# Enhanced renoprotective effect of IGF-1 modified human umbilical cord-derived mesenchymal stem cells on gentamicin-induced acute kidney injury

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# Supplementary File 1

## Genes up-regulated in UC-MSCs-IGF-1

| ProbeName | GeneSymbol | UC-MSCs | UC-MSCs-vector | UC-MSCs-IGF-1 |
|---|---|---|---|---|
| A_23_P43504 | ABCA2 | 143.00017 | 144.9118 | 324.24133 |
| A_23_P82249 | ABCB8 | 111.96739 | 105.19628 | 228.14723 |
| A_33_P3376947 | ABCB9 | 33.770687 | 33.0744 | 67.897484 |
| A_23_P128094 | ABCB9 | 33.542255 | 43.84322 | 118.340515 |
| A_23_P72584 | ACBD7 | 362.07004 | 240.36584 | 791.1804 |
| A_33_P3250730 | ACCN4 | 760.10706 | 626.6783 | 1520.4312 |
| A_23_P138881 | ACTN3 | 980.22864 | 753.5732 | 1785.7445 |
| A_33_P3864411 | ACTR3BP5 | 2410.9546 | 1120.9977 | 9312.506 |
| A_23_P115011 | ADAMTSL4 | 40.150295 | 49.596252 | 121.02768 |
| A_33_P3242383 | AFF1 | 8.383349 | 9.48024 | 14.392249 |
| A_33_P3253628 | AGXT2L2 | 38.195442 | 32.53493 | 69.54955 |
| A_33_P3368560 | AHSA2 | 339.60925 | 297.68933 | 842.3194 |
| A_33_P3260053 | AIF1L | 840.24005 | 745.17834 | 2082.4993 |
| A_33_P3238433 | ALDH3A1 | 40.597485 | 35.37849 | 65.37298 |
| A_24_P131580 | ALPPL2 | 1037.5648 | 850.5033 | 2010.5139 |
| A_33_P3291279 | ANKRD56 | 4.9999995 | 15.662179 | 58.75549 |
| A_33_P3278455 | ANKRD6 | 7.2751503 | 7.164659 | 14.865142 |
| A_32_P148345 | ANXA2 | 4853.517 | 2675.2837 | 10414.334 |
| A_24_P87931 | APOL1 | 1212.4629 | 1217.6804 | 3086.375 |
| A_23_P73511 | ARAF | 585.19934 | 486.83337 | 1193.5731 |
| A_24_P33895 | ATF3 | 19.885704 | 27.230991 | 48.695602 |
| A_24_P307626 | ATP1A4 | 700.2628 | 728.724 | 1525.9015 |
| A_23_P146146 | ATP6V0D2 | 8.045739 | 6.7342277 | 18.346968 |
| A_24_P276932 | ATP6V1C2 | 183.98972 | 158.33847 | 375.15375 |
| A_33_P3282978 | BAALC | 188.81126 | 168.63252 | 641.60706 |
| A_33_P3285470 | BAI1 | 32.718124 | 29.61538 | 54.659824 |
| A_33_P3251932 | BCL2L11 | 304.18738 | 213.02867 | 821.37335 |
| A_32_P69849 | BEX5 | 35.98655 | 32.56157 | 295.44547 |
| A_24_P57898 | BHLHE23 | 1148.1241 | 941.11127 | 3000.5298 |
| A_24_P231829 | BHMT2 | 16.252262 | 17.593092 | 33.894016 |
| A_33_P3503284 | BOD1P | 6.8263745 | 5.981133 | 12.527021 |
| A_23_P254797 | BPIFB2 | 90.760704 | 83.15059 | 237.89432 |
| A_23_P89973 | BRSK1 | 32.37556 | 26.66769 | 91.67442 |
| A_33_P3288431 | C12orf50 | 10.746909 | 17.05764 | 35.182755 |
| A_33_P3403459 | C14orf167 | 512.9974 | 441.87592 | 981.4865 |
| A_33_P3396275 | C15orf62 | 194.47903 | 140.84279 | 357.31705 |
| A_24_P456490 | C1orf204 | 8.098513 | 15.395879 | 25.641928 |
| A_23_P3956 | C1QTNF1 | 349.87204 | 345.52832 | 1020.1469 |
| A_33_P3380772 | C20orf160 | 3756.2148 | 3655.0544 | 11135.831 |
| A_23_P132139 | C21orf58 | 347.93884 | 290.62076 | 1085.799 |

