

Figure e1: Let7i microRNA expressed in leukocytes of patients with ischemic stroke (n=106) compared to controls (n=106) divided by time after stroke onset. Let7i was significantly lower in ischemic stroke compared to controls (p=0.00001). Participants acquired within the first 24 hours of stroke onset (fold change -1.52) and continued to be decreased from 24-48hrs (fold change -1.72) and 48-72 hours (fold change -1.79). While a trend of let7i to decrease over time was present this did not reach statistical significance.

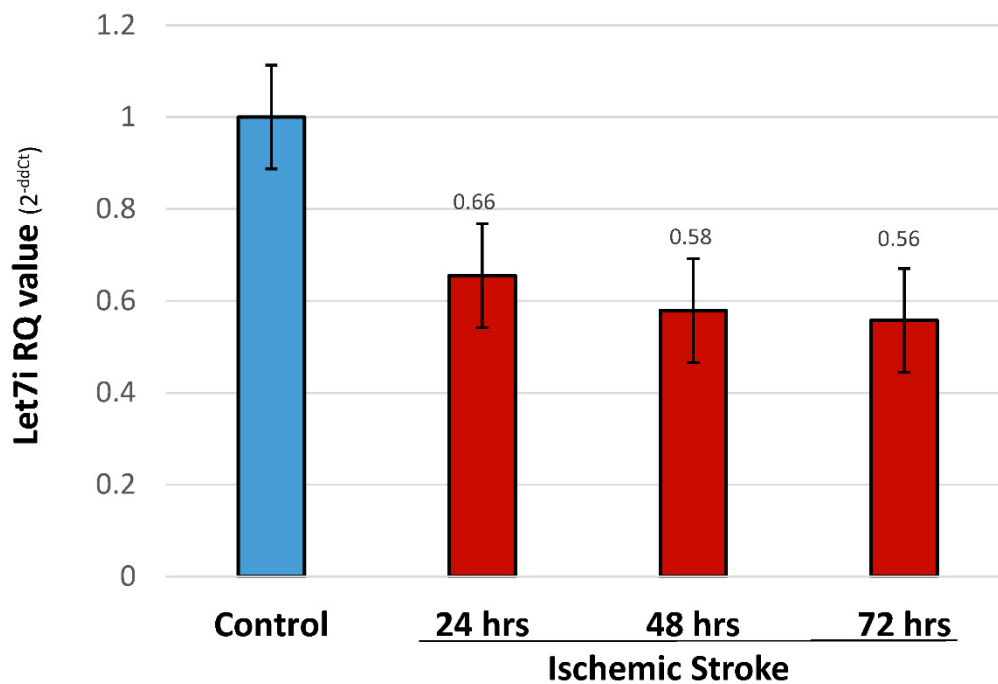


Table e1: Gene targets of let7i that inversely correlate with let7i expression in leukocytes of patients with acute ischemic stroke. Targets are predicted with a cumulative weighted context++ score <-0.2 (TargetScan 7.0).

