

**Table S1. KL and OCL assignments for all isolates in the diverse panel**

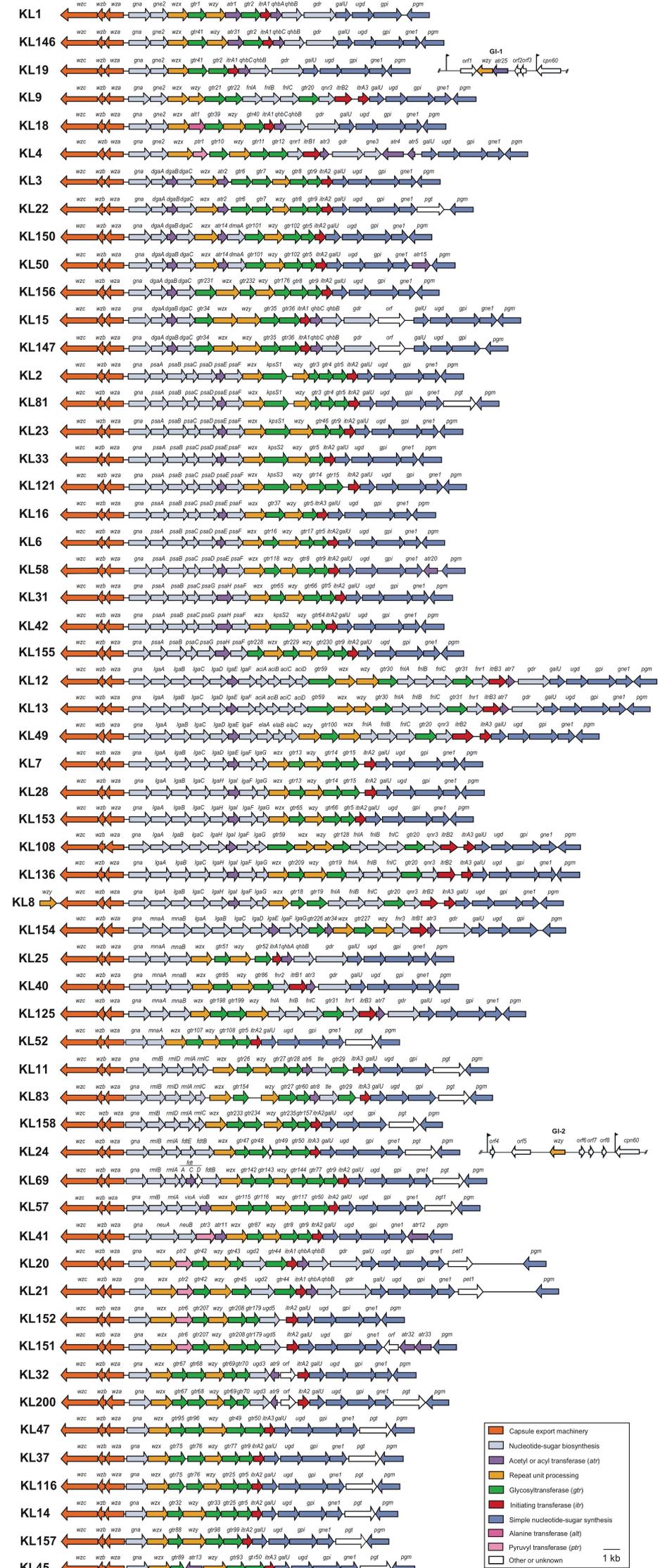
MRSN ID	GenBank Accession	Assembly number	Previously assigned KL	Confirmed KL <sup>1</sup>	Previously assigned OCL	Confirmed OCL <sup>1</sup>
6541	VHEK00000000	GCA_006492195.1	KL1	KL1-v*	OCL1	OCL1
7213	VHEE00000000	GCA_006492065.1	KL1	KL1	OCL1	OCL1
960	VHDR00000000	GCA_006491965.1	KL1	KL1-v*	OCL1	OCL1
31196	VHFU00000000	GCA_006491855.1	KL1	KL1-v* + GI-1	OCL1	OCL1
11695	VHHI00000000	GCA_006493765.1	KL1	KL1-v <sup>2</sup>	OCL1	OCL1
1551	VHGQ00000000	GCA_006493835.1	KL108	KL108	OCL2	OCL2
31461	VHFT00000000	GCA_006491865.1	KL11	KL11	OCL8	OCL8
32875	VHFD00000000	GCA_006492475.1	KL11	KL11	OCL8	OCL8
31937	VHFP00000000	GCA_006492985.1	KL116	KL116	OCL6	OCL6
7067	VHEJ00000000	GCA_006492575.1	KL12	KL12	OCL2	OCL2
15049	VHGW00000000	GCA_006494155.1	KL12	KL12	OCL2	OCL2-v*
15075	VHGU00000000	GCA_006494055.1	KL46	KL121	OCL6	OCL6
11663	VHHK00000000	GCA_006494665.1	KL125	KL125	OCL7	OCL7
32865	VHFF00000000	GCA_006492735.1	KL125	KL125	OCL5	OCL5
32892	VHFC00000000	GCA_006492425.1	KL125	KL125	OCL7	OCL7
1171	VHHG00000000	GCA_006493925.1	KL13	KL13	OCL1	OCL1-v*
32104	VHFL00000000	GCA_006492805.1	KL13	KL13	OCL5	OCL5
32842	VHFG00000000	GCA_006492855.1	KL8	KL136	OCL2	OCL2
7460	VHEA00000000	GCA_006492615.1	KL14	KL14	OCL6	OCL6
31523	VHFR00000000	GCA_006492335.1	KL14	KL14	OCL6	OCL6
31915	VHFQ00000000	GCA_006492315.1	KL14	KL14	OCL6	OCL6
32304	VHFI00000000	GCA_006492945.1	KL14	KL14	OCL7	OCL15
480561	VHEQ00000000	GCA_006492265.1	KL14	KL14	OCL6	OCL6
14193	VHGX00000000	GCA_006494215.1	KL19	KL146	OCL1	OCL1
489678	VHEN00000000	GCA_006492055.1	KL15	KL147	OCL5	OCL5-v <sup>4</sup>
30000	VHGB00000000	GCA_006493705.1	KL15	KL15	OCL7	OCL7
30896	VHFZ00000000	GCA_006494075.1	KL15	KL15	OCL1	OCL1
351162	VHEX00000000	GCA_006492905.1	KL50	KL150	OCL6	OCL6
7153	VHEF00000000	GCA_006492295.1	novel	KL151	OCL5	OCL5
15574	VHGP00000000	GCA_006494565.1	novel	KL152	OCL6	OCL6
