

Supplemental Figure 1: Sequences and contexts of SDR1 elements

High SDR1 (copy number >= 3) elements found by mismatches

Replicon	Dir	Site	Ctx	Left	Right	SDR and flanking regions
SDR1.1 (10)						
Npun.chrom	F	1418941	P	170	77	ATCTTTT TTGGGGCATTGGGCA CTTG TACTGAGCGAAGTCGAAGTA TTGGGCATTG AAAACTTTT
Npun.chrom	F	1518598	P	31	85	TGGGCA TTGGGGCATGGGGCA CTTG TACTGAGCGAAGTCGAAGTA TTGGGCATTGG TTATAGGTCA
Npun.chrom	B	2027856	P	462	71	GGGTTTTAGGAGACCATAGT CTTG TACTGAGCGAAGTCGAAGTA GCTGAAACTTTTAAGCCACTT
Npun.chrom	F	2695318	I	11119	532	TGAAGATACCCAGGTGATCTTG TACTGAGCGAAGTCGAAGTA AACGCTTAGTTGCCTACGTGC
Npun.chrom	B	3756502	I	6458	7389	AGAAGATATTCAGGAGACACTTG TACTGAGCGAAGTCGAAGTA AACGTTTAGTTGCTTATCTTG
Npun.chrom	B	3961044	C	426	71	GGGTTTTAGGAGACCATAGT CTTG TACTGAGCGAAGTCGAAGTA GCTGAAACTTTTAAGCCACTT
Npun.chrom	F	4444408	P	6	140	CTTCTGGATTTTCAT GTCTCA CTTG TACTGAGCGAAGTCGAAGTA TTGGTCATTAGTCATTGGTCG
Npun.chrom	F	4531003	I	1512	113	ATTCAG TCCAAATCCAAAT CTTG TACTGAGCGAAGTCGAAGTA TCATAATCCAGATTCAGAT
Npun.chrom	F	5748997	P	42	86	TAGTCATTTGTCTTTGTCTCA CTTG TACTGAGCGAAGTCGAAGTA TTTGTCTTTGTCTTTGTCTCA
Npun.chrom	F	5893843	I	1195	952	TTTGGATTTTGGATTTTGGATT CTTG TACTGAGCGAAGTCGAAGTA TTGGCAATTTCTCCCTGCT
SDR1.2 (8)						
Npun.chrom	B	251521	P	15	151	GTCACCTTA CCCCCTGCCCC CTTG TACTGAGCGCAGTCGAAGTA TGCCCTCTCTCTATTGA
Npun.chrom	B	280249	P	63	47	TTGAG ATGGGGAATGGGGAA CTTG TACTGAGCGCAGTCGAAGTA TGGGGAATGGGG TATAGATT
Npun.chrom	B	733553	P	293	40	ACATAG TTGGGGAATGGGGAA CTTG TACTGAGCGCAGTCGAAGTA TGGGCAATAGGCAATAGGAAC
Npun.chrom	B	3109442	P	229	64	TGGGAAATGGGC CATAAG GAATGGGAA CTTG TACTGAGCGCAGTCGAAGTA TGGGGAATGGG CTAATAATCA
Npun.chrom	F	3458731	P	101	51	ACTGTT TTGGGGAATGGGGAA CTTG TACTGAGCGCAGTCGAAGTA TGGGGAATGGGG CATTGGGAA
Npun.chrom	F	4987565	I	1199	675	TCGTAGAGAAGT ATGGGGAA CTTG TACTGAGCGCAGTCGAAGTA TGGGGAATGGG TAATACTTG
Npun.chrom	F	5322359	C	43	109	TT GGAATGGGGAATGGGGAA CTTG TACTGAGCGCAGTCGAAGTA TGGGGAATGGGGAATGGG ACT
pNpB	F	168856	D	241	153	CGAACGAGCGAAAAAGC GAACTTG TACTGAGCGCAGTCGAAGTA TTGCGAATTGGAGTTGACAAG
SDR1.3 (7)						
Npun.chrom	B	20611	P	192	380	CAGTCTTT CCCCCTGCCCC CTTG TACTGAGCGCAGTCGAAGTA CGTAAAGCCTGCGGCATAGCTACGCTTA
Npun.chrom	F	2460662	P	117	427	CTACGATGGTCACTGAGCTT CTTG TACTGAGCGCAGTCGAAGTA CGTAAAGCCTGCGGCATAGCTACGCTTA
Npun.chrom	B	3180274	P	1379	133	GGGGAATGGGGAATGGGAA CTTG TACTGAGCGCAGTCGAAGTA CGTAAAGCCTGCGGCATAGCTACGCTTA
Npun.chrom	F	4998149	P	26	135	TGGGAATGGGGAATGGGAA CTTG TACTGAGCGCAGTCGAAGTA CGTAAAGCCTGCGGCATAGCTACGCTTA
Npun.chrom	F	5891999	D	43	349	GGGGAATGGGGAATGGGAA CTTG TACTGAGCGCAGTCGAAGTA CGTAAAGCCTGCGGCATAGCTACGCTTA
Npun.chrom	F	6104334	C	28	156	GGGAATTTGGGAAATGGGGAA CTTG TACTGAGCGCAGTCGAAGTA CGTAAAGCCTGCGGCATAGCTACGCTTA
Npun.chrom	B	6135493	P	259	49	GGGTAGTAG GGGAATGGGGAA CTTG TACTGAGCGCAGTCGAAGTA CGTAAAGCCTGCGGCATAGCTACGCTTA
SDR1.4 (5)						
Npun.chrom	F	2676566	I	9361	3808	TGTGCCTCAAGAAGAGCAGACTTG TACTGAGCGGAGTCGAAGTA CACTCACAGTCAGCTTTGTGC
Npun.chrom	F	2679764	I	12559	610	TGAAGAAATTCAGGTAATACTTG TACTGAGCGGAGTCGAAGTA AGCGCTTAGTCGCTTACGTAG
Npun.chrom	F	2679827	I	12622	547	AGTGCCGATTTACACGCGACTTG TACTGAGCGGAGTCGAAGTA CACCCACAACGGACGAAGTGC
Npun.chrom	B	3507463	C	51	49	GGGGCATTGGGCA GT GGGCA CTTG TACTGAGCGGAGTCGAAGTA TGGGGCATTGG CTTTTCTCAG
Npun.chrom	B	7692801	I	611	0	GGGATGAT TTGGGCATTGGGCA CTTG TACTGAGCGGAGTCGAAGTA TGGGGCATGAGGCA ATGACGA
SDR1.5 (5)						
Npun.chrom	F	633285	D	181	120	GGC TGAGGGTTGAGCGCAG CGAT GCACTGAGCGCAGTCGAAGTG TGAAATCG CGTCTGGT TTGGGA
Npun.chrom	F	1746277	P	237	210	GGC TGAGGGTTGAGCGCAG CGAT GCACTGAGCGCAGTCGAAGTG TGAAATCG TGCTGGT TTGGGA
Npun.chrom	B	8086727	D	119	511	GGC TGAGGGTTGAGCGCAG CGAT GCACTGAGCGCAGTCGAAGTG TGAAATCG CGTCTGGT TTGGGA
Npun.chrom	F	1811886	P	110	186	CAT CGAGAGTTGAGCGCAG CGAT GCACTGAGCGCAGTCGAAGTG TGAAATCG CGGTTTACTAGTA
Npun.chrom	F	7091801	C	66	126	CAT CGAGAGTTGAGCGCAG CGAT GCACTGAGCGCAGTCGAAGTG TGAAATCG CGGTTTACTGGTA

SDR1.6 (4)

Npun.chrom	B	693819	P	143	225
Npun.chrom	F	3532618	P	139	364
Npun.chrom	F	2669959	I	2754	10415
Npun.chrom	B	2670447	I	3242	9927

GGG**GAGCAGG**CTTGCCGTGACTTGTGCCGAGCGGAGCCGAGGTAGCGTAGCCGAACGG**GAGCAGA**
 GGG**GAGCAGC**CTTGCCGTGACTTGTGCCGAGCGGAGCCGAGGTAGCGTAGCCGAACGG**GAGCAGT**
 GTGATACTTG**TA**CTGAGCGACTTGTGCCGAGCGGAGCCGAGGTAGT**CGAAGTA**AACGTTTAGTC
 CTAAGTCTTG**TA**CTGAGCGACTTGTGCCGAGCGGAGCCGAGGTAGT**CGAAGTG**CCTGTTGCTGT

SDR1.7 (3)

Npun.chrom	F	5646889	C	187	57
Npun.chrom	B	5647865	D	179	311
pNpB	B	192986	I	1916	1830

CAATTTCTCATT**GCTCCCG**CGGT**TACTGAGCGCAGTCGAAGTA**T**GCTCCCG**TGG**ACCGT**T**GCT**T
 AACTCTTCT**CT**TTTGC**CCCG**CGGT**TACTGAGCGCAGTCGAAGTA**T**GC**AT**CCG**TGG**CCCG**T**GCT**T
 CTGTTAATTCTT**CTTTACG**CGGT**TACTGAGCGCAGTCGAAGTA**T**CCCGTTTACCGTTT**AAGAG

nod-004	B	75986			
nod-008	F	62540			
nod-009	B	57772			
nod-048	F	24328			
nod-089	F	6788			
nod-202	F	860			
nod-032	B	17555			
nod-087	F	1239			

