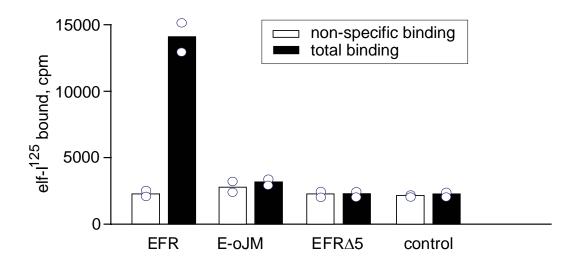


Suppl. Fig. 1. Expression of GFP-tagged EFR variants in *N. benthamiana* leaves. GFP-tagged EFR, EFR-variants and EFR-FLS2 chimeras were expressed in *N. benthamiana* leaves and expression was monitored after ~36-48 h with a fluorescence microscope. Pictures show typical epidermal cells from the lower surface of the leaf. Bar indicates $10 \,\mu\text{m}$.



Suppl. Fig. 2. Binding of elf-I¹²⁵ to binding sites adsorbed to ConA-beads. Leaves of *N. ben-thamiana* expressing intact or truncated forms of EFR were extracted by solubilization in 25 mM Tris pH 8.0, 150 mM NaCl, 1% (w/v) Nonidet NP40 and 0.5% (w/v) Deoxycholate. Glyco-proteins were absorbed to ConA-beads (Sigma). Binding of elf-I¹²⁵ was determined in the absence (total binding) or presence (non-specific binding) of 1 μ M unlabeled elf18. Measurements were done in duplicate with bars indicating the mean of the two values.

