Table S1: Seesaw domain level sequences. Here and elsewhere all sequences start from the 5' end.

c	= CA		t	= TCT	
c*	= TG		t*	= AGA	
S1	= CATCCATTCCACTCA	S2	= CAAAACAAAACCTCA	S3	= CACCCTAAAATCTCA
S1*	= TGAGTGGAATGGATG	S2*	= TGAGGTTTTGTTTTG	S3*	= TGAGATTTTAGGGTG
S4	= CACATAACAACCACA	S5	= CACCACCAAACTTCA	S6	= CATAACACAATCACA
S4*	= TGTGGTTGTTATGTG	S5*	= TGAAGTTTGGTGGTG	S6*	= TGTGATTGTGTTATG
S7	= CAACATATCAATTCA	S8	= CACTAACATACAACA	S9	= CACCATCAAATAACA
S7*	= TGAATTGATATGTTG	S8*	= TGTTGTATGTTAGTG	S9*	= TGTTATTTGATGGTG
S10	= CATACAACATCTACA	S11	= CAATATCCATAACCA	S12	= CATCAATCAACACCA
S10*	= TGTAGATGTTGTATG	S11*	= TGGTTATGGATATTG	S12*	= TGGTGTTGATTGATG
S13	= CACAACTCATTACCA	S14	= CATTATTCAAACCCA	S15	= CACACTATAATTCCA
S13*	= TGGTAATGAGTTGTG	S14*	= TGGGTTTGAATAATG	S15*	= TGGAATTATAGTGTG
S16	= CACTTCATAAATCCA	S17	= CAACTCCTAATATCA	S18	= CATCTTCTAACATCA
S16*	= TGGATTTATGAAGTG	S17*	= TGATATTAGGAGTTG	S18*	= TGATGTTAGAAGATG
S19	= CACCTCTTAAACACA	S20	= CAATCTAACACTCCA	S21	= CAACCATACTAAACA
S19*	= TGTGTTTAAGAGGTG	S20*	= TGGAGTGTTAGATTG	S21*	= TGTTTAGTATGGTTG
S22	= CATTCCTACATTTCA	S23	= CAAATCTTCATCCCA	S24	= CACTCATCCTTTACA
S22*	= TGAAATGTAGGAATG	S23*	= TGGGATGAAGATTTG	S24*	= TGTAAAGGATGAGTG
S25	= CAATTCACTCAATCA	S26	= CATTCATTACCTCCA	S27	= CAAACACTCTATTCA
S25*	= TGATTGAGTGAATTG	S26*	= TGGAGGTAATGAATG	S27*	= TGAATAGAGTGTTTG
S28	= CATCTACAATTCACA	S29	= CACCAATACTCCTCA	S30	= CACCATTACAATCCA
S28*	= TGTGAATTGTAGATG	S29*	= TGAGGAGTATTGGTG	S30*	= TGGATTGTAATGGTG
S31	= CAATCCACACTTCCA	S32	= CACACTTCAAACTCA	S33	= CAACTCAAACATACA
S31*	= TGGAAGTGTGGATTG	S32*	= TGAGTTTGAAGTGTG	S33*	= TGTATGTTTGAGTTG
S34	= CACATAACAAAACCA	S35	= CACTCTCCATCACCA	S36	= CAAACTAAACAACCA
S34*	= TGGTTTTGTTATGTG	S35*	= TGGTGATGGAGAGTG	S36*	= TGGTTGTTTAGTTTG
S37	= CACCTCTTCCCTTCA	S38	= CATACCCTTTTCTCA	S39	= CACTATACACACCCA
S37*	= TGAAGGGAAGAGGTG	S38*	= TGAGAAAAGGGTATG	S39*	= TGGGTGTGTATAGTG
S40	= CAATACAAATCCACA	S41	= CAACAAACCATTACA	S42	= CACTTTTCACTATCA
S40*	= TGTGGATTTGTATTG	S41*	= TGTAATGGTTTGTTG	S42*	= TGATAGTGAAAAGTG
S43	= CATCATACCTACTCA	S44	= CAAAACTCTCTCTCA	S45	= CACCCAAAACCCACA
S43*	= TGAGTAGGTATGATG	S44*	= TGAGAGAGAGTTTTG	S45*	= TGTGGGTTTTGGGTG
S46	= CAAACCCAACTCACA	S47	= CATTCTCCCACCTCA	S48	= CATCACCACTATACA
S46*	= TGTGAGTTGGGTTTG	S47*	= TGAGGTGGGAGAATG	S48*	= TGTATAGTGGTGATG
S49	= CATCCTTAACTCCCA	S50	= CATTACCAACCACCA	S51	= CACAAACTACATCCA
S49*	= TGGGAGTTAAGGATG	S50*	= TGGTGGTTGGTAATG	S51*	= TGGATGTAGTTTGTG
S52	= CACTTCACAACTACA	S53	= CATATCTAATCTCCA	Sf	= CATTTTTTTTTTTCA
S52*	= TGTAGTTGTGAAGTG	S53*	= TGGAGATTAGATATG		

