	-----						
BRA1 Sequence 2	-----						
BRA2 sequence 2.1	-----						
BRA2 sequence 2.2	-----						
BRA2 sequence 4.2	-----						
BRA2 sequence 5.2	-----						
BRA2 sequence 3.2	-----						
BRA2 sequence 6.2	-----						
BRA1 Sequence 1	-----						
BRA2 sequence 1.1	-----						
BRA1 Sequence 4	-----						
BRA2 sequence 3.1	-----						
BRA1 Sequence 2	-----						
BRA1	GCGTACCTGAAAGAAGATGCAGAAGAAAATGCAAAGAAGAGAAACAATGACTGGTGGAAA						
BRA1 Sequence 3	GCGTACCTGAAAGAAGATGCAGAAGAAAATGCAAAGAAGAGAAACAATGACTGGTGGAAA						
BRA2 sequence 4.1	-----						
BRA1 Sequence 1	-----						
BRA2 sequence 5.1	-----						
BRA1 Sequence 2	-----						
BRA2 sequence 2.1	-----						
BRA2 sequence 2.2	-----						
BRA2 sequence 4.2	-----						
BRA2 sequence 5.2	-----						
BRA2 sequence 3.2	-----						
BRA2 sequence 6.2	-----						

BRA1	Sequence	1	-----
BRA2	sequence	1.1	-----
BRA1	Sequence	4	-----
BRA2	sequence	3.1	-----
BRA1	Sequence	2	-----
BRA1			ATAGGTATGTTTATGCTATGTTTAAATGGGAGCAACAGGAGGAATGCTCTGGTGGTATGAG
BRA1	Sequence	3	ATAGGTATGTTTATGCTATGTTTAAATGGGAGCAACAGGAGGAATACTCTGGTGGTATGAG
BRA2	sequence	4.1	-----
BRA1	Sequence	1	-----
BRA2	sequence	5.1	-----
BRA1	Sequence	2	-----
BRA2	sequence	2.1	-----
BRA2	sequence	2.2	-----
BRA2	sequence	4.2	-----
BRA2	sequence	5.2	-----
BRA2	sequence	3.2	-----
BRA2	sequence	6.2	-----
BRA1	Sequence	1	-----
BRA2	sequence	1.1	-----
BRA1	Sequence	4	-----
BRA2	sequence	3.1	-----
BRA1	Sequence	2	-----
BRA1			GATGTGGCACACCCACAATATATAGGATTGATTACTGTTGGTGGGAAATTGGAAGGATCT
BRA1	Sequence	3	GATGTGGCACACCCACAATATATAGGATTGATTACTGTTGGTGGGAAATTGGAAGGATCT
BRA2	sequence	4.1	-----
BRA1	Sequence	1	-----
BRA2	sequence	5.1	-----
BRA1	Sequence	2	-----
BRA2	sequence	2.1	-----
BRA2	sequence	2.2	-----
BRA2	sequence	4.2	-----
BRA2	sequence	5.2	-----
BRA2	sequence	3.2	-----
BRA2	sequence	6.2	-----
BRA1	Sequence	1	-----
BRA2	sequence	1.1	-----
BRA1	Sequence	4	-----
BRA2	sequence	3.1	-----
BRA1	Sequence	2	-----
BRA1			GGAATGACTAGTGCTATAGAATGTTGGGGT-AAGTTTCCTGGCTGTAGACCGTTTGATAA
BRA1	Sequence	3	GGAATGACTAGTGCTATAGAATGTTGGGGTNAAGTTTCCTGGCTGTAGACCGTTTGATAA
BRA2	sequence	4.1	-----
BRA1	Sequence	1	-----
BRA2	sequence	5.1	-----
BRA1	Sequence	2	-----
BRA2	sequence	2.1	-----
BRA2	sequence	2.2	-----
BRA2	sequence	4.2	-----
BRA2	sequence	5.2	-----
BRA2	sequence	3.2	-----
BRA2	sequence	6.2	-----
BRA1	Sequence	1	-----
BRA2	sequence	1.1	-----
BRA1	Sequence	4	-----
BRA2	sequence	3.1	-----
BRA1	Sequence	2	-----
BRA1			TTATTTTAGTTACATGACTAACAGACGTATACATGTACAAAATAACACTGTTTCA-TTAT
BRA1	Sequence	3	TTATTTTAGTTACATGACTAACAGACGTATACATGTACAAAATAACACTGTTTTCMWTAT
BRA2	sequence	4.1	-----
BRA1	Sequence	1	TATATTAGCTTCAGTAACCAGCAGAAGTAGACATGTACAAAATAACACTGTTTCA-TTAT
BRA2	sequence	5.1	-----
BRA1	Sequence	2	-----CAGTAGTAGACATGTACAAAATAACACTGTTTCA-TTAT
BRA2	sequence	2.1	-----
BRA2	sequence	2.2	-----
BRA2	sequence	4.2	-----
BRA2	sequence	5.2	-----
BRA2	sequence	3.2	-----
BRA2	sequence	6.2	-----
BRA1	Sequence	1	-----
BRA2	sequence	1.1	-----
BRA1	Sequence	4	-----
BRA2	sequence	3.1	-----
BRA1	Sequence	2	-----

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BRA2 sequence 3.1 -----
BRA1 Sequence 2 -----

BRA1
BRA1 Sequence 3 TAG-AGTCATATCATAGAGAGATAACATATATATATATAAAA-CAATGTGTACAGATAGTGA
BRA2 sequence 4.1 TAG-AGTCATATCATAGAGAGATAACATATATATATATATAAAAACAATGTGTACAGATAGTGA
BRA1 Sequence 1 TAG-AGTCATATCGTAGAGAGATAGCATTTTATATATACAA-CAATGTCTACTGGTAGTGA
BRA2 sequence 5.1 -----
BRA1 Sequence 2 CAGGAGTCATATCATAGAGAGATAACATATATATATATACAA-CAATGTGTACTGATAGTGA
BRA2 sequence 2.1 -----
BRA2 sequence 2.2 -----TGTGTACAGATAGTGA
BRA2 sequence 4.2 -----TGTGTACAGATAGTGA
BRA2 sequence 5.2 -----TGTGTACAGATAGTGA
BRA2 sequence 3.2 -----TGTGTACAGATAGTGA
BRA2 sequence 6.2 -----GTGTACAGATAGTGA
BRA1 Sequence 1 -----AGTGA
BRA2 sequence 1.1 -----
BRA1 Sequence 4 -----
BRA2 sequence 3.1 -----
BRA1 Sequence 2 -----

BRA1
BRA1 Sequence 3 TCATTGTCAAGAA-TAT-GAGTGT-----AGAAACG--TACAACTGACT
BRA2 sequence 4.1 TCATTGTCAAGAANTATNGAGTGT-----YMAAGAGGGTACAACCTGACTA
BRA1 Sequence 1 TCATCGTCAAGAT-TAT-GAGKWT-----RAARAGG--TACAACTGACT-
BRA2 sequence 5.1 -----
BRA1 Sequence 2 TCATTATCAAGAT-TAT-GAGTGT-----GAGGAGG--TACAACTGACT-
BRA2 sequence 2.1 -----
BRA2 sequence 2.2 TCATTGTCAAGAC-TAT-GAGTGC---GAAAGGGTCCAACATAAAAAACA-CTAGTAAATATA-
BRA2 sequence 4.2 TCATTGTCAAGAC-TAT-GAGTGC-----GAAAGGG--TCCAACATAAA-
BRA2 sequence 5.2 TCATTGTCAAGAC-TAT-GAGTGC-----AAAAGGG--TCCAACATAAAA-
BRA2 sequence 3.2 TCATTGTCAASAC-TAT-GAGTGC-----GAAAGGG--TCCGATTAAT-
BRA2 sequence 6.2 TCATTGTCAAGAC-TAT-GAGTGC-----AAAAGGG--TCCAACATAAAA-
BRA1 Sequence 1 TCATTGTCAAGAA-TAT-GAGTGT-----AAAAGG--AACAACTGCCT-
BRA2 sequence 1.1 -----
BRA1 Sequence 4 -----
BRA2 sequence 3.1 -----
BRA1 Sequence 2 -----

BRA1
BRA1 Sequence 3 G----G-----TAAT----GGGTAAAA-GTG--AATATAA-GCTACACCTTACTA
BRA2 sequence 4.1 G----G-----TATR----TGGGTCNAA-GTGTGACTATAAAGCTACAACG--CTA
BRA1 Sequence 1 A----G-----TART----GGTCAAGT-GTG--ACTATAA-GCTACAAC--RCTA
BRA2 sequence 5.1 -----
BRA1 Sequence 2 G----G-----TGAG----TAGTTGTAGTGTG--AATATAA-CCTACAAC--ACTA
BRA2 sequence 2.1 -----
BRA2 sequence 2.2 T----A-----ATAA----ATGTGACGG-TTA--GTAATAA-TAGTGGTAATAGTG
BRA2 sequence 4.2 GAGAA-----TAAT----AGTGAAGT-GTG--GAGATTA-GTGGTAA--TAGCA
BRA2 sequence 5.2 G----AGACTAAAAA---TAAT----ATAATAAAT-GTG--AGTAATA-GTGGTAA--TAGTA
BRA2 sequence 3.2 G----G-----GAATTTTAGTGATAGAA-TAA--GTGTGGA-GGATAATAATAATA
BRA2 sequence 6.2 G----AGACTAAAAA---TAAT----ATAATAAAT-GTG--AGTAATA-GTGGTAA--TAGTA
BRA1 Sequence 1 A----G-----TAAT----GGGTCCCGT-GTG--AATATAA-GCTACAACG--CTA
BRA2 sequence 1.1 -----
BRA1 Sequence 4 -----
BRA2 sequence 3.1 -----
BRA1 Sequence 2 -----

BRA1
BRA1 Sequence 3 ACACATC--AT----TGGAA-TTTCAAATGGTT--GGTATGTAATCAAACCTGAGAATCAA
BRA2 sequence 4.1 GCACATC--TTAATTTGGAANTTTCAAATGGGTTGGGTATGTAATCAAACCTGRAGAATCAA
BRA1 Sequence 1 GCACATCTTAT----TGGAA-TTTCAAATGGTT--GGTATGTAATCAAACCTGAGAATCAA
BRA2 sequence 5.1 -----
BRA1 Sequence 2 MCACATCTTAT----TGGAA-TTTCAAATGGTT--GGTATGTAATCAAATGAGAATCAA
BRA2 sequence 2.1 -----
BRA2 sequence 2.2 ACACATC--AT----TGGGA-TTTCACATGGTT--ATTATGTAATCAAACCTGAGAATAAA
BRA2 sequence 4.2 GCACATC--AT----TGGAA-TTTCACATGGTT--ATTATGTAATCAAACCTGAGAATAAA
BRA2 sequence 5.2 GCACATC--AT----TGGGA-TTTCACATGGTT--ATTATGTAATCAAGCTGAGAATACA
BRA2 sequence 3.2 GCACATC--AT----TGGGA-TTTCACATGGTT--ATTATGTAATCAAACCTGAGAATAAA
BRA2 sequence 6.2 GCACATC--AT----TGGGA-TTTCACATGGTT--ATTATGTAATCAAGCTGAGAATACA
BRA1 Sequence 1 GCACATCTTAT----TGGAA-TTTCAAATGGTT--GGTATGTAATCAAACCTGAGAATCAA
BRA2 sequence 1.1 -----
BRA1 Sequence 4 -----
BRA2 sequence 3.1 -----
BRA1 Sequence 2 -----

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BRA1 AAGGCAATTC-TTATTCCA-GAAGAAG-AAATGGTACAG---AA-TGATAATAATACTT-
BRA1 Sequence 3 AAGGCAATTCYTTATTCCAAGAAGAAGNAAATGGTACAG---AAATGATAATAATACYTT
BRA2 sequence 4.1 -----
BRA1 Sequence 1 AAGGCAATTC-TTATTCCA-GAAGAAG-AAATGGTACAG---AA-TGATAATAATACTT-
BRA2 sequence 5.1 -----
BRA1 Sequence 2 AAGGCAATTC-TTATTSCA-GAAGAAG-AAGTGGTACAG---AA-TGATAATAATACTT-
BRA2 sequence 2.1 -----
BRA2 sequence 2.2 AAGACAATTC-TTGTTCCTA-GAAGAAG-AAATGATACTG---TA-CAATGGCACCACCTT-
BRA2 sequence 4.2 AAGACAATTC-TTGTTCCTA-GAAGAAG-AAATGATACTG---TACAA-TGACAATCGCACTT-
BRA2 sequence 5.2 AAGACAATTC-TTGTTCCTA-GAGGAAG-AAATGCAGGAC---AG-TGACAATGGCACCCTT-
BRA2 sequence 3.2 AAGACGATTC-TTGTTCCTA-GAAGAAG-AAATGATACTG---TACAA-TGACAATCGCACTT-
BRA2 sequence 6.2 AAGACAATTC-TTGTTCCTA-GAGGAAG-AAATGCAGGAC---AG-TGACAATGGCACCCTT-
BRA1 Sequence 1 AAGGCAATTC-TTATTCCA-GAAGAAG-AAATGGTACAG---AA-TGATAATAATACTT-
BRA2 sequence 1.1 -----
BRA1 Sequence 4 -----ATAATAACTT-
BRA2 sequence 3.1 -----
BRA1 Sequence 2 -----ATAATAACTT-

BRA1 -GGTCCCCTAGGGGAT-GTAATAGCA--CATGGG-CAAGGGTGAAACATT-GTCC-AGCG
BRA1 Sequence 3 GGGTCCCCTAGGGGATGTAATAGCCACCATGGGGCAAAGGGGAAACACTTGTCSAGCCA
BRA2 sequence 4.1 -----
BRA1 Sequence 1 -GGTCCCCTAGGGGAT-GTAATAGCA--CATGGG-CAAAGGTGAAACATT-GTCC-AGCG
BRA2 sequence 5.1 -----
BRA1 Sequence 2 -GGTCTCGTAGGGGAT-GTARTAGCA--CATGGR-CAAAGGTGAAACATT-GTCC-AGCT
BRA2 sequence 2.1 -----
BRA2 sequence 2.2 -GGGCCCCTAAGGGAT-GTAATGACA--CATGGG-CAAAGTAAAACATT-GTCC-AATG
BRA2 sequence 4.2 -GGGCCCCTAAGGGAT-GTAATGACA--CATGGG-CAAAGTAAAACATT-GTCC-AATG
BRA2 sequence 5.2 -GGGCCCCTAAGGGAT-GTAATGACA--CATGGG-CAAAGTAAAACATT-GTCC-AATG
BRA2 sequence 3.2 -GGGCCCCTAAGGGAT-GTAATGACA--CATGGG-CAAAGTAAAACATT-GTCC-AATG
BRA2 sequence 6.2 -GGGCCCCTAAGGGAT-GTAATGACA--CATGGG-CAAAGTAAAACATT-GTCC-AATG
BRA1 Sequence 1 NGGTCCCCTAGGGGAT-GTAATAGCA--CATGGG-CAAAGGTGAAACATT-GTCC-AGCG
BRA2 sequence 1.1 -----
BRA1 Sequence 4 -GGTCCCCTAGGGGAT-GTAATAGCA--CATGGG-CAAAGGTGAAACATTTGTCCCAGCG
BRA2 sequence 3.1 -----
BRA1 Sequence 2 -GGTCCCCTAGGGGAT-GTAATAGCA--CATGGG-CAAAGGTGAAACATTTGTCCCAGCG

BRA1 GAT-CTGTTGTATGGGATACATCCTATTAGGCTATGTGTGCAGCCACCATTTTCTGGT
BRA1 Sequence 3 GATCGGRWTCATGCGATACATCCTATAAGGCCATGTGTGTGCAGCCACATTTTCTGGT
BRA2 sequence 4.1 -----
BRA1 Sequence 1 GAT-YTGTTGTATGGGATACATCCTATTAGGCTATGTGTGCAGCCACCATTTTCTGGT
BRA2 sequence 5.1 -----
BRA1 Sequence 2 GAT-STGTTKTATGGGATTCATCYTATTAGGCTATGTGTGCAGCCACCATTTTCTGGT
BRA2 sequence 2.1 -----
BRA2 sequence 2.2 GAC-TTGTTGTATGGGCTGCATCCTATTAGGTTATGTGTACAGCCACCATTTTCTGGT
BRA2 sequence 4.2 GAC-TTGTTGTATGGGCTGCATCCTATTAGGTTATGTGTACAGCCACCATTTTCTGGT
BRA2 sequence 5.2 GAC-TTGTTGTATGGGCTGCATCCTATTAGGTTATGTGTACAGCCACCATTTTCTGGT
BRA2 sequence 3.2 GAC-TTGTTGTATGGGCTGCATCCTATTAGGTTATGTGTACAGCCACCATTTTCTGGT
BRA2 sequence 6.2 GAC-TTGTTGTATGGGCTGCATCCTATTAGGTTATGTGTACAGCCACCATTTTCTGGT
BRA1 Sequence 1 GATTYGTTGTATGGGATACATCCTATTAGGCTATGTGTGCAGCCACCATTTTCTGGT
BRA2 sequence 1.1 -----
BRA1 Sequence 4 GAT-TTGTTGTATGGGATACATCCTATTAGGCTATGTGTGCAGCCACCATTTTCTGGT
BRA2 sequence 3.1 -----
BRA1 Sequence 2 GAT-TTGTTGTATGGGATACATCCTATTAGGCTATGTGTGCAGCCACCATTTTCTGGT

