

Appendix A. Primers used in this study

Gene	Forward Primer	Reverse Primer	Application
PGSC0003DMP 400052768	GGAGGCCAGTGAATTCATGG GAAAGAACATGTGGAGT	CGAGCTCGATGGATCCTCAAA AACATCTAAGTTCTTCGAAA	AD vector
PGSC0003DMP 400000374	GGAGGCCAGTGAATTCATGGC AAAGAGATCACATCGCC	CGAGCTCGATGGATCCTTACT GGTCCACGCTACTCTCAG	AD vector
PGSC0003DMP 400000617	GGAGGCCAGTGAATTCATGTAC AGATCATTTGTCACTTGTG	CGAGCTCGATGGATCCCTATA GTGTGAGTTCAGTAAGTGC	AD vector
PGSC0003DMP 400002653	GGAGGCCAGTGAATTCATGTCA GCAAGAATGTTATCTTCT	CGAGCTCGATGGATCCTTAGT TGGTAAATAGTTGCCTACAA	AD vector
PGSC0003DMP 400002841	GGAGGCCAGTGAATTCATGGC AAGGAAGTTTCTTTTACA	CGAGCTCGATGGATCCTTATG ACAACATATCCTTGATCACT	AD vector
PGSC0003DMP 400004790	GGAGGCCAGTGAATTCATGGC ACAGAAGCATTTACATGA	CGAGCTCGATGGATCCTTAG GCCAAAACCTTTATTGAAATT	AD vector
PGSC0003DMP 400005078	GGAGGCCAGTGAATTCATGGA GGTTGAAAAGAGAACTTCA	CGAGCTCGATGGATCCTCACA TTAGGGCACCGATCA	AD vector
PGSC0003DMP 400019433	GGAGGCCAGTGAATTCATGCC GCTGGAACAACT	CGAGCTCGATGGATCCCTAAT AAACGTCGATGAATATTAGC	AD vector
PGSC0003DMP 400021574	GGAGGCCAGTGAATTCATGGA GAAAAAGAGATCATCAAGAA	CGAGCTCGATGGATCCTTAGC TACACAAGAAAAAGGTATGA	AD vector
PGSC0003DMP 400026354	GGAGGCCAGTGAATTCATGGTT GTTGAGAAACAGGGTTCC	CGAGCTCGATGGATCCTTAGA GTAGCAAGATGTCAGCAAC	AD vector
PGSC0003DMP 400027391	GGAGGCCAGTGAATTCATGCC TCCAGACAGTCTG	CGAGCTCGATGGATCCCTATA GCATGAAGTCGGTCAAC	AD vector
PGSC0003DMP 400029803	GGAGGCCAGTGAATTCATGGC TTCTTCATCTCCTAG	CGAGCTCGATGGATCCCTAAT TATGAGAAAAAACATCTTCC	AD vector
PGSC0003DMP 400034825	GGAGGCCAGTGAATTCATGAAT GGGTTTCAGAATGGAAAAA	CGAGCTCGATGGATCCTCAC GCTCTACCTGTCAATTCAATG	AD vector
PGSC0003DMP 400039456	GGAGGCCAGTGAATTCATGGA TTCGAAATTGATGAAACCA	CGAGCTCGATGGATCCCTAG CTCAACATGACATCAACT	AD vector
PGSC0003DMP 400039853	GGAGGCCAGTGAATTCATGGA TGGTATGGATGATAGGAGA	CGAGCTCGATGGATCCTTAGA AAACTAACTTCCTACGGGA	AD vector
PGSC0003DMP 400040702	GGAGGCCAGTGAATTCATGGA AAGGAAGCAGCACACAC	CGAGCTCGATGGATCCTCAAT GCAAAGCTAATTCTGCAAC	AD vector
PGSC0003DMP 400041331	GGAGGCCAGTGAATTCATGGA GAAAAGTCGTCACAGG	CGAGCTCGATGGATCCCTAG ATTGCACCTACAACCTTCTTC	AD vector
PGSC0003DMP 400041952	GGAGGCCAGTGAATTCATGGG TAGAGAGTGGTTATACTGGG	CGAGCTCGATGGATCCTCACA CAGTATCATGCACCAC	AD vector
PGSC0003DMP 400042454	GGAGGCCAGTGAATTCATGGC TGCCAAGCTTTTACATTC	CGAGCTCGATGGATCCCTACT TTGCAAAGAGCTGTCTACGC	AD vector

