Supplementary material associated with the publication:

SmithRNAs: a common feature among Metazoa

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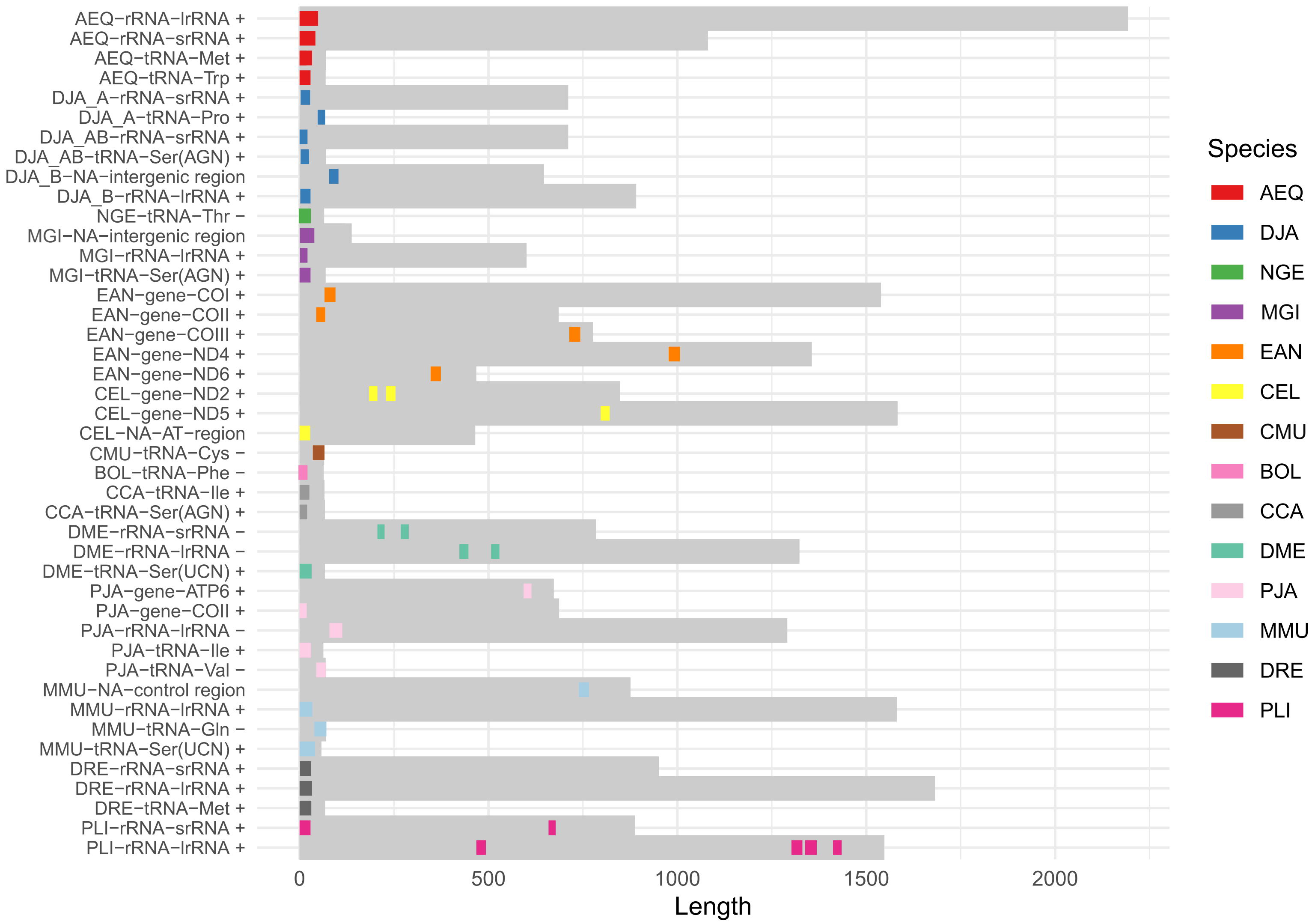

Figure S1: Position of smithRNAs relative to the genomic region where they are encoded. Grey and colored boxes represent the genomic region and smithRNAs, respectively. Species are color coded. Gene strandedness is indicated as + (sequenced strand) or – (complement strand).

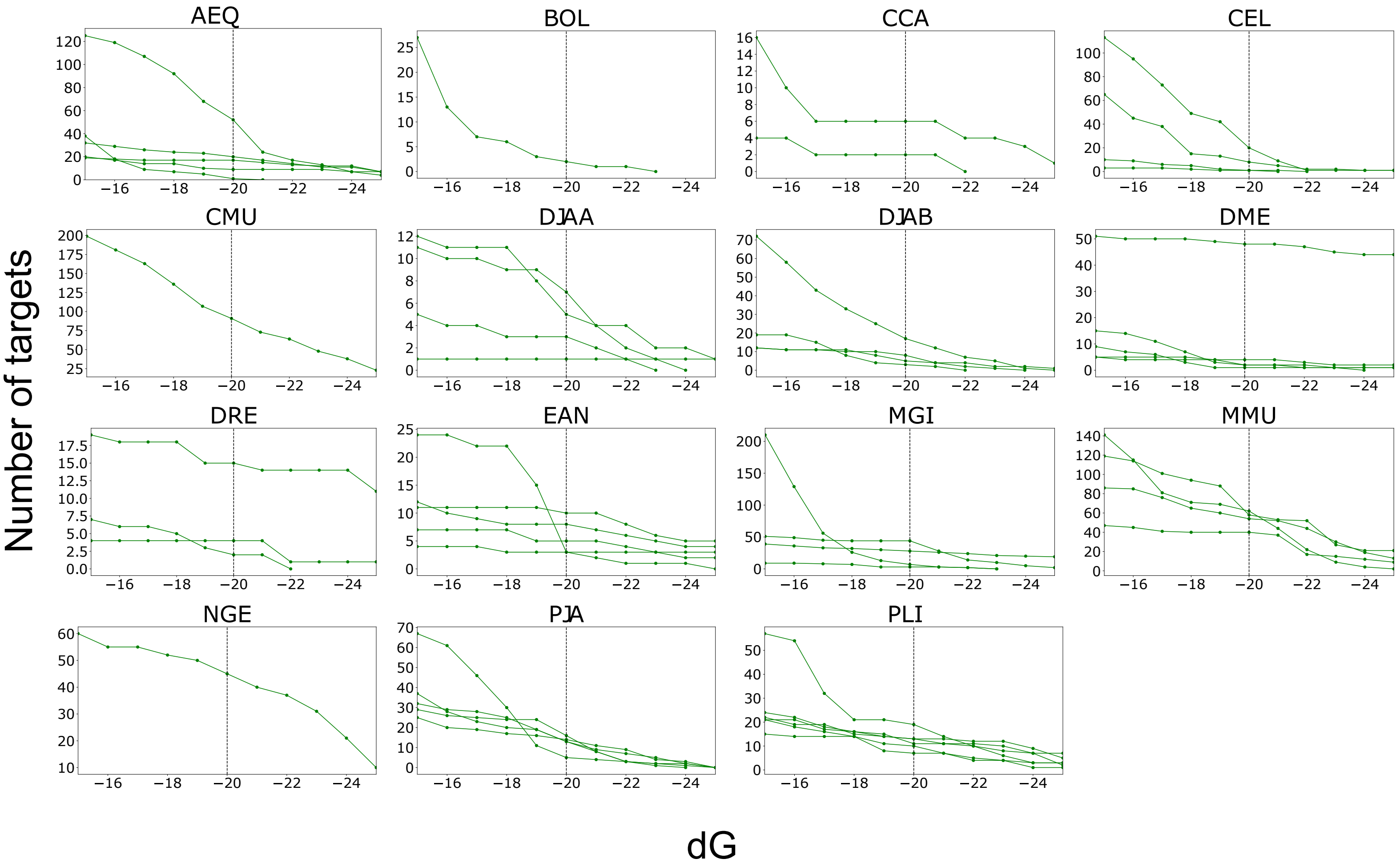

Figure S2: Number of identified nuclear targets as a function of smithRNA-target binding energy. Each green line identifies a different smithRNA.

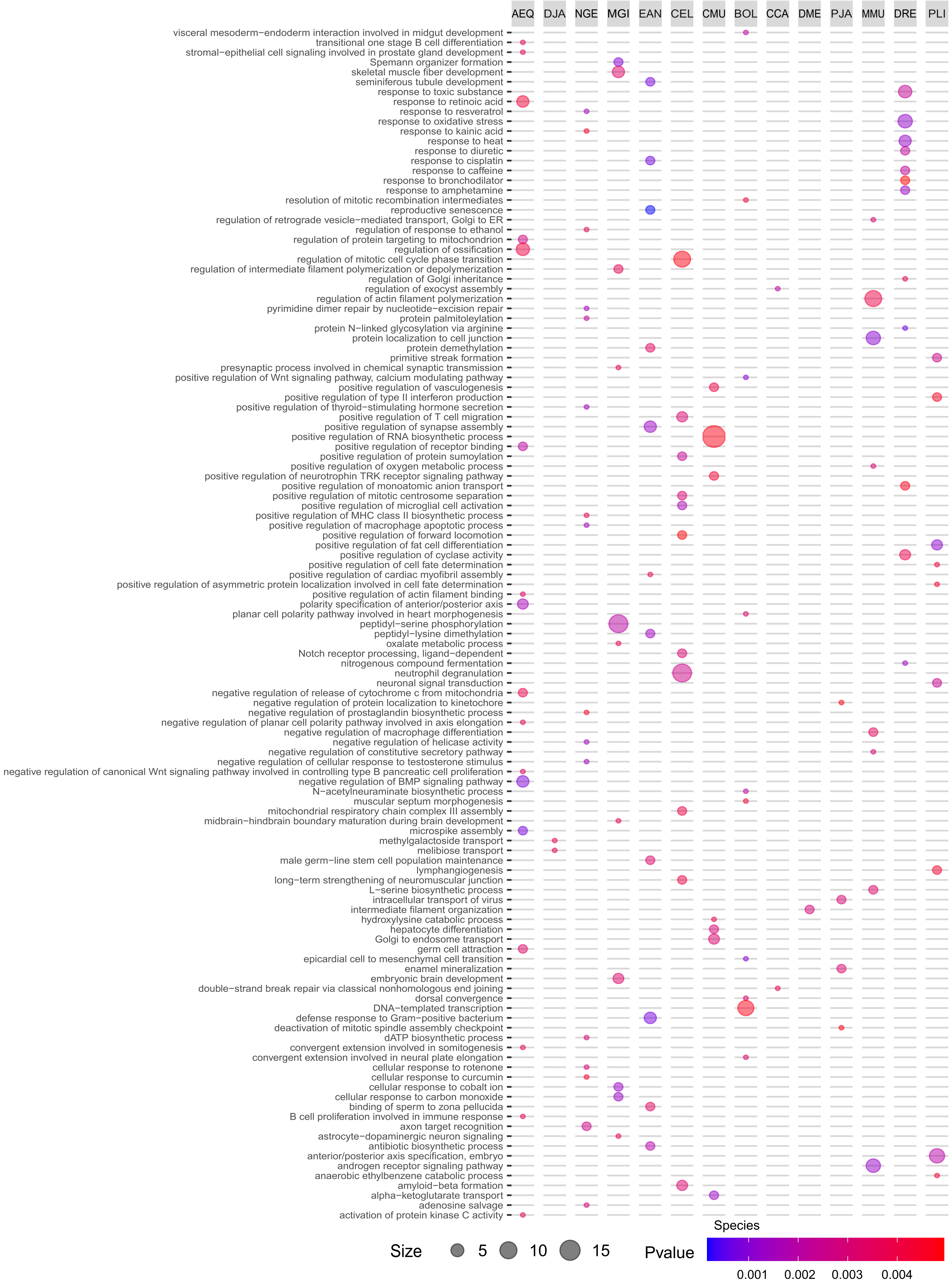

Figure S3: GO enrichment analysis of biological processes performed on the supposed nuclear targets of smithRNAs, by species. See Fig. S4 for molecular functions and cellular components. Circle area represent the number of genes, the p-value is color coded. See Table 1 for species abbreviations

Figure S4: GO enrichment analysis of molecular functions (A) and cellular components (B) performed on the supposed nuclear targets of smithRNAs by species. See Figure 5 and Figure S3 for biological processes. Circle area represent the number of genes, the p-value is color coded

Table S1: transcriptome sequencing. Accession numbers (SRA), biological origin, and the number of raw and filtered reads are indicated for each library. The total number of raw and filtered reads is indicated per species.

Species	SRA accession	Tissue	Raw (read pairs)	Total raw (read pairs)	Filtered (reads pairs)	Total filtered (read pairs)
A. equina	SRR28330942	whole body	35.295.370		5.501.922	
	SRR28330941	whole body	35.453.947		33.134.786	
	SRR28330940	whole body	33.906.265		31.493.426	
	SRR28330939	whole body	35.343.874		33.240.197	
	SRR28330938	whole body	35.064.132	175.063.588	32.969.535	136.339.866
B. oleae	SRR8800824	whole body	34.849.995		24.583.040	
	SRR8800826	whole body	40.630.107		31.532.742	
	SRR8800835	whole body	38.678.071		27.468.455	
	SRR8800833	whole body	37.651.087	151.809.260	29.022.804	112.607.041
Cae. elegans	SRR7443965	hypodermis	37.717.253		2.117.657	
	SRR7443967	neurons	31.348.071		7.252.421	
	SRR7443968	neurons	33.110.795		7.435.022	
	SRR7443975	neurons	32.346.851	134.522.970	2.964.308	19.769.408
Car. multidentata	SRR28330958	whole body	39.609.960		35.007.681	
	SRR28330957	whole body	39.034.511		35.216.020	
	SRR28330956	whole body	36.448.034		31.006.198	
	SRR28330955	whole body	35.244.991		31.488.607	
	SRR28330954	whole body	35.930.691	186.268.187	31.772.868	164.491.374
Ce. capitata	SRR836188	whole body	27.777.737		5.219.824	
	SRR836189	whole body	25.891.361		5.421.987	
	SRR836190	whole body	31.016.416	84.685.514	6.216.464	16.858.275
Da. rerio	SRR5181405	gonads	40.090.189		29.551.196	
	SRR5181406	gonads	37.897.175		27.536.049	
	SRR5181411	gonads	38.346.079		25.503.458	
	SRR5181412	gonads	33.550.183	149.883.626	22.347.735	104.938.438
Dr. melanogaster	SRR5181405	gonads	12.157.192		7.575.689	
	SRR5181406	gonads	10.144.040		6.312.856	
	SRR5181411	gonads	6.868.154		3.973.422	
	SRR5181412	gonads	10.341.764	39.511.150	6.915.772	24.777.739
Du. japonica	SRR28330935	whole body	37.439.968		34.657.203	
	SRR28330934	whole body	35.985.210		33.170.338	
	SRR28330933	whole body	38.664.038		35.703.103	
	SRR28330932	whole body	35.703.235		33.097.739	
	SRR28330931	whole body	42.317.149	190.109.600	39.110.851	175.739.234
E. andrei	SRR28330960	whole body	42.035.147		39.028.360	
	SRR28330959	whole body	40.333.571		37.990.828	
	SRR28330948	whole body	42.274.042		39.949.408	
	SRR28330937	whole body	35.142.458		33.078.754	
	SRR28330936	whole body	32.989.091	192.774.309	31.169.563	181.216.913
Ma. gigas	SRR13528977	gonads	55.680.106		47.427.817	
	SRR13528978	gonads	47.608.066		39.912.255	
	SRR13528979	gonads	47.772.090		41.250.563	
	SRR13528980	gonads	63.158.655		43.569.069	
	SRR13528983	gonads	43.471.193		37.079.882	
	SRR13528984	gonads	50.260.430	307.950.540	42.897.930	252.137.516
Mu. musculus	SRR16832607	gonads	37.861.037		30.449.676	
	SRR16832608	gonads	39.905.457		32.216.464	
	SRR16832609	gonads	38.364.179		31.394.377	
	SRR16832610	gonads	41.127.811		30.266.048	
	SRR16832611	gonads	40.789.383		33.227.390	
	SRR16832612	gonads	36.632.747	234.680.614	27.423.844	184.977.799
N. geniculatus	SRR5811964	gonads	17.233.380		14.564.966	
	SRR5811966	gonads	17.250.875		16.154.404	
	SRR5811967	gonads	16.130.732		15.187.895	
	SRR5811970	gonads	16.473.717	67.088.704	15.330.559	61.237.824
Pa. lividus	SRR28330943	gonads	38.270.799		36.128.014	
	SRR28330947	gonads	33.187.852		31.379.661	
	SRR28330946	gonads	34.967.849		31.958.121	
	SRR28330945	gonads	40.025.085		37.765.963	
	SRR28330944	gonads	33.289.808		31.151.480	
	SRR28330943	gonads	39.115.050		36.719.822	
	SRR28330952	gonads	39.022.595		36.782.161	
	SRR28330951	gonads	39.366.661		36.720.744	
	SRR28330950	gonads	37.032.699		33.640.372	
	SRR28330949	gonads	39.787.721	374.066.119	37.373.548	349.619.886
Po. japonica	SRR20647943	whole body	46.697.613		34.010.274	
	SRR20647941	whole body	51.997.688		44.228.788	
	SRR20647945	whole body	43.120.800		38.558.938	
	SRR20647948	whole body	43.680.037		38.997.322	
	SRR20647950	whole body	41.568.118		35.096.751	
	SRR20647932	whole body	51.649.684		42.629.648	
	SRR20647936	whole body	41.014.055		34.752.395	
	SRR20647934	whole body	45.901.875	365.629.870	39.950.256	308.224.372

Table S2: transcriptome assembly and annotation. Assembly information for all species is reported as: transcriptome size, number of contigs, average contig size and N50, BUSCO completeness statistics, percentage of properly remapping reads. BUSCO statistics are indicated as percentage of 'Complete [Single copy, Duplicated], Fragmented, Missing'. Annotation information is reported as: number of genes, number of isoforms, number of UTRs

Species	Transcript size (bp)	n° of contigs	Aver. contig size (bp)	N50 (bp)	BUSCO	Properly mapping reads (%)	n° genes	n° isoforms	n° UTRs
A. equina	251862622	243629	1033	2168	C:96.8%[S:41.5%,D:55.3%],F:1.2%,M:2.0%	91,55	26018	71398	102793
B. oleae	115706881	90631	1276	2998	C:95.3%[S:61.3%,D:34.0%],F:0.3%,M:4.4%	96,99	12861	28775	48135
Cae. elegans	47979731	45481	1055	1875	C:63.8%[S:35.6%,D:28.2%],F:9.7%,M:26.5%	86,96	13341	21776	28316
Car. multidentata	347221602	267470	1298	3241	C:98.1%[S:37.5%,D:60.6%],F:0.6%,M:1.3%	95,06	25080	71878	112211
Ce. capitata	167719830	203846	822	1538	C:93.8%[S:64.0%,D:29.8%],F:1.2%,M:5.0%	92,27	15405	29486	43700
Da. rerio	127959264	115414	1108,70	2253	C:98.9%[S:61.2%,D:37.7%],F:0.6%,M:0.5%	90,57	23123	42883	63774
Dr. melanogaster	76100984	72514	1049,47	2059	C:89.2%[S:60.3%,D:28.9%],F:7.9%,M:2.9%	91,57	14166	27296	37278
Du. japonica	59356547	64267	923	1627	C:96.8%[S:41.5%,D:55.3%],F:1.2%,M:2.0%	91,85	16939	34510	41507
E. andrei	223980358	275628	812	1478	C:92.0%[S:47.8%,D:44.2%],F:4.7%,M:3.3%	90,38	39508	83710	92503
Ma. gigas	478101424	554331	862,48	1695	C:98.5%[S:37.1%,D:61.4%],F:1.4%,M:0.1%	95,77	38587	104641	145566
Mu. musculus	1009106044	1568414	643,39	884	C:98.7%[S:20%,D:78.7%],F:0.8%,M:0.5%	91,8	74674	151227	226316
N. geniculatus	305559287	334915	912,35	1825	C:98.9%[S:25.4%,D:73.5%],F:0.7%,M:0.4%	88,86	31131	80721	112193
Pa. lividus	724935223	1099158	659	936	C:96.7%[S:12.7%,D:84.0%],F:2.2%,M:1.1%	91,16	46806	153757	164988
Po. japonica	279438688	278215	1004	2495	C:98.3%[S:30.8%,D:67.5%],F:0.1%,M:1.6%	98,5	34896	79707	112879

Table S3: mitochondrial genome sequencing and annotation. Accession numbers (SRA) and the number of reads are indicated for newly sequenced genomes. *sequenced as a pool library with two unrelated species. **two supposedly heteroplasmic variants were sequenced. Consult the database records for credits/citations of the genomes

Species	SRA	Read pairs (raw)	Assembly/annotation	GenBank
A. equina	SRR28211702	85.304.786	Complete, 20691 bp, 17 genes	PP438735
B. oleae	n/a	n/a	Complete, 15815 bp, 37 genes	AY210703
Cae. elegans	n/a	n/a	Complete, 13794 bp, 36 genes	NC_001328
Car. multidentata	SRR28211704	78.339.420	Complete, 15825 bp, 37 genes	PP438739
Ce. capitata	SRR28211706	73.588.649	Complete, 15983 bp, 37 genes	PP438740
Da. rerio	n/a	n/a	Complete, 16596 bp, 37 genes	NC_002333
Dr. melanogaster	n/a	n/a	Complete, 19524 bp, 37 genes	NC_024511
*Du. japonica***	SRR28211705	79.986.910	A type, incomplete 15103 bp, 36 genes	PP484941
			B type, incomplete 15036 bp, 36 genes	PP484942
*E. andrei**	SRR28211706	73.588.649	Complete, 15715 bp, 37 genes	PP438738
Ma. gigas	n/a	n/a	Complete, 18224 bp, 39 genes	NC_001276
Mu. musculus	n/a	n/a	Complete, 16299 bp, 37 genes	NC_005089
N. geniculatus	n/a	n/a	Complete, 15180 bp, 38 genes	NC_042687
Pa. lividus	SRR28211703	80.972.420	Complete, 15706 bp, 37 genes	PP438737
Po. japonica	n/a	n/a	Complete, 18406 bp, 37 genes	OP974626

Table S4: nuclear genomes. The name of the species, name and ID of the assembly, database, sequencing technology, level of assembly and the year of production are indicated. Consult the database records for credits/citations of the genomes

Species	Assembly	ID	Database	Method	Level	Year
A. equina	*equina_smartden.arrow4.noredun*	GCA_011057435.1	NCBI	PacBio	contigs	2020
B. oleae	*MU_Boleae_v2*	GCA_001188975.4	NCBI	Illumina, PacBio, ONT	scaffolds	2019
Cae. elegans	*WBcel235*	GCA_000002985.3	NCBI	illumina	chromosomes	2013
Car. multidentata	*Cmul_gen_Assembly01*	GCA_002091895.1	NCBI	Illumina	scaffolds	2107
Ce. capitata	Ccap_2.1	GCA_000347755.4	NCBI	Illumina	scaffolds	2017
Da. rerio	*GRCz11*	GCA_000002035.4	NCBI	Overlapping BAC clones + WGS	chromosomes	2017
Dr. melanogaster	*Release 6 plus ISO1 MT*	GCA_000001215.4	NCBI	Overlapping BAC clones + WGS	chromosomes	2014
Du. japonica	*Djap assembly v1*	GCA_001938525.1	NCBI	Illumina	scaffolds	2017
E. andrei	Ean_1	GWHACBE00000000	CNCB	PacBio, Illumina, Hi-C	chromosomes	2020
Ma. gigas	*xbMagGiga1.1*	GCA_963853765.1	NCBI	PacBio, Hi-C	chromosomes	2023
Mu. musculus	*GRCm39*	GCA_000001635.9	NCBI	Overlapping BAC clones	chromosomes	2020
N. geniculatus	*ASM263302v1*	GCA_002633025.1	NCBI	Illumina	scaffolds	2017
Pa. lividus	*Pliv_v1*	GCA_940671915.1	NCBI	Illumina, PacBio, Hi-C	scaffolds	2022
Po. japonica	*PoJapo1.0*	GCA_040143775.1	NCBI	Illumina, ONT	scaffolds	2024

Table S5: small RNAs sequencing. For each species and replicate are reported: the SRA accession, the number of raw read pairs, the number and percentage of reads remaining after trimming, the number and percentage of reads mapping to the mitochondrial genome, the number and percentage of reads uniquely mapping to the mitochondrial genome, the percentage of mitochondrial uniquely mapping over mitochondrial mapping reads. For each species, the global number of reads and average mapping/trimming percentages are shown

Species	**SRA**	**raw**	**trimmed**	**%trimmed**	**mitoch.**	**%mitoch.**	**mito-unique**	**%mito-unique**	**%mito-unique/%mito**
A. equina	SRR28406998	36.304.952	33.636.779	92,65	73.081	0,22	44.751	0,13	61,23
	SRR28406997	34.762.440	33.536.554	96,47	70.525	0,21	51.140	0,15	72,51
	SRR28406996	36.555.203	36.188.002	99,00	48.217	0,13	43.503	0,12	90,22
	SRR28406995	36.574.767	36.092.208	98,68	35.838	0,10	33.680	0,09	93,98
	SRR28406994	36.289.299	35.928.766	99,01	97.073	0,27	93.577	0,26	96,40
	overall	***180.486.661***	***175.382.309***	***97,17***	***324.734***	***0,19***	***266.651***	***0,15***	***82,11***
B. oleae	SRR28407026	28.207.227	28.078.213	99,54	1.234	0,00	229	0,00	18,56
	SRR28407025	27.553.765	27.431.889	99,56	1.895	0,01	291	0,00	15,36
	SRR28407024	29.991.158	28.691.004	95,66	232.562	0,81	37.233	0,13	16,01
	SRR28407023	29.418.879	29.249.627	99,42	3.815	0,01	685	0,00	17,96
	SRR28407022	36.524.092	36.423.120	99,72	945	0,00	146	0,00	15,45
	overall	***151.695.121***	***149.873.853***	***98,80***	***240.451***	***0,16***	***38.584***	***0,03***	***16,05***
Cae. elegans	SRR10573443_1	30.691.620	16.821.619	54,81	7.695	0,05	7.222	0,04	93,85
	SRR10573444_1	30.887.212	17.520.685	56,72	12.210	0,07	11.575	0,07	94,80
	SRR10573445_1	26.677.379	14.234.649	53,36	6.547	0,05	6.097	0,04	93,13
	overall	***88.256.211***	***48.576.953***	***55,04***	***26.452***	***0,05***	***24.894***	***0,05***	***94,11***
Car. multidentata	SRR28407020	36.235.679	34.562.296	95,38	53.089	0,15	28.461	0,08	53,61
	SRR28407019	30.563.445	29.201.477	95,54	13.362	0,05	6.436	0,02	48,17
	SRR28407018	28.759.776	26.212.869	91,14	24.451	0,09	11.488	0,04	46,98
	SRR28407017	33.019.481	31.666.112	95,90	21.793	0,07	12.847	0,04	58,95
	SRR28407016	36.717.633	34.240.273	93,25	28.902	0,08	13.868	0,04	47,98
	overall	***165.296.014***	***155.883.027***	***94,31***	***141.597***	***0,09***	***73.100***	***0,05***	***51,63***
Ce. capitata	SRR28407033	89.820.793	86.782.312	96,62	25.968	0,03	3.129	0,00	12,05
	SRR28407032	84.505.707	81.746.038	96,73	16.157	0,02	3.073	0,00	19,02
	SRR28407021	89.759.257	86.726.652	96,62	18.795	0,02	3.732	0,00	19,86
	SRR28407010	80.665.934	79.051.363	98,00	70.950	0,09	19.042	0,02	26,84
	SRR28406999	79.038.962	77.313.299	97,82	8.467	0,01	1.643	0,00	19,40
	overall	***423.790.653***	***411.619.664***	***97,13***	***140.337***	***0,03***	***30.619***	***0,01***	***21,82***
Da. rerio	SRR1265755_1	9.559.974	8.869.516	92,78	4.666	0,05	3.834	0,04	82,17
	SRR1265756_1	15.008.224	14.194.837	94,58	9.330	0,07	8.003	0,06	85,78
	SRR1265757_1	27.666.784	25.980.300	93,90	16.711	0,06	13.884	0,05	83,08
	SRR1265759_1	20.562.446	19.313.126	93,92	10.524	0,05	9.779	0,05	92,92
	SRR1265760_1	14.426.153	13.604.704	94,31	8.928	0,07	8.297	0,06	92,93
	overall	***87.223.581***	***81.962.483***	***93,97***	***50.159***	***0,06***	***43.797***	***0,05***	***87,32***
Dr. melanogaster	SRR5181429_1	15.972.213	7.572.506	47,41	16.567	0,22	14.395	0,19	86,89
	SRR5181430_1	16.986.054	8.006.801	47,14	35.098	0,44	30.358	0,38	86,49
	SRR5181435_1	18.089.388	6.773.710	37,45	7.880	0,12	5.734	0,08	72,77
	SRR5181436_1	22.454.670	9.097.679	40,52	19.589	0,22	16.783	0,18	85,68
	overall	***73.502.325***	***31.450.696***	***42,79***	***129.293***	***0,41***	***111.067***	***0,35***	***85,90***
Du. japonica	SRR28407031	29.802.571	21.821.828	73,22	57.982	0,27	52.634	0,24	90,78
	SRR28407030	26.608.922	25.629.105	96,32	67.493	0,26	56.636	0,22	83,91
	SRR28407029	26.443.598	25.608.764	96,84	219.853	0,86	168.270	0,66	76,54
	SRR28407028	27.434.100	26.664.623	97,20	210.052	0,79	181.222	0,68	86,27
	SRR28407027	26.791.613	19.563.305	73,02	58.639	0,30	50.576	0,26	86,25
	overall	***137.080.804***	***119.287.625***	***87,02***	***614.019***	***0,51***	***509.338***	***0,43***	***82,95***
E. andrei	SRR28406993	30.308.959	29.364.051	96,88	257.064	0,88	223.688	0,76	87,02
	SRR28406992	24.917.613	22.192.955	89,07	50.718	0,23	40.758	0,18	80,36
	SRR28406991	30.393.789	28.255.439	92,96	52.847	0,19	44.409	0,16	84,03
	SRR28406990	25.769.514	19.416.174	75,35	21.768	0,11	16.412	0,08	75,40
	SRR28406989	30.230.288	27.169.661	89,88	52.350	0,19	43.940	0,16	83,94
	overall	***141.620.163***	***126.398.280***	***89,25***	***434.747***	***0,34***	***369.207***	***0,29***	***84,92***
Ma. gigas	SRR13077202_1	13.192.369	13.015.594	98,66	108.375	0,83	96.041	0,74	88,62
	SRR13077216_1	11.067.436	8.419.762	76,08	32.450	0,39	23.156	0,28	71,36
	SRR13077217_1	13.405.415	13.192.690	98,41	27.613	0,21	25.961	0,20	94,02
	SRR13077218_1	11.682.172	11.392.761	97,52	78.674	0,69	58.284	0,51	74,08
	SRR13077219_1	12.723.841	12.591.483	98,96	13.257	0,11	13.087	0,10	98,72
	SRR13077220_1	11.944.890	11.381.224	95,28	17.940	0,16	15.165	0,13	84,53
	overall	***74.016.123***	***69.993.514***	***94,57***	***278.309***	***0,40***	***231.694***	***0,33***	***83,25***
Mu. musculus	SRR5519787_1	11.911.367	9.113.217	76,51	134.226	1,47	57.225	0,63	42,63
	SRR5519788_1	10.456.943	7.327.021	70,07	113.499	1,55	57.738	0,79	50,87
	SRR5519789_1	11.856.890	8.966.218	75,62	65.072	0,73	25.290	0,28	38,86
	SRR5519790_1	11.781.014	8.882.451	75,40	110.115	1,24	51.484	0,58	46,75
	SRR5519791_1	13.853.068	10.859.853	78,39	243.486	2,24	113.411	1,04	46,58
	SRR5519792_1	10.523.396	8.257.814	78,47	178.940	2,17	76.040	0,92	42,49
	overall	***70.382.678***	***53.406.574***	***75,88***	***845.338***	***1,58***	***381.188***	***0,71***	***45,09***
N. geniculatus	NoGe_F1_1	30.721.728	28.263.708	92,00	46.121	0,16	33.363	0,12	72,34
	NoGe_F2_1	24.660.255	23.928.478	97,03	30.964	0,13	27.107	0,11	87,54
	NoGe_F3_1	29.389.076	27.164.421	92,43	15.482	0,06	7.565	0,03	48,86
	NoGe_M1_1	30.824.611	19.286.898	62,57	73.018	0,38	59.196	0,31	81,07
	NoGe_M2_1	31.006.142	30.020.393	96,82	89.240	0,30	77.255	0,26	86,57
	NoGe_M3_1	32.302.091	29.300.210	90,71	42.773	0,15	37.419	0,13	87,48
	overall	***178.903.903***	***157.964.108***	***88,30***	***297.598***	***0,19***	***241.905***	***0,15***	***81,29***
Pa. lividus	SRR28407015	37.384.455	27.725.962	74,16	374.085	1,35	334.040	1,20	89,30
	SRR28407014	38.342.219	30.292.735	79,01	325.441	1,07	291.349	0,96	89,52
	SRR28407013	33.305.417	24.879.206	74,70	30.674	0,12	22.762	0,09	74,21
	SRR28407012	37.204.140	29.236.979	78,59	412.596	1,41	374.191	1,28	90,69
	SRR28407011	38.448.741	30.090.014	78,26	277.354	0,92	225.260	0,75	81,22
	overall	***184.684.972***	***142.224.896***	***77,01***	***1.420.150***	***1,00***	***1.247.602***	***0,88***	***87,85***
Po. japonica	SRR28407004	34.994.643	32.645.206	93,29	132.777	0,41	75.012	0,23	56,49
	SRR28407003	26.877.468	23.189.209	86,28	135.011	0,58	60.073	0,26	44,49
	SRR28407001	38.711.795	34.650.411	89,51	212.697	0,61	94.940	0,27	44,64
	SRR28407002	28.325.478	25.353.796	89,51	88.975	0,35	43.184	0,17	48,53
	SRR28407000	34.934.667	32.016.648	91,65	115.949	0,36	54.532	0,17	47,03
	overall	***163.844.051***	***147.855.270***	***90,24***	***685.409***	***0,46***	***327.741***	***0,22***	***47,82***