4943	VHEM00000000	GCA_006492305.1	novel	KL153	OCL1	OCL1
10372	VHHM00000000	GCA_006493855.1	novel	KL154	OCL4	OCL4
21660	VHGL00000000	GCA_006494015.1	novel	KL155	OCL1	OCL1
11816	VHHE00000000	GCA_006494285.1	novel	KL156	OCL6	OCL6
15093	VHGS00000000	GCA_006494575.1	novel	KL157	OCL6	OCL6
32076	VHFM00000000	GCA_006493005.1	novel	KL158	OCL9	OCL9
1187	VHHC00000000	GCA_006494255.1	KL16	KL16	OCL7	OCL7
3360	VHEZ00000000	GCA_006492795.1	KL18	KL18	OCL3	OCL3
11703	VHHH00000000	GCA_006494005.1	KL18	KL18-v*	OCL1	OCL1
32108	VHFK00000000	GCA_006492525.1	KL18	KL18	OCL3	OCL3
843	VH DU00000000	GCA_006492125.1	KL19	KL19 + GI-1	OCL1	OCL1
3874	VHET00000000	GCA_006492705.1	KL19	KL19 + GI-1	OCL1	OCL1
30945	VHFW00000000	GCA_006493045.1	KL19	KL19 + GI-1	OCL1	OCL1
3692	VHEU00000000	GCA_006492785.1	KL2	KL2	OCL6	OCL6
7431	VHEC00000000	GCA_006492385.1	KL2	KL2	OCL1	OCL1
7735	VHDV00000000	GCA_006492865.1	KL2	KL2	OCL1	OCL1
30909	VH FY00000000	GCA_006491885.1	KL2	KL2	OCL6	OCL6
31947	VHFN00000000	GCA_006492775.1	KL2	KL2	OCL6	OCL6
2821	VHGE00000000	GCA_006493845.1	KL20	KL20	OCL4	OCL4
14237	VHGY00000000	GCA_006494225.1	KL32	KL200-v*	OCL7	OCL15
4484	VHER00000000	GCA_006492085.1	KL21	KL21	OCL5	OCL5
1174	VHHF00000000	GCA_006493655.1	KL22	KL22	OCL3	OCL3-v*
14427	VHGX00000000	GCA_006494175.1	KL22	KL22	OCL1	OCL1
423159	VHES00000000	GCA_006492625.1	KL22	KL22-v*	novel	OCL3-v*
7113	VHEI00000000	GCA_006492505.1	KL23	KL23	OCL5	OCL13
7725	VHDW00000000	GCA_006492405.1	KL23	KL23	OCL6	OCL6
11669	VHHJ00000000	GCA_006493685.1	KL24	KL24 + GI-2	OCL7	OCL7
21681	VH GK00000000	GCA_006658595.1	KL24	KL24 + GI-2	OCL7	OCL7
959	VHDS00000000	GCA_006491985.1	KL25	KL25	OCL2	OCL2
11224	VHHL00000000	GCA_006493645.1	KL25	KL25	OCL1	OCL1
25547	VHGF00000000	GCA_006493745.1	KL25	KL25	OCL1	OCL1
15070	VHGV00000000	GCA_006494115.1	KL28	KL28	OCL7	OCL7
15129	VHGR00000000	GCA_006494085.1	KL3	KL3	OCL2	OCL2
29999	VHGC00000000	GCA_006493955.1	KL31	KL31	OCL6	OCL6