BRA1 AAAAAATAATGATGGGAACCTCACAAATGGGAACCCACACACTTAGCAACTGTGGTCCACA
BRA1 Sequence 3 AAAAAATAGGATGGGAACCTCACGAATATGGGAACCTCAACCACTCCTA-----
BRA2 sequence 4.1 -----
BRA1 Sequence 1 RAAAAATAATGATGGGAACCTCACAAATGGGAACCCACACACTTAGCAACTGTGGTCCACA
BRA2 sequence 5.1 -----
BRA1 Sequence 2 AAAAAATAATGATGGGAACCTCACATTTGGGAACCCACACTYAGCAAYTGTGGTCCACA
BRA2 sequence 2.1 -----
BRA2 sequence 2.2 AAGAAAAGAAGAT-----AATCATAGCCGCACACTTAGTAATTGTGGTCCACA
BRA2 sequence 4.2 AAGAAAAGAAGAT-----AATCATAGCCGCACACTTAGTAATTGTGGTCCACA
BRA2 sequence 5.2 AAGAAAAGAAGAT-----AATCATAGCCGCACACTTAGTAATTGTGGTCCACA
BRA2 sequence 3.2 AAGAAAAGAAGAT-----AATCATAGCCGCACACTTAGTAATTGTGGTCCACA
BRA2 sequence 6.2 AAGAAAAGAAGAT-----AATCATAGCCGCACACTTAGTAATTGTGGTCCACA
BRA1 Sequence 1 GAAAAATAATGATGGGAACCTCACAAATGGGAACCCACACACTTAGCAACTGTGGTCCACA
BRA2 sequence 1.1 -----
BRA1 Sequence 4 GAAAAATAATGATGGGAACCTCACAAATGGGAACCCACACACTTAGCAACTGTGGTCCACA
BRA2 sequence 3.1 -----
BRA1 Sequence 2 GAAAAATAATGATGGGAACCTCACAAATGGGAACCCACACACTTAGCAACTGTGGTCCACA

BRA1 AATATCACTGGGGATATTAGATGAAAAATAAGCTGTTACAAGGGAGGTCAACTGCACTGT
BRA1 Sequence 3 -----
BRA2 sequence 4.1 -----

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BRA1 Sequence 1 AATATCACTGGGGATATTAGATGAAAATAAAGCTGTTACAAGGGGGGTCAACTGCACTGT
 BRA2 sequence 5.1 -----
 BRA1 Sequence 2 AAYAYMACTGGGGATATTRGATGAAAATAAAGCTGTTACAAGGGGGGTCAACTTCACTGT
 BRA2 sequence 2.1 -----
 BRA2 sequence 2.2 AATATCATTAGGGATATTAGATAACAATAAAGCTGCTGTAAGAGATGCCAGCTGCCAGGT
 BRA2 sequence 4.2 AATATCATTAGGGATATTAGATGACAATAAAGCTGCTGTAAGAGATGCCAACTGCGTGGT
 BRA2 sequence 5.2 AATATCACTAGGGATATTAGATAACAATAAAGCTGCTGTAAGAAATGCCAACTGCAGCGT
 BRA2 sequence 3.2 AATATCATTAGGGATATTAGATAGCAATAAAGCTGCTGTAAGAAATGCCAGCTGCCAGGT
 BRA2 sequence 6.2 AATATCACTAGGGATATTAGATAACAATAAAGCTGCTGTAAGAAATGCCAACTGCAGCGT
 BRA1 Sequence 1 AATATCACTGGGGATATTAGATGAAAATAAAGCTGTTACAAGGGGGGTCAACTGCACTGT
 BRA2 sequence 1.1 -----
 BRA1 Sequence 4 AATATCACTGGGGATATTAGATGAAAATAAAGCTGTTATAAGGGAGGTCAACTGCACTGT
 BRA2 sequence 3.1 -----
 BRA1 Sequence 2 AATATCACTGGGGATATTAGATGAAAATAAAGCTGTTATAAGGGAGGTCAACTGCACTGT

 BRA1 GGCTAAAAAA-GTTTTTCATTTT---AAT---GACTATTCTGGACAGTTTATAAGTCCTA
 BRA1 Sequence 3 -----
 BRA2 sequence 4.1 -----
 BRA1 Sequence 1 GGCTAAAAAA-AGTTTTAATTTT---CAT---GACTATTCTGGACAGTTTATAAGYCCTA
 BRA2 sequence 5.1 -----
 BRA1 Sequence 2 GGCTAAAAAA-AGTTATAATTTT---CAT---GACTATTCTGGACAGWTTATAAGTCTAA
 BRA2 sequence 2.1 -----
 BRA2 sequence 2.2 GGAGAGAAAAG-ACTGTTTCAGATT---CCTAAAGAATATCTGGACAGCTTATAGTTCCTA
 BRA2 sequence 4.2 GGAAAAAAG-ACTGTTTCAGATT---CCTAAAGAATATCTGGACAGCTTATAGTTCCTA
 BRA2 sequence 5.2 AGAGAAAAAG-ACTGTTTCAGACT---AAA---GACTATTCTGGACAGCTTATAGTTCCTA
 BRA2 sequence 3.2 GGAGAAAAAG-ACTTTTCAGTTTCTAAA---GGCCATTCTGGACAGCTTATAGTTCCTA
 BRA2 sequence 6.2 AGAGAAAAAG-ACTGTTTCAGACT---AAA---GACTATTCTGGACAGCTTATAGTTCCTA
 BRA1 Sequence 1 GGCTAAAAAAAGTTTTNAATTTT---CAT---GACTATTCTGGACAGTTTATAAGCCCTA
 BRA2 sequence 1.1 -----
 BRA1 Sequence 4 GGCTAAAAAA-AGTTTTAATTTT---CAT---GACTATTCTGGACAGTTTATAAGTCCTA
 BRA2 sequence 3.1 -----
 BRA1 Sequence 2 GGCTAAAAAA-AGTTTTAATTTT---CAT---GACTATTCTGGACAGTTTATAAGTCCTA

 BRA1 TATTTTATCAATGTAATCTTAGC---CTAACACCTTGTAATGGGACAAAACCTCACC-----
 BRA1 Sequence 3 -----
 BRA2 sequence 4.1 -----
 BRA1 sequence 1 TATTTTATCAATGTAATCTTAGC---CTAAAACCTTGTAATGGGACAAAACCTCATC-----
 BRA2 sequence 5.1 -----
 BRA1 Sequence 2 TATTTTATCAATGTAATCTTAGY---CTAAAMCCTTGTAATGGGACAAAACCTCATC-----
 BRA2 sequence 2.1 -----
 BRA2 sequence 2.2 TATTTTATAAGTGTACTATTA-----CTAATCTGACAAGGTGCTATAACAACAGCTCAAC
 BRA2 sequence 4.2 TATTTTATAAGTGTACTATTA-----CTAATCTGACAAGGTGCAATAACGACAACCTCAAC
 BRA2 sequence 5.2 TATTTTATAAGTGTACTATTTACTGGTCTGACAAGGTGCGATAACAACAACCTCAAC-----
 BRA2 sequence 3.2 TATTTTATAAGTGTACTATTTACTAATCTGACAAGGTGCTATAACAACAGCTCAAC-----
 BRA2 sequence 6.2 TATTTTATAAGTGTACTATTTACTGGTCTGACAAGGTGCGATAACAACAACCTCAAC-----
 BRA1 Sequence 1 TATTTTATCAATGTAATCTTAGC---CTAAAACCTTGTAATGGGACAAAACCTCATC-----
 BRA2 sequence 1.1 -----
 BRA1 Sequence 4 TATTTTATCAATGTAATCTTAGC---CTAAAACCTTGTAATGGGACAAAACCTCATC-----
 BRA2 sequence 3.1 -----
 BRA1 Sequence 2 TATTTTATCAATGTAATCTTAGC---CTAAAACCTTGTAATGGGACAAAACCTCATC-----

 BRA1 AGTAAGTATTATCAGATATGATGAGGACACTGTTGAATATTTGATAAGAAACACTGTTGA
 BRA1 Sequence 3 -----
 BRA2 sequence 4.1 -----
 BRA1 Sequence 1 AGTAAGTATTATCAGATATGATGAG-----AACACTGTTGA
 BRA2 sequence 5.1 -----
 BRA1 Sequence 2 AGTAAGTATTATCAGATATGATGAGGACGCTGTYGAATATGTGATA-----
 BRA2 sequence 2.1 -----
 BRA2 sequence 2.2 AATAAGTATTATCAGGTATGATGAGAAAAATGTTCAATATTTGTTATGTAAAACAAATAA
 BRA2 sequence 4.2 AATAAGTATTATCAGATATGATAAGGACAAATGTTCAATATTTGTTATGTAAAATAATAC
 BRA2 sequence 5.2 AATAAGTATTATCAGGTATGATGAGAACAGTGTTCATATTTGTTATGTAAAACAAATAA
 BRA2 sequence 3.2 AATAAGTATTATCAGGTATGATGAG-----AAAA-TGTTCA
 BRA2 sequence 6.2 AATAAGTATTATCAGGTATGATGAGAACAGTGTTCATATTTGTTATGTAAAACAAATAA
 BRA1 Sequence 1 AGTAAGTATTATCAGATATGATGAG-----AA-CACTGTTGA
 BRA2 sequence 1.1 -----
 BRA1 Sequence 4 AGTAAGTATTATCAGATATGATGAGAACACTGTTGAGTATTTGATA-----
 BRA2 sequence 3.1 -----
 BRA1 Sequence 2 AGTAAGTATTATCAGATATGATGAGAACACTGTTGAGTATTTGATA-----

 BRA1 ATATTTGATATGCAAGGCTAAAAACATCACTGAAAA-----A-----
 BRA1 Sequence 3 -----
 BRA2 sequence 4.1 -----
 BRA1 Sequence 1 ATATTTGATATGCAAGGCTAATAGCACCCTGAAAAACCCACTGAAGGA-----
 BRA2 sequence 5.1 -----
 BRA1 Sequence 2 -----TGCAAGGMTAATAGCAACACTGAAAAACCCACTGAAGGA-----

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BRA2 sequence 2.1 -----
BRA2 sequence 2.2 TACAGATGCAGGTAAT-----
BRA2 sequence 4.2 AGATGCAGGT-----
BRA2 sequence 5.2 TACAGATGCAGGTAAT-----
BRA2 sequence 3.2 ATATTTGTTATGTAAAACAAATAATACAGATGCAGG-----T-----
BRA2 sequence 6.2 TACAGATGCAGGTAAT-----
BRA1 Sequence 1 ATATTTGATATGCAAGGCTAATAGCACCCTGAAAACACCCTGAAGGA-----
BRA2 sequence 1.1 -----
BRA1 Sequence 4 -----TGCAAGGCTAATAACATCACT-AAAA-----ACACCGCTGAAA
BRA2 sequence 3.1 -----
BRA1 Sequence 2 -----TGCAAGGCTAATAACATCACT-AAAA-----ACACCGCTGAAA

BRA1 -----AACTTTTTCATGTGTAGTACAAACTTTTGGAAACAATAGGACAGGCAC
BRA1 Sequence 3 -----
BRA2 sequence 4.1 -----
BRA1 Sequence 1 -----AGCTTTTTTCATGTGTAGTACAAACTTTTGGAAACAATAGGACAGGCAC
BRA2 sequence 5.1 -----
BRA1 Sequence 2 -----AACTTTTTCATGTGTAGTACAAACTTTTGGAAACAATAGGACAGGCAC
BRA2 sequence 2.1 -----
BRA2 sequence 2.2 -----TTTTTCATGTGTAGTACAAACTTTTGGGAAAAATAGGACAGGCAC
BRA2 sequence 4.2 -----AATTTTTTCATGTGTAGTACAAACTTTTGGGAAAAATAGGACAGGCAC
BRA2 sequence 5.2 -----TTTTTCATGTGTAGTACAAACTTTTGGGAAAAATAGGACAGGCAC
BRA2 sequence 3.2 -----AATTTTTTCATGTGTAGTACAAACTTTTGGGAAAAATAGGACAGGCAC
BRA2 sequence 6.2 -----TTTTTCATGTGTAGTACAAACTTTTGGGAAAAATAGGACAGGCAC
BRA1 Sequence 1 -----AGCTTTTTTCATGTGTAGTACAAACTTTTGGAAACAATAGGACAGGCAC
BRA2 sequence 1.1 -----
BRA1 Sequence 4 GCACCCTGAAGGAAACTTTTTTCATGTGTAGTACAAACTTTTGGAAACAATAGGACAGGCAC
BRA2 sequence 3.1 -----
BRA1 Sequence 2 GCACCCTGAAGGAAACTTTTTTCATGTGTAGTACAAACTTTTGGAAACAATAGGACAGGCAC

BRA1 ATATAGAACTACCCAGAAAAAATAAAAAGATAATTGGAAACCAGTTCACACAATATAAATT
BRA1 Sequence 3 -----
BRA2 sequence 4.1 -----
BRA1 Sequence 1 ATATAGAACTACCCAGAAAAAATAAAAAGATAATTGGAGACCGGTTACACACAATATAAATT
BRA2 sequence 5.1 -----
BRA1 Sequence 2 ATATAGAACTACCCAGAAAAAATAAAAAGATAATTGGAAACCAGTTCACACAATATGATT
BRA2 sequence 2.1 -----
BRA2 sequence 2.2 ATATAGAGTTACCCAGAAACAATAAAAAGGATAAGAGAGAACAATTCACACAGTATAAATT
BRA2 sequence 4.2 ATATAGAGTTACCCAGAAACAATAAAAAGGATAAGAGAGAACAATTCACACAGTATAAATT
BRA2 sequence 5.2 ATATAGAGTTACCCAGAAACAATAAAAAGGATAAGAGAGAACAATTCACACAGTATAAATT
BRA2 sequence 3.2 ATATAGAGTTACCCAGAAACAATAAAAAGGATAAGAGAGAACAATTCACACAGTATAAATT
BRA2 sequence 6.2 ATATAGAGTTACCCAGAAACAATAAAAAGGATAAGAGAGAACAATTCACACAGTATAAATT
BRA1 Sequence 1 ATATAGAACTACCCAGAAAAAATAAAAAGATAATTGGAGACCGGTTACACACAATATAAATT
BRA2 sequence 1.1 -----
BRA1 Sequence 4 ATATAGAACTACCCAGAAAAAATAAAAAGATAATTGGAGACCGGTTACACACAATATAAATT
BRA2 sequence 3.1 -----
BRA1 Sequence 2 ATATAGAACTACCCAGAAAAAATAAAAAGATAATTGGAGACCGGTTACACACAATATAAATT

BRA1 GTTCAATAAATGATAAAGACAGAGTTAGAAAAATGGAAGTTGGTAAAAA-GTTCAGGTATT
BRA1 Sequence 3 -----
BRA2 sequence 4.1 -----
BRA1 Sequence 1 GTTCAATAAATAATAAAGACAGAGTTAGAAAAATGGAAGTTGGTAAAAA-GTTCAGGTATT
BRA2 sequence 5.1 -----
BRA1 Sequence 2 GTTCAATAAATAATAAAGACAGAGTTAGAAAAATGGAAGTN-----
BRA2 sequence 2.1 -----
BRA2 sequence 2.2 GTTCAATAAATAATCAGACAGAGTTAAAAGAATGGAATGATAAAGAG-GTTCGGGTATT
BRA2 sequence 4.2 GTTCAATAAATAATCAGACAGAGTTAAAAGAATGGAATGATAAAGAG-GTTCGGGTATT
BRA2 sequence 5.2 GTTCAATAAATAATCAGACAGAGTTAAAAGAATGGAATGATAAAGAG-GTTCGGGTATT
BRA2 sequence 3.2 GTTCAATAAATAATCAGACAGAGTTAAAAGAATGGAATGATAAAGAG-GTTCGGGTATT
BRA2 sequence 6.2 GTTCAATAAATAATCAGACAGAGTTAAAAGAATGGAATGATAAAGAG-GTTCGGGTATT
BRA1 Sequence 1 GTTCAATAAATAATAAAGACAGAGTTAGAAAAATGGAAGTTGGTAAAAANGTTCAGGTATT
BRA2 sequence 1.1 -----
BRA1 Sequence 4 GTTCAATAAATGATAAAGACAGAGTTAGAAAAATGGAAGTTGGTAAAAA-GTTCAGGTATT
BRA2 sequence 3.1 -----
BRA1 Sequence 2 GTTCAATAAATGATAAAGACAGAGTTAGAAAAATGGAAGTTGGTAAAAA-GTTCAGGTATT

BRA1 ACTCCTTTTCTGTTACTTCTCGGGCCAATACAGGACTAGTTAGATACAAAAGAGATTTT
BRA1 sequence 3 -----
BRA2 sequence 4.1 -----
BRA1 Sequence 1 ACTCCTTTTCTGTTACTTCTCGGGC-----
BRA2 sequence 5.1 -----
BRA1 Sequence 2 -----
BRA2 sequence 2.1 -----
BRA2 sequence 2.2 ACTCCTATTCTTACTTCTCAGGCTAACACAGGATTAATTAGATACAAAAGAGATTTT
BRA2 sequence 4.2 ACTCCTGTTCTTACTTCTCAGGCTAACACAGGATTAATTAGATACAAAAGAGATTTT

