Table S5 Spectrum of mutations identified in the dwarfing candidate genes

Gene	Freq[a]	Position	WT_Nu[b]	Mu_Nu[c]	WT_AA[d]	Mu_AA[e]	Function[f]	SIFT[f]	Superpool	EMS[g]	Validation[h]
dw3a	5	89	A	G	E	G	missense	0	sp2	1.5%	
dw3a	7	104	C	T	P	L	missense	0	sp19	1.5%	
dw3a	3	200	A	G	N	S	missense	0	sp11	1.5%	
dw3a	17	238	A	G	S	G	missense	0.4	sp6	1.0%	
dw3a	19	503	C	T	A	V	missense	1	sp19	1.5%	YES
dw3a	11	582	C	T	R	R	silent	1	sp14	1.5%	
dw3a	6	628	A	T	T	S	missense	0	sp9	1.0%	
dw3a	3	677	T	A	V	D	missense	0	sp17	1.5%	
dw3a	3	730	G	A	A	T	missense	0.2	sp2	1.5%	
dw3a	10	742	G	A	A	T	missense	0	sp19	1.5%	YES
dw3a	3	838	G	A	A	T	missense	0.2	sp3	1.0%	
dw3a	6	840	G	A	A	A	silent	1	sp19	1.5%	
dw3a	9	863	G	A	R	Q	missense	0.1	sp11	1.5%	
dw3a	3	1023	G	A	G	G	silent	1	sp17	1.5%	
dw3a	6	1105	C	T	R	C	missense	0.1	sp14	1.5%	YES
dw3a	11	1124	G	A	G	D	missense	0	sp7	1.0%	
dw3a	4	1139	C	T	T	I	missense	0.1	sp7	1.0%	YES
dw3a	3	1177	C	T	Q	*	Stop codon	0	sp14	1.5%	NO
dw3a	9	1185	G	A	P	P	silent	1	sp9	1.0%	
dw3a	13	1189	A	T	S	C	missense	0.2	sp1	1.0%	
dw3a	5	1200	C	T	F	F	silent	1	sp14	1.5%	
dw3a	3	1228	A	G	K	E	missense	0	sp19	1.5%	
dw3a	4	1270	G	A	D	N	missense	0.5	sp16	1.5%	
dw3a	3	1294	A	G	T	A	missense	0.8	sp22	1.5%	
dw3a	8	1295	C	T	T	M	missense	0.1	sp14	1.5%	
dw3a	5	1315	G	A	G	S	missense	0.1	sp22	1.5%	
dw3a	10	1526	T	A	L	H	missense	0	sp17	1.5%	
dw3a	5	1564	C	T	L	L	silent	1	sp21	1.5%	
dw3a	9	1594	C	T	L	L	silent	1	sp21	1.5%	
dw3a	4	1606	G	A	D	N	missense	0.2	sp15	1.5%	
dw3a	7	1642	G	A	A	T	missense	0	sp23	1.5%	
dw3a	8	1811	G	A	S	N	missense	0	sp9	1.0%	
dw3a	3	1814	C	A	A	E	missense	0	sp15	1.5%	
dw3a	11	1840	G	A	V	M	missense	0	sp16	1.5%	
dw3a	3	1849	G	A	A	T	missense	0	sp2	1.5%	
dw3a	3	1960	A	T	I	F	missense	0.6	sp7	1.0%	
dw3a	4	1964	G	A	G	E	missense	0	sp23	1.5%	

dw3a	3	1999	G	A	G	S	missense	0.1	sp5	1.0%	
dw3a	3	2288	G	A	R	K	missense	0.2	sp17	1.5%	
dw3a	3	2451	G	A	Y	Y	silent	1	sp12	1.0%	
dw3a	6	2593	G	A	A	T	missense	0	sp14	1.5%	
dw3a	5	2855	C	T	A	V	missense	0	sp14	1.5%	
dw3a	3	2863	C	T	R	C	missense	0	sp6	1.0%	
dw3a	5	2867	C	T	A	V	missense	0	sp23	1.5%	
dw3a	3	2922	C	A	A	A	silent	1	sp10	1.0%	
dw3b	14	48	C	T	G	G	silent	1	sp18	1.5%	
dw3b	4	76	C	T	P	S	missense	0	sp18	1.5%	
dw3b	6	95	A	T	H	L	missense	0	sp15	1.5%	
dw3b	4	106	C	T	P	S	missense	0	sp20	1.5%	YES
dw3b	3	118	C	T	Q	*	Stop codon	0	sp19	1.5%	NO
dw3b	6	127	G	A	G	R	missense	0.2	sp21	1.5%	
dw3b	6	230	C	T	S	F	missense	0.1	sp18	1.5%	
dw3b	4	266	A	G	Q	R	missense	0	sp9	1.0%	
dw3b	9	377	C	T	A	V	missense	0	sp11	1.5%	
dw3b	4	427	C	T	L	F	missense	0	sp7	1.0%	NO
dw3b	3	478	C	T	L	L	silent	1	sp11	1.5%	
dw3b	3	495	G	A	L	L	silent	1	sp2	1.5%	
dw3b	3	499	T	G	Y	D	missense	0.9	sp2	1.5%	
dw3b	11	513	G	A	G	G	silent	1	sp19	1.5%	
dw3b	4	517	G	A	A	T	missense	0.1	sp20	1.5%	NO
dw3b	3	530	C	T	A	V	missense	1	sp16	1.5%	
dw3b	4	642	C	T	T	T	silent	1	sp16	1.5%	
dw3b	19	689	C	T	A	V	missense	0.1	sp20	1.5%	
dw3b	8	746	C	T	A	V	missense	0.2	sp22	1.5%	
dw3b	4	764	T	A	F	Y	missense	0.1	sp21	1.5%	
dw3b	5	813	C	T	V	V	silent	1	sp14	1.5%	
dw3b	4	829	G	A	A	T	missense	0	sp22	1.5%	
dw3b	3	843	C	T	L	L	silent	1	sp10	1.0%	
dw3b	8	850	G	A	A	T	missense	0.3	sp19	1.5%	
dw3b	10	855	G	A	A	A	silent	1	sp19	1.5%	
dw3b	8	920	A	T	Q	L	missense	0	sp23	1.5%	
dw3b	6	929	C	T	A	V	missense	0.1	sp1	1.0%	
dw3b	5	1041	C	T	L	L	silent	1	sp18	1.5%	
dw3b	4	1051	G	A	G	S	missense	0	sp21	1.5%	
dw3b	3	1143	C	T	A	A	silent	1	sp13	1.5%	
dw3b	3	1146	C	T	I	I	silent	1	sp20	1.5%	

