

Table S1. GenBank accession numbers, sample IDs and genotypes of the BLV full-length *env* and *gag* nucleotide sequences of the South African isolates used in this study.

Gene	GenBank accession number	Sample ID	Genotype
<i>env</i>	MN966688.1	K1170	4
	MN966689.1	K1194	4
	MN966690.1	L3401	4
	MN966691.1	M1878	4
	MN966692.1	M2746	1
	MN966693.1	P2152	4
	MN966694.1	P2677	4
	MN966695.1	P591	4
<i>gag</i>	MN966696.1	K1170	4
	MN966697.1	K1194	4
	MN966698.1	L3401	4
	MN966699.1	M1878	4
	MN966700.1	M2746	1
	MN966701.1	P2152	4
	MN966702.1	P2677	4
	MN966703.1	P591	4

Table S2. GenBank accession numbers, country of origin (2-letter country code), genotypes and phylogenetic analyses conducted for each BLV isolate in this study.

Genotype	GenBank accession number	Country of origin	Phylogenetic analyses	References
1	AB934282.1	Japan (JP)	<i>gag</i>	Direct submission by Mekata and Norimine (2014)
	AF399703.3	Brazil (BR)	Full-length <i>env</i> , partial <i>env</i>	[1]
	AF547184.2	Brazil (BR)	Full-length <i>env</i> , partial <i>env</i>	[2]
	AP018006.1	Japan (JP)	<i>gag</i>	[3]
	AP018007.1	Japan (JP)	Full-length <i>env</i> , partial <i>env</i> , <i>gag</i>	[3]
	AP018008.1	Japan (JP)	<i>gag</i>	[3]
	AP018012.1	Japan (JP)	Full-length <i>env</i> , partial <i>env</i>	[3]
	AP018019.1	Japan (JP)	<i>gag</i>	[3]
	AP018029.1	Japan (JP)	<i>gag</i>	[3]
	AP019589.1	Japan (JP)	<i>gag</i>	Direct submission by Murakami and Sato (2019)
	AY078387.1	USA (US)	Full-length <i>env</i> , partial <i>env</i>	[4]
	AY151262.2	Brazil (BR)	Full-length <i>env</i> , partial <i>env</i>	Direct submission by Stancek et al. (2002)
	D00647.1	Australia (AU)	Full-length <i>env</i> , partial <i>env</i> , <i>gag</i>	[5]
	EF065637.1	Costa Rica (CR)	Full-length <i>env</i> , partial <i>env</i>	[6]
	EF065640.1	Costa Rica (CR)	Full-length <i>env</i> , partial <i>env</i>	[6]
	EF065641.1	USA (US)	Full-length <i>env</i> , partial <i>env</i>	[6]
	EF065642.1	USA (US)	Full-length <i>env</i> , partial <i>env</i>	[6]
	EF065644.1	USA (US)	Full-length <i>env</i> , partial <i>env</i>	[6]
	EF065656.1	USA (US)	Full-length <i>env</i> , partial <i>env</i>	[6]
	EF065661.1	Japan (JP)	Full-length <i>env</i> , partial <i>env</i>	[6]
	EF600696.1	USA (US)	<i>gag</i>	[7]
	EU266060.1	Iran (IR)	Partial <i>env</i>	[8]
	FJ808578.1	Argentina (AR)	Partial <i>env</i>	[9]
	HE967301.1	Uruguay (UY)	Full-length <i>env</i> , partial <i>env</i> , <i>gag</i>	Direct submission by Cristina (2012)
	HE967302.1	Uruguay (UY)	Full-length <i>env</i>	Direct submission by Cristina (2012)
	HE967303.1	Uruguay (UY)	Full-length <i>env</i> , partial <i>env</i> , <i>gag</i>	Direct submission by Cristina (2012)
	K02120.1	Japan (JP)	Full-length <i>env</i> , partial <i>env</i> , <i>gag</i>	[10]
	KJ707242.1	South Korea (KR)	Partial <i>env</i>	Direct submission by Kim (2014)
	KX674367.1	Saint Kitts and Nevis (KN)	Full-length <i>env</i> , partial <i>env</i>	[11]

	KX674370.1	Saint Kitts and Nevis (KN)	Full-length <i>env</i> , partial <i>env</i>	[11]
	KX674372.1	Dominica (DM)	Full-length <i>env</i> , partial <i>env</i>	[11]
	KX674373.1	Dominica (DM)	Full-length <i>env</i> , partial <i>env</i>	[11]
	LC060799.1	Mongolia (MN)	Partial <i>env</i>	[12]
	LC060800.1	Mongolia (MN)	Partial <i>env</i>	[12]
	LC075543.1	Peru (PE)	Partial <i>env</i>	[13]
	LC075568.1	Bolivia (BO)	Partial <i>env</i>	[13]
	LC080651.1	Paraguay (PY)	Full-length <i>env</i> , partial <i>env</i> , <i>gag</i>	[13]
	LC080652.1	Paraguay (PY)	<i>gag</i>	[13]
	LC080653.1	Paraguay (PY)	Full-length <i>env</i> , partial <i>env</i>	[13]
	LC164085.1	Japan (JP)	<i>gag</i>	[14]
	LC440653.1	Zambia (ZM)	Partial <i>env</i>	[15]
	LC440663.1	Zambia (ZM)	Partial <i>env</i>	[15]
	LC440666.1	Zambia (ZM)	Partial <i>env</i>	[15]
	MH170027.1	Vietnam (VN)	Full-length <i>env</i> , partial <i>env</i>	[16]
	MH170028.1	Vietnam (VN)	Full-length <i>env</i> , partial <i>env</i>	[16]
2	AF257515.1	Argentina (AR)	Full-length <i>env</i> , partial <i>env</i> , <i>gag</i>	[17]
	AF399704.3	Brazil (BR)	Full-length <i>env</i> , partial <i>env</i>	[1]
	FJ808590.1	Argentina (AR)	Partial <i>env</i>	[9]
	FJ914764.1	Argentina (AR)	Full-length <i>env</i> , partial <i>env</i> , <i>gag</i>	[18]
	LC075544.1	Peru (PE)	Partial <i>env</i>	[13]
	LC075577.1	Bolivia (BO)	Partial <i>env</i>	[13]
	LC080654.1	Peru (PE)	Full-length <i>env</i> , partial <i>env</i> , <i>gag</i>	[13]
	LC080655.1	Paraguay (PY)	Full-length <i>env</i> , partial <i>env</i> , <i>gag</i>	[13]
3	EF065647.1	USA (US)	Full-length <i>env</i> , partial <i>env</i>	[6]
	EF065649.1	USA (US)	Full-length <i>env</i> , partial <i>env</i>	[6]
	EF065650.1	Japan (JP)	Full-length <i>env</i> , partial <i>env</i>	[6]
	KP201464.1	South Korea (KR)	Partial <i>env</i>	[19]
4	AF033818.1	USA (US)	Full-length <i>env</i> , partial <i>env</i> , <i>gag</i>	Direct submission by Chappey (1997)
	AF067081.1	Poland (PL)	Partial <i>env</i>	Direct submission by Mikiewicz et al. (1998)
	AF503581.1	Belgium (BE)	Full-length <i>env</i> , partial <i>env</i>	[20]
	AY515278.1	Chile (CL)	Partial <i>env</i>	[21]
	EF065638.1	Belgium (BE)	Full-length <i>env</i> , partial <i>env</i>	[6]

	EU262575.2	Poland (PL)	Partial <i>env</i>	Direct submission by Kuzmak et al. (2007)
	FJ808596.1	Argentina (AR)	Partial <i>env</i>	[9]
	HQ902258.1	Belarus (BY)	Partial <i>env</i>	[22]
	IN695878.1	Russia (RU)	Full-length <i>env</i> , partial <i>env</i>	Direct submission by Lomakina et al. (2011)
	IQ686097.1	Russia (RU)	Partial <i>env</i>	Direct submission by Lomakina et al. (2011)
	IQ686101.1	Russia (RU)	Partial <i>env</i>	Direct submission by Lomakina et al. (2012)
	K02251.1	Belgium (BE)	Full-length <i>env</i> , partial <i>env</i>	[23]
	KT122858.1	Belgium (BE)	<i>gag</i>	Direct submission by Rosewick et al. (2015)
	LC060795.1	Mongolia (MN)	Partial <i>env</i>	[12]
	LC060797.1	Mongolia (MN)	Partial <i>env</i>	[12]
	LC193462.1	Zambia (ZM)	Partial <i>env</i>	[24]
	M35238.1	France (FR)	Partial <i>env</i>	[25]
	MK820044.1	China (CN)	Full-length <i>env</i> , partial <i>env</i>	[26]
	MK840877.1	China (CN)	Full-length <i>env</i> , partial <i>env</i>	[26]
	MK840879.1	China (CN)	Full-length <i>env</i> , partial <i>env</i>	[26]
	U87872.1	Germany (GE)	Partial <i>env</i>	[27]
5	AF399702.3	Brazil (BR)	Partial <i>env</i>	[1]
	EF065635.1	Costa Rica (CR)	Full-length <i>env</i> , partial <i>env</i>	[6]
	EF065639.1	Costa Rica (CR)	Full-length <i>env</i> , partial <i>env</i>	[6]
	EF065643.1	Costa Rica (CR)	Full-length <i>env</i> , partial <i>env</i>	[6]
	EF065645.1	Costa Rica (CR)	Full-length <i>env</i> , partial <i>env</i>	[6]
	EF065654.1	Costa Rica (CR)	Full-length <i>env</i> , partial <i>env</i>	[6]
	EF065655.1	Costa Rica (CR)	Full-length <i>env</i> , partial <i>env</i>	[6]
6	AY185360.2	Brazil (BR)	Full-length <i>env</i> , partial <i>env</i>	[2]
	FJ808582.1	Argentina (AR)	Partial <i>env</i>	[9]
	LC080656.1	Paraguay (PY)	Full-length <i>env</i> , partial <i>env</i> , <i>gag</i>	[13]
	LC080657.1	Paraguay (PY)	Full-length <i>env</i> , partial <i>env</i> , <i>gag</i>	[13]
	LC080658.1	Paraguay (PY)	Full-length <i>env</i> , partial <i>env</i> , <i>gag</i>	[13]
	MH341524.1	India (IN)	Partial <i>env</i>	[28]
	MF580991.1	China (CN)	<i>gag</i>	[29]
	MF580992.1	China (CN)	<i>gag</i>	[29]
	MG800834.1	China (CN)	Full-length <i>env</i> , partial <i>env</i>	[30]
	MH170029.1	Vietnam (VN)	Full-length <i>env</i> , partial <i>env</i> , <i>gag</i>	[16]