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BRA2 sequence 5.2 ACTCCTATTCTTACTTTCTCAGGCTAACACAGGATTAATTAGATACAAAAGAGATTTT
 BRA2 sequence 3.2 ACTCCTATTCTTACTTTCTCAGGCTAACACAGGATTAATTAGATACAAAAGAGATTTT
 BRA2 sequence 6.2 ACTCCTATTCTTACTTTCTCAGGCTAACACAGGATTAATTAGATACAAAAGAGATTTT
 BRA1 Sequence 1 ACTCCTTTTCTGTTACTTTCTCGGGC-----
 BRA2 sequence 1.1 -----
 BRA1 Sequence 4 ACTCCTTTTCTGTTACTTTCTCGGGC-----
 BRA2 sequence 3.1 -----
 BRA1 Sequence 2 ACTCCTTTTCTGTTACTTTCTCGGGC-----

 BRA1 GGAATATCAGCAATAGTGGCGGCAATAGTGGCTGCAACTGCTATTGCTGCTAGTGTACT
 BRA1 Sequence 3 -----
 BRA2 sequence 4.1 -----GCTATTGCTGCTAGTGTACTACC
 BRA1 Sequence 1 -----
 BRA2 sequence 5.1 -----
 BRA1 Sequence 2 -----
 BRA2 sequence 2.1 -----
 BRA2 sequence 2.2 GGAATATCAGCAATAGTGGCGGCAATAGTGGCTGCAACCGCTATTGCTGCTAGTGTACTACC
 BRA2 sequence 4.2 GGAATATCAGCAATAGTGGCGGCAATAGTGGCTGCAACCGCTATTGCTGCTAGTGTACTACC
 BRA2 sequence 5.2 GGAATATCAGCAATAGTGGCGGCAATAGTGGCTGCAACCGCTATTGCTGCTAGTGTACTACC
 BRA2 sequence 3.2 GGAATATCAGCAATAGTGGCGGCAATAGTGGCTGCAACCGCTATTGCTGCTAGTGTACTACC
 BRA2 sequence 6.2 GGAATATCAGCAATAGTGGCGGCAATAGTGGCTGCAACCGCTATTGCTGCTAGTGTACTACC
 BRA1 Sequence 1 -----
 BRA2 sequence 1.1 -----
 BRA1 Sequence 4 -----
 BRA2 sequence 3.1 -----
 BRA1 Sequence 2 -----

 BRA1 ATGTCCTTATATTGCCTTAACTGAAACAAATAAAATGAGTGATGTAATGAATCATACATTT
 BRA1 Sequence 3 -----
 BRA2 sequence 4.1 ATGTCCTTATATTGCCTTGACTGAAGCAAGTAAAGTTACTAATGCCATGAATCATACATTT
 BRA1 Sequence 1 -----
 BRA2 sequence 5.1 -----TAATGCCATGAATCATACMTTT
 BRA1 Sequence 2 -----
 BRA2 sequence 2.1 -----TTT
 BRA2 sequence 2.2 ATGTCCTTATATTGCCTTGACTGAAGCAAGTAAAGTTACTAATGCCATGAATCATACCTTT
 BRA2 sequence 4.2 ATGTCCTTATATTGCCTTGACTGAAGCAAGTAAAGTTACTAATGCCATGAATCATACCTTT
 BRA2 sequence 5.2 ATGTCCTTATATTGCCTTGACTGAGGCAAGTAAAGTTAGTAATGCCATGAATCATACATTT
 BRA2 sequence 3.2 ATGTCCTTATATTGCCTTGACTGAAGCAAGTAAAGTTAGTAATGCCATGAATCATACATTT
 BRA2 sequence 6.2 ATGTCCTTATATTGCCTTGACTGAGGCAAGTAAAGTTAGTAATGCCATGAATCATACATTT
 BRA1 Sequence 1 -----
 BRA2 sequence 1.1 -----
 BRA1 Sequence 4 -----
 BRA2 sequence 3.1 -----
 BRA1 Sequence 2 -----

 BRA1 GTAGTGAAAAATGATACAATCAGAGCAACGGAAATGATAGAAAAACAGATACATATATTA
 BRA1 Sequence 3 -----
 BRA2 sequence 4.1 GAAGTAGAGAATAACACAATCCATGCAACAGAGATGATAGAAAAACAAATGCATATATTA
 BRA1 Sequence 1 -----
 BRA2 sequence 5.1 GAAGTAGAGAATAACACAATCCATGCAACAGAGATGATAGAAAAACAAATGCATATATTA
 BRA1 Sequence 2 -----
 BRA2 sequence 2.1 GAAGTAGAGAATAACACAATCCATGCAACAGAGATGATAGAAAAACAAATGCATATATTA
 BRA2 sequence 2.2 GAAGTAGAGAATAACACAATCCATGCAACAGAGATGATAGAAAAACAAATGCATATATTA
 BRA2 sequence 4.2 GAAGTAGAGAATAACACAATCCATGCAACAGAGATGATAGAAAAACAAATGCACATATTA
 BRA2 sequence 5.2 GAGGTAGAGAATAACACAATCCATGCAACAGAGATGATAGAAAAACAAATGCATATATTA
 BRA2 sequence 3.2 GAGGTAGAGAATAACACAATCCATGCAACAGAGATGATAGAAAAACAAATGCATATATTA
 BRA2 sequence 6.2 GAGGTAGAGAATAACACAATCCATGCAACAGAGATGATAGAAAAACAAATGCATATATTA
 BRA1 Sequence 1 -----
 BRA2 sequence 1.1 ---GTAGAGAATAACACAATCCATGCAACAGAGATGATAGAAAAACAAATGCATRTATTA
 BRA1 Sequence 4 -----
 BRA2 sequence 3.1 -----AAAAACAAATGCATATATTA
 BRA1 Sequence 2 -----

 BRA1 TATGCAATGGTTCTTCAGACCCATGCAGATGTCC-AGTTACTAAAAGAAAGACAAAAAAT
 BRA1 Sequence 3 -----
 BRA2 sequence 4.1 TATGCAATGATTCTTCAGACCCATGCAGATGTCC-AGTTACTAAAAGAAAGACAAAAAAT
 BRA1 Sequence 1 -----
 BRA2 sequence 5.1 TATGCAATGATTCTTCAGACCCATGCAGATGTCC-AGTTACTAAAAGAAAGACAAAAAAT
 BRA1 Sequence 2 -----
 BRA2 sequence 2.1 TATGCAATGATTCTTCAGACCCATGCAGATGTCC-AGTTACTAAAAGAAAGACAAAAAAT
 BRA2 sequence 2.2 TATGCAATGATTCTTCAGACCCATGCAGATGTCC-AGTTACTAAA-----
 BRA2 sequence 4.2 TATGCAATGATTCTTCAGACCCATGCAGATGTCC-AGTTACTAAA-----
 BRA2 sequence 5.2 TATGCAATGATTCTTCAGACCCATGCAGATGTCC-AGTTA-----
 BRA2 sequence 3.2 TATGCAATGATTCTTCAGACCCATGCAGATGTCC-AGTTACTAAA-----
 BRA2 sequence 6.2 TATGCAATGATTCTTCAGACCCATGCAGATGTCC-AG-----


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BRA1 Sequence 1 -----
BRA2 sequence 1.1 TATGCAATGATTCTTCAGACCCATGCAGATGTCC-AGTTACTAAAAGAAAGACAAAAAT
BRA1 Sequence 4 -----
BRA2 sequence 3.1 TATGCAATGATTCTTCAGACCCATGCAGATGTCCCAGTTACTAAAAGAAAGACAAAAAT
BRA1 Sequence 2 -----

BRA1
BRA1 Sequence 3 AGAGGAAACATTTAATTTG-ATAGGGTGTGTTGAGAGGTCACATACATTCTGCCATACTG
BRA2 sequence 4.1 AGAGGAAACATTTAATTTG-ATAGGGTGTGTTGAAAGATCACATACATTCTGCCATACTG
BRA1 Sequence 1 -----
BRA2 sequence 5.1 AGATGAAACATTTAATTTG-ATAGGGTGTGTTGAAAGATCACATACATTCTGTCATACTG
BRA1 Sequence 2 -----
BRA2 sequence 2.1 AGATGAAACATTTAATTTG-ATAGGGTGTGTTGAAAGATCACATACATTCTGTCATACTG
BRA2 sequence 2.2 -----
BRA2 sequence 4.2 -----
BRA2 sequence 5.2 -----
BRA2 sequence 3.2 -----
BRA2 sequence 6.2 -----
BRA1 Sequence 1 -----
BRA2 sequence 1.1 AGATGAAACATTTAATTTG-ATAGGGTGTGTTGAAAGATCACATACATTCTGTCATACTG
BRA1 Sequence 4 -----
BRA2 sequence 3.1 AGATGAAACATTTAATTTG-ATAGGGTGTGTTGAAAGATCACATACATTCTGTCATACTG
BRA1 Sequence 2 -----

BRA1
BRA1 Sequence 3 GACA-TCCATGGAATGAATCTTGGGGCAAT-TGAATGAAACAACAGAATGGGA
BRA2 sequence 4.1 GACA-TCCATGGAATGATTCTTGGGGACAAT-TAAATGACTCAACACAATGGGA
BRA1 Sequence 1 -----
BRA2 sequence 5.1 GACA-TCCATGGAATGATTCTTGGGGACAAT-TAAATGACTCAACACAATGGGA
BRA1 Sequence 2 -----
BRA2 sequence 2.1 GACA-TCCATGGAATGATTCTTGGGGACAAT-TAAATGACTCAACACAATGGGA
BRA2 sequence 2.2 -----
BRA2 sequence 4.2 -----
BRA2 sequence 5.2 -----
BRA2 sequence 3.2 -----
BRA2 sequence 6.2 -----
BRA1 Sequence 1 -----
BRA2 sequence 1.1 GACA-TCCATGGAATGATTCTTGGGGACAAT-TAAATGACTCAACACAATGGGA
BRA1 Sequence 4 -----
BRA2 sequence 3.1 GACA-TCCATGGAATGATTCTTGGGGACAAT-TAAATGACTCAACACAATGGGA
BRA1 Sequence 2 -----

BRA1
BRA1 Sequence 3 TGATTGGATAACTAAAATGAATAGGCTTGAAACGGAGATATTGACTACTCTGCATGCAGC
BRA2 sequence 4.1 TGATTGGGTAAACAAAATGAATGAGTATGAACAGGACATATTAACAACCTCTTCATGCAGC
BRA1 Sequence 1 -----
BRA2 sequence 5.1 TGATTGGGTAAACAAAATGAATGAGTATGAACAGGACATATTAACAACCTCTTCATGCAGC
BRA1 Sequence 2 -----
BRA2 sequence 2.1 TGATTGGGTAAACAAAATGAATGAGTATGAACAGGACATATTAACAACCTCTTCATGCAGC
BRA2 sequence 2.2 -----
BRA2 sequence 4.2 -----
BRA2 sequence 5.2 -----
BRA2 sequence 3.2 -----
BRA2 sequence 6.2 -----
BRA1 Sequence 1 -----
BRA2 sequence 1.1 TGATTGGGTAAACAAAATGAATGAGTATGAACAGGACATATTAACAACCTCTTCATGCAGC
BRA1 Sequence 4 -----
BRA2 sequence 3.1 TGATTGGGTAAACAAAATGAATGAGTATGAACAGGACATATTAACAACCTCTTCATGCAGC
BRA1 Sequence 2 -----

BRA1
BRA1 Sequence 3 TAAAAATAATTTAGAACAAGCGATGATTACTTTTAATACACCTGATAGTATAGCTCAATT
BRA2 sequence 4.1 TAGAAATAATTTAGAACAGGCTATGATTACTTTTAATACACCTGATAGTATAGCTCAATT
BRA1 Sequence 1 -----
BRA2 sequence 5.1 TAGAAATAATTTAGAACAGGCTATGATTACTTTTAATACACCTGATAGTATAGCTCAATT
BRA2 sequence 2.1 TAGAAATAATTTAGAACAGGCTATGATTACTTTTAATACACCTGATAGTATAGCTCAATT
BRA2 sequence 2.2 -----
BRA2 sequence 4.2 -----
BRA2 sequence 5.2 -----
BRA2 sequence 3.2 -----
BRA2 sequence 6.2 -----
BRA1 Sequence 1 -----
BRA2 sequence 1.1 TAGAAATAATTTAGAACAGGCTATGATTACTTTTAATACACCTGATAGTATAGCTCAATT
BRA1 Sequence 4 -----

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BRA2 sequence 3.1	TAGAAATAATTTAGAACAGGCTATGATTACTTTTAATACACCTGATAGTATAGCTCAATT
BRA1 Sequence 2	-----
BRA1	TGGAAGAAATATTTGGAGTCATATAGCAAACCTGGATTCCGGGACTAGGAGCTTCTATAAT
BRA1 Sequence 3	-----
BRA2 sequence 4.1	CGGAAAAAATATTTGGAGTCATATAGCAAACCTGGATTCCAGGACTGGGAGCTTCAATAAT
BRA1 Sequence 1	-----
BRA2 sequence 5.1	TGGAAAAAATATTTGGAGTCATATAGCAAACCTGGATTCCAGGACTGGGAGCTTCAATAAT
BRA1 Sequence 2	-----
BRA2 sequence 2.1	TGGAAAAAATATTTGGAGTCATATAGCAAACCTGGATTCCAGGACTGGGAGCTTCAATAAT
BRA2 sequence 2.2	-----
BRA2 sequence 4.2	-----
BRA2 sequence 5.2	-----
BRA2 sequence 3.2	-----
BRA2 sequence 6.2	-----
BRA1 Sequence 1	-----
BRA2 sequence 1.1	YGGAAAAAATATTTGGAGTCATATAGCAAACCTGGATTCCAGGACTGGGAGCTTCAATAAT
BRA1 Sequence 4	-----
BRA2 sequence 3.1	YGGAAAAAATATTTGGAGTCATATAGCAAACCTGGATTCCAGGACTGGGAGCTTCAATAAT
BRA1 Sequence 2	-----
BRA1	AAAAATATATAATAATGTTGTTATTGTGTTATGTGGTACTAACCTCTTCACCTAAGATCCT
BRA1 Sequence 3	-----
BRA2 sequence 4.1	AAAAATATATAGTAATGCTATTATTGTGTTATGTGGTACTAACCTCTTCACCTAAGATCCC
BRA1 Sequence 1	-----
BRA2 sequence 5.1	AAAAATATATAGTAATGCTATTATTGTGTTATGTGGTACTAACCTCTTCACCTAAGATCCT
BRA1 Sequence 2	-----
BRA2 sequence 2.1	AAAAATATATAGTAATGCTATTATTGTGTTATGTGGTACTAACCTCTTCACCTAAGATCCT
BRA2 sequence 2.2	-----
BRA2 sequence 4.2	-----
BRA2 sequence 5.2	-----
BRA2 sequence 3.2	-----
BRA2 sequence 6.2	-----
BRA1 Sequence 1	-----
BRA2 sequence 1.1	AAAAATATATAGTAATGCTATTATTGTGTTATGTGGTACTAACCTCTTCACCTAAGATCCT
BRA1 Sequence 4	-----
BRA2 sequence 3.1	AAAAATATATAGTAATGCTATTATTGTGTTATGTGGTACTAACCTCTTCACCTAAGATCCT
BRA1 Sequence 2	-----
BRA1	CAGAAACCTCTTGAGAATGATGAGTGGTGCAGGATCCTCCGTCAATCGCTACCTGAAGAG
BRA1 Sequence 3	-----
BRA2 sequence 4.1	CAGAAACCTCTTGACAACGATGAGTGGTGCAGGATCCTCCGTCAATCACTTCCTGAAGAA
BRA1 Sequence 1	-----
BRA2 sequence 5.1	CAGAAACCTCTTGACAACGATGAGTGGTGCAGGATCCTCCGTCAATCACTTCCTGAAGAA
BRA1 Sequence 2	-----
BRA2 sequence 2.1	CAGAAACCTCTTGACAACGATGAGTGGTGCAGGATCCTCCGTCAATCACTTCCTGAAGAA
BRA2 sequence 2.2	-----
BRA2 sequence 4.2	-----
BRA2 sequence 5.2	-----
BRA2 sequence 3.2	-----
BRA2 sequence 6.2	-----
BRA1 Sequence 1	-----
BRA2 sequence 1.1	CAGAAACCTCTTGACAACGATGAGTGGTGCAGGATCCTCCGTCAATCACTTCCTGAAGAA
BRA1 Sequence 4	-----
BRA2 sequence 3.1	CAGAAACCTCTTGACAACGATGAGTGGTGCAGGATCCTCCGTCAATCACTTCCTGAAGAA
BRA1 Sequence 2	-----
BRA1	ACAACACCATCAGAAACATGCATGGAAAGAAGATGCCTGGGACCAGGACCAGTACAGAAT
BRA1 Sequence 3	-----
BRA2 sequence 4.1	GAAACACCATCAGAAACATGCATGGAAAGAAGATCCTGGGACCAGGACCAGTACAGTGT
BRA1 Sequence 1	-----
BRA2 sequence 5.1	GAAACACCATCAGAAACATGCATGGAAAGAAGATCCTGGGACCAGGACCAGTACAGTGT
BRA1 Sequence 2	-----
BRA2 sequence 2.1	GAAACACCATCAGAAACATGCATGGAAAGAAGATCCTGGGACCAGGACCAGTACAGTGT
BRA2 sequence 2.2	-----
BRA2 sequence 4.2	-----
BRA2 sequence 5.2	-----
BRA2 sequence 3.2	-----
BRA2 sequence 6.2	-----
BRA1 Sequence 1	-----
BRA2 sequence 1.1	GAAACACCATCAGAAACATGCATGGAAAGAAGATCCTGGGACCAGGACCAGTACAGTGT
BRA1 Sequence 4	-----
BRA2 sequence 3.1	GAAACACCATCAGAAACATGCATGGAAAGAAGATCCTGGGACCAGGACCAGTACAGTGT
BRA1 Sequence 2	-----

