

## BLASTx Search Outputs of the 3' End Border Sequences against GenBank Non-redundant Protein Sequences (nr)

BLASTX 2.2.21 [Jun-14-2009]

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Query= Region4  
(1868 letters)

Database: /usr/local/blast/db/blastlibs/nr  
10,862,569 sequences; 3,701,345,023 total letters

Searching.....done

Sequences producing significant alignments:		Score	E
		(bits)	Value
gb AAP94585.1	putative gag-pol precursor [Zea mays]	384	e-155
gb ABA97656.1	retrotransposon protein, putative, Ty3-gypsy subc...	97	9e-18
gb ADB85414.1	putative retrotransposon protein [Phyllostachys e...	96	2e-17
ref XP_002465565.1	hypothetical protein SORBIDRAFT_01g041205 [S...	96	2e-17
gb ABA97860.1	retrotransposon protein, putative, Ty3-gypsy subc...	96	2e-17
ref NP_001068452.1	Os11g0677500 [Oryza sativa (japonica cultiva...	89	2e-17
gb ABA95343.1	retrotransposon protein, putative, Ty3-gypsy subc...	89	2e-17
gb ABA98729.1	retrotransposon protein, putative, Ty3-gypsy subc...	89	2e-17
gb AAS90648.1	putative polyprotein [Oryza sativa Japonica Group...	89	3e-17
emb CAE03913.2	OSJNBb0015G09.7 [Oryza sativa (japonica cultivar...	89	3e-17
gb AAU43931.1	putative polyprotein [Oryza sativa Japonica Group]	89	3e-17
gb ABA92884.2	retrotransposon protein, putative, unclassified, ...	91	3e-17
gb AAV43881.1	putative polyprotein [Oryza sativa Japonica Group]	89	4e-17
gb AAV25234.1	putative polyprotein [Oryza sativa Japonica Group]	88	5e-17
ref XP_002436649.1	hypothetical protein SORBIDRAFT_10g006600 [S...	94	8e-17
emb CAD39962.2	OSJNBa0072D08.9 [Oryza sativa (japonica cultivar...	94	8e-17
gb ABA96533.1	retrotransposon protein, putative, Ty3-gypsy subc...	94	8e-17
emb CAE02993.2	OSJNBa0043L09.12 [Oryza sativa (japonica cultiva...	93	1e-16
emb CAD40441.1	OSJNBa0035B13.14 [Oryza sativa (japonica cultiva...	89	1e-16
gb AAT77397.1	putative polyprotein [Oryza sativa Japonica Group]	93	1e-16
gb AAK52121.1	AC079936_17 Putative retroelement [Oryza sativa Ja...	93	1e-16
gb ABB47490.1	retrotransposon protein, putative, Ty3-gypsy subc...	93	1e-16
emb CAE01888.2	OSJNBa0035O13.7 [Oryza sativa (japonica cultivar...	91	1e-16
emb CAJ86273.1	H0901F07.10 [Oryza sativa (indica cultivar-group)]	92	2e-16
emb CAE05745.1	OSJNBb0017I01.25 [Oryza sativa (japonica cultiva...	92	2e-16
gb ABA93980.1	retrotransposon protein, putative, Ty3-gypsy subc...	92	2e-16
gb AAL31060.1	AC090120_6 putative gag-pol precursor [Oryza sativ...	92	2e-16
gb ABF97190.1	retrotransposon protein, putative, Ty3-gypsy subc...	92	2e-16
emb CAD40114.1	OSJNBa0035O13.3 [Oryza sativa (japonica cultivar...	92	2e-16
gb ABA96683.1	retrotransposon protein, putative, Ty3-gypsy subc...	92	3e-16
gb AAT69666.1	putative polyprotein [Oryza sativa Japonica Group]	91	4e-16
gb ABA99121.1	transposon protein, putative, unclassified [Oryza...	91	4e-16
gb ABA92092.1	retrotransposon protein, putative, Ty3-gypsy subc...	91	4e-16
gb AAP52584.2	retrotransposon protein, putative, Ty3-gypsy subc...	91	5e-16
gb ABA98874.2	retrotransposon protein, putative, Ty3-gypsy subc...	91	5e-16
gb ABF94999.1	retrotransposon protein, putative, Ty3-gypsy subc...	91	5e-16
gb ABA97230.1	retrotransposon protein, putative, Ty3-gypsy subc...	91	5e-16
gb AAN09865.1	putative polyprotein [Oryza sativa Japonica Group]	91	5e-16

gb	AAK92558.1	AC051624_16 Putative retroelement [Oryza sativa Ja...	91	6e-16
gb	AAG59655.1	AC084319_13 putative gypsy-type retrotransposon [O...	91	6e-16
gb	ABB47110.1	retrotransposon protein, putative, Ty3-gypsy subc...	91	6e-16
emb	CAH66342.1	OSIGBa0104J13.2 [Oryza sativa (indica cultivar-g...	90	8e-16
gb	AAP54205.2	retrotransposon protein, putative, Ty3-gypsy subc...	90	8e-16
gb	ABF99975.1	retrotransposon protein, putative, Ty3-gypsy subc...	90	8e-16
gb	AAT93843.1	putative polyprotein [Oryza sativa Japonica Group]	90	8e-16
gb	AAT81721.1	putative retrotransposon protein [Oryza sativa Ja...	90	8e-16
gb	AAT77312.1	putative polyprotein [Oryza sativa Japonica Group...	90	8e-16
gb	AAS01973.1	retrotransposon protein, putative, Ty3-gypsy sub...	90	8e-16
emb	CAE03254.1	OSJNBa0011J08.9 [Oryza sativa (japonica cultivar...	90	8e-16
emb	CAD39396.2	OSJNBb0089K24.6 [Oryza sativa (japonica cultivar...	90	8e-16
gb	AAM00991.1	AC090482_20 Putative retroelement [Oryza sativa Ja...	90	8e-16
gb	ABB47210.1	retrotransposon protein, putative, Ty3-gypsy subc...	90	8e-16
gb	ABA92237.1	retrotransposon protein, putative, Ty3-gypsy subc...	90	8e-16
gb	AAK27822.1	AC022457_25 putative gag-pol precursor [Oryza sati...	90	8e-16
emb	CAE04437.2	OSJNBa0018J19.4 [Oryza sativa (japonica cultivar...	90	8e-16
gb	ABF99249.1	retrotransposon protein, putative, Ty3-gypsy subc...	90	1e-15
emb	CAE03068.2	OSJNBa0089E12.6 [Oryza sativa (japonica cultivar...	90	1e-15
gb	AAV44132.1	putative polyprotein [Oryza sativa Japonica Group]	90	1e-15
gb	AAT75246.1	putative gag-pol precursor [Oryza sativa Japonica...	90	1e-15
emb	CAE04995.2	OSJNBb0093G06.3 [Oryza sativa (japonica cultivar...	90	1e-15
gb	ABA97324.1	retrotransposon protein, putative, unclassified [...	90	1e-15
ref	NP_001061573.1	Os08g0334300 [Oryza sativa (japonica cultiva...	89	1e-15
gb	ABG65980.1	retrotransposon protein, putative, Ty3-gypsy subc...	89	1e-15
gb	AAU10736.1	putative polyprotein [Oryza sativa Japonica Group...	89	1e-15
gb	AAS98430.1	putative polyprotein [Oryza sativa Japonica Group]	89	1e-15
gb	AAS79740.1	putative polyprotein [Oryza sativa Japonica Group]	89	1e-15
gb	AAS90646.1	putative polyprotein [Oryza sativa Japonica Group]	89	1e-15
gb	ABA98213.1	retrotransposon protein, putative, Ty3-gypsy subc...	89	1e-15
gb	ABA98134.1	retrotransposon protein, putative, Ty3-gypsy subc...	89	1e-15
gb	AAL82662.1	AC092387_10 retrotransposon protein, putative, Ty3...	89	1e-15
gb	AAN08247.1	putative GAG-POL precursor [Oryza sativa Japonica...	89	1e-15
emb	CAE02263.2	OSJNBb0049I21.2 [Oryza sativa (japonica cultivar...	89	1e-15
emb	CAE01988.1	OSJNBb0033G08.4 [Oryza sativa (japonica cultivar...	89	1e-15
dbj	BAB19768.1	putative gypsy-type retrotransposon RIRE2 [Oryza...	89	1e-15
emb	CAH65837.1	OSIGBa0124C14.4 [Oryza sativa (indica cultivar-g...	89	2e-15
emb	CAH66795.1	H0215F08.6 [Oryza sativa (indica cultivar-group)]	89	2e-15
emb	CAH66866.1	H0307D04.11 [Oryza sativa (indica cultivar-group)]	89	2e-15
ref	NP_001062707.1	Os09g0261200 [Oryza sativa (japonica cultiva...	89	2e-15
gb	AAP52501.2	retrotransposon protein, putative, Ty3-gypsy subc...	89	2e-15
gb	AAP52640.2	retrotransposon protein, putative, Ty3-gypsy subc...	89	2e-15
gb	AAP52499.2	retrotransposon protein, putative, Ty3-gypsy subc...	89	2e-15
gb	ABA93602.2	retrotransposon protein, putative, Ty3-gypsy subc...	89	2e-15
gb	ABA96243.2	retrotransposon protein, putative, unclassified [...	89	2e-15
gb	ABA98926.2	retrotransposon protein, putative, Ty3-gypsy subc...	89	2e-15
gb	ABF93731.1	retrotransposon protein, putative, Ty3-gypsy subc...	89	2e-15
gb	AAT73678.1	putative polyprotein [Oryza sativa Japonica Group]	89	2e-15
gb	AAT44267.1	hypothetical protein [Oryza sativa Japonica Group]	89	2e-15
gb	AAT01309.1	putative gag-pol polyprotein [Oryza sativa Japoni...	89	2e-15
gb	AAR96234.1	putative polyprotein [Oryza sativa Japonica Group...	89	2e-15
emb	CAE04320.1	OSJNBb0016D16.11 [Oryza sativa (japonica cultiva...	89	2e-15
emb	CAE03508.2	OSJNBa0053K19.16 [Oryza sativa (japonica cultiva...	89	2e-15
emb	CAE05063.1	OSJNBa0094P09.2 [Oryza sativa (japonica cultivar...	89	2e-15
emb	CAE02298.2	OSJNBa0042F21.5 [Oryza sativa (japonica cultivar...	89	2e-15
emb	CAE02180.2	OSJNBa0080E14.11 [Oryza sativa (japonica cultiva...	89	2e-15
gb	AAL58229.1	AC084762_3 putative gag-pol precursor [Oryza sativ...	89	2e-15
gb	AAN04936.1	Putative retroelement [Oryza sativa Japonica Group]	89	2e-15
gb	ABA97070.1	retrotransposon protein, putative, Ty3-gypsy subc...	89	2e-15
gb	ABA97957.1	retrotransposon protein, putative, Ty3-gypsy subc...	89	2e-15
gb	ABA99219.1	retrotransposon protein, putative, Ty3-gypsy subc...	89	2e-15
gb	ABA97102.1	retrotransposon protein, putative, Ty3-gypsy subc...	89	2e-15
gb	ABA95029.1	retrotransposon protein, putative, Ty3-gypsy subc...	89	2e-15

gb	ABA95254.1	retrotransposon protein, putative, Ty3-gypsy subc...	89	2e-15
gb	ABA93599.1	retrotransposon protein, putative, Ty3-gypsy subc...	89	2e-15
gb	ABA94908.1	retrotransposon protein, putative, Ty3-gypsy subc...	89	2e-15
gb	ABA95079.1	retrotransposon protein, putative, Ty3-gypsy subc...	89	2e-15
gb	AAP54065.1	retrotransposon protein, putative, Ty3-gypsy subc...	89	2e-15
gb	AAM00949.1	AC021892_13 Putative retroelement [Oryza sativa Ja...	89	2e-15
gb	AAN08252.1	putative GAG-POL precursor [Oryza sativa Japonica...	89	2e-15
gb	AAM92798.1	putative gag-pol precursor [Oryza sativa Japonica...	89	2e-15
gb	AAD27551.1	AF111709_5 gag-pol protein [Oryza sativa Indica Gr...	89	2e-15
gb	AAM22011.1	AC093178_6 Putative gag-pol precursor [Oryza sativ...	89	2e-15
gb	AAM92802.1	putative gag-pol precursor [Oryza sativa Japonica...	89	2e-15
emb	CAD39529.2	OSJNBa0027001.4 [Oryza sativa (japonica cultivar...	89	2e-15
dbj	BAB00646.1	unnamed protein product [Oryza sativa Japonica G...	89	2e-15
gb	ABG66296.1	retrotransposon protein, putative, Ty3-gypsy subc...	89	2e-15
gb	ABG22603.1	retrotransposon protein, putative, unclassified [...	89	2e-15
gb	ABF98055.1	retrotransposon protein, putative, unclassified [...	89	2e-15
gb	ABF96608.1	retrotransposon protein, putative, Ty3-gypsy subc...	89	2e-15
gb	AAX95359.1	Retrotransposon gag protein, putative [Oryza sati...	89	2e-15
gb	AAV31353.1	putative polyprotein [Oryza sativa Japonica Group]	89	2e-15
gb	AAU90208.1	putative polyprotein [Oryza sativa Japonica Group]	89	2e-15
gb	AAS07318.1	putative polyprotein [Oryza sativa Japonica Group]	89	2e-15
gb	AAS07074.1	putative retrotransposon gag protein [Oryza sativ...	89	2e-15
gb	AAR88606.1	putative polyprotein [Oryza sativa Japonica Group]	89	2e-15
gb	AAR00629.1	putative reverse transcriptase [Oryza sativa Japo...	89	2e-15
emb	CAD40482.1	OSJNBa0067G20.4 [Oryza sativa (japonica cultivar...	89	2e-15
gb	ABA98178.1	retrotransposon protein, putative, Ty3-gypsy subc...	89	2e-15
gb	ABA97627.1	retrotransposon protein, putative, Ty3-gypsy subc...	89	2e-15
gb	ABA97049.1	retrotransposon protein, putative, Ty3-gypsy subc...	89	2e-15
gb	ABA98182.1	retrotransposon protein, putative, Ty3-gypsy subc...	89	2e-15
gb	AAX96254.1	transposon protein, putative, unclassified [Oryza...	89	2e-15
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emb	CAE02527.2	OSJNBb0003A12.14 [Oryza sativa (japonica cultiva...	89	2e-15
emb	CAH66285.1	OSIGBa0161P06.2 [Oryza sativa (indica cultivar-g...	88	3e-15
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gb	ABF96555.1	retrotransposon protein, putative, Ty3-gypsy subc...	88	3e-15
gb	ABF99143.1	retrotransposon protein, putative, Ty3-gypsy subc...	88	3e-15
gb	AAR06299.1	putative gag-pol protein [Oryza sativa Japonica G...	88	3e-15
gb	AAN65036.1	putative RIRE2 retrotransposon protein [Oryza sat...	88	3e-15
gb	ABA96009.1	retrotransposon protein, putative, unclassified [...	88	3e-15
gb	AAX96872.1	retrotransposon protein, putative, Ty3-gypsy sub-...	88	3e-15
gb	AAK43497.1	AC020666_7 gag-pol precursor [Oryza sativa Japonic...	88	3e-15
gb	AAT44283.1	putative polyprotein [Oryza sativa Japonica Group]	88	4e-15
gb	AAO66548.1	retrotransposon protein, putative, Ty3-gypsy sub-...	88	4e-15
gb	ABA98154.1	retrotransposon protein, putative, Ty3-gypsy subc...	88	4e-15
gb	AAV31300.1	putative polyprotein [Oryza sativa Japonica Group...	87	5e-15
emb	CAE01788.1	OSJNBa0039K24.7 [Oryza sativa (japonica cultivar...	87	5e-15
gb	ABA94416.2	retrotransposon protein, putative, Ty3-gypsy subc...	87	7e-15
gb	ABA97931.2	retrotransposon protein, putative, Ty3-gypsy subc...	87	7e-15
gb	ABA92141.1	retrotransposon protein, putative, Ty3-gypsy subc...	87	7e-15
gb	ABA94084.1	retrotransposon protein, putative, Ty3-gypsy subc...	87	7e-15
gb	AAK43513.1	AC020666_23 putative gag-pol precursor [Oryza sati...	87	7e-15
gb	AAM18733.1	AC092548_11 putative polyprotein [Oryza sativa Jap...	87	7e-15
emb	CAH66219.1	OSIGBa0157N01.5 [Oryza sativa (indica cultivar-g...	87	9e-15
emb	CAE02238.2	OSJNBb0054B09.2 [Oryza sativa (japonica cultivar...	87	9e-15
emb	CAE05337.1	OSJNBa0079M09.7 [Oryza sativa (japonica cultivar...	87	9e-15
gb	ABA97384.2	retrotransposon protein, putative, Ty3-gypsy subc...	86	1e-14
gb	AAU10764.1	putative polyprotein [Oryza sativa Japonica Group]	86	1e-14
gb	AAX96740.1	retrotransposon protein, putative, Ty3-gypsy sub-...	86	1e-14
gb	AAX92783.1	retrotransposon protein, putative, Ty3-gypsy sub-...	86	1e-14
emb	CAD39844.2	OSJNBb0072N21.13 [Oryza sativa (japonica cultiva...	86	1e-14
gb	AAT77889.1	putative polyprotein [Oryza sativa Japonica Group...	86	2e-14
gb	AAP06922.1	Putative gag-pol precursor [Oryza sativa Japonica...	86	2e-14
gb	ABA97679.1	retrotransposon protein, putative, Ty3-gypsy subc...	86	2e-14

gb ABA98116.1	retrotransposon protein, putative, Ty3-gypsy subc...	86	2e-14
dbj BAA84457.1	GAG-POL precursor [Oryza sativa Japonica Group]	86	2e-14
gb ABA97602.2	retrotransposon protein, putative, Ty3-gypsy subc...	86	2e-14
gb AAV43893.1	putative polyprotein [Oryza sativa Japonica Group...	86	2e-14
gb AAU90124.1	putative polyprotein [Oryza sativa Japonica Group]	86	2e-14
gb ABA99509.1	retrotransposon protein, putative, Ty3-gypsy subc...	86	2e-14
gb ABF99467.1	retrotransposon protein, putative, unclassified [...	85	3e-14
gb ABF98317.1	retrotransposon protein, putative, Ty3-gypsy subc...	85	3e-14
gb AAT77916.1	putative polyprotein [Oryza sativa Japonica Group]	85	3e-14
gb AAR87220.1	retrotransposon protein, putative, Ty3-gypsy sub...	85	3e-14
gb AAP20843.1	retrotransposon protein, putative, Ty3-gypsy sub...	85	3e-14
gb AAO38507.1	putative GAG-POL precursor [Oryza sativa Japonica...	85	3e-14
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gb ABA93786.1	retrotransposon protein, putative, Ty3-gypsy subc...	85	3e-14
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gb ABA95741.2	retrotransposon protein, putative, unclassified [...	85	4e-14
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ref XP_002448893.1	hypothetical protein SORBIDRAFT_05g000983 [S...	84	5e-14
emb CAH66736.1	H0404F02.12 [Oryza sativa (indica cultivar-group)]	84	5e-14
ref NP_001046396.1	Os02g0237300 [Oryza sativa (japonica cultiva...	84	5e-14
gb ABF93514.1	retrotransposon protein, putative, unclassified [...	84	5e-14
gb AAT94049.1	putative polyprotein [Oryza sativa Japonica Group]	84	5e-14
emb CAD39484.2	OSJNBa0039G19.13 [Oryza sativa (japonica cultiva...	84	5e-14
gb AAS75250.2	putative polyprotein [Oryza sativa Japonica Group]	84	5e-14
gb ABA97822.1	retrotransposon protein, putative, Ty3-gypsy subc...	84	5e-14
gb ABA94226.1	retrotransposon protein, putative, unclassified [...	84	5e-14
gb ABF93909.1	retrotransposon protein, putative, Ty3-gypsy subc...	84	6e-14
gb ABF98885.1	retrotransposon protein, putative, unclassified [...	84	6e-14
gb ABF99476.1	retrotransposon protein, putative, unclassified [...	84	6e-14
gb AAX95836.1	predicted protein [Oryza sativa Japonica Group]	84	6e-14
gb AAU90238.1	putative polyprotein [Oryza sativa Japonica Group]	84	6e-14
gb AAT77917.1	putative polyprotein [Oryza sativa Japonica Group]	84	6e-14
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gb ABA99910.2	retrotransposon protein, putative, unclassified [...	84	8e-14
gb ABF98607.1	retrotransposon protein, putative, unclassified [...	84	8e-14
gb ABF99688.1	retrotransposon protein, putative, unclassified [...	84	8e-14
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gb AAV32231.1	putative polyprotein [Oryza sativa Japonica Group]	84	8e-14
gb AAU44305.1	putative polyprotein [Oryza sativa Japonica Group]	84	8e-14
gb AAT81661.1	putative retrotransposon protein [Oryza sativa Ja...	84	8e-14
gb AAX95687.1	RNase H, putative [Oryza sativa Japonica Group]	84	8e-14
gb AAS07175.1	putative reverse transcriptase [Oryza sativa Jap...	84	8e-14
emb CAD41940.2	OSJNBa0070M12.17 [Oryza sativa (japonica cultiva...	84	8e-14
emb CAE03879.1	OSJNBb0015N08.7 [Oryza sativa (japonica cultivar...	84	8e-14
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gb AAO39874.1	putative gag-pol precursor [Oryza sativa Japonica...	84	8e-14
gb AAX96554.1	retrotransposon protein, putative, Ty3-gypsy sub...	84	8e-14
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emb CAH67479.1	H0805A05.9 [Oryza sativa (indica cultivar-group)]	83	1e-13
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emb CAH66724.1	OSIGBa0118P15.14 [Oryza sativa (indica cultivar-...	83	1e-13
gb ABA93826.2	retrotransposon protein, putative, unclassified [...	83	1e-13
gb ABA91113.2	retrotransposon protein, putative, unclassified [...	83	1e-13
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gb	ABF95088.1	transposon protein, putative, unclassified [Oryza...	83	1e-13
gb	ABF96139.1	retrotransposon protein, putative, unclassified [...	83	1e-13
gb	ABF97875.1	retrotransposon protein, putative, unclassified [...	83	1e-13
gb	ABF98199.1	retrotransposon protein, putative, unclassified [...	83	1e-13
gb	ABF95508.1	retrotransposon protein, putative, unclassified [...	83	1e-13
gb	ABF96344.1	retrotransposon protein, putative, unclassified [...	83	1e-13
gb	ABF93464.1	retrotransposon protein, putative, unclassified [...	83	1e-13
gb	AAV32176.1	putative polyprotein [Oryza sativa Japonica Group...	83	1e-13
gb	AAV25049.1	putative polyprotein [Oryza sativa Japonica Group]	83	1e-13
gb	AAU44275.1	putative polyprotein [Oryza sativa Japonica Group]	83	1e-13
gb	AAU44223.1	putative polyprotein [Oryza sativa Japonica Group]	83	1e-13
gb	AAU44127.1	putative polyprotein [Oryza sativa Japonica Group]	83	1e-13
gb	AAT75253.1	putative gag-pol precursor [Oryza sativa Japonica...	83	1e-13
gb	AAT07608.1	putative polyprotein [Oryza sativa Japonica Group...	83	1e-13
gb	AAR06355.1	putative polyprotein [Oryza sativa Japonica Group]	83	1e-13
gb	AAR01632.1	putative retrotransposon gag protein [Oryza sati...	83	1e-13
emb	CAD40221.2	OSJNBa0019J05.19 [Oryza sativa (japonica cultiva...	83	1e-13
emb	CAE05289.2	OSJNBa0084N21.7 [Oryza sativa (japonica cultivar...	83	1e-13
emb	CAE03695.2	OSJNBb0026E15.13 [Oryza sativa (japonica cultiva...	83	1e-13
emb	CAE05493.2	OSJNBa0022H21.13 [Oryza sativa (japonica cultiva...	83	1e-13
emb	CAE04563.1	OSJNBb0039L24.2 [Oryza sativa (japonica cultivar...	83	1e-13
gb	AAK26119.1	AC084406_2 putative gag-pol precursor [Oryza sativ...	83	1e-13
emb	CAD40917.1	OSJNBa0088K19.3 [Oryza sativa (japonica cultivar...	83	1e-13
gb	AAO24901.1	putative gag-pol precursor [Oryza sativa Japonica...	83	1e-13
gb	AAO17025.1	Putative gag-pol precursor [Oryza sativa Japonica...	83	1e-13
gb	ABA98426.1	retrotransposon protein, putative, unclassified [...	83	1e-13
gb	ABA98055.1	retrotransposon protein, putative, unclassified [...	83	1e-13
gb	ABA99541.1	retrotransposon protein, putative, unclassified [...	83	1e-13
gb	ABA91263.1	retrotransposon protein, putative, unclassified [...	83	1e-13
gb	ABA94639.1	retrotransposon protein, putative, unclassified [...	83	1e-13
gb	AAX96829.1	retrotransposon protein, putative, unclassified [...	83	1e-13
gb	AAX96438.1	retrotransposon protein, putative, Ty3-gypsy sub-...	83	1e-13
gb	AAL75973.1	AF466203_2 putative gypsy-type retrotransposon RIR...	83	1e-13
emb	CAE04928.2	OSJNBa0017P10.5 [Oryza sativa (japonica cultivar...	83	1e-13
emb	CAH67964.1	OSIGBa0142I02-OSIGBa0101B20.7 [Oryza sativa (ind...	83	1e-13
gb	ABB47352.2	retrotransposon protein, putative, unclassified [...	83	1e-13
gb	AAV59295.1	putative polyprotein [Oryza sativa Japonica Group]	83	1e-13
emb	CAE04690.1	OSJNBb0015D13.5 [Oryza sativa (japonica cultivar...	83	1e-13
emb	CAE01723.2	OSJNBb0050003.13 [Oryza sativa (japonica cultiva...	83	1e-13
gb	AAM08617.1	AC107314_8 Putative retroelement [Oryza sativa Jap...	83	1e-13
gb	AAO38003.1	putative polyprotein [Oryza sativa Japonica Group...	83	1e-13
gb	ABA99415.1	retrotransposon protein, putative, unclassified [...	83	1e-13
gb	AAN01247.1	Putative retroelement [Oryza sativa Japonica Grou...	83	1e-13
gb	AAL75981.1	AF466203_10 putative gag-pol precursor -orf1 [Zea ...	83	1e-13
gb	AAL75984.1	AF466203_13 putative prpol [Zea mays]	83	1e-13
emb	CAD39863.2	OSJNBa0036B17.4 [Oryza sativa (japonica cultivar...	83	1e-13
emb	CBG76438.1	OO_Ba0013J05-OO_Ba0033A15.25 [Oryza officinalis]	82	2e-13
emb	CAH66144.1	OSIGBa0114M03.2 [Oryza sativa (indica cultivar-g...	82	2e-13
gb	ABA91954.2	retrotransposon protein, putative, unclassified [...	82	2e-13
gb	ABF94908.1	retrotransposon protein, putative, unclassified [...	82	2e-13
emb	CAJ86094.1	H0818H01.16 [Oryza sativa (indica cultivar-group)]	82	2e-13
gb	AAV33321.1	putative polyprotein [Oryza sativa Japonica Group]	82	2e-13
gb	AAS07367.1	putative polyprotein [Oryza sativa Japonica Group...	82	2e-13
gb	ABA94156.1	retrotransposon protein, putative, unclassified [...	82	2e-13
gb	ABA93961.1	retrotransposon protein, putative, unclassified, ...	82	2e-13
gb	AAX95171.1	retrotransposon protein, putative, Ty3-gypsy sub-...	82	2e-13
gb	AAP54093.1	retrotransposon protein, putative, unclassified [...	82	2e-13
emb	CAE04960.2	OSJNBa0070D17.11 [Oryza sativa (japonica cultiva...	82	2e-13
emb	CAE01792.1	OSJNBa0039K24.11 [Oryza sativa (japonica cultiva...	82	2e-13
emb	CAH66086.1	H0209A05.3 [Oryza sativa (indica cultivar-group)]	82	2e-13
gb	AAV43898.1	putative polyprotein [Oryza sativa Japonica Group]	82	2e-13
emb	CAE05649.2	OSJNBa0038O10.15 [Oryza sativa (japonica cultiva...	82	2e-13
emb	CAE02013.3	OSJNBa0079A21.2 [Oryza sativa (japonica cultivar...	82	2e-13

gb	ABA97009.1	retrotransposon protein, putative, unclassified [...	82	2e-13
gb	ABA95992.1	retrotransposon protein, putative, unclassified [...	82	2e-13
gb	ABA94348.1	retrotransposon protein, putative, unclassified [...	82	2e-13
gb	AAX96721.1	retrotransposon protein, putative, unclassified [...	82	2e-13
emb	CAH66523.1	H0502B11.3 [Oryza sativa (indica cultivar-group)]	82	3e-13
gb	ABF95018.1	retrotransposon protein, putative, unclassified [...	82	3e-13
emb	CAE04098.3	OSJNBa0096F01.7 [Oryza sativa (japonica cultivar...	82	3e-13
emb	CAE03621.3	OSJNBb0003B01.12 [Oryza sativa (japonica cultiva...	82	3e-13
gb	ABA97229.1	retrotransposon protein, putative, unclassified [...	82	3e-13
gb	AAP52619.1	retrotransposon protein, putative, unclassified [...	82	3e-13
emb	CAE04538.2	OSJNBa0040D17.6 [Oryza sativa (japonica cultivar...	82	3e-13
emb	CAE01797.2	OSJNBa0039K24.16 [Oryza sativa (japonica cultiva...	82	3e-13
emb	CAH67840.1	OSIGBa0159H11-OSIGBa0137A07.3 [Oryza sativa (ind...	81	4e-13
emb	CAH67813.1	OSIGBa0138H21-OSIGBa0138E01.4 [Oryza sativa (ind...	81	4e-13
emb	CAH66336.1	OSIGBa0097I24.4 [Oryza sativa (indica cultivar-g...	81	4e-13
emb	CAH66864.1	H0307D04.9 [Oryza sativa (indica cultivar-group)]	81	4e-13
gb	ABF94245.1	transposon protein, putative, unclassified [Oryza...	81	4e-13
gb	ABF96052.1	transposon protein, putative, unclassified [Oryza...	81	4e-13
gb	ABF93468.1	retrotransposon protein, putative, unclassified [...	81	4e-13
gb	ABF94159.1	retrotransposon protein, putative, unclassified [...	81	4e-13
emb	CAH68539.2	OSJNBa0009P12.6 [Oryza sativa (japonica cultivar...	81	4e-13
gb	AAV44039.1	putative polyprotein [Oryza sativa Japonica Group]	81	4e-13
gb	AAV31310.1	putative polyprotein [Oryza sativa Japonica Group]	81	4e-13
gb	AAU44314.1	putative polyprotein [Oryza sativa Japonica Group]	81	4e-13
gb	AAT93919.1	putative polyprotein [Oryza sativa Japonica Group...	81	4e-13
gb	AAT85261.1	putative polyprotein [Oryza sativa Japonica Group]	81	4e-13
gb	AAS98497.1	putative polyprotein [Oryza sativa Japonica Group]	81	4e-13
gb	AAS75222.1	putative polyprotein [Oryza sativa Japonica Group...	81	4e-13
emb	CAD41428.2	OSJNBb0032E06.10 [Oryza sativa (japonica cultiva...	81	4e-13
emb	CAD40289.2	OSJNBb0062H02.6 [Oryza sativa (japonica cultivar...	81	4e-13
emb	CAD39933.2	OSJNBa0091C12.11 [Oryza sativa (japonica cultiva...	81	4e-13
emb	CAD41616.1	OSJNBa0091D06.19 [Oryza sativa (japonica cultiva...	81	4e-13
emb	CAE04174.2	OSJNBa0029C04.4 [Oryza sativa (japonica cultivar...	81	4e-13
emb	CAE05074.2	OSJNBa0094P09.13 [Oryza sativa (japonica cultiva...	81	4e-13
emb	CAD41181.1	OSJNBb0002J11.5 [Oryza sativa (japonica cultivar...	81	4e-13
emb	CAE03002.2	OSJNBa0043L09.21 [Oryza sativa (japonica cultiva...	81	4e-13
emb	CAE03902.2	OSJNBb0026I12.10 [Oryza sativa (japonica cultiva...	81	4e-13
emb	CAE05078.2	OSJNBa0094P09.17 [Oryza sativa (japonica cultiva...	81	4e-13
emb	CAE02878.1	OSJNBb0022F23.15 [Oryza sativa (japonica cultiva...	81	4e-13
emb	CAE01728.2	OSJNBb0050O03.18 [Oryza sativa (japonica cultiva...	81	4e-13
gb	AAP44696.1	putative GAG-POL precursor [Oryza sativa Japonica...	81	4e-13
gb	AAP06924.1	hypothetical protein [Oryza sativa Japonica Group...	81	4e-13
gb	AAM08627.1	AC107314_18 Unknown protein [Oryza sativa Japonica...	81	4e-13
gb	AAN06868.1	Putative polyprotein [Oryza sativa Japonica Group...	81	4e-13
gb	AAK55774.1	AC079038_8 Putative polyprotein [Oryza sativa]	81	4e-13
gb	AAO66539.1	retrotransposon protein, putative, unclassified [...	81	4e-13
gb	ABA97562.1	retrotransposon protein, putative, unclassified [...	81	4e-13
gb	ABA98262.1	transposon protein, putative, unclassified [Oryza...	81	4e-13
gb	ABA99331.1	retrotransposon protein, putative, unclassified [...	81	4e-13
gb	ABA99771.1	retrotransposon protein, putative, unclassified [...	81	4e-13
gb	ABA99567.1	retrotransposon protein, putative, unclassified [...	81	4e-13
gb	ABA96833.1	retrotransposon protein, putative, unclassified [...	81	4e-13
gb	ABA98939.1	transposon protein, putative, unclassified [Oryza...	81	4e-13
gb	ABA96776.1	transposon protein, putative, unclassified [Oryza...	81	4e-13
gb	ABA94515.1	retrotransposon protein, putative, unclassified [...	81	4e-13
gb	ABA95011.1	transposon protein, putative, unclassified [Oryza...	81	4e-13
gb	AAX96861.1	retrotransposon protein, putative, unclassified [...	81	4e-13
gb	AAX96377.1	retrotransposon protein, putative, unclassified [...	81	4e-13
gb	AAX96572.1	transposon protein, putative, unclassified [Oryza...	81	4e-13
gb	AAX96661.1	retrotransposon protein, putative, unclassified [...	81	4e-13
gb	AAP53950.1	transposon protein, putative, unclassified [Oryza...	81	4e-13
gb	AAN31788.1	Putative polyprotein [Oryza sativa Japonica Group...	81	4e-13
emb	CAE05339.2	OSJNBa0079M09.11 [Oryza sativa (japonica cultiva...	81	4e-13

emb	CAE02761.1	OSJNBb0085F13.8 [Oryza sativa (japonica cultivar...	81	4e-13
emb	CAE04877.2	OSJNBa0086006.25 [Oryza sativa (japonica cultiva...	81	4e-13
emb	CAE01816.2	OSJNBa0041A02.3 [Oryza sativa (japonica cultivar...	81	4e-13
gb	ABA94871.2	retrotransposon protein, putative, unclassified [...	81	5e-13
gb	AAD38291.1	AC007789_17 putative polyprotein [Oryza sativa Jap...	81	5e-13
gb	AAM19013.1	AC084748_3 putative gag-pol precursor protein [Ory...	81	5e-13
gb	ABA98790.1	retrotransposon protein, putative, unclassified [...	81	5e-13
gb	AAX95955.1	retrotransposon protein, putative, Ty3-gypsy sub-...	81	5e-13
gb	AAX95959.1	retrotransposon protein, putative, Ty3-gypsy sub-...	81	5e-13
emb	CAE03836.3	OSJNBb0013J13.13 [Oryza sativa (japonica cultiva...	81	5e-13
dbj	BAC05657.1	putative retrotransposon Cinfu1 [Oryza sativ...	81	5e-13
emb	CAD39523.2	OSJNBa0027001.10 [Oryza sativa (japonica cultiva...	81	5e-13
gb	ABA93149.2	retrotransposon protein, putative, Ty3-gypsy subc...	80	7e-13
gb	ABA96229.2	retrotransposon protein, putative, unclassified [...	80	7e-13
gb	AAU43927.1	putative polyprotein [Oryza sativa Japonica Group]	80	7e-13
gb	AAR01644.1	retrotransposon protein, putative, unclassified [...	80	7e-13
emb	CAE02825.2	OSJNBa0043A12.30 [Oryza sativa (japonica cultiva...	80	7e-13
emb	CAE03070.2	OSJNBa0089E12.8 [Oryza sativa (japonica cultivar...	80	7e-13
gb	AAM01165.2	AC113336_17 Hypothetical protein similar to putati...	80	7e-13
gb	ABA96681.1	retrotransposon protein, putative, unclassified [...	80	7e-13
gb	AAX96464.1	retrotransposon protein, putative, unclassified [...	80	7e-13
emb	CAE05254.2	OSJNBb0115I09.16 [Oryza sativa (japonica cultiva...	80	7e-13
emb	CAE03136.1	OJ000114_01.17 [Oryza sativa (japonica cultivar-...	80	7e-13
emb	CAH66808.1	OSIGBa0135C13.3 [Oryza sativa (indica cultivar-g...	80	9e-13
gb	AAU44318.1	putative polyprotein [Oryza sativa Japonica Group]	80	9e-13
emb	CAE06012.3	OSJNBa0016002.22 [Oryza sativa (japonica cultiva...	80	9e-13
gb	ABA97995.1	retrotransposon protein, putative, Ty3-gypsy subc...	80	9e-13
gb	ABA98027.2	retrotransposon protein, putative, unclassified [...	80	1e-12
gb	AAT07583.1	putative polyprotein [Oryza sativa Japonica Group]	80	1e-12
emb	CAD39966.2	OSJNBa0072D08.5 [Oryza sativa (japonica cultivar...	80	1e-12
gb	AAS88834.1	putative polyprotein [Oryza sativa Japonica Group]	80	1e-12
gb	AAK92547.1	AC051624_5 Putative retroelement [Oryza sativa Jap...	80	1e-12
emb	CAE05102.2	OSJNBa0009K15.22 [Oryza sativa (japonica cultiva...	80	1e-12
emb	CAH67380.1	OSIGBa0159F11.4 [Oryza sativa (indica cultivar-g...	79	1e-12
gb	ABF96045.1	transposon protein, putative, unclassified [Oryza...	79	1e-12
gb	ABF93729.1	retrotransposon protein, putative, Ty3-gypsy subc...	79	1e-12
gb	ABA99783.1	retrotransposon protein, putative, unclassified [...	79	1e-12
gb	ABA95291.1	transposon protein, putative, unclassified [Oryza...	79	1e-12
gb	ABA95175.1	retrotransposon protein, putative, unclassified [...	79	1e-12
gb	ABA94864.1	retrotransposon protein, putative, unclassified [...	79	1e-12
ref	XP_850639.1	PREDICTED: similar to F44E2.2b [Canis familiaris]	79	1e-12
gb	ABF97431.1	retrotransposon protein, putative, unclassified [...	79	2e-12
gb	AAU10818.1	putative polyprotein [Oryza sativa Japonica Group]	79	2e-12
emb	CAE76060.1	B1248C03.19 [Oryza sativa (japonica cultivar-gro...	79	2e-12
emb	CAD39796.2	OSJNBa0071G03.9 [Oryza sativa (japonica cultivar...	79	2e-12
emb	CAE01613.2	OSJNBa0067G20.11 [Oryza sativa (japonica cultiva...	79	2e-12
gb	AAN08230.1	putative gag-pol protein [Oryza sativa Japonica G...	79	2e-12
gb	AAO38019.1	putative gag-pol polyprotein [Oryza sativa Japoni...	79	2e-12
emb	CAH67052.1	OSIGBa0127A14.4 [Oryza sativa (indica cultivar-g...	79	3e-12
gb	AAL66751.1	AF464738_2 putative gag-pol precursor [Zea mays] >...	79	3e-12
gb	AAX95025.1	retrotransposon protein, putative, unclassified [...	78	3e-12
gb	AAT85160.1	putative polyprotein [Oryza sativa Japonica Group]	78	3e-12
gb	AAQ56480.1	putative polyprotein [Oryza sativa Japonica Group]	78	3e-12
gb	AAP06851.1	putative polyprotein [Oryza sativa Japonica Group...	78	3e-12
gb	AAO66535.1	transposon protein, putative, unclassified [Oryza...	78	3e-12
ref	XP_848677.1	PREDICTED: similar to Retrovirus-related Pol po...	78	3e-12
gb	AAX95002.1	transposon protein, putative, unclassified [Oryza...	78	3e-12
emb	CAE04515.1	OSJNBb0059K02.25 [Oryza sativa (japonica cultiva...	78	3e-12
gb	AAL58168.1	AC093181_14 putative gag-pol protein [Oryza sativa...	78	4e-12
gb	AAX95884.1	retrotransposon protein, putative, unclassified [...	78	4e-12
gb	AAN08658.1	putative gag-pol precursor [Oryza sativa Japonica...	78	4e-12
gb	AAU10826.1	putative polyprotein [Oryza sativa Japonica Group]	77	6e-12
gb	AAP03396.1	putative GAG-POL precursor [Oryza sativa Japonica...	77	6e-12