Table S2: Seesaw small circuit sequences (part one). Shading indicates which strands were used in which circuits. P indicates PAGE purification by IDT, used only for input strands. H indicates HPLC purification by IDT, used only for reporter strand with fluorophores or quenchers. All other strands were ordered without any purification. See Fig. S16 for details of the clamp design that modifies the toehold T implementation.

		Circuit number	1	2	3	4	5	6	7	8	9
$w_{5,6}$	= S6 T S5	= CATAACACAATCACA TCT CACCACCAAACTTCA									
G_5-b	= T* S5* T*	= TG AGA TGAAGTTTGGTGGTG AGA TG									
$w_{5,7}$	= S7 T S5	= CAACATATCAATTCA TCT CACCACCAAACTTCA									
$Th_{2,5:5}$-t	= S5	= CACCACCAAACTTCA									
$Th_{2,5:5}$-b	= s2* T* S5*	= TGTTTTG AGA TGAAGTTTGGTGGTG									
$w_{2,5}$	= S5 T S2	= CACCACCAAACTTCA TCT CAAAACAAAACCTCA	P	P							
G_2-b	= T* S2* T*	= TG AGA TGAGGTTTTGTTTTG AGA TG									
$w_{1,2}$	= S2 T S1	= CAAAACAAAACCTCA TCT CATCCATTCCACTCA				P					
G_1-b	= T* S1* T*	= TG AGA TGAGTGGAATGGATG AGA TG									
$w_{1,10}$	= S10 T S1	= CATACAACATCTACA TCT CATCCATTCCACTCA									
$Th_{4,1:1}$-t	= S1	= CATCCATTCCACTCA									
$Th_{4,1:1}$-b	= s4* T* S1*	= TTATGTG AGA TGAGTGGAATGGATG									
$w_{4,1}$	= S1 T S4	= CATCCATTCCACTCA TCT CACATAACAACCACA									
G_4-b	= T* S4* T*	= TG AGA TGTGGTTGTTATGTG AGA TG									
$w_{3,2}$	= S2 T S3	= CAAAACAAAACCTCA TCT CACCCTAAAATCTCA			P	P	P	P			
G_3-b	= T* S3* T*	= TG AGA TGAGATTTTAGGGTG AGA TG									
$w_{3,11}$	= S11 T S3	= CAATATCCATAACCA TCT CACCCTAAAATCTCA									
$Th_{12,3:3}$-t	= S3	= CACCCTAAAATCTCA									
$Th_{12,3:3}$-b	= s12* T* S3*	= ATTGATG AGA TGAGATTTTAGGGTG									
$w_{12,3}$	= S3 T S12	= CACCCTAAAATCTCA TCT CATCAATCAACACCA									
G_{12}-b	= T* S12* T*	= TG AGA TGGTGTTGATTGATG AGA TG									
$w_{8,4}$	= S4 T S8	= CACATAACAACCACA TCT CACTAACATACAACA					P				
G_8-b	= T* S8* T*	= TG AGA TGTTGTATGTTAGTG AGA TG									
$w_{8,15}$	= S15 T S8	= CACACTATAATTCCA TCT CACTAACATACAACA									
$Th_{16,8:8}$-t	= S8	= CACTAACATACAACA									
$Th_{16,8:8}$-b	= s16* T* S8*	= TGAAGTG AGA TGTTGTATGTTAGTG									
$w_{16,8}$	= S8 T S16	= CACTAACATACAACA TCT CACTTCATAAATCCA									
G_{16}-b	= T* S16* T*	= TG AGA TGGATTTATGAAGTG AGA TG									
$w_{17,16}$	= S16 T S17	= CACTTCATAAATCCA TCT CAACTCCTAATATCA							P		
G_{17}-b	= T* S17* T*	= TG AGA TGATATTAGGAGTTG AGA TG									
$w_{17,19}$	= S19 T S17	= CACCTCTTAAACACA TCT CAACTCCTAATATCA									
$Th_{20,17:17}$-t	= S17	= CAACTCCTAATATCA									
$Th_{20,17:17}$-b	= s20* T* S17*	= TAGATTG AGA TGATATTAGGAGTTG									
$w_{20,17}$	= S17 T S20	= CAACTCCTAATATCA TCT CAATCTAACACTCCA									
G_{20}-b	= T* S20* T*	= TG AGA TGGAGTGTTAGATTG AGA TG									

