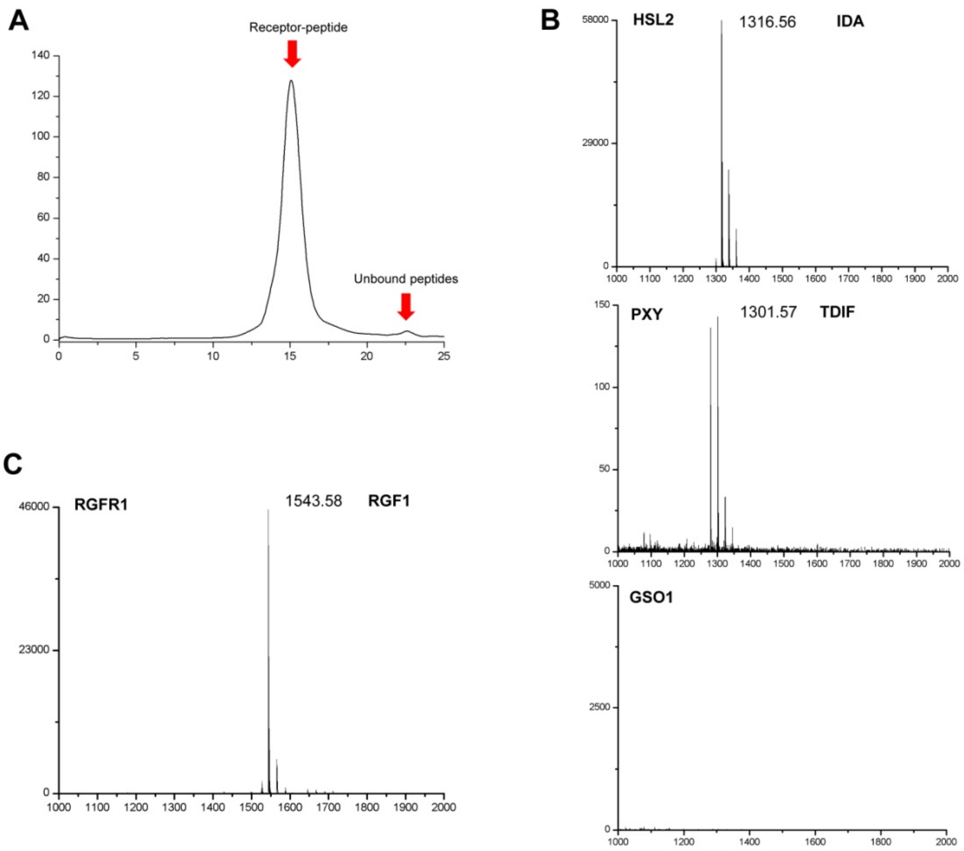

Figure S1 Identification of the LRR-RK At4g26540 as a receptor of RGF1 by Gel-filtration and MS.

(A) Gel-filtration chromatogram of the extracellular LRR domain protein of At4g26540 (RGFR1^{LRR}) and a pool of peptides. The red arrows indicate the elution positions of RGFR1^{LRR}-peptide and the unbound peptides. The vertical and horizontal axes represent UV absorbance (280 nm) and elution volume (ml) respectively. **(B)** MALDI-TOF MS of the peak fractions of HSL2^{LRR}-peptides, PXY^{LRR}-peptides and GSO1^{LRR}-peptides. The vertical and horizontal axes represent the intensity and molecular weight of MS, respectively. **(C)** MALDI-TOF MS of the peak fraction of RGFR1^{LRR}-peptide. The molecular weight of the peptide from the peak fraction (1543.58) as indicated is equivalent to the calculated weight (1623.64) of RGF1 with loss of the sulfate group (80.06).