

**Table S1.** Gene profiling of Dicer KO versus Dicer Het T reg cells

Probe set ID	Gene symbol	p-value	Dicer KO vs. Het fold change
1417898_a_at	Gzma	0.018	308.60
1455900_x_at	Tgm2	0.003	125.40
1425324_x_at	Igh-6	0.004	115.60
1425247_a_at	Igh-6	0.005	97.43
1451632_a_at	Igh-6	0.007	72.57
1424800_at	Enah	0.002	55.29
1433428_x_at	Tgm2	0.008	51.17
1424305_at	Igj	0.025	51.08
1460423_x_at	Igh-V7183 /// Igk-V1 /// Igkv1-117 /// Cr1	0.002	49.91
1437277_x_at	Tgm2	0.003	47.47
1417500_a_at	Tgm2	0.007	46.05
1427756_x_at	Igh-6	0.014	40.02
1420394_s_at	Gp49a /// Lilrb4	0.000	37.73
1435436_at	Epas1	0.044	35.27
1449280_at	Esm1 /// LOC632677	0.030	32.08
1453008_at	2300002D11Rik	0.023	31.07
1422280_at	Gzmk	0.007	28.76
1430523_s_at	Igl-V1	0.049	27.12
1451335_at	Plac8	0.009	26.92
1427076_at	Mpeg1 /// LOC671359	0.015	24.80
1442223_at	Enah	0.001	23.91
1436578_at	A330104H05Rik	0.025	22.96
1424254_at	Ifitm1	0.003	19.58
1427870_x_at	Igh-6	0.009	19.41
1439831_at	EG240327	0.003	18.57
1453715_at	Sv2c	0.002	18.34
1423754_at	Ifitm3	0.006	16.79
1428614_at	Ldhd	0.002	15.77
1419060_at	Gzmb	0.001	15.75
1444254_at	Tns4	0.005	15.01
1423909_at	Tmem176a	0.014	12.73
1441428_at	---	0.004	12.13
1425603_at	Tmem176a	0.000	11.83
1417023_a_at	Fabp4	0.022	11.69
1449864_at	Il4	0.024	11.61
1424471_at	Rapgef3	0.005	10.73
1416094_at	Adam9	0.003	10.52
1424801_at	Enah	0.036	10.48
1419647_a_at	Ier3	0.038	10.44
1436912_at	Cacnb4	0.037	10.20
1447285_at	---	0.032	10.15
1417928_at	Pdlim4	0.040	9.61
1452535_at	Igh-6	0.013	9.07
1427038_at	Penk1	0.019	9.02
1417821_at	D17H6S56E-5	0.016	8.58
1453196_a_at	Oasl2	0.015	8.56
1419042_at	Iigp1	0.004	8.22
1450330_at	Il10	0.005	7.99
1435172_at	Eomes	0.024	7.73
1429404_at	2010317E24Rik	0.040	7.66
1422527_at	H2-DMa	0.010	7.66
1434789_at	Depdc1b	0.034	7.64

1448656_at	Cacnb3	0.002	7.62
1420697_at	Slc15a3	0.020	7.33
1433942_at	Myo6	0.044	7.25
1416514_a_at	Fscn1	0.037	7.22
1451798_at	Il1rn	0.000	7.07
1417460_at	Ifitm2	0.008	7.07
1424356_a_at	Metrn1	0.038	6.93
1453683_a_at	Cep55	0.005	6.82
1440400_at	---	0.001	6.79
1418004_a_at	Tmem176b	0.003	6.73
1424470_a_at	Rapgef3	0.011	6.45
1435494_s_at	Dsp	0.025	6.44
1458089_at	Fkbp5	0.019	6.40
1425609_at	Ncf1	0.005	6.28
1451767_at	Ncf1	0.002	6.25
1416576_at	Socs3	0.002	6.22
1421134_at	Areg	0.002	6.08
1437208_at	10-Sep	0.035	6.03
1435354_at	Kcnj15	0.013	6.02
1427509_at	Baiap3	0.007	5.95
1421688_a_at	Ccl1	0.009	5.86
1419043_a_at	Iigp1	0.014	5.83
1456772_at	Ncf1	0.001	5.75
1426774_at	Parp12	0.004	5.74
1417822_at	D17H6S56E-5	0.003	5.73
1441811_x_at	Tmem176a	0.001	5.71
1453851_a_at	Gadd45g	0.008	5.65
1449911_at	Lag3	0.024	5.61
1427962_at	Ccdc102a /// LOC672218	0.028	5.48
1417153_at	Btbd14a	0.000	5.39
1424923_at	Serpina3g	0.038	5.36
1425787_a_at	Syt13	0.006	5.32
1425583_at	Coro2a	0.006	5.07
1427445_a_at	Ttn	0.006	5.06
1453416_at	Gas2l3	0.033	5.05
1451119_a_at	Fbln1	0.024	5.03
1438316_a_at	Ccdc102a /// LOC672218	0.012	5.00
1434427_a_at	Rnf157	0.015	5.00
1423524_at	Mastl	0.032	4.99
1455990_at	Kif23	0.044	4.96
1418403_at	Adam19	0.024	4.94
1435355_at	Neb	0.000	4.92
1435906_x_at	Gbp2	0.002	4.84
1458427_at	Brip1	0.035	4.78
1444443_at	Lcorl	0.011	4.71
1460250_at	Sostdc1	0.022	4.70
1442160_at	7530404M11Rik	0.035	4.67
1439669_at	6430571L13Rik	0.018	4.61
1418240_at	Gbp2	0.001	4.59
1423271_at	Gjb2	0.044	4.59
1430394_a_at	Abcb9	0.006	4.57
1449090_a_at	Yes1	0.025	4.56
1425584_x_at	Coro2a	0.002	4.50
1449361_at	Tbx21	0.006	4.44
1459872_x_at	H2-DMa	0.008	4.40
1416558_at	Melk	0.031	4.36

1424638_at	Cdkn1a	0.003	4.32
1424733_at	P2ry14	0.008	4.31
1437033_a_at	Skp2	0.008	4.30
1434754_at	Garnl4	0.034	4.24
1434557_at	Hip1	0.007	4.23
1422537_a_at	Id2	0.002	4.19
1419212_at	Icosl	0.012	4.18
1418901_at	Cebpb	0.020	4.14
1455104_at	Mxd1	0.012	4.06
1425947_at	Ifng	0.005	4.06
1456495_s_at	Osbp16	0.022	4.04
1428444_at	Asb2	0.028	4.04
1421992_a_at	Igfbp4	0.024	4.04
1429570_at	Mlkl	0.047	4.02
1458589_at	---	0.048	4.01
1417323_at	Psrc1	0.004	4.00
1424704_at	Runx2	0.013	3.98
1423401_at	Etv6	0.008	3.96
1429566_a_at	Hipk2	0.001	3.95
1441799_at	6030422H21Rik	0.006	3.94
1418969_at	Skp2	0.001	3.92
1455899_x_at	Socs3	0.001	3.92
1448231_at	Fkbp5	0.018	3.92
1418402_at	Adam19	0.031	3.91
1429734_at	4632434I11Rik	0.033	3.88
1431358_at	4930547N16Rik	0.030	3.87
1416041_at	Sgk	0.000	3.87
1434298_at	Zfhx1b	0.019	3.85
1455089_at	Gng12	0.005	3.84
1433623_at	Zfp367	0.008	3.82
1421679_a_at	Cdkn1a	0.008	3.81
1449164_at	Cd68	0.034	3.80
1437012_x_at	Rapgef3	0.022	3.80
1455980_a_at	Gas2l3	0.020	3.79
1459903_at	Sema7a	0.004	3.79
1418944_at	Cysltr1	0.008	3.76
1419599_s_at	Ms4a6d	0.030	3.69
1422601_at	Serpinb9	0.004	3.69
1419569_a_at	Isg20	0.018	3.68
1436000_a_at	Skp2	0.010	3.65
1448291_at	Mmp9	0.036	3.63
1454953_at	Rnf157	0.016	3.61
1432478_a_at	Ibrdc3	0.006	3.57
1448472_at	Vars2	0.036	3.56
1440156_s_at	AI851523	0.024	3.56
1428737_s_at	Gramd3	0.010	3.51
1416871_at	Adam8	0.016	3.51
1435773_at	4930547N16Rik	0.029	3.50
1456080_a_at	Serinc3	0.034	3.49
1453600_at	Ccdc18	0.024	3.48
1439347_at	Tns4	0.044	3.46
1441315_s_at	Slc19a2	0.017	3.42
1455983_at	Cdca2	0.039	3.41
1435342_at	Kcnk6	0.003	3.41
1448830_at	Dusp1	0.036	3.40
1438606_a_at	Clic4	0.002	3.39

