Supplementary Tables

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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

Note: Energy values in miRNA:target pairs are represented by high-throughput studies (Helwak et al. 2013; Moore et al. 2015) which are utilized in this study. On the other hand, we have specified the other interaction factors, seed type and location of binding region on the target, as numeric values based on the previous studies.(Grimson et al. 2007) have compared the seed types' effect on target repression with few miRNA had canonical seed pairing in their study. Additionally, (Bartel 2009) and (Betel et al. 2010) have studied on functional and non-functional seed interactions. Based on results of these studies we have arranged seed types of miRNA:target interactions as numeric values. We also have redefined location of binding region on the target as numeric values, based on studies of (Hausser et al. 2013) and (Helwak et al. 2013). With this process, we have handled this entegrated dataset in context of competitor behaviours and functionality of interactions.

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

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		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

Table S4: Example of E9GE_mirnagenenormal dataset.

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: miRNA:target pairs supported by High-throughput Experiments

Variable	Structure	Means
cluster	character	Barcode from experimentally method
chromosome	character	Chromosome of Terget gene from raw data
start_position	numeric	Gene start position from raw data
end_position	numeric	Gene end position from raw data
strand	chracter	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 vesion 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
Genom_build	character	Genom 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 graph object during the process.

Variables	Structure	Means
Node Variables		
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)
Edge Variables		
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)
afff 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 reppressive effect on individual target at previous iteration ; current: miRNA reppressive effect on individual target at present iteration
effect_list	list	list of miRNA reppressive effect on individual target for each iteration

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