gb ABA98553.1	retrotransposon protein, putative, unclassified [...	77	6e-12
gb AAU90115.1	putative polyprotein [Oryza sativa Japonica Group]	77	7e-12
gb ABB46880.2	retrotransposon protein, putative, unclassified [...	77	1e-11
gb AAU10733.1	hypothetical protein [Oryza sativa Japonica Group]	76	1e-11
emb CAE03547.2	OSJNBa0060D06.13 [Oryza sativa (japonica cultivar...	76	1e-11
gb ABA92306.2	retrotransposon protein, putative, unclassified [...	76	2e-11
emb CAE05270.2	OSJNBb0014D23.4 [Oryza sativa (japonica cultivar...	75	4e-11
emb CAD40314.2	OSJNBb0013003.9 [Oryza sativa (japonica cultivar...	75	4e-11
emb CAH67337.1	OSIGBa0157A06.6 [Oryza sativa (indica cultivar-g...	74	5e-11
emb CAH66189.1	OSIGBa0144J05.1 [Oryza sativa (indica cultivar-g...	74	5e-11
ref NP_001042548.1	Os01g0240700 [Oryza sativa (japonica cultivar...	74	5e-11
gb ABF95742.1	retrotransposon protein, putative, unclassified [...	74	5e-11
gb ABA99805.1	retrotransposon protein, putative, unclassified [...	74	5e-11
emb CAE05341.2	OSJNBa0079M09.16 [Oryza sativa (japonica cultivar...	74	5e-11
emb CAH66232.1	H0825G02.9 [Oryza sativa (indica cultivar-group)]	74	8e-11
gb AAN40029.1	putative gag-pol precursor [Zea mays]	74	8e-11
gb AAX96012.1	retrotransposon protein, putative, Ty3-gypsy sub...	74	8e-11
gb ABF97049.1	retrotransposon protein, putative, Ty3-gypsy subc...	72	2e-10
gb AAP44595.1	putative polyprotein [Oryza sativa Japonica Group]	72	2e-10
gb AAN11193.1	Putative gag-pol precursor [Oryza sativa Japonica...	72	2e-10
gb ABA98574.1	retrotransposon protein, putative, Ty3-gypsy subc...	72	3e-10
gb ABA97299.1	transposon protein, putative, unclassified [Oryza...	71	4e-10
gb ABB47013.1	retrotransposon protein, putative, Ty3-gypsy subc...	71	5e-10
emb CAI44627.1	B1168G10.11 [Oryza sativa (japonica cultivar-gro...	70	7e-10
gb AAC01574.1	hypothetical protein [Zea mays]	70	9e-10
gb AAL75989.1	AF466204_4 putative GAG-POL precursor -orf1 protei...	70	9e-10
gb AAT77321.1	putative polyprotein [Oryza sativa Japonica Group...	70	1e-09
emb CAE05529.2	OSJNBa0053B21.3 [Oryza sativa (japonica cultivar...	69	2e-09
ref XP_002462065.1	hypothetical protein SORBIDRAFT_02g015765 [S...	69	2e-09
emb CAE02225.2	OSJNBb0015C06.3 [Oryza sativa (japonica cultivar...	69	2e-09
gb ABA99729.1	retrotransposon protein, putative, unclassified [...	69	2e-09
gb AAQ56293.1	putative gag-pol precursor [Oryza sativa Japonica...	69	3e-09
emb CAH67624.1	OSIGBa0140J09.5 [Oryza sativa (indica cultivar-g...	68	3e-09
emb CAE02343.1	OSJNBb0072M01.4 [Oryza sativa (japonica cultivar...	68	3e-09
emb CAE02456.1	OSJNBa0042D13.9 [Oryza sativa (japonica cultivar...	68	4e-09
gb ABA99442.1	retrotransposon protein, putative, Ty3-gypsy subc...	68	4e-09
gb AAO23086.1	putative gag-pol precursor [Oryza sativa Japonica...	67	6e-09
gb ABB47056.1	retrotransposon protein, putative, Ty3-gypsy subc...	67	6e-09
gb AAN64455.1	putative GAG-POL precursor [Oryza sativa Japonica...	67	8e-09
gb AAK50400.1	AC021891_1 Putative retroelement [Oryza sativa Jap...	67	1e-08
gb AAW56896.1	putative polyprotein [Oryza sativa Japonica Group]	67	1e-08
gb ABB46838.1	retrotransposon protein, putative, unclassified [...	67	1e-08
gb AAM01123.1	AC108884_5 Putative retroelement [Oryza sativa Jap...	67	1e-08
emb CAH67733.1	H0522A01.4 [Oryza sativa (indica cultivar-group)...	66	1e-08
gb AAK16189.1	AC079887_21 putative polyprotein [Oryza sativa Ja...	66	1e-08
gb AAO73254.1	putative GAG-POL precursor [Oryza sativa Japonica...	66	1e-08
gb AAO37471.1	putative polyprotein [Oryza sativa Japonica Group...	66	1e-08
gb ABA93613.1	retrotransposon protein, putative, Ty3-gypsy subc...	66	1e-08
dbj BAB39950.1	putative polyprotein [Oryza sativa Japonica Group]	66	2e-08
gb AAP52380.2	retrotransposon protein, putative, Ty3-gypsy subc...	65	2e-08
gb ABA96696.1	retrotransposon protein, putative, Ty3-gypsy subc...	65	3e-08
gb EEC73059.1	hypothetical protein OsI_07016 [Oryza sativa Indi...	65	4e-08
gb AAT47104.1	hypothetical protein [Oryza sativa Japonica Group]	65	4e-08
gb AAX95475.1	Integrase core domain, putative [Oryza sativa Jap...	65	4e-08
gb AAP53331.2	retrotransposon protein, putative, Ty3-gypsy subc...	64	5e-08
gb AAL58173.1	AC093181_19 putative polyprotein [Oryza sativa Jap...	64	5e-08
gb AAK52571.1	AC079685_2 Putative Gypsy-Ty3 type retrotransposon...	64	6e-08
emb CAE05833.1	OSJNBa0028M15.25 [Oryza sativa (japonica cultivar...	64	6e-08
emb CAE01996.2	OSJNBb0033G08.12 [Oryza sativa (japonica cultivar...	64	6e-08
emb CAH66268.1	OSIGBa0136B09.4 [Oryza sativa (indica cultivar-g...	64	8e-08
gb AAV24920.1	putative polyprotein [Oryza sativa Japonica Group...	64	8e-08
emb CAD40452.2	OSJNBa0041M21.10 [Oryza sativa (japonica cultivar...	64	8e-08
emb CAH66306.1	OSIGBa0135K14.3 [Oryza sativa (indica cultivar-g...	63	1e-07



gb AAV25276.1	hypothetical protein [Oryza sativa Japonica Group]	63	1e-07
gb AAT77832.1	putative gag-pol precursor [Oryza sativa Japonica...	63	1e-07
gb AAT47025.1	hypothetical protein [Oryza sativa Japonica Group]	63	1e-07
gb AAQ56482.1	putative gag-pol protein [Oryza sativa Japonica G...	63	1e-07
gb AAM01044.1	AC091735_17 Putative retroelement [Oryza sativa Ja...	63	1e-07
gb ABA98749.1	retrotransposon protein, putative, Ty3-gypsy subc...	63	1e-07
emb CAD40750.1	OSJNBa0081G05.3 [Oryza sativa (japonica cultivar...	63	1e-07
gb ABG65975.1	retrotransposon protein, putative, Ty3-gypsy subc...	63	1e-07
emb CAE02097.1	OSJNBa0020I02.4 [Oryza sativa (japonica cultivar...	63	1e-07
gb ABF98840.1	retrotransposon protein, putative, unclassified [...	62	2e-07
gb AAV32123.1	putative polyprotein [Oryza sativa Japonica Group]	62	2e-07
gb AAT77381.1	putative polyprotein [Oryza sativa Japonica Group]	62	2e-07
emb CAE03482.2	OSJNBa0065017.7 [Oryza sativa (japonica cultivar...	62	2e-07
gb ABA98293.1	retrotransposon protein, putative, Ty3-gypsy subc...	62	2e-07
ref NP_001056437.1	Os05g0582200 [Oryza sativa (japonica cultiva...	62	2e-07
gb ABF96473.1	retrotransposon protein, putative, Ty3-gypsy subc...	62	2e-07
gb AAT44202.1	putative polyprotein [Oryza sativa Japonica Group]	62	2e-07
gb AAK52140.1	AC084380_13 retrotransposon protein, putative, Ty3...	62	2e-07
gb AAW56879.1	putative polyprotein [Oryza sativa Japonica Group]	62	2e-07
gb AAK13087.1	AC078839_3 Similar to Zea mays retrotransposon Cin...	62	3e-07
gb ABB47459.1	retrotransposon protein, putative, Ty3-gypsy subc...	62	3e-07

>gb|AAP94585.1| putative gag-pol precursor [Zea mays]  
Length = 1833

Score = 384 bits (987), Expect(2) = e-155  
Identities = 222/403 (55%), Positives = 247/403 (61%)  
Frame = +2

Query: 107 MTITSKCKIALRPGTMFCFGTISSIADEEGTLHRIADLLEKKLSSEISRGARAEQRVAPS 286  
M +T KIA+RPG++FCFGTISS+ADEEG LH +ADL E+K S A  
Sbjct: 1 MAVTFHSKI AVRPGSVFCFGTISSVADEEGILHHLADLPEQKSPPTNS ENAGKTLL---- 56

Query: 287 PAPQAKMTSYKPKVGSSPTRKTPPLSTSPTEWTRITRKKEASVPSQGTGTRQAIFFPTPSP 466  
PA + K+ S + SS TRK+PLSTSPTEWTR+ RKKE T RQ + P P  
Sbjct: 57 PALRKKIVSGEAGARSSLTRKSPPLSTSPTEWTRVVRKKE-----TRERQIVLPVPPT 109

Query: 467 SNEDGKKSAIALAPFYDPDLFIRGRLELAPVFNDDEPTMQGEXXXXXXXXXXXXXXXXXXXXX 646  
S E+GKK A A PFYDPDLFI GR E V +DEPT GE  
Sbjct: 110 SKENGKKVAAAAIPFYDPDLFI-GRAESLAVSDDEPTAPGEEPPQRESRRRRNRNRNVRR 168

Query: 647 HHEAGERDPAQPVS RDEALEVGKTPDEWVHXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX 826  
HH AGE DP QPVS RDE EVG+TP+E V  
Sbjct: 169 HHAAGEWDPEQPVS RDEVSEVGETPEERVFRERRNSRRDRRRRTQEQAQDARQRE--- 225

Query: 827 XNALFARNLYPDFARAMNTPSEVGGVLAQIADGLPRTLDTGYRRLLTRAVNHLLPITNP 1006  
N LF RNL PDFARAMNTPSEVGGVLA IADGLPRT D EGYRRL T+A NHLLP+ +P  
Sbjct: 226 -NPLFGRNLNPDFARAMNTPSEVGGVLAWIADGLPRTDPAEGYRRLFTQAANHLLPLAHP 284

Query: 1007 PSDLRHAINSRDRTRSSINASRDR\*HESEIGNREEYVRDHAILA\*SHATRAESVAASTSV 1186  
P+DLRH INSRD RSSINASR+R HE+EI REEY RDH S ATR ES AST  
Sbjct: 285 PNDLRHTINSRRDARSSINASRERRHENEIRREEYDRDHGFPTQSQATRTE SATASTGG 344

Query: 1187 PFQGRSR\*HTTGSPWDRPHERRHEDTCGVFALTPCLRAIQWP 1315  
+GRSR SPP DR H RR EDTCGV ALTP LRAIQWP  
Sbjct: 345 TTRGRSRNRHHSPPRDRRHPRRQEDTCGVSA LTPRLRAIQWP 387

Score = 190 bits (482), Expect(2) = e-155  
Identities = 90/116 (77%), Positives = 96/116 (82%)  
Frame = +1

Query: 1315 PNFKVSNNVSKYERKQDLGGWLAITYTIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQH 1494  
PNFKVSN KYE KQD GGWLA+YT AAGA+EDVMT Y PIVLGQDA+QWLRHLP+H  
Sbjct: 388 PNFKVSNNFDKYEPKQDPGGWLAIVYTTAARAAGASEDVMTAYLPIVLGQDALQWLRHLPRH 447

Query: 1495 CIDNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRLYLKRF\*TMRNHTPE 1662  
CID+W DFS FIANFQSL DKPAQPWDLKSI +GDETLR YLKRF TMRN PE  
Sbjct: 448 CIDDWGDFSRRFIANFQSLSDKPAQPWDLKSIKRRGDETLRSYLKRFQTMNRRIPE 503

>gb|ABA97656.1| retrotransposon protein, putative, Ty3-gypsy subclass [Oryza sativa  
(japonica cultivar-group)]  
Length = 874

Score = 96.7 bits (239), Expect = 9e-18  
Identities = 50/148 (33%), Positives = 76/148 (51%)  
Frame = +1

Query: 1321 FKVSNNVSKYERKQDLGGWLAITYTIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
F+ + KY+ DL +L +Y+ + +AAGA ++ + Y P L A WL HLP + I  
Sbjct: 262 FRPGAIEKYDGGSTDL EEFLQVYSTILYAAGADDNALANYLPTALKGSARSWLMHLPYYSI 321

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W+D FIANFQ + + A DL + H E+LR Y++ F RN PE+ +A V  
Sbjct: 322 SSWADLWQQFIANFQGTYKRHAIEDDLHVLTHNSGESLREYVRHFNECRNTIPEITDASV 381

Query: 1681 IEDFYRGSNDSAFVRAILQKSVGHLRTL 1764  
I F G D + + + + R L  
Sbjct: 382 IRAFKSGVRDRYTTQELATRRITTTTRRL 409

>gb|ADB85414.1| putative retrotransposon protein [Phyllostachys edulis]  
Length = 1429

Score = 95.9 bits (237), Expect = 2e-17  
Identities = 55/127 (43%), Positives = 71/127 (55%), Gaps = 1/127 (0%)  
Frame = +1

Query: 1315 PN-FKVSNNVSKYERKQDLGGWLAITYTIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQ 1491  
PN F+ +N+ K+ ++ +L IYT AAG E+VM Y P VL A WL +LP  
Sbjct: 444 PNRFRPANLDKFNKTNPLEFLQIYTTTIRAAGGDENVMANLYLPTVLEGSARSWLLNLPV 503

Query: 1492 HCIDNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRLYLKRF\*TMRNHTPEVAE 1671  
I W IANFQ +D+P + DL I DETLR Y+KRF +RN PEVAE  
Sbjct: 504 ESIYTWEQLCDLLIANFQGTYDRPGKEDDLHRIRQGSDETLRQYIKRFSQVRNSLPEVAE 563

Query: 1672 AGVIEDF 1692  
+ VI+ F  
Sbjct: 564 SYVIQAF 570

>ref|XP\_002465565.1| hypothetical protein SORBIDRAFT\_01g041205 [Sorghum bicolor]  
gb|EER92563.1| hypothetical protein SORBIDRAFT\_01g041205 [Sorghum bicolor]  
Length = 1072

Score = 95.9 bits (237), Expect = 2e-17  
Identities = 51/143 (35%), Positives = 77/143 (53%), Gaps = 1/143 (0%)  
Frame = +1

Query: 1276 LRTYSVSPGHPVAP-NFKVSNNVSKYERKQDLGGWLAITYTIVTWAAGATEDVMTVYFPIVL 1452  
LR +S V P NFK+ + KY+ K++ W+ +Y I +A E VM YFP+VL  
Sbjct: 474 LRQFSSHLRQVWVPRNFKLEKLLKKYDGKENPENWITLYEIAVRSAGDEHVMANYFPVVL 533

Query: 1453 GQDAMQWLRHLPQH CIDNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRLYLKR 1632

Q QWL LP+ D+W + FI NF + ++P +DL+ I + +E LR Y++R  
Sbjct: 534 DQAGHQWLLGLPEDSFDSWEELRQAFIDNFIATCEQPGNKYDLERIRDRKNEPLRDYIRR 593

Query: 1633 F\*TMRNHTPEVAEAGVIEDFYRG 1701

F MR P+++ I F +G  
Sbjct: 594 FSDMRLKIPKISHDEAISAFIKG 616

>gb|ABA97860.1| retrotransposon protein, putative, Ty3-gypsy subclass [Oryza sativa  
(japonica cultivar-group)]  
Length = 955

Score = 95.5 bits (236), Expect = 2e-17  
Identities = 55/181 (30%), Positives = 91/181 (50%), Gaps = 5/181 (2%)  
Frame = +1

Query: 1237 PTSRTPT\*RHVRSRLRTYSVSPGHPVAPN-----FKVSNVSKYERKQDLGGWLAIYTIVTW 1401  
P ++T T + + T ++ +A N F+ ++ KY+ D +L +Y+IV +  
Sbjct: 6 PPTKTETVGPIMTDATTTIEIRRIIADNRRGTFKFRPGSIDKYDGSTDPEEFLQVYSIVLY 65

Query: 1402 AAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCHIDNWSDFSWCFIANFQSLFDKPAQPWDL 1581  
AAGA ++ + Y P+VL A W HLP + I +W D F+ANFQ + A DL  
Sbjct: 66 AAGADDNALANYLPVVLKGFARTWFWHLPPNSISSWEDLWQQFVANFQGTNKRHAIEDDL 125

Query: 1582 KSIGHQGDETLRLYLKRF\*TMRNHTPEVAEAGVIEDFYRGSNDSAFVRAILQKSVGHLRT 1761  
++ E+LR Y++RF +N PE+ +A VI F G D + + + + + R  
Sbjct: 126 HTLSQNPGESLRDYIRRFNECKNTIPEITDASVIRAFKSGDRDRYTTQELATRRITYARK 185

Query: 1762 L 1764  
L  
Sbjct: 186 L 186

>ref|NP\_001068452.1| Os11g0677500 [Oryza sativa (japonica cultivar-group)]  
Length = 2381

Score = 89.4 bits (220), Expect(2) = 2e-17  
Identities = 42/127 (33%), Positives = 67/127 (52%)  
Frame = +1

Query: 1321 FKVSNVSKYERKQDLGGWLAIYTIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCHI 1500  
FK + + KY+ + WL +Y + AAG M Y P+ L A WL LP+ I  
Sbjct: 947 FKPTGIEKYDGTTPNESWLTVYGLAIRAAGDNKAMANYLPVALADSARSWLHGLPRGTI 1006

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W++ FIANFQ F++P +DL ++ + E+LR Y++RF RN ++ + +  
Sbjct: 1007 GSWAELRDHFIANFQGTFERPGTQYDLYNVIQSGESLREYIRRFSEQRNKISDITDDVI 1066

Query: 1681 IEDFYRG 1701  
I F +G  
Sbjct: 1067 IAAFTKG 1073

Score = 26.6 bits (57), Expect(2) = 2e-17  
Identities = 11/23 (47%), Positives = 14/23 (60%)  
Frame = +2

Query: 1247 ERRHEDTCGVFALTPCLRAIQWP 1315  
+RR +D GV A T LR + WP  
Sbjct: 922 DRRDDDLGVAaftddLRRVDWP 944

>gb|ABA95343.1| retrotransposon protein, putative, Ty3-gypsy subclass [Oryza sativa  
(japonica cultivar-group)]  
Length = 2289

Score = 89.4 bits (220), Expect(2) = 2e-17  
Identities = 42/127 (33%), Positives = 67/127 (52%)  
Frame = +1

Query: 1321 FKVSNSVSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
FK + + KY+ + WL +Y + AAG M Y P+ L A WL LP+ I  
Sbjct: 707 FKPTGIEKYDGTTPESWLTIVYGLAIRAAGGDNKAMANYLPVALADSARSWLHGLPRGTI 766

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W++ FIANFQ F++P +DL ++ + E+LR Y++RF RN ++ + +  
Sbjct: 767 GSWAELRDHFIANFQGTFERPGTQYDLYNVIQKSGESLREYIRRFSEQRNKISDITDDVI 826

Query: 1681 IEDFYRG 1701  
I F +G  
Sbjct: 827 IAAFTKG 833

Score = 26.6 bits (57), Expect(2) = 2e-17  
Identities = 11/23 (47%), Positives = 14/23 (60%)  
Frame = +2

Query: 1247 ERRHEDTCGVFALTPCLRAIQWP 1315  
+RR +D GV A T LR + WP  
Sbjct: 682 DRRDDDLGVAFTDDLRRVDWP 704

>gb|ABA98729.1| retrotransposon protein, putative, Ty3-gypsy subclass [Oryza sativa  
(japonica cultivar-group)]  
Length = 1964

Score = 89.4 bits (220), Expect(2) = 2e-17  
Identities = 42/127 (33%), Positives = 67/127 (52%)  
Frame = +1

Query: 1321 FKVSNSVSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
FK + + KY+ + WL +Y + AAG M Y P+ L A WL LP+ I  
Sbjct: 434 FKPTGIEKYDGTTPESWLTIVYGLAIRAAGGDNKAMANYLPVALADSARSWLHGLPRGTI 493

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W++ FIANFQ F++P +DL ++ + E+LR Y++RF RN ++ + +  
Sbjct: 494 GSWAELRDHFIANFQGTFERPGTQYDLYNVIQKSGESLREYIRRFSEQRNKISDITDDVI 553

Query: 1681 IEDFYRG 1701  
I F +G  
Sbjct: 554 IAAFTKG 560

Score = 26.6 bits (57), Expect(2) = 2e-17  
Identities = 11/23 (47%), Positives = 14/23 (60%)  
Frame = +2

Query: 1247 ERRHEDTCGVFALTPCLRAIQWP 1315  
+RR +D GV A T LR + WP  
Sbjct: 409 DRRDDDLGVAFTDDLRRVDWP 431

>gb|AAS90648.1| putative polyprotein [Oryza sativa Japonica Group]

gb|AAS98432.1| putative polyprotein [Oryza sativa Japonica Group]  
Length = 2000

Score = 89.0 bits (219), Expect(2) = 3e-17  
Identities = 42/127 (33%), Positives = 67/127 (52%)  
Frame = +1

Query: 1321 FKVSNSVSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
FK + + KY+ + WL +Y + AAG M Y P+ L A WL LP+ I  
Sbjct: 434 FKPTGIEKYDGTTPESWLTIVYGLAIRAAGGDNKAMANYLPVALADSARSWLHGLPRGTI 493

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W++ FIANFQ F++P +DL ++ + E+LR Y++RF RN ++ + +  
Sbjct: 494 GSWAELRDHFIANFQGTFERPGTQYDLYNVIQKSGESLRDYIRRFSEQRNKISDITDDVI 553

Query: 1681 IEDFYRG 1701  
I F +G  
Sbjct: 554 IAAFTKG 560

Score = 26.6 bits (57), Expect(2) = 3e-17  
Identities = 11/23 (47%), Positives = 14/23 (60%)  
Frame = +2

Query: 1247 ERRHEDTCGVFALTPCLRAIQWP 1315  
+RR +D GV A T LR + WP  
Sbjct: 409 DRRDDDLGVAAF'TDDLRRVDWP 431

>emb|CAE03913.2| OSJNBb0015G09.7 [Oryza sativa (japonica cultivar-group)]  
Length = 1991

Score = 89.0 bits (219), Expect(2) = 3e-17  
Identities = 42/127 (33%), Positives = 67/127 (52%)  
Frame = +1

Query: 1321 FKVSNSVSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
FK + + KY+ + WL +Y + AAG M Y P+ L A WL LP+ I  
Sbjct: 434 FKPTGIEKYDGTTPESWLTIVYGLAIRAAGGDNKAMANYLPVALADSARSWLHGLPRGTI 493

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W++ FIANFQ F++P +DL ++ + E+LR Y++RF RN ++ + +  
Sbjct: 494 GSWAELRDHFIANFQGTFERPGTQYDLYNVIQKSGESLRDYIRRFSEQRNKISDITDDVI 553

Query: 1681 IEDFYRG 1701  
I F +G  
Sbjct: 554 IAAFTKG 560

Score = 26.6 bits (57), Expect(2) = 3e-17  
Identities = 11/23 (47%), Positives = 14/23 (60%)  
Frame = +2

Query: 1247 ERRHEDTCGVFALTPCLRAIQWP 1315  
+RR +D GV A T LR + WP  
Sbjct: 409 DRRDDDLGVAAF'TDDLRRVDWP 431

>gb|AAU43931.1| putative polyprotein [Oryza sativa Japonica Group]  
Length = 927

Score = 89.0 bits (219), Expect(2) = 3e-17  
Identities = 42/127 (33%), Positives = 67/127 (52%)  
Frame = +1

Query: 1321 FKVSNVSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
FK ++ KY+ + WL +Y + AAG M Y P+ L A WL LP+ I  
Sbjct: 434 FKPTGIEKYDGTTPESWLTIVYGLAIRAAGGDNKAMANYLPVALADSARSWLHGLPRGTI 493

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W++ FIANFQ F++P +DL ++ + E+LR Y++RF RN ++ + +  
Sbjct: 494 GSWAELRDHFIANFQGTFERPGTQYDLYNVIQKSGESLRDYIRRFSEQRNKISDITDDVI 553

Query: 1681 IEDFYRG 1701  
I F +G  
Sbjct: 554 IAAFTKG 560

Score = 26.6 bits (57), Expect(2) = 3e-17  
Identities = 11/23 (47%), Positives = 14/23 (60%)  
Frame = +2

Query: 1247 ERRHEDTCGVFALTPCLRAIQWP 1315  
+RR +D GV A T LR + WP  
Sbjct: 409 DRRDDDLGVAAFDTDDLRRVDWP 431

>gb|ABA92884.2| retrotransposon protein, putative, unclassified, expressed [Oryza  
sativa (japonica cultivar-group)]  
Length = 715

Score = 90.5 bits (223), Expect(2) = 3e-17  
Identities = 44/124 (35%), Positives = 68/124 (54%)  
Frame = +1

Query: 1321 FKVSNVSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
F++ + KY+R D +L +Y+ V +AAG ++ + Y P L WL HLP + I  
Sbjct: 323 FRLGTIEKYDRSTDPEEFLQVYSTVLYAAGVDDNALANYLPAALKGSTRSWLVHLPPLYI 382

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W+D F+ANFQ + + A DL ++ E+LR Y++RF RN PE+ +A V  
Sbjct: 383 SSWTDLWQQFVANFQGTYKRHAIEDDLHALKQNPGESLRDYIRRFNECRNTIPEITDASV 442

Query: 1681 IEDF 1692  
I F  
Sbjct: 443 IRAF 446

Score = 25.0 bits (53), Expect(2) = 3e-17  
Identities = 25/108 (23%), Positives = 41/108 (37%)  
Frame = +2

Query: 992 PITNPPSDLRHAINSRDRTRSSINASRDR\*HESEIGNREEYVRDHAILA\*SHATRAESVA 1171  
P+ SDLR +N RR+ R S E + R+ ++ + S +  
Sbjct: 237 PLPRGTSDLRDHLNGRREARRS-----QEPERHPRNRTPKPSDSSSSSSSSSS 283

Query: 1172 ASTSVPFQGRSR\*HTTGSPWPDRPHERRHEDTCGVFALTPCLRAIQWP 1315  
+S+S R+ H + P + G A T LR ++WP  
Sbjct: 284 SSSSNRHPRAHDHRQPTAP-----SGGCRAFTRFLREVWVP 320

>gb|AAV43881.1| putative polyprotein [Oryza sativa Japonica Group]

Length = 1551

Score = 89.0 bits (219), Expect(2) = 4e-17  
Identities = 44/127 (34%), Positives = 66/127 (51%)  
Frame = +1

Query: 1321 FKVSNVSKYERKQDLGGWLAITYTIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
FK + + KYE + WL Y + AAG M Y P+ L A WL LP+ I  
Sbjct: 420 FKPTGIEKYEGTTNPESWLTAYGLAIRAAGGDSKAMANYLPVALADSAQSWLHGLPRGTI 479

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W++ FIANFQ F++P +DL +I + E+LR Y++RF RN ++ + +  
Sbjct: 480 GSWAELRDHFIANFQGTFERPGTQFDLYNIIQKSGESLRDYIRRFSEQRNKISDITDNVI 539

Query: 1681 IEDFYRG 1701  
I F +G  
Sbjct: 540 IAAFTKG 546

Score = 26.2 bits (56), Expect(2) = 4e-17  
Identities = 14/34 (41%), Positives = 17/34 (50%)  
Frame = +2

Query: 1214 TTGSPPWDRPHERRHEDTCGVFALTPCLRAIQWP 1315  
T G P P +R +D GV A T LR + WP  
Sbjct: 385 TRGYAPHHSP-DRYDDVDVGAAFTSDLRRVDWP 417

>gb|AAV25234.1| putative polyprotein [Oryza sativa Japonica Group]  
Length = 1953

Score = 88.2 bits (217), Expect(2) = 5e-17  
Identities = 42/127 (33%), Positives = 67/127 (52%)  
Frame = +1

Query: 1321 FKVSNVSKYERKQDLGGWLAITYTIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
FK + + KY+ + WL +Y + AAG M Y P+ L A WL LP+ I  
Sbjct: 434 FKPTGIEKYDGTNPESWLTVYGLAIRAAGGDNKAMANYLPVALADSARSWLHGLPRGTI 493

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W++ FIANFQ F++P +DL ++ + E+LR Y++RF RN ++ + +  
Sbjct: 494 GSWAELRDHFIANFQGTFERPGTQYDLNVIQKPGESLRDYIRRFSEQRNKISDITDDVI 553

Query: 1681 IEDFYRG 1701  
I F +G  
Sbjct: 554 IAAFTKG 560

Score = 26.6 bits (57), Expect(2) = 5e-17  
Identities = 11/23 (47%), Positives = 14/23 (60%)  
Frame = +2

Query: 1247 ERRHEDTCGVFALTPCLRAIQWP 1315  
+RR +D GV A T LR + WP  
Sbjct: 409 DRRDDDLDGVAFTDDLRRVDWP 431

>ref|XP\_002436649.1| hypothetical protein SORBIDRAFT\_10g006600 [Sorghum bicolor]  
gb|EER88016.1| hypothetical protein SORBIDRAFT\_10g006600 [Sorghum bicolor]  
Length = 638

Score = 93.6 bits (231), Expect = 8e-17  
Identities = 45/128 (35%), Positives = 71/128 (55%)  
Frame = +1

Query: 1318 NFKVSNVSKYERKQDLGGWLAITYTIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHC 1497  
NFK+ + KY+ K++ W+ +Y I +A E +M YFP+VL Q QWL LP+  
Sbjct: 472 NFKLEKLKKYDGENPENWITLYEIAVRSAGDEHIMANYFPVVLQAGHQWLLGLPEDS 531

Query: 1498 IDNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEVAEAG 1677  
D+W + FI NF + ++P +DL+ I + +E LR Y++RF MR P+++  
Sbjct: 532 FDSWEELRQAFIDNFIATCEQPGNKYDLERIRDRKNEPLRDYIRRFSYMRLKIPKISHDE 591

Query: 1678 VIEDFYRG 1701  
I F +G  
Sbjct: 592 AISAFIKG 599

>emb|CAD39962.2| OSJNBa0072D08.9 [Oryza sativa (japonica cultivar-group)]  
Length = 880

Score = 93.6 bits (231), Expect = 8e-17  
Identities = 50/148 (33%), Positives = 77/148 (52%)  
Frame = +1

Query: 1321 FKVSNVSKYERKQDLGGWLAITYTIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
F+ + KY+R D +L +Y+ V +AAGA ++++ Y P L A WL HLP + I  
Sbjct: 432 FRPGAIEKYDRSTDPEEFLQVYSKVLAAAGANDNMLVNYLPAALKGSARSWLHLPPYSI 491

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W+D F+ANFQ + + A DL + E+LR Y++RF RN PE+ +A V  
Sbjct: 492 SSWADLWQQFVANFQGTYKRHAIEDDLHVLTONPGESLRDYVRRFNECRNTIPEITDASV 551

Query: 1681 IEDFYRGSNDSAFVRAILQKSVGHLRTL 1764  
I F G D + + + + R L  
Sbjct: 552 IRAFKTGVRDRYTTQELATRRITTTARKL 579

>gb|ABA96533.1| retrotransposon protein, putative, Ty3-gypsy subclass [Oryza sativa  
(japonica cultivar-group)]  
Length = 770

Score = 93.6 bits (231), Expect = 8e-17  
Identities = 53/159 (33%), Positives = 81/159 (50%)  
Frame = +1

Query: 1288 SVSPGHPVAPNFKVSNVSKYERKQDLGGWLAITYTIVTWAAGATEDVMTVYFPIVLGQDAM 1467  
S+S H F+ + KY+ D +L +Y+ V +AAGA ++V+ Y P L A  
Sbjct: 227 SISTPHE---RFRPGAIEKYDGSTDPEEFLQVYSTVLYAAGANDNVLANYLPTALKGSAR 283

Query: 1468 QWLRHLPQHCIDNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMR 1647  
WL HLP + I +W+D F+ANF+ + + A DL ++ E+LR Y++RF R  
Sbjct: 284 SWLMHLPPYSSISWADLWQQFVANFKGTYKRHAIEDDLHALTONPGESLRDYVQRFNECR 343

Query: 1648 NHTPEVAEAGVIEDFYRGSNDSAFVRAILQKSVGHLRTL 1764  
N PE+ +A VI F G D + + + V R L  
Sbjct: 344 NTIPEITDASVIRAFKSGVRDRYTTQELATRRVTTRRL 382

>emb|CAE02993.2| OSJNBa0043L09.12 [Oryza sativa (japonica cultivar-group)]  
Length = 1120

Score = 93.2 bits (230), Expect = 1e-16  
Identities = 50/158 (31%), Positives = 79/158 (50%)



Frame = +1

Query: 1291 VSPGHPVAPNFKVSNVSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQ 1470  
+ GH +A N + KY+ D +L +Y+ V +AAGA ++ + Y P L A  
Sbjct: 270 IHEGHTIADNPPPPALEKYDGSTDPEEFLQVYSTVLYAAGADDNALANYLPTALKGSARS 329

Query: 1471 WLRHLPQH CIDNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGD ETLRLYLKRF\*TM RN 1650  
WL HLP + I +W+D F+ANFQ + + A DL ++ E+LR Y++ F +N  
Sbjct: 330 WLMHLPPYSSISWADLWQQFVANFQGT YKRHAIEDDLHALTQNSGESLREYVQCFNECKN 389

Query: 1651 HTP EVAEAGVIEDFYRGSNDSAFVRAILQKSVGHLRTL 1764  
PE+ +A VI F G D + + + + R L  
Sbjct: 390 TIPEITDASVIRAFKSGVRDRYTTQELATRRITTT RRL 427

>emb|CAD40441.1| OSJNBa0035B13.14 [Oryza sativa (japonica cultivar-group)]  
Length = 1736

Score = 89.0 bits (219), Expect(2) = 1e-16  
Identities = 42/127 (33%), Positives = 67/127 (52%)  
Frame = +1

Query: 1321 FKVSNVSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQH CI 1500  
FK + + KY+ + WL +Y + AAG M Y P+ L A WL LP+ I  
Sbjct: 339 FKPTRIEKYDGTTPESWLT VYGLAIRAAGDNKAMANYLPVALADSARSWLHGLPRGTI 398

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGD ETLRLYLKRF\*TM RNHTPEVAEAGV 1680  
+W++ FIANFQ F++P +DL ++ + E+LR Y++RF RN ++ + +  
Sbjct: 399 GSWAELRDHF IANFQGTFERPGTQYDLYNVIQKSGESLRDYIRRFSEQRNKISDITDDVI 458

Query: 1681 IEDFYRG 1701  
I F +G  
Sbjct: 459 IAAFTKG 465

Score = 24.6 bits (52), Expect(2) = 1e-16  
Identities = 10/23 (43%), Positives = 14/23 (60%)  
Frame = +2

Query: 1247 ERRHEDTCGVFALTPCLRAIQWP 1315  
+RR ++ GV A T LR + WP  
Sbjct: 314 DRRDDNLDGVAAFTDDLRRVDWP 336

>gb|AAT77397.1| putative polyprotein [Oryza sativa Japonica Group]  
Length = 1194

Score = 92.8 bits (229), Expect = 1e-16  
Identities = 49/148 (33%), Positives = 75/148 (50%)  
Frame = +1

Query: 1321 FKVSNVSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQH CI 1500  
F+ + KY+ D +L +Y+ V +AAGA ++ + Y P L A WL HLP + I  
Sbjct: 447 FRPGAIEKYDGSTDPEKEFLQVYSTVLYAAGADDNALANYLPTALKGSARSWLHMLPPYSI 506

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGD ETLRLYLKRF\*TM RNHTPEVAEAGV 1680  
+W+D FIANFQ + + A DL ++ E+LR Y++R RN PE+ +A V  
Sbjct: 507 SSWADLRQQFIANFQGT YKRHAIEDDLHALTQNSGESLREYVRRLNECRNTIPEITDASV 566

Query: 1681 IEDFYRGSNDSAFVRAILQKSVGHLRTL 1764  
I F G D + + + + R L  
Sbjct: 567 IRAFKSGVRDRYTTQELATRRITTT RRL 594

>gb|AAK52121.1|AC079936\_17 Putative retroelement [Oryza sativa Japonica Group]  
Length = 2079

Score = 92.8 bits (229), Expect = 1e-16  
Identities = 49/148 (33%), Positives = 76/148 (51%)  
Frame = +1

Query: 1321 FKVSNVSKYERKQDLGGWLAIYTIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
F+ + KY+ D +L +Y+ V +AAGA ++ + Y P L A WL HLP + I  
Sbjct: 578 FRPGAIEKYDGSIDPEEFLQVYSTVLYAAGADDAVANYLPTALKGSARSWLMHLPPYSI 637

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W+D F+ANFQ + + A DL ++ E+LR Y++RF RN PE+ +A V  
Sbjct: 638 SSWADLWQQFVANFQGTYKRHAIEDDLHALTQNSGESLREYVRRFNECRNTIPEITDASV 697

Query: 1681 IEDFYRGSNDSAFVRAILQKSVGHLRTL 1764  
I F G D + + + + R L  
Sbjct: 698 IRAFKSGVRDRYTTQELATRHITTTTRL 725

>gb|ABB47490.1| retrotransposon protein, putative, Ty3-gypsy subclass [Oryza sativa  
(japonica cultivar-group)]  
Length = 1783

Score = 92.8 bits (229), Expect = 1e-16  
Identities = 49/148 (33%), Positives = 76/148 (51%)  
Frame = +1

Query: 1321 FKVSNVSKYERKQDLGGWLAIYTIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
F+ + KY+ D +L +Y+ V +AAGA ++ + Y P L A WL HLP + I  
Sbjct: 522 FRPGAIEKYDGSIDPEEFLQVYSTVLYAAGADDAVANYLPTALKGSARSWLMHLPPYSI 581

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W+D F+ANFQ + + A DL ++ E+LR Y++RF RN PE+ +A V  
Sbjct: 582 SSWADLWQQFVANFQGTYKRHAIEDDLHALTQNSGESLREYVRRFNECRNTIPEITDASV 641

Query: 1681 IEDFYRGSNDSAFVRAILQKSVGHLRTL 1764  
I F G D + + + + R L  
Sbjct: 642 IRAFKSGVRDRYTTQELATRHITTTTRL 669

>emb|CAE01888.2| OSJNBa0035013.7 [Oryza sativa (japonica cultivar-group)]  
Length = 1421

Score = 91.3 bits (225), Expect(2) = 1e-16  
Identities = 48/130 (36%), Positives = 69/130 (53%)  
Frame = +1

Query: 1321 FKVSNVSKYERKQDLGGWLAIYTIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
F+ + KY+ D +L +Y+ V +AAGA ++ + Y P A WL HLP + I  
Sbjct: 109 FRPGAIEKYDGSTDPEEFLQVYSTVLYAAGADDAVANYLPTAWKGSARSWLMHLPSYSI 168

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
+WSD F+ANFQ + A DL ++ H E+LR Y++RF RN PE+ +A V  
Sbjct: 169 SSWSDLWQQFVANFQGTNKRHAIEDDLHALTHNSGESLRGYVRRFNECRNTIPEITDASV 228

Query: 1681 IEDFYRGSND 1710  
I F G D  
Sbjct: 229 ICAFKSGVRD 238

Score = 21.9 bits (45), Expect(2) = 1e-16  
Identities = 9/26 (34%), Positives = 14/26 (53%)  
Frame = +2

Query: 1238 RPHERRHEDTCGVFALTPCLRAIQWP 1315  
R H + + G AL+ LR ++WP  
Sbjct: 81 RDHRQPTAPSAGCRALSRSRLRDVRWP 106

>emb|CAJ86273.1| H0901F07.10 [Oryza sativa (indica cultivar-group)]  
Length = 1884

Score = 92.4 bits (228), Expect = 2e-16  
Identities = 50/148 (33%), Positives = 75/148 (50%)  
Frame = +1

Query: 1321 FKVSNVSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
F+ + KY+ D +L +Y+ V +AAGA + + Y P L A WL HLP + I  
Sbjct: 429 FRPGAIEKYDGTDPPEEFLQVYSTVLYAAGADNNALANYLPTALKGSARSWLMHLPPYSI 488

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W+D FIANFQ + + A DL ++ E+LR Y++RF RN PE+ +A V  
Sbjct: 489 SSWADLWQQFIANFQGTYKRHAIEDDLHALTQNSGESLREYVRRFNECRNTIPEITDASV 548

Query: 1681 IEDFYRGSNDSAFVRAILQKSVGHLRTL 1764  
I F G D + + + + R L  
Sbjct: 549 IRAFKSGVRDRYTTQELATRRITTTTRRL 576

>emb|CAE05745.1| OSJNBb0017I01.25 [Oryza sativa (japonica cultivar-group)]  
emb|CAE03420.1| OSJNBa0032F06.3 [Oryza sativa (japonica cultivar-group)]  
Length = 1728

