

		<u>1st exon</u>	<u>2nd exon</u>	
<i>O. glaberrima</i>	1	MNPTTAAAADQPSKPS	AAAARKRKSSAKPKASSSSLPTATAAT	NASPKRSKVAAGAGDD 59
<i>O. sativa</i>	1	MNPTTAAAADQPSKPSA	AAAARKRKSSAKPKASSSSLPTATAAT	TNASPKRSKVAAGAGDD 60
		Ins(GCC)	Sub(GCG -> ACG)	
			<u>3rd exon</u>	<u>4th exon</u>
<i>O. glaberrima</i>	60	GDGDADAAE EKPEPAKDYIHVRARRGQATDSHSLAERVRRERISERMKLLQLQSLVPGCNKI		119
<i>O. sativa</i>	61	GDADADAAE EKPEPAKDYIHVRARRGQATDSHSLAERVRRERISERMKLLQLQSLVPGCNKI		120
		Sub(GGC -> GCC)		
			<u>5th exon</u>	<u>6th exon</u>
<i>O. glaberrima</i>	120	TGKALMLDEIINYVQSLQRQVEFLSMKLATMNPQLDFDSHYMPSKDMSHMPVPAYPSGDP		179
<i>O. sativa</i>	121	TGKALMLDEIINYVQSLQRQVEFLSMKLATMNPQLDFDSHYMPSKDMSHMPVPAYPSDDP		180
			Sub(GGC -> AGC)	
<i>O. glaberrima</i>	180	TTTTAFSYTGSPATADPFTVYNCWELDLHTAMQMGATT	VGLSQDGPIATMAPSPSPLPHH	239
<i>O. sativa</i>	181	TTTTAFSYTGSPATADPFTVYNCWELDLHTAMQMGATT	GLSQDGPIATMAPSPSPLPHH	239
		<u>7th exon</u>	Del(TCG)	
<i>O. glaberrima</i>	240	PPLHGFYGGQQQQGTTVNHMKAEP		263
<i>O. sativa</i>	240	PPLHGFYGGQQQQGTTVNHMKAEP		263

Figure S1 Amino acid sequences of RAE1/An-1 in *O. glabeerima* and *O. sativa*

Amino acid sequences of RAE1/An-1 in *O. glaberrima* and *O. sativa* are aligned by ClustalW. Mutations in the DNA sequence are shown below the mutation sites. The thick gray bar under the aligned sequences represents a conserved bHLH domain. The thin black bars and gray bars above the aligned sequences indicate the region of exons.