

Supplementary Figure 1. Western blot analysis of the presence of Dicer in the cell extract. Total proteins extracted from the zebrafish embryos (Cell extract) and the cell extract in which Dicer was depleted by immunoprecipitation of anti-Dicer antiserum (Dicer-) were separated on a 6% polyacrylamide gel. After sodium dodecyl sulfate-polyacrylamide gel electrophoresis, Western blot analysis was performed by using anti-Dicer (Santa Cruz). Dicer was present in the cell extract and in the dissolved immunoprecipitate (IP), whereas Dicer was completely depleted in the cell extract after anti-Dicer immunoprecipitation was treated.

Supplementary Figure 2. Western blot analysis of the presence of Ago protein. Total proteins were obtained from the affinity purification of DIG-tagged miR-1 (miR-1), DIG-tagged mutated miR-1 (Mutated miR-1) and DIG-tagged mutated let-7 (Mutated let-7) from cell extracts and separated on the SDS-PAGE. The anti-Ago antibody was used to perform Western blot analysis. The immuno-positive band against Ago was shown on all the extracts from miR-1, mutated miR-1 and mutated let-7.

Supplementary Figure 3. The matching sequences between *miR-1* and its target mRNA of zebrafish *hand2*. The mir-blast software was used to analyze the alignment between miR-1 and zebrafish *hand2*. Results indicate that there is a binding site located at the 3' untranslated region of *hand2*, where the conserved residues match miRNA sequences (indicated in red).

Supplementary Table 2. Microarray data for top 302 mRNAs from miR-1 pull-down experiments and the corresponding detection values for miR-1 MUT, showing Probe ID, common name and normalized detection values from two experiments.

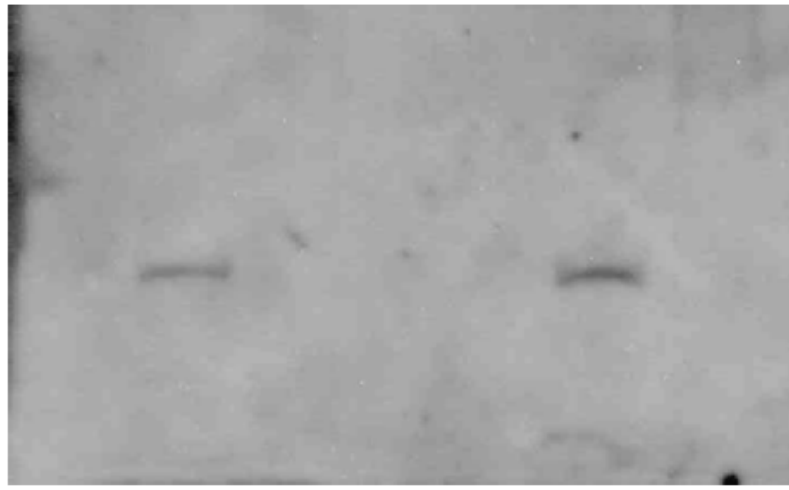
Cell extract

Cell extract (Dicer-)