Score = 92.4 bits (228), Expect = 2e-16  
Identities = 50/148 (33%), Positives = 75/148 (50%)  
Frame = +1

Query: 1321 FKVSNVSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
F+ + KY+ D +L +Y+ V +AAGA + + Y P L A WL HLP + I  
Sbjct: 417 FRPGAIEKYDGTDPPEEFLQVYSTVLYAAGADNNALANYLPTALKGSARSWLMHLPPYSI 476

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W+D FIANFQ + + A DL ++ E+LR Y++RF RN PE+ +A V  
Sbjct: 477 PSWADLWQQFIANFQVITYKRHAIEDDLHALTQNSGESLREYVRRFNECRNTIPEITDASV 536

Query: 1681 IEDFYRGSNDSAFVRAILQKSVGHLRTL 1764  
I F G D + + + + R L  
Sbjct: 537 IRAFKSGVRDRYTTQELATRRITTTTRRL 564

>gb|ABA93980.1| retrotransposon protein, putative, Ty3-gypsy subclass [Oryza sativa  
(japonica cultivar-group)]  
Length = 1567

Score = 92.4 bits (228), Expect = 2e-16  
Identities = 49/148 (33%), Positives = 76/148 (51%)  
Frame = +1

Query: 1321 FKVSNVSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
F+ + KY+ D +L +Y+ V +AAGA ++ + Y P L A WL HLP + I  
Sbjct: 321 FRPRAIEKYDGTDPPEEFLQVYSTVLYAAGADNNALANYLPTALKGFARSWLMHLPPYSI 380

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W+D F+ANFQ + + A DL ++ E+LR Y++RF RN PE+ +A V  
Sbjct: 381 SSWADLWQQFVANFQGTYKRHAIEDDLHTLTQNSGESLREYVRRFNECRNTIPEITDASV 440

Query: 1681 IEDFYRGSNDSAFVRAILQKSVGHLRTL 1764  
I F G D + + + + R L  
Sbjct: 441 IRAFKSGVRDRYTTQELATTRITTRKL 468

>gb|AAL31060.1|AC090120\_6 putative gag-pol precursor [Oryza sativa Japonica Group]  
gb|AAP54365.1| retrotransposon protein, putative, Ty3-gypsy subclass [Oryza sativa  
(japonica cultivar-group)]  
Length = 698

Score = 92.4 bits (228), Expect = 2e-16  
Identities = 49/148 (33%), Positives = 75/148 (50%)  
Frame = +1

Query: 1321 FKVSNVSKYERKQDLGGWLAIYITIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
F+ + KY+ D +L +Y+ V +AAGA ++ + Y P L A WL HLP + I  
Sbjct: 215 FRPGAIAKKYDGSTDPPEFLQVYSTVLYAAGADDNALANYLPTALKGSARSWLMHLPPIYSI 274

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W+D FIANFQ + + A DL ++ E+LR Y++ F RN PE+ +A V  
Sbjct: 275 SSWADLWQQFIANFQGTYKRHAIEDDLHALTQNSGESLREYVRHFNECRNTIPEITDASV 334

Query: 1681 IEDFYRGSNDSAFVRAILQKSVGHLRTL 1764  
I F G D + + + + R L  
Sbjct: 335 IRAFKSGVRDRYTTQELATTRITTRRL 362

>gb|ABF97190.1| retrotransposon protein, putative, Ty3-gypsy subclass [Oryza sativa  
(japonica cultivar-group)]  
Length = 1773

Score = 92.0 bits (227), Expect = 2e-16  
Identities = 45/135 (33%), Positives = 69/135 (51%)  
Frame = +1

Query: 1321 FKVSNVSKYERKQDLGGWLAIYITIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
FK + + KY+ +L WL +Y + AAG M Y P+ L A WL LP+ I  
Sbjct: 525 FKPTGIEKYDGTTNLESWLTVYGLAIRAAGGDSKAMANYLPVALADSARSWLHGLPRGMI 584

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W+ FIANFQ F++P +DL ++ + E+LR Y++RF RN ++ + +  
Sbjct: 585 GSWAKLRDHFIANFQGTFERPGTQFDLYNVIQKSGESLRDYIRRFSEQRNKISDITDDVI 644

Query: 1681 IEDFYRGSNDSAFVR 1725  
I F +G VR  
Sbjct: 645 IATFTKGIRHEDLVR 659

>emb|CAD40114.1| OSJNBa0035013.3 [Oryza sativa (japonica cultivar-group)]  
Length = 2008

Score = 92.0 bits (227), Expect = 2e-16  
Identities = 43/127 (33%), Positives = 68/127 (53%)  
Frame = +1

Query: 1321 FKVSNVSKYERKQDLGGWLAIYITIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
FK + + KY+ + G WL +Y + AAG M Y P+ L A WL LP+ I  
Sbjct: 434 FKPTGIEKYDGTTPGWSLTVYGLAIRAAGGDNKAMANYLPVALADSARSWLHGLPRGTI 493

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W++ FIANFQ F++P +DL ++ + E+LR Y++RF RN ++ + +  
Sbjct: 494 GSWAELRDHFIANFQGTFERPGTQYDLYNVIQKSGESLRDYIRRFSEQRNKISDITDDVI 553

Query: 1681 IEDFYRG 1701  
I F +G  
Sbjct: 554 IAAFTKG 560

>gb|ABA96683.1| retrotransposon protein, putative, Ty3-gypsy subclass [Oryza sativa  
(japonica cultivar-group)]  
Length = 1844

Score = 91.7 bits (226), Expect = 3e-16  
Identities = 43/127 (33%), Positives = 68/127 (53%)  
Frame = +1

Query: 1321 FKVSNSVSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPPIVLGQDAMQWLRHLPQHCI 1500  
FK + + KY+ +L WL +Y + AAG M Y P+ L A WL LP+ I  
Sbjct: 438 FKPTGIEKYDGTTNLESWLTVYGLAIRAAGGDNKAMANYLPVALADSARSWLHGLPRGTI 497

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W++ FIANFQ F++P +DL ++ + E+LR Y++RF RN ++ + +  
Sbjct: 498 GSWAELRDHFIANFQGTFERPGTQYDLYNVIQKSGESLRDYIRRFSEQRNKISDITDDVI 557

Query: 1681 IEDFYRG 1701  
I F +G  
Sbjct: 558 IAAFTKG 564

>gb|AAT69666.1| putative polyprotein [Oryza sativa Japonica Group]  
Length = 973

Score = 91.3 bits (225), Expect = 4e-16  
Identities = 44/127 (34%), Positives = 68/127 (53%)  
Frame = +1

Query: 1321 FKVSNSVSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPPIVLGQDAMQWLRHLPQHCI 1500  
FK + + KY+ + WL +Y + AAG MT Y P+ L A WL LP+ I  
Sbjct: 440 FKPTGIKKYDGTNPESWLTVYGLAIRAAGGDSKAMTNYLPVALADSASWSWLHGLPRDTI 499

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W++ FIANFQ F++P +DL +I + E+LR Y++RF RN ++ + +  
Sbjct: 500 GSWAELRDHFIANFQGTFERPGTHFDLYNIVQKSGESLRDYIRRFSEQRNKISDITDDVI 559

Query: 1681 IEDFYRG 1701  
I F +G  
Sbjct: 560 IAAFTKG 566

>gb|ABA99121.1| transposon protein, putative, unclassified [Oryza sativa (japonica  
cultivar-group)]  
Length = 1681

Score = 91.3 bits (225), Expect = 4e-16  
Identities = 45/128 (35%), Positives = 70/128 (54%)  
Frame = +1

Query: 1321 FKVSNSVSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPPIVLGQDAMQWLRHLPQHCI 1500  
F+ + KY+ D +L +Y+ V +AAGA ++ + Y P L A WL H+P + I  
Sbjct: 397 FRPGAIEKYDGSTDP EEFLQVYSTVLYAAGADDNALANYLP TALKGSARSWLMHIPPYSI 456

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEVAEAGV 1680

+W+D      F+ANFQ  +  +  A      DL  ++          E+LR Y++RF     RN  PE+  +A V  
Sbjct: 457  SSWADLWQQFVANFQGTYKRHAIEDDLHALTQNSGESLREYVRRFNECRNTIPEITDASV 516

Query: 1681  IEDFYRGS 1704

          I   F   G+  
Sbjct: 517  IRAFKSGA 524

>gb|ABA92092.1| retrotransposon protein, putative, Ty3-gypsy subclass [Oryza sativa  
          (japonica cultivar-group)]  
          Length = 1658

Score = 91.3 bits (225), Expect = 4e-16  
Identities = 46/130 (35%), Positives = 69/130 (53%)  
Frame = +1

Query: 1321  FKVSNVSKYERKQDLGGWLAIYTIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500

          F+   + KY+   D   +L +Y+ V +AAGA ++ +  Y P  L   A  WL HLP + I  
Sbjct: 302  FRPRAIEKYDGSTDPEEFLQVYSTVLYAAGADDNALANYLPTALKGSARSWLMHLPPYSI 361

Query: 1501  DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEVAEAGV 1680

          +W+D      F+ NFQ  +  +  A      DL  ++          E+LR Y++RF     RN  PE+  +A V  
Sbjct: 362  SSWADLWQQFVTNFQGTYKRHAIEDDLHALTQNSGESLREYVRRFNECRNTIPEITDASV 421

Query: 1681  IEDFYRGSND 1710

          I   F   G   D  
Sbjct: 422  IHAFKSGVRD 431

>gb|AAP52584.2| retrotransposon protein, putative, Ty3-gypsy subclass [Oryza sativa  
          (japonica cultivar-group)]  
          Length = 1486

Score = 90.9 bits (224), Expect = 5e-16  
Identities = 46/130 (35%), Positives = 69/130 (53%)  
Frame = +1

Query: 1321  FKVSNVSKYERKQDLGGWLAIYTIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500

          F+   + KY+   D   +L +Y+ V +AAGA ++ +  Y P  L   A  WL HLP + I  
Sbjct: 342  FRPRAIKKYDGSTDPEEFLQVYSTVLYAAGADDNALANYLPTALKGSARSWLMHLPPYSI 401

Query: 1501  DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEVAEAGV 1680

          +W+D      F+ANFQ  +  A      DL  ++          E+LR Y++RF     RN  PE+  ++ V  
Sbjct: 402  SSWADLWQQFVANFQGTYKHHAIEDDLHALTQNSGESLREYVRRFNECRNTIPEITDSSV 461

Query: 1681  IEDFYRGSND 1710

          I   F   G   D  
Sbjct: 462  IRTFKSGVRD 471

>gb|ABA98874.2| retrotransposon protein, putative, Ty3-gypsy subclass [Oryza sativa  
          (japonica cultivar-group)]  
          Length = 893

Score = 90.9 bits (224), Expect = 5e-16  
Identities = 47/127 (37%), Positives = 68/127 (53%)  
Frame = +1

Query: 1321  FKVSNVSKYERKQDLGGWLAIYTIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500

          F+   + KY+   D   +L +Y+ V +AAGA ++ +  Y P  L   A  WL HLP + I  
Sbjct: 465  FRPGAIEKYDGSTDPEEFLQVYSTVLYAAGADDNALANYLPTALKGSARSWLMHLPPYSI 524

Query: 1501  DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEVAEAGV 1680

+W+D      FIANFQ  +  +  A      DL  +          E+LR Y++RF      RN  PE+  +A V  
Sbjct: 525  SSWADLWQQFIANFQGTYKRHAIEDDLHVLVTQNSGESLREYVRRFNECRNTIPEITDASV 584

Query: 1681  IEDFYRG 1701

          I  F  G  
Sbjct: 585  IHAFKSG 591

>gb|ABF94999.1| retrotransposon protein, putative, Ty3-gypsy subclass [Oryza sativa  
          (japonica cultivar-group)]  
          Length = 786

Score = 90.9 bits (224), Expect = 5e-16  
Identities = 48/148 (32%), Positives = 74/148 (50%)  
Frame = +1

Query: 1321  FKVSNVSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500

          F+      + KY+      D      +L +Y+ V +AAGA ++ +  Y P  L      A  WL HLP + I  
Sbjct: 358  FRPGAIEKYDGSTDPEEFLQVYSTVLYAAGADDNALANYLPTALKGSACSWLMHLPPYSI 417

Query: 1501  DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEVAEAGV 1680

          +W+D      FI NFQ  +  +  A      DL ++          E+LR Y++ F      RN  PE+  +A V  
Sbjct: 418  SSWADLWQQFIVNFQGTYKRHAIEDDLHALTQNSGESLREYVRHFNECRNTIPEITDASV 477

Query: 1681  IEDFYRGSNDSAFVRAILQKSVGHLRTL 1764

          I  F  G  D      +  +  +  +      R L  
Sbjct: 478  IRAFKSGVRDRYTTQELATTRITTTTRL 505

>gb|ABA97230.1| retrotransposon protein, putative, Ty3-gypsy subclass [Oryza sativa  
          (japonica cultivar-group)]  
          Length = 1807

Score = 90.9 bits (224), Expect = 5e-16  
Identities = 43/128 (33%), Positives = 69/128 (53%)  
Frame = +1

Query: 1318  NFKVSNVSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHC 1497

          +FK +  + KY+      +      WL +Y++      AAG      M  Y P+ L      A  WL  LP+  
Sbjct: 257  SFKPTGIEKYDGTTPESWLTVYSLAICAAGGDSKAMANYLPVALADSARSWLHGLPRGT 316

Query: 1498  IDNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEVAEAG 1677

          I +W++      FIANFQ  F++P      +DL +I  +  E+LR Y++RF      RN      ++  +  
Sbjct: 317  IGSWAELRDHFIANFQGTFFERPGTHFDLYNIVQKSGESLRDYIRRFSEQRNKISDITDDV 376

Query: 1678  VIEDFYRG 1701

          +I  F  +G  
Sbjct: 377  IIAAFTKG 384

>gb|AAN09865.1| putative polyprotein [Oryza sativa Japonica Group]  
          Length = 1469

Score = 90.9 bits (224), Expect = 5e-16  
Identities = 46/130 (35%), Positives = 69/130 (53%)  
Frame = +1

Query: 1321  FKVSNVSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500

          F+      + KY+      D      +L +Y+ V +AAGA ++ +  Y P  L      A  WL HLP + I  
Sbjct: 342  FRPRAIKKYDGSTDPEEFLQVYSTVLYAAGADDNALANYLPTALKGSARSWLMHLPPYSI 401

Query: 1501  DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEVAEAGV 1680

          +W+D      F+ANFQ  +      A      DL ++          E+LR Y++RF      RN  PE+  ++ V

Sbjct: 402 SSWADLWQQFVANFQGTYPKHHAIEDDLHALTQNSGESLREYVRRFNECRNTIPEITDSSV 461

Query: 1681 IEDFYRGSND 1710  
I F G D

Sbjct: 462 IRTFKSGVRD 471

>gb|AAK92558.1|AC051624\_16 Putative retroelement [Oryza sativa Japonica Group]  
Length = 1429

Score = 90.5 bits (223), Expect = 6e-16  
Identities = 44/134 (32%), Positives = 69/134 (51%)  
Frame = +1

Query: 1321 FKVSNNVSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
FK + + KY+ + WL +Y + AAG M Y P+ L A WL LP+ I  
Sbjct: 285 FKPTGIEKYDGTTPESWLTIVYGLAIHAAGGDSKAMANYLPVALADSARSWLHGLPRGTI 344

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W++ FIANFQ F+ P+ +DL ++ + E+LR Y++RF RN ++ + +  
Sbjct: 345 GSWAELRDHFIANFQGTFEHPSTQFDLYNVIQKSGESLRDYIRRFSEQRNKISDITDDVI 404

Query: 1681 IEDFYRGSNDSAFV 1722  
I F +G D V  
Sbjct: 405 IAAFTKGIRDEDLV 418

>gb|AAG59655.1|AC084319\_13 putative gypsy-type retrotransposon [Oryza sativa Japonica Group]  
Length = 1185

Score = 90.5 bits (223), Expect = 6e-16  
Identities = 43/127 (33%), Positives = 67/127 (52%)  
Frame = +1

Query: 1321 FKVSNNVSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
FK + + KY+ +L WL +Y + AAG M Y P+ L A WL LP+ I  
Sbjct: 383 FKPTGIEKYDGTTPNLESWLTIVYGLAIRAAGGDSKAMANYLPVALADSARSWLHGLPRGMI 442

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W+ FIANFQ F++P +DL ++ + E+LR Y++RF RN ++ + +  
Sbjct: 443 GSWAKLRDHFIANFQGTFERPGTQFDLYNVIQKSGESLRDYIRRFSEQRNKISDITDDVI 502

Query: 1681 IEDFYRG 1701  
I F +G  
Sbjct: 503 IATFTKG 509

>gb|ABB47110.1| retrotransposon protein, putative, Ty3-gypsy subclass [Oryza sativa (japonica cultivar-group)]  
Length = 1326

Score = 90.5 bits (223), Expect = 6e-16  
Identities = 44/134 (32%), Positives = 69/134 (51%)  
Frame = +1

Query: 1321 FKVSNNVSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
FK + + KY+ + WL +Y + AAG M Y P+ L A WL LP+ I  
Sbjct: 248 FKPTGIEKYDGTTPESWLTIVYGLAIHAAGGDSKAMANYLPVALADSARSWLHGLPRGTI 307

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W++ FIANFQ F+ P+ +DL ++ + E+LR Y++RF RN ++ + +  
Sbjct: 308 GSWAELRDHFIANFQGTFEHPSTQFDLYNVIQKSGESLRDYIRRFSEQRNKISDITDDVI 367



Query: 1681 IEDFYRGSNDSAFV 1722  
I F +G D V  
Sbjct: 368 IAAFTKGIRDEDLV 381

>emb|CAH66342.1| OSIGBa0104J13.2 [Oryza sativa (indica cultivar-group)]  
Length = 1582

Score = 90.1 bits (222), Expect = 8e-16  
Identities = 48/143 (33%), Positives = 73/143 (51%)  
Frame = +1

Query: 1273 SLRTYSVSPGHPVAPNFKVSNVSKYERKQDLGGWLAIYTIVTWAAGATEDVMTVYFPIVL 1452  
S+ S S P A FK + + KY+ + WL +Y + AAG M Y P+ L  
Sbjct: 580 SVPANSASTRTPA-GFKPTGIEKYDGTTPNESWLTVYGLAIRAAGGDSKAMANYLPVAL 638

Query: 1453 GQDAMQWLRHLPQHCHIDNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKR 1632  
A WL LP+ I +W++ FIANFQ F++P+ +DL +I + E+LR Y++R  
Sbjct: 639 ADSARSWLHGLPRGTIGSWAELRDHFIANFQGTFERPSTHFDLYNIVQKSGESLREYIRR 698

Query: 1633 F\*TMRNHTPEVAEAGVIEDFYRG 1701  
F RN + + +I F +G  
Sbjct: 699 FSEQRNKISNITDDVIIAAFTKG 721

>gb|AAP54205.2| retrotransposon protein, putative, Ty3-gypsy subclass [Oryza sativa  
(japonica cultivar-group)]  
Length = 1734

Score = 90.1 bits (222), Expect = 8e-16  
Identities = 44/127 (34%), Positives = 66/127 (51%)  
Frame = +1

Query: 1321 FKVSNVSKYERKQDLGGWLAIYTIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
FK + + KY + WL +Y I AAG M Y P+ L A WL LP+ I  
Sbjct: 349 FKPTGIEKYNGTTNPESWLTVYGLAIRAAGGDSKAMANYLPVALADSARSWLHGLPRRTI 408

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W++ FIANFQ F++P +DL +I + E+LR Y++RF RN ++ + +  
Sbjct: 409 GSWAELRDHFIANFQGTFERPGTQFDLYNIVQKSGESLTDYIRRFSEQRNKISDITDDVI 468

Query: 1681 IEDFYRG 1701  
I F +G  
Sbjct: 469 IAAFTKG 475

>gb|ABF99975.1| retrotransposon protein, putative, Ty3-gypsy subclass [Oryza sativa  
(japonica cultivar-group)]  
Length = 1413

Score = 90.1 bits (222), Expect = 8e-16  
Identities = 49/141 (34%), Positives = 74/141 (52%)  
Frame = +1

Query: 1288 SVSPGHPVAPNFKVSNVSKYERKQDLGGWLAIYTIVTWAAGATEDVMTVYFPIVLGQDAM 1467  
+ + HP P +N KY+ D +L +Y+ V +AAGA ++ + Y P L A  
Sbjct: 325 AAAAHPPEQPPTGDAN-EKYDGSTDPPEEFLQVYSTVLYAAGADDNALANYLPTALKGSAR 383

Query: 1468 QWLRHLPQHCHIDNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMR 1647  
WL HLP + I +W+D F+ANFQ + + A DL ++ E+LR Y++RF R  
Sbjct: 384 SWLMHLPPYSSISWADLWQQFVANFQGTYKRHAIEDDLHALTQNPGESLREYVQRFNECR 443

Query: 1648 NHTPEVAEAGVIEDFYRGSND 1710  
N P++ +A VI F G D  
Sbjct: 444 NTIPKITDASVIRAFKSGVRD 464

>gb|AAT93843.1| putative polyprotein [Oryza sativa Japonica Group]  
Length = 1723

Score = 90.1 bits (222), Expect = 8e-16  
Identities = 48/148 (32%), Positives = 75/148 (50%)  
Frame = +1

Query: 1321 FKVSNVSKYERKQDLGGWLAIYTIWTAAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
F+ + KY+ D +L +Y+ V +AAGA ++ + Y P L A WL HLP + I  
Sbjct: 326 FRPGAIEKYDGSTDPEEFLLQVYSTVLYAAGADDNALANYLPTALKGSAHSWLMHLPYYSI 385

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W D FI NFQ + + A DL ++ E+LR Y++RF RN P++ +A V  
Sbjct: 386 SSWVDLWQQFITNFQGTYKRHAIEDDLHALTQNPGESLRDYYRRFNECRNTIPDITDASV 445

Query: 1681 IEDFYRGSNDSAFVRAILQKSVGHLRTL 1764  
I F G D + + + + + R L  
Sbjct: 446 IRAFKTGVKDRYTTQELATRRITNTRRL 473

>gb|AAT81721.1| putative retrotransposon protein [Oryza sativa Japonica Group]  
gb|ABF98276.1| retrotransposon protein, putative, Ty3-gypsy subclass [Oryza sativa  
(japonica cultivar-group)]  
Length = 1002

Score = 90.1 bits (222), Expect = 8e-16  
Identities = 46/130 (35%), Positives = 68/130 (52%)  
Frame = +1

Query: 1321 FKVSNVSKYERKQDLGGWLAIYTIWTAAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
F+ + KY+ D +L +Y+ V +AAGA ++ + Y P L WL H P + I  
Sbjct: 533 FRPGAIEKYDGSTDPEEFLLQVYSTVLYAAGADDNALANYLPSALKGSTRSWLMHFPPYYSI 592

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRRLYLKRF\*TMRNHTPEVAEAGV 1680  
W+D FIANFQ + + A DL ++ H E+LR +++RF RN PE+ +A V  
Sbjct: 593 SLWADLWQQFIANFQGTYKRHAIEDDLHALTHNSGESLREFVRRFNECRNTIPEITDASV 652

Query: 1681 IEDFYRGSND 1710  
I F G D  
Sbjct: 653 IRAFKSGVRD 662

>gb|AAT77312.1| putative polyprotein [Oryza sativa Japonica Group]  
gb|AAT77333.1| putative polyprotein [Oryza sativa Japonica Group]  
Length = 1551

Score = 90.1 bits (222), Expect = 8e-16  
Identities = 48/143 (33%), Positives = 73/143 (51%)  
Frame = +1

Query: 1336 VSKYERKQDLGGWLAIYTIWTAAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCIDNWS 1515  
+ KY+ D +L +Y+ V +AAGA ++ + Y P L A WL HLP + I +W D  
Sbjct: 397 IEKYDGSTDPEEFLLQVYSTVLYAAGADDNALANYLPTALKGSARSWLMHLPYYSISSWID 456

Query: 1516 FSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRRLYLKRF\*TMRNHTPEVAEAGVIEDFY 1695  
F+ANFQ + + A DL ++ E+LR Y++RF RN PE+ +A VI F  
Sbjct: 457 LWQQFVANFQGTYKRHAIEDDLTLTQNSGESLREYVRRFNECRNTIPEITDAFVIRAFK 516

Query: 1696 RGSNDSAFVRAILQKSVGHLRTL 1764  
G D + + + + R L  
Sbjct: 517 SGVRDRYTTQELATRRITTTTRRL 539

>gb|AAS01973.1| retrotransposon protein, putative, Ty3-gypsy sub-class [Oryza sativa Japonica Group]  
Length = 1403

Score = 90.1 bits (222), Expect = 8e-16  
Identities = 49/141 (34%), Positives = 74/141 (52%)  
Frame = +1

Query: 1288 SVSPGHPVAPNFKVSNVSKYERKQDLGGWLAIYTIWTWAAGATEDVMTVYFPIVLGQDAM 1467  
+ + HP P +N KY+ D +L +Y+ V +AAGA ++ + Y P L A  
Sbjct: 315 AAAAAHPEQPPTGDAN-EKYDGSTDPEEFLQVYSTVLYAAGADDNALANYLPTALKGSAR 373

Query: 1468 QWLRHLPQHCHIDNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRLYLKRF\*TMR 1647  
WL HLP + I +W+D F+ANFQ + + A DL ++ E+LR Y++RF R  
Sbjct: 374 SWLMHLPPYSSISWADLWQQFVANFQGTYKRHAIEDDLHALTQNPGESLREYVQRFNECR 433

Query: 1648 NHTPEVAEAGVIEDFYRGSND 1710  
N P++ +A VI F G D  
Sbjct: 434 NTIPKITDASVIRAFKSGVRD 454

>emb|CAE03254.1| OSJNBa0011J08.9 [Oryza sativa (japonica cultivar-group)]  
Length = 878

Score = 90.1 bits (222), Expect = 8e-16  
Identities = 43/127 (33%), Positives = 68/127 (53%)  
Frame = +1

Query: 1321 FKVSNVSKYERKQDLGGWLAIYTIWTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
FK + + KY+ + WL +Y++ AAG M Y P+ L A WL LP+ I  
Sbjct: 419 FKPTRIEKYDGTTPESWLTVYSLAIHAAGGDSKAMANYLPVALADSARSWLHGLPRGTI 478

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W++ FIANFQ F++P +DL +I + E+LR Y++RF RN ++ + +  
Sbjct: 479 GSWAELHDHFIANFQGTFERPGTHFDLYNIIQKSGESLRDYIRRFSEQRNKISDITDDVI 538

Query: 1681 IEDFYRG 1701  
I F +G  
Sbjct: 539 IAAFTKG 545

>emb|CAD39396.2| OSJNBb0089K24.6 [Oryza sativa (japonica cultivar-group)]  
Length = 1400

Score = 90.1 bits (222), Expect = 8e-16  
Identities = 48/148 (32%), Positives = 75/148 (50%)  
Frame = +1

Query: 1321 FKVSNVSKYERKQDLGGWLAIYTIWTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
F+ + KY+ D +L +Y+ V +AAGA ++ + Y P L A WL HLP + I  
Sbjct: 442 FRPRAIEKYDGSTDPEEFLQVYSTVLYAAGADDNALANYLPTALKGYARSWLMHLPPYSI 501

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W+D F+ANFQ + + A DL ++ E+LR Y++RF RN PE+ +A V  
Sbjct: 502 SSWADLWQQFVANFQGTYKRHAIEDDLHALTQNSGESLREYVRRFNECRNTIPEITDASV 561

Query: 1681 IEDFYRGSNDSAFVRAILQKSVGHLRTL 1764  
I G D + + + + R L

Sbjct: 562 IRALKSGVRDRYTTQELATRRITTTTRRL 589

>gb|AAM00991.1|AC090482\_20 Putative retroelement [Oryza sativa Japonica Group]  
Length = 2017

Score = 90.1 bits (222), Expect = 8e-16  
Identities = 42/127 (33%), Positives = 68/127 (53%)  
Frame = +1

Query: 1321 FKVSNSVSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
FK + + KY+ + WL +Y + AAG M Y P+ L A WL LP+ I  
Sbjct: 438 FKPTGIEKYDGTNPESWLTVYGLAIRAAGGDSKAMANYLPVALADSARSWLHGLPRGTI 497

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
++W++ FIANFQ F++P +DL ++ + E+LR Y++RF RN ++ + +  
Sbjct: 498 ESWAELRDHFIANFQGTFERPGTQYDLYNVIQKSGESLRDYIRRFSEQRNKISDITDDVI 557

Query: 1681 IEDFYRG 1701  
I F +G  
Sbjct: 558 IAAFTKG 564

>gb|ABB47210.1| retrotransposon protein, putative, Ty3-gypsy subclass [Oryza sativa  
(japonica cultivar-group)]  
Length = 1995

Score = 90.1 bits (222), Expect = 8e-16  
Identities = 42/127 (33%), Positives = 68/127 (53%)  
Frame = +1

Query: 1321 FKVSNSVSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
FK + + KY+ + WL +Y + AAG M Y P+ L A WL LP+ I  
Sbjct: 438 FKPTGIEKYDGTNPESWLTVYGLAIRAAGGDSKAMANYLPVALADSARSWLHGLPRGTI 497

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
++W++ FIANFQ F++P +DL ++ + E+LR Y++RF RN ++ + +  
Sbjct: 498 ESWAELRDHFIANFQGTFERPGTQYDLYNVIQKSGESLRDYIRRFSEQRNKISDITDDVI 557

Query: 1681 IEDFYRG 1701  
I F +G  
Sbjct: 558 IAAFTKG 564

>gb|ABA92237.1| retrotransposon protein, putative, Ty3-gypsy subclass [Oryza sativa  
(japonica cultivar-group)]  
Length = 1646

Score = 90.1 bits (222), Expect = 8e-16  
Identities = 42/128 (32%), Positives = 69/128 (53%)  
Frame = +1

Query: 1318 NFKVSNSVSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHC 1497  
+FK++ + KY+ + WL +Y + AAG M Y P+ L A WL LP+  
Sbjct: 440 SFKLTRIEKYDGTNPESWLTVYGLAIRAAGGDSKAMANYLPVALADSARSWLHGLPRGT 499

Query: 1498 IDNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRLYLKRF\*TMRNHTPEVAEAG 1677  
I +W++ FIANFQ F++P +DL ++ + E+LR Y++RF RN ++ + +  
Sbjct: 500 IGSWAELRDHFIANFQGTFERPGTQFDLYNVIQKSGESLRDYIRRFSEQRNKISDITDDV 559

Query: 1678 VIEDFYRG 1701  
+I F +G  
Sbjct: 560 IIAAFTKG 567

>gb|AAK27822.1|AC022457\_25 putative gag-pol precursor [Oryza sativa Japonica Group]  
Length = 1720

Score = 90.1 bits (222), Expect = 8e-16  
Identities = 44/127 (34%), Positives = 66/127 (51%)  
Frame = +1

Query: 1321 FKVSNVSKYERKQDLGGWLAIYTIWTAAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
FK + + KY + WL +Y I AAG M Y P+ L A WL LP+ I  
Sbjct: 314 FKPTGIEKYNGTTNPESWLTVYGLAIRAAGGDSKAMANYLPVALADSARSWLHGLPRRTI 373

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W++ FIANFQ F++P +DL +I + E+LR Y++RF RN ++ + +  
Sbjct: 374 GSWAELRDHFIANFQGTFERPGTQFDLYNIVQKSGESLRDYIRRFSEQRNKISDITDDVI 433

Query: 1681 IEDFYRG 1701  
I F +G  
Sbjct: 434 IAAFTKG 440

>emb|CAE04437.2| OSJNBa0018J19.4 [Oryza sativa (japonica cultivar-group)]  
Length = 1527

Score = 90.1 bits (222), Expect = 8e-16  
Identities = 48/143 (33%), Positives = 73/143 (51%)  
Frame = +1

Query: 1273 SLRTYSVSPGHPVAPNFKVSNVSKYERKQDLGGWLAIYTIWTAAAGATEDVMTVYFPIVL 1452  
S+ S S P A FK + + KY+ + WL +Y + AAG M Y P+ L  
Sbjct: 462 SVPANSASTRTPTA-GFKPTGIEKYDGTNPESWLTVYGLAIRAAGGDSKAMANYLPVAL 520

Query: 1453 GQDAMQWLRHLPQHCIDNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKR 1632  
A WL LP+ I +W++ FIANFQ F++P+ +DL +I + E+LR Y++R  
Sbjct: 521 ADSARSWLHGLPRGTIGSWAELRDHFIANFQGTFERPSTHFDLYNIVQKSGESLREYIRR 580

Query: 1633 F\*TMRNHTPEVAEAGVIEDFYRG 1701  
F RN + + +I F +G  
Sbjct: 581 FSEQRNKISNITDDVIIAAFTKG 603

>gb|ABF99249.1| retrotransposon protein, putative, Ty3-gypsy subclass [Oryza sativa  
(japonica cultivar-group)]  
Length = 1552

Score = 89.7 bits (221), Expect = 1e-15  
Identities = 42/128 (32%), Positives = 68/128 (53%)  
Frame = +1

Query: 1318 NFKVSNVSKYERKQDLGGWLAIYTIWTAAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHC 1497  
+FK + + KY+ + WL +Y + AAG M Y P+ L A WL LP+  
Sbjct: 384 SFKPTGIEKYDGTNPESWLTVYGLAIRAAGGDSKAMANYLPVALADSAQSWLNGLPRGT 443

Query: 1498 IDNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEVAEAG 1677  
I +W++ FIANFQ F++P +DL ++ + E+LR Y++RF RN ++ +  
Sbjct: 444 IGSWAELRDHFIANFQGTFERPGTQFDLYNVVQKSGESLRDYIRRFSEQRNKISDITDDV 503

Query: 1678 VIEDFYRG 1701  
+I F +G  
Sbjct: 504 IIAAFTKG 511

>emb|CAE03068.2| OSJNBa0089E12.6 [Oryza sativa (japonica cultivar-group)]  
Length = 1939

Score = 89.7 bits (221), Expect = 1e-15  
Identities = 42/128 (32%), Positives = 68/128 (53%)  
Frame = +1

Query: 1318 NFKVSNVSKYERKQDLGGWLAIYITVWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHC 1497  
+FK + + KY+ + WL +Y + AAG M Y P+ L A WL LP+  
Sbjct: 438 SFKPTGIEKYDGTNPESWLTVYGLAIRAAGGDNKAMANYLPVALADSARSWLHGLPRGT 497

Query: 1498 IDNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEVAEAG 1677  
I +W++ FIANFQ F++P +DL ++ + E+LR Y++RF RN ++ +  
Sbjct: 498 IGSWAELRDHFIANFQGTFERPGTQYDLYNVIQKSGESLREYIRRFSEQRNKISDITDDV 557

Query: 1678 VIEDFYRG 1701  
+I F +G  
Sbjct: 558 IIAAFTKG 565

>gb|AAV44132.1| putative polyprotein [Oryza sativa Japonica Group]  
Length = 1185

Score = 89.7 bits (221), Expect = 1e-15  
Identities = 56/175 (32%), Positives = 83/175 (47%), Gaps = 18/175 (10%)  
Frame = +1

Query: 1240 TSRTPT\*RHVRSRLRTYSVSPGHPVAPN-----FKVSNVSKYERKQDL 1365  
+S + + RH R RTY HP AP+ F+ + KY+ D  
Sbjct: 282 SSSSSSGRHPR--RTYDRQ--HPTAPSAGCRAFNRLRDVWRPERFRPGAIEKYDGSTDP 337

Query: 1366 GGWLAIYITVWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCCIDNWSDFSWCFIANFQ 1545  
+L +Y+ V +AAGA ++ + Y P L A WL HLP + I +W+D F+ NFQ  
Sbjct: 338 EEFLQVYSTVPYAAAGADDNALANYLPTALKGSARSWLMHLPPYSISSWADLWQQFVGNFQ 397

Query: 1546 SLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEVAEAGVIEDFYRGSND 1710  
+ + DL ++ E+LR Y++RF RN PE+ +A VI F G D  
Sbjct: 398 GTYKRHMIEDDLHALTQNPGESLRDYVRRFNDRCNTIPEITDASVIRAFKTGVRD 452

>gb|AAT75246.1| putative gag-pol precursor [Oryza sativa Japonica Group]  
Length = 1512

Score = 89.7 bits (221), Expect = 1e-15  
Identities = 42/128 (32%), Positives = 68/128 (53%)  
Frame = +1

Query: 1318 NFKVSNVSKYERKQDLGGWLAIYITVWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHC 1497  
+FK + + KY+ + WL +Y + AAG M Y P+ L A WL LP+  
Sbjct: 384 SFKPTGIEKYDGTNPESWLTVYGLAIRAAGGDSKAMANYLPVALADSAQSWLNGLPRGT 443

Query: 1498 IDNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEVAEAG 1677  
I +W++ FIANFQ F++P +DL ++ + E+LR Y++RF RN ++ +  
Sbjct: 444 IGSWAELRDHFIANFQGTFERPGTQFDLYNVVQKSGESLRDYIRRFSEQRNKISDITDDV 503

Query: 1678 VIEDFYRG 1701  
+I F +G  
Sbjct: 504 IIAAFTKG 511

>emb|CAE04995.2| OSJNBb0093G06.3 [Oryza sativa (japonica cultivar-group)]  
Length = 1986

Score = 89.7 bits (221), Expect = 1e-15  
Identities = 42/127 (33%), Positives = 68/127 (53%)  
Frame = +1

Query: 1321 FKVSNVSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
FK + + KY+ + WL +Y + AAG M Y P+ L A WL LP+ I  
Sbjct: 434 FKPTGIEKYDGTTPESWLTIVYGLAIRAAGGDNKAMANYLPVALADSARSWLHGLPRGTI 493

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W++ FIANFQ F++P +DL ++ + E+LR Y++RF RN ++++ +  
Sbjct: 494 GSWAELRDHFIANFQGTFERPGTQYDLYNVIQKSGESLREYIRRFSEQRNKISDISDDVI 553

Query: 1681 IEDFYRG 1701  
I F +G  
Sbjct: 554 IAAFTKG 560

>gb|ABA97324.1| retrotransposon protein, putative, unclassified [Oryza sativa  
(japonica cultivar-group)]  
Length = 553

Score = 89.7 bits (221), Expect = 1e-15  
Identities = 47/148 (31%), Positives = 74/148 (50%)  
Frame = +1

Query: 1321 FKVSNVSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
F+ V KY+ D +L +Y+ V +A G+ ++ + Y P L A WL HLP + I  
Sbjct: 405 FRPGAVEKYDGSTDPPEEFLQVYSTVLYAVGSDDNALANYLPTALKGSARSWLMHLPPYSI 464

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W+D F+ANFQ + + A DL ++ E+LR Y++ F RN PE+ +A V  
Sbjct: 465 SSWADLWQQFVANFQGTYKRHAIEDDLHALTQSSGESLREYVRHFNECRNTIPEITDASV 524

Query: 1681 IEDFYRGSNDSAFVRAILQKSVGHLRTL 1764  
I F G D + + + + R L  
Sbjct: 525 IRAFKSGVRDRYTTQELATRRITTTTRRL 552

>ref|NP\_001061573.1| Os08g0334300 [Oryza sativa (japonica cultivar-group)]  
Length = 2100

Score = 89.4 bits (220), Expect = 1e-15  
Identities = 42/127 (33%), Positives = 67/127 (52%)  
Frame = +1

Query: 1321 FKVSNVSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
FK + + KY+ + WL +Y + AAG M Y P+ L A WL LP+ I  
Sbjct: 601 FKPTGIEKYDGTTPESWLTIVYGLAIRAAGGDNKAMANYLPVALADSARSWLHGLPRGTI 660

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W++ FIANFQ F++P +DL ++ + E+LR Y++RF RN ++ + +  
Sbjct: 661 GSWAELRDHFIANFQGTFERPGTQYDLYNVIQKSGESLREYIRRFSEQRNKISDITDDVI 720

Query: 1681 IEDFYRG 1701  
I F +G  
Sbjct: 721 IAAFTKG 727

>gb|ABG65980.1| retrotransposon protein, putative, Ty3-gypsy subclass [Oryza sativa  
(japonica cultivar-group)]  
Length = 975

Score = 89.4 bits (220), Expect = 1e-15

Identities = 42/127 (33%), Positives = 67/127 (52%)  
Frame = +1

Query: 1321 FKVSNVSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
FK + + KY+ + WL +Y + AAG M Y P+ L A WL LP+ I  
Sbjct: 431 FKPTGIEKYDGTTPNESWLTVYGLAIRAAGGDNKAMANYLPVALADSARSWLHGLPRGTI 490

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W++ FIANFQ F++P +DL ++ + E+LR Y++RF RN ++ + +  
Sbjct: 491 GSWAELRDYFIANFQGTFERPGTQYDLYNVIQKSGESLRDYIRRFSEQRNKISDITDDVI 550

Query: 1681 IEDFYRG 1701  
I F +G  
Sbjct: 551 IAAFTKG 557

>gb|AAU10736.1| putative polyprotein [Oryza sativa Japonica Group]  
gb|AAU43942.1| putative polyprotein [Oryza sativa Japonica Group]  
Length = 1995

Score = 89.4 bits (220), Expect = 1e-15  
Identities = 42/127 (33%), Positives = 68/127 (53%)  
Frame = +1