	MH170030.1	Vietnam (VN)	Full-length <i>env</i> , partial <i>env</i> , <i>gag</i>	[16]
7	AY515274.1	Chile (CL)	Partial <i>env</i>	[21]
	AY515280.1	Chile (CL)	Partial <i>env</i>	[21]
	EU262555.2	Poland (PL)	Partial <i>env</i>	Direct submission by Kuzmak and Olech. (2010)
	HM563758.3	Ukraine (UA)	Partial <i>env</i>	Direct submission by Kuzmak and Olech. (2010)
	JN695879.1	Russia (RU)	Full-length <i>env</i> , partial <i>env</i>	Direct submission by Lomakina et al (2012)
	JN695880.1	Russia (RU)	Full-length <i>env</i> , partial <i>env</i>	Direct submission by Lomakina et al (2012)
	KF801457.1	Moldova (MD)	Full-length <i>env</i> , partial <i>env</i>	[31]
	KF801458.1	Moldova (MD)	Full-length <i>env</i> , partial <i>env</i>	[31]
	LC060801.1	Mongolia (MN)	Partial <i>env</i>	[12]
	S83530.1	Italy (IT)	Partial <i>env</i>	[32]
8	GU724606.1	Croatia (HR)	Partial <i>env</i>	[33]
	HM563764.3	Ukraine (UA)	Partial <i>env</i>	[22]
	JF713455.1	Russia (RU)	Partial <i>env</i>	Direct submission by Shaeva et al. (2011)
	JN990071.1	Croatia (HR)	Partial <i>env</i>	[33]
9	LC080659.1	Bolivia (BO)	Full-length <i>env</i> , partial <i>env</i> , <i>gag</i>	[13]
	LC080662.1	Bolivia (BO)	Full-length <i>env</i> , partial <i>env</i> , <i>gag</i>	[13]
	LC080663.1	Bolivia (BO)	Full-length <i>env</i> , partial <i>env</i> , <i>gag</i>	[13]
	LC080666.1	Bolivia (BO)	Full-length <i>env</i> , partial <i>env</i> , <i>gag</i>	[13]
	LC080667.1	Bolivia (BO)	Full-length <i>env</i> , partial <i>env</i> , <i>gag</i>	[13]
	LC080668.1	Bolivia (BO)	Full-length <i>env</i> , partial <i>env</i>	[13]
	LC080671.1	Bolivia (BO)	Full-length <i>env</i> , partial <i>env</i> , <i>gag</i>	[13]
10	KU233527.1	Thailand (TH)	Partial <i>env</i>	[34]
	KU233535.1	Thailand (TH)	Partial <i>env</i>	[34]
	KU233554.1	Thailand (TH)	Partial <i>env</i>	[34]
	LC154848.1	Myanmar (MM)	Full-length <i>env</i> , partial <i>env</i> , <i>gag</i>	[35]
	LC154849.1	Myanmar (MM)	Full-length <i>env</i> , partial <i>env</i> , <i>gag</i>	[35]
	MF580994.1	China (CN)	Full-length <i>env</i> , partial <i>env</i> , <i>gag</i>	[29]
	MF580995.1	China (CN)	Full-length <i>env</i> , partial <i>env</i> , <i>gag</i>	[29]

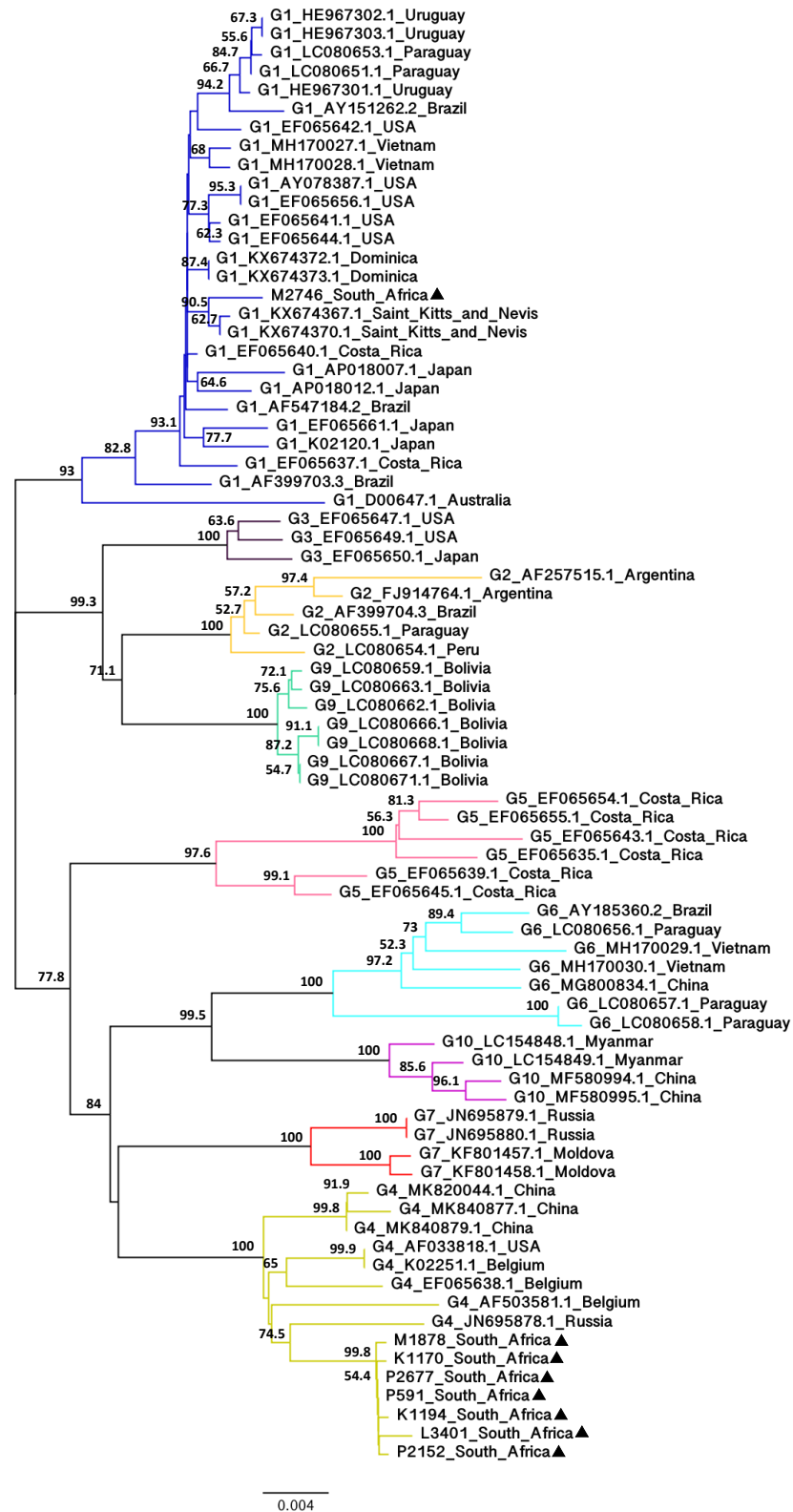


Figure S1. Neighbour-joining phylogenetic tree based on the alignment of BLV full-length *env* nucleotide sequences (1,548 bp) from South Africa and other geographic regions worldwide. The South African BLV isolates identified in this study are indicated by filled triangles (▲) followed by their sample ID. Other BLV strains are shown by genotype followed by GenBank accession number and country of origin. Numbers at the branches denote bootstrap support (1000 iterations). Bootstrap values of $\geq 50\%$ are shown. The bar at the bottom of the figure denotes genetic distance.

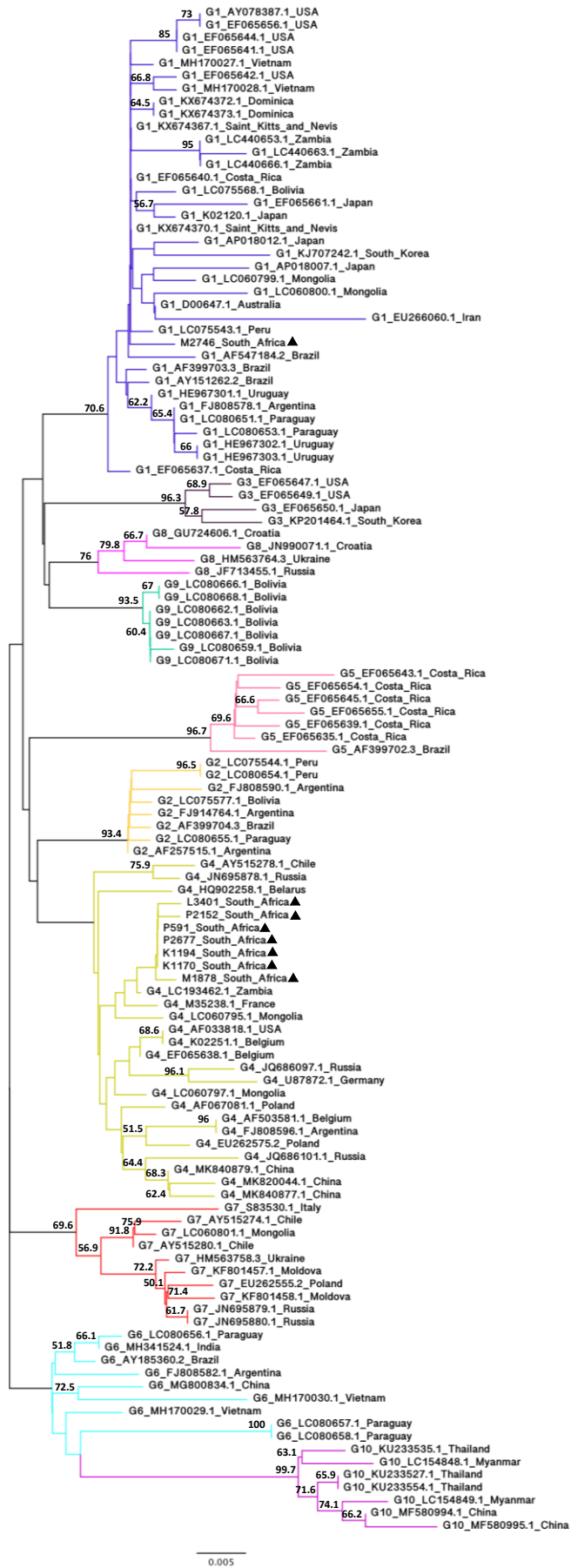


Figure S3. Neighbour-joining phylogenetic tree based on the alignment of BLV partial *env* nucleotide sequences (444 bp) from South Africa and other geographic regions worldwide. The South African BLV strains identified in this study are indicated by filled triangles (▲) followed by their sample ID. Other strains are indicated by their genotype, GenBank accession number and country of origin. Numbers at the branches denote bootstrap support (1000 iterations). Bootstrap values of $\geq 50\%$ are shown. The bar at the bottom of the figure denotes genetic distance.