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Table S3: Seesaw small circuit sequences (part two). Shading indicates which strands were used in which circuits. P indicates PAGE purification by IDT, used only for input strands. H indicates HPLC purification by IDT, used only for reporter strand with fluorophores or quenchers. All other strands were ordered without any purification. See Fig. S16 for details of the clamp design that modifies the toehold T implementation.

		Circuit number	1	2	3	4	5	6	7	8	9
$w_{21,20}$	= S20 T S21	= CAATCTAACACTCCA TCT CAACCATACTAAACA						P	P	P	P
$w_{22,20}$	= S20 T S22	= CAATCTAACACTCCA TCT CATTCCTACATTTCA						P	P	P	
$w_{18,16}$	= S16 T S18	= CACTTCATAAATCCA TCT CATCTTCTAACATCA					P	P	P	P	P
$w_{9,4}$	= S4 T S9	= CACATAACAACCACA TCT CACCATCAAATAACA			P	P	P	P	P	P	P
$w_{13,12}$	= S12 T S13	= CATCAATCAACACCA TCT CACAACTCATTACCA							P	P	P
$w_{14,12}$	= S12 T S14	= CATCAATCAACACCA TCT CATTATTCAAACCCA							P	P	P
$w_{8,2}$	= S2 T S8	= CAAAACAAAACCTCA TCT CACTAACATACAACA									
$w_{17,2}$	= S2 T S17	= CAAAACAAAACCTCA TCT CAACTCCTAATATCA									
$w_{23,4}$	= S4 T S23	= CACATAACAACCACA TCT CAAATCTTCATCCCA							P		
$w_{24,16}$	= S16 T S24	= CACTTCATAAATCCA TCT CACTCATCCTTTACA							P		
$w_{3,4}$	= S4 T S3	= CACATAACAACCACA TCT CACCCTAAAATCTCA									
$w_{3,16}$	= S16 T S3	= CACTTCATAAATCCA TCT CACCCTAAAATCTCA									
$w_{3,20}$	= S20 T S3	= CAATCTAACACTCCA TCT CACCCTAAAATCTCA									
$w_{1,23}$	= S23 T S1	= CAAATCTTCATCCCA TCT CATCCATTCCACTCA									
$w_{8,24}$	= S24 T S8	= CACTCATCCTTTACA TCT CACTAACATACAACA									
$w_{17,25}$	= S25 T S17	= CAATTCACTCAATCA TCT CAACTCCTAATATCA									
$w_{22,2}$	= S2 T S22	= CAAAACAAAACCTCA TCT CATTCCTACATTTCA									P
Rep$_6$-t	= RQ S6	= /5IAbRQ/ CATAACACAATCACA	H	H	H	H	H	H	H	H	H
Rep$_6$-b	= T* S6* ROX	= TG AGA TGTGATTGTGTTATG /3ROXN/	H	H	H	H	H	H	H	H	H
Rep$_{23}$-t	= FQ S23	= /5IAbFQ/ CAAATCTTCATCCCA									H
Rep$_{23}$-b	= T* S23* FAM	= TG AGA TGGGATGAAGATTTG /36-FAM/									H
Rep$_{24}$-t	= RQ S24	= /5IAbRQ/ CACTCATCCTTTACA									H
Rep$_{24}$-b	= T* S24* TYE563	= TG AGA TGTAAAGGATGAGTG /3TYE563/									H
Rep$_{25}$-t	= RQ S25	= /5IAbRQ/ CAATTCACTCAATCA									H
Rep$_{25}$-b	= T* S25* TYE665	= TG AGA TGATTGAGTGAATTG /3TYE665/									H

Table S4: Seesaw square root circuit sequences (part one).

