

Library Number	RMK024
Library Name	Nuclear Receptors Library (Sundrud)
Old Document Name	
Library Purpose	CRISPR/Cas9 Knockout of genes encoding nuclear receptors and co-activators/repressors in CD4 positive T cells. Genes were identified from previously utilized shRNA screen in CD4 positive T cells.
Location	
Designer Name	Zach Bacigalupa (for Sundrud Lab)
Designing Date	Aug-23
Design Reference	
Usage Reference	n/a

Species	Mouse (Mus musculus)
Total Gene #	82
Total Target #	328
Gene Group	
1. Negative Controls	targeting controls from BRIE library) + 6 user supplied (4 guides each) =28
2. Positive Controls	2 (4 guides each) = 8
3. NR Genes	81
Target Number	
1. Negative Controls	28
2. Positive Controls	8
3. IEM Genes	82*4=328

Note: The Nuclear Receptors Library was designed from genes that support nuclear receptor signaling critical to CD4 T cell programs and was inspired by a previously published screen (doi: 10.1038/s41586-021-03421-6). Genes without mouse orthologs, mitochondrial DNA-encoded genes, genes encoding noncoding RNAs, and genes without guides in either the BRIE or Gecko libraries were excluded. 4 NTCs (~1%) were added from the BRIE library controls, as well as 28 additional negative control guides (7 genes, 4 guides each) and 8 positive controls (2 genes, 4 guides each). This brings total # of guides to 364 guides. Available in GFP and BFP vectors.

Target Gene ID	Target Gene Symbol	sgRNA Target Sequence	Notes
11835	Ar	GGTGGAAAGTAATAGTCGAT	
11835	Ar	ACCAGGATACCACACTTCGG	
11835	Ar	GACTTGGGTAGTCTACATGG	
11835	Ar	GCTCCTGGGAGGTCCACCCG	
13982	Esr1	GGCATACGGAAAGACCGCCG	
13982	Esr1	CACTGTGTTCAACTACCCCG	
13982	Esr1	TATTCAGAATAGATCATGGG	
13982	Esr1	AGAGGCATAGTCATTGCACA	
13983	Esr2	TGGCGCTTGGACTAGTAACA	
13983	Esr2	TTCGTGACGGCTCTCTACAT	
13983	Esr2	GAAGTAGGAATGGTCAAGTG	
13983	Esr2	CGGCTCACTAGCACATTGGG	
26379	Esrra	CTACGGTGTGGCATCCTGTG	
26379	Esrra	CAGCGGGGAGGTGTCCATCG	
26379	Esrra	TGTACTTCTGCCGTCCGCCG	
26379	Esrra	CGACACCAGAGCGTTCCTG	
not found in Brie	Esrrb		
	Esrrb		
	Esrrb		
	Esrrb		
26381	Esrrg	TGGCGTCGGAAGACCCACCA	
26381	Esrrg	GGTCTGGGGATCCTCTACGA	
26381	Esrrg	CCAAGTCACAGAGTGTGGTG	
26381	Esrrg	TGTGTGGCGACATCGCCTCT	
15378	Hnf4a	GCAATGACTACATCGTCCCT	
15378	Hnf4a	AATGTGCAGGTGTTGACCAT	
15378	Hnf4a	AGCGGGACCGGATCAGCACG	
15378	Hnf4a	GGTCCGTAGTGTGGCCGG	
30942	Hnf4g	TACAAGAAGAAGTACCTACG	
30942	Hnf4g	TGTTGCGGTGAATAACATAG	
30942	Hnf4g	TCCAGCATGGGCTCTCAAGA	
30942	Hnf4g	GCATGTTCTTAATCTTCACA	
11614	Nr0b1	GCCAACTCAAGCATGAGTAG	
11614	Nr0b1	CAGGGTCTTCAACAGGCCAG	
11614	Nr0b1	CGTTGGTGAGCATAGAGTAG	
11614	Nr0b1	CTTACC GCACACATAGCTG	
23957	Nr0b2	ACTTAAGAAGATCCTGCTAG	
23957	Nr0b2	GGATGCTGTGACCTTCGAGG	
23957	Nr0b2	TGCCCATGAGGATCAGCGG	
23957	Nr0b2	AGAAGTGCATACAGAATAGT	
217166	Nr1d1	GTTGCGATTGATGCGAACGA	
217166	Nr1d1	GAGTAGGTGAGGTCTCTAGA	
217166	Nr1d1	CACAACAGCTGACACCACCC	
217166	Nr1d1	TTCTGGGGCCGAATATACGT	

Target Gene ID	Target Gene Symbol	sgRNA Target Sequence	Notes
not found in Brie	Nr1d2		
	Nr1d2		
	Nr1d2		
	Nr1d2		
22260	Nr1h2	TTCCTTAATAGTGGGTGACG	
22260	Nr1h2	CACCGAGCTAGCCATCATCT	
22260	Nr1h2	CGGCGCAGTGTGGTCCACGG	
22260	Nr1h2	CTCCGACCAGCCCAAAGTCA	
22259	Nr1h3	AAAGCAACCCAGTTGACTG	
22259	Nr1h3	CAAGTACCGTGACGCGCAGG	
22259	Nr1h3	AATCTCCTGCACGGACACGA	
22259	Nr1h3	TTCCGCCGAGTGCATCAA	
20186	Nr1h4	AAACGGGACATTGTTGTATG	
20186	Nr1h4	TGATGGACATGTACATGCGC	
20186	Nr1h4	TGTGACAAAGAAGCCGCGAA	
20186	Nr1h4	AGTGTAATCTAAACGGCTA	
not found in Brie	Nr1h5		
	Nr1h5		
	Nr1h5		
	Nr1h5		
18171	Nr1i2	GTTCAACACGATGTTTCGACA	
18171	Nr1i2	TGTAGGTTGACACATCGGCC	
18171	Nr1i2	TGGCCTTGTCACACATACA	
18171	Nr1i2	TGATCTCGCAGGTTCCCTTG	
12355	Nr1i3	TGCATGAACAGATAGGCCGG	
12355	Nr1i3	GGCGAGCCAGACAGGCACAG	
12355	Nr1i3	AAACGGACAGATGGGACCAA	
12355	Nr1i3	ACACAGGTCCCTAACCATGG	
22025	Nr2c1	GGTGCAGAGCTTACGCAATG	
22025	Nr2c1	ACAGTCTTGCTTCATCCCGA	
22025	Nr2c1	GTTCACTTGGCAAACACG	
22025	Nr2c1	ACGTGCGACTCGCTCAGCAG	
22026	Nr2c2	GATCCAGATAGTCAACGCAG	
22026	Nr2c2	AGGGACAAGGTTGTCCGAGG	
22026	Nr2c2	GTACCATCCTCACGTATCAA	
22026	Nr2c2	TGGAGGTGAAGCACTATCTG	
21907	Nr2e1	CACTTCGTAGAGATACATTG	
21907	Nr2e1	AGGACCCCGCTCGTGCTGCA	
21907	Nr2e1	AGTGTTAGCATCAACCGAA	
21907	Nr2e1	TTCTGTGTGTCTTGTCTACG	
23958	Nr2e3	TGACCCCGATCAGAACCAG	
23958	Nr2e3	CAGTTTAGCACAAGTTTCGG	
23958	Nr2e3	GCCTCCAAGAAGGAGTCTCC	
23958	Nr2e3	TCCTTCTTGAGCCATACAG	
13865	Nr2f1	CCAGTATGCACTCACAACG	
13865	Nr2f1	GGCTGCCATAACGCGACGTG	

Target Gene ID	Target Gene Symbol	sgRNA Target Sequence	Notes
13865	Nr2f1	CGAGCTGTTTCGTGCTCAACG	
13865	Nr2f1	GATGTTGCGGGCCCACTCGA	
11819	Nr2f2	GCAGTTTGCCCTGACCAACG	
11819	Nr2f2	CTACGGCCAGTTCACGTGCG	
11819	Nr2f2	GGCGCTGAAGAGCATCCGTG	
11819	Nr2f2	CTCAAAAAGTGCCTCAAAGT	
13864	Nr2f6	GAGCTACCCACGCGCGACCG	
13864	Nr2f6	GCATGCGCTCCCCGGTCCAG	
13864	Nr2f6	CGGGCGACGAGGAGCGTCCG	
13864	Nr2f6	CATCGACAACGTGTGCGAGT	
14815	Nr3c1	CATTATGGGGTGCTGACGTG	
14815	Nr3c1	AGCTTGCTGGCAATAAACC	
14815	Nr3c1	AAAGCCGTTTCACTGTCCAT	
14815	Nr3c1	AAAAGTGAATAGGTGCCAA	
110784	Nr3c2	GATGATTGGGCTCTTAACGA	
110784	Nr3c2	CAAGGAACTTTCAGCCACGG	
110784	Nr3c2	TCCACTAATGCATTGACAGG	
110784	Nr3c2	GAATGGAAATGGGTTGACTG	
15370	Nr4a1	GGAAGTGTACGGTTCGGAG	
15370	Nr4a1	TGCTTCGTGTCAGCACTATG	
15370	Nr4a1	GGCAAACAAGGATTGCCCTG	
15370	Nr4a1	GCCTTCATAAGTCTGGCTCG	
18227	Nr4a2	TGTCAAGCAACTGCGATGCG	
18227	Nr4a2	TGCCGGATTGGAATCGACGT	
18227	Nr4a2	AGTACTGACAACGATTTCCGG	
18227	Nr4a2	TAGTAAACCGACCCGCTGTG	
18124	Nr4a3	GCATTCATCATAACAGATCGG	
18124	Nr4a3	ACCAAGCTGACCATGGACCT	
18124	Nr4a3	CGGCCGTGGGGTCATAGCCG	
18124	Nr4a3	AGTGTGCGGATGGTTAAGGA	
26423	Nr5a1	TGGAGACCGGACCACCGATG	
26423	Nr5a1	GTGCGTGCTGATCGAATGCG	
26423	Nr5a1	CGCACGTGAGCAGCCCGTAG	
26423	Nr5a1	CCATTGTGCGACTGGGCACGA	
26424	Nr5a2	TGTGTGGCGATAAAGTGTCT	
26424	Nr5a2	GTAAGAGCCGACCGCATGCG	
26424	Nr5a2	TCGCCACTCCCCAAACGTG	
26424	Nr5a2	CTTCTGTCATAGTCTGTCCG	
14536	Nr6a1	CCTTACCCACCGTTGCGCGG	
14536	Nr6a1	CATAGTGCAAGCCCGTAGCG	
14536	Nr6a1	CCAGAATAGCTAAAAAGGTG	
14536	Nr6a1	CACCTATGTTGATTGAAGAT	
18667	Pgr	CTCTGGCCGACTCATGAGCG	
18667	Pgr	AGGAGGAGTCGCAGCCAACG	
18667	Pgr	GGCGGAACGAACCCTGCGT	
18667	Pgr	CAGTCTGGGAAGTCACCGCA	

Target Gene ID	Target Gene Symbol	sgRNA Target Sequence	Notes
19013	Ppara	CATCGAGTGTCTGAATATGTG	
19013	Ppara	GATTTCTCAGTCCATCGGTG	
19013	Ppara	TCTGTCGGGATGTCACACAA	
19013	Ppara	CTGCTGCCAGTGCATGTCCG	
19015	Ppard	CCTCCGGCATCCGTCCAAAG	
19015	Ppard	GGCCTCGGGCTTCCACTACG	
19015	Ppard	TCGAGTATGAGAAGTGCAT	
19015	Ppard	CCTCAAGTATGGCGTGACG	
19016	Pparg	AATGCTGGAGAAATCAACTG	
19016	Pparg	AGAACCTTCTAACTCCCTCA	
19016	Pparg	GCACCCTTGAAAAATTCGGA	
19016	Pparg	CTGCCTATGAGCACTTCACA	
19401	Rara	GAGCTACACGCTGACGCCTG	
19401	Rara	ATCATCCGGCTACCACTATG	
19401	Rara	AGATTCTGCGAATCTGCACG	
19401	Rara	CAAGTGCATCATTAAGACTG	
218772	Rarb	AAGCAGGGCTTGTACACCCG	
218772	Rarb	CCAAGTCCAATCGGACCCGG	
218772	Rarb	ACCGGCATACTGCTCAATGT	
218772	Rarb	TGACGCAGTTCTTATCTCGA	
19411	Rarg	TGGGCAAGTACACCACGGTG	
19411	Rarg	AAGCATGGCTTATAGACCCG	
19411	Rarg	GCTACAAAAGTGTTCGAAG	
19411	Rarg	ACACTATGACATTCTCGGAT	
19883	Rora	TTGGCTGAGATGTTGTAGGT	
19883	Rora	CATTGATGTCCAATCCCGAC	
19883	Rora	GAGAGACAGCTTGTACGCCG	
19883	Rora	AGCTATGCGAGCTCCAGCCG	
225998	Rorb	CACCACGTA CTGGATAGCAT	
225998	Rorb	GGAGACATGTCAGTACACCA	
225998	Rorb	TCCCAGCTGTAAAGTTCGGG	
225998	Rorb	ACAAGTTGGGTACAGATGTG	
19885	Rorc	CTTGAGTATAGTCCAGAACG	
19885	Rorc	GTCATCTGGGATCCACTACG	
19885	Rorc	TCTGGGGCACTGCAGAACT	
19885	Rorc	GACAAGCAGAGGCCTCGGGT	
20181	Rxra	CAAGACTGAGACATACGTGG	
20181	Rxra	AGGACGCCATTGAGGCCTAG	
20181	Rxra	CATGGGCCCGCACTCCATGT	
20181	Rxra	GGGGCAGCTCAGAAAAGTGT	
20182	Rxrb	ATTGTGGGGTCGCGTCCCGG	
20182	Rxrb	GCTGTTCACTCGTTGAGT	
20182	Rxrb	GTTCAGGAGGAGCGTCAACG	
20182	Rxrb	TCCACAGTGTGCTCCCTGG	
20183	Rxrg	TAGCCACGAAGACATGCCCC	
20183	Rxrg	TGCGTTTGGCCCACTCAACG	

Target Gene ID	Target Gene Symbol	sgRNA Target Sequence	Notes
20183	Rxrg	TCGTAACCAGGGAAGCACTA	
20183	Rxrg	CACAGCACTCAGCGTCCGAG	
21833	Thra	ACAGCGGTAGTGATAACCGG	
21833	Thra	TGTCACTCTCAGGGTCGTAG	
21833	Thra	TCTAGATGATTCTGAAGCGGG	
21833	Thra	AAAACCTGCCCATGTTCTCCG	
21834	Thrb	GAAGACAGTCCGGCTCTCAG	
21834	Thrb	CCCATCGTGAATGCCCCAGA	
21834	Thrb	CATCTTTGTCTAAATAGCTG	
21834	Thrb	CAGGTTTCCAGGGTAACTAC	
22337	Vdr	TGGAGATTGCCGCATCACCA	
22337	Vdr	AGCGTTGAAGTGAAGCCCCG	
22337	Vdr	TTCTTCATTCAGATCCATCG	
22337	Vdr	TTCGTGCAGACGTAAGTACA	
17977	Ncoa1	TTGACTGAGGGATTTATTCG	
17977	Ncoa1	GATGCTAATTCACCCTCCAG	
17977	Ncoa1	ACCACTAGTAATGCCAACTG	
17977	Ncoa1	AGTTTGGACAACCAGGAGCG	
17978	Ncoa2	AGTGCATAGTTACTACCCTG	
17978	Ncoa2	GGGAGGATTCATATTAAGT	
17978	Ncoa2	AGTCAGATGTGTCGTCCACG	
17978	Ncoa2	CTTTGCAAAGTGATGTCAAG	
17979	Ncoa3	CAAGGAGAAACGATACACGG	
17979	Ncoa3	TCGTCCTCCATATAACCGAG	
17979	Ncoa3	AGAACATCATGATTTCCCCT	
17979	Ncoa3	ACGTGCTCCTCCGACGACCG	
27057	Ncoa4	CGTCGCTGATTGTTGCGCCG	
27057	Ncoa4	TTCAAGAAGTCAGCATCCAG	
27057	Ncoa4	GGTCTTAAGGGATCCAAATG	
27057	Ncoa4	AATTAAGATAATTTACGAG	
228869	Ncoa5	GGGTGGATGACTATTGCCGG	
228869	Ncoa5	GTAGAGAGGAGCTTTATCGT	
228869	Ncoa5	CTGCGGTCCCPCAAATCCCG	
228869	Ncoa5	TAACAGATACCTCACTGCCG	
56406	Ncoa6	TGAACCATAGGATTCCGACC	
56406	Ncoa6	GCTGTTATGACGCCCCAGGG	
56406	Ncoa6	CAATGACTACAAATCAAGGG	
56406	Ncoa6	TGTGCCCAACTTGTTACACA	
211329	Ncoa7	AGGCCTTAAAACCCATCGAG	
211329	Ncoa7	AGTTCAACGTTACAGCAGAG	
211329	Ncoa7	GGTACACTCTGGGTAAAAGG	
211329	Ncoa7	CTAAGGGATCGGACTTATGA	
170826	Ppargc1b	AGGGCTTGCTAACATCACAG	
170826	Ppargc1b	TGGACGAGCTTTCACTGGTG	
170826	Ppargc1b	GGCCTTGACTACTGTCTGTG	
170826	Ppargc1b	TCCTGTGCTAGGGAGTCTTG	

Target Gene ID	Target Gene Symbol	sgRNA Target Sequence	Notes
19017	Ppargc1a	GAATGAGGCAAACCTTGCTAG	
19017	Ppargc1a	TATTGAGCGAACCTTAAGTG	
19017	Ppargc1a	TTGCATGCGCACCTTAACAA	
19017	Ppargc1a	AAGACCAGTGAACCTAAGGGA	
19018	Scand1	AGCGCTGGCGAAAGGTCTCG	
19018	Scand1	TTCGCTACCAGGACGCGGCC	
19018	Scand1	GCTCCCGGAATCGGGCGACG	
19018	Scand1	CGCGCCCGCAGCTTTGAACA	
20185	Ncor1	GGCTTACGGAAACCCCGTG	
20185	Ncor1	GGCCTAGCAAACCTACCCCG	
20185	Ncor1	ATATGCCGAGCATTACCCAG	
20185	Ncor1	CCCTACCAAAGCCGACTCCG	
20602	Ncor2	GCCATCTCGACTGTCCAAGG	
20602	Ncor2	GCATAGAGAACAATCCGCGA	
20602	Ncor2	GCTACCACACCCTCGTGAGT	
20602	Ncor2	TACCGACTGAGCCCCACGC	
11622	Ahr	AGCTGTGCACAAGAGGATCG	
11622	Ahr	GTATAATAGACTGCTGCCTG	
11622	Ahr	TCTCCGGTAGCAAACATGAA	
11622	Ahr	GTGGAAAGAATCCTTACTTG	
18671	Abcb1a	ACTGAATGCTCCAATTAACA	
18671	Abcb1a	CAGGAAGCTTAGTACCAAAG	
18671	Abcb1a	CAAAGATCAGCATCATAAGT	
18671	Abcb1a	AATGACGTCAGCATTACGAA	
18669	Abcb1b	AGCCTTTGCAAACGCACGAG	
18669	Abcb1b	TGATGCTTCTAGTGTTAAAG	
18669	Abcb1b	TCATCTCTTGAAAAACCTG	
18669	Abcb1b	CAGATGACAATCCAATAAGA	
65256	Asb2	GGAGACAGACTCGTGCAATG	
65256	Asb2	CAGTGCATCAGCCCTCTACG	
65256	Asb2	CGAGCGCGCCCGCCTCTACG	
65256	Asb2	CCTCCAAGAAGGGCAACTAT	
58208	Bcl11b	GTTGTGCAAATGTAGCTGGA	
58208	Bcl11b	CTGAGAGCCCGTCTGTCTGAG	
58208	Bcl11b	GCGGGAAGTTCATCTGACAC	
58208	Bcl11b	CAGAGGTGAAGTAATCACGG	
22042	Tfr3	CTACACGCTTACAATAGCCC	
22042	Tfr3	GAATACATACACTCCTCGTG	
22042	Tfr3	GGGCTCCTACTACAACATAA	
22042	Tfr3	AACCCTCGGGAGACTCCACT	
13813	Eomes	GCCATACGCCGGAACCTCAG	
13813	Eomes	GCTGTCCATGGAGTAGCGCG	
13813	Eomes	CACCCAGAATCTCCTAACAC	
13813	Eomes	TTCCACGAAAACATTGTAGT	
20371	Foxp3	CATACCTGATGCATGAAGTG	
20371	Foxp3	TCTACCCACAGGGATCAATG	