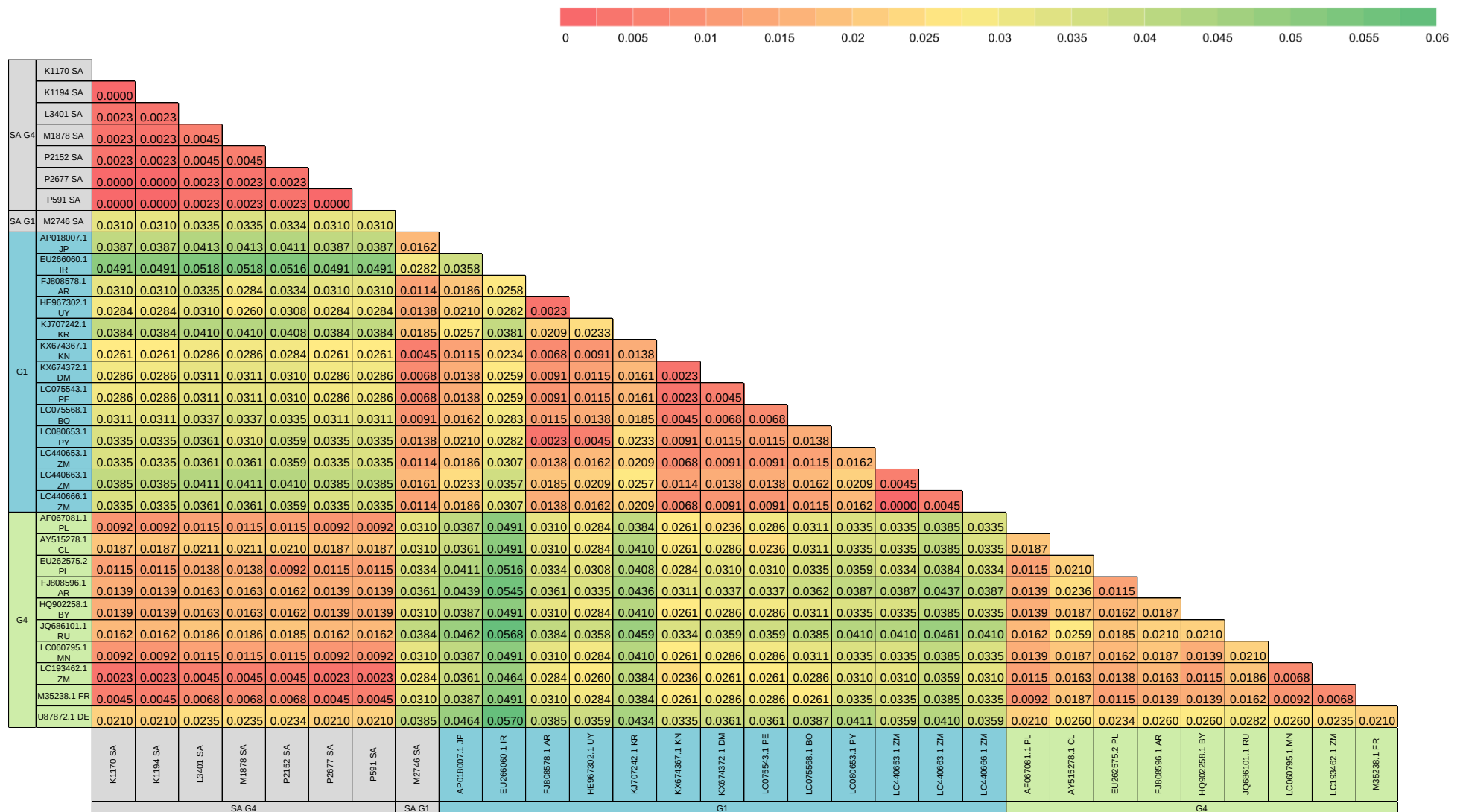


Figure S4. Pairwise evolutionary distance of BLV partial *env* nucleotide sequences (444 bp) between G1 and G4 isolates from South Africa and other geographic regions worldwide. The values indicate the number of base substitutions per site between sequences. The country of origin is indicated by 2-letter country codes (See Table S2). SA, South Africa.

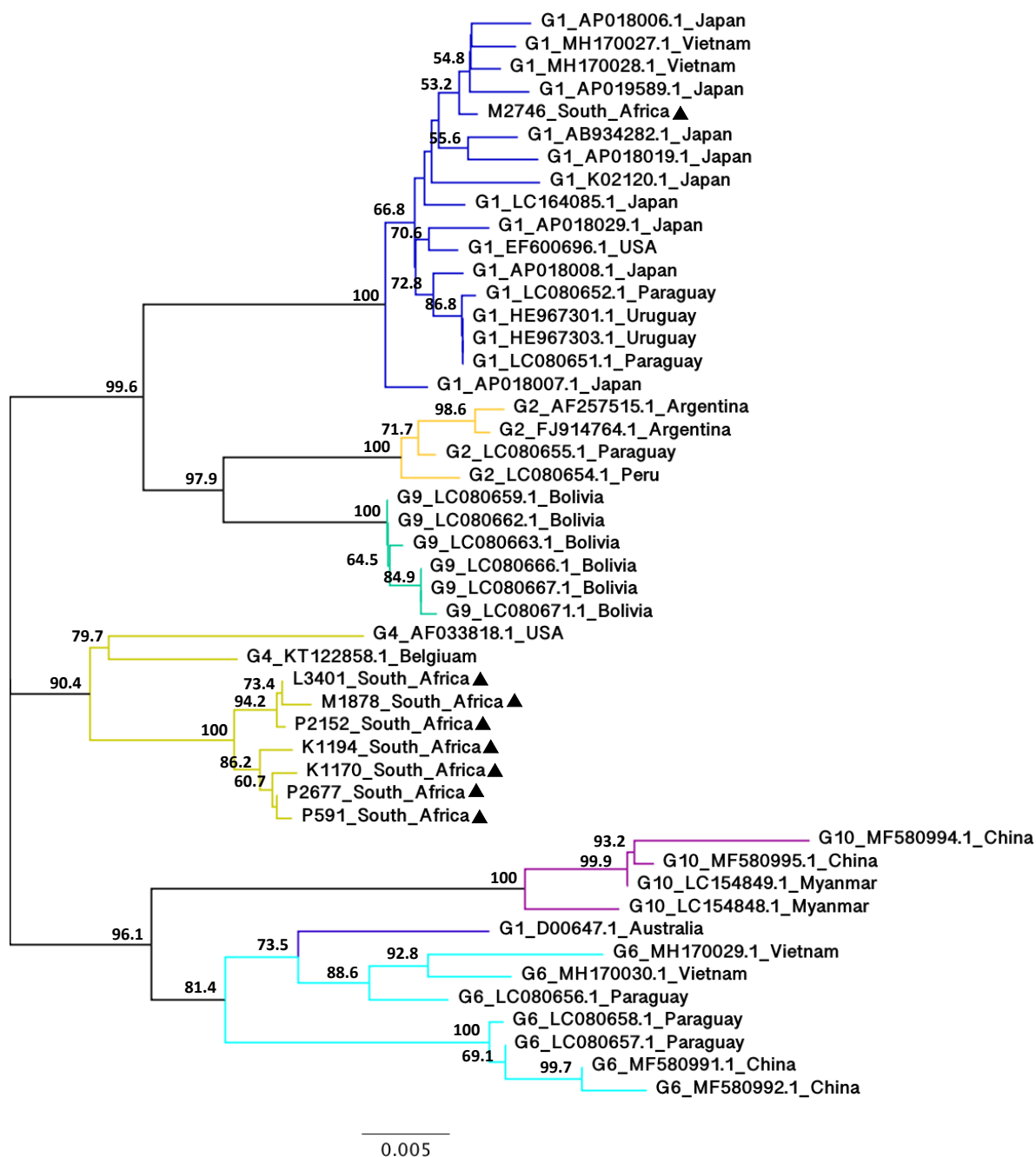


Figure S5. Neighbour-joining phylogenetic tree based on the alignment of BLV full-length *gag* nucleotide sequences (1,182 bp) from South Africa and other geographic regions worldwide. The South African BLV strains identified in this study are indicated by filled triangles (▲) followed by their sample ID. Other strains are indicated by their genotype, GenBank accession number and country of origin. Numbers at the branches denote bootstrap support (1000 iterations). Bootstrap values of $\geq 50\%$ are shown. The bar at the bottom of the figure denotes genetic distance.