Gate strands (IDT unpurified)		
$w_{1,23}$	= S23 T S1	= CAAATCTTCATCCCA TCT CATCCATTCCACTCA
$w_{1,f}$	= Sf T S1	= CATTTTTTTTTTTCA TCT CATCCATTCCACTCA
G_1-b	= T* S1* T*	= TG AGA TGAGTGGAATGGATG AGA TG
$Th_{10,1:1}$-t	= S1	= CATCCATTCCACTCA
$Th_{10,1:1}$-b	= s10* T* S1*	= TTGTATG AGA TGAGTGGAATGGATG
$w_{10,1}$	= S1 T S10	= CATCCATTCCACTCA TCT CATACAACATCTACA
G_{10}-b	= T* S10* T*	= TG AGA TGTAGATGTTGTATG AGA TG
$w_{5,6}$	= S6 T S5	= CATAACACAATCACA TCT CACCACCAAACTTCA
$w_{5,f}$	= Sf T S5	= CATTTTTTTTTTTCA TCT CACCACCAAACTTCA
G_5-b	= T* S5* T*	= TG AGA TGAAGTTTGGTGGTG AGA TG
$Th_{53,5:5}$-t	= S5	= CACCACCAAACTTCA
$Th_{53,5:5}$-b	= s53* T* S5*	= AGATATG AGA TGAAGTTTGGTGGTG
$w_{53,5}$	= S5 T S53	= CACCACCAAACTTCA TCT CATATCTAATCTCCA
G_{53}-b	= T* S53* T*	= TG AGA TGGAGATTAGATATG AGA TG
$w_{8,25}$	= S25 T S8	= CAATTCACTCAATCA TCT CACTAACATACAACA
$w_{8,f}$	= Sf T S8	= CATTTTTTTTTTTCA TCT CACTAACATACAACA
G_8-b	= T* S8* T*	= TG AGA TGTTGTATGTTAGTG AGA TG
$Th_{20,8:8}$-t	= S8	= CACTAACATACAACA
$Th_{20,8:8}$-b	= s20* T* S8*	= TAGATTG AGA TGTTGTATGTTAGTG
$w_{20,8}$	= S8 T S20	= CACTAACATACAACA TCT CAATCTAACACTCCA
G_{20}-b	= T* S20* T*	= TG AGA TGGAGTGTTAGATTG AGA TG
$w_{13,24}$	= S24 T S13	= CACTCATCCTTTACA TCT CACAACTCATTACCA
$w_{13,f}$	= Sf T S13	= CATTTTTTTTTTTCA TCT CACAACTCATTACCA
G_{13}-b	= T* S13* T*	= TG AGA TGGTAATGAGTTGTG AGA TG
$Th_{26,13:13}$-t	= S13	= CACAACTCATTACCA
$Th_{26,13:13}$-b	= s26* T* S13*	= ATGAATG AGA TGGTAATGAGTTGTG
$w_{26,13}$	= S13 T S26	= CACAACTCATTACCA TCT CATTCATTACCTCCA
G_{26}-b	= T* S26* T*	= TG AGA TGGAGGTAATGAATG AGA TG
$w_{18,53}$	= S53 T S18	= CATATCTAATCTCCA TCT CATCTTCTAACATCA
$w_{18,f}$	= Sf T S18	= CATTTTTTTTTTTCA TCT CATCTTCTAACATCA
G_{18}-b	= T* S18* T*	= TG AGA TGATGTTAGAAGATG AGA TG
$Th_{34,18:18}$-t	= S18	= CATCTTCTAACATCA
$Th_{34,18:18}$-b	= s34* T* S18*	= TTATGTG AGA TGATGTTAGAAGATG
$w_{34,18}$	= S18 T S34	= CATCTTCTAACATCA TCT CACATAACAAAACCA
G_{34}-b	= T* S34* T*	= TG AGA TGGTTTTGTTATGTG AGA TG

Table S5: Seesaw square root circuit sequences (part two).

