Supplementary figure 1. PV Alignment of six isolates of PvLSA and their SNP

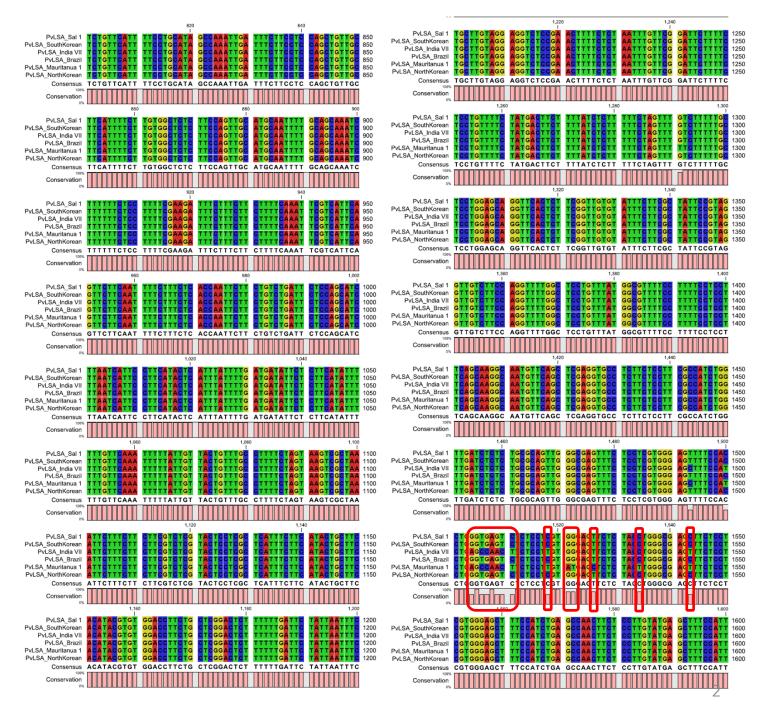
: SNP

lintron part

20 40	
PVLSA_Sal 1 PVLSA_SouthKorean TCACTGCAAC PVLSA_NourikKorean TCACTGCAAC TCGTCCGCCC PVLSA_Mauritanua 1 TCACTGCAAC TCGTCCGCCC TCGTCGCCC TCGTCCGCCC TCGTCCGCCC TCGTCGCCC TCGTCGCCC TCGTCGCCCC TCGTCGCCCC TCGTCGCCC TCGTCGCCC TCGTCGCCC TCGTCGCCC TCG	PVLSA_Sal1 TTGCTTTGCT CCTGTCGCT GCTGTTCAGG TGGCGCTTT GCGTGGCCAC 450 PVLSA_SouthKorean TTGCTTTGCT CCTGTCGCT GCTGTTCAGG TGGCGCTTT GCCTGCCCAC 450 PVLSA_India VII TTGCTTTGCT CCTGTCGCG GCGTTTCAGG TGGCGCTTT GCCTGCCCAC 450 PVLSA_Brazi TGCTTTGCT CCTGTGCGCT GCTGTTCAGG TGGCGCTTT GCCTGCCCAC 450 PVLSA_Maurianua 1 TGCTTTGCT CCTGTGTCGCT GCTGTTCAGG TGGCGCTTTT GCCTGCCCAC 450 PVLSA_Ndurianua 1 TGCTTTGCT CCTGTGTCGCT GCTGTTCAGG TGGCGCTTTT GCCTGCCCAC 450 PVLSA_Ndurianua 1 TGCTTTGCT CCTGTGTCGCT GCTGTTCAGG TGGCGCTTTT GCCTGCCCAC 450 CCTGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
PVLSA_Sal1 CCCGAATGCT GGCTCGATG AAGCTGAGTC GCTTGGTGAA GCTGTCGAGG 100 PVLSA_SouthKorean CCCGAATGCT GGCTCGATG AAGCTGAGTC GCTTGGTGAA GCTGTCGAGG 100 PVLSA_Brazi CCCGAATGCT GGCTCGATG AAGCTGAGTC GCTTGGTGAA CCTGTCGAGG 100 PVLSA_Brazi CCCGAATGCT GGCTCGATG AAGCTGAGTC GCTTGGTGAA CCTGTCGAGG 100 PVLSA_Mauritanua 1 CCCGAATGCT GGCTCGATG AAGCTGAGTC GCTTGGTGAA CCTGTCGAGG 100 PVLSA_NorthKorean CCCGAATGCT GGCTCGATG AAGCTGAGTC GCTTGGTGAA CCTGTCGAGG 100 Consensus CCCGAATGCT GGCTCGATG AAGCTGAGTC GCTTGGTGAA CCTGTCGAGG 100 CCnservation 0 T20 140	PvLSA_Sal1 CTGCTCGTAC TGCCTTGCA GGGAGGCCAC TTCCTCCTTG ACTTCGTTCA 500 PvLSA_SouthKorean CTGCTCGTAC TGCCTTGCA GGGAGGCCAC TTCCTCCTTG ACTTCGTTCA 500 PvLSA_Mauritanua 1 CTGCTCGTAC TGCCTTGCA GGGAGGCCAC TTCCTCGTCTTC ACTTCGTTCA 500 PvLSA_Mauritanua 1 CTGCTCGTAC TGCCTTCCA GGGAGGCCAC TTCCTCGTCTTG ACTTCGTTCA 500 PvLSA_Mauritanua 1 CTGCTCGTAC TGCCTTCCA GGGAGGCCAC TTCCTCGTCTTG ACTTCGTTCA 500 PvLSA_MouthKorean CTGCTCGTAC TGCCTTCCA GGGAGGCCAC TTCCTCGTTC ACTTCGTTCA 500 Conservation of tGCTCGTAC TGCCTTCCA GGGAGGCCAC TTCGTCCTTG ACTTCGTTCA 500 Conservation of tGCTCGTAC TGCCTTCCA GGGAGGCCAC TTCGTCCTTG ACTTCGTTCA 500 500 CONSERVATION OF 500 500 500 500 500 500 500 500 500 50