Table S6: candidate smithRNAs identified. SmithRNAs are named based on the species of origin and the corresponding cluster number from the SmithHunter pipeline. Origin from heteroplasmic variant A or B in *Du. japonica* is indicated. For each smithRNA, the species, genomic location, strandedness of the gene/region where the smithRNA is encoded as well as strandedness of the smithRNA, smithRNA sequence and length are indicated. SmithRNAs are ordered by genomic region. Intergenic regions were indicated as + if both preceding and following gene are encoded in + orientation. * smithRNA AEQ_smith3 largely overlaps with smithRNA AEQ_smith2 and has a lower depth.** smithRNA DJA_A_smith199 largely overlaps with smithRNA DJA_AB_smith0 and has a lower depth

smithRNA ID	**species**	**genomic origin**	**strand origin**	**strand smithRNA**	**smithRNA sequence**	**Length (bp)**
AEQ_smith1	*A. equina*	lrRNA	+	+	TCAATTAAATTAAAAAGAGGAACGAATGGCGAGCTAGGGTGCACTAATA	49
AEQ_smith0	*A. equina*	srRNA	+	+	GTCCTTTGATTTTGGGGAATGTAGAAGGCGAGTGGCCCTTTT	42
AEQ_smith2	*A. equina*	tRNA-Met	+	+	CGTAGAGTGGACTAATGGTAAGTCACCAGACTC	33
AEQ_smith3*	*A. equina*	tRNA-Met	+	+	CGTAGAGTGGACTAATGA	18
AEQ_smith4	*A. equina*	tRNA-Trp	+	+	AGGAGGTTAGGTTAAGGTAGACCGTTAGC	29
BOL_smith0	*B. oleae*	tRNA-Phe	-	-	TGGTATCCAAGAATTAAACAATTA	24
CEL_smith0	*Cae. elegans*	NAD2	+	+	TATTTCTTCTTTGTAGAGGAGG	22
CEL_smith1	*Cae. elegans*	NAD2	+	+	TATTGAAAATTGGTGTAGCACCGCT	25
CEL_smith2	*Cae. elegans*	NAD5	+	+	AATAGTTACTTTGGGCCTAGGGCT	24
CEL_smith4	*Cae. elegans*	control region	na	+	GATAGTTTTACACGCGCGTATACGCGCG	28
CMU_smith2	*Car. multidentata*	tRNA-Cys	-	-	AGTCTAATGTCTTTCTTTCCACCACAAAGCC	31
CCA_smith2	*Ce. capitata*	tRNA-Ile	+	+	AATGAATTCCCTGATAAAAAGGATTA	26
CCA_smith0	*Ce. capitata*	tRNA-Ser(AGN)	+	+	GAAGTATGACGTTCAAGAAA	20
MGI_smith0	*Ma. gigas*	intergenic region	+	+	AAAGAGAATTTTTATAGTGGTAGTTGAAATAAAGGGGG	38
MGI_smith5	*Ma. gigas*	intergenic region	+	+	ACTACTGAGCGTTAGGTTCGTAGAGGCTAGGGC	33
MGI_smith2	*Ma. gigas*	lrRNA	+	+	ATACCAAAGGTATGGGGACT	20
MGI_smith8	*Ma. gigas*	tRNA-Ser(AGN)	+	+	GGAGGGATGAGTGGTCTTACACTGTGACT	29
DRE_smith1	*Da. rerio*	srRNA	+	+	AAAGGCATGGTCCCGACCTTTTGATCAGC	29
DRE_smith5	*Da. rerio*	lrRNA	+	+	GCTAAATAGCTAGCTTAACCATCAAGATCAACT	33
DRE_smith6	*Da. rerio*	tRNA-Met	+	+	GATGAGGTCAGCTAATTAAGCTACCGGGCCC	31
DME_smith3	*Dr. melanogaster*	srRNA	-	-	TCAGATCAAGGTGTAGCTT	19
DME_smith6	*Dr. melanogaster*	srRNA	-	-	TACCGTCGTTATCAGAATATT	21
DME_smith11	*Dr. melanogaster*	lrRNA	-	-	GGAATGAATGGTTGGACGAAAT	22
DME_smith4	*Dr. melanogaster*	lrRNA	-	-	TATTTAAAAGACGAGAAGACCCTA	24
DME_smith0	*Dr. melanogaster*	tRNA-Ser(UCN)	+	+	GAAATATGATGATCAAGTAAAAGCTGCTAACT	32
DJA_A _smith199**	*Du. japonica* var. A	srRNA	+	+	CTGTTTGGTTCTGGCATAATAAATT	25
DJA_A _smith19	*Du. japonica* var. A	tRNA-Pro	+	+	TCTCCCTCTGTTTTATGGCC	20
DJA_AB_smith0	*Du. japonica* var A and B	srRNA	+	+	TTTCTGTTTGGTTCTGGCATA	21
DJA_B_smith13	*Du. japonica* var B	intergenic region	+	+	TTTTCTAATCTAAATCCGAACTTCT	25
DJA_B_smith6	*Du. japonica* var B	lrRNA	+	+	AGATTTTATTGGTTGTATTTTTTCCTT	27
DJA_AB_smith18	*Du. japonica* var A and B	tRNA-Ser(AGN)	+	+	TTGGAAACTTTGCATGAGGGTA	22
EAN_smith1	*E. andrei*	COX1	+	+	CCAGTTTGATTCTAGCTGAGAACTTAGCT	29
EAN_smith2	*E. andrei*	COX2	+	+	ATTGTGGGCTAGAATGAAAGGACT	24
EAN_smith5	*E. andrei*	COX3	+	+	GGTACAGCGCCGGATGAACGGATAACTCT	29
EAN_smith14	*E. andrei*	NAD4	+	+	CTTGACTCTAGGCCTCCCCATCTGATTTAG	30
EAN_smith0	*E. andrei*	NAD6	+	+	AGATTAGCCGGGATACATAAGAACTTC	27
MMU_smith2	*Mu. musculus*	control region	na	-	GAATTGATCAGGACATAGGGTTTGATA	27
MMU_smith0	*Mu. musculus*	lrRNA	+	+	ACTAATCCTAGCCCTAGCCCTACACAAATATAAT	34
MMU_smith4	*Mu. musculus*	tRNA-Gln	-	-	TAGGATAAGGTGTTTAGGTAGCACGGAGAATT	32
MMU_smith1	*Mu. musculus*	tRNA-Ser(UCN)	+	+	AAGAAAGATTGCAAGAACTGCTAATTCATGCTTCCATGTTT	41
NGE_smith2	*N. geniculatus*	tRNA-Thr	-	-	ATTGGAGGAAGAACTACGTTCCGTCCGCTCCA	32
PLI_smith4	*Pa. lividus*	srRNA	+	+	CATAAGCTGGGAATGAGTG	19
PLI_smith7	*Pa. lividus*	srRNA	+	+	ACCGATTTGGTCCTAGTCCTAACTTTAGC	29
PLI_smith10	*Pa. lividus*	lrRNA	+	+	AAAATGGAAACCCCCAATTCTGATA	25
PLI_smith14	*Pa. lividus*	lrRNA	+	+	CAGCGTTATCTTTTCTGAGAGTTCACATT	29
PLI_smith1	*Pa. lividus*	lrRNA	+	+	AGGTTTGCGACCTCGATGTTGGATCGGGACA	31
PLI_smith28	*Pa. lividus*	lrRNA	+	+	TTAAAGTCCTACGTGATCTGAGT	23
PJA_smith9	*Po. japonica*	ATP6	+	+	AATTTTAGAATCTGCTGTTGC	21
PJA_smith11	*Po. japonica*	COX2	+	+	ATAGCTACTTGAAACACCA	19
PJA_smith5	*Po. japonica*	lrRNA	-	-	TCCAACCTGGCTCACGCCGGTTTAAACTCAGATC	34
PJA_smith14	*Po. japonica*	tRNA-Ile	+	+	AATGAAGTGTCTGACTATAGAGTTACTTTA	30
PJA_smith1	*Po. japonica*	tRNA-Val	-	-	TATGCTTTATTACAAGCTCTAATTTG	26

Table S7: smithRNAs and their targets. For each species, and separately for *Du. japonica* heteroplasmic variant A and B, the association is shown between individual smithRNAs and their putative targets as identified by the SmithHunter pipeline. Bound free energy is reported.

***Actinia equina* (5 candidates, 235 targets)**				
smithID	**transcriptID**	**Blastx**	**dG PITA**	**dG RNAHybrid**
AEQ_smith0	TRINITY_DN10043_c0_g1_i2	Protein pelota homolog	-26	-20
AEQ_smith0	TRINITY_DN1008_c0_g1_i10	Transcription elongation regulator 1	-28	-22
AEQ_smith0	TRINITY_DN1021_c0_g1_i3	.	-25	-17
AEQ_smith0	TRINITY_DN10230_c0_g1_i1	.	-29	-18
AEQ_smith0	TRINITY_DN104_c0_g1_i14	3-hydroxy-3-methylglutaryl-coenzyme A reductase	-22	-20
AEQ_smith0	TRINITY_DN1067_c0_g1_i1	Presenilin-associated rhomboid-like protein, mitochondrial	-28	-17
AEQ_smith0	TRINITY_DN10916_c0_g1_i10	.	-31	-20
AEQ_smith0	TRINITY_DN11057_c0_g1_i5	Succinate--hydroxymethylglutarate CoA-transferase	-27	-29
AEQ_smith0	TRINITY_DN11081_c0_g1_i11	NBAS subunit of NRZ tethering complex	-27	-18
AEQ_smith0	TRINITY_DN11084_c0_g1_i4	ATP-binding cassette sub-family D member 3	-20	-18
AEQ_smith0	TRINITY_DN11169_c0_g1_i10	Dynein axonemal heavy chain 10	-26	-15
AEQ_smith0	TRINITY_DN11694_c0_g1_i12	.	-27	-21
AEQ_smith0	TRINITY_DN11694_c0_g3_i1	.	-30	-21
AEQ_smith0	TRINITY_DN12516_c0_g2_i3	.	-22	-19
AEQ_smith0	TRINITY_DN1269_c1_g1_i1	SEC14-like protein 2	-23	-20
AEQ_smith0	TRINITY_DN12876_c0_g1_i11	.	-23	-19
AEQ_smith0	TRINITY_DN1325_c1_g3_i1	AN1-type zinc finger protein 3 homolog	-23	-17
AEQ_smith0	TRINITY_DN13296_c0_g1_i1	.	-25	-20
AEQ_smith0	TRINITY_DN1383_c0_g1_i10	Uncharacterized protein C15orf61	-18	-17
AEQ_smith0	TRINITY_DN1387_c0_g1_i13	Laminin subunit alpha-3	-25	-16
AEQ_smith0	TRINITY_DN14070_c0_g1_i1	Histamine H2 receptor	-21	-18
AEQ_smith0	TRINITY_DN14335_c1_g2_i1	Probable G-protein coupled receptor No9	-23	-17
AEQ_smith0	TRINITY_DN1449_c0_g1_i12	Glucuronokinase 1	-20	-18
AEQ_smith0	TRINITY_DN14832_c0_g2_i1	GATA zinc finger domain-containing protein 1	-28	-26
AEQ_smith0	TRINITY_DN14844_c0_g1_i1	Phosphoethanolamine N-methyltransferase 1	-24	-16
AEQ_smith0	TRINITY_DN15388_c0_g2_i4	Octopamine receptor beta-2R	-28	-16
AEQ_smith0	TRINITY_DN155_c0_g1_i2	Methylenetetrahydrofolate reductase (NADPH)	-37	-23
AEQ_smith0	TRINITY_DN15634_c0_g1_i1	E3 ubiquitin-protein ligase RNF213	-28	-19
AEQ_smith0	TRINITY_DN1572_c0_g1_i1	DnaJ homolog subfamily C member 5	-28	-19
AEQ_smith0	TRINITY_DN1597_c0_g1_i1	.	-25	-17
AEQ_smith0	TRINITY_DN1618_c0_g2_i1	Chromatin structure-remodeling complex subunit RSC4	-20	-19
AEQ_smith0	TRINITY_DN1623_c1_g1_i1	Coadhesin	-30	-16
AEQ_smith0	TRINITY_DN165_c2_g1_i1	LON peptidase N-terminal domain and RING finger protein 3	-32	-18
AEQ_smith0	TRINITY_DN17486_c0_g1_i1	Polypeptide N-acetylgalactosaminyltransferase 11	-22	-18
AEQ_smith0	TRINITY_DN18482_c0_g1_i1	Nephrocystin-3	-22	-17
AEQ_smith0	TRINITY_DN1870_c0_g1_i10	Cytoplasmic polyadenylation element-binding protein 2	-21	-15
AEQ_smith0	TRINITY_DN188_c1_g1_i1	.	-25	-20
AEQ_smith0	TRINITY_DN1914_c0_g6_i1	Tubulin-specific chaperone D	-21	-16
AEQ_smith0	TRINITY_DN19721_c0_g1_i2	Metabotropic glutamate receptor 3	-24	-20
AEQ_smith0	TRINITY_DN1_c1_g1_i3	Amyloid beta precursor protein binding family B member 1	-20	-19
AEQ_smith0	TRINITY_DN2111_c0_g1_i1	Epithelial splicing regulatory protein 2	-26	-15
AEQ_smith0	TRINITY_DN21279_c0_g1_i1	Centrosomal protein of 120 kDa	-17	-18
AEQ_smith0	TRINITY_DN2135_c0_g2_i1	Peptidyl-prolyl cis-trans isomerase FKBP8	-26	-20
AEQ_smith0	TRINITY_DN21543_c0_g1_i1	Secreted frizzled-related protein 1	-27	-18
AEQ_smith0	TRINITY_DN2186_c0_g1_i2	Cation-independent mannose-6-phosphate receptor	-32	-20
AEQ_smith0	TRINITY_DN22344_c0_g1_i2	Protein DD3-3	-32	-29
AEQ_smith0	TRINITY_DN2246_c0_g1_i10	Serrate RNA effector molecule homolog	-26	-18
AEQ_smith0	TRINITY_DN22975_c0_g1_i4	.	-26	-18
AEQ_smith0	TRINITY_DN2402_c0_g1_i2	5'-3' exonuclease PLD3	-22	-17
AEQ_smith0	TRINITY_DN24724_c1_g1_i1	.	-28	-20
AEQ_smith0	TRINITY_DN2509_c0_g1_i2	Matrix metalloproteinase-9	-31	-18
AEQ_smith0	TRINITY_DN258_c1_g1_i10	Protein FAM72A	-17	-16
AEQ_smith0	TRINITY_DN2673_c0_g1_i1	Protocadherin Fat 4	-27	-20
AEQ_smith0	TRINITY_DN27948_c0_g1_i11	Receptor-type tyrosine-protein kinase FLT3	-24	-19
AEQ_smith0	TRINITY_DN2796_c0_g2_i8	Aminopeptidase A	-29	-18
AEQ_smith0	TRINITY_DN283_c0_g1_i1	Cathepsin Z	-25	-21
AEQ_smith0	TRINITY_DN28646_c0_g1_i10	Serine/threonine-protein kinase pdik1l	-24	-18
AEQ_smith0	TRINITY_DN2877_c0_g1_i1	Glycogen phosphorylase, muscle form	-27	-18
AEQ_smith0	TRINITY_DN2922_c0_g1_i2	.	-25	-18
AEQ_smith0	TRINITY_DN2945_c0_g2_i3	DDRGK domain-containing protein 1	-20	-19
AEQ_smith0	TRINITY_DN3093_c0_g3_i1	Pro-interleukin-16	-31	-18
AEQ_smith0	TRINITY_DN312_c0_g1_i10	Serine/arginine-rich splicing factor 12	-30	-20
AEQ_smith0	TRINITY_DN31579_c0_g1_i3	Serine/threonine-protein kinase Kist	-30	-20
AEQ_smith0	TRINITY_DN32604_c0_g1_i2	G-protein coupled receptor 135	-22	-18
AEQ_smith0	TRINITY_DN3297_c0_g1_i15	Complement C3	-15	-20
AEQ_smith0	TRINITY_DN3483_c0_g1_i1	Protein zyg-11 homolog B	-32	-22
AEQ_smith0	TRINITY_DN3590_c0_g2_i4	.	-24	-19
AEQ_smith0	TRINITY_DN368_c1_g2_i1	.	-20	-23
AEQ_smith0	TRINITY_DN3769_c0_g1_i11	.	-27	-20
AEQ_smith0	TRINITY_DN398_c0_g4_i1	.	-20	-23
AEQ_smith0	TRINITY_DN4194_c0_g1_i1	Metalloprotease TIKI homolog	-24	-20
AEQ_smith0	TRINITY_DN4209_c0_g1_i2	Lipoxygenase homology domain-containing protein 1	-18	-18
AEQ_smith0	TRINITY_DN4268_c0_g1_i1	Deoxyribonuclease TATDN1	-17	-19
AEQ_smith0	TRINITY_DN427_c2_g3_i1	Tubulin-specific chaperone cofactor E-like protein	-24	-20
AEQ_smith0	TRINITY_DN435_c1_g1_i1	Stromal membrane-associated protein 2	-22	-23
AEQ_smith0	TRINITY_DN4480_c0_g1_i2	Tyrosine-protein kinase ABL1	-30	-20
AEQ_smith0	TRINITY_DN4577_c1_g1_i1	.	-32	-21
AEQ_smith0	TRINITY_DN4584_c0_g1_i2	Protein inturned	-28	-29
AEQ_smith0	TRINITY_DN462_c0_g2_i2	.	-18	-19
AEQ_smith0	TRINITY_DN4696_c0_g1_i5	Counting factor associated protein D	-24	-16
AEQ_smith0	TRINITY_DN4755_c0_g2_i1	Eukaryotic peptide chain release factor subunit 1	-27	-20
AEQ_smith0	TRINITY_DN484_c1_g7_i1	.	-26	-15
AEQ_smith0	TRINITY_DN4856_c0_g2_i1	ZP domain-containing protein	-24	-19
AEQ_smith0	TRINITY_DN5036_c0_g1_i1	.	-23	-22
AEQ_smith0	TRINITY_DN5063_c0_g1_i11	Protein MTSS 1	-25	-16
AEQ_smith0	TRINITY_DN51516_c0_g3_i1	Sentrin-specific protease 2	-28	-17
AEQ_smith0	TRINITY_DN5229_c0_g1_i1	Outer dynein arm-docking complex subunit 4	-23	-18

AEQ_smith0	TRINITY_DN5255_c0_g1_i1	Neuropeptide SIFamide receptor	-31	-18
AEQ_smith0	TRINITY_DN5358_c0_g1_i1	Spectrin beta chain, non-erythrocytic 5	-25	-20
AEQ_smith0	TRINITY_DN5359_c0_g1_i12	Exosome complex component RRP43	-20	-15
AEQ_smith0	TRINITY_DN5365_c0_g1_i14	Probable E3 ubiquitin-protein ligase HECTD2	-29	-16
AEQ_smith0	TRINITY_DN5507_c0_g4_i1	Transposon Tf2-6 polyprotein	-17	-15
AEQ_smith0	TRINITY_DN5539_c0_g1_i11	UPF0462 protein C4orf33 homolog	-31	-20
AEQ_smith0	TRINITY_DN55_c0_g1_i4	Myoblast growth factor receptor egl-15	-21	-17
AEQ_smith0	TRINITY_DN5655_c0_g1_i5	Tetratricopeptide repeat protein 28	-30	-19
AEQ_smith0	TRINITY_DN5728_c1_g1_i1	Cell division cycle protein 23 homolog	-26	-16
AEQ_smith0	TRINITY_DN5832_c0_g1_i12	Deleted in malignant brain tumors 1 protein	-27	-16
AEQ_smith0	TRINITY_DN58487_c0_g2_i5	SH3 and PX domain-containing protein 2A	-23	-16
AEQ_smith0	TRINITY_DN5926_c0_g5_i1	Heat shock protein HSP 90-alpha	-24	-18
AEQ_smith0	TRINITY_DN6052_c0_g2_i1	.	-20	-21
AEQ_smith0	TRINITY_DN6309_c1_g2_i2	Progestin and adipoQ receptor family member 3	-21	-25
AEQ_smith0	TRINITY_DN633_c0_g1_i6	.	-27	-19
AEQ_smith0	TRINITY_DN6416_c2_g1_i10	Orexin receptor type 2	-35	-26
AEQ_smith0	TRINITY_DN704_c1_g2_i10	GTPase IMAP family member 4	-24	-17
AEQ_smith0	TRINITY_DN7095_c0_g1_i1	.	-21	-20
AEQ_smith0	TRINITY_DN7376_c0_g1_i4	GRIP and coiled-coil domain-containing protein 1	-25	-18
AEQ_smith0	TRINITY_DN7715_c0_g1_i2	RNA-directed DNA polymerase from mobile element jockey	-31	-20
AEQ_smith0	TRINITY_DN775_c0_g1_i2	.	-31	-20
AEQ_smith0	TRINITY_DN7891_c0_g2_i1	Steryl-sulfatase	-35	-17
AEQ_smith0	TRINITY_DN790_c2_g1_i3	Pancreatic triacylglycerol lipase	-32	-23
AEQ_smith0	TRINITY_DN79_c1_g1_i11	Gamma-aminobutyric acid type B receptor subunit 2	-30	-23
AEQ_smith0	TRINITY_DN8246_c0_g1_i1	Cyclic nucleotide-binding domain-containing protein 2	-30	-21
AEQ_smith0	TRINITY_DN833_c0_g2_i1	Ribonuclease P protein subunit p25-like protein	-20	-17
AEQ_smith0	TRINITY_DN8375_c0_g1_i3	Sulfiredoxin	-22	-22
AEQ_smith0	TRINITY_DN8413_c0_g2_i10	CCR4-NOT transcription complex subunit 4	-30	-17
AEQ_smith0	TRINITY_DN8707_c0_g1_i10	Tachykinin-like peptides receptor 86C	-25	-20
AEQ_smith0	TRINITY_DN8886_c0_g1_i12	Tyrosine-protein kinase BTK	-28	-18
AEQ_smith0	TRINITY_DN8996_c0_g1_i1	Disks large-associated protein 1	-31	-29
AEQ_smith0	TRINITY_DN9036_c0_g1_i2	.	-30	-17
AEQ_smith0	TRINITY_DN9057_c0_g1_i2	3-oxo-5-alpha-steroid 4-dehydrogenase 1	-26	-19
AEQ_smith0	TRINITY_DN9209_c0_g1_i3	Kinesin-like protein KIF28P	-24	-20
AEQ_smith0	TRINITY_DN9211_c0_g2_i10	Probable RNA-directed DNA polymerase from transposon BS	-34	-21
AEQ_smith0	TRINITY_DN9432_c0_g1_i2	Putative uncharacterized transposon-derived protein F54H12.3	-26	-20
AEQ_smith0	TRINITY_DN9535_c0_g1_i1	Protein LZIC	-20	-18
AEQ_smith0	TRINITY_DN960_c0_g1_i13	Lipoxygenase homology domain-containing protein 1	-24	-20
AEQ_smith0	TRINITY_DN9616_c0_g1_i1	Fibrillin-2	-17	-20
AEQ_smith1	TRINITY_DN10851_c0_g1_i1	ADP-ribosylation factor-like protein 8B-A	-20	-15
AEQ_smith1	TRINITY_DN1168_c0_g1_i3	.	-10	-15
AEQ_smith1	TRINITY_DN1171_c0_g1_i3	Myocyte-specific enhancer factor 2C	-34	-15
AEQ_smith1	TRINITY_DN14233_c0_g1_i4	Proton-coupled folate transporter	-17	-16
AEQ_smith1	TRINITY_DN14474_c0_g1_i1	Mu-type opioid receptor	-21	-17
AEQ_smith1	TRINITY_DN1578_c0_g1_i1	Fatty acid synthase	-16	-16
AEQ_smith1	TRINITY_DN1583_c0_g1_i9	.	-25	-15
AEQ_smith1	TRINITY_DN16460_c0_g2_i1	Frizzled-1	-29	-16
AEQ_smith1	TRINITY_DN1740_c0_g1_i16	Electrogenic aspartate/glutamate antiporter SLC25A12, mitochondrial	-14	-15
AEQ_smith1	TRINITY_DN178_c1_g1_i1	Probable ribosome biogenesis protein RLP24	-18	-19
AEQ_smith1	TRINITY_DN1795_c0_g4_i1	.	-24	-16
AEQ_smith1	TRINITY_DN1821_c0_g6_i1	.	-12	-15
AEQ_smith1	TRINITY_DN21501_c0_g1_i1	Zinc finger protein 724	-14	-19
AEQ_smith1	TRINITY_DN2207_c0_g1_i10	Polcalcin Cup a 4	-22	-15
AEQ_smith1	TRINITY_DN2421_c0_g1_i10	ATP-dependent DNA helicase PIF1	-22	-15
AEQ_smith1	TRINITY_DN2728_c0_g1_i4	Cyclic AMP receptor-like protein A	-22	-19
AEQ_smith1	TRINITY_DN27863_c0_g1_i1	Homeobox protein AHox1	-20	-15
AEQ_smith1	TRINITY_DN28502_c0_g1_i2	von Willebrand factor D and EGF domain-containing protein	-14	-15
AEQ_smith1	TRINITY_DN2916_c0_g1_i3	NACHT domain- and WD repeat-containing protein 1	-30	-20
AEQ_smith1	TRINITY_DN2938_c0_g1_i1	Protein FAM117B	-32	-15
AEQ_smith1	TRINITY_DN29_c1_g1_i1	Solute carrier family 12 member 9	-21	-15
AEQ_smith1	TRINITY_DN3447_c0_g1_i15	Uridine-cytidine kinase-like 1	-19	-16
AEQ_smith1	TRINITY_DN347_c0_g1_i1	.	-24	-17
AEQ_smith1	TRINITY_DN3576_c0_g1_i1	OTU domain-containing protein 7B	-20	-15
AEQ_smith1	TRINITY_DN379_c2_g1_i2	Small ribosomal subunit protein mS33	-28	-15
AEQ_smith1	TRINITY_DN4343_c0_g2_i1	3-hydroxyisobutyrate dehydrogenase, mitochondrial	-23	-15
AEQ_smith1	TRINITY_DN474_c0_g1_i7	Muscleblind-like protein 1	-23	-15
AEQ_smith1	TRINITY_DN4814_c0_g1_i1	Amiloride-sensitive sodium channel subunit beta	-25	-18
AEQ_smith1	TRINITY_DN50156_c0_g1_i1	.	-23	-15
AEQ_smith1	TRINITY_DN5062_c0_g1_i6	Calcium-activated potassium channel subunit alpha-1	-16	-15
AEQ_smith1	TRINITY_DN533_c0_g1_i1	TAF5-like RNA polymerase II p300/CBP-associated factor-associated factor 65 kDa subunit 5L	-19	-15
AEQ_smith1	TRINITY_DN583_c0_g1_i3	Scavenger receptor cysteine-rich type 1 protein M130	-17	-16
AEQ_smith1	TRINITY_DN637_c0_g1_i12	.	-25	-15
AEQ_smith1	TRINITY_DN6608_c0_g1_i1	TBC1 domain family member 30	-27	-19
AEQ_smith1	TRINITY_DN662_c1_g1_i10	Neuronal growth regulator 1	-9	-15
AEQ_smith1	TRINITY_DN8981_c0_g3_i5	Major facilitator superfamily domain-containing protein 12	-24	-18
AEQ_smith1	TRINITY_DN9568_c0_g2_i1	.	-26	-16
AEQ_smith1	TRINITY_DN9806_c0_g1_i3	Gamma-aminobutyric acid receptor subunit rho-1	-14	-16
AEQ_smith2	TRINITY_DN10484_c0_g1_i1	.	-32	-25
AEQ_smith2	TRINITY_DN1108_c2_g1_i3	.	-24	-21
AEQ_smith2	TRINITY_DN11104_c0_g1_i9	DNA replication complex GINS protein PSF2	-25	-22
AEQ_smith2	TRINITY_DN11135_c0_g1_i1	Interferon-induced helicase C domain-containing protein 1	-19	-24
AEQ_smith2	TRINITY_DN1259_c0_g1_i11	.	-28	-25
AEQ_smith2	TRINITY_DN15433_c0_g2_i1	Pyridoxal 5'-phosphate synthase subunit SNZERR	-27	-24
AEQ_smith2	TRINITY_DN1719_c0_g1_i4	.	-20	-19
AEQ_smith2	TRINITY_DN1870_c0_g1_i10	Cytoplasmic polyadenylation element-binding protein 2	-16	-21
AEQ_smith2	TRINITY_DN19874_c0_g1_i12	Exonuclease mut-7 homolog	-28	-22
AEQ_smith2	TRINITY_DN20916_c1_g1_i9	THAP domain-containing protein 11	-12	-18
AEQ_smith2	TRINITY_DN2113_c0_g1_i1	2-oxoglutarate dehydrogenase-like, mitochondrial	-21	-27
AEQ_smith2	TRINITY_DN21710_c0_g1_i13	Agrin	-29	-25
AEQ_smith2	TRINITY_DN22304_c0_g1_i2	Ankyrin repeat and MYND domain-containing protein 1	-21	-24
AEQ_smith2	TRINITY_DN225_c0_g2_i2	.	-28	-20
AEQ_smith2	TRINITY_DN2447_c0_g1_i10	Low-density lipoprotein receptor-related protein 6	-28	-26
AEQ_smith2	TRINITY_DN2787_c0_g1_i10	.	-18	-16
AEQ_smith2	TRINITY_DN27890_c0_g1_i4	Talin-1	-22	-22

AEQ_smith2	TRINITY_DN30091_c1_g1_i1	.	-28	-15
AEQ_smith2	TRINITY_DN3331_c0_g1_i2	Coiled-coil domain-containing protein 186	-17	-19
AEQ_smith2	TRINITY_DN34312_c0_g1_i4	[F-actin]-monooxygenase MICAL3	-22	-16
AEQ_smith2	TRINITY_DN3732_c0_g1_i4	TBC1 domain family member 1	-26	-15
AEQ_smith2	TRINITY_DN4298_c0_g1_i1	.	-16	-15
AEQ_smith2	TRINITY_DN46497_c0_g1_i1	.	-20	-17
AEQ_smith2	TRINITY_DN4688_c0_g1_i9	Sorting nexin-25	-33	-25
AEQ_smith2	TRINITY_DN46_c0_g1_i8	.	-18	-21
AEQ_smith2	TRINITY_DN552_c0_g2_i1	Serine/threonine-protein kinase/endoribonuclease IRE2	-23	-16
AEQ_smith2	TRINITY_DN5683_c0_g1_i10	S-adenosylmethionine-dependent nucleotide dehydratase RSAD2	-24	-25
AEQ_smith2	TRINITY_DN6127_c0_g1_i7	Receptor-type tyrosine-protein phosphatase delta	-23	-19
AEQ_smith2	TRINITY_DN7231_c0_g1_i1	Tiggy-winkle hedgehog protein	-25	-20
AEQ_smith2	TRINITY_DN746_c1_g2_i9	ADP-ribosylation factor-like protein 3	-21	-17
AEQ_smith2	TRINITY_DN816_c0_g1_i3	Nuclear pore complex protein Nup98-Nup96	-25	-24
AEQ_smith2	TRINITY_DN8648_c0_g1_i2	Polycystin-1-like protein 2	-22	-20
AEQ_smith3	TRINITY_DN10484_c0_g1_i1	.	-21	-25
AEQ_smith3	TRINITY_DN1108_c2_g1_i3	.	-21	-21
AEQ_smith3	TRINITY_DN11135_c0_g1_i1	Interferon-induced helicase C domain-containing protein 1	-18	-24
AEQ_smith3	TRINITY_DN1259_c0_g1_i11	.	-20	-25
AEQ_smith3	TRINITY_DN15433_c0_g2_i1	Pyridoxal 5'-phosphate synthase subunit SNZERR	-16	-24
AEQ_smith3	TRINITY_DN1870_c0_g1_i10	Cytoplasmic polyadenylation element-binding protein 2	-11	-21
AEQ_smith3	TRINITY_DN19874_c0_g1_i12	Exonuclease mut-7 homolog	-20	-22
AEQ_smith3	TRINITY_DN2113_c0_g1_i1	2-oxoglutarate dehydrogenase-like, mitochondrial	-17	-27
AEQ_smith3	TRINITY_DN21710_c0_g1_i13	Agrin	-21	-25
AEQ_smith3	TRINITY_DN22304_c0_g1_i2	Ankyrin repeat and MYND domain-containing protein 1	-20	-24
AEQ_smith3	TRINITY_DN225_c0_g2_i2	.	-21	-20
AEQ_smith3	TRINITY_DN2447_c0_g1_i10	Low-density lipoprotein receptor-related protein 6	-21	-26
AEQ_smith3	TRINITY_DN2787_c0_g1_i10	.	-12	-16
AEQ_smith3	TRINITY_DN30091_c1_g1_i1	.	-20	-15
AEQ_smith3	TRINITY_DN31319_c0_g2_i24	.	-21	-24
AEQ_smith3	TRINITY_DN4688_c0_g1_i9	Sorting nexin-25	-25	-25
AEQ_smith3	TRINITY_DN5683_c0_g1_i10	S-adenosylmethionine-dependent nucleotide dehydratase RSAD2	-21	-25
AEQ_smith3	TRINITY_DN816_c0_g1_i3	Nuclear pore complex protein Nup98-Nup96	-19	-24
AEQ_smith3	TRINITY_DN8648_c0_g1_i2	Polycystin-1-like protein 2	-13	-20
AEQ_smith4	TRINITY_DN1067_c0_g1_i2	Presenilin-associated rhomboid-like protein, mitochondrial	-18	-16
AEQ_smith4	TRINITY_DN10898_c0_g1_i2	Cyclin-dependent kinase 5	-14	-15
AEQ_smith4	TRINITY_DN11665_c0_g1_i1	Superkiller complex protein 2	-25	-23
AEQ_smith4	TRINITY_DN14289_c0_g1_i4	TraB domain-containing protein	-28	-25
AEQ_smith4	TRINITY_DN22147_c0_g1_i1	Beta-1,3-glucosyltransferase	-28	-24
AEQ_smith4	TRINITY_DN231_c0_g1_i1	Sodium/calcium exchanger NCL1	-22	-23
AEQ_smith4	TRINITY_DN248_c0_g1_i2	Follistatin-related protein 1	-18	-19
AEQ_smith4	TRINITY_DN248_c1_g1_i2	Prosaposin	-18	-18
AEQ_smith4	TRINITY_DN24963_c0_g2_i2	Toxin CrTX-A	-31	-26
AEQ_smith4	TRINITY_DN250_c0_g3_i1	Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	-21	-18
AEQ_smith4	TRINITY_DN26841_c0_g1_i1	Putative uncharacterized transposon-derived protein F54H12.3	-19	-18
AEQ_smith4	TRINITY_DN2966_c0_g1_i1	D(5)-like dopamine receptor	-25	-27
AEQ_smith4	TRINITY_DN3159_c0_g1_i1	Scaffold attachment factor B2	-12	-18
AEQ_smith4	TRINITY_DN3445_c0_g1_i2	Mitochondrial import inner membrane translocase subunit Tim29	-31	-16
AEQ_smith4	TRINITY_DN39247_c0_g1_i2	60 kDa lysophospholipase	-28	-25
AEQ_smith4	TRINITY_DN6187_c0_g1_i3	.	-23	-24
AEQ_smith4	TRINITY_DN6733_c0_g1_i2	Collagen-like protein 2	-22	-15
AEQ_smith4	TRINITY_DN7335_c0_g1_i1	.	-23	-24
AEQ_smith4	TRINITY_DN7891_c0_g2_i1	Steryl-sulfatase	-22	-15
AEQ_smith4	TRINITY_DN80_c12_g1_i1	Transcription initiation factor TFIID subunit 1	-24	-16
		***Bactrocera oleae* (1 candidate, 28 targets)**		
smithID	**transcriptID**	**Blastx**	**dG PITA**	**dG RNAHybrid**
BOL_smith0	TRINITY_DN10294_c0_g1_i1	.	-10	-15
BOL_smith0	TRINITY_DN1090_c0_g1_i1	Trafficking protein particle complex subunit 2-like protein	-10	-16
BOL_smith0	TRINITY_DN1505_c0_g1_i1	E3 ubiquitin-protein ligase TRIM33	-16	-15
BOL_smith0	TRINITY_DN1529_c1_g1_i14	Mitoguardin	-18	-16
BOL_smith0	TRINITY_DN16384_c1_g1_i2	Peptide-N(4)-(N-acetyl-beta-glucosaminyl)asparagine amidase	-11	-15
BOL_smith0	TRINITY_DN18184_c0_g1_i1	Immunoglobulin domain-containing protein oig-4	-13	-16
BOL_smith0	TRINITY_DN2665_c5_g1_i1	Neurobeachin	-15	-15
BOL_smith0	TRINITY_DN2884_c1_g1_i1	TATA-binding protein-associated factor 172	-14	-18
BOL_smith0	TRINITY_DN2966_c0_g2_i5	ADP-ribose glycohydrolase OARD1	-13	-16
BOL_smith0	TRINITY_DN3107_c0_g2_i1	Vam6/Vps39-like protein	-12	-15
BOL_smith0	TRINITY_DN3216_c0_g1_i2	Protein artichoke	-15	-16
BOL_smith0	TRINITY_DN32_c0_g1_i1	Protein yippee	-18	-22
BOL_smith0	TRINITY_DN3387_c0_g1_i1	DNA repair protein XRCC3	-15	-15
BOL_smith0	TRINITY_DN3585_c0_g1_i1	Cuticle protein 7	-11	-17
BOL_smith0	TRINITY_DN38005_c0_g1_i1	Protein Abitram	-10	-15
BOL_smith0	TRINITY_DN3951_c0_g1_i1	.	-14	-19
BOL_smith0	TRINITY_DN4190_c0_g1_i2	Polycomb protein Su(z)12	-16	-20
BOL_smith0	TRINITY_DN4432_c0_g1_i1	D-glucuronyl C5-epimerase B	-15	-16
BOL_smith0	TRINITY_DN4596_c0_g3_i1	N-acylneuraminate-9-phosphatase	-10	-15
BOL_smith0	TRINITY_DN53_c0_g2_i1	Cuticular protein 47Eg	-13	-15
BOL_smith0	TRINITY_DN5514_c0_g1_i1	Serine/threonine-protein phosphatase 5	-10	-18
BOL_smith0	TRINITY_DN5737_c0_g1_i1	.	-10	-15
BOL_smith0	TRINITY_DN612_c0_g2_i4	Probable multidrug resistance-associated protein lethal(2)03659	-9	-15
BOL_smith0	TRINITY_DN681_c1_g3_i1	Transcription factor grauzone	-13	-15
BOL_smith0	TRINITY_DN699_c0_g1_i12	Protein CIMAP1D	-10	-15
BOL_smith0	TRINITY_DN7188_c0_g1_i1	Vang-like protein 1	-14	-15
BOL_smith0	TRINITY_DN7878_c1_g1_i1	Gamma-butyrobetaine dioxygenase	-15	-15
BOL_smith0	TRINITY_DN8044_c0_g1_i1	.	-12	-16
		***Caenorhabditis elegans* (4 candidates, 197 targets)**		
smithID	**transcriptID**	**Blastx**	**dG PITA**	**dG RNAHybrid**
CEL_smith0	TRINITY_DN1007_c1_g1_i11	.	-18	-21
CEL_smith0	TRINITY_DN1056_c0_g2_i1	Transcription factor dcp-66	-11	-15
CEL_smith0	TRINITY_DN1073_c2_g1_i1	Protein strawberry notch homolog	-17	-21
CEL_smith0	TRINITY_DN10910_c0_g1_i1	DNA damage-binding protein 1	-15	-16
CEL_smith0	TRINITY_DN10939_c0_g1_i2	Histone-lysine N-methyltransferase set-6	-15	-17
CEL_smith0	TRINITY_DN11184_c0_g1_i2	.	-12	-16
CEL_smith0	TRINITY_DN1141_c0_g1_i6	Octopamine receptor 1	-13	-15

