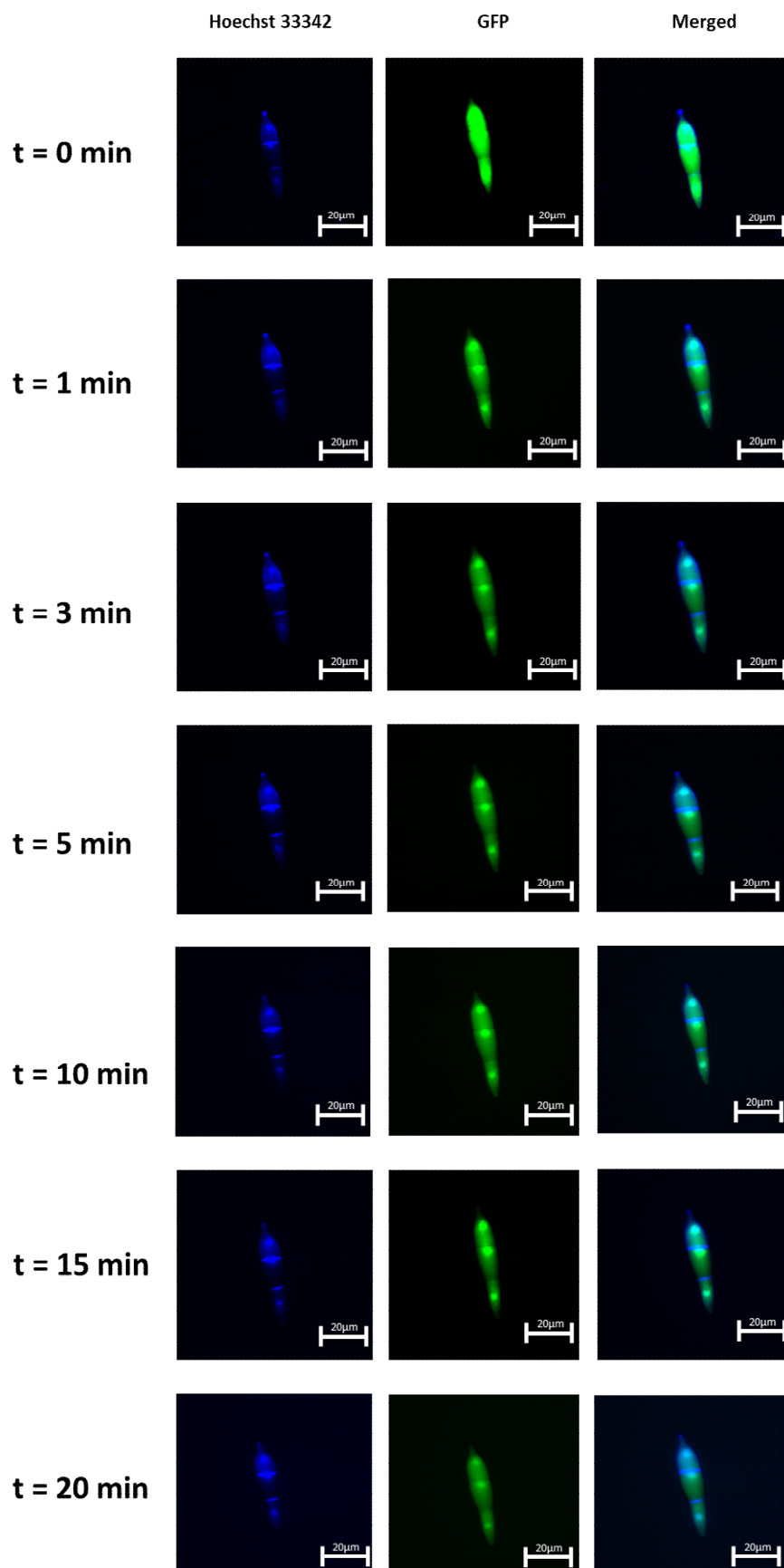


1 **Supplementary data**

2



3

Figure S1: Localization of GFP-fused total MoYpd1p in conidia of $\Delta Moypd1::GFP-MoYPD1$ before and after 1 M KCl treatment.