Gene Symbol	r	p-value (corr)	Total context++ score
ACER3	-0.25	2.28E-02	-0.27
ACTR10	-0.65	1.98E-11	-0.4
ACVR2A	-0.29	8.48E-03	-0.62
ANAPC13	-0.45	2.10E-05	-0.39
ANAPC15	-0.58	5.36E-09	-0.26
ANKRA2	-0.64	8.31E-11	-0.37
ANKRD49	-0.74	5.18E-16	-0.74
AP5M1	-0.60	2.02E-09	-0.38
AP5M1	-0.60	2.14E-09	-0.38
ARL5A	-0.57	1.89E-08	-0.36
ARL5B	-0.50	1.70E-06	-0.26
ARL6IP6	-0.58	8.67E-09	-0.55
ARL6IP6	-0.49	2.19E-06	-0.55
ARL8B	-0.55	6.86E-08	-0.21
ARMC10	-0.59	4.19E-09	-0.26
ARPP19	-0.28	9.71E-03	-0.56
ATG12	-0.67	3.93E-12	-0.42
ATG12	-0.64	4.55E-11	-0.42
ATP5G3	-0.58	9.03E-09	-0.3
ATP6V1C1	-0.35	1.30E-03	-0.38
ATP6V1G1	-0.73	1.86E-15	-0.34
ATP8B4	-0.32	3.06E-03	-0.38
AURKA	-0.24	3.07E-02	-0.27
BCAP29	-0.52	5.22E-07	-0.41
BCAP29	-0.50	1.29E-06	-0.41
BCAS2	-0.64	6.37E-11	-0.21
BLOC1S6	-0.51	7.88E-07	-0.34
BMPRI1A	-0.30	4.94E-03	-0.21
BORA	-0.58	1.00E-08	-0.21
BTF3L4	-0.69	3.03E-13	-0.41
BZW1	-0.48	4.48E-06	-0.76
BZW1	-0.35	1.15E-03	-0.76
C11orf57	-0.70	1.22E-13	-0.43
C11orf58	-0.60	1.61E-09	-0.3
C12orf4	-0.63	9.70E-11	-0.26
C14orf2	-0.77	1.36E-17	-0.6
C14orf28	-0.53	2.78E-07	-1.63
C18orf21	-0.64	4.02E-11	-0.72
C1GALT1	-0.38	3.28E-04	-0.38
C3orf38	-0.61	7.53E-10	-0.42
C4orf29	-0.58	9.87E-09	-0.41
C4orf33	-0.46	8.52E-06	-0.3
C6orf120	-0.72	1.50E-14	-0.29
C6orf211	-0.67	3.06E-12	-0.3
C7orf60	-0.41	1.18E-04	-0.23
C9orf156	-0.56	2.34E-08	-0.22
C9orf85	-0.58	5.49E-09	-0.24
CASP3	-0.62	4.13E-10	-0.52
CCDC71L	-0.43	4.00E-05	-0.46
CCNT2	-0.63	1.76E-10	-0.32
CCNT2	-0.60	1.21E-09	-0.32
CD164	-0.66	9.46E-12	-0.34
CD28	-0.34	1.57E-03	-0.22
CD300E	-0.22	4.83E-02	-0.24
CD86	-0.44	3.06E-05	-0.34
CDKN2AIP	-0.70	1.88E-13	-0.24
CELFI	-0.33	1.89E-03	-0.21
CEP57	-0.64	5.72E-11	-0.21
CEP57L1	-0.42	5.60E-05	-0.21
CHUK	-0.40	1.58E-04	-0.38
CLOCK	-0.38	4.23E-04	-0.28
CNIH1	-0.76	9.90E-17	-0.26
CNIH4	-0.55	7.62E-08	-0.25
COX6B1	-0.40	1.48E-04	-0.24
CRBN	-0.67	3.54E-12	-0.28
CRCP	-0.65	1.70E-11	-0.23
CRK	-0.23	3.37E-02	-0.24
CRTAP	-0.55	6.41E-08	-0.26
CTDSPL2	-0.46	1.32E-05	-0.6
CUZD1	-0.27	1.37E-02	-0.31
CXCL8	-0.23	2.90E-02	-0.28
CYSLTR1	-0.37	5.34E-04	-0.23
DENND2D	-0.39	2.52E-04	-0.25
DET1	-0.34	1.56E-03	-0.22