CEL_smith0	TRINITY_DN1148_c2_g1_i1	85/88 kDa calcium-independent phospholipase A2	-9	-19
CEL_smith0	TRINITY_DN1154_c0_g1_i1	.	-14	-17
CEL_smith0	TRINITY_DN1208_c0_g1_i1	SWI/SNF complex subunit SMARCC2	-11	-16
CEL_smith0	TRINITY_DN1252_c0_g2_i11	.	-19	-19
CEL_smith0	TRINITY_DN1282_c0_g1_i2	Nuclear hormone receptor family member daf-12	-11	-17
CEL_smith0	TRINITY_DN1282_c2_g1_i2	Uncharacterized protein F13E6.1	-14	-17
CEL_smith0	TRINITY_DN1288_c0_g1_i1	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A containing DEAD/H box 1 homolog	-20	-20
CEL_smith0	TRINITY_DN130_c0_g1_i1	Casein kinase II subunit beta	-14	-17
CEL_smith0	TRINITY_DN1395_c0_g1_i1	Protein odd-skipped-related 2	-13	-17
CEL_smith0	TRINITY_DN1416_c1_g1_i2	Mediator of RNA polymerase II transcription subunit 13	-14	-19
CEL_smith0	TRINITY_DN141_c0_g1_i4	Phosphatidylinositol 4-phosphate 5-kinase type-1 alpha	-11	-17
CEL_smith0	TRINITY_DN1420_c1_g1_i1	Glucosidase 2 subunit beta	-18	-20
CEL_smith0	TRINITY_DN1432_c0_g1_i3	.	-22	-20
CEL_smith0	TRINITY_DN1505_c0_g1_i15	E3 ubiquitin-protein ligase hecd-1	-16	-19
CEL_smith0	TRINITY_DN1507_c0_g1_i1	Translational repressor ifet-1	-18	-16
CEL_smith0	TRINITY_DN1514_c0_g4_i1	Uridine 5'-monophosphate synthase	-17	-20
CEL_smith0	TRINITY_DN1540_c0_g4_i1	Protein let-418	-11	-20
CEL_smith0	TRINITY_DN157_c0_g2_i12	Mesocentin	-15	-15
CEL_smith0	TRINITY_DN1676_c0_g1_i1	FMRFamide-like neuropeptides 14	-16	-16
CEL_smith0	TRINITY_DN169_c0_g1_i6	Ankyrin-2	-15	-19
CEL_smith0	TRINITY_DN1723_c0_g1_i2	2-oxoisovalerate dehydrogenase subunit alpha, mitochondrial	-11	-15
CEL_smith0	TRINITY_DN174_c0_g1_i5	.	-10	-19
CEL_smith0	TRINITY_DN1774_c1_g1_i3	WD repeat-containing protein 20 homolog	-19	-15
CEL_smith0	TRINITY_DN1803_c0_g1_i2	ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial	-11	-15
CEL_smith0	TRINITY_DN192_c0_g2_i1	Myotubularin-related protein 3	-16	-21
CEL_smith0	TRINITY_DN195_c0_g2_i1	Germline survival defective-1	-13	-16
CEL_smith0	TRINITY_DN195_c3_g1_i1	Tyrosine--tRNA ligase, cytoplasmic	-17	-17
CEL_smith0	TRINITY_DN19830_c0_g1_i1	Probable pre-mRNA-splicing factor ATP-dependent RNA helicase mog-1	-11	-17
CEL_smith0	TRINITY_DN1995_c0_g1_i5	NPC intracellular cholesterol transporter 1 homolog 1	-15	-19
CEL_smith0	TRINITY_DN19_c2_g1_i2	Amyloid-beta-like protein	-16	-21
CEL_smith0	TRINITY_DN1_c0_g1_i1	Oligopeptidase A	-12	-16
CEL_smith0	TRINITY_DN200_c0_g1_i2	.	-9	-15
CEL_smith0	TRINITY_DN20244_c0_g1_i2	General transcription and DNA repair factor IIH helicase subunit XPB	-14	-15
CEL_smith0	TRINITY_DN204_c0_g1_i15	Protein unc-80	-13	-16
CEL_smith0	TRINITY_DN2148_c0_g1_i5	Solute carrier family 4 member 11	-13	-15
CEL_smith0	TRINITY_DN23065_c0_g1_i1	TWiK family of potassium channels protein 9	-14	-19
CEL_smith0	TRINITY_DN2480_c0_g3_i3	Ester hydrolase C11orf54 homolog	-9	-17
CEL_smith0	TRINITY_DN24_c1_g1_i2	Calmodulin-like protein	-10	-20
CEL_smith0	TRINITY_DN2577_c0_g2_i9	.	-10	-17
CEL_smith0	TRINITY_DN26014_c0_g1_i1	Suppressor/enhancer of lin-12 protein 9	-11	-16
CEL_smith0	TRINITY_DN2690_c0_g1_i1	.	-14	-16
CEL_smith0	TRINITY_DN2732_c1_g3_i4	.	-16	-20
CEL_smith0	TRINITY_DN273_c0_g1_i1	.	-17	-18
CEL_smith0	TRINITY_DN277_c0_g1_i1	Spectrin alpha chain	-20	-19
CEL_smith0	TRINITY_DN2919_c0_g1_i7	Glycogenin-1	-11	-16
CEL_smith0	TRINITY_DN2993_c0_g1_i19	Protein skinhead-1	-15	-20
CEL_smith0	TRINITY_DN307_c0_g1_i12	Calcitonin receptor-like protein 1	-15	-16
CEL_smith0	TRINITY_DN3125_c0_g1_i5	Stress activated transcription factor atfs-1	-14	-15
CEL_smith0	TRINITY_DN32_c0_g1_i15	Prostaglandin reductase 2	-13	-16
CEL_smith0	TRINITY_DN3466_c0_g2_i3	Macoilin	-16	-21
CEL_smith0	TRINITY_DN349_c0_g1_i2	Uncharacterized protein R10E11.6	-15	-16
CEL_smith0	TRINITY_DN36_c1_g1_i1	Integrin beta pat-3	-15	-19
CEL_smith0	TRINITY_DN3720_c1_g1_i1	Secretory carrier-associated membrane protein 1	-14	-19
CEL_smith0	TRINITY_DN3807_c0_g1_i4	Serine/threonine-protein kinase WNK	-11	-19
CEL_smith0	TRINITY_DN3818_c0_g1_i2	Microtubule-associated serine/threonine-protein kinase 3	-14	-17
CEL_smith0	TRINITY_DN393_c0_g1_i1	.	-14	-19
CEL_smith0	TRINITY_DN3967_c0_g1_i1	Suppressor of Ty 6 homolog	-9	-18
CEL_smith0	TRINITY_DN3996_c0_g1_i1	Deoxynucleoside triphosphate triphosphohydrolase sahd-1	-21	-21
CEL_smith0	TRINITY_DN3997_c0_g1_i2	.	-9	-19
CEL_smith0	TRINITY_DN4064_c0_g1_i1	Nuclear anchorage protein 1	-20	-21
CEL_smith0	TRINITY_DN4142_c0_g1_i2	.	-17	-15
CEL_smith0	TRINITY_DN4238_c0_g1_i1	.	-11	-15
CEL_smith0	TRINITY_DN4245_c0_g1_i2	Sop-2-related protein 1	-18	-17
CEL_smith0	TRINITY_DN4256_c0_g2_i1	Dynein, cytoplasmic 1, intermediate chain 2a	-12	-15
CEL_smith0	TRINITY_DN427_c0_g1_i2	CAP-Gly domain-containing linker protein 1 homolog	-17	-20
CEL_smith0	TRINITY_DN4449_c0_g1_i4	Endoplasmic reticulum resident protein 44.2	-11	-17
CEL_smith0	TRINITY_DN445_c0_g1_i13	Muscarinic acetylcholine receptor gar-2	-12	-17
CEL_smith0	TRINITY_DN4518_c0_g1_i1	Ubiquitin-like modifier-activating enzyme 1	-15	-20
CEL_smith0	TRINITY_DN453_c0_g1_i13	V-type proton ATPase 116 kDa subunit a 1	-15	-17
CEL_smith0	TRINITY_DN4628_c0_g2_i5	Cell division cycle protein 27 homolog	-16	-16
CEL_smith0	TRINITY_DN466_c0_g2_i22	Triple functional domain protein	-12	-18
CEL_smith0	TRINITY_DN468_c0_g1_i1	Cyclin-dependent kinase 17	-12	-18
CEL_smith0	TRINITY_DN469_c2_g1_i2	Calmodulin	-15	-18
CEL_smith0	TRINITY_DN5057_c4_g1_i1	Condensin complex subunit capg-1	-13	-15
CEL_smith0	TRINITY_DN5202_c0_g1_i1	Uncharacterized ATP-dependent helicase C05C10.2	-12	-17
CEL_smith0	TRINITY_DN5224_c0_g2_i1	.	-14	-16
CEL_smith0	TRINITY_DN524_c1_g1_i2	DnaJ homolog subfamily A member 2	-9	-16
CEL_smith0	TRINITY_DN5650_c0_g2_i1	.	-13	-16
CEL_smith0	TRINITY_DN576_c0_g1_i10	Sex peptide receptor	-15	-19
CEL_smith0	TRINITY_DN585_c0_g1_i1	High mobility group protein 1.2	-10	-15
CEL_smith0	TRINITY_DN58_c0_g1_i4	.	-13	-17
CEL_smith0	TRINITY_DN592_c0_g1_i2	Influenza virus NS1A-binding protein	-11	-18
CEL_smith0	TRINITY_DN629_c0_g1_i17	Rho GTPase-activating protein 29	-13	-15
CEL_smith0	TRINITY_DN648_c0_g2_i4	Protein seu-1	-18	-16
CEL_smith0	TRINITY_DN6502_c0_g1_i1	Uncharacterized protein F10E9.3	-15	-15
CEL_smith0	TRINITY_DN651_c0_g2_i1	Chromo domain-containing protein cec-4	-19	-19
CEL_smith0	TRINITY_DN652_c0_g1_i1	Serine/threonine kinase NLK	-13	-17
CEL_smith0	TRINITY_DN653_c0_g1_i10	.	-18	-17
CEL_smith0	TRINITY_DN6834_c0_g1_i10	Calmodulin-binding transcription activator homolog 1	-16	-19
CEL_smith0	TRINITY_DN7185_c0_g1_i1	Cytosolic carboxypeptidase 1	-12	-17
CEL_smith0	TRINITY_DN718_c0_g1_i1	Probable aconitate hydratase, mitochondrial	-17	-16
CEL_smith0	TRINITY_DN720_c0_g1_i1	Glutamate receptor 2	-14	-15
CEL_smith0	TRINITY_DN7267_c1_g1_i1	V-type proton ATPase 16 kDa proteolipid subunit c 1	-14	-16
CEL_smith0	TRINITY_DN7545_c0_g1_i1	Chaperone protein dnaJ 16	-13	-17

CEL_smith0	TRINITY_DN7765_c0_g1_i1	Putative transmembrane protein INAFM2	-15	-19
CEL_smith0	TRINITY_DN8000_c1_g1_i3	.	-14	-20
CEL_smith0	TRINITY_DN8022_c0_g1_i1	Armadillo repeat-containing protein 1	-14	-19
CEL_smith0	TRINITY_DN8143_c0_g1_i2	Midasin	-12	-17
CEL_smith0	TRINITY_DN8517_c0_g1_i1	N-glycosidase R617	-15	-21
CEL_smith0	TRINITY_DN860_c0_g7_i1	.	-20	-18
CEL_smith0	TRINITY_DN861_c0_g1_i1	Neuroendocrine convertase 2	-11	-17
CEL_smith0	TRINITY_DN866_c0_g1_i2	cAMP-dependent protein kinase regulatory subunit	-16	-17
CEL_smith0	TRINITY_DN869_c0_g1_i6	Spectrin beta chain	-17	-19
CEL_smith0	TRINITY_DN8943_c0_g1_i1	Signal transducer and activator of transcription 1	-16	-19
CEL_smith0	TRINITY_DN917_c0_g1_i1	Protein tfg-1	-14	-19
CEL_smith0	TRINITY_DN9217_c1_g1_i4	Dynein heavy chain, cytoplasmic	-17	-19
CEL_smith0	TRINITY_DN940_c0_g2_i2	Guanine nucleotide-binding protein-like 3 homolog	-21	-17
CEL_smith0	TRINITY_DN9617_c0_g1_i1	Multiple C2 and transmembrane domain-containing protein 1	-12	-16
CEL_smith0	TRINITY_DN995_c0_g1_i14	.	-23	-25
CEL_smith1	TRINITY_DN10360_c0_g1_i1	.	-22	-15
CEL_smith1	TRINITY_DN11078_c0_g1_i2	Nuclear hormone receptor family member nhr-90	-22	-16
CEL_smith1	TRINITY_DN11164_c0_g1_i1	.	-16	-15
CEL_smith1	TRINITY_DN1129_c0_g3_i2	.	-11	-15
CEL_smith1	TRINITY_DN1140_c0_g1_i3	.	-18	-15
CEL_smith1	TRINITY_DN1162_c0_g1_i1	Paramyosin	-14	-18
CEL_smith1	TRINITY_DN116_c0_g1_i7	Band 4.1-like protein 1	-11	-17
CEL_smith1	TRINITY_DN1288_c0_g1_i1	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A containing DEAD/H box 1 homolog	-9	-17
CEL_smith1	TRINITY_DN1480_c0_g1_i3	Acyl-CoA	-13	-15
CEL_smith1	TRINITY_DN1509_c0_g1_i1	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	-21	-27
CEL_smith1	TRINITY_DN1550_c0_g1_i1	Golgi to ER traffic protein 4 homolog B	-12	-16
CEL_smith1	TRINITY_DN1585_c0_g1_i11	5'-AMP-activated protein kinase subunit gamma-1	-12	-20
CEL_smith1	TRINITY_DN1591_c0_g1_i1	Actin-binding LIM protein 2	-11	-15
CEL_smith1	TRINITY_DN1655_c0_g1_i9	Synaptotagmin 2	-14	-17
CEL_smith1	TRINITY_DN1679_c0_g1_i13	.	-14	-17
CEL_smith1	TRINITY_DN168_c1_g1_i1	.	-16	-15
CEL_smith1	TRINITY_DN1895_c0_g2_i1	Tetratricopeptide repeat protein 19, mitochondrial	-13	-15
CEL_smith1	TRINITY_DN19807_c0_g1_i1	UBX domain-containing protein 2	-14	-15
CEL_smith1	TRINITY_DN2010_c0_g3_i1	WD repeat-containing protein 47	-14	-16
CEL_smith1	TRINITY_DN2226_c0_g1_i1	Ankyrin repeat domain-containing protein 50	-9	-18
CEL_smith1	TRINITY_DN2237_c0_g1_i1	.	-13	-17
CEL_smith1	TRINITY_DN2311_c0_g1_i1	.	-16	-15
CEL_smith1	TRINITY_DN2517_c0_g2_i1	Enhancer of polycomb homolog 1	-23	-21
CEL_smith1	TRINITY_DN25490_c0_g1_i1	Putative glycerophosphocholine phosphodiesterase GPCPD1 homolog 2	-14	-15
CEL_smith1	TRINITY_DN2577_c0_g2_i12	Nuclear hormone receptor family member nhr-41	-15	-17
CEL_smith1	TRINITY_DN25897_c0_g1_i1	Target of rapamycin complex subunit lst8	-18	-20
CEL_smith1	TRINITY_DN2601_c0_g1_i1	Acyl-coenzyme A thioesterase 8	-20	-15
CEL_smith1	TRINITY_DN26259_c0_g1_i1	Ras-related protein rab-39	-18	-17
CEL_smith1	TRINITY_DN2731_c1_g1_i1	.	-18	-17
CEL_smith1	TRINITY_DN2736_c0_g2_i2	RNA-binding protein 26	-9	-15
CEL_smith1	TRINITY_DN2784_c0_g1_i2	Dedicator of cytokinesis protein 7	-11	-17
CEL_smith1	TRINITY_DN2812_c0_g1_i2	Trafficking protein particle complex subunit 11	-18	-17
CEL_smith1	TRINITY_DN2877_c0_g1_i8	Protein lin-14	-10	-17
CEL_smith1	TRINITY_DN2889_c0_g1_i3	Kinesin-like protein klpA	-12	-19
CEL_smith1	TRINITY_DN2972_c0_g2_i2	Phospholipase A2 inhibitor beta	-27	-21
CEL_smith1	TRINITY_DN3023_c0_g1_i1	Probable inactive acireductone dioxygenase 2	-15	-19
CEL_smith1	TRINITY_DN3023_c0_g3_i1	Probable inactive acireductone dioxygenase 2	-15	-19
CEL_smith1	TRINITY_DN3167_c0_g1_i3	Mitochondrial import inner membrane translocase subunit Tim21	-14	-17
CEL_smith1	TRINITY_DN3334_c0_g1_i3	Toll-interacting protein	-13	-16
CEL_smith1	TRINITY_DN3613_c0_g1_i1	Deubiquitinase OTUD6B	-17	-23
CEL_smith1	TRINITY_DN367_c0_g2_i10	Oxidation resistance protein 1	-17	-17
CEL_smith1	TRINITY_DN36_c1_g1_i1	Integrin beta pat-3	-17	-19
CEL_smith1	TRINITY_DN4034_c0_g2_i1	Zinc finger transcription factor family protein 17	-15	-17
CEL_smith1	TRINITY_DN4259_c0_g1_i1	.	-13	-17
CEL_smith1	TRINITY_DN463_c0_g1_i1	MOB kinase activator-like 2	-10	-15
CEL_smith1	TRINITY_DN5028_c0_g1_i3	Inositol hexakisphosphate kinase 1	-17	-17
CEL_smith1	TRINITY_DN528_c0_g1_i2	Heat shock protein 110	-20	-17
CEL_smith1	TRINITY_DN539_c0_g1_i1	Propionyl-CoA carboxylase beta chain, mitochondrial	-12	-15
CEL_smith1	TRINITY_DN5_c0_g1_i3	Phosphoenolpyruvate carboxykinase [GTP]	-17	-17
CEL_smith1	TRINITY_DN6018_c0_g1_i1	mRNA export factor rae-1	-11	-20
CEL_smith1	TRINITY_DN6026_c0_g1_i3	Cell cycle checkpoint protein RAD1 homolog mrt-2	-14	-15
CEL_smith1	TRINITY_DN6071_c0_g1_i3	Collagenase 3	-17	-17
CEL_smith1	TRINITY_DN6340_c0_g1_i1	Synembryn	-15	-16
CEL_smith1	TRINITY_DN658_c0_g1_i11	Multidrug resistance-associated protein 1	-12	-16
CEL_smith1	TRINITY_DN71_c2_g1_i1	Arrestin domain-containing protein 17	-21	-17
CEL_smith1	TRINITY_DN730_c0_g2_i5	Early growth response protein 1	-13	-15
CEL_smith1	TRINITY_DN7580_c0_g1_i2	Multifunctional protein pyr-1	-17	-17
CEL_smith1	TRINITY_DN7766_c0_g1_i1	Heme transporter hrg-1	-14	-15
CEL_smith1	TRINITY_DN789_c0_g1_i3	Adenylate cyclase type 9	-12	-17
CEL_smith1	TRINITY_DN792_c1_g1_i10	.	-15	-17
CEL_smith1	TRINITY_DN79_c1_g1_i1	Glutamate receptor ionotropic, kainate glr-3	-17	-20
CEL_smith1	TRINITY_DN8062_c0_g1_i1	Sulfotransferase ssu-1	-13	-21
CEL_smith1	TRINITY_DN8159_c0_g1_i2	Nicastrin	-21	-19
CEL_smith1	TRINITY_DN8188_c1_g1_i5	32 kDa beta-galactoside-binding lectin lec-3	-16	-16
CEL_smith1	TRINITY_DN81_c0_g3_i1	cGMP-dependent protein kinase egl-4	-14	-15
CEL_smith1	TRINITY_DN8708_c0_g1_i1	Protein flightless-1 homolog	-12	-15
CEL_smith1	TRINITY_DN9577_c0_g1_i3	Aurora/IPL1-related protein kinase 2	-15	-17
CEL_smith2	TRINITY_DN17480_c0_g1_i2	.	-19	-21
CEL_smith2	TRINITY_DN204_c0_g1_i15	Protein unc-80	-11	-16
CEL_smith2	TRINITY_DN2081_c0_g1_i1	Nuclear hormone receptor family member nhr-71	-17	-18
CEL_smith2	TRINITY_DN2147_c0_g1_i4	TBC1 domain family member 22B	-17	-17
CEL_smith4	TRINITY_DN129_c0_g1_i2	Folliculin	-17	-19
CEL_smith4	TRINITY_DN141_c0_g1_i4	Phosphatidylinositol 4-phosphate 5-kinase type-1 alpha	-13	-18
CEL_smith4	TRINITY_DN149_c0_g1_i1	Potassium voltage-gated channel unc-103	-26	-20
CEL_smith4	TRINITY_DN2200_c0_g2_i10	Eyes absent homolog 1	-10	-18
CEL_smith4	TRINITY_DN23176_c0_g1_i1	Autophagic-related protein 16.2	-18	-16
CEL_smith4	TRINITY_DN320_c0_g2_i17	E3 SUMO-protein ligase gei-17	-16	-18
CEL_smith4	TRINITY_DN3718_c0_g1_i2	.	-15	-17
CEL_smith4	TRINITY_DN6776_c0_g1_i1	Semaphorin-1A	-16	-16

CEL_smith4	TRINITY_DN8375_c0_g1_i1	.	-11	-16
CEL_smith4	TRINITY_DN9171_c0_g1_i1	Disintegrin and metalloproteinase domain-containing protein 10 homolog	-22	-15

***Caridina multidentata* (1 candidate, 200 targets)**

smithID	transcriptID	Blastx	dG PITA	dG RNAHybrid
CMU_smith2	TRINITY_DN10011_c0_g1_i1	Protein yippee-like 2	-25	-22
CMU_smith2	TRINITY_DN100184_c0_g1_i1	.	-16	-19
CMU_smith2	TRINITY_DN10087_c0_g1_i1	Protein arginine N-methyltransferase 6	-21	-16
CMU_smith2	TRINITY_DN10097_c0_g1_i7	Uncharacterized protein CG43867	-21	-24
CMU_smith2	TRINITY_DN10130_c0_g1_i1	Protein prenyltransferase alpha subunit repeat-containing protein 1	-18	-19
CMU_smith2	TRINITY_DN102_c0_g1_i2	DNA polymerase subunit gamma-1, mitochondrial	-18	-22
CMU_smith2	TRINITY_DN1048_c0_g1_i10	NADP-dependent malic enzyme	-23	-26
CMU_smith2	TRINITY_DN10672_c0_g1_i1	.	-14	-17
CMU_smith2	TRINITY_DN1070_c0_g1_i1	Ras-related protein Rap-1b	-17	-15
CMU_smith2	TRINITY_DN11098_c0_g1_i3	.	-25	-17
CMU_smith2	TRINITY_DN1109_c0_g1_i10	Poly(rC)-binding protein 3	-13	-24
CMU_smith2	TRINITY_DN11320_c0_g2_i3	Transcriptional repressor CTCF	-18	-21
CMU_smith2	TRINITY_DN11640_c0_g1_i1	Solute carrier organic anion transporter family member 74D	-20	-18
CMU_smith2	TRINITY_DN116_c0_g1_i7	MOB kinase activator-like 2	-12	-17
CMU_smith2	TRINITY_DN11864_c0_g1_i11	Atrial natriuretic peptide-converting enzyme	-12	-16
CMU_smith2	TRINITY_DN11912_c0_g1_i1	.	-18	-15
CMU_smith2	TRINITY_DN11967_c0_g1_i10	Peptidyl-prolyl cis-trans isomerase-like 3	-14	-19
CMU_smith2	TRINITY_DN12105_c0_g1_i1	Hypoxia-inducible factor 1-alpha inhibitor	-12	-15
CMU_smith2	TRINITY_DN12168_c0_g2_i10	Probable RNA-directed DNA polymerase from transposon X-element	-14	-16
CMU_smith2	TRINITY_DN1251_c0_g1_i10	Carboxyl-terminal PDZ ligand of neuronal nitric oxide synthase protein	-23	-25
CMU_smith2	TRINITY_DN12572_c0_g1_i13	Protein bric-a-brac 2	-24	-24
CMU_smith2	TRINITY_DN1264_c0_g2_i1	Pseudouridylate synthase RPUSD2	-14	-18
CMU_smith2	TRINITY_DN1265_c0_g1_i1	.	-14	-16
CMU_smith2	TRINITY_DN12839_c0_g1_i1	Solute carrier family 25 member 35	-14	-17
CMU_smith2	TRINITY_DN12919_c0_g1_i2	Methylthioribulose-1-phosphate dehydratase	-14	-15
CMU_smith2	TRINITY_DN1302_c0_g1_i6	Sodium leak channel NALCN	-13	-16
CMU_smith2	TRINITY_DN1352_c0_g1_i10	Phenoloxidase-activating factor 2	-17	-15
CMU_smith2	TRINITY_DN1384_c1_g3_i1	Death-associated inhibitor of apoptosis 1	-17	-19
CMU_smith2	TRINITY_DN13856_c0_g1_i10	SET and MYND domain-containing protein 4	-21	-23
CMU_smith2	TRINITY_DN1397_c0_g1_i1	.	-20	-22
CMU_smith2	TRINITY_DN1415_c0_g1_i1	Metaxin-1	-16	-18
CMU_smith2	TRINITY_DN14174_c0_g1_i3	.	-15	-15
CMU_smith2	TRINITY_DN14227_c0_g1_i3	F-box/WD repeat-containing protein 7	-14	-19
CMU_smith2	TRINITY_DN1442_c0_g1_i10	Copper-transporting ATPase 1	-15	-19
CMU_smith2	TRINITY_DN14482_c0_g1_i10	Eukaryotic translation initiation factor eIF1	-21	-23
CMU_smith2	TRINITY_DN1477_c0_g1_i2	Translocation protein SEC63 homolog	-17	-24
CMU_smith2	TRINITY_DN14827_c0_g1_i3	.	-24	-20
CMU_smith2	TRINITY_DN15179_c0_g1_i1	.	-25	-18
CMU_smith2	TRINITY_DN1536_c0_g1_i4	Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	-26	-15
CMU_smith2	TRINITY_DN153_c0_g1_i2	Thrombospondin-3	-19	-17
CMU_smith2	TRINITY_DN15513_c0_g2_i1	.	-15	-19
CMU_smith2	TRINITY_DN1561_c1_g1_i10	Longitudinals lacking protein, isoforms H/M/V	-16	-17
CMU_smith2	TRINITY_DN1576_c0_g1_i1	Glypican-5	-18	-19
CMU_smith2	TRINITY_DN15891_c0_g1_i10	.	-13	-18
CMU_smith2	TRINITY_DN16191_c1_g1_i1	Small ribosomal subunit protein uS8	-12	-17
CMU_smith2	TRINITY_DN16266_c0_g1_i5	Zinc finger and BTB domain-containing protein 17	-13	-20
CMU_smith2	TRINITY_DN16315_c0_g1_i1	Calcium-independent phospholipase A2-gamma	-12	-16
CMU_smith2	TRINITY_DN163_c0_g1_i10	Spectrin beta chain, non-erythrocytic 5	-22	-18
CMU_smith2	TRINITY_DN16526_c0_g1_i16	VPS35 endosomal protein-sorting factor-like	-17	-17
CMU_smith2	TRINITY_DN1675_c0_g1_i2	NFX1-type zinc finger-containing protein 1	-15	-18
CMU_smith2	TRINITY_DN1690_c0_g1_i2	Cold shock domain-containing protein E1	-24	-22
CMU_smith2	TRINITY_DN17181_c0_g1_i1	Gastrula zinc finger protein XlCGF8.2DB	-27	-24
CMU_smith2	TRINITY_DN17387_c0_g1_i1	.	-13	-18
CMU_smith2	TRINITY_DN1749_c0_g1_i3	Eukaryotic translation initiation factor 3 subunit I	-15	-21
CMU_smith2	TRINITY_DN1852_c0_g1_i12	Acetyl-CoA carboxylase	-14	-18
CMU_smith2	TRINITY_DN18575_c0_g1_i1	E3 ubiquitin-protein ligase TRIM9	-23	-22
CMU_smith2	TRINITY_DN1882_c0_g1_i2	Protein suppressor of sable	-16	-17
CMU_smith2	TRINITY_DN1883_c3_g1_i3	AP2-associated protein kinase 1	-17	-18
CMU_smith2	TRINITY_DN1884_c1_g1_i3	Muscle-specific protein 300 kDa	-15	-15
CMU_smith2	TRINITY_DN1924_c0_g1_i10	R3H domain-containing protein 4	-21	-22
CMU_smith2	TRINITY_DN19323_c0_g1_i4	Meiosis regulator and mRNA stability factor 1	-12	-18
CMU_smith2	TRINITY_DN1936_c0_g1_i2	.	-20	-27
CMU_smith2	TRINITY_DN1938_c0_g1_i11	Chloride channel protein 2	-19	-18
CMU_smith2	TRINITY_DN1939_c0_g1_i2	Papilin	-17	-23
CMU_smith2	TRINITY_DN1964_c0_g1_i12	Sodium/calcium exchanger 1	-15	-25
CMU_smith2	TRINITY_DN2000_c0_g1_i1	.	-20	-17
CMU_smith2	TRINITY_DN20091_c0_g1_i11	GRAM domain-containing protein 4	-16	-18
CMU_smith2	TRINITY_DN200_c0_g1_i2	.	-10	-18
CMU_smith2	TRINITY_DN205_c0_g1_i7	Actin-related protein 2/3 complex subunit 1A-B	-20	-15
CMU_smith2	TRINITY_DN20628_c0_g1_i13	Acetylcholine receptor subunit alpha-like	-16	-17
CMU_smith2	TRINITY_DN2080_c1_g1_i5	Neurogenic locus notch homolog protein 1	-29	-31
CMU_smith2	TRINITY_DN20872_c0_g1_i4	GTP-binding protein 128up	-20	-22
CMU_smith2	TRINITY_DN21294_c0_g1_i13	Ubiquitin-like domain-containing CTD phosphatase 1	-17	-16
CMU_smith2	TRINITY_DN21637_c0_g1_i13	N-acetyltransferase 9-like protein	-23	-26
CMU_smith2	TRINITY_DN22124_c0_g1_i2	Neprilysin-1	-18	-25
CMU_smith2	TRINITY_DN2263_c0_g1_i12	RNA-binding protein 45	-17	-20
CMU_smith2	TRINITY_DN227_c0_g1_i10	Glucoside xylosyltransferase 1	-21	-25
CMU_smith2	TRINITY_DN2299_c0_g1_i1	Mitochondrial ribosome-associated GTPase 1	-18	-18
CMU_smith2	TRINITY_DN2386_c0_g1_i1	Protein cornichon	-16	-20
CMU_smith2	TRINITY_DN2398_c0_g1_i16	Tau-tubulin kinase homolog Asator	-18	-28
CMU_smith2	TRINITY_DN24921_c0_g1_i2	Serine/threonine-protein phosphatase 6 regulatory ankyrin repeat subunit C	-15	-20
CMU_smith2	TRINITY_DN2499_c0_g1_i1	Rab proteins geranylgeranyltransferase component A 2	-16	-22
CMU_smith2	TRINITY_DN25734_c0_g1_i2	.	-20	-16
CMU_smith2	TRINITY_DN2600_c0_g1_i4	Leucine-rich repeats and immunoglobulin-like domains protein 3	-19	-22
CMU_smith2	TRINITY_DN2673_c0_g1_i8	Cytoplasmic dynein 1 intermediate chain 2	-18	-18
CMU_smith2	TRINITY_DN2727_c0_g1_i1	Ubiquitin carboxyl-terminal hydrolase 19	-17	-17
CMU_smith2	TRINITY_DN27_c0_g1_i5	Transcriptional adapter 2-beta	-19	-24
CMU_smith2	TRINITY_DN2817_c0_g1_i1	.	-22	-22
CMU_smith2	TRINITY_DN2901_c0_g1_i2	Calcium-binding mitochondrial carrier protein Aralar1	-17	-20
CMU_smith2	TRINITY_DN29999_c0_g1_i4	Polyamine-transporting ATPase 13A3	-20	-25