PVLSA_Sal1 GCCCCCCACA TGGTCTCCCT TTTCGTAGCT ATCTCCTCAT TTTCGAATTT 150 PVLSA_SouthKorean GCCCCCCACA TGGTCTCCCT TTTCGTAGCT ATCTCCTCAT TTTCGCAATTT 150 PVLSA_Brazi GCCCCCGCACA TGGTCTCGCT TTTCGTAGCT ATCTCCTCAT TTTGCAATTT 150 PVLSA_Brazi GCCCCGCACA TGGTCTCGCT TTTCGTAGCT ATCTCCTCAT TTTGCAATTT 150 PVLSA_Mauritanua 1 GCCCCGCGACA TGGTCTCGCT TTTCGTAGCT ATCTCCTCAT TTTGCAATTT 150 PVLSA_Mauritanua 1 GCCCCGCGACA TGGTCTCGCT TTTCGTAGCT ATCTCCTCAT TTTGCAATTT 150 PVLSA_Mauritanua 1 GCCCCCGCACA TGGTCTCGCT TTTCGTAGCT ATCTCCTCAT TTTGCAATTT 150 Consensus GCCCCCGCACA TGGTCTCGCT TTTCGTAGCT ATCTCCTCAT TTTGCAATTT 150 Consensus GCCCCCGCACA TGGTCTCGCT TTTCGTAGCT ATCTCCTCAT TTTGCAATTT 150 Consensus GCCCCCGCACA TGGTCTCGCT TTTCGTAGCT ATCTCCTCAT TTTGCAATTT 150 CONSensensus GCCCCCGCACA TGGTCTCGCT TTTCGTAGCT ATCTCCTCAT TTTGCAATTT 150 CONSENSUS GCCCCCGCACA TGGTCTCGCT TTTCGTAGCT ATCTCCTCAT TTTGCAATTT 150 CONSENSUS GCCCCCCGCACA TGGTCTCGCT TTTCGTAGCT ATCTCCTCAT TTTGCAATTT 150 CONSENSUS GCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	PVLSA_Sal1 GCTTGTGCGT GAGGTGGTGA TTCTTAAAAG TTAGCTGGTC GTTCTGGGTG 550 PVLSA_SouthKorean GCTTGTGCGT CAGGTGGTGA TTCTTAAAAG TTAGCTGGTG GTTCTGGGTG 550 PVLSA_India VII GCTTGTGCGT CAGGTGGTGA TTCTTAAAAG TTAGCTGGTG GTTCTGGGTG 550 PVLSA_Brazil GGTTGTGCGT CAGGTGGTGA TTCTTAAAAG TTAGCTGGTG GTTCTGGGTG 550 PVLSA_Maurianua 1 GGTTGTGCGT CAGGTGGTGA TTCTTAAAAG TTAGCTGGTG GTTCTGGGTG 550 PVLSA_NorthKorean GCTTGTCGCT CAGGTGGTGA TTCTTAAAAG TTAGCTGGTG GTTCTGGGTG 550 Conservation 0 0 550 580 600