7251	VHED00000000	GCA_006492175.1	KL32	KL32	OCL6	OCL6-v*
7576	VHDY00000000	GCA_006492515.1	KL32	KL32	OCL6	OCL6
1196	VHHB00000000	GCA_006494265.1	KL33	KL33	OCL1	OCL1
7137	VHEG00000000	GCA_006492635.1	KL37	KL37	OCL7	OCL7
31159	VHFV00000000	GCA_006494615.1	KL37	KL37	OCL6	OCL6
19482	VHGM00000000	GCA_006493735.1	KL4	KL4-v <sup>3</sup>	OCL10	OCL10
337038	VHEY00000000	GCA_006492395.1	KL40	KL40	OCL2	OCL2
32142	VHFJ00000000	GCA_006492215.1	KL41	KL41	OCL5	OCL5
3658	VHEV00000000	GCA_006492495.1	KL42	KL42-v*	OCL6	OCL6
32797	VHFH00000000	GCA_006492965.1	KL42	KL42	OCL6	OCL6
30885	VHGA00000000	GCA_006493945.1	KL45	KL45	OCL6	OCL6
480622	VHEP00000000	GCA_006492585.1	KL45	KL45	OCL5	OCL5
15088	VHGT00000000	GCA_006493915.1	KL47	KL47	OCL5	OCL5
918	VHDT00000000	GCA_006492155.1	KL49	KL49	OCL1	OCL1
1311	VHHA00000000	GCA_006494165.1	KL49	KL49	OCL3	OCL3
7124	VHEH00000000	GCA_006492375.1	KL49	KL49	OCL2	OCL2
16880	VHGO00000000	GCA_006494585.1	KL49	KL49	OCL2	OCL2
30912	VHFX00000000	GCA_006492715.1	KL50	KL50	OCL6	OCL6
22112	VHGJ00000000	GCA_006493975.1	KL52	KL52	OCL6	OCL6
32915	VHFB00000000	GCA_006492925.1	KL52	KL52	OCL1	OCL1
5969	VHEL00000000	GCA_006491955.1	KL57	KL57	OCL5	OCL5-v*
31468	VHFS00000000	GCA_006491875.1	KL58	KL58	OCL6	OCL6
7521	VHDZ00000000	GCA_006492165.1	KL6	KL6	OCL1	OCL1
17493	VHGN00000000	GCA_006494065.1	KL6	KL6-v*	OCL1	OCL1
351524	VHEW00000000	GCA_006492685.1	novel	KL69	OCL7	OCL7
29908	VHGD00000000	GCA_006493755.1	KL7	KL7	OCL1	OCL1
7690	VHDX00000000	GCA_006491975.1	KL8	KL8	OCL2	OCL2
31942	VHFO00000000	GCA_006493035.1	KL81	KL81-v*	OCL6	OCL6
24603	VHGG00000000	GCA_006493875.1	KL83	KL83	OCL5	OCL5-v*
334	VHFA00000000	GCA_006492245.1	KL9	KL9	OCL1	OCL1
1183	VHHD00000000	GCA_006494305.1	KL9	KL9	OCL2	OCL2
7446	VHEB00000000	GCA_006492885.1	KL9	KL9	OCL6	OCL6
23390	VHGI00000000	GCA_006658565.1	KL9	KL9	OCL7	OCL7
24008	VHGH00000000	GCA_006493815.1	KL9	KL9	OCL1	OCL1
32866	VHFE00000000	GCA_006492675.1	KL9	KL9	OCL1	OCL1
489669	VHEO00000000	GCA_006492075.1	KL9	KL9	OCL1	OCL1

