### Supplementary Tables

#### Supplementary Table 1. miRNA enrichment of CASP1 co-expressed genes.

| Geneset | Enrichment score | Normalized enrichment score | pvalue | FDR | Size | Leading EdgeNum |
|---------|------------------|-----------------------------|--------|-----|------|-----------------|
| CAGTCAC,MIR-134 | -0.5356147 | -1.5057118 | 0.012397 | 0.307969 | 46 | 15 |
| GGGATGC,MIR-324-5P | -0.5395772 | -1.5411925 | 0.004405 | 0.308328 | 46 | 13 |
| CGCTGCT,MIR-503 | -0.5996193 | -1.4712781 | 0.041667 | 0.322831 | 22 | 13 |
| TGACGCA,MIR-517A,MIR-517C | -0.6180279 | -1.4177299 | 0.044898 | 0.438749 | 16 | 3 |
| TCTAGAG,MIR-517 | -0.4748998 | -1.3425616 | 0.075556 | 0.535813 | 45 | 12 |
| GGTAAACC,MIR-409-5P | -0.5314163 | -1.3730561 | 0.069767 | 0.547899 | 27 | 5 |
| GGCCAGT,MIR-193A,MIR-193B | -0.4799717 | -1.5457977 | 0.004926 | 0.575831 | 83 | 19 |
| AGTCAGC,MIR-345 | -0.4490602 | -1.3434165 | 0.06278 | 0.608981 | 54 | 17 |
| GTGTGTG,MIR-197 | -0.379348 | -1.1863224 | 0.156951 | 0.629742 | 67 | 18 |
| CTCGGCT,MIR-214 | -0.3322383 | -1.1932098 | 0.055249 | 0.629751 | 220 | 44 |
| CAGCTTC,MIR-485-5P | -0.3823391 | -1.2927548 | 0.028846 | 0.639001 | 131 | 35 |
| ATGTTC,MIR-494 | -0.3414139 | -1.1966772 | 0.089474 | 0.646199 | 141 | 36 |
| GCGGGCA,MIR-371 | -0.7508409 | -1.3047399 | 0.136531 | 0.649839 | 5 | 3 |
| CAGGGTC,MIR-504 | -0.3825697 | -1.1988028 | 0.116279 | 0.671615 | 78 | 21 |
| AAGGCCA,MIR-328 | -0.4041804 | -1.2586383 | 0.09375 | 0.684516 | 73 | 24 |
| GTGTCA,MIR-514 | -0.4130576 | -1.2703542 | 0.093617 | 0.68502 | 59 | 16 |
| CCCAGAG,MIR-326 | -0.3471427 | -1.2023533 | 0.09596 | 0.690066 | 141 | 25 |
| TCCCCAC,MIR-491 | -0.4121849 | -1.2101717 | 0.132159 | 0.692994 | 55 | 15 |
| CAGCACT,MIR-512-3P | -0.3292829 | -1.135226 | 0.15311 | 0.700912 | 143 | 43 |
| TCGATGG,MIR-213 | -0.6772519 | -1.1432002 | 0.310714 | 0.712765 | 5 | 4 |
| AATGGAG,MIR-136 | -0.3630656 | -1.13698 | 0.181818 | 0.718277 | 74 | 18 |
| GTGTGT,MIR-495 | -0.3044444 | -1.1160896 | 0.147541 | 0.719442 | 235 | 69 |
| AGGGTGT,MIR-483 | -0.4095191 | -1.2127934 | 0.120773 | 0.720192 | 61 | 16 |
| CAGCAGG,MIR-370 | -0.3218814 | -1.1096571 | 0.176768 | 0.722945 | 137 | 17 |
| ACAGGGT,MIR-10A,MIR-10B | -0.3334561 | -1.1202692 | 0.190217 | 0.724158 | 119 | 20 |
| AAGCGT,MIR-135A,MIR-135B | 0.33712366 | 1.19216267 | 0.065672 | 0.818531 | 310 | 43 |
| GTGACTT,MIR-224 | 0.36301753 | 1.19240037 | 0.130872 | 0.857659 | 150 | 31 |
| CTTTGCA,MIR-527 | 0.32108688 | 1.082235 | 0.254386 | 0.86316 | 221 | 29 |
| ATTCTT,MIR-186 | 0.31759521 | 1.09460462 | 0.248387 | 0.86323 | 251 | 49 |
| GTCTACCA,MIR-379 | 0.51560807 | 1.19760904 | 0.206349 | 0.871802 | 20 | 3 |
| CTCCAAG,MIR-432 | 0.3607626 | 1.06810144 | 0.29588 | 0.874074 | 74 | 16 |
| GGTACC,MIR-127 | 0.58680985 | 1.21240622 | 0.231441 | 0.875448 | 10 | 3 |
| AATGTGA,MIR-23A,MIR-23B | 0.30464776 | 1.08335814 | 0.25731 | 0.878253 | 388 | 64 |
| TAATAA,MIR-126 | 0.32201754 | 1.08721064 | 0.269841 | 0.878776 | 207 | 34 |
| TTTGCAG,MIR-518A-2 | 0.32615264 | 1.0958745 | 0.231013 | 0.879395 | 193 | 33 |
| ATGTAA,MIR-302C | 0.35198092 | 1.20279444 | 0.09090 | 0.887306 | 228 | 35 |
| GTGCCAA,MIR-96 | 0.30565774 | 1.06837271 | 0.29582 | 0.892419 | 283 | 53 |
| TACTT,G,MIR-26A,MIR-26B | 0.31273251 | 1.09627075 | 0.215873 | 0.901719 | 285 | 55 |
| CTCAAGG,MIR-125B,MIR-125A | 0.34406849 | 1.21625446 | 0.058282 | 0.904954 | 303 | 89 |
| TCTGGAC,MIR-198 | 0.33218434 | 1.0140016 | 0.409894 | 0.906819 | 82 | 16 |
| ACCAAG,MIR-9 | 0.29584667 | 1.0691252 | 0.240331 | 0.910421 | 458 | 57 |
| CAGTATT,MIR-200B,MIR-200C,MIR-429 | 0.29035348 | 1.05676528 | 0.261838 | 0.912723 | 440 | 69 |
| CTGAGCC,MIR-24 | 0.29625819 | 1.00895049 | 0.460064 | 0.913255 | 219 | 31 |