1435226_at	Ibrdc3	0.009	3.39
1419759_at	Abcb1a	0.047	3.39
1452565_x_at	LOC641050	0.014	3.38
1424727_at	Ccr5	0.042	3.37
1456212_x_at	Socs3	0.003	3.36
1447926_at	Arl5a	0.019	3.35
1418930_at	Cxcl10	0.029	3.33
1422141_s_at	Csprs	0.046	3.33
1448914_a_at	Csf1	0.008	3.32
1460255_at	Tnfsf13b	0.021	3.28
1450424_a_at	Il18bp	0.006	3.27
1436725_at	E130306D19Rik	0.019	3.27
1429778_at	Optn	0.037	3.27
1449293_a_at	Skp2	0.049	3.24
1459840_s_at	Ccdc28b	0.002	3.24
1416263_at	Abcb9	0.006	3.23
1441241_at	9630013D21Rik	0.038	3.23
1451458_at	Tmem2	0.000	3.23
1435444_at	Atf6	0.013	3.22
1454809_at	Ncoa7	0.012	3.22
1459546_s_at	Enpp1	0.009	3.21
1439496_at	4921524J06Rik	0.050	3.21
1452937_s_at	Ccdc28b	0.016	3.21
1452210_at	Dna2l	0.024	3.20
1423326_at	Entpd1	0.035	3.20
1460247_a_at	Skp2	0.004	3.20
1422970_at	Mxd3	0.017	3.19
1428736_at	Gramd3	0.000	3.18
1439221_s_at	Cd40	0.017	3.18
1453129_a_at	Rgs12	0.005	3.17
1436271_at	BC085284 /// LOC666348	0.001	3.16
1434830_at	Mxd1	0.022	3.12
1448847_at	Serinc3	0.011	3.12
1437291_at	2700081O15Rik	0.005	3.11
1448110_at	Sema4a	0.034	3.10
1456145_at	Dleu2	0.018	3.09
1426594_at	Frmd4b	0.022	3.08
1423525_at	Mastl	0.047	3.07
1444524_at	---	0.004	3.07
1420874_at	Twf1	0.002	3.06
1436714_at	Lpp	0.004	3.05
1456951_at	Mybl1	0.006	3.05
1453053_at	2610036L11Rik	0.003	3.05
1415949_at	Cpe	0.011	3.05
1419276_at	Enpp1	0.003	3.04
1423393_at	Clic4	0.005	3.03
1451755_a_at	Apobec1	0.018	3.02
1426343_at	Stt3b	0.037	3.02
1424354_at	Tmem140	0.021	3.01
1449235_at	Fasl	0.009	3.01
1417594_at	Gkap1	0.038	3.01
1417021_a_at	Spo11 /// LOC675982	0.014	3.00
1438307_at	Hmgb2	0.014	2.99
1443626_at	Chn2	0.008	2.97
1443481_at	Tube1	0.044	2.97
1417152_at	Btbd14a	0.012	2.97

1448576_at	Il7r	0.042	2.97
1424895_at	Gpsm2	0.027	2.96
1415694_at	Wars	0.007	2.96
1423847_at	Ncapd2	0.037	2.95
1454736_at	Ankrd57	0.018	2.95
1437514_at	B430306N03Rik	0.003	2.95
1435792_at	Csprs /// EG665338	0.011	2.93
1450028_a_at	Lancl2	0.017	2.93
1434548_at	Serinc3	0.019	2.92
1419168_at	Mapk6	0.006	2.92
1423757_x_at	Igfbp4	0.016	2.91
1455314_at	Lpp	0.001	2.90
1435998_at	Gm288	0.002	2.90
1449551_at	Myo1c	0.040	2.89
1421546_a_at	Racgap1	0.045	2.88
1430802_at	H2-Q8	0.014	2.88
1433605_at	Inpp5a	0.028	2.88
1418203_at	Pmaip1	0.013	2.86
1450117_at	Tcf3	0.033	2.86
1418191_at	Usp18	0.036	2.85
1426063_a_at	Gem	0.020	2.85
1448380_at	Lgals3bp	0.011	2.82
1449578_at	Supt16h	0.033	2.80
1428574_a_at	Chn2	0.007	2.80
1417902_at	Slc19a2	0.004	2.78
1417445_at	Kntc2	0.030	2.78
1449110_at	Rhob	0.021	2.76
1424629_at	Brca1	0.040	2.76
1439790_at	Serpinb9	0.016	2.75
1418448_at	Rras	0.000	2.75
1456245_x_at	Vamp3	0.006	2.74
1428655_at	Ccdc128	0.029	2.74
1428197_at	Tspan9	0.045	2.74
1417101_at	Hspa2	0.049	2.74
1429400_at	Clcn5	0.005	2.74
1417816_s_at	Serinc3	0.024	2.73
1426275_a_at	Uxs1	0.021	2.72
1440363_at	---	0.016	2.71
1450821_at	Pcaf	0.016	2.71
1444484_at	A130009E19Rik	0.039	2.70
1420875_at	Twf1	0.001	2.70
1456545_at	Il18rap	0.017	2.69
1425469_a_at	Coro2a	0.013	2.69
1420660_at	Lrrc6	0.039	2.68
1436678_at	Sgcb	0.006	2.68
1436200_at	Lonrf3	0.004	2.68
1444405_at	E430029J22Rik	0.026	2.67
1442167_at	Cyfip2	0.023	2.67
1425084_at	Gimap7	0.047	2.65
1452011_a_at	Uxs1	0.000	2.65
1449925_at	Cxcr3	0.044	2.65
1457944_at	Etv6	0.042	2.65
1448681_at	Il15ra	0.038	2.65
1435526_at	Tor1aip2	0.002	2.64
1435176_a_at	Id2	0.003	2.63
1443964_at	Tmie	0.007	2.63