Target Gene ID	Target Gene Symbol	sgRNA Target Sequence	Notes
20371	Foxp3	AGGTCGGGACCTGCGAAGTG	screen-specific control or presumed activity
20371	Foxp3	GCAAGAGCTCTGTCCATTG	
14462	Gata3	CTACTACGGAAACTCCGTCA	
14462	Gata3	CCGGGTTCGGATGTAAGTCG	
14462	Gata3	GCAGCTGCACCTGATACTTG	
14462	Gata3	TCCAAGACGTCCATCCACCA	
16153	Il10	GCTAACCGACTCCTTAATGC	
16153	Il10	AACTGCACCCACTTCCCAGT	
16153	Il10	AAGGAGCATTTGAATCCCT	
16153	Il10	ACTGGCATGAGGATCAGCAG	
16171	Il17a	CTCAGCGTGTCCAAACTG	
16171	Il17a	GAACGGTTGAGGTAGTCTGA	
16171	Il17a	CTTACGTAAGGAGAGTCCA	
16171	Il17a	CTGAGCTTCCCAGATCACAG	
212391	Lcor	ACAGCACTTAATCTTATCCA	
212391	Lcor	ATCTGCAGAGATCGAGCCAG	
212391	Lcor	GATACCACAAGTTCGAGGAA	
212391	Lcor	TCCATCCAATTAGGCGACCT	
17132	Maf	GTGGCTTCGATGGCTATGCG	
17132	Maf	GACCGCATCATCAGCCAGTG	
17132	Maf	GGTGTCCGCCGTGATCGCCG	
17132	Maf	ACCACCACCACCACGCCGCG	
19014	Med1	CCAACCAACACCTTCCGGG	
19014	Med1	AGGTGTATCCAGCGGTCAG	
19014	Med1	TAACTTACCCCCACTCCGCG	
19014	Med1	GTGAGCTGTAAACTCTACAA	
not found in Brie	Nrip1		
	Nrip1		
	Nrip1		
	Nrip1		
12142	Prdm1	TTGGAACTAATGCCGTACGG	
12142	Prdm1	GGATAGGATAAACCACCCGA	
12142	Prdm1	GTGTAGACTTCACCGATGAG	
12142	Prdm1	TTGTACCACGTGTTCTGACG	
17128	Smad4	TGAATCCATATCACTATGAG	
17128	Smad4	GGTGGCGTTAGACTCTGCCG	
17128	Smad4	TGTCACCATACAGAGAACAT	
17128	Smad4	CAAAAGCGATCTCTCCCGA	
20846	Stat1	GGATAGACGCCAGCCACTG	
20846	Stat1	TGTGATGTTAGATAAACAGA	
20846	Stat1	TTAATGACGAGCTCGTGAG	
20846	Stat1	GAAAAGCAAGCGTAATCTCC	
not found in Brie	Stat2		
	Stat2		
	Stat2		
	Stat2		

Target Gene ID	Target Gene Symbol	sgRNA Target Sequence	Notes	
20848	Stat3	CCAACAAATTAAGAAACTGG		
20848	Stat3	CTGCTTCTCTGCTACTACGG		
20848	Stat3	GTTTACCACGAAAGTCAGGT		
20848	Stat3	CAAAGAGTCACATGCCACGT		
20849	Stat4	AATGTCTAAACTCCACTGAG		
20849	Stat4	GCATGCCAACGCACCCTCAG		
20849	Stat4	AAATCCAATGCATGTAGCTG		
20849	Stat4	TGGCCTCACCATTAACCTAG		
20850	Stat5a	CATGGACGATAACGACCACA		
20850	Stat5a	GTTTCGTTGTACAGAATGTGA		
20850	Stat5a	AGTGGATCGAGAGCCAGCCG		
20850	Stat5a	GTGGGCGCTGAGCGTGCCAG		
20851	Stat5b	CTGATTCGCAGTGATTACAG		
20851	Stat5b	TACAGCGAACCAGTCCATG		
20851	Stat5b	GGCGTTGTCCCAGAGGACAG		
20851	Stat5b	AGTGGATCGAAAGCCAAGCC		
20852	Stat6	ATAAAGCGCTGTGAGCGGAA		
20852	Stat6	GCTGAAAGGCCTCCACACTG		
20852	Stat6	AGAAAGCATCTGAACCGACC		
20852	Stat6	CATCAGACAAATACTTCAAG		
57765	Tbx21	AGTCTGGGTGGACATATAAG		
57765	Tbx21	AGGACTACGCATTGCCCGCG		
57765	Tbx21	GACCCGACCGATCGCCGCGC		
57765	Tbx21	GGCTTCCAACAATGTGACCC		
12525	Cd8a	TGGGTGAGTCGATTATCCTG		negative controls
12525	Cd8a	ATCCCACAACAAGATAACGT		
12525	Cd8a	GTGTTGGGGTCCGTTTCGCA		
12525	Cd8a	GGACGCCGA ACTTGGTCAGA		
12478	Cd19	GAATGACTGACCCCGCCAGG		
12478	Cd19	AATGTCTCAGACCATATGGG		
12478	Cd19	GGCACCTATTATTGTCTCCG		
12478	Cd19	TTTAGCCACACATACAGCT		
not found in Brie	dsRed			
	dsRed			
	dsRed			
	dsRed			
	EGFP			
	EGFP			
	EGFP			
	EGFP			
	Fluc			
	Fluc			
	Fluc			
	mCherry			
mCherry				

Target Gene ID	Target Gene Symbol	sgRNA Target Sequence	Notes
	mCherry		

Target Gene ID	Target Gene Symbol	sgRNA Target Sequence	Notes
	mCherry		negative controls
17879	Myh1	GCTGCCAGTGTATAACGCAG	
17879	Myh1	TGACCTCGCTAGTAACATGG	
17879	Myh1	AGTTGGCCCAGCTTATAACC	
17879	Myh1	TAAAACATGACTTACATCTG	
19373	Rag1	ACACCAAAGCAGAGTCGTAG	
19373	Rag1	TGAAACGATTCCCACAGATG	
19373	Rag1	TCCC GC CAAGATTGCAATG	
19373	Rag1	TGGGAAGTAGACCTGACTGT	
19374	Rag2	CATCAATATATCATTACGG	
19374	Rag2	ATTGACGTGGTGTATAGTCG	
19374	Rag2	TAAC TTGTATAGAATAAGAG	
19374	Rag2	CATACCAGGAGACAATAAGC	
11657	Alb	ACAAGAGTGAGATCGCCCAT	
11657	Alb	TACTCACTGTCCATAAAGG	
11657	Alb	TCCCGCATGCTACGGCACAG	
11657	Alb	GCTCCACCTCACTAAGACAG	
12504	Cd4	TCAAAACGATCAA ACTGCGA	positive control
12504	Cd4	TATCACGGCCTATAAGAGTG	
12504	Cd4	ACTCACCTCAAGATACCCC	
12504	Cd4	TTCTTCTGGGAACTCTCGCA	
21838	Thy1	CCTTGGTGTTATTCTCATGG	positive control
21838	Thy1	TAAGGACCTTGATATAGGGC	
21838	Thy1	CAGTCTTG CAGGTG TCCCGA	
21838	Thy1	CGTGTGCTCGGGTATCCCAA	
BRDN0000737505	NTC	AAAAAGTCCGCGATTACGTC	negative controls
BRDN0000737693	NTC	AAAACGGCTCGATCGGTGAT	
BRDN0000737637	NTC	AAAACGTAATTATACCGAGC	
BRDN0000738185	NTC	AAAATTGCACCTTCCCGGCC	
BRDN0000737801	NTC	AAACCCCCGCGGGAGCGTC	
BRDN0000737467	NTC	AAACCTAGCGTAGATTCGGC	
BRDN0000737848	NTC	AAACGAGGCTGTTCGTACAC	
BRDN0000737609	NTC	AAACTCATACGTAGCGAATC	

Original Doc Name: Nuclear Receptors Library (Sundr

*Oligo name	guide sequence
example 1	
Ar	GGTGGAAAGTAATAGTCGAT
Ar	ACCAGGATACCACACTTCGG
Ar	GACTTGGGTAGTCTACATGG
Ar	GCTCCTGGGAGGTCCACCCG
Esr1	GGCATA CGGAAAGACCGCCG
Esr1	CACTGTGTTCAACTACCCCG
Esr1	TATTCAGAATAGATCATGGG
Esr1	AGAGGCATAGTCATTGCACA
Esr2	TGGCGCTTGGACTAGTAACA
Esr2	TTCGTGACGGCTCTCTACAT
Esr2	GAAGTAGGAATGGTCAAGTG
Esr2	CGGCTCACTAGCACATTGGG
Esrra	CTACGGTGTGGCATCCTGTG
Esrra	CAGCGGGGAGGTGTCCATCG
Esrra	TGTA CT TCTGCCGTC CGCCG
Esrra	CGACACCAGAGCGTTC ACTG
Esrrg	TGGCGTCGGAAGACCCACCA
Esrrg	GGTCTGGGGATCCTCTACGA
Esrrg	CCAAGTCACAGAGTGTGGTG
Esrrg	TGTGTGGCGACATCGCCTCT
Hnf4a	GCAATGACTACATCGTCCCT
Hnf4a	AATGTGCAGGTGTTGACCAT
Hnf4a	AGCGGGACCGGATCAGCACG
Hnf4a	GGCTCCGTAGTGTTCGCGG
Hnf4g	TACAAGAAGAAGTACCTACG
Hnf4g	TGTTGCGGTGAATAACATAG
Hnf4g	TCCAGCATGGGCTCTCAAGA
Hnf4g	GCATGTTCTTAATCTTCACA
Nr0b1	GCCAACTCAAGCATGAGTAG
Nr0b1	CAGGGTCTTCAACAGGCCAG
Nr0b1	CGTTGGTGAGCATAGAGTAG
Nr0b1	CTTACC GCACACATAGCTG
Nr0b2	ACTTAAGAAGATCCTGCTAG
Nr0b2	GGATGCTGTGACCTTCGAGG
Nr0b2	TGCCCCATGAGGATCAGCGG
Nr0b2	AGAAGTGCATACAGAATAGT
Nr1d1	GTTGCGATTGATGCGAACGA
Nr1d1	GAGTAGGTGAGGTCTCTAGA
Nr1d1	CACAACAGCTGACACCACCC
Nr1d1	TTCTGGGGCCGAATATACGT
Nr1h2	TTCCTTAATAGTGGGTGACG
Nr1h2	CACCGAGCTAGCCATCATCT
Nr1h2	CGGCGCAGTGTGGTCCACGG

*Oligo name	guide sequence
Nr1h2	CTCCGACCAGCCCAAAGTCA
Nr1h3	AAAGCAACCCCAGTTGACTG
Nr1h3	CAAGTACCGTGACGCGCAGG
Nr1h3	AATCTCCTGCACGGACACGA
Nr1h3	TTCCGCCGACAGTGCATCAA
Nr1h4	AAACGGGACATTGTTGTATG
Nr1h4	TGATGGACATGTACATGCGC
Nr1h4	TGTGACAAAGAAGCCGCGAA
Nr1h4	AGTGTAATCTAAACGGCTA
Nr1i2	GTTCAACACGATGTTGACA
Nr1i2	TGTAGTTGACACATCGGCC
Nr1i2	TGGCCTTGTCACACATAACA
Nr1i2	TGATCTCGCAGTTCCCTTG
Nr1i3	TGCATGAACAGATAGGCCGG
Nr1i3	GGCGAGCCAGACAGGCACAG
Nr1i3	AAACGGACAGATGGGACCAA
Nr1i3	ACACAGGTCCCTAACCATGG
Nr2c1	GGTGCAGAGCTTACGCAATG
Nr2c1	ACAGTCTTGCTTCATCCCGA
Nr2c1	GTTCAATTCTGGCAAACCACG
Nr2c1	ACGTGCGACTCGCTCAGCAG
Nr2c2	GATCCAGATAGTCACCGCAG
Nr2c2	AGGGACAAGGTTGTCCGAGG
Nr2c2	GTACCATCCTCACGTATCAA
Nr2c2	TGGAGGTGAAGCACTATCTG
Nr2e1	CACTTCGTAGAGATACATTG
Nr2e1	AGGACCCCGCTCGTGCTGCA
Nr2e1	AGTGTTAGCATCAACCGGAA
Nr2e1	TTCTGTGTGTCTTGTCTACG
Nr2e3	TGACCCCGATCAGAACCAG
Nr2e3	CAGTTTAGCACAAGTTTCGG
Nr2e3	GCCTCCAAGAAGGAGTCTCC
Nr2e3	TCCTTCTGGAGCCATACAG
Nr2f1	CCAGTATGCACTCACAAACG
Nr2f1	GGCTGCCATAACGCGACGTG
Nr2f1	CGAGCTGTTCTGTGCTCAACG
Nr2f1	GATGTTGCGGGCCCACTCGA
Nr2f2	GCAGTTTGCCCTGACCAACG
Nr2f2	CTACGGCCAGTTCACGTGCG
Nr2f2	GGCGCTGAAGAGCATCCGTG
Nr2f2	CTCAAAAAGTGCCTCAAAGT
Nr2f6	GAGTACCCACGCGCGACCG
Nr2f6	GCATGCGCTCCCCGGTCCAG
Nr2f6	CGGGCGACGAGGAGCGTCCG
Nr2f6	CATCGACAACGTGTGCGAGT
Nr3c1	CATTATGGGGTGCTGACGTG

*Oligo name	guide sequence
Nr3c1	AGCTTGCCTGGCAATAAACC
Nr3c1	AAAGCCGTTTCACTGTCCAT
Nr3c1	AAAAGTGAATAGGTGCCAA
Nr3c2	GATGATTGGGCTCTTAACGA
Nr3c2	CAAGGAACTTTCAGCCACGG
Nr3c2	TCCACTAATGCATTGACAGG
Nr3c2	GAATGGAAATGGGTTGACTG
Nr4a1	GGAAGTGTCACGGTTCGGAG
Nr4a1	TGCTTCGTGTCAGCACTATG
Nr4a1	GGCAAACAAGGATTGCCCTG
Nr4a1	GCCTTCATAAGTCTGGCTCG
Nr4a2	TGTCAAGCAACTGCGATGCG
Nr4a2	TGCCGGATTGGAATCGACGT
Nr4a2	AGTACTGACAACGATTTCCGG
Nr4a2	TAGTAAACCGACCCGCTGTG
Nr4a3	GCATTCATCATAACAGATCGG
Nr4a3	ACCAAGCTGACCATGGACCT
Nr4a3	CGGCCGTGGGGTCATAGCCG
Nr4a3	AGTGTCGGGATGGTTAAGGA
Nr5a1	TGGAGACCGGACCACCGATG
Nr5a1	GTGCGTGCTGATCGAATGCG
Nr5a1	CGCACGTGAGCAGCCCGTAG
Nr5a1	CCATTGTCGACTGGGCACGA
Nr5a2	TGTGTGGCGATAAAGTGTCT
Nr5a2	GTAAGAGCCGACCGCATGCG
Nr5a2	TCGCCACTCCCCAAACGTG
Nr5a2	CTTCTGTCATAGTCTGTCCGG
Nr6a1	CCTTACCACCGTTGCGCGG
Nr6a1	CATAGTGCAAGCCCGTAGCG
Nr6a1	CCAGAATAGCTAAAAAGGTG
Nr6a1	CACCTATGTTGATTGAAGAT
Pgr	CTCTGGCCGACTCATGAGCG
Pgr	AGGAGGAGTCGCAGCCAACG
Pgr	GGCGGAACGAACCCTGCGT
Pgr	CAGTCTGGGAAGTCACCGCA
Ppara	CATCGAGTGTCGAATATGTG
Ppara	GATTTCTCAGTCCATCGGTG
Ppara	TCTGTCGGGATGTCACACAA
Ppara	CTGCTGCCAGTGCATGTCCG
Ppard	CCTCCGGCATCCGTCCAAAG
Ppard	GGCCTCGGGCTTCCACTACG
Ppard	TCGAGTATGAGAAGTGCATG
Ppard	CCTCAAGTATGGCGTGCACG
Pparg	AATGCTGGAGAAATCAACTG
Pparg	AGAACCTTCTAACTCCCTCA
Pparg	GCACCCTGAAAAATTCGGA

*Oligo name	guide sequence
Pparg	CTGCCTATGAGCACTTCACA
Rara	GAGCTACAGCTGACGCCTG
Rara	ATCATCCGGCTACCACTATG
Rara	AGATTCTGCGAATCTGCACG
Rara	CAAGTGCATCATTAAAGACTG
Rarb	AAGCAGGGCTTGTACACCCG
Rarb	CCAAGTCCAATCGGACCCGG
Rarb	ACCGGCATACTGCTCAATGT
Rarb	TGACGCAGTTCTTATCTCGA
Rarg	TGGGCAAGTACACCACGGTG
Rarg	AAGCATGGCTTATAGACCCG
Rarg	GCTACAAAAGTGTTCGAAG
Rarg	ACACTATGACATTCTCGGAT
Rora	TTGGCTGAGATGTTGTAGGT
Rora	CATTGATGTCCAATCCCGAC
Rora	GAGAGACAGCTTGTACGCCG
Rora	AGCTATGCGAGCTCCAGCCG
Rorb	CACCACGTAAGGATAGCAT
Rorb	GGAGACATGTCAGTACACCA
Rorb	TCCCAGCTGTAAAGTTCGGG
Rorb	ACAAGTTGGGTACAGATGTG
Rorc	CTTGAGTATAGTCCAGAACG
Rorc	GTCATCTGGGATCCACTACG
Rorc	TCTGGGGCACTGCAGAACT
Rorc	GACAAGCAGAGGCCTCGGGT
Rxra	CAAGACTGAGACATACGTGG
Rxra	AGGACGCCATTGAGGCCTAG
Rxra	CATGGGCCCCTCCATGT
Rxra	GGGGCAGCTCAGAAAAGTGT
Rxrb	ATTGTGGGGTCGCGTCCCGG
Rxrb	GCTGTTCACTCGTTGAGT
Rxrb	GTTCAGGAGGAGCGTCAACG
Rxrb	TCCACAGTGTGCTCCCTGG
Rxrg	TAGCCACGAAGACATGCCCG
Rxrg	TGCGTTTGGCCCACTCAACG
Rxrg	TCGTAACCAGGGAAGCACTA
Rxrg	CACAGCACTCAGCGTCCGAG
Thra	ACAGCGGTAGTGATAACCGG
Thra	TGTCACTCTCAGGGTCGTAG
Thra	TCTAGATGATTCTGAAGCGGG
Thra	AAAAGTCCCATGTTCTCCG
Thrb	GAAGACAGTCCGGCTCTCAG
Thrb	CCCATCGTGAATGCCCCAGA
Thrb	CATCTTTGTCTAAATAGCTG
Thrb	CAGGTTTCCAGGGTAACTAC
Vdr	TGGAGATTGCCGCATCACCA

