

Supplementary tables

Table S1 EBI/ENA sequence information

Line	Sequence type	Library tag	Library and distance information	Seq. multiplexing barcode	EBI Project ID (primary)	EBI Sample ID	EBI Sample Name
Lo7	paired end	PE350	PE; 150-350 bp	CTTGTA	PRJEB6214	ERS446995	Rye_Lo7
Lo7	paired end	PE450	PE; 250-500 bp	CTTGTA	PRJEB6214	ERS446995	Rye_Lo7
Lo7	paired end	METH	PE; 100-600 bp	CAGATC	PRJEB6214	ERS446995	Rye_Lo7
Lo7	paired end	METH	PE; 100-600 bp	TTGA	PRJEB6214	ERS446995	Rye_Lo7
Lo7	mate pair	LJD3	LJD; 3.2 kbp	TAGCTT	PRJEB6214	ERS446995	Rye_Lo7
Lo7	mate pair	LJD3	LJD; 3.3 kbp	GGCTAC	PRJEB6214	ERS446995	Rye_Lo7
Lo7	mate pair	LJD8	LJD; 8 kbp	ACTTGA	PRJEB6214	ERS446995	Rye_Lo7
Lo7	mate pair	LJD20	LJD; 20 kbp	CAGATC	PRJEB6214	ERS446995	Rye_Lo7
Lo7	mate pair	LJD3	UJD; -	TAGCTT	PRJEB6214	ERS446995	Rye_Lo7
Lo7	mate pair	LJD3	UJD, -	GGCTAC	PRJEB6214	ERS446995	Rye_Lo7
Lo7	mate pair	LJD8	UJD, -	ACTTGA	PRJEB6214	ERS446995	Rye_Lo7
Lo7	mate pair	LJD20	UJD, -	CAGATC	PRJEB6214	ERS446995	Rye_Lo7
Lo7	mate pair	LJD3	Singleton; -	TAGCTT	PRJEB6214	ERS446995	Rye_Lo7
Lo7	mate pair	LJD3	Singleton; -	GGCTAC	PRJEB6214	ERS446995	Rye_Lo7
Lo7	mate pair	LJD8	Singleton; -	ACTTGA	PRJEB6214	ERS446995	Rye_Lo7
Lo7	mate pair	LJD20	Singleton; -	CAGATC	PRJEB6214	ERS446995	Rye_Lo7
Lo90	paired end	-	PE; 250-500 bp	ATCACG	PRJEB6215	ERS455621	Rye_Lo90
Lo115	paired end	-	PE; 250-500 bp	CGATGT	PRJEB6215	ERS455622	Rye_Lo115
Lo117	paired end	-	PE; 250-500 bp	TTAGGC	PRJEB6215	ERS455623	Rye_Lo117
Lo176	paired end	-	PE; 250-500 bp	TGACCA	PRJEB6215	ERS455624	Rye_Lo176
Lo191	paired end	-	PE; 250-500 bp	ACAGTG	PRJEB6215	ERS455625	Rye_Lo191
Lo282	paired end	-	PE; 250-500 bp	GCCAAT	PRJEB6215	ERS455626	Rye_Lo282
Lo298	paired end	-	PE; 250-500 bp	CAGATC	PRJEB6215	ERS455627	Rye_Lo298
Lo310	paired end	-	PE; 250-500 bp	ACTTGA	PRJEB6215	ERS455628	Rye_Lo310
Lo348	paired end	-	PE; 250-500 bp	GATCAG	PRJEB6215	ERS455629	Rye_Lo348
Lo351	paired end	-	PE; 250-500 bp	TAGCTT	PRJEB6215	ERS455630	Rye_Lo351
S.vavilovii	paired end	-	PE; 250-500 bp	GGCTAC	PRJEB6215	ERS455631	Rye_Svavi

Table S2 Statistics of the WGS sequencing and read quality processing of reference line Lo7