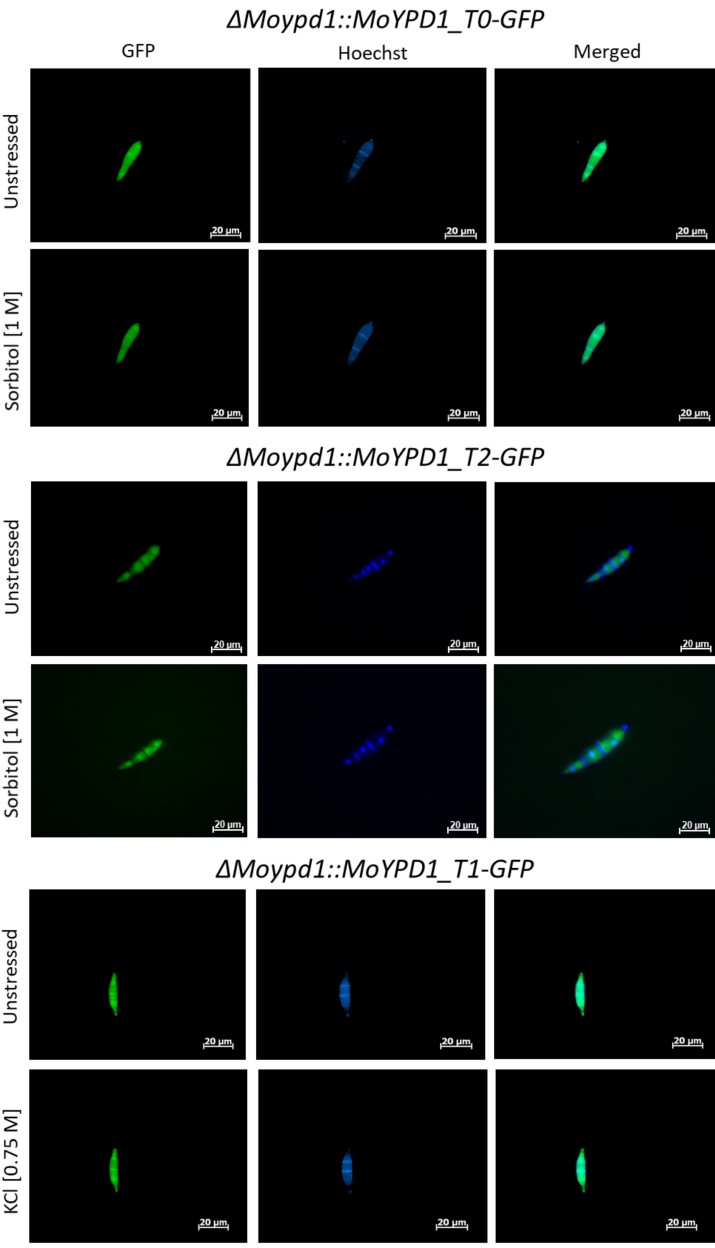


Figure S2: Localization of GFP-fused MoYpd1p isoforms. After treatment with sorbitol [1 M], no translocation into the nucleus was observed for MoYpd1p_T0 and MoYpd1p_T2. However, MoYpd1p_T1 did not accumulate in the nucleus upon KCl stress [0,75 M].