BRA1 ACACCTAGCAGACGCGACCGGTGGCTCAGAGGACAAATACAACAAGCCGAAATGCTCCAA
 BRA1 Sequence 3 -----
 BRA2 sequence 4.1 ACACCTAGCAGGCGTAACCGGTGGATTAGAGGACAAATACAACAAGCTGAAATACTCCAA
 BRA1 Sequence 1 -----
 BRA2 sequence 5.1 ACACCTAGCAGGCGTAACCGGTGGATTAGAGGACAAATACAACAAGCTGAAATACTCCAA
 BRA1 Sequence 2 -----
 BRA2 sequence 2.1 ACACCTAGCAGGCGTAACCGGTGGATTAGAGGACAAATACAACAAGCTGAAATACTCCAA
 BRA2 sequence 2.2 -----
 BRA2 sequence 4.2 -----
 BRA2 sequence 5.2 -----
 BRA2 sequence 3.2 -----
 BRA2 sequence 6.2 -----
 BRA1 Sequence 1 -----
 BRA2 sequence 1.1 ACACCTAGCAGGCGTAACCGGTGGATTAGAGGACAAATACAACAAGCTGAAATACTCCAA
 BRA1 Sequence 4 -----
 BRA2 sequence 3.1 ACACCTAGCAGGCGTAACCGGTGGATTAGAGGACAAATACAACAAGCTGAAATACTCCAA
 BRA1 Sequence 2 -----

BRA1 GAGAAATTACARTGGCGGATTAAGGGGTTCAACAGACAGCCAAAGAATTGGAAGAACTC
 BRA1 Sequence 3 -----
 BRA2 sequence 4.1 GAGAAATTACAATGGCGGATCAAAGGAGTTCAACAAACGGCCCAAGAGCTGGGAGACCTT
 BRA1 Sequence 1 -----
 BRA2 sequence 5.1 GAGAAATTACAATGGCGGATCAAAGGAGTTCAACAAACGGCCCAAGAGCTGGGAGACCTT
 BRA1 Sequence 2 -----
 BRA2 sequence 2.1 GAGAAATTACAATGGCGGATCAAAGGAGTTCAACAAACGGCCCAAGAGCTGGGAGACCTT
 BRA2 sequence 2.2 -----
 BRA2 sequence 4.2 -----
 BRA2 sequence 5.2 -----
 BRA2 sequence 3.2 -----
 BRA2 sequence 6.2 -----
 BRA1 Sequence 1 -----
 BRA2 sequence 1.1 GAGAAATTACAATGGCGGATCAAAGGAGTTCAACAAACGGCCCAAGAGCTGGGAGACCTT
 BRA1 Sequence 4 -----
 BRA2 sequence 3.1 GAGAAATTACAATGGCGGATCAAAGGAGTTCAACAAACGGCCCAAGAGCTGGGAGACCTT
 BRA1 Sequence 2 -----

BRA1 AACAGAAAGATCAGAAGTGAAGTCTGACTGGACTAGGAGAACACATGGAGACTTCTCATCT
 BRA1 Sequence 3 -----
 BRA2 sequence 4.1 AATAGACGCATCAGGAAAGAACTCGACTGGACCCGGGCCAGCATGGGGATTACTCTTCC
 BRA1 Sequence 1 -----
 BRA2 sequence 5.1 AATAGACGCATCAGGAAAGAACTCGACTGGACCCGGGCCAGCATGGGGATTACTCTTCC
 BRA1 Sequence 2 -----
 BRA2 sequence 2.1 AATAGACGCATCAGGAAAGAACTCGACTGGACCCGGGCCAGCATGGGGATTACTCTTCC
 BRA2 sequence 2.2 -----
 BRA2 sequence 4.2 -----
 BRA2 sequence 5.2 -----
 BRA2 sequence 3.2 -----
 BRA2 sequence 6.2 -----
 BRA1 Sequence 1 -----
 BRA2 sequence 1.1 AATAGACGCATCAGGAAAGAACTCGACTGGACCCGGGCCAGCATGGGGATTACTCTTCC
 BRA1 Sequence 4 -----
 BRA2 sequence 3.1 AATAGACGCATCAGGAAAGAACTCGACTGGACCCGGGCCAGCATGGGGATTACTCTTCC
 BRA1 Sequence 2 -----

BRA1 TTCCATAGCTATCGCCGAGAACA---GCGTCTCTGGGGACAATGCTCAGAGAACGTCTAC
 BRA1 Sequence 3 -----
 BRA2 sequence 4.1 TTCGATGGCTATCGGCGAGACCAAGAGCGTCGCTGGGGACAATGCCCAACAAGCATCGGC
 BRA1 Sequence 1 -----
 BRA2 sequence 5.1 TTCGATGGCTATCGGCGAGACCAAGAGCGTCGCTGGGGACAATGCCCAACAAGCATCGGC
 BRA1 Sequence 2 -----
 BRA2 sequence 2.1 TTCGATGGCTATCGGCGAGACCAAGAGCGTCGCTGGGGACAATGCCCAACAAGCATCGGC
 BRA2 sequence 2.2 -----
 BRA2 sequence 4.2 -----
 BRA2 sequence 5.2 -----
 BRA2 sequence 3.2 -----
 BRA2 sequence 6.2 -----
 BRA1 Sequence 1 -----
 BRA2 sequence 1.1 TTCGATGGCTATCGGCGAGACCAAGAGCGTCGCTGGGGACAATGCCCAACAAGCATCGGC
 BRA1 Sequence 4 -----
 BRA2 sequence 3.1 TTCGATGGCTATCGGCGAGACCAAGAGCGTCGCTGGGGACAATGCCCAACAAGCATCGGC
 BRA1 Sequence 2 -----

BRA1 AAGTCTGAAGATCCAAAGCGAAGGAGGAAACATCTATGACTGTTGCATCAAAGCCCAAGA
 BRA1 Sequence 3 -----
 BRA2 sequence 4.1 AAACCTGGAGATTCCAAGCGAAGGAGGAAACATCTATGACTGTTGCATTAAGCTCAGGA

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BRA1 Sequence 1 -----
BRA2 sequence 5.1 AAACCTGGAGATTCGAAGCGAAGGAGGAAACATCTATGACTGTTGCATTAAGCTCAGGA
BRA1 Sequence 2 -----
BRA2 sequence 2.1 AAACCTGGAGATTCGAAGCGAAGGAGGAAACATCTATGACTGTTGCATTAAGCTCAGGA
BRA2 sequence 2.2 -----
BRA2 sequence 4.2 -----
BRA2 sequence 5.2 -----
BRA2 sequence 3.2 -----
BRA2 sequence 6.2 -----
BRA1 Sequence 1 -----
BRA2 sequence 1.1 AAACCTGGAGATTCGAAGCGAAGGAGGAAACATCTATGACTGTTGCATTAAGCTCAGGA
BRA1 Sequence 4 -----
BRA2 sequence 3.1 AAACCTGGAGATTCGAAGCGAAGGAGGAAACATCTATGACTGTTGCATTAAGCTCAGGA
BRA1 Sequence 2 -----

BRA1 GGGGACTCTTGCTATTCCTTGCTGCGGGTTCCCACTATGGCTATTCTGGGGACTCATAAT
BRA1 Sequence 3 -----
BRA2 sequence 4.1 GGGGACTCTTGCTATTCCTTGCTGTTGGGTTTCCACTGTGGTTATTCTGGGGATTTGTGAT
BRA1 Sequence 1 -----
BRA2 sequence 5.1 GGGGACTCTTGCTATTCCTTGCTGTTGGGTTTCCACTGTGGTTATTCTGGGGATTTGTGAT
BRA1 Sequence 2 -----
BRA2 sequence 2.1 GGGGACTCTTGCTATTCCTTGCTGTTGGGTTTCCACTGTGGTTATTCTGGGGATTTGTGAT
BRA2 sequence 2.2 -----
BRA2 sequence 4.2 -----
BRA2 sequence 5.2 -----
BRA2 sequence 3.2 -----
BRA2 sequence 6.2 -----
BRA1 Sequence 1 -----
BRA2 sequence 1.1 GGGGACTCTTGCTATTCCTTGCTGTTGGGTTTCCACTGTGGTTATTCTGGGGATTTGTGAT
BRA1 Sequence 4 -----
BRA2 sequence 3.1 GGGGACTCTTGCTATTCCTTGCT-----
BRA1 Sequence 2 -----

BRA1 CATAATGGGACGTTTGTTCGGCTATGGGTTGCGAGGGATTGCTATGATACTGTCCTATTG
BRA1 Sequence 3 -----
BRA2 sequence 4.1 CATAATAGGGCGATTATTAGGCTATGGACTGCGAGGCGTTGCTATGATACTGCTCTATTG
BRA1 Sequence 1 -----
BRA2 sequence 5.1 CATAATAGGGCGATTATTAGGCTATGGACTGCG-----
BRA1 Sequence 2 -----
BRA2 sequence 2.1 CATAATAGGGCGATTATTAGGCTATGGACTGCGAGGC-----
BRA2 sequence 2.2 -----
BRA2 sequence 4.2 -----
BRA2 sequence 5.2 -----
BRA2 sequence 3.2 -----
BRA2 sequence 6.2 -----
BRA1 Sequence 1 -----
BRA2 sequence 1.1 CATAATAGGGCGATTATTAGGCTATGGACTGCGRGGCRTYGCTATGATACTGYTCTATTG
BRA1 Sequence 4 -----
BRA2 sequence 3.1 -----
BRA1 Sequence 2 -----

BRA1 TGAAAAAGGATTGACTATGCTATTTATAATGCTAAA
BRA1 Sequence 3 -----
BRA2 sequence 4.1 TGGGAAAGGATTAACATATGCTGTTTATTATGTAAAA
BRA1 Sequence 1 -----
BRA2 sequence 5.1 -----
BRA1 Sequence 2 -----
BRA2 sequence 2.1 -----
BRA2 sequence 2.2 -----
BRA2 sequence 4.2 -----
BRA2 sequence 5.2 -----
BRA2 sequence 3.2 -----
BRA2 sequence 6.2 -----
BRA1 Sequence 1 -----
BRA2 sequence 1.1 TGGGAAAGGATTAACATATGCTGTTTATTA-----
BRA1 Sequence 4 -----
BRA2 sequence 3.1 -----
BRA1 Sequence 2 -----

```

Supplementary Figure S2: Alignment of nucleotide sequences in EIAV LTR using MUSCLE. U3 is in black, R in red, and U5 in blue. Methylated DNA-binding protein site (MDBP) is in the red box, PEA1/AP-1 site in pink, transactivation response element (TAR) is in the green box, initiation site of transcription is in gray, and PU.1 binding sites is in yellow.

BRA1	TGTGGGGTTAATAT-AAAATGGCTGTAGAAAAGAAAGTTGCTGATGATTATAAGTA-----AATATGCTGA
BRA2G.....A.A.....G.....
LiaoningA.....C...G...TCT.A.....AG.....GT.....
KY411969A.....G...TCT.A.....AG.....GT.....
KY411970A.....G...TCT.A.....AG.....GT.....
KY411971A.....G...TCT.A.....AG.....GT.....
KY411972A.....G...TCT.A.....AG.....GT.....
KY411973A.....G...TCT.A.....AG.....GT.....
KY411974A.....G...TCT.A.....AG.....GT.....
KY411975A.....G...TCT.A.....AG.....GT.....
KY411976A.....G...TCT.A.....AG.....GT.....
KY412097A.....G...TCT.A.....AG.....GT.....
KY412098A.....G...TCT.A.....AG.....GT.....
DLV9-7A.....G...TCT.A.....AG...A...G.AAGTTGCTGATGCTCTC...GT.....
DV10-3A.....G...TCT.A.....AG...A...G.....GT.....
IRE_F2A.....-----ATAA.G-----AG.AC...G...AA.GA-----CT.....
IRE_F3A.....-----ATAA.G-----AG.AC...G...AA.GA-----CT.....
IRE_F4A.....-----ATAA.G-----AG.AC...G...AA.GA-----CT.....
IRE_H3A.....-----ATAA.G-----AG.AC...G...AA.GA-----CT.....
WyomingTT...G.GGGGTTT.A.....A.....AGTAAAAAG-----A...GT.....
MiyazakiA.A.....-----A.....TG.AT...G...TA-----AC.....
BRA1	TGCTCT-CATAACCGCGTGAACCTAGAAG-CTA-GCTCATGTTGCTAGGCAACTAAACTGTAATAACCT-GTTAGTTC
BRA2-.....-.....A.....-.....A.A.A.....A.....-.....
Liaoning-.....TTA.....C.A.A.....-.....C.....G.....-.....T.....
KY411969-.....TTA.....C.A.A.....-.....C.....-.....T.....
KY411970-.....TTA.....C.A.A.....-.....C.....-.....T.....
KY411971-.....TTA.....C.A.A.....-.....C.....-.....T.....
KY411972-.....TTA.....C.A.A.....-.....C.....-.....T.....
KY411973-.....TTA.....C.A.A.....-.....C.....-.....T.....
KY411974-.....TTA.....C.A.A.....-.....C.....-.....T.....
KY411975-.....TTA.....C.A.A.....-.....C.....-.....T.....
KY411976-.....TTA.....C.A.A.....-.....C.C.....-.....T.....
KY412097-.....TTA.....C.A.A.....-.....C.C.....G.....-.....T.....
KY412098-.....TTA.....C.A.A.....-.....C.C.....CG.C.....-.....T.....
DLV9-7-.....TTA.....-----A.....-.....C.....G.....G.....-.....T.....
DV10-3-.....TTA.....C.A.G.A.....-.....C.....G.....-.....T.....
IRE_F2-T.....T.A.....A.....G.....G.....A.G.....-.....A.....
IRE_F3-T.....T.A.....A.....G.....G.....A.....-.....A.....
IRE_F4-T.....T.A.....A.....G.....G.....A.G.....-.....A.....
IRE_H3-T.....T.A.....A.....G.....G.....A.G.....-.....A.....
Wyoming-.....TT...A.....C.A.G.A.....-.....C.C.....GCA...T...GA
MiyazakiA.....TT...A.....C.T.TAA...G...AGGC.....A.....G...AAT.....-A.....
BRA1	TCATTATTGT-----TCCTGTTTTTACACATATATAAGTACATGTAT
BRA2-----G.....G.....G.....
LiaoningA.....-----TCCGCTTTTGTGACGCGTTAAGT.....G.....T.....
KY411969A.....-----TCCGCTTTTGTGACGCGTTAAGT.....G.....G.T.....
KY411970A.....-----TCCGCTTTTGTGACGCGTTAAGT.....G...C.....G.T.....
KY411971A.....-----TCCGCTTTTGTGACGCGTTAAGT.....G.....G.T.....
KY411972A.....-----TCCGCTTTTGTGACGCGTTAAGT.....G.....G.T.....
KY411973A.....-----TCCGCTTTTGTGACGCGTTAAGT.....G.....G.T.....
KY411974A.....-----TCCGCTTTTGTGACGCGTTAAGT.....G.....G.T.....
KY411975A.....-----TCCGCTTTTGTGACGCGTTAAGT.....G.....G.T.....
KY411976A.....-----TCCGCTTTTGTGACGCGTTAAGT.....G.....G.T.....
KY412097A.....-----TCCGCTTTTGTGACGCGTTAAGT.....G.....T.....
KY412098A.....-----TCCGCTTTTGTGACGCGTTAAGT.....G.....T.....
DLV9-7A...TCCGCTTTTGTATAGTTCCGCTTTTGTGACGCGTTAAGT.....G.....G.T.....
DV10-3A.....-----TCCGCTTTTGTGACGCGTTAAGT.....G.....G.T.....
IRE_F2A.....-----TCCGCTTTTGTGACGCGTTAAGT...CAAA...A.....C.T.....
IRE_F3A.....-----TCCGCTTTTGTGACGCGTTAAGT...CAAA...A.....C.T.....
IRE_F4A.....-----TCCGCTTTTGTGACGCGTTAAGT...CAAA...A.....C.T.....
IRE_H3A.....-----TCCGCTTTTGTGACGCGTTAAGT...CAAA...A.....C.T.....
Wyoming	G.G---A.....-----TCCCATTTGGTACGCGTTAAGT.....G.....G.T.....
Miyazaki	CT...TAA.....-----TCCGCTTTTGTGACGCGTTAAGT...A.....A.....G.T.A.....