*Oligo name	guide sequence
Vdr	AGCGTTGAAGTGGAAGCCCG
Vdr	TTCTTCATTCAGATCCATCG
Vdr	TTCGTGCAGACGTAAGTACA
Ncoa1	TTGACTGAGGGATTTATTCG
Ncoa1	GATGCTAATTCACCCTCCAG
Ncoa1	ACCACTAGTAATGCCAACTG
Ncoa1	AGTTTGGACAACCAGGAGCG
Ncoa2	AGTGCATAGTTACTACCCTG
Ncoa2	GGGAGGATTCATATTAAGT
Ncoa2	AGTCAGATGTGTCTCCACG
Ncoa2	CTTTGCAAAGTGATGTCAAG
Ncoa3	CAAGGAGAAACGATACACGG
Ncoa3	TCGTCCTCCATATAACCGAG
Ncoa3	AGAACATCATGATTTCCCT
Ncoa3	ACGTGCTCCTCCGACGACCG
Ncoa4	CGTCGCTGATTGTTGCGCCG
Ncoa4	TTCAAGAAGTCAGCATCCAG
Ncoa4	GGTCTTAAGGGATCCAAATG
Ncoa4	AATTAAGATAATTTACGAG
Ncoa5	GGGTGGATGACTATTGCCGG
Ncoa5	GTAGAGAGGAGCTTTATCGT
Ncoa5	CTGCGGTCCCGCAAATCCCG
Ncoa5	TAACAGATACCTCACTGCCG
Ncoa6	TGAACCATAGGATTCCGACC
Ncoa6	GCTGTTATGACGCCCCAGGG
Ncoa6	CAATGACTACAAATCAAGGG
Ncoa6	TGTGCCCAACTTGTTACACA
Ncoa7	AGGCCTTAAAACCCATCGAG
Ncoa7	AGTTCAACGTTACAGCAGAG
Ncoa7	GGTACTCTGGGTAAAAGG
Ncoa7	CTAAGGGATCGGACTTATGA
Ppargc1b	AGGGCTTGCTAACATCACAG
Ppargc1b	TGGACGAGCTTTCCTGCTG
Ppargc1b	GGCCTTGACTACTGTCTGTG
Ppargc1b	TCCTGTGCTAGGGAGTCTG
Ppargc1a	GAATGAGGCAAACCTTGCTAG
Ppargc1a	TATTGAGCGAACCTTAAGTG
Ppargc1a	TTGCATGCGCACCTTAACAA
Ppargc1a	AAGACCAGTGAACCTAAGGGA
Scand1	AGCGCTGGCGAAAGGTCTCG
Scand1	TTGCTACCAGGACGCGGCC
Scand1	GCTCCCGAATCGGGCGACG
Scand1	CGCGCCCGCAGCTTTGAACA
Ncor1	GGCTTCACGGAAACCCCGTG
Ncor1	GGGCCTAGCAAACCTACCCCG
Ncor1	ATATGCCGAGCATTACCCAG

*Oligo name	guide sequence
Ncor1	CCCTACCAAAGCCGACTCCG
Ncor2	GCCATCTCGACTGTCCAAGG
Ncor2	GCATAGAGAACAATCCGCGA
Ncor2	GCTACCACACCCTCGTGAGT
Ncor2	TACCGACTGAGCCCCACGC
Ahr	AGCTGTGCACAAGAGGATCG
Ahr	GTATAATAGACTGCTGCCTG
Ahr	TCTCCGGTAGCAAACATGAA
Ahr	GTGGAAAGAATCCTTACTTG
Abcb1a	ACTGAATGCTCCAATTAACA
Abcb1a	CAGGAAGCTTAGTACCAAAG
Abcb1a	CAAAGATCAGCATCATAAGT
Abcb1a	AATGACGTCAGCATTACGAA
Abcb1b	AGCCTTTGCAAACGCACGAG
Abcb1b	TGATGCTTCTAGTGTTAAAG
Abcb1b	TCATCTCTTGAAAAACCTG
Abcb1b	CAGATGACAATCCAATAAGA
Asb2	GGAGACAGACTCGTGCAGTG
Asb2	CAGTGCATCAGCCCTCTACG
Asb2	CGAGCGCGCCCGCCTCTACG
Asb2	CCTCCAAGAAGGGCAACTAT
Bcl11b	GTTGTGCAAATGTAGCTGGA
Bcl11b	CTGAGAGCCCGTCGTCTGAG
Bcl11b	GCGGGAAGTTCATCTGACAC
Bcl11b	CAGAGGTGAAGTAATCACGG
Tfr3	CTACACGCTTACAATAGCCC
Tfr3	GAATACATACACTCCTCGTG
Tfr3	GGGCTCCTACTACAACATAA
Tfr3	AACCCTCGGGAGACTCCACT
Eomes	GCCATACGCCGGAACCTCAG
Eomes	GCTGTCCATGGAGTAGCGCG
Eomes	CACCCAGAATCTCCTAACAC
Eomes	TTCCACGAAAACATTGTAGT
Foxp3	CATACCTGATGCATGAAGTG
Foxp3	TCTACCCACAGGGATCAATG
Foxp3	AGGTCGGGACCTGCGAAGTG
Foxp3	GCAAGAGCTCTTGCCATTG
Gata3	CTACTACGGAAACTCCGTC
Gata3	CCGGGTTCCGATGTAAGTCG
Gata3	GCAGCTGCACCTGATACTTG
Gata3	TCCAAGACGTCCATCCACCA
Il10	GCTAACCGACTCCTTAATGC
Il10	AACTGCACCCACTTCCCAGT
Il10	AAGGAGCATTGAATTCCCT
Il10	ACTGGCATGAGGATCAGCAG
Il17a	CTCAGCGTGCCAACACTG

*Oligo name	guide sequence
Il17a	GAACGGTTGAGGTAGTCTGA
Il17a	CTTACGTA CTGGAGAGTCCA
Il17a	CTGAGCTTCCCAGATCACAG
Lcor	ACAGCACTTAATCTTATCCA
Lcor	ATCTGCAGAGATCGAGCCAG
Lcor	GATACCACAAGTTCGAGGAA
Lcor	TCCATCCAATTAGGCGACCT
Maf	GTGGCTTCGATGGCTATGCG
Maf	GACCGCATCATCAGCCAGTG
Maf	GGTGTCCGCCGTGATCGCCG
Maf	ACCACCACCACCACGCCGCG
Med1	CCAACCAACACCTTTCCGGG
Med1	AGGTGTATCCAGCGCGTCAG
Med1	TAACTTACCCCCACTCCGCG
Med1	GTGAGCTGTAAACTCTACAA
Prdm1	TTGGA ACTAATGCCGTACGG
Prdm1	GGATAGGATAAACCACCCGA
Prdm1	GTGTAGACTTCACCGATGAG
Prdm1	TTGTACCACGTGTTCTGACG
Smad4	TGAATCCATATCACTATGAG
Smad4	GGTGGCGTTAGACTCTGCCG
Smad4	TGTCACCATACAGAGAACAT
Smad4	CAAAAGCGATCTCCTCCCGA
Stat1	GGATAGACGCCAGCCACTG
Stat1	TGTGATGTTAGATAAACAGA
Stat1	TTAATGACGAGCTCGTGGAG
Stat1	GAAAAGCAAGCGTAATCTCC
Stat3	CCAACAAATTAAGAACTGG
Stat3	CTGCTTCTCTGTCACTACGG
Stat3	GTTTACCACGAAAGTCAGGT
Stat3	CAAAGAGTCACATGCCACGT
Stat4	AATGTCTAAACTCCACTGAG
Stat4	GCATGCCAACGCACCCTCAG
Stat4	AAATCCAATGCATGTAGCTG
Stat4	TGGCCTCACCATTAACCTAG
Stat5a	CATGGACGATAACGACCACA
Stat5a	GTTTCGTTGTACAGAATGTGA
Stat5a	AGTGGATCGAGAGCCAGCCG
Stat5a	GTGGGCGCTGAGCGTGCCAG
Stat5b	CTGATTCGCAGTGATTACAG
Stat5b	TACAGCGAACCACTCCATG
Stat5b	GGCGTTGTCCCAGAGGACAG
Stat5b	AGTGGATCGAAAGCCAAGCC
Stat6	ATAAAGCGCTGTGAGCGGAA
Stat6	GCTGAAAGGCCTCCCACTG
Stat6	AGAAAGCATCTGAACCGACC

*Oligo name	guide sequence
Stat6	CATCAGACAAATACTTCAAG
Tbx21	AGTCTGGGTGGACATATAAG
Tbx21	AGGACTACGCATTGCCCGCG
Tbx21	GACCCGACCGATCGCCGCGC
Tbx21	GGCTTCCAACAATGTGACCC
Cd8a	TGGGTGAGTCGATTATCCTG
Cd8a	ATCCCACAACAAGATAACGT
Cd8a	GTGTTGGGGTCCGTTTCGCA
Cd8a	GGACGCCGAACTGGTCAGA
Cd19	GAATGACTGACCCCGCCAGG
Cd19	AATGTCTCAGACCATATGGG
Cd19	GGCACCTATTATTGTCTCCG
Cd19	TTTAGCCACACATACAGCT
Myh1	GCTGCCAGTGTATAACGCAG
Myh1	TGACCTCGCTAGTAACATGG
Myh1	AGTTGGCCCAGCTTATAACC
Myh1	TAAAACATGACTTACATCTG
Rag1	ACACCAAAGCAGAGTCGTAG
Rag1	TGAAACGATTCCCACAGATG
Rag1	TCCCGCGCAAGATTGCAATG
Rag1	TGGGAAGTAGACCTGACTGT
Rag2	CATCAATATATCATTACGG
Rag2	ATTGACGTGGTGTATAGTCG
Rag2	TAACCTGTATAGAATAAGAG
Rag2	CATACCAGGAGACAATAAGC
Alb	ACAAGAGTGAGATCGCCCAT
Alb	TACTCACTGTCCATAAAGG
Alb	TCCCGCATGCTACGGCACAG
Alb	GCTCCACCTCACTAAGACAG
Cd4	TCAAAACGATCAAACCTGCGA
Cd4	TATCACGGCCTATAAGAGTG
Cd4	ACTCACCTCAAGATACCCC
Cd4	TTCTTCTGGGAACCTCTCGCA
Thy1	CCTTGGTGTTATTCTCATGG
Thy1	TAAGGACCTTGATATAGGGC
Thy1	CAGTCTTGAGGTGTCCCGA
Thy1	CGTGTGCTCGGGTATCCCAA
NTC	AAAAAGTCCGCGATTACGTC
NTC	AAAACGGCTCGATCGGTGAT
NTC	AAAACGTAATTATACCGAGC
NTC	AAAATTGCACCTTCCCGGCC
NTC	AAACCCCGCGCGGAGCGTC
NTC	AAACCTAGCGTAGATTCCGGC
NTC	AAACGAGGCTGTTTCGTACAC
NTC	AAACTCATACGTAGCGAATC

Original Doc Name: Nuclear Receptors Library (Sundrud)

No.	*Oligo name	*Oligo name	*Sequence (5' to 3')	nt#	Remarks	5'	guide sequence	3'
Example row, don't delete	example 1	example 1	AATATTTAAGGTCTGCTTAACTGATCCCATGCTGTAATTTACCTCTGACTCCA	59		GGAAAGGACGAAACACCGG		GTTTGTAGAGCTAGAAATAGCAAGTTAAATAAGGC
1	Ar	Ar_1	GGAAAGGACGAAACACCGGGTGGAAAGTAATAGTCGATGTTTTAGAGCTAGAAATAGCAAGTTAAATAA	73			GGTGAAAGTAATAGTCGAT	
2	Ar	Ar_2	GGAAAGGACGAAACACCGACCAGGATACCACACTCCGGTTTTAGAGCTAGAAATAGCAAGTTAAATAA	73			ACCAGGATACCACACTCCGG	
3	Ar	Ar_3	GGAAAGGACGAAACACCGGACTTGGGTAGTCTACATGGGTTTTAGAGCTAGAAATAGCAAGTTAAATAA	73			GACTTGGGTAGTCTACATGG	
4	Ar	Ar_4	GGAAAGGACGAAACACCGGCTCTGGGAGTCCACCCGGTTTTAGAGCTAGAAATAGCAAGTTAAATAA	73			GCTCTGGGAGTCCACCCGG	
5	Esr1	Esr1_1	GGAAAGGACGAAACACCGGCATACGGAAGACCGCCGTTTTAGAGCTAGAAATAGCAAGTTAAATAA	73			GGCATAAGGAAAGACCGCCG	
6	Esr1	Esr1_2	GGAAAGGACGAAACACCGCACTGTCTCACTACCCCGTTTTAGAGCTAGAAATAGCAAGTTAAATAA	73			CACTGTGTCTCACTACCCCG	
7	Esr1	Esr1_3	GGAAAGGACGAAACACCGTATTGAGATATGATGCGGTTTTAGAGCTAGAAATAGCAAGTTAAATAA	73			TATTGAGATATGATGCGG	
8	Esr1	Esr1_4	GGAAAGGACGAAACACCGAGAGGCATAGTCATTGCACAGTTTTAGAGCTAGAAATAGCAAGTTAAATAA	73			AGAGGCATAGTCATTGCACA	
9	Esr2	Esr2_1	GGAAAGGACGAAACACCGTGGCGCTTGACTAGTAAACAGTTTTAGAGCTAGAAATAGCAAGTTAAATAA	73			TGGCGCTTGACTAGTAAACA	
10	Esr2	Esr2_2	GGAAAGGACGAAACACCGTTCGTCAGCGCTCTACATGTTTTAGAGCTAGAAATAGCAAGTTAAATAA	73			TTCGTGACGGCTCTACATG	
11	Esr2	Esr2_3	GGAAAGGACGAAACACCGGAAGTAGAATGTCAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAATAA	73			GAAAGTAGAATGTCAGTGG	
12	Esr2	Esr2_4	GGAAAGGACGAAACACCGCGCTCACTAGCACATTTGGGTTTTAGAGCTAGAAATAGCAAGTTAAATAA	73			CGGCTCACTAGCACATTTGGG	
13	Esrra	Esrra_1	GGAAAGGACGAAACACCGCTACGGTGTGGCATCTGTGTTTTAGAGCTAGAAATAGCAAGTTAAATAA	73			CTACGGTGTGGCATCTGTG	
14	Esrra	Esrra_2	GGAAAGGACGAAACACCGCAGCGGGAGGTGCCATCGTTTTAGAGCTAGAAATAGCAAGTTAAATAA	73			CAGCGGGAGGTGCCCATCG	
15	Esrra	Esrra_3	GGAAAGGACGAAACACCGTGTACTTCTGCGCTCGCGTTTTAGAGCTAGAAATAGCAAGTTAAATAA	73			TGTACTTCTGCGCTCGCGCG	
16	Esrra	Esrra_4	GGAAAGGACGAAACACCGCGACACAGAGCTTCACTGTTTTAGAGCTAGAAATAGCAAGTTAAATAA	73			CGACACAGAGCTTCACTG	
17	Esrrg	Esrrg_1	GGAAAGGACGAAACACCGTGGCGTGGAGAGCCACAGTTTTAGAGCTAGAAATAGCAAGTTAAATAA	73			TGGCGTGGAGAGCCACCA	
18	Esrrg	Esrrg_2	GGAAAGGACGAAACACCGGCTGCGGATCCTACGAGTTTTAGAGCTAGAAATAGCAAGTTAAATAA	73			GGTCTGGGATCCTACGAG	
19	Esrrg	Esrrg_3	GGAAAGGACGAAACACCGCAAGTACAGAGTGGTGGTTTTAGAGCTAGAAATAGCAAGTTAAATAA	73			CCAAGTACAGAGTGGTGGT	
20	Esrrg	Esrrg_4	GGAAAGGACGAAACACCGTGTGGCGCATCGCTCTGTTTTAGAGCTAGAAATAGCAAGTTAAATAA	73			TGTGTGGCATCGCTCT	
21	Hnf4a	Hnf4a_1	GGAAAGGACGAAACACCGCAATGACTACATCGTCCCTGTTTTAGAGCTAGAAATAGCAAGTTAAATAA	73			GCAATGACTACATCGTCCCT	
22	Hnf4a	Hnf4a_2	GGAAAGGACGAAACACCGAATGTGCAGGTGTGACCATTTTTAGAGCTAGAAATAGCAAGTTAAATAA	73			AATGTGCAGGTGTGACCAT	
23	Hnf4a	Hnf4a_3	GGAAAGGACGAAACACCGAGCGGGACCGTATCGAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAATAA	73			AGCGGACCGGATCGACAG	
24	Hnf4a	Hnf4a_4	GGAAAGGACGAAACACCGGCTCGTGTGTTGCGGTTTTAGAGCTAGAAATAGCAAGTTAAATAA	73			GGTCCGTGTGTTGCGGG	
25	Hnf4g	Hnf4g_1	GGAAAGGACGAAACACCGTACAAGAAGAAGTCACTACGTTTTAGAGCTAGAAATAGCAAGTTAAATAA	73			TACAAGAAGAAGTCACTACG	
26	Hnf4g	Hnf4g_2	GGAAAGGACGAAACACCGTGTGGGTGAATAACATAGTTTTAGAGCTAGAAATAGCAAGTTAAATAA	73			TGTTGGTGAATAACATAG	
27	Hnf4g	Hnf4g_3	GGAAAGGACGAAACACCGTCCAGCATGGGCTCTCAAGTTTTAGAGCTAGAAATAGCAAGTTAAATAA	73			TCCAGCATGGGCTCTCAAGA	
28	Hnf4g	Hnf4g_4	GGAAAGGACGAAACACCGGCATGTTCTTAATCTCACAGTTTTAGAGCTAGAAATAGCAAGTTAAATAA	73			GCATGTTCTTAATCTCAC	
29	Nr0b1	Nr0b1_1	GGAAAGGACGAAACACCGCCAATCAAGCATGAGTAGTTTTAGAGCTAGAAATAGCAAGTTAAATAA	73			GCCAATCAAGCATGAGTAG	
30	Nr0b1	Nr0b1_2	GGAAAGGACGAAACACCGCAGGTTCTCAACAGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAATAA	73			CAGGTTCTCAACAGGCCAG	
31	Nr0b1	Nr0b1_3	GGAAAGGACGAAACACCGCTTGGTGGCATAGTAGTTTTAGAGCTAGAAATAGCAAGTTAAATAA	73			CGTTGGTGGCATAGTAGTAG	
32	Nr0b1	Nr0b1_4	GGAAAGGACGAAACACCGCTTCAACCGCACATAGTGTGTTTTAGAGCTAGAAATAGCAAGTTAAATAA	73			CTTCAACCGCACATAGTGTG	
33	Nr0b2	Nr0b2_1	GGAAAGGACGAAACACCGACTTAAAGAAATCCTGCTAGTTTTAGAGCTAGAAATAGCAAGTTAAATAA	73			ACTTAAAGAAATCCTGCTAG	
34	Nr0b2	Nr0b2_2	GGAAAGGACGAAACACCGGGATGCTGTGACCTTCGAGGTTTTAGAGCTAGAAATAGCAAGTTAAATAA	73			GGATGCTGTGACCTTCGAGG	
35	Nr0b2	Nr0b2_3	GGAAAGGACGAAACACCGTGGCCATGAGGATCAGCGGTTTTAGAGCTAGAAATAGCAAGTTAAATAA	73			TGCCCATGAGGATCAGCGG	
36	Nr0b2	Nr0b2_4	GGAAAGGACGAAACACCGAGAAGTGATACAGAAATAGTTTTAGAGCTAGAAATAGCAAGTTAAATAA	73			AGAAGTGATACAGAAATAGT	
37	Nr1d1	Nr1d1_1	GGAAAGGACGAAACACCGGTTGCGATTGATGCGAACGAGTTTTAGAGCTAGAAATAGCAAGTTAAATAA	73			GTTGCGATTGATGCGAACGA	
38	Nr1d1	Nr1d1_2	GGAAAGGACGAAACACCGGAGTAGGTGAGGCTCTAGAGTTTTAGAGCTAGAAATAGCAAGTTAAATAA	73			GAGTAGGTGAGGCTCTAGAG	
39	Nr1d1	Nr1d1_3	GGAAAGGACGAAACACCGCACACAGCTGACACCCCGTTTTAGAGCTAGAAATAGCAAGTTAAATAA	73			CACACAGCTGACACCCCG	
40	Nr1d1	Nr1d1_4	GGAAAGGACGAAACACCGTCTGGGGCGAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAATAA	73			TCTGGGGCGAATACCTG	
41	Nr1h2	Nr1h2_1	GGAAAGGACGAAACACCGTCTCTAATAGTGGGTGACGGTTTTAGAGCTAGAAATAGCAAGTTAAATAA	73			TTCTTAATAGTGGGTGACG	
42	Nr1h2	Nr1h2_2	GGAAAGGACGAAACACCGCAGGCTAGCCATCATCTGTTTTAGAGCTAGAAATAGCAAGTTAAATAA	73			CACCGAGTAGCCATCATCT	
43	Nr1h2	Nr1h2_3	GGAAAGGACGAAACACCGCGCAGTGTGGTCCACGGTTTTAGAGCTAGAAATAGCAAGTTAAATAA	73			CGGCGAGTGTGGTCCACGG	
44	Nr1h2	Nr1h2_4	GGAAAGGACGAAACACCGCTCCGACCGCCAAAGTCAAGTTTTAGAGCTAGAAATAGCAAGTTAAATAA	73			CTCCGACGACCCAAAGTCA	
45	Nr1h3	Nr1h3_1	GGAAAGGACGAAACACCGAAGCAACCCCAAGTTGACTGTTTTAGAGCTAGAAATAGCAAGTTAAATAA	73			AAAGCAACCCCAAGTTGAA	
46	Nr1h3	Nr1h3_2	GGAAAGGACGAAACACCGCAAGTACCGTACGCGCAGGTTTTAGAGCTAGAAATAGCAAGTTAAATAA	73			CAAGTACCGTACGCGCAGG	
47	Nr1h3	Nr1h3_3	GGAAAGGACGAAACACCGAATCTCTGCGCAGGACAGTTTTAGAGCTAGAAATAGCAAGTTAAATAA	73			AATCTCTGCGCAGGACAGCA	
48	Nr1h3	Nr1h3_4	GGAAAGGACGAAACACCGTTCGCGCATGTCATCAAGTTTTAGAGCTAGAAATAGCAAGTTAAATAA	73			TTCCCGCGAGTGTCAACAA	
49	Nr1h4	Nr1h4_1	GGAAAGGACGAAACACCGAACCGGACATTTGTTGATGTTTTAGAGCTAGAAATAGCAAGTTAAATAA	73			AAACGGGACATTTGTTGATG	
50	Nr1h4	Nr1h4_2	GGAAAGGACGAAACACCGTGATGGACATGTACATGCGCTTTTTAGAGCTAGAAATAGCAAGTTAAATAA	73			TGATGGACATGTACATGCGC	
51	Nr1h4	Nr1h4_3	GGAAAGGACGAAACACCGTGTGACAAAGAACCGCGAAGTTTTAGAGCTAGAAATAGCAAGTTAAATAA	73			TGTGACAAAGAACCGCGAA	
52	Nr1h4	Nr1h4_4	GGAAAGGACGAAACACCGAGTGAATCTAAACGGCTAGTTTTAGAGCTAGAAATAGCAAGTTAAATAA	73			AGTGTAAATCTAAACGGCTA	
53	Nr1i2	Nr1i2_1	GGAAAGGACGAAACACCGGTTCAACACGATGTTGACAGTTTTAGAGCTAGAAATAGCAAGTTAAATAA	73			GTTCAACAGATGTTGACAG	
54	Nr1i2	Nr1i2_2	GGAAAGGACGAAACACCGTGTAGGTTGACACATCGGCGTTTTAGAGCTAGAAATAGCAAGTTAAATAA	73			TGAGTTGACACATCGGCC	
55	Nr1i2	Nr1i2_3	GGAAAGGACGAAACACCGTGGCTTGTCCCCACATACGTTTTAGAGCTAGAAATAGCAAGTTAAATAA	73			TGGCTTGTCCCCACATACA	
56	Nr1i2	Nr1i2_4	GGAAAGGACGAAACACCGTGATCTGCGAGTTCCTTGTGTTTTAGAGCTAGAAATAGCAAGTTAAATAA	73			TGATCTGCGAGTTCCTCTG	
57	Nr1i3	Nr1i3_1	GGAAAGGACGAAACACCGTGCATGAACAGATAGCCGGTTTTAGAGCTAGAAATAGCAAGTTAAATAA	73			TGCATGAACAGATAGCCGG	
58	Nr1i3	Nr1i3_2	GGAAAGGACGAAACACCGGGCAGCCAGACAGGCCAGGTTTTAGAGCTAGAAATAGCAAGTTAAATAA	73			GGCGCAGCCAGCAGGACAG	
59	Nr1i3	Nr1i3_3	GGAAAGGACGAAACACCGAACCGACAGATGGACCAAGTTTTAGAGCTAGAAATAGCAAGTTAAATAA	73			AAACGGACAGATGGACCA	