Library *	Library tag	Raw reads						Quality-trimmed reads				
		Number of reads	Total bases	Mean seq. length (bp)	Duplicated reads [%]	GC content [%]	X-fold genome coverage	Paired-end / single-end reads	Total bases	PE reads after trimming [%]	Bases after trimming [%]	X-fold genome coverage
Lo7 PE350	PE350	821,006,993	164,201,398,600	100	9.35	46.35	20.8	669,048,585	127,531,668,707	81.5	77.7	16.1
Lo7 PE450	PE450	690,272,201	138,054,440,200	100	10.34	45.96	17.5	587,756,529	111,875,472,517	85.1	81.0	14.2
Lo7 METH	METH	414,692,471	82,938,494,200	100	8.37	44.87	10.5	289,131,699	53,749,859,381	69.7	64.8	6.8
Lo7 PE Singletons	-	-	-	-	-	-	-	205,657,016	18,214,098,332	-	-	-
Lo7 PE500 (total) **		3,851,943,330	385,194,333,000	-	-	-	48.8	3,297,530,642	311,371,098,937	85.6	80.8	39.4
Lo7 MP3k LJD_32	LJD3	81,134,356	12,468,667,579	77	9.90	44.45	1.6	75,710,959	11,500,441,743	93.3	92.2	1.5
Lo7 MP3k LJD_33	LJD3	84,757,593	13,061,192,079	77	10.24	44.45	1.7	79,348,607	12,106,026,066	93.6	92.7	1.5
Lo7 MP3k UJD_32	LJD3	84,953,613	16,201,026,849	95	9.63	44.32	2.1	76,186,806	14,428,630,418	89.7	89.1	1.8
Lo7 MP3k UJD_33	LJD3	102,605,814	19,680,060,012	96	9.85	44.30	2.5	93,068,995	17,734,995,864	90.7	90.1	2.2
Lo7 MP3k Singleton_32	LJD3	228,282,290	16,831,768,621	74	16.70	44.00	2.1	227,025,876	16,278,041,666	-	-	2.1
Lo7 MP3k Singleton_33	LJD3	200,312,984	14,749,768,091	74	18.03	45.07	1.9	188,896,210	13,537,322,348	-	-	1.7
Lo7 MP3k (total) **		1,135,498,026	92,992,483,231	-	-	-	11.8	1,064,552,820	85,585,458,105	93.8	92.0	10.8
Lo7 MP8k LJD	LJD8	79,444,680	12,238,474,299	77	13.67	44.66	1.5	74,076,747	11,355,803,315	93.2	92.8	1.4
Lo7 MP8k UJD	LJD8	96,488,366	18,433,744,254	96	12.18	44.41	2	86,753,408	16,599,378,289	89.9	90.0	2.1
Lo7 MP8k Singleton	LJD8	161,371,692	11,957,446,374	74	11.77	44.52	1.5	161,866,929	11,808,567,131	-	-	1.5
Lo7 MP8k (total) **		513,237,784	42,629,664,927	-	-	-	5.4	483,527,239	39,763,748,735	94.2	93.3	5.0
Lo7 MP20k LJD	LJD20	54,280,556	8,141,957,185	75	77.06	45.55	1.0	46,083,863	6,875,103,025	84.9	84.4	0.9
Lo7 MP20k UJD	LJD20	62,952,601	11,289,963,553	90	63.35	45.37	1.4	46,460,553	8,671,687,245	73.8	76.8	1.1
Lo7 MP20k Singleton	LJD20	433,413,132	31,299,915,086	72	13.48	46.05	4.0	370,989,638	27,105,565,546	-	-	3.4
Lo7 MP20k (total) **		667,879,446	50,731,835,824	-	-	-	6.4	556,078,470	42,652,355,816	83.3	84.1	5.4
Total		6,168,558,586	571,548,316,982	-	-	-	72.35	5,401,689,171	479,372,661,593	87.6	83.9	60.68

* Abbreviations: PE (paired end); MP (mate pair); METH (methylation-filtrated libraries); LJD (long jumping distance libraries); UJD (Unknown jumping distance)

** For counting the total number of reads the number of PE reads was doubled and number of SE reads was counted singular.

Table S3 High-confidence gene set of rye

HC1 to HC3 are three classes of high-confidence genes. LCG are low-confidence genes and PGGF are pseudogenes and gene fragments. For a detailed description see Experimental procedures.