GGTT**TACTGAGCGCAGTCGAAGTA**CGGT**TACTGAGCGCAGTCGAAGTA**ACT**CCCGACTCGG**TACCTACG
 TTTCCACAGGA**CCACTCCCG**CGGT**TACTGAGCGCAGTCGAAGTA**ACT**CCCGACTCGG**TACCTACG
 TTTCCACAGGA**CCACTCCCG**CGGT**TACTGAGCGCAGTCGAAGTA**ACT**CCCGACTCGG**TACCTACG
 TTTCCACAGGA**CCACTCCCG**CGGT**TACTGAGCGCAGTCGAAGTA**ACT**CCCGACTCGG**TACCTACG
 TTTCCACAGGA**CCACTCCCG**CGGT**TACTGAGCGCAGTCGAAGTA**ACT**CCCGACTCGG**TACCTACG
 AAAGCTGT**TTCCCACTCCCG**CGGT**TACTGAGCGCAGTCGAAGTA**ACT**CCCGACTCGG**TACCTACG
 CT**CCCGACTCGG**CGGT**TACTGAGCGCAGTCGAAGTA**ACT**CCCGACTCGG**TACCTACG
 GT**CCCGACTCGG**CGGT**TACTGAGCGCAGTCGAAGTA**ACT**CCCGACTCGG**TACCTACG

SDR1.8 (3)

Npun.chrom	F	2688069	I	3870	7781
Npun.chrom	F	2699441	I	3594	4013
Npun.chrom	B	8021940	P	190	141

ACTTGAAGCATTTATCAACA**CTTGTACTGAGCGAAGC**CGTTGGCGTT**CGCGTAGCGTCTC**CGTTA
 ACTTGAAGCATTTATCAACA**CTTGTACTGAGCGAAGC**CGTTGGCGTT**CGCGTAGCGTCTC**CGTTA
 ACGCTCAGGGCAAGTGGAAC**CTTGTACTGAGCGAAGC**CGTTGGCGTAGCGTCTC**CGTTAGAGAACT**

SDR1.9 (3)

Npun.chrom	F	4987513	I	1147	727
Npun.chrom	B	5873244	P	237	46
Npun.chrom	F	6813642	P	21	114

TCGTAGAGAAGT**ATGGGGAA**CTTGT**TACTGAGCGCAGT**CGTTGGCGCAGCCTCTCGT-AGAG**AACTA**
 GGGGAC**TGGGGAATGGGGAA**CTTGT**TACTGAGCGCAGT**CGTTGGCGTAGCCTCTCGTTAGAG**AACT**
 GGGGAA**TAGGGAATGGGGAA**CTTGT**TACTGAGCGCAGT**CGTTGGCGTAGCCTCTCGT-AGAG**AACTA**

SDR1.10 (3)

Npun.chrom	B	1468715	P	209	485
Npun.chrom	B	4499200	C	98	35
Npun.chrom	F	4750549	I	1117	331

CCCTTAGTTGGTTGAGCGAA**CTTGTACTGAGCGTAGTCGAAGTA**GTCGAAACCAACGGTGGCGGT
 TGGAATTAG**GC**AA**TGGGGAA**CTTGT**TACTGAGCGTAGTCGAAGTA**TGGGGAA**TGGGGAA**TAATTA
 TATAGAAG**AGTCATTAGTCA**CTTGT**TACTGAGCGTAGTCGAAGTA**TTAGTCATTCTCGT**CA**TTGGTAA

nod-041	F	30888	D		
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CCTAATCAGGGCGGGCAAGA**CTTGTACTGAGCGTAGTCGAAGTA**TGCCCTCCCCACAATAATTT

SDR1.11 (3)

Npun.chrom	B	5070629	P	133	113
Npun.chrom	B	6371569	P	228	55
Npun.chrom	F	7201691	P	11	121

TAGTCATTGGTCATTGGTCACTTGT**TACTGAGCGTATC**GGTAAAGG**GAAAGCTCCGCTAACGCGCA**
 TTGT**CA**TTAGTCATTGGGCACTTGT**TACTGAGCGTATC**GGTAAAGG**GAAAGCTCCGCTAACGCGTA**
 AACC**GA**TTAGTCATTGGGCACTTGT**TACTGAGCGTATC**GGTAAAGG**GAAAGCTCCGCTAACGCGCA**

SDR1.12 (3)

Npun.chrom	B	1433728	D	420	533
Npun.chrom	F	2352190	P	46	267
Npun.chrom	F	4592990	P	48	153

TAAGTCA**CGACTATACAGA**CTTGT**TTGAGCGGAGTCGAAATA**CAAAACC**AG**CT**CA**GTGGGT**T**
 AGAAGTCGCGGCTATACAGA**CTTGT**TTGAGCGGAGTCGAAATA**CAAAACC**CACT**CG**GTGGGT**T**
 AGAAGTCGCGGCTATACAGA**CTTGT**TTGAGCGGAGTCGAAATA**CAAAACC**TGCTCC**CA**GGT**T**

Genome	Accession	Position	Length	Sequence
Npun.chrom	B 1476382	P 45	64	GAAGGGGAGCAGGGGGCAGGTGGTCACTGAGCGTAGCCGAAAGTGGGGCAGGGGGAAAATGACAAA
Npun.chrom	F 3690844	P 18	141	TAATGAAGGTAGAAGGCAGGTGGTCACTGAGCGTAGCCGAAAGTGAAGGCAGAAGGCAGGAGTTAGT
Npun.chrom	F 7695617	D 722	369	GAACGGGGGCAGAGGGCAGGTGGTCACTGAGCGTAGCCGAAAGTGGAGCAAGGGAAAAATGTTGAAG

Npun.chrom	F	2245647	D	173	49	CCTGC	GATGTCTACGACGGGTGGTT	CCTGAGCGCAGCCG	TACCACTT	CCCTACGGGACGCTACGC
Npun.chrom	F	4994933	D	245	729	TTTGT	GATGTCTACAGCGGTGGTT	CCTGAGCGCAGCCG	TACCACTT	CCCTATAGGACGCTACGC
Npun.chrom	B	6276593	C	73	305	GAAGC	GATGTCTACGAGGGGTGGTT	CCTGAGCGCAGCCG	TACCACTT	CGTGGGAAGCAAGCTACGC

Replicon	Site	SDR and flanking region
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Npun.chrom 593573F GATCCCAAGGCTGAGAAAAAGCAACTTATGAGATAGGGGCTGGGGCAGGCTTGGCGTGAGCGTAGCCGAACGGGAGCAGGAAAGGATTAGGGGACGAGGGGGACAAGGAGGACAAGGGGAAAT
 Npun.chrom 1141711F GAGAATGACAGGCACTTGTGCGACGGTATTGGCAGAAAGTAGGGAGCAGGCTTGGCGTGAGCGTAGCCGAACGGGGGAGGGGGCAGAGGAGCAGGGGAGCAGAGGAGAGTTTTGTG
 Npun.chrom 1567039B CGATACCTGCGACGGGCTTTGTCAACGCCCAATGATTCAAGGAGCGGGCTTGGCGTGAGCGTAGCCGAACGGGAGCAGGAGGAGCAGAGGAGATGGAAGATAGGGAGATGAGGAAATGG
 Npun.chrom 4549647F TTAGTGAGGAGTGATGAGAGCGCATTAATCACGCTCTACTGAGTGGGCTTGGCGTGAGCGTAGCCGAACGGGAGTGCTGAGTTTTATTAGCTTTTGTAAATCCTTCGCAACAGTCGCAAT
 Npun.chrom 4605964F TTAACCTTGGCAAGAATTGAGGGAAAAGAGAGGGGAGCAGGGAGCAGGCTTGGCGTGAGCGTAGCCGAACGGGAGCAGGAGCAGGGGAGGAGGCAGGGGGAGAAAATCTTTATACTCCGCACTC
 Npun.chrom 5017961B TAGCCATCCGGTGACAGTACGGGGATGAGGGAGAAAGGAGCAGGGAGCAGGCTTGGCGTGAGCGTAGCCGAACGGGAGCAGGGGGCGGGGGAGAGTAAGGGGGATAAGGGGACAA
 Npun.chrom 6279883F GGGAAACAATTGCAATTTTGTGAGATCGCCATAAAGACAGCAGGGGAGCAGGCTTGGCGTGAGCGTAGCCGAACGGGAGCAGGGGAATGGAAAAAGAACCAATTATCGGACAGAAATTCATTCTAT
 Npun.chrom 7695579F TAAAAAGTGCCCTTAGAGGTTGAAAAAGAGGCAAGGAGCAGGAGCAGGCTTGGCGTGAGCGTAGCCGAACGGGGGAGGGGAGGCTGGTCACTGAGCGTAGCCGAAGTGAGGCAAGGAAAA
 Npun.chrom 7739603F ATACTTTAGTCAAGGTACTGCTGAGTCGAATAGTAGGGAGGGGAGGCTTGGCGTGAGCGTAGCCGAACGGGGGAGGAGAGATAAAAACTACTTTATATATGTGATCTGAGCTGCTGAT
 Npun.chrom 7758894B CGCAGTTTAGGGAATTGGGGAATGGGGAAGAAGCAAGGGGAGCAGGGGGAGGCTTGGCGTGAGCGTAGCCGAACGGGGGAGGAGAGCAAGGAGGAAAGCAGGAGGAAAGAGAACTATT