dw3b	3	1163	C	T	S	F	missense	0	sp14	1.5%	
dw3b	6	1273	C	T	L	F	missense	0.1	sp20	1.5%	
dw3b	3	1318	G	A	V	M	missense	0	sp10	1.0%	
dw3b	3	1322	C	T	T	M	missense	0.1	sp17	1.5%	
dw3b	3	1354	G	A	A	T	missense	0.2	sp21	1.5%	
dw3b	7	1460	C	T	T	M	missense	0	sp19	1.5%	
dw3b	11	1481	G	A	R	K	missense	0	sp17	1.5%	
dw3b	3	1604	G	A	S	N	missense	0	sp8	1.0%	
dw3b	4	1621	C	T	L	L	silent	1	sp2	1.5%	
dw3b	6	1683	C	T	N	N	silent	1	sp14	1.5%	
dw3b	6	1738	G	T	E	*	Stop codon	0	sp14	1.5%	
dw3b	5	1739	A	G	E	G	missense	0	sp14	1.5%	
dw3b	4	1760	G	A	G	D	missense	0	sp18	1.5%	
dw3b	5	1831	G	A	A	T	missense	0	sp18	1.5%	
dw3b	5	1841	C	T	A	V	missense	0	sp11	1.5%	
dw3b	8	1867	G	A	V	M	missense	0	sp2	1.5%	
dw3b	3	1884	C	T	R	R	silent	1	sp16	1.5%	
dw3b	5	1899	G	A	R	R	silent	1	sp11	1.5%	
dw3b	3	1941	C	T	K	K	silent	1	sp6	1.0%	
dw3b	6	1984	G	A	E	K	missense	0	sp18	1.5%	
dw3b	3	2077	G	A	A	T	missense	0.7	sp19	1.5%	
dw3b	3	2210	T	C	F	S	missense	0.3	sp3	1.0%	
dw3b	14	2238	G	A	E	E	silent	1	sp19	1.5%	
dw3b	10	2257	A	T	M	L	missense	0.7	sp2	1.5%	
dw3b	3	2284	G	A	A	T	missense	0.6	sp17	1.5%	
dw3b	5	2287	G	A	G	R	missense	0.6	sp3	1.0%	
dw3b	11	2289	G	A	A	A	silent	1	sp15	1.5%	
dw3b	3	2387	C	G	A	G	missense	0	sp1	1.0%	
dw3b	7	2440	C	T	P	S	missense	0.5	sp5	1.0%	
dw3b	5	2772	G	A	R	R	silent	1	sp14	1.5%	
dw3b	10	2784	G	A	V	V	silent	1	sp18	1.5%	
dw3b	3	2797	G	A	V	M	missense	0	sp4	1.0%	
dw3b	5	2803	C	T	P	S	missense	0	sp23	1.5%	
dw3b	3	2892	G	A	I	I	silent	1	sp16	1.5%	
dw3b	8	2925	C	T	V	V	silent	1	sp20	1.5%	
dw3b	5	3035	G	A	G	E	missense	0	sp20	1.5%	
dw3b	3	3059	C	T	A	V	missense	0	sp6	1.0%	
dw3b	4	3133	C	T	R	C	missense	0	sp21	1.5%	
rht1a	4	358	C	T	P	S	missense	0	sp18	1.5%	YES

rht1a	3	408	C	T	G	G	silent	1	sp2	1.5%
rht1b	5	108	G	A	V	V	silent	1	sp21	1.5%
rht1b	3	160	G	A	A	T	missense	0.1	sp13	1.5%
rht1b	3	184	C	T	Q	*	Stop codon	0	sp23	1.5%
rht1b	4	219	C	A	A	A	silent	1	sp5	1.0%

[a] The mutation frequency in the total dataset
[b] The wild type nucleotide
[c] The mutated nucleotide
[d] The wild type amino acid
[e] The mutated amino acid
[f] Function and SIFT represent predicted protein function effect and the scores, respectively. A score value < 0.05 is usually predicted as damaging effect
[g] The EMS concentration used to treat the seeds
[h] PCR validation of selected mutations. YES indicates that a mutation was validated by Sanger sequencing. NO indicates that a mutation was found to be a false positive by Sanger sequencing