PGSC0003DMP	GGAGGCCAGTGAATTCATGAAT	CGAGCTCGATGGATCCTTAGC	AD
400045837	GATAGTTTAGCCATAACAG	TAGAACTGTAGAGGTCC	vector
PGSC0003DMP	GGAGGCCAGTGAATTCATGGC	CGAGCTCGATGGATCCTTAG	AD
400049129	ACAGAAGCATTTGC	GAGTGAGCTAAATGAATTAGC	vector
PGSC0003DMP	GGAGGCCAGTGAATTCATGGC	CGAGCTCGATGGATCCTCATT	AD
400052652	TAAAAATCCAAAAGACACA	GTGCAAAGATTACGAGT	vector
PGSC0003DMP	GGAGGCCAGTGAATTCATGGC	CGAGCTCGATGGATCCTCAC	AD
400054403	TGTCTCAAGTGATGATC	CAGCATCTTCCATATTTTC	vector
StOFP20	GGCGAATTCATGGGGAATTATA	GGCGGATCCTTACTTCAGTCG	BD
	GGTTTAGATTATCA	AATTTCAGTGATG	vector
StTRM5	GGAGGCCAGTGAATTCATGGA	CGAGCTCGATGGATCCTCAAA	AD
	TGGTATGGATGATAGGAG	CCTTGAACATTTACTAAAA	vector
StOFP20-BD	CATGGAGGCCGAATTCATGGG	GCAGGTCGACGGATCCTTACT	BD
	GAATTATAGGTTTAGATT	TGAGTCGAATTTCACTGA	vector
StTON1-AD	GGAGGCCAGTGAATTCATGGA	CGAGCTCGATGGATCCCTATT	AD
	CGATTACACTAGAGAAATG	CCATCCTGCCATCATCC	vector
StTON2-AD	GGAGGCCAGTGAATTCATGTAC	CACCCGGGTGGAATTCTCATC	AD
	AGTGGCTCAAGCG	CTTCTTCTTGGGGTTCTTCC	vector
StTON1-BD	CATGGAGGCCGAATTCATGGA	GCAGGTCGACGGATCCCTATT	BD
	CGATTACACTAGAGAAATG	CCATCCTGCCATCATCC	vector
StTON2-BD	CATGGAGGCCGAATTCATGTAC	GCAGGTCGACGGATCCTCAT	BD
	AGTGGCTCAAGCG	CCTTCTTCTTGGGGTTCTTCC	vector
StOFP20-M1-F	CATGGAGGCCGAATTCATGGG	GCAGGTCGACGGATCCTGAT	BD
	GAATTATAGGTTTAGATTATCA	TTCACCACTGCAAAGCTC	vector
	G		
StOFP20-M2-F	CATGGAGGCCGAATTCTCAAGA	GCAGGTCGACGGATCCGATG	BD
	AATCCTCAGAAAGATTTC	TCGAACCAGATTTGCTT	vector
StTRM20-M-1	GGAGGCCAGTGAATTCATGAAT	ATCAATATTCCACCCTGGTGC	AD
	GGGTTTCAGAATGGAAAAA		vector
StTRM20-M-2	GGGTGGAATATTGATAGTCTTA	CGAGCTCGATGGATCCTCAC	AD
	GCAAGACACACAACTGC	GCTCTACCTGTCAATTCAATG	vector
StTRM5-M-1	GGAGGCCAGTGAATTCATGGA	AGGATCATATACAAAATTCCG	AD
	TGGTATGGATGATAGGAGA	GTG	vector
StTRM5-M-2	TTTGTATATGATCCTTCGAGAT	CGAGCTCGATGGATCCTTAGA	AD
	CAGTTTCACCAAGC	AACTAACTTCCTACGGGA	vector
StTRM19-M-1	GGAGGCCAGTGAATTCATGGA	CTTCCCTTCAGAAAGAACCGG	AD
	GAAAAGTCGTCACAGG		vector
StTRM19-M-2	CTTTCTGAAGGGAAGAACCCTTG	CGAGCTCGATGGATCCCTAG	AD
	GGATAACACAAAGTAATAT	ATTGCACCTACAACCTTCTTC	vector
StOFP20	CGGGGGACGAGCTCGGTACCA	ACGAGATCTGGTCGACCTTCA	nLuc
	TGGGGAATTATAGGTTTAGATT	GTGCAATTTCACTGATGT	vector
	ATCAG		

StTRM20	ACGCGTCCCGGGGCGGTACCA TGAATGGGTTTCAGAATGGAAA	ACGCGTCCCGGGGCGGTACC ATGAATGGGTTTCAGAATGGA AA	cLuc vector
StTRM5	ACGCGTCCCGGGGCGGTACCA TGGATGGTATGGATGATAGGA GA	AGCTCTGCAGGTCGACTTAGA AACTAACTTCCTACGGGAAG	cLuc vector
StTRM19	ACGCGTCCCGGGGCGGTACCA TGGAGAAAAGTCGTCACAGGA	AGCTCTGCAGGTCGACCTAG ATTGCACCTACAACTTCTTCTA TG	cLuc vector
StTRM11	ACGCGTCCCGGGGCGGTACCA TGGCTTCTTCATCTCCTAG	AGCTCTGCAGGTCGACCTAAT TATGAGAAAAAACATCTTCC	cLuc vector
StOFP20	GAGCTTTGCAGTGGTGAAATCA T	TCGAACCAGATTTGCTTGAAG AC	qPCR
Cas9	GCAGCTCTCCAAGGACACAT	CGTGAGTTCTTCTGGCCCTT	PCR

Appendix B. Coding sequence and amino acid sequence alignment of StOFP20 and SLOFP20.