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PVLSA_Sal 1 PVLSA_SouthKorean PVLSA_SouthKorean PVLSA_SouthKorean PVLSA_India VII PVLSA_Sal ndia VII PVLSA_Brazil TATICCTIGT ATAAGCTGCT TIGTTCCTTT ATTITGTGCTT CCAAAGATTT 300 PVLSA_Mauritanua 1 PVLSA_Mauritanua 1 PVLSA_Mauritanua 1 PVLSA_NorthKorean TATICCTIGT ATAAGCTCCT TIGTTCCTTT ATTITGTGCTT CCAAAGATTT 300 PVLSA_NorthKorean TATICCTIGT ATAAGCTCCT TIGTTCCTTT ATTITGTGCTT CCAAAGATTT 300 TATICCTIGT ATAAGCTCCT TIGTTCCTTT ATTITGTGCTT CCAAAGATTT 300 TATICCTIGT ATAAGCTCCT TIGTTCCTTT ATTITGTGCTT CCAAAGATTT 300 Consensus TATICCTIGT ATAAGCTCCT TIGTTCCTTT ATTITGTGCTT CCAAAGATTT 300 300 320 340	PvLSA_Sall I GCCCTCCCC TCCCCCCCCAT CATCCATCCCTCC 700 PvLSA_brainda VII I CCCCTCCCC TCCCCCCCCAC A CCCCCCCAT CATCTCCTCC 700 PvLSA_brain I CCCCTCCCC TCCCCCCCAC A CCCCCCCAT CATCTCCTCC 700 PvLSA_brain I CCCCTCCCC TCCCCCCCAC A CCCCCCCAT CATCTCCTCC 700 PvLSA_brain I CCCCTCCCC TCCCCCCCAC A CCCCCCCAT CATCTCCTCC 700 PvLSA_brain I CCCCCCCCCCCCCCCCCCAT CATCTCCCCCCCCCCC
PVLSA_Sal 1 PVLSA_SouthKorean PVLSA_SouthKorean PVLSA_SouthKorean PVLSA_SouthKorean PVLSA_SouthKorean PVLSA_MOUTH I TATAATGCTC ACATITITITA TGTTTAATTC TGTGTCCTTT TGTGTAAGTC 350 PVLSA_Brazil TATAATGCTC ACATITITITA TGTTTAATTC TGTGTCCTTT TGTGTAGTC 350 PVLSA_Mauritanua 1 TATAATGCTC ACATITITITA TGTTTAATTC TGTGTCCTTT TGTGTAGTC 350 PVLSA_NouthKorean TATAATGCTC ACATITITITA TGTTTAATTC TGTGTCCTTT TGTGTAGTC 350 PVLSA_NouthKorean TATAATGCTC ACATITITITA TGTTTAATTC TGTGTCCTTT TGTGTAGTC 350 TGTGTCCTTT TGTGTAGTC 350 TGTGTCCTCCTTT TGTGTAGTC 350 TGTGTCCTCCTTT TGTGTAGTC 350 TGTGTCCTCCTTT TGTGTAGTC 350 TGTGTCCTCCTTT TGTGTAGTC 350 TGTGTCCTCCTTT TGTGTAGTC 350 TGTGTCCTCCTCCTTT TGTGTAGTC 350 TGTGTCCTCCTCCTTT TGTGTAGTC 350 TGTGTCCTCCTCCTTT TGTGTAGTC 350 TGTGTCCTCCTCCTTT TGTGTAGTC 350 TGTGTCCTCCTCCTTT TGTGTAGTC 350 TGTGTCCTCCTCCTTT TGTGTAGTC 350 TGTGTCCCTCCTCCTTT TGTGTAGTC 350 TGTGTCCCTCCTCCTTT 70 TGTGTCCCTCCTCCTTT 70 TGTGTCCCTCCTCCTTT 70 TGTGTCCCTCCTCCTTT 70 TGTGTCCCTCCTCCTTT 70 TGTGTCCCTCCTCCTTT 70 TGTGTCCCCTCCTCCTTT 70 TGTGTCCCCTCCTCCTTT 70 TGTGTCCCTCCTCCTTT 