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|---|---|---|---|---|
| A_33_P3394252 | C2orf67 | 34.688705 | 27.868618 | 55.686687 |
| A_33_P3347869 | C3 | 410.73798 | 502.32687 | 1140.1812 |
| A_23_P2431 | C3AR1 | 6571.2256 | 7387.1514 | 15021.205 |
| A_23_P312383 | C5orf64 | 7.9948153 | 8.896511 | 14.6351 |
| A_24_P100650 | C9orf11 | 4.9999995 | 5.2086687 | 6.9475245 |
| A_24_P401870 | C9orf139 | 15.436991 | 10.972792 | 28.59563 |
| A_33_P3359223 | C9orf173 | 1308.318 | 1155.6991 | 2545.752 |
| A_23_P307502 | C9orf53 | 216.41455 | 189.42609 | 1053.3795 |
| A_24_P303874 | C9orf62 | 815.2112 | 502.31094 | 2717.0735 |
| A_33_P3334398 | CA6 | 635.76227 | 648.6666 | 1358.1013 |
| A_33_P3318646 | CALY | 7464.1274 | 7242.137 | 22848.09 |
| A_24_P292929 | CAMKK1 | 10.118651 | 12.004202 | 23.50445 |
| A_23_P138835 | CAPN1 | 1877.1244 | 2085.2048 | 5174.0835 |
| A_23_P217570 | CAPN6 | 7.224693 | 10.600702 | 16.244148 |
| A_23_P152406 | CAPNS2 | 784.1337 | 653.3245 | 1506.6105 |
| A_23_P126752 | CAPZB | 5667.146 | 5453.0312 | 12272.863 |
| A_24_P3045 | CASP10 | 12.08541 | 15.1755705 | 23.889343 |
| A_33_P3257594 | CCDC103 | 19.160599 | 13.386822 | 34.54912 |
| A_33_P3261054 | CCDC114 | 11.218641 | 22.625563 | 39.943283 |
| A_33_P3246613 | CCDC78 | 6842.084 | 7136.498 | 16831.371 |
| A_23_P207456 | CCL8 | 6.340178 | 19.452358 | 33.151234 |
| A_23_P343398 | CCR7 | 26.99001 | 31.058153 | 41.94847 |
| A_33_P3234292 | CD244 | 23.800396 | 22.742418 | 41.29029 |
| A_33_P3245439 | CD40 | 10.8409 | 16.876284 | 33.906578 |
| A_23_P40192 | CDH22 | 2244.1453 | 2382.2957 | 5369.2783 |
| A_23_P154050 | CDK15 | 36.533554 | 33.27653 | 292.59503 |
| A_24_P118376 | CEACAM20 | 4669.6055 | 3786.65 | 10017.041 |
| A_33_P3671378 | CERCAM | 383.16586 | 312.1826 | 805.84625 |
| A_23_P5679 | CFC1 | 4.9999995 | 8.237859 | 11.970499 |
| A_33_P3376965 | CHAC1 | 2152.0273 | 1435.451 | 4717.5127 |
| A_23_P349463 | CHP2 | 7.8933153 | 9.4271 | 15.345508 |
| A_33_P3345186 | CHST13 | 110.01203 | 76.172874 | 216.62065 |
| A_33_P3299739 | CLDN19 | 1793.792 | 1176.0189 | 3568.879 |
| A_33_P3775848 | CLIC2 | 5.8539605 | 8.739239 | 14.199943 |
| A_23_P215479 | CLIP2 | 1139.3367 | 930.72015 | 2098.9053 |
| A_24_P269551 | CLVS1 | 4.9999995 | 4.9999995 | 10.914868 |
| A_23_P37718 | CNGB1 | 56.267166 | 39.023045 | 96.37552 |
| A_33_P3220347 | CNPY1 | 30.522774 | 26.130253 | 49.027847 |
| A_33_P3216448 | COL11A2 | 202.21225 | 215.1566 | 785.67316 |
| A_33_P3269539 | COL6A2 | 5323.8877 | 5579.7944 | 15041.038 |
| A_33_P3210488 | COL6A3 | 8308.847 | 6329.138 | 15648.159 |
| A_23_P2474 | COPS7A | 1487.7974 | 1373.6381 | 2840.3655 |
| A_33_P3378284 | COX6B2 | 3868.9683 | 2975.1443 | 9286.767 |
| A_33_P3343196 | CP | 6.6754756 | 5.836154 | 18.808216 |

