Table S4: SAMD9 and SAMD9L amino acid properties under positive selection determined in TreeSAAP

Protein	**Property**	**Category**[a]	**z-Score**[b]
SAMD9	Isoelectric point	8	8.218***
	Equilibrium constant (ionization of COOH)	8	5.001***
	Power to be at the C-terminal	7	4.032***
	Alpha-helical tendencies	6	5.581***
SAMD9L	Isoelectric point	8	6.922***
	Equilibrium constant (ionization of COOH)	8	4.797***
	Solvent accessible reduction ratio	7	4.366***
	Power to be at the middle of alpha-helix	7	3.554***
	Power to be at the C-terminal	6	10.442***
	Alpha-helical tendencies	6	5.228***
	Surrounding hydrophobicity	6	3.921***

[a] Between 6 and 8 (the most radical values denoting positive destabilizing selection).

[b] z-Score > 3.09, level of significance $p<0.001$ (***).