70 TGTGTCCCCTCCTC	PvLSA_Sal 1 PvLSA_SouthKorean TCCTCATCT TCACCTCCT CACTCACTCATCT TCACCTCCTCCTCCATCACCACCTCACTCACCACCT PvLSA_India VII TCCTCATCT TCACCTCCCTCCATCCT TCACCTCCCTCCATCCT TCCTCATCT TCACCTCCCTCCATCCT TCACCTCCCTCCATCCT TCCTCATCT TCCTCATCT TCCTCATCT TCCTCATCT TCCTCATCT TCCTCATCT TCCTCATCT TCCTCATCT TCCTCATCT TCCTCATCT TCCTCCATCTC TCCTCCATCTC TCCTCCATCTC TCCTCCATCTC TCCTCCATCTC TCCTCCATCTC TCCTCCATCTC TCCTCCATCTC TCCTCCATCTC TCCTCCATCTC TCCTCCATCTC TCCTCCATCTC TCCTCCATCTC TCCTCCATCTCCATCTC TCCTCCATCTC T
PVLSA_Sal 1 GAATCAAGTC CCTATITATT GTTTCCAGGT GGTCAATCT GTGGTGAGT 400 PVLSA_SouthKorean CAATCAAGTC CCTATITATT GTTTCCAGGT GGTCAATCT GTGGTGAGT 400 PVLSA_India VI GAATCAAGTC CCTATITATT GTTTCCAGGT GGTCAATCT GTGGTGAGT 400 PVLSA_Brazi GAATCAAGTC CCTATITATT GTTTCCAGGT GGTCAATCT GTGGTGAGT 400 PVLSA_Mauritanua 1 GAATCAAGTC CCTATITATT GTTTCCAGGT GGTCAATCT GTGGTGAGT 400 PVLSA_NorthKorean GAATCAAGTC CCTATITATT GTTTCCAGGT GGTCAATCT GTGGTGAGT 400 Consensus GAATCAAGTC CCTATITATT GTTTCCAGGT GGTCAATCT GTGGTGAGT 400 Conservation	PVLSA_Sall CTCCATCTCG TGCACCCTGG ACTCCTACCT ATTGCTAATG CGCACCATGT 800 PVLSA_SultKorean CTCCATCTCG TGCACCCTGG ACTCCTACCT ATTGCTAATG CGCACCATGT 800 PVLSA_India VII CTCCATCTCG TGCACCCTGG ACTCCTACCT ATTGCTAATG CGCACCATGT 800 PVLSA_BTR2II CTCCATCTCG TGCACCCTGG ACTCCTACCT ATTGCTAATG CGCACCATGT 800 PVLSA_BTR2II CTCCATCTCG TGCACCCTGG ACTCCTACCT ATTGCTAATG CGCACCATGT 800 PVLSA_Munitanua 1 CTCCATCTCG TGCACCCTGG ACTCCTACCT ATTGCTAATG CGCACCATGT 800 POLSA_MUNITANUA 1 CTCCATCTCG TGCACCCTGG ACTCCTACGT ATTGCTAATG CGCACCATGT 800 POLSA_MUNITANUA 1 CTCCATCTCG TGCACCCTGG ACTCCTACGT ATTGCTAATG CGCACGATGT 800 POLSA_MUNITANUA 1 CTCCATCTCG TGCACCCTGG ACTCGTACGT ATTGCTAATG CGCACGATGT 800 POLSA_MUNITANUA 1 CTCCATCTCG TGCACCCTGG ACTCGTACGT ATTGCTAATGCTAATGCTAATGCTAATGCTAATGCTACGT 800 POLSA_MUNITANUA 1 CTCCATCTCG ACTCCTGACGACGATGT 800 POLSA_MUNITANUA 1 CTCCATCTGG ACTCCTACGT ATTGC