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|---|---|---|---|---|
| A_33_P3222424 | CSF3 | 1371.932 | 314.37628 | 2423.5107 |
| A_23_P170453 | CST5 | 775.81476 | 723.8127 | 1700.8323 |
| A_33_P3357979 | CTBP1 | 335.72968 | 316.92584 | 755.501 |
| A_32_P86150 | CTRB2 | 1457.7062 | 1178.489 | 3076.1238 |
| A_33_P3355580 | CTSL3 | 20.808908 | 17.952648 | 296.6196 |
| A_33_P3712341 | CXCL12 | 333.33563 | 291.34283 | 521.9166 |
| A_33_P3261132 | CYCSP52 | 53.63392 | 30.849384 | 118.466606 |
| A_33_P3285868 | CYGB | 2332.327 | 1731.1384 | 5620.17 |
| A_23_P215997 | CYP11B2 | 6.2548456 | 10.37883 | 16.32613 |
| A_23_P208373 | CYP2B6 | 123.29476 | 106.20361 | 346.0602 |
| A_33_P3303474 | CYP4A11 | 17.328028 | 11.14476 | 27.112778 |
| A_23_P146198 | CYP7A1 | 4.9999995 | 8.6325655 | 11.785751 |
| A_23_P115161 | DARC | 5.345743 | 8.400822 | 11.821681 |
| A_23_P212105 | DAZL | 12.177572 | 13.180187 | 24.480429 |
| A_23_P50399 | DCAF15 | 184.45161 | 103.592285 | 392.43973 |
| A_33_P3768992 | DCAF4L2 | 5.226402 | 35.004555 | 85.459 |
| A_33_P3346083 | DCDC1 | 7.397402 | 11.853419 | 32.4891 |
| A_33_P3264577 | DCTN1 | 2288.6152 | 2004.3037 | 4507.34 |
| A_23_P93311 | DDR1 | 379.52832 | 568.3353 | 747.24023 |
| A_33_P3724155 | DERL3 | 1200.8143 | 933.4657 | 3122.8887 |
| A_33_P3330125 | DIABLO | 3109.8345 | 3258.4724 | 6955.773 |
| A_24_P236251 | DLK1 | 22.837652 | 18.52143 | 42.196243 |
| A_23_P359457 | DNAH2 | 99.43101 | 79.95397 | 188.62851 |
| A_23_P255876 | DNAI1 | 10.05623 | 11.767361 | 28.286093 |
| A_33_P3285629 | DNAI2 | 7.440089 | 9.154515 | 13.9415 |
| A_24_P50091 | DNM1P46 | 23.73833 | 24.388523 | 43.50886 |
| A_24_P359405 | DTX3 | 60.98432 | 59.700737 | 119.94491 |
| A_23_P347432 | DVL1 | 446.7325 | 319.22818 | 819.4416 |
| A_23_P171132 | EDA2R | 28.928463 | 22.62024 | 75.50574 |
| A_32_P83049 | EFR3B | 888.5846 | 887.48865 | 2168.9597 |
| A_23_P20894 | EHMT1 | 153.00508 | 131.25917 | 285.66022 |
| A_33_P3402116 | EIF2C1 | 1908.3202 | 1505.8757 | 3985.8862 |
| A_33_P3268478 | ENO4 | 4.9999995 | 12.885479 | 19.461363 |
| A_23_P351 | EPB41 | 13.601318 | 19.226429 | 32.341446 |
| A_24_P63537 | ERAP1 | 4.9999995 | 7.1176586 | 10.30415 |
| A_24_P314585 | ERAS | 24.75101 | 26.317026 | 57.728813 |
| A_33_P3235432 | ESYT3 | 238.95398 | 218.05273 | 662.5407 |
| A_23_P8820 | FABP4 | 9.245049 | 13.43238 | 26.16549 |
| A_33_P3424861 | FAM118A | 1041.5835 | 970.2659 | 3412.0127 |
| A_33_P3279124 | FAM21C | 3599.1353 | 2845.782 | 7034.3105 |
| A_24_P941898 | FAM22D | 28.064476 | 23.07835 | 43.95513 |
| A_23_P45488 | FAM3A | 278.0447 | 309.96448 | 680.29156 |
| A_32_P70203 | FAM41C | 8.87177 | 13.453199 | 25.558752 |
| A_23_P21560 | FAM49A | 26.225498 | 31.623318 | 63.61314 |