Query: 1321 FKVSNVSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
FK + + KY+ + WL +Y + AAG M Y P+ L A WL LP+ I  
Sbjct: 436 FKPTGIEKYDGTTPNESWLTVYGLAIRAAGGDSKAMANYLPVALADSARSWLHGLPRGTI 495

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W++ FIANFQ F++P+ +DL ++ + E+LR Y++RF RN ++ + +  
Sbjct: 496 GSWAELRDHFIANFQGTFERPSTQYDLYNVIQKSGESLRDYIRRFSEQRNKISDITDDVI 555

Query: 1681 IEDFYRG 1701  
I F +G  
Sbjct: 556 IAAFTKG 562

>gb|AAS98430.1| putative polyprotein [Oryza sativa Japonica Group]  
Length = 2004

Score = 89.4 bits (220), Expect = 1e-15  
Identities = 42/127 (33%), Positives = 67/127 (52%)  
Frame = +1

Query: 1321 FKVSNVSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
FK + + KY+ + WL +Y + AAG M Y P+ L A WL LP+ I  
Sbjct: 439 FKPTGIEKYDGTTPNESWLTVYGLAIRAAGGDNKAMANYLPVALADSARSWLHGLPRGTI 498

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W++ FIANFQ F++P +DL ++ + E+LR Y++RF RN ++ + +  
Sbjct: 499 GSWAELRDHFIANFQGTFERPGTQYDLYNVIQKSGESLREYIRRFSEQRNKISDITDDVI 558

Query: 1681 IEDFYRG 1701  
I F +G  
Sbjct: 559 IAAFTKG 565

>gb|AAS79740.1| putative polyprotein [Oryza sativa Japonica Group]  
Length = 1756

Score = 89.4 bits (220), Expect = 1e-15  
Identities = 43/134 (32%), Positives = 69/134 (51%)  
Frame = +1



Query: 1300 GHPVAPNFKVSNVSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLR 1479  
 G + FK + + KY+ + WL +Y + AAG M Y P+ L A WL  
 Sbjct: 170 GVTTSAGFKPTGIEKYDGTTPESWLTVYGLAIRAAGGDSKAMANYLPVALADSARSWLH 229

Query: 1480 HLPQHCIDNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTP 1659  
 LP+ I +W++ FIANFQ F++P +DL ++ + E+LR Y++RF RN  
 Sbjct: 230 GLPRGTIRSWAELRDHFIANFQGTFERPGTQYDLYNVIQKSGESLRDYIRRFSEQRNKIS 289

Query: 1660 EVAEAGVIEDFYRG 1701  
 ++ + +I F +G  
 Sbjct: 290 DITDDVIIAAFTKG 303

>gb|AAS90646.1| putative polyprotein [Oryza sativa Japonica Group]  
 Length = 1991

Score = 89.4 bits (220), Expect = 1e-15  
 Identities = 42/127 (33%), Positives = 67/127 (52%)  
 Frame = +1

Query: 1321 FKVSNVSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
 FK + + KY+ + WL +Y + AAG M Y P+ L A WL LP+ I  
 Sbjct: 439 FKPTGIEKYDGTTPESWLTVYGLAIRAAGGDNKAMANYLPVALADSARSWLHGLPRGTI 498

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
 +W++ FIANFQ F++P +DL ++ + E+LR Y++RF RN ++ + +  
 Sbjct: 499 GSWAELRDHFIANFQGTFERPGTQYDLYNVIQKSGESLREYIRRFSEQRNKISDITDDVI 558

Query: 1681 IEDFYRG 1701  
 I F +G  
 Sbjct: 559 IAAFTKG 565

>gb|ABA98213.1| retrotransposon protein, putative, Ty3-gypsy subclass [Oryza sativa  
 (japonica cultivar-group)]  
 Length = 1964

Score = 89.4 bits (220), Expect = 1e-15  
 Identities = 42/127 (33%), Positives = 67/127 (52%)  
 Frame = +1

Query: 1321 FKVSNVSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
 FK + + KY+ + WL +Y + AAG M Y P+ L A WL LP+ I  
 Sbjct: 434 FKPTGIEKYDGTTPESWLTVYGLAIRAAGGDNKAMANYLPVALADSARSWLHGLPRGTI 493

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
 +W++ FIANFQ F++P +DL ++ + E+LR Y++RF RN ++ + +  
 Sbjct: 494 GSWAELRDHFIANFQGTFERPGTQYDLYNVIQKSGESLREYIRRFSEQRNKISDITDDVI 553

Query: 1681 IEDFYRG 1701  
 I F +G  
 Sbjct: 554 IAAFTKG 560

>gb|ABA98134.1| retrotransposon protein, putative, Ty3-gypsy subclass [Oryza sativa  
 (japonica cultivar-group)]  
 Length = 1956

Score = 89.4 bits (220), Expect = 1e-15  
 Identities = 43/134 (32%), Positives = 69/134 (51%)  
 Frame = +1

Query: 1321 FKVSNNVSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
 FK + + KY+ + WL +Y + AAG M Y P+ L A WL LP+ I  
 Sbjct: 438 FKPTGIEKYDGTTPESWLTIVYGLAIRAAGGDSKAMANYLPVALADSARSWLHGLPRGTI 497

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
 +W++ FIANFQ F++P +DL ++ + E+LR Y++RF RN ++ + +  
 Sbjct: 498 GSWAELRDHFIANFQGTFERPGTQYDLYNVIQKSGESLRDYIRRFSEQRNKISDITDDVI 557

Query: 1681 IEDFYRGSNDSAFV 1722  
 I F +G + V  
 Sbjct: 558 IAAFTKGISPEELV 571

>gb|AAL82662.1|AC092387\_10 retrotransposon protein, putative, Ty3-gypsy sub-class [Oryza sativa

Japonica Group]  
 gb|AAM18149.1|AC092172\_9 Putative gag-pol precursor [Oryza sativa Japonica Group]  
 gb|AAP52743.1| retrotransposon protein, putative, Ty3-gypsy subclass [Oryza sativa  
 (japonica cultivar-group)]  
 Length = 1964

Score = 89.4 bits (220), Expect = 1e-15  
 Identities = 42/127 (33%), Positives = 67/127 (52%)  
 Frame = +1

Query: 1321 FKVSNNVSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
 FK + + KY+ + WL +Y + AAG M Y P+ L A WL LP+ I  
 Sbjct: 434 FKPTGIEKYDGTTPESWLTIVYGLAIRAAGGDNKAMANYLPVALADSARSWLHGLPRGTI 493

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
 +W++ FIANFQ F++P +DL ++ + E+LR Y++RF RN ++ + +  
 Sbjct: 494 GSWAELRDHFIANFQGTFERPGTQYDLYNVIQKSGESLREYIRRFSEQRNKISDITDDVI 553

Query: 1681 IEDFYRG 1701  
 I F +G  
 Sbjct: 554 IAAFTKG 560

>gb|AAN08247.1| putative GAG-POL precursor [Oryza sativa Japonica Group]  
 Length = 1696

Score = 89.4 bits (220), Expect = 1e-15  
 Identities = 42/127 (33%), Positives = 67/127 (52%)  
 Frame = +1

Query: 1321 FKVSNNVSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
 FK + + KY+ + WL +Y + AAG M Y P+ L A WL LP+ I  
 Sbjct: 389 FKPTGIEKYDGTTPESWLTIVYGLAIRAAGGDNKAMANYLPVALADSARSWLHGLPRGTI 448

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
 +W++ FIANFQ F++P +DL ++ + E+LR Y++RF RN ++ + +  
 Sbjct: 449 GSWAELRDYFIANFQGTFERPGTQYDLYNVIQKSGESLRDYIRRFSEQRNKISDITDDVI 508

Query: 1681 IEDFYRG 1701  
 I F +G  
 Sbjct: 509 IAAFTKG 515

>emb|CAE02263.2| OSJNBb0049I21.2 [Oryza sativa (japonica cultivar-group)]  
 Length = 1843

Score = 89.4 bits (220), Expect = 1e-15  
 Identities = 42/127 (33%), Positives = 67/127 (52%)

Frame = +1

Query: 1321 FKVSNVSKYERKQDLGGWLAIYTIWTAAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
FK + + KY+ + WL +Y + AAG M Y P+ L A WL LP+ I  
Sbjct: 440 FKPTGIEKYDGTNPESWLT VYGLAIRAAGGDSKAMANYLPVALADSARSWLHGLPRGTI 499

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W++ FIANFQ F++P +DL ++ + E+LR Y++RF RN ++ + +  
Sbjct: 500 GSWAELRDRFIANFQGTFERPGTQYDLYNVIQKSGESLREYIRRFSEQRNKISDITDDVI 559

Query: 1681 IEDFYRG 1701  
I F +G  
Sbjct: 560 IAAFTKG 566

>emb|CAE01988.1| OSJNBb0033G08.4 [Oryza sativa (japonica cultivar-group)]  
Length = 701

Score = 89.4 bits (220), Expect = 1e-15  
Identities = 48/148 (32%), Positives = 75/148 (50%)  
Frame = +1

Query: 1321 FKVSNVSKYERKQDLGGWLAIYTIWTAAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
F+ + KY+ D +L +Y+IV +AA A ++ + Y P L A WL HLP + I  
Sbjct: 185 FRPGAIEKYDGSTDPEEFQVYSIVLYAAEADDNALANYLPAALKGSARSWLHLPPLYI 244

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W D F+ANFQ + + A DL ++ E+LR Y++RF RN PE+ A +  
Sbjct: 245 SSWVDLWQQFVANFQGTYKRHAIEDDLHALTQNPGESLRDYIRRFNECRNTIPEITNASM 304

Query: 1681 IEDFYRGSNDSAFVRAILQKSVGHLRTL 1764  
I F G D + ++ + + R L  
Sbjct: 305 IRAFKTGVRDRYTTQELVTRQITTARKL 332

>dbj|BAB19768.1| putative gypsy-type retrotransposon RIRE2 [Oryza sativa Japonica  
Group]  
Length = 983

Score = 89.4 bits (220), Expect = 1e-15  
Identities = 42/127 (33%), Positives = 67/127 (52%)  
Frame = +1

Query: 1321 FKVSNVSKYERKQDLGGWLAIYTIWTAAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
FK + + KY+ + WL +Y + AAG M Y P+ L A WL LP+ I  
Sbjct: 438 FKPTGIEKYDGTNPESWLT VYGLAIHAAGGDSKAMANYLPVALADSARSWLHGLPRGTI 497

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W++ FIANFQ F++P +DL ++ + E+LR Y++RF RN ++ + +  
Sbjct: 498 GSWAELRDHFIANFQGTFERPGTQFDLYNVVQKSGESLRDYIRRFQSKQRNKISDITDDVI 557

Query: 1681 IEDFYRG 1701  
I F +G  
Sbjct: 558 IAAFTKG 564

>emb|CAH65837.1| OSIGBa0124C14.4 [Oryza sativa (indica cultivar-group)]  
Length = 1802

Score = 89.0 bits (219), Expect = 2e-15  
Identities = 42/127 (33%), Positives = 67/127 (52%)  
Frame = +1

Query: 1321 FKVSNVSKYERKQDLGGWLAIYITIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
FK + + KY+ + WL +Y + AAG M Y P+ L A WL LP+ I  
Sbjct: 438 FKPTGIEKYDGTTPESWLTVYGLAIRAAGGDSKAMANYLPVALADSARSWLHGLPRGTI 497

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W++ FIANFQ F++P +DL ++ + E+LR Y++RF RN ++ + +  
Sbjct: 498 GSWAELRDHFIANFQGTTFERPQTQFDLYNVVQKSGESLRDYIRRFSEQRNKISDITDDVI 557

Query: 1681 IEDFYRG 1701  
I F +G  
Sbjct: 558 IAAFTKG 564

>emb|CAH66795.1| H0215F08.6 [Oryza sativa (indica cultivar-group)]  
Length = 1991

Score = 89.0 bits (219), Expect = 2e-15  
Identities = 42/127 (33%), Positives = 67/127 (52%)  
Frame = +1

Query: 1321 FKVSNVSKYERKQDLGGWLAIYITIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
FK + + KY+ + WL +Y + AAG M Y P+ L A WL LP+ I  
Sbjct: 412 FKPTGIEKYDGTTPESWLTVYGLAIRAAGGDSKAMANYLPVALADSARSWLHGLPRGTI 471

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W++ FIANFQ F++P +DL ++ + E+LR Y++RF RN ++ + +  
Sbjct: 472 GSWAELHDHFIANFQGTTFERPQTQYDLYNVIQKSGESLRDYIRRFSEQRNKISDITDDVI 531

Query: 1681 IEDFYRG 1701  
I F +G  
Sbjct: 532 IAAFTKG 538

>emb|CAH66866.1| H0307D04.11 [Oryza sativa (indica cultivar-group)]  
Length = 2017

Score = 89.0 bits (219), Expect = 2e-15  
Identities = 42/127 (33%), Positives = 67/127 (52%)  
Frame = +1

Query: 1321 FKVSNVSKYERKQDLGGWLAIYITIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
FK + + KY+ + WL +Y + AAG M Y P+ L A WL LP+ I  
Sbjct: 438 FKPTGIEKYDGTTPESWLTVYGLAIRAAGGDSKAMANYLPVALADSARSWLHGLPRGTI 497

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W++ FIANFQ F++P +DL ++ + E+LR Y++RF RN ++ + +  
Sbjct: 498 GSWAELRDHFIANFQGTTFERPQTQYDLYNVIQKSGESLRDYIRRFSEQRNKISDITDDVI 557

Query: 1681 IEDFYRG 1701  
I F +G  
Sbjct: 558 IAAFTKG 564

>ref|NP\_001062707.1| Os09g0261200 [Oryza sativa (japonica cultivar-group)]  
Length = 1747

Score = 89.0 bits (219), Expect = 2e-15  
Identities = 42/127 (33%), Positives = 67/127 (52%)  
Frame = +1

Query: 1321 FKVSNVSKYERKQDLGGWLAIYITIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
FK + + KY+ + WL +Y + AAG M Y P+ L A WL LP+ I  
Sbjct: 434 FKPTGIEKYDGTTPESWLTVYGLAIRAAGGDNKAMANYLPVALADSARSWLHGLPRGTI 493

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W++ FIANFQ F++P +DL ++ + E+LR Y++RF RN ++ + +  
Sbjct: 494 GSWAELRDHFIANFQGTFERPGTQYDLYNVIQKSGESLRDYIRRFSEQRNKISDITDDVI 553

Query: 1681 IEDFYRG 1701  
I F +G  
Sbjct: 554 IAAFTKG 560

>gb|AAP52501.2| retrotransposon protein, putative, Ty3-gypsy subclass [Oryza sativa  
(japonica cultivar-group)]  
Length = 1964

Score = 89.0 bits (219), Expect = 2e-15  
Identities = 42/127 (33%), Positives = 67/127 (52%)  
Frame = +1

Query: 1321 FKVSNVSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
FK + + KY+ + WL +Y + AAG M Y P+ L A WL LP+ I  
Sbjct: 434 FKPTGIEKYDGTTPESWLTIVYGLAIRAAGGDNKAMANYLPVALADSARSWLHGLPRGTI 493

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W++ FIANFQ F++P +DL ++ + E+LR Y++RF RN ++ + +  
Sbjct: 494 GSWAELRDHFIANFQGTFERPGTQYDLYNVIQKSGESLRDYIRRFSEQRNKISDITDDVI 553

Query: 1681 IEDFYRG 1701  
I F +G  
Sbjct: 554 IAAFTKG 560

>gb|AAP52640.2| retrotransposon protein, putative, Ty3-gypsy subclass [Oryza sativa  
(japonica cultivar-group)]  
Length = 808

Score = 89.0 bits (219), Expect = 2e-15  
Identities = 42/127 (33%), Positives = 67/127 (52%)  
Frame = +1

Query: 1321 FKVSNVSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
FK + + KY+ + WL +Y + AAG M Y P+ L A WL LP+ I  
Sbjct: 354 FKPTGIEKYDGTTPESWLTIVYGLAIRAAGGDNKAMANYLPVALADSARSWLHGLPRGTI 413

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W++ FIANFQ F++P +DL ++ + E+LR Y++RF RN ++ + +  
Sbjct: 414 GSWAELRDHFIANFQGTFERPGTQYDLYNVIQKSGESLRDYIRRFSEQRNKISDITDDVI 473

Query: 1681 IEDFYRG 1701  
I F +G  
Sbjct: 474 IAAFTKG 480

>gb|AAP52499.2| retrotransposon protein, putative, Ty3-gypsy subclass [Oryza sativa  
(japonica cultivar-group)]  
Length = 1995

Score = 89.0 bits (219), Expect = 2e-15  
Identities = 42/127 (33%), Positives = 67/127 (52%)  
Frame = +1

Query: 1321 FKVSNVSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
FK + + KY+ + WL +Y + AAG M Y P+ L A WL LP+ I  
Sbjct: 438 FKPTGIEKYDGTTPESWLTIVYGLAIRAAGGDNKAMANYLPVALADSARSWLHGLPRGTI 497

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W++ FIANFQ F++P +DL ++ + E+LR Y++RF RN ++ + +  
Sbjct: 498 GSWAELRDHFIANFQGTFERPGTQYDLYNVIQKSGESLRDYIRRFSEQRNKISDITDDVI 557

Query: 1681 IEDFYRG 1701  
I F +G  
Sbjct: 558 IAAFTKG 564

>gb|ABA93602.2| retrotransposon protein, putative, Ty3-gypsy subclass [Oryza sativa  
(japonica cultivar-group)]  
Length = 1761

Score = 89.0 bits (219), Expect = 2e-15  
Identities = 42/127 (33%), Positives = 67/127 (52%)  
Frame = +1

Query: 1321 FKVSNSVSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
FK + + KY+ + WL +Y + AAG M Y P+ L A WL LP+ I  
Sbjct: 438 FKPTGIEKYDGTTPESWLTIVYGLAIRAAGGDNKAMANYLPVALADSARSWLHGLPRGTI 497

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W++ FIANFQ F++P +DL ++ + E+LR Y++RF RN ++ + +  
Sbjct: 498 GSWAELRDHFIANFQGTFERPGTQYDLYNVIQKSGESLRDYIRRFSEQRNKISDITDDVI 557

Query: 1681 IEDFYRG 1701  
I F +G  
Sbjct: 558 IAAFTKG 564

>gb|ABA96243.2| retrotransposon protein, putative, unclassified [Oryza sativa  
(japonica cultivar-group)]  
Length = 1419

Score = 89.0 bits (219), Expect = 2e-15  
Identities = 48/148 (32%), Positives = 74/148 (50%)  
Frame = +1

Query: 1321 FKVSNSVSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
F+ + KY+ D +L IY+ V +AAG ++ + Y P L A W HLP + I  
Sbjct: 391 FRPGAIEKYDGSTDPEKFLQIYSTVLYAAGVDDNALANYLPTALKGSARSWPMHLPPYSI 450

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W+D F+ANFQ + + A DL ++ E+LR Y++RF RN PE+ +A V  
Sbjct: 451 SSWADLWQQFVANFQGTYKRHAIEDDLHALTQNSGESLRGYVRRFNECRNTIPEITDASV 510

Query: 1681 IEDFYRGSNDSAFVRAILQKSVGHLRTL 1764  
I F G D + + + + R L  
Sbjct: 511 IRAFKFGVRDRYTTQELATTRITTTTRRL 538

>gb|ABA98926.2| retrotransposon protein, putative, Ty3-gypsy subclass [Oryza sativa  
(japonica cultivar-group)]  
Length = 1991

Score = 89.0 bits (219), Expect = 2e-15  
Identities = 42/127 (33%), Positives = 67/127 (52%)  
Frame = +1

Query: 1321 FKVSNSVSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
FK + + KY+ + WL +Y + AAG M Y P+ L A WL LP+ I  
Sbjct: 434 FKPTGIEKYDGTTPESWLTIVYGLAIRAAGGDSKAMANYLPVALADSARSWLHGLPRGTI 493

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W++ FIANFQ F++P +DL ++ + E+LR Y++RF RN ++ + +  
Sbjct: 494 GSWAELRDHFIANFQGTFERPGTQYDLYNVIQKSGESLRDYIRRFSEQRNKISDITDDVI 553

Query: 1681 IEDFYRG 1701  
I F +G  
Sbjct: 554 IAAFTKG 560

>gb|ABF93731.1| retrotransposon protein, putative, Ty3-gypsy subclass [Oryza sativa  
(japonica cultivar-group)]  
Length = 1953

Score = 89.0 bits (219), Expect = 2e-15  
Identities = 42/127 (33%), Positives = 67/127 (52%)  
Frame = +1

Query: 1321 FKVSNVSKYERKQDLGGWLAIYITIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
FK + + KY+ + WL +Y + AAG M Y P+ L A WL LP+ I  
Sbjct: 396 FKPTGIEKYDGTTPESWLTIVYGLAIRAAGGDSKAMANYLPVALADSARSWLHGLPRGTI 455

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W++ FIANFQ F++P +DL ++ + E+LR Y++RF RN ++ + +  
Sbjct: 456 GSWAELRDHFIANFQGTFERPGTQYDLYNVIQKSGESLRDYIRRFSEQRNKISDITDDVI 515

Query: 1681 IEDFYRG 1701  
I F +G  
Sbjct: 516 IAAFTKG 522

>gb|AAT73678.1| putative polyprotein [Oryza sativa Japonica Group]  
Length = 1992

Score = 89.0 bits (219), Expect = 2e-15  
Identities = 42/127 (33%), Positives = 67/127 (52%)  
Frame = +1

Query: 1321 FKVSNVSKYERKQDLGGWLAIYITIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
FK + + KY+ + WL +Y + AAG M Y P+ L A WL LP+ I  
Sbjct: 431 FKPTGIEKYDGTTPESWLTIVYGLAIRAAGGDSKAMANYLPVALADSARSWLHGLPRGTI 490

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W++ FIANFQ F++P +DL ++ + E+LR Y++RF RN ++ + +  
Sbjct: 491 GSWAELRDHFIANFQGTFERPGTQYDLYNVIQKSGESLRDYIRRFSEQRNKISDITDDVI 550

Query: 1681 IEDFYRG 1701  
I F +G  
Sbjct: 551 IAAFTKG 557

>gb|AAT44267.1| hypothetical protein [Oryza sativa Japonica Group]  
Length = 1315

Score = 89.0 bits (219), Expect = 2e-15  
Identities = 44/134 (32%), Positives = 70/134 (52%)  
Frame = +1

Query: 1321 FKVSNVSKYERKQDLGGWLAIYITIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
FK + + KY+ + WL +Y++ AAG M Y P+ L A WL LP+ I  
Sbjct: 270 FKPTGIEKYDGTTPETWLTIVYSLAIRAAGGDIKAMANYLPVALADSARSWLHGLPRGTI 329

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEVAEAGV 1680

+W++      FIANFQ  F++P   +DL +I  +  E+LR Y++RF   RN   ++ +  +  
Sbjct: 330  GSWAELRDHFIANFQGTFERPGTQFDLYNIVQKSGESLRDYIRRFSEQRNKISDITDDVI 389

Query: 1681  IEDFYRGSNDSAFV 1722

          I  F  +G  +      V  
Sbjct: 390  IAAFTKGIHDDLVLV 403

>gb|AAT01309.1| putative gag-pol polyprotein [Oryza sativa Japonica Group]  
gb|AAU03118.1| putative polyprotein [Oryza sativa Japonica Group]  
          Length = 1149

Score = 89.0 bits (219), Expect = 2e-15  
Identities = 42/127 (33%), Positives = 67/127 (52%)  
Frame = +1

Query: 1321  FKVSNVSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPPIVLGQDAMQWLRHLPQHCI 1500  
          FK  +  +  KY+      +  WL  +Y  +  AAG      M  Y  P+  L   A  WL  LP+  I  
Sbjct: 431  FKPTGIEKYDGTTPESWLTVYGLAIRAAGGDNKAMANYLPVALADSARSWLHGLPRGTI 490

Query: 1501  DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
          +W++      FIANFQ  F++P   +DL ++  +  E+LR Y++RF   RN   ++ +  +  
Sbjct: 491  GSWAELRDHFIANFQGTFERPGTQFDLYNVIQKSGESLRDYIRRFSEQRNKISDITDDVI 550

Query: 1681  IEDFYRG 1701  
          I  F  +G  
Sbjct: 551  IAAFTKG 557

>gb|AAR96234.1| putative polyprotein [Oryza sativa Japonica Group]  
gb|ABF96264.1| retrotransposon protein, putative, Ty3-gypsy subclass [Oryza sativa  
          (japonica cultivar-group)]  
          Length = 2004

Score = 89.0 bits (219), Expect = 2e-15  
Identities = 42/127 (33%), Positives = 67/127 (52%)  
Frame = +1

Query: 1321  FKVSNVSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPPIVLGQDAMQWLRHLPQHCI 1500  
          FK  +  +  KY+      +  WL  +Y  +  AAG      M  Y  P+  L   A  WL  LP+  I  
Sbjct: 438  FKPTGIEKYDGTTPESWLTVYGLAIRAAGGDSKAMANYLPVALADSARSWLHGLPRGTI 497

Query: 1501  DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
          +W++      FIANFQ  F++P   +DL ++  +  E+LR Y++RF   RN   ++ +  +  
Sbjct: 498  GSWAELRDHFIANFQGTFERPGTQFDLYNVVQKSGESLRDYIRRFSEQRNKISDITDDVI 557

Query: 1681  IEDFYRG 1701  
          I  F  +G  
Sbjct: 558  IAAFTKG 564

>emb|CAE04320.1| OSJNBb0016D16.11 [Oryza sativa (japonica cultivar-group)]  
          Length = 1748

Score = 89.0 bits (219), Expect = 2e-15  
Identities = 42/127 (33%), Positives = 67/127 (52%)  
Frame = +1

Query: 1321  FKVSNVSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPPIVLGQDAMQWLRHLPQHCI 1500  
          FK  +  +  KY+      +  WL  +Y  +  AAG      M  Y  P+  L   A  WL  LP+  I  
Sbjct: 438  FKPTGIEKYDGTTPESWLTVYGLAIRAAGGDSKAMANYLPVALADSARSWLHGLPRGTI 497

Query: 1501  DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEVAEAGV 1680



+W++ FIANFQ F++P +DL ++ + E+LR Y++RF RN ++ + +  
Sbjct: 498 GSWAELRDHFIANFQGTFERPGTQFDLYNVVQKSGESLRDYIRRFSEQRNKISDITDDVI 557

Query: 1681 IEDFYRG 1701

I F +G  
Sbjct: 558 IAAFTKG 564

>emb|CAE03508.2| OSJNBa0053K19.16 [Oryza sativa (japonica cultivar-group)]  
Length = 2010

Score = 89.0 bits (219), Expect = 2e-15  
Identities = 42/127 (33%), Positives = 67/127 (52%)  
Frame = +1

Query: 1321 FKVSNVSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
FK + + KY+ + WL +Y + AAG M Y P+ L A WL LP+ I  
Sbjct: 431 FKPTGIEKYDGTTPESWLTVMYGLAIRAAGGDNKAMANYLPVALADSARSWLHGLPRGTI 490

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W++ FIANFQ F++P +DL ++ + E+LR Y++RF RN ++ + +  
Sbjct: 491 GSWAELRDHFIANFQGTFERPGTQYDLYNVIQKSGESLRDYIRRFSEQRNKISDITDDVI 550

Query: 1681 IEDFYRG 1701  
I F +G  
Sbjct: 551 IAAFTKG 557

>emb|CAE05063.1| OSJNBa0094P09.2 [Oryza sativa (japonica cultivar-group)]  
emb|CAD39817.3| OSJNBa0079F16.18 [Oryza sativa (japonica cultivar-group)]  
Length = 1802

Score = 89.0 bits (219), Expect = 2e-15  
Identities = 42/127 (33%), Positives = 67/127 (52%)  
Frame = +1

Query: 1321 FKVSNVSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
FK + + KY+ + WL +Y + AAG M Y P+ L A WL LP+ I  
Sbjct: 438 FKPTGIEKYDGTTPESWLTVMYGLAIRAAGGDSKAMANYLPVALADSARSWLHGLPRGTI 497

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W++ FIANFQ F++P +DL ++ + E+LR Y++RF RN ++ + +  
Sbjct: 498 GSWAELRDHFIANFQGTFERPGTQYDLYNVIQKSGESLRDYIRRFSEQRNKISDITDDVI 557

Query: 1681 IEDFYRG 1701  
I F +G  
Sbjct: 558 IAAFTKG 564

>emb|CAE02298.2| OSJNBa0042F21.5 [Oryza sativa (japonica cultivar-group)]  
Length = 1950

Score = 89.0 bits (219), Expect = 2e-15  
Identities = 42/127 (33%), Positives = 67/127 (52%)  
Frame = +1

Query: 1321 FKVSNVSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
FK + + KY+ + WL +Y + AAG M Y P+ L A WL LP+ I  
Sbjct: 371 FKPTGIEKYDGTTPESWLTVMYGLAIRAAGGDNKAMANYLPVALADSARSWLHGLPRGTI 430

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W++ FIANFQ F++P +DL ++ + E+LR Y++RF RN ++ + +  
Sbjct: 431 GSWAELRDHFIANFQGTFERPGTQYDLYNVIQKSGESLRDYIRRFSEQRNKISDITDDVI 490

Query: 1681 IEDFYRG 1701  
I F +G  
Sbjct: 491 IAAFTKG 497

>emb|CAE02180.2| OSJNBa0080E14.11 [Oryza sativa (japonica cultivar-group)]  
Length = 2001

Score = 89.0 bits (219), Expect = 2e-15  
Identities = 42/127 (33%), Positives = 67/127 (52%)  
Frame = +1

Query: 1321 FKVSNVSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
FK + + KY+ + WL +Y + AAG M Y P+ L A WL LP+ I  
Sbjct: 438 FKPTGIEKYDGTTPNESWLTVYGLAIRAAGGDSKAMVNYLPVALADSARSWLHGLPRGTI 497

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W++ FIANFQ F++P +DL ++ + E+LR Y++RF RN ++ + +  
Sbjct: 498 GSWAELRDHFIANFQGTTFERPQTQFDLYNVVQKSGESLTDYIRRFSEQRNKISDITDDVI 557

Query: 1681 IEDFYRG 1701  
I F +G  
Sbjct: 558 IAAFTKG 564

>gb|AAL58229.1|AC084762\_3 putative gag-pol precursor [Oryza sativa Japonica Group]  
Length = 2026

Score = 89.0 bits (219), Expect = 2e-15  
Identities = 42/127 (33%), Positives = 67/127 (52%)  
Frame = +1

Query: 1321 FKVSNVSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
FK + + KY+ + WL +Y + AAG M Y P+ L A WL LP+ I  
Sbjct: 438 FKPTGIEKYDGTTPNESWLTVYGLAIRAAGGDSKAMANYLPVALADSARSWLHGLPRGTI 497

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W++ FIANFQ F++P +DL ++ + E+LR Y++RF RN ++ + +  
Sbjct: 498 GSWAELRDHFIANFQGTTFERPQTQFDLYNVVQKSGESLTDYIRRFSEQRNKISDITDDVI 557

Query: 1681 IEDFYRG 1701  
I F +G  
Sbjct: 558 IAAFTKG 564

>gb|AAN04936.1| Putative retroelement [Oryza sativa Japonica Group]  
Length = 1479

Score = 89.0 bits (219), Expect = 2e-15  
Identities = 42/127 (33%), Positives = 67/127 (52%)  
Frame = +1

Query: 1321 FKVSNVSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
FK + + KY+ + WL +Y + AAG M Y P+ L A WL LP+ I  
Sbjct: 434 FKPTGIEKYDGTTPNESWLTVYGLAIRAAGGDSKAMANYLPVALADSARSWLHGLPRGTI 493

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W++ FIANFQ F++P +DL ++ + E+LR Y++RF RN ++ + +  
Sbjct: 494 GSWAELRDHFIANFQGTTFERPQTQYDLYNVIQKSGESLTDYIRRFSEQRNKISDITDDVI 553

Query: 1681 IEDFYRG 1701  
I F +G

Sbjct: 554 IAAFTKG 560

>gb|ABA97070.1| retrotransposon protein, putative, Ty3-gypsy subclass [Oryza sativa  
(japonica cultivar-group)]  
Length = 1988

Score = 89.0 bits (219), Expect = 2e-15  
Identities = 42/127 (33%), Positives = 67/127 (52%)  
Frame = +1

Query: 1321 FKVSNSVSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
FK + + KY+ + WL +Y + AAG M Y P+ L A WL LP+ I  
Sbjct: 431 FKPTGIEKYDGTTPESWLTIVYGLAIRAAGGDNKAMANYLPVALADSARSWLHGLPRGTI 490

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W++ FIANFQ F++P +DL ++ + E+LR Y++RF RN ++ + +  
Sbjct: 491 GSWAELRDHFIANFQGTFERPGTQYDLYNVIQKSGESLRDYIRRFSEQRNKISDITDDVI 550

Query: 1681 IEDFYRG 1701  
I F +G  
Sbjct: 551 IAAFTKG 557

>gb|ABA97957.1| retrotransposon protein, putative, Ty3-gypsy subclass [Oryza sativa  
(japonica cultivar-group)]  
Length = 1984

Score = 89.0 bits (219), Expect = 2e-15  
Identities = 42/127 (33%), Positives = 67/127 (52%)  
Frame = +1

Query: 1321 FKVSNSVSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
FK + + KY+ + WL +Y + AAG M Y P+ L A WL LP+ I  
Sbjct: 431 FKPTGIEKYDGTTPESWLTIVYGLAIRAAGGDNKAMANYLPVALADSARSWLHGLPRGTI 490

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W++ FIANFQ F++P +DL ++ + E+LR Y++RF RN ++ + +  
Sbjct: 491 GSWAELRDHFIANFQGTFERPGTQYDLYNVIQKSGESLRDYIRRFSEQRNKISDITDDVI 550

Query: 1681 IEDFYRG 1701  
I F +G  
Sbjct: 551 IAAFTKG 557

>gb|ABA99219.1| retrotransposon protein, putative, Ty3-gypsy subclass [Oryza sativa  
(japonica cultivar-group)]  
Length = 2360

Score = 89.0 bits (219), Expect = 2e-15  
Identities = 42/127 (33%), Positives = 67/127 (52%)  
Frame = +1

Query: 1321 FKVSNSVSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
FK + + KY+ + WL +Y + AAG M Y P+ L A WL LP+ I  
Sbjct: 1816 FKPTGIEKYDGTTPESWLTIVYGLAIRAAGGDSKAMANYLPVALADSARSWLHGLPRGTI 1875

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W++ FIANFQ F++P +DL ++ + E+LR Y++RF RN ++ + +  
Sbjct: 1876 GSWAELRDHFIANFQGTFERPGTQYDLYNVIQKSGESLRDYIRRFSEQRNKISDITDDVI 1935

Query: 1681 IEDFYRG 1701  
I F +G

Sbjct: 1936 IAAFTKG 1942

>gb|ABA97102.1| retrotransposon protein, putative, Ty3-gypsy subclass [Oryza sativa  
(japonica cultivar-group)]  
Length = 1233

Score = 89.0 bits (219), Expect = 2e-15  
Identities = 42/127 (33%), Positives = 67/127 (52%)  
Frame = +1

Query: 1321 FKVSNVSKYERKQDLGGWLAIYTIWTAAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
FK + + KY+ + WL +Y + AAG M Y P+ L A WL LP+ I  
Sbjct: 438 FKPTGIEKYDGTTPESWLTIVYGLAIRAAGGDNKAMANYLPVALADSARSWLHGLPRGTI 497

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W++ FIANFQ F++P +DL ++ + E+LR Y++RF RN ++ + +  
Sbjct: 498 GSWAELHDHFIANFQGTFERPGTQYDLYNVIQKSGESLRDYIRRFSEQRNKISDITDDVI 557

Query: 1681 IEDFYRG 1701  
I F +G  
Sbjct: 558 IAAFTKG 564

>gb|ABA95029.1| retrotransposon protein, putative, Ty3-gypsy subclass [Oryza sativa  
(japonica cultivar-group)]  
Length = 1995

Score = 89.0 bits (219), Expect = 2e-15  
Identities = 42/127 (33%), Positives = 67/127 (52%)  
Frame = +1

Query: 1321 FKVSNVSKYERKQDLGGWLAIYTIWTAAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
FK + + KY+ + WL +Y + AAG M Y P+ L A WL LP+ I  
Sbjct: 438 FKPTGIEKYDGTTPESWLTIVYGLAIRAAGGDSKAMANYLPVALADSARSWLHGLPRGTI 497

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W++ FIANFQ F++P +DL ++ + E+LR Y++RF RN ++ + +  
Sbjct: 498 GSWAELRDHFIANFQGTFERPGTQYDLYNVIQKSGESLRDYIRRFSEQRNKISDITDDVI 557

Query: 1681 IEDFYRG 1701  
I F +G  
Sbjct: 558 IAAFTKG 564

>gb|ABA95254.1| retrotransposon protein, putative, Ty3-gypsy subclass [Oryza sativa  
(japonica cultivar-group)]  
Length = 823

Score = 89.0 bits (219), Expect = 2e-15  
Identities = 42/127 (33%), Positives = 67/127 (52%)  
Frame = +1

Query: 1321 FKVSNVSKYERKQDLGGWLAIYTIWTAAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
FK + + KY+ + WL +Y + AAG M Y P+ L A WL LP+ I  
Sbjct: 365 FKPTGIEKYDGTTPESWLTIVYGLAIRAAGGDSKAMANYLPVALADSARSWLHGLPRGTI 424

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W++ FIANFQ F++P +DL ++ + E+LR Y++RF RN ++ + +  
Sbjct: 425 GSWAELRDHFIANFQGTFERPGTQFDLYNVVQKSGESLRDYIRRFSEQRNKISDITDDVI 484

Query: 1681 IEDFYRG 1701  
I F +G

Sbjct: 485 IAAFTKG 491

>gb|ABA93599.1| retrotransposon protein, putative, Ty3-gypsy subclass [Oryza sativa  
(japonica cultivar-group)]  
Length = 1912

Score = 89.0 bits (219), Expect = 2e-15  
Identities = 42/127 (33%), Positives = 67/127 (52%)  
Frame = +1

Query: 1321 FKVSNSVSKYERKQDLGGWLAIYTIWTAAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
FK + + KY+ + WL +Y + AAG M Y P+ L A WL LP+ I  
Sbjct: 434 FKPTGIEKYDGTTPESWLTVYGLAIRAAGGDSKAMANYLPVALADSARSWLHGLPRGTI 493

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W++ FIANFQ F++P +DL ++ + E+LR Y++RF RN ++ + +  
Sbjct: 494 GSWAELRDHFIANFQGTFERPGTQYDLYNVIQKSGESLRDYIRRFSEQRNKISDITDDVI 553

Query: 1681 IEDFYRG 1701  
I F +G  
Sbjct: 554 IAAFTKG 560

>gb|ABA94908.1| retrotransposon protein, putative, Ty3-gypsy subclass [Oryza sativa  
(japonica cultivar-group)]  
Length = 1994

Score = 89.0 bits (219), Expect = 2e-15  
Identities = 42/127 (33%), Positives = 67/127 (52%)  
Frame = +1

Query: 1321 FKVSNSVSKYERKQDLGGWLAIYTIWTAAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
FK + + KY+ + WL +Y + AAG M Y P+ L A WL LP+ I  
Sbjct: 434 FKPTGIEKYDGTTPESWLTVYGLAIRAAGGDNKAMANYLPVALADSARSWLHGLPRGTI 493

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W++ FIANFQ F++P +DL ++ + E+LR Y++RF RN ++ + +  
Sbjct: 494 GSWAELRDHFIANFQGTFERPGTQYDLYNVIQKSGESLRDYIRRFSEQRNKISDITDDVI 553

Query: 1681 IEDFYRG 1701  
I F +G  
Sbjct: 554 IAAFTKG 560

>gb|ABA95079.1| retrotransposon protein, putative, Ty3-gypsy subclass [Oryza sativa  
(japonica cultivar-group)]  
Length = 1966

Score = 89.0 bits (219), Expect = 2e-15  
Identities = 42/127 (33%), Positives = 67/127 (52%)  
Frame = +1

Query: 1321 FKVSNSVSKYERKQDLGGWLAIYTIWTAAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
FK + + KY+ + WL +Y + AAG M Y P+ L A WL LP+ I  
Sbjct: 434 FKPTGIEKYDGTTPESWLTVYGLAIRAAGGDNKAMANYLPVALADSARSWLHGLPRGTI 493

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W++ FIANFQ F++P +DL ++ + E+LR Y++RF RN ++ + +  
Sbjct: 494 GSWAELRDHFIANFQGTFERPGTQYDLYNVIQKSGESLRDYIRRFSEQRNKISDITDDVI 553

Query: 1681 IEDFYRG 1701  
I F +G

Sbjct: 554 IAAFTKG 560

>gb|AAP54065.1| retrotransposon protein, putative, Ty3-gypsy subclass [Oryza sativa (japonica cultivar-group)]  
Length = 1995

Score = 89.0 bits (219), Expect = 2e-15  
Identities = 42/127 (33%), Positives = 67/127 (52%)  
Frame = +1

Query: 1321 FKVSNSVSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
FK + + KY+ + WL +Y + AAG M Y P+ L A WL LP+ I  
Sbjct: 438 FKPTGIEKYDGTTPESWLTIVYGLAIRAAGGDSKAMANYLPVALADSARSWLHGLPRGTI 497