Supplementary figure 1. Alignment of six isolates of PvLSA and their SNP

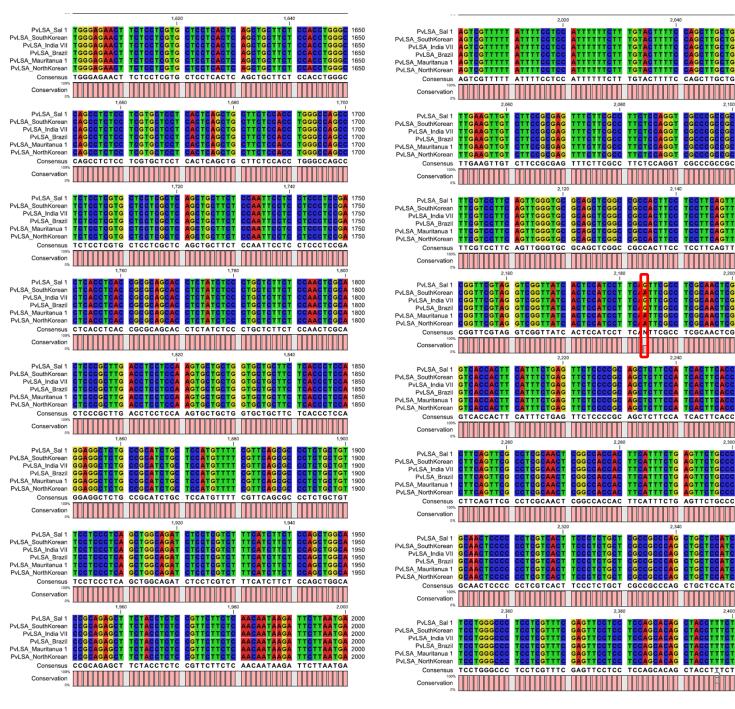




Supplementary figure 1. Alignment of six isolates of PvLSA and their SNP

: SNP

: Intron part



2,040

2,140

NTTCGCC TCGCAACTCG

GT

2.340

2.240

2.080

2,180

2,280

2,380

тс/

T 2150

T 2150

2.200

2400 2400

2,40

2,300

G 2200

CG 2200

TG 2050

GCTG 2050

2,10

Supplementary figure 1. PvLSA_Sal 1 PvLSA_Sal 1 2450 2450 2450 Alignment of six isolates PvLSA SouthKorean PvLSA SouthKorean PvI SA India VII PvI SA India VII 2450 PvLSA_Brazil PvLSA Brazil of PvLSA and their SNP PvLSA Mauritanua 1 2450 PvLSA Mauritanua 1 тg PvLSA NorthKorean PvLSA NorthKorean GCACT GACTCGACT 2450 AGCATGTTGT CTCCGCTTCG Consensus AGCATGTTGT GCACTTCGGA CTGTTCCTCC TCCCCCTCGG CTTCTCCCCC Consensus CTCCGCTTCG GACTCGACTT TCTTCAGCTC CTCCTTCAGC GCGGCCTCCT Conservation Conservation 2,460 2,480 2,500 2,860 2,880 2,900 PvLSA_Sal 1 2500 PvLSA_Sal 1 CTG 2900 CTG 2900 2500 PvLSA_SouthKorean PvLSA SouthKorean TAGAGACGCT 2500 TAGAGACGCT 2500 TAGAGACGCT 2500 TAGAGACGCT 2500 PvLSA India VII PvLSA India VII PvLSA Brazil PvLSA Brazil PvI SA Mauritanua 1 CTG 2900 PvI SA Mauritanua 1 TGGGT PvLSA_NorthKorean PvLSA NorthKorean CTTCTG 2900 ACCT TGGGTGGCG Consensus TTGGGTGGCG CTACCCTCCT CGTCTAACTG CGACGCGGTT ACCACTTCTG Consensus TCTCCCTCAT CGCTCTCTCC AACTCCTCTT CCTTCACCTT TAGAGACGCT Conservation Conservation 2,540 2,920 2,940 PvLSA_Sal 1 2550 PvLSA_Sal 