Npun.chrom 733392B ACGAGAGGCTGCGCCCTAAGCGTAGCTATGCCGACAGGCTTTACGACTGCGGGTAGTTGAGCGCAGTCGAAAC CAGTACAAGTCCCAATTCCCACTTGCCCTGAGCGTATCGCTAAAGCGAA

Npun.chrom 1111726F ACGAGAGGCTGCGTCCTAAGCGTAGCTATGCCGACAGGCTTTACGATTACG GGTAGTTGAGCGCAGTCGAAAC CAGTACAAATGAGTAATGACTATGAGATTACTAATAGCAACGACGACGG

Npun.chrom 1996810F ACGAGAGGCTGCGCCCTAAGCGTAGCTATGCCGACAGGCTTTACGACTGCGGGTAGTTGAGCGCAGTCGAAAC CAGTACAAGTCCCAATTCCCAATTCCGAATTAAGTACTTAGAAGGTG

Npun.chrom 2248585B TGGAGAGGCTGCGCCCTAAGCGTA-CTATGCCGACAGGCTT-ACGCGTTTCG GGTAGTTGAGCGCAGTCGAAAC CAGTACAAGTGCCTCGTGCCCAATCCCTAATACCCCATTAATTAAGAAAG

Npun.chrom 2294380F ACGAGAGGCTGCGCCCTAAGCGTAGCTATGCCGACAGGCTTTACGACTGCGGGTAGTTGAGCGCAGTCGAAAC CAGTACAAGTCCGAATTCCCAATTCCGTAAATTC

Npun.chrom 4548957F ATTTCCAATTCCCACTA-CTCTCAACGAGAGGCTACGCCAATGACTGCGGGTAGTTGAGCGCAGTCGAAAC CAGTACAAGTCCCAATTCCCAATTTCCCAATTTTAAATTTACGGCTTAC

Npun.chrom 6128349F ACGAGAGGCTGCGCCCTAAGCGTAGCTATGCCGACAGGCTTTACGACTGCGGGTAGTTGAGCGCAGTCGAAAC CAGTACAAGTCCGATTACCATTAAGCTGCAAACTTGCCACTC

Npun.chrom 7182586B TTTGTGAATTAACATA-CTCTCAACGAGAGGCTACGCCAATGACTACG GGTAGTTGAGCGCAGTCGAAAC CAGTACAAGTACCAATGACTAATGACCAATGACTAATGACCAATGACT

Npun.chrom 585618F TTATGTCATTGGTCA**TTAGTCATTGGTCACTTATACTGAGTTTCGACTGCGGGAATCGAGCGAAAGTCGAGATCAACTACCGCGTAGT****CGTAAAGTCTGCGCATAGCTAGGCTTAG**GACGCA
 Npun.chrom 5690304B ACCACAAATAGTCA**TTAGTCATTAGTCACTTGTACTGAGTTTCGACTGCGGGAATCGAGCGAAAGTCGAGATCAACTACCGCGTAGT****CGTA---CTGCGCATAGCTCCGCTTAG**GGCGCA
 Npun.chrom 5750725B ACAATTATTGGTCA**TTAGTCATTAGTCACTTGTAAATGAGTTTCGACTGCGGGAATCGAGCGAAAGTCGAGATCAACTACCGCGTAGT****CGTAAAGCTGCTGCTAGATAGCTAGGCTTAG**GGCGCA
 Npun.chrom 7754298B AGAGGCTGCACAA**CGGCTACGCTCAGGACAACTCAGTGCATCGCTGCGGGAATCGAGCGAAAGTCGAGATCAACTACCGCTTGTGCTCGCGTAGT****CGAGCATAGCGCAAGCGAAGT**AGCCTC
 Npun.chrom 7840565B ATATAAATTAT**TCATTGGTCACTGGTCACTTGTACTGAGTTTTCGACTGCGGGAATCGAGCGAAAGTCGAGATCAACTACCGCGTAGT****CGTAAAGCTGAGCATAGCTAGCTCTTAGGGTGA**

Npun.chrom 50801B **TCGACACTTCGA**-----**CTGCGCTCAACCCTCA**GCCAT**CGAGAGTTGAGCGCAGTCGAAACT**CGGTTTACTGGTACTTTATTTTCACGCAAGTCCTTAAGCACATAAAATTTA
 Npun.chrom 633239B **TCGACACTTCGACTGCGCTCAGTGCATC**G**CTGCGCTCAACCCTCA**GCCAT**CGAGAGTTGAGCGCAGTCGAAACT**CGGTTTACTGGTACTTTATTTTCATGCAAGTCCTTAAGCGATCGCCTGGA
 Npun.chrom 1746231B **TCGACACTTCGACTGCGCTCAGTGCATC**G**CTGCGCTCAACCCTCA**GCCAT**CGAGAGTTGAGCGCAGTCGAAACT**CGGTTTACTGGTACTTTATTTTCACGCAAGTCCTTAATTGGTTTTTTTTTG
 Npun.chrom 2564961F **TCGACACTTCGACTGCGCTCAGTACATC**G**CTGCGCTCAACCCTCA**GCCAT**CGAGAGTTGAGCGCAGTCGAAACT**CGGTTTACTGGTACTTTATTTTCATGCAAGTCCTTAATTGTGACATAACC

SDR1.19 (4)

Npun.chrom	1266794B	AGTCAGGAGTCAGAATACAGGAAAGGTATTCTGTACGACACAACGACCGG	CGGTAGTTGAGCGTAGCCGAAACT	AAGTGCATCGCTGGCGGATAGCGT	CGGCGGCAAGCGAGTCCGC	GAGCGTC
Npun.chrom	2215533F	CGTCAGTCGTCAGAATACAGGAAAGGTATTTGTGCGACACAACGATCGA	CGGTAGTTGAGCGTAGCCGAAACT	CAGTGCATCACTGGTGGATGAAT	CCAGGGCTTTAAGACCCCACTAAATC	
Npun.chrom	6273884B	AGTCAGGAGTCAGAATTCAG - -AATGAATCTGTACGACACAACGACCTG	CGGTAGTTGAGCGTAGCCGAAACT	CAGTGCATCGCTGGTGGATGAATAAATCGG	TTAAGACGCTCGGGACTC	
Npun.chrom	7633752B	AGTCAGGAGTCAGAATTCAG - TTGGGTATTCTGTACGACAGAACGACCGA	CGGTAGTTGAGCGTAGCCGAAACT	CAGTGCATCGCTGGCGGATAGCGC	CGGCGGCAAGCGAGTCCGC	AATAGCG

SDR1.20 (4)

Npun.chrom	1270159F	ATGAAATAATCAGTCTGCAATGACCAAT	TACTTCGACTTACCTCGGCTCCG	GTTCCATCGAGCGAAGTCGAGATG	CTCGGCACGAGTC-CTCAGTACAAG	TCACCAATGACAAATGACTAATGACT
Npun.chrom	2687195B	GTGCTACCACGTAGGCGACTAAACGTT	TACTTCGACTTACCTCGGCTCCG	GTTCCATCGAGCGAAGTCGAGATG	CTCGGCACAAGTCGCTCAGTACAAG	TATCACCAGGGCTATCCTCACGGGC
Npun.chrom	2687709F	AATCGATTGGGCAATTACAGCAACAGG	TACTTCGACTTACCTCGGCTCCG	GTTCCATCGAGCGAAGTCGAGATG	CTCGGCACGAGTCGCTCAGTACAAG	ACTTAGAACTTTCTACACCATTTCAT
Npun.chrom	3368676F	GCGTAAAAATAAAGTACCAGTAAACCG	AGTTTCGACTTACCTCGGCTCCG	GTTCCATCGAGCGAAGTCGAGATG	CTCGGCACGAGTCGCTCAACTCTCG	ATGGCTGAGGGTTGAGCGCAGCGAT
nod-022	33060F	CTCCTACAGCAGAGACGGCTGAACCTTCCGCCTTGAT	CCCTTCGGCTTCG	GTTCCATCGAGCGAAGTCGAGATG	CTCAGGGCAAG	CATTCTGATCCCTCGGCTCTAATATTGAGCGCTGCGTT
nod-062	16565F	CTCCTACAGCAGAGACGGCTGAACCTTCCGCCTTGAT	CATTTCGACTGCG	GTTCCATCGAGCGAAGTCGAGATG	CTCAATGCAAG	CATTCTGATCCCTCGGCTCTAATATTGAGCGCTGCGTT

SDR1.21 (3)