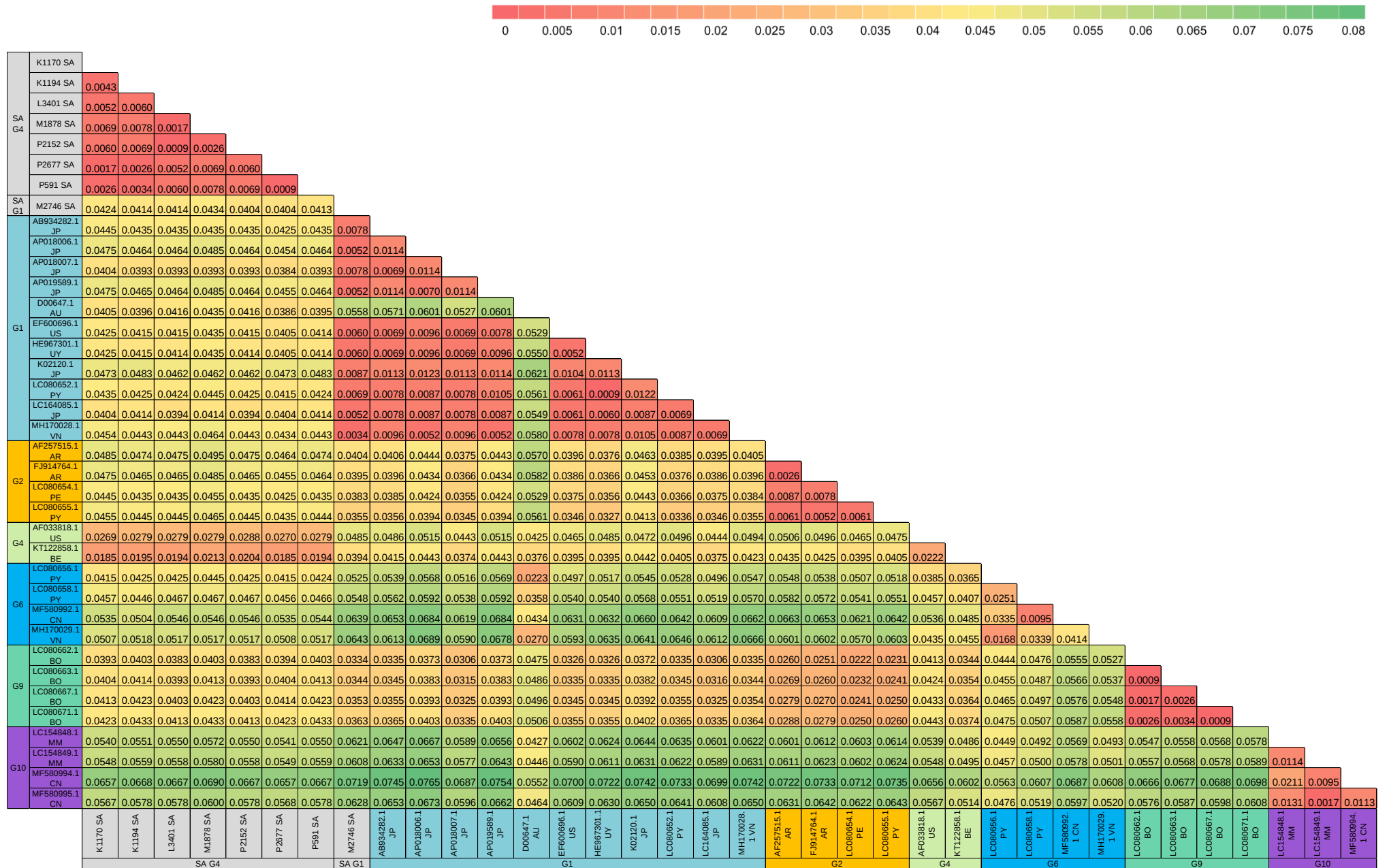


Figure S6. Pairwise evolutionary distance of BLV full-length *gag* nucleotide sequences (1,182 bp) from the South African isolates and 29 isolates from other geographic regions worldwide. The number of base substitutions per site from between sequences are shown. The country of origin is indicated by 2-letter country codes (See Table S2). SA, South Africa.

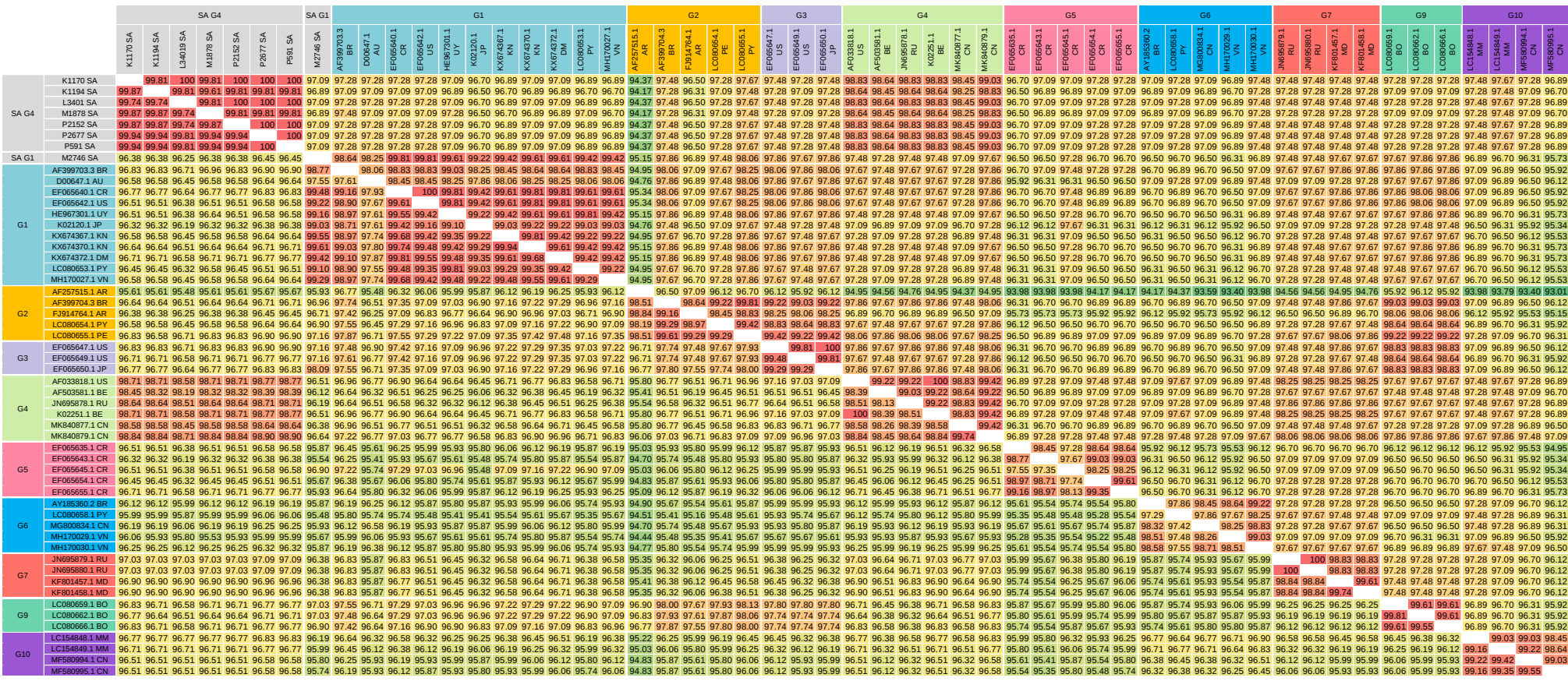


Figure S7. Pairwise percent identity of BLV full-length Env nucleotide (1,548 bp) and amino acid sequences (515 amino acids) between the South African isolates and 46 selected isolates from other geographic regions worldwide. Low matrix shows percent identity of nucleotide sequences and the upper matrix shows percent identity of amino acid sequences. The country of origin is indicated by 2-letter country codes (See Table S2). SA, South Africa.

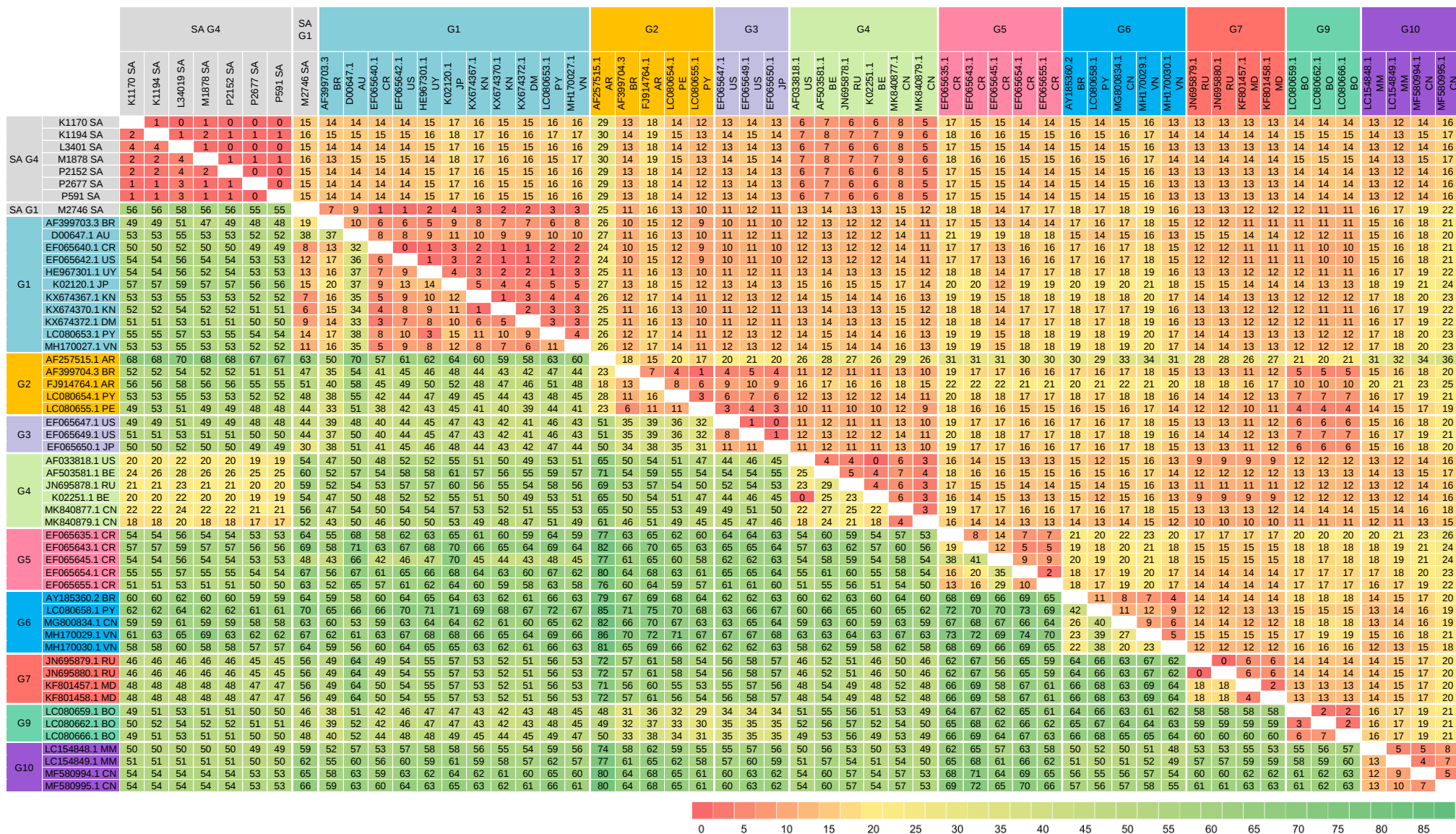


Figure S8. Pairwise comparison of BLV full-length Env nucleotide (1,548 bp) and amino acid (515 amino acids) differences between the South African isolates and 46 selected isolates from other geographic regions worldwide. Lower matrix shows the number of nucleotide differences and the upper matrix shows the number of amino acid differences. The country of origin is indicated by 2-letter country codes (See Table S2). SA, South Africa.