>Nucleotide alignment 8 Alignment of 2 sequences: St0FP20, Sl0FP20

Score = 3774.0, Identities = 887/1056 (83%),
Positives = 887/1056 (83%), Gaps = 105/1056 (9%)

St0FP20	1	ATGGGGAATTATAGGTTTAGATTATCAGATATGATGCCAAATGCTTGGTTTTACAACCTC	60
		ATGGGGAATTATAGGTTTAGATTATCAGATATGATGCCAAA GCTTGGTTTTACAA CTC	
SLOFP20	1	ATGGGGAATTATAGGTTTAGATTATCAGATATGATGCCAAACGCTTGGTTTTACAAGCTC	60
St0FP20	61	AAAGAAATAGGCAAAAGCAGCAGCAGCAGCAGCAGCAAGAACCCATAGCCACACA	120
		AAAGA AT G CAAAAGCAG CAGCAGAAG CATAGCCACA	
SLOFP20	61	AAAGACATGGCCAAAAGCAG-----CAGCAGAAGACATAGCCACA---	100
St0FP20	121	ACTTCATCAACATCAACATCATCATCAAATCTACAGCCAGACAAAAAAGACAACCCC---	178
		CAACATCATCATCAAATCT CA C AGACAAAAAAGACAACCCC	
SLOFP20	101	-----CAACATCATCATCAAATCTTCAACTAGACAAAAAAGACAACCCCAT	147
St0FP20	179	-ATAACCTTGGTTGTCAAAGAAAATCATATTACATTTCAAGAAACCTCACTAGTAGTAGT	237
		ATAACCTTGGTTGTCAAAGAAAATCATATTACATTTCAAGAAACCTCACTA TA TAG	
SLOFP20	148	AATAACCTTGGTTGTCAAAGAAAATCATATTACATTTCAAGAAACCTCACTATTACTAG-	206
St0FP20	238	CCACCTGAACATTTTCTCAGAATCCTTATCTTCTTCAACAGCCCAAAACCCGAT-----	291
		TCC ATCTCTTCTAACAG CCAAAAC CGAT	
SLOFP20	207	-----TCCCATCTCTTCTAACAGTCCAAAACCTCGATCACAAAC	243
St0FP20	292	---CATTTCACTGAGCCATCAAGAAAGTCTTGAAGAAAAGGCGTAGTACCAATTCAGG	348
		CA TCACTGAGCCATCAAGAAAGTCTT CAAGAAAAGGCGTAGTAC AATT CAGG	
SLOFP20	244	GTCACATCACTGAGCCATCAAGAAAGTCTTACAAGAAAAGGCGTAGTACAAATTCAGG	303
St0FP20	349	AAGAGAAATTCCTCCAAACTTGTCAATCCCTCTGTTTCAGCCAATTGTAGTTGCCGCGCT	408
		A GAGAAATTCCTC AAAC TGTCAAT CCTCT GCT	
SLOFP20	304	AGGAGAAATTCCTCGAAACCTGTCAATTCCTCT-----GCT	339
St0FP20	409	TCTGTTGAATCTGTCTGGACTAAAGCTGATTCACCCCTGAAGAATACCCAAATTCATCT	468
		TCTGTTGAATCTGTCTGGAC AAA CTGATTC ACCCTGAA AATACCCAAATTCATC	
SLOFP20	340	TCTGTTGAATCTGTCTGGACGAAACCTGATTCACCCCTGAACAAATACCCAAATTCATCG	399
St0FP20	469	TCCTCTTCGTCGTCTCATCACCATCTTCAATTTTGCTGAAAAATCAAAACCCATTACT	528
		TC TC TCGTCGTCTCATCACCATCTTCAATTTTGCT A AATCAAAACCCATT CT	
SLOFP20	400	TCTTCTCGTCGTCTCATCACCATCTTCAATTTTGCTCATAAATCAAAACCCATTGCT	459
St0FP20	529	TCAATTACACCGTCTTGTGACTGCAGAAGTATTACATGAATCAAGATTGAGCCAATCTT	588
		TCAATT CACCGTCTTG GACTG AGAAGTATTACA GAATCAA ATTCAGCCAATCTT	
SLOFP20	460	TCAATTCACCGTCTTGGACTGTAGAAGTATTACAGCAATCAAAATTCAGCCAATCTT	519
St0FP20	589	GATCATGGGGTTCACTCTGTTTCCAAAATTGACCTTCTCTGATCATAAACAAACCCGAA	648
		GATC TGGGGTTCACTCTGTTTCCAAAATTGACCTTCTCTGATCATAAACAA CCCGAA	
SLOFP20	520	GATCTCGGGTTCACTCTGTTTCCAAAATTGACCTTCTCTGATCATAAACCAAGCCGAA	579
St0FP20	649	AAATTCGATGAAAAAAGAGAAAAAAGAGGAGTGTGAAACAAGAACAGGAGGATGTG	708
		AAATTC A GAAAA A AAGAAAAACAGAGGATGTGAAACAAGAACAGGAGGAT GTG	
SLOFP20	580	AAATTCACGAAAAAGATCCAGAAAAACAGAGGATGTGAAACAAGAACAGGAGGATGTG	639
St0FP20	709	AGAAGAGTATCAACAAATGGTGTGAAGCTGAGAACAATTCACCAAGAATAACAACAAAC	768
		AGAAGAGTATCAACAAATGGTGTGAAGCTGAGAACAATTCACCAAGAATAACAACAA	
SLOFP20	640	AGAAGAGTATCAACAAATGGTGTGAAGCTGAGAACAATTCACCAAGAATAACAACAA---	697
St0FP20	769	AGCAAGAAGATTCAAGGAAGCAGAAAGAGTGTTCATCAAAAAGGACAAGTGTGA---CA	825
		CAA A CAA AGCAGAAAGAGTGTTCATCAAAAAG ACAAGTGTGA CA	
SLOFP20	698	---CAACCA---CA--ACAGCAGAAAGAGTGTTCATCAAAAAGACAAGTGTTCACGACA	750
St0FP20	826	GAGAGCTTTGCAAGTGGTGAATCATCAAGAAATCCTCAGAAAGATTTTCAGAGAATCAATG	885
		GA AGCTTTGCAAGTGGTGAATCATC AGAAATCCTCA AAAGATTTTCAGAGAATCAATG	
SLOFP20	751	GACAGCTTTGCAAGTGGTGAATCATCAGAAATCCTCAAAAAGATTTTCAGAGAATCAATG	810
St0FP20	886	GTGGAAATGATAGTTGAGAATAATATAAGAACATCAAGGATTTTGAAGAAGTCTTCTGCT	945
		GTGGAAATGAT TTGAGAA AATATAA AACATCAAGGATTTTGAAGAAGTCTTCTGCT	
SLOFP20	811	GTGGAAATGATCATTGAGAACAATATAACAACATCAAGGATTTTGAAGAAGTCTTCTGCT	870
St0FP20	946	TGCTATCTTTTCAATTAATTCAGATGAGTATCATGATCTAATCATCAAGTCTTCAAGCAA	1005
		TGCTATCTTTTCAATTAATTCAGATGA TATCATGAT TAATCATCAAGT TTCAAGCAA	
SLOFP20	871	TGCTATCTTTTCAATTAATTCAGATGAATATCATGATATATAATCATCAAGATTTCAAGCAA	930
St0FP20	1006	ATCTGGTTCGACATCACTGAAATTCGACTGAAGTAA 1041	
		ATCTGGTTCGA ATCACTGAAATTCGACT AAGTAA	

