

# Supplementary Tables

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2019-12-27

Table S1: *minsamp* sample dataset that includes interaction factors. The parameters which affect miRNA:target interactions (i.e. seed type, region, energy) are provided in sample dataset.

competing	miRNA	Competing_expression	miRNA_expression	seed_type	region	energy
Gene1	Mir1	10000	1000	0.43	0.30	-20
Gene2	Mir1	10000	1000	0.43	0.01	-15
Gene3	Mir1	5000	1000	0.32	0.40	-14
Gene4	Mir1	10000	1000	0.23	0.50	-10
Gene4	Mir2	10000	2000	0.35	0.90	-12
Gene5	Mir2	5000	2000	0.05	0.40	-11
Gene6	Mir2	10000	2000	0.01	0.80	-25

Table S2: Efficiency factors for seed types.

	seed_type	seed_type_effect
1	6-mer_noncanonical	0.05
2	9-mer	0.43
3	6-mer	0.07
4	8-mer	0.43
5	7-mer	0.23
6	none	0.01
7	5-mer_noncanonical	0.04
8	5-mer	0.05
9	6-merA1_noncanonical	0.05
10	7-mer-8m_noncanonical	0.21
11	7-mer-8m	0.25
12	8-mer_noncanonical	0.35
13	7-merA1_noncanonical	0.16
14	7-merA1	0.19
15	6-merA1	0.07

Some of information about miRNA:target interactions were exhibited directly by high-throughput studies. On the other haned, we were examined other interacion factors based on different studies.

- Helwak et al. (2013) and Moore et al.(- Moore et al. 2015) reported the energy values in miRNA:target interactions.
- Comparisons of canonical seed types were evaluated by study of Grimson et al. (2007), while functional and non-functional seed interactions were studied by Bartel et al. (2009) and Betel et al. (2010) (Table S2).

Table S3: Efficiency factors for binding regions on targets

	region	region_effect
1	3UTR	0.84
2	CDS	0.42
3	3UTRCDS	0.93
4	5UTR	0.01
5	5UTRCDS	0.42
6	none	0.01
7	intron	0.01
8	CDS3UTR	0.93
9	CDS5UTR	0.42
10	exon_unclassified	0.20
11	CDS3UTRintron	0.93
12	3UTRintron	0.84
13	CDSintron	0.42
14	5UTRintron	0.01
15	5UTR3UTR	0.93
16	CDS5UTR3UTR	0.93

- Numeric definition of target region location effect was performed based on studies of Hausser et al. (2013) and Helwak et al. (2013) (Table S3).

Table S4: Example of E9GE\_mirnagenenormal dataset. Hugo Symbol, gene symbol; miRNA name, name of miRNA that interacted with specified gene; mirna RPM; mirna count in read per million; seed type and region effect, numeric seed type and region coefficients for specified miRNA:gene interactions based on Table S2 and S3.

Hugo Symbol	miRNA name	mirna RPM	GE normal	energy	seed type effect	region effect
ENAH	hsa-let-7a-5p	111204.15	7540	-22.70	0.01	0.00
GALNT2	hsa-let-7a-5p	111204.15	2824	-20.50	0.14	0.00
RLF	hsa-let-7a-5p	111204.15	1144	-18.00	0.03	0.20
MAST2	hsa-let-7a-5p	111204.15	2640	-22.60	0.24	0.00
DOCK1	hsa-let-7a-5p	111204.15	4826	-20.50	0.01	0.00
ZBTB16	hsa-let-7a-5p	111204.15	315	-24.30	0.14	0.00

Table S5: Context of miRNA:target pairs dataset supported by High-throughput Experiments

Variable	Structure	Means
cluster	character	Barcode from experimentally method
chromosome	character	Chromosome of Target gene from raw data
start_position	numeric	Gene start position from raw data
end_position	numeric	Gene end position from raw data
strand	character	Gene strand
hgnc_symbol	character	Gene name (Symbol)
Ensembl_Gene_Id	character	Ensembl Gene Id of gene
Ensembl_Transcript_Id	character	Ensembl transcript id of mRNA of Target gene
target_seq	character	mRNA sequences targeted by miRNA
miRNA	character	miRNA id (from miRBase version 21 )
miR_seq	character	miRNA sequence
seed_type	character	seed type of miRNA:target interaction
Energy	numeric	Energy of miRNA:target binding
HG38build_loc	character	Recent chromosomal location of Gene
Genome_build	character	Genome build of given chromosome, start and end positions
region	character	interaction location on target
region_effect	numeric	Coefficient of location on target
seed_type_effect	numeric	Coefficient for seed sequence of miRNA:target interaction

As a result of simulation a dataset, a graph object is obtained that includes various variables in edge and node data. A graph object includes variables at following.

Table S6: The context of graph object during the process.

Variables	Structure	Means
<i>Node Variables</i>		
name	character	node name
type	character	Competing or miRNA
node_id	numeric	in on graph object
initial_count	numeric	Initial Expression value of node
count_pre	numeric	Expression value of node at previous regulation
count_current	numeric	Existing expression value of node
changes_variable	character	Regulation of node (Up, down or steady)
<i>Edge Variables</i>		
Competing name	character	name of genes
miRNA name	character	name of miRNAs
Competing expression	numeric	Expression values of competing elements at steady-state
miRNA expression	numeric	Expression values of miRNA elements at steady-state
energy	numeric	coefficient of miRNA:target interactions (binding affinity)
seed type	numeric	coefficient of miRNA:target interactions (binding affinity)
region	numeric	coefficient of miRNA:target interactions (degradation efficiency)
aff factor	numeric	coefficient scaled and combined affinity factor
degg factor	numeric	coefficient scaled and combined degradation factor
comp_count_list	list	list of competing expression for each iteration
comp_count	numeric	pre: competing expression at previous iteration; current: competing expression at present iteration
mirna_count_list	list	list of miRNA expression for each iteration
mirna_count	numeric	pre: miRNA expression at previous iteration; current: miRNA expression at present iteration
effect	numeric	pre: total miRNA repressive effect on individual target at previous iteration ; current: miRNA repressive effect on individual target at present iteration
effect_list	list	list of miRNA repressive effect on individual target for each iteration

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