

Table 7 The orthologous candidate genes of *ZIK4* in three species of Legume

Species	Gene name	ID No of gene	If the gene was Full-Length	Similarity	Evidence of EST
<i>Medicago truncatula</i>	<i>MtZIK4a</i>	AC171498_31	Yes	56.7%	E
	<i>MtZIK4b</i>	AC135565_12	Yes	56.9%	E
<i>Lotus japonicas</i>	<i>MtZIK4c</i>	AC202374_9	Yes	52.4%	E
<i>Glycine max</i>	<i>LjZIK4a</i>	LjB12P21_90_nc	Yes	55.3%	E
	<i>LjZIK4b</i>	chr5_CM0357_880_nc	Yes	50.6%	E
	<i>GmZIK4a</i>	Glyma20g37180	Yes	61.1%	E
	<i>GmZIK4b</i>	Glyma19g43210	Yes	57.6%	F
	<i>GmZIK4c</i>	Glyma03g40550	Yes	43.7%	F
	<i>GmZIK4d</i>	Glyma10g30210	Yes	53.5%	F
	<i>GmZIK4e</i>	Glyma10g39390	Yes	55.8%	E

Note: F: the whole candidate gene was covered by PUT sequence, or both ends were covered by PUT sequence and 80% of the whole gene sequences were covered by PUT sequence; E: a certain part or several parts of the gene were covered by suitable PUT sequence, but had not reached the standard of F