$w_{21,10}$	= S10 T S21	= CATACAACATCTACA TCT CAACCATACTAAACA
$w_{21,f}$	= Sf T S21	= CATTTTTTTTTTTCA TCT CAACCATACTAAACA
G_{21}-b	= T* S21* T*	= TG AGA TGTTTAGTATGGTTG AGA TG
$Th_{36,21:21}$-t	= S21	= CAACCATACTAAACA
$Th_{36,21:21}$-b	= s36* T* S21*	= TAGTTTG AGA TGTTTAGTATGGTTG
$w_{36,21}$	= S21 T S36	= CAACCATACTAAACA TCT CAAACTAAACAACCA
G_{36}-b	= T* S36* T*	= TG AGA TGGTTGTTTAGTTTG AGA TG
$w_{22,53}$	= S53 T S22	= CATATCTAATCTCCA TCT CATTCCTACATTTCA
$w_{22,f}$	= Sf T S22	= CATTTTTTTTTTTCA TCT CATTCCTACATTTCA
G_{22}-b	= T* S22* T*	= TG AGA TGAAATGTAGGAATG AGA TG
$Th_{39,22:22}$-t	= S22	= CATTCCTACATTTCA
$Th_{39,22:22}$-b	= s39* T* S22*	= TATAGTG AGA TGAAATGTAGGAATG
$w_{39,22}$	= S22 T S39	= CATTCCTACATTTCA TCT CACTATACACACCCA
G_{39}-b	= T* S39* T*	= TG AGA TGGGTGTGTATAGTG AGA TG
$w_{27,10}$	= S10 T S27	= CATACAACATCTACA TCT CAAACACTCTATTCA
$w_{27,f}$	= Sf T S27	= CATTTTTTTTTTTCA TCT CAAACACTCTATTCA
G_{27}-b	= T* S27* T*	= TG AGA TGAATAGAGTGTTTG AGA TG
$Th_{40,27:27}$-t	= S27	= CAAACACTCTATTCA
$Th_{40,27:27}$-b	= s40* T* S27*	= TGTATTG AGA TGAATAGAGTGTTTG
$w_{40,27}$	= S27 T S40	= CAAACACTCTATTCA TCT CAATACAAATCCACA
G_{40}-b	= T* S40* T*	= TG AGA TGTGGATTTGTATTG AGA TG
$w_{28,34}$	= S34 T S28	= CACATAACAAAACCA TCT CATCTACAATTCACA
$w_{28,40}$	= S40 T S28	= CAATACAAATCCACA TCT CATCTACAATTCACA
$w_{28,f}$	= Sf T S28	= CATTTTTTTTTTTCA TCT CATCTACAATTCACA
G_{28}-b	= T* S28* T*	= TG AGA TGTGAATTGTAGATG AGA TG
$Th_{41,28:28}$-t	= S28	= CATCTACAATTCACA
$Th_{41,28:28}$-b	= s41* T* S28*	= TTTGTTG AGA TGTGAATTGTAGATG
$w_{41,28}$	= S28 T S41	= CATCTACAATTCACA TCT CAACAAACCATTACA
G_{41}-b	= T* S41* T*	= TG AGA TGTAATGGTTTGTTG AGA TG
$w_{29,36}$	= S36 T S29	= CAAACTAAACAACCA TCT CACCAATACTCCTCA
$w_{29,39}$	= S39 T S29	= CACTATACACACCCA TCT CACCAATACTCCTCA
$w_{29,f}$	= Sf T S29	= CATTTTTTTTTTTCA TCT CACCAATACTCCTCA
G_{29}-b	= T* S29* T*	= TG AGA TGAGGAGTATTGGTG AGA TG
$Th_{42,29:29}$-t	= S29	= CACCAATACTCCTCA
$Th_{42,29:29}$-b	= s42* T* S29*	= AAAAGTG AGA TGAGGAGTATTGGTG
$w_{42,29}$	= S29 T S42	= CACCAATACTCCTCA TCT CACTTTTCACTATCA
G_{42}-b	= T* S42* T*	= TG AGA TGATAGTGAAAAGTG AGA TG

Table S6: Seesaw square root circuit sequences (part three).