Npun.chrom	479677B	CACAAAATACTTAATTTTGTCAATTAGTTATTGGTCA	CTTGACTGAGCGACTTG	CCTTGAGCGAAGTCGAAAGG	AGCCGAAGTA	TTAGTCATTAGTGAATAACAAAGGACAAATGACGAAGGAC	
Npun.chrom	540567F	ATTTGTCAATTAGTCATTAT	CATTGTCAATTAGTCA	CTTGACTGAGCGACTTG	CCTTGAGCGAAGTCGAAAGG	AGTCGAAGTA	TTTGTCAATTATCCTCCGCCCTTAACGTGGGAAGATTATT
Npun.chrom	7336699F	GGGACACAATAATTATTGTCAATTGGGATTGGGCA	CTTGACTGAGCGACTTG	CCTTGAGCGAAGTCGAAAGG	AGCCGAAGTA	TGGGGCATTGGGCATTGG	ATTGGACTAATGACCAATGAC

SDR1.22 (3)

Npun.chrom	781655B	TTAAAAAATCATTCTCTAATAATGTCCTTTAATCTAAAAATCCAAATG	GTTGACTGAGCGAAGCCGAAGTC	CAAAATCCAAAT	TAGGGGAGTATCAGTGTTAGCTGACCTAAATTTATT	
Npun.chrom	6852716F	TAAGATTTTTTGGGATTTTTGGAAAGCTTTTAAATTC	CAAAATCCAAATG	GTTGACTGAGCGAAGCCGAAGTC	CAAAATCCGAAT	CTGGTATAAGGTAACCTTTTAGAGAACCTACAGAA
Npun.chrom	7099877B	GGGATGCAGGGGATGCAGGGGAAGCGAGGAAGAAC	CAAAATCCAAATG	GTTGACTGAGCGAAGCCGAAGTC	CAAAAGCCAAAT	GGCAGAGTGGAGTGTTACTAGAAGGCTGCGAGTCAC

Low SDR1 (copy number < 3) elements found by mismatches

Replicon	Dir	Site	Ctx	Left	Right	SDR and flanking regions
Doubles						
Npun.chrom	F	6448505	I	100	163	AACCGAGTTTCGACACTTCGACTGCACTGAGCGCAGTCGAAGTGTCGAAACCCATCT-GGTTGGGA
Npun.chrom	F	8020788	C	277	147	AACCGAGTTTCGACACTTCGACTGCACTGAGCGCAGTCGAAGTGTCGAAACCCGCTAGGTTGGG
Npun.chrom	B	969271	P	277	102	AACTACAGCGATGTCTACGACGGTCACTGAGCGCAGCCGAAGTGCGGGCTACGCCCTACGC
Npun.chrom	B	4106906	I	242	1065	TCCCAAGCGATGTCTACGACGGTCACTGAGCGCAGCCGAAGTGCGGGCTGCGCCTACGC
Npun.chrom	B	2676278	I	9073	4096	CCCTCTGCTCCCTGCTCATCGGTCACTGAGCGTAGCCGAAGTGCTGCTCCTGCTTCTTTTAA
Npun.chrom	B	7039631	I	152	864	TAACGCTACGATGCTACGCGGTCACTGAGCGTAGCCGAAGTGCGGGCTACACCTACGC
Npun.chrom	F	1247050	P	87	182	CTCTGCCTCCCTGCTCCCGGTACTGAGCGTAGTGGTAAAGCCTGCGGCATAGCTACGCTTA
Npun.chrom	B	4586661	P	69	87	CCTGCTTCTCTGCTACCCCGGTACTGAGCGTAGTGGTAAAGCCTGCGGCATAGCTACGCTTA
Npun.chrom	B	2673672	I	6467	6702	GTAAGTCTTGACTGAGCGACTCGTGCCGAGCGGAGCCGAAGTAAGTCGAAGTACTTGTTGCTGT
Npun.chrom	B	3409045	P	131	60	TAGTCACTTGACTGAGCGACTCGTGCCGAGCGGAGCCGAAGTAAGTCGAAGTATTAGTTTTAGA
Npun.chrom	F	4829404	P	132	93	GGGGAATGGGGCATTGGGCACTTGACTGAGCGAAGCCGAAGTATTGGGCATTAGTTATTTTTC
Npun.chrom	B	7764635	C	46	86	TCACTCAGGGCAAGTGGGAACCTTGACTGAGCGAAGCCGAAGTATTGGGAATTGGGAATTGGGCA

Npun.chrom	B	5013918	P	40	30	TTAG	ATTTTGTCA	TTTGTACTGAGCGGAGCCGAAGTA	TTTGTCA	TTTGGTCATTGGTCATTGGTCA
Npun.chrom	B	6256790	I	8	2256	TTGGGATTGGGAATGGGGCA	CTTGTACTGAGCGGAGCCGAAGTA	TTGGGCATGGGGCATTGGGA		
Npun.chrom	B	732545	P	8	209	TACGAATTACGAATTACGAA	CTTGTACTGAGCGTAGCCGAAGTA	TTACGAA	TTATTTTAATTGTG	
Npun.chrom	F	4618473	I	503	165	CATATCAAGAAATGCGGGTGT	CTTGTACTGAGCGTAGCCGAAGTA	TGGGTTT	GAGCGCATCGCGT	
Npun.chrom	F	5615555	P	35	139	GGGGAATGGGGAATGGGGAA	CTTGTACTGAGCGTAGT	CGTAAAGCCTGCGGCATAGCTACGCTTA		
Npun.chrom	B	6158943	P	59	138	TACGAATTACGAATTGCGAA	CTTGTACTGAGCGTAGT	CGTAAAGCCTGCGGCATAGCTACGCTTA		
Npun.chrom	B	2700466	I	4619	2988	ATACACCCACCAGTCCATTA	CTTGTACTGAGCGTAGT	CGTTGGCGTTCCGCTAGCGTCTC	CGTTA	
Npun.chrom	F	4736580	I	643	2035	TGGTCATTTGTCTTGGTCA	CTTGTACTGAGCGTAGT	CGTTGGCG	CAGCCTCTCGTAGAGAAGTA	
Npun.chrom	B	4524254	P	107	409	CACTGAGCGACTTGCCCTTGAC	CTTGTG	CGCCGAGCGAAGCCGAGGTA	GCGAAGCCGA	GGTAGCGAAGT
Npun.chrom	B	4757199	P	222	65	TACTGAGCGACTTGCCCTTGAC	CTTGTG	CGCCGAGCGAAGCCGAGGTA	GCGAAGTCGAAAGGAGTCGAA	
Npun.chrom	B	2564915	C	125	340	GGC	TGAGGGTTGAGCGCAGC	GATGTACTGAGCGCAGTCGAAGTGT	CGAAACC	CGTCTGGTTGGGA
Npun.chrom	F	3368747	P	129	892	GGC	TGAGGGTTGAGCGCAGC	GATGTACTGAGCGCAGTCGAAGTGT	CGAAACC	CGTCTAGTTGGGA
Npun.chrom	B	5929905	P	289	45	ACAAGAA	GCGATGTCTACGA	TGGTCACTGAGCCTTGT	CGTAAAGCCTGCGGCATAGCTACGCTTA	
Npun.chrom	B	6650831	P	219	69	GGTTGGT	GCGATGTCTACGA	TGGTCACTGAGCCTTGT	CGTAAAGCCTGCGGCATAGCTACGCTTA	
Npun.chrom	F	3625023	I	268	2287	TCCAGCAGCGATGCCTGCGGT	TGGTCACTGAGCGCAGCCGAAGTG	CGGGCGGCCATGCCTACGCGA		
Npun.chrom	B	5532957	P	96	566	ATACATAGCGATGCCTGCGGT	TGGTCACTGAGCGCAGCCGAAGTG	CGGGCTATACTACGCATTTTC		
Npun.chrom	F	1932884	P	119	95	AAATTC	TGCAATGCCTACGGT	TGGTCACTGAGCCTTTGT	CGAAGTG	CGGGT
Npun.chrom	B	4402500	P	42	1011	TATAGT	TGCGATGTCTACGAT	TGGTCACTGAGCCTTTGT	CGAAGTG	CGGGCTACGCTACGCAGCTA
Npun.chrom	F	1381406	I	36	635	TGAATA	AGGCAGGAGGCAGG	TGGTCGCCGAGCGCAGCCGAGGTG	AGGCAGG	GAGCAGGGGCAAG
Npun.chrom	F	2773154	P	114	678	GGCAGGAGGCAGGAGGCAGG	TGGTCGCCGAGCGCAGCCGAGGTG	AGGCAGGAGGCAG	ATCGCGCA	