CMU_smith2	TRINITY_DN303_c0_g1_i10	Protein enabled	-17	-18
CMU_smith2	TRINITY_DN3064_c0_g1_i1	Fibrillin-2	-16	-22
CMU_smith2	TRINITY_DN307_c0_g1_i10	F-actin-uncapping protein LRRC16A	-28	-33
CMU_smith2	TRINITY_DN3080_c0_g3_i1	Inositol hexakisphosphate and diphosphoinositol-pentakisphosphate kinase	-18	-16
CMU_smith2	TRINITY_DN3156_c0_g1_i1	Large ribosomal subunit protein mL40	-14	-23
CMU_smith2	TRINITY_DN32857_c0_g2_i1	Galactosylgalactosylxylosylprotein 3-beta-glucuronosyltransferase S	-21	-24
CMU_smith2	TRINITY_DN3336_c0_g2_i2	.	-18	-23
CMU_smith2	TRINITY_DN3485_c0_g1_i2	Sideroflexin-2	-21	-15
CMU_smith2	TRINITY_DN353_c0_g1_i13	Dystonin	-16	-15
CMU_smith2	TRINITY_DN3562_c0_g1_i1	.	-19	-15
CMU_smith2	TRINITY_DN3643_c0_g1_i1	Integrin beta-PS	-23	-26
CMU_smith2	TRINITY_DN3651_c0_g1_i3	Unconventional myosin-IXb	-15	-21
CMU_smith2	TRINITY_DN3741_c0_g1_i10	Synapsin	-16	-17
CMU_smith2	TRINITY_DN3822_c0_g1_i12	.	-23	-21
CMU_smith2	TRINITY_DN3856_c0_g1_i3	GEL complex subunit OPTI	-11	-17
CMU_smith2	TRINITY_DN389_c0_g1_i17	Basement membrane-specific heparan sulfate proteoglycan core protein	-16	-20
CMU_smith2	TRINITY_DN3935_c0_g1_i1	THO complex subunit 4-A	-18	-18
CMU_smith2	TRINITY_DN407_c0_g1_i4	Tissue factor pathway inhibitor	-21	-22
CMU_smith2	TRINITY_DN4241_c0_g1_i2	Mitochondrial 2-oxodicarboxylate carrier	-20	-25
CMU_smith2	TRINITY_DN42579_c0_g2_i1	RNA-directed DNA polymerase from mobile element jockey	-9	-19
CMU_smith2	TRINITY_DN4278_c0_g1_i1	Ras-related protein Rab-14	-22	-23
CMU_smith2	TRINITY_DN4375_c0_g1_i2	Kelch-like protein 18	-14	-17
CMU_smith2	TRINITY_DN440_c1_g1_i4	Partner of Y14 and mago	-18	-22
CMU_smith2	TRINITY_DN4413_c0_g1_i10	Splicing factor 3A subunit 1	-15	-17
CMU_smith2	TRINITY_DN4449_c0_g1_i2	BTB/POZ domain-containing protein 10	-23	-24
CMU_smith2	TRINITY_DN4482_c0_g1_i1	Homeobox protein prospero	-25	-27
CMU_smith2	TRINITY_DN448_c0_g1_i3	Eye-specific diacylglycerol kinase	-14	-23
CMU_smith2	TRINITY_DN45033_c0_g1_i1	Golgi-associated plant pathogenesis-related protein 1	-23	-24
CMU_smith2	TRINITY_DN4549_c0_g1_i1	Zinc finger protein 850	-25	-26
CMU_smith2	TRINITY_DN4601_c1_g1_i1	SREBP regulating gene protein	-13	-16
CMU_smith2	TRINITY_DN4645_c0_g1_i1	Protein kinase C, brain isozyme	-18	-16
CMU_smith2	TRINITY_DN4740_c0_g1_i4	.	-17	-20
CMU_smith2	TRINITY_DN4761_c0_g1_i1	Developmentally-regulated GTP-binding protein 2	-17	-26
CMU_smith2	TRINITY_DN480_c0_g1_i1	Tetratricopeptide repeat protein 33	-11	-17
CMU_smith2	TRINITY_DN4853_c0_g1_i2	Homeobox protein Mohawk	-15	-17
CMU_smith2	TRINITY_DN4864_c0_g1_i6	KICSTOR complex protein kaptin	-19	-20
CMU_smith2	TRINITY_DN5014_c0_g1_i14	Cholesterol uptake protein 1	-19	-17
CMU_smith2	TRINITY_DN5048_c0_g1_i1	Flotillin-1	-20	-17
CMU_smith2	TRINITY_DN5093_c0_g1_i5	Dual specificity protein phosphatase CDC14A	-17	-25
CMU_smith2	TRINITY_DN514_c0_g1_i12	Calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type	-20	-25
CMU_smith2	TRINITY_DN5164_c0_g1_i10	.	-17	-24
CMU_smith2	TRINITY_DN528_c0_g1_i10	Muscle calcium channel subunit alpha-1	-15	-24
CMU_smith2	TRINITY_DN5406_c0_g1_i1	Peroxisomal membrane protein PEX16	-19	-17
CMU_smith2	TRINITY_DN5408_c0_g1_i2	LIM domain kinase 1	-20	-20
CMU_smith2	TRINITY_DN5524_c0_g1_i8	Arginyl-tRNA--protein transferase 1	-18	-20
CMU_smith2	TRINITY_DN5543_c0_g2_i1	Protein pinocchio	-24	-26
CMU_smith2	TRINITY_DN5549_c0_g1_i1	Apoptosis-stimulating of p53 protein 1	-24	-17
CMU_smith2	TRINITY_DN5579_c0_g1_i3	Regulator of microtubule dynamics protein 1	-17	-31
CMU_smith2	TRINITY_DN5589_c0_g1_i12	.	-19	-22
CMU_smith2	TRINITY_DN5637_c0_g1_i1	Dual specificity phosphatase 29	-15	-15
CMU_smith2	TRINITY_DN574_c0_g1_i1	.	-16	-21
CMU_smith2	TRINITY_DN579_c0_g1_i24	Probable methylmalonate-semialdehyde/malonate-semialdehyde dehydrogenase [acylating], mitochondrial	-17	-22
CMU_smith2	TRINITY_DN5827_c0_g1_i11	Mitochondrial 2-oxoglutarate/malate carrier protein	-20	-19
CMU_smith2	TRINITY_DN5957_c0_g1_i10	Kinesin-like protein Klp98A	-22	-29
CMU_smith2	TRINITY_DN6002_c0_g1_i10	Forkhead box protein P4	-14	-18
CMU_smith2	TRINITY_DN6025_c0_g1_i1	Glutaryl-CoA dehydrogenase, mitochondrial	-22	-25
CMU_smith2	TRINITY_DN6122_c0_g1_i1	DENN domain-containing protein Crag	-14	-18
CMU_smith2	TRINITY_DN6430_c1_g1_i1	.	-12	-17
CMU_smith2	TRINITY_DN643_c1_g1_i12	Serine/threonine-protein kinase N	-16	-17
CMU_smith2	TRINITY_DN6561_c0_g1_i10	Protein phosphatase 1 regulatory subunit 16A	-14	-16
CMU_smith2	TRINITY_DN6675_c0_g1_i3	.	-15	-16
CMU_smith2	TRINITY_DN66_c0_g1_i25	BET1-like protein	-14	-17
CMU_smith2	TRINITY_DN6752_c0_g1_i1	.	-19	-18
CMU_smith2	TRINITY_DN6776_c1_g1_i9	Ecdysone receptor	-17	-18
CMU_smith2	TRINITY_DN6814_c0_g1_i3	Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit epsilon isoform	-14	-20
CMU_smith2	TRINITY_DN6829_c0_g1_i1	Lysosomal protective protein	-17	-24
CMU_smith2	TRINITY_DN6842_c0_g1_i3	TBC1 domain family member 7	-16	-18
CMU_smith2	TRINITY_DN6868_c0_g1_i1	Ubiquinone biosynthesis monooxygenase COQ6, mitochondrial	-22	-19
CMU_smith2	TRINITY_DN6875_c0_g1_i1	Ras-related protein Rab-4B	-17	-21
CMU_smith2	TRINITY_DN6986_c0_g1_i12	.	-14	-21
CMU_smith2	TRINITY_DN7075_c0_g1_i5	Esterase FE4	-22	-24
CMU_smith2	TRINITY_DN7112_c0_g1_i1	Protein flightless-1	-16	-20
CMU_smith2	TRINITY_DN7116_c0_g1_i10	Zinc finger protein 341	-16	-16
CMU_smith2	TRINITY_DN7182_c0_g1_i1	5'-3' exoribonuclease 1	-20	-19
CMU_smith2	TRINITY_DN7395_c0_g1_i1	Potassium channel subfamily K member 18	-17	-15
CMU_smith2	TRINITY_DN741_c1_g1_i10	Stromal interaction molecule homolog	-17	-20
CMU_smith2	TRINITY_DN7444_c0_g1_i11	Pleckstrin homology domain-containing family G member 5	-21	-19
CMU_smith2	TRINITY_DN7450_c0_g1_i12	ATPase family AAA domain-containing protein 2B	-15	-18
CMU_smith2	TRINITY_DN7469_c0_g1_i6	Ribosome quality control complex subunit TCF25	-12	-15
CMU_smith2	TRINITY_DN752_c1_g1_i3	E3 SUMO-protein ligase PIAS2	-20	-15
CMU_smith2	TRINITY_DN76504_c0_g1_i1	.	-21	-15
CMU_smith2	TRINITY_DN7692_c0_g1_i10	NGFI-A-binding protein homolog	-14	-16
CMU_smith2	TRINITY_DN7707_c0_g1_i10	Luc7-like protein 3	-18	-16
CMU_smith2	TRINITY_DN7950_c0_g2_i1	Heterogeneous nuclear ribonucleoprotein M	-19	-20
CMU_smith2	TRINITY_DN8178_c0_g1_i1	Serine/threonine-protein kinase WNK3	-14	-24
CMU_smith2	TRINITY_DN819_c0_g1_i11	Homeobox protein homothorax	-19	-19
CMU_smith2	TRINITY_DN825_c0_g3_i1	Protein BTG3	-26	-23
CMU_smith2	TRINITY_DN832_c0_g1_i1	.	-26	-22
CMU_smith2	TRINITY_DN839_c0_g1_i10	RNA-binding protein 10	-20	-17
CMU_smith2	TRINITY_DN8449_c0_g1_i3	Protein dopey-1 homolog	-16	-16
CMU_smith2	TRINITY_DN8673_c0_g1_i1	.	-15	-18
CMU_smith2	TRINITY_DN8797_c0_g1_i6	.	-19	-23
CMU_smith2	TRINITY_DN8850_c0_g2_i8	Dedicator of cytokinesis protein 3	-21	-18
CMU_smith2	TRINITY_DN890_c0_g1_i22	Xaa-Pro aminopeptidase 1	-12	-19

CMU_smith2	TRINITY_DN905_c0_g1_i16	RNA-binding protein squid	-18	-18
CMU_smith2	TRINITY_DN9083_c0_g1_i11	Arf-GAP domain and FG repeat-containing protein 1	-14	-15
CMU_smith2	TRINITY_DN9109_c0_g1_i2	Zinc finger protein ZXDC	-16	-17
CMU_smith2	TRINITY_DN910_c0_g1_i13	Serine/threonine-protein phosphatase PP1-beta catalytic subunit	-19	-18
CMU_smith2	TRINITY_DN918_c0_g1_i1	Bromodomain-containing protein 8	-21	-20
CMU_smith2	TRINITY_DN922_c0_g1_i4	Twinfilin-2	-16	-16
CMU_smith2	TRINITY_DN9599_c0_g1_i11	Solute carrier family 35 member E2A	-15	-20
CMU_smith2	TRINITY_DN9613_c1_g1_i3	Proton channel OtopLc	-13	-20
CMU_smith2	TRINITY_DN9738_c0_g1_i1	Cysteine protease ATG4C	-14	-15
CMU_smith2	TRINITY_DN976_c0_g1_i2	Serine-arginine protein 55	-17	-23
CMU_smith2	TRINITY_DN9772_c0_g1_i3	Longitudinals lacking protein, isoforms H/M/V	-17	-21
CMU_smith2	TRINITY_DN9807_c0_g2_i2	Palmitoyltransferase ZDHHC16	-24	-27
CMU_smith2	TRINITY_DN9818_c0_g1_i1	.	-17	-17
CMU_smith2	TRINITY_DN9876_c0_g1_i10	Unc-112-related protein	-22	-19
CMU_smith2	TRINITY_DN9879_c0_g1_i10	Actin-binding protein WASF1	-11	-21
CMU_smith2	TRINITY_DN994_c2_g1_i1	Transcription initiation factor TFIID subunit 3	-23	-24
***Ceratitis capitata* (2 candidates, 21 targets)**				
smithID	**transcriptID**	**Blastx**	**dG PITA**	**dG RNAHybrid**
CCA_smith0	TRINITY_DN10758_c3_g1_i1	.	-14	-21
CCA_smith0	TRINITY_DN243_c1_g1_i1	Histone-lysine N-methyltransferase SETMAR	-16	-21
CCA_smith0	TRINITY_DN3056_c0_g1_i3	Guanine nucleotide-releasing factor 2	-13	-16
CCA_smith0	TRINITY_DN943_c5_g1_i2	.	-13	-16
CCA_smith2	TRINITY_DN14518_c0_g1_i1	UPF0389 protein CG9231	-16	-21
CCA_smith2	TRINITY_DN15_c0_g1_i10	Twitchin	-15	-16
CCA_smith2	TRINITY_DN1803_c0_g1_i17	Recombination repair protein 1	-9	-16
CCA_smith2	TRINITY_DN2150_c0_g1_i2	G protein-activated inward rectifier potassium channel 4	-16	-21
CCA_smith2	TRINITY_DN3291_c0_g1_i3	Citron Rho-interacting kinase	-14	-15
CCA_smith2	TRINITY_DN351_c0_g1_i19	Protein Gawky	-11	-15
CCA_smith2	TRINITY_DN37462_c0_g1_i2	.	-14	-16
CCA_smith2	TRINITY_DN449_c0_g1_i14	.	-18	-24
CCA_smith2	TRINITY_DN561_c0_g1_i3	Krueppel homolog 1	-11	-15
CCA_smith2	TRINITY_DN5923_c0_g1_i1	UV radiation resistance-associated gene protein	-9	-23
CCA_smith2	TRINITY_DN612_c0_g2_i2	Retrovirus-related Env polyprotein from transposon gypsy	-12	-15
CCA_smith2	TRINITY_DN624_c0_g1_i4	Hillarin	-22	-24
CCA_smith2	TRINITY_DN7455_c0_g1_i2	Homeodomain-interacting protein kinase 2	-13	-15
CCA_smith2	TRINITY_DN836_c1_g1_i10	Fasciclin-2	-11	-16
CCA_smith2	TRINITY_DN8748_c0_g1_i3	Serine protease easter	-18	-21
CCA_smith2	TRINITY_DN937_c0_g1_i12	.	-27	-25
CCA_smith2	TRINITY_DN973_c1_g1_i2	F-box/LRR-repeat protein 20	-13	-15
***Magallana gigas* (4 candidates, 314 targets)**				
smithID	**transcriptID**	**Blastx**	**dG PITA**	**dG RNAHybrid**
MGI_smith0	TRINITY_DN10006_c0_g1_i1	.	-14	-17
MGI_smith0	TRINITY_DN10050_c0_g1_i5	Protein patched homolog 1	-17	-15
MGI_smith0	TRINITY_DN10261_c0_g1_i2	Putative inhibitor of apoptosis	-16	-15
MGI_smith0	TRINITY_DN10303_c0_g1_i12	Katanin p60 ATPase-containing subunit A-like 2	-21	-15
MGI_smith0	TRINITY_DN10335_c0_g1_i11	.	-19	-17
MGI_smith0	TRINITY_DN10408_c0_g1_i11	.	-28	-16
MGI_smith0	TRINITY_DN1071_c0_g1_i1	Arginine-glutamic acid dipeptide repeats protein	-20	-15
MGI_smith0	TRINITY_DN107241_c1_g1_i1	.	-15	-16
MGI_smith0	TRINITY_DN10835_c0_g1_i3	Activating molecule in BECN1-regulated autophagy protein 1	-14	-16
MGI_smith0	TRINITY_DN10888_c0_g1_i1	Ras-related protein Rap-2b	-14	-21
MGI_smith0	TRINITY_DN1098_c0_g1_i5	Microtubule-associated serine/threonine-protein kinase 4	-18	-16
MGI_smith0	TRINITY_DN1137_c0_g1_i10	Dynamin-1	-18	-15
MGI_smith0	TRINITY_DN11886_c0_g1_i4	.	-15	-16
MGI_smith0	TRINITY_DN12099_c0_g2_i2	Jouberin	-21	-18
MGI_smith0	TRINITY_DN12161_c0_g1_i2	.	-25	-17
MGI_smith0	TRINITY_DN12184_c0_g1_i11	Transposon Ty3-G Gag-Pol polyprotein	-20	-16
MGI_smith0	TRINITY_DN122370_c1_g1_i5	.	-19	-15
MGI_smith0	TRINITY_DN12401_c0_g1_i11	Kinesin-like protein KIFC3	-17	-16
MGI_smith0	TRINITY_DN1240_c0_g1_i10	PTB domain-containing engulfment adapter protein 1	-19	-15
MGI_smith0	TRINITY_DN1285_c0_g1_i11	Single-stranded DNA-binding protein 3	-19	-16
MGI_smith0	TRINITY_DN12889_c0_g1_i1	Sodium-dependent neutral amino acid transporter B(0)AT1	-17	-16
MGI_smith0	TRINITY_DN1326_c0_g1_i1	MYND-type zinc finger-containing chromatin reader ZMYND8	-18	-15
MGI_smith0	TRINITY_DN134788_c0_g1_i1	.	-20	-18
MGI_smith0	TRINITY_DN1368_c0_g1_i3	Sestrin-1	-18	-17
MGI_smith0	TRINITY_DN137471_c0_g1_i1	.	-17	-17
MGI_smith0	TRINITY_DN13798_c0_g1_i11	Cornifelin homolog	-15	-15
MGI_smith0	TRINITY_DN14006_c1_g1_i2	Tripartite motif-containing protein 2	-17	-15
MGI_smith0	TRINITY_DN14155_c0_g1_i2	Tyramine beta-hydroxylase	-25	-15
MGI_smith0	TRINITY_DN14186_c0_g1_i10	Ceramide kinase	-14	-16
MGI_smith0	TRINITY_DN14341_c0_g1_i4	Vasoactive intestinal polypeptide receptor 1	-23	-15
MGI_smith0	TRINITY_DN14386_c0_g2_i2	.	-16	-16
MGI_smith0	TRINITY_DN1457_c0_g1_i4	Mitogen-activated protein kinase kinase kinase kinase 3	-21	-19
MGI_smith0	TRINITY_DN14774_c0_g1_i10	GATOR2 complex protein MIOS	-23	-16
MGI_smith0	TRINITY_DN1503_c0_g1_i10	WD repeat-containing protein 5	-18	-15
MGI_smith0	TRINITY_DN15109_c0_g1_i1	Arginine-hydroxylase NDUFAF5, mitochondrial	-26	-15
MGI_smith0	TRINITY_DN1515_c0_g1_i1	.	-18	-16
MGI_smith0	TRINITY_DN1532_c0_g1_i8	Cytosolic phospholipase A2	-21	-16
MGI_smith0	TRINITY_DN15506_c0_g1_i1	.	-22	-15
MGI_smith0	TRINITY_DN16016_c5_g1_i5	Protein asteroid homolog 1	-18	-16
MGI_smith0	TRINITY_DN1648_c0_g1_i10	DNA damage-regulated autophagy modulator protein 1	-15	-16
MGI_smith0	TRINITY_DN1718_c0_g1_i2	Nuclear pore complex protein Nup50	-15	-15
MGI_smith0	TRINITY_DN17245_c0_g2_i1	Deformed epidermal autoregulatory factor 1	-16	-15
MGI_smith0	TRINITY_DN1727_c0_g1_i10	FERM domain-containing protein 5	-15	-16
MGI_smith0	TRINITY_DN1780_c0_g1_i2	Glycine dehydrogenase (decarboxylating), mitochondrial	-16	-15
MGI_smith0	TRINITY_DN17814_c0_g1_i6	Phosphatidylinositol polyphosphate 5-phosphatase type IV	-15	-15
MGI_smith0	TRINITY_DN17950_c0_g1_i2	.	-19	-15
MGI_smith0	TRINITY_DN18607_c0_g1_i1	Probable protein phosphatase 2C T23F11.1	-25	-17
MGI_smith0	TRINITY_DN18658_c0_g1_i6	LINE-1 retrotransposable element ORF2 protein	-21	-15
MGI_smith0	TRINITY_DN189223_c0_g1_i2	Transient receptor potential cation channel subfamily V member 5	-16	-16
MGI_smith0	TRINITY_DN1902_c1_g1_i11	Pericentrin	-28	-17
MGI_smith0	TRINITY_DN1919_c0_g1_i1	.	-29	-15
MGI_smith0	TRINITY_DN1943_c0_g1_i5	Ral GTPase-activating protein subunit alpha-1	-15	-15

MGI_smith0	TRINITY_DN1967_c0_g1_i2	Genetic suppressor element 1	-21	-17
MGI_smith0	TRINITY_DN1975_c0_g1_i14	StAR-related lipid transfer protein 13	-18	-15
MGI_smith0	TRINITY_DN199_c0_g1_i10	RNA binding protein fox-1 homolog 3	-18	-15
MGI_smith0	TRINITY_DN20274_c1_g1_i6	.	-23	-20
MGI_smith0	TRINITY_DN20596_c0_g1_i5	Ras-like protein family member 10B	-16	-16
MGI_smith0	TRINITY_DN2101_c0_g1_i10	Pleckstrin homology-like domain family B member 2	-17	-16
MGI_smith0	TRINITY_DN2112_c0_g1_i4	INO80 complex subunit B	-18	-16
MGI_smith0	TRINITY_DN2128_c0_g1_i2	Tyrosine-protein phosphatase non-receptor type 9	-19	-18
MGI_smith0	TRINITY_DN21305_c0_g1_i1	S-adenosylmethionine-dependent methyltransferase Rv2258c	-21	-17
MGI_smith0	TRINITY_DN2133_c0_g1_i17	Cytohesin-1	-18	-17
MGI_smith0	TRINITY_DN2137_c0_g2_i3	Tetraspanin-33	-24	-18
MGI_smith0	TRINITY_DN2138_c0_g3_i1	mRNA export factor	-24	-15
MGI_smith0	TRINITY_DN2156_c0_g1_i10	Putative molluscan insulin-related peptide(s) receptor	-16	-15
MGI_smith0	TRINITY_DN2166_c0_g1_i2	Serine/threonine-protein phosphatase 1 regulatory subunit 10	-13	-15
MGI_smith0	TRINITY_DN22396_c0_g1_i6	.	-9	-16
MGI_smith0	TRINITY_DN2242_c0_g1_i8	One cut domain family member 2	-19	-16
MGI_smith0	TRINITY_DN2267_c0_g1_i11	Nuclear envelope phosphatase-regulatory subunit 1	-24	-17
MGI_smith0	TRINITY_DN23075_c0_g1_i2	Zinc finger protein 236	-23	-19
MGI_smith0	TRINITY_DN2326_c0_g1_i6	.	-25	-15
MGI_smith0	TRINITY_DN2380_c0_g1_i3	FMRFamide peptide receptor frpr-18	-24	-17
MGI_smith0	TRINITY_DN24235_c0_g1_i1	.	-11	-15
MGI_smith0	TRINITY_DN2563_c0_g1_i10	Mitogen-activated protein kinase kinase kinase 15	-17	-16
MGI_smith0	TRINITY_DN2565_c0_g1_i10	Protein kinase C delta type	-19	-16
MGI_smith0	TRINITY_DN26185_c0_g1_i1	Atlastin-1	-17	-17
MGI_smith0	TRINITY_DN26311_c0_g1_i10	Zinc finger C2HC domain-containing protein 1A	-17	-16
MGI_smith0	TRINITY_DN264_c0_g1_i1	Heat shock 70 kDa protein 12B	-22	-16
MGI_smith0	TRINITY_DN27395_c0_g1_i1	Tripartite motif-containing protein 2	-17	-15
MGI_smith0	TRINITY_DN27609_c0_g1_i4	Putative nuclease HARBI1	-16	-15
MGI_smith0	TRINITY_DN2785_c1_g2_i1	Renin receptor	-21	-16
MGI_smith0	TRINITY_DN27864_c1_g1_i2	.	-17	-15
MGI_smith0	TRINITY_DN28064_c0_g1_i6	Putative enzymatic polyprotein	-15	-15
MGI_smith0	TRINITY_DN2845_c0_g1_i5	Patatin-like phospholipase domain-containing protein 2	-16	-16
MGI_smith0	TRINITY_DN2856_c0_g1_i9	G-protein coupled receptor 157	-14	-15
MGI_smith0	TRINITY_DN2880_c0_g1_i5	SEC14-like protein 5	-12	-15
MGI_smith0	TRINITY_DN2918_c0_g1_i10	Calcineurin B homologous protein 1	-17	-15
MGI_smith0	TRINITY_DN29377_c0_g1_i2	.	-15	-16
MGI_smith0	TRINITY_DN2955_c0_g1_i1	.	-16	-16
MGI_smith0	TRINITY_DN2968_c0_g1_i5	Allatostatin-A receptor	-20	-15
MGI_smith0	TRINITY_DN2975_c0_g1_i2	Myeloid-derived growth factor	-17	-15
MGI_smith0	TRINITY_DN2984_c0_g1_i10	C-Jun-amino-terminal kinase-interacting protein 4	-17	-16
MGI_smith0	TRINITY_DN29895_c0_g1_i1	Protein Wnt-1	-22	-15
MGI_smith0	TRINITY_DN29_c0_g1_i1	Collagen alpha-2(IV) chain	-31	-19
MGI_smith0	TRINITY_DN3053_c0_g3_i1	Glutamine-rich protein 2	-21	-16
MGI_smith0	TRINITY_DN3262_c0_g1_i1	TNF receptor-associated factor 6	-14	-15
MGI_smith0	TRINITY_DN326_c0_g1_i11	Nucleolysin TIAR	-20	-17
MGI_smith0	TRINITY_DN3334_c0_g1_i3	Mucolipin-3	-20	-17
MGI_smith0	TRINITY_DN33435_c0_g1_i5	.	-21	-16
MGI_smith0	TRINITY_DN35872_c0_g1_i1	.	-16	-16
MGI_smith0	TRINITY_DN3617_c0_g1_i4	TBC1 domain family member 1	-21	-16
MGI_smith0	TRINITY_DN3619_c0_g3_i2	Interferon-induced protein 44-like	-14	-16
MGI_smith0	TRINITY_DN3630_c3_g2_i1	.	-13	-20
MGI_smith0	TRINITY_DN36575_c0_g3_i1	.	-19	-15
MGI_smith0	TRINITY_DN3661_c0_g1_i6	.	-18	-15
MGI_smith0	TRINITY_DN3704_c0_g1_i10	Rabankyrin-5	-12	-16
MGI_smith0	TRINITY_DN37356_c0_g1_i1	.	-23	-15
MGI_smith0	TRINITY_DN37519_c0_g1_i2	.	-23	-17
MGI_smith0	TRINITY_DN38634_c0_g1_i2	.	-18	-15
MGI_smith0	TRINITY_DN40498_c0_g2_i1	Transcription initiation factor IIA subunit 2	-21	-16
MGI_smith0	TRINITY_DN40985_c0_g1_i1	Tripartite motif-containing protein 3	-9	-15
MGI_smith0	TRINITY_DN4149_c0_g1_i1	CD2-associated protein	-13	-15
MGI_smith0	TRINITY_DN42525_c1_g1_i12	.	-20	-16
MGI_smith0	TRINITY_DN43089_c0_g2_i2	Malignant fibrous histiocytoma-amplified sequence 1 homolog	-16	-18
MGI_smith0	TRINITY_DN43296_c0_g1_i12	Polycystin-1-like protein 3	-20	-18
MGI_smith0	TRINITY_DN4361_c0_g1_i3	.	-24	-22
MGI_smith0	TRINITY_DN44003_c0_g1_i1	Bromodomain adjacent to zinc finger domain protein 1A	-21	-15
MGI_smith0	TRINITY_DN44140_c0_g3_i1	.	-21	-16
MGI_smith0	TRINITY_DN44768_c0_g1_i2	.	-22	-18
MGI_smith0	TRINITY_DN4496_c0_g1_i2	UBX domain-containing protein 4	-20	-15
MGI_smith0	TRINITY_DN4536_c0_g1_i1	Adenylosuccinate synthetase isozyme 1 A	-21	-17
MGI_smith0	TRINITY_DN4583_c0_g1_i10	Transcription initiation factor IIA subunit 1	-19	-22
MGI_smith0	TRINITY_DN4584_c0_g1_i5	.	-22	-15
MGI_smith0	TRINITY_DN4612_c0_g1_i4	RILP-like protein 1	-21	-15
MGI_smith0	TRINITY_DN4662_c0_g1_i1	Sodium/hydrogen exchanger 1	-22	-19
MGI_smith0	TRINITY_DN4690_c0_g1_i2	MORN repeat-containing protein 4	-18	-16
MGI_smith0	TRINITY_DN4707_c0_g1_i1	Serine/threonine-protein kinase PLK2	-12	-15
MGI_smith0	TRINITY_DN47127_c0_g2_i1	Bardet-Biedl syndrome 2 protein homolog	-16	-16
MGI_smith0	TRINITY_DN47675_c0_g1_i1	.	-25	-18
MGI_smith0	TRINITY_DN4776_c1_g1_i1	Cyclin-dependent kinase 5	-15	-15
MGI_smith0	TRINITY_DN4849_c2_g1_i1	4-hydroxy-2-oxoglutarate aldolase, mitochondrial	-16	-16
MGI_smith0	TRINITY_DN4985_c0_g2_i1	Sorting nexin-16	-14	-15
MGI_smith0	TRINITY_DN4999_c0_g1_i10	Pre-mRNA-splicing regulator WTAP	-17	-16
MGI_smith0	TRINITY_DN500_c0_g1_i1	EGF-like domain-containing protein 2	-24	-20
MGI_smith0	TRINITY_DN504_c0_g4_i2	BCL2/adenovirus E1B 19 kDa protein-interacting protein 3	-17	-15
MGI_smith0	TRINITY_DN51335_c0_g1_i7	.	-18	-16
MGI_smith0	TRINITY_DN5362_c0_g1_i10	Gametogenetin-binding protein 2	-16	-15
MGI_smith0	TRINITY_DN548_c0_g1_i10	Dual specificity protein kinase CLK2	-25	-16
MGI_smith0	TRINITY_DN549_c0_g1_i12	Protein scribble homolog	-17	-16
MGI_smith0	TRINITY_DN55424_c0_g1_i1	Sodium/potassium/calcium exchanger 2	-28	-19
MGI_smith0	TRINITY_DN557_c0_g1_i3	QRFP-like peptide receptor	-17	-16
MGI_smith0	TRINITY_DN56588_c0_g1_i3	.	-19	-16
MGI_smith0	TRINITY_DN5799_c0_g1_i11	Glutamate carboxypeptidase 2	-24	-15
MGI_smith0	TRINITY_DN5835_c0_g1_i3	.	-18	-16
MGI_smith0	TRINITY_DN5891_c0_g1_i10	Coiled-coil domain-containing protein CG32809	-16	-17
MGI_smith0	TRINITY_DN598_c1_g2_i1	PX domain-containing protein kinase-like protein	-17	-17
MGI_smith0	TRINITY_DN604_c0_g1_i17	Rap guanine nucleotide exchange factor 2	-18	-16

MGI_smith0	TRINITY_DN61519_c0_g1_i2	.	-21	-16
MGI_smith0	TRINITY_DN6153_c0_g1_i6	Putative ferric-chelate reductase 1 homolog	-18	-15
MGI_smith0	TRINITY_DN6208_c0_g1_i8	.	-14	-15
MGI_smith0	TRINITY_DN6215_c0_g2_i1	.	-22	-20
MGI_smith0	TRINITY_DN6217_c0_g1_i12	Smoothelin-like protein 1	-27	-16
MGI_smith0	TRINITY_DN6254_c0_g1_i12	Glutamate receptor ionotropic, kainate 3	-10	-17
MGI_smith0	TRINITY_DN6272_c0_g2_i11	.	-15	-18
MGI_smith0	TRINITY_DN6314_c0_g2_i1	Myosin light chain kinase, smooth muscle	-18	-16
MGI_smith0	TRINITY_DN6316_c0_g1_i6	Ras-related protein R-Ras2	-15	-15
MGI_smith0	TRINITY_DN63978_c0_g1_i1	GPI ethanolamine phosphate transferase 1	-23	-16
MGI_smith0	TRINITY_DN64417_c0_g1_i1	.	-14	-16
MGI_smith0	TRINITY_DN6441_c0_g1_i4	Sodium- and chloride-dependent glycine transporter 1	-15	-16
MGI_smith0	TRINITY_DN6582_c0_g1_i1	cAMP-dependent protein kinase catalytic subunit 3	-20	-16
MGI_smith0	TRINITY_DN6603_c0_g1_i1	Endonuclease/exonuclease/phosphatase family domain-containing protein 1	-15	-17
MGI_smith0	TRINITY_DN6656_c0_g1_i4	Band 4.1-like protein 4A	-22	-15
MGI_smith0	TRINITY_DN6677_c0_g1_i10	Putative ATP-dependent RNA helicase TDRD12	-14	-15
MGI_smith0	TRINITY_DN667_c0_g1_i5	Prolow-density lipoprotein receptor-related protein 1	-17	-16
MGI_smith0	TRINITY_DN6698_c0_g1_i1	Polyamine-transporting ATPase 13A3	-20	-17
MGI_smith0	TRINITY_DN67002_c1_g1_i2	.	-14	-15
MGI_smith0	TRINITY_DN6762_c0_g1_i1	.	-23	-15
MGI_smith0	TRINITY_DN68338_c0_g1_i2	.	-18	-16
MGI_smith0	TRINITY_DN6835_c0_g1_i4	U11/U12 small nuclear ribonucleoprotein 25 kDa protein	-17	-16
MGI_smith0	TRINITY_DN685_c0_g1_i11	Tyrosine-protein phosphatase non-receptor type 4	-22	-16
MGI_smith0	TRINITY_DN6999_c0_g1_i11	Kinesin heavy chain	-19	-16
MGI_smith0	TRINITY_DN7005_c0_g1_i2	MYCBP-associated protein	-22	-17
MGI_smith0	TRINITY_DN7071_c0_g1_i1	.	-15	-17
MGI_smith0	TRINITY_DN709_c1_g1_i26	Phospholipid-transporting ATPase ID	-15	-18
MGI_smith0	TRINITY_DN7210_c0_g1_i4	Short transient receptor potential channel 7	-22	-15
MGI_smith0	TRINITY_DN7296_c0_g1_i10	Nuclear RNA export factor 1	-24	-15
MGI_smith0	TRINITY_DN73495_c0_g1_i1	Integrator complex subunit 10	-22	-17
MGI_smith0	TRINITY_DN7391_c0_g1_i1	Peroxiredoxin-like 2A	-18	-16
MGI_smith0	TRINITY_DN73_c0_g1_i1	4-aminobutyrate aminotransferase, mitochondrial	-14	-16
MGI_smith0	TRINITY_DN740_c0_g1_i2	Ryanodine receptor	-20	-15
MGI_smith0	TRINITY_DN743_c0_g1_i1	DnaJ homolog subfamily B member 3	-12	-15
MGI_smith0	TRINITY_DN7440_c0_g1_i4	.	-16	-15
MGI_smith0	TRINITY_DN746_c0_g1_i2	Sodium/glucose cotransporter 4	-14	-17
MGI_smith0	TRINITY_DN75194_c1_g1_i1	Tripartite motif-containing protein 3	-16	-15
MGI_smith0	TRINITY_DN7591_c0_g1_i12	.	-20	-15
MGI_smith0	TRINITY_DN77490_c0_g1_i1	Dynein heavy chain	-23	-18
MGI_smith0	TRINITY_DN7792_c0_g2_i5	Ankyrin repeat and MYND domain-containing protein 2	-13	-17
MGI_smith0	TRINITY_DN7795_c0_g1_i2	Allantoicase	-16	-15
MGI_smith0	TRINITY_DN7861_c0_g1_i6	.	-25	-16
MGI_smith0	TRINITY_DN786_c0_g3_i1	Adhesion G protein-coupled receptor A3	-22	-15
MGI_smith0	TRINITY_DN788_c0_g1_i5	Sodium- and chloride-dependent glycine transporter 1	-18	-15
MGI_smith0	TRINITY_DN7976_c0_g1_i4	Protein naked cuticle homolog 1	-23	-15
MGI_smith0	TRINITY_DN8021_c0_g2_i1	Ankyrin repeat domain-containing protein 29	-16	-15
MGI_smith0	TRINITY_DN8324_c1_g1_i1	Elongator complex protein 3	-19	-16
MGI_smith0	TRINITY_DN8328_c0_g1_i4	.	-20	-17
MGI_smith0	TRINITY_DN8349_c2_g1_i3	.	-12	-16
MGI_smith0	TRINITY_DN8354_c0_g1_i3	.	-18	-15
MGI_smith0	TRINITY_DN83_c0_g1_i17	Protein muscleblind	-18	-16
MGI_smith0	TRINITY_DN8452_c0_g1_i3	Adhesion G-protein coupled receptor G6	-24	-18
MGI_smith0	TRINITY_DN8526_c0_g1_i3	Centrosomal protein of 128 kDa	-17	-15
MGI_smith0	TRINITY_DN8541_c0_g2_i10	.	-11	-16
MGI_smith0	TRINITY_DN8709_c0_g1_i2	DEP domain-containing protein 7	-17	-15
MGI_smith0	TRINITY_DN875_c0_g1_i2	SH3 and multiple ankyrin repeat domains protein 2	-22	-19
MGI_smith0	TRINITY_DN8910_c0_g1_i1	Pyroglutamyl-peptidase 1	-24	-16
MGI_smith0	TRINITY_DN897_c0_g1_i1	Voltage-gated hydrogen channel 1	-23	-15
MGI_smith0	TRINITY_DN901_c0_g1_i11	Pyruvate carboxylase, mitochondrial	-17	-16
MGI_smith0	TRINITY_DN91501_c0_g1_i1	.	-13	-16
MGI_smith0	TRINITY_DN9433_c0_g1_i1	.	-16	-18
MGI_smith0	TRINITY_DN943_c0_g1_i3	Alpha-1,3-mannosyl-glycoprotein 4-beta-N-acetylglucosaminyltransferase C	-15	-15
MGI_smith0	TRINITY_DN9627_c0_g1_i2	.	-24	-17
MGI_smith0	TRINITY_DN9635_c0_g1_i1	26S proteasome regulatory subunit 6B	-14	-15
MGI_smith0	TRINITY_DN9638_c0_g1_i6	Ubiquitin carboxyl-terminal hydrolase 15	-14	-15
MGI_smith0	TRINITY_DN96624_c0_g1_i2	.	-16	-15
MGI_smith0	TRINITY_DN975_c0_g1_i10	Lysine-specific demethylase 6A	-19	-15
MGI_smith2	TRINITY_DN100388_c0_g1_i1	.	-15	-21
MGI_smith2	TRINITY_DN10381_c0_g1_i12	Glycerol kinase 3	-23	-21
MGI_smith2	TRINITY_DN11403_c0_g1_i5	.	-25	-28
MGI_smith2	TRINITY_DN11886_c0_g1_i4	.	-19	-22
MGI_smith2	TRINITY_DN1219_c0_g2_i10	Roquin-1	-16	-20
MGI_smith2	TRINITY_DN1251_c0_g1_i2	Nuclear receptor coactivator 4	-21	-24
MGI_smith2	TRINITY_DN13142_c0_g1_i7	Asparagine-rich protein	-16	-15
MGI_smith2	TRINITY_DN15085_c0_g1_i2	Probable RNA-directed DNA polymerase from transposon BS	-20	-17
MGI_smith2	TRINITY_DN16294_c0_g1_i10	ELAV-like protein 2	-17	-21
MGI_smith2	TRINITY_DN16937_c0_g1_i6	.	-18	-20
MGI_smith2	TRINITY_DN17058_c0_g1_i2	.	-13	-15
MGI_smith2	TRINITY_DN17311_c0_g1_i5	.	-19	-20
MGI_smith2	TRINITY_DN17377_c0_g1_i7	Probable serine/threonine-protein kinase pats1	-21	-26
MGI_smith2	TRINITY_DN174835_c0_g1_i1	Uncharacterized protein in xynA 3'region	-19	-22
MGI_smith2	TRINITY_DN19084_c0_g2_i1	.	-19	-21
MGI_smith2	TRINITY_DN19215_c0_g1_i1	.	-21	-23
MGI_smith2	TRINITY_DN21372_c0_g1_i1	Sex peptide receptor	-19	-21
MGI_smith2	TRINITY_DN2294_c0_g1_i1	.	-17	-22
MGI_smith2	TRINITY_DN2295_c0_g1_i7	Influenza virus NS1A-binding protein homolog	-15	-20
MGI_smith2	TRINITY_DN2389_c0_g1_i3	Dual specificity mitogen-activated protein kinase kinase 1	-20	-24
MGI_smith2	TRINITY_DN24567_c0_g2_i1	.	-21	-21
MGI_smith2	TRINITY_DN25471_c0_g3_i1	PDZ and LIM domain protein Zasp	-18	-20
MGI_smith2	TRINITY_DN28350_c0_g2_i2	.	-16	-20
MGI_smith2	TRINITY_DN2872_c0_g1_i1	Fasciculation and elongation protein zeta-2	-20	-23
MGI_smith2	TRINITY_DN28735_c0_g1_i10	.	-20	-24
MGI_smith2	TRINITY_DN31168_c0_g1_i3	.	-18	-20
MGI_smith2	TRINITY_DN3476_c0_g1_i1	Cadherin EGF LAG seven-pass G-type receptor 1	-25	-21
MGI_smith2	TRINITY_DN35441_c0_g2_i1	Ankyrin repeat domain-containing protein 23	-17	-22