>Protein alignment Alignment of 2 sequences: St0FP20 , Sl0FP20

Score = 1266.0, Identities = 282/351 (80%),
Positives = 296/351 (84%), Gaps = 35/351 (9%)

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St0FP20      1 MGNYRFRLSDMMPNAWFYKLKEIGKSSSSSRNSRSHSHTTSSTSTSSSNLQPDKKRQPH  60
               MGNYRFRLSDMMPNAWFYKLK++ KSS      SR HSHT      TSSSNLQ DKKRQPH
Sl0FP20      1 MGNYRFRLSDMMPNAWFYKLKDMAKSS-----SRRHSHT-----TSSSNLQLDKKRQPH  49

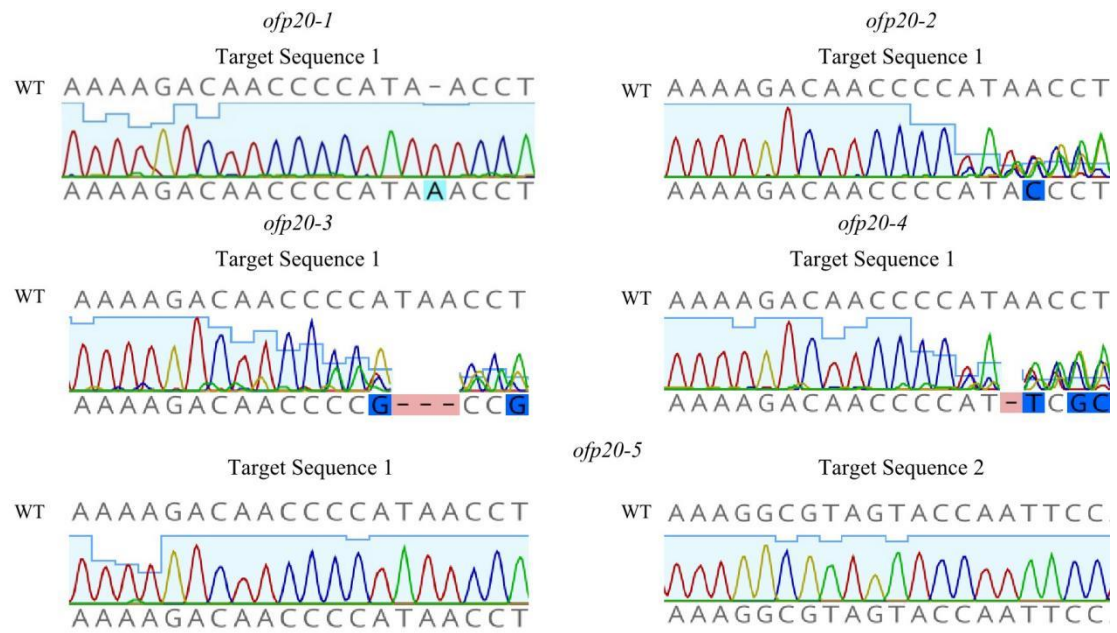
St0FP20     61 -NLGCQRKSYYSISRNLTSSSPPETFSQNPISSNSPKPDH---FTEPSRKSCCKRRSTNSR 116
               NLGCQRKSYYSISRNLT +S      PISSNSPK DH      TEPsrks KKRSTN R
Sl0FP20     50 NNLGCQRKSYYSISRNLTITS-----PISSNSPKLDHNVHITEPSRKSYKKRRSTNFR 101

