PFC	Dist to 3' gene	Length	Sequence
$DreD_{AC}1_{b}$	12,618	296	ATTCATCAAAAAGTGGTTTGCGCCTTCGTCGTTAAAGGTGCGCGTG ACGCGGCTCGAATGATCATTTATTGTAACAGGTTTATAAGCAAATA AATAGGAGAGAGACTGTCATCGGTTGATAGAGTCGGCCCTTGATCG GCCAGACGCGTATATCCAGGTGGAGAGAGAGAGGAGAAGTGAGGA GAGAGCAGCTTCTGATCTGAGTCTGTTTTAGATGGCTCCTGGGGTTG GCCTCTGGGGTGAAATTGACAGTCTGATTAATAAAATGAGCGCGGC AACATTTCCCTCTTCATTTA
$DreD_{CD}2$	2,475	27	ATTTTAGACTCGGTGTCTGAATAAGTT
$DreD_{CD}4$	111	75	TACTTTGCATATCACGTGATGGTGCATTAACAAATCAACAATTACCT TGCTCGTATTCTTTAGGGGTAACTAAAA
$DreD_{DE}7$	3,509	53	ATTAATTGCAATAATCTAAAACAAGTATATGGAACAGGACAAACGG GAGAAGA
$DreD_{DE}9_{abcde}$	249	152	TAATGACTGATATTGATATATGGTAATTTTTTTACCGGATCACATGA CACAATTACCTCAAGAATCGATCAAGATGAATTGCACGTCAGCGTA CGTTTCCGATTTTTTCTTCCTCGCGAGTCCTATCCGCACGCATATGG TGCAATAGATGG
$DreD_{DE}10_{cd}$	2,061	28	GGGGCGCCAATACAAAGTTAAGGTCAAG
$DreD_{EF}11_{b}$	5,617	20	AAACCTTGAACAGTCTAGAC
$DreD_{EF}13$	5,259	49	TTTGAACTTCTGTAATGTCAAGGTCGTCACCCTTAACCTTTTTGAAT AA
$DreD_{EF}16$	4,948	46	TGCAAAACAAACAAAGCCGTAATATGCTTATAGTGATCGAGCAGAG
$DreD_{EF}19_{abc}$	226	179	GTCGCTGTTGACCACGTCTGAAACTTCAAATCATGTGTCAATCCGCC CACGTGACGGGGAAGAGCCTGCGTCTCAAGGCCATTTTCAAATTTC ATTGGTGAGAGTGTCATGTGGTTGCAGAGAGACTCGCTGGGTTATA CAGGGATTGTTTTGCTAGATATGTCAGCTTACAGAGGACA
$DreD_{FG}21_{abc}$	713	58	TTTTATTAAGGGAACATTAATACATAATCAAATGCACCTCATAAAAT GTTTTATTGAT
$DreD_{FG}22$	476	33	TTTACAGCATGTTATTACATTTATTTTACGAGG
$DreD_{FG}23_{bcd}$	127	111	GTAAATATGATCACGTGATTCATGTAACCAATCACTGAAGGTGAAG GCAGCAAAAATACTACGATTGTTCGGAGGCAAGGTTTCGGAAACAG AGTACCGTTTTATATGAGT
$DreD_{GL}29$	12,865	81	CAGGAAGAAACGGGGTCCAATAAAGCTATAGAAAGAGCTAGACGT CTGGACTAAATGAGTTTATGGTACACGACTGTAATT
$DreD_{GL}30$	11,317	29	ATGTGTGTGTTTTAAAACAGCGAGGCAAC
$DreD_{GL}31$	10,723	34	TAATTTTATCTGTTTGGGAAATCTGCGGCACAGA
$DreD_{GL}35_{bcd}$	8,951	135	AATTTACAGCTTCGTAATAGATCTTTTTATGAGCCTATTTCGTCTGT CATTGGATGCCACTGGTCATGTGCAGCACGCAAACGTCTTCATGAC CCCTTTTCCTGATTTCCCAAGCGATTTTTCCACTACATTCTG
$DreD_{GL}36$	7,359	31	AATAAGTTATGCATGCTTTAATATATATTTG
$DreD_{GL}37_{abcd}$	5,107	136	TATTGAATAAGTGCAACTTTCAGGATTATTTATGGCACCCGCGCGCT GTCATGAATGGCTGTGGGGAAGCACGTGATACCATTAAACTTTGTTT TATGGCCAGGGAGTTGACAAGCCAAAATATAATTCACATTGT