MGI_smith2	TRINITY_DN36660_c0_g1_i4	.	-20	-16
MGI_smith2	TRINITY_DN36850_c0_g1_i2	.	-22	-16
MGI_smith2	TRINITY_DN390_c0_g1_i11	Glycoprotein 3-alpha-L-fucosyltransferase A	-18	-20
MGI_smith2	TRINITY_DN42735_c0_g1_i4	ADP-ribosyl cyclase/cyclic ADP-ribose hydrolase 2	-17	-21
MGI_smith2	TRINITY_DN5036_c0_g1_i12	Centrosome-associated protein 350	-15	-20
MGI_smith2	TRINITY_DN51534_c0_g1_i6	.	-18	-20
MGI_smith2	TRINITY_DN52563_c0_g1_i1	Torsin-1A-interacting protein 1	-18	-20
MGI_smith2	TRINITY_DN5434_c0_g1_i12	.	-16	-21
MGI_smith2	TRINITY_DN56009_c2_g1_i1	.	-17	-21
MGI_smith2	TRINITY_DN5778_c2_g1_i1	.	-20	-16
MGI_smith2	TRINITY_DN5796_c0_g1_i1	Short-chain dehydrogenase/reductase family 42E member 1	-16	-21
MGI_smith2	TRINITY_DN60325_c0_g1_i2	.	-16	-20
MGI_smith2	TRINITY_DN6217_c0_g1_i12	Smoothelin-like protein 1	-21	-18
MGI_smith2	TRINITY_DN6447_c0_g2_i1	Ataxin-7-like protein 1	-17	-21
MGI_smith2	TRINITY_DN6570_c0_g1_i11	.	-18	-20
MGI_smith2	TRINITY_DN676_c0_g1_i1	.	-18	-23
MGI_smith2	TRINITY_DN6980_c1_g2_i1	Calexcitin-1	-17	-16
MGI_smith2	TRINITY_DN7107_c0_g1_i1	.	-20	-21
MGI_smith2	TRINITY_DN7143_c0_g1_i2	Kinesin-like protein KIF28P	-23	-23
MGI_smith2	TRINITY_DN718_c0_g2_i3	Coadhesin	-18	-20
MGI_smith2	TRINITY_DN843_c0_g1_i3	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-1	-21	-21
MGI_smith2	TRINITY_DN8662_c0_g1_i15	Protein draper	-17	-20
MGI_smith2	TRINITY_DN929_c0_g1_i3	.	-18	-21
MGI_smith2	TRINITY_DN975_c0_g1_i10	Lysine-specific demethylase 6A	-15	-20
MGI_smith5	TRINITY_DN13474_c0_g1_i1	Retrovirus-related Pol polyprotein from transposon 17.6	-22	-17
MGI_smith5	TRINITY_DN13564_c0_g1_i10	.	-21	-21
MGI_smith5	TRINITY_DN3279_c0_g1_i10	.	-16	-18
MGI_smith5	TRINITY_DN3410_c1_g1_i10	E3 ubiquitin-protein ligase rnf213-alpha	-19	-18
MGI_smith5	TRINITY_DN343_c0_g1_i12	Neurofibromin	-22	-18
MGI_smith5	TRINITY_DN3950_c0_g1_i3	Nuclear receptor-binding protein	-23	-18
MGI_smith5	TRINITY_DN41831_c0_g1_i3	cGMP-dependent protein kinase	-23	-22
MGI_smith5	TRINITY_DN4289_c0_g1_i2	.	-15	-16
MGI_smith5	TRINITY_DN71564_c0_g2_i3	.	-23	-22
MGI_smith8	TRINITY_DN10148_c0_g1_i4	.	-17	-20
MGI_smith8	TRINITY_DN10835_c0_g1_i2	ATP-dependent RNA helicase DHX33	-26	-26
MGI_smith8	TRINITY_DN11192_c0_g1_i11	.	-26	-22
MGI_smith8	TRINITY_DN13752_c0_g1_i7	Malignant fibrous histiocytoma-amplified sequence 1 homolog	-27	-28
MGI_smith8	TRINITY_DN14255_c0_g1_i2	Mediator of RNA polymerase II transcription subunit 18	-20	-19
MGI_smith8	TRINITY_DN14821_c0_g1_i4	FMRFamide-activated amiloride-sensitive sodium channel	-24	-29
MGI_smith8	TRINITY_DN16266_c0_g1_i9	THAP domain-containing protein 2	-24	-20
MGI_smith8	TRINITY_DN1654_c0_g1_i2	Netrin receptor UNC5C	-22	-21
MGI_smith8	TRINITY_DN17011_c0_g1_i8	Putative phosphatidate phosphatase	-26	-25
MGI_smith8	TRINITY_DN22099_c0_g1_i1	Probable U3 small nucleolar RNA-associated protein 11	-25	-28
MGI_smith8	TRINITY_DN2515_c0_g1_i15	DENN domain-containing protein 1B	-28	-26
MGI_smith8	TRINITY_DN25736_c0_g1_i1	.	-31	-28
MGI_smith8	TRINITY_DN2635_c0_g1_i1	Pumilio homolog 2	-20	-28
MGI_smith8	TRINITY_DN2773_c0_g1_i3	Inositol polyphosphate-4-phosphatase type I A	-33	-31
MGI_smith8	TRINITY_DN31547_c1_g1_i1	Vertnin	-19	-16
MGI_smith8	TRINITY_DN31665_c0_g1_i10	Formin-like protein 3	-27	-31
MGI_smith8	TRINITY_DN33836_c0_g1_i1	Putative uncharacterized transposon-derived protein F54H12.3	-26	-18
MGI_smith8	TRINITY_DN3857_c0_g1_i5	RNA polymerase II-associated protein 1	-36	-18
MGI_smith8	TRINITY_DN387_c0_g1_i7	Ras-specific guanine nucleotide-releasing factor RalGPS1	-26	-16
MGI_smith8	TRINITY_DN3922_c0_g1_i13	.	-12	-21
MGI_smith8	TRINITY_DN39517_c0_g1_i11	Mitochondrial Rho GTPase 1	-26	-26
MGI_smith8	TRINITY_DN4549_c0_g1_i3	Dehydrogenase/reductase SDR family member 1	-28	-29
MGI_smith8	TRINITY_DN4552_c0_g1_i1	Syntenin-1	-23	-22
MGI_smith8	TRINITY_DN5054_c0_g1_i4	Phosphatidylinositol 3,4,5-trisphosphate 3-phosphatase and dual-specificity protein phosphatase PTEN	-18	-22
MGI_smith8	TRINITY_DN5418_c0_g2_i1	Mannose-6-phosphate isomerase	-23	-15
MGI_smith8	TRINITY_DN5505_c0_g2_i2	Dual 3',5'-cyclic-AMP and -GMP phosphodiesterase 11A	-15	-19
MGI_smith8	TRINITY_DN558_c0_g1_i1	Cytoplasmic FMR1-interacting protein	-19	-16
MGI_smith8	TRINITY_DN5666_c0_g1_i8	Protein Mdm4	-13	-26
MGI_smith8	TRINITY_DN6290_c0_g1_i1	.	-23	-26
MGI_smith8	TRINITY_DN7142_c0_g1_i1	PDZ and LIM domain protein 3	-21	-23
MGI_smith8	TRINITY_DN769_c0_g1_i10	Casein kinase I isoform gamma-3	-33	-29
MGI_smith8	TRINITY_DN7784_c0_g1_i1	Serine/threonine-protein kinase H1 homolog	-23	-22
MGI_smith8	TRINITY_DN7843_c0_g2_i1	Breast cancer anti-estrogen resistance protein 1	-17	-15
MGI_smith8	TRINITY_DN79432_c0_g1_i3	Beta-1,3-galactosyl-O-glycosyl-glycoprotein beta-1,6-N-acetylglucosaminyltransferase	-32	-27
MGI_smith8	TRINITY_DN8218_c0_g1_i1	DnaJ homolog subfamily C member 22	-25	-27
MGI_smith8	TRINITY_DN883_c0_g1_i13	DNA-directed RNA polymerase II subunit RPB1	-29	-31
MGI_smith8	TRINITY_DN94268_c0_g1_i6	Vesicle transport through interaction with t-SNAREs homolog 1A	-26	-15
MGI_smith8	TRINITY_DN9661_c0_g1_i10	ATP-dependent DNA helicase RecQ	-31	-26
MGI_smith8	TRINITY_DN9817_c0_g1_i1	Hypoxia-inducible factor 1-alpha	-17	-17
		***Danio rerio* (3 candidates, 31 targets)**		
smithID	**transcriptID**	**Blastx**	**dG PITA**	**dG RNAHybrid**
DRE_smith1	TRINITY_DN24146_c0_g1_i1	Adenosine receptor A2a	-32	-26
DRE_smith1	TRINITY_DN2661_c0_g1_i1	Translational activator of cytochrome c oxidase 1	-20	-21
DRE_smith1	TRINITY_DN3695_c1_g1_i1	Golgin subfamily A member 7	-19	-21
DRE_smith1	TRINITY_DN5491_c0_g1_i10	Guanine nucleotide-binding protein G(olf) subunit alpha	-20	-21
DRE_smith5	TRINITY_DN10915_c1_g3_i1	Zinc finger transcription factor Trps1	-19	-18
DRE_smith5	TRINITY_DN1264_c0_g2_i1	Anaphase-promoting complex subunit 1	-13	-21
DRE_smith5	TRINITY_DN1416_c0_g1_i3	N-sulphoglucosamine sulphohydrolase	-14	-17
DRE_smith5	TRINITY_DN30703_c0_g1_i2	Phosphatidylinositol 4-phosphate 5-kinase type-1 alpha	-15	-15
DRE_smith5	TRINITY_DN3904_c0_g1_i1	Paralemmin-1	-15	-18
DRE_smith5	TRINITY_DN5958_c0_g1_i10	NEDD4-like E3 ubiquitin-protein ligase WWP2	-17	-19
DRE_smith5	TRINITY_DN6208_c0_g1_i2	Homeobox protein cut-like 1	-14	-21
DRE_smith6	TRINITY_DN12073_c0_g1_i1	Menin	-24	-27
DRE_smith6	TRINITY_DN12298_c0_g4_i3	Regulator of G-protein signaling 12	-18	-20
DRE_smith6	TRINITY_DN12804_c2_g1_i1	.	-18	-24
DRE_smith6	TRINITY_DN13345_c1_g5_i1	Mucin-12	-23	-25
DRE_smith6	TRINITY_DN1728_c3_g1_i4	Cyclin-J	-18	-20
DRE_smith6	TRINITY_DN2390_c0_g3_i1	Mitogen-activated protein kinase 1	-31	-25
DRE_smith6	TRINITY_DN2538_c0_g2_i1	Ribosomal protein S6 kinase beta-1	-25	-18

DRE_smith6	TRINITY_DN2649_c0_g1_i1	L-lactate dehydrogenase A chain	-30	-27
DRE_smith6	TRINITY_DN2790_c0_g1_i6	E3 ubiquitin-protein ligase TTC3	-25	-28
DRE_smith6	TRINITY_DN30118_c0_g1_i9	ATP synthase mitochondrial F1 complex assembly factor 1	-34	-25
DRE_smith6	TRINITY_DN3143_c0_g4_i1	Glycogen phosphorylase, brain form	-15	-18
DRE_smith6	TRINITY_DN3551_c0_g1_i2	RUN domain-containing protein 3A	-21	-24
DRE_smith6	TRINITY_DN3742_c0_g1_i1	Keratinocyte-associated protein 2	-21	-25
DRE_smith6	TRINITY_DN4820_c0_g1_i3	85/88 kDa calcium-independent phospholipase A2	-22	-27
DRE_smith6	TRINITY_DN5128_c1_g1_i2	E3 ubiquitin-protein ligase znrf2	-26	-26
DRE_smith6	TRINITY_DN5189_c0_g2_i2	Protein ILRUN	-22	-15
DRE_smith6	TRINITY_DN5769_c1_g1_i7	.	-22	-18
DRE_smith6	TRINITY_DN7722_c1_g1_i1	Desmin	-25	-27
DRE_smith6	TRINITY_DN8603_c0_g1_i1	Very long chain fatty acid elongase 4	-27	-25
DRE_smith6	TRINITY_DN924_c0_g1_i4	Calpain-15	-21	-24

***Drosophila melanogaster* (5 candidates, 87 targets)**

smithID	transcriptID	Blastx	dG PITA	dG RNAHybrid
DME_smith0	TRINITY_DN1392_c0_g1_i1	.	-15	-18
DME_smith0	TRINITY_DN1507_c0_g2_i1	tRNA (cytosine(72)-C(5))-methyltransferase NSUN6	-16	-17
DME_smith0	TRINITY_DN1891_c0_g1_i2	Putative serine protease F56F10.1	-17	-16
DME_smith0	TRINITY_DN2194_c0_g1_i1	Transcription factor Dp	-17	-16
DME_smith0	TRINITY_DN22487_c0_g1_i1	Cell death protein hid	-14	-16
DME_smith0	TRINITY_DN2433_c0_g1_i2	TBC1 domain family member whacked	-13	-18
DME_smith0	TRINITY_DN2528_c0_g7_i1	.	-11	-17
DME_smith0	TRINITY_DN262_c0_g1_i21	Retrovirus-related Env polyprotein from transposon 297	-11	-15
DME_smith0	TRINITY_DN3014_c0_g1_i10	.	-21	-18
DME_smith0	TRINITY_DN4512_c1_g1_i1	.	-15	-17
DME_smith0	TRINITY_DN4781_c0_g2_i1	.	-16	-21
DME_smith0	TRINITY_DN4936_c0_g1_i1	Nucleic-acid-binding protein from transposon X-element	-16	-17
DME_smith0	TRINITY_DN5749_c0_g1_i1	UDP-glycosyltransferase UGT5	-25	-23
DME_smith0	TRINITY_DN591_c0_g1_i10	Putative protein disulfide-isomerase C1F5.02	-13	-19
DME_smith0	TRINITY_DN6803_c0_g1_i1	.	-17	-18
DME_smith11	TRINITY_DN10006_c0_g1_i1	Dynein axonemal heavy chain 2	-33	-42
DME_smith11	TRINITY_DN10722_c0_g6_i1	Protein dpy-30 homolog	-33	-42
DME_smith11	TRINITY_DN11026_c0_g2_i4	C-mannosyltransferase dpy-19 homolog	-33	-42
DME_smith11	TRINITY_DN1205_c0_g2_i1	Protein clueless	-9	-25
DME_smith11	TRINITY_DN1398_c0_g1_i1	Epidermal growth factor receptor kinase substrate 8	-33	-42
DME_smith11	TRINITY_DN1530_c0_g1_i2	Leucine-rich repeat-containing protein 70	-33	-42
DME_smith11	TRINITY_DN1714_c0_g1_i6	.	-33	-42
DME_smith11	TRINITY_DN1804_c0_g2_i2	Raf homolog serine/threonine-protein kinase Raf	-33	-42
DME_smith11	TRINITY_DN1865_c0_g2_i18	Kinesin-like protein KIF13B	-33	-42
DME_smith11	TRINITY_DN1893_c0_g1_i3	Glutathione S-transferase D1	-33	-42
DME_smith11	TRINITY_DN2014_c0_g1_i1	Choline-phosphate cytidylyltransferase B	-33	-42
DME_smith11	TRINITY_DN201_c0_g1_i4	Macoilin-1	-17	-21
DME_smith11	TRINITY_DN212_c0_g1_i10	Probable multidrug resistance-associated protein lethal(2)03659	-20	-25
DME_smith11	TRINITY_DN2202_c0_g2_i3	Apolipoprotein D	-33	-42
DME_smith11	TRINITY_DN2303_c0_g2_i2	Superkiller complex protein 2	-33	-42
DME_smith11	TRINITY_DN2305_c1_g1_i4	.	-33	-42
DME_smith11	TRINITY_DN2307_c0_g1_i1	Transforming growth factor beta-1-induced transcript 1 protein	-33	-42
DME_smith11	TRINITY_DN2308_c1_g2_i8	Syndecan	-33	-42
DME_smith11	TRINITY_DN2407_c0_g1_i5	Decapping nuclease DXO homolog	-15	-15
DME_smith11	TRINITY_DN2502_c0_g1_i5	.	-33	-42
DME_smith11	TRINITY_DN2743_c0_g3_i2	Galactosylgalactosylxylosylprotein 3-beta-glucuronosyltransferase I	-33	-42
DME_smith11	TRINITY_DN2774_c0_g1_i5	.	-33	-42
DME_smith11	TRINITY_DN29628_c0_g1_i1	Sex-regulated protein janus-B	-32	-41
DME_smith11	TRINITY_DN3022_c0_g5_i1	.	-33	-42
DME_smith11	TRINITY_DN3058_c0_g1_i1	PAX-interacting protein 1	-33	-42
DME_smith11	TRINITY_DN3306_c0_g1_i1	Nucleolar GTP-binding protein 1	-33	-42
DME_smith11	TRINITY_DN3308_c0_g1_i2	.	-12	-22
DME_smith11	TRINITY_DN3360_c0_g1_i1	Protein EFR3 homolog cmp44E	-27	-36
DME_smith11	TRINITY_DN372_c0_g1_i3	.	-15	-22
DME_smith11	TRINITY_DN40329_c0_g1_i1	Metallothionein-2	-33	-42
DME_smith11	TRINITY_DN4057_c0_g1_i1	TBC1 domain family member 13	-33	-41
DME_smith11	TRINITY_DN4586_c0_g2_i1	.	-31	-40
DME_smith11	TRINITY_DN4631_c0_g1_i1	Zinc finger protein weckle	-33	-42
DME_smith11	TRINITY_DN4640_c0_g1_i2	Leucine--tRNA ligase, cytoplasmic	-33	-42
DME_smith11	TRINITY_DN482_c0_g2_i1	Serine protease inhibitor 42Dd	-33	-42
DME_smith11	TRINITY_DN54_c0_g2_i8	Calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type	-33	-42
DME_smith11	TRINITY_DN5555_c0_g2_i5	Aminopeptidase Ey	-33	-42
DME_smith11	TRINITY_DN595_c0_g1_i2	Acetylcholine receptor subunit beta	-31	-40
DME_smith11	TRINITY_DN6125_c0_g1_i5	Myeloid leukemia factor	-33	-42
DME_smith11	TRINITY_DN6391_c0_g3_i1	.	-33	-42
DME_smith11	TRINITY_DN6549_c0_g4_i5	Zinc finger CCCH domain-containing protein 18	-33	-42
DME_smith11	TRINITY_DN657_c0_g1_i5	Phosphofurin acidic cluster sorting protein 1	-33	-42
DME_smith11	TRINITY_DN6676_c1_g1_i3	.	-33	-42
DME_smith11	TRINITY_DN6903_c1_g1_i1	U6 snRNA phosphodiesterase 1	-18	-23
DME_smith11	TRINITY_DN7261_c0_g4_i2	Ubiquilin-1	-33	-42
DME_smith11	TRINITY_DN7967_c0_g1_i3	Protein Malvolio	-10	-17
DME_smith11	TRINITY_DN829_c0_g2_i2	Cytochrome P450 4e3	-33	-42
DME_smith11	TRINITY_DN8319_c0_g1_i13	Cryptochrome-1	-33	-42
DME_smith11	TRINITY_DN884_c0_g6_i1	ATP synthase subunit beta, mitochondrial	-33	-42
DME_smith11	TRINITY_DN92_c0_g3_i2	Vacuolar protein sorting-associated protein 33A	-33	-42
DME_smith11	TRINITY_DN9376_c0_g5_i1	MPN domain-containing protein CG4751	-33	-41
DME_smith11	TRINITY_DN9477_c0_g2_i3	Zwei Ig domain protein zig-8	-17	-19
DME_smith3	TRINITY_DN1128_c1_g3_i11	Golgi-associated plant pathogenesis-related protein 1	-27	-33
DME_smith3	TRINITY_DN2615_c0_g1_i14	ATP-binding cassette sub-family C member 3	-16	-22
DME_smith3	TRINITY_DN484_c0_g1_i10	Centrosome-associated zinc finger protein Cp190	-17	-21
DME_smith3	TRINITY_DN518_c0_g1_i10	Mitochondrial pyruvate carrier 1	-11	-15
DME_smith3	TRINITY_DN6560_c0_g4_i2	.	-22	-27
DME_smith4	TRINITY_DN10431_c0_g1_i4	Protein tolkin	-11	-15
DME_smith4	TRINITY_DN1488_c0_g2_i1	NAD(P)H-hydrate epimerase	-36	-42
DME_smith4	TRINITY_DN216_c1_g1_i1	Importin subunit alpha-4	-20	-17
DME_smith4	TRINITY_DN227_c0_g1_i11	Serine protease grass	-11	-16
DME_smith4	TRINITY_DN2502_c0_g1_i5	.	-16	-21
DME_smith4	TRINITY_DN390_c0_g2_i1	DnaJ homolog subfamily B member 2	-14	-18
DME_smith4	TRINITY_DN5_c0_g1_i2	.	-11	-15

DME_smith4	TRINITY_DN803_c0_g1_i11	E3 ubiquitin-protein ligase Ubr3	-16	-17
DME_smith4	TRINITY_DN868_c2_g1_i10	Sodium-dependent nutrient amino acid transporter 1	-16	-17
DME_smith4	TRINITY_DN999_c0_g3_i1	Tetraspanin-33	-11	-18
DME_smith6	TRINITY_DN173_c0_g1_i12	Heterogeneous nuclear ribonucleoprotein Q	-17	-22
DME_smith6	TRINITY_DN1846_c2_g3_i6	Histone-lysine N-methyltransferase trithorax	-10	-19
DME_smith6	TRINITY_DN3039_c0_g1_i10	Potassium/sodium hyperpolarization-activated cyclic nucleotide-gated channel 4	-17	-26
DME_smith6	TRINITY_DN3787_c0_g1_i1	Protein SPT2 homolog	-18	-19
DME_smith6	TRINITY_DN5333_c0_g1_i4	Protein singed wings 2	-13	-18

***Dugesia japonica* var. A (4 candidates, 33 targets)**

smithID	transcriptID	Blastx	dG PITA	dG RNAHybrid
DJAA_smith0	TRINITY_DN11044_c0_g1_i4	PAN2-PAN3 deadenylation complex catalytic subunit PAN2	-12	-24
DJAA_smith0	TRINITY_DN11746_c0_g1_i1	F-box only protein 16	-16	-22
DJAA_smith0	TRINITY_DN14683_c0_g1_i1	Zinc finger protein 782	-17	-20
DJAA_smith0	TRINITY_DN2259_c0_g2_i4	Potassium channel subfamily T member 1	-17	-19
DJAA_smith0	TRINITY_DN3482_c0_g1_i10	Adhesion G-protein coupled receptor D1	-15	-20
DJAA_smith0	TRINITY_DN3777_c0_g1_i1	.	-18	-17
DJAA_smith0	TRINITY_DN6079_c0_g1_i4	AP2-associated protein kinase 1	-17	-20
DJAA_smith0	TRINITY_DN6507_c0_g2_i2	AMMECR1-like protein	-20	-15
DJAA_smith0	TRINITY_DN6837_c0_g1_i3	Solute carrier family 13 member 1	-20	-19
DJAA_smith0	TRINITY_DN7310_c0_g1_i1	Condensin complex subunit 1	-20	-22
DJAA_smith0	TRINITY_DN7712_c0_g1_i1	Protein HIRA	-16	-20
DJAA_smith0	TRINITY_DN9527_c0_g1_i1	.	-22	-27
DJAA_smith18	TRINITY_DN141_c0_g1_i3	THO complex subunit 2	-17	-20
DJAA_smith18	TRINITY_DN15845_c1_g1_i3	Large ribosomal subunit protein mL65	-21	-23
DJAA_smith18	TRINITY_DN1769_c0_g1_i12	WD repeat and FYVE domain-containing protein 3	-18	-21
DJAA_smith18	TRINITY_DN18174_c0_g3_i4	Vitellogenin	-13	-21
DJAA_smith18	TRINITY_DN20239_c0_g1_i1	LIM/homeobox protein Awh	-15	-18
DJAA_smith18	TRINITY_DN266_c0_g2_i1	.	-15	-19
DJAA_smith18	TRINITY_DN3072_c0_g1_i5	.	-17	-19
DJAA_smith18	TRINITY_DN3482_c0_g1_i10	Adhesion G-protein coupled receptor D1	-14	-18
DJAA_smith18	TRINITY_DN4687_c0_g1_i2	.	-19	-18
DJAA_smith18	TRINITY_DN5725_c0_g1_i1	Tripeptidyl-peptidase 2	-18	-22
DJAA_smith18	TRINITY_DN7076_c0_g2_i5	Mediator of RNA polymerase II transcription subunit 13-like	-12	-15
DJAA_smith18	TRINITY_DN9303_c0_g1_i1	Zinc phosphodiesterase ELAC protein 1	-15	-19
DJAA_smith18	TRINITY_DN9661_c0_g1_i1	Stabilizer of axonemal microtubules 2	-14	-18
DJAA_smith199	TRINITY_DN11044_c0_g1_i4	PAN2-PAN3 deadenylation complex catalytic subunit PAN2	-23	-25
DJAA_smith199	TRINITY_DN1157_c1_g1_i8	Protein PRRC2C	-11	-23
DJAA_smith199	TRINITY_DN17975_c0_g1_i1	Signal peptidase complex subunit 1	-14	-17
DJAA_smith199	TRINITY_DN2405_c0_g1_i1	Innexin unc-9	-20	-15
DJAA_smith199	TRINITY_DN3243_c0_g2_i9	.	-17	-20
DJAA_smith199	TRINITY_DN9527_c0_g1_i1	.	-17	-22
DJAA_smith199	TRINITY_DN9988_c1_g1_i8	Potassium voltage-gated channel subfamily H member 7	-18	-25
DJAA_smith19	TRINITY_DN2819_c0_g2_i3	Probable ATP-dependent RNA helicase DHX37	-16	-21

***Dugesia japonica* var. B (4 candidates, 118 targets)**

smithID	transcriptID	Blastx	dG PITA	dG RNAHybrid
DJAB_smith0	TRINITY_DN11044_c0_g1_i4	PAN2-PAN3 deadenylation complex catalytic subunit PAN2	-12	-24
DJAB_smith0	TRINITY_DN11746_c0_g1_i1	F-box only protein 16	-16	-22
DJAB_smith0	TRINITY_DN14683_c0_g1_i1	Zinc finger protein 782	-17	-20
DJAB_smith0	TRINITY_DN2259_c0_g2_i4	Potassium channel subfamily T member 1	-17	-19
DJAB_smith0	TRINITY_DN3482_c0_g1_i10	Adhesion G-protein coupled receptor D1	-15	-20
DJAB_smith0	TRINITY_DN3777_c0_g1_i1	.	-18	-17
DJAB_smith0	TRINITY_DN6079_c0_g1_i4	AP2-associated protein kinase 1	-17	-20
DJAB_smith0	TRINITY_DN6507_c0_g2_i2	AMMECR1-like protein	-20	-15
DJAB_smith0	TRINITY_DN6837_c0_g1_i3	Solute carrier family 13 member 1	-20	-19
DJAB_smith0	TRINITY_DN7310_c0_g1_i1	Condensin complex subunit 1	-20	-22
DJAB_smith0	TRINITY_DN7712_c0_g1_i1	Protein HIRA	-16	-20
DJAB_smith0	TRINITY_DN9527_c0_g1_i1	.	-22	-27
DJAB_smith18	TRINITY_DN141_c0_g1_i3	THO complex subunit 2	-17	-20
DJAB_smith18	TRINITY_DN15845_c1_g1_i3	Large ribosomal subunit protein mL65	-21	-23
DJAB_smith18	TRINITY_DN1769_c0_g1_i12	WD repeat and FYVE domain-containing protein 3	-18	-21
DJAB_smith18	TRINITY_DN18174_c0_g3_i4	Vitellogenin	-13	-21
DJAB_smith18	TRINITY_DN20239_c0_g1_i1	LIM/homeobox protein Awh	-15	-18
DJAB_smith18	TRINITY_DN266_c0_g2_i1	.	-15	-19
DJAB_smith18	TRINITY_DN3072_c0_g1_i5	.	-17	-19
DJAB_smith18	TRINITY_DN3482_c0_g1_i10	Adhesion G-protein coupled receptor D1	-14	-18
DJAB_smith18	TRINITY_DN4687_c0_g1_i2	.	-19	-18
DJAB_smith18	TRINITY_DN5725_c0_g1_i1	Tripeptidyl-peptidase 2	-18	-22
DJAB_smith18	TRINITY_DN7076_c0_g2_i5	Mediator of RNA polymerase II transcription subunit 13-like	-12	-15
DJAB_smith18	TRINITY_DN9303_c0_g1_i1	Zinc phosphodiesterase ELAC protein 1	-15	-19
DJAB_smith18	TRINITY_DN9661_c0_g1_i1	Stabilizer of axonemal microtubules 2	-14	-18
DJAB_smith13	TRINITY_DN11550_c0_g1_i1	TNF receptor-associated factor 2	-18	-20
DJAB_smith13	TRINITY_DN11860_c0_g1_i2	.	-12	-17
DJAB_smith13	TRINITY_DN1606_c0_g1_i6	Cathepsin B	-12	-17
DJAB_smith13	TRINITY_DN1606_c0_g2_i2	Cathepsin B	-12	-17
DJAB_smith13	TRINITY_DN1640_c0_g1_i4	Centriolin	-12	-17
DJAB_smith13	TRINITY_DN17825_c0_g2_i10	Inositol polyphosphate-5-phosphatase A	-16	-16
DJAB_smith13	TRINITY_DN21195_c0_g1_i1	Homeobox protein aristaless-like 3	-13	-17
DJAB_smith13	TRINITY_DN2628_c1_g1_i1	Heme-binding protein 2	-12	-16
DJAB_smith13	TRINITY_DN3287_c0_g1_i2	Hsc70-interacting protein	-17	-21
DJAB_smith13	TRINITY_DN3445_c0_g1_i1	.	-13	-17
DJAB_smith13	TRINITY_DN3501_c0_g1_i1	Centrosomal protein of 131 kDa	-18	-19
DJAB_smith13	TRINITY_DN403_c0_g1_i3	.	-15	-18
DJAB_smith13	TRINITY_DN4490_c0_g2_i2	Spectrin beta chain, non-erythrocytic 1	-14	-16
DJAB_smith13	TRINITY_DN4916_c0_g1_i3	.	-9	-18
DJAB_smith13	TRINITY_DN5481_c0_g1_i2	Muscle calcium channel subunit alpha-1	-22	-21
DJAB_smith13	TRINITY_DN58_c1_g1_i1	Trypsin-1	-12	-18
DJAB_smith13	TRINITY_DN7727_c0_g1_i12	LIM and calponin homology domains-containing protein 1	-12	-16
DJAB_smith13	TRINITY_DN846_c0_g1_i3	Serine/threonine kinase SAD-1	-16	-18
DJAB_smith13	TRINITY_DN957_c0_g1_i1	Dual specificity tyrosine-phosphorylation-regulated kinase 2	-12	-16
DJAB_smith6	TRINITY_DN10205_c0_g1_i1	Cadherin-11	-22	-23
DJAB_smith6	TRINITY_DN10205_c0_g2_i1	Progranulin	-22	-23
DJAB_smith6	TRINITY_DN1131_c0_g1_i3	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-1	-14	-17