Singles

Npun.chrom	B	3108875	I	1254	338	AGCAGG	TGGTCACTGAGCGT	CCTGCCCTGAGCGAAGC	CGTTGGCGCAGCCTCTCGTAGAG	AAGG
Npun.chrom	F	6397710	P	59	230	CG	TTGGGCA	CTTGTACTGAGCCTGTGCTGAGCGTAGC	CGTAAAGCCTGTGGCATAGCTACGCTTA	
Npun.chrom	F	7891980	I	117	713	TGTCTACGA	TAGTCACTGAGCCTGTGCTGAGCGTAGC	CGTTGGCGCAGCCTCTCGTAGAG	AAGG	
Npun.chrom	F	708238	I	493	481	TGGTATGCGATGTCTACGGC	GGTCACTGAACCGCAGTCGAAGT	GCTGGCTACGCCACGCATTG		
Npun.chrom	F	4591508	D	303	216	AATGCGAT	CGATGCTCCGA	CGGTCACTGAGCGCAGC	CGTAAAGCCTGCGGCATAGCTACGCTTA	
Npun.chrom	F	3841985	I	482	1623	CCCT	CTGCTTCCGCTGCTGCT	CGGTCACTGAGCGTAGTCGAAGTG	CTGCCCTCTGCTTTCTTCTA	
Npun.chrom	F	7336192	I	895	463	TATTTTCTCCTTT	GCTCCCC	CGGT	TACTGAGCGCAGT	CGTTGGCGCAGCCTCTCGTGGAG
Npun.chrom	F	4292951	I	1537	1369	ATTTT	CTGCCGCTGCTGCCG	CGGT	TACTGAGCGTAGTCGAAGTA	TGCTCCCCCTGCTCTCTCACC
Npun.chrom	B	1243442	I	1589	1758	CGGCTGCTGCCGCTGCTGCCG	CGGT	TACTGAGCGTAGTC	CGTTGGCACAGCCTCTCGTAGAG	AAGTA
Npun.chrom	B	3732630	I	10512	2864	GCGATA	CTTGACTGAGCGA	CTGTCGCGAGCGCAGCCGAGGTA	AGTCGAAGTA	AACGCTTAGTT
Npun.chrom	B	2686180	I	1981	9670	ACAAAC	CTTGTACTGAGCGG	CTTGCCCTGAGCGGAGC	CGTTCGCGTAGCGTCCCGTAGGG	AAGG
Npun.chrom	B	733346	P	86	247	GTACAAG	TTCCGAATTCCCA	CTTGCCCTGAGCGTATCGC	TAAAGT	GAAAGCTCCGCTAACGCGTA
Npun.chrom	B	6265488	I	97	160	GGGGA	AATTGGGAATGGGGAA	CTTGTACTAAGCCAGT	CGTAAAGCCTGCGGCATAGCTACGCTTA	
Npun.chrom	B	5106444	P	96	41	TAGTT	ATTGGGAATTGGGAA	CTTGTACTAAGCGCAGT	CGTAAAGCCTGCGGTATAGCTACGCTTA	
Npun.chrom	F	1021335	I	453	392	GGAGTATTGGGAAC	TAAAGA	CTTGTACTGAGCAAGTCGAAGTA	TTGGGAA	CTAGGTAAAATAAA
Npun.chrom	F	2677306	I	10101	3068	AATTCAAGCATTTATCTAC	CTTGTACTGAGCGAAGA	CGTTGGCGAAGCCT	CTGCCT	CAGC
Npun.chrom	B	481149	P	78	45	TAGTCATTAGTCATTGGTCA	CTTGTACTGAGCGAAGC	CGTTCGCGTAGCGTCTCGCAGAG	AAGTA	
Npun.chrom	B	3747194	I	6953	2775	AGTTGATACCCAGGAGATA	CTTGTACTGAGCGAAGT	CAAAGTA	AACGTTTAGTTGCTTACTTAG	
Npun.chrom	F	5099498	P	7	131	ATCT	CACCTAGTCATTAGTCA	CTTGTACTGAGCGCAGCCGAAGTA	TTAGTCATTTATCATTAGCCA	
Npun.chrom	F	1021297	I	415	430	GTAATA	AATAGGGAC	TGGAG	CTTGTACTGAGCGCAGCCGAGTA	TTGGGAA
									CTAAAGACTTGTAC	

Npun.chrom	B	7659643	P	238	46	TCGTGATTAGTCATTATTCACCTTGACTGAGCGTAATCCTTCGCGTAGCGTCTCGTAGAGAGTA
Npun.chrom	F	1436686	I	2425	403	TTTAGAAGAATTCATTGTCCTTGACTGAGCGTAGCCGTACCACTTCGTGGAAGCAAGCTACGC
Npun.chrom	B	5369756	P	45	144	TAAACTGTTTAAATTCGAACTTGACTGAGCGTAGCCCTTGCGCAGCGCTCTCGCAGAGAGTA
Npun.chrom	F	5596464	C	15	157	TTTTGATTTGGCATTGGGCACTTGACTGAGCGTATCCCATAAGGAAAGCTTCGCTAACGCGTA
Npun.chrom	B	5620377	C	51	285	ATCTAAAATCGTTCAACTGACTTGACTGAGCGTTGTCGAAGTAACGCTCACGACAAGCTCTAAAA
Npun.chrom	B	3424416	C	210	49	TGGGCATTGGGCATTGGGAACTTGACTGAGGGTATCGCTAAAGCGAAAGCTCCGCTAACGCGTA
Npun.chrom	B	5087575	P	281	84	ATGCTACGATGGTCACTGACTTGACTGAGTGCAAGTCAAGCAGCTTTGTCTGTAACCACTTCATA
Npun.chrom	F	187272	D	830	10	GGGCAAGTGGGAATTGGGAACTTGACTGAGTGCAAGTGAAGTATGGGGAATTGGTGATTGGTAG
Npun.chrom	F	1888202	C	19	77	AATTAAATACGAATTACGAACTTGACTGTGCGTAGTCTGTAAGCCCTGCAGCATAGCTACGCTTA
Npun.chrom	B	5940638	P	151	194	CTGTCAATTTGTCCATTGTCCTTGACTTAGCGTAGTCGTACCACTTCCCTACGGGACGCTACGC
Npun.chrom	B	3205476	I	1070	2472	TCTCAACCATTTTCGCCACCCTTGATTGAGCGAAGTCGAAATATCCCTCAAGGAGTTTGATTCTG
Npun.chrom	B	1246971	P	8	261	GCCCATTACGAATTACGAACTTGATTGAGCGCAGTCGAAATATACGAATTACGAATTAGTTA
Npun.chrom	F	4987461	I	1095	779	CACTCTTGGGGAATGGGGAACTTGATTGAGCGCAGTCTTGGCGCAGCCTCTCGTAGAGAGTA
Npun.chrom	F	7754339	P	209	950	CCGCGCAGCGATGCACTGAGCTTGCTGAGCGTAGCCCTTGGCGCAGCCTCTAGTATAGAGGG
Npun.chrom	B	2919046	I	2546	1665	AGGGCGGGCTTGCCGTGAGCTTGCTGAGCGTAGTCTTGGCGCAGCTTCTCGTAGAGAGGG
Npun.chrom	F	4760907	I	747	5228	GGGAGCAGGCTTGCCATGAGCTTGCTGAGCGTAGTCTTGGCGCAGCCTCTCGTAGAGAGGG
Npun.chrom	B	703666	P	104	48	AGGGAGTAGGCTTGCCGTGACTTGTCGCGAGCAAAAGCCGAGGTAGCGTAGTCGAACGGGAGTAGG
Npun.chrom	B	5405409	C	79	53	TTGTCACTTGACTGAGCGACTTGTCGCGAGCGAAGTCGAGGTAGCCGAAGTATTGGTCATTTG
Npun.chrom	B	5646796	C	94	150	CACTGAGCGACTTGCTTGACTTGCTGAGTGAAAGCCGAGGTAGCGAAGTCGAAAGGAGTCGAA
Npun.chrom	F	3117984	P	195	213	AAAACACTTGTTGAGCGGCTTCCCTGAGCGTAGCCGTAAGCCCTGCGGCATAGCTACGCTTA
Npun.chrom	B	7754253	P	123	1036	AACTACCGCTTGTCGTTTCGCGCAGTACTGAGCGAAGCCGAAGTAGCCTCTCGTAGAGAAGTGTC
Npun.chrom	B	1500168	I	209	75	TCAAAGAAGCGATGCTACGAGGGCCACTGAGCGCAGCCGAAGTGCAGGCTACGCTTATGCTTTCT
Npun.chrom	B	4548821	P	21	198	CTGCTCCCTCTGCCTACCCGGTATACTGAGCGTAGTCTTGGCGCAGCCTCTCGTAGAGAGTA
Npun.chrom	B	5176302	I	1234	889	AATCGCTACATGATGGTTTGTGTTAACAGAGCCCTTGTCGAAGTGTAGAATTATGATTTGTTGCG
Npun.chrom	B	1458042	P	290	958	GATCGCAGCAATGCCTGCGGTGGTCACTGAACCGCAGCCGTACCACTTCCCTACGGGACGCTACGC
Npun.chrom	B	4660888	I	350	261	CGATGGTCCGATGCTACGATGGTCACTGAGCCCTTGTCGAAGTGCAGGCTACACCTACGCAGTTT
Npun.chrom	B	1636453	P	142	248	ATGCTGTCCGATGCTACGATGGTCACTGAGCGCAGCCGTACCACTTCGTGGAAGCAAGCTACGC
Npun.chrom	F	1214036	I	1069	37	TGTGGCAACGATATCTACAATGGTCACTGAGCGCAGCCCTTCGCGCAGCGTCTCGTAGAGAGTG
Npun.chrom	F	2179989	I	47	1530	GGATTCTCCCCCTTGCTCCTTGGTCACTGAGCGCAGTCGAAGTGTGCCCTGCCCCCTCTTCTTG
Npun.chrom	F	1185336	I	3458	621	TCTGCTGCCCCCTGCTCCTTGGTCACTGAGCGTAGCCCTTCGCGCAGCGTCTCGTAGAGAGTG
Npun.chrom	F	3691866	P	24	220	AGGTGAAGGTACAAGGCAGGTGGTCACTGAGCGTAGCCCTTGGCGTAGCCTCTCGTAGAGAGTG
Npun.chrom	B	313248	P	102	131	GAGCGTCGGCAGGGGGCAGGTGGTCACTGAGCGTAGTCGAAGTGAAGGCAGGGAGTAGGTGGAAAA
Npun.chrom	B	1186339	I	287	1764	TTTCTGCCCCCTGCTCCTTGGTCACTGAGCGTAGTCTTCGCGCAGCGTCTCGTAGAGAGTG
Npun.chrom	F	6486170	P	96	61	ACATGGGAGAGGTTTCCCTCTGGTCACTGAGCGTAGTCTTGGCGCAGCCTCTCGTAGAGAGTG
Npun.chrom	F	4103984	P	27	139	AGAAGATTTCAGAATTTCAGTGGTCACTGAGCTTAGTCGAAGTGAATCAGAATTTCAGTATGAATT
Npun.chrom	B	8012695	P	424	109	CACATTATGCCGATGCCGTGCGGTGGTCACTGAGCTTTGTCTTCGCGGAGCGTCTCGTAGAGAGTG
Npun.chrom	F	2145725	P	115	120	CAAGCCCTAAATTTATTTATGGTTACTGAGCGTAGCCGTAAGCCCTGCGGCATAGCTACGCTTA
Npun.chrom	F	6385170	D	136	279	GGAGCGATGCTCCGACGGGTGGTTCTGAGCGCAACCGTACCCTTCGTGGAAGCAAGCTACGC
Npun.chrom	B	8203396	D	339	118	AAAGCGATGCTACGACGAGTGGTTCTGAGCGCAGCCGTAAGCCCTGCGGCATAGCTACGCTTA
Npun.chrom	B	353441	P	315	310	AGCAGTGTCGCTGACTAAGATTTCACACTGAGCGTAGCCGAAGTGTATATACATCTAAACATTTT
Npun.chrom	F	5303193	D	21	315	TTGTTCTTTGTCTTTGTCTTTGTTACTGAGCGTAGCCGTAAGCCAAAGCTCCGCTAACGCGTA
Npun.chrom	F	3242326	I	408	554	TGGACACTTGTTGTTGAGCGAATTGCTGAGCGGAGTCGAAGTGAAGTCGAACAATCAGCAGACAT