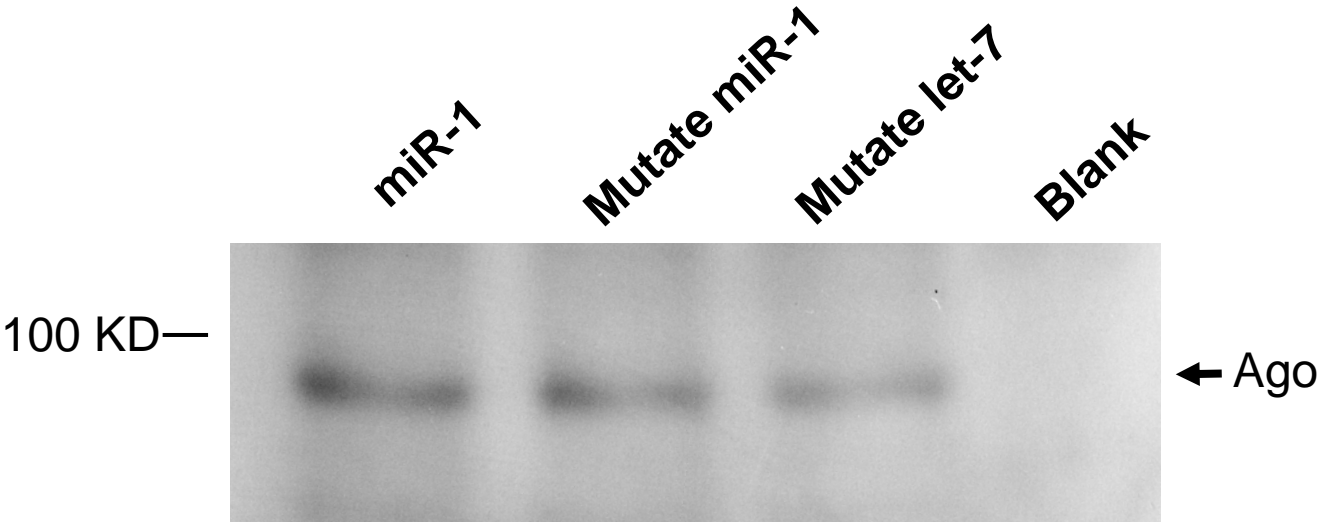
IP: Dicer

250 kDa →

130 kDa →



← Dicer



miR-1: AUGUAUGAAGAAU-----GUAAGGU
 || ||||| |||||
hand2 3'UTR: GACAUUAGAUUUUGAGGAAAACCAUCCAUUU

Table S1 Primer sequences

Name	oligonucleotide sequences (5'→3')	description
Cel-Pre-lin4-1F	ATGCTTCCGGCTGTTCCCTGAGACCTCAAGTGTGAGTG	nt 499- 538
Cel-Pre-lin4-2F	AAGTGTGAGTGACTATTGATGCTTCACACCTGGGCTCT	nt 527-566
Cel-Pre-lin4-1R	ATCTGCTCAAACCGTCCTGGTACCCGGAGAGCCCAGGTG	nt 592-555
Cel-Pre-let7-1F	TACTGTGGATCCGGTGAGGTAGTAGTTGTATAGTTT	nt 1747-1789
Cel-Pre-let7-2F	TGTATAGTTTGAATATTACCACCGGTGAACTATGCAAT	nt 1775-1814
Cel-Pre-let7-1R	TCGAAGAGTTCTGTCTCCGGTAAGGTAGAAAATTGCAA	nt 1845-1806
Cel-Pre-let7M-1F	TACTGTGGATCCGGTGAGGTAGAACGAAGTATAGTTT	
Cel-Pre-let7M-2F	AGTATAGTTTGAATATTACCACCGGTGAACTATGCAAT	
Cel-Pre-let7M-1R	TCGAAGAGTTCTGTCTCCGGTAAGGTAGAAAATTGCATA	
ZF-Pre-let7-1F	GAGGTAGTAGGTTGTATAGTTTTAGGGTCACACCCACC	nt 143959-143920
ZF-Pre-let7-2F	TAGTTTTAGGGTCACACCCACCACTGGGAGATAACTATA	nt 143942-143903
ZF-Pre-let7-1R	GGGTGGTGACCCTCTATTGATATGTTAGATGACAGAAAG	nt143881-143910
ZF-Pre-miR1-1F	GCCCATATATCCCGCTGGTAGACATACTTCTTTATATG	nt 166173-166134
ZF-Pre-miR1-1R	TTTATATGCCCATATGAACAAGAGCAGCTATG	nt 166141-166102
ZF-Pre-miR1-1R	TGGGATACATACTTCTTTACATTCCATAG	nt 166110-166071
ZF-Pre-miR1-2R	GCCCCGTTTTTCTCTCACCTGGGATACA	nt 166068-166080
ZF-Pre-miR1M-2F	TTTATATGCCCATATGAACAAGAGCAGCTAT _c	
ZF-Pre-miR1M-1R	TGGGATACATACTTCTTTAC _{ta} TgCATAG	
Cel-lin41F	GATCCCTTGATCCTTCTTGC	nt 3519-3499
Cel-lin41R	CGGAGCCATATGAATGGATG	nt 3920-3911
Cel-Hbl-1F	GGACGTCCTCGTTAAGGAAAC	nt 3079-3099
Cel-Hbl-1R	ATCCCGAAGTTAATAAGAGG	nt 3540-3521
Cel-lin14F	CAATGTTCGAAATCCCCGTTT	nt 1337-1356
Cel-lin14R	GCTTCAGGCGATACTGTTC	nt 1833-1812
Cel-lin28F	CCTCTGATGAATAGAATCACTC	nt 696-716
Cel-lin28R	GATGATTCTATTCATCAGAGG	nt 991-1010
Cel-ef2F	GTCAACTTCACGGTCGATG	nt 34-52
Cel-ef2R	TCCGAGCTTCTCAACAAGAGC	nt 972-952
ZF-lin41F	ATAAGACTGCTGCAAGCTGAGAG	nt 1-23
ZF-lin41R	TCAGGGATATAACTTGCGTTC	nt 379-358
ZF-hand2-3' UTR-F	GGCCATCTGAACTATTTTATG	nt1141-1162
ZF-hand2-3' UTR-R	GTTTGTGTCTTCGGACGGAAG	nt1565-1585
ZF-β-actinF	GGCACGAGAGATCTTCACTCCC	nt 1-22
ZF-β-actinR	CCGATCCAGACGGAGTATTTGCG	nt 1078-1056
TS primer	AAGCAGTGGTAACAACGCAGAGTACGCGGG	