```

BRA1      TCTGATAACAAGACACTCAGATTCTGCGGTCTGAGTCCCTTCTCTGCTGGGCCTAATA--AGCCTTGA-AATAA--ATAT
BRA2      .T..T.....C.--.A.G.....
Liaoning  ....C.TTTG.....T-.CTCT.....GT.....
KY411969  ....C.TTTG.....T-G.CTCT.....GT.....
KY411970  ....C.TTTG.....T-G.CTCT.....GT.....
KY411971  ....C.TTTG.....T-G.CTCT.....GT.....
KY411972  ....C.TTTG.....T-G.CTCT.....GT.....
KY411973  ....C.TTTG.....T-G.CCCT.....GT.....
KY411974  ....C.TTTG.....T-G.CTCT.....GT.....
KY411975  ....C.TTTG.....T-G.CTCT.....GT.....
KY411976  ....C.TTTG.....T-G.CTCT.....GT.....
KY412097  ....C.TTTG.....T-.CTCT.....GT.....
KY412098  ....C.TTTG.....T-.CTCT.....GT.....
DLV9-7    ....C.TTTG..T.G.....TA..CTCT.....GT.....
DV10-3    ....C.TTTG.....TA..CTCT.....GT.....
IRE_F2    ....C.CTGG.....TA..A---.....CTT.....
IRE_F3    ....C.CTGG.....TA..A---.....CTT.....
IRE_F4    ....C.CTGG.....TA..A---.....CTT.....
IRE_H3    ....C.CTGG.....TA..A---.....CTT.....
Wyoming   ....C..TTG..G.....TG..A--G.....TGT.....
Miyazaki  ....TC.TTTG..G.....TA.....C.....AT.....

```

```

BRA1      AATTCTCTA-CTCAGTCCCTTGCTCAACTTGT--TGGTTTTAA-GATCCTACA
BRA2      .....GA.....A.....-T..A.....-.....
Liaoning  .....G-.....GT...T.GTC..CT..T..C..-..G..TA...
KY411969  .....G-T.....GT...T.GT...CT..T..C..-...TA...
KY411970  .....G-T.....GT...T.GT...CT..T..C..-...TA...
KY411971  .....G-T.....GT...T.GT...CT..T..C..-...TA...
KY411972  .....G-T.....GT...T.GT...CT..T..C..-...TA...
KY411973  .....G-T.....GT...T.GT...CT..T..C..-...TA...
KY411974  .....G-T.....GT...T.GT...CT..T..C..-...TA...
KY411975  .....G-T.....GT...T.GT...CT..T..C..-...TA...
KY411976  .....G-T.....GT...T.GT...CT..T..C..-...TA...
KY412097  .....CG-.....GT...T.GTC..CT..T..C..-...TA...
KY412098  .....G-.....GT...T.GTC..CT..T..C..-...TA...
DLV9-7    .....G-..A.....GT...T.GT...CT..T..C..-...TA...
DV10-3    .....G-..A.....GT...T.GT...CT..T..C..-...TA...
IRE_F2    .....-.....T...GTGT.....A.CTCTTGG.....-.....
IRE_F3    .....-.....T...GTGT.....A.CTCTTGG.....-.....
IRE_F4    .....-.....T...GTGT.....A.CTCTTGG.....-.....
IRE_H3    .....-.....T...GTGT.....A.CTCTTGG.....-.....
Wyoming   .....-.....GTCTCT.GT...C--TG..CG..-.....
Miyazaki  .....G-T.....GTGT.....TT..C..AC.GCA.C..A...

```

Supplementary Figure S3: Alignment of EIAV gag polyprotein. The proteins p15, p26, p11 and p9 are separated by blue arrows. Amino acid variations between BRA1 and BRA2 are in yellow. A leucine-rich-type nuclear export signal is in the green box (p15), major homology region is in the red box (p26), two zinc binding domains are in the blue boxes (p11), and YPDL late domain is in the orange box (p9).

BRA1 MGDPV TWSKAL LKKLEKVTV SSGS QKLN SGNCN WALSLVDLY HDTN YL KEKDWQLRN V I P L L E D V T Q T L S G Q
 BRA2 L T T E F T D S L
 DLV9-7_HM141922 S L Q T N F F C D V S
 DV10-3_HM141910 S L Q T N F F C D S
 IRE_F2_JX480631 Q K A S L L F S D I L S T
 IRE_F3_JX480632 Q K A S L L F S D I L S T
 IRE_F4_JX480633 Q K A S L L F S D I L S T
 IRE_H3_JX480634 Q K A S L L F S D I L S T
 ITA_DE_KM247554 Q K A S L L F S D I L S T
 ITA_SA_KM247555 Q K A S L L F S D I L S T
 Liaoning_AF327877 -----
 Miyazaki_JX003263 S L N Q Q P F F M K D A E P
 Wyoming_AF033820 L Q T T F F V D P

BRA1 E R E A F E K T W W A I S A V K M G M Q I N N V A D G K A S F Q L L K A K Y D K R D - - T G K K Q P E P P E E F P I M I D G A G N R N F R P
 BRA2 L A G V E K A R Y
 DLV9-7_HM141922 A L T . N . A . T T . S I F E R K T V N . T S . M . Y
 DV10-3_HM141910 A L T . N . A . T . T I F E R K T A N . T S . E . Y
 IRE_F2_JX480631 K V K . L . G H . G . R . T Y E R A P - - S K . Q H . . Q . Y
 IRE_F3_JX480632 K V K . L . G H . G . R . T Y E R A P - - S K . Q H . . Q . Y
 IRE_F4_JX480633 K V K . L . G H . G . R . T Y E R A P - - S K . Q H . . Q . Y
 IRE_H3_JX480634 K R V K . L . G H . G . R . T Y E R A P - - S K . Q H . . T Q . Y
 ITA_DE_KM247554 K V K . L . G H . G . R . T Y E R A P - - S K . Q H . . Q . Y
 ITA_SA_KM247555 K V K . L . G H . G . R . T Y E R A P - - S K . Q H . . Q . Y
 Liaoning_AF327877 ----- . L . . T . N . A . T . T I . . . F E R K T A N . T . . . S . M . Y
 Miyazaki_JX003263 K R T . I M . . . H . . . T G . G A - - . . . T N . Q . A Y . . . I T . G . . T . . .
 Wyoming_AF033820 R L V R E . K T - - A N . . . S . S . Y

p15 ← → p26

BRA1 L T P R G Y T T W V N T I Q Q N L L N E A S V N L F G I L S V D C T S E E M N A F L D V V P G Q A G Q K Q V L L D L L D K M A E D W D N R
 BRA2 I
 DLV9-7_HM141922 N V E R
 DV10-3_HM141910 N I E R
 IRE_F2_JX480631 I Q A
 IRE_F3_JX480632 E I Q A
 IRE_F4_JX480633 I Q A
 IRE_H3_JX480634 I Q A
 ITA_DE_KM247554 E I Q A
 ITA_SA_KM247555 E I Q A
 Liaoning_AF327877 N I E R
 Miyazaki_JX003263 S T I N E I E R
 Wyoming_AF033820 T G Q I A I I D

BRA1 H P L P N P P L V A P A Q G P I P M T A R F I R G L G V P R E R Q M E P A F D Q F R Q T Y R Q W I E A M T E G I K I M I G K P K A Q N I R
 BRA2 M
 DLV9-7_HM141922 M P M
 DV10-3_HM141910 M P M
 IRE_F2_JX480631 A . M . . . P
 IRE_F3_JX480632 A . M . . . P
 IRE_F4_JX480633 A . M . . . P
 IRE_H3_JX480634 A . M . . . P
 ITA_DE_KM247554 A . M . . . P
 ITA_SA_KM247555 A . M . . . P
 Liaoning_AF327877 M P
 Miyazaki_JX003263 N . I . . . M . . . P
 Wyoming_AF033820 A P S V

```

BRA1 QGPKEPYPEFVDRLLSQIKSEGHPSSEITKFLTDTLTIQNANEECRNAMRHLRPEDSLEEKLYACRDIGTV
BRA2 .....T.....K.....T.....T
DLV9-7_HM141922 .....I.....AD.....D.K.....T...M.....M
DV10-3_HM141910 .....AD.....D.K.....T...M.....
IRE_F2_JX480631 .....D.....V.....KA.....T.....T
IRE_F3_JX480632 .....D.....V.....KA.....T.....T
IRE_F4_JX480633 .....D.....V.....KA.....T.....T
IRE_H3_JX480634 .....D.....V.....KA.....T.....T
ITA_DE_KM247554 .....D.....V.....KA.....T.....T
ITA_SA_KM247555 .....D.....V.....KA.....T.....T
Liaoning_AF327877 .....AD.....D.KS.....T...M.....M
Miyazaki_JX003263 .....D.....SPD.....H.....S.....T...M.....V.SQ
Wyoming_AF033820 ..A.....Q..S.....T...M.....T

```

p26 ← → p11

```

BRA1 KQKMLLLAKALQTGLAGPMKGGTMRGGPLKAKQTCYNCGKPGHLSQCRAPKVCFKCKEPGHFSKQCRAP
BRA2 .....M.F.....A.S.....I.IK.....PR.....K.L
DLV9-7_HM141922 .....A.....IFK.....G.....F.....K.....I.....R.....Q.....NA
DV10-3_HM141910 .....A.....IFK.....S.G.....F.....K.....Q.....NA
IRE_F2_JX480631 .....M...R...S...S...ICK...P.....Q.....NA
IRE_F3_JX480632 .....M...R...S...S...ICK...P.....Q.....NA
IRE_F4_JX480633 .....M...R...S...S...ICK...P.....Q.....NA
IRE_H3_JX480634 .....M...R...S...T...ICK...S.....Q.....NA
ITA_DE_KM247554 .....M...R...S...S...ICK...P.....Q.....NA
ITA_SA_KM247555 .....M...R...S...S...ICK...S...P.....Q.....NA
Liaoning_AF327877 .....A.....IFK.....G.....F.....K.....Q.....NA
Miyazaki_JX003263 R..A.....V...A.VLK.....KQN
Wyoming_AF033820 .....M.....F...ALK.....A.....Q.....SV

```

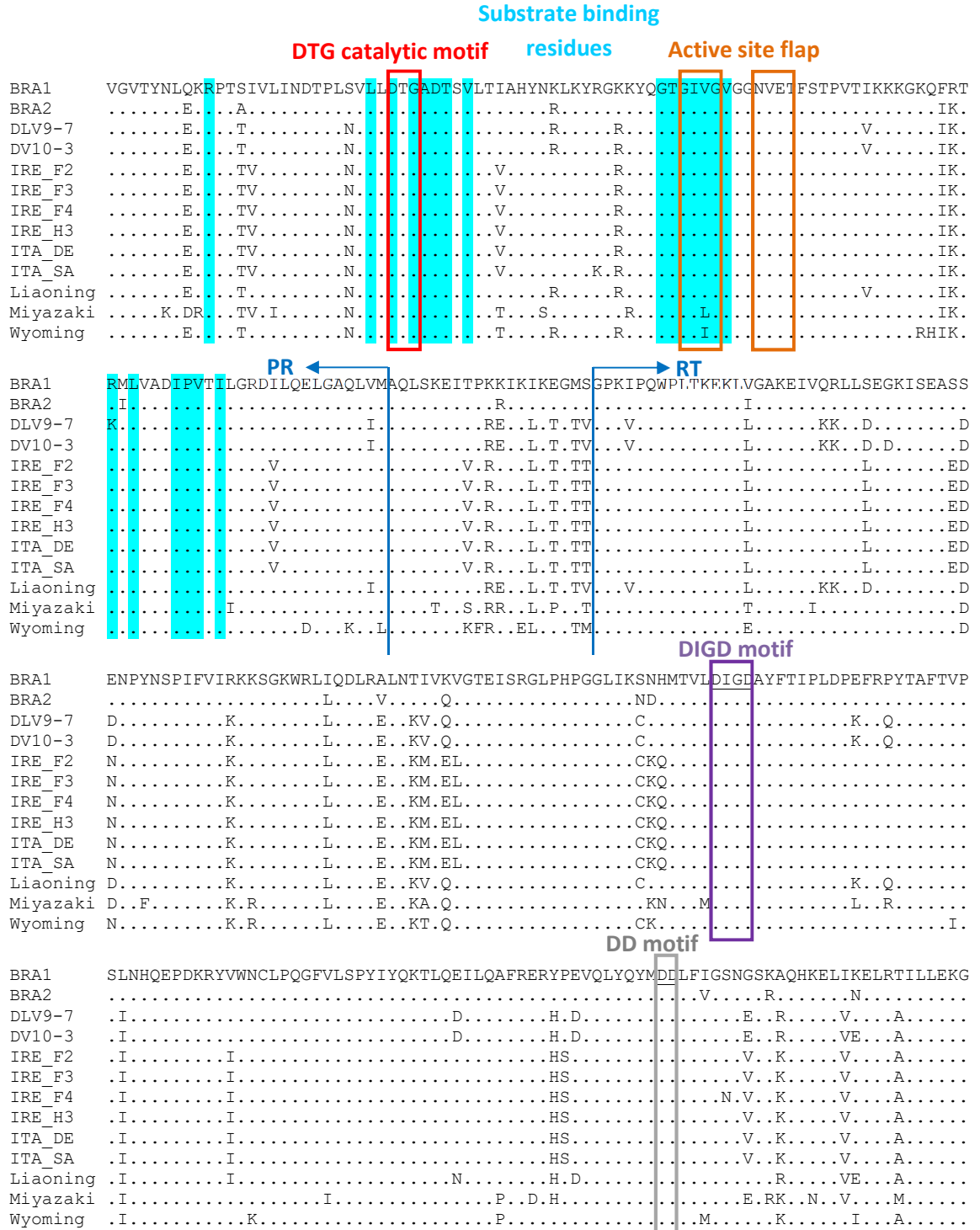
p11 ← → p9

```

BRA1 PKNGKKGAGRPOKQTFPVQSSSAENKQRNTVE-TQNLYPDLTQMKEEYQIETKVPQDPEDLNLSSLWE
BRA2 .....Q.....HE.KSN.GER.Q.....D.....GKEA
DLV9-7_HM141922 .....Q.....K-G.MDKT.MEEKQ-QGT.....S.....K.KEE--ENQ.....D...G
DV10-3_HM141910 .....Q.....K-G.MNKT.-EEKQ-QGT.....S.....K.KEE--ENQ.....D...
IRE_F2_JX480631 .....Q.....I..KGQMTQ.GGPKE-S.G.....KL.K.SQEEV.....N...
IRE_F3_JX480632 .....Q.....I..KGQMTQ.GGPKE-S.G.....KL.K.SQEEV.....N...
IRE_F4_JX480633 .....Q.....I..KGQMTQ.GGPKE-S.G.....KL.K.SQEEV.....N...
IRE_H3_JX480634 .....Q.....I..KGQMTQ.GGPKE-S.G.....KL.K.SQEEV.....N...
ITA_DE_KM247554 .....Q.....I..KGQMTQ.GGPKE-S.G.....KL.K.SQEEV.....N...
ITA_SA_KM247555 .....Q.....I..KGQMTQ.GGPKE-S.G.....KL.K.SQEEV.....N...
Liaoning_AF327877 .....Q.....K-E.MNKT.KEEKQ-QGT.....S.....K.KEE--ENQ.....D...
Miyazaki_JX003263 .....N.....H.K...H.-QETA.PAKTAT.-.S.....S.....D.K.K.--EEV.....D...G
Wyoming_AF033820 .....Q.....I..K.QHNKSVVQET.Q.....SEI.K..NVKE.--DQV.....D...

```


Supplementary Figure S4: Alignment of EIAV pol polyprotein. In PR, the catalytic motif DTG is in the red box, substrate-binding sites are in cyan and active sites flap are in the box orange. In RT, DIGD motif is in the purple box and DD motif is in the gray box. In RNase H, invariant residues are in cyan and the glycine-rich motif is in the dark green box. In DU, the conserved motifs MI-MV are in the dark blue boxes, with the conserved residue D72 in MIII in cyan. In IN, the zinc finger-binding motif (H12, H16, C40, C43) are in green, hydrophobic core residues (I5, A8, L22, A33 and I36) are in pink, and central catalytic core residues (D64, D116 and E152) are in blue.



RT ←

```

BRA1  FETPDDKVKQEEAPYNWLGYYQIKPSSWKVQKMQLEMVQEPFLNDVQKLMGNITWMSSGVPGLTVKQIAATTGKCLDLNQKV
BRA2  .....L.T.....
DLV9-7  ...E.L.....S.GN.....L.K.....
DV10-3  ...E.L.....S.GN.....L.K.....
IRE_F2  .....L.P.....C.DN.....L.K.....
IRE_F3  .....L.P.....C.DN.....L.K.....
IRE_F4  .....L.P.....C.DN.....L.K.....
IRE_H3  .....L.P.....C.DN.....L.K.....
ITA_DE  .....L.P.....C.DN.....L.K.....
ITA_SA  .....L.P.....C.DN.....L.K.....
Liaoning  ...E.L.....S.GN.....L.K.....
Miyazaki  ...EE.L.D...G...F.NN.MPTV...LAK.....I.I.....H.....E..
Wyoming  .....L.VP..S.....C.EN.....D..KN.....I.....H.....E.....

```