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W++ FIANFQ F++P +DL ++ + E+LR Y++RF RN ++ + +  
Sbjct: 498 GSWAELRDHFIANFQGTFERPGTQYDLYNVIQKSGESLRDYIRRFSEQRNKISDITDDVI 557

Query: 1681 IEDFYRG 1701  
I F +G  
Sbjct: 558 IAAFTKG 564

>gb|AAM00949.1|AC021892\_13 Putative retroelement [Oryza sativa Japonica Group]  
gb|AAP52913.1| retrotransposon protein, putative, Ty3-gypsy subclass [Oryza sativa (japonica cultivar-group)]  
Length = 1945

Score = 89.0 bits (219), Expect = 2e-15  
Identities = 42/127 (33%), Positives = 67/127 (52%)  
Frame = +1

Query: 1321 FKVSNSVSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
FK + + KY+ + WL +Y + AAG M Y P+ L A WL LP+ I  
Sbjct: 434 FKPTGIEKYDGTTPESWLTIVYGLAIRAAGGDSKAMANYLPVALADSARSWLHGLPRGTI 493

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W++ FIANFQ F++P +DL ++ + E+LR Y++RF RN ++ + +  
Sbjct: 494 GSWAELRDHFIANFQGTFERPGTQYDLYNVIQKSGESLRDYIRRFSEQRNKISDITDDVI 553

Query: 1681 IEDFYRG 1701  
I F +G  
Sbjct: 554 IAAFTKG 560

>gb|AAN08252.1| putative GAG-POL precursor [Oryza sativa Japonica Group]  
Length = 792

Score = 89.0 bits (219), Expect = 2e-15  
Identities = 42/127 (33%), Positives = 67/127 (52%)  
Frame = +1

Query: 1321 FKVSNSVSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
FK + + KY+ + WL +Y + AAG M Y P+ L A WL LP+ I  
Sbjct: 338 FKPTGIEKYDGTTPESWLTIVYGLAIRAAGGDNKAMANYLPVALADSARSWLHGLPRGTI 397

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W++ FIANFQ F++P +DL ++ + E+LR Y++RF RN ++ + +  
Sbjct: 398 GSWAELRDHFIANFQGTFERPGTQYDLYNVIQKSGESLRDYIRRFSEQRNKISDITDDVI 457

Query: 1681 IEDFYRG 1701  
I F +G

Sbjct: 458 IAAFTKG 464

>gb|AAM92798.1| putative gag-pol precursor [Oryza sativa Japonica Group]  
Length = 1986

Score = 89.0 bits (219), Expect = 2e-15  
Identities = 42/127 (33%), Positives = 67/127 (52%)  
Frame = +1

Query: 1321 FKVSNVSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
FK + + KY+ + WL +Y + AAG M Y P+ L A WL LP+ I  
Sbjct: 434 FKPTGIEKYDGTNPESWLTVYGLAIRAAGGDNKAMANYLPVALADSARSWLHGLPRGTI 493

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W++ FIANFQ F++P +DL ++ + E+LR Y++RF RN ++ + +  
Sbjct: 494 GSWAELRDHFIANFQGTFERPGTQYDLYNVIQKSGESLRDYIRRFSEQRNKISDITDDVI 553

Query: 1681 IEDFYRG 1701  
I F +G  
Sbjct: 554 IAAFTKG 560

>gb|AAD27551.1|AF111709\_5 gag-pol protein [Oryza sativa Indica Group]  
Length = 1016

Score = 89.0 bits (219), Expect = 2e-15  
Identities = 42/127 (33%), Positives = 67/127 (52%)  
Frame = +1

Query: 1321 FKVSNVSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
FK + + KY+ + WL +Y + AAG M Y P+ L A WL LP+ I  
Sbjct: 434 FKPTGIEKYDGTNPESWLTVYGLAIRAAGGDNKAMANYLPVALADSARSWLHGLPRGTI 493

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W++ FIANFQ F++P +DL ++ + E+LR Y++RF RN ++ + +  
Sbjct: 494 GSWAELRDHFIANFQGTFERPGTQYDLYNVIQKSGESLRDYIRRFSEQRNKISDITDDVI 553

Query: 1681 IEDFYRG 1701  
I F +G  
Sbjct: 554 IAAFTKG 560

>gb|AAM22011.1|AC093178\_6 Putative gag-pol precursor [Oryza sativa Japonica Group]  
gb|AAP52687.1| retrotransposon protein, putative, Ty3-gypsy subclass [Oryza sativa  
(japonica cultivar-group)]  
Length = 1933

Score = 89.0 bits (219), Expect = 2e-15  
Identities = 42/127 (33%), Positives = 67/127 (52%)  
Frame = +1

Query: 1321 FKVSNVSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
FK + + KY+ + WL +Y + AAG M Y P+ L A WL LP+ I  
Sbjct: 438 FKPTGIEKYDGTNPESWLTVYGLAIRAAGGDSKAMANYLPVALADSARSWLHGLPRGTI 497

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W++ FIANFQ F++P +DL ++ + E+LR Y++RF RN ++ + +  
Sbjct: 498 GSWAELRDHFIANFQGTFERPGTQFDLYNVVQKSGESLRDYIRRFSEQRNKISDITDDVI 557

Query: 1681 IEDFYRG 1701  
I F +G  
Sbjct: 558 IAAFTKG 564

>gb|AAM92802.1| putative gag-pol precursor [Oryza sativa Japonica Group]  
Length = 2017

Score = 89.0 bits (219), Expect = 2e-15  
Identities = 42/127 (33%), Positives = 67/127 (52%)  
Frame = +1

Query: 1321 FKVSNVSKYERKQDLGGWLAIYTIWTAAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
FK + + KY+ + WL +Y + AAG M Y P+ L A WL LP+ I  
Sbjct: 438 FKPTGIEKYDGTTPESWLTIVYGLAIRAAGDNKAMANYLPVALADSARSWLHGLPRGTI 497

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W++ FIANFQ F++P +DL ++ + E+LR Y++RF RN ++ + +  
Sbjct: 498 GSWAELRDHFIANFQGTFERPGTQYDLYNVIQKSGESLRDYIRRFSEQRNKISDITDDVI 557

Query: 1681 IEDFYRG 1701  
I F +G  
Sbjct: 558 IAAFTKG 564

>emb|CAD39529.2| OSJNBa0027001.4 [Oryza sativa (japonica cultivar-group)]  
Length = 2013

Score = 89.0 bits (219), Expect = 2e-15  
Identities = 42/127 (33%), Positives = 67/127 (52%)  
Frame = +1

Query: 1321 FKVSNVSKYERKQDLGGWLAIYTIWTAAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
FK + + KY+ + WL +Y + AAG M Y P+ L A WL LP+ I  
Sbjct: 434 FKPTGIEKYDGTTPESWLTIVYGLAIRAAGDNKAMANYLPVALADSARSWLHGLPRGTI 493

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W++ FIANFQ F++P +DL ++ + E+LR Y++RF RN ++ + +  
Sbjct: 494 GSWAELRDHFIANFQGTFERPGTQYDLYNVIQKSGESLRDYIRRFSEQRNKISDITDDVI 553

Query: 1681 IEDFYRG 1701  
I F +G  
Sbjct: 554 IAAFTKG 560

>dbj|BAB00646.1| unnamed protein product [Oryza sativa Japonica Group]  
dbj|BAB17742.1| GAG-POL precursor [Oryza sativa Japonica Group]  
Length = 1473

Score = 89.0 bits (219), Expect = 2e-15  
Identities = 55/169 (32%), Positives = 80/169 (47%)  
Frame = +1

Query: 1234 GPTSRTPT\*RHVRSRLRTYSVSPGHPVAPNFKVSNVSKYERKQDLGGWLAIYTIWTAAAGA 1413  
GP SR P R R P+AP + KY+ + +L IYT AAG+  
Sbjct: 40 GPASRVPGWR-CRLSSLCGEPSERPLAPKVPAAHHRKYDGSVNPAEFLQIYTTGIEAAGS 98

Query: 1414 TEDVMTVYFPIVLGQDAMQWLRHLPQHCIDNWSDFSWCFIANFQSLFDKPAQPWDLKSIG 1593  
+ VMT +FP+ L A WL +LP + +W D F NFQ + +P + DL ++  
Sbjct: 99 DDRVMTNFFPMALKGQARGWLMNLPASVHSHWEDLCQQFTMNFGQTYPRPGEEADLHAVQ 158

Query: 1594 HQGDETLRLYLKRF\*TMRNHTPEVAEAGVIEDFYRGSNDSAFVRAILQK 1740  
+ DE+LR Y++RF +RN P + VI F G + + I K  
Sbjct: 159 RRDDESLRSYIQRFCQVRNTIPCIHAHAVIYAFRGGVRHNRMLEKIASK 207



>gb|ABG66296.1| retrotransposon protein, putative, Ty3-gypsy subclass [Oryza sativa (japonica cultivar-group)]  
Length = 1658

Score = 88.6 bits (218), Expect = 2e-15  
Identities = 42/127 (33%), Positives = 67/127 (52%)  
Frame = +1

Query: 1321 FKVSNVSKYERKQDLGGWLAIYTIWTAAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
FK + + KY+ + WL +Y + AAG M Y P+ L A WL LP+ I  
Sbjct: 430 FKPTGIEKYDGTTPESWLTIVYGLAIRAAGGDSKAMANYLPVALANSARSWLHGLPRGTI 489

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W++ FIANFQ F++P +DL ++ + E+LR Y++RF RN ++ + +  
Sbjct: 490 GSWAELRDHFIANFQGTFERPGTQFDLYNVVQKSGESLRDYIRRFSEQRNKISDITDDII 549

Query: 1681 IEDFYRG 1701  
I F +G  
Sbjct: 550 IAAFTKG 556

>gb|ABG22603.1| retrotransposon protein, putative, unclassified [Oryza sativa (japonica cultivar-group)]  
Length = 539

Score = 88.6 bits (218), Expect = 2e-15  
Identities = 47/148 (31%), Positives = 75/148 (50%)  
Frame = +1

Query: 1321 FKVSNVSKYERKQDLGGWLAIYTIWTAAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
F+ + KY+ D +L +Y+ + +AAGA ++ + Y P L A WL HLP + I  
Sbjct: 365 FRPGAIEKYDGSTDPPEEFLQVYSTILYAAGADDNALANYLPAALKGSARSWLVHLPPLYI 424

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W+D F+ANFQ + + +L ++ E+LR Y++RF RN PE+ +A V  
Sbjct: 425 SSWADLWQQFVANFQGTYKRHEIEDNLHALTQNPGESLRDYIRRFNECRNTIPEITDASV 484

Query: 1681 IEDFYRGSNDSAFVRAILQKSVGHLRTL 1764  
I F G D + + K + R L  
Sbjct: 485 IRVFKSGVRDHYTTQELATKRIVTARKL 512

>gb|ABF98055.1| retrotransposon protein, putative, unclassified [Oryza sativa (japonica cultivar-group)]  
Length = 1890

Score = 88.6 bits (218), Expect = 2e-15  
Identities = 54/180 (30%), Positives = 82/180 (45%)  
Frame = +1

Query: 1201 IKMTHNWLPSLGPTSRTPT\*RHVRSRLTYSVSPGHPVAPNFKVSNVSKYERKQDLGGWLA 1380  
++ H P + P V SLR P F+ + KY+R + +L  
Sbjct: 142 LRSGHGGRPPVSPVGGAGCRAFVASLRNVRWPP-----RFRPTITEKYDRSVNPAEFLQ 195

Query: 1381 IYTIWTAAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCIDNWSDFSWCFIANFQSLFDK 1560  
IYT AAG + VM +FP+ L A WL +LP + +W D F NFQ ++ +  
Sbjct: 196 IYTTGIEAAGGDDRVMANFFPMALKGQARGWLMNLPPASVHSWEDLCQQFTTNFQGIYPR 255

Query: 1561 PAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEVAEAGVIEDFYRGSNDSAFVRAILQK 1740  
P + DL ++ + DE+LR Y++RF +RN P + VI F G + + I K  
Sbjct: 256 PGEEADLHAVQRRNDESLRSYIQRFCQVRNTIPCIPAHAVIYAFRGGVRHNRMLEKIASK 315

>gb|ABF96608.1| retrotransposon protein, putative, Ty3-gypsy subclass [Oryza sativa (japonica cultivar-group)]  
Length = 828

Score = 88.6 bits (218), Expect = 2e-15  
Identities = 41/127 (32%), Positives = 67/127 (52%)  
Frame = +1

Query: 1321 FKVSNVSKYERKQDLGGWLAIYTIWTAAAGATEDVMTVYFPPIVLGQDAMQWLRHLPQHCI 1500  
FK + + KY+ + WL +Y + AG M Y P+ L A WL LP+ I  
Sbjct: 299 FKPTGIEKYDGTTPESWLTIVYGLAIRTAGGDSKAMANYLPVALADSARSWLHGLPRGTI 358

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W++ FIANFQ F++P +DL ++ + +E+LR Y++RF RN ++ + +  
Sbjct: 359 GSWAELRDHFIANFQGTFERPGTQFDLYNVVQKSEESLRDYIRRFSEQRNKISDITDDVI 418

Query: 1681 IEDFYRG 1701  
I F +G  
Sbjct: 419 IAAFTKG 425

>gb|AAX95359.1| Retrotransposon gag protein, putative [Oryza sativa Japonica Group]  
Length = 635

Score = 88.6 bits (218), Expect = 2e-15  
Identities = 47/148 (31%), Positives = 75/148 (50%)  
Frame = +1

Query: 1321 FKVSNVSKYERKQDLGGWLAIYTIWTAAAGATEDVMTVYFPPIVLGQDAMQWLRHLPQHCI 1500  
F+ + KY+ D +L +Y+ + +AAGA ++ + Y P L A WL HLP + I  
Sbjct: 365 FRPGAIEKYDGSTDPEEFLQVYSTILYAAGADDNALANYLPAALKGSARSWLHGLPPYLI 424

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W+D F+ANFQ + + +L ++ E+LR Y++RF RN PE+ +A V  
Sbjct: 425 SSWADLWQQFVANFQGTYKRHEIEDNLHALTQNPGESLRDYIRRFNECRNTIPEITDASV 484

Query: 1681 IEDFYRGSNDSAFVRAILQKSVGHLRTL 1764  
I F G D + + K + R L  
Sbjct: 485 IRVFKSGVRDHYTTQELATKRIVTARKL 512

>gb|AAV31353.1| putative polyprotein [Oryza sativa Japonica Group]  
Length = 1799

Score = 88.6 bits (218), Expect = 2e-15  
Identities = 42/127 (33%), Positives = 67/127 (52%)  
Frame = +1

Query: 1321 FKVSNVSKYERKQDLGGWLAIYTIWTAAAGATEDVMTVYFPPIVLGQDAMQWLRHLPQHCI 1500  
FK + + KY+ + WL +Y + AAG M Y P+ L A WL LP+ I  
Sbjct: 233 FKPTGIEKYDGTTPESWLTIVYGLAIRAAGDSKAMANYLPVALADSARSWLHGLPRGTI 292

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W++ FIANFQ F++P +DL ++ + E+LR Y++RF RN ++ + +  
Sbjct: 293 RSWAELRDHFIANFQGTFERPGTQYDLYNVIQKSGESLRDYIRRFSEQRNKISDITDDVI 352

Query: 1681 IEDFYRG 1701  
I F +G  
Sbjct: 353 IAAFTKG 359

>gb|AAU90208.1| putative polyprotein [Oryza sativa Japonica Group]  
Length = 1862

Score = 88.6 bits (218), Expect = 2e-15  
Identities = 55/180 (30%), Positives = 82/180 (45%)  
Frame = +1

Query: 1201 IKMTHNWLPSLGPTSRTPT\*RHVRSRLRTYSVSPGHPVAPNFKVSNVSKYERKQDLGGWLA 1380  
++ H P + P T V SLR P F+ + KY+ + +L  
Sbjct: 203 LRSGHGGRPPVSPVGGTGCRTFVASLRNVRWPP-----RFRPTITEKYDGSVNPAEFLQ 256

Query: 1381 IYTIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCDNWSDFSWCFIANFQSLFDK 1560  
IYT AAG + VM +FP+ L A WL +LP + +W D F NFQ ++ +  
Sbjct: 257 IYTTGIEAAGGDDRVMANFFPMALKGQARGWLMNLPPASVHSWEDLCQQFTTNFQGIYPR 316

Query: 1561 PAQPWDLKSIGHQGETLRLLYLKRF\*TMRNHTPEVAEAGVIEDFYRGSNDSAFVRAILQK 1740  
P + DL ++ + DE+LR Y++RF +RN P + VI F G + V I K  
Sbjct: 317 PGEEADLHAVQRRDDESLRSYIQRFCQVRNTIPCIPAHAVIYAFRGGVRHNRNMEKIASK 376

>gb|AAS07318.1| putative polyprotein [Oryza sativa Japonica Group]  
Length = 968

Score = 88.6 bits (218), Expect = 2e-15  
Identities = 54/180 (30%), Positives = 82/180 (45%)  
Frame = +1

Query: 1201 IKMTHNWLPSLGPTSRTPT\*RHVRSRLRTYSVSPGHPVAPNFKVSNVSKYERKQDLGGWLA 1380  
++ H P + P V SLR P F+ + KY+R + +L  
Sbjct: 142 LRSGHGGRPPVSPVGGAGCRAFVASLRNVRWPP-----RFRPTITEKYDRSVNPAEFLQ 195

Query: 1381 IYTIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCDNWSDFSWCFIANFQSLFDK 1560  
IYT AAG + VM +FP+ L A WL +LP + +W D F NFQ ++ +  
Sbjct: 196 IYTTGIEAAGGDDRVMANFFPMALKGQARGWLMNLPPASVHSWEDLCQQFTTNFQGIYPR 255

Query: 1561 PAQPWDLKSIGHQGETLRLLYLKRF\*TMRNHTPEVAEAGVIEDFYRGSNDSAFVRAILQK 1740  
P + DL ++ + DE+LR Y++RF +RN P + VI F G + + I K  
Sbjct: 256 PGEEADLHAVQRRNDESLRSYIQRFCQVRNTIPCIPAHAVIYAFRGGVRHNRMLEKIASK 315

>gb|AAS07074.1| putative retrotransposon gag protein [Oryza sativa Japonica Group]  
Length = 776

Score = 88.6 bits (218), Expect = 2e-15  
Identities = 41/127 (32%), Positives = 67/127 (52%)  
Frame = +1

Query: 1321 FKVSNVSKYERKQDLGGWLAIYTIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
FK + + KY+ + WL +Y + AG M Y P+ L A WL LP+ I  
Sbjct: 299 FKPTGIEKYDGTNPESWLTVYGLAIRTAGGDSKAMANYLPVALADSARSWLHGLPRGTI 358

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRLLYLKRF\*TMRNHTPEVAEAGV 1680  
+W++ FIANFQ F++P +DL ++ + +E+LR Y++RF RN ++ + +  
Sbjct: 359 GSWAELRDHFIANFQGTFERPGTQFDLYNVVQKSEESLRDYIRRFSEQRNKISDITDDVI 418

Query: 1681 IEDFYRG 1701  
I F +G  
Sbjct: 419 IAAFTKG 425

>gb|AAR88606.1| putative polyprotein [Oryza sativa Japonica Group]  
Length = 1871

Score = 88.6 bits (218), Expect = 2e-15  
Identities = 54/180 (30%), Positives = 82/180 (45%)

Frame = +1

```
Query: 1201 IKMTHNWLPSLGPTSRTPT*RHVRSRLRTYSVSPGHPVAPNFKVSNVSKYERKQDLGGWLA 1380
      ++ H P + P V SLR P F+ + KY+R + +L
Sbjct: 142 LRS GHGGRPPVSPVGGAGCRA FVASLRNVRWPP-----RFRPTITEKYDRSVNPAEFLQ 195

Query: 1381 IYTIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQH CIDNWSDFSWCFIANFQSLFDK 1560
      IYT AAG + VM +FP+ L A WL +LP + +W D F NFQ ++ +
Sbjct: 196 IYTTGIEAAGGDDRVMANFFPMALKGQARGWLMNLPASVH SWEDLCQQFTTNFQGIYPR 255

Query: 1561 PAQPWDLKSIGHQGD ETLRLYLKRF*TM RNHTPEVAEAGVIEDFYRGSNDSAFVRAILQK 1740
      P + DL ++ + DE+LR Y++RF +RN P + VI F G + + I K
Sbjct: 256 PGEEADLHAVQRRNDESLRSYIQRFQVRNTIPCIPAHAVIYAFRGGVRHNRMLEKIASK 315
```

>gb|AAR00629.1| putative reverse transcriptase [Oryza sativa Japonica Group]  
Length = 1445

Score = 88.6 bits (218), Expect = 2e-15  
Identities = 50/148 (33%), Positives = 74/148 (50%)  
Frame = +1

```
Query: 1321 FKVSNVSKYERKQDLGGWLAIYTIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQH CI 1500
      F+ + KY+ D +L +Y+ V +AAGA ++ + Y P L A WL HLP + I
Sbjct: 183 FRSGAIEKYDGSTDPEEF LQVYSTVLYAAGADDNALANYLPTALKGSARSWLMHLLPYSI 242

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGD ETLRLYLKRF*TM RNHTPEVAEAGV 1680
      W+D F+ANFQ + + A DL + E+LR Y++RF RN PE+ +A V
Sbjct: 243 SLWADLWQQFVANFQGT YKRHAIEDDLHASTQNPGESLRDYVRRFNECRNTIPEITDASV 302

Query: 1681 IEDFYRGSNDSAFVRAILQKSVGHLRTL 1764
      I F G D + + + V R L
Sbjct: 303 ICAFKSGVRDRYTTQELATRRVTTTRRL 330
```

>emb|CAD40482.1| OSJNBa0067G20.4 [Oryza sativa (japonica cultivar-group)]  
emb|CAE03321.2| OSJNBa0032I19.15 [Oryza sativa (japonica cultivar-group)]  
emb|CAH66332.1| H0813E03.9 [Oryza sativa (indica cultivar-group)]  
Length = 554

Score = 88.6 bits (218), Expect = 2e-15  
Identities = 46/130 (35%), Positives = 68/130 (52%)  
Frame = +1

```
Query: 1321 FKVSNVSKYERKQDLGGWLAIYTIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQH CI 1500
      F+ + KY+ D +L +Y V +AAGA ++ + Y P L A WL HL + I
Sbjct: 421 FRPGAIEKYDGSTDSEEF LQVYFTVLYAAGADDNALANYLPTALKGSARSWLMHLLPYSI 480

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGD ETLRLYLKRF*TM RNHTPEVAEAGV 1680
      +W+D F+ANFQ + + A DL ++ E+LR Y++RF RN PE+ +A V
Sbjct: 481 SSWADLWQQFVANFQGT YKRHAIEDDLHALTQNSGESLREYVRRFNECRNTIPEITDASV 540

Query: 1681 IEDFYRGSND 1710
      I F G D
Sbjct: 541 IHAFKSGVRD 550
```

>gb|ABA98178.1| retrotransposon protein, putative, Ty3-gypsy subclass [Oryza sativa  
(japonica cultivar-group)]  
Length = 1271

Score = 88.6 bits (218), Expect = 2e-15  
Identities = 42/127 (33%), Positives = 66/127 (51%)

Frame = +1

Query: 1321 FKVSNVSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
FK + + KY+ + WL +Y + AAG M Y P+ L A WL LP I  
Sbjct: 438 FKPTGIEKYDGTTPESWLTIVYGLAIRAAGGDNKAMANYLPVALADSARSWLHGLPHGTI 497

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W++ FIANFQ F++P +DL ++ + E+LR Y++RF RN ++ + +  
Sbjct: 498 GSWAELRDHFIANFQGTFERPGTQYDLYNVIQKSGESLRDYIRRFSEQRNKISDITDDVI 557

Query: 1681 IEDFYRG 1701  
I F +G  
Sbjct: 558 IAAFTKG 564

>gb|ABA97627.1| retrotransposon protein, putative, Ty3-gypsy subclass [Oryza sativa  
(japonica cultivar-group)]  
Length = 2010

Score = 88.6 bits (218), Expect = 2e-15  
Identities = 42/127 (33%), Positives = 67/127 (52%)  
Frame = +1

Query: 1321 FKVSNVSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
FK + + KY+ + WL +Y + AAG M Y P+ L A WL LP+ I  
Sbjct: 431 FKPTGIEKYDGTTPESWLTIVYGLAIRAAGGDNKAMANYLPVALADSARSWLHGLPRGTI 490

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W++ FIANFQ F++P +DL ++ + E+LR Y++RF RN ++ + +  
Sbjct: 491 GSWAELRDHFIANFQGTFERPGTQYDLYNVIQKSRESLRDYIRRFSEQRNKISDITDDVI 550

Query: 1681 IEDFYRG 1701  
I F +G  
Sbjct: 551 IAAFTKG 557

>gb|ABA97049.1| retrotransposon protein, putative, Ty3-gypsy subclass [Oryza sativa  
(japonica cultivar-group)]  
Length = 1399

Score = 88.6 bits (218), Expect = 2e-15  
Identities = 42/127 (33%), Positives = 67/127 (52%)  
Frame = +1

Query: 1321 FKVSNVSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
FK + + KY+ + WL +Y + AAG M Y P+ L A WL LP+ I  
Sbjct: 311 FKPTGIEKYDGTTPESWLTIVYGLAIRAAGGDSKAMANYLPVALADSARSWLHGLPRGMI 370

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W++ FIANFQ F++P +DL ++ + E+LR Y++RF RN ++ + +  
Sbjct: 371 GSWAELRDHFIANFQGTFERPGTQYDLYNVIQKSGESLRDYIRRFSEQRNKISDITDDVI 430

Query: 1681 IEDFYRG 1701  
I F +G  
Sbjct: 431 IAAFTKG 437

>gb|ABA98182.1| retrotransposon protein, putative, Ty3-gypsy subclass [Oryza sativa  
(japonica cultivar-group)]  
Length = 1940

Score = 88.6 bits (218), Expect = 2e-15  
Identities = 42/127 (33%), Positives = 66/127 (51%)

Frame = +1

Query: 1321 FKVSNVSKYERKQDLGGWLAIYITIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
FK + + KY+ + WL +Y + AAG M Y P+ L A WL LP I  
Sbjct: 438 FKPTGIEKYDGTTPESWLTIVYGLAIRAAGDNKAMANYLPVALADSARSWLHGLPHGTI 497

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W++ FIANFQ F++P +DL ++ + E+LR Y++RF RN ++ + +  
Sbjct: 498 GSWAELRDHFIANFQGTFERPGTQYDLYNVIQKSGESLRDYIRRFSEQRNKISDITDDVI 557

Query: 1681 IEDFYRG 1701  
I F +G  
Sbjct: 558 IAAFTKG 564

>gb|AA96254.1| transposon protein, putative, unclassified [Oryza sativa Japonica Group]  
gb|ABA93300.1| transposon protein, putative, unclassified [Oryza sativa (japonica cultivar-group)]  
Length = 631

Score = 88.6 bits (218), Expect = 2e-15  
Identities = 47/148 (31%), Positives = 74/148 (50%)  
Frame = +1

Query: 1321 FKVSNVSKYERKQDLGGWLAIYITIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
F+ + KY+ D +L +Y+ V +AAGA ++ + Y P+ L WL HLP + I  
Sbjct: 278 FQPGAIEKYDGTDPPEEFLQVYSTVLYAAGADDNALANYLPMALKGSTRSWLMHLPPYSI 337

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W+D FIANFQ + + A DL ++ E+LR Y++RF RN P++ V  
Sbjct: 338 SSWADLWQQFIANFQGTYKRHAIEDDLHALTQNPGESLRDYVRRFNECRNTIPDITNVSV 397

Query: 1681 IEDFYRGSNDSAFVRAILQKSVGHLRTL 1764  
I F G D + + + + R L  
Sbjct: 398 IHAFKTGVRDCYTTQELATTRITTTTRL 425

>gb|AAG46174.1|AC018727\_26 putative gypsy-type retrotransposon GAG-POL precursor [Oryza sativa Japonica Group]  
Length = 785

Score = 88.6 bits (218), Expect = 2e-15  
Identities = 42/127 (33%), Positives = 67/127 (52%)  
Frame = +1

Query: 1321 FKVSNVSKYERKQDLGGWLAIYITIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
FK + + KY+ + WL +Y + AAG M Y P+ L A WL LP+ I  
Sbjct: 287 FKPTGIEKYDGTTPESWLTIVYGLAIRAAGGDSKAMANYLPVALANSARSWLHGLPRGTI 346

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W++ FIANFQ F++P +DL ++ + E+LR Y++RF RN ++ + +  
Sbjct: 347 GSWAELRDHFIANFQGTFERPGTQFDLYNVVQKSGESLRDYIRRFSEQRNKISDITDDII 406

Query: 1681 IEDFYRG 1701  
I F +G  
Sbjct: 407 IAAFTKG 413

>emb|CAE02527.2| OSJNBb0003A12.14 [Oryza sativa (japonica cultivar-group)]  
Length = 1863

Score = 88.6 bits (218), Expect = 2e-15  
Identities = 42/127 (33%), Positives = 67/127 (52%)  
Frame = +1

Query: 1321 FKVSNSVSKYERKQDLGGWLAIIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
FK + + KY+ + WL +Y + AAG M Y P+ L A WL LP+ I  
Sbjct: 419 FKPTGIEKYDGTTPESWLTIVYGLAIRAAGGDSKAMANYLPVALADSARSWLHGLPRGTI 478

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W++ FIANFQ F++P +DL ++ + E+LR Y++RF RN ++ + +  
Sbjct: 479 GSWAELRDHFIANFQGTFERPGTQFDLYNVIQKSGESLRDYIRRFSEQRNKISDITDDVI 538

Query: 1681 IEDFYRG 1701  
I F +G  
Sbjct: 539 IAAFTKG 545

>emb|CAH66285.1| OSIGBa0161P06.2 [Oryza sativa (indica cultivar-group)]  
Length = 1987

Score = 88.2 bits (217), Expect = 3e-15  
Identities = 42/127 (33%), Positives = 67/127 (52%)  
Frame = +1

Query: 1321 FKVSNSVSKYERKQDLGGWLAIIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
FK + + KY+ + WL +Y + AAG M Y P+ L A WL LP+ I  
Sbjct: 434 FKPTGIEKYDGTTPESWLTIVYGLAIRAAGGDSKAMANYLPVALADSARSWLHGLPRGTI 493

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W++ FIANFQ F++P +DL ++ + E+LR Y++RF RN ++ + +  
Sbjct: 494 GSWAELRDHFIANFQGTFERPGTQYDLYNVIQKPGESLRDYIRRFSEQRNKISDITDDVI 553

Query: 1681 IEDFYRG 1701  
I F +G  
Sbjct: 554 IAAFTKG 560

>gb|AAP54912.2| retrotransposon protein, putative, Ty3-gypsy subclass [Oryza sativa  
(japonica cultivar-group)]  
Length = 1995

Score = 88.2 bits (217), Expect = 3e-15  
Identities = 43/127 (33%), Positives = 66/127 (51%)  
Frame = +1

Query: 1321 FKVSNSVSKYERKQDLGGWLAIIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
FK + + KY+ + WL IY + AAG M Y P+ L A WL LP+ I  
Sbjct: 438 FKPTGIEKYDGTTPESWLTIIYGLAIRAAGGDSKAMANYLPVALADSARSWLHGLPRGTI 497

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W++ FIANFQ F+ P +DL ++ + E+LR Y++RF RN ++ + +  
Sbjct: 498 GSWAELRDHFIANFQGTFEHPGTQYDLYNVIQKSGESLRDYIRRFSEQRNKISDITDDVI 557

Query: 1681 IEDFYRG 1701  
I F +G  
Sbjct: 558 IAAFTKG 564

>gb|ABF96555.1| retrotransposon protein, putative, Ty3-gypsy subclass [Oryza sativa  
(japonica cultivar-group)]  
Length = 1659

Score = 88.2 bits (217), Expect = 3e-15

Identities = 42/128 (32%), Positives = 67/128 (52%)  
Frame = +1

Query: 1318 NFKVSNVSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHC 1497  
+FK + + KY+ + WL +Y + A G M Y P+ L A WL LP+  
Sbjct: 348 DFKPTGIEKYDGTNPESWLTVYGLAVRAVGDSKAMANYLPVALADSARSWLHGLPRGT 407

Query: 1498 IDNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLLYLKRF\*TMRNHTPEVAEAG 1677  
I +W++ FIANFQ F++P +DL +I + E+LR Y++RF RN ++ +  
Sbjct: 408 IGSWAELRDHFIANFQGTFERPGTHFDLYNIVQKSGESLRDYIRRFQSKQRNKISDITDDV 467

Query: 1678 VIEDFYRG 1701  
+I F +G  
Sbjct: 468 IIAAFTKG 475

>gb|ABF99143.1| retrotransposon protein, putative, Ty3-gypsy subclass [Oryza sativa  
(japonica cultivar-group)]  
Length = 1318

Score = 88.2 bits (217), Expect = 3e-15  
Identities = 51/172 (29%), Positives = 81/172 (47%), Gaps = 12/172 (6%)  
Frame = +1

Query: 1222 LPSLGPTSRTPTR-HVRSLRTYSVSPGHPVA-----PNFKVSNVSKYERKQDL 1365  
+P+ ++RTPT R H S Y A FK + + KY+ +  
Sbjct: 199 VPANSASTRTPTARGHRHSPNLYDDVDVGVAFTNDLRRVDWPAGFKSTGIEKYDSTTNP 258

Query: 1366 GGWLAIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCIDNWSDFSWCFIANFQ 1545  
WL +Y + AAG M Y P+ L A WL LP+ I +W++ FIANFQ  
Sbjct: 259 ESWLTVYGLAIRAAGGDSKAMANYLPVALADSARSWLHGLPRGTIGSWAELRDHFIANFQ 318

Query: 1546 SLFDKPAQPWDLKSIGHQGDETLRLLYLKRF\*TMRNHTPEVAEAGVIEDFYRG 1701  
F++P +DL ++ + E+LR Y++RF +RN ++ + +I +G  
Sbjct: 319 GTFERPGTQFDLYNVVQKSGESLRDYIRRFSELRNKISDITDDVIIAALTKG 370

>gb|AAR06299.1| putative gag-pol protein [Oryza sativa Japonica Group]  
Length = 1653

Score = 88.2 bits (217), Expect = 3e-15  
Identities = 42/128 (32%), Positives = 67/128 (52%)  
Frame = +1

Query: 1318 NFKVSNVSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHC 1497  
+FK + + KY+ + WL +Y + A G M Y P+ L A WL LP+  
Sbjct: 348 DFKPTGIEKYDGTNPESWLTVYGLAVRAVGDSKAMANYLPVALADSARSWLHGLPRGT 407

Query: 1498 IDNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLLYLKRF\*TMRNHTPEVAEAG 1677  
I +W++ FIANFQ F++P +DL +I + E+LR Y++RF RN ++ +  
Sbjct: 408 IGSWAELRDHFIANFQGTFERPGTHFDLYNIVQKSGESLRDYIRRFQSKQRNKISDITDDV 467

Query: 1678 VIEDFYRG 1701  
+I F +G  
Sbjct: 468 IIAAFTKG 475

>gb|AAN65036.1| putative RIRE2 retrotransposon protein [Oryza sativa Japonica Group]  
Length = 1300

Score = 88.2 bits (217), Expect = 3e-15  
Identities = 51/172 (29%), Positives = 81/172 (47%), Gaps = 12/172 (6%)  
Frame = +1



Query: 1222 LPSLGPTSRTPTR-HVRSRLRTYSVSPGHPVA-----PNFKVSNVSKYERKQDL 1365  
 +P+ ++RTPT R H S Y A FK + + KY+ +  
 Sbjct: 181 VPANSASTRTPRTARGHRHSPNLYDDDDVDGVAAFTNDLRRVDWPAGFKSTGIEKYDSTTNP 240

Query: 1366 GGWLAIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCHIDNWSDFSWCFIANFQ 1545  
 WL +Y + AAG M Y P+ L A WL LP+ I +W++ FIANFQ  
 Sbjct: 241 ESWLTVYGLAIRAAGGDSKAMANYLPVALADSARSWLHGLPRGTIGSWAELRDHFIANFQ 300

Query: 1546 SLFDKPAQPWDLKSIGHQGDETLRRLYLKRF\*TMRNHTPEVAEAGVIEDFYRG 1701  
 F++P +DL ++ + E+LR Y++RF +RN ++ + +I +G  
 Sbjct: 301 GTFERPQTQFDLYNVVQKSGESLRDYIRRFSELRNKISDITDDVIIAALTKG 352

>gb|ABA96009.1| retrotransposon protein, putative, unclassified [Oryza sativa  
 (japonica cultivar-group)]  
 Length = 280

Score = 88.2 bits (217), Expect = 3e-15  
 Identities = 57/187 (30%), Positives = 85/187 (45%), Gaps = 4/187 (2%)  
 Frame = +1

Query: 1162 VGCGLDQCPVPGTIKMTHN----WLPSLGPTSRTPTRHVRSRLRTYSVSPGHPVAPNFKV 1329  
 + C D+ P + HN ++P G + TPT R +R F+  
 Sbjct: 107 LSCSSDRPP-----RRCHNHGPPFVPGGCRAFTPTLRDIRW-----PEKFRP 149

Query: 1330 SNVSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCHIDNW 1509  
 + KY+ D +L +Y + +AAGA ++ + Y P L A WL HLP I +W  
 Sbjct: 150 GVIEKYDGSTDPEEFLQVYYTILYAAGADDNALANYLPAALKGSARSWLHLPSPRSISSW 209

Query: 1510 SDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRRLYLKRF\*TMRNHTPEVAEAGVIED 1689  
 D F+ANF + + A DL ++ E+LR Y++RF RN PE+ +A VI  
 Sbjct: 210 EDLWQQFVANFHGTYKRHAIEDDLHTLTQNPGESLRDYIRRFNKRNTIPEITDASVIRA 269

Query: 1690 FYRGSND 1710  
 F G D  
 Sbjct: 270 FKSGIRD 276

>gb|AAK96872.1| retrotransposon protein, putative, Ty3-gypsy sub-class [Oryza sativa  
 Japonica Group]  
 gb|ABA92512.1| retrotransposon protein, putative, Ty3-gypsy subclass [Oryza sativa  
 (japonica cultivar-group)]  
 Length = 1945

Score = 88.2 bits (217), Expect = 3e-15  
 Identities = 42/127 (33%), Positives = 67/127 (52%)  
 Frame = +1

Query: 1321 FKVSNVSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCH 1500  
 FK + + KY+ + WL +Y + AAG M Y P+ L A WL LP+ I  
 Sbjct: 438 FKPTGIEKYDGTNPESWLTVYGLAIRAAGGDSKAMANYLPVALVDSARSWLHGLPRGTI 497

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRRLYLKRF\*TMRNHTPEVAEAGV 1680  
 +W++ FIANFQ F++P +DL ++ + E+LR Y++RF RN ++ + +  
 Sbjct: 498 GSWAELRDHFIANFQGTFERPQTQYDLNVVQKSGESLRDYIRRFSEQRNKISDITDDVI 557

Query: 1681 IEDFYRG 1701  
 I F +G  
 Sbjct: 558 IAAFTKG 564

>gb|AAK43497.1|AC020666\_7 gag-pol precursor [Oryza sativa Japonica Group]

Length = 2017

Score = 88.2 bits (217), Expect = 3e-15  
Identities = 43/127 (33%), Positives = 66/127 (51%)  
Frame = +1

```
Query: 1321 FKVSNVSKYERKQDLGGWLAITYTIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500
          FK + + KY+   +   WL IY +   AAG      M Y P+ L   A WL LP+ I
Sbjct: 438 FKPTGIEKYDGTTPNESWLTIIYGLAIRAAGGDSKAMANYLPVALADSARSWLHGLPRGTI 497

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF*TMRNHTPEVAEAGV 1680
          +W++   FIANFQ F+ P   +DL ++   +   E+LR Y++RF   RN   ++ + +
Sbjct: 498 GSWAELRDHFIANFQGTTFEHPGTQYDLYNVIQKSGESLRDYIRRFSEQRNKISDITDDVI 557

Query: 1681 IEDFYRG 1701
          I   F +G
Sbjct: 558 IAAFTKG 564
```

>gb|AAT44283.1| putative polyprotein [Oryza sativa Japonica Group]  
Length = 1741

Score = 87.8 bits (216), Expect = 4e-15  
Identities = 42/127 (33%), Positives = 67/127 (52%)  
Frame = +1

```
Query: 1321 FKVSNVSKYERKQDLGGWLAITYTIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500
          FK + + KY+   +   WL +Y +   AAG      M Y P+ L   A WL LP+ I
Sbjct: 389 FKPTGIEKYDGTTPNESWLTIVYGLAIRAAGGDSKAMENYLPVALADSARSWLHGLPRGTI 448

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF*TMRNHTPEVAEAGV 1680
          +W++   FIANFQ F++P   +DL ++   +   E+LR Y++RF   RN   ++ + +
Sbjct: 449 GSWAELRDHFIANFQGTTFERPQTQFDLYNVIQKSRESLRDYIRRFSEQRNKISDITDNVI 508

Query: 1681 IEDFYRG 1701
          I   F +G
Sbjct: 509 IAAFTKG 515
```

>gb|AA066548.1| retrotransposon protein, putative, Ty3-gypsy sub-class [Oryza sativa Japonica Group]  
Length = 1380