St0FP20     117 KRNSPKLVNPSVSANCSRASVESVWTKADSTPEEYPNSSSSSSSSSPSSILPEKSNPIT 176
               +RNSPK VN S      ASVESVWTK DSTPE+YPNSSSSSSSSSPSSILP KSNPI
Sl0FP20     102 RRNSPKPVNSS-----ASVESVWTKPDSTPEQYPNSSSSSSSSSPSSILPHKSNPIA 153

St0FP20     177 SITPSCDCRTDYMNQDSANLDHGVHSVSKIDLPRIITKPEKFDEKKEEKQRIVKQEQRIV 236
               SI+PSCDCRTDY NQ+SANLD GVHSVSKIDLPRIITKPEKF+EK +EKQRIVKQEQRIV
Sl0FP20     154 SISPSCDCRTDYNQNSANLDPGVHSVSKIDLPRIITKPEKFNEKIQEKQRIVKQEQRIV 213

St0FP20     237 RRVSTNGVKLRTNSPRITTNSKKIQGSRKSVSSKRTSV-TESFAVVKSSRNPQKDFRESM 295
               RRVSTNGVKLRTNSPRITT +      SRKSVSSKRTSV T+SFAVVKSSRNPQKDFRESM
Sl0FP20     214 RRVSTNGVKLRTNSPRITTTT---TNSRKSVSSKRTSVTTDSFAVVKSSRNPQKDFRESM 270

St0FP20     296 VEMIVENNIRTSKDLEELLACYLSLNSDEYHDLIIKVKQIWF DITEIRLK 346
               VEMI+ENNI TSKDLEELLACYLSLNSDEYHD+IIKVKQIWF+ITEIRLK
Sl0FP20     271 VEMIIENNITT SKDLEELLACYLSLNSDEYHDIIKVKQIWF EITEIRLK 321
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Appendix C. Mutation profiles for the first target in sequencing chromatogram

Appendix D. Mutations of OFP20 induced by CRISPR/Cas9

>OFP20 WT

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TAGTAGTCCACCTGAAACATTTTCTCAGAATCCTATCTCTTCTAACAGCCCAAAACCC
GATCATTTCACTGAGCCATCAAGAAAGTCTTGCAAGAAAAGGCGTAGTACCAATTCC
AGGAAGAGAAATTCTCCCAAACCTTGTCATCCCTCTGTTTCAGCCAATTGTAGTTGC
CGCGCTTCTGTTGAATCTGTCTGGACTAAAGCTGATTCCACCCCTGAAGAATACCCA
AATTCATCTTCCTCTTCGTCGTCCTCATCACCATCTTCAATTTTGCCTGAAAAATCAA
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>ofp20-1

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>ofp20-2-1

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>ofp20-2-2

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>ofp20-2-3

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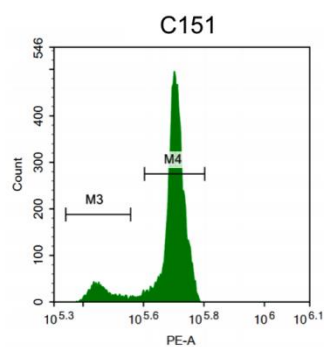
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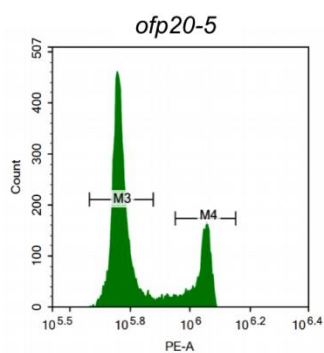
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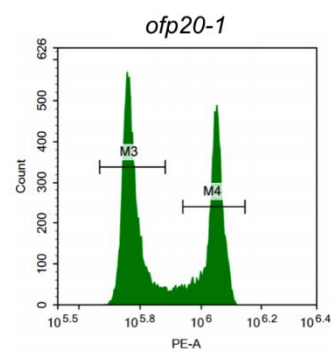
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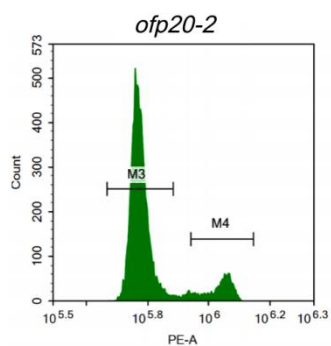
Gate	Mean X
P2	486,851
M3	292,571
M4	511,326