	High-confidence genes				LCG	PGGF
	HC1-3	HC1	HC2	HC3		
Genes (#)	27,784	16,407	4,863	6,514	3,395	147,075
Single exon (#)	9,234	4,662	1,534	3,038	1,978	132,257
Single exon (%)	33	28	32	47	58.3	89.9
Multi exon (#)	18,550	11,745	3,329	3,476	1,417	14,818
Multi exon (%)	67	72	68	53	41.7	10.1
Max. exons per gene	64	64	31	35	28	16
Mean exons per gene	3.6	4.1	3.4	2.5	1.93	1.15
Min. gene size (bp)	72	81	87	72		
Max. gene size (bp)	15,366	15,366	7,035	7,251		
Average gene size (bp)	930.2	1,130.3	781.8	537.2		

Table S4 BUSCO analysis of genome (WGS assembly), protein and transcript data sets

Type	No. of elements analyzed	Complete BUSCOs	Fragmented BUSCOs	Missing BUSCOs	Complete duplicated BUSCOs	Total
genome	1,581,707	723	131	102	117	956
proteins	27,784	590	122	244	198	956
CDS*	27,784	542	124	290	108	956

*CDS: coding sequence derived from high-confidence genes

Table S5 Transposable element composition of the rye genome in the Lo7 WGS assembly and in 800 Mbp of random Illumina reads

The log2-fold change of the WGS assembly versus Illumina reads is shown.

	Lo7 WGS assembly (%)	Illumina reads (%)	WGS vs Illumina
Mobile Element (TXX)	50.30	71.61	-0.51
Class I: Retroelement (RXX)	38.16	60.19	-0.66
LTR Retrotransposon (RLX)	37.20	59.78	-0.68
Ty1/copia (RLC)	6.58	14.13	-1.10
Ty3/gypsy (RLG)	23.31	33.70	-0.53
unclassified LTR (RLX)	7.31	11.96	-0.71
non-LTR Retrotransposon (RXX)	0.95	0.41	1.23
LINE (RIX)	0.92	0.40	1.21
SINE (RSX)	0.03	0.01	2.20
Class II: DNA Transposon (DXX)	10.31	7.09	0.54
DNA Transposon Superfamily (DTX)	9.87	6.97	0.50
CACTA superfamily (DTC)	8.93	6.61	0.43
hAT superfamily (DTA)	0.02	0.02	0.51
Mutator superfamily (DTM)	0.27	0.13	1.07
Tc1/Mariner superfamily (DTT)	0.17	0.05	1.71
PIF/Harbinger (DTH)	0.33	0.11	1.59
unclassified (DTX)	0.15	0.05	1.64
MITE (DXX)	0.42	0.11	1.99
Helitron (DHH)	0.02	0.01	0.36
Unclassified Element (TXX)	1.84	4.34	-1.24
<i>Retro-TE/DNA-TE ratio</i>	<i>3.7</i>	<i>8.5</i>	<i>-1.20</i>
<i>Gypsy/Copia ratio</i>	<i>3.5</i>	<i>2.4</i>	<i>0.54</i>

Table S6 Statistics for resequencing results and read alignment statistics of the 10 rye inbred lines and *S. vavilovii*

See Excel file TableS6_resequencing_alignment_statistics.xlsx

Table S7 Functional annotation of SNVs discovered in 10 resequenced rye inbred lines and *S. vavilovii*

See Excel file TableS7_functional_annotation_variants.xlsx

Table S8 Classification of SNVs on the Rye600k array according to Affymetrix SNV categories

Affymetrix SNV category	Number	%
Poly High Resolution	236,216	39.3
OTV (= off-target variant)	45,365	7.6
No Minor Homozygote	34,965	5.8
Mono High Resolution	45,139	7.5
Other	238,181	39.6
Call Rate Below Threshold	977	0.2
Total	600,843	100

Table S9 Overview statistics for the Lo7 x Lo225 high-density genetic map

Chromosome	1R	2R	3R	4R	5R	6R	7R	Total
Map length [cM]	154.3	180.9	166.7	206.8	214.6	181.7	139.9	1244.9
No. of mapped markers	12,340	13,050	10,055	10,517	13,382	15,525	12,951	87,820
No. of represented sequence contigs	6,570	6,786	5,156	5,900	6,740	8,722	7,519	47,393
No. of represented Lo7 WGS contigs	6,125	6,255	4,773	5,531	6,262	8,322	7,103	44,371
No. of unique loci*	290	280	290	324	362	302	230	2,078
Average map distance between loci [cM]	0.532	0.646	0.575	0.638	0.593	0.602	0.608	0.599
Maximum gap between loci [cM]	2.03	3.76	2.87	3.89	3.92	5.28	2.43	5.28

* Loci represent unique positions on the genetic map and may contain cosegregating markers.