Score = 87.8 bits (216), Expect = 4e-15  
Identities = 45/123 (36%), Positives = 67/123 (54%)  
Frame = +1

```
Query: 1342 KYERKQDLGGWLAITYTIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCIDNWSDFS 1521
          KY+   D   +L +Y+ V +AAGA ++ +   Y P L   A WL HLP + I +W+D
Sbjct: 309 KYDGSTDPEEFLLQVYSTVLYAAGADDNALANYLPTALKGSARSWLMHLPYPYSSISWADLW 368

Query: 1522 WCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF*TMRNHTPEVAEAGVIEDFYRG 1701
          F+ANFQ   + + A   DL ++   E+LR Y++RF   RN P++ +A VI F G
Sbjct: 369 QQFVANFQGTYKRHAIEDDLHALTQNPGESLREYVQRFNECRNTIPKITDASVIRAFKSG 428

Query: 1702 SND 1710
          D
Sbjct: 429 VRD 431
```

>gb|ABA98154.1| retrotransposon protein, putative, Ty3-gypsy subclass [Oryza sativa (japonica cultivar-group)]  
Length = 662

Score = 87.8 bits (216), Expect = 4e-15  
Identities = 43/134 (32%), Positives = 70/134 (52%)  
Frame = +1

Query: 1300 GHPVAPNFKVSNVSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLR 1479  
G + +FK + + KY+ + WL +Y + AAG M Y P+ L A WL  
Sbjct: 348 GDMMNASFKPTGIEKYDGTTPESWLTIVYGLAIRAAGGDNKAMANYLPVALADSARSWLH 407

Query: 1480 HLPQHCIDNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLLYLKRF\*TMRNHTP 1659  
LP+ I +W++ FIANFQ F +P+ +DL ++ + E+LR Y++RF RN  
Sbjct: 408 GLPRGTIGSWAELRDHFIANFQGTFFKRPTQFDLYNVVQKPGESLRDYIRRFSEKRNKIS 467

Query: 1660 EVAEAGVIEDFYRG 1701  
++ + +I F +G  
Sbjct: 468 DITDDVIIAAFTKG 481

>gb|AAV31300.1| putative polyprotein [Oryza sativa Japonica Group]  
gb|AAV32108.1| putative polyprotein [Oryza sativa Japonica Group]  
Length = 1988

Score = 87.4 bits (215), Expect = 5e-15  
Identities = 41/127 (32%), Positives = 66/127 (51%)  
Frame = +1

Query: 1321 FKVSNVSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
FK + + KY+ + WL +Y + AAG M Y P+ L WL LP+ I  
Sbjct: 438 FKPTGIEKYDGTTPESWLTIVYGLAIRAAGGDSKAMANYLPVALADSTRSWLHGLPRGTI 497

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLLYLKRF\*TMRNHTPEVAEAGV 1680  
+W++ FIANFQ F++P +DL ++ + E+LR Y++RF RN ++ + +  
Sbjct: 498 GSWAELRDHFIANFQGTFFRPGTQFDLYNVVQKSGESLRDYIRRFSEQRNKISDITDDVI 557

Query: 1681 IEDFYRG 1701  
I F +G  
Sbjct: 558 IAAFTKG 564

>emb|CAE01788.1| OSJNBa0039K24.7 [Oryza sativa (japonica cultivar-group)]  
Length = 1818

Score = 87.4 bits (215), Expect = 5e-15  
Identities = 42/127 (33%), Positives = 67/127 (52%)  
Frame = +1

Query: 1321 FKVSNVSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
FK + + KY+ + WL +Y + AAG M Y P+ L A WL LP+ I  
Sbjct: 438 FKPTRIEKYDGTTPNELWLTIVYGLAIRAAGGDSKAMANYLPVALADSARSWLHGLPRGTI 497

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLLYLKRF\*TMRNHTPEVAEAGV 1680  
+W++ FIANFQ F++P +DL ++ + E+LR Y++RF RN ++ + +  
Sbjct: 498 GSWAELRDHFIANFQGTFFRPGTQYDLNVIQKSGESLRDYIRRFSEQRNKISDITDDVI 557

Query: 1681 IEDFYRG 1701  
I F +G  
Sbjct: 558 IAAFTKG 564

>gb|ABA94416.2| retrotransposon protein, putative, Ty3-gypsy subclass [Oryza sativa  
(japonica cultivar-group)]  
Length = 1714

Score = 87.0 bits (214), Expect = 7e-15  
Identities = 44/124 (35%), Positives = 66/124 (53%)  
Frame = +1

Query: 1321 FKVSNSVSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
F+ + KY+ D +L +Y+ V + AGA ++ + Y P L A WL HLP + I  
Sbjct: 435 FRPGVIEKYDGSTDPEEFLQVYSTVLYTAGADDNALANYLPTALKGSARSWLMHLPYYSI 494

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W+D F+ANFQ + A DL ++ E+LR Y++RF RN PE+ +A V  
Sbjct: 495 SSWADLWQQFVANFQETYKHHAIEDDLHALTQNSGESLREYVRRFNECRNTIPEIIDASV 554

Query: 1681 IEDF 1692  
I F  
Sbjct: 555 IRAF 558

>gb|ABA97931.2| retrotransposon protein, putative, Ty3-gypsy subclass [Oryza sativa  
(japonica cultivar-group)]  
Length = 1082

Score = 87.0 bits (214), Expect = 7e-15  
Identities = 42/127 (33%), Positives = 67/127 (52%)  
Frame = +1

Query: 1321 FKVSNSVSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
FK + + KY+ + WL +Y + AAG M Y P+ L A WL LP+ I  
Sbjct: 437 FKPTGIEKYDGTNPESWLTIVYGLAIRAAGGDSKAMANYLPVALADFAFSWHLGLPRGTI 496

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W++ FIANFQ F++P +DL ++ + E+LR Y++RF RN ++ + +  
Sbjct: 497 GSWAELRDHFIANFQGTFERPGTQFDLYNVIQKSRESLRDYIRRFQSKQRNKISDITDDVI 556

Query: 1681 IEDFYRG 1701  
I F +G  
Sbjct: 557 IAAFTKG 563

>gb|ABA92141.1| retrotransposon protein, putative, Ty3-gypsy subclass [Oryza sativa  
(japonica cultivar-group)]  
Length = 1929

Score = 87.0 bits (214), Expect = 7e-15  
Identities = 53/176 (30%), Positives = 82/176 (46%), Gaps = 16/176 (9%)  
Frame = +1

Query: 1222 LPSLGPTSRTP\*T\*RHVRSRLRTYSV-----SPGHPVAP-----NFKVSNSVSKYER 1353  
+P+ ++RTPT V + S+ S GH FK + + KY+  
Sbjct: 359 VPANSASSTRPTGSRVPHQPSLSIAGAESSRRSRGHDRLRRVDWPAGFKPTGIEKYDG 418

Query: 1354 KQDLGGWLAIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCDNWSDFSWCFI 1533  
+ WL +Y + AAG M Y P+ L A WL LP I +W++ FI  
Sbjct: 419 TTNPESWLTIVYGLAIRAAGGDSKAMANYLPVALADSARSWLHGLPCGTIASWAELLDFHI 478

Query: 1534 ANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEVAEAGVIEDFYRG 1701  
ANFQ F++P +DL +I + E+LR Y++RF RN ++ + +I F +G  
Sbjct: 479 ANFQGTFERPGTHFDLYNIVQKSGESLRDYIRRFQQRNKISDITDDVIIAAFTKG 534

>gb|ABA94084.1| retrotransposon protein, putative, Ty3-gypsy subclass [Oryza sativa  
(japonica cultivar-group)]  
Length = 1756

Score = 87.0 bits (214), Expect = 7e-15  
Identities = 42/127 (33%), Positives = 66/127 (51%)  
Frame = +1

Query: 1321 FKVSNVSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
FK + + KY+ + WL +Y+ AG M Y P+ L A WL LP+ I  
Sbjct: 382 FKSTGIEKYDGTTPESWLTIVYGLAIRVAGGDSKAMANYLPVALADSARSWLHGLPRGTI 441

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRLYLKRF\*TMNRHTPEVAEAGV 1680  
+W++ FIANFQ F++P +DL +I + E+LR Y++RF RN ++ + +  
Sbjct: 442 GSWAELRDHFIANFQGTTFERPGETHFDLYNIIQKSGESLRDYIRRFSEQRNKISDITDDVI 501

Query: 1681 IEDFYRG 1701  
I F +G  
Sbjct: 502 IAAFTKG 508

>gb|AAK43513.1|AC020666\_23 putative gag-pol precursor [Oryza sativa Japonica Group]  
gb|AAP54915.1| retrotransposon protein, putative, Ty3-gypsy subclass [Oryza sativa  
(japonica cultivar-group)]  
Length = 1519

Score = 87.0 bits (214), Expect = 7e-15  
Identities = 46/148 (31%), Positives = 75/148 (50%)  
Frame = +1

Query: 1321 FKVSNVSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
F+ + KY+ + +L +Y+ V +AAGA ++ + Y L A WL HLP + I  
Sbjct: 295 FRPGAIEKYDGSTNPEEFLQVYSTVLYAAGADDNALANYLSTALKGSARSWLMHLPPYSI 354

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRLYLKRF\*TMNRHTPEVAEAGV 1680  
+W+D F+ANFQ + + A +L ++ E+LR Y++RF RN PE+ +A V  
Sbjct: 355 SSWADLWQQFVANFQGTYKRHAIEDNLHALTQNSGESLREYVRRFNECRNTIPEITDASV 414

Query: 1681 IEDFYRGSNDSAFVRAILQKSVGHLRTL 1764  
I F G D + + + + R L  
Sbjct: 415 IRAFKSGVRDRYTTQELATRRITTTTRL 442

>gb|AAM18733.1|AC092548\_11 putative polyprotein [Oryza sativa Japonica Group]  
gb|AAP53314.1| retrotransposon protein, putative, Ty3-gypsy subclass [Oryza sativa  
(japonica cultivar-group)]  
Length = 724

Score = 87.0 bits (214), Expect = 7e-15  
Identities = 47/148 (31%), Positives = 74/148 (50%)  
Frame = +1

Query: 1321 FKVSNVSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
F+ + KY+ D +L +Y+ V +AAG + + Y P L A WL HL + I  
Sbjct: 234 FRPGAIEKYDGSTDPEEFLQVYSTVFYAAGVDNNALANYLPTTLKGSARSWLIHLAPYSI 293

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRLYLKRF\*TMNRHTPEVAEAGV 1680  
+W+D F+ANFQ + A DL+++ DE+LR Y++RF RN PE+ ++ V  
Sbjct: 294 SSWADLWQQFVANFQGTYKCHAIDDDQLALTQNPDESRLDYVRRFNECRNTIPEITDSSV 353

Query: 1681 IEDFYRGSNDSAFVRAILQKSVGHLRTL 1764  
I F G D + + + + R L  
Sbjct: 354 IRTFKSGVRDCYTTQELATRCITTTTRL 381

>emb|CAH66219.1| OSIGBa0157N01.5 [Oryza sativa (indica cultivar-group)]  
Length = 720

Score = 86.7 bits (213), Expect = 9e-15  
Identities = 41/127 (32%), Positives = 66/127 (51%)  
Frame = +1

Query: 1321 FKVSNVSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
FK + + KY+ + WL +Y + AAG M Y P+ L A WL LP+ I  
Sbjct: 346 FKPTGIEKYDGTTPESWLTVYGLAIRAAGGDSKAMANYLPVALADSAWSWLHGLPRGTI 405

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W++ FI NFQ F++P +DL ++ + E+LR Y++RF RN ++ + +  
Sbjct: 406 GSWAELRDHFITNFQGTFERPGTQFDLYNVIQKSGESLRDYIRRFSEQRNKISDITDDVI 465

Query: 1681 IEDFYRG 1701  
I F +G  
Sbjct: 466 IVAFTKG 472

>emb|CAE02238.2| OSJNBb0054B09.2 [Oryza sativa (japonica cultivar-group)]  
emb|CAH66179.1| OSIGBa0130015.3 [Oryza sativa (indica cultivar-group)]  
emb|CAH66204.1| OSIGBa0148D14.10 [Oryza sativa (indica cultivar-group)]  
Length = 1992

Score = 86.7 bits (213), Expect = 9e-15  
Identities = 41/127 (32%), Positives = 66/127 (51%)  
Frame = +1

Query: 1321 FKVSNVSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
FK + + KY+ + WL +Y + A G M Y P+ L A WL LP+ I  
Sbjct: 433 FKPTGIEKYDGTTPESWLTVYGLAIRAVGGDSKAMANYLPVALEDSARSWLHGLPRGTI 492

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W++ FIANFQ F++P +DL ++ + E+LR Y++RF RN ++ + +  
Sbjct: 493 GSWAELRDHFIANFQGTFERPGTQYDLYNVIQKSGESLRDYIRRFSEQRNKISDITDDVI 552

Query: 1681 IEDFYRG 1701  
I F +G  
Sbjct: 553 IAAFTKG 559

>emb|CAE05337.1| OSJNBa0079M09.7 [Oryza sativa (japonica cultivar-group)]  
Length = 877

Score = 86.7 bits (213), Expect = 9e-15  
Identities = 41/127 (32%), Positives = 66/127 (51%)  
Frame = +1

Query: 1321 FKVSNVSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
FK + + KY+ + WL +Y + AAG M Y P+ L A WL LP+ I  
Sbjct: 346 FKPTGIEKYDGTTPESWLTVYGLAIRAAGGDSKAMANYLPVALADSAWSWLHGLPRGTI 405

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W++ FI NFQ F++P +DL ++ + E+LR Y++RF RN ++ + +  
Sbjct: 406 GSWAELRDHFITNFQGTFERPGTQFDLYNVIQKSGESLRDYIRRFSEQRNKISDITDDVI 465

Query: 1681 IEDFYRG 1701  
I F +G  
Sbjct: 466 IVAFTKG 472

>gb|ABA97384.2| retrotransposon protein, putative, Ty3-gypsy subclass [Oryza sativa  
(japonica cultivar-group)]  
Length = 627

Score = 86.3 bits (212), Expect = 1e-14  
Identities = 41/124 (33%), Positives = 65/124 (52%)  
Frame = +1

Query: 1321 FKVSNVSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
FK + + KY+ + WL +Y + AAG M Y P+ L A WL LP+ I  
Sbjct: 262 FKPTGIEKYDGTTPESWLTIVYGLTIRAAGGDSKAMANYLPVALADSARSWLHGLPRGTI 321

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W++ FIANFQ F++P +DL ++ + E+LR Y++RF RN ++ + +  
Sbjct: 322 GSWAELRDHFIANFQGTFERPGTQFDLYNVIQKSGESLRDYIRRFSEQRNKISDITDDVI 381

Query: 1681 IEDF 1692  
I F  
Sbjct: 382 IAAF 385

>gb|AAU10764.1| putative polyprotein [Oryza sativa Japonica Group]  
Length = 1743

Score = 86.3 bits (212), Expect = 1e-14  
Identities = 47/142 (33%), Positives = 72/142 (50%)  
Frame = +1

Query: 1315 PNFKVSNSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQH 1494  
P F+ + KY+ + +L IYT AAG + VM +FP+ L A WL +LP  
Sbjct: 122 PRFRPTITEKYDGSVNPAEFLQIYTTRIEAAGGDDRVMANFFPMALKGQARGWLMNLPPI 181

Query: 1495 CIDNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRRLYLKRF\*TMRNHTPEVAEA 1674  
+ +W D F NFQ ++ +P + DL ++ + DE+LRLY++RF +RN P +  
Sbjct: 182 SVHSWEDLCQQFTTNFQGIYLRPGEEADLHAVQRRDDESLRLYIQRFCQVRNTKPCIPAH 241

Query: 1675 GVIEDFYRGSNDSAFVRAILQK 1740  
VI F G + + I K  
Sbjct: 242 AVIYAFRGGVRHNRMLEKIASK 263

>gb|AAX96740.1| retrotransposon protein, putative, Ty3-gypsy sub-class [Oryza sativa Japonica Group]  
gb|ABA91942.1| retrotransposon protein, putative, Ty3-gypsy subclass [Oryza sativa (japonica cultivar-group)]  
Length = 1372

Score = 86.3 bits (212), Expect = 1e-14  
Identities = 48/148 (32%), Positives = 75/148 (50%)  
Frame = +1

Query: 1321 FKVSNVSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
F+ + KY+ D +L +Y+ V +AA A ++ + Y P L A WL HLP + I  
Sbjct: 195 FRPGAIEKYDGSTDPEEFLQVYSTVLYAARADDNALANYLPTALKGSARSWLMHLPPIYSI 254

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRRLYLKRF\*TMRNHTPEVAEAGV 1680  
+ +D FIANFQ + + A DL ++ E+LR Y++RF RN PE+ +A V  
Sbjct: 255 SSCADLCQQFIANFQGTYKRHAIEDDLHALTQNSGESLREYVRRFNECRNTIPEITDASV 314

Query: 1681 IEDFYRGSNDSAFVRAILQKSVGHLRTL 1764  
I F G D + + + + R L  
Sbjct: 315 ICAFKSGVRDRYTTQELVTRRITTTTRL 342

>gb|AAX92783.1| retrotransposon protein, putative, Ty3-gypsy sub-class [Oryza sativa Japonica Group]

gb|ABA93327.1| retrotransposon protein, putative, Ty3-gypsy subclass [Oryza sativa (japonica cultivar-group)]  
Length = 1288

Score = 86.3 bits (212), Expect = 1e-14  
Identities = 42/127 (33%), Positives = 68/127 (53%)  
Frame = +1

Query: 1321 FKVSNSVSKYERKQDLGGWLAIYTIWTAAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
FK + + KY+ + WL +Y + AAG M Y P+ L A WL LP+ I  
Sbjct: 300 FKPTRIEKYDGTTPESWLTIVYGLAIRAAGGDSKAMANYLPVALVDSARSWLHGLPRGTI 359

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W++ FIANFQS F++P +DL ++ + E+LR Y++RF N ++++ +  
Sbjct: 360 GSWAELRDHFIANFQSTFERPGAQFDLYNVIQKSGESLRDYIRRFSEQCNKISDISDDVI 419

Query: 1681 IEDFYRG 1701  
I F +G  
Sbjct: 420 IAAFTKG 426

>emb|CAD39844.2| OSJNBb0072N21.13 [Oryza sativa (japonica cultivar-group)]  
emb|CAE05407.2| OSJNBa0036B17.1 [Oryza sativa (japonica cultivar-group)]  
Length = 1070

Score = 86.3 bits (212), Expect = 1e-14  
Identities = 48/142 (33%), Positives = 69/142 (48%)  
Frame = +1

Query: 1315 PNFKVSNSVSKYERKQDLGGWLAIYTIWTAAAGATEDVMTVYFPIVLGQDAMQWLRHLPQH 1494  
P F+ + KY+ + +L IYT V AAG VM YFP+ L A WL P  
Sbjct: 246 PKFRPNLTEKYDGSINPSEFLQIYTTVIVAAGGDNRMANYFPMALKGQARGWLMTPPD 305

Query: 1495 CIDNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEVAEA 1674  
I +W D FI NFQ + +P + DL ++ + DE+LR Y++RF +RN P +  
Sbjct: 306 SIHSWEDLCQQFITNFQGTYP RPGEADLHAVRRKDDESLRSYIQRFCQVRNTIPCIPAH 365

Query: 1675 GVIEDFYRGSNDSAFVRAILQK 1740  
V+ F G + + I K  
Sbjct: 366 AVVYAFRNGVRHNMLEKIASK 387

>gb|AAT77889.1| putative polyprotein [Oryza sativa Japonica Group]  
gb|ABF98704.1| retrotransposon protein, putative, unclassified [Oryza sativa (japonica cultivar-group)]  
Length = 1851

Score = 85.9 bits (211), Expect = 2e-14  
Identities = 53/180 (29%), Positives = 81/180 (45%)  
Frame = +1

Query: 1201 IKMTHNWLPSLGPTSRTPT\*RHVRSRLTYSVSPGHPVAPNFKVSNSVSKYERKQDLGGWLA 1380  
++ H P + P V SLR P F+ + KY+ + +L  
Sbjct: 203 LRSGHGGRPPVSPVGGAGCRAFVASLRNVRWPP-----RFRPTITEKYDGSVNPAEFLQ 256

Query: 1381 IYTIWTAAAGATEDVMTVYFPIVLGQDAMQWLRHLPQH CIDNWSDFSWCFIANFQSLFDK 1560  
IYT AAG + VM +FP+ L A WL +LP + +W D F NFQ ++ +  
Sbjct: 257 IYTTGIEAAGDDRVMANFFPMALKGQARGWLMNLPPASVHSEDLCQQFTTNFQGIYPR 316

Query: 1561 PAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEVAEAGVIEDFYRGSNDSAFVRAILQK 1740  
P + DL ++ + DE+LR Y++RF +RN P + VI F G + + I K  
Sbjct: 317 PGEEADLHAVQRDDESLRSYIQRFCQVRNTIPCIPAHAVIYAFRGGMRHNRMLEKIASK 376



>gb|AAP06922.1| Putative gag-pol precursor [Oryza sativa Japonica Group]  
gb|ABF95196.1| retrotransposon protein, putative, unclassified [Oryza sativa  
(japonica cultivar-group)]  
Length = 438

Score = 85.9 bits (211), Expect = 2e-14  
Identities = 46/142 (32%), Positives = 71/142 (50%)  
Frame = +1

Query: 1315 PNFKVSNSVSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQH 1494  
P F+ + KY+ + +L +YT AAG + VM +FP+ L A WL +LP  
Sbjct: 88 PRFRPTIAEKYDGSVNPAEFLQVYTTGIEAAGGDDRVMANFFPMALKGQARGWLMNLPPA 147

Query: 1495 CIDNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRLYLKRF\*TMRNHTPEVAEA 1674  
+ +W D F NFQ + +P + DL ++ + DE+LR Y++RF +RN P +  
Sbjct: 148 SVHSWEDLCQQFTMNFQGTYP RPGEADLHAVQRRDDESLRSYIQRFCQVRNTIPCI PAH 207

Query: 1675 GVIEDFYRGSNDSAFVRAILQK 1740  
VI F RG + + I K  
Sbjct: 208 AVIYAFRRGVRHNRMLEKIASK 229

>gb|ABA97679.1| retrotransposon protein, putative, Ty3-gypsy subclass [Oryza sativa  
(japonica cultivar-group)]  
Length = 890

Score = 85.9 bits (211), Expect = 2e-14  
Identities = 41/127 (32%), Positives = 66/127 (51%)  
Frame = +1

Query: 1321 FKVSNSVSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQH CI 1500  
FK + + KY+ + WL +Y + AAG M Y P+ L A WL L + I  
Sbjct: 438 FKPTGIEKYDGTNPESWLT VYGLAIRAAGGDSKAMANYLPVALADSARSWLHGLTRGTI 497

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W++ FIANFQ F++P +DL ++ + E+LR Y++RF RN ++ + +  
Sbjct: 498 GSWAELRDHFIANFQGTFERPGTQYDLYNVIQKSGESLRDYIRRFSEQRNKISDITDDVI 557

Query: 1681 IEDFYRG 1701  
I F +G  
Sbjct: 558 IAAFTKG 564

>gb|ABA98116.1| retrotransposon protein, putative, Ty3-gypsy subclass [Oryza sativa  
(japonica cultivar-group)]  
Length = 640

Score = 85.9 bits (211), Expect = 2e-14  
Identities = 42/127 (33%), Positives = 66/127 (51%)  
Frame = +1

Query: 1321 FKVSNSVSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQH CI 1500  
FK + + KY+ + WL +Y + AAG M Y P+ L A WL LP+ I  
Sbjct: 325 FKPTGIEKYDGTNPESWLT VYGLAIRAAGGDSKAMVNYLPVALADSARSWLHGLPRGTI 384

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W++ FIANFQ F++P +DL +I + E+LR Y++ F RN ++ + +  
Sbjct: 385 GSWTEL RDHFIANFQGTFERPGTHFDLYNIIQKSGESLRDYIRHFSKERNKISDITDDVI 444

Query: 1681 IEDFYRG 1701  
I F +G  
Sbjct: 445 IAAFTKG 451

>dbj|BAA84457.1| GAG-POL precursor [Oryza sativa Japonica Group]  
Length = 983

Score = 85.9 bits (211), Expect = 2e-14  
Identities = 41/127 (32%), Positives = 66/127 (51%)  
Frame = +1

Query: 1321 FKVSNSVSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
FK + + KY+ + WL +Y + AAG M Y P+ L A WL L + I  
Sbjct: 439 FKPTGIEKYDGTTPESWLTIVYGLAIRAAGGDSKAMANYLPVALADSARSWLHGLTRGTI 498

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W++ FIANFQ F++P +DL ++ + E+LR Y++RF RN ++ + +  
Sbjct: 499 GSWAELRDHFIANFQGTFERPGTQYDLYNVIQKSGESLRDYIRRFSEQRNKISDITDDVI 558

Query: 1681 IEDFYRG 1701  
I F +G  
Sbjct: 559 IAAFTKG 565

>gb|ABA97602.2| retrotransposon protein, putative, Ty3-gypsy subclass [Oryza sativa  
(japonica cultivar-group)]  
Length = 721

Score = 85.5 bits (210), Expect = 2e-14  
Identities = 41/128 (32%), Positives = 67/128 (52%)  
Frame = +1

Query: 1318 NFKVSNSVSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHC 1497  
+FK + + K + + WL +Y + AAG M Y P+ L A WL LP+  
Sbjct: 295 SFKPTGIEKDDGTTPESWLTIVYGLAIRAAGGDSKAMANYLPVALADSARSWLPGLPRGT 354

Query: 1498 IDNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEVAEAG 1677  
I +W++ FIANFQ F++P +DL ++ + E+LR Y++RF RN ++ +  
Sbjct: 355 IGSWAELRDHFIANFQGTFERPGTQFDLYNLSQKSGESLRDYIRRFSEQRNKISDITDDV 414

Query: 1678 VIEDFYRG 1701  
+I F +G  
Sbjct: 415 IIAAFTKG 422

>gb|AAV43893.1| putative polyprotein [Oryza sativa Japonica Group]  
gb|AAV43934.1| putative polyprotein [Oryza sativa Japonica Group]  
Length = 1565

Score = 85.5 bits (210), Expect = 2e-14  
Identities = 44/124 (35%), Positives = 67/124 (54%)  
Frame = +1

Query: 1321 FKVSNSVSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
F+ + KY+ D +L +Y+ V +AAGA ++ + Y P L A WL HLP + I  
Sbjct: 362 FRPGAIEKYDGSTDP EEFLQVYSTVLYAAGADDNTLANYLPTALKGSARSWLMHLPPIYSI 421

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W+D FIANFQ +++ A DL ++ E+LR Y+ F RN P++ +A V  
Sbjct: 422 SSWADLWQQFIANFQGTYERHAIEDDLHALTQDSGESLREYVWCFNECRNTIPKITDASV 481

Query: 1681 IEDF 1692  
I F  
Sbjct: 482 IRAF 485

>gb|AAU90124.1| putative polyprotein [Oryza sativa Japonica Group]  
Length = 1796

Score = 85.5 bits (210), Expect = 2e-14  
Identities = 46/142 (32%), Positives = 71/142 (50%)  
Frame = +1

Query: 1315 PNFKVSNSVSKYERKQDLGGWLAIYTIWTAAAGATEDVMTVYFPIVLGQDAMQWLRHLPQH 1494  
P F+ + KY+ + +L IYT AAG + VM +FP+ L A WL +LP  
Sbjct: 257 PRFRPTITEKYDGSVNPAEFLQIYTTGIEAAGGDDRVMANFFPMALKGQAQGWLMLNPPA 316

Query: 1495 CIDNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRLYLKRF\*TMRNHTPEVAEA 1674  
+ +W D F NFQ ++ +P + DL ++ + DE+LR Y++RF +RN P +  
Sbjct: 317 SVHSWEDLCQQFTTNFQGIYPRPGEEADLHAVQRRDDESLRSYIQRFCQVRNTIPCIPAH 376

Query: 1675 GVIEDFYRGSNDSAFVRAILQK 1740  
VI F G + + I K  
Sbjct: 377 AVIYAFRGGVRHNRMLEKIASK 398

>gb|ABA99509.1| retrotransposon protein, putative, Ty3-gypsy subclass [Oryza sativa  
(japonica cultivar-group)]  
Length = 2003

Score = 85.5 bits (210), Expect = 2e-14  
Identities = 42/127 (33%), Positives = 65/127 (51%)  
Frame = +1

Query: 1321 FKVSNSVSKYERKQDLGGWLAIYTIWTAAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
FK + + KY+ + WL +Y + AAG M Y P+ L A WL LP+ I  
Sbjct: 857 FKPTGIEKYDGTANPESWLTVYGLAIRAAGGDSKAMANYLPVALADSAWSWLHGLPRGTI 916

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W++ FIANFQ F++P +DL +I + E LR Y++RF RN ++ + +  
Sbjct: 917 GSWAELRDHFIANFQGTFERPGTHFDLYNIVQKSREFLRDYIRRFSEQRNKISDITDDVI 976

Query: 1681 IEDFYRG 1701  
F +G  
Sbjct: 977 TAAFTKG 983

>gb|ABF99467.1| retrotransposon protein, putative, unclassified [Oryza sativa  
(japonica cultivar-group)]  
Length = 1992

Score = 85.1 bits (209), Expect = 3e-14  
Identities = 54/172 (31%), Positives = 79/172 (45%)  
Frame = +1

Query: 1225 PSLGPTSRTPT\*RHVRSLRTYSVSPGHPVAPNFKVSNSVSKYERKQDLGGWLAIYTIWTWA 1404  
PS+ P V SLR SP F+ + KY+ + +L +YT A  
Sbjct: 211 PSVPPVGGVGCRAFVASLRNVWSP-----RFRPTIAEKYDGSVNPAEFLQVYTTGIEA 264

Query: 1405 AGATEDVMTVYFPIVLGQDAMQWLRHLPQH CIDNWSDFSWCFIANFQSLFDKPAQPWDLK 1584  
AG + VM +FP+ L A WL +LP I +W D F NFQ + +P + DL  
Sbjct: 265 AGGDDRVMANFFPMALKGQARGWLMLNPPASIHSWEDLCQQFTMNFQGTYPYPGEEADLH 324

Query: 1585 SIGHQGETLRLYLKRF\*TMRNHTPEVAEAGVIEDFYRGSNDSAFVRAILQK 1740  
++ + DE+LR Y++RF +RN P + VI F G + + I K  
Sbjct: 325 AVQRRDDESLRSYIQRFCQVRNTIPCIPAHAVIYAFRGGVRHNRMLEKIASK 376

>gb|ABF98317.1| retrotransposon protein, putative, Ty3-gypsy subclass [Oryza sativa (japonica cultivar-group)]  
Length = 1375

Score = 85.1 bits (209), Expect = 3e-14  
Identities = 48/148 (32%), Positives = 72/148 (48%)  
Frame = +1

Query: 1321 FKVSNVSKYERKQDLGGWLAIYTIWTAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
F+ + KY+ + +L +Y+ V +AAGA + + Y P L A WL HLP + I  
Sbjct: 350 FRPGAIEKYDGSSTNPEEFLQVYSTVLYAAGADDSALVNYLPTALKGSARSWLMHLPYISI 409

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRRLYLKRF\*TMRNHTPEVAEAGV 1680  
W+D F+ANFQ + + A DL ++ E+L Y+ RF RN PE+ +A V  
Sbjct: 410 SLWADLWQQFVANFQGTQYKRHAIEDDLHALTQNPGESLSDYVWRFNECRNTIPEITDASV 469

Query: 1681 IEDFYRGSNDSAFVRAILQKSVGHLRTL 1764  
I F G D + + + V R L  
Sbjct: 470 IRAFKSGVRDRYTTQELATRRVTTRRL 497

>gb|AAT77916.1| putative polyprotein [Oryza sativa Japonica Group]  
Length = 2010

Score = 85.1 bits (209), Expect = 3e-14  
Identities = 54/172 (31%), Positives = 79/172 (45%)  
Frame = +1

Query: 1225 PSLGPTSRTPT\*RHVRSRLRTYSVSPGHPVAPNFKVSNVSKYERKQDLGGWLAIYTIWTA 1404  
PS+ P V SLR SP F+ + KY+ + +L +YT A  
Sbjct: 211 PSVPPVGGVGCRAFVASLRNVRWSP-----RFRPTIAEKYDGSVNPAEFLQVYTTGIEA 264

Query: 1405 AGATEDVMTVYFPIVLGQDAMQWLRHLPQHCIDNWSDFSWCFIANFQSLFDKPAQPWDLK 1584  
AG + VM +FP+ L A WL +LP I +W D F NFQ + +P + DL  
Sbjct: 265 AGGDDRVMANFFPMALKGQARGWLMNLPASIHSWEDLCQQFTMNFQGTYP RPGE EADLH 324

Query: 1585 SIGHQGETLRRLYLKRF\*TMRNHTPEVAEAGVIEDFYRGSNDSAFVRAILQK 1740  
++ + DE+LR Y++RF +RN P + VI F G + + I K  
Sbjct: 325 AVQRRDDESLRSYIQRFCQVRNTIPCI PAHAVIYA FRGGVRHNRMLEKIASK 376

>gb|AAR87220.1| retrotransposon protein, putative, Ty3-gypsy sub-class [Oryza sativa Japonica Group]

gb|AAT78756.1| putative retrotansposon gag protein [Oryza sativa Japonica Group]  
gb|ABF97527.1| retrotransposon protein, putative, Ty3-gypsy subclass [Oryza sativa (japonica cultivar-group)]  
Length = 1389

Score = 85.1 bits (209), Expect = 3e-14  
Identities = 43/141 (30%), Positives = 71/141 (50%)  
Frame = +1

Query: 1321 FKVSNVSKYERKQDLGGWLAIYTIWTAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
FK + + KY+ + WL +Y + AAG M Y P+ L A WL LP+ I  
Sbjct: 326 FKPTGIEKYDGTNPESWLTVYGLAIRAAGGDSKAMANYLPVALADSARSWLHGLPRGTI 385

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W++ FIANFQ F++P +DL ++ + ++LR Y++ F RN ++ + +  
Sbjct: 386 GSWAELHDHFIANFQGTFERPGTQFDLYNVIQKTGKSLRDYIRCFSEQRNKISDITDDVI 445

Query: 1681 IEDFYRGSNDSAFVRAILQKS 1743  
I F +G + V +KS  
Sbjct: 446 IAAFTKGIHHEDLVGKFRRKS 466

>gb|AAP20843.1| retrotransposon protein, putative, Ty3-gypsy sub-class [Oryza sativa Japonica Group]  
gb|ABF96690.1| retrotransposon protein, putative, Ty3-gypsy subclass [Oryza sativa (japonica cultivar-group)]  
Length = 1547

Score = 85.1 bits (209), Expect = 3e-14  
Identities = 43/130 (33%), Positives = 67/130 (51%)  
Frame = +1

Query: 1321 FKVSNSVSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
F+ + KY+ D +L +Y+ V +AA A + + Y P L A WL HLP + +  
Sbjct: 299 FRPRAIEKYDGSTDP EEFLQVYSTVLYAAQADNNALANYLPTALKGSARSWLMHLPPLYV 358

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGD ETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W++ F+ANFQ + + DL ++ E+LR Y++RF RN PE+ +A V  
Sbjct: 359 SSWANLWQQFVANFQGTYKRHTIEDDLHALTQNSGESLRDYVRRFDECRNTIPEITDASV 418

Query: 1681 IEDFYRGSND 1710  
I F G D  
Sbjct: 419 IRTFKSGFRD 428

>gb|AA038507.1| putative GAG-POL precursor [Oryza sativa Japonica Group]  
Length = 831

Score = 85.1 bits (209), Expect = 3e-14  
Identities = 48/148 (32%), Positives = 72/148 (48%)  
Frame = +1

Query: 1321 FKVSNSVSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
F+ + KY+ + +L +Y+ V +AAGA + + Y P L A WL HLP + I  
Sbjct: 350 FRPGAIEKYDGSTNP EEFLQVYSTVLYAAGADDSALVNYLPTALKGSARSWLMHLPPIYSI 409

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGD ETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
W+D F+ANFQ + + A DL ++ E+L Y+ RF RN PE+ +A V  
Sbjct: 410 SLWADLWQQFVANFQGTYKRHAIEDDLHALTQNPGESLSDYVWRFNECRNTIPEITDASV 469

Query: 1681 IEDFYRGSNDSAFVRAILQKSVGHLRTL 1764  
I F G D + + + V R L  
Sbjct: 470 IRAFKSGVRDRYTTQELATTRVTTTRRL 497

>gb|ABA99731.1| retrotransposon protein, putative, Ty3-gypsy subclass [Oryza sativa (japonica cultivar-group)]  
Length = 1752

Score = 85.1 bits (209), Expect = 3e-14  
Identities = 42/127 (33%), Positives = 66/127 (51%)  
Frame = +1

Query: 1321 FKVSNSVSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
FK + + KY+ + WL +Y + AAG M Y + L A WL LP+ I  
Sbjct: 350 FKPTGIEKYDGTTPNESWLT VYGLAIRAAGGDSKAMANYLLVALADSARSWLHGLPRGTI 409

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGD ETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W++ FIANFQ F++P +DL +I + E+LR Y++RF RN ++ + +  
Sbjct: 410 GSWAELRDHFIANFQGTFERPGTHFDLYNIVQKSGESLRDYIRRFSEQRNKISDITDDVI 469

Query: 1681 IEDFYRG 1701  
I F +G

Sbjct: 470 IAAFTKG 476

>gb|ABA93786.1| retrotransposon protein, putative, Ty3-gypsy subclass [Oryza sativa (japonica cultivar-group)]  
Length = 1498

Score = 85.1 bits (209), Expect = 3e-14  
Identities = 41/128 (32%), Positives = 67/128 (52%)  
Frame = +1

Query: 1318 NFKVSNVSKYERKQDLGGWLAIYTIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHC 1497  
+FK++ + KY+ + WL +Y + AAG M Y + L A WL LP+  
Sbjct: 379 SFKLTGIEKYDGTNPESWLTIVYRLAIRAAGGDSKAMANYLLVALADSARSWLHGLPRGT 438

Query: 1498 IDNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEVAEAG 1677  
I +W++ FIANFQ F++P +DL + + E+LR Y++RF RN ++ +  
Sbjct: 439 IGSWAELRDHFIANFQGTFERPDTQFDLYNFVQKSGESLRDYIRRFSEQRNKISDITDNV 498

Query: 1678 VIEDFYRG 1701  
+I F +G  
Sbjct: 499 IIAAFTKG 506

>gb|AAP53804.1| retrotransposon protein, putative, unclassified [Oryza sativa (japonica cultivar-group)]  
Length = 1765

Score = 85.1 bits (209), Expect = 3e-14  
Identities = 48/151 (31%), Positives = 72/151 (47%)  
Frame = +1

Query: 1288 SVSPGHPVAPNFKVSNVSKYERKQDLGGWLAIYTIVTWAAGATEDVMTVYFPIVLGQDAM 1467  
S P P F+ + KY + +L IYT AAGA + VM + P+ L A  
Sbjct: 162 STPPTQEYPPRFRPTITEKYNGSVNPAEFLQIYTTGIEAAGADDRVMANFIPMALKGQAR 221

Query: 1468 QWLRHLPQHCIDNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMR 1647  
WL +LP + +W D F NFQ + +P + DL ++ + DE+LR Y++RF +R  
Sbjct: 222 GWLMNLPPASVHSEWEDLCQQFTTNFQGTYPGEEADLHAVQRRDDESLRSYIQRFCQVR 281

Query: 1648 NHTPEVAEAGVIEDFYRGSNDSAFVRAILQK 1740  
N P + VI F G + ++ I K  
Sbjct: 282 NTIPCIPAHAVIYAFRGGVVRHNRMLKKIASK 312

>emb|CAH67521.1| OSIGBa0131L05.2 [Oryza sativa (indica cultivar-group)]  
Length = 1770

Score = 84.7 bits (208), Expect = 4e-14  
Identities = 46/142 (32%), Positives = 71/142 (50%)  
Frame = +1

Query: 1315 PNFKVSNVSKYERKQDLGGWLAIYTIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQH 1494  
P F+ + KY+ + +L IYT AAG + VM +FP+ L A WL +LP  
Sbjct: 235 PRFRPTITEKYDGSVNPAEFLQIYTTGIEAAGDDRVMANFFPMALKGQARGWLMNLPPA 294

Query: 1495 CIDNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEVAEA 1674  
+ +W D F NFQ ++ +P + DL ++ + DE+LR Y++RF +RN P +  
Sbjct: 295 SVHSEWEDLCQQFTTNFQGIYPRPGEEADLHAVQRRDDESLRSYIQRFCQVRNTIPCIPAH 354

Query: 1675 GVIEDFYRGSNDSAFVRAILQK 1740  
VI F G + + I K  
Sbjct: 355 AVIYVFRGGVVRHNRMLEKIASK 376

>gb|ABA95741.2| retrotransposon protein, putative, unclassified [Oryza sativa (japonica cultivar-group)]  
Length = 1809

Score = 84.7 bits (208), Expect = 4e-14  
Identities = 45/142 (31%), Positives = 71/142 (50%)  
Frame = +1

Query: 1315 PNFKVSNSVSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQH 1494  
P F+ ++ KY+ + +L +YT AAG + VM +FP+ L A WL +LP  
Sbjct: 122 PRFRPTSAEKYDGSVNPAEFLQVYTTGIEAAGGDDRVMANFFPMALKGQARGWLMNLPPA 181