A signal peptide	FLS2 1 kl-1sktflitltffffgiala 23 . . . EFR 1 klsfslvfnaltllqvcifaqa 24
LRRNT	FLS2 qsfepeiealksfkngis-ndplgvlsdwtiigslrhanwtgitöd-stghvvsvsllekqlegv ::::::::::::::::::::::::
LRR domain	
FLS2 s EFR s	LERI LERI LERI LERI LERI LERI LERI LERI
FLS2 v EFR v	LRR4 LRR5 LRR5 LRR5 LRR6 ^{FO/E} esickssivligfdymnitgk ipecigdivligmfungs prosigtianitdidisgrq1tgk isisis
FLS2	LRR25
EFR	LRR7 to LRR24 prslqacknvftldfsgnnlsgn LRR7 to LRR17 fpeevgkleling(sasynklsgk LRR8
FLS2	LRR26 LRR27 LRR28 devrqumdmiislnisrnsfsge ipgsfunnthlvsldissnitge ipgslantlikhklasnikuh
outer juxtamembrane	domain transmembrane domain
FLS2 V	pesgvfkninasdlmgntdlegskkplkpctikqksshfskrtr vil-iilgsaaalllvlllvliltcc 831 .: : :. :: . : .:: : :. .: .:. ::
	pttgvfrnatavsvfgntnicggvremqlkpcivqasprkrkplsvrkk vvsgicigiasllliiivaslcwfm 674
в	E-21/F E-oJM/F
inner juxtamembrane dom	in kinase domain>
FIS2 832 KKREKKIENSESSESDDDUSALKLARFERKELEGATDERNSAHIGSSELTYKGCI-DECTVINVEVINLEKERSESDEMYTAR EFR 675 KREKKINASIONSEDSTILAMFEKVEVEELEASTESSESTILISSENFUNFEGLIGPENKUNVEVINLEKERSESDEMPAAC ELI 667 REKKINKEINNETDSTLEVLHEKISYCILENAINCESSENULSSENFUTYSALI-DECKUVAVUNUKUKERSENPAAC PEDRI 794 PARKCEPEKVAN PARKCEPEKVAN BEII 854 KEALSINL	
EFR ETFKGTRRRNINKLITM ELI ESIKDIRHRNINKLITM PEDRI DIGKVRRRNINIILGEF BRII ETIGKNKRRNINSLIGY PSKRI ETIGKNKRPNUNSLIGY PSKRI ETISRAGHPNIVILRGF BAM2 OTIGRIRRRHIVELIGFT HAESA ETIGTRRKSIVELMOOD	RESCRITEAL FULPHENRICH EDTIMGSAAP TOSLERID (CVHILSGIDYHHSCVOPP UP DIVE DURANILLISD SSLDSEGNÜFRALDIS HYKGS LIMH OLEDLERNNDHSRS: TPAEKINI ALDV SALEYI MUH HUP TAC DURS WILLOD SSIDDORNE FRALTISH INKSL IMM HIP EVEN HINSSRITTLEBILMI ALDVA SVLD FLIMH HEP TAK DURS MULD LRKDC MILGYI HKSS IVM HIP EVEN HINSSRITTLEBILMI ALDVA SVLD FLIMH HEP TAK DURS MULD SSIDDORNE FRALTISH INKSL IMM HIP EVEN HINSSRITTLEBILMI ALDVA SVLD FLIMH HEP TAK DURS MULD SSIDDORNE FRALTISH INKSL IMM HIP EVEN HINSSRITTLEBILMI ALDVA SVLD FLIMH HEP TAK DURS MULD SSIDDORNE FRALTISH HINSSL IMM HIP EVEN HINSSRITTLEBILMI ALDVA SVLD FLIMH HEP TAK DURS MULD SSIDDORNE FRALTISH HINSSL IMM HIP EVEN HINSSRITTLEBILMI ALDVA SVLD FLIMH HINSSRITTLISH SSIDDORNE FRALTISH HINSSL IMM HINSSRITTLEBILMI ALDVA SVLD FLIMH SSIDTLISH SSIDDORNE FRALTISH HINSSL IMM HINSSRITTLEBILMI ALDVA SVLD FLIMH SSIDTLISH SSIDDORNE FRALTISH HINSSL IMM HINSSRITTLEBILMI ALDVA SVLD FLIMH SSIDTLISH SSIDDORNE FRALTISH SSIDTLESS SSIDTLESS SSIDTLESS SSIDTLESS SSIDTLISH HINSSRITTLESS SSIDDORNE FRALTISH SSIDTLESS SSIDTLESS SSIDTLESS SSIDTLISH SSIDTLING SSIDTLISH SSIDTLESS SSIDTLESS SSIDTLESS SSIDTLESS SSIDTLESS SSIDTLESS SSIDTLESS SSITTLISS SSITTLISS
FLS2 RVARVSDRGTARILGFREDGS-TTATSTAFFCTIFVLAPEFAYRGKVTTKADVFSBGTIFMEUMEKONETSL-NEDEDGONTLGDLVESSIGNRAG ERF LIAAVSDRGTARILGFREDGS-TTATSTAFFCTIFVLAPEFAYRGKPOFICOUVFSBGTIFLEFAFGKGTDESFAGDYNLBFYKSISGESGS	
EFR GGSNA] ELI IVDES-ILHIGLRVGFPV	EEAIEDFLKLCLFUTSSRØEDROMNEILTHIMKLRGKANSFREDRNEDREV 1173 DEGLELVLQVCIKCSEEVIRDRARTDERVREIISIRSKFFSKTITIESPRDAPQSSPQEWMLNTDMHTM 1031 VECLTMVFEVGLRGCEESEMMRLATSIVVKEIISIRERFFKASRITWR 1010 REQVMVVTELALSTQODARMETMRDAVKLEDVKHLARSCSSDSVR
BRI1VFDPELMKEDPAL EMS1 AVDVIDPLLVSVALKNSC	EIELLQHLKVAVACLDDRAWRRPTMVQVMANFKEIQAGSGIDSQSTIRSIEDGGFSTIEMVDMSIKEVPEGKL 1196 LRLLQIAMLCLAETPAKRPNMLDVLKA <mark>L</mark> KEI
PSKR1EVFDPLIYSKEN BAM2 VLKVIDLRLSSVEN HAESA LEPVIDPKLDLKFM	DKEMERVLËTACLILSENEKOSTTOOUUSWIDOV INEVTNEVYLALUVEROXEPTMEEVVOITEIPKIPLSKQQAAESDVTEKAPAINESSPDGSSPPDLLSN 1002 -EEISKVIHIGLLITSPLEINE SHRKVVIM QEVSGAVPCSSPNTSKREKTOCKLSPYTTELNSV 999 DEEVEQLIQVALLITOSSIMEPDYMSEVVPMICGDGLAERWEENGKEEMFRQDFNYPTHHPAVSGWIIGDSTSQIENEYPSGPR 615

Suppl. Fig. 3. Sequence comparisons. A) Comparison of the ectodomains from EFR and FLS2. Residues that correspond to the consensus of plant LRRs and the conserved cysteine pairs in the LRRNT and the outer juxtamembrane domain are shaded in grey, positions used for swapping in the different chimeric receptors are indicated in red. B) Comparison of the cytoplasmic domains from a subgroup of RLKs attributed with the induction of defense responses [dark blue shading: EFR (At5g20480), FLS2 (At5g46330), ELI (EFR-like, the closest homolog of EFR At3g47570) and PEPR1 (At1g73080)] with six additional RLKs that have well characterized functions in regulation of processes other than defense responses [light blue shading: BRI1, At4g39400; EMS1, At5g07280; PSKR1, At2g02220; BAM2 At3g49670; BAK1, At4g33430; HAESA, At4g28490]. Light green and green shading indicate positions with high and very high conservation in all RLKs, respectively. EFR, FLS2 and ELI are so-called non-RD kinases while PEPR1 and the other kinases have RD at the position indicated by an asteriks.