Table S10 Rice orthologs for selection candidates

The table lists hits from a tBLASTX search of Lo7 WGS contigs harbouring SNVs identified as selection candidates based on the overlap of Lositan (F_{ST}) outliers with the top 1% of $X^T X$ values against cloned and functionally characterized rice genes. Results are shown for the comparisons of i) seed and pollen parent pools, ii) seed parent pool and genetic resources (GR), and iii) pollen parent pool and GR.

See Excel file TableS10_CGunderSelection.xlsx

Table S11 Nucleotide diversity π for 22 contigs harbouring SNVs which were under selection

For each contig from Table S10 which gave hit(s) to rice orthologs, π values were calculated for all SNVs per contig for each of the three groups (seed and pollen parent pool and GR). The lowest π value per contig is shown in red, the highest in green and intermediate values in yellow.

Contig	chr	pos_cM	Number of SNVs per contig	Os_Gene(s)	Candidate SNVs found in comparison(s)	Seed_pi (*10 ⁻³)	Pollen_pi (*10 ⁻³)	GR_pi (*10 ⁻³)
Lo7_v2_contig_60281	1	77.09200398	7	gid1	pollen - GR	0.20593200	0.09839069	0.26431730
Lo7_v2_contig_2869846	1	142.2424682	8	DCW11	seed - GR	0.29577020	0.33030690	0.33894330
Lo7_v2_contig_1346031	2	65.4900965	12	ObgC	seed - pollen	0.31518080	0.00000000	0.73900370
Lo7_v2_contig_1354214	2	70.2492276	11	SIT1; SIT2	seed - pollen, seed - GR	0.81776080	0.34738200	0.58515720
Lo7_v2_contig_2869793	2	75.7710711	15	d11	pollen - GR	0.41961270	0.46090910	0.50018030
Lo7_v2_contig_63401	2	87.28342787	9	OsGPX1 // OsGPX3	seed - pollen	0.12646260	0.37388070	0.51614580
Lo7_v2_contig_63575	2	87.28342787	8	OsPIP1;1 // RWC3	seed - pollen, pollen - GR	0.00000000	0.17180240	0.13871310
Lo7_v2_contig_1350830	2	90.0934742	10	rlin1	seed - GR	0.45268450	0.58837550	0.77054130
Lo7_v2_contig_1345318	3	72.95919645	4	OsGSK2/BIN2	seed - GR	0.03035398	0.00999979	0.14388270
Lo7_v2_contig_63978	3	73.35290537	5	OsGAE1	seed - GR	0.08476150	0.28291680	0.33799350
Lo7_v2_contig_1346414	3	86.49173766	18	OsWRKY13	seed - pollen	0.73668580	0.10666490	0.44766910
Lo7_v2_contig_1355272	4	70.6310735	15	SP1	seed - GR	0.35438800	0.72020950	0.88249870
Lo7_v2_contig_1350051	4	71.4247409	3	kch1	pollen - GR	0.00000000	0.00000000	0.00000000
Lo7_v2_contig_145752	4	72.2090828	3	OsDOG	pollen - GR	0.06470709	0.15482110	0.09246184
Lo7_v2_contig_1372217	5	51.8078509	5	NAC1 // OMTN3	pollen - GR	0.22981150	0.13612250	0.28954310
Lo7_v2_contig_1354407	5	114.124518	11	DHS	pollen - GR	0.45680760	0.56390980	0.72281710
Lo7_v2_contig_4740	5	126.2107894	6	OsPH1	seed - pollen, pollen - GR	0.12173950	0.25799710	0.29581270
Lo7_v2_contig_1365212	5	139.7813379	11	el1	pollen - GR	0.11665850	0.44173750	0.53726530
Lo7_v2_contig_171174	5	172.9130459	10	rim1	seed - GR	0.11208180	0.15882030	0.18330420
Lo7_v2_contig_1351758	6	60.73602851	8	OsPIN1 // OsPIN3t	pollen - GR	0.37105920	0.21785060	0.42132370
Lo7_v2_contig_4902	6	89.48103351	10	Dwarf 1 gene	seed - pollen	0.44523740	0.41883790	0.46453000
Lo7_v2_contig_126830	6	155.6950513	10	OVP1	pollen - GR	0.18875280	0.15263440	0.24763650