$w_{30,40}$	= S40 T S30	= CAATACAAATCCACA TCT CACCATTACAATCCA
$w_{30,f}$	= Sf T S30	= CATTTTTTTTTTTCA TCT CACCATTACAATCCA
G_{30}-b	= T* S30* T*	= TG AGA TGGATTGTAATGGTG AGA TG
$Th_{43,30:30}$-t	= S30	= CACCATTACAATCCA
$Th_{43,30:30}$-b	= s43* T* S30*	= TATGATG AGA TGGATTGTAATGGTG
$w_{43,30}$	= S30 T S43	= CACCATTACAATCCA TCT CATCATACCTACTCA
G_{43}-b	= T* S43* T*	= TG AGA TGAGTAGGTATGATG AGA TG
$w_{31,39}$	= S39 T S31	= CACTATACACACCCA TCT CAATCCACACTTCCA
$w_{31,f}$	= Sf T S31	= CATTTTTTTTTTTCA TCT CAATCCACACTTCCA
G_{31}-b	= T* S31* T*	= TG AGA TGGAAGTGTGGATTG AGA TG
$Th_{44,31:31}$-t	= S31	= CAATCCACACTTCCA
$Th_{44,31:31}$-b	= s44* T* S31*	= AGTTTTG AGA TGGAAGTGTGGATTG
$w_{44,31}$	= S31 T S44	= CAATCCACACTTCCA TCT CAAAACTCTCTCTCA
G_{44}-b	= T* S44* T*	= TG AGA TGAGAGAGAGTTTTG AGA TG
$w_{33,34}$	= S34 T S33	= CACATAACAAAACCA TCT CAACTCAAACATACA
$w_{33,43}$	= S43 T S33	= CATCATACCTACTCA TCT CAACTCAAACATACA
$w_{33,26}$	= S26 T S33	= CATTCATTACCTCCA TCT CAACTCAAACATACA
$w_{33,f}$	= Sf T S33	= CATTTTTTTTTTTCA TCT CAACTCAAACATACA
G_{33}-b	= T* S33* T*	= TG AGA TGTATGTTTGAGTTG AGA TG
$Th_{49,33:33}$-t	= S33	= CAACTCAAACATACA
$Th_{49,33:33}$-b	= s49* T* S33*	= AAGGATG AGA TGTATGTTTGAGTTG
$w_{35,36}$	= S36 T S35	= CAAACTAAACAACCA TCT CACTCTCCATCACCA
$w_{35,44}$	= S44 T S35	= CAAAACTCTCTCTCA TCT CACTCTCCATCACCA
$w_{35,20}$	= S20 T S35	= CAATCTAACACTCCA TCT CACTCTCCATCACCA
$w_{35,f}$	= Sf T S35	= CATTTTTTTTTTTCA TCT CACTCTCCATCACCA
G_{35}-b	= T* S35* T*	= TG AGA TGGTGATGGAGAGTG AGA TG
$Th_{50,35:35}$-t	= S35	= CACTCTCCATCACCA
$Th_{50,35:35}$-b	= s50* T* S35*	= GGTAATG AGA TGGTGATGGAGAGTG
$w_{37,34}$	= S34 T S37	= CACATAACAAAACCA TCT CACCTCTTCCCTTCA
$w_{37,44}$	= S44 T S37	= CAAAACTCTCTCTCA TCT CACCTCTTCCCTTCA
$w_{37,26}$	= S26 T S37	= CATTCATTACCTCCA TCT CACCTCTTCCCTTCA
$w_{37,f}$	= Sf T S37	= CATTTTTTTTTTTCA TCT CACCTCTTCCCTTCA
G_{37}-b	= T* S37* T*	= TG AGA TGAAGGGAAGAGGTG AGA TG
$Th_{51,37:37}$-t	= S37	= CACCTCTTCCCTTCA
$Th_{51,37:37}$-b	= s51* T* S37*	= GTTTGTG AGA TGAAGGGAAGAGGTG

Table S7: Seesaw square root circuit sequences (part four).