| Sequence                   | Score 1 | Score 2 | Score 3 | Score 4 | Score 5 |
|----------------------------|---------|---------|---------|---------|---------|
| GTGCAAT,MIR-25,MIR-32,MIR-92,MIR-363,MIR-367 | 0.28211347 | 0.99537175 | 0.461538 | 0.915301 | 294 50 |
| GTGCCTT,MIR-506            | 0.31351677 | 1.15712834 | 0.060526 | 0.917579 | 674 144 |
| TTTTGAG,MIR-373           | 0.32583634 | 1.1026909 | 0.233846 | 0.918391 | 210 28 |
| AGCATT,MIR-155            | 0.35282527 | 1.11720312 | 0.244068 | 0.920096 | 128 29 |
| AAGCAGT,MIR-520F          | 0.30106978 | 1.01432611 | 0.422442 | 0.921389 | 219 44 |
| TACAATT,MIR-508           | 0.41788572 | 1.1689215 | 0.234848 | 0.922923 | 57 14 |
| ATGCAGT,MIR-217           | 0.32340869 | 0.9970131 | 0.468852 | 0.92301 | 103 14 |
Supplementary Table 2. Transcription factor enrichment of CASP1 co-expressed genes.

| Geneset                                      | Enrichment score | Normalized enrichment score | pvalue | FDR   | Size | Leading | EdgeNum |
|----------------------------------------------|------------------|----------------------------|--------|-------|------|---------|---------|
| VSPEA3_Q6                                   | 0.57396322       | 1.96059442                  | 0.0002347 | 64    | 240  | 64      |
| VSE2F_01                                    | -0.5999168       | -1.8352204                  | 0.003574 | 208   | 63   |
| VSPU1_Q6                                    | 0.5411158        | 1.81098492                  | 0.004468 | 220   | 62   |
| VSSRF_01                                    | 0.65959571       | 1.80023909                  | 0.004765 | 228   | 84   |
| VSELF1_Q6                                   | 0.55037567       | 1.86720217                  | 0.005659 | 233   | 76   |
| VSRIF_Q6                                    | 0.53577782       | 1.8177585                   | 0.007914 | 1002  | 222  |
| VSISRE_01                                   | 0.50728611       | 1.74621947                  | 0.010276 | 220   | 54   |
| RYTTCCCTG_VSE2S2_B                          | 0.55066767       | 1.72071227                  | 0.007194 | 1002  | 222  |
| VSTEL2_Q6                                   | 0.49657672       | 1.70003045                  | 0.012834 | 233   | 55   |
| STTTCRNTTT_VSRIF_Q6                         | 0.51339992       | 1.69480119                  | 0.010722 | 175   | 48   |
| RGAGGAARY_VSPU1_Q6                          | 0.46921073       | 1.67433248                  | 0.011765 | 459   | 94   |
| YNTTTNNNANGCARM_UNKNOWN                     | 0.58236407       | 1.68595935                  | 0.017195 | 67    | 10   |
| VSRIF1_Q6                                   | 0.49473696       | 1.67451422                  | 0.018284 | 218   | 91   |
| VSE2F1_Q6_01                                | -0.4839508       | -1.7537136                  | 0.014084 | 218   | 91   |
| VSET2_B                                     | 0.47904718       | 1.65316635                  | 0.014159 | 259   | 55   |
| VSICSBP_Q6                                  | 0.47956267       | 1.62511362                  | 0.019658 | 230   | 62   |
| VSE2F_Q6_01                                 | -0.4632908       | -1.6752839                  | 0.022534 | 218   | 66   |
| VSE2F1_Q4_01                                | -0.4690197       | -1.6876398                  | 0.022887 | 210   | 77   |
| VSCEBPB1                                   | 0.47218528       | 1.60792237                  | 0.02347  | 240   | 54   |
| VSE2F_Q3                                   | 0.46520902       | 1.59344716                  | 0.028369 | 236   | 47   |
| VSET_Q7                                     | 0.45616718       | 1.58251459                  | 0.028791 | 235   | 50   |