Table S12 Assignment of WGS contigs and scaffolds to rye chromosomes based on Carma, 88k genetic map and Rye Genome Zipper

	Type	WGS assembly / scaffolds	1R	2R	3R	4R	5R	6R	7R	0R
Number of sequences	Contigs	1,581,707	98,024	121,210	126,168	138,822	99,608	106,597	115,213	776,065
	Scaffolds	1,286,927	77,039	94,814	97,352	105,939	77,238	81,491	90,656	662,398
N50 number	Contigs	233,728	14,763	18,087	19,352	20,820	14,778	16,499	17,608	175,922
	Scaffolds	68,672	13,055	12,384	12,404	13,117	12,928	13,164	11,970	41,508
N50 length (bp)	Contigs	1,708	2,631	2,473	2,415	2,383	2,609	2,533	2,337	755
	Scaffolds	9,448	4,849	5,891	6,119	6,180	4,826	5,285	5,562	4,513
Total size (Mbp)	Contigs	1,685	147.0	172.3	180.0	192.1	147.2	158.0	158.9	530.0
	Scaffolds	2,804	258.8	294.5	308.2	334.1	249.7	279.0	269.7	809.9
Largest sequence (bp)	Contigs	35,334	33,899	32,214	29,466	28,438	29,500	34,750	30,215	35,334
	Scaffolds	148,970	138,002	148,970	128,743	136,807	120,439	148,047	121,891	104,152

Table S13 List of rye inbred lines and accessions genotyped with the Rye600k array for genome-wide selection screens

The names or codes of inbred lines and accessions, their assignment to the three germplasm groups (seed parent pool, pollen parent pool, genetic resources - GR), information on the country of origin of the source population (origin), DNA sample composition (bulk samples or single plants), information whether a line was included in WGS sequencing (seq.), and the provider of seeds/DNA are given. Lines from the seed parent pool were selfed 5-6 times, lines from the pollen parent pool were selfed 2-3 times. The GR accessions were heterozygous single plants from open-pollinated populations or full-sib families.

Sample name	Group	Origin	DNA sample	Seq.	Provider of seeds/DNA
Lo7	Seed	Germany	bulk	yes	KWS LOCHOW GMBH
Ro_S002	Seed	Germany	bulk		KWS LOCHOW GMBH
Ro_S004	Seed	Germany	bulk		KWS LOCHOW GMBH
Ro_S005	Seed	Germany	bulk		KWS LOCHOW GMBH
Ro_S007	Seed	Germany	bulk		KWS LOCHOW GMBH
Ro_S011 (alias Lo90)	Seed	Germany	bulk	yes	KWS LOCHOW GMBH
Ro_S015	Seed	Germany	bulk		KWS LOCHOW GMBH
Ro_S016 (alias Lo115)	Seed	Germany	bulk	yes	KWS LOCHOW GMBH
Ro_S017 (alias Lo117)	Seed	Germany	bulk	yes	KWS LOCHOW GMBH
Ro_S020	Seed	Germany	bulk		KWS LOCHOW GMBH
Ro_S027	Seed	Germany	bulk		KWS LOCHOW GMBH
Ro_S036	Seed	Germany	bulk		KWS LOCHOW GMBH
Ro_S038	Seed	Germany	bulk		KWS LOCHOW GMBH
Ro_S046	Seed	Germany	bulk		KWS LOCHOW GMBH
Ro_S051	Seed	Germany	bulk		KWS LOCHOW GMBH
Ro_S054	Seed	Germany	bulk		KWS LOCHOW GMBH
Ro_S056	Seed	Germany	bulk		KWS LOCHOW GMBH
Ro_S057	Seed	Germany	bulk		KWS LOCHOW GMBH
Ro_S062	Seed	Germany	bulk		KWS LOCHOW GMBH
Ro_S064	Seed	Germany	bulk		KWS LOCHOW GMBH
Ro_S065	Seed	Germany	bulk		KWS LOCHOW GMBH
Ro_S174	Seed	Germany	bulk		KWS LOCHOW GMBH
Ro_S175	Seed	Germany	bulk		KWS LOCHOW GMBH
Ro_S185	Seed	Germany	bulk		KWS LOCHOW GMBH
Ro_S186	Seed	Germany	bulk		KWS LOCHOW GMBH
Ro_S189	Seed	Germany	bulk		KWS LOCHOW GMBH
Ro_S242	Seed	Germany	bulk		KWS LOCHOW GMBH
Ro_S245	Seed	Germany	bulk		KWS LOCHOW GMBH
Ro_S247	Seed	Germany	bulk		KWS LOCHOW GMBH
Ro_S248	Seed	Germany	bulk		KWS LOCHOW GMBH
Ro_S249 (alias Lo176)	Seed	Germany	bulk	yes	KWS LOCHOW GMBH
Ro_S252	Seed	Germany	bulk		KWS LOCHOW GMBH
Ro_S254 (alias Lo191)	Seed	Germany	bulk	yes	KWS LOCHOW GMBH
Ro_S259	Seed	Germany	bulk		KWS LOCHOW GMBH
Ro_S287	Seed	Germany	bulk		KWS LOCHOW GMBH
Ro_S288	Seed	Germany	bulk		KWS LOCHOW GMBH
Ro12024_00434	Seed	Germany	bulk		KWS LOCHOW GMBH