$w_{38,36}$	= S36 T S38	= CAAACTAAACAACCA TCT CATACCCTTTTCTCA
$w_{38,43}$	= S43 T S38	= CATCATACCTACTCA TCT CATACCCTTTTCTCA
$w_{38,20}$	= S20 T S38	= CAATCTAACACTCCA TCT CATACCCTTTTCTCA
$w_{38,f}$	= Sf T S38	= CATTTTTTTTTTTCA TCT CATACCCTTTTCTCA
G_{38}-b	= T* S38* T*	= TG AGA TGAGAAAGGGTATG AGA TG
$Th_{52,38:38}$-t	= S38	= CATACCCTTTTCTCA
$Th_{52,38:38}$-b	= s52* T* S38*	= TGAAGTG AGA TGAGAAAGGGTATG
Reporter strands (IDT HPLC purified)		
Rep_6-t	= RQ S6	= /5IAbRQ/ CATAACACAATCACA
Rep_6-b	= T* S6* ROX	= TG AGA TGTGATTGTGTTATG /3ROXN/
Rep_{23}-t	= FQ S23	= /5IAbFQ/ CAAATCTTCATCCCA
Rep_{23}-b	= T* S23* FAM	= TG AGA TGGGATGAAGATTTG /36-FAM/
Rep_{24}-t	= RQ S24	= /5IAbRQ/ CACTCATCCTTTACA
Rep_{24}-b	= T* S24* TYE563	= TG AGA TGTAAAGGATGAGTG /3TYE563/
Rep_{25}-t	= RQ S25	= /5IAbRQ/ CAATTCACTCAATCA
Rep_{25}-b	= T* S25* TYE665	= TG AGA TGATTGAGTGAATTG /3TYE665/
Input strands (IDT PAGE purified)		
$x_1^0 : w_{45,42}$	= S42 T S45	= CACTTTTCACTATCA TCT CACCCAAAACCCACA
$x_1^1 : w_{46,41}$	= S41 T S46	= CAACAAACCATTACA TCT CAAACCCAACTCACA
$x_2^0 : w_{47,42}$	= S42 T S47	= CACTTTTCACTATCA TCT CATTCTCCCACCTCA
$x_2^1 : w_{48,41}$	= S41 T S48	= CAACAAACCATTACA TCT CATCACCACTATACA
$x_3^0 : w_{49,33}$	= S33 T S49	= CAACTCAAACATACA TCT CATCCTTAACTCCCA
$x_3^1 : w_{50,35}$	= S35 T S50	= CACTCTCCATCACCA TCT CATTACCAACCACCA
$x_4^0 : w_{51,37}$	= S37 T S51	= CACCTCTTCCCTTCA TCT CACAAACTACATCCA
$x_4^1 : w_{52,38}$	= S38 T S52	= CATACCCTTTTCTCA TCT CACTTCACAACTACA
Internal fan-out strands for readout (IDT unpurified)		
$w_{21,32}$	= S32 T S21	= CACACTTCAAACTCA TCT CAACCATACTAAACA
$w_{28,32}$	= S32 T S28	= CACACTTCAAACTCA TCT CATCTACAATTCACA
$w_{31,32}$	= S32 T S32	= CACACTTCAAACTCA TCT CAATCCACACTTCCA
Internal readout reporter strands (IDT HPLC purified)		
Rep_{32}-t	= RQ S32	= /5IAbRQ/ CACACTTCAAACTCA
Rep_{32}-b	= T* S32* Cy5.5	= TG AGA TGAGTTTGAAGTGTG /3Cy55Sp/

Table S8: Seesaw sequences without clamps.

Domain level sequences						
T	= CTCT	T*	= AGAG			
S1	= CATCCATTCCACTAT	S2	= CCAAACAAAACCTAT	S3	= CACCCTAAAATCTAT	
S1*	= ATAGTGGAATGGATG	S2*	= ATAGGTTTTGTTTGG			
S4	= AACAAAACAACCACT	S5	= AACCACCAAACTTAT	S6	= CCTAACACAATCACT	
S4*	= AGTGGTTGTTTTGTT	S5*	= ATAAGTTTGGTGGTT	S6*	= AGTGATTGTGTTAGG	
S7	= CCACAAAACAAAACT	S8	= CCCAAATAAACAACT	S9	= CACCATCAAATAACT	
S10	= TCAAAACCAACTACT					