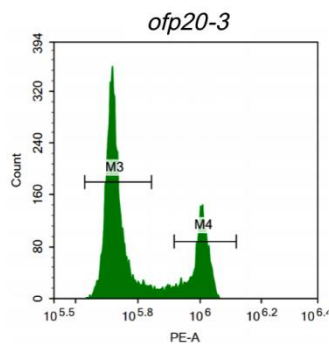
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M3	591,663
M4	1,095,209



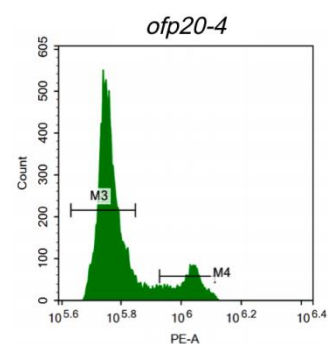
Gate	Mean X
P2	828,149
M3	600,580
M4	1,111,602



Gate	Mean X
P2	669,228
M3	599,031
M4	1,094,164



Gate	Mean X
P2	675,024
M3	538,603
M4	1,005,605



Gate	Mean X
P2	667,203
M3	576,994
M4	1,058,803

Appendix E. Ploidy measurement of transgenic and control plants.

StTRM19 895 CAAAAGTCCTCACC GGTTCTTTCTGAAGGGAAGGAGGAAAACATTCTACCAACAAGAAATTGTTGTTCTGAAGCCAAACCTTGGGATAACACAAAGTAATATTGCTTCT 1002
 CAAAAGTCCTCACC GGTTCTTTCTGAAGGGAAG ----- AACCTTGGGATAACACAAAGTAATATTGCTTCT

StTRM5 1031 CGGAGCAGATTGGCCACC GGAATTTGTATATGATCCTACTTTATCATCTGATGAGTCCCAATAGTCCTTATGAGGCTTCGAGATCAGTTTCACCAAGCCATAGAA 1138
 CGGAGCAGATTGGCCACC GGAATTTGTATATGATCCT ----- TCGAGATCAGTTTCACCAAGCCATAGAA

StTRM20 944 TTGTCTGATTTCCTCCTGCACCA GGGTGGAATATTGATGAAAATCCCGCTCAGCCGACAAAGGATAGTGGTGTGAAACCAAGTCTTAGCAAGACACACAACCTGCAG 1052
 TTGTCTGATTTCCTCCTGCACCA GGGTGGAATATTGAT ----- AGTCTTAGCAAGACACACAACCTGCAG

Appendix F. Alignment of the wildtype and deleted M10 motif in the three TRM proteins.

Appendix G. Amino acid sequence alignment of TON proteins from potato and *Arabidopsis*.

>Protein alignment 4 Alignment of 2 sequences: StTON1, >AT3G55005

Score = 859.0, Identities = 175/261 (67%),
Positives = 205/261 (78%), Gaps = 10/261 (3%)

```

StTON1      1 MDDYTREMMDLKTLLVTRTLEKKGVLAKIRAE LRASVF EAIED EDRVIEKDETLP PALLGS 60
              MDDYTREMMDLKTLLVTRTLEKKGVLAKIRAE LRASVF EAIE+EDRVIE +E LPPALLGS
>AT3G55005  1 MDDYTREMMDLKTLLVTRTLEKKGVLAKIRAE LRASVF EAIEEEDRVIE NNENGLPPALLGS 60

StTON1      61 CNDQAKQLHN SP SGRLLTALICEYLDWAQLNHTLKVYLPECNLPKESWKSELKEFSSKNG 120
              CND+A+QLH SP SGRL+ALICEYLDWAQLNHTLKVY PECN K+SWKSE+++FS NG
>AT3G55005  61 CNDRARQLHASPSGRLLSALICEYLDWAQLNHTLKVYQPECNSAKDSWKSEIRDFSINNG 120

StTON1      121 YDLNRNGDSAPLLLDVLEGFLKYENFSQAKGAGSLSNTEARNV-----RKPSSSSSVAGG 174
              Y+LNRN DS PLLLDVLEGFLK+EN +Q G S +E + P SS +
>AT3G55005  121 YELNRNEDSRPLLDVLEGFLKFENMTQVMGGSSRRESETESSLSLDTRNPPRRSSASDS 180

StTON1      175 LPPLGRPGPAAQSSDRRAGSSISGYRKDEYNWRYENEELSQDVMLASSALENLQLDRKAR 234
              LP R A+Q+S G++ SGYRKDE NWR Y+ E++ ++VM AS+ALENLQLDRK R
>AT3G55005  181 LPHQRRSVSASQAS-----GAATSGYRKDESNWRYDTE DMPEEVMRASTALENLQLDRKTR 236

StTON1      235 NLTTSWRHRG DGI SEDDGRME 255
              NLT+SWR+ DG SE++ +
>AT3G55005  237 NLTSSWRNVK DGTSEEEEGKD 257

```

>Protein alignment 3 Alignment of 2 sequences: StTON1, >AT3G55000

Score = 904.0, Identities = 179/261 (68%),
Positives = 212/261 (81%), Gaps = 7/261 (2%)

```

StTON1      1 MDDYTREMMDLKTLLVTRTLEKKGVLAKIRAE LRASVF EAIED EDRVIEKDETLP PALLGS 60
              MDDYTREMMDLKTLLVTRTLEKKGVLAKIRAE LRASVF EAIE+EDRVIE +E PPALLGS
>AT3G55000  1 MDDYTREMMDLKTLLVTRTLEKKGVLAKIRAE LRASVF EAIEEEDRVIE NNENEGPPPALLGS 60

StTON1      61 CNDQAKQLHN SP SGRLLTALICEYLDWAQLNHTLKVYLPECNLPKESWKSELKEFSSKNG 120
              CND+A++LH SP SGRL+ALICEYLDWAQLNHTL VY PE NLPK+SWKSEL++F+S NG
>AT3G55000  61 CNDRARKLHASPSGRLLSALICEYLDWAQLNHTLIVYQPESNLPKDSWKSEL RDFSNNNG 120

StTON1      121 YDLNRNGDSAPLLLDVLEGFLKYENFSQAKGAGSLSNTEARNV-----RKPSSSSSVAGG 174
              ++LNRNGDS PLLLDVLEGFLK+E+ +Q G+ S ++E + P SS +
>AT3G55000  121 FELNRNGDSGPLLLDVLEGFLKFESMTQGMGSSSRDSETESSSSLESRNPPRRSSASDS 180

StTON1      175 LPPLGRPGPAAQSSDRRAGSSISGYRKDEYNWRYENEELSQDVMLASSALENLQLDRKAR 234
              LPP RP A+Q+SDRRAG S SGYRKDE+NWR N++ ++V AS+ALENLQLDRK R
>AT3G55000  181 LPPQRRPVSASQASDRRAGLSTSGYRKDEFNWRQGNQDTHEEVTRASA ALENLQLDRKTR 240

StTON1      235 NLTTSWRHRG DGI SEDDGRME 255
              NLT+SWR+ DG +E++GR
>AT3G55000  241 NLTSSWRNV R DGTNEEEGRD- 260