Ro12024_03140	Seed	Germany	bulk		KWS LOCHOW GMBH
Ro_S069_rep2 (alias Lo225)	Pollen	Germany	bulk		KWS LOCHOW GMBH
Ro_S072	Pollen	Germany	bulk		KWS LOCHOW GMBH
Ro_S079	Pollen	Germany	bulk		KWS LOCHOW GMBH
Ro_S082	Pollen	Germany	bulk		KWS LOCHOW GMBH
Ro_S094	Pollen	Germany	bulk		KWS LOCHOW GMBH
Ro_S102	Pollen	Germany	bulk		KWS LOCHOW GMBH
Ro_S104 (alias Lo298)	Pollen	Germany	bulk	yes	KWS LOCHOW GMBH
Ro_S111	Pollen	Germany	bulk		KWS LOCHOW GMBH
Ro_S116 (alias Lo310)	Pollen	Germany	bulk	yes	KWS LOCHOW GMBH
Ro_S118	Pollen	Germany	bulk		KWS LOCHOW GMBH
Ro_S119	Pollen	Germany	bulk		KWS LOCHOW GMBH
Ro_S121	Pollen	Germany	bulk		KWS LOCHOW GMBH
Ro_S127	Pollen	Germany	bulk		KWS LOCHOW GMBH
Ro_S131	Pollen	Germany	bulk		KWS LOCHOW GMBH
Ro_S132	Pollen	Germany	bulk		KWS LOCHOW GMBH
Ro_S139	Pollen	Germany	bulk		KWS LOCHOW GMBH
Ro_S141	Pollen	Germany	bulk		KWS LOCHOW GMBH
Ro_S148	Pollen	Germany	bulk		KWS LOCHOW GMBH
Ro_S149	Pollen	Germany	bulk		KWS LOCHOW GMBH
Ro_S153	Pollen	Germany	bulk		KWS LOCHOW GMBH
Ro_S157	Pollen	Germany	bulk		KWS LOCHOW GMBH
Ro_S166	Pollen	Germany	bulk		KWS LOCHOW GMBH
Ro_S168	Pollen	Germany	bulk		KWS LOCHOW GMBH
Ro_S172	Pollen	Germany	bulk		KWS LOCHOW GMBH
Ro_S191	Pollen	Germany	bulk		KWS LOCHOW GMBH
Ro_S192	Pollen	Germany	bulk		KWS LOCHOW GMBH
Ro_S195	Pollen	Germany	bulk		KWS LOCHOW GMBH
Ro_S198	Pollen	Germany	bulk		KWS LOCHOW GMBH
Ro_S209	Pollen	Germany	bulk		KWS LOCHOW GMBH
Ro_S211	Pollen	Germany	bulk		KWS LOCHOW GMBH
Ro_S216	Pollen	Germany	bulk		KWS LOCHOW GMBH
Ro_S220	Pollen	Germany	bulk		KWS LOCHOW GMBH
Ro_S221	Pollen	Germany	bulk		KWS LOCHOW GMBH
Ro_S224	Pollen	Germany	bulk		KWS LOCHOW GMBH
Ro_S227	Pollen	Germany	bulk		KWS LOCHOW GMBH
Ro_S235	Pollen	Germany	bulk		KWS LOCHOW GMBH
Ro_S272	Pollen	Germany	bulk		KWS LOCHOW GMBH
Ro_S273	Pollen	Germany	bulk		KWS LOCHOW GMBH
Ro_S281	Pollen	Germany	bulk		KWS LOCHOW GMBH
Ro_S282	Pollen	Germany	bulk		KWS LOCHOW GMBH
Ro_S286	Pollen	Germany	bulk		KWS LOCHOW GMBH
Ro11002_00004	Pollen	Germany	bulk		KWS LOCHOW GMBH
Ro11002_00006	Pollen	Germany	bulk		KWS LOCHOW GMBH
Ro13030_00299	Pollen	Germany	bulk		KWS LOCHOW GMBH
Ro13030_00738	Pollen	Germany	bulk		KWS LOCHOW GMBH
Ro13030_01528	Pollen	Germany	bulk		KWS LOCHOW GMBH
5017/4211_St185	GR	Russia	single		KWS LOCHOW GMBH

