

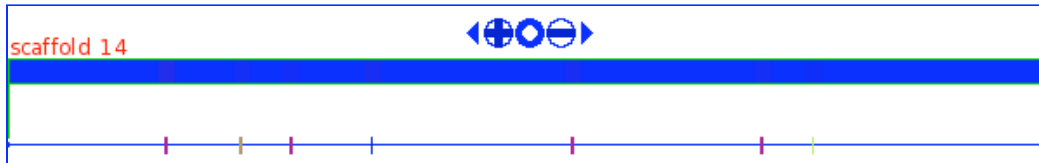


- [Home](#)
- [About GIRI](#)
- [Rebase](#)
- [Repeat Masking](#)
- [Repeat Maps](#)
- [Research](#)

Map of Hits

[SVG viewer](#) is required to view graphical representation of the map as Scalable Vector Graphics (SVG plot).

scaffold_14 ([SVG Plot](#); [Alignments](#); [Masked](#))



Name	From	To	Name	From	To	Class	Dir	Sim	Pos	Score
scaffold_14	15077	15235	MERMITED	1010	1152	DNA	c	0.7143	0.71	279
scaffold_14	22289	22373	Atlantys-2-1 OS	8527	8611	LTR/Gypsy	d	0.6824	0.68	301
scaffold_14	27104	27178	SHOOTER	11	81	DNA/EnSpm	d	0.7432	0.74	258
scaffold_14	34844	34948	BS1	1041	1145	Interspersed_Repeat	d	0.6981	0.70	301
scaffold_14	54126	54228	STOWAWAY50 OS	35	133	DNA	d	0.7624	0.76	302
scaffold_14	72308	72395	EnSpm-9 OS	5111	5189	DNA/EnSpm	c	0.7407	0.74	222
scaffold_14	77278	77331	TREP60	150	203	Simple/Sat/MSAT	d	0.8148	0.81	278