1429749_at	9330180L21Rik	0.016	2.61
1421037_at	Npas2	0.049	2.60
1418166_at	Il12rb1	0.017	2.58
1434200_at	BC010981	0.030	2.58
1416016_at	Tap1	0.006	2.58
1416380_at	Mov10	0.023	2.57
1429947_a_at	Zbp1	0.018	2.56
1442454_at	Top2a	0.045	2.56
1438783_at	LOC637870	0.028	2.56
1428336_at	Agpat4	0.004	2.56
1433769_at	Als2cl	0.026	2.55
1422706_at	LOC637870	0.015	2.54
1455448_at	Nt5dc3	0.008	2.54
1433795_at	Tgfbr3	0.036	2.54
1433916_at	Vamp3	0.000	2.53
1422692_at	Sub1	0.023	2.53
1435338_at	Cdk6	0.010	2.52
1448175_at	Ehd1	0.006	2.52
1426818_at	Arrdc4	0.018	2.51
1432202_a_at	Wdr51a	0.030	2.51
1435493_at	Dsp	0.013	2.50
1441164_at	Pip5k2b	0.041	2.50
1427982_s_at	Syne2	0.001	2.50
1430368_s_at	1700019D03Rik	0.041	2.50
1416757_at	Zwilch	0.040	2.50
1425106_a_at	Wars	0.003	2.50
1418133_at	Bcl3	0.024	2.49
1424864_at	Hipk2	0.005	2.49
1416022_at	Fabp5	0.023	2.49
1416593_at	Glrx	0.013	2.49
1428780_at	Tha1	0.011	2.49
1416125_at	Fkbp5	0.028	2.48
1429046_at	Smurf2	0.028	2.48
1443669_at	Zfyve28	0.024	2.48
1458911_at	C230086A09Rik	0.033	2.47
1437290_at	Impad1	0.008	2.47
1435641_at	9530018I07Rik	0.006	2.47
1460521_a_at	Obfc2a	0.032	2.47
1454894_at	Smurf2	0.002	2.47
1455320_at	---	0.000	2.46
1439520_at	---	0.012	2.46
1419169_at	Mapk6	0.009	2.46
1434903_s_at	Il1rl2	0.007	2.45
1435323_a_at	Mboat1	0.003	2.45
1422705_at	Tmepai	0.013	2.45
1453344_at	1810032O08Rik	0.001	2.44
1418020_s_at	Cpd	0.041	2.44
1447711_x_at	4933412E12Rik	0.002	2.44
1448026_at	---	0.005	2.43
1451053_a_at	Mdm1	0.021	2.43
1448575_at	Il7r	0.009	2.42
1448555_at	D15Ert682e	0.001	2.41
1425934_a_at	B4galt4	0.014	2.41
1440275_at	Runx3	0.001	2.40
1416184_s_at	Hmga1	0.027	2.40
1418350_at	Hbegf	0.007	2.39

1428573_at	Chn2	0.021	2.39
1434909_at	Rragd	0.010	2.39
1434813_x_at	Wars	0.006	2.39
1434240_at	4632434I11Rik	0.039	2.39
1420594_at	Bard1	0.042	2.38
1437942_x_at	Tube1	0.008	2.38
1445381_at	---	0.007	2.38
1417616_at	St6galnac2	0.026	2.38
1427736_a_at	Ccrl2	0.011	2.38
1427141_at	2700099C18Rik	0.049	2.37
1453596_at	Id2	0.026	2.37
1425145_at	Il1rl1	0.013	2.37
1430150_at	Dcp2	0.019	2.36
1429683_at	5830472M02Rik	0.035	2.36
1440167_s_at	Lpp	0.007	2.36
1439768_x_at	Sema4f	0.012	2.36
1416011_x_at	Ehd1	0.003	2.35
1444155_at	Nin	0.044	2.35
1419649_s_at	Myo1c	0.003	2.35
1443445_at	Diap3	0.013	2.34
1448436_a_at	Irf1	0.004	2.34
1454899_at	Lpp	0.013	2.34
1418066_at	Cfl2	0.002	2.34
1425471_x_at	---	0.042	2.33
1426903_at	Fndc3a	0.000	2.33
1451340_at	Arid5a	0.010	2.33
1438075_at	Fem1c	0.041	2.33
1452540_a_at	Hist1h2bc /// Hist1h2be /// Hist1h2bl /// Hist1h2bm /// Hist1h2bp /// LOC665596 /// LOC665622 /// LOC671645	0.013	2.32
1426028_a_at	Cit	0.013	2.32
1435529_at	LOC667373 /// LOC669129	0.040	2.32
1448883_at	Lgmn	0.035	2.31
1460220_a_at	Csf1	0.009	2.31
1458130_at	1110001A07Rik	0.014	2.31
1422966_a_at	Tfrc	0.022	2.29
1435187_at	Tomm20	0.036	2.29
1448618_at	Mvp	0.002	2.29
1449851_at	Per1	0.033	2.28
1452742_at	Trak1	0.036	2.28
1426733_at	Itpk1	0.004	2.28
1424711_at	Tmem2	0.023	2.28
1416343_a_at	Lamp2	0.010	2.28
1418825_at	Irgm	0.003	2.28
1448452_at	Irf8	0.030	2.27
1429582_at	Btbd14a	0.047	2.27
1459026_at	Snw1	0.031	2.27
1424775_at	Oas1a	0.004	2.27
1418154_at	BC004022	0.007	2.26
1451584_at	Havcr2	0.029	2.26
1416543_at	Nfe2l2	0.000	2.26
1450685_at	Arpp19	0.003	2.26
1423632_at	Gpr146	0.007	2.26
1456635_at	---	0.033	2.25
1448728_a_at	Nfkbiz	0.036	2.25
1428346_at	Trafd1	0.008	2.25
1416469_at	Luzp1	0.013	2.24

1439802_at	Stk35	0.047	2.23
1431873_a_at	Tube1	0.048	2.23
1450744_at	Ell2	0.007	2.22
1450048_a_at	Idh2	0.002	2.22
1433951_at	Arl5a	0.015	2.22
1418067_at	Cfl2	0.001	2.22
1439141_at	Gpr18	0.012	2.21
1416492_at	Ccne1	0.026	2.21
1417546_at	Il2rb	0.005	2.21
1443099_at	BC087945	0.030	2.20
1418012_at	Sh3glb1	0.001	2.20
1419711_at	Cd7	0.035	2.20
1460415_a_at	Cd40	0.016	2.20
1452202_at	Pde2a	0.014	2.20
1436882_at	Ubl5 /// EG435336 /// LOC673926	0.005	2.20
1437085_at	D630039A03Rik	0.018	2.20
1435448_at	Bcl2l11	0.046	2.20
1429049_at	Nuak2	0.016	2.20
1416592_at	Glrx	0.014	2.19
1449009_at	Tgtp	0.015	2.19
1421517_at	St6galnac1	0.016	2.19
1455228_at	Whsc1	0.014	2.18
1453392_at	1810054D07Rik	0.019	2.18
1428735_at	Cd69	0.028	2.18
1431017_at	Rcbtb2	0.034	2.18
1422880_at	Sypl	0.020	2.18
1418803_a_at	Fasl	0.016	2.18
1422879_at	Sypl	0.005	2.17
1433885_at	Iqgap2	0.012	2.17
1430623_s_at	Obfc2a	0.003	2.17
1419328_at	Sema4f	0.021	2.16
1439218_at	Ust	0.002	2.16
1452132_at	Tlcd1	0.020	2.16
1417172_at	Ube2l6	0.016	2.15
1421237_at	Tmpo	0.028	2.15
1418856_a_at	Fanca	0.037	2.15
1427819_at	---	0.007	2.15
1430533_a_at	Ctnnb1	0.020	2.15
1455606_at	BC004022	0.014	2.15
1423392_at	Clic4	0.019	2.15
1419668_at	Sgcb	0.019	2.14
1435694_at	Arhgap26	0.019	2.14
1420886_a_at	Xbp1	0.006	2.14
1417010_at	Zfp238	0.004	2.14
1429390_at	Acpl2	0.019	2.13
1435956_at	Frmf5	0.017	2.13
1428938_at	Gnaq	0.002	2.13
1422804_at	Serpinb6b	0.020	2.12
1424841_s_at	Rbks	0.009	2.12
1436654_at	5830483C08Rik	0.040	2.12
1417793_at	Iigp2	0.002	2.12
1416697_at	Dpp4	0.006	2.12
1423630_at	Cygb	0.015	2.11
1435223_at	Spfh2	0.014	2.11
1451079_at	Adpgk	0.007	2.11
1419648_at	Myo1c	0.037	2.11