```

>Protein alignment 2 Alignment of 2 sequences: StTON2 , >AT5G18580

Score = 2303.0, Identities = 437/480 (91%),
Positives = 453/480 (94%), Gaps = 2/480 (0%)

```
StTON2      1 MYSGSSDGE GPDAPAQRKIPPPSSMLWVRNLRRYIGSGAGLGSEALMELETKRILLDIFK  60
              MYSGSSDGE  D   QRKIPP SSMLWVRNLRRYIGSGAGLGSEALMELETKRILL+IFK
>AT5G18580   1 MYSGSSDGESHDTSTQRKIPPASSMLWVRNLRRYIGSGAGLGSEALMELETKRILLEIFK  60

StTON2      61 EKQKQSAEAGTIPSFYKKKPEEGSISHRVQRLAKYRFLKKQSDLLLNADDLDAMWVCLRE 120
              EKQQKS  EAGTIPSFYKKKPEEGSIS RVQ+LAKYRFLKKQSDLLLNADDL AMWVCLRE
>AT5G18580   61 EKQKQSQEAGTIPSFYKKKPEEGSISQRVQKLAKYRFLKKQSDLLLNADDLAAMWVCLRE 120

StTON2      121 NCVIDDATGAEKMNIEDFCHIASVCTEQIGPKCRRFFSPSNFMKFEKDESGRIAILPFYL 180
              NCVIDDATGAEKMNIEDFCHIASVCTEQIGPKCRRFFSPSNFMKFEKDE+GRIAILPFYL
>AT5G18580   121 NCVIDDATGAEKMNIEDFCHIASVCTEQIGPKCRRFFSPSNFMKFEKDEAGRIAILPFYL 180

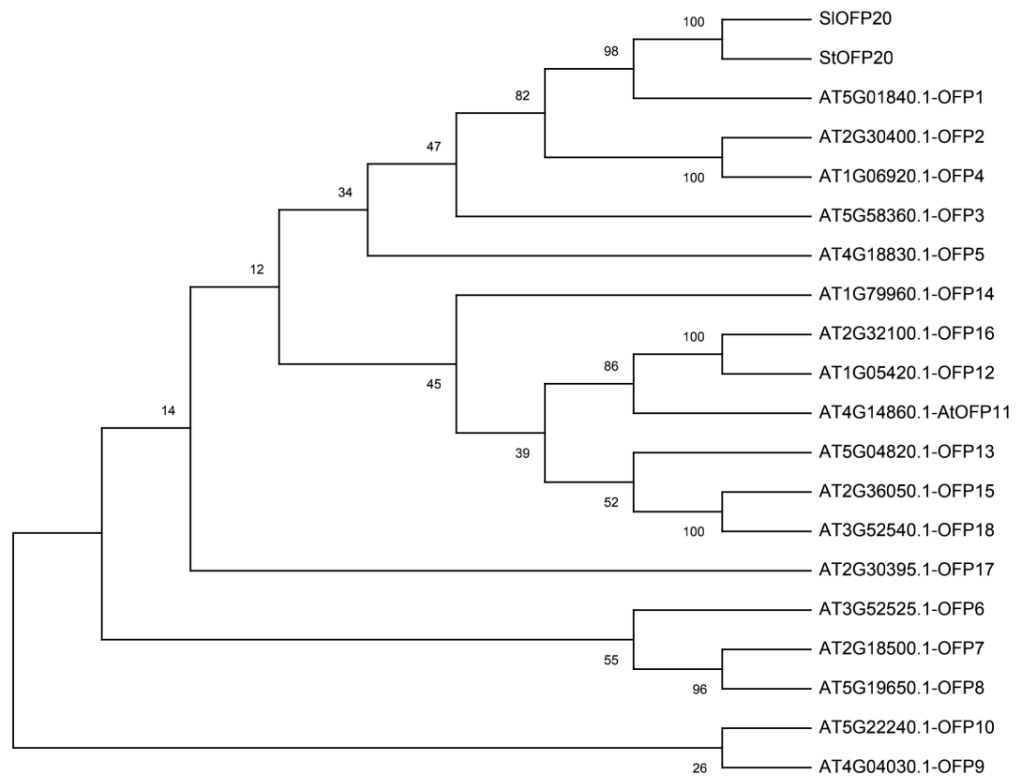
StTON2      181 YVMRTVSLTQARIDMSELEDSDGFLQPHEMEAYIRGLIPNLAQLRDMPAAFVQMYCRIA 240
              YVMRTVSLTQARIDMSELEDSDGFL  EME+YI GLIPNLAQLRDMP AF QMYCRIA
>AT5G18580   181 YVMRTVSLTQARIDMSELEDSDGFLHSDMESYIGGLIPNLAQLRDMPPAFNQMYCRIA 240

StTON2      241 AHKFFFCDPHRRGKACIKKILLSNCLQELMELHQETEEVTDTEQAENWFSLTSAQRIC 300
              + KFFFCDPHRRG+ACIKKILLSNCLQELMELHQE+EEVTDTEQAENWFSLTSAQRIC
>AT5G18580   241 SQKFFFCDPHRRGRACIKKILLSNCLQELMELHQESEEVTDTEQAENWFSLTSAQRIC 300

StTON2      301 DMFLALDKDMNGTLSKQELREYADGTLTDIFIERVFDEHVRRGKIGGGNAREMDFESFLD 360
              DMFLALDKDM+G+L KQEL+EYADGTLT+IFIERVFDEHVRRGKI GN+REMDF+SFLD
>AT5G18580   301 DMFLALDKDMSGSLCKQELKEYADGTLTEIFIERVFDEHVRRGKIVAGNSREMDFDSFLD 360

StTON2      361 FVLALENKDAPEGLTYLFRCLDLQGRGFLTADIIHLFRDVHQWIEGGNYELCIEDVRD 420
              FVLALENKD  PEGLTLYLFRCLDLQGRGFLTADIIH+LFRDVHQWIEGGNYELCIEDVRD
>AT5G18580   361 FVLALENKDTPEGLTYLFRCLDLQGRGFLTADIIHSLFRDVHQWIEGGNYELCIEDVRD 420

StTON2      421 EIWDMVKPSDSLRLISLADLLSCKQGGTVASMLIDVRGFWAHDNRENLLQEEEEPQEEG--- 478
              EIWDMVKPSD L+I+L DLL CKQGGTVASMLIDVRGFWAHDNRENLLQEEEEP EE
>AT5G18580   421 EIWDMVKPSDPLKITLGDLGCKQGGTVASMLIDVRGFWAHDNRENLLQEEEEPPEEESQ 480
```



Appendix H. Phylogenetic analysis of SIOFP20, StOFP20 and OFP proteins in *Arabidopsis*.



Appendix I. Yeast two-hybrid analysis of the interactions between StOFP20 and two putative TON proteins.