No.	*Oligo name	*Oligo name	*Sequence (5' to 3')	nt#	Remarks	5'	guide sequence	3'
60	Nr1i3	Nr1i3_4	GGAAAGGACGAAACACCGACACAGGTCCTAACCATGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			ACACAGGTCCCTAACCATGG	
61	Nr2c1	Nr2c1_1	GGAAAGGACGAAACACCGGGTGCAGAGCTTACGCAATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			GGTGCAGAGCTTACGCAATG	
62	Nr2c1	Nr2c1_2	GGAAAGGACGAAACACCGACAGTCTTCTTCATCCCGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			ACAGTCTTGCATCCCGA	
63	Nr2c1	Nr2c1_3	GGAAAGGACGAAACACCGGTTCAATCTGGCAAACACCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			GTTCAATCTGGCAAACACCG	
64	Nr2c1	Nr2c1_4	GGAAAGGACGAAACACCGACGTGCGACTGCTCAGCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			ACGTGCGACTGCTCAGCAG	
65	Nr2c2	Nr2c2_1	GGAAAGGACGAAACACCGGATCCAGATAGTACCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			GATCCAGATAGTACCAGCAG	
66	Nr2c2	Nr2c2_2	GGAAAGGACGAAACACCGAGGGACAAGGTTTCCGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			AGGGACAAGGTTGTCGAGG	
67	Nr2c2	Nr2c2_3	GGAAAGGACGAAACACCGGTACCATCCTCACGTATCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			GTACCATCCTCAGTATCAA	
68	Nr2c2	Nr2c2_4	GGAAAGGACGAAACACCGTGGAGGTGAAGCACTACTCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			TGGAGGTGAAGCACTATCTG	
69	Nr2e1	Nr2e1_1	GGAAAGGACGAAACACCGCACTCTCGTAGAGATACATTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			CACTCTGTAGAGATACATTG	
70	Nr2e1	Nr2e1_2	GGAAAGGACGAAACACCGAGGACCCCGCTGCTGCTGCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			AGGACCCCGCTGCTGCTGCA	
71	Nr2e1	Nr2e1_3	GGAAAGGACGAAACACCGAGTGTAGCATCAACCGGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			AGTGTAGCATCAACCGGAA	
72	Nr2e1	Nr2e1_4	GGAAAGGACGAAACACCGTCTGTGTCTTGTCTACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			TTCTGTGTCTTGTCTACG	
73	Nr2e3	Nr2e3_1	GGAAAGGACGAAACACCGTGACCCCGATCAGAACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			TGACCCCGATCAGAACAG	
74	Nr2e3	Nr2e3_2	GGAAAGGACGAAACACCGCAGTTAGCACAAAGTTTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			CAGTTAGCACAAAGTTTCGG	
75	Nr2e3	Nr2e3_3	GGAAAGGACGAAACACCGGCTCCAAAGAGGAGTCTCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			GCTCCAAAGAGGAGTCTCC	
76	Nr2e3	Nr2e3_4	GGAAAGGACGAAACACCGTCTCTTGGAGCCATACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			TCCTTCTGGAGCCATACAG	
77	Nr2f1	Nr2f1_1	GGAAAGGACGAAACACCGCAGTATGCACTACAAACCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			CCAGTATGCACTACAAACG	
78	Nr2f1	Nr2f1_2	GGAAAGGACGAAACACCGGCTGCCATAACCGCAGCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			GGCTGCCATAACCGCAGCTG	
79	Nr2f1	Nr2f1_3	GGAAAGGACGAAACACCGCAGCTGTTCTGCTCAACCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			CGAGCTGTTCTGCTCAACG	
80	Nr2f1	Nr2f1_4	GGAAAGGACGAAACACCGGATGTTGCGGGCCACTCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			GATGTTGCGGGCCACTCGA	
81	Nr2f2	Nr2f2_1	GGAAAGGACGAAACACCGCAGTTTGCCTGACCAACCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			CGAGTTTGCCTGACCAACG	
82	Nr2f2	Nr2f2_2	GGAAAGGACGAAACACCGTACCGCAGTTCACGTGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			CTACGGCCAGTTCACGTGCG	
83	Nr2f2	Nr2f2_3	GGAAAGGACGAAACACCGGCGCTGAAGAGCATCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			GGCGCTGAAGAGCATCCGTTG	
84	Nr2f2	Nr2f2_4	GGAAAGGACGAAACACCGCTCAAAAAGTCCCTCAAAGTGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			CTCAAAAAGTCCCTCAAAGT	
85	Nr2f6	Nr2f6_1	GGAAAGGACGAAACACCGGAGTACCCACGCGCACCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			GAGTACCCACGCGCACCG	
86	Nr2f6	Nr2f6_2	GGAAAGGACGAAACACCGGCATGCGTCCCCGGTCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			GCATGCGTCCCCGGTCCAG	
87	Nr2f6	Nr2f6_3	GGAAAGGACGAAACACCGGGCGCAGGAGCGTCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			CGGGCGCAGGAGCGTCCG	
88	Nr2f6	Nr2f6_4	GGAAAGGACGAAACACCGCATCGACAAACGTTGCGAGTGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			CATCGACAAACGTTGCGAGT	
89	Nr3c1	Nr3c1_1	GGAAAGGACGAAACACCGCATTATGGGGTCTGACGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			CATTATGGGGTCTGACGTG	
90	Nr3c1	Nr3c1_2	GGAAAGGACGAAACACCGAGCTTGCTGCAATAAACCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			AGCTTGCTGCAATAAAC	
91	Nr3c1	Nr3c1_3	GGAAAGGACGAAACACCGAAAGCCGTTTCACTGCTCATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			AAAGCCGTTTCACTGCTCAT	
92	Nr3c1	Nr3c1_4	GGAAAGGACGAAACACCGAAAACCTGGAATAGGTGCCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			AAAACCTGGAATAGGTGCCAA	
93	Nr3c2	Nr3c2_1	GGAAAGGACGAAACACCGGATGATTTGGGCTTAAACGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			GATGATTTGGGCTTAAACGA	
94	Nr3c2	Nr3c2_2	GGAAAGGACGAAACACCGCAAGGAACTTTCAGCCACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			CAAGGAACTTTCAGCCACGG	
95	Nr3c2	Nr3c2_3	GGAAAGGACGAAACACCGTCCACTAATGCATTGACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			TCCACTAATGCATTGACAGG	
96	Nr3c2	Nr3c2_4	GGAAAGGACGAAACACCGGAATGGAAATGGGTTGACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			GAATGGAAATGGGTTGACTG	
97	Nr4a1	Nr4a1_1	GGAAAGGACGAAACACCGGGAAGTGTACCGTTCCGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			GGAAAGTGTACCGTTCCGAGG	
98	Nr4a1	Nr4a1_2	GGAAAGGACGAAACACCGTCTCTGTGTGACGACTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			TGCTCTGTGTGACGACTATG	
99	Nr4a1	Nr4a1_3	GGAAAGGACGAAACACCGGGCAACAAAGGATTCGCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			GGCAAAACAAAGGATTCGCTG	
100	Nr4a1	Nr4a1_4	GGAAAGGACGAAACACCGCTTCATAAGTCTGGCTCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			GCCTTCATAAGTCTGGCTG	
101	Nr4a2	Nr4a2_1	GGAAAGGACGAAACACCGTGTCAAGCACTGCGATGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			TGTCAAGCACTGCGATGCG	
102	Nr4a2	Nr4a2_2	GGAAAGGACGAAACACCGTGCAGGATTGGAATCGAGCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			TGCCGATTGGAATCGAGCT	
103	Nr4a2	Nr4a2_3	GGAAAGGACGAAACACCGAGTACTGACAACGATTTCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			AGTACTGACAACGATTTCCG	
104	Nr4a2	Nr4a2_4	GGAAAGGACGAAACACCGTAGTAAACCGACCCGCTGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			TAGTAAACCGACCCGCTGTG	
105	Nr4a3	Nr4a3_1	GGAAAGGACGAAACACCGGCAATCATACAGATCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			GCATTCATACAGATCGG	
106	Nr4a3	Nr4a3_2	GGAAAGGACGAAACACCGACCAAGCTGACCATGGACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			ACCAAGTCAAGTCAAGTAA	
107	Nr4a3	Nr4a3_3	GGAAAGGACGAAACACCGCGCTGGGTCATAGCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			CGGCCGTGGGTCATAGCCG	
108	Nr4a3	Nr4a3_4	GGAAAGGACGAAACACCGAGTGTCCGGATGGTTAAGGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			AGTGTCCGGATGGTTAAGGA	
109	Nr5a1	Nr5a1_1	GGAAAGGACGAAACACCGTGGAGACCGGACCCGATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			TGGAGCCGGACCCGATG	
110	Nr5a1	Nr5a1_2	GGAAAGGACGAAACACCGTGCCTGCTGATCGAATGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			GTGCGTCTGATCGAATGCG	
111	Nr5a1	Nr5a1_3	GGAAAGGACGAAACACCGCGCAGTGTGACGAGCCCGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			CGCACGTGACGAGCCCGTAG	
112	Nr5a1	Nr5a1_4	GGAAAGGACGAAACACCGCAATGTCGACTGGGCACGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			CCAATGTCGACTGGGCACGA	
113	Nr5a2	Nr5a2_1	GGAAAGGACGAAACACCGTGTGGGCGATAAAAGTGTCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			TGTGTGGCGATAAAAGTGTCT	
114	Nr5a2	Nr5a2_2	GGAAAGGACGAAACACCGTAAGAGCCGACCGCATGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			GTAAGAGCCGACCCGATGCG	
115	Nr5a2	Nr5a2_3	GGAAAGGACGAAACACCGTGCCTCCCCAACCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			TGCCACTCCCCAACCTGG	
116	Nr5a2	Nr5a2_4	GGAAAGGACGAAACACCGCTTCTGTACATGCTCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			CTTCTGTACATGCTCGGG	
117	Nr6a1	Nr6a1_1	GGAAAGGACGAAACACCGCTTACCACCGTTGCGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			CTTACCACCGTTGCGCGG	
118	Nr6a1	Nr6a1_2	GGAAAGGACGAAACACCGCATAGTGCAGCCCGTAGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			CATAGTGCAGCCCGTAGCG	
119	Nr6a1	Nr6a1_3	GGAAAGGACGAAACACCGCAGAATAGCTAAAAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			CCAGAATAGCTAAAAGTGG	
120	Nr6a1	Nr6a1_4	GGAAAGGACGAAACACCGCACCTATGTTGATTGAAGATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			CACCTATGTTGATTGAAGAT	
121	Pgr	Pgr_1	GGAAAGGACGAAACACCGCTGCGGCACTCATGAGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAG	73			CTCTGCGCACTCATGAGCG	