Low SDR1 (copy number < 3) elements found by pattern (but not mismatches)

Replicon	Site	SDR and flanking region
Npun.chrom	3561922B	GTATATTTAACTAATGCTTAACCTTGC GCGATACCTGCGGT GTTCACTGAGCGGCTGGTGAGCGGAAGTCGAACCA TGCCCTCTCGTAGAGAAG TCGGGGCTACGCTGCGCATTTGCAAGTTGAGT
Npun.chrom	7282024B	GGCAGGAGCTACGCCCACTTTATA GCGATGCTGCGGT GTTCACTGAGCGGCTGGTGAGCGGAAGTCGAACCA TGTCGTAAGCCGTGCGGCATAGCTACGCTTAACGCGGAGCGTCTCGTAGA
Npun.chrom	672537B	AAGAAGCAGGGGAGCAGGGAAGAAGAGTTTTCTCCCATA CCCCAATCC TCA CTTGCCCTGAGCGGAGCGGAAGGG ATA CCCCAATCCCCAATCCCC AAAATCCTGATGTGCAACTGCTCCAAGCCTT
Npun.chrom	4699921F	TAATCACCAATACCCATGCCAATCCCCAGT CCCCAATGCCCAATGCCCA CTTGCCCTGAGCGGAGCGGAAGGG AT TGCCCAATACCCAATGCCAATGTGCCAAT ACCCAAAGATTGCAAGATTT
Npun.chrom	3298573B	CGCAGACGCTATGCTATCGCTAT TGCAGTCTCGCTC AACTCTCGACCATACT AGTTGGTTGAGCGAAAGTCGAACCA AAATGGCTATGGTAAATTTATTACTAGAAATTCACCTAAACCCCTTTGATTCA
Npun.chrom	7049918B	TTTCGACTTCTCGAGACGCTACGCCAA GCGCTC AACTCTCGATTCCTT AGTTGGTTGAGCGGAAGTCGAACCA AACCGGCAGACGATAGTTATTAAACGGAAATTCGCTTAACAGAGAAAGGAG
Npun.chrom	899833F	CTACGCGTAGCTTGCTTCCCGGAGGGGTCA GCGCTC AATCAACTGAGTGGT CGAAGATTGAGCGGAAGTCGAAACT CATCAACCTGGGTATATCTTTGTG CAAAAATACCTTTAACATTAGCTTGAA
Npun.chrom	7851476B	TTTATAGTTAAGCGATCGCTTTTGTAGCGATGTCTACGA TGGTCACTGAGCGGCTGGTGAGCGCAGTCGAACCA TGT GTTTCGCGGAGCGCTCTCGTAGAG AGTG CGGGCTACGCTTCTGCGCT
Npun.chrom	1268284F	ATAGCAATACGCTTGGATTAAAGCATTTATTTTCTCTCTGTTGT CGGTATTGAGCGGAGCGGCAAA TA CTGCACCTCTGTGGTAGTCTGCGGCAAGCCGCTGACGCTCCTTTGTGCGCT
Npun.chrom	1729894B	TGGAAGTTGACCTTCTA ACTCTCCCTCATCCCCCTTATCTCCCATCCCT CGGTGGTGAGCGGAAGTCGAACCA AACTCTCCCCAAAGCCCTCCCCAATCTTCGCGCAGTTAGTATAAAC
Npun.chrom	4672301B	GGAGCAGCAGTCGCATCCGTGTTGAGGATCGGGAAGAGGAAGGGGCGAGG CTTACCCTGAGCGTAGCCGAACGG GAGCAGGGGAGGAATAACTAATCTCAATTCTAATTACCAATTTACTAATC
Npun.chrom	6488795F	GAGCAGAGGAGCAGGAGAGAAGTAACAACAACCT GAATGCCCAATTCGGAC TTG CCCTGAGCGGAAGCGGAAGGG AT TGCCCAAT ATAGGAAAATAACGTGTCAATAACAGAACATAAAATCCATG
Npun.chrom	1275865F	TTTGTAATTTACGAATACGAACATGAATACGAA CTTGTACTGAGCGCACTTGCCCTGAGCGCAGTCGAAGGG AGCCGAAGTA ATTACGAATTAAGTATGTGCATCTGATGATATTTCCACAGC
Npun.chrom	5490593B	GTCTGTGGCAAATACCTGTATTAGGAAGAGTCA GGGGAGCAGGGAGCAAGGCTTGCCGTGAGCGTAGACGAACGG GAGCAGGGAG ATATGAATAGTGTGAGTTAAAGACTACTCACAAGGAGC
Npun.chrom	3283624B	GCCCACTTATACTATTGTGGATTTAGACTTCGGCTTACCTCGGCTCTGGCT TCCATC GAGCGGAAGTCGA GATG CTGCGCACAAAGTCGCTCAATCGAACGATTTTAGATTGCAAATCGTCCAAG
Npun.chrom	3261593F	AGACGAGTCAACGCCGAGAAAACCGGGGGTGCTGGCCTGAATAACTCTCAGGG TTCCATC GAGCGGAAGTCGA GATG GTTTCACAGCTTGTCAACAGAGATAAATGTCGTCAAGAAAACATAGTTATC
Npun.chrom	5873033B	TTCTCCATGCCAATGCCGCTGCGCTCTTTGCAATACCC AACTCTAAATGTTGCACTGAGCGGAAGTCGAAGTC CAAAATCTAAATCTAAAT GTTTTATGGCTTCTACATTTCTCTTGACA
Npun.chrom	6930570B	GATTAACCTCTCAGCAGGTGTGCGTTGGATTTAAGATTTT ATCTCAAATCGTTGCACTGAGCGGAGCGCAAGT CCATATCTCAAATCCAAAT AAAATCTATGCCAGACCCCAATCTCTG
Npun.chrom	2948356F	TAATTTATGCGCTATACGAACATATATGACAAATGGATCG TCCAAATCGTTGCACTGAGCGTAGTCGAAGTC CAAAATCCAAAT CGGATCGTGGGTATTGTGTTGTTAGTAACCTTAG
Npun.chrom	6197745B	GTTTAAATTTATGGCGCATTTGGGCAAGAAGCAGAGAGGCAACAACTCGGTT GTCCGTGAGCGTAGCCGAACGG GAGCAGAGGGGAAAGAGCTAATTTATCTCCCCCTTGCCCCCTGCTCCC
Npun.chrom	1367429B	TCATCGGTAAAGATAAAGTCAGATGATTTGA CCCTTCGCGCTCGCGCTCAGAGTCAACAG TAGGAGCGGAAGCGCAACTGTTGACTTACCTAAAGGGTTTAGGCTGACCAATCTGCAATATTATTAAC
Npun.chrom	1811840B	TCCGACACTTCGACTGCGCTCAGTGCATCGCTGCGCTCAACTCT CGATGGCTGA GGGTTGAGCGCAGTCGAACCC CAACTTACATTTAATGCACAAATTTAAGCTTGACACGGCACTATATTTAT
Npun.chrom	3057877F	CAATAGATGGACGGTTATTTCAAGTAATCCACCCAGCGGAAGCAATCAGGT TACATC GAGCGGAGCG AGATG TTCACAGTTATAGACCTCCAGACATTTCTGAGTCTGAGCAAGAAGCAGA
Npun.chrom	1243491B	AGAGACGACGTTAAAGTTTGTGATTCGGGACTGGAGACTAGGTGCTGGG CTTGCCGTGAGCGTAGTCGAATGGG GACTCGGAGTTAAGAAATTTCTCCCTCTGCTCCCTGCTCCTCATCCCC
Npun.chrom	1367359B	TTGTGACGCTCAAAACCTTTAGTTAAGTCAAG CAGTTCGCGCTTCGCTCAGGTT GACTGAGCGGAGCGGAAGGG CTCATATCGATCAGTTTATCTTACCGATGAAATAAAAAATCACTTAACTTT
Npun.chrom	2647900B	ATGTAATCTGTAATTGGTAAATTGCCGGATTAATAAGGCTAGAATGTTGT TTTTTGTGAGCGTAGCGGAATAA ACTCACTCTAAAAGGTAATAATGAAGGCTTTTGAAAAATCATCTAAAT
Npun.chrom	2743932B	TTCTACGATACGCTACGTTGATCTGCTTCCACGAGTGGTACGCGCTACG CGGTTCCTGAGCGGAAGTCGAAGGG CAGTACAAAGTTCGTAAATCCGATCTGCAAGCCTTCATGATTTGGAAT
Npun.chrom	4939098B	GGGGAAACA GGGGAAACA GGAAATA AACCATA CCCCAATTCGCAATTCGCAAT TGCCCTGAGCGGAAGCGGAAGG ATTCGCAAT CCCCAATTCGCAAT CCCCAATTCGCAAT CCCCAATTCGCAAT
Npun.chrom	8086723F	TCCGACACTTCGACTGCGCTCAGTGCATCGCTGCGCTCAACCC CTAGCCAT CGAAGAGCTGAGCGCAGTCGAAACT CGGTTTACTGGTACTTTTTCACACAAGTCCCTACTGTGTGGAGTTCG