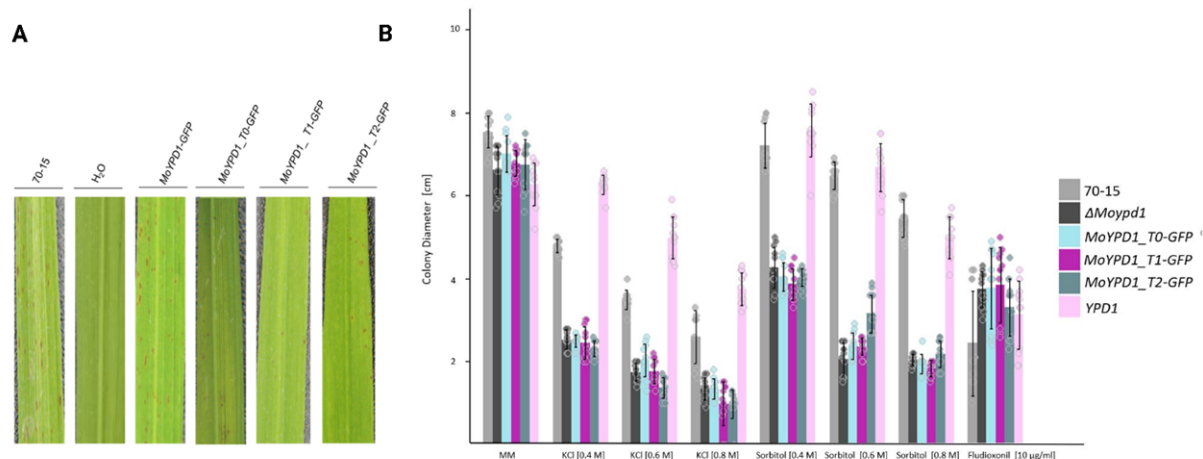


Figure S3: A: Rice leaves with blast lesions. Rice plants inoculated with conidia suspension of the mutant strains producing only one isoform show disease symptoms on the leaves. B: Vegetative growth of *Magnaporthe oryzae* 70-15 strain, the loss-of-function mutant Δ MoYpd1 and the GFP-tagged MoYpd1p-producing isoform strains under KCl, sorbitol and fludioxonil stress.

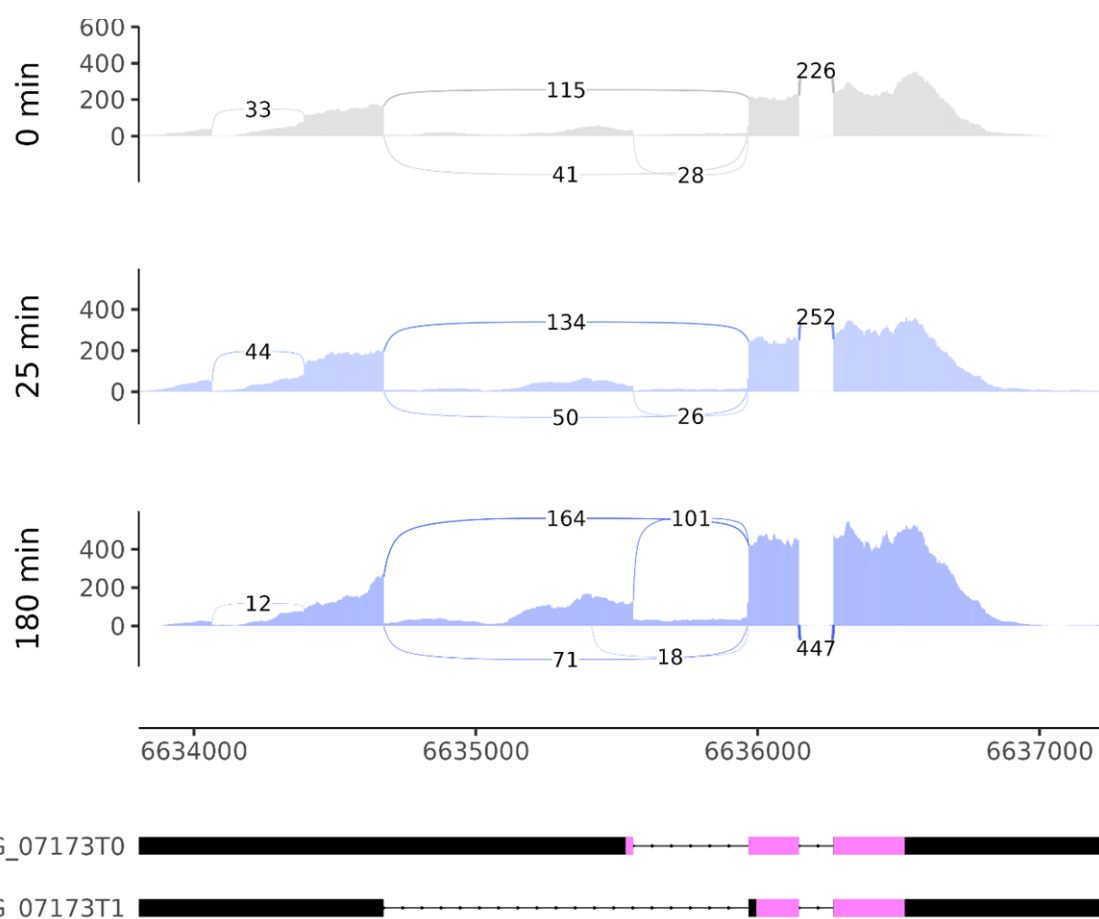


Figure S4: Sashimi plots of *MoYPD1* before and after 0.5 M sorbitol treatment. Sashimi plots visualize the read coverage (y-axis) for corresponding *MoYPD1* genomic region (x-axis). Arcs represent splice junctions of *MoYPD1*. Beneath the sashimi plot annotated transcripts are shown with the CDS highlighted in pink.