```

BRA1  TWTEEAQKELEENNEKIRNAOGLQYYDPKKEEICEIELTKNYEAIYMIKQFQGIWAGKKIMKANKGWSAAKNMLLLQH
BRA2  V.....R.....K.....L.....H.....R.....
DLV9-7  V.....K.QE.....N.E.V.....I.....T.I...S.....R.....
DV10-3  V.....K.QE.....N.E.V.....I.....T.I...S.....R.....
IRE_F2  I..K..I.....K...H.N.E.T...I.....IVR.S.K.....R.....T.....
IRE_F3  I..K..I.....K...H.N.E.T...I.....IVR.S.K.....R.....VV.....
IRE_F4  I..K..I.....K...H.N.E.T...I.....IVR.S.K.....R.....
IRE_H3  I..K..I.....K...H.N.E.T...I.....IVR.S.K.....R.....T.....
ITA_DE  I..K..I.....K...H.N.E.T...I.....IVR.S.K.....R.....
ITA_SA  I..K..I.....K...H.N.E.T...I.....IVR.S.K.....R.....
Liaoning  V.....K.QE.....N.E.V.....I.....T.I...S.....R.....
Miyazaki  N..A...Q..Q...VQK.....N.D.V...N..C.T.IV.S.....R.TV.....
Wyoming  I.....K.....N.E..ML..V.I.....T.V...S.....T.V.....

```

RN →

```

BRA1  VATESITRVGVC PKFKVPFTKEQVMWEMQKGWYYSWLPEIYSNQVVHDSWRMKLVEQPTAGITTYTDGGKKNEGIAAY
BRA2  .....Q.....
DLV9-7  ...V.I.T...K.E...DM..H...D.L...S...Q.E.V...
DV10-3  ...V.I.T...K.E...DM..H...D.KL...S...Q.E.V...
IRE_F2  .....I.....I.....A.....S..F.D.KL...S...Q.....
IRE_F3  .....I.....I.....A.....S..F.D.KL...S...Q.....
IRE_F4  .....I.....I.....A.....S..F.D.KL...S...Q.....
IRE_H3  .....I.....I.....A.....S..F.D.KL...S...Q.....
ITA_DE  .....I.....I.....A.....S..F.D.KL...S...Q.....
ITA_SA  .....I.....I.....A.....S..F.D.KL...S...Q.....
Liaoning  ...V.I.T...K.E...DMV..H...D.KL...S...Q.E.V...
Miyazaki  .....I.I.T...S..K.....S...E.KL...E.S...Q..R.V...
Wyoming  .....K..T.....V.TH...D...E.S...Q.....

```

Glycine-rich motif

```

BRA1  VTSDGKTKQRQLGLTTHQAAERIAIQMALEDIRDKQVNI V TDSYYCWKNITEGLGLEGPDSPWWP I ICNIQDKDAVYFAW
BRA2  .....PV..T..V.....K.....F.....I.....
DLV9-7  ...N...KR..PV..T...TEETL.....Q..RA.EM...
DV10-3  ...N...KR..PV..T...TEETL.....Q..RA.EM...
IRE_F2  I..K..K..KL..PV..T...SEE..I.....Q..KT.E.I...
IRE_F3  I..K..K..KL..PV..T...SEE..I.....Q..KT.E.I...
IRE_F4  I..K..K..KL..PV..T...SEE..I.....Q..KT.E.I...
IRE_H3  I..K..K..KL..PV..T...SEE..I.....Q..KT.E.I...
ITA_DE  I..K..K..KL..PV..I...SEE..I.....Q..KT.E.I...
ITA_SA  I..K..K..KL..PV..I...SEE..I.....Q..KT.E.I...
Liaoning  ...N...KR..PV..T...TEETL.....Q..RA.EM...
Miyazaki  ...T...K...PV..R..M...YN..L...Q..YN.ETI...
Wyoming  ...N.R...KR..PV..V...M...T...Q...Q..RE.EI...

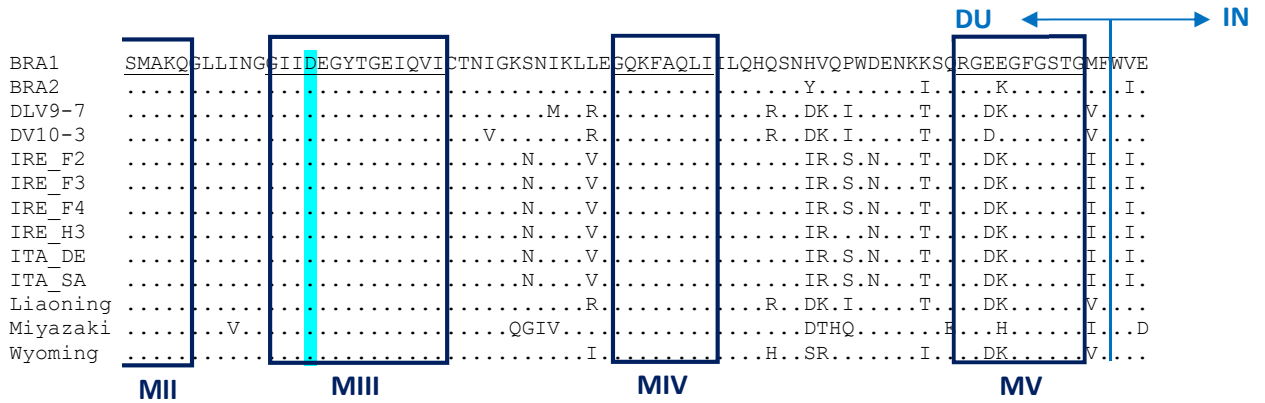
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RT ← **DU** → **MI**