No.	*Oligo name	*Oligo name	*Sequence (5' to 3')	nt#	Remarks	5'	guide sequence	3'
122	Pgr	Pgr_2	GGAAAGGACGAAACACCGAGGAGTTCGACGCCAACCGTTTTAGAGCTAGAAATAGCAAGTAAAAATAA	73			AGGAGGAGTCGACGCCAACG	
123	Pgr	Pgr_3	GGAAAGGACGAAACACCGGGCGGCAACCAACCGCTGCTTTTTAGAGCTAGAAATAGCAAGTAAAAATAA	73			GGCGGCAACGCAACCGCTGCT	
124	Pgr	Pgr_4	GGAAAGGACGAAACACCGCAGTCTGGGAAGTCCACCGCAGTTTTAGAGCTAGAAATAGCAAGTAAAAATAA	73			CAGTCTGGGAAGTCCACCGCA	
125	Ppara	Ppara_1	GGAAAGGACGAAACACCGCATCGAGTGTGCAATATGTGTTTTAGAGCTAGAAATAGCAAGTAAAAATAA	73			CATCGAGTGTGCAATATGTG	
126	Ppara	Ppara_2	GGAAAGGACGAAACACCGGATTTCTCAGTCCATCGGTGTTTTAGAGCTAGAAATAGCAAGTAAAAATAA	73			GATTTCTCAGTCCATCGGTG	
127	Ppara	Ppara_3	GGAAAGGACGAAACACCGTCTGTCGGGATGTCACACAAGTTTTAGAGCTAGAAATAGCAAGTAAAAATAA	73			TCTGTGGGATGTCACACAAG	
128	Ppara	Ppara_4	GGAAAGGACGAAACACCGCTCGTCCAGTGCATGTCGGTTTTAGAGCTAGAAATAGCAAGTAAAAATAA	73			CTGCTGGAGTGCATGTCGG	
129	Ppard	Ppard_1	GGAAAGGACGAAACACCGCTCCGCGCATCGTCCAAAGTTTTAGAGCTAGAAATAGCAAGTAAAAATAA	73			CCTCCGCGCATCGTCCAAAG	
130	Ppard	Ppard_2	GGAAAGGACGAAACACCGGGCTCGGGTCCACTACCGTTTTAGAGCTAGAAATAGCAAGTAAAAATAA	73			GGCTCGGGTCCACTACG	
131	Ppard	Ppard_3	GGAAAGGACGAAACACCGTCGAGTATGAGAAAGTGCAGTGTGTTTTAGAGCTAGAAATAGCAAGTAAAAATAA	73			TCGAGTATGAGAAAGTGCAGT	
132	Ppard	Ppard_4	GGAAAGGACGAAACACCGCTCAAGTATGCGGTGTCACGGTTTTAGAGCTAGAAATAGCAAGTAAAAATAA	73			CCTCAAGTATGGCGTGCAGC	
133	Pparg	Pparg_1	GGAAAGGACGAAACACCGAATGCTGGAGAAATCACTGGTTTTAGAGCTAGAAATAGCAAGTAAAAATAA	73			AATGCTGGAGAAATCAACTG	
134	Pparg	Pparg_2	GGAAAGGACGAAACACCGAGAACCTTCTAACTCCCTCAGTTTTAGAGCTAGAAATAGCAAGTAAAAATAA	73			AGAACCTTCTAACTCCCTCA	
135	Pparg	Pparg_3	GGAAAGGACGAAACACCGGACCCCTTAAAAAATTCGAGTTTTAGAGCTAGAAATAGCAAGTAAAAATAA	73			GCACCTTAAAAAATTCGGGA	
136	Pparg	Pparg_4	GGAAAGGACGAAACACCGCTGCCTATGAGCACTTCCAGTTTTAGAGCTAGAAATAGCAAGTAAAAATAA	73			CTGCCATGAGCACTTCCACA	
137	Rara	Rara_1	GGAAAGGACGAAACACCGGAGCTACACGCTGACGCGTGGTTTTAGAGCTAGAAATAGCAAGTAAAAATAA	73			GAGCTACACGCTGACGCGCT	
138	Rara	Rara_2	GGAAAGGACGAAACACCGATCATCCGGTACCACTATGTTTTAGAGCTAGAAATAGCAAGTAAAAATAA	73			ATCATCCGGTACCACTATG	
139	Rara	Rara_3	GGAAAGGACGAAACACCGAGATTCTGCGAATCTGACGCGTTTTAGAGCTAGAAATAGCAAGTAAAAATAA	73			AGATTCTGCGAATCTGACG	
140	Rara	Rara_4	GGAAAGGACGAAACACCGCAAGTGCATCATTAAAGACTGTTTTAGAGCTAGAAATAGCAAGTAAAAATAA	73			CAAGTGCATCATTAAAGACT	
141	Rarb	Rarb_1	GGAAAGGACGAAACACCGAAGCAGGCTGTACACCGTTTTAGAGCTAGAAATAGCAAGTAAAAATAA	73			AAGCAGGCTGTACACCGG	
142	Rarb	Rarb_2	GGAAAGGACGAAACACCGCCAAGTCCAATCGGACCCGGTTTTAGAGCTAGAAATAGCAAGTAAAAATAA	73			CCAAGTCCAATCGGACCCGG	
143	Rarb	Rarb_3	GGAAAGGACGAAACACCGACCGCATCTGCTCAATGTGTTTTAGAGCTAGAAATAGCAAGTAAAAATAA	73			ACCGGCATCTGCTCAATGT	
144	Rarb	Rarb_4	GGAAAGGACGAAACACCGTGACGCACTTCTATCTCGAGTTTTAGAGCTAGAAATAGCAAGTAAAAATAA	73			TGACGCACTTCTATCTCGA	
145	Rarg	Rarg_1	GGAAAGGACGAAACACCGTGGGCAAGTACACCAACCGTTTTAGAGCTAGAAATAGCAAGTAAAAATAA	73			TGGGCAAGTACACCAACCGG	
146	Rarg	Rarg_2	GGAAAGGACGAAACACCGAAGCTGCTTATAGACCCGTTTTAGAGCTAGAAATAGCAAGTAAAAATAA	73			AAGCATGGCTTATAGACCCG	
147	Rarg	Rarg_3	GGAAAGGACGAAACACCGGCTACAAAAGTGTTCGAAAGTTTTAGAGCTAGAAATAGCAAGTAAAAATAA	73			GCTACAAAAGTGTTCGAAAG	
148	Rarg	Rarg_4	GGAAAGGACGAAACACCGACACTATGACATCTCGGATGTTTTAGAGCTAGAAATAGCAAGTAAAAATAA	73			ACACTATGACATCTCGGAT	
149	Rora	Rora_1	GGAAAGGACGAAACACCGTGGCTGAGATGTTGAGGTTTTAGAGCTAGAAATAGCAAGTAAAAATAA	73			TGGCTGAGATGTTGAGGAT	
150	Rora	Rora_2	GGAAAGGACGAAACACCGCATTGATGTCCAATCCGACGTTTTAGAGCTAGAAATAGCAAGTAAAAATAA	73			CATTGATGTCCAATCCGAC	
151	Rora	Rora_3	GGAAAGGACGAAACACCGGAGAGACAGCTGTACGCGGTTTTAGAGCTAGAAATAGCAAGTAAAAATAA	73			GAGAGACAGCTGTACGCGG	
152	Rora	Rora_4	GGAAAGGACGAAACACCGAGCTATGCGAGCTCCAGCCGTTTTAGAGCTAGAAATAGCAAGTAAAAATAA	73			AGCTATGCGAGCTCCAGCCG	
153	Rorb	Rorb_1	GGAAAGGACGAAACACCGCACCACTGCTGATGATGTTTTAGAGCTAGAAATAGCAAGTAAAAATAA	73			CACCACTGCTGATGATGAT	
154	Rorb	Rorb_2	GGAAAGGACGAAACACCGGAGACATGTCAGTACACCAAGTTTTAGAGCTAGAAATAGCAAGTAAAAATAA	73			GGAGACATGTCAGTACACCA	
155	Rorb	Rorb_3	GGAAAGGACGAAACACCGTCCAGCTGTAAAGTTCGGGTTTTAGAGCTAGAAATAGCAAGTAAAAATAA	73			TCCAGCTGTAAAGTTCGGG	
156	Rorb	Rorb_4	GGAAAGGACGAAACACCGACAAGTTGGGTACAGATGTTTTAGAGCTAGAAATAGCAAGTAAAAATAA	73			ACAAGTTGGGTACAGATGTT	
157	Rorc	Rorc_1	GGAAAGGACGAAACACCGCTTGAATAGTCCAGAACCGTTTTAGAGCTAGAAATAGCAAGTAAAAATAA	73			CTTGAGTATAGTCCAGAACG	
158	Rorc	Rorc_2	GGAAAGGACGAAACACCGGTCTCTGGGATCCACTACCGTTTTAGAGCTAGAAATAGCAAGTAAAAATAA	73			GTCATCTGGGATCCACTACG	
159	Rorc	Rorc_3	GGAAAGGACGAAACACCGTCTGGGGCACTGCAGAACTGTTTTAGAGCTAGAAATAGCAAGTAAAAATAA	73			TCTGGGGCACTGCAGAACTG	
160	Rorc	Rorc_4	GGAAAGGACGAAACACCGGACAGCAGAGGCTCGGGTTTTAGAGCTAGAAATAGCAAGTAAAAATAA	73			GACAAGCAGAGGCTCGGGT	
161	Rxra	Rxra_1	GGAAAGGACGAAACACCGCAAGTCTGAGACATACGTTGGTTTTAGAGCTAGAAATAGCAAGTAAAAATAA	73			CAAGACTGAGACATACGTTG	
162	Rxra	Rxra_2	GGAAAGGACGAAACACCGAGGACGCCATTGAGGCTAGGTTTTAGAGCTAGAAATAGCAAGTAAAAATAA	73			AGGACGCCATTGAGGCTAG	
163	Rxra	Rxra_3	GGAAAGGACGAAACACCGCATGGGCCGCTCCATGTGTTTTAGAGCTAGAAATAGCAAGTAAAAATAA	73			CATGGGCCGCTCCATGT	
164	Rxra	Rxra_4	GGAAAGGACGAAACACCGGGGCACTGAGAAAAGTGTGTTTTAGAGCTAGAAATAGCAAGTAAAAATAA	73			GGGGCAGCTGAGAAAAGTGT	
165	Rxrb	Rxrb_1	GGAAAGGACGAAACACCGATTGTGGGGTTCGCGTCCCGGTTTTAGAGCTAGAAATAGCAAGTAAAAATAA	73			ATTGTGGGGTTCGCGTCCCG	
166	Rxrb	Rxrb_2	GGAAAGGACGAAACACCGGCTTTCACACTCGTTGAGTGTGTTTTAGAGCTAGAAATAGCAAGTAAAAATAA	73			GCTGTTCACTCGTTGAGT	
167	Rxrb	Rxrb_3	GGAAAGGACGAAACACCGGTTCCAGGAGGCGTCAACGGTTTTAGAGCTAGAAATAGCAAGTAAAAATAA	73			GTTCCAGGAGGCGTCAACGG	
168	Rxrb	Rxrb_4	GGAAAGGACGAAACACCGTCCACAGTGTGCTCCCTGGGTTTTAGAGCTAGAAATAGCAAGTAAAAATAA	73			TCCAGATGTGCTCCCTGG	
169	Rxrg	Rxrg_1	GGAAAGGACGAAACACCGTAGCCACGAAAGACATGCCCGTTTTAGAGCTAGAAATAGCAAGTAAAAATAA	73			TAGCCACGAAAGACATGCCCG	
170	Rxrg	Rxrg_2	GGAAAGGACGAAACACCGTGGCTTGGGCCCACTCAACGGTTTTAGAGCTAGAAATAGCAAGTAAAAATAA	73			TGGCTTGGGCCCACTCAACG	
171	Rxrg	Rxrg_3	GGAAAGGACGAAACACCGTCTGTAACCGGAAAGCAGTATGTTTTAGAGCTAGAAATAGCAAGTAAAAATAA	73			TCGTAACCGGAAAGCAGTAT	
172	Rxrg	Rxrg_4	GGAAAGGACGAAACACCGCACAGCACTCAGCTCCGAGTTTTAGAGCTAGAAATAGCAAGTAAAAATAA	73			CACAGCACTCAGCTCCGAG	
173	Thra	Thra_1	GGAAAGGACGAAACACCGACAGCGGTAGTATAACCGGTTTTAGAGCTAGAAATAGCAAGTAAAAATAA	73			ACAGCGGTAGTATAACCGG	
174	Thra	Thra_2	GGAAAGGACGAAACACCGTGTCACTCTCAGGCTGTTAGGTTTTAGAGCTAGAAATAGCAAGTAAAAATAA	73			TGTCACCTCAGGCTGTTAG	
175	Thra	Thra_3	GGAAAGGACGAAACACCGTCTAGATGATTCGAAAGCGGGTTTTAGAGCTAGAAATAGCAAGTAAAAATAA	73			TCTAGATGATTCGAAAGCGGG	
176	Thra	Thra_4	GGAAAGGACGAAACACCGAAAACCTGCCATGTTCTCCGGTTTTAGAGCTAGAAATAGCAAGTAAAAATAA	73			AAAACCTGCCATGTTCTCCG	
177	Thrb	Thrb_1	GGAAAGGACGAAACACCGAAGACAGTCCGGCTCTCAGTTTTAGAGCTAGAAATAGCAAGTAAAAATAA	73			GAAAGACAGTCCGGCTCTCAG	
178	Thrb	Thrb_2	GGAAAGGACGAAACACCGCCATCGTGAATGCCCAAGTTTTAGAGCTAGAAATAGCAAGTAAAAATAA	73			CCCATCGTGAATGCCCAAG	
179	Thrb	Thrb_3	GGAAAGGACGAAACACCGCATCTTGTCTAAATAGCTGTTTTAGAGCTAGAAATAGCAAGTAAAAATAA	73			CATCTTGTCTAAATAGCTG	
180	Thrb	Thrb_4	GGAAAGGACGAAACACCGCAGTTTTCCAGGGTAACTACGTTTTAGAGCTAGAAATAGCAAGTAAAAATAA	73			CAGTTTTCCAGGGTAACTAC	
181	Vdr	Vdr_1	GGAAAGGACGAAACACCGTGGAGATTCCGCAATCCCAAGTTTTAGAGCTAGAAATAGCAAGTAAAAATAA	73			TGGAGATTCCGCAATCCCA	
182	Vdr	Vdr_2	GGAAAGGACGAAACACCGAGCTTGAAGTGGAGCCCGTTTTAGAGCTAGAAATAGCAAGTAAAAATAA	73			AGCGTTGAAGTGGAGCCCG	
183	Vdr	Vdr_3	GGAAAGGACGAAACACCGTCTCTCATTGATGATCCATCGTTTTAGAGCTAGAAATAGCAAGTAAAAATAA	73			TCTCTCATTGATGATCCATC	

No.	*Oligo name	*Oligo name	*Sequence (5' to 3')	nt#	Remarks	5'	guide sequence	3'
184	Vdr	Vdr_4	GGAAAGGACGAAACACCGTTTCGTGCAGACGTAAGTACAGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			TTCGTGCAGACGTAAGTACA	
185	Ncoa1	Ncoa1_1	GGAAAGGACGAAACACCGTTGACTGAGGGATTTATTCGGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			TTGACTGAGGGATTTATTCG	
186	Ncoa1	Ncoa1_2	GGAAAGGACGAAACACCGATGCTAATTACCCCTCCAGGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			GATGCTAATTCACCCCTCCAG	
187	Ncoa1	Ncoa1_3	GGAAAGGACGAAACACCGACCTAGTAAATGCAACTGGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			ACCACTAGTAAATGCCAACTG	
188	Ncoa1	Ncoa1_4	GGAAAGGACGAAACACCGAGTTGGACAACCCAGGAGCGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			AGTTTGGACAACCCAGGAGCG	
189	Ncoa2	Ncoa2_1	GGAAAGGACGAAACACCGAGTGCATAGTTACTACCTCGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			AGTGCATAGTTACTACCTCG	
190	Ncoa2	Ncoa2_2	GGAAAGGACGAAACACCGGGAGGATTCATATTAACCTGGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			GGGAGGATTCATATTAACCTG	
191	Ncoa2	Ncoa2_3	GGAAAGGACGAAACACCGAGTGCAGTGTCTGCCACCGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			AGTCAGATGTCTGCCACCG	
192	Ncoa2	Ncoa2_4	GGAAAGGACGAAACACCGCTTTCGCAAGTGATGTCAGGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			CTTTGCAAGTGATGTCAGG	
193	Ncoa3	Ncoa3_1	GGAAAGGACGAAACACCGCAAGGAGAAACGATACACCGGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			CAAGGAGAAACGATACACCGG	
194	Ncoa3	Ncoa3_2	GGAAAGGACGAAACACCGCTCCTCATATAACCGAGGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			TCGTCTCCATATAACCGGAG	
195	Ncoa3	Ncoa3_3	GGAAAGGACGAAACACCGGAGAACATCATGATTTCCCTGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			AGAACATCATGATTTCCCTG	
196	Ncoa3	Ncoa3_4	GGAAAGGACGAAACACCGACGCTCCTCCGACGACCGGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			ACGTGCTCCTCCGACGACCGG	
197	Ncoa4	Ncoa4_1	GGAAAGGACGAAACACCGCTGCTGATTGTTGCGCGGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			CGTCTGCTGATTGTTGCGCGG	
198	Ncoa4	Ncoa4_2	GGAAAGGACGAAACACCGTTCAGAAGTACGATCCAGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			TTCAAGAAGTACGATCCAG	
199	Ncoa4	Ncoa4_3	GGAAAGGACGAAACACCGGCTTAAAGGATCCAAATGGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			GGTCTTAAAGGATCCAAATG	
200	Ncoa4	Ncoa4_4	GGAAAGGACGAAACACCGAATTAAGATAATTTACGAGGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			AATTAAGATAATTTACGAG	
201	Ncoa5	Ncoa5_1	GGAAAGGACGAAACACCGGGTGGATGACTATTGCGGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			GGGTGGATGACTTTGCGCGG	
202	Ncoa5	Ncoa5_2	GGAAAGGACGAAACACCGGTAGAGAGGAGCTTTATCTGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			GTAGAGAGGAGCTTTATCTG	
203	Ncoa5	Ncoa5_3	GGAAAGGACGAAACACCGCTGCGTCCCGCAATCCCGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			CTGCGTCCCGCAATCCCG	
204	Ncoa5	Ncoa5_4	GGAAAGGACGAAACACCGTAAACAGATACCTACTGCCGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			TAAACAGATACCTACTGCCG	
205	Ncoa6	Ncoa6_1	GGAAAGGACGAAACACCGTGAACCATAGGATTCGACCGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			TGAACCATAGGATTCGACCG	
206	Ncoa6	Ncoa6_2	GGAAAGGACGAAACACCGGCTTATGACGCCCCAGGGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			GCTGTTATGACGCCCCAGGG	
207	Ncoa6	Ncoa6_3	GGAAAGGACGAAACACCGCAATGACTACAAATCAAGGGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			CAATGACTACAAATCAAGGG	
208	Ncoa6	Ncoa6_4	GGAAAGGACGAAACACCGTGTGCCAACTGTTACACAGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			TGTGCCAACTTTGTTACACA	
209	Ncoa7	Ncoa7_1	GGAAAGGACGAAACACCGAGGCTTAAACCCATCGAGGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			AGGCCCTTAAACCCATCGAG	
210	Ncoa7	Ncoa7_2	GGAAAGGACGAAACACCGAGTTCAACGTTACAGCAGGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			AGTTCAACGTTACAGCAGAG	
211	Ncoa7	Ncoa7_3	GGAAAGGACGAAACACCGGTACACTCTGGGTTAAAGGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			GGTCACTCTGGGTTAAAGG	
212	Ncoa7	Ncoa7_4	GGAAAGGACGAAACACCGCTAAGGGATCGGACTTATGAGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			CTAAGGGATCGGACTTATGA	
213	Ppargc1b	Ppargc1b_1	GGAAAGGACGAAACACCGAGGCTTGCTAACATCAACAGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			AGGGCTTGCTAACATCACAG	
214	Ppargc1b	Ppargc1b_2	GGAAAGGACGAAACACCGTGGACGAGCTTCTACTGGTGGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			TGGACGAGCTTCTACTGGTG	
215	Ppargc1b	Ppargc1b_3	GGAAAGGACGAAACACCGGGCTTGACTACTGCTGTGGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			GGCCTGACTACTGCTGTG	
216	Ppargc1b	Ppargc1b_4	GGAAAGGACGAAACACCGTCTGCTGCTAGGAGTCTTGGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			TCCTGTGCTAGGGAGTCTTG	
217	Ppargc1a	Ppargc1a_1	GGAAAGGACGAAACACCGGAATGAGGCAAACTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			GAATGAGGCAAACTGTCTAG	
218	Ppargc1a	Ppargc1a_2	GGAAAGGACGAAACACCGTATTGAGCGAACCTTAAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			TATTGAGCGAACCTTAAAGT	
219	Ppargc1a	Ppargc1a_3	GGAAAGGACGAAACACCGTGTGATGCGCACCTTAAACAGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			TTGCATGCGCACCTTAAACA	
220	Ppargc1a	Ppargc1a_4	GGAAAGGACGAAACACCGAAGACCACTAAGGGAGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			AAGACCAGTGAACCTAAGGGA	
221	Scand1	Scand1_1	GGAAAGGACGAAACACCGAGCGCTGGCGAAAGGTTCTCGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			AGCGCTGGCGAAAGGTTCTCG	
222	Scand1	Scand1_2	GGAAAGGACGAAACACCGTTCGCTACAGGACGCGCGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			TTGCTACAGGACGCGCGCC	
223	Scand1	Scand1_3	GGAAAGGACGAAACACCGGCTCCCGGAATCGGGCAGCGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			GCTCCGGAATCGGGCAGCG	
224	Scand1	Scand1_4	GGAAAGGACGAAACACCGCGCGCCGCGACTTTGAACAGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			CGCGCCGCGACTTTGAACA	
225	Ncor1	Ncor1_1	GGAAAGGACGAAACACCGGCTTACGGAACCCCGTGGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			GGCTTACGGAACCCCGTG	
226	Ncor1	Ncor1_2	GGAAAGGACGAAACACCGGGCTAGCAAACTACCCGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			GGGCTAGCAAACTACCCCG	
227	Ncor1	Ncor1_3	GGAAAGGACGAAACACCGATATGCCGAGCATTACCAGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			ATATGCCGAGCATTACCCAG	
228	Ncor1	Ncor1_4	GGAAAGGACGAAACACCGCCCTACCAAGCCGACTCCGGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			CCCTACCAAGCCGACTCCG	
229	Ncor2	Ncor2_1	GGAAAGGACGAAACACCGGCTTCTGACTGTCCAAAGGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			GGCATCTGACTGTCCAAAG	
230	Ncor2	Ncor2_2	GGAAAGGACGAAACACCGGCATAGAGAACCAATCCGCGAGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			GCATAGAGAACCAATCCGCGA	
231	Ncor2	Ncor2_3	GGAAAGGACGAAACACCGGCTACACACCTCGTGAAGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			GCTACACACCTCGTGAAG	
232	Ncor2	Ncor2_4	GGAAAGGACGAAACACCGTACCAGTACGCCCCACGCGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			TACCGACTGAGCCCCACGCG	
233	Ahr	Ahr_1	GGAAAGGACGAAACACCGAGCTGTGCACAAGAGGATCGGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			AGCTGTGCACAAGAGGATCG	
234	Ahr	Ahr_2	GGAAAGGACGAAACACCGGTATAATAGACTGCTGCTGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			GTATAATAGACTGCTGCTG	
235	Ahr	Ahr_3	GGAAAGGACGAAACACCGTCTCCGCTAGCAAACTAAGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			TCTCCGCTAGCAAACTAAG	
236	Ahr	Ahr_4	GGAAAGGACGAAACACCGGTGAAAGAAATCTTACTTGGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			GTGAAAGAAATCTTACTTGG	
237	Abcb1a	Abcb1a_1	GGAAAGGACGAAACACCGACTGAATGCTCCAATTAACAGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			ACTGAATGCTCCAATTAACA	
238	Abcb1a	Abcb1a_2	GGAAAGGACGAAACACCGCAGGAAGCTTAGTACCAAGGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			CAGGAAGCTTAGTACCAAAG	
239	Abcb1a	Abcb1a_3	GGAAAGGACGAAACACCGCAAGATCAGATCATAAGTGTTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			CAAAGATCAGATCATAAAG	
240	Abcb1a	Abcb1a_4	GGAAAGGACGAAACACCGAATGACGTCAGCATTACGAAAGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			AATGACGTCAGCATTACGAA	
241	Abcb1b	Abcb1b_1	GGAAAGGACGAAACACCGAGCCTTTGCAACCGCAGGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			AGCCTTTGCAACCGCAGG	
242	Abcb1b	Abcb1b_2	GGAAAGGACGAAACACCGTGATGCTTCTAGTGTAAAGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			TGATGCTTCTAGTGTAAAG	
243	Abcb1b	Abcb1b_3	GGAAAGGACGAAACACCGTTCATCTTGAAAAACTGGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			CATCTTGAAAAACTG	
244	Abcb1b	Abcb1b_4	GGAAAGGACGAAACACCGCAGTGAACAATCAAGAGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			CAGATGAACAATCAAGAGA	
245	Asb2	Asb2_1	GGAAAGGACGAAACACCGGAGACAGACTGTCGAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			GGAGACAGACTGTCGAGTG	