DNAJA2	-0.51	7.94E-07	-0.36
DNAJB14	-0.55	7.46E-08	-0.28
DNAJB9	-0.56	3.87E-08	-0.31
DPH3	-0.55	4.49E-08	-0.77
DR1	-0.49	2.00E-06	-0.27

Gene Symbol	r	p-value (corr)	Total context++ score
DTWD1	-0.63	1.75E-10	-0.23
DUSP22	-0.51	8.99E-07	-0.46
DYNC2L1	-0.44	2.27E-05	-0.53
E2F6	-0.36	8.02E-04	-0.65
ECHDC1	-0.69	3.29E-13	-0.52
EFCAB2	-0.23	3.27E-02	-0.21
EIF2S2	-0.64	5.31E-11	-0.41
ELOVL4	-0.22	4.52E-02	-0.41
EMB	-0.60	1.15E-09	-0.32
ENY2	-0.73	2.64E-15	-0.3
ENY2	-0.67	3.39E-12	-0.3
ERCC8	-0.56	4.05E-08	-0.22
ERGIC2	-0.65	2.31E-11	-0.36
ERO1L	-0.22	4.38E-02	-0.65
ETFDH	-0.46	1.35E-05	-0.32
ETV3	-0.25	2.23E-02	-0.34
EVI2B	-0.22	4.75E-02	-0.27
EXOC5	-0.41	1.18E-04	-0.27
FAM103A1	-0.45	1.99E-05	-0.77
FAM105A	-0.55	4.88E-08	-0.22
FAM122A	-0.35	1.11E-03	-0.48
FAM206A	-0.50	1.05E-06	-0.23
FAM208A	-0.36	8.16E-04	-0.23
FAM72C	-0.30	5.21E-03	-0.33
FAS	-0.39	2.39E-04	-0.58
FAS	-0.39	2.69E-04	-0.58
FBXO30	-0.25	1.98E-02	-0.27
FKBP3	-0.72	1.19E-14	-0.38
FOPNL	-0.65	1.80E-11	-0.28
FSD1L	-0.29	8.48E-03	-0.23
FUNDC2	-0.41	1.19E-04	-0.22
FUT4	-0.35	1.09E-03	-0.23
GALNT1	-0.58	7.08E-09	-0.69
GALNT12	-0.27	1.14E-02	-0.24
GDPD1	-0.56	2.23E-08	-0.37
GHITM	-0.51	6.51E-07	-0.22
GLRX	-0.61	6.12E-10	-0.43
GMNN	-0.32	2.98E-03	-0.28
GOLGA7	-0.36	7.15E-04	-0.36
GOLT1B	-0.63	1.07E-10	-0.59
GPCPD1	-0.25	2.06E-02	-0.57
GRAMD3	-0.24	2.70E-02	-0.23
GTF2A2	-0.56	3.35E-08	-0.27
GTPBP8	-0.62	4.75E-10	-0.38
H2AFJ	-0.59	4.94E-09	-0.21
HCFC2	-0.51	9.04E-07	-0.34
HDX	-0.23	3.49E-02	-0.56
HECTD2	-0.26	1.56E-02	-0.28
HMGB1	-0.72	1.67E-14	-0.26
HMGB1	-0.68	1.43E-12	-0.26
HMGB2	-0.59	4.02E-09	-0.24
HNRNPC	-0.56	2.64E-08	-0.25
HNRNPLL	-0.32	2.65E-03	-0.34
HSD17B11	-0.42	6.96E-05	-0.26
IFT80	-0.60	2.01E-09	-0.36
IGFBP7	-0.55	7.89E-08	-0.51
KATNBL1	-0.28	1.02E-02	-0.43
KCNE3	-0.22	3.96E-02	-0.28
KIAA0391	-0.52	4.38E-07	-0.46
KIAA1143	-0.58	8.34E-09	-0.23
KIAA1328	-0.35	1.02E-03	-0.48
KIAA1715	-0.45	1.53E-05	-0.21
LCORL	-0.31	4.08E-03	-0.33
LONRF3	-0.23	3.63E-02	-0.38
LOXL4	-0.22	4.30E-02	-0.29
LYRM2	-0.54	1.42E-07	-0.24
LYRM2	-0.52	3.63E-07	-0.24
LZIC	-0.42	5.72E-05	-0.22
MAP2K6	-0.31	3.58E-03	-0.33