nucleotide (nt)

Table S2 Microarray analysis presented by LAMIPAS for zebrafish miR-1 probe

Probe ID	WT Raw Signal	MT Raw Signal	normalized Ratio (WT/MT)	Common Name
A_15_P195461	112737.6	6.744765	53,163	hand2
A_15_P139791	211485	30.94004	21,741	hsp70-4
A_15_P138581	261974.2	48.39565	17,217	NCN
A_15_P191111	4596.214	6.138789	2,381	epn4
A_15_P584272	3809.017	7.05483	1,717	
A_15_P580728	2111.8	6.142564	1,093	
A_15_P149826	3791.559	12.11153	995.7	nedd4a
A_15_P546627	2045.285	6.998787	929.5	LOC798015
A_15_P426210	23029.81	81.32103	900.7	
A_15_P215281	1570.749	6.226203	802.4	LOC553494
A_15_P169516	10298.77	41.15472	795.9	fb61d02
A_15_P584142	1562.155	6.796371	731.1	
A_15_P100163	1729.736	7.897229	696.7	zgc:103521
A_15_P299911	5867.391	27.6957	673.8	
A_15_P131451	5017.448	25.20416	633.2	isl2
A_15_P610062	6524.688	36.26974	572.2	
A_15_P201236	1282.604	7.152338	570.4	entgLOC571027
A_15_P515886	1118.904	6.567261	541.9	
A_15_P460980	1062.729	6.242546	541.5	LOC559212
A_15_P575367	9828.417	50.58489	511.7	suclg1
A_15_P578547	1873.737	11.67252	510.6	LOC561142
A_15_P241486	11963.17	76.02713	500.5	LOC100000804
A_15_P612242	930.1458	6.207293	476.6	LOC100000556
A_15_P596992	892.7289	6.034088	470.6	zgc:158387
A_15_P177256	1005.584	7.138385	448.1	nr5a5
A_15_P444815	1812.052	13.28376	433.9	
A_15_P382130	3676.944	29.20111	400.5	zgc:110313
A_15_P289026	778.8423	6.482828	382.1	LOC565834
A_15_P371420	4617.821	39.87967	368.3	
A_15_P452770	618.9743	5.653852	348.2	
A_15_P498812	2673.045	24.68297	344.4	LOC100007541
A_15_P161386	986.3221	9.318299	336.7	pvalb3b
A_15_P119814	592.9164	5.715904	329.9	zgc:77659
A_15_P590252	799.3277	7.749044	328.1	