No.	*Oligo name	*Oligo name	*Sequence (5' to 3')	nt#	Remarks	5'	guide sequence	3'
246	Asb2	Asb2_2	GGAAAGGACGAAACACCCGAGTGCATCAGCCCTCTACGGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			CAGTGCATCAGCCCTCAGC	
247	Asb2	Asb2_3	GGAAAGGACGAAACACCCGAGCGAGCGCCGCTCTACGGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			CGAGCGCGCCGCTCAGC	
248	Asb2	Asb2_4	GGAAAGGACGAAACACCCGCTCCAAGAGGGCAACTATGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			CCTCCAAGAGGGCAACTAT	
249	Bcl11b	Bcl11b_1	GGAAAGGACGAAACACCCGTTGTGCAAAATGAGCTGGAGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			GTGTGCAAAATGAGCTGGA	
250	Bcl11b	Bcl11b_2	GGAAAGGACGAAACACCCGCTGAGAGCCCGTCTGTAGGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			CTGAGAGCCCGTCTGAG	
251	Bcl11b	Bcl11b_3	GGAAAGGACGAAACACCCGCGGGAAGTTTCATCTGACACGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			GCGGGAAGTTTCATCTGACAC	
252	Bcl11b	Bcl11b_4	GGAAAGGACGAAACACCCGAGAGGTGAAGTAACTACCGGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			CAGAGGTGAAGTAACTACCGG	
253	Tfrc	Tfrc_1	GGAAAGGACGAAACACCCGCTACACGCTTACAATAGCCGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			CTACACGCTTACAATAGCCG	
254	Tfrc	Tfrc_2	GGAAAGGACGAAACACCCGGAATACATACACTCCTCGTGGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			GAATACATACACTCCTCGTG	
255	Tfrc	Tfrc_3	GGAAAGGACGAAACACCCGGGCTCTACTACAACATAAGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			GGGCTCTACTACAACATAA	
256	Tfrc	Tfrc_4	GGAAAGGACGAAACACCCGAACCTCGGGAGACTCCACTGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			AACCTCGGGAGACTCCACT	
257	Eomes	Eomes_1	GGAAAGGACGAAACACCCGCCATACCCGGAACTCAGGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			GCCATACGCGGAACTCAG	
258	Eomes	Eomes_2	GGAAAGGACGAAACACCCGGTGTCCATGGAGTAGCGCGGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			GCTGTCATGGAGTAGCGCG	
259	Eomes	Eomes_3	GGAAAGGACGAAACACCCGACCCAGAATCTCTACAACGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			CACCCAGAATCTCTAACAC	
260	Eomes	Eomes_4	GGAAAGGACGAAACACCCGTTCCACGAAACATTTGAGTGTGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			TTCCACGAAACATTTGAGT	
261	Foxp3	Foxp3_1	GGAAAGGACGAAACACCCGATACCTGATGTCATGAAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			CATACCTGATGTCATGAAGT	
262	Foxp3	Foxp3_2	GGAAAGGACGAAACACCCGTTACCCACAGGATCAATGGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			TCTACCCACAGGATCAATG	
263	Foxp3	Foxp3_3	GGAAAGGACGAAACACCCGAGTCCGGACCTCGGAAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			AGGTCCGGACTCGGAAGTG	
264	Foxp3	Foxp3_4	GGAAAGGACGAAACACCCGCAAGAGCTCTGTCCATTTGGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			GCAAGAGCTCTGTCCATTG	
265	Gata3	Gata3_1	GGAAAGGACGAAACACCCGCTACTACGAAACTCCGTCAGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			CTACTACGAAACTCCGTC	
266	Gata3	Gata3_2	GGAAAGGACGAAACACCCGCGGTTCCGATGTAAGTCGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			CCGGTTCCGATGTAAGTCG	
267	Gata3	Gata3_3	GGAAAGGACGAAACACCCGCACTGACCTGATCTGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			GCAGTCCGACTGATACTG	
268	Gata3	Gata3_4	GGAAAGGACGAAACACCCGTCACAGCTCCATCCACCAGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			TCCAAGACGTCATCCACCA	
269	Il10	Il10_1	GGAAAGGACGAAACACCCGGTAAACCGACTCTTAATGCGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			GCTAACCGACTCTTAATGC	
270	Il10	Il10_2	GGAAAGGACGAAACACCCGAACTGCACCCACTCCAGTGTGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			AACTGCACCCACTCCAGT	
271	Il10	Il10_3	GGAAAGGACGAAACACCCGAAGGAGCATTGAATCCCTGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			AAGGAGCATTGAATCCCT	
272	Il10	Il10_4	GGAAAGGACGAAACACCCGACTGGCATGAGGATCAGCAGGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			ACTGGCATGAGGATCAGCAG	
273	Il17a	Il17a_1	GGAAAGGACGAAACACCCGCTCAGCGTGTCCAACACTGGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			CTCAGCGTGTCCAACACTG	
274	Il17a	Il17a_2	GGAAAGGACGAAACACCCGGAACGGTTGAGGTAGTCTGAGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			GAAAGGTTGAGGTAGTCTGA	
275	Il17a	Il17a_3	GGAAAGGACGAAACACCCGCTTACGTACTGGAGAGTCCAGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			CTTACGTACTGGAGAGTCCA	
276	Il17a	Il17a_4	GGAAAGGACGAAACACCCGCTGAGTCTCCAGATCAGAGGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			CTGAGTCTCCAGATCAGCAG	
277	Lcor	Lcor_1	GGAAAGGACGAAACACCCGACAGCACTTAATCTTATCCAGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			ACAGCACTTAATCTTATCCA	
278	Lcor	Lcor_2	GGAAAGGACGAAACACCCGATCTGCAGAGATCAGAGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			ATCTGCAGAGATCAGAGCAG	
279	Lcor	Lcor_3	GGAAAGGACGAAACACCCGGATACCACAAGTTCGAGGAAGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			GATACCAAGTTCGAGGAA	
280	Lcor	Lcor_4	GGAAAGGACGAAACACCCGTTCCATCAATTAGCGACCTGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			TCCATCAATTAGCGACCT	
281	Maf	Maf_1	GGAAAGGACGAAACACCCGGTGGCTTCGATGGCTATGCGGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			GTGGCTTCGATGGCTATGCG	
282	Maf	Maf_2	GGAAAGGACGAAACACCCGGACCGCATCATCAGCCAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			GACCGCATCATCAGCCAGTG	
283	Maf	Maf_3	GGAAAGGACGAAACACCCGGGTGTCGCGGTGATCGCCGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			GGTGTCCCGGTGATCGCCG	
284	Maf	Maf_4	GGAAAGGACGAAACACCCGACCCACCCACCGCCGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			ACCACCCACCCAGCCCGG	
285	Med1	Med1_1	GGAAAGGACGAAACACCCGCAACCAACCTTCCGGGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			CCAACCAACCTTCCGGG	
286	Med1	Med1_2	GGAAAGGACGAAACACCCGAGGTGTATCCAGCGCTCAGGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			AGGTGTATCCAGCGCTCAG	
287	Med1	Med1_3	GGAAAGGACGAAACACCCGTAACCTACCCCACTCCGCGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			TAACCTACCCCACTCCGCG	
288	Med1	Med1_4	GGAAAGGACGAAACACCCGGTGTGAGCTGTAACCTCTACAAGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			GTGAGCTGTAACCTCTACAA	
289	Prdm1	Prdm1_1	GGAAAGGACGAAACACCCGTTGGAACCTAATGCCGTACGGGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			TTGGAACCTAATGCCGTACGG	
290	Prdm1	Prdm1_2	GGAAAGGACGAAACACCCGGATAGGATAAACCCAGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			GGATAGGATAAACCCCGGA	
291	Prdm1	Prdm1_3	GGAAAGGACGAAACACCCGGTGTAGACTTACCAGTGTAGGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			GTGTAGACTTACCAGTGTAG	
292	Prdm1	Prdm1_4	GGAAAGGACGAAACACCCGTTGTACCAGTGTCTGACGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			TTGTACCAGTGTCTGAGAG	
293	Smad4	Smad4_1	GGAAAGGACGAAACACCCGTAATCCATATCACTATGAGGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			TGAATCCATATCACTATGAG	
294	Smad4	Smad4_2	GGAAAGGACGAAACACCCGGTGGCGTTAGACTCTGCCGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			GGTGGGTTAGACTTGTCCG	
295	Smad4	Smad4_3	GGAAAGGACGAAACACCCGTGTCCATACAGAGAACATGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			TGTCCATACAGAGAACAT	
296	Smad4	Smad4_4	GGAAAGGACGAAACACCCGAAAGCGATCTCTCCGAGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			CAAAAGCGATCTCTCCGGA	
297	Stat1	Stat1_1	GGAAAGGACGAAACACCCGGATAGAGCCCAAGCTGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			GGATAGAGCCCAAGCTG	
298	Stat1	Stat1_2	GGAAAGGACGAAACACCCGTTGATGTTAGATAAACAGAGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			TGTGATGTTAGATAAACAGA	
299	Stat1	Stat1_3	GGAAAGGACGAAACACCCGTTAATGACGAGCTCGTGGAGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			TTAATGACGAGCTCGTGGAG	
300	Stat1	Stat1_4	GGAAAGGACGAAACACCCGAAAGCAAGCGTAATCTCCGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			GAAAAGCAAGCGTAATCTCC	
301	Stat3	Stat3_1	GGAAAGGACGAAACACCCCAACAATAAAGAACTGGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			CCAACAATAAAGAACTGG	
302	Stat3	Stat3_2	GGAAAGGACGAAACACCCGCTGTTCTCTGCTACCGGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			CTGCTCTGCTCACTACGG	
303	Stat3	Stat3_3	GGAAAGGACGAAACACCCGTTTACCAGGAAAGTCAAGTGTGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			GTTTACCAGGAAAGTCAAGT	
304	Stat3	Stat3_4	GGAAAGGACGAAACACCCGAAAGAGTCAATGCCAGTGTGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			CAAAGAGTCAATGCCAGT	
305	Stat4	Stat4_1	GGAAAGGACGAAACACCCGAAATGTCTAACTCCACTGAGGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			AATGTCTAACTCCACTGAG	
306	Stat4	Stat4_2	GGAAAGGACGAAACACCCGATGCCAACCGCCCTCAGGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			GCATGCCAACCGCCCTCAG	
307	Stat4	Stat4_3	GGAAAGGACGAAACACCCGAAATCCAATGCATGTAGCTGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			AAATCCAATGCATGTAGCTG	

No.	*Oligo name	*Oligo name	*Sequence (5' to 3')	nt#	Remarks	5'	guide sequence	3'
308	Stat4	Stat4_4	GGAAAGGACGAAACACCGTGGCCCTACCATTAACTAGGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			TGGCCTCACCTAACCTAG	
309	Stat5a	Stat5a_1	GGAAAGGACGAAACACCGCATGGACGATAACACCACAGCTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			CATGGACGATAACGACCACA	
310	Stat5a	Stat5a_2	GGAAAGGACGAAACACCGTTGTTGTACAGAAATGAGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			GTTCTGTACAGAAATGTA	
311	Stat5a	Stat5a_3	GGAAAGGACGAAACACCGAGTGGATCGAGAGCCAGCCGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			AGTGGATCGAGAGCCAGCCG	
312	Stat5a	Stat5a_4	GGAAAGGACGAAACACCGTGGCGCTGAGCGTCCAGGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			GTGGCGCTGAGCGTCCAG	
313	Stat5b	Stat5b_1	GGAAAGGACGAAACACCGCTGATTCGCAGTATTACAGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			CTGATTCGCAGTATTACAG	
314	Stat5b	Stat5b_2	GGAAAGGACGAAACACCGTACAGCAACCAAGTCCATGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			TACAGCGAACCAAGTCCATG	
315	Stat5b	Stat5b_3	GGAAAGGACGAAACACCGGGCTGTCCAGAGGACAGGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			GGCGTTGTCCAGAGGACAG	
316	Stat5b	Stat5b_4	GGAAAGGACGAAACACCGAGTGGATCGAAAGCCAGCCGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			AGTGGATCGAAAGCCAGCC	
317	Stat6	Stat6_1	GGAAAGGACGAAACACCGCATCAAGCAAACTTCAAGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			ATAAAGCGCTGTGAGCGGAA	
318	Stat6	Stat6_2	GGAAAGGACGAAACACCGGCTGAAGGCCCTCCACACTGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			GCTGAAAGGCCCTCCACTG	
319	Stat6	Stat6_3	GGAAAGGACGAAACACCGAGAAAGCATCTGAAACCCGCTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			AGAAAGCATCTGAAACCGACC	
320	Stat6	Stat6_4	GGAAAGGACGAAACACCGCATCAGACAAACTTCAAGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			CATCAGACAAACTCTCAAG	
321	Tbx21	Tbx21_1	GGAAAGGACGAAACACCGAGTCTGGGTGGACATATAAGGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			AGTCTGGGTGGACATATAAG	
322	Tbx21	Tbx21_2	GGAAAGGACGAAACACCGAGGACTACGCATTGCCCGGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			AGGACTACGCATTGCCCGCG	
323	Tbx21	Tbx21_3	GGAAAGGACGAAACACCGGACCCGACCCGCTGCGCGCTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			GACCCGACCGATCGCCGCGC	
324	Tbx21	Tbx21_4	GGAAAGGACGAAACACCGGCTTCCAACAATGTGACCCGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			GGCTTCCAACAATGTGACCC	
325	Cd8a	Cd8a_1	GGAAAGGACGAAACACCGTGGGTGAGTGCATTACTCTGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			TGGGTGAGTGCATTATCTCTG	
326	Cd8a	Cd8a_2	GGAAAGGACGAAACACCGATCCCAACAAGATAACGTGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			ATCCCAACAAGATAAAGCT	
327	Cd8a	Cd8a_3	GGAAAGGACGAAACACCGTGTGGGGTCCGTTTCGCAAGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			GTGTTGGGGTCCGTTCCGA	
328	Cd8a	Cd8a_4	GGAAAGGACGAAACACCGGGACCCGAACCTTGGTGCAGATTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			GGACGCCGAACCTTGGTCAGA	
329	Cd19	Cd19_1	GGAAAGGACGAAACACCGGAATGACTGACCCGCCAGGGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			GAATGACTGACCCGCCAGG	
330	Cd19	Cd19_2	GGAAAGGACGAAACACCGAATGTCTCAGACCATATGGGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			AATGTCTCAGACCATATGGG	
331	Cd19	Cd19_3	GGAAAGGACGAAACACCGGGACCTATTATGTCTCCGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			GGCACCTATTATGTCTCCG	
332	Cd19	Cd19_4	GGAAAGGACGAAACACCGTTTTAGCCACACATACAGCTGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			TTTAGCCACACATACAGCT	
333	Myh1	Myh1_1	GGAAAGGACGAAACACCGGTGCCAGTGTATAACGCAGGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			GCTGCCAGTGTATAACGCAG	
334	Myh1	Myh1_2	GGAAAGGACGAAACACCGTGACCTCGCTAGTAACTGGGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			TGACCTCGCTAGTAACTAGG	
335	Myh1	Myh1_3	GGAAAGGACGAAACACCGAGTTGGCCAGCTTAAACCGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			AGTTGGCCAGCTTAAACC	
336	Myh1	Myh1_4	GGAAAGGACGAAACACCGTAAACATGACTTACATCTGGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			TAAACATGACTTACATCTG	
337	Rag1	Rag1_1	GGAAAGGACGAAACACCGACACCAAAGCAGAGTCTGAGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			ACACCAAAGCAGAGTCTGATG	
338	Rag1	Rag1_2	GGAAAGGACGAAACACCGTGAACAGTTCACACAGATGGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			TGAAACGATTCACACAGATG	
339	Rag1	Rag1_3	GGAAAGGACGAAACACCGTCCCGCAGATTGCAATGGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			TCCCGCAGATTGCAATG	
340	Rag1	Rag1_4	GGAAAGGACGAAACACCGTGGGAAGTAGACCTGCTGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			TGGGAAGTAGACCTGACTGT	
341	Rag2	Rag2_1	GGAAAGGACGAAACACCGCATCAATATATCATTACGGGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			CATCAATATATCATTACCGG	
342	Rag2	Rag2_2	GGAAAGGACGAAACACCGATTGACGTGTTATAGTCGGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			ATTGACGTGTTATAGTCG	
343	Rag2	Rag2_3	GGAAAGGACGAAACACCGTAACTTGTATAGAATAAGAGGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			TAACCTGTATAGAATAAGAG	
344	Rag2	Rag2_4	GGAAAGGACGAAACACCGCATACCAGGAGACAATAAGCGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			CATACCAGGAGACAATAAGC	
345	Alb	Alb_1	GGAAAGGACGAAACACCGACAAGAGTGAGATCGCCATGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			ACAAGAGTGAGATCGCCAT	
346	Alb	Alb_2	GGAAAGGACGAAACACCGTACTCACTGTCCCATAAAGGGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			TACTCACTGTCCCATAAAGG	
347	Alb	Alb_3	GGAAAGGACGAAACACCGTCCCGCATGTACGGCACAGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			TCCCGCATGTACGGCACAG	
348	Alb	Alb_4	GGAAAGGACGAAACACCGGCTCCACCTCACTAAGACAGGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			GCTCCACCTCACTAAGACAG	
349	Cd4	Cd4_1	GGAAAGGACGAAACACCGTCAAAACGATCAAACTGCGAGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			TCAAAACGATCAAACTGCGA	
350	Cd4	Cd4_2	GGAAAGGACGAAACACCGTATCACGGCCTAAGAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			TATCACGGCCTAAGAGTGG	
351	Cd4	Cd4_3	GGAAAGGACGAAACACCGACTCACCTCAAGATACCCCGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			ACTCACCTCAAGATACCCCG	
352	Cd4	Cd4_4	GGAAAGGACGAAACACCGTCTCTGGAAGTCTCGAGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			TTCTCTGGAAGTCTCGCA	
353	Thy1	Thy1_1	GGAAAGGACGAAACACCGCCTTGGTGTATTCTCATGGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			CTTGGTGTATTCTCATGG	
354	Thy1	Thy1_2	GGAAAGGACGAAACACCGTAAGGACCTTGATATAGGGCGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			TAAGGACCTTGATATAGGGC	
355	Thy1	Thy1_3	GGAAAGGACGAAACACCGCAGTCTGACAGGTGCCGAGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			CAGTCTGACAGTGTCCCGA	
356	Thy1	Thy1_4	GGAAAGGACGAAACACCGCGTGTGCTCGGGTATCCCAAGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			CGTGTGCTCGGGTATCCCAA	
357	NTC	NTC_1	GGAAAGGACGAAACACCGAAAAGTCCGCGATTACGCTCGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			AAAAGTCCGCGATTACGTC	
358	NTC	NTC_2	GGAAAGGACGAAACACCGAAAACGGCTCGATCGGTGATTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			AAAACGGCTCGATCGGTGAT	
359	NTC	NTC_3	GGAAAGGACGAAACACCGAAAACGTAATTATACCGAGCGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			AAAACGTAATTATACCGAGC	
360	NTC	NTC_4	GGAAAGGACGAAACACCGAAAATTGACCTTCCCGCCGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			AAAATTGACCTTCCCGCC	
361	NTC	NTC_5	GGAAAGGACGAAACACCGAAACCCCGCGGGAGCGTCTTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			AAACCCCGCGGGAGCGTC	
362	NTC	NTC_6	GGAAAGGACGAAACACCGAAAACCTAGCCTAGATTGCGCGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			AAACCTAGCCTAGATTCCGGC	
363	NTC	NTC_7	GGAAAGGACGAAACACCGAAAACGAGGCTTTCGTACACGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			AAACGAGGCTTTCGTACAC	
364	NTC	NTC_8	GGAAAGGACGAAACACCGAAACTCATACGTAGCGAATCGTTTTAGAGCTAGAAATAGCAAGTTAAATAAG	73			AAACTCATACGTAGCGAATC	