MAP4K3	-0.58	5.33E-09	-0.55
MAPK6	-0.61	5.36E-10	-0.51
MCTS1	-0.64	7.95E-11	-0.22
METTL14	-0.64	3.55E-11	-0.47
MFF	-0.66	1.11E-11	-0.41
MFSD1	-0.43	4.66E-05	-0.27
MKKS	-0.71	3.47E-14	-0.22
MOB1A	-0.34	1.38E-03	-0.26
MOB4	-0.75	2.60E-16	-0.33
MRPL17	-0.59	4.66E-09	-0.24

Gene Symbol	r	p-value (corr)	Total context++ score
MRPS11	-0.33	1.90E-03	-0.22
MTHFD2	-0.53	2.79E-07	-0.21
MTHFD2	-0.51	9.45E-07	-0.21
NAA20	-0.68	6.97E-13	-0.26
NAA38	-0.69	4.26E-13	-0.59
NABP1	-0.24	2.49E-02	-0.33
NBN	-0.25	2.21E-02	-0.3
NDUFA4	-0.77	1.10E-17	-0.79
NECAP2	-0.50	1.37E-06	-0.27
NFU1	-0.70	1.05E-13	-0.3
NIPAL2	-0.35	1.17E-03	-0.22
LONRF3	-0.23	3.63E-02	-0.38
LOXL4	-0.22	4.30E-02	-0.29
LYRM2	-0.54	1.42E-07	-0.24
LYRM2	-0.52	3.63E-07	-0.24
LZIC	-0.42	5.72E-05	-0.22
MAP2K6	-0.31	3.58E-03	-0.33
MAP4K3	-0.58	5.33E-09	-0.55
MAPK6	-0.61	5.36E-10	-0.51
MCTS1	-0.64	7.95E-11	-0.22
METTL14	-0.64	3.55E-11	-0.47
MFF	-0.66	1.11E-11	-0.41
MFSD1	-0.43	4.66E-05	-0.27
MKKS	-0.71	3.47E-14	-0.22
MOB1A	-0.34	1.38E-03	-0.26
MOB4	-0.75	2.60E-16	-0.33
MRPL17	-0.59	4.66E-09	-0.24

Gene Symbol	r	p-value (corr)	Total context++ score
RNFT1	-0.64	5.84E-11	-0.72
RPAP3	-0.38	3.00E-04	-0.26
RPF1	-0.68	7.03E-13	-0.21
RPL34	-0.79	3.61E-19	-0.58
RPL38	-0.60	1.14E-09	-0.29
RPL9	-0.78	4.84E-18	-0.23
RPL9	-0.76	2.52E-17	-0.23
RPL9	-0.76	2.95E-17	-0.23
RTCA	-0.61	6.77E-10	-0.4
RWDD1	-0.74	7.65E-16	-0.26
SAP30L	-0.27	1.36E-02	-0.26
SCOC	-0.67	5.12E-12	-0.25
SELT	-0.64	8.72E-11	-0.26
SENP5	-0.49	2.23E-06	-0.29
SERF2	-0.50	1.52E-06	-0.23
SERF2	-0.24	2.65E-02	-0.23
SERPINI1	-0.31	4.50E-03	-0.32
SFT2D3	-0.69	5.49E-13	-0.43
SKIL	-0.45	1.66E-05	-0.77
SKIL	-0.25	2.42E-02	-0.77
SLC25A24	-0.42	5.78E-05	-0.41
SLC25A40	-0.45	1.95E-05	-0.38
SLC30A1	-0.48	4.32E-06	-0.37
SLC31A2	-0.22	4.08E-02	-0.24
SMDT1	-0.51	6.98E-07	-0.26
SMIM8	-0.30	5.60E-03	-0.32
SNX16	-0.53	2.91E-07	-0.4
SNX6	-0.55	5.86E-08	-0.38
SOCS4	-0.62	4.60E-10	-0.67
SPCS3	-0.47	5.89E-06	-0.35
SREK1IP1	-0.62	3.92E-10	-0.78
SRGN	-0.48	3.47E-06	-0.27
SRGN	-0.42	7.22E-05	-0.27
SRI	-0.51	8.00E-07	-0.27
STARD3NL	-0.61	7.33E-10	-0.36
STARD4	-0.44	3.50E-05	-0.42
SUB1	-0.71	3.11E-14	-0.54