A_15_P289151	709.4306	7.084238	318.5	LOC792877
A_15_P313551	1536.355	15.41215	317.1	
A_15_P391435	739.4811	7.426985	316.7	
A_15_P107534	3121.57	33.96794	292.3	zgc:103443
A_15_P141466	3573.355	39.26662	289.4	fut9
A_15_P111524	1601.287	17.80825	286	olfr2.8
A_15_P369610	6460.729	72.31904	284.1	
A_15_P449735	3445.134	39.18846	279.6	LOC799448
A_15_P551227	2813.233	32.66784	273.9	si:dkey-76p14.2
A_15_P554632	1194.867	14.34012	265	LOC798934
A_15_P203841	512.8302	6.196714	263.2	
A_15_P118156	1991.086	24.69777	256.4	zgc:136280
A_15_P307921	812.4374	10.16774	254.1	
A_15_P215911	4056.863	52.08939	247.7	LOC563327
A_15_P388960	2072.211	26.67683	247.1	LOC793696
A_15_P517182	580.192	7.620772	242.1	wu:fc06h10
A_15_P441985	2698.655	35.57912	241.2	LOC100000720
A_15_P567317	4314.466	57.37854	239.2	
A_15_P559122	557.1886	7.759026	228.4	
A_15_P462165	837.5907	11.7026	227.6	LOC100008273
A_15_P391225	522.4305	7.29933	227.6	LOC796852
A_15_P174911	4193.81	58.70719	227.2	lect2
A_15_P107891	609.3993	8.897997	217.8	LOC558924
A_15_P524512	533.3239	7.940948	213.6	
A_15_P232661	667.9069	11.35441	187.1	
A_15_P409800	1090.465	18.81411	184.3	LOC799775
A_15_P269656	542.4277	9.595135	179.8	entg LOC566073
A_15_P589087	4451.406	80.98185	174.8	
A_15_P119253	923.6432	16.81963	174.7	wu:fe01a10
A_15_P328421	4117.614	76.64507	170.9	
A_15_P397705	2254.214	43.74457	163.9	LOC100005987
A_15_P490937	737.7007	14.31151	163.9	LOC100004123
A_15_P132286	1011.515	21.19531	151.8	zgc:91947
A_15_P461670	1221.573	27.42701	141.7	
A_15_P398975	2305.448	51.79372	141.6	LOC556262
A_15_P452315	1848.454	43.65344	134.7	entg zgc:171516
A_15_P208331	599.6405	14.2022	134.3	pop1; zgc:86887
A_15_P503742	608.9254	15.71751	123.2	zgc:66008

A_15_P156261	783.5289	20.29741	122.8	
A_15_P435080	842.4722	21.95199	122.1	entg LOC556826
A_15_P146286	1730.875	45.75627	120.3	parvalbumin 4
A_15_P171917	606.4738	16.95807	113.7	z-28; hoxd9
A_15_P408365	1223.904	35.39129	110	MGC64051
A_15_P480855	547.3127	16.49761	105.5	
A_15_P553017	1695.573	52.46911	102.8	
A_15_P268401	1051.189	33.17826	100.8	
A_15_P516407	654.3865	20.76135	100.3	wu:fc02a12
A_15_P565662	625.1946	19.90524	99.9	zgc:92808
A_15_P229006	551.7773	18.43202	95.21	zgc:76878
A_15_P242391	657.9025	22.00142	95.11	LOC796345
A_15_P243276	669.9573	22.63853	94.13	si:dkey-94n12.2
A_15_P238026	2305.476	78.43646	93.49	
A_15_P193851	1723.051	58.69859	93.36	MGC110031
A_15_P551847	774.0115	26.37196	93.35	
A_15_P536627	702.8545	24.03226	93.02	entg LOC571844
A_15_P106795	1454.765	50.44018	91.73	zgc:112439
A_15_P362343	899.0071	31.45905	90.89	
A_15_P251921	1155.918	42.25878	87	
A_15_P552352	2142.268	83.01441	82.08	
A_15_P142506	1302.95	51.75174	80.08	zgc:64086
A_15_P133961	914.9298	36.76261	79.16	AA-NAT
A_15_P587652	5128.692	206.7739	78.89	entg zgc:110158
A_15_P131501	523.6769	22.14466	75.22	wt1; zwt1
A_15_P316776	1128.656	48.07121	74.68	
A_15_P100468	806.0082	34.5574	74.18	zgc:85935
A_15_P160741	1179.386	51.95231	72.2	zgc:110576
A_15_P156016	537.6212	24.16306	70.77	LOC100003810
A_15_P188286	3601.382	167.5536	68.36	zgc:56524
A_15_P161631	1330.908	62.44604	67.79	zgc:55577
A_15_P610562	1081.304	53.40516	64.4	LOC100000391
A_15_P162711	1643.503	82.16133	63.62	sdca4
A_15_P393815	503.1127	25.31691	63.21	
A_15_P171126	732.0505	37.55036	62.01	si:dkey-12h9.2
A_15_P196596	1654.551	85.06415	61.86	zgc:101085
A_15_P367530	3033.936	156.2681	61.75	Tal; MGC56232
A_15_P121060	840.082	44.17083	60.49	zgc:103711