1424759_at	Arrdc4	0.020	2.10
1448661_at	Plcb3	0.011	2.10
1434680_at	Plekhg3	0.037	2.10
1433693_x_at	Vamp3	0.011	2.10
1429244_at	2610524H06Rik	0.018	2.10
1419620_at	Pttg1	0.027	2.10
1455551_at	Uevld	0.018	2.09
1452196_a_at	Nckap1	0.014	2.09
1420849_at	Crnk11	0.003	2.09
1434817_s_at	4930535B03Rik	0.042	2.08
1429422_at	4933412E12Rik	0.015	2.07
1427446_s_at	Ttn	0.026	2.07
1456735_x_at	Acpl2	0.049	2.06
1431810_a_at	Tmco4	0.032	2.06
1449222_at	Ebi3	0.013	2.05
1425198_at	Ptpn2	0.000	2.05
1431008_at	0610037M15Rik	0.039	2.05
1453913_a_at	Tap2	0.006	2.05
1460314_s_at	Hist2h3c1 /// Hist2h3c2 /// Hist1h3g /// Hist1h3f /// Hist1h3c /// Hist1h3d /// Hist1h3b /// Hist1h3e /// Hist1h3h /// Hist1h3i /// Hist2h3b /// Hist1h3a	0.048	2.04
1456111_at	D930028F11Rik	0.028	2.04
1417508_at	Rnf19	0.029	2.04
1419811_at	D16Wsu65e	0.022	2.04
1455679_at	Obfc2a	0.042	2.04
1418050_at	Gpld1	0.003	2.04
1438811_at	Dlg7	0.033	2.04
1427992_a_at	Rab12	0.012	2.03
1434891_at	Ptgfrn	0.020	2.03
1420987_at	Kif3b	0.050	2.03
1420376_a_at	H3f3b	0.001	2.03
1417182_at	Dnaja2	0.000	2.02
1423161_s_at	Spred1	0.025	2.02
1417719_at	Sap30	0.034	2.01
1449840_at	Sntb2	0.010	2.01
1455294_at	1110029L17Rik	0.002	2.01
1436747_at	1110014K08Rik /// EG664786 /// LOC664849 /// LOC672175	0.007	2.01
1416691_at	Gtpbp2	0.004	2.01
1436182_at	---	0.016	2.01
1431050_at	Rps6ka5	0.004	2.00
1438937_x_at	Ang1	0.037	-2.01
1430662_at	9430091E24Rik	0.029	-2.01
1439586_at	LOC548102	0.009	-2.01
1437234_x_at	Prmt2	0.008	-2.01
1456174_x_at	Ndrp1	0.010	-2.02
1437651_a_at	Dtnb	0.009	-2.02
1439059_at	BC031748	0.005	-2.02
1437366_at	AI608492	0.034	-2.02
1418301_at	Irf6	0.011	-2.02
1437367_at	H2-K1	0.001	-2.02
1439729_at	A930038B10Rik	0.040	-2.03
1451063_at	Stxbp4	0.034	-2.04
1446006_at	Immp11	0.008	-2.04
1417234_at	Mmp11	0.009	-2.04
1435987_x_at	1110059G02Rik	0.022	-2.05
1458077_at	---	0.008	-2.05

1450512_at	Ntn4	0.007	-2.05
1433242_at	5830415B17Rik	0.021	-2.06
1435840_x_at	LOC625360	0.016	-2.06
1436833_x_at	Till1	0.009	-2.06
1442039_at	Tox	0.002	-2.06
1446509_at	Smox	0.049	-2.07
1452678_a_at	Ccbl1	0.045	-2.07
1434690_at	Lycat	0.023	-2.07
1434793_at	Wdr78	0.021	-2.08
1439503_at	Zfp28	0.032	-2.08
1434642_at	Hsd17b11	0.002	-2.09
1433595_at	---	0.017	-2.10
1442920_at	Klf3	0.040	-2.10
1437877_at	Ttc14	0.020	-2.11
1419940_at	C030018P15Rik	0.049	-2.11
1445618_at	---	0.007	-2.11
1421430_at	Rad51l1	0.037	-2.11
1445664_at	Igf1r	0.016	-2.12
1434581_at	---	0.013	-2.12
1417441_at	Dnajc12	0.002	-2.12
1424613_at	Gprc5b	0.033	-2.13
1422620_s_at	Ppap2a	0.033	-2.14
1427682_a_at	Egr2	0.009	-2.14
1426934_at	Nhsl1	0.047	-2.14
1425484_at	Tox	0.003	-2.15
1418084_at	Nrp1	0.001	-2.15
1446911_at	Itsn2	0.021	-2.16
1433542_at	Inpp5f	0.004	-2.16
1456430_at	Ttc14	0.036	-2.16
1435078_at	Tanc2	0.028	-2.16
1429418_at	Cdc14b	0.012	-2.16
1417388_at	Bex2	0.001	-2.16
1449520_at	Ttc28	0.039	-2.18
1441482_at	---	0.008	-2.19
1445600_at	Igf1r	0.014	-2.19
1442704_at	---	0.030	-2.20
1440847_at	Mtss1	0.002	-2.21
1439013_x_at	Acyp1	0.003	-2.21
1441965_at	Ccdc38	0.042	-2.22
1436759_x_at	Cnn3	0.009	-2.22
1434591_at	4732460K03Rik	0.003	-2.22
1417481_at	Ramp1	0.003	-2.23
1447421_at	Pam	0.001	-2.23
1439654_at	EG319225 /// LOC633385	0.019	-2.23
1416419_s_at	Gabarapl1	0.006	-2.23
1449835_at	Pdcd1	0.004	-2.24
1428704_at	Zfp661	0.009	-2.24
1428142_at	Etv5	0.025	-2.25
1436122_at	Zfp667	0.036	-2.25
1444541_at	Myo9a	0.040	-2.26
1432057_a_at	Prdm5	0.000	-2.26
1434036_at	Mtss1	0.001	-2.27
1455621_at	BC066107	0.022	-2.27
1429316_at	Rasgef1a	0.008	-2.27
1429093_at	Ddi2	0.049	-2.28
1435931_at	E130308A19Rik	0.008	-2.28

1428326_s_at	Hrsp12	0.008	-2.29
1455570_x_at	Cnn3	0.004	-2.29
1423544_at	Ptpn5	0.000	-2.29
1436729_at	2600003E23Rik	0.027	-2.30
1438331_at	Ypel2	0.023	-2.31
1455953_x_at	Pstk	0.020	-2.31
1460069_at	Smc6	0.024	-2.32
1454942_at	Niban	0.001	-2.32
1437070_at	Cdc14b	0.006	-2.34
1439632_at	---	0.021	-2.35
1457884_at	4732496C06Rik	0.033	-2.35
1454084_a_at	Senp8	0.006	-2.36
1445370_at	Vapb	0.012	-2.36
1427182_s_at	D18Ertd653e	0.007	-2.36
1427167_at	Armcx4	0.007	-2.37
1420980_at	Pak1	0.021	-2.38
1445613_at	Nr2c2	0.017	-2.38
1424826_s_at	Mtss1	0.005	-2.39
1454745_at	Arhgap29	0.018	-2.40
1434148_at	Tcf4	0.043	-2.41
1424268_at	Smox	0.017	-2.42
1428329_a_at	Ift80	0.032	-2.43
1456891_at	Dennd2c	0.015	-2.44
1421022_x_at	Acyp1	0.002	-2.44
1454231_a_at	Rpgrip1	0.001	-2.46
1452679_at	Tubb2b	0.043	-2.46
1445612_at	---	0.040	-2.47
1459595_at	---	0.023	-2.48
1451718_at	Plp1	0.027	-2.49
1457445_at	Trps1	0.012	-2.49
1439558_at	Zfp75	0.005	-2.49
1452366_at	4732435N03Rik	0.017	-2.51
1437868_at	BC023892	0.005	-2.51
1442024_at	Ppp1r3e	0.002	-2.51
1437168_at	Srrp	0.028	-2.51
1440188_at	Aco2	0.010	-2.51
1456593_at	Sytl2	0.045	-2.54
1457528_at	Slc4a7	0.003	-2.54
1427752_a_at	Tcrb-V13 /// LOC665446 /// LOC669809 /// LOC674045 /// LOC676754	0.044	-2.54
1436692_at	---	0.009	-2.54
1458802_at	Hivep3	0.005	-2.55
1450095_a_at	Acyp1	0.015	-2.56
1424455_at	Gprasp1	0.008	-2.56
1458974_at	Tox	0.005	-2.60
1450136_at	Cd38	0.021	-2.62
1416418_at	Gabarapl1	0.020	-2.63
1424433_at	Msrb2	0.001	-2.63
1421144_at	Rpgrip1	0.024	-2.65
1457376_at	Itga4	0.014	-2.65
1458082_at	---	0.015	-2.65
1419616_at	Bmpr2	0.022	-2.66
1419595_a_at	Ggh /// LOC667301	0.002	-2.67
1456420_at	Arid4a	0.021	-2.70
1420842_at	Ptprf	0.019	-2.70
1438931_s_at	Sesn1	0.002	-2.72

