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CORRECTION
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Corrigendum: Strategies for Efficient Gene Editing in Protoplasts of *Solanum tuberosum* Theme: Determining gRNA Efficiency Design by Utilizing Protoplast (Research)

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A Corrigendum on

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In the original article, there were various errors present throughout the main text. These errors have been corrected in the original article.

Additionally, **Figure 1** and **Table 1** have been updated. The updated figure and table are shown below. The Funding statement has also been updated and is shown below.

FUNDING

Kartoffelafgiftfonden (2021) "Samtidig introduktion af flere egenskaber i kartoffel vha. DNA-fri CRISPR". Kartoffelafgiftfonden (2022)" Reduceret miljø og klima aftryk gennem præcis forædling af skimmel resistens i stivelses kartofler". Novo Nordisk Foundation (2020) "Gene edited potatoes for reduced pesticide usage" (NNF19OC0057208). Grønt Udviklings-og Demonstrations program (GUDP) (2020) "KRISPS Kartofler med Resistens og Innovativ Stivelse som Platform for Synergi

mellem grøn og økonomisk bæredygtighed" (34009-19-1531). DFF/ Independent Research Fund Denmark (2022) "Green CRISPR production platform for new starch qualities" (1032-00399B).

The authors apologize for these errors and state that they do not change the scientific conclusions of the article in any way. The original article has been updated.