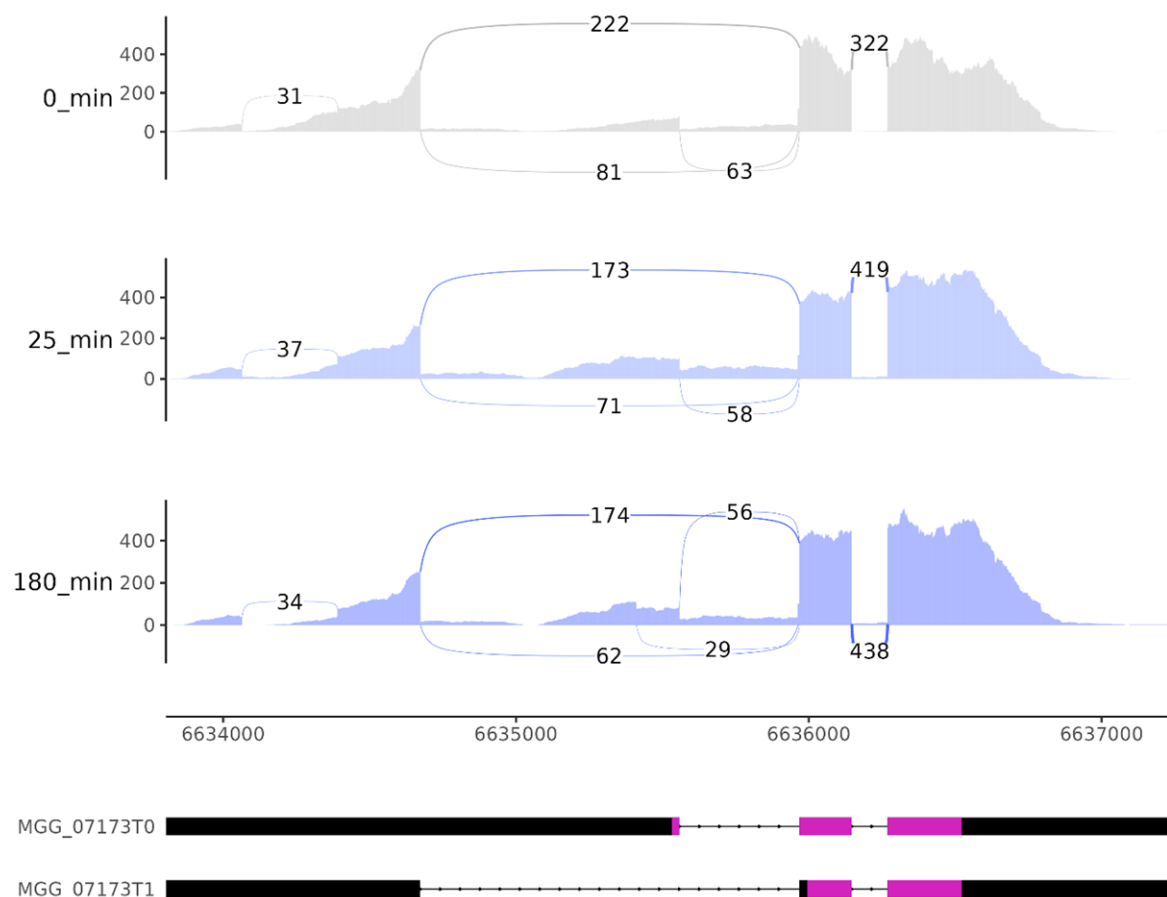


Figure S5: Sashimi plots of *MoYPD1* before and after 10 µg/ml fludioxonil treatment. Sashimi plots visualize the read coverage (y-axis) for corresponding *MoYPD1* genomic region (x-axis). Arcs represent splice junctions of *MoYPD1*. Beneath the sashimi plot annotated transcripts are shown with the CDS highlighted in pink.