Query: 1495 CIDNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRLYLKRF\*TMRNHTPEVAEA 1674  
+ +W D F NFQ + +P + DL ++ + DE+LR Y++RF +RN P +  
Sbjct: 182 SVHSWEDLCQQFTMNFQGTYP RPGEADLHAVQRRDDESLRSYIQRFCQVRNTIPCIPAH 241

Query: 1675 GVIEDFYRGSNDSAFVRAILQK 1740  
VI F G + + I K  
Sbjct: 242 AVIYAFRGGVRHNRMLEKIASK 263

>emb|CAE05311.2| OSJNBa0056L23.9 [Oryza sativa (japonica cultivar-group)]  
Length = 836

Score = 84.7 bits (208), Expect = 4e-14  
Identities = 40/127 (31%), Positives = 66/127 (51%)  
Frame = +1

Query: 1321 FKVSNSVSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
FK + + KY+ + WL +Y + AAG + Y P+ L A WL LP+ I  
Sbjct: 358 FKPTGIEKYDGSTNPESWLTVYGLAIRAAGGDSKALANYLPVALADSARSWLHGLPRGTI 417

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W++ FIANFQ F++P +DL ++ + E+LR Y++RF N ++ + +  
Sbjct: 418 GSWAELRDHFIANFQGTFERPGTQFDLYNVIQKSGESLRDYIRRFSEQCNKISDITDDVI 477

Query: 1681 IEDFYRG 1701  
I F +G  
Sbjct: 478 IAAFTKG 484

>gb|ABA94658.1| retrotransposon protein, putative, unclassified [Oryza sativa (japonica cultivar-group)]  
Length = 1965

Score = 84.7 bits (208), Expect = 4e-14  
Identities = 45/144 (31%), Positives = 72/144 (50%)  
Frame = +1

Query: 1315 PNFKVSNSVSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQH 1494  
P F+ + KY+ + +L +YT AAG + VM +FP+ L A WL +LP  
Sbjct: 229 PRFRPTIAEKYDGSVNPAEFLQVYTTGIEAAGGDDRVMANFFPMALKGQARGWLMNLPPA 288

Query: 1495 CIDNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRLYLKRF\*TMRNHTPEVAEA 1674  
+ +W D F NFQ ++ +P + DL ++ + DE+LR Y++RF +RN P +  
Sbjct: 289 SVHSWEDLCQQFTMNFQGIYPRPGEADLHAVQRRDDESLRSYIQRFCQVRNTIPCIPAH 348

Query: 1675 GVIEDFYRGSNDSAFVRAILQKSV 1746  
VI F G + + I K +  
Sbjct: 349 AVIYAFRGGVRHNRMLEKIASKEL 372

>gb|AAL83337.1|AC074282\_4 Putative gag-pol polyprotein [Oryza sativa Japonica Group]  
gb|AAM08726.1|AC116601\_19 Putative gag-pol polyprotein [Oryza sativa Japonica Group]  
gb|AAP51915.1| transposon protein, putative, unclassified [Oryza sativa (japonica  
cultivar-group)]  
Length = 276

Score = 84.7 bits (208), Expect = 4e-14  
Identities = 46/144 (31%), Positives = 70/144 (48%)  
Frame = +1

Query: 1336 VSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCIDNWS 1515  
+ KY+ D +L +++ V +AAGA + + Y P L A WL HLP I +W D  
Sbjct: 88 IEKYDGSTDPEEFLHVFSTVLYAAGANDHALANYLPAALKGSARSWLHLPPCSISWED 147

Query: 1516 FSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEVAEAGVIEDFY 1695  
F+ANFQ + + A DL ++ E+LR Y++RF RN PE+ A VI F  
Sbjct: 148 LWQQFVANFQGTYKRHAIEDDLHALVQNPGESLRDYIRRFNECRNTIPEITNASVIRTFK 207

Query: 1696 RGSNDSAFVRAILQKSVGHLRTL 1767  
G D + + + + L+  
Sbjct: 208 LGIRDYTTQELATRRITS AHKLI 231

>emb|CAE03745.1| OSJNBa0019D11.11 [Oryza sativa (japonica cultivar-group)]  
Length = 1770

Score = 84.7 bits (208), Expect = 4e-14  
Identities = 46/142 (32%), Positives = 71/142 (50%)  
Frame = +1

Query: 1315 PNFKVSNSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQH 1494  
P F+ + KY+ + +L IYT AAG + VM +FP+ L A WL +LP  
Sbjct: 235 PRFRPTITEKYDGSVNPAEFLQIYTTGIEAAGDDRVMANFFPMALKGQARGWLMNLP 294

Query: 1495 CIDNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEVAEA 1674  
+ +W D F NFQ ++ +P + DL ++ + DE+LR Y++RF +RN P +  
Sbjct: 295 SVHSWEDLCQFTTNFQGIYPRPGEEADLHAVQRRDDESLRSYIQRFCQVRNTIPCIPAH 354

Query: 1675 GVIEDFYRGSNDSAFVRAILQK 1740  
VI F G + + I K  
Sbjct: 355 AVIYVFRGGVRHNRMLEKIASK 376

>ref|XP\_002448893.1| hypothetical protein SORBIDRAFT\_05g000983 [Sorghum bicolor]  
gb|EES07881.1| hypothetical protein SORBIDRAFT\_05g000983 [Sorghum bicolor]  
Length = 855

Score = 84.3 bits (207), Expect = 5e-14  
Identities = 43/139 (30%), Positives = 71/139 (51%), Gaps = 1/139 (0%)  
Frame = +1

Query: 1330 SNVSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVY-FPIVLGQDAMQWLRHLPQHCIDN 1506  
+N++KY + + WLA Y + GA +D++ + P+ L A WL HLP I +  
Sbjct: 533 ANLTKYSGETNPWLADYRLACQLGGADDDLLIIRNLPPLHLADTARAWLEHLPDRMIHD 592

Query: 1507 WSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEVAEAGVIE 1686  
W+D F+ NFQ + +P WDL+S + DE+LR ++KRF + ++ VI  
Sbjct: 593 WADLVKIFVGNFQGTYYVRPGNSWDLRSCRQKPDESLRDFIKRFSKQCTELTNITDSDVIG 652

Query: 1687 DFYRGSNDSAFVRAILQKS 1743  
F G+ V + +K+  
Sbjct: 653 AFISGTTCKELVHELGRKT 671



>emb|CAH66736.1| H0404F02.12 [Oryza sativa (indica cultivar-group)]  
Length = 780

Score = 84.3 bits (207), Expect = 5e-14  
Identities = 42/127 (33%), Positives = 66/127 (51%)  
Frame = +1

Query: 1321 FKVSNVSKYERKQDLGGWLAITYTIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
FK + + KY+ + WL +Y + AAG M Y P+ L A WL LP+ I  
Sbjct: 419 FKPTRIKKYDGTNPESWLTIVYGLAIRAAGGDSKAMANYLPVALADSARSWLHGLPRGTI 478

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W++ FIANFQ F++P +DL +I + E+LR Y++RF N ++ + +  
Sbjct: 479 GSWAELHDHFIANFQGTFERPGTHFDLYNIIQKYGESLRDYIRRFSEQCNKISDITDDVI 538

Query: 1681 IEDFYRG 1701  
I F +G  
Sbjct: 539 IAAFTKG 545

>ref|NP\_001046396.1| Os02g0237300 [Oryza sativa (japonica cultivar-group)]  
Length = 1377

Score = 84.3 bits (207), Expect = 5e-14  
Identities = 47/140 (33%), Positives = 69/140 (49%)  
Frame = +1

Query: 1321 FKVSNVSKYERKQDLGGWLAITYTIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
F+ + KY+ + +L IYT V AAG + VM YFP+ L A WL P I  
Sbjct: 248 FRPNLTEKYDGNINPSEFLQIYTTVIVAAGGDDRVMANYPFPMALKGQACGWLMTPPDSI 307

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W D S FI NFQ + +P + DL ++ + DE+LR Y++RF +RN P + V  
Sbjct: 308 HSWEDLSQQFITNFQGTYPGPGEADLHAVRQKDDDESLRSYIQRFCQVRNTIPCIPAHAV 367

Query: 1681 IEDFYRGSNDSAFVRAILQK 1740  
+ F + + I K  
Sbjct: 368 VYAFRNSVRHNRMLEKITSK 387

>gb|ABF93514.1| retrotransposon protein, putative, unclassified [Oryza sativa (japonica cultivar-group)]  
Length = 776

Score = 84.3 bits (207), Expect = 5e-14  
Identities = 53/180 (29%), Positives = 80/180 (44%)  
Frame = +1

Query: 1201 IKMTHNWLPSLGPTSRTP\*T\*RHVRSRLTYSVSPGHPVAPNFKVSNVSKYERKQDLGGWLA 1380  
++ H P + P V SLR P F+ + KY+ + +L  
Sbjct: 203 LRSEHGGQPPVSPVGGAGCRAFVASLRNVRWPP-----RFRPTITEKYDGSVNPAEFLQ 256

Query: 1381 IYTIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCHIDNWSDFSWCFIANFQSLFDK 1560  
IYT AAG + VM +FP+ L A WL +LP + +W D F NFQ + +  
Sbjct: 257 IYTTGIEAAGGDDRVMANFFPMALKGQARGWLMNLPPASVHSHWEDLCQQFTMNFQGTYP 316

Query: 1561 PAQPWDLKSIGHQGETLRLYLKRF\*TMRNHTPEVAEAGVIEDFYRGSNDSAFVRAILQK 1740  
P + DL ++ + DE+LR Y++RF +RN P + VI F G + + I K  
Sbjct: 317 PGEEADLHAVQRRDDESLRSYIQRFCQVRNTIPCIPAHAVIYAFRGGVRHNRMLEKIASK 376

>gb|AAT94049.1| putative polyprotein [Oryza sativa Japonica Group]  
Length = 1844

Score = 84.3 bits (207), Expect = 5e-14  
Identities = 42/134 (31%), Positives = 68/134 (50%)  
Frame = +1

Query: 1321 FKVSNVSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
FK + + KY+ + WL +Y + AAG M Y + L A WL LP+ I  
Sbjct: 438 FKPAGIEKYDGTTPNELWLTVYGLAIRAAGGDSKAMANYLSVALADSARSWLHGLPRGTI 497

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W++ FIANFQ F++P +DL ++ + E+LR Y++RF RN ++ + +  
Sbjct: 498 GSWAELRDHFIANFQGTFERPGTQFDLYNVIQKSGESLRDYIRRFSEQRNKISDITDDVI 557

Query: 1681 IEDFYRGSNDSAFV 1722  
I F +G + V  
Sbjct: 558 IAAFTKGIHHEELV 571

>emb|CAD39484.2| OSJNBa0039G19.13 [Oryza sativa (japonica cultivar-group)]  
Length = 714

Score = 84.3 bits (207), Expect = 5e-14  
Identities = 43/127 (33%), Positives = 67/127 (52%)  
Frame = +1

Query: 1321 FKVSNVSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
FK + + KY+ + WL +Y +V AAG M Y P+ L A L LP+ I  
Sbjct: 237 FKPTGIEKYDGTINPESWLTVDLVIRAAGGDSKAMANYLPVALVDFARSRLHGLPRGTI 296

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W++ FIANFQ F++P +DL ++ + E+LR Y++RF RN ++ E +  
Sbjct: 297 GSWAELCGHFIANFQGTFERPGTQFDLYNVIQKSGESLRNYIRRFSEQRNKISDITEDVI 356

Query: 1681 IEDFYRG 1701  
I F +G  
Sbjct: 357 IAAFTKG 363

>gb|AAS75250.2| putative polyprotein [Oryza sativa Japonica Group]  
Length = 1744

Score = 84.3 bits (207), Expect = 5e-14  
Identities = 41/127 (32%), Positives = 66/127 (51%)  
Frame = +1

Query: 1321 FKVSNVSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
FK + + KY+ + WL +Y + AAG M Y P+ L A WL LP+ I  
Sbjct: 315 FKPTGIEKYDGTTPNPESWLTVDLVIRAAGGDSKAMANYLPVALADSAQSWLHGLPRGTI 374

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W++ FIANFQ F++P ++L +I + E+LR Y++RF N ++ + +  
Sbjct: 375 GSWAELRDHFIANFQGTFERPGTQFNLYNIIQKSGESLRDYIRRFSEQCNKISDITDDVI 434

Query: 1681 IEDFYRG 1701  
I F +G  
Sbjct: 435 IAAFTKG 441

>gb|ABA97822.1| retrotransposon protein, putative, Ty3-gypsy subclass [Oryza sativa  
(japonica cultivar-group)]  
Length = 1379

Score = 84.3 bits (207), Expect = 5e-14  
Identities = 40/127 (31%), Positives = 66/127 (51%)  
Frame = +1

Query: 1321 FKVSNVSKYERKQDLGGWLAITYTIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
FK + + KY+ + WL +Y + AAG M Y P+ L A WL LP+ I  
Sbjct: 242 FKPTGIEKYDGTTPESWLTIVYGLAIRAAGGDSKAMANYLPVALADSARSWLHGLPRGTI 301

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W++ FIANFQ F++P +DL ++ + +L+ Y++RF RN ++ + +  
Sbjct: 302 GSWAELRDHFIANFQGTFERPGTQFDLYNVVQKSRGSLQDYIRRFSEQRNKISDITDDVI 361

Query: 1681 IEDFYRG 1701  
I F +G  
Sbjct: 362 IAAFTKG 368

>gb|ABA94226.1| retrotransposon protein, putative, unclassified [Oryza sativa  
(japonica cultivar-group)]  
Length = 1739

Score = 84.3 bits (207), Expect = 5e-14  
Identities = 53/180 (29%), Positives = 80/180 (44%)  
Frame = +1

Query: 1201 IKMTHNWLP SLGPTSRTPT\*RHVRS LR TYSVSPGHPVAPNFKVSNVSKYERKQDLGGWLA 1380  
++ H P + P V SLR P F+ + KY+ + +L  
Sbjct: 95 LRS GHGGQPPVSPVGGAGCRA FVASLRNVRWPP-----RFRPTITEKYDGSVNP AEFLQ 148

Query: 1381 IYTIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQH CIDNWSDFSWCFIANFQSLFDK 1560  
IYT AAG + VM +FP+ L A WL +LP + +W D F NFQ + +  
Sbjct: 149 IYTTGIEAAGGDDRVMANFFPMALRGQARGWLMNLPPASVHSWEDLCQQFTMNFQGTYP R 208

Query: 1561 PAQPWDLKSIGHQGETLRLYLKRF\*TMRNHTPEVAEAGVIEDFYRGSNDSAFVRAILQK 1740  
P + DL ++ + DE+LR Y++RF +RN P + VI F G + + I K  
Sbjct: 209 PGEEADLHAVQRRDDESLRSYIQRFCQVRNTVPCIPAHAVIYAFRGGVRHNRMLEKIAS K 268

>gb|ABF93909.1| retrotransposon protein, putative, Ty3-gypsy subclass [Oryza sativa  
(japonica cultivar-group)]  
Length = 882

Score = 84.0 bits (206), Expect = 6e-14  
Identities = 39/127 (30%), Positives = 65/127 (51%)  
Frame = +1

Query: 1321 FKVSNVSKYERKQDLGGWLAITYTIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCI 1500  
FK++ + KY+ + WL +Y + AAG + Y P+ L A WL +P I  
Sbjct: 415 FKLTGIEKYDGTTPKSWLTIVYGLTIRAAGGDSKAIANYLPVALADSARSWLHGVPHGTI 474

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W+ FIANFQ F++P +DL ++ + E+LR Y++RF N ++ + +  
Sbjct: 475 GSWAKLRDHFIANFQGTFERPGTQFDLYNVVQKSGESLRDYIRRFSEQHNKISDITDDVI 534

Query: 1681 IEDFYRG 1701  
I F +G  
Sbjct: 535 IAAFTKG 541

>gb|ABF98885.1| retrotransposon protein, putative, unclassified [Oryza sativa  
(japonica cultivar-group)]  
Length = 2012

Score = 84.0 bits (206), Expect = 6e-14  
Identities = 46/142 (32%), Positives = 71/142 (50%)  
Frame = +1

Query: 1315 PNFKVSNSKYERKQDLGGWLAIYTIWTAAAGATEDVMTVYFPIVLGQDAMQWLRHLPQH 1494  
P F+ + KY+ + +L +YT AAG + VM +FP+ L A WL +LP  
Sbjct: 235 PRFRPTISEKYDGSVNPAEFLQVYTTGIEAAGGDDRVMANFFPMALKGQARGWLMNLPPA 294

Query: 1495 CIDNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEVAEA 1674  
+ +W D F NFQ + +P + DL ++ + DE+LRLY++RF +RN P +  
Sbjct: 295 SVYSWEDLCQQFTMNFQGTYP RPGEEDLHAVQRRDDESLRLYIQRFCQVRNTIPCI PAH 354

Query: 1675 GVIEDFYRGSNDSAFVRAILQK 1740  
VI F G + + I K  
Sbjct: 355 AVIYAFRGGVRHNRMLEKIASK 376

>gb|ABF99476.1| retrotransposon protein, putative, unclassified [Oryza sativa  
(japonica cultivar-group)]  
Length = 1840

Score = 84.0 bits (206), Expect = 6e-14  
Identities = 45/142 (31%), Positives = 71/142 (50%)  
Frame = +1

Query: 1315 PNFKVSNSKYERKQDLGGWLAIYTIWTAAAGATEDVMTVYFPIVLGQDAMQWLRHLPQH 1494  
P F+ + KY+ + +L +YT AAG + VM +FP+ L A WL +LP  
Sbjct: 159 PRFRPTITEKYDGSVNPAEFLQVYTTGIEAAGGDDRVMANFFPMALKGQARGWLMNLPPA 218

Query: 1495 CIDNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEVAEA 1674  
+ +W D F NFQ + +P + DL ++ + DE+LR Y++RF +RN P +  
Sbjct: 219 SVHSWEDLCQQFTMNFQGTYP RPGEEDLHAVQRRDDESLRSYIQRFCQVRNTIPCI PAH 278

Query: 1675 GVIEDFYRGSNDSAFVRAILQK 1740  
VI F G + ++ I K  
Sbjct: 279 AVIYAFRGGVRHNRMLKKIASK 300

>gb|AAX95836.1| predicted protein [Oryza sativa Japonica Group]  
Length = 1179

Score = 84.0 bits (206), Expect = 6e-14  
Identities = 42/127 (33%), Positives = 63/127 (49%)  
Frame = +1

Query: 1321 FKVSNSKYERKQDLGGWLAIYTIWTAAAGATEDVMTVYFPIVLGQDAMQWLRHLPQH CI 1500  
FK + KY+ + WL +Y + AAG M Y P+ L A WL LP+ I  
Sbjct: 409 FKPFGIEKYDGTTPNESWLTVYGLAIRAAGGDNKAMANYLPVALADSARSWLHGLPRGTI 468

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W++ FIANFQ F+ P +DL + + E+LR Y++RF RN ++ + +  
Sbjct: 469 GSWAELRDHFIANFQGTFECPGTQFDLYIVIQKSRESLRDYIRRFSEQRNKISDITDDVI 528

Query: 1681 IEDFYRG 1701  
I F G  
Sbjct: 529 IASFTNG 535

>gb|AAU90238.1| putative polyprotein [Oryza sativa Japonica Group]  
Length = 1923

Score = 84.0 bits (206), Expect = 6e-14

Identities = 45/142 (31%), Positives = 71/142 (50%)  
Frame = +1

Query: 1315 PNFKVSNSVSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQH 1494  
P F+ + KY+ + +L +YT AAG + VM +FP+ L A WL +LP  
Sbjct: 235 PRFRPTIAEKYDGSVNPAEFLQVYTTGIEAAGGDDRVMANFFPMALKGQARGWLMNLPPA 294

Query: 1495 CIDNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRLYLKRF\*TMRNHTPEVAEA 1674  
+ +W D F NFQ ++ +P + DL ++ + DE+LR Y++RF +RN P +  
Sbjct: 295 SVHSWEDLCQQFTMNFQGIYPRPGEEADLHAVQRRDDESLRSYIQRFCQVRNTIPCI PAH 354

Query: 1675 GVIEDFYRGSNDSAFVRAILQK 1740  
VI F G + + I K  
Sbjct: 355 AVIYA FRGGVRHNMLEKIASK 376

>gb|AAT77917.1| putative polyprotein [Oryza sativa Japonica Group]  
Length = 1898

Score = 84.0 bits (206), Expect = 6e-14  
Identities = 45/142 (31%), Positives = 71/142 (50%)  
Frame = +1

Query: 1315 PNFKVSNSVSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQH 1494  
P F+ + KY+ + +L +YT AAG + VM +FP+ L A WL +LP  
Sbjct: 217 PRFRPTITEKYDGSVNPAEFLQVYTTGIEAAGGDDRVMANFFPMALKGQARGWLMNLPPA 276

Query: 1495 CIDNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRLYLKRF\*TMRNHTPEVAEA 1674  
+ +W D F NFQ + +P + DL ++ + DE+LR Y++RF +RN P +  
Sbjct: 277 SVHSWEDLCQQFTMNFQGTYP RPGEADLHAVQRRDDESLRSYIQRFCQVRNTIPCI PAH 336

Query: 1675 GVIEDFYRGSNDSAFVRAILQK 1740  
VI F G + ++ I K  
Sbjct: 337 AVIYA FRGGVRHNRMLKKIASK 358

>emb|CAE04380.1| OSJNBa0027G07.22 [Oryza sativa (japonica cultivar-group)]  
emb|CAE02561.2| OSJNBa0006M15.4 [Oryza sativa (japonica cultivar-group)]  
Length = 359

Score = 84.0 bits (206), Expect = 6e-14  
Identities = 47/144 (32%), Positives = 70/144 (48%)  
Frame = +1

Query: 1315 PNFKVSNSVSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQH 1494  
P F+ + KY+ + +L IYT AAG + VM +FP+ L A WL +LP  
Sbjct: 214 PRFRPTITEKYDGSVNPAEFLQIYTTGIEAAGGDDRVMANFFPMALKGQARGWLMNLPPA 273

Query: 1495 CIDNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRLYLKRF\*TMRNHTPEVAEA 1674  
+ +W D F NFQ + +P + DL ++ DE+LR Y++RF +RN P +  
Sbjct: 274 SVHSWEDLCQQFTMNFQGTYP RPGEADLHAVQRGDDESLRSYIQRFCQVRNTIPCI PAH 333

Query: 1675 GVIEDFYRGSNDSAFVRAILQKSV 1746  
VI F G + + I K V  
Sbjct: 334 AVIYA FRGGVRHNRMLEKIASKDV 357

>gb|AAK55777.1|AC079038\_11 Putative polyprotein [Oryza sativa]  
Length = 1992

Score = 84.0 bits (206), Expect = 6e-14  
Identities = 46/142 (32%), Positives = 69/142 (48%)  
Frame = +1

Query: 1315 PNFKVSNSVSKYERKQDLGGWLAIYTIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQH 1494  
P F+ + KY+ + +L +YT AAG + VM +FP+ L A WL +LP  
Sbjct: 235 PRFRPTIAEKYDGSVNPAEFLQVYTTGIEAAGGDDRVMANFFPMALKGQARGWLMNLPPA 294

Query: 1495 CIDNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEVAEA 1674  
+ +W D F NFQ + +P + DL ++ + DETLR Y++RF RN P +  
Sbjct: 295 SVHSWEDLCQQFTMNFQGTYP RPGEEDLHAVQRRDDETLRSYIQRFCQARNTIPCIPAH 354

Query: 1675 GVIEDFYRGSNDSAFVRAILQK 1740  
VI F G + + I K  
Sbjct: 355 AVIYAFRGGVRHNRMLEKIASK 376

>gb|AAL58969.1|AC091811\_18 putative gag-pol precursor [Oryza sativa Japonica Group]  
Length = 1997

Score = 84.0 bits (206), Expect = 6e-14  
Identities = 46/142 (32%), Positives = 71/142 (50%)  
Frame = +1

Query: 1315 PNFKVSNSVSKYERKQDLGGWLAIYTIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQH 1494  
P F+ + KY+ + +L +YT AAG + VM +FP+ L A WL +LP  
Sbjct: 235 PRFRPTISEKYDGSVNPAEFLQVYTTGIEAAGGDDRVMANFFPMALKGQARGWLMNLPPA 294

Query: 1495 CIDNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEVAEA 1674  
+ +W D F NFQ + +P + DL ++ + DE+LRLY++RF +RN P +  
Sbjct: 295 SVYSWEDLCQQFTMNFQGTYP RPGEEDLHAVQRRDDESLRLYIQRFCQVRNTIPCIPAH 354

Query: 1675 GVIEDFYRGSNDSAFVRAILQK 1740  
VI F G + + I K  
Sbjct: 355 AVIYAFRGGVRHNRMLEKIASK 376

>emb|CAD40172.2| OSJNBa0061A09.11 [Oryza sativa (japonica cultivar-group)]  
Length = 2030

Score = 84.0 bits (206), Expect = 6e-14  
Identities = 45/142 (31%), Positives = 71/142 (50%)  
Frame = +1

Query: 1315 PNFKVSNSVSKYERKQDLGGWLAIYTIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQH 1494  
P F+ + KY+ + +L +YT AAG + VM +FP+ L A WL +LP  
Sbjct: 235 PRFRPTIAEKYDGSVNPAEFLQVYTTGIEAAGGDDRVMANFFPMALKGQARGWLMNLPPA 294

Query: 1495 CIDNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEVAEA 1674  
+ +W D F NFQ + +P + DL+++ + DE+LR Y++RF +RN P +  
Sbjct: 295 SVHSWEDLCQQFTMNFQGTYP RPGEEDLQAVQRRDDESLRSYIQRFCQVRNTIPCIPAH 354

Query: 1675 GVIEDFYRGSNDSAFVRAILQK 1740  
VI F G + + I K  
Sbjct: 355 AVIYAFRGGVRHNRMLEKIASK 376

>gb|ABA93606.2| retrotransposon protein, putative, unclassified [Oryza sativa  
(japonica cultivar-group)]  
Length = 1939

Score = 83.6 bits (205), Expect = 8e-14  
Identities = 46/142 (32%), Positives = 70/142 (49%)  
Frame = +1

Query: 1315 PNFKVSNSVSKYERKQDLGGWLAIYTIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQH 1494

P F+ + KY+ + +L +YT AAG + VM +FP+ L A WL +LP  
 Sbjct: 180 PRFRPTIAEKYDGSVNPAEFLQVYTTGIEAAGDDRVMANFFPMALKGQARGWLMNLPPA 239  
 Query: 1495 CIDNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRLYLKRF\*TMRNHTPEVAEA 1674  
 I +W D F NFQ + +P + DL ++ + DE+LR Y++RF +RN P +  
 Sbjct: 240 SIHSWEDLCQQFTMNFQGTYP RPGEADLHAVQRRDDESLRSYIQRFCQVRNTIPCIPAH 299  
 Query: 1675 GVIEDFYRGSNDSAFVRAILQK 1740  
 VI F G + + I K  
 Sbjct: 300 AVIYAFRGGVRHNRMLEKIASK 321

>gb|ABA99910.2| retrotransposon protein, putative, unclassified [Oryza sativa  
 (japonica cultivar-group)]  
 Length = 1757

Score = 83.6 bits (205), Expect = 8e-14  
 Identities = 53/180 (29%), Positives = 80/180 (44%)  
 Frame = +1

Query: 1201 IKMTHNWLPSLGPTSRTPTRHVRSLRTYSVSPGHPVAPNFKVSNVSKYERKQDLGGWLA 1380  
 ++ H P + P V SLR P F+ + KY+ + +L  
 Sbjct: 202 LRSGHGGRPPVSPVGGAGCRAFVASLRNVWP-----RFRPTITEKYDGSFNPAEFLQ 255  
 Query: 1381 IYTIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQH CIDNWSDFSWCFIANFQSLFDK 1560  
 IYT AAG + VM +FP+ L A WL +LP + +W D F NFQ + +  
 Sbjct: 256 IYTTGIEAAGDDRVMANFFPMALKGQARGWLMNLPPASVHSWEDLCQQFTTNFQGTYP 315  
 Query: 1561 PAQPWDLKSIGHQGETLRLYLKRF\*TMRNHTPEVAEAGVIEDFYRGSNDSAFVRAILQK 1740  
 P + DL ++ + DE+LR Y++RF +RN P + VI F G + + I K  
 Sbjct: 316 PGEDADLHAVQRRDDESLRSYIQRFCQVRNTIPCIPAHAVIYAFRGGVRHNRMLEKIASK 375

>gb|ABF98607.1| retrotransposon protein, putative, unclassified [Oryza sativa  
 (japonica cultivar-group)]  
 Length = 1748

Score = 83.6 bits (205), Expect = 8e-14  
 Identities = 44/132 (33%), Positives = 68/132 (51%)  
 Frame = +1

Query: 1315 PNFKVSNSVSKYERKQDLGGWLA IYTIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQH 1494  
 P F+ + KY+ + +L +YT AAG + VM +FP+ L A WL +LP  
 Sbjct: 235 PRFRPTIAEKYDGSVNPAEFLQVYTTGIEAAGDDRVMANFFPMALKGQARGWLMNLPPA 294  
 Query: 1495 CIDNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRLYLKRF\*TMRNHTPEVAEA 1674  
 + +W D F NFQ + +P + DL ++ + DE+LR Y++RF +RN P +  
 Sbjct: 295 SVHSWEDLCQQFTMNFQGTYP RPGEADLHAVQRRDDESLRSYIQRFCQVRNTIPCIPAH 354  
 Query: 1675 GVIEDFYRGSND 1710  
 VI F G +D  
 Sbjct: 355 AVIYAFRGGGRHD 366

>gb|ABF99688.1| retrotransposon protein, putative, unclassified [Oryza sativa  
 (japonica cultivar-group)]  
 Length = 1629

Score = 83.6 bits (205), Expect = 8e-14  
 Identities = 46/144 (31%), Positives = 70/144 (48%)  
 Frame = +1

Query: 1315 PNFKVSNSVSKYERKQDLGGWLA IYTIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQH 1494

P F+ + KY+ + +L IYT V AAG+ + VM YFP+ L A WL P  
 Sbjet: 246 PKFRPNLTEKYDGSINPSEFLQIYTTVIVAAGSDDRVMANYFPMALKGQARGWLMTPPG 305  
 Query: 1495 CIDNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEVAEA 1674  
 I +W D FI NFQ + +P + DL ++ + DE+LR Y++ F +RN P +  
 Sbjet: 306 SIHSWEDLCQQFITNFQGTYP RPGEVDLHAVRRKDDESLRSYIQHFCQVRNTIPCIPAH 365  
 Query: 1675 GVIEDFYRGSNDSAFVRAILQKSV 1746  
 V+ F + + I K +  
 Sbjet: 366 AVVYAFRNSVRHNRMLEKIASKE 389

>emb|CAH67689.1| H0510A06.14 [Oryza sativa (indica cultivar-group)]  
 emb|CAH66966.1| H0525D09.6 [Oryza sativa (indica cultivar-group)]  
 Length = 2027

Score = 83.6 bits (205), Expect = 8e-14  
 Identities = 46/142 (32%), Positives = 70/142 (49%)  
 Frame = +1

Query: 1315 PNFKVSNNVSKYERKQDLGGWLAIYTTIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQH 1494  
 P F+ + KY+ + +L +YT AAG + VM +FP+VL A WL +LP  
 Sbjet: 235 PRFRPTITEKYDGSVNPTFLQVYTTGIEAAGDDRVMANFFPMVLKGQARGWLMNLPPA 294  
 Query: 1495 CIDNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEVAEA 1674  
 + +W D F NFQ + +P + DL ++ DE+LR Y++RF +RN P +  
 Sbjet: 295 SVHSWEDLCQQFTMNFQGTYP RPGEADLHAVQRSDDDESLRSYIQRFCQVRNTIPCIPAH 354  
 Query: 1675 GVIEDFYRGSNDSAFVRAILQK 1740  
 VI F G + + I K  
 Sbjet: 355 AVIYAFRGGVRHNRMLEKIASK 376

>gb|AAV32231.1| putative polyprotein [Oryza sativa Japonica Group]  
 Length = 3092

Score = 83.6 bits (205), Expect = 8e-14  
 Identities = 46/132 (34%), Positives = 68/132 (51%), Gaps = 5/132 (3%)  
 Frame = +1

Query: 1321 FKVSNNVSKYERKQDLGG-----WLAIYTTIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHL 1485  
 F+ + KY + G +L +Y+ V +AAGA ++ Y P VL A WL HL  
 Sbjet: 1724 FRPGAIEKYSTLLNDGSTDPEEFQVYSTVLVYAAAGADNANFANYLPTVLKGSARSWLMHL 1783  
 Query: 1486 PQHCIDNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEV 1665  
 P + I +W+D F+ANFQ + A DL ++ E+LR Y++RF RN P++  
 Sbjet: 1784 PPYSISSWADLWQQFVANFQGTYPKHHAIKDDLHALTONSGESLREYVRRFNECRNTIPKI 1843  
 Query: 1666 AEAGVIEDFYRG 1701  
 +A VI F G  
 Sbjet: 1844 TDASVIRAFKSG 1855

>gb|AAU44305.1| putative polyprotein [Oryza sativa Japonica Group]  
 Length = 912

Score = 83.6 bits (205), Expect = 8e-14  
 Identities = 40/127 (31%), Positives = 63/127 (49%)  
 Frame = +1

Query: 1321 FKVSNNVSKYERKQDLGGWLAIYTTIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQH 1500  
 FK + + KY+ + WL + + A G M Y P+ L A WL LP+ I  
 Sbjet: 267 FKPTGIEKYDGTTPNESWLTVCGLAIRATGGDSKAMANYLPVALADSAWSWLHGLPRGTI 326



Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEVAEAGV 1680  
+W + FIANFQ F++P +DL ++ + E+LR Y++RF RN ++ +  
Sbjct: 327 GSWHEELREHFIANFQGTFERPGTQFDLYNVTQKSGESLRDYIRRFFEQRNKISDITNDVI 386

Query: 1681 IEDFYRG 1701  
I F +G  
Sbjct: 387 IAAFTKG 393

>gb|AAT81661.1| putative retrotransposon protein [Oryza sativa Japonica Group]  
gb|ABF97633.1| retrotransposon protein, putative, unclassified [Oryza sativa  
(japonica cultivar-group)]  
Length = 1878

Score = 83.6 bits (205), Expect = 8e-14  
Identities = 53/180 (29%), Positives = 80/180 (44%)  
Frame = +1

Query: 1201 IKMTHNWLPSLGPTSRTPT\*RHVRSRLRTYSVSPGHPVAPNFKVSNVSKYERKQDLGGWLA 1380  
++ H P + P V SLR P F+ + KY+ + +L  
Sbjct: 203 LRSGHGGRPPVSPVGGAGCRAFVASLRNVRWPP-----RFRPTITEKYDGSVNPAEFLQ 256

Query: 1381 IYTIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQH CIDNWSDFSWCFIANFQSLFDK 1560  
IYT AAG + VM +FP+ L A WL +LP + +W D F NFQ ++  
Sbjct: 257 IYTTGIEAAGGDDRVMANFFPMALKGQARGWLMNLPPASVYSWEDLCQQFTTNFQGIYPH 316

Query: 1561 PAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEVAEAGVIEDFYRGSNDSAFVRAILQK 1740  
P + DL ++ + DE+LR Y++RF +RN P + VI F G + + I K  
Sbjct: 317 PGEEADLHAVQRRDDESLRSYIQRFCQVRNTIPCIPAHAVIYAFRGGVRHNRMLEKIASK 376

>gb|AAX95687.1| RNase H, putative [Oryza sativa Japonica Group]  
Length = 1775

Score = 83.6 bits (205), Expect = 8e-14  
Identities = 44/132 (33%), Positives = 68/132 (51%)  
Frame = +1

Query: 1315 PNFKVSNNVSKYERKQDLGGWLAIYTIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQH 1494  
P F+ + KY+ + +L +YT AAG + VM +FP+ L A WL +LP  
Sbjct: 235 PRFRPTIAEKYDGSVNPAEFLQVYTTGIEAAGGDDRVMANFFPMALKGQARGWLMNLPPA 294

Query: 1495 CIDNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEVAEA 1674  
+ +W D F NFQ + +P + DL ++ + DE+LR Y++RF +RN P +  
Sbjct: 295 SVHSWEDLCQQFTMNFQGTYP RPGEADLHAVQRRDDESLRSYIQRFCQVRNTIPCIPAH 354

Query: 1675 GVIEDFYRGSND 1710  
VI F G +D  
Sbjct: 355 AVIYAFRGGGRHD 366

>gb|AAS07175.1| putative reverse transcriptase [Oryza sativa Japonica Group]  
gb|ABF97312.1| retrotransposon protein, putative, unclassified [Oryza sativa  
(japonica cultivar-group)]  
Length = 2002

Score = 83.6 bits (205), Expect = 8e-14  
Identities = 46/142 (32%), Positives = 70/142 (49%)  
Frame = +1

Query: 1315 PNFKVSNNVSKYERKQDLGGWLAIYTIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQH 1494  
P F+ + KY+ + +L IYT AAG + VM +FP+ L A WL +LP

Sbjct: 235 PRFRPTITEKYDGSVNPAEFLQIYTTGIEAAGGDDRVMANFFPMALKGQARGWLMNLPPA 294

Query: 1495 CIDNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEVAEA 1674  
 + +W D F NFQ + +P + DL ++ + DE+LR Y++RF +RN P +

Sbjct: 295 SVHSWEDLCQQFTMNFQGTYP RPGE EADLHAVQRRDDESLRSYIQRFCQVRNTIPCIPAH 354

Query: 1675 GVIEDFYRGSNDSAFVRAILQK 1740  
 VI F G + + I K

Sbjct: 355 AVIYAFRGGVRHNRMLEKIASK 376

>emb|CAD41940.2| OSJNBa0070M12.17 [*Oryza sativa* (japonica cultivar-group)]  
 Length = 1709

Score = 83.6 bits (205), Expect = 8e-14  
 Identities = 45/142 (31%), Positives = 70/142 (49%)  
 Frame = +1

Query: 1315 PNFKVSNSKYERKQDLGGWLAIYTI VTWAAGATEDVMTVYFPIVLGQDAMQWLRHL PQH 1494  
 P F+ + KY+ + +L +YT AAG + VM +FP+ L A WL +LP

Sbjct: 122 PRFRPTITEKYDGSVN PADFLQVYTTGIKAAGGDDRVMANFFPMALKGQARGWLMNLPLA 181

Query: 1495 CIDNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEVAEA 1674  
 + +W D F NFQ + +P + DL ++ + DE+LR Y++RF +RN P +

Sbjct: 182 SVHSWEDLCQQFTMNFQGTYP RPGE EADLHAVQRRNDESLRSYIQRFCQVRNTIPCIPAH 241

Query: 1675 GVIEDFYRGSNDSAFVRAILQK 1740  
 VI F G + + I K

Sbjct: 242 AVIYAFRGGVRHNRMLEKIASK 263

>emb|CAE03879.1| OSJNBb0015N08.7 [*Oryza sativa* (japonica cultivar-group)]  
 Length = 1975

Score = 83.6 bits (205), Expect = 8e-14  
 Identities = 45/142 (31%), Positives = 70/142 (49%)  
 Frame = +1

Query: 1315 PNFKVSNSKYERKQDLGGWLAIYTI VTWAAGATEDVMTVYFPIVLGQDAMQWLRHL PQH 1494  
 P F+ + KY+ + +L +YT AAG + VM +FP+ L A WL +LP

Sbjct: 235 PRFRATIAEKYDGSVNPAEFLQVYTTGIEAAGGDDRV MENFFPMALKGQARGWLMNLPPA 294

Query: 1495 CIDNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEVAEA 1674  
 + +W D F NFQ + +P + DL ++ + DE+LR Y++RF +RN P +

Sbjct: 295 SVHSWEDLCQQFTMNFQGTYP RPGE EADLHAVQRRDDESLRSYIQRFCQVRNTIPCIPAH 354

Query: 1675 GVIEDFYRGSNDSAFVRAILQK 1740  
 VI F G + + I K

Sbjct: 355 AVIYAFRGGVRHNRMLEKIASK 376

>gb|AAP46242.1| putative gag-pol precursor, 3'-partial [*Oryza sativa* Japonica Group]  
 Length = 948

Score = 83.6 bits (205), Expect = 8e-14  
 Identities = 46/144 (31%), Positives = 70/144 (48%)  
 Frame = +1

Query: 1315 PNFKVSNSKYERKQDLGGWLAIYTI VTWAAGATEDVMTVYFPIVLGQDAMQWLRHL PQH 1494  
 P F+ + KY+ + +L IYT V AAG+ + VM YFP+ L A WL P

Sbjct: 246 PKFRPNLTEKYDGSINPSEFLQIYTTVIVAAGSDDRV MANYFPMALKGQARGWLMTQPPG 305

Query: 1495 CIDNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEVAEA 1674

I +W D     FI NFQ   + +P +   DL ++   + DE+LR Y++ F   +RN   P +  
Sbjct: 306 SIHSWEDLCQQFITNFQGTYP RPGEEDLHAVRRKDDESLRSYIQHFCQVRNTIPCIPAH 365

Query: 1675 GVIEDFYRGSNDSAFVRAILQKSV 1746

          V+   F           +   +   I   K +  
Sbjct: 366 AVVYAFRNSVRHNRMLEKIASKEL 389

>gb|AA039874.1| putative gag-pol precursor [Oryza sativa Japonica Group]  
          Length = 1635