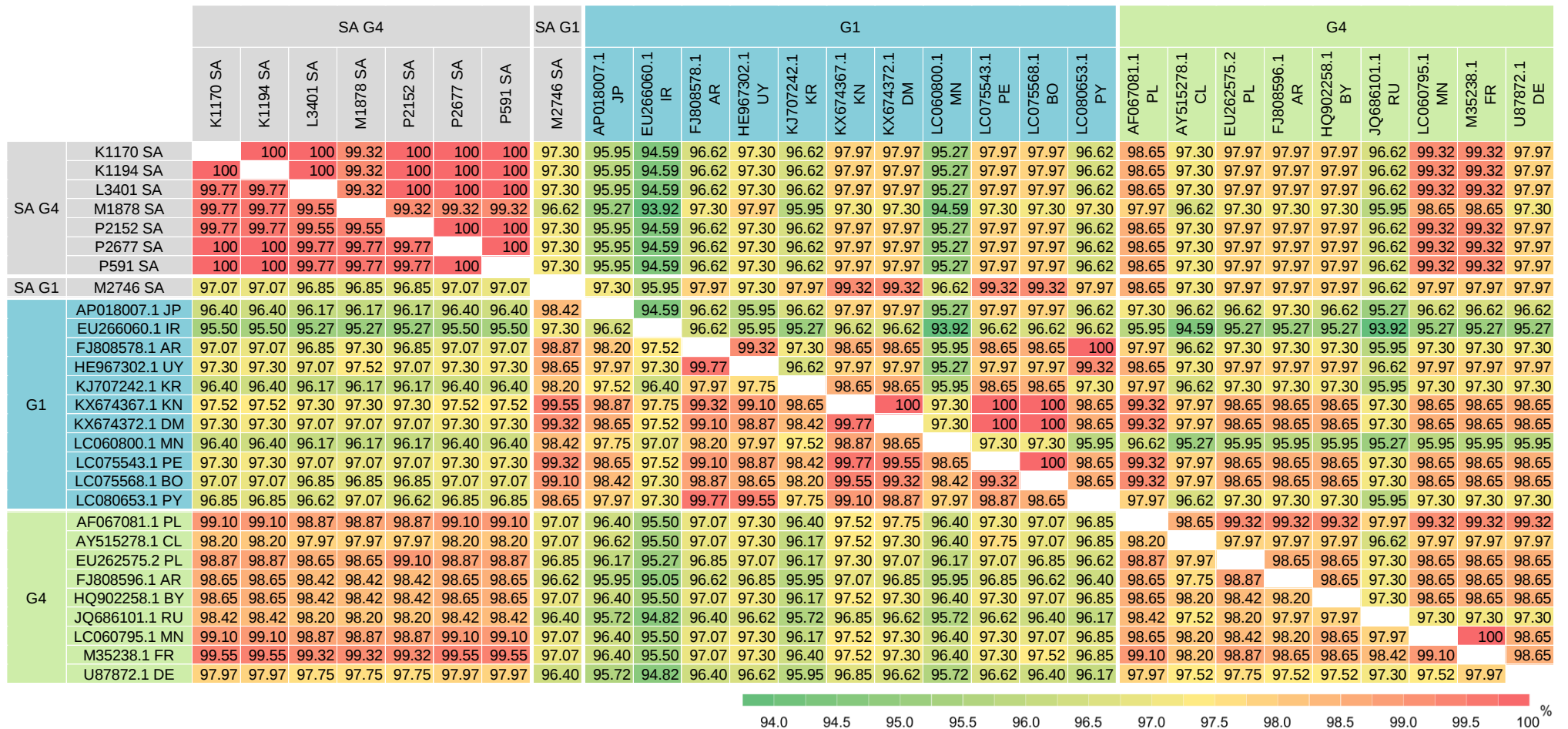


Figure S9. Pairwise percent identity of the BLV partial Env nucleotide (444 bp) and amino acid (148 amino acids) sequences between G1 and G4 isolates from South Africa and other geographic regions worldwide. Lower matrix shows percent identity of nucleotide sequences and the upper matrix shows percent identity of amino acid sequences. The country of origin is indicated by 2-letter country codes (See Table S2). SA, South Africa.

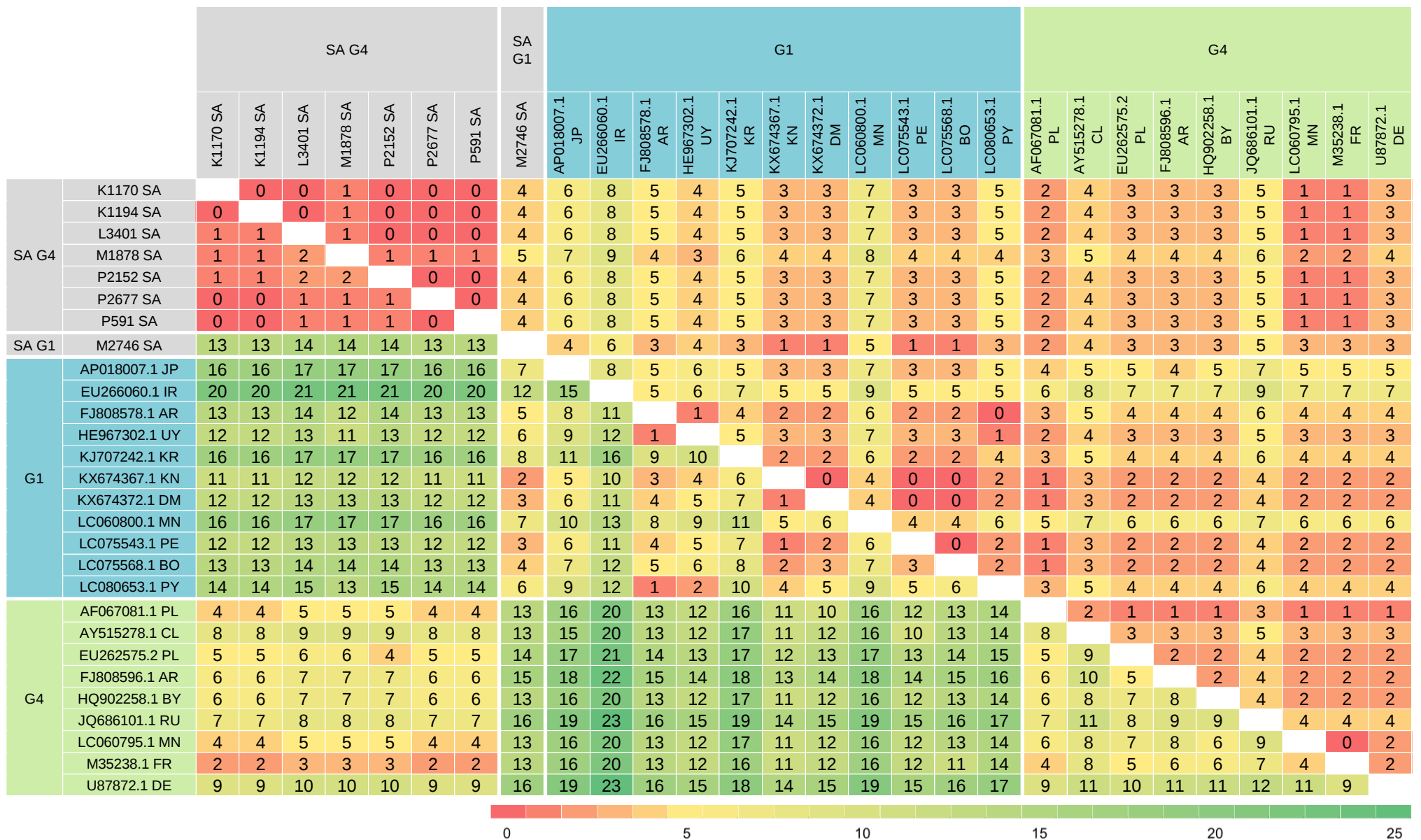


Figure S10. Pairwise comparison of BLV partial Env nucleotide (444 bp) and amino acid (148 amino acids) differences between G1 and G4 isolates from South Africa and other geographic regions worldwide. Lower matrix shows the number of nucleotide differences and the upper matrix shows the number of amino acid differences. The country of origin is indicated by 2-letter country codes (See Table S2). SA, South Africa.

Table S2. Pairwise comparison of BLV partial Env nucleotide and amino acid sequences between G1 South African and Zambian sequences.