DJAB_smith6	TRINITY_DN11449_c0_g1_i5	Ryanodine receptor	-14	-15
DJAB_smith6	TRINITY_DN11671_c0_g1_i4	ATP-dependent RNA helicase TDRD9	-17	-17
DJAB_smith6	TRINITY_DN12064_c0_g1_i3	DmX-like protein 1	-11	-15
DJAB_smith6	TRINITY_DN1229_c0_g2_i3	Collagen alpha-1(IV) chain	-15	-19
DJAB_smith6	TRINITY_DN1256_c0_g1_i1	La-related protein 6	-17	-22
DJAB_smith6	TRINITY_DN1257_c0_g1_i4	Ubiquitin-conjugating enzyme E2 D3	-20	-16
DJAB_smith6	TRINITY_DN12930_c0_g1_i1	Calpain-7	-15	-17
DJAB_smith6	TRINITY_DN1315_c0_g1_i4	Myosin-9	-9	-17
DJAB_smith6	TRINITY_DN1324_c0_g1_i3	.	-17	-16
DJAB_smith6	TRINITY_DN13445_c0_g1_i3	GRIP and coiled-coil domain-containing protein 2	-13	-16
DJAB_smith6	TRINITY_DN13_c0_g2_i2	Serine/threonine-protein kinase MARK1	-17	-20
DJAB_smith6	TRINITY_DN1453_c0_g1_i1	Serine/threonine-protein kinase DCLK1	-11	-16
DJAB_smith6	TRINITY_DN14821_c0_g2_i1	SH3 and cysteine-rich domain-containing protein 3	-19	-22
DJAB_smith6	TRINITY_DN15260_c0_g4_i1	.	-13	-19
DJAB_smith6	TRINITY_DN15871_c0_g1_i1	.	-13	-15
DJAB_smith6	TRINITY_DN16679_c1_g1_i1	Nischarin	-16	-15
DJAB_smith6	TRINITY_DN1669_c0_g1_i9	Homeobox protein dve-1	-17	-18
DJAB_smith6	TRINITY_DN166_c0_g1_i10	TNF receptor-associated factor 6	-14	-17
DJAB_smith6	TRINITY_DN17207_c0_g1_i8	Secretory carrier-associated membrane protein 3	-15	-18
DJAB_smith6	TRINITY_DN1746_c0_g1_i3	Golgi to ER traffic protein 4 homolog B	-15	-18
DJAB_smith6	TRINITY_DN1769_c0_g1_i12	WD repeat and FYVE domain-containing protein 3	-15	-18
DJAB_smith6	TRINITY_DN17706_c0_g1_i1	Hepatic sodium/bile acid cotransporter	-12	-15
DJAB_smith6	TRINITY_DN18060_c0_g2_i1	Alpha-actinin-4	-18	-20
DJAB_smith6	TRINITY_DN1859_c0_g1_i1	.	-13	-16
DJAB_smith6	TRINITY_DN185_c0_g1_i5	Sodium-dependent lysophosphatidylcholine symporter 1	-15	-16
DJAB_smith6	TRINITY_DN1988_c0_g1_i5	.	-17	-17
DJAB_smith6	TRINITY_DN20167_c1_g1_i1	.	-16	-16
DJAB_smith6	TRINITY_DN2098_c0_g1_i1	Monocarboxylate transporter 4	-15	-15
DJAB_smith6	TRINITY_DN2134_c0_g1_i1	.	-13	-16
DJAB_smith6	TRINITY_DN2185_c0_g1_i1	Serine/threonine-protein kinase ULK3	-16	-18
DJAB_smith6	TRINITY_DN22528_c1_g1_i1	Lysine-specific demethylase 4B	-13	-21
DJAB_smith6	TRINITY_DN2269_c1_g1_i3	Protein dopey-1	-11	-17
DJAB_smith6	TRINITY_DN2340_c0_g2_i3	.	-13	-19
DJAB_smith6	TRINITY_DN24236_c0_g1_i2	Bestrophin-1	-16	-21
DJAB_smith6	TRINITY_DN2531_c0_g1_i1	Cytochrome c oxidase assembly protein COX11, mitochondrial	-17	-21
DJAB_smith6	TRINITY_DN2601_c0_g1_i1	.	-13	-15
DJAB_smith6	TRINITY_DN2603_c0_g2_i2	Putative aminopeptidase W07G4.4	-11	-15
DJAB_smith6	TRINITY_DN2955_c0_g3_i1	14-3-3-like protein GF14 iota	-13	-19
DJAB_smith6	TRINITY_DN298_c0_g2_i1	Hepatocyte nuclear factor 6	-10	-16
DJAB_smith6	TRINITY_DN3245_c0_g1_i5	.	-20	-15
DJAB_smith6	TRINITY_DN3875_c0_g1_i2	Nck-associated protein 1	-18	-19
DJAB_smith6	TRINITY_DN3997_c0_g1_i4	Receptor-type guanylate cyclase gcy-28	-19	-16
DJAB_smith6	TRINITY_DN406_c0_g1_i1	Choline-phosphate cytidylyltransferase B	-14	-24
DJAB_smith6	TRINITY_DN40_c0_g3_i3	Rab-like protein 6	-18	-16
DJAB_smith6	TRINITY_DN4398_c0_g2_i1	Phosphatidylinositol-binding clathrin assembly protein LAP	-17	-20
DJAB_smith6	TRINITY_DN448_c1_g1_i7	Potassium/sodium hyperpolarization-activated cyclic nucleotide-gated channel 1	-18	-18
DJAB_smith6	TRINITY_DN4870_c0_g1_i10	IQ domain-containing protein H	-12	-18
DJAB_smith6	TRINITY_DN4964_c0_g1_i1	Major facilitator superfamily domain-containing protein 1	-13	-17
DJAB_smith6	TRINITY_DN4964_c0_g2_i1	Protein lin-54 homolog	-13	-17
DJAB_smith6	TRINITY_DN4968_c0_g1_i11	.	-19	-23
DJAB_smith6	TRINITY_DN5246_c0_g2_i3	DDB1- and CUL4-associated factor 12-like protein 1	-19	-21
DJAB_smith6	TRINITY_DN5403_c0_g1_i4	Sushi, nidogen and EGF-like domain-containing protein 1	-14	-16
DJAB_smith6	TRINITY_DN5491_c0_g1_i3	Leucine--tRNA ligase, cytoplasmic	-17	-20
DJAB_smith6	TRINITY_DN5990_c0_g1_i3	Sodium/hydrogen exchanger 9B2	-16	-15
DJAB_smith6	TRINITY_DN5998_c0_g1_i1	NEDD8 ultimate buster 1	-15	-16
DJAB_smith6	TRINITY_DN6714_c0_g1_i1	.	-16	-21
DJAB_smith6	TRINITY_DN6774_c0_g1_i1	Mitochondrial potassium channel	-16	-17
DJAB_smith6	TRINITY_DN6967_c0_g1_i4	NF-kappa-B inhibitor alpha	-20	-18
DJAB_smith6	TRINITY_DN700_c0_g1_i1	Voltage-gated hydrogen channel 1	-11	-15
DJAB_smith6	TRINITY_DN7245_c1_g1_i2	Adiponectin receptor protein	-16	-15
DJAB_smith6	TRINITY_DN738_c0_g1_i1	Anion exchange protein 3	-9	-15
DJAB_smith6	TRINITY_DN74_c0_g1_i20	Probable glutamine--tRNA ligase	-22	-15
DJAB_smith6	TRINITY_DN7623_c0_g2_i3	Dysferlin	-16	-16
DJAB_smith6	TRINITY_DN8295_c0_g1_i2	.	-17	-20
DJAB_smith6	TRINITY_DN8714_c0_g1_i3	TNF receptor-associated factor 2	-9	-23
DJAB_smith6	TRINITY_DN8877_c0_g2_i2	Protein TFG	-14	-19
DJAB_smith6	TRINITY_DN8983_c0_g1_i1	Stromal cell-derived factor 2	-13	-18
DJAB_smith6	TRINITY_DN9208_c0_g2_i2	Laminin subunit gamma-1	-14	-16
DJAB_smith6	TRINITY_DN9216_c0_g1_i2	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase epsilon-1	-18	-19
DJAB_smith6	TRINITY_DN922_c0_g1_i3	Metabotropic glutamate receptor 5	-9	-15
DJAB_smith6	TRINITY_DN92_c0_g3_i3	Serine/threonine-protein kinase SMU1	-19	-19
		***Eisenia andrei* (5 candidates, 60 targets)**		
smithID	**transcriptID**	**Blastx**	**dG PITA**	**dG RNAHybrid**
EAN_smith0	TRINITY_DN11392_c2_g1_i1	Active breakpoint cluster region-related protein	-26	-29
EAN_smith0	TRINITY_DN207_c0_g1_i2	Lysine-specific demethylase 3A	-20	-25
EAN_smith0	TRINITY_DN26536_c0_g1_i1	.	-12	-17
EAN_smith0	TRINITY_DN3894_c0_g1_i4	Glycerol-3-phosphate dehydrogenase, mitochondrial	-18	-20
EAN_smith0	TRINITY_DN42622_c0_g1_i1	.	-23	-25
EAN_smith14	TRINITY_DN1087_c2_g1_i2	.	-20	-25
EAN_smith14	TRINITY_DN11856_c1_g1_i10	Adhesion G protein-coupled receptor L3	-56	-64
EAN_smith14	TRINITY_DN12802_c0_g1_i7	Protein SON	-22	-16
EAN_smith14	TRINITY_DN14830_c0_g1_i7	.	-16	-17
EAN_smith14	TRINITY_DN23549_c0_g1_i3	Receptor expression-enhancing protein 5	-11	-20
EAN_smith14	TRINITY_DN26193_c0_g3_i1	Protein HGV2	-26	-30
EAN_smith14	TRINITY_DN32107_c0_g1_i4	Receptor-transporting protein 3	-21	-22
EAN_smith14	TRINITY_DN34071_c0_g1_i2	.	-16	-21
EAN_smith14	TRINITY_DN4162_c0_g2_i1	52 kDa repressor of the inhibitor of the protein kinase	-21	-23
EAN_smith14	TRINITY_DN5406_c1_g1_i6	Neuron navigator 2	-23	-25
EAN_smith14	TRINITY_DN5854_c0_g1_i11	.	-23	-15
EAN_smith14	TRINITY_DN71496_c0_g1_i1	Protein-L-histidine N-pros-methyltransferase	-22	-15
EAN_smith1	TRINITY_DN11526_c0_g1_i1	Maternal embryonic leucine zipper kinase	-14	-19
EAN_smith1	TRINITY_DN12127_c0_g1_i5	.	-22	-19
EAN_smith1	TRINITY_DN13507_c0_g1_i3	Alpha/beta hydrolase domain-containing protein 17C	-14	-19
EAN_smith1	TRINITY_DN153_c0_g2_i1	ADAM 17-like protease	-19	-19

EAN_smith1	TRINITY_DN15842_c0_g1_i2	T-complex protein 1 subunit zeta	-19	-19
EAN_smith1	TRINITY_DN18004_c0_g1_i2	Dynein axonemal heavy chain 10	-16	-19
EAN_smith1	TRINITY_DN20275_c0_g1_i1	MICAL-like protein 1	-19	-19
EAN_smith1	TRINITY_DN207_c0_g1_i1	Lysine-specific demethylase 3A	-16	-15
EAN_smith1	TRINITY_DN21924_c0_g1_i2	Liprin-alpha-1	-18	-21
EAN_smith1	TRINITY_DN24127_c0_g1_i7	Serine/threonine-protein kinase TBK1	-19	-20
EAN_smith1	TRINITY_DN24290_c0_g1_i1	Large ribosomal subunit protein mL48	-17	-19
EAN_smith1	TRINITY_DN26330_c0_g2_i1	Eukaryotic elongation factor 2 kinase	-19	-18
EAN_smith1	TRINITY_DN336_c1_g1_i5	Guanine nucleotide-binding protein G(q) subunit alpha	-14	-16
EAN_smith1	TRINITY_DN33769_c0_g2_i1	Uncharacterized protein C7orf57	-17	-19
EAN_smith1	TRINITY_DN34135_c1_g1_i1	Peptidyl-prolyl cis-trans isomerase Fkbp12	-20	-18
EAN_smith1	TRINITY_DN38282_c0_g1_i2	.	-13	-18
EAN_smith1	TRINITY_DN41260_c0_g1_i1	Interleukin-12 receptor subunit beta-2	-12	-18
EAN_smith1	TRINITY_DN43900_c0_g2_i1	Cyclin-dependent kinase 8	-20	-24
EAN_smith1	TRINITY_DN4936_c0_g2_i1	ER degradation-enhancing alpha-mannosidase-like protein 1	-22	-19
EAN_smith1	TRINITY_DN51662_c0_g1_i1	Proteasome subunit alpha type-1	-15	-19
EAN_smith1	TRINITY_DN61878_c0_g1_i1	.	-18	-18
EAN_smith1	TRINITY_DN7501_c0_g1_i5	Muscle cell intermediate filament protein AV71	-16	-18
EAN_smith1	TRINITY_DN766_c0_g1_i14	.	-21	-18
EAN_smith1	TRINITY_DN808_c0_g1_i12	Macrophage mannose receptor 1	-19	-19
EAN_smith1	TRINITY_DN8608_c0_g1_i1	.	-19	-16
EAN_smith2	TRINITY_DN10345_c0_g2_i1	Methylosome protein WDR77	-21	-21
EAN_smith2	TRINITY_DN10477_c0_g1_i2	Ubiquitin carboxyl-terminal hydrolase 16	-18	-22
EAN_smith2	TRINITY_DN10707_c0_g1_i1	Dual specificity mitogen-activated protein kinase kinase 6	-24	-27
EAN_smith2	TRINITY_DN13267_c0_g2_i2	.	-21	-23
EAN_smith2	TRINITY_DN3460_c0_g2_i1	.	-24	-22
EAN_smith2	TRINITY_DN5530_c1_g1_i1	Myosin regulatory light chain, striated muscle, 25 kDa isoform	-24	-26
EAN_smith2	TRINITY_DN62244_c0_g1_i1	.	-24	-25
EAN_smith2	TRINITY_DN6629_c0_g3_i1	BAG domain-containing protein Samui	-25	-27
EAN_smith2	TRINITY_DN86249_c0_g1_i1	Regulator of G-protein signaling egl-10	-14	-19
EAN_smith2	TRINITY_DN945_c0_g1_i2	Protein CNPPD1	-23	-25
EAN_smith2	TRINITY_DN9517_c0_g1_i1	Alpha-L-fucosidase	-21	-21
EAN_smith5	TRINITY_DN16540_c1_g2_i1	Linear primary-alkylsulfatase	-22	-22
EAN_smith5	TRINITY_DN17598_c0_g2_i1	Zinc finger protein 236	-29	-23
EAN_smith5	TRINITY_DN203_c0_g1_i2	E3 ubiquitin-protein ligase TRIM56	-14	-18
EAN_smith5	TRINITY_DN42259_c0_g1_i1	Synaptogyrin-1	-27	-21
EAN_smith5	TRINITY_DN5433_c0_g1_i1	Eukaryotic translation initiation factor 3 subunit A	-16	-18
EAN_smith5	TRINITY_DN654_c1_g3_i4	NADP-dependent malic enzyme	-26	-28
EAN_smith5	TRINITY_DN7862_c0_g1_i2	Putative phosphoenolpyruvate synthase	-29	-31
		***Mus musculus* (4 candidates, 402 targets)**		
smithID	**transcriptID**	**Blastx**	**dG PITA**	**dG RNAHybrid**
MMU_smith0	TRINITY_DN10871_c0_g1_i10	Oxytocin receptor	-22	-19
MMU_smith0	TRINITY_DN10895_c0_g1_i2	Glycerate kinase	-20	-19
MMU_smith0	TRINITY_DN110554_c0_g1_i1	.	-22	-22
MMU_smith0	TRINITY_DN11177_c1_g1_i1	.	-19	-22
MMU_smith0	TRINITY_DN11707_c0_g3_i1	.	-22	-22
MMU_smith0	TRINITY_DN127893_c0_g1_i1	.	-24	-25
MMU_smith0	TRINITY_DN12890_c0_g1_i1	b(0,+)-type amino acid transporter 1	-23	-22
MMU_smith0	TRINITY_DN129192_c0_g2_i1	.	-21	-23
MMU_smith0	TRINITY_DN132774_c0_g1_i1	.	-22	-19
MMU_smith0	TRINITY_DN136243_c0_g1_i2	Complement C1q subcomponent subunit A	-30	-19
MMU_smith0	TRINITY_DN1401_c0_g2_i7	Dynein axonemal heavy chain 10	-19	-17
MMU_smith0	TRINITY_DN1407_c0_g1_i12	Tight junction protein ZO-1	-19	-22
MMU_smith0	TRINITY_DN1468_c0_g1_i6	Ataxin-2-like protein	-34	-26
MMU_smith0	TRINITY_DN150529_c1_g1_i4	.	-25	-26
MMU_smith0	TRINITY_DN15301_c0_g1_i16	UDP-GlcNAc	-24	-19
MMU_smith0	TRINITY_DN153527_c0_g1_i2	Protein lin-7 homolog A	-22	-26
MMU_smith0	TRINITY_DN158141_c1_g1_i5	Spectrin alpha chain, erythrocytic 1	-21	-22
MMU_smith0	TRINITY_DN1630_c0_g1_i20	Adenosine kinase	-14	-19
MMU_smith0	TRINITY_DN1635_c0_g1_i4	RNA-binding protein 15	-17	-19
MMU_smith0	TRINITY_DN18032_c0_g1_i1	.	-19	-19
MMU_smith0	TRINITY_DN180885_c0_g1_i5	.	-19	-22
MMU_smith0	TRINITY_DN1809_c1_g1_i3	Sulfhydryl oxidase 1	-17	-16
MMU_smith0	TRINITY_DN18668_c0_g1_i1	LINE-1 retrotransposable element ORF2 protein	-27	-15
MMU_smith0	TRINITY_DN1869_c4_g2_i3	Zinc finger protein 709	-22	-28
MMU_smith0	TRINITY_DN19006_c3_g1_i1	.	-19	-19
MMU_smith0	TRINITY_DN2125_c1_g1_i1	DNA-directed RNA polymerase III subunit RPC2	-22	-25
MMU_smith0	TRINITY_DN2130_c0_g1_i14	Coiled-coil domain-containing protein 110	-25	-23
MMU_smith0	TRINITY_DN2146_c2_g1_i2	.	-25	-19
MMU_smith0	TRINITY_DN21760_c0_g1_i10	.	-30	-31
MMU_smith0	TRINITY_DN2210_c0_g1_i1	.	-21	-22
MMU_smith0	TRINITY_DN2294_c0_g1_i5	Pre-mRNA-processing factor 19	-21	-19
MMU_smith0	TRINITY_DN2355_c0_g1_i2	FK506-binding protein 15	-17	-16
MMU_smith0	TRINITY_DN2363_c1_g1_i10	Paternally-expressed gene 3 protein	-23	-19
MMU_smith0	TRINITY_DN2364_c0_g3_i3	Protein O-mannosyl-transferase 2	-21	-25
MMU_smith0	TRINITY_DN23723_c0_g1_i1	Calcium-independent phospholipase A2-gamma	-14	-16
MMU_smith0	TRINITY_DN2453_c0_g2_i1	Nucleolar protein 4-like	-18	-15
MMU_smith0	TRINITY_DN2546_c0_g1_i3	Histone deacetylase complex subunit SAP18	-21	-16
MMU_smith0	TRINITY_DN2666_c0_g1_i13	Peroxiredoxin-like 2C	-23	-28
MMU_smith0	TRINITY_DN2671_c0_g1_i10	DNA repair protein XRCC3	-17	-22
MMU_smith0	TRINITY_DN27103_c1_g4_i3	Ras-related protein Rab-33A	-22	-18
MMU_smith0	TRINITY_DN27142_c1_g1_i3	HLA class II histocompatibility antigen, DO beta chain	-33	-28
MMU_smith0	TRINITY_DN27944_c0_g1_i2	.	-26	-18
MMU_smith0	TRINITY_DN2796_c0_g1_i21	Transmembrane channel-like protein 3	-38	-42
MMU_smith0	TRINITY_DN29231_c0_g6_i1	.	-17	-19
MMU_smith0	TRINITY_DN29827_c0_g1_i12	Zinc finger protein 445	-19	-17
MMU_smith0	TRINITY_DN3003_c0_g2_i1	NMDA receptor synaptonuclear signaling and neuronal migration factor	-26	-20
MMU_smith0	TRINITY_DN3036_c0_g1_i4	Zinc finger CCCH domain-containing protein 14	-15	-17
MMU_smith0	TRINITY_DN3105_c1_g3_i4	Inactive serine/threonine-protein kinase TEX14	-22	-19
MMU_smith0	TRINITY_DN3138_c0_g2_i1	Germ cell-less protein-like 1	-16	-20
MMU_smith0	TRINITY_DN3164_c1_g2_i20	Kinesin-like protein KIF2A	-18	-16
MMU_smith0	TRINITY_DN319_c0_g6_i3	Mediator of RNA polymerase II transcription subunit 14	-27	-22
MMU_smith0	TRINITY_DN3247_c0_g1_i12	Signal peptidase complex subunit 1	-16	-19
MMU_smith0	TRINITY_DN33077_c0_g2_i12	Golgi integral membrane protein 4	-15	-16

MMU_smith0	TRINITY_DN33099_c0_g4_i1	Small ribosomal subunit protein eS25	-18	-22
MMU_smith0	TRINITY_DN33287_c0_g2_i1	.	-23	-28
MMU_smith0	TRINITY_DN333_c0_g1_i6	SLIT-ROBO Rho GTPase-activating protein 2	-24	-19
MMU_smith0	TRINITY_DN336_c0_g3_i2	.	-21	-17
MMU_smith0	TRINITY_DN3415_c0_g1_i10	.	-24	-28
MMU_smith0	TRINITY_DN34228_c1_g1_i2	.	-10	-23
MMU_smith0	TRINITY_DN34346_c0_g1_i1	.	-23	-18
MMU_smith0	TRINITY_DN3495_c1_g1_i19	Protein SHQ1 homolog	-17	-22
MMU_smith0	TRINITY_DN350_c0_g1_i8	Ubiquitin carboxyl-terminal hydrolase isozyme L5	-18	-23
MMU_smith0	TRINITY_DN35429_c0_g1_i2	Homeobox protein TGIF2	-16	-20
MMU_smith0	TRINITY_DN36850_c0_g1_i1	.	-29	-17
MMU_smith0	TRINITY_DN37049_c0_g1_i3	Large ribosomal subunit protein uL11m	-26	-22
MMU_smith0	TRINITY_DN3744_c2_g1_i1	Rho guanine nucleotide exchange factor 3	-14	-19
MMU_smith0	TRINITY_DN3836_c1_g1_i6	Mitochondrial adenyl nucleotide antiporter SLC25A23	-37	-16
MMU_smith0	TRINITY_DN3869_c7_g1_i2	.	-25	-22
MMU_smith0	TRINITY_DN38895_c0_g2_i1	.	-20	-25
MMU_smith0	TRINITY_DN38943_c0_g1_i3	.	-22	-22
MMU_smith0	TRINITY_DN409583_c1_g1_i1	.	-19	-19
MMU_smith0	TRINITY_DN41683_c0_g1_i5	Tripeptidyl-peptidase 1	-11	-19
MMU_smith0	TRINITY_DN421052_c0_g1_i1	.	-30	-26
MMU_smith0	TRINITY_DN42499_c0_g2_i1	Calcium release-activated calcium channel protein 1	-23	-19
MMU_smith0	TRINITY_DN4314_c0_g9_i1	.	-19	-19
MMU_smith0	TRINITY_DN433419_c0_g1_i1	.	-28	-23
MMU_smith0	TRINITY_DN43815_c0_g1_i3	Zinc finger protein 330	-20	-15
MMU_smith0	TRINITY_DN4488_c0_g3_i1	.	-28	-18
MMU_smith0	TRINITY_DN45772_c1_g1_i1	.	-37	-41
MMU_smith0	TRINITY_DN4635_c0_g1_i6	.	-25	-17
MMU_smith0	TRINITY_DN4642_c1_g1_i5	Cell division control protein 42 homolog	-20	-22
MMU_smith0	TRINITY_DN46665_c0_g1_i1	.	-19	-22
MMU_smith0	TRINITY_DN4680_c0_g3_i4	Serine/threonine-protein kinase DCLK2	-21	-22
MMU_smith0	TRINITY_DN47046_c0_g1_i1	.	-18	-22
MMU_smith0	TRINITY_DN4753_c0_g1_i1	.	-17	-19
MMU_smith0	TRINITY_DN48006_c0_g1_i2	.	-14	-16
MMU_smith0	TRINITY_DN484_c2_g1_i1	Uncharacterized protein KIAA0930 homolog	-26	-27
MMU_smith0	TRINITY_DN48_c2_g2_i3	Serine hydroxymethyltransferase, cytosolic	-17	-16
MMU_smith0	TRINITY_DN4947_c1_g1_i1	.	-11	-19
MMU_smith0	TRINITY_DN4954_c2_g1_i3	.	-12	-18
MMU_smith0	TRINITY_DN495_c10_g1_i1	.	-22	-27
MMU_smith0	TRINITY_DN5036_c0_g2_i11	Protein PAT1 homolog 1	-16	-19
MMU_smith0	TRINITY_DN50666_c0_g1_i1	.	-23	-15
MMU_smith0	TRINITY_DN5374_c0_g1_i1	Epithelial splicing regulatory protein 2	-21	-23
MMU_smith0	TRINITY_DN5411_c0_g1_i2	.	-22	-19
MMU_smith0	TRINITY_DN55600_c0_g1_i3	Eukaryotic translation initiation factor 4E-binding protein 1	-38	-37
MMU_smith0	TRINITY_DN56_c1_g1_i2	Vacuolar protein sorting-associated protein 4B	-19	-19
MMU_smith0	TRINITY_DN57214_c1_g1_i1	Carbohydrate sulfotransferase 4	-21	-22
MMU_smith0	TRINITY_DN62374_c0_g1_i1	Dickkopf-related protein 3	-17	-29
MMU_smith0	TRINITY_DN6432_c0_g1_i1	.	-27	-16
MMU_smith0	TRINITY_DN643_c0_g1_i13	Fibronectin	-18	-19
MMU_smith0	TRINITY_DN64551_c1_g1_i1	.	-18	-21
MMU_smith0	TRINITY_DN656_c0_g1_i12	IGF-like family receptor 1	-22	-16
MMU_smith0	TRINITY_DN6697_c1_g1_i10	Mitochondrial peptide methionine sulfoxide reductase	-30	-20
MMU_smith0	TRINITY_DN6712_c0_g1_i4	Transcriptional repressor p66-beta	-19	-19
MMU_smith0	TRINITY_DN68778_c0_g2_i1	.	-24	-28
MMU_smith0	TRINITY_DN692521_c0_g1_i1	.	-18	-22
MMU_smith0	TRINITY_DN72158_c0_g2_i2	.	-15	-16
MMU_smith0	TRINITY_DN7258_c0_g1_i6	Myocardin-related transcription factor B	-23	-17
MMU_smith0	TRINITY_DN73097_c1_g1_i1	.	-32	-18
MMU_smith0	TRINITY_DN75596_c0_g2_i1	.	-24	-26
MMU_smith0	TRINITY_DN7983_c2_g1_i1	.	-15	-20
MMU_smith0	TRINITY_DN81247_c0_g1_i7	Nitric oxide-associated protein 1	-27	-22
MMU_smith0	TRINITY_DN8314_c0_g1_i11	Insulin-like growth factor 2 mRNA-binding protein 3	-22	-16
MMU_smith0	TRINITY_DN8465_c10_g1_i1	.	-19	-19
MMU_smith0	TRINITY_DN87303_c0_g2_i1	.	-17	-19
MMU_smith0	TRINITY_DN876_c0_g1_i3	NF-kappa-B-activating protein	-22	-22
MMU_smith0	TRINITY_DN8992_c0_g2_i1	.	-16	-19
MMU_smith0	TRINITY_DN93879_c0_g1_i2	LINE-1 retrotransposable element ORF2 protein	-12	-15
MMU_smith0	TRINITY_DN97632_c0_g1_i2	.	-25	-22
MMU_smith0	TRINITY_DN9927_c0_g1_i1	Centromere protein O	-23	-22
MMU_smith1	TRINITY_DN100454_c1_g1_i13	Glutamate--cysteine ligase catalytic subunit	-28	-22
MMU_smith1	TRINITY_DN10140_c0_g1_i1	.	-11	-17
MMU_smith1	TRINITY_DN10319_c0_g2_i3	Regulator of microtubule dynamics protein 3	-24	-22
MMU_smith1	TRINITY_DN10526_c0_g1_i1	Striatin-interacting proteins 2	-19	-20
MMU_smith1	TRINITY_DN10876_c0_g1_i1	Vacuolar ATPase assembly integral membrane protein Vma21	-19	-19
MMU_smith1	TRINITY_DN109565_c0_g2_i1	.	-13	-16
MMU_smith1	TRINITY_DN1156_c0_g3_i2	Ras-related protein Rab-33B	-17	-15
MMU_smith1	TRINITY_DN11674_c1_g1_i10	.	-21	-22
MMU_smith1	TRINITY_DN116906_c0_g1_i1	.	-22	-20
MMU_smith1	TRINITY_DN12020_c0_g2_i3	Serine incorporator 5	-19	-20
MMU_smith1	TRINITY_DN12122_c0_g1_i2	.	-24	-19
MMU_smith1	TRINITY_DN12326_c0_g6_i3	Sphingosine 1-phosphate receptor 3	-19	-21
MMU_smith1	TRINITY_DN12379_c0_g1_i2	Afadin	-22	-15
MMU_smith1	TRINITY_DN12571_c0_g1_i14	COMM domain-containing protein 8	-20	-15
MMU_smith1	TRINITY_DN128785_c1_g1_i1	.	-24	-22
MMU_smith1	TRINITY_DN131065_c0_g2_i18	Neutral amino acid transporter B(0)	-21	-22
MMU_smith1	TRINITY_DN13123_c0_g2_i2	Gag-Pro polyprotein	-18	-19
MMU_smith1	TRINITY_DN13145_c0_g1_i3	PH domain leucine-rich repeat-containing protein phosphatase 1	-23	-23
MMU_smith1	TRINITY_DN133225_c0_g1_i1	Olfactory receptor 52E4	-22	-22
MMU_smith1	TRINITY_DN13372_c0_g1_i7	PC4 and SFRS1-interacting protein	-18	-15
MMU_smith1	TRINITY_DN1348_c0_g3_i1	Transmembrane protein 265	-25	-16
MMU_smith1	TRINITY_DN13870_c0_g1_i11	Rho guanine nucleotide exchange factor 4	-19	-21
MMU_smith1	TRINITY_DN1404_c0_g3_i1	Kinesin-like protein KIF3C	-30	-21
MMU_smith1	TRINITY_DN14208_c0_g1_i10	Adenylate kinase 4, mitochondrial	-21	-21
MMU_smith1	TRINITY_DN1426_c2_g1_i7	Chromodomain-helicase-DNA-binding protein 1-like	-34	-19
MMU_smith1	TRINITY_DN14906_c0_g1_i2	Fasciculation and elongation protein zeta-1	-25	-21
MMU_smith1	TRINITY_DN149656_c0_g1_i6	Mastermind-like protein 2	-16	-16