Masked Sequence

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TATCAGTGGGCTGAAGAGACTATACAGAACTACTTAAAGATGCTCCTCACATCAGTTACCTTCTCTAT
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FT      AAGALLRHPPVNPETPVQRWLDVANLVTTAQRQLATGGRSAATGTSRT
FT      PITLSSSARRRARRSATXSRRSTAPTSSGASGSRRRHDGLYGEQDARINIE
FT      RRRDERRAARMGEGASSSGVPRSSSRGGPPPTLTPGGTGCRAVVASLRNVR
FT      WPKFRPNLTKYDGSINPSEFLQIYTTIIIVAAGDDRMANYFFPMALKGQ
FT      ARGWLMTOQPPDSIHSWEDLCQOQFITNFOGTYPRPGEEADLHAVRRKDDDSL
FT      RSYIQRFQVRNTIPCIPAHAVVYAFRNGVRHNRMLEKIASKEPKTAELEF
FT      ELADKVARKEEAWAWNSPGTAAAAATPESAPRSKRDRRRGRKPARSDDE
FT      GHVLAADGPTRAPRKGKATGDKPSSSTAPSGEGRSADKWCSVHNTYRHSLAD
FT      CRSVKNLAEFRKADEEKQRREGKAPATSTGDRRGEAKNKAPADDGXDS
FT      EDLDFQIPOGTVATLDRGGGGACAHTSRRGFKAMRRELLAAVPTHEAARKA
FT      RWSEVKLTFDQSDHPTVLRGGKLLLVVSPTIHNVKMKRVLVDGGGPAGSG
FT      FPDTSGDRRHARPGGGGLRSHLSPRLQGHEARASGRXPHARGGPEGALVG
FT      GEHLRPERPSDGARSREVPGGLPDHPQRQDEACPGGRGGASLSIISPA
FT      AFDALKAPGMKLPSPLIIGVTPGHWTWPLGHVELPVTFGDSTNFRTERIDF
FT      DVADLNLPLYNALVGRPALVKFMAATHYAYLQMKMPGAPGITVFGDVKVAL
FT      ACAEQRADNLAVATEPQAPEASASRASKKRLTSADEVVKEIPLGDDPSKT
FT      AKIGGTLDAKESALVSFLRANSDFAWKPSDMPGVPREVIEHRLAVRPDAR
FT      PVRQKRRQAPERQAFIREVARLLEADFIREVIVPEWLANPVVVPKANGK
FT      LRMCIDYTDLNKACPKDPFLPRIDQIVDSTAGCDLLCFLDAYSQYHQIRM
FT      AREDEEKTAFITPVGTFCYTTMPFGLKNAGPTFORMTRITLSNQIGRNVEA
FT      YVDDL VVKTRHQDTLLQDLAETFDLSRSTRVKNLNPDKCVFVGPAGKLLGFL
FT      VSSRGIEANPEKIRAIERMPPSKLRDVQCVTGCMAALSRFISRLGERALP
FT      LFKLLKRSRGPFWTEEAQALNQLKAYLTSSPHLGSPGAGGTVATLLGRDP
FT      PCGECRPSKLTSPPPPILVAPGPEEPLLLYLAATPHVVSAAALVVEREEEXE
FT      PEAPLTRDGPSSPEGPVPKAPSPREDPEAPVGGGEALAGGPEAYDPEMVRD
FT      PPGAPEQGRPGSSAPDNTXRPKRKQRPVYFVSEALRDAKTRYPOAQKMLY
FT      AVLMASRKLRYFQAHRSVVTSYPLGQILHNREGTGRVVKWAIELAEFDL
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FT      ELRHVPRRDNTVADELSRVASARAPLPPGTFEERLAQPSARPNPSRDPNDT
FT      PSAPTGDPRASGPEGVDPPRQVVMWTDIRAYLDGNTLPEDRAEAEKLA
FT      RISKRYVLVEGTYRRAANGILLKCSREQIELIADAHQGECEGASASRT
FT      LVGKAFRQGFYWPTALQDAQEWVRRCKACQFHAKQTHQPAQALQVIPLSWP
FT      FAVWGLDILGPFKAARGGYQHLYVAIDKFTKWPEAYPVVKIDKHSALKFIR
FT      GITSRFGVPNRIITDNGTQFTSELFQDYCDMGIKLFCFASPAPKSNQOQE
FT      RANAELKGLKTKTYNVLKKHGDSWLEELPAVLWANRTTPSRATGETPFFL
FT      VYGAEAVLPSELGLSPRVALYNEANQDDLRRDDLDYLEERRRRAALRAAR
FT      YQOQLRRYHQRHVRARSLQVGDVLVLRVQSRGLGLSKLSPMWEQPYKIVGVP
FT      RPGSVRLTTEDGTLPNPNWIEHLRRFYF"

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XX
SQ Sequence 10783 BP; 1856 A; 3675 C; 3354 G; 1831 T; 67 other;

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ID      BS1          rebase; DNA      ; PLN      ; 3203 BP.
XX
AC      M25397;
XX
DT      11-NOV-1996 (Rel. 1.1, Created)
DT      11-NOV-1996 (Rel. 1.1, Last updated, Version 1)
XX
DE      Maize transposon Bs1.
XX
KW      BS1; insertion element; transposon.
XX
OS      Zea mays
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC      PACCAD clade; Panicoideae; Andropogoneae; Zea.
XX
RN      [1]
RP      1-3203
RA      Jin K.Y., Bennetzen L.J.;
RT      "The structure and coding properties of Bs1, a maize
RT      retrovirus-like transposon.";
RL      Proc. Natl. Acad. Sci. U.S.A 86, 6235-6239 (1989).
XX
DR      GenBank; M25397; Positions      1      3203.
XX

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SQ   Sequence 3203 BP; 738 A; 813 C; 870 G; 782 T; 0 other;