A_15_P269676	1532.97	80.84517	60.31	LOC571255
A_15_P443505	742.6913	40.76455	57.95	entg LOC571836
A_15_P245701	710.6388	39.23662	57.61	
A_15_P120385	7966.934	447.5265	56.62	fj42d12
A_15_P181056	2995.226	172.6526	55.18	entg LOC407683
A_15_P483075	994.0124	62.31622	50.73	entg LOC559281
A_15_P114680	1117.076	71.32021	49.82	zgc:110067
A_15_P454255	751.6255	48.1236	49.68	
A_15_P248956	1508.941	98.18625	48.88	
A_15_P297541	871.2495	56.94965	48.66	cacnb4b
A_15_P323016	530.3931	34.66862	48.66	entg wu:fj51h02
A_15_P370030	639.2548	41.96791	48.45	
A_15_P443140	518.5936	34.0592	48.43	entg LOC558116
A_15_P554637	800.5389	52.59349	48.41	
A_15_P203801	915.4548	60.38067	48.22	MGC123214
A_15_P362115	592.0196	39.13732	48.11	
A_15_P131006	1561.26	104.3067	47.61	zgc:77257
A_15_P315801	1260.746	86.4956	46.36	
A_15_P310786	500.994	36.89783	43.19	
A_15_P588032	802.5982	59.82561	42.67	
A_15_P175296	1660.124	124.6198	42.37	capsl
A_15_P259631	584.3059	44.0435	42.2	MGC65997
A_15_P260641	1459.602	110.3462	42.07	
A_15_P152236	615.6214	46.53729	42.07	zgc:113041
A_15_P583412	79159.22	5989.548	42.04	
A_15_P204506	644.9083	48.9121	41.94	entg LOC567631
A_15_P189306	567.3779	45.86764	39.34	
A_15_P452385	543.267	44.4501	38.87	LOC563791
A_15_P222841	4576.89	384.8388	37.83	
A_15_P497907	910.4883	77.30328	37.46	LOC794516
A_15_P244111	569.9094	48.38465	37.46	
A_15_P219471	1538.885	131.9506	37.09	zgc:162249
A_15_P409970	642.9407	56.09779	36.45	
A_15_P197261	1157.826	101.2058	36.39	
A_15_P369465	630.9089	58.01611	34.59	entg LOC558325
A_15_P160121	822.113	77.18916	33.88	
A_15_P388850	127.5211	12.324	32.7	Sars
A_15_P109869	540.4793	56.31104	30.53	si:ch211-105n9.1

				cb235; fb39c11; fc51e12; zeh1207;
A_15_P206546	746.6943	79.83739	29.75	sb:cb235; hm:zeh1207; wu:fb39c11; wu:fc51e12
A_15_P412475	812.7591	87.81868	29.44	LOC100007149
A_15_P533622	552.2031	60.08588	29.23	LOC570248
A_15_P241356	1101.959	123.0269	28.49	LOC797088
A_15_P404700	867.9293	105.0054	26.29	
A_15_P467290	4894.407	597.1747	26.07	
A_15_P428820	770.5859	94.11853	26.04	
A_15_P104288	513.2694	62.95544	25.93	actr3
A_15_P597697	592.7314	74.22234	25.4	LOC797715
A_15_P518027	543.607	68.8767	25.1	LOC100008150
A_15_P297186	531.7836	68.71512	24.61	LOC798944
A_15_P195576	512.0662	69.88439	23.31	MGC55975; zgc:55975
A_15_P187996	870.3597	120.4484	22.98	
A_15_P413945	607.4908	85.56991	22.58	entg aldh5a1
A_15_P139451	1455.539	209.3156	22.12	zgc:110852
A_15_P330646	713.3187	103.0937	22.01	
A_15_P144191	692.5272	101.5078	21.7	entg LOC569977
A_15_P404905	6859.033	1006.627	21.67	
A_15_P248611	818.8273	121.3037	21.47	
A_15_P333584	2131.703	316.206	21.44	zgc:158463
A_15_P583952	505.873	75.73867	21.24	
A_15_P451105	3140.786	473.0198	21.12	
A_15_P454660	514.6307	77.67033	21.07	
A_15_P116336	503.11	79.61873	20.1	
A_15_P578087	887.4809	144.3246	19.56	
A_15_P114305	630.0089	102.5846	19.53	
A_15_P401690	614.4205	100.5291	19.44	LOC100005868
A_15_P462675	829.6454	146.8089	17.97	
A_15_P451335	1043.889	187.3899	17.72	
A_15_P369685	654.9993	121.236	17.18	
A_15_P507047	1028.331	190.6577	17.15	zgc:158313
A_15_P266491	591.4842	111.5324	16.87	tpma