	Comparison with South African G1 (M2746)	Percent identity	Differences
Zambian G1	LC440653.1	98.87% (98.65%)	5 (2)
	LC440654.1	98.87% (98.65%)	5 (2)
	LC440655.1	98.87% (98.65%)	5 (2)
	LC440656.1	98.87% (98.65%)	5 (2)
	LC440657.1	98.87% (98.65%)	5 (2)
	LC440658.1	98.87% (98.65%)	5 (2)
	LC440659.1	98.87% (98.65%)	5 (2)
	LC440660.1	98.87% (98.65%)	5 (2)
	LC440661.1	98.20% (96.62%)	8 (5)
	LC440662.1	98.87% (98.65%)	5 (2)
	LC440663.1	98.42% (97.30%)	7 (4)
	LC440664.1	98.87% (98.65%)	5 (2)
	LC440665.1	98.87% (98.65%)	5 (2)
	LC440666.1	98.87% (98.65%)	5 (2)

Percent identity of amino acid sequences and the number of amino acid differences are shown in brackets.

Table S3. Pairwise comparison of BLV partial Env nucleotide and amino acid sequences between G4 South African and Zambian sequences.

	Comparison with Zambian G4 (LC193462.1)	Percent identity	Differences
South African G4	K1170	99.77% (100%)	1 (0)
	K1194	99.77% (100%)	1 (0)
	L3401	99.55% (100%)	2 (0)
	M1878	99.55% (99.32%)	2 (1)
	P2152	99.55% (100%)	2 (0)
	P2677	99.77% (100%)	1 (0)
	P591	99.77% (100%)	1 (0)

Percent identity of amino acid sequences and the number of amino acid differences are shown in brackets.

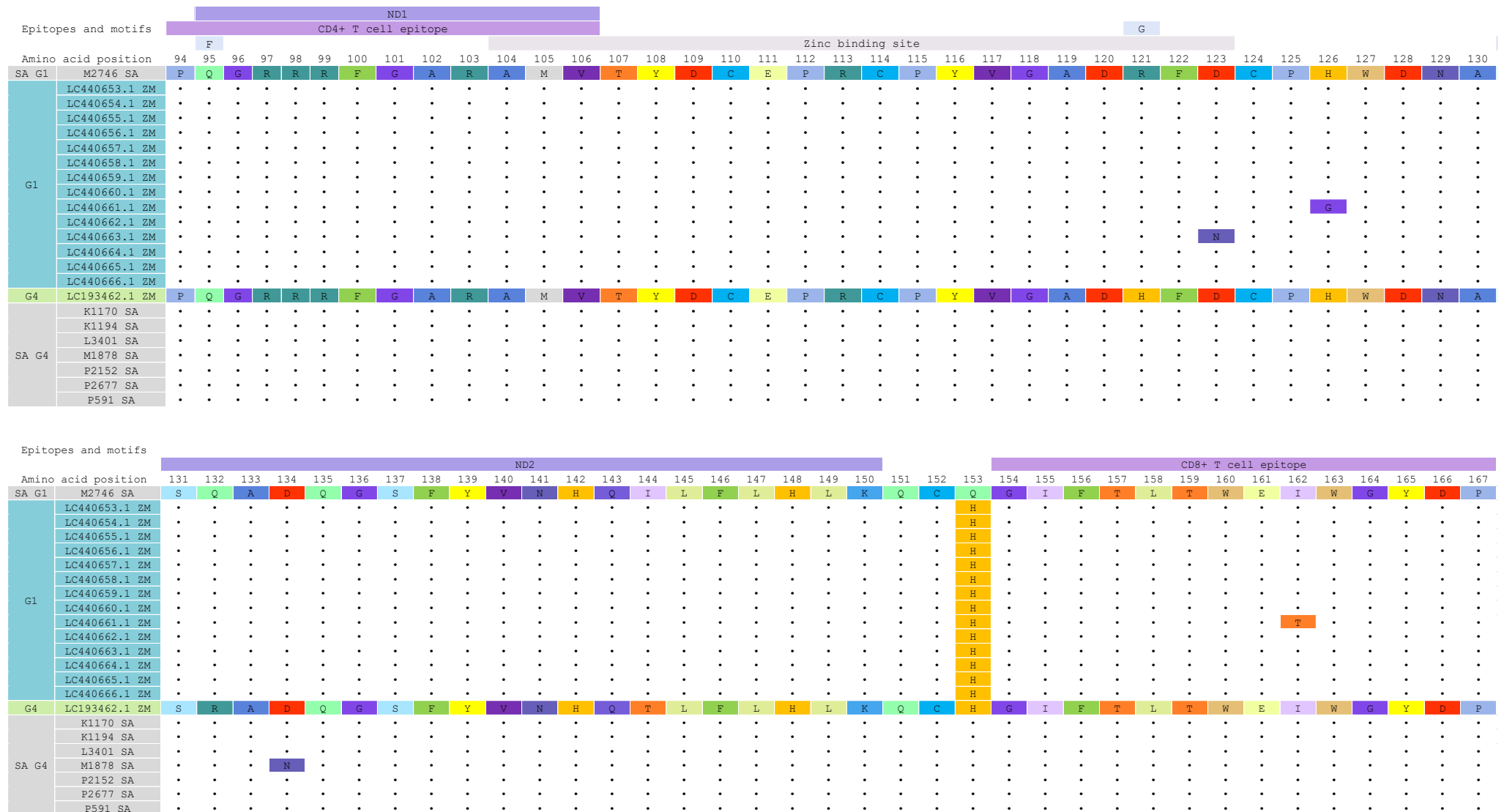


Figure S11. Comparison of 148 amino acid region in the Env gp51 protein between the G1 and G4 South African and Zambian isolates. G1 South African isolate M2746 was used as a consensus sequence for the comparison with other G1 isolates and G4 Zambian isolate LC193462.1 for the comparison with other G4 isolates. A dot indicates homology with the consensus sequence. SA, South Africa; ZM, Zambia. Colour bars above the sequence alignment show positions of epitopes and motifs including neutralising domains (ND1, ND2 and ND3), conformational epitopes (F and G), a linear epitope (E), CD8⁺ T cell epitope, CD4⁺ T cell epitope, a position of disulphide bond formation and a zinc binding site.

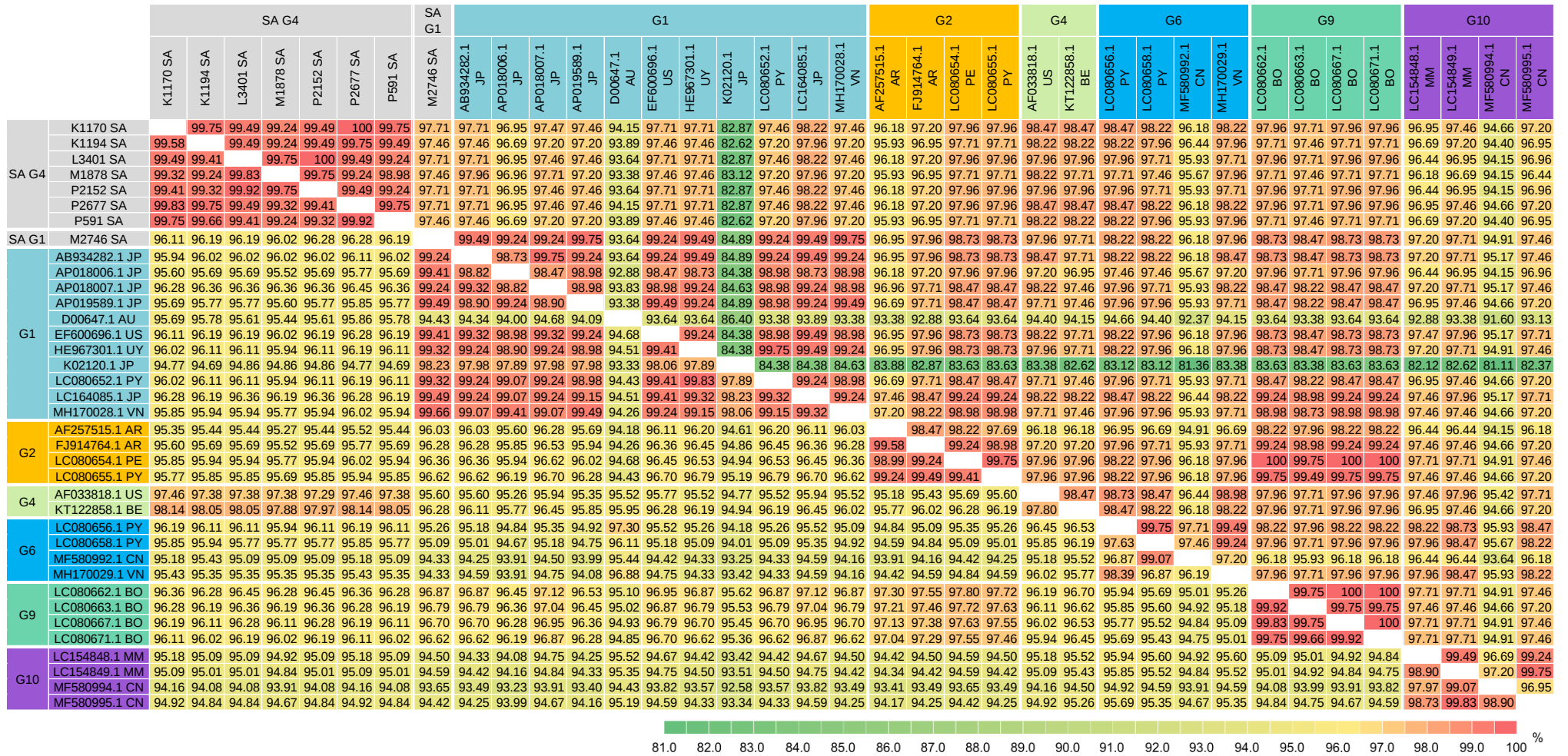


Figure S12. Pairwise percent identity of BLV full-length Gag nucleotide (1,182 bp) and amino acid (393 amino acids) sequences between the South African isolates and 29 selected isolates from other geographic regions worldwide. Lower matrix shows percent identity of nucleotide sequences and the upper matrix shows percent identity of amino acid sequences. The country of origin is indicated by 2-letter country codes (See Table S2). SA, South Africa.