MMU_smith1	TRINITY_DN15009_c0_g1_i1	Arrestin domain-containing protein 3	-16	-18
MMU_smith1	TRINITY_DN15284_c0_g2_i1	Exocyst complex component 3	-14	-16
MMU_smith1	TRINITY_DN15628_c0_g2_i3	Arpin	-19	-16
MMU_smith1	TRINITY_DN15992_c0_g1_i6	Protein diaphanous homolog 3	-22	-16
MMU_smith1	TRINITY_DN161030_c0_g2_i1	.	-30	-24
MMU_smith1	TRINITY_DN161792_c1_g1_i3	.	-18	-16
MMU_smith1	TRINITY_DN164_c0_g1_i9	Transcription initiation factor TFIID subunit 7-like	-19	-16
MMU_smith1	TRINITY_DN1651_c0_g1_i10	Unconventional myosin-Id	-16	-20
MMU_smith1	TRINITY_DN1673_c0_g1_i11	Lysine-specific demethylase 5A	-19	-17
MMU_smith1	TRINITY_DN167766_c0_g1_i2	.	-28	-23
MMU_smith1	TRINITY_DN16990_c0_g2_i10	Src kinase-associated phosphoprotein 2	-27	-21
MMU_smith1	TRINITY_DN17771_c0_g1_i5	AT-rich interactive domain-containing protein 1B	-21	-17
MMU_smith1	TRINITY_DN17820_c0_g3_i1	Ribosomal protein S6 kinase alpha-5	-20	-20
MMU_smith1	TRINITY_DN1788_c0_g1_i4	Glutaredoxin-3	-13	-22
MMU_smith1	TRINITY_DN18465_c1_g3_i1	Rho GTPase-activating protein 17	-20	-21
MMU_smith1	TRINITY_DN19344_c0_g1_i4	MICOS complex subunit Mic26	-27	-16
MMU_smith1	TRINITY_DN19649_c0_g1_i2	Cation-dependent mannose-6-phosphate receptor	-16	-16
MMU_smith1	TRINITY_DN196813_c0_g1_i1	Sorting nexin-19	-20	-16
MMU_smith1	TRINITY_DN2056_c1_g2_i1	.	-20	-21
MMU_smith1	TRINITY_DN21385_c0_g2_i1	.	-22	-16
MMU_smith1	TRINITY_DN21512_c0_g1_i1	Myomegalin	-23	-15
MMU_smith1	TRINITY_DN2169_c0_g3_i2	Rootletin	-22	-21
MMU_smith1	TRINITY_DN2200_c0_g1_i8	Phospholipase A-2-activating protein	-16	-16
MMU_smith1	TRINITY_DN2237_c0_g1_i10	Lysophosphatidic acid receptor 1	-25	-21
MMU_smith1	TRINITY_DN2250_c0_g1_i14	Circadian locomoter output cycles protein kaput	-21	-15
MMU_smith1	TRINITY_DN23614_c1_g1_i1	.	-20	-16
MMU_smith1	TRINITY_DN2363_c1_g1_i13	Paternally-expressed gene 3 protein	-25	-22
MMU_smith1	TRINITY_DN23769_c0_g1_i3	GDP-fucose protein O-fucosyltransferase 1	-17	-20
MMU_smith1	TRINITY_DN239084_c1_g1_i4	.	-25	-20
MMU_smith1	TRINITY_DN2403_c0_g1_i9	Protein transport protein Sec16A	-25	-22
MMU_smith1	TRINITY_DN24083_c0_g1_i7	Sushi, nidogen and EGF-like domain-containing protein 1	-17	-19
MMU_smith1	TRINITY_DN2447_c1_g4_i1	.	-20	-20
MMU_smith1	TRINITY_DN25002_c3_g1_i2	.	-9	-17
MMU_smith1	TRINITY_DN250563_c0_g1_i1	.	-28	-21
MMU_smith1	TRINITY_DN25509_c1_g1_i1	LINE-1 retrotransposable element ORF2 protein	-19	-15
MMU_smith1	TRINITY_DN25736_c0_g2_i1	Centromere protein W	-16	-21
MMU_smith1	TRINITY_DN2819_c0_g1_i2	YTH domain-containing protein 1	-17	-15
MMU_smith1	TRINITY_DN2877_c0_g4_i5	Rap1 GTPase-GDP dissociation stimulator 1	-15	-15
MMU_smith1	TRINITY_DN2912_c0_g1_i5	BTB/POZ domain-containing protein 10	-17	-16
MMU_smith1	TRINITY_DN292_c0_g1_i9	Protein disulfide-isomerase TMX3	-20	-16
MMU_smith1	TRINITY_DN29645_c0_g1_i3	Dipeptidyl peptidase 8	-18	-20
MMU_smith1	TRINITY_DN29892_c0_g2_i4	.	-19	-22
MMU_smith1	TRINITY_DN30604_c0_g1_i1	.	-29	-17
MMU_smith1	TRINITY_DN30954_c5_g1_i1	.	-21	-23
MMU_smith1	TRINITY_DN31934_c0_g4_i5	.	-17	-15
MMU_smith1	TRINITY_DN3213_c0_g1_i11	RRP12-like protein	-25	-22
MMU_smith1	TRINITY_DN3247_c0_g1_i12	Signal peptidase complex subunit 1	-18	-15
MMU_smith1	TRINITY_DN32920_c0_g1_i1	.	-21	-25
MMU_smith1	TRINITY_DN3455_c1_g3_i1	Zinc finger protein 790	-26	-16
MMU_smith1	TRINITY_DN3481_c0_g4_i2	Synaptotagmin-1	-20	-15
MMU_smith1	TRINITY_DN3523_c0_g1_i2	Enhancer of mRNA-decapping protein 3	-15	-15
MMU_smith1	TRINITY_DN3646_c0_g2_i4	Serine/threonine/tyrosine-interacting protein	-17	-19
MMU_smith1	TRINITY_DN3695_c0_g2_i1	F-BAR and double SH3 domains protein 2	-11	-17
MMU_smith1	TRINITY_DN37257_c0_g1_i12	Adhesion G protein-coupled receptor L3	-26	-22
MMU_smith1	TRINITY_DN3787_c0_g1_i10	Hemicentin-1	-19	-22
MMU_smith1	TRINITY_DN3797_c0_g1_i7	.	-20	-16
MMU_smith1	TRINITY_DN379_c0_g2_i12	Lysophosphatidic acid phosphatase type 6	-21	-21
MMU_smith1	TRINITY_DN3843_c0_g1_i3	Synaptojanin-1	-23	-16
MMU_smith1	TRINITY_DN4131_c0_g1_i16	Protein SCAI	-25	-21
MMU_smith1	TRINITY_DN41456_c0_g1_i1	.	-22	-16
MMU_smith1	TRINITY_DN4198_c0_g1_i12	.	-21	-20
MMU_smith1	TRINITY_DN4279_c0_g2_i4	Electroneutral sodium bicarbonate exchanger 1	-20	-17
MMU_smith1	TRINITY_DN432_c0_g1_i1	MMS19 nucleotide excision repair protein homolog	-23	-16
MMU_smith1	TRINITY_DN44071_c0_g2_i3	.	-20	-15
MMU_smith1	TRINITY_DN45497_c0_g1_i10	Probable ATP-dependent RNA helicase DDX59	-27	-16
MMU_smith1	TRINITY_DN4581_c1_g2_i4	Tyrosine-protein phosphatase non-receptor type 14	-17	-20
MMU_smith1	TRINITY_DN4642_c1_g1_i5	Cell division control protein 42 homolog	-16	-15
MMU_smith1	TRINITY_DN4663_c0_g1_i11	Transcription factor 12	-23	-15
MMU_smith1	TRINITY_DN48502_c0_g1_i1	.	-21	-20
MMU_smith1	TRINITY_DN48964_c0_g2_i1	.	-19	-20
MMU_smith1	TRINITY_DN5142_c2_g1_i1	Sodium-dependent proline transporter	-26	-21
MMU_smith1	TRINITY_DN52819_c0_g1_i7	.	-23	-15
MMU_smith1	TRINITY_DN54046_c0_g2_i1	.	-10	-15
MMU_smith1	TRINITY_DN5431_c2_g2_i1	.	-19	-20
MMU_smith1	TRINITY_DN5432_c0_g1_i1	Divergent protein kinase domain 1A	-18	-16
MMU_smith1	TRINITY_DN5444_c2_g1_i1	.	-24	-15
MMU_smith1	TRINITY_DN54_c0_g1_i8	Exocyst complex component 2	-15	-16
MMU_smith1	TRINITY_DN5547_c0_g1_i10	WD repeat-containing protein 11	-25	-20
MMU_smith1	TRINITY_DN5556_c0_g1_i11	Myotubularin-related protein 13	-24	-15
MMU_smith1	TRINITY_DN55963_c0_g2_i2	.	-16	-15
MMU_smith1	TRINITY_DN5703_c0_g1_i12	Inositol hexakisphosphate and diphosphoinositol-pentakisphosphate kinase 1	-12	-15
MMU_smith1	TRINITY_DN57214_c1_g1_i1	Carbohydrate sulfotransferase 4	-21	-17
MMU_smith1	TRINITY_DN580_c0_g1_i11	Integrator complex subunit 2	-24	-21
MMU_smith1	TRINITY_DN5871_c1_g1_i4	Calcineurin B homologous protein 1	-13	-16
MMU_smith1	TRINITY_DN59665_c0_g1_i1	MORC family CW-type zinc finger protein 4	-15	-19
MMU_smith1	TRINITY_DN59_c0_g3_i7	U2 small nuclear ribonucleoprotein B''	-19	-16
MMU_smith1	TRINITY_DN6087_c0_g1_i5	Dynactin subunit 5	-30	-15
MMU_smith1	TRINITY_DN6092_c0_g1_i6	WD repeat-containing protein 17	-19	-15
MMU_smith1	TRINITY_DN6311_c0_g2_i1	Ubiquitin-like modifier-activating enzyme 5	-27	-24
MMU_smith1	TRINITY_DN63484_c2_g1_i1	.	-25	-25
MMU_smith1	TRINITY_DN6400_c0_g2_i10	Zinc finger CCCH domain-containing protein 7A	-17	-23
MMU_smith1	TRINITY_DN64088_c0_g3_i1	Tribbles homolog 2	-22	-21
MMU_smith1	TRINITY_DN6487_c0_g1_i12	.	-13	-15
MMU_smith1	TRINITY_DN6836_c0_g1_i11	FHF complex subunit HOOK-interacting protein 1A	-29	-23
MMU_smith1	TRINITY_DN6852_c0_g2_i2	Adenylate cyclase type 1	-16	-15

MMU_smith1	TRINITY_DN7012_c1_g1_i4	.	-29	-21
MMU_smith1	TRINITY_DN7059_c1_g1_i3	.	-21	-16
MMU_smith1	TRINITY_DN7059_c1_g2_i1	.	-21	-16
MMU_smith1	TRINITY_DN70714_c3_g1_i3	.	-23	-21
MMU_smith1	TRINITY_DN70853_c0_g2_i5	Zinc finger protein Helios	-26	-20
MMU_smith1	TRINITY_DN7095_c0_g1_i10	TBC1 domain family member 14	-20	-17
MMU_smith1	TRINITY_DN7261_c0_g2_i1	.	-12	-16
MMU_smith1	TRINITY_DN7553_c0_g1_i1	E3 ubiquitin-protein ligase RNF113A	-21	-21
MMU_smith1	TRINITY_DN7573_c0_g1_i2	Phosphatidylinositol 4,5-bisphosphate 3-kinase catalytic subunit beta isoform	-20	-15
MMU_smith1	TRINITY_DN7776_c0_g1_i1	Cleavage stimulation factor subunit 2 tau variant	-13	-15
MMU_smith1	TRINITY_DN789_c0_g2_i10	Ubiquitin carboxyl-terminal hydrolase 34	-23	-15
MMU_smith1	TRINITY_DN8080_c0_g2_i7	Coxsackievirus and adenovirus receptor homolog	-20	-16
MMU_smith1	TRINITY_DN8086_c0_g1_i4	Cyclin-dependent kinase 12	-15	-17
MMU_smith1	TRINITY_DN81133_c0_g1_i1	.	-14	-15
MMU_smith1	TRINITY_DN82292_c0_g2_i2	Insulin-like growth factor-binding protein 6	-17	-21
MMU_smith1	TRINITY_DN8598_c0_g2_i1	Golgi-associated PDZ and coiled-coil motif-containing protein	-12	-16
MMU_smith1	TRINITY_DN8668_c4_g2_i1	Zinc finger CCHC domain-containing protein 24	-18	-20
MMU_smith1	TRINITY_DN8822_c0_g1_i13	Pre-mRNA-splicing factor SPF27	-16	-16
MMU_smith1	TRINITY_DN886_c0_g3_i2	Serine/threonine-protein kinase SMG1	-22	-17
MMU_smith1	TRINITY_DN888_c1_g1_i1	Serine/threonine-protein phosphatase 6 regulatory ankyrin repeat subunit B	-13	-18
MMU_smith1	TRINITY_DN90846_c1_g1_i1	.	-25	-21
MMU_smith1	TRINITY_DN926_c0_g1_i15	Zinc finger and SCAN domain-containing protein 18	-16	-16
MMU_smith1	TRINITY_DN92937_c0_g1_i1	.	-19	-16
MMU_smith1	TRINITY_DN975429_c0_g1_i1	.	-22	-20
MMU_smith2	TRINITY_DN1007_c0_g2_i15	Tyrosine-protein phosphatase non-receptor type 13	-18	-25
MMU_smith2	TRINITY_DN1010_c0_g2_i2	Protein PRR14L	-23	-16
MMU_smith2	TRINITY_DN11071_c0_g1_i1	.	-20	-21
MMU_smith2	TRINITY_DN1114_c0_g1_i2	Probable E3 ubiquitin-protein ligase HECTD4	-9	-21
MMU_smith2	TRINITY_DN113938_c0_g1_i1	.	-21	-23
MMU_smith2	TRINITY_DN1208_c0_g1_i3	Zinc finger protein 280D	-12	-16
MMU_smith2	TRINITY_DN12379_c0_g1_i10	Afadin	-21	-23
MMU_smith2	TRINITY_DN13002_c0_g2_i4	.	-23	-24
MMU_smith2	TRINITY_DN1343_c0_g1_i11	Protein kintoun	-26	-27
MMU_smith2	TRINITY_DN141644_c0_g1_i1	Putative olfactory receptor 7A2	-21	-25
MMU_smith2	TRINITY_DN1590_c0_g3_i1	Hepatocyte growth factor receptor	-25	-25
MMU_smith2	TRINITY_DN161446_c0_g1_i2	Large ribosomal subunit protein eL6	-26	-25
MMU_smith2	TRINITY_DN1904_c0_g1_i3	Thioredoxin domain-containing protein 11	-18	-21
MMU_smith2	TRINITY_DN192645_c0_g1_i1	.	-17	-21
MMU_smith2	TRINITY_DN19604_c0_g1_i3	Protein phosphatase 1 regulatory subunit 14A	-21	-21
MMU_smith2	TRINITY_DN2184_c0_g1_i10	.	-20	-20
MMU_smith2	TRINITY_DN2363_c1_g1_i13	Paternally-expressed gene 3 protein	-21	-21
MMU_smith2	TRINITY_DN2780_c0_g1_i11	Translocation protein SEC62	-15	-15
MMU_smith2	TRINITY_DN2932_c0_g1_i11	Macoilin	-22	-21
MMU_smith2	TRINITY_DN297_c0_g1_i11	Protein FAM135A	-19	-21
MMU_smith2	TRINITY_DN3142_c0_g1_i11	Translin-associated protein X	-20	-21
MMU_smith2	TRINITY_DN324669_c0_g1_i1	.	-17	-21
MMU_smith2	TRINITY_DN3475_c0_g1_i1	.	-19	-24
MMU_smith2	TRINITY_DN3880_c0_g2_i4	BTB/POZ domain-containing adapter for CUL3-mediated RhoA degradation protein 2	-15	-15
MMU_smith2	TRINITY_DN3965_c0_g2_i10	GTPase-activating protein and VPS9 domain-containing protein 1	-22	-20
MMU_smith2	TRINITY_DN3993_c0_g1_i1	E3 ubiquitin-protein ligase RMND5A	-16	-17
MMU_smith2	TRINITY_DN409587_c0_g1_i1	.	-16	-20
MMU_smith2	TRINITY_DN425_c0_g1_i8	Calsyntenin-2	-26	-25
MMU_smith2	TRINITY_DN4350_c0_g1_i3	Large ribosomal subunit protein eL19	-17	-21
MMU_smith2	TRINITY_DN4400_c0_g1_i12	Collagen alpha-1(XI) chain	-18	-21
MMU_smith2	TRINITY_DN45390_c0_g1_i1	Mediator of RNA polymerase II transcription subunit 12-like protein	-18	-21
MMU_smith2	TRINITY_DN462_c0_g1_i14	E3 ubiquitin-protein ligase MYCBP2	-10	-21
MMU_smith2	TRINITY_DN4887_c0_g1_i19	tRNA (32-2'-O)-methyltransferase regulator THADA	-13	-16
MMU_smith2	TRINITY_DN5043_c0_g1_i4	Cytoplasmic polyadenylation element-binding protein 4	-16	-21
MMU_smith2	TRINITY_DN55310_c0_g1_i1	.	-17	-23
MMU_smith2	TRINITY_DN5556_c0_g1_i5	Myotubularin-related protein 13	-16	-16
MMU_smith2	TRINITY_DN55617_c0_g2_i2	Zinc fingers and homeoboxes protein 1	-19	-21
MMU_smith2	TRINITY_DN59574_c0_g1_i1	PDZ domain-containing protein 8	-13	-22
MMU_smith2	TRINITY_DN60533_c0_g1_i1	.	-20	-21
MMU_smith2	TRINITY_DN6146_c0_g1_i12	Differentially expressed in FDCP 8	-26	-31
MMU_smith2	TRINITY_DN6508_c0_g1_i10	Lebercilin	-26	-29
MMU_smith2	TRINITY_DN70003_c1_g2_i2	.	-23	-27
MMU_smith2	TRINITY_DN70_c0_g2_i11	Methyl-CpG-binding domain protein 5	-21	-21
MMU_smith2	TRINITY_DN71216_c3_g1_i1	.	-19	-21
MMU_smith2	TRINITY_DN7737_c0_g1_i13	Centlein	-21	-21
MMU_smith2	TRINITY_DN773_c2_g1_i10	Zinc finger ZZ-type and EF-hand domain-containing protein 1	-21	-21
MMU_smith2	TRINITY_DN80_c0_g1_i6	Eukaryotic translation initiation factor 5	-19	-24
MMU_smith2	TRINITY_DN816_c0_g1_i1	.	-20	-22
MMU_smith2	TRINITY_DN9169_c0_g1_i1	.	-20	-16
MMU_smith4	TRINITY_DN10110_c0_g1_i2	FERM, ARHGEF and pleckstrin domain-containing protein 2	-21	-15
MMU_smith4	TRINITY_DN10218_c0_g2_i14	Oxysterol-binding protein-related protein 6	-21	-19
MMU_smith4	TRINITY_DN10613_c0_g1_i4	E3 ubiquitin-protein ligase RNF31	-23	-22
MMU_smith4	TRINITY_DN1097_c0_g1_i18	Formin-binding protein 1-like	-19	-19
MMU_smith4	TRINITY_DN1117_c1_g1_i11	Cytotoxic granule associated RNA binding protein TIA1	-19	-20
MMU_smith4	TRINITY_DN112400_c0_g4_i1	.	-28	-21
MMU_smith4	TRINITY_DN115066_c0_g3_i1	.	-30	-23
MMU_smith4	TRINITY_DN115558_c3_g1_i1	.	-20	-17
MMU_smith4	TRINITY_DN12302_c1_g1_i1	.	-24	-17
MMU_smith4	TRINITY_DN12718_c0_g1_i6	.	-34	-26
MMU_smith4	TRINITY_DN12766_c0_g1_i6	Neuronal acetylcholine receptor subunit alpha-7	-21	-21
MMU_smith4	TRINITY_DN129068_c0_g1_i1	.	-23	-26
MMU_smith4	TRINITY_DN13864_c0_g1_i5	DNA excision repair protein ERCC-6-like 2	-16	-16
MMU_smith4	TRINITY_DN14612_c0_g1_i10	Eukaryotic translation initiation factor 4 gamma 3	-22	-16
MMU_smith4	TRINITY_DN14748_c0_g1_i6	Mitotic spindle assembly checkpoint protein MAD1	-26	-23
MMU_smith4	TRINITY_DN1489_c0_g1_i10	Endoplasmic reticulum membrane-associated RNA degradation protein	-21	-21
MMU_smith4	TRINITY_DN150003_c0_g1_i1	.	-35	-22
MMU_smith4	TRINITY_DN150409_c0_g1_i13	.	-24	-16
MMU_smith4	TRINITY_DN15369_c2_g3_i1	Calcium/manganese antiporter SLC30A10	-27	-27
MMU_smith4	TRINITY_DN16324_c1_g1_i1	.	-19	-19
MMU_smith4	TRINITY_DN167_c1_g2_i1	Nuclear pore complex protein Nup155	-23	-17

MMU_smith4	TRINITY_DN176483_c0_g1_i2	.	-21	-17
MMU_smith4	TRINITY_DN18282_c0_g1_i4	.	-26	-22
MMU_smith4	TRINITY_DN1898_c0_g1_i7	5'-AMP-activated protein kinase subunit beta-2	-31	-23
MMU_smith4	TRINITY_DN194583_c0_g1_i2	.	-25	-23
MMU_smith4	TRINITY_DN19678_c0_g2_i6	Corticotropin-releasing factor receptor 2	-14	-17
MMU_smith4	TRINITY_DN20187_c0_g1_i3	Syntaxin-1B	-27	-24
MMU_smith4	TRINITY_DN20767_c0_g1_i5	WD repeat-containing protein 1	-24	-22
MMU_smith4	TRINITY_DN2096_c0_g1_i1	.	-26	-24
MMU_smith4	TRINITY_DN21109_c0_g1_i2	Eukaryotic translation initiation factor 3 subunit A	-24	-26
MMU_smith4	TRINITY_DN2121_c0_g1_i11	Rapamycin-insensitive companion of mTOR	-26	-17
MMU_smith4	TRINITY_DN2124_c0_g2_i9	SUMO-conjugating enzyme UBC9	-22	-18
MMU_smith4	TRINITY_DN21299_c3_g1_i4	GTPase KRas	-15	-23
MMU_smith4	TRINITY_DN23326_c0_g1_i4	Annexin A8	-19	-19
MMU_smith4	TRINITY_DN2522_c0_g2_i4	Lysine-specific demethylase 3A	-30	-23
MMU_smith4	TRINITY_DN27698_c1_g1_i16	Ankyrin repeat and sterile alpha motif domain-containing protein 1B	-26	-23
MMU_smith4	TRINITY_DN2851_c0_g1_i4	THO complex subunit 5 homolog	-24	-22
MMU_smith4	TRINITY_DN29042_c0_g3_i3	Large ribosomal subunit protein uL3m	-23	-22
MMU_smith4	TRINITY_DN29127_c0_g1_i6	Cyclic AMP-responsive element-binding protein 1	-24	-16
MMU_smith4	TRINITY_DN29569_c0_g1_i1	Endoplasmic reticulum chaperone BiP	-24	-18
MMU_smith4	TRINITY_DN29862_c0_g3_i2	.	-20	-23
MMU_smith4	TRINITY_DN300190_c0_g1_i1	.	-18	-22
MMU_smith4	TRINITY_DN313557_c0_g1_i1	.	-28	-24
MMU_smith4	TRINITY_DN3182_c0_g1_i1	.	-36	-25
MMU_smith4	TRINITY_DN3221_c0_g1_i7	Serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform	-24	-24
MMU_smith4	TRINITY_DN33993_c0_g1_i25	Intraflagellar transport protein 140 homolog	-18	-22
MMU_smith4	TRINITY_DN34898_c0_g1_i7	Arf-GAP with Rho-GAP domain, ANK repeat and PH domain-containing protein 1	-25	-22
MMU_smith4	TRINITY_DN379_c3_g1_i1	.	-21	-24
MMU_smith4	TRINITY_DN3862_c0_g2_i1	DNA mismatch repair protein Msh3	-26	-22
MMU_smith4	TRINITY_DN4103_c0_g1_i6	Gamma-glutamylcyclotransferase	-23	-18
MMU_smith4	TRINITY_DN4105_c0_g2_i2	AN1-type zinc finger protein 1	-27	-25
MMU_smith4	TRINITY_DN4116_c0_g4_i2	Myb/SANT-like DNA-binding domain-containing protein 7	-25	-22
MMU_smith4	TRINITY_DN4233_c0_g1_i1	Transcription elongation factor A protein 3	-32	-21
MMU_smith4	TRINITY_DN4322_c0_g1_i3	Phosphofurin acidic cluster sorting protein 2	-33	-25
MMU_smith4	TRINITY_DN437705_c0_g1_i1	.	-34	-32
MMU_smith4	TRINITY_DN4402_c0_g1_i8	Late secretory pathway protein AVL9 homolog	-21	-22
MMU_smith4	TRINITY_DN44099_c0_g2_i1	Angiopoietin-related protein 1	-20	-17
MMU_smith4	TRINITY_DN447_c0_g2_i1	Tripartite motif-containing protein 6	-16	-16
MMU_smith4	TRINITY_DN4524_c0_g2_i1	Fibronectin type III domain-containing protein 3B	-26	-23
MMU_smith4	TRINITY_DN4604_c0_g2_i2	Carabin	-16	-16
MMU_smith4	TRINITY_DN4606_c0_g2_i9	EF-hand calcium-binding domain-containing protein 11	-24	-18
MMU_smith4	TRINITY_DN466_c10_g1_i1	.	-22	-21
MMU_smith4	TRINITY_DN493_c0_g5_i1	.	-22	-17
MMU_smith4	TRINITY_DN5442_c0_g1_i9	Helicase ARIP4	-22	-21
MMU_smith4	TRINITY_DN55481_c0_g1_i11	Calcyphosin-2	-17	-22
MMU_smith4	TRINITY_DN585_c0_g4_i1	BTB/POZ domain-containing protein 3	-23	-16
MMU_smith4	TRINITY_DN59002_c0_g1_i1	.	-29	-26
MMU_smith4	TRINITY_DN5909_c0_g1_i8	Uncharacterized protein KIAA1671	-26	-17
MMU_smith4	TRINITY_DN6092_c0_g1_i5	WD repeat-containing protein 17	-16	-19
MMU_smith4	TRINITY_DN6374_c0_g2_i15	Glutaminase kidney isoform, mitochondrial	-17	-16
MMU_smith4	TRINITY_DN652_c0_g1_i11	Deleted in azoospermia-like	-18	-15
MMU_smith4	TRINITY_DN693_c0_g2_i3	U3 small nucleolar RNA-interacting protein 2	-21	-24
MMU_smith4	TRINITY_DN6991_c0_g1_i10	Mediator of RNA polymerase II transcription subunit 12	-22	-25
MMU_smith4	TRINITY_DN76153_c0_g1_i1	Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial	-15	-16
MMU_smith4	TRINITY_DN7744_c0_g3_i1	.	-22	-20
MMU_smith4	TRINITY_DN8096_c0_g1_i10	Brain-specific angiogenesis inhibitor 1-associated protein 2-like protein 1	-17	-23
MMU_smith4	TRINITY_DN894_c0_g2_i10	Phosphatidylinositol 4-phosphate 3-kinase C2 domain-containing subunit alpha	-22	-18
MMU_smith4	TRINITY_DN9148_c1_g2_i1	von Willebrand factor A domain-containing protein 5A	-20	-27
MMU_smith4	TRINITY_DN941_c15_g1_i1	Multiple inositol polyphosphate phosphatase 1	-19	-17
MMU_smith4	TRINITY_DN9428_c0_g1_i7	Endogenous retrovirus group FC1 Env polyprotein	-23	-21
MMU_smith4	TRINITY_DN95117_c0_g1_i1	Octanoyl-[acyl-carrier-protein]	-18	-21
MMU_smith4	TRINITY_DN95149_c0_g2_i1	.	-20	-22
MMU_smith4	TRINITY_DN9643_c5_g1_i2	.	-28	-26
MMU_smith4	TRINITY_DN980_c0_g1_i13	Transcription factor E2-alpha	-18	-23
MMU_smith4	TRINITY_DN99871_c0_g1_i1	Ectodysplasin-A receptor-associated adapter protein	-28	-25
MMU_smith4	TRINITY_DN9988_c0_g1_i11	Beta-1,4 N-acetylgalactosaminyltransferase 1	-28	-19

***Notospermus geniculatus* (1 candidate, 61 targets)**

smithID	transcriptID	Blastx	dG PITA	dG RNAHybrid
NGE_smith2	TRINITY_DN10241_c1_g1_i10	Probable RNA-directed DNA polymerase from transposon X-element	-27	-24
NGE_smith2	TRINITY_DN10293_c0_g1_i7	.	-22	-22
NGE_smith2	TRINITY_DN10748_c0_g1_i2	Insulin-like growth factor-binding protein complex acid labile subunit	-24	-22
NGE_smith2	TRINITY_DN10897_c0_g1_i13	Protein AF-9	-30	-23
NGE_smith2	TRINITY_DN11149_c0_g1_i3	.	-27	-25
NGE_smith2	TRINITY_DN1180_c0_g1_i6	Adenosine 5'-monophosphoramidase HINT1	-27	-25
NGE_smith2	TRINITY_DN12440_c0_g1_i2	Protein-serine O-palmitoleoyltransferase porcupine	-28	-20
NGE_smith2	TRINITY_DN129852_c0_g1_i1	.	-24	-27
NGE_smith2	TRINITY_DN13206_c1_g1_i6	.	-22	-22
NGE_smith2	TRINITY_DN13629_c0_g1_i5	Death domain-containing protein 1	-23	-26
NGE_smith2	TRINITY_DN1440_c0_g1_i10	Serpin B11	-28	-23
NGE_smith2	TRINITY_DN14517_c0_g1_i4	Ubiquitin carboxyl-terminal hydrolase 22	-13	-15
NGE_smith2	TRINITY_DN14788_c0_g1_i1	DENN domain-containing protein 5B	-19	-19
NGE_smith2	TRINITY_DN1666_c0_g1_i1	Endoribonuclease LACTB2	-32	-24
NGE_smith2	TRINITY_DN17472_c0_g1_i1	MICAL-like protein 2	-18	-22
NGE_smith2	TRINITY_DN17508_c0_g1_i1	Sex peptide receptor	-19	-19
NGE_smith2	TRINITY_DN18_c0_g1_i10	.	-21	-22
NGE_smith2	TRINITY_DN19517_c0_g1_i1	Cysteine protease ATG4D	-18	-23
NGE_smith2	TRINITY_DN1966_c0_g1_i2	Tektin-1	-25	-24
NGE_smith2	TRINITY_DN19992_c0_g2_i1	Protein O-linked-mannose beta-1,2-N-acetylglucosaminyltransferase 1	-27	-24
NGE_smith2	TRINITY_DN20444_c0_g1_i1	.	-22	-25
NGE_smith2	TRINITY_DN20799_c0_g2_i3	.	-11	-20
NGE_smith2	TRINITY_DN22744_c0_g1_i8	von Willebrand factor D and EGF domain-containing protein	-25	-23
NGE_smith2	TRINITY_DN22764_c0_g1_i1	Adenosine kinase	-16	-23
NGE_smith2	TRINITY_DN2281_c0_g1_i4	.	-21	-15
NGE_smith2	TRINITY_DN22935_c0_g1_i9	Histone H2A deubiquitinase MYSM1	-18	-23
NGE_smith2	TRINITY_DN2315_c2_g1_i3	.	-27	-25

NGE_smith2	TRINITY_DN23438_c0_g1_i10	Liprin-alpha-1	-31	-24
NGE_smith2	TRINITY_DN2469_c0_g1_i1	NAD-dependent protein deacetylase sirtuin-1	-28	-18
NGE_smith2	TRINITY_DN25201_c0_g1_i10	Brain-specific angiogenesis inhibitor 1-associated protein 2	-22	-22
NGE_smith2	TRINITY_DN26556_c0_g1_i2	.	-19	-24
NGE_smith2	TRINITY_DN29026_c1_g1_i1	WW domain-binding protein 4	-13	-17
NGE_smith2	TRINITY_DN3408_c3_g1_i1	UPF0462 protein C4orf33 homolog	-24	-19
NGE_smith2	TRINITY_DN35498_c0_g1_i2	Protein lin-54 homolog	-17	-24
NGE_smith2	TRINITY_DN36481_c0_g1_i2	Guanylate cyclase 2G	-20	-17
NGE_smith2	TRINITY_DN39607_c0_g1_i12	ATP-dependent DNA helicase PIF1	-28	-20
NGE_smith2	TRINITY_DN4041_c0_g1_i2	Nucleolar protein 8	-21	-25
NGE_smith2	TRINITY_DN4074_c0_g1_i1	.	-19	-23
NGE_smith2	TRINITY_DN41159_c0_g1_i1	.	-29	-24
NGE_smith2	TRINITY_DN41955_c0_g1_i1	.	-24	-15
NGE_smith2	TRINITY_DN4196_c0_g1_i14	Harmonin	-20	-23
NGE_smith2	TRINITY_DN45733_c0_g1_i1	Transposon Ty3-I Gag-Pol polyprotein	-25	-19
NGE_smith2	TRINITY_DN47683_c0_g1_i3	MFS-type transporter clz9	-36	-27
NGE_smith2	TRINITY_DN4820_c0_g1_i1	DDB1- and CUL4-associated factor 13	-30	-25
NGE_smith2	TRINITY_DN5088_c1_g1_i1	Zinc finger protein 782	-25	-24
NGE_smith2	TRINITY_DN51784_c0_g1_i1	.	-13	-20
NGE_smith2	TRINITY_DN55757_c0_g1_i1	.	-21	-24
NGE_smith2	TRINITY_DN5971_c0_g1_i10	Pre-mRNA-processing factor 39	-20	-20
NGE_smith2	TRINITY_DN66_c0_g1_i2	Transforming growth factor-beta-induced protein ig-h3	-29	-23
NGE_smith2	TRINITY_DN68160_c0_g1_i15	Transcription factor SPT20 homolog	-26	-21
NGE_smith2	TRINITY_DN69138_c0_g1_i1	.	-28	-15
NGE_smith2	TRINITY_DN70104_c0_g2_i4	.	-35	-27
NGE_smith2	TRINITY_DN7104_c0_g1_i1	Meso-2,3-butanediol dehydrogenase	-25	-19
NGE_smith2	TRINITY_DN7381_c0_g1_i3	RanBP-type and C3HC4-type zinc finger-containing protein 1	-30	-22
NGE_smith2	TRINITY_DN7543_c0_g1_i2	tRNA-dihydrouridine(16/17) synthase [NAD(P)(+)]-like	-10	-15
NGE_smith2	TRINITY_DN948_c0_g2_i12	Proline iminopeptidase	-21	-24
NGE_smith2	TRINITY_DN9673_c0_g1_i11	Cyclin-Y-like protein 1	-22	-22
NGE_smith2	TRINITY_DN97_c0_g1_i1	Twitchin	-27	-21
NGE_smith2	TRINITY_DN9832_c1_g1_i6	.	-9	-17
NGE_smith2	TRINITY_DN992_c2_g1_i1	Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform	-19	-17
NGE_smith2	TRINITY_DN9982_c0_g1_i14	Ceramide kinase	-20	-23
		Paracentrotus lividus **(6 candidates, 166 targets)**		
smithID	**transcriptID**	**Blastx**	**dG PITA**	**dG RNAHybrid**
PLI_smith10	TRINITY_DN1006_c0_g1_i10	Hypoxia-inducible factor 1-alpha inhibitor	-12	-16
PLI_smith10	TRINITY_DN104616_c1_g1_i2	.	-18	-19
PLI_smith10	TRINITY_DN106060_c0_g2_i1	.	-17	-21
PLI_smith10	TRINITY_DN109025_c0_g1_i2	.	-20	-20
PLI_smith10	TRINITY_DN121620_c0_g1_i1	Neuropeptides capa receptor	-11	-16
PLI_smith10	TRINITY_DN126_c0_g1_i13	2-oxoglutarate dehydrogenase complex component E1	-23	-16
PLI_smith10	TRINITY_DN155966_c0_g1_i2	.	-20	-20
PLI_smith10	TRINITY_DN158_c0_g2_i1	Proteasome subunit alpha type-2	-11	-16
PLI_smith10	TRINITY_DN171245_c0_g1_i4	.	-14	-16
PLI_smith10	TRINITY_DN17172_c0_g1_i1	Spermatogenesis-associated protein 24	-11	-17
PLI_smith10	TRINITY_DN180589_c0_g1_i1	.	-17	-16
PLI_smith10	TRINITY_DN1893_c1_g1_i2	.	-17	-16
PLI_smith10	TRINITY_DN190896_c0_g1_i2	Lysosome-associated membrane glycoprotein 5	-14	-16
PLI_smith10	TRINITY_DN1964_c0_g1_i1	Transmembrane protein 19	-14	-15
PLI_smith10	TRINITY_DN20685_c0_g1_i1	Next to BRCA1 gene 1 protein	-21	-22
PLI_smith10	TRINITY_DN210229_c0_g1_i1	.	-17	-20
PLI_smith10	TRINITY_DN21978_c0_g1_i1	G1/S-specific cyclin-D2	-12	-17
PLI_smith10	TRINITY_DN22925_c0_g2_i2	Stabilizer of axonemal microtubules 4	-12	-16
PLI_smith10	TRINITY_DN2328_c1_g1_i1	.	-11	-16
PLI_smith10	TRINITY_DN2339_c0_g1_i8	.	-21	-23
PLI_smith10	TRINITY_DN2432_c0_g1_i11	Probable transmembrane reductase CYB561D1	-15	-16
PLI_smith10	TRINITY_DN25464_c0_g1_i3	.	-17	-23
PLI_smith10	TRINITY_DN2966_c0_g1_i10	Dehydrogenase/reductase SDR family member 12	-15	-16
PLI_smith10	TRINITY_DN29902_c0_g1_i1	Parkin coregulated gene protein homolog	-16	-29
PLI_smith10	TRINITY_DN30197_c0_g1_i2	.	-13	-16
PLI_smith10	TRINITY_DN3084_c0_g1_i10	.	-12	-16
PLI_smith10	TRINITY_DN31318_c0_g1_i1	Fibropellin-1	-16	-16
PLI_smith10	TRINITY_DN3345_c0_g2_i10	Claspin	-16	-21
PLI_smith10	TRINITY_DN3382_c0_g1_i10	U2 small nuclear ribonucleoprotein auxiliary factor 35 kDa subunit-related protein 2	-17	-22
PLI_smith10	TRINITY_DN3431_c0_g1_i10	Vacuolar protein sorting-associated protein 16 homolog	-11	-15
PLI_smith10	TRINITY_DN34571_c1_g1_i3	Thiosulfate sulfurtransferase/rhodanese-like domain-containing protein 2	-9	-19
PLI_smith10	TRINITY_DN36625_c0_g1_i3	Testis-specific serine/threonine-protein kinase 2	-11	-17
PLI_smith10	TRINITY_DN39837_c0_g1_i14	Myosin-10	-11	-16
PLI_smith10	TRINITY_DN3995_c1_g1_i11	LIM and calponin homology domains-containing protein 1	-19	-16
PLI_smith10	TRINITY_DN39963_c0_g1_i12	Tripartite motif-containing protein 59	-11	-17
PLI_smith10	TRINITY_DN409_c0_g1_i1	.	-27	-28
PLI_smith10	TRINITY_DN42158_c0_g1_i11	Medium-chain acyl-CoA ligase ACSF2, mitochondrial	-12	-17
PLI_smith10	TRINITY_DN4312_c0_g1_i1	Probable ATP-dependent RNA helicase DDX6	-9	-16
PLI_smith10	TRINITY_DN4428_c9_g1_i2	Neuronal acetylcholine receptor subunit alpha-3	-14	-16
PLI_smith10	TRINITY_DN52426_c0_g1_i1	.	-19	-23
PLI_smith10	TRINITY_DN52746_c0_g1_i1	Dynein light chain Tctex-type 5	-18	-22
PLI_smith10	TRINITY_DN5280_c0_g1_i1	WD repeat-containing protein 38	-17	-20
PLI_smith10	TRINITY_DN5337_c1_g1_i3	Cryptochrome-1	-12	-15
PLI_smith10	TRINITY_DN5436_c0_g3_i1	Hyalin	-21	-20
PLI_smith10	TRINITY_DN5725_c0_g1_i10	Sarcalumenin	-11	-17
PLI_smith10	TRINITY_DN5742_c0_g1_i16	AP-1 complex subunit sigma-2	-31	-30
PLI_smith10	TRINITY_DN5808_c0_g2_i5	Large ribosomal subunit protein P2	-21	-22
PLI_smith10	TRINITY_DN6277_c0_g2_i2	Tyrosine kinase receptor Cad96Ca	-11	-17
PLI_smith10	TRINITY_DN6553_c0_g2_i2	Endonuclease/exonuclease/phosphatase family domain-containing protein 1	-11	-16
PLI_smith10	TRINITY_DN656_c0_g1_i10	.	-12	-17
PLI_smith10	TRINITY_DN73259_c1_g1_i4	Ubiquitin	-18	-16
PLI_smith10	TRINITY_DN7454_c0_g1_i2	Dehydrogenase/reductase SDR family member 1	-13	-17
PLI_smith10	TRINITY_DN761_c0_g1_i18	Fibropellin-1	-15	-16
PLI_smith10	TRINITY_DN79262_c0_g1_i2	.	-17	-20
PLI_smith10	TRINITY_DN8402_c0_g2_i1	.	-13	-17
PLI_smith10	TRINITY_DN8919_c0_g1_i3	Alpha-N-acetylglucosaminidase	-19	-21
PLI_smith10	TRINITY_DN9514_c0_g1_i1	MAP/microtubule affinity-regulating kinase 3	-13	-16
PLI_smith10	TRINITY_DN9565_c0_g1_i1	Y+L amino acid transporter 2	-20	-21