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BRA1  VPGHGKIYGNQLADATKIVQEI MIAYKGTQIKEKRDEDAGFDLCIPYDMTIKVLTKIISTDVRIQVPPNSFGWVTGKS
BRA2  .....A.....L.....P.....K.....
DLV9-7  ...E..TE..L.Q.....II.P.S...V.Y...K...QKC...
DV10-3  ...E..TE..L.Q.....Y.....I.P.S...V.P...K...HKC...
IRE_F2  ...E..MSE..L.Q...R...H..ILHTG...P...K...QQ...
IRE_F3  ...E..MSE..L.Q...R...H..ILHTG...P...K...QQ...
IRE_F4  ...E..MSE..L.Q...R...H..ILHTG...P...K...QQ...
IRE_H3  ...E..MSE..L.Q...R...H..ILHTG...P...K...QQ...
ITA_DE  ...E..MSE..L.Q...R...H..ILHTG...P...K...QQ...
ITA_SA  ...E..MSE..L.Q...R...H..ILHTG...P...K...QQ...
Liaoning  ...E...TED..L.Q...R...II.P.S...V.P...K...HKC...
Miyazaki  ...E..TE..L.Q...RN..K...S...I.LH.S...P...K...QC...
Wyoming  ...E.A..KE..L.Q...V...IM.P.SD...P...K...

```



Hydrophobic core residues

Zinc finger binding motif

BRA1	N	IQEAQDE	ENW	TSPKII	AKRYGLPIAVAKQ	ITQEC	PH	TKQSGSPAGCVMRSPNHWAQ	D	CTHIENKVI	ILTFVESNSGY
BRA2											
DLV9-7					LT					L	R
DV10-3					LT					L	R
IRE_F2					L			V		LD	I
IRE_F3					L			V		LD	I
IRE_F4					L			V		LD	I
IRE_H3	H				L			V		LD	I
ITA_DE				H	L			V		LD	I
ITA_SA				H	L			V		LD	I
Liaoning					LT			P		L	RI
Miyazaki	D				K	LT				RL	I
Wyoming					RN	KI	LT			LD	I

Central catalytic core residues

BRA1	I	HATLLSKENALCTSLAILEWARLFS	SPRSLHT	D	NGTNFIADTVQNLRLFLKITH	TGIPYHPESQGI	I	RANRTLKEKIQ
BRA2				I		S		V
DLV9-7		V		K	V	ES	A	K
DV10-3		V		K	V	ES	A	K
IRE_F2	A			K	V	E	K	QVK
IRE_F3	A			K	V	E	K	QVK
IRE_F4	A			K	V	E	K	QVK
IRE_H3	A			K	V	E	K	QVK
ITA_DE	A			K	V	E	K	QVK
ITA_SA	A			K	V	E	K	QVK
Liaoning		V		K	V	ES	A	K
Miyazaki	P	H		V	I	K		T
Wyoming				K		V	EP	V

BRA1	S	HRDNTQTLEAALQLALITCNKGR	ESMGQTPWEVFITNQAOVI	HDELLQQA	KSSKFCFYKIPGESD	WKGP	TKVLWKG
BRA2				??	I		Q
DLV9-7	E			T	E		Q
DV10-3	E			T	E		Q
IRE_F2						I	Q
IRE_F3						I	Q
IRE_F4						I	Q
IRE_H3						I	Q
ITA_DE		E				I	Q
ITA_SA						I	Q
Liaoning	E			T	E		Q
Miyazaki	E			V		T	E
Wyoming						E	K

BRA1	D	GAVVVNDEGKGI	IAVPLTRKLLIKPH
BRA2			M
DLV9-7		E	R
DV10-3		E	R
IRE_F2		I	R
IRE_F3		I	R
IRE_F4		I	R
IRE_H3		I	R
ITA_DE		I	R
ITA_SA		I	R
Liaoning		E	R
Miyazaki		E	I
Wyoming			N

Supplementary Figure S5: Alignment of EIAV env. The surface protein and transmembrane protein were aligned using MUSCLE. Hypervariable regions are marked with colors: yellow - V1, green - V2, cyan - V3, blue - V4, orange - V5, purple - V6, dark green - V7, and red - V8. While cysteine residues are with red letters.

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BRA1      MVSIAFYGGI PGGISTPIIQ S---SEEASHT KGD-TIFKPY CSDEKSNRNK TMAEERD---
BRA2      .....V.A.V. .--P...TC. ....YNDN..KD. K...G...
DLV9-7_HM141922 .....E....T. Q--T.STDTQ ...HVMVQ...YNDSHKEE- -...A...
DV10-3_HM141910 .....V....T. Q--T.STDTQ ...HVMVQ...YNDSHKAE- -...A...
IRE_F2_JX480631 .....VQ...V. QSEP.SKGSE .R.YE..Q...Y.SSYKTK- -...G...
IRE_F3_JX480632 .....VQ...V. QSEP.SKGSE .R.YE..Q...Y.SSYKTK- -...G...
IRE_F4_JX480633 .....VQ...V. QSEP.SKGSE .R.YE..Q...Y.SSYKTK- -...G...
IRE_H3_JX480634 .....VQ...V. QSEP.SKGSE .R.YE..Q...Y.SSYKTK- -...G...
ITA_DE_KM247554 .....VQ...V. QSEP.SKGSE .R.YE..Q...Y.SSYKTE- -...G...
ITA_SA_KM247555 .....VQ...V. QSEP.SKGSE .R.YK..Q...Y.SSYKTE- -...G...
Liaoning_AF327877 .....T...T. Q--TKSTDTQ ...HVMVQ...YNDSHKAE- -...A...
Miyazaki_JX003263 .....SS E--.Q.DTD .R.GPMV.Q...YNGSNK.R- -...GKQIP
Wyoming_AF033820 .....T...Q--.KSKCE EN--.M.Q...YNND.KNS- -...SKE---

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```

BRA1      SRERREAYLK EDAEENAKKR NNDWWKIGMF MLCMLMGATGG MLWWYEDVAH PQYIGLITVG
BRA2      P.D...MN.. .P..K.R.. .....T... I....G... .R.....
DLV9-7_HM141922 T.YQE.MNQ. .EK.D.--. R.N..... L..L.T.. F....RQQ. SY...V.I.
DV10-3_HM141910 T.YQE.MNR. .K.D---. R.N..... L..L.T.. F....GQH. SH...V.I.
IRE_F2_JX480631 .YQE.MIP. .ESKGKEE.G R..... .L..A.. I....GTPD VH...VA..
IRE_F3_JX480632 .YQE.MIP. .ESKGKEE.G R..... .L..A.. I....GTPD VH...VA..
IRE_F4_JX480633 .YQE.MIP. .ESKGKEE.G R..... .L..A.. I....GAPD VH...VA..
IRE_H3_JX480634 .YQE.MIP. .ESKGKEE.G RK..... .L..A.. I....GTPD VH...VA..
ITA_DE_KM247554 .YQE.MIP. .ESKGKEE.G R..... .L..A.. I....GAPD VH...VA..
ITA_SA_KM247555 .YQE.MIP. .ESKGKEE.G R..... .L..A.. I....GAPD VH...VA..
Liaoning_AF327877 T.YQE.MNR. .EK.D.--. R.N..... L..L.T.. F....GQK. SH...V.I.
Miyazaki_JX003263 PE..E.LFQG .ELKK---E. R..... L..L.T.. F....GQE. SH...PVA..
Wyoming_AF033820 A.DQ-.MN.. .ESK.E--. R..... L..A.T.. I....GLPQ QH...VAI.

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BRA1      GKLESGMSTS AIECWGKFPFG CRPFDNYSY MTNRRIHVQN NT-VSLLESY HREITYIYKT
BRA2      ...E....T... ..T... E...T.QET. D.-AT.... N??-----
DLV9-7_HM141922 .R.N.....S... ..T... E...TVSRD. --AT..DA. Q..V.N..R.
DV10-3_HM141910 .R.N.....S... ..T... E...TVSRD. --AT..DA. Q...N..R.
IRE_F2_JX480631 .R.N.....N ..T... ..T... K...S..AD. --AT..NA.
IRE_F3_JX480632 .R.N.....N ..T... ..T... K...S..AD. --AT..NA.
IRE_F4_JX480633 .R.N.....N ..T... ..T... K...S..AD. --AT..NA.
IRE_H3_JX480634 .R.N.....N ..T... ..T...R. K...S..AD. --AT..NA.
ITA_DE_KM247554 .R.N.....N ..T... ..T... K...S..AD. --AT..NA.
ITA_SA_KM247555 .R.N.....N ..T... ..T... K...S..AD. --AT..NA.
Liaoning_AF327877 .R.N.....S... ..T... E...T.SRD. --AT..DA. Q..V.N..R.
Miyazaki_JX003263 .G.N.....SS... ..N... E..KT.NID. .AAT..QA. .K.G.L...
Wyoming_AF033820 .R.N...QSN ..S... ..Q... E...SM.MD. --AT..A. ....F...S

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BRA1      MCTDSDHCQE YECRNVQLTG NGLKVNISYN TILDTP--Y WNFKWLVCNQ TENQKAILIP
BRA2      .....? ..ER.R.N. -NFSDR..VE DNNNST--- .D.T..L... ..K.T..V.
DLV9-7_HM141922 S.V.....K .K.KQ...E- -KNSN..IM. NCSNNSCEEF .G.S..E... ..SAI...V.
DV10-3_HM141910 S.V.....K .K.KQ...K- -ENSS..IM. NCSNNSCEEF RG.S..E... ..AIT...V.
IRE_F2_JX480631 S.V.....V.QV.DM.- -DKNNTLTIS I.GNGT--D. .G.Q..E... ..A.T.VV.
IRE_F3_JX480632 S.V.....V.QV.DM.- -DKNNTLTIS I.GNGT--D. .G.Q..E... ..A.T.VV.
IRE_F4_JX480633 S.V.....V.Q.ISM.- -NKGSTLTI. I.G.GT--D. .G.Q..E... ..A.TMVV.
IRE_H3_JX480634 S.V.....V.Q.ISM.- -DNGN..II- -.GNGT--D. .G.Q..E... ..A.T.VV.
ITA_DE_KM247554 S.V.....V.QA.NM.- -DGGNTLTIS I.GNRT--D. .G.R..E... ..A.T.VV.
ITA_SA_KM247555 S.V.....V.QV.NM.- -DRGNTLTIS I.GNGT--D. .G.Q..E... ..A.T.VV.
Liaoning_AF327877 S.V.....K.KQ...R- -ENSS..IM. NCSNNSCEEF .G.S..E... ..AIT...V.
Miyazaki_JX003263 S.V.....T.QKFDADK IDNGST-TI. I.IIS.---- --NL.E..L ..KA.T.VV.
Wyoming_AF033820 S.....Q.KK.N.NS SDSSNSVRVE DVMN.A--E. .G...E... ..F.T..V.

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BRA1      EEEMVQ-NDN NTWSPRGCS TWARVKHCPA DLYGIHPIR ICVQPPFFLV KNNDGNFTNG
BRA2      ...I.Y... R..A.K..D ..K...M .....L... ..RKE.NHS---
DLV9-7_HM141922 .V..Q--SK ..I.KR.KK ..K...M .....NR.. M.....F ..QD.TSNNT-
DV10-3_HM141910 DI..QE-S.. ..I.KR..E .R.....M .....NR.. M.....F ..Q..TSNNT-
IRE_F2_JX480631 IN..RIDNS SS.V.K..E .....Q.V ..... ..DSS.DNSS
IRE_F3_JX480632 IN..RIDNS SS.V.K..E .....Q.V ..... ..DSS.DNSS
IRE_F4_JX480633 IN..I-.. SS.V.K..E .....Q.V ..... ..DSS.DNSS
IRE_H3_JX480634 IN..I-.. SS.V.K..E .....Q.V ..... ..DSS.DNSS

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ITA_DE_KM247554 IN...IDNS SS.V.K...E ...K..Q..VDSS.SNSS
 ITA_SA_KM247555 MN...IDNS SS.V.K...EQ..VDSS.GISS
 Liaoning_AF327877 .V..Q?-S.. ..I.KR..EMNR.. M.....F ..Q..TSNNT-
 Miyazaki_JX003263 .Q...NI--S ..S.Y.K.Y.E ...K....IRK.NDTN---
 Wyoming_AF033820 .N...NI..T D..I.K...ER..I ..I.....QEKGIAD.---

BRA1 NHTLSNCGPQ ISLGILDENK AVTR-EV-NC TVAKKVHFHN D-YSGQFISP IFYQCNLS-L
 BRA2 -R.....S... ..AVK-DA-S. Q.E..T.Q.S KGH..L.V. ...K.TITN.
 DLV9-7_HM141922 -GI.....L VF...ED... AIQ-NG-S. .LHRTNIERP ..F.YQV. ...I...TG.
 DV10-3_HM141910 -GI.....L VF...ED... AVQ-NG-S. .LHRTNIKRP ..F.YQV. ...I...TG.
 IRE_F2_JX480631 .S.....S .F...ED... .VT-.G-. .LHRRNINRP L-.Y..Y.V. ...K.SFN-Y
 IRE_F3_JX480632 .S.....S .F...ED... .VT-.G-. .LHRRNINRP L-.Y..Y.V. ...K.SFN-Y
 IRE_F4_JX480633 .S.....S .F...ED... .VT-KG-. .LH..NINRP L-.Y..Y.V. ...K..F.-Y
 IRE_H3_JX480634 .S.....S .F...ED... .VT-.G-. .LHRRNINRP L-.Y..Y.V. ..N..F.-Y
 ITA_DE_KM247554 .S.....S .F...ED... .VT-.G-S. LHRTSIYRS L-.Y..Y.V. ...N.SFN-Y
 ITA_SA_KM247555 .S.....S .F...ED... .VT-.G-. .LHRTNIKRP L-.Y..Y.V. ...N..F.-Y
 Liaoning_AF327877 -SI.....L VF...ED... AIQ-NG-S. .LHRTNIKRP ..F.YQV. ...I...TG.
 Miyazaki_JX003263VF..V..D. T.VK-SEEK. KIIRFNKRO ..F..Y.T. ...N.YT.N-I
 Wyoming_AF033820 -SRIG...T .F..V.ED.. G.V.GDYTA. N.RRLNINRK ..T..YQV. ...T.TFTNI

BRA1 TPCN-GTNSP VSIIRYEDT VEYLIRNIVE YLICKA---- --KNITEKN F---S...VQT
 BRA2 .R.Y-NNS.T I.....KN .Q----- .L..T---- --N.TDAG. .-----
 DLV9-7_HM141922 QS.--NG.I I...M.ESNN .Q----- .L.NT---- --S.TNST. NANV...S
 DV10-3_HM141910 QS.--NG.I I...M.ESNN .Q----- .L.NT---- --S.TNST. NANV...S
 IRE_F2_JX480631 .S.--DD.L I.V...EP.N .Q----- .L.NI---- --N.TSDT. NA---I..
 IRE_F3_JX480632 .S.--ND.L I.V.M.EP.N .Q----- .L.NINGTN NTSN.TS.I. NA---I..
 IRE_F4_JX480633 .S.D--NDPL I.V.M.EP.N .Q----- .L.NINGTN NTSN.TRNI. NA---I..
 IRE_H3_JX480634 .S.D--NDPL I.V.M.EP.N .Q----- .L.NINGTN NTSN.TSKI. NA---I..
 ITA_DE_KM247554 .S.--ND.L I.V.MHEPGN LQ----- .L.NI---- --N.TSKI. NA---I..
 ITA_SA_KM247555 .S.--ND.L I.V.M.EP.N .Q----- .L.NI---- --N.TSDI. NA---I..
 Liaoning_AF327877 QS.--NG.I I...MSENN .Q----- .L.NT---- --S.TNST. NATV...S
 Miyazaki_JX003263 SR..QKN.KS ..V.M.ESGN IQ----- .L.NVNNEN NNTNITDAIK NY--I.IA.S
 Wyoming_AF033820 .S.--NEPI I.V.M.EPNQ .Q----- .L.NN---- --N.SNNY. -----S

BRA1 FGTIGQAHIE LPRKNNKIIG NOFTQYNC SI NDKTELEKWK LVKSSGITPF PVTSRANTGL
 BRA2 ..K..... .N..R.RE .K..... .NQ...KE.. .I.G....I .I..Q....
 DLV9-7_HM141922 ..V....VARLQS PN..A...T. .N...RQ.Q ..T...L .IS.T....
 DV10-3_HM141910 ..V....VARLQS PK..AH.... .N...RQ.Q ..T...L .IS.T....
 IRE_F2_JX480631 ..I.....LR.AT PN..SH...TV .N...MQE.Q ..T...I .IS..NEK..
 IRE_F3_JX480632 ..I.....LR.TE PN..SH...TV .N...MQE.Q ..T...I .IS..NEE..
 IRE_F4_JX480633LR.AT PN..SH...TV .N...MQE.Q ..T...I .IS..NEE..
 IRE_H3_JX480634 ..I.....LR.AT PN..SH...TV .N...MQE.Q ..T...I .IS..NEK..
 ITA_DE_KM247554 ..I.....LR.AE PG..SH...TV .N...MQE.Q ..T...I .IS..SEK..
 ITA_SA_KM247555LR.AE PD..SH...TV .N...MQE.Q ..T...I .IS..NEK..
 Liaoning_AF327877 ..V....VARLQS PK..AH...T. .N...RQ.Q ..T...L .IS.T....
 Miyazaki_JX003263 ..K.....LPT.G.KQ QN..R..... .QG.MR..T ..T...L .S.SD.S..
 Wyoming_AF033820 ..V....LP..R.RN QS..N..... .N...T... ..T...L .IS.E....



BRA1 VRYKROFGIS AIVAAIVAAT AIAASATMSY IALTETNKMS DVMNHFFVVE NDTIRATEMI
 BRA2 I..... ..AS.V. NA.....E. .N..H....
 DLV9-7_HM141922 .H..... .I..... ..V..LD G.Q....E. .N..NSM.LT
 DV10-3_HM141910 .H..... .I..... ..V..LD S.Q....E. .N..NSM.L.
 IRE_F2_JX480631 .H.....LT..... ..AS.IQ ..V..LN.. .N..LS....
 IRE_F3_JX480632 I.H.....LT..... ..AS.IQ ..V..LN.. .N..LS....
 IRE_F4_JX480633 I.H.....LT..... ..AS.IQ ..V..LN.. .N..LS....
 IRE_H3_JX480634 .H.....LT..... ..AS.IQ ..V..LN.. .N..LS....
 ITA_DE_KM247554 I.H.....LT..... ..AS.IQ ..V..LN.. .N..LS...M
 ITA_SA_KM247555 I.H.....LT..... ..AS.IQ ..V..LN.. .N..LS....
 Liaoning_AF327877 .H..... ..I..... ..V..LD S.Q....E. .N..NGL.LV
 Miyazaki_JX003263 I..... ..I..... ..Q..HLM ..T...E. .N..SGM.L.
 Wyoming_AF033820 I.H..... ..V...V..IM E.Q....E. .S.LNGMDL.

BRA1 EKQIHILYAM VLQTHADVQL LKERQKIEET FNLIGCVERS HTFCHTGHWP NESWGQLNET
 BRA2 ..M..... I..... ..D..... ..D.....DS
 DLV9-7_HM141922 .E..... ..Q..... ..I..... ..I.....DS
 DV10-3_HM141910 .E..... ..Q..... ..I..... ..I.....DS
 IRE_F2_JX480631 .R..N.... I..... ..K.QV... ..I.KTN...L..DS
 IRE_F3_JX480632 .R..N.... I..... ..K.QV... ..I.KTN...F..DS
 IRE_F4_JX480633 .R..N.... I..... ..K.QV... ..I..TN...L..DS
 IRE_H3_JX480634 ..VS..... I..... ..K.QV... ..I.KTN...L..D.
 ITA_DE_KM247554S..... I..... ..K.QV... ..I..TN...L..DS

ITA_SA_KM247555 .R.VS..... I..... .K.QV... ..I..TN...F..DS
Liaoning_AF327877 .E..... .S...Q..... .I..... .DS
Miyazaki_JX003263M.... I..... .Q..... .M...A... .I..... .T...S...DS
Wyoming_AF033820 .R..K..... I..... .QV... ..I..T .V..... .M...H...S

BRA1 TEWDDWITKM NRLETEILTT LHAAKNNLEQ AMITFNTPDS IAQFGRNIWS HIANWIFGLG
BRA2 .Q...VN.. .EY.QD.... .R..... .K.....
DLV9-7_HM141922 .Q...VD.. EN.NHD.... .T.R..... S..... .K.....
DV10-3_HM141910 .Q...VD.. EN.NHD.... .T.R..... S..... .K.....
IRE_F2_JX480631 .Q..T.VGE. EKYNQD.... .I.R..... .K...D
IRE_F3_JX480632 .Q..T.VGE. EKYNQD.... .I.R..... .K...D
IRE_F4_JX480633 .Q..T.VGE. EKYNQD.... .V.R..... .K...D
IRE_H3_JX480634 .Q..T.VGE. EKYNQD.... .V.R..... .K...D
ITA_DE_KM247554 .Q..T.VGE. EKYNQD.... .I.R..... .K...D
ITA_SA_KM247555 .Q..T.VGE. EKYNQD.... .I.R..... .K...D
Liaoning_AF327877 .Q...VD.. EN.NHD.... .T.R..... S..... .K.....
Miyazaki_JX003263 .Q...V.R. .G..H.V... .R..... SI.....TK...V.....
Wyoming_AF033820 .Q...VS.. ED.NQ..... .G.R...A. S..... .KDL.. .G.....

BRA1 ASIIKYIIML LLCYVVLITSS PKILRNLLRM MSGAGSSVNR YLKRQHQQKH AWKEDAWDQD
BRA2V..... .TT.....H F..KK.....ES....
DLV9-7_HM141922VL.. .V..L..AG..T.S. .RKRY.HR. .SRG.I.A.V
DV10-3_HM141910VL.. .V..L..AG..TTAS. .RKRY.HR. .SRG.I.A.V
IRE_F2_JX480631VLF .II.....M .L.H..TT .T.A.AS. ...KL.H.R .SQDGN..R.
IRE_F3_JX480632VLF .II.....M .L.H..TT .T.....AS. ...KL.H.R .SQDGH..R.
IRE_F4_JX480633VLF .II.....M .L.H..TT .T.....AS. ...KL.H.R .SQDGN..R.
IRE_H3_JX480634VLF .II.....M .L.H..TT .T.....AS. ...KL.H.R .SQDGH..R.
ITA_DE_KM247554VLF .II.....M .L.H..TT .T...FASH ...KL.H.R .SQDGH..R.
ITA_SA_KM247555VLF .II.....M .L.H..TT .T.....AS. ...KL.H.R .SQDGH..R.
Liaoning_AF327877VL.. .V..L..AG..TTAS. .RKRY.HR. .SRG.I.A.V
Miyazaki_JX003263 .IT..V.LF .V.....M .F..H..TT I...R..AS. ...ETY.RRR V.Q.GH....
Wyoming_AF033820V.F .I..LL... ..A.WKV T.....GS. ...KKF.H.. .SR..T...A

BRA1 QYRIHLADAT GGSSEDKYNKP KCSKRSYSGG LKGFNRQPKN WKNSTERSEV NSTGLGEHME
BRA2 ..SV...GV. .L.....L .Y...N.N.. S.E..KR..S .ETLIDA.GK ...P.PS.G
DLV9-7_HM141922 ..HAY...E. H..G..S.MR .L.RNNWN.E SEEY..RQ.. .RLIK..GE .YN-----
DV10-3_HM141910 ..HAY...E. H..G..S.MR .LPRNNWN.E PEEY..RQ.. .RLIK..GE .YNTHEDN.G
IRE_F2_JX480631 ...V...SVN D...G.F.RQ RAF.N.W..E SEEYSSRR.H YEK..KEFGK SFN..ADYE.
IRE_F3_JX480632 ...V...SVN D...G.FSRQ RAF.N.W..E SEEYSSRR.H YEK..KEFGK SFN..ADYE.
IRE_F4_JX480633 ...V...SVN D...G.F.RQ RAF.N.W..E SEEYSSRR.H YEK..KEFGK SFN..ANYE.
IRE_H3_JX480634 ...V...SVN D...G.FSRQ RAF.N.W..E SEEYSSRR.H YEK..KEFGK SFN..ANYE.
ITA_DE_KM247554 ...V...GVN D...G.FSRQ RAF.N.W..E SEEYSSRR.H YEA..KKFGE SFN..ADTK.
ITA_SA_KM247555 ...V...SVN D...G.F.RQ RAF.N.W..E SEEYSSRR.H YET..KEFGK SFN..ANNK.
Liaoning_AF327877 ..HAY...E. H..G..S.MR .L.RNNWN.E SEEY..RQ.. .KLIK..GE .YNTHEDN.G
Miyazaki_JX003263 ..N...NV. V...EEF.TQ NNFRNNWN.D S.VYDKLQ.H .RRL.K..GE DWHIP.VNEG
Wyoming_AF033820 .HN....GV. ...G...Y.Q .Y.RNDWN.E SEEY..R..S .VK.I.AFGE SYISEKTKG.

BRA1 TSHLSIAIAE -NS-VSGDNA QRTSTSLKIQ SEGGNIYDCC IKAQEGTLAI PCCGFPLWLF
BRA2 ITLP.M..G. TK.-.A.... .QA.AN.E.R
DLV9-7_HM141922 .MGRLVTT.A EKK-NV.V.P HQG.LN.E..L
DV10-3_HM141910 .MGHL.TT.A EKK-NV.E.P HQG.LN.E..G.....L
IRE_F2_JX480631 ITPAF..PNV KKD-AGEK.P SQG.L..E..
IRE_F3_JX480632 ITPAF..PNV KKD-AGEK.P SQG.L..E..
IRE_F4_JX480633 ITPAF..PNV KKD-AGEK.P SQG.L..E..
IRE_H3_JX480634 ITPAF..PNV KKD-AGEK.P SQG.L..E..
ITA_DE_KM247554 ITPTF..PNV KKD-AGEK.P SQG.L..E..
ITA_SA_KM247555 ITPTF.PPNV KKD-AGEK.P SQG.L..E..
Liaoning_AF327877 .MGRLVTT.A EKK-NV.V.P HQG.LN.E..L
Miyazaki_JX003263 ...HGTTTGA KKK-HI.G.P .QG.LD.E.. .T.....T.....
Wyoming_AF033820 I.QPGA..N. HKNGSG.N.P HQG.LD.E.R

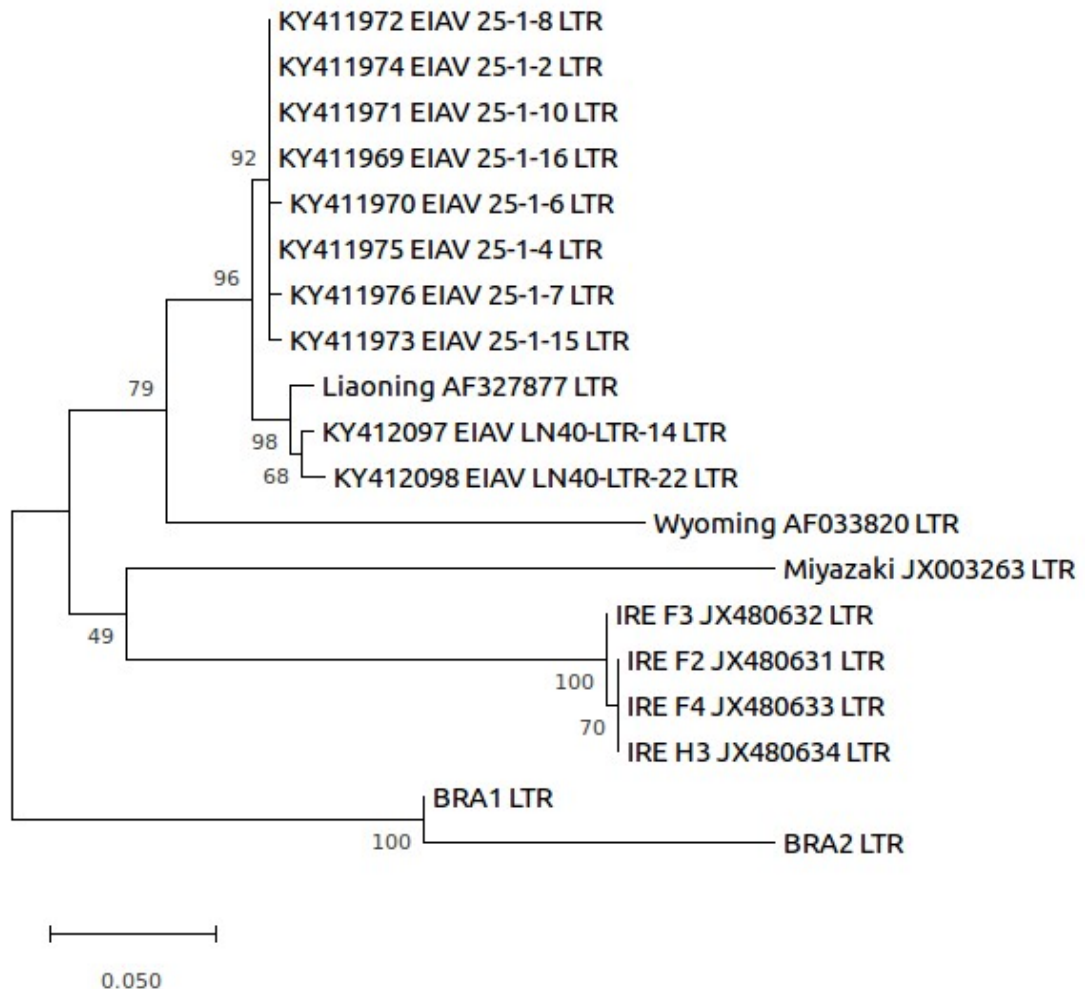
BRA1 WGLIIMGRL FGYGLRGIAM ILSYCEKGLT MLFIMLKRLC DFIGRALNPA TSHVSMQPQV
BRA2 ..FV..I... L.....L..G.... ..?..... .S.....
DLV9-7_HM141922L... L...F....K FIMILG..N VIITG.RK.. .Y..KM.... .T....D
DV10-3_HM141910L... L.....K .IMILG...N VIITG.RK.. .Y..KM.... .T....D
IRE_F2_JX480631L... I.....L.K .IMFSGRVIL LSINW.RKGL .YV.KM...S K...T..C.D
IRE_F3_JX480632L... I.....L.K .IMFSGRVIL LSINW.RKGL .YV.KM...S K...T..C.D
IRE_F4_JX480633L... I.....L.K .IMFSGRVIL LSINW.RKGL .YV.KM...S K...T..C.D
IRE_H3_JX480634L... I...F..L.K .IMFSGRVIL LSINW.RKGL .YV.KM...S K...T..C.D
ITA_DE_KM247554L... I.....L.K .IMFSGRVIL LSINW.RKGL .YV.KM...S K...T..C.D
ITA_SA_KM247555L... I.....L.K .IMFSGRVIL LSINW.RKGL .YV.KM...S K...T..C.D

Liaoning_AF327877L... L.....K .IMILG...N VIITG.RK.. .Y..KM....T....D
Miyazaki_JX003263 ...L..... L....K.L.I M.QIIG...Y G.LN.I.QIF .YM.N.FS.P K..I.....I
Wyoming_AF033820 ...V..V..I A.....L.V .IRI.IR..N LI.EIIRKML .Y.....G

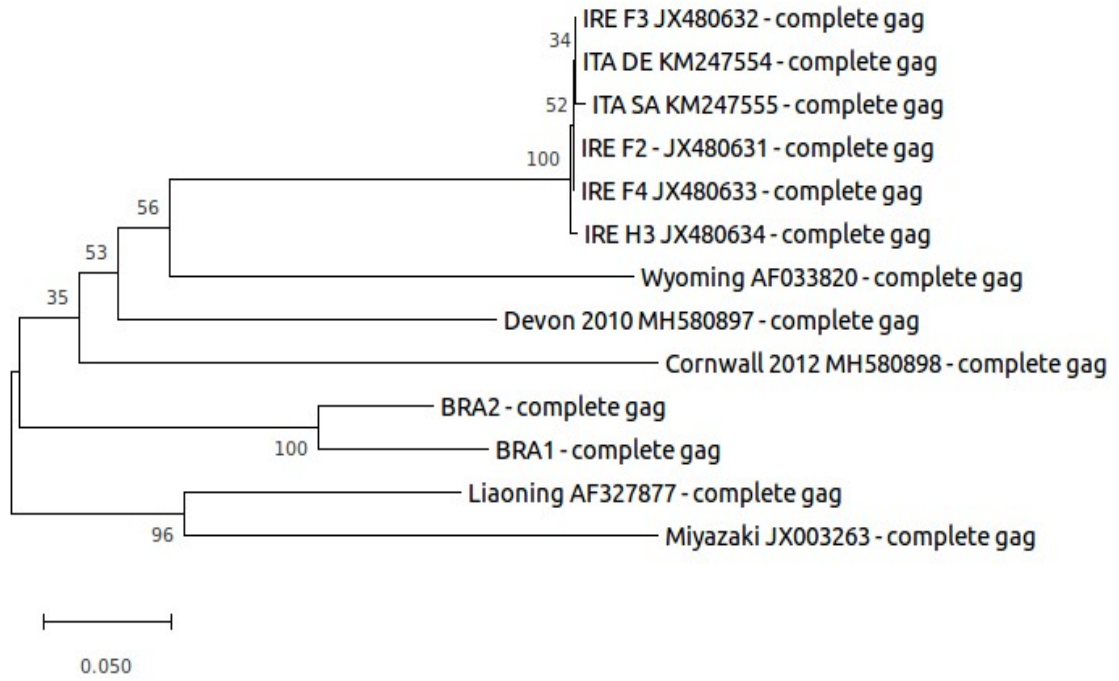
BRA1 --
BRA2 --
DLV9-7_HM141922 V-
DV10-3_HM141910 V-
IRE_F2_JX480631 I-
IRE_F3_JX480632 I-
IRE_F4_JX480633 I-
IRE_H3_JX480634 I-
ITA_DE_KM247554 I-
ITA_SA_KM247555 I-
Liaoning_AF327877 V?
Miyazaki_JX003263 --
Wyoming_AF033820 --

Supplementary Figure S6: Phylogenetic trees of Brazilian field sequences and foreign sequences. Each tree was performed based a genome region or gene: A. LTR; B. Gag; C. Pol; D. Env; E. Env protein. Used sequences: Liaoning (AF327877), Wyoming (AF033820), Miyazaki 2011-A (JX003263), IRE F2 (JX480631) IRE F3 (JX480632), IRE F4 (JX480633), IRE H3 (JX480634), ITA SA (KM247555), ITA DE (KM247554), and LTR sequences from China (KY411969-76; KY412097-98).

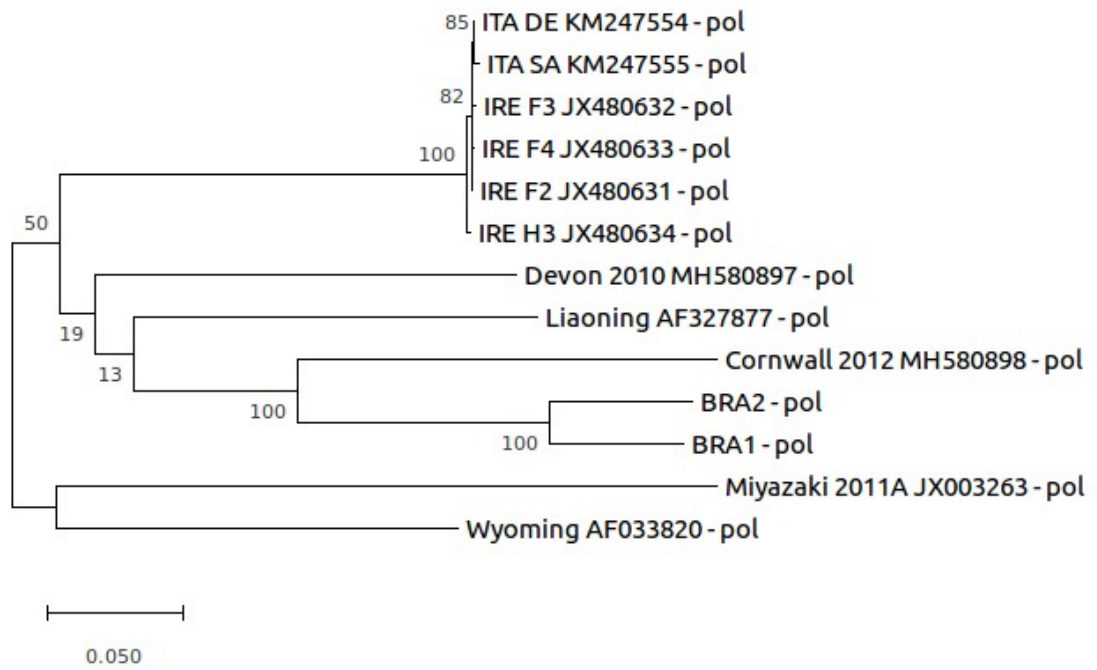
A.



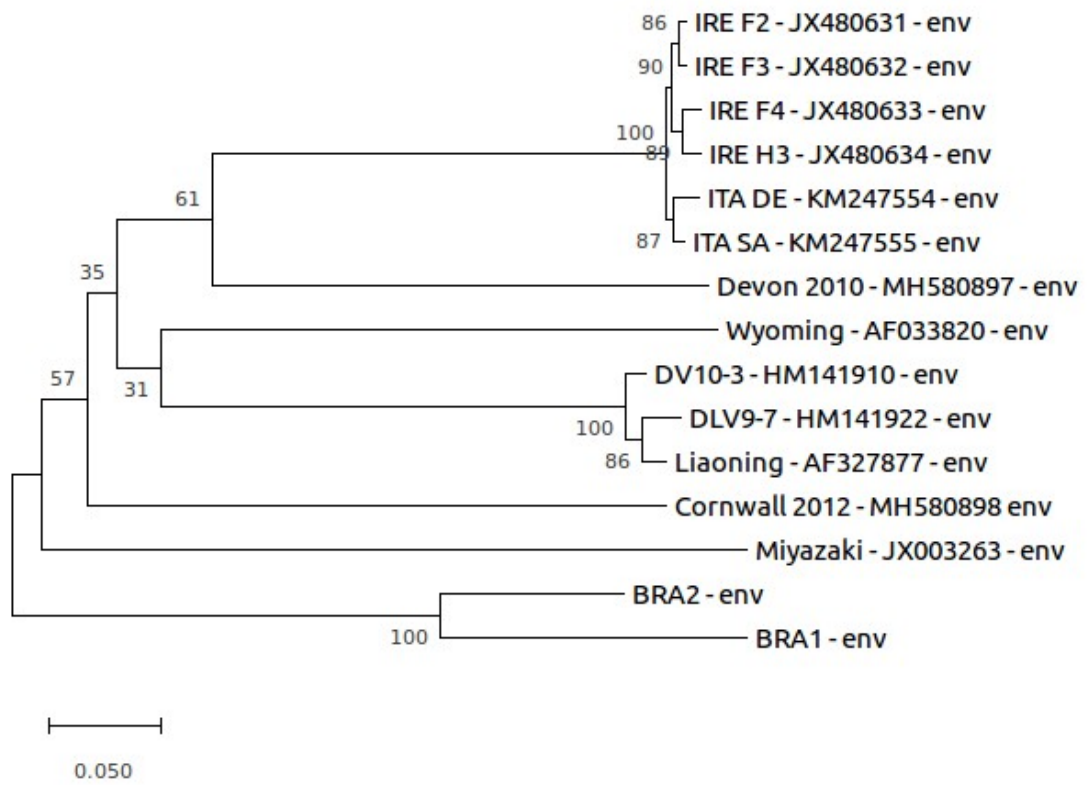
B.



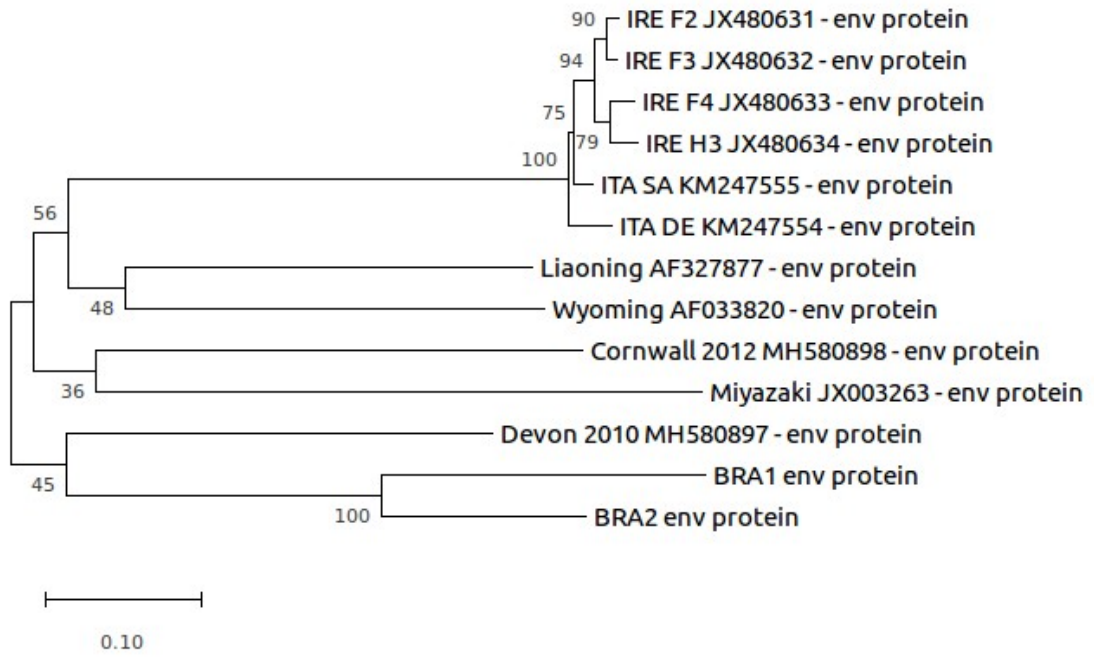
C.



D.



E.



Supplementary Figure S7: Multiple alignment of partial gag sequences from Bahia (Brazil) and BRA1 and 2 from Pantanal (Brazil).