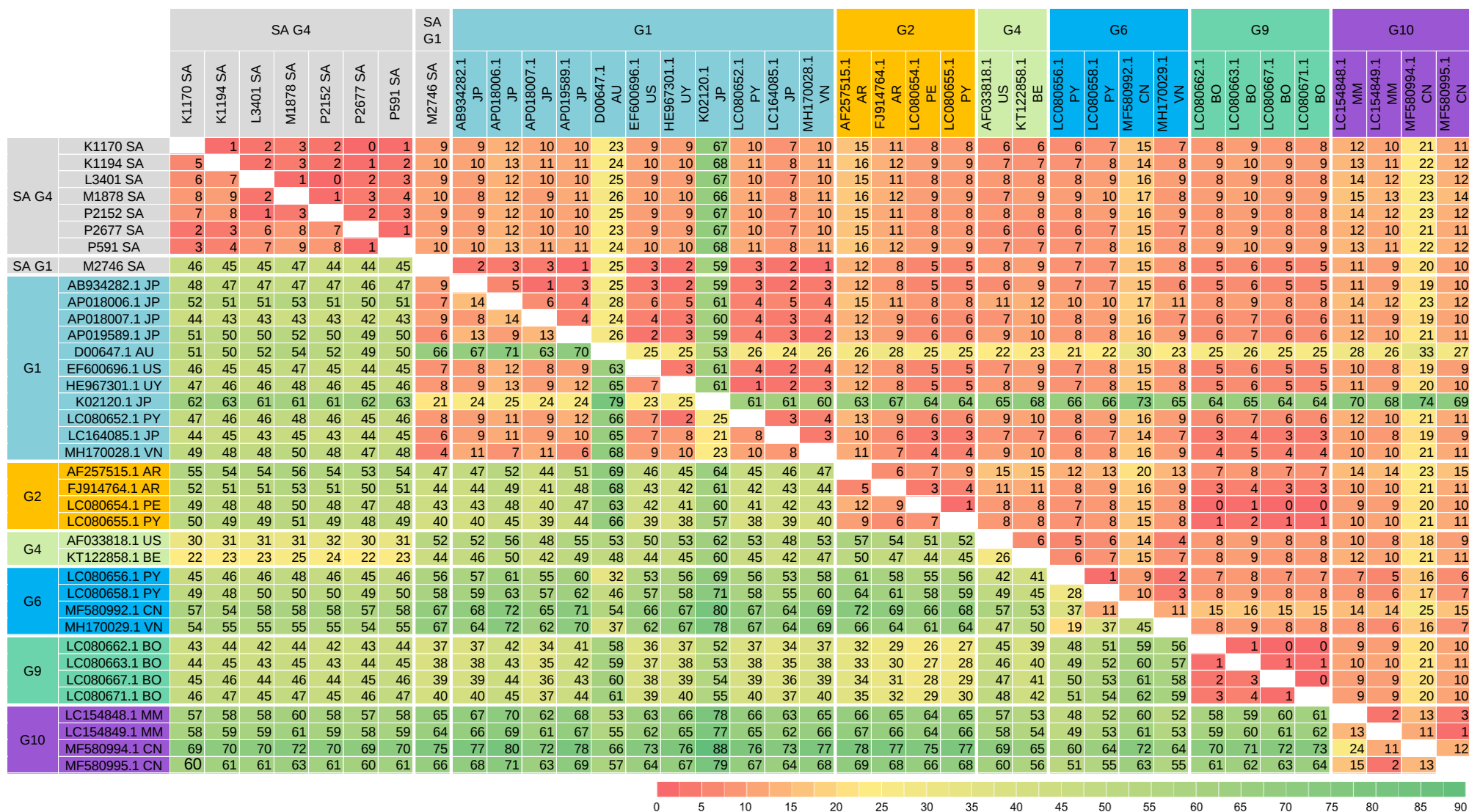


Figure S13. Pairwise comparison of BLV full-length Gag nucleotide (1,182 bp) and amino acid (393 amino acids) differences between the South African isolates and 29 selected isolates from other geographic regions worldwide. Lower matrix shows the number of nucleotide differences and the upper matrix shows the number of amino acid differences. The country of origin is indicated by 2-letter country codes (See Table S2). SA, South Africa.

Table S4. Mean nucleotide and amino acid distances in the BLV full-length Env sequences within (intra-genotype) and between (inter-genotype) BLV strains from South Africa and other geographic regions worldwide.

	SA G1	SA G4	G1	G2	G3	G4	G5	G6	G7	G9	G10
SA G1	N/A	0.0315±0.0080	0.0063±0.0022	0.0309±0.0064	0.0245±0.0066	0.0279±0.0068	0.0346±0.0073	0.0388±0.0072	0.0279±0.0064	0.0225±0.0063	0.0434±0.0075
SA G4	0.0387±0.0054	0.0013±0.0050 0.0011 ±0.0008	0.0330±0.0073	0.0361±0.0075	0.0292±0.0072	0.0141±0.0042	0.0332±0.0070	0.0319±0.0061	0.0280±0.0064	0.0288±0.0073	0.0362±0.0067
G1	0.0082±0.0018	0.0369±0.0051	0.0069±0.0007 0.0079 ±0.0013	0.0327±0.0061	0.0261±0.0062	0.0293±0.0064	0.0359±0.0070	0.0404±0.0068	0.0294±0.0060	0.0243±0.0059	0.0450±0.0071
G2	0.0346±0.0047	0.0383±0.0050	0.0328±0.041	0.0105±0.0017 0.0204±0.0046	0.0193±0.0044	0.0326±0.0064	0.0445±0.0077	0.0454±0.0072	0.0357±0.0067	0.0188±0.0045	0.0494±0.0075
G3	0.0304±0.0044	0.0342±0.0048	0.0302±0.0041	0.0255±0.0038	0.0049±0.0011 0.0031±0.0017	0.0256±0.0062	0.0375±0.0075	0.0387±0.0071	0.0291±0.0067	0.0138±0.0047	0.0432±0.0073
G4	0.0383±0.0049	0.0138±0.0022	0.0365±0.0044	0.0374±0.0045	0.0335±0.0043	0.0129±0.0017 0.0097±0.0026	0.0331±0.0068	0.0323±0.0057	0.0234±0.0059	0.0255±0.0061	0.0372±0.0062
G5	0.0423±0.0052	0.0377±0.0049	0.0397±0.0048	0.0462±0.0055	0.0441±0.0053	0.0389±0.0045	0.0162±0.0023 0.0164±0.0038	0.0443±0.0072	0.0345±0.0066	0.0381±0.0074	0.0487±0.0077
G6	0.0470±0.0051	0.0408±0.0047	0.0456±0.0047	0.0496±0.0050	0.0447±0.0048	0.0421±0.0043	0.0492±0.0048	0.0266±0.0030 0.0248±0.0042	0.0315±0.0056	0.0373±0.0069	0.0309±0.0050
G7	0.0394±0.0054	0.0324±0.0051	0.0377±0.0050	0.0423±0.0055	0.0397±0.0052	0.0341±0.0049	0.0445±0.0054	0.0454±0.049	0.0082±0.0018 0.0085±0.0030	0.0291±0.0067	0.0353±0.0061
G9	0.0313±0.0046	0.0347±0.0052	0.0312±0.0043	0.0239±0.0036	0.0224±0.0035	0.0356±0.0047	0.0448±0.0055	0.0446±0.0050	0.0410±0.0056	0.0016±0.0006 0.0014±0.0009	0.0408±0.0070
G10	0.0490±0.0053	0.0436±0.0049	0.0479±0.0049	0.0513±0.0052	0.0457±0.0049	0.0448±0.0046	0.0519±0.0049	0.0288 ±0.0033	0.0486±0.0052	0.0469±0.0052	0.0273±0.0033 0.0320 ±0.0054

Genetic distances in each column are shown with standard errors. The lower matrix shows intergenotype nucleotide distance and the upper matrix shows intergenotype amino acid distance. Diagonal columns (highlighted in green) show intra-genotype nucleotide (top) and amino acid (bottom) distances. Mean intergenotype nucleotide and amino acid distances between G1 and G4 South African isolates and the G1 and G4 global isolates are highlighted in yellow. N/A, not applicable.

