

RefSeq	#seeds	Target
NM_001001508	6	Rattus norvegicus plasticity related gene 1 (Lppr4), mRNA
NM_001108615	6	Rattus norvegicus myelin transcription factor 1 (Myt1), mRNA
NM_012775	6	Rattus norvegicus transforming growth factor, beta receptor 1 (Tgfbr1), mRNA
NM_022599	6	Rattus norvegicus synaptojanin 2 binding protein (Synj2bp), mRNA
NM_001007688	5	Rattus norvegicus LEA_4 domain containing protein RGD1359600 (RGD1359600), mRNA
NM_001008362	5	Rattus norvegicus zinc finger protein 655 (Znf655), mRNA
NM_001105668	5	Rattus norvegicus MyoD family inhibitor domain containing (Mdfic), mRNA
NM_001105881	5	Rattus norvegicus N-acetyltransferase 13 (Nat13), mRNA
NM_001107213	5	Rattus norvegicus ubiquitin-like modifier activating enzyme 6 (Uba6), mRNA
NM_001107641	5	Rattus norvegicus single-minded homolog 1 (Drosophila) (Sim1), mRNA
NM_001108666	5	Rattus norvegicus structural maintenance of chromosomes 2 (Smc2), mRNA
NM_001109317	5	Rattus norvegicus similar to transmembrane 4 superfamily member 10 (RGD1564799), mRNA
NM_012555	5	Rattus norvegicus v-ets erythroblastosis virus E26 oncogene homolog 1 (avian) (Ets1), mRNA
NM_031841	5	Rattus norvegicus stearyl-CoA desaturase (delta-9-desaturase) (Scd), mRNA
NM_138879	5	Rattus norvegicus selectin, endothelial cell (Sele), mRNA
NM_172066	5	Rattus norvegicus solute carrier family 30 (zinc transporter), member 4 (Slc30a4), mRNA
NM_001009349	4	Rattus norvegicus 5,10-methenyltetrahydrofolate synthetase (5-formyltetrahydrofolate cyclo-ligase) (Mthfs), mRNA
NM_001013434	4	Rattus norvegicus related RAS viral (r-ras) oncogene homolog 2 (Rras2), mRNA
NM_001105880	4	Rattus norvegicus zinc finger and BTB domain containing 20 (Zbtb20), mRNA
NM_001106415	4	Rattus norvegicus Nipped-B homolog (Drosophila) (NIPBL), mRNA

Supplementary Table 1:- mRNA targets of miR200 b/c. Potential targets were obtained through searching 3'UTR sequences of rat mRNAs for the seeds of miRNAs. Rat mRNAs were downloaded from UCSC Genome Browser (<http://genome.ucsc.edu/>). For each 3'UTR, a number of seeds, its flanking nucleotides and position were recorded. Each list of potential targets was screened using specific criteria including high number of seeds, small distance between seeds and physiological function of the targets. Targets presented represent those which have highest number of seeds present.