SDR1 elements in cyanobacteria other than *N. punctiforme* and not sharing its sequence with a multicopy SDR1 from *N. punctiforme*

Replicon	Site	C	SDR and flanking region
<i>Anabaena</i> PCC 7120			
A7120:Chrom	1752691F	D	TAATAGTGTCTCAACCAGCCG G TTTTC G ACT C CGCTCA CA CCCTCACTCTGT CGAGAGTTGAGCGGAGT CGAA ACT CGGTTTACTGGTACTTTATTTTTCATGCAAGTCCCTAAGCTATTACGAGTGT
A7120:pAlpha	168914F	C	TTTGCTGGCTCTACCGCTCCTCGATAAAAGTAAAAATTCAGAACCCAGG CGGTGCGCGAGCGCAGT CGAG GGT GATTCAAGCAATGCTCTAAGCTTGTCTGAAGGGTCAGAAATTTAGAAGTATT
A7120:Chrom	5147756F	C	TGATCAGCTATTACGCTTTTAAATTACATAGACACATGGTTTGTGAGGG CTGACCCTGAGCGTAGT CGA AGGG TACGCCCTCAACTATTAATAAACTACTGTACTCTTGCCTCTAAGCCATTAGAG
A7120:Chrom	1236435F	D	CATTGGTCAGTTGTCAGTGTCTTCTCCTCTGCTCTAGGCTGGTGAGCGA CTTGCTTGAGCGGAGT CGAA AGG AATTTAACTACTGCCTTCTACCTCTTAAGAGTCTTAGTCTAGTCACTACG
A7120:pAlpha	7273F	P	CGCAGCGTGTAAGGAATAATTA TCAGTCACTCAGTCATCACT AT ATCAGTTA CTTG TACTGAGCGGAGT CGA GGTA TCAGTTA AACTCATCCCCCTCATTCAAATATGACTTAGTAAAACTTTAGC
A7120:Chrom	3314882B	I	CCCTAAATCAATACCGCTAAATCTCCCTCCGTAATAGCAGGCTTTTCA CTTGTTGTTGAGCGGAGT CGAA ACA CCCTCTACTTCAGTCAGGATAGATGCCAAGTATTTACCTGATGGTGTTTTA
A7120:Chrom	1752660B	D	AATAAAGTACCATAGCAAA CGAGTTTTCGACTCCGCTCAACTTCG ACAGAT GAGGGTTGAGCGGAGT CGAA CCG CGCTGGTTAGGACACTATTAACCGCGCAGATCCTTTATATATCTTTGTGCGC
A7120:Chrom	1353787F	P	GTAGGCGCGGAGGTACGCGGAGAGTTATACAAATCTTTCTT TGCGTCTTGCGT ACT GAGCGGAGT CGAA AGTA TGCGCCTCTGCGT GAGATAAAAAAGGAATTACTAATGACGACCTTATATC

Anabaena variabilis ATCC 29413

Avar:Chrom 2275336B I AAGACCTGACAGACTTAAGTCTCAAGGGCAGTTGCAAAAAACCCGTAAGGCTTGCCCTTGAGCGTAGCCGAAAGGGACAGAAACAGAAACCTAAGTCGTGAGGCTTAGGAATCCCCGACCGTTCA
Avar:Chrom 4288041F P CCCTCCCGTCTGCACTCTGCGCGCTCGGTCACTGAGCGACTTGCCCTTGAGCTTGCTCTGAGCGTAGTCGAAGGGCGAAGGCGAAAGAGCCGAAGTCTGCGCGCTCTGCGCTCTCAATGATAAG
Avar:Chrom 2101898F P TGCAGAGGTGCAGGGGAGCAGAGGAGAGAAACACCCACACTTCGTCAAGCGGTAGTTGAGCGAGTCGAAACGAGCGTCGGACGCTGCGCCATCGCCAGGGACAAGGCTTTGAACCTGATCT

Nodularia CCY9414

nod-020 41609B P TTAAGTAGTAATTAGTCAATAGTAGCTGACTAAAACTCCTGACTAAAGATTTACCCTGAGCGTAGCCGAAAGGGCTAATGACTAATAACTAATATGCGATTTGCTAACCGTTTACAACCCCTGC
nod-065 18950F D TCTGTAGAAGAAAGTGTGAGTTCATGTTTGATGACCAATGACCAATGATTTACCCTGAGCGTAGCCGAAAGGGCTAATGACTAATGACCAATGACCAATGACCAAGTTAACTGCCCATGAAA
nod-096 15270B C TAATTTTCCACTGGCCACTGACCATTTGGCTAATTACCAATGACCAATTAATTACCCTGAGCGTAGCCGAAAGGGCTAATGACCAATGACCAATGACTAATGACTAATGACTCAATTC

nod-006 91538B P GTACGGACAATAACTTTAGCGTGAAGTCGATATGTGGTCTGATTGATTGGGTGGTTGAGCGAAGTCGAAACACGATACCCCAATCATCTCTAAAACTCTTTGGGGTTATCTTCACCTCAC
nod-006 93946B P AAAGTCAACAAAATCCACAAGAAAGTTGCAAAAACCAAGTCAATTGATTGGGTGGTTGAGCGAAGTCGAAACACGATACCCCAATCATCTCTAAAACTCTTTGGGGTTATCTTCACCTCAC

nod-006 91421F P ACTTAGCTTTTCTTCTAGTCAGATTTTAGCACTTGAAAATTGATTCTTAATGTTCCCTGAGCGAAGTCGAAAGGGAACAATATCAGGGGGAGGAAGTGAGGTGAAGATAACCCCAAGAGATTTTA
nod-006 93829F P GTGATCTGGCGACCACCGGGTTTGGGTTGTGGAATCATCTCACTGCTGATGTTCCCTGAGCGAAGTCGAAAGGGAACAATATCAGGCTGAGGAAGTGAGGTGAAGATAACCCCAAGAGATTTTA