Name	Oligo Sequence
Ar_1	GGAAAGGACGAAACACCGGGTGGAAAGTAATAGTCGATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Ar_2	GGAAAGGACGAAACACCGACCAGGATACCACACTTCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Ar_3	GGAAAGGACGAAACACCGGACTTGGGTAGTCTACATGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Ar_4	GGAAAGGACGAAACACCGGCTCCTGGGAGGTCCACCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Esr1_1	GGAAAGGACGAAACACCGGCATACGGAAAGACCGCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Esr1_2	GGAAAGGACGAAACACCGCACTGTGTTCAACTACCCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Esr1_3	GGAAAGGACGAAACACCGTATTGAGAATAGATCATGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Esr1_4	GGAAAGGACGAAACACCGAGAGGCATAGTCATTGCACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Esr2_1	GGAAAGGACGAAACACCGTGGCGCTTGGACTAGTAACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Esr2_2	GGAAAGGACGAAACACCGTTCGTGACGGCTCTCTACATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Esr2_3	GGAAAGGACGAAACACCGGAAGTAGGAATGGTCAAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Esr2_4	GGAAAGGACGAAACACCGCGCTCACTAGCACATTGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Esr1a_1	GGAAAGGACGAAACACCGCTACGGTGTGGCATCCTGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Esr1a_2	GGAAAGGACGAAACACCGCAGCGGGGAGGTGTCCATCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Esr1a_3	GGAAAGGACGAAACACCGTGTACTTCTGCCGTCGCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Esr1a_4	GGAAAGGACGAAACACCGCGACACCAGAGCGTTCCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Esr1g_1	GGAAAGGACGAAACACCGTGGCGCTCGGAAGACCCACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Esr1g_2	GGAAAGGACGAAACACCGGTCTGGGGATCCTCTACGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Esr1g_3	GGAAAGGACGAAACACCGCAAGTCACAGAGTGTGGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Esr1g_4	GGAAAGGACGAAACACCGTGTGTGGCGACATCGCCTCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Hnf4a_1	GGAAAGGACGAAACACCGCAATGACTACATCGTCCCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Hnf4a_2	GGAAAGGACGAAACACCGAATGTGCAGGTGTTGACCATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Hnf4a_3	GGAAAGGACGAAACACCGAGCGGGACCGGATCAGCACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Hnf4a_4	GGAAAGGACGAAACACCGGGCTCCGTAGTGTGGCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Hnf4g_1	GGAAAGGACGAAACACCGTACAAGAAGAAGTACCTACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Hnf4g_2	GGAAAGGACGAAACACCGTGTGCGGTGAATAACATAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Hnf4g_3	GGAAAGGACGAAACACCGTCCAGCATGGGCTCTCAAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Hnf4g_4	GGAAAGGACGAAACACCGGCATGTTCTTAATCTTCACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Nr0b1_1	GGAAAGGACGAAACACCGGCAACTCAAGCATGAGTAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Nr0b1_2	GGAAAGGACGAAACACCGCAGGGTCTTCAACAGGCCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Nr0b1_3	GGAAAGGACGAAACACCGGCTTGGTGAGCATAGAGTAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Nr0b1_4	GGAAAGGACGAAACACCGCTTACCAGCACACATAGCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Nr0b2_1	GGAAAGGACGAAACACCGACTTAAGAAGATCCTGCTAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Nr0b2_2	GGAAAGGACGAAACACCGGGATGCTGTGACCTTCGAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Nr0b2_3	GGAAAGGACGAAACACCGTGCCTCATGAGGATCAGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Nr0b2_4	GGAAAGGACGAAACACCGAGAAGTGCATACAGAATAGTGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Nr1d1_1	GGAAAGGACGAAACACCGTTGCGATTGATGCGAACGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Nr1d1_2	GGAAAGGACGAAACACCGGAGTAGGTGAGGTCTCTAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Nr1d1_3	GGAAAGGACGAAACACCGCACACAGCTGACACCACCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Nr1d1_4	GGAAAGGACGAAACACCGTCTGGGGCCGAATATACGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Nr1h2_1	GGAAAGGACGAAACACCGTTCCTTAATAGTGGGTGACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Nr1h2_2	GGAAAGGACGAAACACCGCACCGAGCTAGCCATCATCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Nr1h2_3	GGAAAGGACGAAACACCGCGGCGCAGTGTGGTCCACGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Nr1h2_4	GGAAAGGACGAAACACCGCTCCGACCAGCCAAAGTCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Nr1h3_1	GGAAAGGACGAAACACCGAAAGCAACCCAGTTGACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Nr1h3_2	GGAAAGGACGAAACACCGCAAGTACCGTGACGCGCAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC

Name	Oligo Sequence
Nr1h3_3	GGAAAGGACGAAACACCGAATCTCCTGCACGGACACGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Nr1h3_4	GGAAAGGACGAAACACCGTTCGCCGCGAGTGTCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Nr1h4_1	GGAAAGGACGAAACACCGAAACGGGACATTGTTGTATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Nr1h4_2	GGAAAGGACGAAACACCGTGATGGACATGTACATGCGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Nr1h4_3	GGAAAGGACGAAACACCGTGTGACAAAGAAGCCGCGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Nr1h4_4	GGAAAGGACGAAACACCGAGTGTAAATCTAAACGGCTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Nr1i2_1	GGAAAGGACGAAACACCGTTCAACACGATGTTTCGACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Nr1i2_2	GGAAAGGACGAAACACCGTGTAGGTTGACACATCGGCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Nr1i2_3	GGAAAGGACGAAACACCGTGGCCTTGTCACATACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Nr1i2_4	GGAAAGGACGAAACACCGTGATCTCGCAGGTTCCCTTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Nr1i3_1	GGAAAGGACGAAACACCGTGCATGAACAGATAGGCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Nr1i3_2	GGAAAGGACGAAACACCGGGCGAGCCAGACAGGCACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Nr1i3_3	GGAAAGGACGAAACACCGAAACGGACAGATGGGACCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Nr1i3_4	GGAAAGGACGAAACACCGACACAGGTCCCTAACCATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Nr2c1_1	GGAAAGGACGAAACACCGGTGCAGAGCTTACGCAATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Nr2c1_2	GGAAAGGACGAAACACCGACAGTCTTGCTTCATCCCGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Nr2c1_3	GGAAAGGACGAAACACCGTTTATTCTGGCAAACCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Nr2c1_4	GGAAAGGACGAAACACCGACGTGCGACTCGCTCAGCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Nr2c2_1	GGAAAGGACGAAACACCGGATCCAGATAGTCCCGCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Nr2c2_2	GGAAAGGACGAAACACCGAGGGACAAGGTTGTCCGAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Nr2c2_3	GGAAAGGACGAAACACCGGTACCATCCTCACGTATCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Nr2c2_4	GGAAAGGACGAAACACCGTGGAGGTGAAGCACTATCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Nr2e1_1	GGAAAGGACGAAACACCGCACTTCGTAGAGATACATTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Nr2e1_2	GGAAAGGACGAAACACCGAGGACCCCGCTCGTGCTGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Nr2e1_3	GGAAAGGACGAAACACCGAGTGTAGCATCAACCGAAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Nr2e1_4	GGAAAGGACGAAACACCGTTCTGTGTGTCTGTCTACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Nr2e3_1	GGAAAGGACGAAACACCGTGACCCCGATCAGAACCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Nr2e3_2	GGAAAGGACGAAACACCGCAGTTTAGCACAAGTTTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Nr2e3_3	GGAAAGGACGAAACACCGGCCTCCAAGAAGGAGTCTCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Nr2e3_4	GGAAAGGACGAAACACCGTCTTCTTGAGCCATACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Nr2f1_1	GGAAAGGACGAAACACCGCCAGTATGCACTCACAACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Nr2f1_2	GGAAAGGACGAAACACCGGGCTGCCATAACGCGACGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Nr2f1_3	GGAAAGGACGAAACACCGCGAGCTGTTCTGTGCTCAACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Nr2f1_4	GGAAAGGACGAAACACCGGATGTTGCGGGCCACTCGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Nr2f2_1	GGAAAGGACGAAACACCGGCAGTTTGCCTGACCAACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Nr2f2_2	GGAAAGGACGAAACACCGCTACGGCCAGTTCACGTGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Nr2f2_3	GGAAAGGACGAAACACCGGGCGCTGAAGAGCATCCGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Nr2f2_4	GGAAAGGACGAAACACCGTCAAAAAGTGCCTCAAAGTGTTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Nr2f6_1	GGAAAGGACGAAACACCGGAGCTACCCACGCGCGACCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Nr2f6_2	GGAAAGGACGAAACACCGGCATGCGCTCCCCGGTCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Nr2f6_3	GGAAAGGACGAAACACCGCGGGCGACGAGGAGCGTCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Nr2f6_4	GGAAAGGACGAAACACCGCATCGACAACGTGTGCGAGTGTTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Nr3c1_1	GGAAAGGACGAAACACCGCATTATGGGGTGCTGACGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Nr3c1_2	GGAAAGGACGAAACACCGAGCTTGCTGGCAATAAACCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Nr3c1_3	GGAAAGGACGAAACACCGAAAGCCGTTTCACTGTCCATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Nr3c1_4	GGAAAGGACGAAACACCGAAACTGGAATAGGTGCCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC

Name	Oligo Sequence
Nr3c2_1	GGAAAGGACGAAACACCGGATGATTGGGCTCTTAACGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Nr3c2_2	GGAAAGGACGAAACACCGCAAGGAACTTTCAGCCACGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Nr3c2_3	GGAAAGGACGAAACACCGTCCACTAATGCATTGACAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Nr3c2_4	GGAAAGGACGAAACACCGAATGGAAATGGGTTGACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Nr4a1_1	GGAAAGGACGAAACACCGGAAGTGTCCAGGTTCCGGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Nr4a1_2	GGAAAGGACGAAACACCGTGCTTCGTGTCCAGCACTATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Nr4a1_3	GGAAAGGACGAAACACCGGGCAAACAAGGATTGCCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Nr4a1_4	GGAAAGGACGAAACACCGGCCTTCATAAGTCTGGCTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Nr4a2_1	GGAAAGGACGAAACACCGTGTCAAGCAACTGCGATGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Nr4a2_2	GGAAAGGACGAAACACCGTGCCGATTGGAATCGACGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Nr4a2_3	GGAAAGGACGAAACACCGAGTACTGACAACGATTTCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Nr4a2_4	GGAAAGGACGAAACACCGTAGTAAACCGACCCGCTGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Nr4a3_1	GGAAAGGACGAAACACCGGCATTTCATCATAACAGATCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Nr4a3_2	GGAAAGGACGAAACACCGACCAAGCTGACCATGGACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Nr4a3_3	GGAAAGGACGAAACACCGCGGCCGTGGGGTTCATAGCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Nr4a3_4	GGAAAGGACGAAACACCGAGTGTCCGGATGGTTAAGGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Nr5a1_1	GGAAAGGACGAAACACCGTGAGACCGGACCACCGATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Nr5a1_2	GGAAAGGACGAAACACCGGTGCGTGCTGATCGAATGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Nr5a1_3	GGAAAGGACGAAACACCGCGCACGTGAGCAGCCCGTAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Nr5a1_4	GGAAAGGACGAAACACCGCCATTGTGCGACTGGGCACGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Nr5a2_1	GGAAAGGACGAAACACCGTGTGTGGCGATAAAGTGTCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Nr5a2_2	GGAAAGGACGAAACACCGGTAAGAGCCGACCGCATGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Nr5a2_3	GGAAAGGACGAAACACCGTCGCCACTCCCCAAACGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Nr5a2_4	GGAAAGGACGAAACACCGCTTCTGTACATAGTCTGTCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Nr6a1_1	GGAAAGGACGAAACACCGCCTTACCCACCGTTGCGCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Nr6a1_2	GGAAAGGACGAAACACCGCATAGTGCAAGCCCGTAGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Nr6a1_3	GGAAAGGACGAAACACCGCCAGAATAGCTAAAAAGGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Nr6a1_4	GGAAAGGACGAAACACCGCACCTATGTTGATTGAAGATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Pgr_1	GGAAAGGACGAAACACCGCTCTGGCCGACTCATGAGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Pgr_2	GGAAAGGACGAAACACCGAGGAGGAGTCGCAGCCAACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Pgr_3	GGAAAGGACGAAACACCGGGCGGAACGAACCCTGCGTGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Pgr_4	GGAAAGGACGAAACACCGCAGTCTGGGAAGTCACCGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Ppara_1	GGAAAGGACGAAACACCGCATCGAGTGTGCAATATGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Ppara_2	GGAAAGGACGAAACACCGGATTTCTCAGTCCATCGGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Ppara_3	GGAAAGGACGAAACACCGTCTGTCCGGATGTCACACAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Ppara_4	GGAAAGGACGAAACACCGCTGCTGCCAGTGCATGTCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Ppard_1	GGAAAGGACGAAACACCGCCTCCGGCATCCGTCCAAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Ppard_2	GGAAAGGACGAAACACCGGGCCTCGGGCTTCCACTACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Ppard_3	GGAAAGGACGAAACACCGTCCAGTATGAGAAGTGCAGTGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Ppard_4	GGAAAGGACGAAACACCGCCTCAAGTATGGCGTGACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Pparg_1	GGAAAGGACGAAACACCGAATGCTGGAGAAATCAACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Pparg_2	GGAAAGGACGAAACACCGAGAACCTTCTAACTCCCTCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Pparg_3	GGAAAGGACGAAACACCGGCACCTTGAAAAATTCGGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Pparg_4	GGAAAGGACGAAACACCGCTGCCTATGAGCACTTCACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Rara_1	GGAAAGGACGAAACACCGGAGCTACACGCTGACGCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Rara_2	GGAAAGGACGAAACACCGATCATCCGGCTACCACTATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC

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Rara_3	GGAAAGGACGAAACACCGAGATTCTGCGAATCTGCACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Rara_4	GGAAAGGACGAAACACCGCAAGTGCATCATTAAGACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Rarb_1	GGAAAGGACGAAACACCGAAGCAGGGCTTGTACACCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Rarb_2	GGAAAGGACGAAACACCGCCAAGTCCAATCGGACCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Rarb_3	GGAAAGGACGAAACACCGACCGCATACTGCTCAATGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Rarb_4	GGAAAGGACGAAACACCGTGACGCAGTTCCTATCTCGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Rarg_1	GGAAAGGACGAAACACCGTGGGCAAGTACACCACGGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Rarg_2	GGAAAGGACGAAACACCGAAGCATGGCTTATAGACCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Rarg_3	GGAAAGGACGAAACACCGGCTACAAAAGTGTTCGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Rarg_4	GGAAAGGACGAAACACCGACACTATGACATTCTCGGATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Rora_1	GGAAAGGACGAAACACCGTTGGCTGAGATGTTGTAGGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Rora_2	GGAAAGGACGAAACACCGCATTGATGTCCAATCCCGACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Rora_3	GGAAAGGACGAAACACCGGAGAGACAGCTTGTACGCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Rora_4	GGAAAGGACGAAACACCGAGCTATGCGAGCTCCAGCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Rorb_1	GGAAAGGACGAAACACCGCACCACGTACTGGATAGCATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Rorb_2	GGAAAGGACGAAACACCGGGAGACATGTCAGTACACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Rorb_3	GGAAAGGACGAAACACCGTCCCAGCTGTAAAGTTCGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Rorb_4	GGAAAGGACGAAACACCGACAAGTTGGGTACAGATGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Rorc_1	GGAAAGGACGAAACACCGCTTGAGTATAGTCCAGAACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Rorc_2	GGAAAGGACGAAACACCGTCTGCGGATCCACTACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Rorc_3	GGAAAGGACGAAACACCGTCTGGGGCACTGCAGAACTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Rorc_4	GGAAAGGACGAAACACCGGACAAGCAGAGGCCTCGGGTTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Rxra_1	GGAAAGGACGAAACACCGCAAGACTGAGACATACGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Rxra_2	GGAAAGGACGAAACACCGAGGACGCCATTGAGGCCTAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Rxra_3	GGAAAGGACGAAACACCGCATGGGCCCGCACTCCATGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Rxra_4	GGAAAGGACGAAACACCGGGGGCAGCTCAGAAAAGTGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Rxrb_1	GGAAAGGACGAAACACCGATTGTGGGGTCGCGTCCCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Rxrb_2	GGAAAGGACGAAACACCGGCTGTTCACACTCGTTGAGTGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Rxrb_3	GGAAAGGACGAAACACCGTTCCAGGAGGAGCGTCAACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Rxrb_4	GGAAAGGACGAAACACCGTCCACAGTGTGCTCCCTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Rxrg_1	GGAAAGGACGAAACACCGTAGCCACGAAGACATGCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Rxrg_2	GGAAAGGACGAAACACCGTGCGTTTGGCCCACTCAACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Rxrg_3	GGAAAGGACGAAACACCGTCTGAACAGGGAAGCACTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Rxrg_4	GGAAAGGACGAAACACCGCACAGCACTCAGCGTCCGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Thra_1	GGAAAGGACGAAACACCGACAGCGGTAGTGATAACCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Thra_2	GGAAAGGACGAAACACCGTGTCACTCTCAGGGTCTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Thra_3	GGAAAGGACGAAACACCGTCTAGATGATTCGAAGCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Thra_4	GGAAAGGACGAAACACCGAAAACACTGCCATGTTCTCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Thrb_1	GGAAAGGACGAAACACCGAAGACAGTCCGGCTCTCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Thrb_2	GGAAAGGACGAAACACCGCCCATCGTGAATGCCCCAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Thrb_3	GGAAAGGACGAAACACCGCATCTTTGTCTAAATAGCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Thrb_4	GGAAAGGACGAAACACCGCAGGTTCCAGGGTAACTACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Vdr_1	GGAAAGGACGAAACACCGTGGAGATTGCCGCATCACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Vdr_2	GGAAAGGACGAAACACCGAGCGTTGAAGTGAAGCCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Vdr_3	GGAAAGGACGAAACACCGTCTTCATTGAGTCCATCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Vdr_4	GGAAAGGACGAAACACCGTTCGTGCAGACGTAAGTACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC

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Ncoa1_1	GGAAAGGACGAAACACCGTTGACTGAGGGATTTATTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Ncoa1_2	GGAAAGGACGAAACACCGGATGCTAATTCACCCTCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Ncoa1_3	GGAAAGGACGAAACACCGACCACTAGTAATGCCAACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Ncoa1_4	GGAAAGGACGAAACACCGAGTTTGGACAACCAGGAGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Ncoa2_1	GGAAAGGACGAAACACCGAGTGCATAGTTACTACCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Ncoa2_2	GGAAAGGACGAAACACCGGGGAGGATTCATATTAACCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Ncoa2_3	GGAAAGGACGAAACACCGAGTCAGATGTGTCTCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Ncoa2_4	GGAAAGGACGAAACACCGCTTTGCAAAGTGATGTCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Ncoa3_1	GGAAAGGACGAAACACCGCAAGGAGAAACGATACACGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Ncoa3_2	GGAAAGGACGAAACACCGTCTCCTCCATATAACCGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Ncoa3_3	GGAAAGGACGAAACACCGAGAACATCATGATTTCCCCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Ncoa3_4	GGAAAGGACGAAACACCGACGTGCTCCTCCGACGACCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Ncoa4_1	GGAAAGGACGAAACACCGCGTCTGCTGATTGTTGCGCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Ncoa4_2	GGAAAGGACGAAACACCGTTCAAGAAGTCAGCATCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Ncoa4_3	GGAAAGGACGAAACACCGGGTCTTAAGGGATCCAAATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Ncoa4_4	GGAAAGGACGAAACACCGAATTAAGATAATTTACGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Ncoa5_1	GGAAAGGACGAAACACCGGGTGATGACTATTGCCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Ncoa5_2	GGAAAGGACGAAACACCGGTAGAGAGGAGCTTTATCGTGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Ncoa5_3	GGAAAGGACGAAACACCGTCTGCGGTCGCAATCCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Ncoa5_4	GGAAAGGACGAAACACCGTAACAGATACCTCACTGCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Ncoa6_1	GGAAAGGACGAAACACCGTGAACCATAGGATCCGACCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Ncoa6_2	GGAAAGGACGAAACACCGGCTGTTATGACGCCCCAGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Ncoa6_3	GGAAAGGACGAAACACCGCAATGACTACAAATCAAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Ncoa6_4	GGAAAGGACGAAACACCGTGTGCCCACTTGTTACACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Ncoa7_1	GGAAAGGACGAAACACCGAGGCCTTAAAACCCATCGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Ncoa7_2	GGAAAGGACGAAACACCGAGTTCAACGTTACAGCAGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Ncoa7_3	GGAAAGGACGAAACACCGGTACTCTGGGTAAAAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Ncoa7_4	GGAAAGGACGAAACACCGTAAGGGATCGGACTTATGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Ppargc1b_1	GGAAAGGACGAAACACCGAGGGCTTGCTAACATCACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Ppargc1b_2	GGAAAGGACGAAACACCGTGGACGAGCTTCACTGGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Ppargc1b_3	GGAAAGGACGAAACACCGGCCTTGACTACTGTCTGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Ppargc1b_4	GGAAAGGACGAAACACCGTCTGTGCTAGGGAGTCTTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Ppargc1a_1	GGAAAGGACGAAACACCGAATGAGGCAAACCTTGCTAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Ppargc1a_2	GGAAAGGACGAAACACCGTATTGAGCGAACCTTAAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Ppargc1a_3	GGAAAGGACGAAACACCGTTGCATGCGCACCTTAACAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Ppargc1a_4	GGAAAGGACGAAACACCGAAGACCAGTGAACCTAAGGGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Scand1_1	GGAAAGGACGAAACACCGAGCGCTGGCGAAAGGTCTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Scand1_2	GGAAAGGACGAAACACCGTTCGCTACCAGGACGCGGCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Scand1_3	GGAAAGGACGAAACACCGGCTCCCGGAATCGGGCGACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Scand1_4	GGAAAGGACGAAACACCGCGCGCCCGCAGCTTTGAACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Ncor1_1	GGAAAGGACGAAACACCGGGCTTACGGAAACCCCGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Ncor1_2	GGAAAGGACGAAACACCGGGCCTAGCAAACCTACCCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Ncor1_3	GGAAAGGACGAAACACCGATATGCCGAGCATTACCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Ncor1_4	GGAAAGGACGAAACACCGCCCTACCAAAGCCGACTCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Ncor2_1	GGAAAGGACGAAACACCGCCATCTCGACTGTCCAAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Ncor2_2	GGAAAGGACGAAACACCGGCATAGAGAACAATCCGCGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC

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Ncor2_3	GGAAAGGACGAAACACCGGCTACCACACCCTCGTGAGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Ncor2_4	GGAAAGGACGAAACACCGTACCGACTGAGCCCCACGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Ahr_1	GGAAAGGACGAAACACCGAGCTGTGCACAAGAGGATCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Ahr_2	GGAAAGGACGAAACACCGGTATAATAGACTGCTGCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Ahr_3	GGAAAGGACGAAACACCGTCTCCGGTAGCAAACATGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Ahr_4	GGAAAGGACGAAACACCGGTGGAAAGAATCCTTACTTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Abcb1a_1	GGAAAGGACGAAACACCGACTGAATGCTCCAATTAACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Abcb1a_2	GGAAAGGACGAAACACCGCAGGAAGCTTAGTACCAAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Abcb1a_3	GGAAAGGACGAAACACCGCAAAGATCAGCATCATAAGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Abcb1a_4	GGAAAGGACGAAACACCGAATGACGTCAGCATTACGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Abcb1b_1	GGAAAGGACGAAACACCGAGCCTTTGCAAACGCACGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Abcb1b_2	GGAAAGGACGAAACACCGTGATGCTTCTAGTGTTAAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Abcb1b_3	GGAAAGGACGAAACACCGTCATCTCTTGAAAAACCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Abcb1b_4	GGAAAGGACGAAACACCGCAGATGACAATCCAATAAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Asb2_1	GGAAAGGACGAAACACCGGGAGACAGACTCGTGAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Asb2_2	GGAAAGGACGAAACACCGCAGTGCATCAGCCCTCTACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Asb2_3	GGAAAGGACGAAACACCGCGAGCGCGCCCGCCTCTACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Asb2_4	GGAAAGGACGAAACACCGCCTCCAAGAAGGGCAACTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Bcl11b_1	GGAAAGGACGAAACACCGTGTGCAAATGTAGCTGGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Bcl11b_2	GGAAAGGACGAAACACCGCTGAGAGCCCGTCTGCTGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Bcl11b_3	GGAAAGGACGAAACACCGGCGGGAAGTTCATCTGACACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Bcl11b_4	GGAAAGGACGAAACACCGCAGAGGTGAAGTAATCACGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Tfr3_1	GGAAAGGACGAAACACCGCTACACGCTTACAATAGCCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Tfr3_2	GGAAAGGACGAAACACCGGAATACATACACTCCTCGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Tfr3_3	GGAAAGGACGAAACACCGGGCTCCTACTACAACATAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Tfr3_4	GGAAAGGACGAAACACCGAACCCCTCGGGAGACTCCACTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Eomes_1	GGAAAGGACGAAACACCGCCATACGCCGGAACCTCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Eomes_2	GGAAAGGACGAAACACCGGCTGTCCATGGAGTAGCGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Eomes_3	GGAAAGGACGAAACACCGCACCCAGAATCTCCTAACACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Eomes_4	GGAAAGGACGAAACACCGTTCACGAAAACATTGTAGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Foxp3_1	GGAAAGGACGAAACACCGCATACTGATGCATGAAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Foxp3_2	GGAAAGGACGAAACACCGTCTACCCACAGGGATCAATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Foxp3_3	GGAAAGGACGAAACACCGAGGTCGGGACCTGCGAAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Foxp3_4	GGAAAGGACGAAACACCGGCAAGAGCTCTTGTCCATTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Gata3_1	GGAAAGGACGAAACACCGCTACTACGGAAACTCCGTCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Gata3_2	GGAAAGGACGAAACACCGCCGGTTTCGGATGTAAGTTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Gata3_3	GGAAAGGACGAAACACCGGCAGCTGCACCTGATACTTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Gata3_4	GGAAAGGACGAAACACCGTCCAAGACGTCCATCCACCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Il10_1	GGAAAGGACGAAACACCGGCTAACCGACTCCTAATGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Il10_2	GGAAAGGACGAAACACCGAACTGCACCCACTTCCCAGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Il10_3	GGAAAGGACGAAACACCGAAGGAGCATTGAATTCCCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Il10_4	GGAAAGGACGAAACACCGACTGGCATGAGGATCAGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Il17a_1	GGAAAGGACGAAACACCGCTCAGCGTGTCCAAACACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Il17a_2	GGAAAGGACGAAACACCGGAACGGTTGAGGTAGTCTGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Il17a_3	GGAAAGGACGAAACACCGCTTACGTACTGGAGAGTCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Il17a_4	GGAAAGGACGAAACACCGCTGAGCTTCCCAGATCACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC

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Lcor_1	GGAAAGGACGAAACACCGACAGCACTTAATCTTATCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Lcor_2	GGAAAGGACGAAACACCGATCTGCAGAGATCGAGCCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Lcor_3	GGAAAGGACGAAACACCGGATACCACAAGTTTCGAGGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Lcor_4	GGAAAGGACGAAACACCGTCCATCCAATTAGGCGACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Maf_1	GGAAAGGACGAAACACCGGTGGCTTCGATGGCTATGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Maf_2	GGAAAGGACGAAACACCGGACCGCATCATCAGCCAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Maf_3	GGAAAGGACGAAACACCGGTGTCGCGGTGATCGCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Maf_4	GGAAAGGACGAAACACCGACCACCACCACCACGCCGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Med1_1	GGAAAGGACGAAACACCGCCAACCAACACCTTCCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Med1_2	GGAAAGGACGAAACACCGAGGTGTATCCAGCGCGTCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Med1_3	GGAAAGGACGAAACACCGTAACTTACCCCACTCCGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Med1_4	GGAAAGGACGAAACACCGGTGAGCTGTAACCTCTACAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Prdm1_1	GGAAAGGACGAAACACCGTTGGAATAATGCCGTACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Prdm1_2	GGAAAGGACGAAACACCGGATAGGATAAACCACCCGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Prdm1_3	GGAAAGGACGAAACACCGGTGTAGACTTCACCGATGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Prdm1_4	GGAAAGGACGAAACACCGTTGTACCACGTGTTCTGACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Smad4_1	GGAAAGGACGAAACACCGTGAATCCATATCACTATGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Smad4_2	GGAAAGGACGAAACACCGGTGGCGTTAGACTCTGCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Smad4_3	GGAAAGGACGAAACACCGTGTACCATAACAGAGAACATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Smad4_4	GGAAAGGACGAAACACCGCAAAGCGATCTCCTCCCGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Stat1_1	GGAAAGGACGAAACACCGGATAGACGCCAGCCACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Stat1_2	GGAAAGGACGAAACACCGTGTGATGTTAGATAAACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Stat1_3	GGAAAGGACGAAACACCGTAAATGACGAGCTCGTGGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Stat1_4	GGAAAGGACGAAACACCGGAAAAGCAAGCGTAATCTCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Stat3_1	GGAAAGGACGAAACACCGCCAACAAATTAAGAACTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Stat3_2	GGAAAGGACGAAACACCGCTGCTTCTCTGCTACTACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Stat3_3	GGAAAGGACGAAACACCGTTTTACCACGAAAGTCAGGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Stat3_4	GGAAAGGACGAAACACCGCAAAGAGTCACATGCCACGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Stat4_1	GGAAAGGACGAAACACCGAATGTCTAAACTCCACTGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Stat4_2	GGAAAGGACGAAACACCGGCATGCCAACGCACCTCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Stat4_3	GGAAAGGACGAAACACCGAAATCCAATGCATGTAGCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Stat4_4	GGAAAGGACGAAACACCGTGGCCTCACCATTAACCTAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Stat5a_1	GGAAAGGACGAAACACCGCATGGACGATAACGACCACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Stat5a_2	GGAAAGGACGAAACACCGTTCGTTGTACAGAATGTGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Stat5a_3	GGAAAGGACGAAACACCGAGTGGATCGAGAGCCAGCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Stat5a_4	GGAAAGGACGAAACACCGGTGGCGCTGAGCGTGCCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Stat5b_1	GGAAAGGACGAAACACCGCTGATTCGCAGTGATTACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Stat5b_2	GGAAAGGACGAAACACCGTACAGCGAACCAGCTCCATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Stat5b_3	GGAAAGGACGAAACACCGGGCGTTGTCCAGAGGACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Stat5b_4	GGAAAGGACGAAACACCGAGTGGATCGAAAGCCAAGCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Stat6_1	GGAAAGGACGAAACACCGATAAAGCGCTGTGAGCGGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Stat6_2	GGAAAGGACGAAACACCGGCTGAAAGGCCTCCCACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Stat6_3	GGAAAGGACGAAACACCGAGAAAGCATCTGAACCGACCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Stat6_4	GGAAAGGACGAAACACCGCATCAGACAAATACTTCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Tbx21_1	GGAAAGGACGAAACACCGAGTCTGGGTGGACATATAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Tbx21_2	GGAAAGGACGAAACACCGAGGACTACGCATTGCCCGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC

Name	Oligo Sequence
Tbx21_3	GGAAAGGACGAAACACCGGACCCGACCGATCGCCGCGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Tbx21_4	GGAAAGGACGAAACACCGGGCTTCCAACAATGTGACCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Cd8a_1	GGAAAGGACGAAACACCGTGGGTGAGTCGATTATCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Cd8a_2	GGAAAGGACGAAACACCGATCCCACAACAAGATAACGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Cd8a_3	GGAAAGGACGAAACACCGGTGTTGGGGTCCGTTTCGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Cd8a_4	GGAAAGGACGAAACACCGGGACGCCGAACCTGGTCAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Cd19_1	GGAAAGGACGAAACACCGAATGACTGACCCCGCCAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Cd19_2	GGAAAGGACGAAACACCGAATGTCTCAGACCATATGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Cd19_3	GGAAAGGACGAAACACCGGGCACCTATTATTGTCTCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Cd19_4	GGAAAGGACGAAACACCGTTTAGCCACACATACAGCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Myh1_1	GGAAAGGACGAAACACCGGCTGCCAGTGATAACGCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Myh1_2	GGAAAGGACGAAACACCGTGACCTCGCTAGTAACATGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Myh1_3	GGAAAGGACGAAACACCGAGTTGGCCAGCTTATAACCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Myh1_4	GGAAAGGACGAAACACCGTAAAACATGACTTACATCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Rag1_1	GGAAAGGACGAAACACCGACACCAAAGCAGAGTCGTAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Rag1_2	GGAAAGGACGAAACACCGTGAACGATTCCCACAGATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Rag1_3	GGAAAGGACGAAACACCGTCCCGCACAAGATTGCAATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Rag1_4	GGAAAGGACGAAACACCGTGGGAAGTAGACCTGACTGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Rag2_1	GGAAAGGACGAAACACCGCATCAATATATCATTACGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Rag2_2	GGAAAGGACGAAACACCGATTGACGTGGTGTATAGTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Rag2_3	GGAAAGGACGAAACACCGTAACTTGTATAGAATAAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Rag2_4	GGAAAGGACGAAACACCGCATACCAGGAGACAATAAGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Alb_1	GGAAAGGACGAAACACCGACAAGAGTGAGATCGCCATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Alb_2	GGAAAGGACGAAACACCGTACTCACTGTCCCATAAAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Alb_3	GGAAAGGACGAAACACCGTCCCGCATGCTACGGCACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Alb_4	GGAAAGGACGAAACACCGGCTCCACCTACTAAGACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Cd4_1	GGAAAGGACGAAACACCGTCAAACGATCAAACCTGCGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Cd4_2	GGAAAGGACGAAACACCGTATCACGGCCTATAAGAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Cd4_3	GGAAAGGACGAAACACCGACTCACCTCAAGATACCCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Cd4_4	GGAAAGGACGAAACACCGTCTTCTGGGAACCTCTCGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Thy1_1	GGAAAGGACGAAACACCGCCTTGTTGTTATTCTCATGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Thy1_2	GGAAAGGACGAAACACCGTAAGGACCTTGATATAGGGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Thy1_3	GGAAAGGACGAAACACCGCAGTCTTGCAAGGTGTCGGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
Thy1_4	GGAAAGGACGAAACACCGCGTGTGCTCGGGTATCCCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
NTC_1	GGAAAGGACGAAACACCGAAAAAGTCCGCGATTACGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
NTC_2	GGAAAGGACGAAACACCGAAAAACGGCTCGATCGGTGATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
NTC_3	GGAAAGGACGAAACACCGAAAAACGTAATTATACCGAGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
NTC_4	GGAAAGGACGAAACACCGAAAAATTGCACCTTCCCGGCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
NTC_5	GGAAAGGACGAAACACCGAAACCCCGCGCGGAGCGTCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
NTC_6	GGAAAGGACGAAACACCGAAACCTAGCGTAGATTGCGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
NTC_7	GGAAAGGACGAAACACCGAAACGAGGCTGTTGTTACACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC
NTC_8	GGAAAGGACGAAACACCGAAACTCATACGTAGCGAATCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC