

Supplementary Table 1. Differently expressed miRNAs in normal cervix, CIN3 and SCC tissues.

| Transcript Cluster ID | Normal cervix | CIN3 | SCC | FC | ANOVA p-value | Transcript ID | Accession | Sequence Length | Sequence |
|-----------------------|---------------|-------|-------|-------------|---------------|------------------|--------------|-----------------|--------------------------|
| 20500132 | 5.84 | 5.7 | 6.97 | 2.411615655 | 0.011473 | hsa-miR-18a-5p | MIMAT0000072 | 23 | UAAGGUGCAUCUAGUGCAGAUAG |
| 20500133 | 2.54 | 2.63 | 4.11 | 2.969047141 | 0.009958 | hsa-miR-18a-3p | MIMAT0002891 | 23 | ACUGCCCUAAGUGCUCUUCUGG |
| 20500142 | 3.63 | 4.51 | 5.47 | 3.580100284 | 0.002311 | hsa-miR-21-3p | MIMAT0004494 | 21 | CAACACCAGUCGAUGGGCUGU |
| 20500145 | 4.56 | 4.65 | 5.75 | 2.281527432 | 0.010072 | hsa-miR-23a-5p | MIMAT0004496 | 22 | GGGGUCCUGGGGAUGGGAAUUU |
| 20500150 | 3.72 | 4.42 | 5.32 | 3.031433133 | 0.000513 | hsa-miR-25-5p | MIMAT0004498 | 21 | AGGCGGAGACUUGGGCAAUUG |
| 20500156 | 2.51 | 3.86 | 5.64 | 8.75434961 | 0.000411 | hsa-miR-27a-5p | MIMAT0004501 | 22 | AGGGCUUAGCUGCUUGUGAGCA |
| 20500170 | 1.27 | 2.6 | 4.22 | 7.727490631 | 0.000473 | hsa-miR-92a-1-5p | MIMAT0004507 | 23 | AGGUUGGGAUCCGUUGCAAUGCU |
| 20500174 | 4.83 | 4.79 | 5.87 | 2.114036081 | 0.023707 | hsa-miR-93-3p | MIMAT0004509 | 22 | ACUGCUGAGCUAGCACUUCGCCG |
| 20500181 | 11.73 | 11.29 | 9.42 | 4.9588308 | 0.006134 | hsa-miR-99a-5p | MIMAT0000097 | 22 | AACCCGUAGAUCCGAUCUUGUG |
| 20500183 | 10.45 | 10.45 | 8.66 | 3.458148925 | 0.047895 | hsa-miR-100-5p | MIMAT0000098 | 22 | AACCCGUAGAUCCGAACUUGUG |
| 20500393 | 1.54 | 1.28 | 5.53 | 19.02731384 | 0.00429 | hsa-miR-196a-5p | MIMAT0000226 | 22 | UAGGUAGUUUCAUGUUGUUGGG |
| 20500400 | 10.32 | 10.76 | 9.28 | 2.789487333 | 0.012829 | hsa-miR-199a-3p | MIMAT0000232 | 22 | ACAGUAGUCUGCACAUUGGUUA |
| 20500438 | 7.28 | 8.24 | 6.04 | 4.59479342 | 0.019024 | hsa-miR-10a-5p | MIMAT0000253 | 23 | UACCCGUAGAUCCGAAUUUGUG |
| 20500450 | 8.22 | 8.53 | 9.25 | 2.042024251 | 0.038977 | hsa-miR-182-5p | MIMAT0000259 | 24 | UUUGGCAAUGGUAGAACUCACACU |
| 20500452 | 4.59 | 5.97 | 6.62 | 4.084048503 | 0.009666 | hsa-miR-183-5p | MIMAT0000261 | 22 | UAUGGCACUGGUAGAAUUCACU |
| 20500453 | 1.11 | 1.71 | 3.26 | 4.438277888 | 0.010949 | hsa-miR-183-3p | MIMAT0004560 | 22 | GUGAAUUACCGAAGGGCCAUA |
| 20500457 | 4.69 | 4.65 | 1.86 | 7.110741449 | 0.034627 | hsa-miR-199b-5p | MIMAT0000263 | 23 | CCCAGUGUUUAGACUAUCUGUUC |
| 20500458 | 10.32 | 10.76 | 9.28 | 2.789487333 | 0.012829 | hsa-miR-199b-3p | MIMAT0004563 | 22 | ACAGUAGUCUGCACAUUGGUUA |
| 20500463 | 0.91 | 0.85 | 2.67 | 3.530811985 | 0.031006 | hsa-miR-205-3p | MIMAT0009197 | 21 | GAUUUCAGUGGAGUGAAGUUC |
| 20500489 | 4.6 | 5.63 | 6.55 | 3.863745316 | 0.029366 | hsa-miR-224-5p | MIMAT0000281 | 21 | CAAGUCACUAGUGGUUCCGUU |
| 20500555 | 6.25 | 7.91 | 7.46 | 3.160165247 | 0.029931 | hsa-miR-200b-5p | MIMAT0004571 | 22 | CAUCUUACUGGGCAGCAUUGGA |
| 20500556 | 7.5 | 9.13 | 8.4 | 3.095129987 | 0.046326 | hsa-miR-200b-3p | MIMAT0000318 | 22 | UAAUACUGCCUGGUAAUGAUGA |
| 20500722 | 4.01 | 5.01 | 5.77 | 3.386981249 | 0.003796 | hsa-miR-27b-5p | MIMAT0004588 | 22 | AGAGCUUAGCUGAUUGGUGAAC |
| 20500730 | 12.58 | 12.57 | 11.15 | 2.694467154 | 0.003039 | hsa-miR-125b-5p | MIMAT0000423 | 22 | UCCUGAGACCCUAACUUGUGA |
| 20500784 | 3.37 | 3.18 | 0.76 | 6.105036836 | 0.002713 | hsa-miR-154-5p | MIMAT0000452 | 22 | UAGGUUAUCCGUGUUGCCUUCG |
| 20500798 | 10.68 | 10.9 | 8.87 | 4.084048503 | 0.000612 | hsa-miR-195-5p | MIMAT0000461 | 21 | UAGCAGCACAGAAUAUUGGC |
| 20501159 | 3.14 | 2.49 | 1.55 | 3.010493495 | 0.048142 | hsa-miR-29c-5p | MIMAT0004673 | 22 | UGACCGAUUUCUCCUGGUGUUC |
| 20501172 | 1.08 | 1.98 | 0.64 | 2.531513188 | 0.024299 | hsa-miR-299-5p | MIMAT0002890 | 22 | UGGUUUACCGUCCCAUAACAU |
| 20501224 | 4.76 | 4.67 | 2.05 | 6.543216468 | 0.0358 | hsa-miR-376c-3p | MIMAT0000720 | 21 | AACAUAGAGGAAAUCCACGU |

| | | | | | | | | | |
|----------|------|------|------|-------------|----------|-------------------|--------------|----|--------------------------|
| 20501249 | 2.94 | 2.76 | 1.08 | 3.630076621 | 0.038799 | hsa-miR-381-3p | MIMAT0000736 | 22 | UAUACAAGGGCAAGCUCUCUGU |
| 20501281 | 4.72 | 3.77 | 2.02 | 6.498019171 | 0.032777 | hsa-miR-337-5p | MIMAT0004695 | 21 | GAACGGCUUCAUACAGGAGUU |
| 20502125 | 2.8 | 3.54 | 1.21 | 5.028053498 | 0.006824 | hsa-miR-424-5p | MIMAT0001341 | 22 | CAGCAGCAAUUCAUGUUUUGAA |
| 20502235 | 1.79 | 2.34 | 3.9 | 4.316912946 | 0.001094 | hsa-miR-18b-5p | MIMAT0001412 | 23 | UAAGGUGCAUCUAGUGCAGUUAG |
| 20502441 | 2.6 | 3.96 | 1.19 | 6.821079134 | 0.010122 | hsa-miR-433-3p | MIMAT0001627 | 22 | AUCAUGAUGGGCUCUCGGUGU |
| 20503803 | 8.1 | 7.73 | 7.09 | 2.0139111 | 0.021848 | hsa-miR-494-3p | MIMAT0002816 | 22 | UGAAACAUAACACGGGAAACCUC |
| 20503877 | 1.93 | 2.83 | 3.25 | 2.496661098 | 0.025726 | hsa-miR-501-5p | MIMAT0002872 | 22 | AAUCCUUUGUCCUCGGUGAGA |
| 20504325 | 1.8 | 2.85 | 3.45 | 3.138336392 | 0.039014 | hsa-miR-550a-3p | MIMAT0003257 | 22 | UGUCUUACUCCUCAGGCACAU |
| 20504353 | 0.82 | 1.61 | 2.03 | 2.313376368 | 0.038855 | hsa-miR-612 | MIMAT0003280 | 25 | GCUGGGCAGGGCUUCUGAGCUCCU |
| 20504357 | 0.33 | 0.41 | 1.82 | 2.808889751 | 0.006142 | hsa-miR-615-3p | MIMAT0003283 | 22 | UCCGAGCCUGGGUCUCCUCUU |
| 20504362 | 5.89 | 3.7 | 1.12 | 27.28431654 | 0.040973 | hsa-miR-617 | MIMAT0003286 | 22 | AGACUCCCAUUUGAAGGUGGC |
| 20504390 | 1.49 | 2.72 | 2.37 | 2.345669898 | 0.013819 | hsa-miR-637 | MIMAT0003307 | 24 | ACUGGGGGCUUUCGGCUCUGCGU |
| 20504407 | 1.14 | 2.22 | 2.38 | 2.361985323 | 0.004941 | hsa-miR-652-5p | MIMAT0022709 | 25 | CAACCCUAGGAGAGGGUGCCAUUC |
| 20504421 | 4.11 | 3.9 | 1.48 | 6.190259974 | 0.007056 | hsa-miR-654-3p | MIMAT0004814 | 22 | UAUGUCUGCUGACCAUCACCUU |
| 20504434 | 2.03 | 3.01 | 0.72 | 4.890561111 | 0.045974 | hsa-miR-542-5p | MIMAT0003340 | 23 | UCGGGAUCAUCAUGUCACGAGA |
| 20504556 | 2.06 | 3.06 | 3.26 | 2.29739671 | 0.009567 | hsa-miR-550a-3-5p | MIMAT0020925 | 20 | AGUGCCUGAGGGAGUAAGAG |
| 20505789 | 0.96 | 2.6 | 0.75 | 3.60500185 | 0.047856 | hsa-miR-885-5p | MIMAT0004947 | 22 | UCCAUUACACUACCCUGCCUCU |
| 20506002 | 3.41 | 4.67 | 4.58 | 2.394957409 | 0.016407 | hsa-miR-933 | MIMAT0004976 | 22 | UGUGCGCAGGGAGACCUCUCC |
| 20506818 | 1.18 | 1.73 | 4.73 | 11.71268557 | 0.001508 | hsa-miR-1290 | MIMAT0005880 | 19 | UGGAUUUUUGGAUCAGGGA |
| 20506837 | 7.1 | 7.75 | 8.8 | 3.249009585 | 0.009619 | hsa-miR-1246 | MIMAT0005898 | 19 | AAUGGAUUUUUGGAGCAGG |
| 20506887 | 1.92 | 2.64 | 3.04 | 2.173469725 | 0.000435 | hsa-miR-1292-5p | MIMAT0005943 | 25 | UGGGAACGGGUUCCGGCAGACGCU |
| 20509232 | 1.77 | 2.06 | 0.44 | 3.073750363 | 0.027465 | hsa-miR-1912 | MIMAT0007887 | 22 | UACCCAGAGCAUGCAGUGUGAA |
| 20509235 | 0.97 | 2.3 | 2.01 | 2.514026749 | 0.010508 | hsa-miR-1914-3p | MIMAT0007890 | 22 | GGAGGGGUCCGCACUGGGAGG |
| 20515607 | 8.5 | 9.48 | 9.68 | 2.265767771 | 0.002746 | hsa-miR-3178 | MIMAT0015055 | 17 | GGGGCGCGCCGGAUCG |
| 20515610 | 5.38 | 6.39 | 6.43 | 2.070529848 | 0.010024 | hsa-miR-3180-3p | MIMAT0015058 | 22 | UGGGGCGGAGCUUCCGGAGGCC |
| 20515623 | 3.09 | 4.01 | 4.11 | 2.02791896 | 0.013168 | hsa-miR-3187-3p | MIMAT0015069 | 20 | UUGGCAUGGGGUCGCGCGG |
| 20517817 | 0.49 | 1.87 | 1.52 | 2.602683711 | 0.005233 | hsa-miR-3610 | MIMAT0017987 | 20 | GAAUCGAAAGGAGGCGCCG |
| 20517821 | 6.53 | 7.32 | 7.99 | 2.751083636 | 0.02787 | hsa-miR-3613-3p | MIMAT0017991 | 24 | ACAAAAAAAAAAGCCAACCCUUC |
| 20517824 | 2.25 | 3.33 | 3.48 | 2.345669898 | 0.005343 | hsa-miR-3615 | MIMAT0017994 | 21 | UCUCUCGGUCUCCUCGCGGUC |
| 20517916 | 5 | 5.67 | 6.23 | 2.345669898 | 0.008639 | hsa-miR-3663-3p | MIMAT0018085 | 23 | UGAGCACACACAGGCCGGGCGC |
| 20518785 | 4.9 | 6.64 | 6.45 | 3.340351678 | 0.038644 | hsa-miR-4417 | MIMAT0018929 | 18 | GGUGGGCUUCCCGGAGGG |
| 20518818 | 6.23 | 6.88 | 7.36 | 2.188587403 | 0.029035 | hsa-miR-4443 | MIMAT0018961 | 17 | UUGGAGGCGUGGGUUUU |

| | | | | | | | | | |
|----------|------|------|------|-------------|----------|------------------|--------------|----|---------------------------|
| 20518844 | 5.67 | 5.57 | 4.42 | 2.37841423 | 0.046067 | hsa-miR-4462 | MIMAT0018986 | 23 | UGACACGGAGGGUGGCUUGGGAA |
| 20518919 | 4.91 | 4.76 | 6.43 | 3.182145935 | 0.006492 | hsa-miR-4521 | MIMAT0019058 | 22 | GCUAAGGAAGUCCUGUGCUCAG |
| 20519573 | 3.83 | 4.97 | 4.7 | 2.203810232 | 0.030294 | hsa-miR-4730 | MIMAT0019852 | 23 | CUGGCGGAGCCCAUCCAUGCCA |
| 20519588 | 2.33 | 3.82 | 3.77 | 2.808889751 | 0.025629 | hsa-miR-4738-3p | MIMAT0019867 | 22 | UGAAACUGGAGCGCCUGGAGGA |
| 20519670 | 1.75 | 3.22 | 3.29 | 2.907945035 | 0.000201 | hsa-miR-4783-3p | MIMAT0019947 | 23 | CCCCGUGUUGGGGCGGUCUGC |
| 20525414 | 3.44 | 4.6 | 4.86 | 2.67585511 | 0.024649 | hsa-miR-6726-5p | MIMAT0027353 | 21 | CGGGAGCUGGGGUCUGCAGGU |
| 20525432 | 2.51 | 3.88 | 3.39 | 2.584705661 | 0.016537 | hsa-miR-6735-5p | MIMAT0027371 | 25 | CAGGGCAGAGGGCACAGGAAUCUGA |
| 20525442 | 1.59 | 2.64 | 2.46 | 2.070529848 | 0.046065 | hsa-miR-6740-5p | MIMAT0027381 | 22 | AGUUUGGGAUGGAGAGAGGAGA |
| 20525509 | 3.47 | 4.56 | 4.55 | 2.128740365 | 0.001692 | hsa-miR-6774-5p | MIMAT0027448 | 25 | ACUUGGGCAGGAGGGACCCUGUAUG |
| 20525611 | 2.01 | 3.57 | 2.92 | 2.948538435 | 0.039101 | hsa-miR-6825-5p | MIMAT0027550 | 22 | UGGGGAGGUGUGGAGUCAGCAU |
| 20525633 | 4.46 | 5.12 | 5.77 | 2.4794154 | 0.005709 | hsa-miR-6780b-5p | MIMAT0027572 | 23 | UGGGGAAGGCUUGGCAGGGAAGA |
| 20525653 | 3.21 | 4.59 | 4.44 | 2.602683711 | 0.010016 | hsa-miR-6846-5p | MIMAT0027592 | 22 | UGGGGGCUGGAUGGGGUAGAGU |
| 20525701 | 3.9 | 4.71 | 5.08 | 2.265767771 | 0.017735 | hsa-miR-6870-5p | MIMAT0027640 | 19 | UGGGGGAGAUGGGGUUGA |
| 20525731 | 1.13 | 2.26 | 2.16 | 2.188587403 | 0.044783 | hsa-miR-6885-5p | MIMAT0027670 | 25 | AGGGGGGCACUGCGCAAGCAAAGCC |
| 20526180 | 3.94 | 5.03 | 4.71 | 2.128740365 | 0.024455 | hsa-miR-7111-5p | MIMAT0028119 | 22 | UGGGGGAGGAAGGACAGGCCAU |
| 20526182 | 2.29 | 3.45 | 3.64 | 2.549121255 | 0.014317 | hsa-miR-7112-5p | MIMAT0028121 | 22 | ACGGGCAGGGCAGUGCACCCUG |

Fold Change cut-off: 2.0

P-value cut-off: 0.05

Conditions: cervical cancer (SCC)_vs_CIN3_vs_Normal cervix

Column A: Transcript Cluster ID, it represents transcript cluster name.

Column B - D: Bi-weight Avg Signal (log2), Normalized Intensity of each group (averaged normalized intensities of each group, log2 transformed)

Column E: FC, the absolute ratio (no log scale) of normalized intensities between three conditions.

Column F: ANOVA P value (All Conditions), P value calculated from the student's t-test.

Column G: Transcript ID (Array Design).

Column H: Accession.

Column I: Sequence Length.

Column J: Sequence from miRBase.