A_15_P372650	2075.064	394.322	16.74	
A_15_P385280	601.1452	115.8459	16.5	
A_15_P217776	2449.408	482.1613	16.16	MGC153462
A_15_P200281	732.6837	145.8674	15.98	
A_15_P404660	908.9371	185.0196	15.63	LOC100005890
A_15_P401905	1263.177	263.3439	15.26	LOC560678
A_15_P369775	601.8929	126.7054	15.11	
A_15_P597322	616.4723	130.375	15.04	
A_15_P546302	1391.695	296.5127	14.93	LOC100000041
A_15_P119642	1580.127	339.9044	14.79	
A_15_P336640	3475.614	762.124	14.5	setd5
A_15_P220321	551.3976	121.8557	14.39	
A_15_P394305	1191.392	279.5276	13.56	LOC570868
A_15_P461970	2970.575	698.5419	13.53	
A_15_P484155	593.4229	142.3012	13.26	col4a1; fc02g11; wu:fc02g11
A_15_P279816	1712.826	416.3408	13.09	LOC557744
A_15_P402390	730.789	178.4655	13.02	e(r); zgc:86761
A_15_P433400	529.44	129.5557	13	LOC556563
A_15_P204106	637.3677	156.1124	12.99	entg hdac9b
A_15_P144301	2025.582	506.7237	12.71	entg LOC567842
A_15_P318451	1483.493	385.6631	12.23	
A_15_P329921	1258.94	333.524	12.01	
A_15_P469210	685.2981	181.7429	11.99	
A_15_P526407	536.4605	148.1323	11.52	
A_15_P516752	519.7576	145.685	11.35	LOC561758
A_15_P313511	2532.776	711.9219	11.32	
A_15_P113380	1604.906	457.3489	11.16	
A_15_P141861	606.5813	174.0033	11.09	Shfdg1; fb55c02; zgc:56203; zgc:85901; wu:fb55c02
A_15_P277501	1432.457	414.524	10.99	zgc:110070
A_15_P308106	1220.293	364.9511	10.64	
A_15_P247981	979.0344	303.4516	10.26	
A_15_P576647	533.9608	169.0651	10.05	
A_15_P113908	700.7125	226.8046	9.827	
A_15_P575042	1621.177	541.1687	9.528	

A_15_P141781	692.1289	236.1989	9.32	MGC136325
A_15_P117663	781.9702	268.0876	9.277	entg CH211-198N5.11
A_15_P238216	623.0198	218.012	9.089	
A_15_P161006	7578.78	2738.865	8.801	MGC153954
A_15_P291361	1536.189	582.9856	8.381	entg LOC792944
A_15_P115713	530.9062	202.0089	8.359	entg LOC563577
A_15_P326866	2537.123	978.8559	8.244	
A_15_P350755	920.6272	361.8256	8.093	
A_15_P443160	1002.47	407.3737	7.827	LOC795217
A_15_P253856	1628.621	662.8839	7.814	
				odc; fc54f04; fi06d08;
A_15_P170821	2170.17	910.7068	7.579	CHUNP6922; wu:fc54f04; wu:fi06d08
A_15_P547182	585.298	253.2537	7.351	
A_15_P583252	618.2911	271.2504	7.25	
A_15_P556347	610.1992	269.8315	7.193	entg LOC568122
A_15_P523692	625.6119	279.2233	7.126	
A_15_P172471	626.7649	281.8995	7.072	MGC123321
A_15_P118768	740.0267	346.4795	6.793	MGC55887; zgc:55887
A_15_P555972	984.0913	471.4651	6.639	LOC572258
A_15_P439095	614.5045	294.9222	6.627	entg KIAA0261
A_15_P351555	1085.583	557.9819	6.188	
A_15_P215991	960.147	494.1694	6.18	tri; stbm; vang fb99h10; tdsbc_2c6;
A_15_P102849	732.1453	383.7244	6.069	wu:fb99h10; ik:tdsbc_2c6; xx:tdsbc_2c6
A_15_P282626	1807.671	974.9644	5.897	
A_15_P577747	4344.616	2587.896	5.34	
A_15_P446415	973.438	610.388	5.072	zgc:103631
A_15_P462330	1194.541	787.5543	4.824	LOC100007650
A_15_P519412	502.3961	343.1029	4.657	
A_15_P262221	506.4832	355.7664	4.528	wu:fk52g02
A_15_P358625	2197.587	1605.579	4.353	
A_15_P597267	535.0222	410.6529	4.144	c20orf149
A_15_P309326	574.0817	441.9062	4.132	