AND15	GR	Poland	single		KWS LOCHOW GMBH
AND15_6378	GR	Poland	single		KWS LOCHOW GMBH
Armand_6474	GR	Poland	single		KWS LOCHOW GMBH
C463	GR	Germany	single		KWS LOCHOW GMBH
DankAmber_6605	GR	Poland	single		KWS LOCHOW GMBH
DC26	GR	Poland	single		KWS LOCHOW GMBH
EstafetaTatarstana	GR	Russia	single		KWS LOCHOW GMBH
Florida_Black_1	GR	U.S.A.	single		KWS LOCHOW GMBH
H_1225	GR	Russia	single		KWS LOCHOW GMBH
H_149	GR	Russia	single		KWS LOCHOW GMBH
H_29	GR	Russia	single		KWS LOCHOW GMBH
H_809	GR	Russia	single		KWS LOCHOW GMBH
Hp1	GR	Russia	single		KWS LOCHOW GMBH
HVG_3079	GR	Russia	single		KWS LOCHOW GMBH
Iran3009	GR	Iran	single		KWS LOCHOW GMBH
LN370	GR	Russia	single		KWS LOCHOW GMBH
LN-720/2	GR	Russia	single		KWS LOCHOW GMBH
Lp1	GR	Russia	single		KWS LOCHOW GMBH
Lp2	GR	Russia	single		KWS LOCHOW GMBH
Luta_6665	GR	Russia	single		KWS LOCHOW GMBH
Nem20085/1/5	GR	Russia	single		KWS LOCHOW GMBH
P45_Radzima	GR	Belarus	single		KWS LOCHOW GMBH
Puma_HOH_1	GR	Canada	single		KWS LOCHOW GMBH
Puma_WOH_1	GR	Canada	single		KWS LOCHOW GMBH
R1119_S.strictum	GR	Turkey	single		IPK Gatersleben Genebank
R6	GR	Germany	single		KWS LOCHOW GMBH
R801_S.sylvestre	GR	Russia	single		IPK Gatersleben Genebank
Radon	GR	Russia	single		KWS LOCHOW GMBH
Radoncopy	GR	Russia	single		KWS LOCHOW GMBH
RU_VGF_785	GR	Russia	single		KWS LOCHOW GMBH
RU_VGF_807	GR	Russia	single		KWS LOCHOW GMBH
S.vavilovii	GR	unknown	single	yes	T. Miedaner, University of Hohenheim
Saratovskaja7_1	GR	Russia	single		KWS LOCHOW GMBH
Saratovskaja7_2	GR	Russia	single		KWS LOCHOW GMBH
Saratovskaja7_3	GR	Russia	single		KWS LOCHOW GMBH
Sodmia_6674	GR	Balticum	single		KWS LOCHOW GMBH
Tatjana	GR	Russia	single		KWS LOCHOW GMBH
UniWRO_187	GR	Poland	single		KWS LOCHOW GMBH
UniWRO_191_typ1	GR	Poland	single		KWS LOCHOW GMBH
UniWRO_224_typ2	GR	Poland	single		KWS LOCHOW GMBH
UniWRO_247	GR	Poland	single		KWS LOCHOW GMBH
UniWRO_249	GR	Poland	single		KWS LOCHOW GMBH
UniWRO_283	GR	Poland	single		KWS LOCHOW GMBH
V861	GR	Germany	single		KWS LOCHOW GMBH
Vila_Pouca_1	GR	Portugal	single		KWS LOCHOW GMBH