1425914_a_at	Armcx1	0.004	-2.72
1457548_at	Adamts6	0.001	-2.72
1440355_at	Kctd12b	0.020	-2.74
1427568_a_at	Ift80	0.014	-2.74
1441286_at	LOC328483	0.044	-2.74
1455265_a_at	Rgs16	0.041	-2.75
1416638_at	Sall2	0.033	-2.75
1445711_at	BB163080	0.007	-2.75
1429113_at	2900092E17Rik /// 1500031I19Rik	0.002	-2.75
1426775_s_at	Scamp1	0.020	-2.76
1460444_at	Arrb1	0.037	-2.76
1460242_at	Cd55	0.009	-2.77
1422438_at	Ephx1	0.012	-2.80
1447757_x_at	Inpp5f	0.006	-2.81
1433335_at	4930405G09Rik	0.020	-2.82
1422010_at	Tlr7	0.002	-2.82
1435669_at	Zfp532	0.024	-2.82
1453252_at	Dus4l	0.018	-2.87
1444402_at	Zc3h12c	0.021	-2.91
1433823_at	AW456874	0.010	-2.92
1448944_at	Nrp1	0.004	-2.92
1433711_s_at	Sesn1	0.003	-2.99
1449283_a_at	Mapk12	0.015	-2.99
1441305_at	---	0.019	-3.01
1457701_at	Tmem136	0.013	-3.03
1456178_at	Bambi-ps1	0.000	-3.03
1418762_at	Cd55	0.005	-3.04
1451620_at	C1ql3	0.018	-3.05
1436223_at	Itgb8	0.035	-3.07
1446950_at	Tox	0.007	-3.07
1425745_a_at	Tacc2	0.008	-3.08
1437506_at	---	0.001	-3.14
1429065_at	1200009F10Rik	0.018	-3.15
1450070_s_at	Pak1	0.001	-3.17
1454699_at	Sesn1	0.002	-3.23
1454768_at	Kcnf1	0.005	-3.25
1422542_at	Gpr34	0.006	-3.27
1440837_at	H2-Ob	0.030	-3.28
1450344_a_at	Ptger3	0.022	-3.31
1416111_at	Cd83	0.000	-3.31
1438466_at	Dnahc7c /// Dnahc7b /// LOC433299	0.007	-3.39
1438701_at	Bicd1	0.001	-3.44
1433741_at	Cd38	0.045	-3.50
1452583_s_at	Galm	0.007	-3.55
1455746_at	Kif13a	0.014	-3.57
1457198_at	Nrp1	0.001	-3.79
1433575_at	LOC672274	0.031	-3.85
1417951_at	Eno3	0.007	-3.86
1419709_at	Stfa3	0.044	-3.92
1440986_at	Rpap1	0.005	-3.97
1444376_at	Sesn1	0.002	-3.97
1446606_at	LOC625175	0.013	-4.05
1448501_at	Tspan6	0.012	-4.12
1418171_at	Tceal8	0.017	-4.17
1443906_at	Cd55	0.002	-4.20
1419117_at	Slc22a2	0.008	-4.22

1416630_at	Id3	0.005	-4.31
1429918_at	Arhgap20	0.019	-4.39
1428393_at	Nrn1	0.042	-4.44
1455633_at	Zfp647	0.000	-4.52
1434073_at	Gprasp2	0.007	-4.61
1437540_at	---	0.010	-4.78
1439995_at	C80638	0.003	-5.18
1420064_s_at	Tktl1	0.011	-5.29
1439304_at	Pam	0.014	-5.32
1439794_at	---	0.026	-5.81
1442740_at	---	0.008	-5.92
1455408_at	Pla2g4f	0.010	-6.06
1449824_at	Prg4	0.010	-6.06
1442262_at	---	0.000	-6.94
1449084_s_at	Sh3d19	0.026	-7.87
1457231_at	Hif1a	0.046	-8.77
1434572_at	Hdac9	0.009	-10.98
1434141_at	Gucy1a3	0.006	-11.31
1420491_at	Eif2s1	0.000	-12.05
1448665_at	Dmd	0.003	-13.57
1416824_at	B230118H07Rik	0.001	-19.34
1459372_at	Npas4	0.006	-25.58

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The list of genes differentially expressed between Dicer-sufficient and -deficient CD4<sup>+</sup>YFP<sup>+</sup> cells are shown. Based on a *t* test with cut-off p-values of <0.05 and a fold change of >2, 686 probe sets were found to be differentially regulated in these two populations.

**Table S2.** Overlap of the gene expression profile of Dicer KO and FoxP3-deficient T reg cells

Probe set ID	Gene symbol	Dicer KO vs. Het (fold change)	p-value	FoxP3A-GFP vs. FoxP3- GFP (fold change)	p-value
1417898_a_at	Gzma	308.60	0.018	72.99	0.015
1455900_x_at	Tgm2	125.40	0.003	3.33	0.013
1420394_s_at	Gp49a /// Lilrb4	37.73	0.000	19.03	0.023
1435436_at	Epas1	35.27	0.044	56.38	0.024
1422280_at	Gzmk	28.76	0.007	27.12	0.015
1451335_at	Plac8	26.92	0.009	10.94	0.014
1419060_at	Gzmb	15.75	0.001	25.91	0.006
1449864_at	Il4	11.61	0.024	32.12	0.002
1419647_a_at	Ier3	10.44	0.038	3.93	0.031
1417928_at	Pdlim4	9.61	0.040	4.01	0.002
1427038_at	Penk1	9.02	0.019	6.85	0.009
1417821_at	D17H6S56E-5	8.58	0.016	4.89	0.009
1429404_at	2010317E24Rik	7.66	0.040	4.21	0.008
1434789_at	Depdc1b	7.64	0.034	6.63	0.025
1420697_at	Slc15a3	7.33	0.020	3.83	0.003
1433942_at	Myo6	7.25	0.044	7.62	0.007
1417460_at	Ifitm2	7.07	0.008	8.27	0.027
1453683_a_at	Cep55	6.82	0.005	12.45	0.002
1421688_a_at	Ccl1	5.86	0.009	6.67	0.007
1417822_at	D17H6S56E-5	5.73	0.003	4.21	0.004
1449911_at	Lag3	5.61	0.024	4.85	0.000
1424923_at	Serpina3g	5.36	0.038	4.08	0.001
1425787_a_at	Sytl3	5.32	0.006	4.27	0.023
1455990_at	Kif23	4.96	0.044	4.08	0.001
1418403_at	Adam19	4.94	0.024	3.04	0.013
1449361_at	Tbx21	4.44	0.006	10.77	0.019
1416558_at	Melk	4.36	0.031	7.71	0.005
1437033_a_at	Skp2	4.30	0.008	3.28	0.015
1434557_at	Hip1	4.23	0.007	3.48	0.016
1425947_at	Ifng	4.06	0.005	15.81	0.027
1417323_at	Psrc1	4.00	0.004	4.74	0.004
1424704_at	Runx2	3.98	0.013	5.17	0.026
1448231_at	Fkbp5	3.92	0.018	3.15	0.026
1418402_at	Adam19	3.91	0.031	3.33	0.033
1440156_s_at	AI851523	3.56	0.024	3.97	0.000
1435773_at	4930547N16Rik	3.50	0.029	4.99	0.020
1455983_at	Cdca2	3.41	0.039	3.19	0.000
1424727_at	Ccr5	3.37	0.042	4.28	0.004
1418930_at	Cxcl10	3.33	0.029	5.84	0.006
1460255_at	Tnfsf13b	3.28	0.021	5.90	0.006
1416263_at	Abcb9	3.23	0.006	2.64	0.000