nod-004 76007B P TTACAATCTCGGTATAACACAAAAAGGTTTTTTCCTACTCCGCACTCCGCGGTACTGAGCGCAGTCGAAGTAACCTCCCACTCCCTACCTACGCTGTGTGT
nod-010 45423F I AGTGGTATAAAAAATCAGAGAATCAGCAAAATTTCCGACTCCGCACTCCGCGGTACTGAGCGCAGTCGAAGTAACCTCCGCACTCCGCGGTACTGAGCGCAGTCGAAGTAACCTCCCACTCCCTACCTACGCTGTGTGT
nod-139 5240F C CTGCAAAAATCCTCTTTCCCTGCTCCCAAGGACTACTCCCTACTCCGCGGTACTGAGCGCAGTCGAAGTAACCTCCGCACTCCGCGGTACTGAGCGCAGTCGAAGTAACCTCCCACTCCCTACCTACGCTGTGTGT
nod-029 19128F D TCCTGAGATGGTTAGTCACAAATCTGCCAGTATTTGTGAGAAAAATTTCTAGCCCTGAGCGTAGCCGAAAGGGAGCGCAGCCGAAGGACTAAATTTGCTTCCCTGAGAAATACATAAAATAAC
nod-081 23468F P CGCCGCTAGAAGTCGCGGAACCATCTACACAAATTCGCGGCTCAACTGACTTGACTGAGCGTAGTCGAAGTAACCTCCGCACTCCGCGGTACTGAGCGCAGTCGAAGTAACCTCCCACTCCCTACCTACGCTGTGTGT
nod-096 4511F C TAAATTACAGGGAATTTCTCTAAATAAGGTATATGCGTAGCGGCAAGAATTGTTGACTGAGGGTAGTCGAAGTAACCTCCGCACTACACGATTTGTATCATTATGTTTATACTTCATTTACTTG
nod-077 18304F P ATTGTTCTAGTTTCTCTAGCAGTAGGTAAGATTCATAGGGGCTAGACTTTGTTGAGCGAAGTCGAAGTAACCTCCGCACTACACGATTTGTATCATTATGTTTATACTTCATTTACTTG
nod-173 355F D ACTCTATCAGTCTACTGTTACCAAGTCAATGAATTAGGCGAATAAATTCGTTGGTCAAGTGAAGTCGAAGTAACCTCCGCTGCTTATATCTCAGGTCTAAAGACACTGAGCTTTACGCTTACC
nod-102 6354F I CCATCGGGTAAATAACGTGCTAAATCTCCTGTTTATAGAGGTAATGGGATGGTTGGTGAAGTCGAAGTAACCTCCGCTGCTTATATCTCAGGTCTAAAGACACTGAGCTTTACGCTTACC
nod-015 15509F C CGAGATGGTGAACGGGAAGTAGGAAGAAGCAAGGAGCAGGCGCAGGCTTGCCCTGAGCGCAGTCGTTAGCGAAGCTTCCGAAAGGGTAGGGGAGCAGAGGGAAAGATTGTGACTTACCAA
nod-029 33209F I CCGGAGGTTCTACTACAGGTTTAAACGGCTCCACTTTGGTCACCTTAGTAGTTGATTGAGAGCAGCGAAGTCGTTCTGCGCTTTTATGCCAACCTGATTTGCCCAAATTGGGAGAAGGTAT

Crocospaera watsonii

Cwat:225 8372B D GGAGACTGGGAGCAGAATATTAATATTATTTTAGTCTTCCGACCTTCTGCTTACTGAGCGAAGTCGAAGTAACCTCCGCACTCCGCGGTACTGAGCGCAGTCGAAGTAACCTCCCACTCCCTACCTACGCTGTGTGT
Cwat:259 5488B P CCACACTTCTCTGTACTGAGCGAAGTCGAAGTAACCTCCGCACTCCGCGGTACTGAGCGCAGTCGAAGTAACCTCCGCACTCCGCGGTACTGAGCGCAGTCGAAGTAACCTCCCACTCCCTACCTACGCTGTGTGT
Cwat:259 5528B P AGCTTTCTTGAGCAGAATATTAATATTGTTTCTAGTCTTCCGACACTTCTGCTTACTGAGCGAAGTCGAAGTAACCTCCGCACTCCGCGGTACTGAGCGCAGTCGAAGTAACCTCCCACTCCCTACCTACGCTGTGTGT
Cwat:356 39100F P TACCAATCCGATTGTCAAACCTCTTTATAGTTTTGCTCTCTTTCCCTGCTTACTGAGCGAAGTCGAAGTAACCTCCGCACTCCGCGGTACTGAGCGCAGTCGAAGTAACCTCCCACTCCCTACCTACGCTGTGTGT
Cwat:361 314386F C GAGATGGGGGAGCAGAATATTAATATTGCTTCTAGTCTTCCGACCTTCTGCTTACTGAGCGAAGTCGAAGTAACCTCCGCACTCCGCGGTACTGAGCGCAGTCGAAGTAACCTCCCACTCCCTACCTACGCTGTGTGT

Cwat:285 4857B D TTTATACTTGTGTTTAGGTGTTAAAGTCCCCCTAATTCTCCACCACTCCGCGGTACTGAGCGAAGTCGAAGTAACCTCCGCACTCCGCGGTACTGAGCGCAGTCGAAGTAACCTCCCACTCCCTACCTACGCTGTGTGT
Cwat:327 11425F C AGAGGGGGAAGGCTGGAAAGAGAAAACATTATGTATTGCTTAATTCTCCGCTTACTGAGCGAAGTCGAAGTAACCTCCGCACTCCGCGGTACTGAGCGCAGTCGAAGTAACCTCCCACTCCCTACCTACGCTGTGTGT
Cwat:360 32195F P TCAAAGGATTACAAAAATCATAGATTAAATATAAAATCCCAATACTCCGCTTACTGAGCGAAGTCGAAGTAACCTCCGCACTCCGCGGTACTGAGCGCAGTCGAAGTAACCTCCCACTCCCTACCTACGCTGTGTGT
Cwat:361 74433F I CTCACCGGAGGGGGAACCTGAAGGGGGTGGTGTCTGCTCCCTAGAGGGTAAACGCTGAGCGTAGTCGAAGCGTTTACCCTACAAAGATCAAAATACTATTAAATCTTTTCTCATACCTA
Cwat:362 165517F P CTTTAAAGAAAAAACCGTTTTTTCGTAGTAAATATTATATTGAGGGGTCAACACTGAGCGTAGTCGAAGCGTTTACCCTACAAAGATCAAAATACTATTAAATCTTTTCTCATACCTA
Cwat:319 6678F C TCTTTGACTCTAATAACATTAATATAACCTTAGTTTAAACAGCACTAGGGGTCAACCTGAGCGTAGTCGAAGCGTTTACCCTACAAAGATCAAAATACTATTAAATCTTTTCTCATACCTA
Cwat:346 7200F C AATTTTTGAAAGCGATCGCTAATAATAACTATTATCACTTTCCCTAGGGGTCAACGCTGAGCGTAGTCGAAGCGTTTACCCTACAAATATAGAGTTTGTATAGTCAAGACATATAACTCTG
Cwat:300 12049F P TATAATACCATTTTTATCAACTGAAACCACAGATATTAAACCTGAGGGGTCAACGCTGAGCGTAGTCGAAGCGTTTACCCTACCAATTGAAATAGATATTAACTGATGTATAATTGGAGTA
Cwat:354 16158F P TCGGCATAGCCGAGAGTCCTCTCTGACATTTAAGATAAAAAGATAGGGGTGAACGCTGAGCGTAGTCGAAGCGTTTACCCTACAAATTTCTACATCTTCTCAAGTATTATTCAATTATAT
Cwat:297 13456B P GTCCTAAGCGTTTTGGCGACTGCTATATTAGAAATTAAGCCTTACGGATACTTGCACTGAGGGAGTCGAAGTTCTTAAGAATGGAGAATTTTTAAATAGATATAATGACCAATTCTAAATAC

Synechococcus WH8102

S8102.Chrom 1011877B I TCGCGCAAGGCCTCGGCAGAGAAACCACCGAACACAACGGAATGGGGGGCAACGATGCGAGCGCAGGCGAGCATCGCAATGGCGGCCTCTGGAATCATCGGCATGTAGAGGGCGACCAAGATCGC

Supplemental Figure 1: Sequences and contexts of SDR1 elements. All instances of SDR1 in the genomes of the cyanobacteria listed in Figure 5 of the main text are indicated. The **replicon** in each case is given by the organism abbreviation (see Figure 5) followed either by "chrom" to indicate the chromosome or by the name of a plasmid. In the case of genomes that have not been completely sequenced, the name of the contig is given instead. The **site** is the low-order coordinate of the SDR element in the replicon or contig, followed by "F" or "B" to indicate that the sequence shown was taken from the upper (forward) strand or lower (backward) strand, respectively. The **context (Ctx or C)** of the reference point (the left-most nucleotide of an element), when given, is: **I**, inside a gene; **C**, between convergent genes; **D**, between divergent genes; **PP**, between genes oriented in parallel, with the element also in parallel; **PA**, between genes oriented in parallel, with the element antiparallel. **Left** and **right** refer to the number of nucleotides between the reference point and the nearest left- or right-hand gene boundary, including the gene containing the reference point (if the context is **I**). The **sequence** shown includes the SDR element, in bold and highlighted by its characteristic color and flanking sequence, following the conventions described in Figure 1 of the main text. In addition, gene sequences are sometimes shown italicized and in dark cyano (forward) or magenta (backward).