Table S1: Primer Gibson Assembly®

Primer ID	Oligonucleotide sequences (5'→3')
Plasmid 1	
SJ1561	ttactgatcactgattaagtactgatatcggtacgaaaaaaaaacccctcaaagccctc
SJ1562	ttttttctcgctctcagcaacaaccgtaaagatgtgagttc
SJ1563	atctttacgggtgtttgctgagagcgagaaaaaaaaaactcttcgctc
SJ1564	ctcctcctcctccgacatggtggcgggttggtgctctctttt
SJ1565	agcaccaaaccgccaccatgtcggaggaggaggaggagaaca
SJ1566	tcctcgcccttgctcacaggatcgatcacgaaaaactcattgagaagtttc
SJ1567	ttttcgtgatcgatcctgtgagcaagggcgaggagctgttca
SJ1568	tgctcctcaatatcaggatctagtaacatagatgacaccgcgcgc
SJ1569	catctatgttactagatcctgatattgaaggagcatttttgggc
SJ1570	gtttgaagtttctgaattcagaagaactcgtcaagaaggcgatag
SJ1571	ttgacgagttctctgaattcaagaaactcaaacgaaagac
SJ1572	cgaagaactcctccgctcaagtcaagaatgcgcaacgctgaagggtatgaatcaataatg
Plasmid 2	
SJ1714	taagtactgatatcggtacgCTCGAGCTTGCTGGCTGTG

SJ1715	tcgctctcagTCGTGTACGCTCTGCTAGC
SJ1716	gcgtacacgaCTGAGAGCGAGAAAAAAAAC
SJ1717	acgcggccgcCTTGTACAGCTCGTCCATG
SJ1718	gctgtacaagGCGGCCGCGTACTCTGTAAAG
SJ1719	gatcgaattcCGCGGCCGCTAAGGATC
SJ1720	ggcggccgcgGAATTCGATCGTTCAAAC
SJ1721	ttgaatctaaGAATTCTCAGAAGAACTCG
SJ1722	ctgagaattcTTAGATTCAAGAACTTCAAAC
SJ1723	cttcaagtcaagaatgcgcaCTGAAGGGTATGAATCAATAATG
Plasmid 3	
SJ2359	ttactgatcactgattaagtactgatatcggtacgTTTAGAATGATAATGCTTTGTCAGCCACC
SJ2360	tttttctcgctcagTTCCTTGTTCCTTGCGCGTATGCTCA
SJ2361	accgccaagaacaaggaaCTGAGAGCGAGAAAAAAAACCTCTTCGTC
SJ2362	gtcctttacagagtacatctcgagTGGCGGTTTGGTGTCTCTTTTTGA
SJ2363	ccaaaccgccactcgagATGTACTCTGTAAAGGACTCTGAAAAG
SJ2364	ccctgtcacagatctAGGATCGATCACGAAAAAATCATTG
SJ2365	ttttcgtgatcgtctagatctGTGAGCAAGGGCGAGGAGCTGTTCA
SJ2366	atcaataatgacttgcctcCATCATGCAACATGCATGTACTGTCTGATGTATTAAGAGTATAG
SJ2367	atgcatgttgcgatgGAGCAAGTCATTATTGATTTCATACC
SJ2368	cgaagaactcctcgctcaagtcaagaatgcgcaTAGTCGACAATTAATCATCTGTGCTAG
Plasmid 4	
SJ2369	atcatcaaaaagagagcaccaaacgccaccctcgagATGCCCCGATTTTGGAGCCCA
SJ2370	ccggtgaacagctcctcgcccttgctcacaagatctttAGGATCGATCACGAAAAAATCATTGAG
Plasmid 5	
SJ2371	caaaaagagagcaccaaacgccaccctcgagATGTCCGAGGAGGAGGAGGAGAAC
SJ2372	gaacagctcctcgcccttgctcacaagatctttAGGATCGATCACGAAAAAATCATTGAGAAG

Table S2: Overview of the predicted proteins with the UniprotID and the length of the assumed amino acid sequence (n.a. indicates not available)

Protein	Uniprot ID	Length (AA)
MoYpd1p_T0	G4MTK9	153
MoYpd1p_T1	G4MTL0	135
MoYpd1p_T2	n.a.	162

Table S3: cDNA sequences of isoformT0, T1 and T2.