1454809_at	Ncoa7	3.22	0.012	3.32	0.029
1452210_at	Dna21	3.20	0.024	6.90	0.010
1423326_at	Entpd1	3.20	0.035	2.79	0.002
1422970_at	Mxd3	3.19	0.017	4.11	0.000
1448110_at	Sema4a	3.10	0.034	2.94	0.012
1444524_at	EST	3.07	0.004	2.95	0.047
1423525_at	Mastl	3.07	0.047	2.55	0.000
1449235_at	Fasl	3.01	0.009	2.94	0.006
1424895_at	Gpsm2	2.96	0.027	4.93	0.003
1423847_at	Ncapd2	2.95	0.037	6.76	0.000
1421546_a_at	Racgap1	2.88	0.045	6.89	0.005
1448380_at	Lgals3bp	2.82	0.011	2.60	0.001
1428574_a_at	Chn2	2.80	0.007	5.17	0.019
1417445_at	Kntc2	2.78	0.030	3.94	0.005
1424629_at	Bra1	2.76	0.040	5.42	0.012
1429400_at	Cln5	2.74	0.005	2.29	0.008
1456545_at	Il18rap	2.69	0.017	4.09	0.006
1435176_a_at	Id2	2.63	0.003	3.16	0.010
1435338_at	Cdk6	2.52	0.010	4.24	0.003
1448175_at	Ehd1	2.52	0.006	2.91	0.002
1432202_a_at	Wdr51a	2.51	0.030	3.41	0.005
1427982_s_at	Syne2	2.50	0.001	3.00	0.003
1430368_s_at	1700019D03Rik	2.50	0.041	14.38	0.018
1416757_at	Zwilch	2.50	0.040	5.07	0.006
1416022_at	Fabp5	2.49	0.023	3.19	0.006
1416125_at	Fkbp5	2.48	0.028	3.36	0.021
1439768_x_at	Sema4f	2.36	0.012	3.60	0.000
1416011_x_at	Ehd1	2.35	0.003	2.67	0.002
1451584_at	Havcr2	2.26	0.029	10.56	0.048
1431873_a_at	Tube1	2.23	0.048	5.57	0.020
1450744_at	Ell2	2.22	0.007	2.98	0.043
1416492_at	Ccne1	2.21	0.026	4.48	0.003
1455228_at	Whsc1	2.18	0.014	2.50	0.350
1418856_a_at	Fanca	2.15	0.037	2.61	0.003
1422804_at	Serpinb6b	2.12	0.020	3.61	0.028
1429244_at	2610524H06Rik	2.10	0.018	3.79	0.000
1449222_at	Ebi3	2.05	0.013	6.76	0.019
1434891_at	Ptgfrn	2.03	0.020	3.15	0.014
1456174_x_at	Ndr1	-2.02	0.010	-3.21	0.016
1450512_at	Ntn4	-2.05	0.007	-5.00	0.015
1433595_at	EST	-2.10	0.017	-3.43	0.008
1434581_at	EST	-2.12	0.013	-3.13	0.012
1433542_at	Inpp5f	-2.16	0.004	-4.32	0.006
1429418_at	Cdc14b	-2.16	0.012	-2.93	0.000
1436759_x_at	Cnn3	-2.22	0.009	-4.36	0.048
1417481_at	Ramp1	-2.23	0.003	-2.35	0.005

1434036_at	Mtss1	-2.27	0.001	-2.93	0.005
1436729_at	2600003E23Rik	-2.30	0.027	-3.24	0.000
1437070_at	Cdc14b	-2.34	0.006	-2.54	0.000
1424826_s_at	Mtss1	-2.39	0.005	-3.04	0.007
1428329_a_at	Ift80	-2.43	0.032	-4.27	0.000
1452679_at	Tubb2b	-2.46	0.043	-6.64	0.031
1437868_at	BC023892	-2.51	0.005	-5.16	0.044
1427752_a_at	Tcrb-V13	-2.54	0.044	-3.07	0.005
1424455_at	Gprasp1	-2.56	0.008	-3.01	0.002
1438931_s_at	Sesn1	-2.72	0.002	-6.54	0.041
1427568_a_at	Ift80	-2.74	0.014	-3.78	0.000
1460444_at	Arrb1	-2.76	0.037	-2.68	0.037
1460242_at	Cd55	-2.77	0.009	-10.72	0.001
1422438_at	Ephx1	-2.80	0.012	-3.19	0.000
1447757_x_at	Inpp5f	-2.81	0.006	-6.05	0.012
1433711_s_at	Sesn1	-2.99	0.003	-8.71	0.004
1456178_at	Bambi-ps1	-3.03	0.000	-3.63	0.027
1418762_at	Cd55	-3.04	0.005	-8.23	0.017
1437506_at	EST	-3.14	0.001	-3.48	0.018
1454699_at	Sesn1	-3.23	0.002	-11.67	0.018
1440837_at	H2-Ob	-3.28	0.030	-23.79	0.022
1429918_at	Arhgap20	-4.39	0.019	-2.94	0.002
1437540_at	EST	-4.78	0.010	-3.34	0.001
1439794_at	EST	-5.81	0.026	-7.41	0.000
1449824_at	Prg4	-6.06	0.010	-17.92	0.033

All of the probe sets from the differentially-regulated Dicer KO and the FoxP3-deficient (reference 24) T reg cells were compared, and the 112 probe sets similarly dysregulated in the miRNA-deficient T reg cells as compared to FoxP3-deficient T reg cells are listed.



**Table S3.** miRNA target prediction in T reg cells

<b>miRNA name</b>	<b>Target score</b>	<b>Gene symbol</b>	<b>Gene description</b>
mmu-miR-297a	50	1810054D07Rik	RIKEN cDNA 1810054D07 gene
mmu-miR-24	55	1810054D07Rik	RIKEN cDNA 1810054D07 gene
mmu-miR-125a-3p	66	1810054D07Rik	RIKEN cDNA 1810054D07 gene
mmu-miR-297a	86	2610036L11Rik	RIKEN cDNA 2610036L11 gene
mmu-miR-27b	69	4632434I11Rik	RIKEN cDNA 4632434I11 gene
mmu-miR-214	53	4933412E12Rik	RIKEN cDNA 4933412E12 gene
mmu-miR-16	70	6430571L13Rik	RIKEN cDNA 6430571L13 gene
mmu-miR-15b	71	6430571L13Rik	RIKEN cDNA 6430571L13 gene
mmu-miR-214	73	A330104H05Rik	RIKEN cDNA A330104H05 gene
mmu-miR-27b	60	Abca1	ATP-binding cassette, sub-family A (ABC1), member 1
mmu-miR-23a	54	Adam19	a disintegrin and metallopeptidase domain 19 (meltrin beta)
mmu-miR-23b	56	Adam19	a disintegrin and metallopeptidase domain 19 (meltrin beta)
mmu-miR-30a	61	Adam19	a disintegrin and metallopeptidase domain 19 (meltrin beta)
mmu-miR-30a	66	Adam9	a disintegrin and metallopeptidase domain 9 (meltrin gamma)
mmu-miR-23a	68	Ankrd57	ankyrin repeat domain 57
mmu-miR-23b	70	Ankrd57	ankyrin repeat domain 57
mmu-miR-103	57	Arhgap26	Rho GTPase activating protein 26
mmu-miR-24	51	Arid5a	AT rich interactive domain 5A (Mrf1 like)
mmu-miR-223	78	Arl5a	ADP-ribosylation factor-like 5A
mmu-miR-214	53	Arpp19	cAMP-regulated phosphoprotein 19
mmu-miR-16	72	Atf6	activating transcription factor 6
mmu-miR-15b	74	Atf6	activating transcription factor 6
mmu-miR-23a	91	BC004022	cDNA sequence BC004022
mmu-miR-23b	91	BC004022	cDNA sequence BC004022
mmu-miR-103	95	BC004022	cDNA sequence BC004022
mmu-miR-16	99	BC004022	cDNA sequence BC004022
mmu-miR-24	53	Bcl2l11	BCL2-like 11 (apoptosis facilitator)
mmu-miR-214	70	Bcl2l11	BCL2-like 11 (apoptosis facilitator)
mmu-miR-125a-3p	53	Brca1	breast cancer 1
mmu-miR-149	67	Brca1	breast cancer 1
mmu-miR-30a	50	Btbd14a	BTB (POZ) domain containing 14A
mmu-miR-23a	98	Btbd14a	BTB (POZ) domain containing 14A
mmu-miR-23b	99	Btbd14a	BTB (POZ) domain containing 14A
mmu-miR-103	72	Cacnb4	calcium channel, voltage-dependent, beta 4 subunit
mmu-miR-27b	51	Ccdc28b	coiled coil domain containing 28B
mmu-miR-15b	87	Ccne1	cyclin E1
mmu-miR-16	91	Ccne1	cyclin E1
mmu-miR-103	53	Cdk6	cyclin-dependent kinase 6
mmu-miR-191	57	Cebpb	CCAAT/enhancer binding protein (C/EBP), beta
mmu-miR-155	60	Cebpb	CCAAT/enhancer binding protein (C/EBP), beta
mmu-miR-103	51	Cfl2	cofilin 2, muscle
mmu-miR-15b	56	Cfl2	cofilin 2, muscle
mmu-miR-16	61	Cfl2	cofilin 2, muscle
mmu-miR-30a	71	Cfl2	cofilin 2, muscle
mmu-miR-125a-3p	64	Cpd	carboxypeptidase D
mmu-miR-146a	65	Cpd	carboxypeptidase D
mmu-miR-16	70	Cpd	carboxypeptidase D