2550 2550 2550 PvLSA_SouthKorean PvLSA_SouthKorean PvLSA_India VII PvLSA India VII CATAATTT PvLSA Brazil PvLSA Brazil 2550 PvLSA Mauritanua 1 PvLSA Mauritanua 1 PvLSA_NorthKorean PvLSA_NorthKorean 2550 Consensus TCCCGCTCCC GCGTCGCTCG CTGC. ACTCC TCCTCACGAT TCATAATTTC Consensus CACCTTCGCT CTCCTCTTTT ATGCTTTTCA ACTGGCTCAT TTTCCTATAC Conservation Conservation 2.560 2.580 2.600 2,960 2,980 PvLSA_Sal 1 PvLSA_Sal 1 2600 PvLSA_SouthKorean 2600 2600 PvLSA SouthKorean PvLSA India VII PvLSA India VII PvLSA_Brazil AG TGG 2600 PvLSA Brazil GTI PvLSA Mauritanua 1 GAG GG 2600 PvLSA Mauritanua 1 PvLSA NorthKorean CTTGG PvLSA NorthKorean GCTGGAGG тсст TATTGCTTCT 2600 GGTGAA Consensus CAGCTGGAGG TTCCTTTTTC CCTCTAAGAT CTCCTCTTGG TATTGCTTCT Consensus AGAGCGTCCA ACGCGCTCTC CTTCTCTGCA GCCAGGTGAA GTTTCTCCGC Conservation Conservation 2,620 2,640 3.020 3,040 PvLSA_Sal 1 2650 PvLSA_Sal 1 PvLSA_SouthKorean 2650 PvLSA SouthKorean 2650 PvLSA India VII PvLSA_India VII GTT 2650 PvLSA_Brazil GTTAAT PvLSA_Brazil PvI SA Mauritanua 1 2650 PvI SA Mauritanua 1 AAAGA GTT PvLSA NorthKorean 2650 PvLSA NorthKorean Consensus CCTTCTTTTT AAAAGAGGCG CTCCTCCTTC TCTCCTTTTC CTCCATCTCC Consensus TTCTAACTTT AGCCGGCCCT TAAAAGCTTC GTCCTCTTTT GTTAATCCCT Conservation Conservation 2,660 2,680 2,700 3,060 3,080 3,100 PvLSA_Sal 1 2700 PvLSA_Sal 1 GGGGG 3100 PvLSA_SouthKorean 2700 PvLSA_SouthKorean TGC TGC TGC TGC TGC **GGGG** 3100 ATGGT 2700 GGGGG 3100 PvLSA India VII PvLSA