Gate strands (IDT unpurified)		
$w_{5,6}$	= S6 T S5	= CCTAACACAATCACT CTCT AACCACCAAACTTAT
G_5-b	= T* S5* T*	= AGAG ATAAGTTTGGTGGTT AGAG
$w_{5,7}$	= S7 T S5	= CCACAAAACAAAACT CTCT AACCACCAAACTTAT
$Th_{2,5:5}$-t	= S5	= AACCACCAAACTTAT
$Th_{2,5:5}$-b	= s2* T* S5*	= TTTGG AGAG ATAAGTTTGGTGGTT
$w_{2,5}$	= S5 T S2	= AACCACCAAACTTAT CTCT CCAAACAAAACCTAT
G_2-b	= T* S2* T*	= AGAG ATAGGTTTTGTTTGG AGAG
$w_{1,2}$	= S2 T S1	= CCAAACAAAACCTAT CTCT CATCCATTCCACTAT
G_1-b	= T* S1* T*	= AGAG ATAGTGGAATGGATG AGAG
$w_{1,10}$	= S10 T S1	= TCAAAACCAACTACT CTCT CATCCATTCCACTAT
$Th_{4,1:1}$-t	= S1	= CATCCATTCCACTAT
$Th_{4,1:1}$-b	= s4* T* S1*	= TTGTT AGAG ATAGTGGAATGGATG
$w_{4,1}$	= S1 T S4	= CATCCATTCCACTAT CTCT AACAAAACAACCACT
G_4-b	= T* S4* T*	= AGAG AGTGGTTGTTTTGTT AGAG

Reporter strands (IDT HPLC purified)		
$Rep_{5,6}$-t	= RQ S6 T	= /5IAbRQ/ CCTAACACAATCACT CTCT
$Rep_{5,6}$-b	= s5* T* S6* ROX	= TGGTT AGAG AGTGATTGTGTTAGG/3ROXN/

Input strands (IDT PAGE purified)		
$w_{3,2}$	= S2 T S3	= CCAAACAAAACCTAT CTCT CACCCTAAAATCTAT
$w_{8,4}$	= S4 T S8	= AACAAAACAACCACT CTCT CCCAAATAAACAACT
$w_{9,4}$	= S4 T S9	= AACAAAACAACCACT CTCT CACCATCAAATAACT

Table S9: Seesaw hairpin sequences.

Domain level sequences						
T	= TGAGG	T*	= CCTCA			
S1	= TAGTTGGAAGAGGGC	S3	= GATGTAAGTATTTGC	S4	= AGTATGTAGTGTGGC	
S1*	= GCCCTCTTCCAACTA	S3*	= GCAAATACTTACATC	S4*	= GCCACACTACATACT	
S2	= GGATTAGGGGGTAGC					

Excised hairpin sequences with restriction enzyme recognition sites	
EH-HgaI	= NNNNNNNNNNGCGTCNTTTTNGACGCNNNNN
EH-MlyI	= NNNNNGACTCNTTTTNGAGTCNNNNN

Gate strands (IDT unpurified)		
G_{3:3,1}-h	= S1 T S3 EH-HgaI T* S3* T*	= TAGTTGGAAGAGGGC TGAGG GATGTAAGTATTTGC TGAGGCGCTGGCGTCGTTTTCGACGCCAGCG CCTCA GCAAATACTTACATC CCTCA
w_{3,2}	= S2 T S3	= GGATTAGGGGGTAGC TGAGG GATGTAAGTATTTGC
Th_{4,3:3}-h	= s4* T* S3* EH-MlyI S3	= ACT CCTCA GCAAATACTTACATC AACCAGACTCGTTTTCGAGTCTGGTT GATGTAAGTATTTGC

Reporter strands (IDT HPLC purified)		
Rep₁-t	= TET S1	= /5TET/ TAGTTGGAAGAGGGC
Rep₁-b	= T* S1* BHQ	= CCTCA GCCCTCTTCCAACTA /3BHQ_1/

Input strands (IDT unpurified)		
w_{4,3}	= S3 T S4	= GATGTAAGTATTTGC TGAGG AGTATGTAGTGTGGC

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