mmu-miR-15b	75	Cpd	carboxypeptidase D
mmu-miR-27b	80	Csf1	colony stimulating factor 1 (macrophage)
mmu-miR-214	54	Ctnnb1	catenin (cadherin associated protein), beta 1
mmu-miR-30a	67	Cysltr1	cysteinyl leukotriene receptor 1
mmu-miR-24	66	Dcp2	DCP2 decapping enzyme homolog ( <i>S. cerevisiae</i> )
mmu-miR-27b	88	Dcp2	DCP2 decapping enzyme homolog ( <i>S. cerevisiae</i> )
mmu-miR-22	54	Dpp4	dipeptidylpeptidase 4
mmu-miR-30a	58	Ell2	elongation factor RNA polymerase II 2
mmu-miR-297a	100	Ell2	elongation factor RNA polymerase II 2
mmu-miR-223	52	Enpp1	ectonucleotide pyrophosphatase/phosphodiesterase 1
mmu-miR-207	51	Eomes	eomesodermin homolog ( <i>Xenopus laevis</i> )
mmu-miR-23a	54	Eomes	eomesodermin homolog ( <i>Xenopus laevis</i> )
mmu-miR-23b	54	Eomes	eomesodermin homolog ( <i>Xenopus laevis</i> )
mmu-miR-146a	54	Fabp5	fatty acid binding protein 5, epidermal
mmu-miR-24	61	Fasl	Fas ligand (TNF superfamily, member 6)
mmu-miR-30a	69	Fndc3a	fibronectin type III domain containing 3a
mmu-miR-149	95	Frm4a	FERM domain containing 4A
mmu-miR-23a	61	Frm5	FERM domain containing 5
mmu-miR-23b	61	Frm5	FERM domain containing 5
mmu-miR-297a	66	Gas2l3	growth arrest-specific 2 like 3
mmu-miR-30a	53	Gem	GTP binding protein (gene overexpressed in skeletal muscle)
mmu-miR-297a	96	Gnaq	guanine nucleotide binding protein, alpha q polypeptide
mmu-miR-29c	52	Gng12	guanine nucleotide binding protein (G protein), gamma 12
mmu-miR-23a	62	Gng12	guanine nucleotide binding protein (G protein), gamma 12
mmu-miR-23b	62	Gng12	guanine nucleotide binding protein (G protein), gamma 12
mmu-miR-27b	59	Gpld1	glycosylphosphatidylinositol specific phospholipase D1
mmu-miR-21	71	Gramd3	GRAM domain containing 3
mmu-miR-22	78	H3f3b	H3 histone, family 3B
mmu-miR-214	50	Hbegf	heparin-binding EGF-like growth factor
mmu-miR-27b	77	Hbegf	heparin-binding EGF-like growth factor
mmu-miR-15b	66	Hmga1	high mobility group AT-hook 1
mmu-miR-16	68	Hmga1	high mobility group AT-hook 1
mmu-miR-23a	67	Hmgb2	high mobility group box 2
mmu-miR-23b	71	Hmgb2	high mobility group box 2
mmu-miR-27b	69	Ifng	interferon gamma
mmu-miR-23a	57	Igfbp4	insulin-like growth factor binding protein 4
mmu-miR-23b	59	Igfbp4	insulin-like growth factor binding protein 4
mmu-miR-24	69	Il15ra	interleukin 15 receptor, alpha chain
mmu-miR-24	50	Il1rl1	interleukin 1 receptor-like 1
mmu-miR-214	51	Il7r	interleukin 7 receptor
mmu-miR-27b	73	Il7r	interleukin 7 receptor
mmu-miR-30a	55	Impad1	inositol monophosphatase domain containing 1
mmu-miR-23a	60	Inpp5a	inositol polyphosphate-5-phosphatase A
mmu-miR-23b	65	Inpp5a	inositol polyphosphate-5-phosphatase A
mmu-miR-23a	65	Irf1	interferon regulatory factor 1
mmu-miR-23b	65	Irf1	interferon regulatory factor 1
mmu-miR-207	70	Irf8	interferon regulatory factor 8
mmu-miR-23a	61	Irgm	immunity-related GTPase family, M
mmu-miR-23b	63	Irgm	immunity-related GTPase family, M
mmu-miR-214	64	Itpk1	inositol 1,3,4-triphosphate 5/6 kinase