India VII TGTACA 2700 PvI SA Brazil TGGGGGG 3100 PvLSA Brazil GGTTT AATGG PvLSA Mauritanua 1 PvLSA Mauritanua 1 GGGGG 3100 AATT ATGGT 2700 AGGTTTT PvLSA_NorthKorean TTTTGTACA AATGGT 2700 PvLSA NorthKorean GATTA CTACCTTTT ттттт Consensus CTTAGAATTT CTAGGTTTTT TTTTTCCCTT TTTTTGTACA ACCGAATGGT Consensus TTTTCAGTGC ACTTAGAATA TGCTCGATTA GCTCCTTTTC CTTCTGGGGG Conservation Conservation 2,720 2.740 3.120 3,140 PvLSA_Sal 1 PvLSA_Sal 2750 2750 2750 PvLSA_SouthKorean PvLSA SouthKorean TTTG 3150 TTTTG 3150 PvLSA India VII PvLSA India VII PvLSA Brazil TCG 2750 PvLSA Brazil GGAAGGG TTG 3150 AAATO PvLSA Mauritanua 1 2750 PvLSA Mauritanua 1 PvLSA NorthKorean TTCG 2750 PvLSA NorthKorean TTTG 3150 Consensus TTCTTCGTTT TTCGCTTTCG CCCTTCTCAA TTCGTTGCAA AAATGAGCAA Consensus AGGAAGCCTC CTGGGTAGTT GCCGCTCATC GGAAGGGCCT TCTCCTTTTG Conservation Conservation 2.760 2,780 2,800 3,160 3,180 3.200 GGGGGG 3200 PvLSA_Sal 1 2800 PvLSA Sal 1 GATTAGGTGT 2800 GATTAGGTGT 2800 GGGGGGG 3200 PvLSA_SouthKorean PvLSA SouthKorean TGG AGGGGGGGG 3200 СТТАТ TTGG PvLSA India VII PvLSA India VII PvLSA Brazil GATTAGGTGT 2800 PvLSA Brazil TGG GGGAACAT TAGGGGGGGG 3200 GGTGT 2800 GGGGGGGG 3200 PvLSA Mauritanua 1 PvLSA Mauritanua 1 TGG AGGTGT 2800 TGGGAACATA PvLSA NorthKorean TTTTG PvLSA NorthKorean TTTGGT TAGGGGGGG 3200 Consensus ACGTTTCCAC CTCTCTTTG ATTTTCTTAT TTTTACTGTT GATTAGGTGT Consensus TTCGCTCACC CCTTCTGCCA TCGTTTTGGT TGGGAACATA CTAGGGGGGGG Conservation Conservation