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ID   EnSpm-9_OS   rebase; DNA   ; PLN   ; 8955 BP.
XX
AC   TREP3418;
XX
DT   21-JUL-2008 (Rel. 13.09, Created)
DT   11-SEP-2008 (Rel. 13.09, Last updated, Version 1)
XX
DE   EnSpm element from Oryza sativa - a consensus sequence.
XX
KW   EnSpm; DNA transposon; Transposable Element; CACTA; TIR;
KW   transposon; DNA; DTC_Baldur_consensus-1; TREP3418; EnSpm-9_OS.
XX
OS   Oryza sativa
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC   BEP clade; Ehrhartoideae; Oryzeae; Oryza.
XX
RN   [1]
RP   1-8955
RA   Wicker T.;
RT   "EnSpm element from Oryza sativa.";
RL   Direct Submission to Repbase Update (10-SEP-2008).
XX
DR   TREP; TREP3418; Positions      1      8955.
XX
FH   Key          Location/Qualifiers
FT   CDS           1527..3722
FT               /product="EnSpm-9_OS_1p"
FT               /translation="MTSREWMYSGWTRGKAPTNEWIDNTTQFLNRAFSMQE
FT               VVKDGTIKCPAQCRNYFRHKRDTIELHLCKYGYKENYGIWTSHERPVIN
FT               DNDPGPSLIDHEGFGESDRMDNMLVDLASAQPPESSEPAHYAKAFYRMVA
FT               SADELIHENTHSCLSAVARLLAMKSQYNMSVAHYDDVLGIHEFLPPESK
FT               LAKDFYRSKLLLEGLGMPYVKIDVCYNNCMLYKEDHEHKEKDFCGTSRYE
FT               NGQNKTPRKVLRYPKIDRLQRLYAHEE IARLLQSHSRSQSGNMVHPCDGE
FT               AWQQFDEDFQDFAQDPRNVRLALATDGFTPYSLGAAPYSCWPVFI TPLNFP
FT               PGVCMRPEYTF LTLVIPGPEHPGKKLSVLMQPLVDELLKLWEGVETWDASR
FT               KQNFMTRAIFLWSIHDFPAYGIFAGWSTHGRLACPICMGDSQSFQLRNGRK
FT               PCWFDCHRRFLPNEHEFR TQLNAFRKNTFMLEPPRILTGE EIKEEMYACV
FT               DDTENFGKTHHWHTHISCFWQLPYFDKLRHNIDLMHNEKNVAESIWN TCF
FT               DIQDKTKDNVKARKDLAEICSRPLLQLVSKGNGKWHKPRASF CIDRNDKTT
FT               ILKWFQELKFPDGYAANIRRGVNLLQRKIFGLKSHDYHVFMERLLPVAFRG
FT               FIPESVWKCLAELSFFYRQLCAKELNKDTIRSL EENVAVLICKLEKIFPPG
FT               FFNPMQHLLIIHLPYEARLGGPVQFRWNYPYER"
XX
SQ   Sequence 8955 BP; 2754 A; 1630 C; 1847 G; 2724 T; 0 other;

//
ID   MERMITED     rebase; DNA   ; PLN   ; 1572 BP.
XX
AC   .
XX
DT   06-NOV-2002 (Rel. 7.1, Created)
DT   06-NOV-2002 (Rel. 7.1, Last updated, Version 1)
XX
DE   Rice non-autonomous DNA transposon MERMITED - a consensus.
XX
KW   DNA transposon; Transposable Element; Nonautonomous; MERMITED;
KW   target site duplication.
XX
OS   Oryza sativa
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC   BEP clade; Ehrhartoideae; Oryzeae; Oryza.
XX
RN   [1]
RA   Tarchini R., Biddle P., Wineland R., Tingey S., Rafalski A.;

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RT "The complete sequence of 340 kb of DNA around the rice Adh1-adh2
RT region reveals interrupted colinearity with maize chromosome 4.";
RL Plant Cell 12(3), 381-391 (2000).
XX
RN [2]
RP 1-1572
RA Jurka J., Drazkiewicz A.;
RT "MERMITED: a non-autonomous DNA transposon from Oryza sativa.";
RL Direct Submission to Repbase Update (29-MAR-2002).
XX
CC [2] (Consensus)
XX
CC 8bp target site duplications.
XX
SQ Sequence 1572 BP; 253 A; 570 C; 505 G; 244 T; 0 other;