mmu-miR-297a	80	Lamp2	lysosomal membrane glycoprotein 2
mmu-miR-297a	50	Lcor1	ligand dependent nuclear receptor corepressor-like
mmu-miR-30a	51	Lcor1	ligand dependent nuclear receptor corepressor-like
mmu-miR-155	60	Lcor1	ligand dependent nuclear receptor corepressor-like
mmu-miR-103	66	LOC637870	similar to Nedd4 WW binding protein 4
mmu-miR-23a	67	Lonrf3	LON peptidase N-terminal domain and ring finger 3
mmu-miR-23b	70	Lonrf3	LON peptidase N-terminal domain and ring finger 3
mmu-miR-214	68	Lrrc6	leucine rich repeat containing 6 (testis)
mmu-miR-23a	72	Lrrc6	leucine rich repeat containing 6 (testis)
mmu-miR-23b	72	Lrrc6	leucine rich repeat containing 6 (testis)
mmu-miR-214	72	Luzp1	leucine zipper protein 1
mmu-miR-149	76	Luzp1	leucine zipper protein 1
mmu-miR-16	79	Luzp1	leucine zipper protein 1
mmu-miR-15b	86	Luzp1	leucine zipper protein 1
mmu-miR-30a	54	Mboat1	membrane bound O-acyltransferase domain containing 1
mmu-miR-27b	51	Melk	maternal embryonic leucine zipper kinase
mmu-miR-149	65	Mmp9	matrix metalloproteinase 9
mmu-miR-21	68	Mybl1	myeloblastosis oncogene-like 1
mmu-miR-23b	60	Myo6	myosin VI
mmu-miR-23a	61	Myo6	myosin VI
mmu-miR-30a	55	Ncoa7	nuclear receptor coactivator 7
mmu-miR-27b	84	Ncoa7	nuclear receptor coactivator 7
mmu-miR-27b	52	Neb	nebulin
mmu-miR-125a-3p	52	Neb	nebulin
mmu-miR-155	59	Nfe2l2	nuclear factor, erythroid derived 2, like 2
mmu-miR-27b	71	Nfe2l2	nuclear factor, erythroid derived 2, like 2
mmu-miR-23a	60	Nuak2	NUAK family, SNF1-like kinase, 2
mmu-miR-23b	60	Nuak2	NUAK family, SNF1-like kinase, 2
mmu-miR-16	82	Nuak2	NUAK family, SNF1-like kinase, 2
mmu-miR-15b	85	Nuak2	NUAK family, SNF1-like kinase, 2
mmu-miR-27b	89	Obfc2a	oligonucleotide/oligosaccharide-binding fold containing 2A
mmu-miR-23a	50	Osbpl6	oxysterol binding protein-like 6
mmu-miR-23b	50	Osbpl6	oxysterol binding protein-like 6
mmu-miR-146a	80	Osbpl6	oxysterol binding protein-like 6
mmu-miR-23b	53	Pip5k2b	phosphatidylinositol-4-phosphate 5-kinase, type II, beta
mmu-miR-30a	60	Pip5k2b	phosphatidylinositol-4-phosphate 5-kinase, type II, beta
mmu-miR-30a	58	Pmaip1	phorbol-12-myristate-13-acetate-induced protein 1
mmu-miR-155	63	Pmaip1	phorbol-12-myristate-13-acetate-induced protein 1
mmu-miR-30a	80	Ptgfrn	prostaglandin F2 receptor negative regulator
mmu-miR-223	80	Rhob	ras homolog gene family, member B
mmu-miR-29c	65	Rnf19	ring finger protein (C3HC4 type) 19
mmu-miR-27b	54	Rps6ka5	ribosomal protein S6 kinase, polypeptide 5
mmu-miR-155	88	Rps6ka5	ribosomal protein S6 kinase, polypeptide 5
mmu-miR-30a	92	Runx2	runt related transcription factor 2
mmu-miR-149	57	Sema4a	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4A
mmu-miR-24	56	Sema7a	sema domain, immunoglobulin domain (Ig), and GPI membrane anchor, (semaphorin) 7A
mmu-miR-27b	85	Sema7a	sema domain, immunoglobulin domain (Ig), and GPI membrane anchor, (semaphorin) 7A
mmu-miR-16	57	Serinc3	serine incorporator 3

mmu-miR-15b	63	Serinc3	serine incorporator 3
mmu-miR-30a	61	Serpib6b	serine (or cysteine) peptidase inhibitor, clade B, member 6b
mmu-miR-23a	86	Serpib9	serine (or cysteine) peptidase inhibitor, clade B, member 9
mmu-miR-23b	86	Serpib9	serine (or cysteine) peptidase inhibitor, clade B, member 9
mmu-miR-16	50	Sgcb	sarcoglycan, beta (dystrophin-associated glycoprotein)
mmu-miR-27b	51	Sgcb	sarcoglycan, beta (dystrophin-associated glycoprotein)
mmu-miR-15b	57	Sgcb	sarcoglycan, beta (dystrophin-associated glycoprotein)
mmu-miR-21	58	Sgcb	sarcoglycan, beta (dystrophin-associated glycoprotein)
mmu-miR-146a	84	Sgcb	sarcoglycan, beta (dystrophin-associated glycoprotein)
mmu-miR-30a	87	Sgcb	sarcoglycan, beta (dystrophin-associated glycoprotein)
mmu-miR-15b	81	Sgk	serum/glucocorticoid regulated kinase
mmu-miR-16	82	Sgk	serum/glucocorticoid regulated kinase
mmu-miR-23a	57	Skp2	S-phase kinase-associated protein 2 (p45)
mmu-miR-23b	57	Skp2	S-phase kinase-associated protein 2 (p45)
mmu-miR-21	62	Skp2	S-phase kinase-associated protein 2 (p45)
mmu-miR-30a	64	Skp2	S-phase kinase-associated protein 2 (p45)
mmu-miR-223	58	Smurf2	SMAD specific E3 ubiquitin protein ligase 2
mmu-miR-23a	66	Smurf2	SMAD specific E3 ubiquitin protein ligase 2
mmu-miR-23b	66	Smurf2	SMAD specific E3 ubiquitin protein ligase 2
mmu-miR-23a	50	Sntb2	syntrophin, basic 2
mmu-miR-23b	50	Sntb2	syntrophin, basic 2
mmu-miR-30a	88	Socs3	suppressor of cytokine signaling 3
mmu-miR-103	72	Sostdc1	sclerostin domain containing 1
mmu-miR-30a	75	Stk35	serine/threonine kinase 35
mmu-miR-23b	51	Stt3b	STT3, subunit of the oligosaccharyltransferase complex, homolog B ( <i>S. cerevisiae</i> )
mmu-miR-155	66	Sypl	synaptophysin-like protein
mmu-miR-16	74	Sypl	synaptophysin-like protein
mmu-miR-15b	76	Sypl	synaptophysin-like protein
mmu-miR-30a	78	Sypl	synaptophysin-like protein
mmu-miR-23b	55	Tgfbr3	transforming growth factor, beta receptor III
mmu-miR-23a	56	Tgfbr3	transforming growth factor, beta receptor III
mmu-miR-103	61	Tgfbr3	transforming growth factor, beta receptor III
mmu-miR-16	65	Tgfbr3	transforming growth factor, beta receptor III
mmu-miR-15b	66	Tgfbr3	transforming growth factor, beta receptor III
mmu-miR-214	52	Tgm2	transglutaminase 2, C polypeptide
mmu-miR-23a	90	Tmem2	transmembrane protein 2
mmu-miR-23b	90	Tmem2	transmembrane protein 2
mmu-miR-23a	66	Tmpo	thymopoietin
mmu-miR-23b	71	Tmpo	thymopoietin
mmu-miR-155	69	Tomm20	translocase of outer mitochondrial membrane 20 homolog (yeast)
mmu-miR-149	65	Tspan9	tetraspanin 9
mmu-miR-30a	92	Twf1	twinfilin, actin-binding protein, homolog 1 ( <i>Drosophila</i> )
mmu-miR-155	71	Ust	uronyl-2-sulfotransferase
mmu-miR-297a	52	Vamp3	vesicle-associated membrane protein 3
mmu-miR-30a	68	Vamp3	vesicle-associated membrane protein 3
mmu-miR-24	51	Whsc1	Wolf-Hirschhorn syndrome candidate 1 (human)
mmu-miR-214	60	Whsc1	Wolf-Hirschhorn syndrome candidate 1 (human)
mmu-miR-23a	62	Whsc1	Wolf-Hirschhorn syndrome candidate 1 (human)
mmu-miR-23b	62	Whsc1	Wolf-Hirschhorn syndrome candidate 1 (human)

mmu-miR-297a	75	Whsc1	Wolf-Hirschhorn syndrome candidate 1 (human)
mmu-miR-30a	58	Zfp238	zinc finger protein 238
mmu-miR-23a	60	Zfp238	zinc finger protein 238
mmu-miR-23b	60	Zfp238	zinc finger protein 238
mmu-miR-21	74	Zfp367	zinc finger protein 367

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20 T reg cell-specific miRNAs (miR-15b, miR-16, miR-21, miR-22, miR-23a, miR-23b, miR-24, miR-27b, miR-29c, miR-30a, miR-103, miR-125a-3p, miR-146a, miR-149, miR-155, miR-191, miR-207, miR-214, miR-223, and miR-297a) were selected. miRNA target prediction used miRDB, an miRNA target prediction and functional annotation database. 114 genes that were observed to be unregulated in Dicer KO T reg cells and also have potential targets for these 20 miRNAs are shown.