SUPT4H1	-0.37	4.63E-04	-0.22
SWSAP1	-0.45	1.96E-05	-0.74
SWT1	-0.22	4.61E-02	-0.34
TAF5	-0.33	1.92E-03	-0.32
TAF9B	-0.59	4.26E-09	-0.34
TFEC	-0.54	1.14E-07	-0.25
TGDS	-0.64	8.60E-11	-0.41
THAP2	-0.57	1.33E-08	-0.22
THAP9	-0.32	2.61E-03	-0.5
TIMM17B	-0.43	5.00E-05	-0.37
TMBIM4	-0.53	2.61E-07	-0.27
TMED5	-0.60	2.07E-09	-0.44
TMED5	-0.48	4.27E-06	-0.44
TMEM167A	-0.59	3.56E-09	-0.62
TMEM251	-0.30	5.60E-03	-0.34
TMEM65	-0.46	1.36E-05	-0.34
TMOD2	-0.43	4.51E-05	-0.36
TNFSF10	-0.42	6.78E-05	-0.53
TNFSF10	-0.42	7.19E-05	-0.53
TTC14	-0.62	3.28E-10	-0.38
UBE2W	-0.48	4.57E-06	-0.38
UBXN4	-0.54	8.80E-08	-0.21
UCHL5	-0.55	6.05E-08	-0.29
UCHL5	-0.53	1.76E-07	-0.29
UFC1	-0.62	4.51E-10	-0.24
UFM1	-0.72	1.63E-14	-0.6
UFM1	-0.69	3.16E-13	-0.6
UGCG	-0.42	5.94E-05	-0.48
UQCR10	-0.62	2.98E-10	-0.37
UQCRB	-0.74	1.31E-15	-0.22
USO1	-0.43	5.28E-05	-0.22
USP49	-0.36	6.61E-04	-0.42
UTP6	-0.60	1.37E-09	-0.25
VPS25	-0.61	5.94E-10	-0.44
WDFY2	-0.42	5.74E-05	-0.28
WDR41	-0.42	6.10E-05	-0.57
YAE1D1	-0.61	5.50E-10	-0.35
YAF2	-0.42	6.61E-05	-0.34
YIPF1	-0.22	4.09E-02	-0.47
YWHAE	-0.54	1.05E-07	-0.22
YWHAE	-0.48	4.89E-06	-0.22
ZBTB37	-0.50	1.10E-06	-0.51
ZBTB5	-0.23	3.34E-02	-0.33
ZBTB8OS	-0.72	1.39E-14	-0.38
ZBTB8OS	-0.57	1.07E-08	-0.38

Gene Symbol	r	p-value (corr)	Total context score
ZCCHC9	-0.61	5.30E-10	-0.65
ZFAND5	-0.25	2.14E-02	-0.24
ZNF141	-0.64	7.72E-11	-0.21
ZNF169	-0.22	4.28E-02	-0.25
ZNF226	-0.69	3.04E-13	-0.58
ZNF226	-0.66	6.91E-12	-0.58
ZNF24	-0.46	8.76E-06	-0.25
ZNF268	-0.68	8.41E-13	-0.52
ZNF322	-0.73	2.71E-15	-0.51
ZNF322	-0.63	1.24E-10	-0.51
ZNF33A	-0.24	2.94E-02	-0.24
ZNF347	-0.36	8.82E-04	-0.24
ZNF354A	-0.60	1.36E-09	-0.38
ZNF410	-0.61	8.45E-10	-0.29
ZNF410	-0.59	4.69E-09	-0.29
ZNF431	-0.50	1.18E-06	-0.22
ZNF432	-0.59	4.43E-09	-0.36
ZNF436	-0.45	1.54E-05	-0.23
ZNF443	-0.54	8.82E-08	-0.27
ZNF493	-0.69	2.34E-13	-0.39
ZNF557	-0.68	1.16E-12	-0.25
ZNF583	-0.40	1.63E-04	-0.47
ZNF622	-0.60	1.24E-09	-0.34
ZNF644	-0.55	5.68E-08	-0.48
ZNF678	-0.67	3.41E-12	-0.34
ZNF70	-0.27	1.23E-02	-0.57
ZNF738	-0.69	6.18E-13	-0.36
ZNF738	-0.68	1.04E-12	-0.36
ZNF79	-0.30	5.17E-03	-0.3
ZSWIM5	-0.27	1.39E-02	-0.4