Score = 83.6 bits (205), Expect = 8e-14  
Identities = 46/144 (31%), Positives = 70/144 (48%)  
Frame = +1

Query: 1315 PNFKVSNSVSKYERKQDLGGWLAIYTIWTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQH 1494

          P F+ +   KY+   +   +L IYT V   AAG+ + VM   YFP+ L   A   WL   P  
Sbjct: 246 PKFRPNLTEKYDGSINPSEFLQIYTTVIVAAGSDDRVMANYFPMALKGQARGWLMTPPG 305

Query: 1495 CIDNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRLYLKRF\*TMRNHTPEVAEA 1674

          I +W D     FI NFQ   + +P +   DL ++   + DE+LR Y++ F   +RN   P +  
Sbjct: 306 SIHSWEDLCQQFITNFQGTYP RPGEEDLHAVRRKDDESLRSYIQHFCQVRNTIPCIPAH 365

Query: 1675 GVIEDFYRGSNDSAFVRAILQKSV 1746

          V+   F           +   +   I   K +  
Sbjct: 366 AVVYAFRNSVRHNRMLEKIASKEL 389

>gb|AAX96554.1| retrotransposon protein, putative, Ty3-gypsy sub-class [Oryza sativa  
          Japonica Group]  
gb|ABA93240.1| retrotransposon protein, putative, Ty3-gypsy subclass [Oryza sativa  
          (japonica cultivar-group)]  
          Length = 1701

Score = 83.6 bits (205), Expect = 8e-14  
Identities = 41/127 (32%), Positives = 65/127 (51%)  
Frame = +1

Query: 1321 FKVSNSVSKYERKQDLGGWLAIYTIWTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQH 1500

          FK + + KY+   +   WL +Y +   AAG   M   Y P+ L   A   WL   LP+   I  
Sbjct: 360 FKPTGIEKYDGTNPESWLTVYGLAIRAAGGDSKAMANYLPVALADSARSWLHGLPRGTI 419

Query: 1501 DNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRLYLKRF\*TMRNHTPEVAEAGV 1680

          +W++     FIANFQ   F+ P   +DL ++   +   E+L   Y++RF   RN   ++ + +  
Sbjct: 420 GSWAELRDHFIFIANFQGTFECPGTQFDLYNVIQKSRESLGDYIRRFSEQRNKISDITDDVI 479

Query: 1681 IEDFYRG 1701

          I   F +G  
Sbjct: 480 IAAFTKG 486

>emb|CAH67128.1| H0315E07.6 [Oryza sativa (indica cultivar-group)]  
          Length = 1891

Score = 83.2 bits (204), Expect = 1e-13  
Identities = 44/132 (33%), Positives = 67/132 (50%)  
Frame = +1

Query: 1315 PNFKVSNSVSKYERKQDLGGWLAIYTIWTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQH 1494

          P F+ +   KY+   +   +L +YT   AAG + VM   +FP+ L   A   WL +LP  
Sbjct: 235 PRFRPTIAEKYDGSVNPAEFLQVYTTGIEAAGGDDRVMANFFPMALKGQARGWLMNLP 294

Query: 1495 CIDNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRLYLKRF\*TMRNHTPEVAEA 1674

+ +W D     F   NFQ   + +P +   DL ++   + DE+LR Y++RF   +RN   P +  
Sbjct: 295   SVHSWEDLCQQFTMNFQGTYP RPGE EADLHAVQRRDDESLRSYIQRFCQVRNTIPCI PAH 354

Query: 1675   GVIEDFYRGSND 1710

          VI   F   G   D  
Sbjct: 355   AVIYA FRGGRRD 366

>emb|CAH67900.1| OSIGBa0115K01-H0319F09.6 [Oryza sativa (indica cultivar-group)]  
Length = 1917

Score = 83.2 bits (204), Expect = 1e-13  
Identities = 45/142 (31%), Positives = 70/142 (49%)  
Frame = +1

Query: 1315   PNFKVSNVSKYERKQDLGGWLAIYTIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQH 1494  
          P F+ +   KY+   +   +L +YT     AAG + VM   +FP+ L   A   WL +LP  
Sbjct: 229   PRFRPTIAEKYDGSVNPAEFLQVYTTGIEAAGDDRVMANFFPMALKGQARGWLMNLPPT 288

Query: 1495   CIDNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRLYLKRF\*TMRNHTPEVAEA 1674  
          + +W D     F   NFQ   + +P +   DL ++   + DE+LR Y++RF   +RN   P +  
Sbjct: 289   SVHSWEDLCQQFTMNFQGTYP RPGE EADLHAVQRRDDESLRSYIQRFCQVRNTIPCI PAH 348

Query: 1675   GVIEDFYRGSNDSAFVRAILQK 1740  
          VI   F   G   +   +   I   K  
Sbjct: 349   AVIYA FRGGVRHNRMLEKIASK 370

>emb|CAH67479.1| H0805A05.9 [Oryza sativa (indica cultivar-group)]  
Length = 1930

Score = 83.2 bits (204), Expect = 1e-13  
Identities = 45/142 (31%), Positives = 70/142 (49%)  
Frame = +1

Query: 1315   PNFKVSNVSKYERKQDLGGWLAIYTIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQH 1494  
          P F+ +   KY+   +   +L +YT     AAG + VM   +FP+ L   A   WL +LP  
Sbjct: 174   PRFRPTIAEKYDGSVNPAEFLQVYTTGIEAAGDDRVMANFFPMALKGQARGWLMNLP PA 233

Query: 1495   CIDNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRLYLKRF\*TMRNHTPEVAEA 1674  
          + +W D     F   NFQ   + +P +   DL ++   + DE+LR Y++RF   +RN   P +  
Sbjct: 234   SVHSWEDLCQQFTMNFQGTYP RPGE EADLHAVQRRDDESLRSYIQRFCQVRNTIPCI PAH 293

Query: 1675   GVIEDFYRGSNDSAFVRAILQK 1740  
          VI   F   G   +   +   I   K  
Sbjct: 294   AVIYA FRGGVRHNRMLEKIASK 315

>emb|CAH66280.1| OSIGBa0116004.2 [Oryza sativa (indica cultivar-group)]  
Length = 1465

Score = 83.2 bits (204), Expect = 1e-13  
Identities = 46/150 (30%), Positives = 73/150 (48%)  
Frame = +1

Query: 1252   PT\*RHVRSRLRTYSVSPGHPVAPNFKVS NVSKYERKQDLGGWLAIYTIVTWAAGATEDVMT 1431  
          P+ +H R   R   S   G     FK + + KY+   +   WL +Y +   AAG   M  
Sbjct: 300   PSLQH-RRRRIQSQEQGVDPAGFKPTRIEKYDGTNPESWLT VYGLAIHAAGGDNKAMA 358

Query: 1432   VYFPIVLGQDAMQWLRHLPQH CIDNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGET 1611  
          Y   + L   A   WL   LP+   I +W++   FIANFQ   F++P   +DL ++   +   E+  
Sbjct: 359   NYLLVALANSARSWLHGLPRGTIGSWAELRDHF IANFQGTFERPGTHFDLYNVIQKSGES 418

Query: 1612 LRLYLKRF\*TMRNHTPEVAEAGVIEDFYRG 1701  
LR Y++ F RN ++ + +I F +G  
Sbjct: 419 LRDYIRCFSEQRNKISDITDDVIIAAFTKG 448

>emb|CAH66724.1| OSIGBa0118P15.14 [Oryza sativa (indica cultivar-group)]  
Length = 1951

Score = 83.2 bits (204), Expect = 1e-13  
Identities = 45/142 (31%), Positives = 70/142 (49%)  
Frame = +1

Query: 1315 PNFKVSINVSKYERKQDLGGWLAIYTIWTAAAGATEDVMTVYFPIVLGQDAMQWLRHLPQH 1494  
P F+ + KY+ + +L +YT AAG + VM +FP+ L A WL +LP  
Sbjct: 235 PRFRPTIAEKYDGSVNPAEFLQVYTTGIEAAGGDDRVMANFFPMALKGQARGWLMNLPPA 294

Query: 1495 CIDNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRLYLKRF\*TMRNHTPEVAEA 1674  
+ +W D F NFQ + +P + DL ++ + DE+LR Y++RF +RN P +  
Sbjct: 295 SVHSWEDLCQQFTMNFQGTYPGEEADLHAVQRRDDESLRSYIQRFCQVRNTIPCIPIAH 354

Query: 1675 GVIEDFYRGSNDSAFVRAILQK 1740  
VI F G + + I K  
Sbjct: 355 AVIYAFRGGVRHNRMLEKIASK 376

>gb|ABA93826.2| retrotransposon protein, putative, unclassified [Oryza sativa  
(japonica cultivar-group)]  
Length = 1739

Score = 83.2 bits (204), Expect = 1e-13  
Identities = 45/142 (31%), Positives = 70/142 (49%)  
Frame = +1

Query: 1315 PNFKVSINVSKYERKQDLGGWLAIYTIWTAAAGATEDVMTVYFPIVLGQDAMQWLRHLPQH 1494  
P F+ + KY+ + +L +YT AAG + VM +FP+ L A WL +LP  
Sbjct: 122 PRFRPTITEKYDGSVNPAEFLQVYTTGIEAAGGDDRVMANFFPMALKGQARGWLMNLPPA 181

Query: 1495 CIDNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRLYLKRF\*TMRNHTPEVAEA 1674  
+ +W D F NFQ + +P + DL ++ + DE+LR Y++RF +RN P +  
Sbjct: 182 SVHSWEDLCQQFTMNFQGTYPGEEADLHAVQRRDDESLRSYIQRFCQVRNTIPCIPIAH 241

Query: 1675 GVIEDFYRGSNDSAFVRAILQK 1740  
VI F G + + I K  
Sbjct: 242 AVIYAFRGGVRHNRMLEKIASK 263

>gb|ABA91113.2| retrotransposon protein, putative, unclassified [Oryza sativa  
(japonica cultivar-group)]  
Length = 1981

Score = 83.2 bits (204), Expect = 1e-13  
Identities = 45/142 (31%), Positives = 70/142 (49%)  
Frame = +1

Query: 1315 PNFKVSINVSKYERKQDLGGWLAIYTIWTAAAGATEDVMTVYFPIVLGQDAMQWLRHLPQH 1494  
P F+ + KY+ + +L +YT AAG + VM +FP+ L A WL +LP  
Sbjct: 235 PRFRPTIAEKYDGSVNPAEFLQVYTTGIEAAGGDDRVMANFFPMALKGQARGWLMNLPPA 294

Query: 1495 CIDNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRLYLKRF\*TMRNHTPEVAEA 1674  
+ +W D F NFQ + +P + DL ++ + DE+LR Y++RF +RN P +  
Sbjct: 295 SVHSWEDLCQQFTMNFQGTYPGEEADLHAVQRRDDESLRSYIQRFCQVRNTIPCILAH 354

Query: 1675 GVIEDFYRGSNDSAFVRAILQK 1740

VI F G + + I K  
Sbjct: 355 AVIYAFRGGVRHNRMLEKITSK 376

>gb|ABF96026.1| retrotransposon protein, putative, unclassified [Oryza sativa  
(japonica cultivar-group)]  
Length = 1977

Score = 83.2 bits (204), Expect = 1e-13  
Identities = 45/142 (31%), Positives = 70/142 (49%)  
Frame = +1

Query: 1315 PNFKVSNSVSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQH 1494  
P F+ + KY+ + +L +YT AAG + VM +FP+ L A WL +LP  
Sbjct: 208 PRFRPTIAEKYDGSVNPAEFLQVYTTGIEAAGGDDRVMANFFPMALKGQARGWLMNLPPA 267

Query: 1495 CIDNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRLYLKRF\*TMRNHTPEVAEA 1674  
+ +W D F NFQ + +P + DL ++ + DE+LR Y++RF +RN P +  
Sbjct: 268 SVHSWEDLCQQFTMNFQGTYP RPGEADLHAVQRRDDESLRSYIQRFCQVRNTIPCI PAH 327

Query: 1675 GVIEDFYRGSNDSAFVRAILQK 1740  
VI F G + + I K  
Sbjct: 328 AVIYAFRGGVRHNRMLEKIASK 349

>gb|ABF95088.1| transposon protein, putative, unclassified [Oryza sativa (japonica  
cultivar-group)]  
Length = 1965

Score = 83.2 bits (204), Expect = 1e-13  
Identities = 45/142 (31%), Positives = 70/142 (49%)  
Frame = +1

Query: 1315 PNFKVSNSVSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQH 1494  
P F+ + KY+ + +L +YT AAG + VM +FP+ L A WL +LP  
Sbjct: 235 PRFRPTIAEKYDGSVNPAEFLQVYTTGIEAAGGDDRVMANFFPMALKGQARGWLMNLPPA 294

Query: 1495 CIDNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRLYLKRF\*TMRNHTPEVAEA 1674  
+ +W D F NFQ + +P + DL ++ + DE+LR Y++RF +RN P +  
Sbjct: 295 SVHSWEDLCQQFTMNFQGTYP RPGEADLHAVQRRDDESLRSYIQRFCQVRNTIPCILAH 354

Query: 1675 GVIEDFYRGSNDSAFVRAILQK 1740  
VI F G + + I K  
Sbjct: 355 AVIYAFRGGVRHNRMLEKIASK 376

>gb|ABF96139.1| retrotransposon protein, putative, unclassified [Oryza sativa  
(japonica cultivar-group)]  
Length = 260

Score = 83.2 bits (204), Expect = 1e-13  
Identities = 46/145 (31%), Positives = 70/145 (48%)  
Frame = +1

Query: 1306 PVA PNFKVSNSVSKYERKQDLGGWLAIYTIIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHL 1485  
P P F+ + KY+ + +L +YT AAG + VM +FP+ L A WL +L  
Sbjct: 27 PPYPFRPTIAEKYDGSVNPAEFLQVYTTGIEAAGGDDRVMANFFPMALRGQARGWLMNL 86

Query: 1486 PQHCIDNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRLYLKRF\*TMRNHTPEV 1665  
P + +W D F NFQ + +P + DL + + DE+LR Y++RF +RN P +  
Sbjct: 87 PPASVHSWEDLCQQFTMNFQGTYP RPGEADLHVQRRDDESLRSYIQRFCQVRNTIPCI 146

Query: 1666 AEAGVIEDFYRGSNDSAFVRAILQK 1740

VI F G + + I K  
Sbjct: 147 PAHAVIYAFRGGVRHNRMLEKIASK 171

>gb|ABF97875.1| retrotransposon protein, putative, unclassified [Oryza sativa  
(japonica cultivar-group)]  
Length = 1881

Score = 83.2 bits (204), Expect = 1e-13  
Identities = 53/180 (29%), Positives = 80/180 (44%)  
Frame = +1

Query: 1201 IKMTHNWLPSLGPTSRTPT\*RHVRSRLRTYSVSPGHPVAPNFKVSNVSKYERKQDLGGWLA 1380  
++ H P + P V SLR P F+ + KY+ + +L  
Sbjct: 203 LRSGHGGQPPVSPVGGAGCRAFAVSLRNVWRPP-----RFRPTITEKYDGSVNPAEFLH 256

Query: 1381 IYTIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCHIDNWSDFSWCFIANFQSLFDK 1560  
IYT AAG + VM +FP+ L A WL +LP + +W D F NFQ + +  
Sbjct: 257 IYTTGIEAAGGDDRVMANFFPMALKGQARGWLMNLPPASVHSWEDLCQQFTMNFQGTYPH 316

Query: 1561 PAQPWDLKSIGHQGETLRLYLKRF\*TMRNHTPEVAEAGVIEDFYRGSNDSAFVRAILQK 1740  
P + DL ++ + DE+LR Y++RF +RN P + VI F G + + I K  
Sbjct: 317 PGEEADLHAVQRRDDESLRSYIQRFCQVRNTIPCIPAHAVIYAFRGGVRHNYMLEKIASK 376

>gb|ABF98199.1| retrotransposon protein, putative, unclassified [Oryza sativa  
(japonica cultivar-group)]  
Length = 1887

Score = 83.2 bits (204), Expect = 1e-13  
Identities = 53/180 (29%), Positives = 79/180 (43%)  
Frame = +1

Query: 1201 IKMTHNWLPSLGPTSRTPT\*RHVRSRLRTYSVSPGHPVAPNFKVSNVSKYERKQDLGGWLA 1380  
++ H P + P V SLR P F+ + KY+ + +L  
Sbjct: 161 LRSGHGGRPPVSPVGGAGCRAFAVSLRNVWRPP-----RFRPTITEKYDGSVNPAEFLQ 214

Query: 1381 IYTIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQHCHIDNWSDFSWCFIANFQSLFDK 1560  
IYT AAG + VM +FP+ L A WL +LP + +W D F NFQ + +  
Sbjct: 215 IYTTGIEAAGGDDRVMANFFPMALKGQARGWLMNLPPASVHSWEDLCQQFTTNFQGTYPH 274

Query: 1561 PAQPWDLKSIGHQGETLRLYLKRF\*TMRNHTPEVAEAGVIEDFYRGSNDSAFVRAILQK 1740  
P + DL ++ DE+LR Y++RF +RN P + VI F G + + I K  
Sbjct: 275 PGEEADLHAVQRGDDDESLRSYIQRFCQVRNTIPCIPAHAVIYAFRGGVRHNRMLEKIASK 334

>gb|ABF95508.1| retrotransposon protein, putative, unclassified [Oryza sativa  
(japonica cultivar-group)]  
Length = 735

Score = 83.2 bits (204), Expect = 1e-13  
Identities = 45/142 (31%), Positives = 70/142 (49%)  
Frame = +1

Query: 1315 PNFKVSNNVSKYERKQDLGGWLAITYTIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQH 1494  
P F+ + KY+ + +L +YT AAG + VM +FP+ L A WL +LP  
Sbjct: 235 PRFRPTIAEKYDGSVNPAEFLQVYTTGIEAAGGDDRVMANFFPMALKGQARGWLMNLPPA 294

Query: 1495 CIDNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRLYLKRF\*TMRNHTPEVAEA 1674  
+ +W D F NFQ + +P + DL ++ + DE+LR Y++RF +RN P +  
Sbjct: 295 SVHSWEDLCQQFTMNFQGTYPHPRGEEADLHAVQRRDDESLRSYIQRFCQVRNTIPCIPAH 354

Query: 1675 GVIEDFYRGSNDSAFVRAILQK 1740

VI F G + + I K  
Sbjct: 355 AVIYAFRGGVRHNRMLEKIASK 376

>gb|ABF96344.1| retrotransposon protein, putative, unclassified [Oryza sativa  
(japonica cultivar-group)]  
Length = 1841

Score = 83.2 bits (204), Expect = 1e-13  
Identities = 45/142 (31%), Positives = 70/142 (49%)  
Frame = +1

Query: 1315 PNFKVSNSVSKYERKQDLGGWLAIYTIWTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQH 1494  
P F+ + KY+ + +L +Y AAG + VM +FP+ L A WL +LP  
Sbjct: 235 PRFRPTITEKYDGSVNPAEFLQVYMTGIEAAGGDDKVMANFFPMALKGQARGWLMNLPPA 294

Query: 1495 CIDNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRLYLKRF\*TMRNHTPEVAEA 1674  
+ +W D F NFQ + +P + DL ++ + DE+LRLY++RF +RN P +  
Sbjct: 295 SVHSWEDLCQQFTMNFQGTYPGEEADLHAVQRREDESLRLYIQRFCQVRNTIPCIPIAH 354

Query: 1675 GVIEDFYRGSNDSAFVRAILQK 1740  
VI F G + + I K  
Sbjct: 355 AVIYAFRGGVRHNRMLEKIASK 376

>gb|ABF93464.1| retrotransposon protein, putative, unclassified [Oryza sativa  
(japonica cultivar-group)]  
Length = 1037

Score = 83.2 bits (204), Expect = 1e-13  
Identities = 47/149 (31%), Positives = 72/149 (48%)  
Frame = +1

Query: 1294 SPGHPVAPNFKVSNSVSKYERKQDLGGWLAIYTIWTWAAGATEDVMTVYFPIVLGQDAMQW 1473  
S G P F+ + KY+ + +L +YT AAG + VM +FP+ L A W  
Sbjct: 198 SSGAPFRFGFRPTITEKYDGSVNPAEFLQVYTTGIEAAGGDDRVMANFFPMALKGQARGW 257

Query: 1474 LRHLPQH CIDNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRLYLKRF\*TMRNH 1653  
L +LP + +W D F NFQ + +P + DL ++ + DE+LR Y++RF +RN  
Sbjct: 258 LMNLPPASVHSWEDLCQQFTMNFQGTYPVEEADLHAVQRRDDESLRSYIQRFCQVRNT 317

Query: 1654 TPEVAEAGVIEDFYRGSNDSAFVRAILQK 1740  
P + VI F G + + I K  
Sbjct: 318 QPCIPAHAVIYAFRGGVRHNRMLENIASK 346

>gb|AAV32176.1| putative polyprotein [Oryza sativa Japonica Group]  
gb|AAV43954.1| putative polyprotein [Oryza sativa Japonica Group]  
Length = 1230

Score = 83.2 bits (204), Expect = 1e-13  
Identities = 45/142 (31%), Positives = 70/142 (49%)  
Frame = +1

Query: 1315 PNFKVSNSVSKYERKQDLGGWLAIYTIWTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQH 1494  
P F+ + KY+ + +L +YT AAG + VM +FP+ L A WL +LP  
Sbjct: 235 PRFRPTIAEKYDGSVNPAEFLQVYTTGIEAAGGDDRVMANFFPMALKGQARGWLMNLPPA 294

Query: 1495 CIDNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRLYLKRF\*TMRNHTPEVAEA 1674  
+ +W D F NFQ + +P + DL ++ + DE+LR Y++RF +RN P +  
Sbjct: 295 SVHSWEDLCQQFTMNFQGTYPGEEADLHAVQRRDDESLRSYIQRFCQVRNTIPCIPIAH 354

Query: 1675 GVIEDFYRGSNDSAFVRAILQK 1740



VI F G + + I K  
Sbjct: 355 AVIYAFRGGVRHNRMLEKIASK 376

>gb|AAV25049.1| putative polyprotein [Oryza sativa Japonica Group]  
Length = 1869

Score = 83.2 bits (204), Expect = 1e-13  
Identities = 45/142 (31%), Positives = 70/142 (49%)  
Frame = +1

Query: 1315 PNFKVSNSKYERKQDLGGWLAIYTIWTAAAGATEDVMTVYFPIVLGQDAMQWLRHLPQH 1494  
P F+ + KY+ + +L +YT AAG + VM +FP+ L A WL +LP  
Sbjct: 108 PRFRPTIAEKYDGSVNPAEFLQVYTTGIEAAGGDDRVMANFFPMALKGQARGWLMNLPPA 167

Query: 1495 CIDNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEVAEA 1674  
+ +W D F NFQ + +P + DL ++ + DE+LR Y++RF +RN P +  
Sbjct: 168 SVHSWEDLCQQFTMNFQGTYP RPGEADLHAVQRRDDESLRSYIQRFCQVRNTIPCI PAH 227

Query: 1675 GVIEDFYRGSNDSAFVRAILQK 1740  
VI F G + + I K  
Sbjct: 228 AVIYAFRGGVRHNRMLEKIASK 249

>gb|AAU44275.1| putative polyprotein [Oryza sativa Japonica Group]  
Length = 2027

Score = 83.2 bits (204), Expect = 1e-13  
Identities = 45/142 (31%), Positives = 70/142 (49%)  
Frame = +1

Query: 1315 PNFKVSNSKYERKQDLGGWLAIYTIWTAAAGATEDVMTVYFPIVLGQDAMQWLRHLPQH 1494  
P F+ + KY+ + +L +YT AAG + VM +FP+ L A WL +LP  
Sbjct: 235 PRFRPTIAEKYDGSVNPAEFLQVYTTGIEAAGGDDRVMANFFPMTLKGQARGWLMNLPPA 294

Query: 1495 CIDNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEVAEA 1674  
+ +W D F NFQ + +P + DL ++ + DE+LR Y++RF +RN P +  
Sbjct: 295 SVHSWEDLCQQFTMNFQGTYP RPGEADLHAVQRRDDESLRSYIQRFCQVRNTIPCI PAH 354

Query: 1675 GVIEDFYRGSNDSAFVRAILQK 1740  
VI F G + + I K  
Sbjct: 355 AVIYAFRGGVRHNRMLEKIASK 376

>gb|AAU44223.1| putative polyprotein [Oryza sativa Japonica Group]  
Length = 1823

Score = 83.2 bits (204), Expect = 1e-13  
Identities = 45/142 (31%), Positives = 70/142 (49%)  
Frame = +1

Query: 1315 PNFKVSNSKYERKQDLGGWLAIYTIWTAAAGATEDVMTVYFPIVLGQDAMQWLRHLPQH 1494  
P F+ + KY+ + +L +YT AAG + VM +FP+ L A WL +LP  
Sbjct: 235 PRFRPTITEKYDGSVNPAEFLQVYTTGIEAAGGDDRVMVNFFPMALKGQARGWLMNLPPA 294

Query: 1495 CIDNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEVAEA 1674  
+ +W D F NFQ + +P + DL ++ + DE+LR Y++RF +RN P +  
Sbjct: 295 SVHSWEDLCQQFTMNFQGTYP RPGEADLHAVQRRDDESLRSYIQRFCQVRNTIPCI PAH 354

Query: 1675 GVIEDFYRGSNDSAFVRAILQK 1740  
VI F G + + I K  
Sbjct: 355 AVIYAFRGGVRHNRMLEKIASK 376

>gb|AAU44127.1| putative polyprotein [Oryza sativa Japonica Group]  
Length = 1991

Score = 83.2 bits (204), Expect = 1e-13  
Identities = 45/142 (31%), Positives = 70/142 (49%)  
Frame = +1

Query: 1315 PNFKVSNSVSKYERKQDLGGWLAIYTIWTAAAGATEDVMTVYFPIVLGQDAMQWLRHLPQH 1494  
P F+ + KY+ + +L +YT AAG + VM +FP+ L A WL +LP  
Sbjct: 235 PRFRPTIAEKYDGSVNPAEFLQVYTTGIEAAGGDDRVMANFFPMALKGQARGWLMNLPPA 294

Query: 1495 CIDNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRLYLKRF\*TMRNHTPEVAEA 1674  
+ +W D F NFQ + +P + DL ++ + DE+LR Y++RF +RN P +  
Sbjct: 295 SVHSWEDLCQQFTMNFQGTYP RPGE EADLHAVQRRDDESLRSYIQRFCQVRNTIPCIPAH 354

Query: 1675 GVIEDFYRGSNDSAFVRAILQK 1740  
VI F G + + I K  
Sbjct: 355 AVIYAFRGGVRHNRMLEKIASK 376

>gb|AAT75253.1| putative gag-pol precursor [Oryza sativa Japonica Group]  
gb|ABF99259.1| retrotransposon protein, putative, unclassified [Oryza sativa  
(japonica cultivar-group)]  
Length = 1980

Score = 83.2 bits (204), Expect = 1e-13  
Identities = 45/142 (31%), Positives = 70/142 (49%)  
Frame = +1

Query: 1315 PNFKVSNSVSKYERKQDLGGWLAIYTIWTAAAGATEDVMTVYFPIVLGQDAMQWLRHLPQH 1494  
P F+ + KY+ + +L +YT AAG + VM +FP+ L A WL +LP  
Sbjct: 229 PRFRPTIAEKYDGSVNPAEFLQVYTTGIEAAGGDDRVMANFFPMALKGQARGWLMNLPPA 288

Query: 1495 CIDNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRLYLKRF\*TMRNHTPEVAEA 1674  
+ +W D F NFQ + +P + DL ++ + DE+LR Y++RF +RN P +  
Sbjct: 289 SVHSWEDLCQQFTMNFQGTYP RPGE EADLHAVQRRDDESLRSYIQRFCQVRNTIPCIPAH 348

Query: 1675 GVIEDFYRGSNDSAFVRAILQK 1740  
VI F G + + I K  
Sbjct: 349 AVIYAFRGGVRHNRMLEKIASK 370

>gb|AAT07608.1| putative polyprotein [Oryza sativa Japonica Group]  
gb|AAV59311.1| putative polyprotein [Oryza sativa Japonica Group]  
Length = 2021

Score = 83.2 bits (204), Expect = 1e-13  
Identities = 45/142 (31%), Positives = 70/142 (49%)  
Frame = +1

Query: 1315 PNFKVSNSVSKYERKQDLGGWLAIYTIWTAAAGATEDVMTVYFPIVLGQDAMQWLRHLPQH 1494  
P F+ + KY+ + +L +YT AAG + VM +FP+ L A WL +LP  
Sbjct: 235 PRFRPTIAEKYDGSVNPAEFLQVYTTGIEAAGGDDRVMANFFPMALKGQARGWLMNLPPA 294

Query: 1495 CIDNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRLYLKRF\*TMRNHTPEVAEA 1674  
+ +W D F NFQ + +P + DL ++ + DE+LR Y++RF +RN P +  
Sbjct: 295 SVHSWEDLCQQFTMNFQGTYP RPGE EADLHAVQRRDDESLRSYIQRFCQVRNTIPCIPAH 354

Query: 1675 GVIEDFYRGSNDSAFVRAILQK 1740  
VI F G + + I K  
Sbjct: 355 AVIYAFRGGVRHNRMLEKIASK 376

>gb|AAR06355.1| putative polyprotein [Oryza sativa Japonica Group]  
Length = 1809

Score = 83.2 bits (204), Expect = 1e-13  
Identities = 45/142 (31%), Positives = 70/142 (49%)  
Frame = +1

Query: 1315 PNFKVSNSVSKYERKQDLGGWLAIYTIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQH 1494  
P F+ + KY+ + +L +Y AAG + VM +FP+ L A WL +LP  
Sbjct: 235 PRFRPTITEKYDGSVNPAEFLQVYMTGIEAAGDDKVMANFFPMALKGQARGWLMNLPPA 294

Query: 1495 CIDNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEVAEA 1674  
+ +W D F NFQ + +P + DL ++ + DE+LRLY++RF +RN P +  
Sbjct: 295 SVHSWEDLCQQFTMNFQGTYP RPGEADLHAVQRRDESRLRYIQRFCQVRNTIPCIPAH 354

Query: 1675 GVIEDFYRGSNDSAFVRAILQK 1740  
VI F G + + I K  
Sbjct: 355 AVIYAFRGGVRHNRMLEKIASK 376

>gb|AAR01632.1| putative retrotransposon gag protein [Oryza sativa Japonica Group]  
gb|AAx95682.1| Retrotransposon gag protein, putative [Oryza sativa Japonica Group]  
gb|ABF98612.1| retrotransposon protein, putative, unclassified [Oryza sativa  
(japonica cultivar-group)]  
Length = 735

Score = 83.2 bits (204), Expect = 1e-13  
Identities = 45/142 (31%), Positives = 70/142 (49%)  
Frame = +1

Query: 1315 PNFKVSNSVSKYERKQDLGGWLAIYTIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQH 1494  
P F+ + KY+ + +L +YT AAG + VM +FP+ L A WL +LP  
Sbjct: 235 PRFRPTIAEKYDGSVNPAEFLQVYTTGIEAAGDDRVMANFFPMALKGQARGWLMNLPPA 294

Query: 1495 CIDNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEVAEA 1674  
+ +W D F NFQ + +P + DL ++ + DE+LR Y++RF +RN P +  
Sbjct: 295 SVHSWEDLCQQFTMNFQGTYP RPGEKADLHAVQRRDESLSYIQRFCQVRNTIPCIPAH 354

Query: 1675 GVIEDFYRGSNDSAFVRAILQK 1740  
VI F G + + I K  
Sbjct: 355 AVIYAFRGGVRHNRMLEKIASK 376

>emb|CAD40221.2| OSJNBa0019J05.19 [Oryza sativa (japonica cultivar-group)]  
Length = 1969

Score = 83.2 bits (204), Expect = 1e-13  
Identities = 45/142 (31%), Positives = 70/142 (49%)  
Frame = +1

Query: 1315 PNFKVSNSVSKYERKQDLGGWLAIYTIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQH 1494  
P F+ + KY+ + +L +YT AAG + VM +FP+ L A WL +LP  
Sbjct: 235 PRFRPTIAEKYDGSVNPAEFLQVYTTGIEAAGDDRVMANFFPMALKGQARGWLMNLPPA 294

Query: 1495 CIDNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEVAEA 1674  
+ +W D F NFQ + +P + DL ++ + DE+LR Y++RF +RN P +  
Sbjct: 295 SVHSWEDLCQQFTMNFQGTYP RPGEADLHAVQRRDESLSYIQRFCQVRNTIPCIPAH 354

Query: 1675 GVIEDFYRGSNDSAFVRAILQK 1740  
VI F G + + I K  
Sbjct: 355 AVIYAFRGGVRHNRMLEKIASK 376

>emb|CAE05289.2| OSJNBa0084N21.7 [Oryza sativa (japonica cultivar-group)]  
Length = 2023

Score = 83.2 bits (204), Expect = 1e-13  
Identities = 45/142 (31%), Positives = 70/142 (49%)  
Frame = +1

Query: 1315 PNFKVSNVSKYERKQDLGGWLAIYTIWTAAAGATEDVMTVYFPIVLGQDAMQWLRHLPQH 1494  
P F+ + KY+ + +L +YT AAG + VM +FP+ L A WL +LP  
Sbjct: 235 PRFRPTIAEKYDGSVNPAEFLQVYTTGIEAAGGDDRVMANFFPMALKGQARGWLMNLPPA 294

Query: 1495 CIDNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRLYLKRF\*TMRNHTPEVAEA 1674  
+ +W D F NFQ + +P + DL ++ + DE+LR Y++RF +RN P +  
Sbjct: 295 SVHSWEDLCQQFTMNFQGTYPGEEADLHAVQRRDDESLRSYIQRFCQVRNTIPCI PAH 354

Query: 1675 GVIEDFYRGSNDSAFVRAILQK 1740  
VI F G + + I K  
Sbjct: 355 AVIYAFRGGVRHNRMLEKIASK 376

>emb|CAE03695.2| OSJNBb0026E15.13 [Oryza sativa (japonica cultivar-group)]  
Length = 1952

Score = 83.2 bits (204), Expect = 1e-13  
Identities = 45/142 (31%), Positives = 70/142 (49%)  
Frame = +1

Query: 1315 PNFKVSNVSKYERKQDLGGWLAIYTIWTAAAGATEDVMTVYFPIVLGQDAMQWLRHLPQH 1494  
P F+ + KY+ + +L +YT AAG + VM +FP+ L A WL +LP  
Sbjct: 235 PRFRPTITEKYDGSVNPAEFLQVYTTGIEAAGGDDRVMANFFPMALKGQARGWLMNLPPA 294

Query: 1495 CIDNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGETLRLYLKRF\*TMRNHTPEVAEA 1674  
+ +W D F NFQ + +P + DL ++ + DE+LR Y++RF +RN P +  
Sbjct: 295 SVHSWEDLCQQFTMNFQGTYPGEEADLHAVQRRDDESLRSYIQRFCQVRNTIPCI PAH 354

Query: 1675 GVIEDFYRGSNDSAFVRAILQK 1740  
VI F G + + I K  
Sbjct: 355 AVIYAFRGGVRHNRMLEKIASK 376

>emb|CAE05493.2| OSJNBa0022H21.13 [Oryza sativa (japonica cultivar-group)]  
Length = 1993

Score = 83.2 bits (204), Expect = 1e-13  
Identities = 53/176 (30%), Positives = 80/176 (45%)  
Frame = +1

Query: 1213 HNWLP SLGPTSRTPT\*RHVRSRLRTYSVSPGHPVAPNFKVSNVSKYERKQDLGGWLAIYTI 1392  
H PS+ P V SLR P F+ + KY+ + +L +YT  
Sbjct: 207 HGDQPSVPPVGGVGCRAFVASLRNVRWPP-----RFRPTIAEKYDGSINPTEFLQVYTT 260

Query: 1393 VTAAAGATEDVMTVYFPIVLGQDAMQWLRHLPQH CIDNWSDFSWCFIANFQSLFDKPAQP 1572  
AAG + VM +FP+ L A WL +LP + +W D F NFQ + +P +  
Sbjct: 261 GIEAAGGDDRVMANFFPMALKGQARGWLMNLPPASVHSWEDLCQQFTMNFQGTYPGEE 320

Query: 1573 WDLKSIGHQGETLRLYLKRF\*TMRNHTPEVAEAGVIEDFYRGSNDSAFVRAILQK 1740  
DL ++ + DE+LR Y++RF +RN P + VI F G ++ + I K  
Sbjct: 321 ADLHAVQRRDDESLRSYIQRFCQVRNTMPCIPAHAVIYAFRGGVRHNSMLEKIASK 376

>emb|CAE04563.1| OSJNBb0039L24.2 [Oryza sativa (japonica cultivar-group)]  
emb|CAD41151.2| OSJNBa0081C01.21 [Oryza sativa (japonica cultivar-group)]

Length = 2027

Score = 83.2 bits (204), Expect = 1e-13  
Identities = 45/142 (31%), Positives = 70/142 (49%)  
Frame = +1

Query: 1315 PNFKVSNNVSKYERKQDLGGWLAIYITIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQH 1494  
P F+ + KY+ + +L +YT AAG + VM +FP+ L A WL +LP  
Sbjct: 235 PRFRPTIAEKYDGSVNPAEFLQVYTTGIEAAGGDDRVMANFFPMALKGQARGWLMNLPPA 294

Query: 1495 CIDNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEVAEA 1674  
+ +W D F NFQ + +P + DL ++ + DE+LR Y++RF +RN P +  
Sbjct: 295 SVHSWEDLCQQFTMNFQGTYPGEEADLHAVQRRDDESLRSYIQRFCQVRNTIPCIPAH 354

Query: 1675 GVIEDFYRGSNDSAFVRAILQK 1740  
VI F G + + I K  
Sbjct: 355 AVIYAFRGGVRHNRMLEKITSK 376

>gb|AAK26119.1|AC084406\_2 putative gag-pol precursor [Oryza sativa Japonica Group]  
Length = 1901

Score = 83.2 bits (204), Expect = 1e-13  
Identities = 53/180 (29%), Positives = 79/180 (43%)  
Frame = +1

Query: 1201 IKMTHNWLPSLGPTSRTPT\*RHVRSRLRTYSVSPGHPVAPNFKVSNNVSKYERKQDLGGWLA 1380  
++ H P + P V SLR P F+ + KY+ + +L  
Sbjct: 161 LRSGHGGRPPVSPVGGAGCRAFVASLRNVRWPP-----RFRPTITEKYDGSVNPAEFLQ 214

Query: 1381 IYITIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQH CIDNWSDFSWCFIANFQSLFDK 1560  
IYT AAG + VM +FP+ L A WL +LP + +W D F NFQ + +  
Sbjct: 215 IYTTGIEAAGGDDRVMANFFPMALKGQARGWLMNLPPASVHSWEDLCQQFTTNFQGTYP 274

Query: 1561 PAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEVAEAGVIEDFYRGSNDSAFVRAILQK 1740  
P + DL ++ DE+LR Y++RF +RN P + VI F G + + I K  
Sbjct: 275 PGEEADLHAVQRGDDESLRSYIQRFCQVRNTIPCIPAHAVIYAFRGGVRHNRMLEKIASK 334

>emb|CAD40917.1| OSJNBa0088K19.3 [Oryza sativa (japonica cultivar-group)]  
Length = 1882

Score = 83.2 bits (204), Expect = 1e-13  
Identities = 44/132 (33%), Positives = 67/132 (50%)  
Frame = +1

Query: 1315 PNFKVSNNVSKYERKQDLGGWLAIYITIVTWAAGATEDVMTVYFPIVLGQDAMQWLRHLPQH 1494  
P F+ + KY+ + +L +YT AAG + VM +FP+ L A WL +LP  
Sbjct: 235 PRFRPTIAEKYDGSVNPAEFLQVYTTGIEAAGGDDRVMANFFPMALKGQARGWLMNLPPA 294

Query: 1495 CIDNWSDFSWCFIANFQSLFDKPAQPWDLKSIGHQGDETLRLYLKRF\*TMRNHTPEVAEA 1674  
+ +W D F NFQ + +P + DL ++ + DE+LR Y++RF +RN P +  
Sbjct: 295 SVHSWEDLCQQFTMNFQGTYPGEEADLHAVQRRDDESLRSYIQRFCQVRNTIPCIPAH 354

Query: 1675 GVIEDFYRGSND 1710  
VI F G D  
Sbjct: 355 AVIYAFRGGRRD 366

Database: /usr/local/blast/db/blastlibs/nr  
Posted date: Apr 19, 2010 11:58 AM  
Number of letters in database: 3,701,345,023  
Number of sequences in database: 10,862,569

Lambda	K	H
0.318	0.134	0.401

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Sequences: 10862569

Number of Hits to DB: 13,237,956,592

Number of extensions: 317670085

Number of successful extensions: 931859

Number of sequences better than 10.0: 992

Number of HSP's gapped: 928605

Number of HSP's successfully gapped: 1011

Length of query: 622

Length of database: 3,701,345,023

Length adjustment: 144

Effective length of query: 478

Effective length of database: 2,137,135,087

Effective search space: 1021550571586

Effective search space used: 1021550571586

Neighboring words threshold: 12

Window for multiple hits: 40

X1: 16 ( 7.3 bits)

X2: 38 (14.6 bits)

X3: 64 (24.7 bits)

S1: 41 (21.7 bits)

S2: 33 (17.3 bits)