Table2 Tubulin mutants with helical growth phenotypes Root slanting Phenotype[†] Independent Transgene Mutagen **Tubulin Mutation** Position§ Ecotype angle* experiment[‡] isolates Col-0 -4 ± 3 TUA4 R2K 17 ± 6 strong Yes near GAR Col,Ler **EMS** 3 TUA2 T561 NT(R) Yes Lateral Col **EMS** 2 strong

TUA4	T56I	37 ± 4	strong	Yes	Lateral	Col	EMS	1
TUA6	T56I	22 ± 6	strong	Yes	Lateral	Col,WS	EMS	2
TUA4	V62I	25 ± 4	strong	Yes	Lateral	Col	EMS	1
TUA4	S178∆	-46 ± 5	medium	Yes	Intardimer	Col	T-DNA	1
TUA3	D205N	-16±4	weak	Yes	Others	Col	EMS	1
TUA5	D251N	31 ± 5	medium	Yes	GAR	Col	EMS	1
TUA4	M268I	52±5	medium	Yes	Lateral	Col	EMS	1
TUA4	S277F	35 ± 7	medium	Yes	Lateral	Col	EMS	1
TUA6	S277F	13 ± 4	weak	Yes	Lateral	Col,WS	EMS	3
TUA6	A281T	49 ± 6	medium	Yes	Lateral	Col	T-DNA	1

TUA4	M268I	52 ± 5	medium	Yes	Lateral	Col	EMS	1
TUA4	S277F	35 ± 7	medium	Yes	Lateral	Col	EMS	1
TUA6	S277F	13 ± 4	weak	Yes	Lateral	Col,WS	EMS	3
TUA6	A281T	49 ± 6	medium	Yes	Lateral	Col	T-DNA	1
TUA2	E284K	32 ± 8	medium	Yes	Lateral	Col	EMS	1
TUA6	P325S	44 ± 81	medium	Yes	Interdimer	Col	EMS	1
TUA2	T349I	-37 ± 8	medium	NT	Interdimer	Col	EMS	1
TUA4	T349I	NT (L)	strong	NT	Interdimer	Col	EMS	1
TUA3	R390W	-9±5	weak	Yes	Others	Col	EMS	1
TUB1	S96F	33+7	medium	Yes	Interdimer	Col	FMS	1

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TUA2	T349I	-37 ± 8	medium	NT	Interdimer	Col	EMS	1	
TUA4	T349I	NT (L)	strong	NT	Interdimer	Col	EMS	1	
TUA3	R390W	-9±5	weak	Yes	Others	Col	EMS	1	
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TUB1	S96F	33 ± 7	medium	Yes	Interdimer	Col	EMS	1	
TUB4	S95F	NT (R)	strong	Yes	Interdimer	WS	EMS	1	
TUB4	G96D	44 ± 6	medium	NT	Interdimer	Col	EMS	1	
TUB4	T178I	-47 ± 10	medium	Yes	Interdimer	Col	EMS	1	
TUB4	P220S	21 ± 6	medium	Yes	Interdimer	Col	EMS	1	
TUB2	C239Y	NT (L)	strong	Yes	Others	Col	EMS	1	
TUB1	G245E	NT (L)	medium	NT	Others	WS	EMS	1	
THDA	1.2500	30 - 1	modium	Voc	Intardimor	Col	EMC	1	

TUB1	S96F	33 ± 7	medium	Yes	Interdimer	Col	EMS	1
TUB4	S95F	NT (R)	strong	Yes	Interdimer	WS	EMS	1
TUB4	G96D	44 ± 6	medium	NT	Interdimer	Col	EMS	1
TUB4	T178I	-47 ± 10	medium	Yes	Interdimer	Col	EMS	1
TUB4	P220S	21 ± 6	medium	Yes	Interdimer	Col	EMS	1
TUB2	C239Y	NT (L)	strong	Yes	Others	Col	EMS	1
TUB1	G245E	NT (L)	medium	NT	Others	WS	EMS	1
TUB4	L250F	-30 ± 4	medium	Yes	Intardimer	Col	EMS	1
TUB2	P287L	8±5	strong	Yes	Lateral	Col	EMS	1
TUB3	P287L	32 ± 6	strong	Yes	Lateral	Col,WS	EMS	3
TUB4	P287L	NT (R)	strong	Yes	Lateral	Col	EMS	1
TUB4	E288K	-35 ± 8	strong	Yes	Lateral	Col	EMS	1

TUB4	P220S	21 ± 6	medium	Yes	Interdimer	Col	EMS	1
TUB2	C239Y	NT (L)	strong	Yes	Others	Col	EMS	1
TUB1	G245E	NT (L)	medium	NT	Others	WS	EMS	1
TUB4	L250F	-30 ± 4	medium	Yes	Intardimer	Col	EMS	1
TUB2	P287L	8±5	strong	Yes	Lateral	Col	EMS	1
TUB3	P287L	32 ± 6	strong	Yes	Lateral	Col,WS	EMS	3
TUB4	P287L	NT (R)	strong	Yes	Lateral	Col	EMS	1
TUB4	E288K	-35 ± 8	strong	Yes	Lateral	Col	EMS	1
TUB4	A302V	NT (L)	medium	NT	Interdimer	WS	EMS	1
TUB4	S351F	-37 ± 13	medium	Yes	Intardimer	Col	EMS	1

NT(L) NT WS **EMS** A394T medium Interdimer Root slanting angles toward the right side of the agar plates are shown. Minus angles indicate that the

roots skewed to the left. NT, slanting angles were not quantified. (R), right-handed twisting, (L), lefthanded twisting. [†]Severity of the cell expansion defects was arbitrarily classified into four groups; very strong, strong, medium, and weak. The weak-type mutants were semidominant in their growth responses to propyzamide, but their heterozygotes were indistinguishable in growth in the absence of the drug. [‡]"Yes" indicates that the mutant tubulin gene expressed in wild-type *Arabidopsis* plants reproduced the twisting phenotypes. NT; not tested.

§ Mutated residues were mapped on the tubulin heterodimer structure. "Lateral" positions indicate the

interacting regions between adjacent protofilaments. GAR; GTPase-activating region.