//
ID SHOOTER rebase; DNA ; PLN ; 5060 BP.
XX
AC AF136220;
XX
DT 30-MAY-2000 (Rel. 5.04, Created)
DT 30-MAY-2000 (Rel. 5.04, Last updated, Version 1)
XX
DE Zea mays transposon Shooter; putative transposase protein (Sho)
DE gene, partial cds.
XX
KW EnSpm; DNA transposon; Transposable Element; En/Spm superfamily;
KW SHOOTER.
XX
OS Zea mays
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
XX
RN [1]
RP 1-5060
RA Panavas T., Weir J., Walker L.E.;
RT "The structure and paramutagenicity of the R-marbled haplotype of
RT Zea mays.";
RL Genetics 153(2), 979-991 (1999).
XX
RN [2]
RP 1-5060
RA Panavas T., Weir J., Walker L.E.;
RT "SHOOTER.";
RL Direct Submission to Genbank (19-MAR-1999)Biology, U of
RL Massachusetts, Amherst, MA 01003, USA.
XX
DR GenBank; AF136220; Positions 1 5060.
XX
SQ Sequence 5060 BP; 1605 A; 953 C; 1093 G; 1409 T; 0 other;

//
ID STOWAWAY50_OS rebase; DNA ; PLN ; 174 BP.
XX
AC .
XX
DT 06-NOV-2002 (Rel. 7.1, Created)
DT 06-NOV-2002 (Rel. 7.1, Last updated, Version 1)
XX
DE Rice non-autonomous DNA transposon STOWAWAY50_OS - a consensus.
XX
KW DNA transposon; Transposable Element; Nonautonomous;
KW STOWAWAY50_OS; target site duplication.
XX
OS Oryza sativa
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

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OC  BEP clade; Ehrhartoideae; Oryzeae; Oryza.
XX
RN  [1]
RA  Bureau E.T., Wessler R.S.;
RT  "Stowaway: a new family of inverted repeat elements associated
RT  with the genes of both monocotyledonous and dicotyledonous
RT  plants.";
RL  Plant Cell 6(6), 907-916 (1994).
XX
RN  [2]
RP  1-174
RA  Jurka J., Drazkiewicz A.;
RT  "STOWAWAY50_OS: a non-autonomous DNA transposon from Oryza
RT  sativa.";
RL  Direct Submission to Repbase Update (01-APR-2002).
XX
CC  [2] (Consensus)
XX
CC  MITE, TA target site duplications.
XX
SQ  Sequence 174 BP; 71 A; 18 C; 17 G; 68 T; 0 other;

//
ID  TREP60      rebase; DNA      ; PLN      ; 334 BP.
XX
AC  Z50100;
XX
DT  16-OCT-2002 (Rel. 7.09, Created)
DT  16-OCT-2002 (Rel. 7.09, Last updated, Version 1)
XX
DE  Hordeum vulgare microsatellite DNA, TREP60.
XX
KW  MSAT; Satellite; Simple Repeat; GAA repeats; Repetitive sequence;
KW  TREP60; microsatellite; tandem repeat.
XX
OS  Hordeum vulgare
OC  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC  BEP clade; Pooideae; Triticeae; Hordeum.
XX
RN  [1]
RA  Pedersen C., Rasmussen K.S., Linde-Laursen I.;
RT  "Genome and chromosome identification in cultivated barley and
RT  related species of the Triticeae (Poaceae) by in situ
RT  hybridization with the GAA-satellite sequence.";
RL  Genome 39(1), 93-104 (1996).
XX
RN  [2]
RA  Pedersen C.;
RT  "Direct submission.";
RL  Direct Submission to Repbase Update (from TREP) (02-APR-2002)..
XX
DR  Genbank; Z50100; Positions      1      334.
XX
SQ  Sequence 334 BP; 213 A; 1 C; 115 G; 5 T; 0 other;

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Summary Table

Repeat Class	Fragments	Length
Simple Repeat	1	54
Satellite	1	54
MSAT	1	54

Transposable Element	5	510
DNA transposon	4	425
EnSpm	2	163
LTR Retrotransposon	1	85
Gypsy	1	85
Total	7	669

* alignment score for local alignment may not always be equal to alignment score in map of hits because of use of heuristics for stitching fragments reported in map section, and use of different [wu-blast](#) parameters on stage of search and stage of producing local alignments.

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