```

KC213783.1 CCTAGAGGAT ATACTACTTG GGTGAATCCC ATACAGACAA ATGGTCTATT AAATGAAGCT
KC213784.1 .....
KC213785.1 .....
KC213786.1 .....
KC213787.1 .....
KC213788.1 .....
KC213789.1 .....
KC213790.1 .....A..
BRA1 - Gag ..C.....C..C..C.. ..A...A.T .....CA.. ..AA.T.G.. .....G..A
BRA2 - Gag ..C.....C..C..C.. ..A...A.T .....CA.. .CAA...G.. .....G..A

```

```

KC213783.1 AGTCAAAACT TATTTGGGAT ATTATCAGTA GACTGTACTT CTGAAGAAAT GAATGCATTT
KC213784.1 .....
KC213785.1 .....
KC213786.1 .....
KC213787.1 .....
KC213788.1 .....
KC213789.1 .....
KC213790.1 .....C...
BRA1 - Gag ...GT.....G.....A.. T..G.....T..C..A..G.....
BRA2 - Gag ...GT.....G.....A.. ..G.....T..C..A.. ..G.....

```

```

KC213783.1 TTGGATGTGG TACCTGGCCA GGCAGGACAA AAGCAGATAT TACTTGATGC AATTGATAAA
KC213784.1 .....
KC213785.1 .....
KC213786.1 .....
KC213787.1 .....
KC213788.1 .....
KC213789.1 .....
KC213790.1 .....
BRA1 - Gag C.A.....A..A.. A.....A..AG.T..G.....TT..C.A..C..G
BRA2 - Gag C.A.....G..A..A.. A.....G..A..AG.TC.....TT GC.G.....G

```

```

KC213783.1 ATAGCAGATG ATTGGGATAA TAGACATCCA TTACCGAATG CTCCACTGGT GGCACCACCA
KC213784.1 .....
KC213785.1 .....
KC213786.1 .....
KC213787.1 .....
KC213788.1 .....
KC213789.1 .....
KC213790.1 .....
BRA1 - Gag ..G..T..A.. ..C.. ..G..... ..A..CC..A..CT.... ..G..GG..
BRA2 - Gag .....G..A.. ..C.. ..G..... ..G..A..CC..A..TT.... A..G..GG..

```

```

KC213783.1 CAAGGGCCTA TTCCCATGAC AGCAAGGTTT ATTAGAGGTT TAGGAGTACC TAGAGAAAGA
KC213784.1 .....
KC213785.1 .....
KC213786.1 .....
KC213787.1 .....
KC213788.1 .....
KC213789.1 .....
KC213790.1 .....
BRA1 - Gag .....A.... ..T.... G....A.... ..G....T.... ..G....G
BRA2 - Gag .....A.... ..T.... G..G..A.... ..A....T.... ..G....G

```

KC213783.1	CAGATGGAGC	CTGCTTTTGA	TCAGTTTAGG	CAGACATATA	GACAATGGAT	AATAGAAGCC
KC213784.1
KC213785.1
KC213786.1
KC213787.1
KC213788.1
KC213789.1
KC213790.1
BRA1 - GagA.	.A..C.....C..AT.....G.....	...T..G..G
BRA2 - Gag	..A.....A.	.A..C.....C..A	..A..T.....T..G...

KC213783.1	ATGTCAGAAG	GCATCAAAGT	GATGTCGGTA	AAA
KC213784.1
KC213785.1
KC213786.1
KC213787.1
KC213788.1
KC213789.1
KC213790.1ATT.G.	...
BRA1 - Gag	...A.....	.A..A...A.	A...ATT.G.	..G
BRA2 - Gag	...A....G.	.A..A...A.	A...ATA.G.	..G

Supplementary Figure S8: Phylogenetic tree of partial *gag* sequences from Bahia (Brazil), BRA1 and 2 from Pantanal (Brazil), and field sequences of other countries.