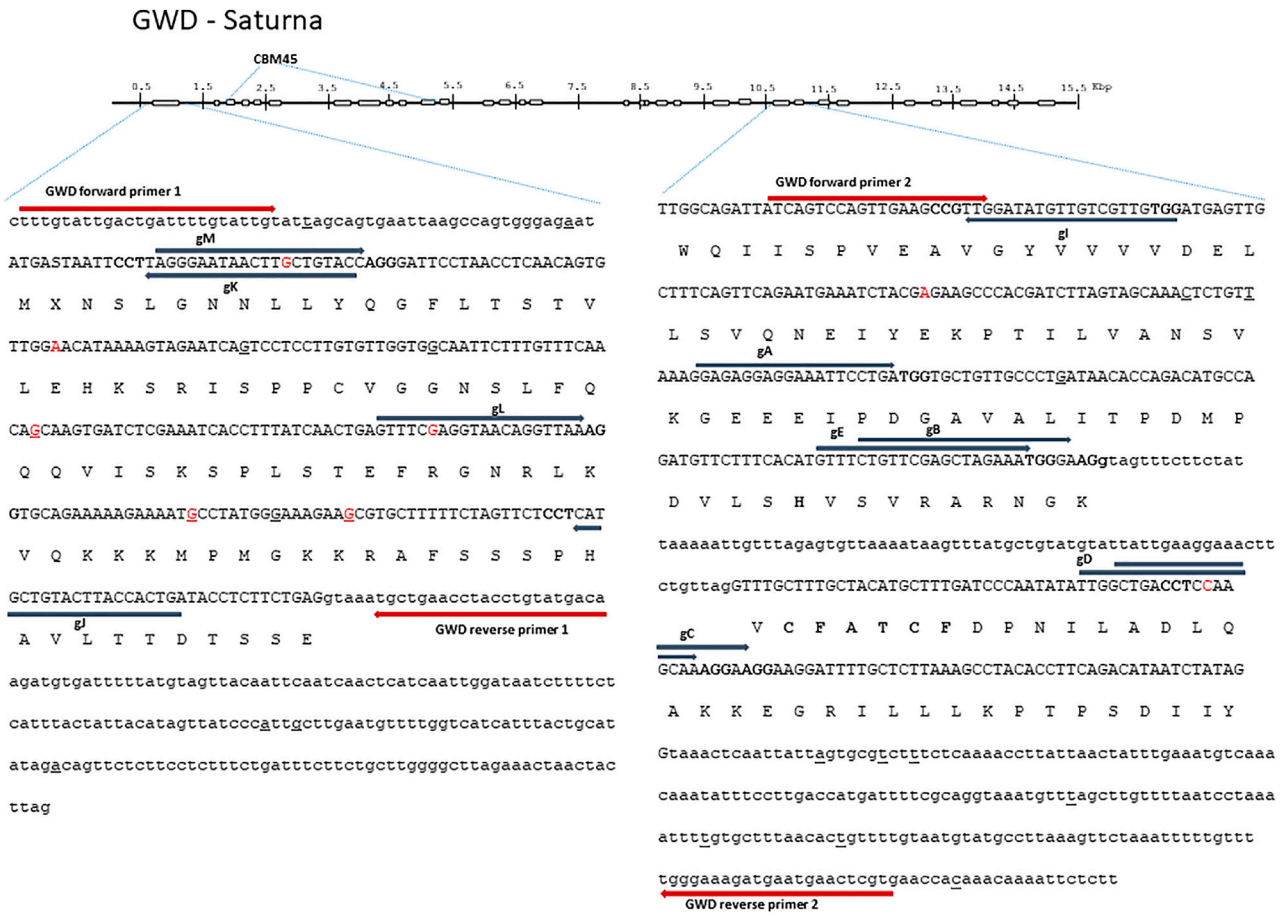

FIGURE 1 | Glucan Water Dikinase (GWD) 1—structure and full allelic sequence of gRNA target regions. Overall gene structure with exons (boxes) and the area containing carbohydrate-binding module (CBM) depicted above. Left: the nucleotide sequence of exon 1 and introns. Right: exon 24 and 25 including introns. Exons are depicted in capital letters with the amino acid sequence indicated. Small nucleotide polymorphisms (SNPs) from cultivars included in the SPUD database are marked with red, and SNPs found in Saturna are underlined. Grey arrows designate gRNAs (gA, gB, gC, gD, gE, gI, gJ, gK, gL, and gM) with PAM sites marked in bold. Red arrows designate diagnostic IDAA PCR primers. The "CFATC" region, containing cysteine's hypothesized to be involved in inter or intra-di-sulfide bond formation and thus in putative redox-state modulation of GWD activity is marked with bold. The active site histidine residue is also marked with bold.

TABLE 1 | gRNAs and diagnostic IDAA primers for each of the four target regions. Scores and first selection of gRNAs were obtained by feeding ca 1 kb regions to the *in silico* prediction servers CHOPCHOP (http://chopchop.cbu.uib.no/), CRISPRater (https://crispr.cos.uniheidelberg.de/) and SSC (http://crispr.dfci.harvard.edu/SSC/).

	Diagnostic PCR(s)	gRNA
GWD—5′ exon 1	GWD Forward primer 1	gJ: TCAGTGGTAAGTACAGCATG
	5′ TTTGTATTGACTGATTTTGTATTGT 3′	gK: AGGGAATAACTTGCTGTACC
	GWD Reverse primer 1	gL: GTTTCGAGGTAACAGGTTAA
	FAM 5′ TAGTTTCTAAGCCCCAAGCA3′	gM: GTACAGCAAGTTATTCCCTA
GWD—3′ exon 24 + 25	GWD Forward primer 2:	gA: GGAGAGGAGGAAATTCCTGA
	5′ TCAGTCCAGTTGAAGCCGTTG 3′	gB: TGTTCGAGCTAGAAATGGGA
	GWD Reverse primer 2:	gC: GCTGACCTCCAAGCAAAGGA
	FAM 5′ TCACGAGTTCATTCATCTTTCCCA 3′	gD: ATTGGCTGACCTCCAAGCAA
		gE: TTTCTGTTCGAGCTAGAAAT
		gI: CACAACGACAACATATCCAA
DMR6—5′ exon 1	DMR6 Forward primer 1	g43: TTTGAGGGAGAGTAGAGTGG
	FAM 5′ CCATGGAAACGAAAGTTATTTC 3′	g44: GTGGCCTATCGGATTCGGGT
	DMR6 Reverse primer primer 1	
	5′ CAACCTAAGTCAATTATTGGAAC 3′	
DMR6—5′ exon 2	DMR6 Forward primer 2	g45: TGGAGAAATATGCTCCTGAA
	*5′ AGCTGACCGGCAGCAAAATTG*GGTAGCTGGGGAATTTTTCA 3′	
	DMR6 Reverse primer 2	
	5′ GGTTACCATGCATAACTATACACAC 3′	
	FAM primer	
	FAM 5′ AGCTGACCGGCAGCAAAATTG 3′	
DMR6—5′ exon 1 + 2	DMR6 Forward primer 1	g43: TTTGAGGGAGAGTAGAGTGG
	FAM 5′ CCATGGAAACGAAAGTTATTTC′3	g44: GTGGCCTATCGGATTCGGGT
	DMR6 Reverse primer 2	g45: TGGAGAAATATGCTCCTGAA
	5′ GGTTACCATGCATAACTATACACAC 3′	
	DMR6 Reverse primer 4	
	FAM 5′ CGATGGATTAGAAGGCCATTC 3′	
DMR6—3′ exon 3	DMR6 Forward primer primer 3	g46: GAAGCCATAGCAGAGAGCCT
	5′ ATCGTGAGCAGATATTGCACG 3′	g47: GAATTTGGATCAGTATGGGC
	DMR6 Reverse primer 3	g48: ATCACCAAGATTAATGACAA
	FAM 5′ GGTTTACCTGCAATTGATCAC 3′	