<sup>1</sup> '-v' denotes 'variant locus' as sequence is found in >1 contig with overhanging sequence at break site matching an IS sequence. '-v\*' denotes 'possible variant locus' as sequence is found in >1 contig though no IS sequence is found.

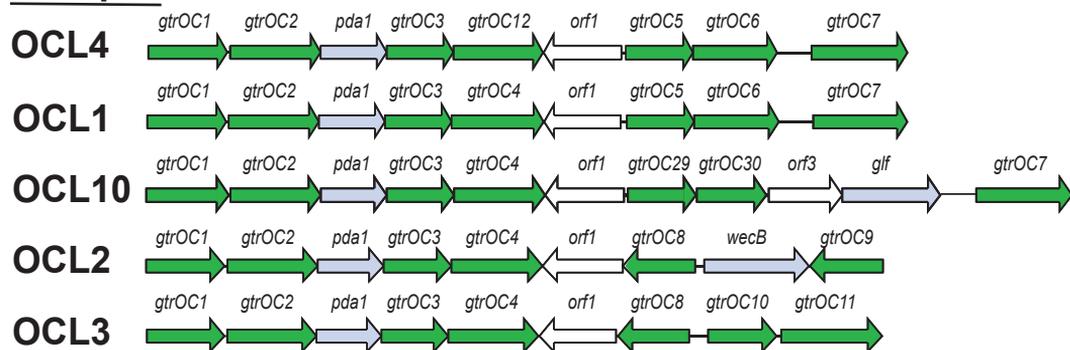
<sup>2</sup> ISAba1 interrupting *atr1* gene

<sup>3</sup> ISAba26 interrupting *gne1* gene



**Figure S1. Organisation of all KL gene clusters identified in the diverse panel**

## Group A



## Group B

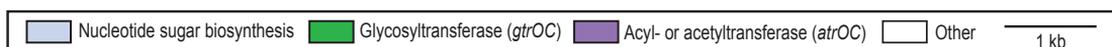
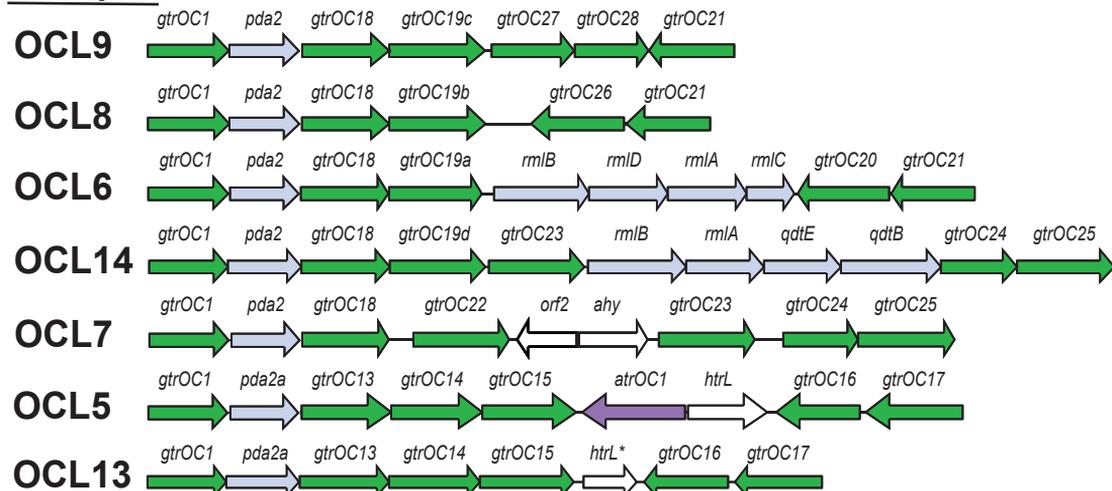


Figure S2. Organisation of all OCL gene clusters identified in the diverse panel