References

1. Camargos, M.F.; Stancek, D.; Rocha, M.A.; Lessa, L.M.; Reis, J.K.; Leite, R.C. Partial sequencing of *env* gene of bovine leukaemia virus from Brazilian samples and phylogenetic analysis. *Journal of veterinary medicine. B, Infectious diseases and veterinary public health* **2002**, *49*, 325-331.
2. Camargos, M.F.; Pereda, A.; Stancek, D.; Rocha, M.A.; dos Reis, J.K.; Greiser-Wilke, I.; Leite, R.C. Molecular characterization of the *env* gene from Brazilian field isolates of Bovine leukemia virus. *Virus Genes* **2007**, *34*, 343-350, doi:10.1007/s11262-006-0011-x.
3. Murakami, H.; Uchiyama, J.; Suzuki, C.; Nikaido, S.; Shibuya, K.; Sato, R.; Maeda, Y.; Tomioka, M.; Takeshima, S.N.; Kato, H., et al. Variations in the viral genome and biological properties of bovine leukemia virus wild-type strains. *Virus Res* **2018**, *253*, 103-111, doi:10.1016/j.virusres.2018.06.005.
4. Johnston, E.R.; Albritton, L.M.; Radke, K. Envelope Proteins Containing Single Amino Acid Substitutions Support a Structural Model of the Receptor-Binding Domain of Bovine Leukemia Virus Surface Protein. *Journal of Virology* **2002**, *76*, 10861-10872, doi:10.1128/jvi.76.21.10861-10872.2002.
5. Coulston, J.; Naif, H.; Brandon, R.; Kumar, S.; Khan, S.; Daniel, R.C.; Lavin, M.F. Molecular cloning and sequencing of an Australian isolate of proviral bovine leukaemia virus DNA: comparison with other isolates. *J Gen Virol* **1990**, *71* 1737-1746, doi:10.1099/0022-1317-71-8-1737.
6. Zhao, X.; Buehring, G.C. Natural genetic variations in bovine leukemia virus envelope gene: possible effects of selection and escape. *Virology* **2007**, *366*, 150-165, doi:10.1016/j.virol.2007.03.058.
7. Derse, D.; Diniak, A.J.; Casey, J.W.; Deininger, P.L. Nucleotide sequence and structure of integrated bovine leukemia virus long terminal repeats. *Virology* **1985**, *141*, 162-166.
8. Hemmatzadeh, F. Sequencing and phylogenetic analysis of gp51 gene of bovine leukaemia virus in Iranian isolates. *Vet Res Commun* **2007**, *31*, 783-789, doi:10.1007/s11259-007-0012-9.
9. Rodriguez, S.M.; Golemba, M.D.; Campos, R.H.; Trono, K.; Jones, L.R. Bovine leukemia virus can be classified into seven genotypes: evidence for the existence of two novel clades. *J Gen Virol* **2009**, *90*, 2788-2797, doi:10.1099/vir.0.011791-0.
10. Sagata, N.; Yasunaga, T.; Tsuzuku-Kawamura, J.; Ohishi, K.; Ogawa, Y.; Ikawa, Y. Complete nucleotide sequence of the genome of bovine leukemia virus: its evolutionary relationship to other retroviruses. *Proc Natl Acad Sci U S A* **1985**, *82*, 677-681.
11. Yang, Y.; Kelly, P.J.; Bai, J.; Zhang, R.; Wang, C. First molecular characterization of bovine leukemia virus infections in the caribbean. *PLoS One* **2016**, *11*, e0168379, doi:10.1371/journal.pone.0168379.
12. Ochirkhuu, N.; Konnai, S.; Odbileg, R.; Nishimori, A.; Okagawa, T.; Murata, S.; Ohashi, K. Detection of bovine leukemia virus and identification of its genotype in Mongolian cattle. *Arch Virol* **2016**, *161*, 985-991, doi:10.1007/s00705-015-2676-8.
13. Polat, M.; Takeshima, S.N.; Hosomichi, K.; Kim, J.; Miyasaka, T.; Yamada, K.; Arainga, M.; Murakami, T.; Matsumoto, Y.; de la Barra Diaz, V., et al. A new genotype of bovine leukemia virus in South America identified by NGS-based whole genome sequencing and molecular evolutionary genetic analysis. *Retrovirology* **2016**, *13*, 4, doi:10.1186/s12977-016-0239-z.
14. Murakami, H.; Uchiyama, J.; Nikaido, S.; Sato, R.; Sakaguchi, M.; Tsukamoto, K. Inefficient viral replication of bovine leukemia virus induced by spontaneous deletion mutation in the G4 gene. *J Gen Virol* **2016**, *97*, 2753-2762, doi:10.1099/jgv.0.000583.
15. Phiri, M.M.; Kaimoyo, E.; Changula, K.; Silwamba, I.; Chambaro, H.M.; Kapila, P.; Kajihara, M.; Simuunza, M.; Muma, J.B.; Pandey, G.S., et al. Molecular detection and characterization of genotype 1 bovine leukemia virus from beef cattle in the traditional sector in Zambia. *Archives of virology* **2019**, *164*, 2531-2536, doi:<https://doi.org/10.1007/s00705-019-04350-6>.
16. Dao, T.D.; Bui, V.N.; Omatsu, T.; Katayama, Y.; Mizutani, T.; Ogawa, H.; Imai, K. Application of the SureSelect target enrichment system for next-generation sequencing to obtain the

- complete genome sequence of bovine leukemia virus. *Arch Virol* **2018**, *163*, 3155-3159, doi:10.1007/s00705-018-3957-9.
17. Dube, S.; Dolcini, G.; Abbott, L.; Mehta, S.; Dube, D.; Gutierrez, S.; Ceriani, C.; Esteban, E.; Ferrer, J.; Poiesz, B. The complete genomic sequence of a BLV strain from a Holstein cow from Argentina. *Virology* **2000**, *277*, 379-386, doi:10.1006/viro.2000.0622.
 18. Dube, S.; Abbott, L.; Dube, D.K.; Dolcini, G.; Gutierrez, S.; Ceriani, C.; Juliarena, M.; Ferrer, J.; Perzova, R.; Poiesz, B.J. The complete genomic sequence of an in vivo low replicating BLV strain. *Virol J* **2009**, *6*, 120, doi:10.1186/1743-422X-6-120.
 19. Lee, E.; Kim, E.J.; Joung, H.K.; Kim, B.H.; Song, J.Y.; Cho, I.S.; Lee, K.K.; Shin, Y.K. Sequencing and phylogenetic analysis of the gp51 gene from Korean bovine leukemia virus isolates. *Virol J* **2015**, *12*, 64, doi:10.1186/s12985-015-0286-4.
 20. Willems, L.; Gatot, J.S.; Mammerickx, M.; Portetelle, D.; Burny, A.; Kerkhofs, P.; Kettmann, R. The YXXL signalling motifs of the bovine leukemia virus transmembrane protein are required for in vivo infection and maintenance of high viral loads. *J Virol* **1995**, *69*, 4137-4141.
 21. Felmer, R.; Munoz, G.; Zuniga, J.; Recabal, M. Molecular analysis of a 444 bp fragment of the bovine leukaemia virus gp51 *env* gene reveals a high frequency of non-silent point mutations and suggests the presence of two subgroups of BLV in Chile. *Veterinary microbiology* **2005**, *108*, 39-47, doi:10.1016/j.vetmic.2005.04.005.
 22. Rola-Luszczak, M.; Pluta, A.; Olech, M.; Donnik, I.; Petropavlovskiy, M.; Gerilovych, A.; Vinogradova, I.; Choudhury, B.; Kuzmak, J. The molecular characterization of bovine leukaemia virus isolates from Eastern Europe and Siberia and its impact on phylogeny. *PLoS One* **2013**, *8*, e58705, doi:10.1371/journal.pone.0058705.
 23. Rice, N.R.; Stephens, R.M.; Couez, D.; Deschamps, J.; Kettmann, R.; Burny, A.; Gilden, R.V. The nucleotide sequence of the *env* gene and post-*env* region of bovine leukemia virus. *Virology* **1984**, *138*, 82-93, doi:[https://doi.org/10.1016/0042-6822\(84\)90149-1](https://doi.org/10.1016/0042-6822(84)90149-1).
 24. Pandey, G.S.; Simulundu, E.; Mwiinga, D.; Samui, K.L.; Mweene, A.S.; Kajihara, M.; Mangani, A.; Mwenda, R.; Ndebe, J.; Konnai, S., et al. Clinical and subclinical bovine leukemia virus infection in a dairy cattle herd in Zambia. *Archives of virology* **2017**, *162*, 1051-1056, doi:10.1007/s00705-016-3205-0.
 25. Mamoun, R.Z.; Morisson, M.; Rebeyrotte, N.; Busetta, B.; Couez, D.; Kettmann, R.; Hospital, M.; Guillemain, B. Sequence variability of bovine leukemia virus *env* gene and its relevance to the structure and antigenicity of the glycoproteins. *J Virol* **1990**, *64*, 4180-4188.
 26. Yang, Y.; Chen, L.; Dong, M.; Huang, W.; Hao, X.; Peng, Y.; Gong, Z.; Qin, A.; Shang, S.; Yang, Z. Molecular characterization of bovine leukemia virus reveals existence of genotype 4 in Chinese dairy cattle. *Virol J* **2019**, *16*, 108, doi:10.1186/s12985-019-1207-8.
 27. Fechner, H.; Blankenstein, P.; Looman, A.C.; Elwert, J.; Geue, L.; Albrecht, C.; Kurg, A.; Beier, D.; Marquardt, O.; Ebner, D. Provirus variants of the bovine leukemia virus and their relation to the serological status of naturally infected cattle. *Virology* **1997**, *237*, 261-269, doi:10.1006/viro.1997.8784.
 28. Gautam, S.; Mishra, N.; Kalaiyarasu, S.; Jhade, S.K.; Sood, R. Molecular characterization of bovine leukaemia virus (BLV) strains reveals existence of genotype 6 in cattle in India with evidence of a new subgenotype. *Transboundary and emerging diseases* **2018**, *65*, 1968-1978, doi:10.1111/tbed.12979.
 29. Wang, M.; Wang, Y.; Baloch, A.R.; Pan, Y.; Xu, F.; Tian, L.; Zeng, Q. Molecular epidemiology and characterization of bovine leukemia virus in domestic yaks (*Bos grunniens*) on the Qinghai-Tibet Plateau, China. *Archives of virology* **2018**, *163*, 659-670, doi:10.1007/s00705-017-3658-9.
 30. Yu, C.; Wang, X.; Zhou, Y.; Wang, Y.; Zhang, X.; Zheng, Y. Genotyping bovine leukemia virus in dairy cattle of Heilongjiang, northeastern China. *BMC Vet Res* **2019**, *15*, doi:<https://doi.org/10.1186/s12917-019-1863-3>.

31. Pluta, A.; Rola-Luszczak, M.; Kubis, P.; Balov, S.; Moskalik, R.; Choudhury, B.; Kuzmak, J. Molecular characterization of bovine leukemia virus from Moldovan dairy cattle. *Archives of virology* **2017**, *162*, 1563-1576, doi:10.1007/s00705-017-3241-4.
32. Molteni, E.; Agresti, A.; Meneveri, R.; Marozzi, A.; Malcovati, M.; Bonizzi, L.; Poli, G.; Ginelli, E. Molecular characterization of a variant of proviral bovine leukaemia virus (BLV). *Zentralblatt fur Veterinarmedizin. Reihe B. Journal of veterinary medicine. Series B* **1996**, *43*, 201-211.
33. Balic, D.; Lojkic, I.; Periskic, M.; Bedekovic, T.; Jungic, A.; Lemo, N.; Roic, B.; Cac, Z.; Barbic, L.; Madic, J. Identification of a new genotype of bovine leukemia virus. *Archives of virology* **2012**, *157*, 1281-1290, doi:10.1007/s00705-012-1300-4.
34. Lee, E.; Kim, E.J.; Ratthanophart, J.; Vitoonpong, R.; Kim, B.H.; Cho, I.S.; Song, J.Y.; Lee, K.K.; Shin, Y.K. Molecular epidemiological and serological studies of bovine leukemia virus (BLV) infection in Thailand cattle. *Infect Genet Evol* **2016**, *41*, 245-254, doi:10.1016/j.meegid.2016.04.010.
35. Polat, M.; Moe, H.H.; Shimogiri, T.; Moe, K.K.; Takeshima, S.N.; Aida, Y. The molecular epidemiological study of bovine leukemia virus infection in Myanmar cattle. *Archives of virology* **2017**, *162*, 425-437, doi:10.1007/s00705-016-3118-y.