Isoform T0 cDNA sequence (5'→3')
ATGTAATCTGTAAAGGACTCTGAAAAGTCCGATTCCGAAGAAAACGCCGACAAGATGCCCGATTTTGGAG CCCATGTCGACAGCAGCAGCTTCGAACAGATCCTGGAAATGGACGAAGATGAGGCCGAAAGGGATTTC GCAAACCTTTAGTCATGGGATTCTTTGAACAAGCAGAGGAGACTTTTGAAAAAATGGACAAGGCCCTGAAA GATCGTGAATTTGAAAGAGCTTTGAGCCTTGCCACTTCCTCAAGGGTTCATCCGCCACTCTGGGCTTTA CAAAGGTCAAGGACAGCTGCCAAGTGATTCAACAGTACGGAACAAGCTGAACTAGACGGCACTGAGGA GCCAAGCGAGGATGTGTGCTATGAGAAGATCGATAAAGCACTTGTGGATGCCAAGAAGGATATGGAGAGT TTGAAGAACTTCTCAATGAGTTTTTCGTGATCGATCCTTAG
Isoform T1 cDNA sequence (5'→3')
ATGCCCGATTTTGGAGCCCATGTGACAGCAGCAGCTTCGAACAGATCCTGGAAATGGACGAAGATGAG GCCGAAAGGGATTTCAGCAAACCTTTAGTCATGGGATTCTTTGAACAAGCAGAGGAGACTTTTGAAAAAAT GGACAAGGCCCTGAAAGATCGTGACTTGAAAGAGCTTTGAGCCTTGCCACTTCCTCAAGGGTTCATCC GCCACTCTGGGCTTTACAAAGGTCAAGGACAGCTGCCAAGTGATTCAACAGTACGGAACAAGCTGAAAC TAGACGGCACTGAGGAGCCAAGCGAGGATGTGTGCTATGAGAAGATCGATAAAGCACTTGTGGATGCCA AGAAGGATATGGAGAGTTTGAAGAACTTCTCAATGAGTTTTTCGTGATCGATCCTTAG
Isoform T2 cDNA sequence (5'→3')
ATGTCGGAGGAGGAGGAGGAGGAGAACAAGAAGACCAAAGTCGTGGGTGGTGTGAATCCGATTC CGAAGAAAACGCCGACAAGATGCCCGATTTTGGAGCCCATGTGACAGCAGCAGCTTCGAAC AGATCCTGGAAATGGACGAAGATGAGGCCGAAAGGGATTTCAGCAAACCTTTAGTCATGGGAT

TCTTTGAACAAGCAGAGGAGACTTTTGAAGGATGGACAAGGCCCTGAAAGATCGTGAAGTGAAGAGCTTTTCGAGCCTTGGCCACTTCCTCAAGGGTTCATCCGCCACTCTGGGCTTTACAAAGGTCAAGGACAGCTGCCAAGTGATTCAACAGTACGGAAACAAGCTGAAACTAGACGGCACTGAGGAGCCAAGCGAGGATGTGTGCTATGAGAAGATCGATAAAGCACTTGTGGATGCCAAGAAGGATATGGAGAGTTTGAAGAACTTCTCAATGAGTTTTTCGTGATCGATCCTTAG

Table S4: Overview of the total AS events in *M. oryzae* via rMATS

Sample	Treatment	5'ASS	3'ASS	SE	IR	MXE	Total
t0	-	1030	1290	434	689	31	3474
t25	KCl [0.5 M]	1129	1415	591	670	46	3851
t180	KCl [0.5 M]	1089	1430	553	697	43	3812
t0	-	1151	1299	464	717	30	3661
t25	sorbitol [0.5 M]	1015	1219	424	612	22	3292
t180	sorbitol [0.5 M]	1012	1281	432	617	25	3367
t0	-	1030	1290	434	689	31	3474
t25	fludioxonil [10 µg/ml]	852	1106	306	490	12	2766
t180	fludioxonil [10 µg/ml]	944	1225	328	621	28	3146

Table S5: ddPCR Primer

Primer ID	Oligonucleotide sequences (5'→3')
SJ2494	GACGTTCGAACAGATCCT
SJ2596	CTCGAAAGCTCTTTCAAGTC