PLI_smith10	TRINITY_DN98320_c0_g1_i2	L-rhamnose-binding lectin CSL3	-11	-17
PLI_smith14	TRINITY_DN11520_c0_g1_i5	Frizzled-5	-22	-16
PLI_smith14	TRINITY_DN12869_c0_g1_i1	Diacylglycerol kinase theta	-21	-26
PLI_smith14	TRINITY_DN13943_c0_g1_i2	GDP-fucose protein O-fucosyltransferase 2	-30	-28
PLI_smith14	TRINITY_DN16506_c0_g1_i11	.	-26	-23
PLI_smith14	TRINITY_DN165_c0_g1_i4	Enzymatic polyprotein	-28	-26
PLI_smith14	TRINITY_DN1749_c0_g1_i7	STE20-related kinase adapter protein alpha	-27	-20
PLI_smith14	TRINITY_DN189091_c0_g1_i10	Glutathione hydrolase 1 proenzyme	-26	-26
PLI_smith14	TRINITY_DN22034_c1_g1_i3	.	-31	-26
PLI_smith14	TRINITY_DN2475_c0_g1_i2	Metal regulatory transcription factor 1	-26	-22
PLI_smith14	TRINITY_DN25202_c0_g1_i4	ATP-binding cassette sub-family C member 9	-17	-17
PLI_smith14	TRINITY_DN281092_c0_g1_i1	.	-27	-20
PLI_smith14	TRINITY_DN2874_c0_g1_i3	DNA damage-inducible transcript 4-like protein	-23	-15
PLI_smith14	TRINITY_DN28958_c0_g1_i10	Glycosyltransferase-like domain-containing protein 1	-31	-26
PLI_smith14	TRINITY_DN29889_c0_g1_i1	Transmembrane protein 179B	-25	-17
PLI_smith14	TRINITY_DN30693_c0_g2_i1	.	-33	-25
PLI_smith14	TRINITY_DN319_c0_g1_i10	Patched domain-containing protein 3	-26	-23
PLI_smith14	TRINITY_DN3507_c0_g2_i1	Gamma-interferon-inducible lysosomal thiol reductase	-23	-18
PLI_smith14	TRINITY_DN3737_c0_g1_i11	Cyclin-T2	-17	-18
PLI_smith14	TRINITY_DN4841_c0_g1_i11	E3 ubiquitin-protein ligase CCNB1IP1	-18	-16
PLI_smith14	TRINITY_DN5385_c0_g1_i12	Golgi apparatus protein 1	-21	-19
PLI_smith14	TRINITY_DN6740_c0_g2_i4	.	-25	-15
PLI_smith14	TRINITY_DN8453_c0_g1_i6	Probable RNA-directed DNA polymerase from transposon BS	-24	-16
PLI_smith14	TRINITY_DN8578_c0_g1_i1	Tubby-related protein 4	-26	-23
PLI_smith1	TRINITY_DN109679_c0_g1_i4	Cytochrome P450 2U1	-19	-16
PLI_smith1	TRINITY_DN11334_c0_g1_i10	Serine/threonine-protein kinase 32B	-24	-25
PLI_smith1	TRINITY_DN11624_c0_g2_i4	.	-16	-21
PLI_smith1	TRINITY_DN1432_c1_g1_i10	Ubiquitin carboxyl-terminal hydrolase 49	-11	-15
PLI_smith1	TRINITY_DN14377_c0_g1_i1	3 beta-hydroxysteroid dehydrogenase/Delta 5-->4-isomerase type 2	-19	-23
PLI_smith1	TRINITY_DN165_c0_g1_i4	Enzymatic polyprotein	-21	-22
PLI_smith1	TRINITY_DN166476_c0_g1_i4	.	-18	-18
PLI_smith1	TRINITY_DN17251_c0_g1_i2	Protein arginine N-methyltransferase 6	-23	-21
PLI_smith1	TRINITY_DN1876_c0_g1_i11	TATA-box-binding protein	-27	-28
PLI_smith1	TRINITY_DN2046_c2_g1_i1	Nocturnin	-19	-18
PLI_smith1	TRINITY_DN23398_c0_g1_i3	.	-18	-18
PLI_smith1	TRINITY_DN23978_c1_g1_i4	.	-18	-18
PLI_smith1	TRINITY_DN2438_c0_g1_i11	Protein Wnt-5a	-18	-19
PLI_smith1	TRINITY_DN315988_c0_g1_i1	Fatty acid-binding protein	-16	-18
PLI_smith1	TRINITY_DN3609_c0_g1_i13	HCLS1-binding protein 3	-13	-19
PLI_smith1	TRINITY_DN44222_c0_g1_i3	.	-18	-18
PLI_smith1	TRINITY_DN593_c0_g1_i1	LanC-like protein 2	-22	-26
PLI_smith1	TRINITY_DN6330_c0_g1_i1	Protocadherin Fat 3	-24	-21
PLI_smith1	TRINITY_DN640_c0_g2_i1	.	-15	-18
PLI_smith1	TRINITY_DN7484_c0_g2_i1	Pyruvate dehydrogenase phosphatase regulatory subunit, mitochondrial	-17	-17
PLI_smith1	TRINITY_DN8571_c2_g1_i11	Tetratricopeptide repeat protein 33	-9	-15
PLI_smith1	TRINITY_DN8692_c0_g1_i7	Mucin-5AC	-19	-16
PLI_smith1	TRINITY_DN92271_c0_g1_i1	.	-22	-21
PLI_smith1	TRINITY_DN948_c0_g2_i7	Deoxyhypusine synthase	-22	-19
PLI_smith28	TRINITY_DN13705_c0_g1_i1	4-hydroxyphenylpyruvate dioxygenase	-20	-23
PLI_smith28	TRINITY_DN13943_c0_g1_i2	GDP-fucose protein O-fucosyltransferase 2	-14	-16
PLI_smith28	TRINITY_DN20633_c0_g1_i13	Aminomethyltransferase, mitochondrial	-15	-17
PLI_smith28	TRINITY_DN2159_c0_g1_i13	Low-density lipoprotein receptor-related protein 5	-19	-23
PLI_smith28	TRINITY_DN2172_c0_g1_i5	Mediator of RNA polymerase II transcription subunit 17	-14	-15
PLI_smith28	TRINITY_DN23213_c0_g1_i10	Transient receptor potential cation channel subfamily A member 1	-18	-23
PLI_smith28	TRINITY_DN2960_c0_g1_i11	Zinc finger protein castor homolog 1	-17	-15
PLI_smith28	TRINITY_DN3292_c1_g1_i11	Guanine nucleotide-binding protein-like 3 homolog	-18	-20
PLI_smith28	TRINITY_DN3367_c0_g1_i1	Histone-binding protein N1/N2	-15	-18
PLI_smith28	TRINITY_DN3908_c0_g1_i12	Univin	-18	-20
PLI_smith28	TRINITY_DN5151_c0_g1_i7	Valine--tRNA ligase	-18	-16
PLI_smith28	TRINITY_DN5249_c0_g4_i10	Isovaleryl-CoA dehydrogenase, mitochondrial	-20	-18
PLI_smith28	TRINITY_DN7756_c0_g1_i14	Cytoplasmic tRNA 2-thiolation protein 1	-21	-20
PLI_smith28	TRINITY_DN7849_c0_g1_i1	.	-24	-21
PLI_smith28	TRINITY_DN95120_c0_g1_i3	LINE-1 retrotransposable element ORF2 protein	-24	-28
PLI_smith28	TRINITY_DN9544_c0_g1_i2	DnaJ homolog subfamily C member 28	-17	-17
PLI_smith4	TRINITY_DN11241_c1_g1_i12	Heparanase	-20	-19
PLI_smith4	TRINITY_DN1174_c0_g1_i2	.	-12	-15
PLI_smith4	TRINITY_DN1305_c1_g1_i9	Retrovirus-related Pol polyprotein from transposon 412	-16	-17
PLI_smith4	TRINITY_DN13156_c0_g1_i10	Histone-lysine N-methyltransferase PRDM9	-21	-26
PLI_smith4	TRINITY_DN15556_c0_g2_i3	Ankyrin repeat domain-containing protein 29	-21	-23
PLI_smith4	TRINITY_DN1633_c0_g1_i10	LLGL scribble cell polarity complex component 2	-23	-18
PLI_smith4	TRINITY_DN18784_c0_g1_i1	Paraneoplastic antigen Ma3 homolog	-19	-24
PLI_smith4	TRINITY_DN19515_c1_g1_i3	Sperm motility kinase X	-19	-24
PLI_smith4	TRINITY_DN234618_c0_g1_i1	.	-18	-26
PLI_smith4	TRINITY_DN25464_c0_g1_i1	.	-18	-18
PLI_smith4	TRINITY_DN27_c0_g1_i1	Collagen alpha-2(I) chain	-21	-26
PLI_smith4	TRINITY_DN3202_c1_g1_i3	Mediator of RNA polymerase II transcription subunit 20	-19	-15
PLI_smith4	TRINITY_DN44158_c0_g1_i5	Retrovirus-related Pol polyprotein from transposon 17.6	-11	-17
PLI_smith4	TRINITY_DN5249_c0_g4_i10	Isovaleryl-CoA dehydrogenase, mitochondrial	-22	-21
PLI_smith4	TRINITY_DN54892_c0_g2_i2	.	-21	-28
PLI_smith4	TRINITY_DN56559_c0_g1_i1	Divergent protein kinase domain 1C	-21	-24
PLI_smith4	TRINITY_DN635_c3_g1_i2	SMC5-SMC6 complex localization factor protein 1	-10	-17
PLI_smith4	TRINITY_DN65945_c0_g1_i1	.	-18	-23
PLI_smith4	TRINITY_DN6684_c0_g2_i3	.	-19	-23
PLI_smith4	TRINITY_DN7207_c0_g1_i11	Serine/threonine-protein phosphatase PP1	-21	-28
PLI_smith4	TRINITY_DN79806_c0_g1_i2	Latent-transforming growth factor beta-binding protein 4	-17	-17
PLI_smith4	TRINITY_DN84988_c0_g2_i1	.	-20	-24
PLI_smith4	TRINITY_DN8582_c0_g1_i10	UPF0415 protein C7orf25 homolog	-9	-15
PLI_smith7	TRINITY_DN10119_c0_g1_i3	E3 ubiquitin-protein ligase UBR2	-22	-24
PLI_smith7	TRINITY_DN10126_c0_g1_i10	.	-17	-16
PLI_smith7	TRINITY_DN10910_c0_g1_i1	Somatomedin-B and thrombospondin type-1 domain-containing protein	-22	-26
PLI_smith7	TRINITY_DN1252_c0_g1_i2	Deleted in malignant brain tumors 1 protein	-18	-19
PLI_smith7	TRINITY_DN1641_c0_g1_i1	.	-13	-19
PLI_smith7	TRINITY_DN177_c0_g2_i11	D-beta-hydroxybutyrate dehydrogenase	-16	-24
PLI_smith7	TRINITY_DN205_c0_g1_i2	Small integral membrane protein 19	-19	-16
PLI_smith7	TRINITY_DN23073_c0_g1_i2	Antiviral innate immune response receptor RIG-I	-15	-21

PLI_smith7	TRINITY_DN2663_c0_g1_i10	Paxillin	-19	-24
PLI_smith7	TRINITY_DN2778_c0_g1_i17	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10	-12	-16
PLI_smith7	TRINITY_DN33200_c0_g1_i4	Myocilin	-19	-24
PLI_smith7	TRINITY_DN36814_c0_g1_i2	Zinc finger protein 605	-28	-25
PLI_smith7	TRINITY_DN4092_c0_g1_i1	Delta-1-pyrroline-5-carboxylate synthase	-20	-18
PLI_smith7	TRINITY_DN44026_c0_g1_i6	.	-15	-19
PLI_smith7	TRINITY_DN4751_c0_g1_i6	Roundabout homolog 2	-26	-17
PLI_smith7	TRINITY_DN6133_c2_g1_i2	.	-21	-22
PLI_smith7	TRINITY_DN61926_c0_g1_i1	Ras-related protein Rab-10	-24	-16
PLI_smith7	TRINITY_DN6553_c0_g2_i2	Endonuclease/exonuclease/phosphatase family domain-containing protein 1	-28	-23
PLI_smith7	TRINITY_DN6701_c0_g2_i1	Methylosome protein WDR77	-23	-24
PLI_smith7	TRINITY_DN7338_c0_g1_i10	Ubiquitin-conjugating enzyme E2 L3	-21	-19
PLI_smith7	TRINITY_DN833_c0_g1_i10	Presenilin-1	-9	-22
		***Popillia japonica* (5 candidates, 194 targets)**		
smithID	**transcriptID**	**Blastx**	**dG PITA**	**dG RNAHybrid**
PJA_smith11	TRINITY_DN10495_c0_g1_i2	.	-16	-15
PJA_smith11	TRINITY_DN11249_c0_g1_i1	.	-17	-22
PJA_smith11	TRINITY_DN1133_c0_g2_i1	Serine/threonine-protein phosphatase 2B catalytic subunit 3	-10	-19
PJA_smith11	TRINITY_DN1462_c0_g1_i1	Exportin-1	-18	-22
PJA_smith11	TRINITY_DN1579_c0_g1_i13	V-type proton ATPase 116 kDa subunit a1	-16	-17
PJA_smith11	TRINITY_DN1754_c0_g1_i10	Extracellular serine/threonine protein CG31145	-13	-16
PJA_smith11	TRINITY_DN18023_c0_g1_i3	Retrovirus-related Pol polyprotein from transposon 297	-18	-23
PJA_smith11	TRINITY_DN1864_c0_g1_i11	Transposon Tf2-11 polyprotein	-12	-18
PJA_smith11	TRINITY_DN21502_c0_g1_i10	Copper transport protein ATOX1	-18	-24
PJA_smith11	TRINITY_DN2457_c0_g1_i6	Palmitoyltransferase app	-15	-20
PJA_smith11	TRINITY_DN2658_c1_g1_i1	Androgen-dependent TFPI-regulating protein	-16	-21
PJA_smith11	TRINITY_DN30209_c0_g1_i5	Peptidoglycan-recognition protein 3	-18	-19
PJA_smith11	TRINITY_DN3120_c0_g2_i1	Initiator protein NS1	-10	-15
PJA_smith11	TRINITY_DN3307_c0_g1_i2	Metabotropic glycine receptor	-20	-24
PJA_smith11	TRINITY_DN38860_c0_g1_i1	.	-15	-15
PJA_smith11	TRINITY_DN4407_c0_g1_i15	Coatomer subunit gamma	-10	-15
PJA_smith11	TRINITY_DN4680_c0_g1_i6	Transmembrane protein 203	-16	-21
PJA_smith11	TRINITY_DN4711_c0_g1_i10	RNA-directed DNA polymerase from mobile element jockey	-12	-15
PJA_smith11	TRINITY_DN4892_c0_g1_i2	Thioredoxin, mitochondrial	-18	-22
PJA_smith11	TRINITY_DN551_c0_g1_i10	Adenylate kinase 7	-11	-17
PJA_smith11	TRINITY_DN6854_c0_g1_i3	NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial	-10	-20
PJA_smith11	TRINITY_DN6972_c0_g1_i2	RAB6A-GEF complex partner protein 2	-15	-20
PJA_smith11	TRINITY_DN7026_c0_g1_i1	Serine protease snake	-16	-22
PJA_smith11	TRINITY_DN70980_c0_g1_i1	UPF0669 protein C6orf120 homolog	-17	-22
PJA_smith11	TRINITY_DN7235_c0_g1_i3	.	-18	-17
PJA_smith11	TRINITY_DN811_c0_g1_i3	Mannosyl-oligosaccharide glucosidase	-16	-24
PJA_smith1	TRINITY_DN1239_c0_g1_i1	Cytoplasmic polyadenylation element-binding protein 1-B	-18	-18
PJA_smith1	TRINITY_DN1286_c0_g1_i10	Solute carrier organic anion transporter family member 74D	-14	-17
PJA_smith1	TRINITY_DN13080_c0_g1_i1	Transposable element Tc1 transposase	-16	-19
PJA_smith1	TRINITY_DN14952_c0_g1_i2	Phenoloxidase-activating factor 3	-12	-15
PJA_smith1	TRINITY_DN15949_c0_g1_i1	Proton-coupled zinc antiporter SLC30A9, mitochondrial	-13	-18
PJA_smith1	TRINITY_DN1680_c0_g1_i14	.	-19	-16
PJA_smith1	TRINITY_DN18410_c0_g1_i1	.	-17	-22
PJA_smith1	TRINITY_DN1885_c0_g1_i13	Protein strawberry notch	-18	-18
PJA_smith1	TRINITY_DN2275_c0_g1_i10	Protein chiffon	-16	-21
PJA_smith1	TRINITY_DN2287_c0_g1_i10	Kinesin-associated protein 3	-18	-20
PJA_smith1	TRINITY_DN23860_c0_g1_i2	Serine protease Hayan	-20	-20
PJA_smith1	TRINITY_DN2547_c1_g1_i5	Regucalcin	-10	-19
PJA_smith1	TRINITY_DN2894_c0_g4_i1	Retrovirus-related Pol polyprotein from transposon TNT 1-94	-20	-23
PJA_smith1	TRINITY_DN291_c1_g1_i15	.	-16	-18
PJA_smith1	TRINITY_DN2936_c0_g1_i2	Chitin deacetylase 1	-12	-15
PJA_smith1	TRINITY_DN30763_c0_g1_i10	Importin subunit alpha-7	-16	-18
PJA_smith1	TRINITY_DN37106_c1_g1_i3	Transposable element Tcb1 transposase	-21	-21
PJA_smith1	TRINITY_DN3783_c0_g1_i1	.	-19	-19
PJA_smith1	TRINITY_DN3939_c0_g1_i4	DEAD-box helicase Dbp80	-13	-15
PJA_smith1	TRINITY_DN466_c0_g1_i11	Neurogenic locus notch homolog protein 1	-11	-21
PJA_smith1	TRINITY_DN4754_c0_g1_i10	Retrovirus-related Pol polyprotein from transposon TNT 1-94	-15	-19
PJA_smith1	TRINITY_DN4998_c0_g1_i11	KICSTOR complex protein SZT2	-15	-20
PJA_smith1	TRINITY_DN5122_c0_g1_i1	Fasciclin-1	-17	-19
PJA_smith1	TRINITY_DN57013_c0_g1_i2	UPF0488 protein CG14286	-17	-21
PJA_smith1	TRINITY_DN6226_c0_g1_i2	DNA-directed RNA polymerase III subunit RPC2	-17	-17
PJA_smith1	TRINITY_DN642_c0_g1_i1	X-box-binding protein 1	-17	-21
PJA_smith1	TRINITY_DN694_c0_g1_i2	Disks large-associated protein 1	-16	-19
PJA_smith1	TRINITY_DN7329_c0_g1_i1	Small G protein signaling modulator 3	-18	-24
PJA_smith1	TRINITY_DN7546_c0_g1_i1	.	-17	-18
PJA_smith1	TRINITY_DN7638_c0_g1_i14	Splicing factor 3B subunit 3	-20	-20
PJA_smith1	TRINITY_DN8715_c0_g1_i10	TBC1 domain family member 12	-18	-17
PJA_smith1	TRINITY_DN999_c0_g1_i10	Uroporphyrinogen decarboxylase	-16	-20
PJA_smith14	TRINITY_DN10437_c0_g2_i10	EH domain-binding protein 1	-13	-16
PJA_smith14	TRINITY_DN10462_c0_g1_i1	DNA-directed RNA polymerase I subunit RPA43	-18	-20
PJA_smith14	TRINITY_DN1118_c0_g2_i2	Tyrosine-protein kinase Btk	-11	-19
PJA_smith14	TRINITY_DN11827_c0_g1_i1	Malate dehydrogenase, glyoxysomal	-16	-17
PJA_smith14	TRINITY_DN126390_c0_g1_i1	Xaa-Pro dipeptidase	-16	-19
PJA_smith14	TRINITY_DN1496_c0_g3_i2	Restin homolog	-10	-15
PJA_smith14	TRINITY_DN1881_c0_g1_i1	Putative tricarboxylate transport protein, mitochondrial	-14	-20
PJA_smith14	TRINITY_DN1919_c0_g2_i3	CTD nuclear envelope phosphatase 1 homolog	-13	-15
PJA_smith14	TRINITY_DN216_c0_g1_i10	.	-18	-21
PJA_smith14	TRINITY_DN2203_c0_g1_i1	.	-19	-22
PJA_smith14	TRINITY_DN22327_c0_g2_i1	.	-18	-19
PJA_smith14	TRINITY_DN2260_c0_g1_i3	Serine protease snake	-16	-19
PJA_smith14	TRINITY_DN23134_c0_g1_i1	Zinc finger protein 280D	-20	-15
PJA_smith14	TRINITY_DN244_c0_g1_i10	Serine/threonine-protein kinase Genghis Khan	-15	-16
PJA_smith14	TRINITY_DN262_c0_g2_i1	Complexin	-14	-16
PJA_smith14	TRINITY_DN27105_c0_g4_i1	PGC-1 and ERR-induced regulator in muscle protein 1	-24	-23
PJA_smith14	TRINITY_DN2829_c0_g1_i9	Endothelin-converting enzyme homolog	-18	-20
PJA_smith14	TRINITY_DN37065_c0_g1_i6	Sodium-coupled monocarboxylate transporter 2	-20	-17
PJA_smith14	TRINITY_DN40490_c0_g1_i1	.	-16	-16
PJA_smith14	TRINITY_DN4201_c0_g1_i1	Adenosine receptor A2a	-13	-15

PJA_smith14	TRINITY_DN436_c0_g1_i12	A disintegrin and metalloproteinase with thrombospondin motifs 20	-18	-16
PJA_smith14	TRINITY_DN4789_c0_g1_i2	Leucine-rich repeat-containing protein 20	-15	-21
PJA_smith14	TRINITY_DN526_c1_g1_i10	Tropomyosin-2	-21	-24
PJA_smith14	TRINITY_DN5331_c0_g1_i1	Probable pseudouridine-5'-phosphatase	-28	-23
PJA_smith14	TRINITY_DN5395_c0_g2_i2	Mariner Mos1 transposase	-13	-18
PJA_smith14	TRINITY_DN543_c0_g1_i19	5'-nucleotidase domain-containing protein 3	-19	-15
PJA_smith14	TRINITY_DN551_c0_g1_i10	Adenylate kinase 7	-13	-16
PJA_smith14	TRINITY_DN564_c0_g2_i2	Chymotrypsin-2	-14	-15
PJA_smith14	TRINITY_DN5764_c0_g1_i7	Transposable element Tcb2 transposase	-20	-19
PJA_smith14	TRINITY_DN6853_c0_g1_i13	RNA-directed DNA polymerase from mobile element jockey	-20	-24
PJA_smith14	TRINITY_DN69215_c0_g2_i8	BTB/POZ domain-containing protein KCTD3	-18	-15
PJA_smith14	TRINITY_DN718_c0_g1_i2	Scaffold attachment factor B2	-15	-15
PJA_smith14	TRINITY_DN749_c0_g1_i10	PH and SEC7 domain-containing protein	-20	-24
PJA_smith14	TRINITY_DN7541_c0_g1_i1	MFS-type transporter clz9	-26	-23
PJA_smith14	TRINITY_DN9134_c0_g1_i10	Zinc finger homeobox protein 3	-14	-20
PJA_smith14	TRINITY_DN92412_c0_g1_i1	.	-11	-15
PJA_smith14	TRINITY_DN92_c0_g2_i11	Heterogeneous nuclear ribonucleoprotein R	-12	-16
PJA_smith14	TRINITY_DN94716_c0_g1_i1	Retrovirus-related Pol polyprotein from transposon 17.6	-20	-22
PJA_smith5	TRINITY_DN10017_c0_g1_i12	Tigger transposable element-derived protein 4	-30	-19
PJA_smith5	TRINITY_DN10594_c0_g2_i1	.	-23	-22
PJA_smith5	TRINITY_DN161225_c0_g1_i1	.	-27	-19
PJA_smith5	TRINITY_DN17928_c0_g1_i2	.	-24	-23
PJA_smith5	TRINITY_DN21580_c1_g1_i13	.	-27	-20
PJA_smith5	TRINITY_DN2288_c0_g1_i1	.	-20	-21
PJA_smith5	TRINITY_DN2358_c0_g1_i18	Ca(2+)/calmodulin-responsive adenylate cyclase	-21	-20
PJA_smith5	TRINITY_DN2545_c0_g1_i1	Sialin	-24	-19
PJA_smith5	TRINITY_DN2945_c1_g5_i1	Actin-related protein 6	-20	-21
PJA_smith5	TRINITY_DN297_c0_g1_i1	.	-23	-20
PJA_smith5	TRINITY_DN3110_c1_g1_i2	.	-20	-20
PJA_smith5	TRINITY_DN3760_c1_g1_i11	PHAF1 protein CG7083	-24	-17
PJA_smith5	TRINITY_DN42345_c0_g1_i4	Retrovirus-related Pol polyprotein from transposon TNT 1-94	-27	-19
PJA_smith5	TRINITY_DN4641_c0_g1_i1	.	-24	-19
PJA_smith5	TRINITY_DN48850_c0_g1_i4	DDB1- and CUL4-associated factor 15	-25	-20
PJA_smith5	TRINITY_DN4945_c0_g1_i5	Potassium channel subfamily K member 9	-23	-16
PJA_smith5	TRINITY_DN4973_c0_g1_i3	Leucine-rich repeat-containing protein 49	-25	-20
PJA_smith5	TRINITY_DN5197_c0_g1_i9	Zinc finger protein 271	-27	-21
PJA_smith5	TRINITY_DN523_c0_g1_i10	Nuclear receptor coactivator 7	-16	-19
PJA_smith5	TRINITY_DN5321_c0_g1_i5	Protein yellow	-14	-19
PJA_smith5	TRINITY_DN5744_c0_g1_i1	RILP-like protein homolog	-14	-15
PJA_smith5	TRINITY_DN578_c0_g1_i11	Protein muscleblind	-23	-20
PJA_smith5	TRINITY_DN6246_c0_g1_i1	Organic cation transporter protein	-26	-15
PJA_smith5	TRINITY_DN7253_c0_g1_i3	Proton channel OtopLc	-25	-20
PJA_smith5	TRINITY_DN83471_c0_g1_i1	Phosphoenolpyruvate carboxykinase [GTP]	-15	-21
PJA_smith5	TRINITY_DN83_c0_g3_i1	Protein FAM76A	-22	-15
PJA_smith5	TRINITY_DN93_c1_g1_i10	Zinc finger FYVE domain-containing protein 26 homolog	-21	-19
PJA_smith5	TRINITY_DN9723_c0_g1_i2	Thymidylate kinase	-21	-22
PJA_smith5	TRINITY_DN992_c0_g1_i12	Carnitine O-acetyltransferase	-22	-21
PJA_smith9	TRINITY_DN10453_c0_g3_i1	.	-15	-18
PJA_smith9	TRINITY_DN11205_c0_g1_i10	Arginine/serine-rich protein PNISR	-16	-17
PJA_smith9	TRINITY_DN1128_c0_g3_i1	.	-10	-15
PJA_smith9	TRINITY_DN1150_c0_g1_i10	Probable peroxisomal acyl-coenzyme A oxidase 1	-15	-18
PJA_smith9	TRINITY_DN1155_c0_g1_i11	Transposable element Tcb1 transposase	-9	-17
PJA_smith9	TRINITY_DN12058_c0_g1_i3	ATP-binding cassette subfamily G member 4	-17	-16
PJA_smith9	TRINITY_DN12206_c0_g1_i4	.	-17	-24
PJA_smith9	TRINITY_DN12303_c0_g1_i19	Uncharacterized protein K02A2.6	-9	-16
PJA_smith9	TRINITY_DN1234_c0_g1_i6	Ubiquitin carboxyl-terminal hydrolase 32	-13	-18
PJA_smith9	TRINITY_DN12557_c0_g2_i1	Dual specificity testis-specific protein kinase 2	-14	-17
PJA_smith9	TRINITY_DN1257_c0_g1_i15	E3 SUMO-protein ligase PIAS3	-14	-16
PJA_smith9	TRINITY_DN1275_c0_g1_i15	Copia protein	-14	-16
PJA_smith9	TRINITY_DN1341_c0_g1_i9	TBC1 domain family member 4	-13	-16
PJA_smith9	TRINITY_DN137_c0_g3_i2	2-methoxy-6-polyprenyl-1,4-benzoquinol methylase, mitochondrial	-13	-18
PJA_smith9	TRINITY_DN1473_c0_g1_i10	Protein ILRUN	-10	-17
PJA_smith9	TRINITY_DN15166_c0_g2_i1	Vesicle-fusing ATPase 1	-12	-17
PJA_smith9	TRINITY_DN1546_c0_g1_i5	CCHC-type zinc finger nucleic acid binding protein	-14	-18
PJA_smith9	TRINITY_DN15_c0_g2_i1	Probable 4-coumarate--CoA ligase 3	-17	-19
PJA_smith9	TRINITY_DN160054_c0_g1_i1	3-hydroxyacyl-CoA dehydrogenase type-2	-18	-22
PJA_smith9	TRINITY_DN160_c0_g2_i1	Protein ROP	-14	-16
PJA_smith9	TRINITY_DN16132_c0_g1_i7	Focal adhesion kinase 1	-13	-17
PJA_smith9	TRINITY_DN1628_c0_g1_i1	Sodium-dependent neutral amino acid transporter SLC6A17	-12	-18
PJA_smith9	TRINITY_DN17335_c0_g1_i1	.	-15	-17
PJA_smith9	TRINITY_DN1750_c0_g1_i10	Unconventional myosin-Ib	-11	-17
PJA_smith9	TRINITY_DN1780_c0_g1_i12	Protein SERAC1	-14	-17
PJA_smith9	TRINITY_DN1883_c0_g1_i6	Toll-like receptor Tollo	-12	-18
PJA_smith9	TRINITY_DN1967_c0_g1_i5	Mannosyl-oligosaccharide alpha-1,2-mannosidase IA	-13	-18
PJA_smith9	TRINITY_DN19708_c0_g1_i10	.	-16	-18
PJA_smith9	TRINITY_DN20197_c0_g1_i7	Regulator of G-protein signaling 7	-12	-19
PJA_smith9	TRINITY_DN2066_c0_g3_i2	Autophagy-related protein 101	-10	-18
PJA_smith9	TRINITY_DN2112_c0_g1_i4	Multiple inositol polyphosphate phosphatase 1	-9	-18
PJA_smith9	TRINITY_DN21_c1_g2_i2	Cytochrome P450 4C1	-14	-16
PJA_smith9	TRINITY_DN23286_c0_g1_i1	.	-14	-19
PJA_smith9	TRINITY_DN24070_c0_g1_i3	.	-23	-18
PJA_smith9	TRINITY_DN26423_c0_g1_i1	DNA polymerase eta	-19	-15
PJA_smith9	TRINITY_DN2697_c0_g1_i2	Chitin deacetylase 7	-13	-16
PJA_smith9	TRINITY_DN2788_c0_g1_i8	Peptidyl-prolyl cis-trans isomerase-like 3	-20	-18
PJA_smith9	TRINITY_DN3095_c0_g1_i23	SET and MYND domain-containing protein 4	-15	-16
PJA_smith9	TRINITY_DN3182_c0_g1_i3	H(+)/Cl(-) exchange transporter 3	-17	-20
PJA_smith9	TRINITY_DN3341_c0_g1_i1	Mediator of RNA polymerase II transcription subunit 12-like protein	-12	-15
PJA_smith9	TRINITY_DN343_c0_g2_i1	SRSF protein kinase 3	-13	-17
PJA_smith9	TRINITY_DN36313_c0_g1_i1	Mediator of RNA polymerase II transcription subunit 1	-15	-16
PJA_smith9	TRINITY_DN3686_c0_g1_i10	Molybdenum cofactor biosynthesis protein 1	-15	-15
PJA_smith9	TRINITY_DN37619_c0_g1_i5	Heparan-alpha-glucosaminide N-acetyltransferase	-16	-19
PJA_smith9	TRINITY_DN398_c0_g2_i2	Putative ankyrin repeat protein RF_0381	-11	-17
PJA_smith9	TRINITY_DN4212_c0_g1_i1	Protein obstructor-E	-13	-17
PJA_smith9	TRINITY_DN435_c0_g1_i11	Ubiquinone biosynthesis protein COQ4 homolog, mitochondrial	-11	-16
			-12	-17

PJA_smith9	TRINITY_DN4705_c0_g1_i7	Protein salivary glands marred		
PJA_smith9	TRINITY_DN4752_c0_g2_i2	.	-11	-18
PJA_smith9	TRINITY_DN5026_c0_g2_i10	Actin-binding protein IPP	-16	-18
PJA_smith9	TRINITY_DN5070_c0_g1_i10	Threonine aspartase 1	-12	-15
PJA_smith9	TRINITY_DN5086_c0_g1_i11	Sodium- and chloride-dependent GABA transporter 1	-11	-16
PJA_smith9	TRINITY_DN5794_c0_g1_i13	Homeobox protein Hox-A1a	-15	-18
PJA_smith9	TRINITY_DN5836_c0_g1_i1	SREBP regulating gene protein	-15	-19
PJA_smith9	TRINITY_DN6108_c0_g1_i1	XK-related protein 4	-13	-18
PJA_smith9	TRINITY_DN6606_c0_g1_i1	Lysosomal acid glucosylceramidase	-19	-24
PJA_smith9	TRINITY_DN667_c0_g1_i11	Echinoderm microtubule-associated protein-like 2	-17	-21
PJA_smith9	TRINITY_DN7253_c0_g1_i1	RanBP-type and C3HC4-type zinc finger-containing protein 1	-14	-18
PJA_smith9	TRINITY_DN72815_c0_g1_i1	.	-12	-17
PJA_smith9	TRINITY_DN7546_c0_g1_i1	.	-15	-18
PJA_smith9	TRINITY_DN7641_c0_g1_i5	Golgi-associated plant pathogenesis-related protein 1	-16	-18
PJA_smith9	TRINITY_DN7701_c0_g1_i1	3-hydroxyisobutyrate dehydrogenase, mitochondrial	-17	-16
PJA_smith9	TRINITY_DN777_c0_g1_i1	Retrovirus-related Pol polyprotein from transposon 297	-16	-19
PJA_smith9	TRINITY_DN8583_c0_g1_i5	.	-19	-18
PJA_smith9	TRINITY_DN871_c0_g2_i3	27 kDa hemolymph protein	-10	-15
PJA_smith9	TRINITY_DN8820_c0_g1_i11	Tetratricopeptide repeat protein 5	-17	-17
PJA_smith9	TRINITY_DN88_c0_g1_i4	Chromodomain-helicase-DNA-binding protein 7	-9	-16
PJA_smith9	TRINITY_DN921_c0_g1_i1	PHD finger protein rhinoceros	-11	-17
PJA_smith9	TRINITY_DN9733_c0_g1_i9	Activity-regulated cytoskeleton associated protein 1	-21	-16