2.820

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TG 3150

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TG 2900

2,420

: SNP

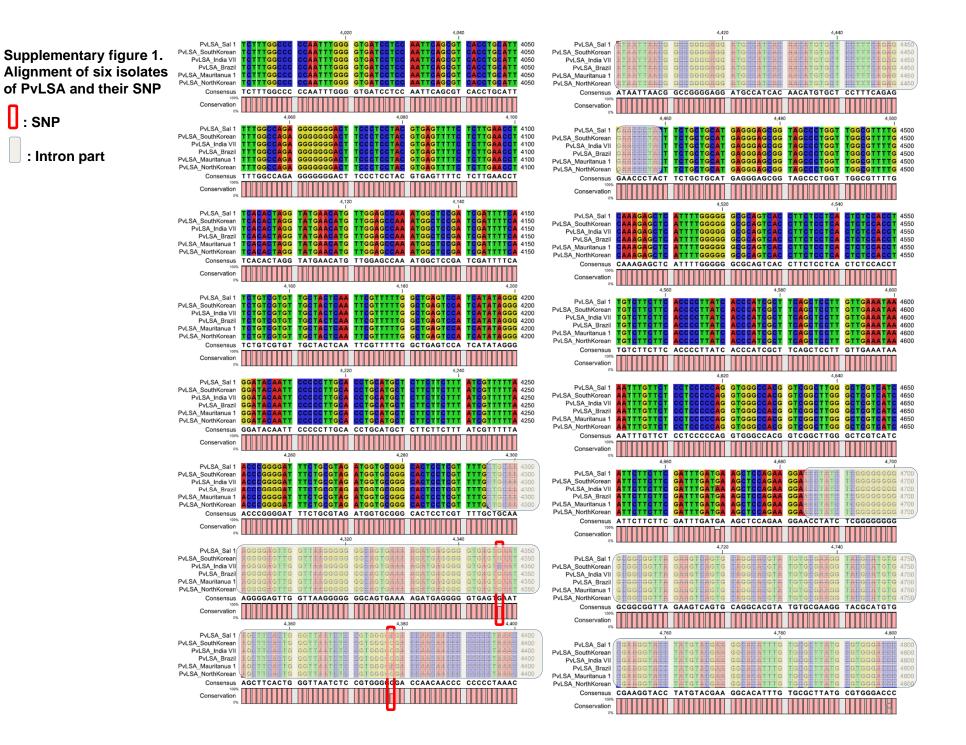
: Intron part

Supplementary figure 1. Alignment of six isolates of PvLSA and their SNP



lintron part

3,220 3,240		3,620 3,640
	TCCAG 3250 PvLSA_Brazil GGGTGGTATG TCCAG 3250 PvLSA_Mauritanua 1 GGGTGGTATG TCCAG 3250 PvLSA_NorthKorean GGGTGGTATG	TTAACCCCAC TTGGCGCGTT AAAACTGTCG AACTTCCTT 3650 TTAACCCCAC TTGGCGCGTT AAAACTGTCG AACGTTCCTT 3650
	TGGGA 3300 PVLSA_India VII TCAGTTCGAG TGGGA 3300 PVLSA_BraziI TCAGTTCGAG TGGGA 3300 PVLSA_Mauritanua 1 TCAGTTCGAG TGGGA 3300 PVLSA_NorthKorean TCAGTTCGAG	ACCTTGGGG ATGCTTTCAC TAGACGCTCC AATTCCCACG 3700 ACCTTGGGG ATGCTTTCAC TAGACGCTCC AATTCCCACG 3700 ACCCTTGGGG ATGCTTTCAC TAGACGCTCC AATTCCCACG 3700 ACCCTTGGGG ATGCTTTCAC TAGACGCTCC AATTCCCACG 3700
PvLSA_Mauritanua 1 GCCTTCCATT GCGCGCCCGT TGTAGGTGCC ATTCGGCATG GTCGCG	SAATT 3350 PvLSA_Brazil TAACTCTCTT SAATT 3350 PvLSA_Mauritanua 1 TAACTCTCTT SAATT 3350 PvLSA_Mauritanua 1 TAACTCTCTT SAATT 3350 PvLSA_Mouritanua 1 TAACTCTCTT	GEATGGGICE TCCCCTGT TCCAATITGG 3750 GEATGGCTCE TCCCTCTC TTCCTCCTAT TCCAATITGG 3750 GEATGGCTCE TCCCTCTC TTCCTCCTAT TCCAATITGG 3750 GCATGGCTCE TCCCTCTC TTCCTCCTAT TCCAATITGG 3750 GCATGGCTCE TCCCTCTC TTCCTCCTAT TCCAATITGG 3750 GCATGGGTCC TCCCCTGTCG TTCCTCCTAT TCGAATITGG
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Supplementary figure 1. Alignment of six isolates of PvLSA and their SNP