$DreD_{GL}38$	615	191	TTATTGATTGGCACGGCGCATTGATGGCGAACCAGGGCGCCCTATA CAGCGAGCTGAAAGGATGAGAAGCGCTGGAACGATGAGACTCCAG TAACTTCTGTGTGACCTCTACATGACAAAGACGGTCTTCATCAATTG TCTGCAGGCTTTATGCGTCTCTTTTTGTGCCCTGGACCGTTTTTATCT TTTGT

$DreD_{GL}40_{ab}$	7,758	72	GAACAAAGACAGTATTTCACAGTCAGCTGACAGGCCGCTGCAGAG GTATTTACAACCTCTCTGCAATGCGGC
$DreD_{GL}46_{bcd}$	3,372	63	GGCTTTGACCCGCCTGAACAAGTCGCAATTCAAGGTGAAACACAGG TCACGCTGTCTAACAAA
$DreD_{GL}47_{b}$	2,771	39	AAAAATAATGAAACATTGTGATGTGTGTTGTAAATGATT
$DreD_{GL}48_{abcde}$	2,257	82	GTCTATATATACCCTGTAGAACCGAATTTGTGTGAAAAAATAACATT CACAGATTCGATTCTAGGGGAGTATATGGTCGATG
$DreD_{GL}49_{b}$	63	60	ATTGGCCAAGCTGGTCACATGGTAGGCTAACTTTATTCAGTTGACA GCAAGTAGGAGGGC
$DreD_{LM}50$	9,100	89	CAGGTTCATCCAGAGGACACAGTTTCTGTTGCATTACAGACGCTTTT CAGCCGCGAGCACTGACCTCTACACTCGTGACCCGATGGACC
$DreD_{LM}51$	9,979	15	TATAATAAAAAAATA
$DreD_{LM}56_{c}$	9,100	65	CAGGTTCATCCAGAGGACACAGTTTCTGTTGCATTACAGACGCTTTT CAGCCGCGAGCACTGACC
$DreD_{LM}58_{abcd}$	6,965	432	TGACCTGGATGTCTGAACAGAATAAATGGGAGCCATACGCAGTTCC ATTTGCAATGACACTGCACCGACTACCACCGCCGCTCTCACAATGC CTCTCAAACGGCCATTTTTGATTTCCAGCTGTTCGCTGAAAATGTGT TCGCCCATCGAGACCAGCCGTTAAGATAAATCAAACTGCGCTGTCG ACATCCCGAGACAGAATTCGGTATATGGTTCCGTTCTATATCTTTTT TTGTTTGACCACGTGATTGTCTAAATAATTAATGCAGCACGTCCCCT AGAAACACGGCATCGTCATTAATCGCGAGGACTCTATCAGACTTGA AAACTGAAGAGATCCAAGAAAATAATATCCAAACGGTCCTGTTTCT CACACCACCGCAGCCTGCACATTCGTACAGCTTTTCATCCAATGGA AGATCGGTAGGTAAA
$DreD_{LM}59$	5,325	19	GTCATTGCCTAAACCATAA
$DreD_{LM}60$	3,333	29	CAAACTTACCGTGGGAGTGCGTAGGCGAA
$DreD_{LM}61_{abcd}$	2,922	70	GTTCATTAATCAGTGAGTTATTGGAGAGCAAGCCAAAGGTCACCCA AAAGGCTTATGAGTGCTAAATATT
$DreD_{LM}62_{ab}$	1,724	45	GTCATAAATTTTGTCGGGCTCCACAATGACAGGTGCATTGATATG
$DreD_{LM}67_{bc}$	5,816	95	TAAATCATGCTCAGTAATTCCTGAAAGGGTGAGAGGCTGTTGGGGG CCGGGCGTGGACTGTAAATCTTTCACTTTTATTAGCCCGTGAACATA TG
$DreD_{LM}69_{abcd}$	4,802	90	CTCAATCAGGACAATCTGCGATCCGGATCACGTGAACAAATATGCT TGTATTTTAAGGCAGCGCCTTTATTTGTCATGATAAGGTTTCCG
$DreD_{LM}70_{ab}$	4,600	231	TTTATTGGTAGCTGAGTGAGTGGCTCCCATTCTTTCGGGAATACTGT CTGCATTGGTATATGGAAATGCCTGGAAAAGCGCGAGATCAGTTTT AAGACAGTACTGTCTATAGACAAAGGGTGAAGGATATATCCGAGCA GCTGAACTGAGAGATATTGAGACTAAGAAGCACGGCTATATAATAA ATTGACATCACAGGTAAGCAATTGCATTGCAAAACGTAACCTTTAA