



Appendix A Genomic *in situ* hybridization analysis of root tip cells of wheat-*P.huashania* introgression line H148. In root tip cells of H148, 42 chromosomes were counterstained with DAPI (blue), and no chromosome fragment with green fluorescence signals was found by using *P. huashania* genomic DNA as the probe.

Appendix B The information of Kompetitive Allele Specific PCR (KASP) primers used to genotype F₂ individual plant for mapping the take-all resistance QTL in H148.

Probe ID	SNP Position	Primer Sequence (5'–3')	
		FAM+A	GAAGGTGACCAAGTTCATGCTgatcaccatgaatgacTttgtgC
AX-108769147	2A:52574077	HEX+B	GAAGGTCGGAGTCAACGGATTgatcaccatgaatgacTttgtgA
		Common	gCcagatgaaaacatccactaaT
		FAM+A	GAAGGTGACCAAGTTCATGCTcGgAcGGcTagagatTAattcAtT
AX-110444395	2A:68813311	HEX+B	GAAGGTCGGAGTCAACGGATTcGgAcGGcTagagatTAattcAtC
		Common	ctaccgcaccgagatctT
		FAM+A	GAAGGTGACCAAGTTCATGCTggacgtttgtgccgtgG
AX-111495892	2A:70032510	HEX+B	GAAGGTCGGAGTCAACGGATTggacgtttgtgccgtgC
		Common	CGAtaCtAcaaacgtctctGtC
		FAM+A	GAAGGTGACCAAGTTCATGCTgtatgattggtttctccAtgTtgT
AX-110582753	2A:116169618	HEX+B	GAAGGTCGGAGTCAACGGATTgtatgattggtttctccAtgTtgC
		Common	agtctttaactcaaccaTacaccA
		FAM+A	GAAGGTGACCAAGTTCATGCTacaagtcattatgatgacaggtA
AX-108849129	2A:178571864	HEX+B	GAAGGTCGGAGTCAACGGATTacaagtcattatgatgacaggtG
		Common	agccaaaagtgcaCtgcgA
		FAM+A	GAAGGTGACCAAGTTCATGCTgcgacacatgtgtaaagatGgG
AX-108981754	2A:182891486	HEX+B	GAAGGTCGGAGTCAACGGATTgcgacacatgtgtaaagatGgT
		Common	atcgacctaatctgtgagcA
		FAM+A	GAAGGTGACCAAGTTCATGCTcaaacgaactgacatgcctG
AX-109412276	2A:198754354	HEX+B	GAAGGTCGGAGTCAACGGATTcaaacgaactgacatgcctC
		Common	GctagaactggcctgtggG
		FAM+A	GAAGGTGACCAAGTTCATGCTaccggaaaagatgcaggacC
AX-110616107	2A:201797717	HEX+B	GAAGGTCGGAGTCAACGGATTaccggaaaagatgcaggacG

Probe ID	SNP Position	Primer Sequence (5'-3')
		Common cgcCacatcaccaTcaaaataCTA
		FAM+A GAAGGTGACCAAGTTCATGCTacttacttggtcatgtcaaccG
AX-109856076	2A:485045387	HEX+B GAAGGTCTGGAGTCAACGGATTacttacttggtcatgtcaaccA
		Common accacagatcactaatagagtcaaA
		FAM+A GAAGGTGACCAAGTTCATGCTctgcCgccgaaTgagacG
AX-111049184	2A:523864943	HEX+B GAAGGTCTGGAGTCAACGGATTctgcCgccgaaTgagacA
		Common agtaactgaagtgacaacaggaG
		FAM+A GAAGGTGACCAAGTTCATGCTgccttctcgccatttccG
AX-111205512	2A:602439035	HEX+B GAAGGTCTGGAGTCAACGGATTgccttctcgccatttccT
		Common cggaagccacaagatccaC