| VSE2F1_Q6_01                                | -0.4701195       | -1.6921283                  | 0.02895  | 215   | 78   |
| VSAP1_Q4_01                                 | 0.46035093       | 1.58408106                  | 0.030065 | 243   | 58   |
| ACTAYRNNNCCCR_UNKNOWN                       | -0.4214518      | -1.6043698                  | 0.035503 | 408   | 121  |
| VSCEBP_Q2_01                                | 0.45789441       | 1.56208554                  | 0.035647 | 247   | 51   |
| VSE2F_03                                    | -0.449346       | -1.6225953                  | 0.038731 | 224   | 68   |
| VSE2F_Q4_01                                 | -0.4471581       | -1.6057194                  | 0.039905 | 215   | 66   |
| VSRIF1_Q7                                   | 0.45553697       | 1.54190145                  | 0.040336 | 231   | 49   |
| SGCGSSAAA_VSE2F1DP2_01                       | -0.4473325       | -1.5812434                  | 0.040426 | 155   | 71   |
| VSMAF_Q6                                    | 0.45346044       | 1.54239303                  | 0.042174 | 239   | 50   |
| VSE2F1_Q6                                   | -0.4312803       | -1.5668496                  | 0.043191 | 213   | 77   |
| VSE2F1DP1_01                                | -0.4161494       | -1.5071466                  | 0.043426 | 218   | 82   |
| VSE2F1DP2_01                                | -0.4161494       | -1.5071466                  | 0.043426 | 218   | 82   |
| VSE2F4DP2_01                                | -0.4161494       | -1.5071466                  | 0.043426 | 218   | 82   |
| VSE2F_Q6                                    | -0.4276823       | -1.5559191                  | 0.043532 | 211   | 85   |
| VSMYMAX_Q1                                 | -0.4205049       | -1.5483221                  | 0.043621 | 236   | 66   |
| VSSRF_C                                    | 0.44992831       | 1.53071115                  | 0.044189 | 197   | 41   |
| VSE2F_Q4                                   | -0.4241098       | -1.5337775                  | 0.045683 | 212   | 87   |
| WCTCNATGGY_UNKNOWN                          | -0.4877758       | -1.5119369                  | 0.047085 | 71    | 28   |
| GGAMTNNNNTCCY_UNKNOWN                       | -0.4533504       | -1.4950502                  | 0.048176 | 104   | 36   |
| VSE2F_02                                    | -0.4157139       | -1.513259                   | 0.049441 | 218   | 82   |
| VSE2F1DP1RB_01                              | -0.418954        | -1.5160793                  | 0.050702 | 209   | 76   |
| VSZF5_B                                    | -0.4153122       | -1.5217067                  | 0.050971 | 225   | 52   |
| VSNMYC_01                                   | -0.4036861       | -1.4760014                  | 0.056656 | 252   | 69   |
| MCAATNNNNGCG_UNKNOWN                        | -0.4717761       | -1.4586272                  | 0.062596 | 76    | 24   |
| VSMYMAX_B                                   | -0.3940211       | -1.4621286                  | 0.063072 | 245   | 89   |
| VSMYMAX_B                                   | 0.43094581       | 1.48271613                  | 0.069993 | 246   | 55   |
| Gene Name          | Value1 | Value2     | Value3 | Value4 | Value5 | Value6 | Value7 | Value8 | Value9 |
|-------------------|--------|------------|--------|--------|--------|--------|--------|--------|--------|
| VSAML1_Q6         | 0.43094581 | 1.48271613 | 0.003155 | 0.069993 | 246    | 55     |
| VSE2F4DP1_01      | -0.3957904 | -1.4443529 | 0      | 0.070608 | 219    | 84     |
| TGANTCA_V$AP1_C   | 0.38701162 | 1.47565026 | 0      | 0.073769 | 1035   | 221    |