A_15_P464870	622.6881	490.5413	4.037	
A_15_P376420	571.1636	473.4774	3.837	
A_15_P114676	1363.153	1156.893	3.748	
A_15_P152906	1691.816	1441.074	3.734	zgc:158280
A_15_P430240	699.0459	612.3196	3.631	
A_15_P564517	1232.146	1325.136	2.957	entg COX1
A_15_P307641	1402.378	1514.03	2.946	
A_15_P111288	783.2648	877.2008	2.84	sb:cb794; id:ibd3393
A_15_P476815	591.7214	695.6127	2.706	
A_15_P536027	556.5851	654.8063	2.704	
A_15_P520142	696.7422	822.1862	2.695	sb:cb597
A_15_P237256	716.7628	868.8485	2.624	
A_15_P609917	833.0049	1021.274	2.594	
A_15_P400345	722.0431	963.5673	2.383	LOC796736
A_15_P141801	519.9757	704.8384	2.346	MGC114157
A_15_P409225	4201.538	5753.578	2.323	LOC794331
A_15_P286756	1593.408	2330.464	2.175	Ptk; tec; ZFPtk
A_15_P386375	502.4079	753.0919	2.122	
A_15_P283386	796.5646	1200.733	2.11	
A_15_P595322	642.8374	1111.424	1.84	
A_15_P591817	1408.812	2488.809	1.8	SH3BGRL; MGC64130
A_15_P101439	1023.596	1816.089	1.793	zgc:136505
A_15_P560162	570.0735	1041.125	1.742	
A_15_P262961	601.594	1132.377	1.69	
A_15_P106403	1461.7	2754.554	1.688	cb326; fb36c12; wu:fb36c12 cTnT; zeh0954;
A_15_P192466	93019.07	176096	1.68	MGC123151; hm:zeh0954 cTnT; zeh0954;
A_15_P260616	30446.78	57669.35	1.679	MGC123151; hm:zeh0954
A_15_P283861	551.9881	1090.878	1.609	
A_15_P255041	535.6234	1060.366	1.607	
A_15_P428615	738.808	1504.818	1.562	
A_15_P193236	544.8239	1143.552	1.515	zeh0819; MGC77664; zgc:73129;

zgc:77664;

hm:zeh0819

A_15_P427195	1793.23	3792.965	1.504	
GE_BrightCorner	2663.7874	5719.4614	1.481	
A_15_P411085	541.1392	1174.168	1.466	MGC111960
A_15_P574142	514.2937	1122.541	1.457	LOC565141
A_15_P571557	581.2514	1293.976	1.429	entgLOC799508
A_15_P370160	651.6943	1508.844	1.374	
A_15_P359895	744.7673	1731.351	1.368	
A_15_P520127	521.3237	1303.492	1.272	
A_15_P536267	876.2537	2215.968	1.258	
A_15_P109273	602.846	1545.618	1.241	MGC73262
A_15_P354405	617.2427	1665.014	1.179	
A_15_P390895	563.4147	1527.451	1.173	
A_15_P335940	1784.431	4950.619	1.146	
A_15_P546442	1158.545	3428.299	1.075	LOC798405
A_15_P372475	520.2233	1573.787	1.051	
A_15_P390815	556.2657	1756.853	1.007	