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|---|---|---|---|---|
| A_23_P364444 | FAM65C | 17.32068 | 8.565667 | 28.717138 |
| A_32_P6221 | FAM86C2P | 38.568775 | 39.663002 | 85.20486 |
| A_33_P3257513 | FAT3 | 1244.7169 | 921.11993 | 2725.9192 |
| A_23_P200637 | FBXO44 | 92.87148 | 86.60386 | 241.66374 |
| A_23_P160849 | FCER1G | 739.4592 | 645.2411 | 1353.8069 |
| A_24_P276576 | FCRLA | 6.772625 | 10.02719 | 20.165169 |
| A_33_P3380797 | FGF3 | 36.10452 | 27.773647 | 70.079445 |
| A_23_P316447 | FGFR1 | 22.48515 | 19.525677 | 40.070698 |
| A_24_P147540 | FLJ22184 | 5640.107 | 4369.0483 | 17799.59 |
| A_33_P3739870 | FLJ31183 | 26.138071 | 8.483534 | 54.025085 |
| A_33_P3325843 | FLJ40039 | 419.46707 | 355.61554 | 1111.001 |
| A_33_P3421084 | FLJ42289 | 6.7124248 | 8.458752 | 11.590111 |
| A_24_P252996 | FOLR3 | 8.877824 | 11.708019 | 18.41986 |
| A_33_P3264331 | FOXD3 | 5.0444684 | 6.34313 | 9.387477 |
| A_33_P3269403 | FOXI1 | 4.9999995 | 4.9999995 | 10.23001 |
| A_33_P3249793 | FOXO4 | 10.272988 | 12.979392 | 47276.707 |
| A_33_P3284019 | FOXP4 | 3569.4924 | 2918.8525 | 13327.459 |
| A_24_P738168 | FREM3 | 4.9999995 | 5.218929 | 6.9840865 |
| A_32_P160896 | FTMT | 222.89832 | 174.24857 | 643.5457 |
| A_24_P393740 | FYB | 5.612754 | 4.9999995 | 17.933393 |
| A_23_P252462 | GALNT9 | 69.66866 | 45.429695 | 140.73468 |
| A_33_P3323822 | GATAD2B | 36.991116 | 34.954185 | 77.28077 |
| A_23_P130642 | GBP6 | 2018.7867 | 1626.5309 | 3773.9456 |
| A_32_P197621 | GEMIN8P4 | 4.9999995 | 4.9999995 | 11.29536 |
| A_33_P3377100 | GHRH | 22.98347 | 16.921608 | 50.116623 |
| A_33_P3273767 | GJB7 | 4.9999995 | 4.9999995 | 23.264036 |
| A_33_P3264790 | GJD4 | 17.29674 | 18.477417 | 30.238426 |
| A_33_P3285715 | GLI4 | 6679.593 | 6092.8467 | 17635.752 |
| A_23_P67913 | GMPPA | 356.6344 | 340.1793 | 752.49054 |
| A_24_P319374 | GPA33 | 4.9999995 | 4.9999995 | 6.577977 |
| A_23_P416686 | GPR137 | 166.3395 | 167.98088 | 380.02615 |
| A_33_P3302586 | GPR153 | 38.81 | 31.637514 | 71.5682 |
| A_23_P142096 | GPR32 | 113.4688 | 101.21466 | 423.48154 |
| A_33_P3369371 | GPX3 | 8.7216835 | 11.86791 | 27.992579 |
| A_32_P380675 | GRIP2 | 8.769227 | 7.167501 | 26.132267 |
| A_23_P58869 | GSTM2P1 | 100.991066 | 104.038315 | 253.492 |
| A_23_P41304 | GYPE | 8.134949 | 11.92808 | 19.527039 |
| A_23_P28697 | HAAO | 236.46577 | 184.64052 | 506.16745 |
| A_33_P3319640 | HDGFRP2 | 219.68857 | 165.88336 | 459.1838 |
| A_23_P149221 | HECTD3 | 204.83034 | 185.30913 | 405.3724 |
| A_24_P213950 | HEPACAM | 21.585857 | 25.094572 | 43.366066 |
| A_24_P51201 | HERC3 | 13.438958 | 12.767268 | 25.85841 |
| A_23_P250358 | HERC6 | 4.9999995 | 9.303241 | 15.611818 |
| A_33_P3322859 | HES6 | 2110.1333 | 2018.0422 | 4911.6807 |

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|---|---|---|---|---|
| A_33_P3338152 | HIF3A | 2066.5056 | 1635.9553 | 4688.3984 |
| A_23_P40347 | HM13 | 2015.8291 | 1705.0525 | 3789.189 |
| A_33_P3598466 | HSP90AB6P | 187.85297 | 104.694405 | 404.59015 |
| A_33_P3331120 | HSPBAP1 | 4.9999995 | 9.592722 | 13.867079 |
| A_33_P3212665 | HTATSF1P2 | 96.94246 | 102.5124 | 234.17934 |
| A_33_P3421984 | HYAL4 | 1735.94 | 1566.4999 | 3500.5132 |
| A_33_P3423551 | IER3 | 4740.129 | 2456.847 | 5840.357 |
| A_23_P13907 | IGF1 | 22.903273 | 19.563646 | 90486.32 |
| A_24_P382187 | IGFBP4 | 5180.8223 | 6726.9834 | 15495.363 |
| A_33_P3371954 | IGSF8 | 104.29571 | 103.85911 | 223.25415 |
| A_23_P166775 | IL17RC | 238.94522 | 288.94693 | 776.5726 |
| A_33_P3374190 | INPP5A | 124.050064 | 101.09239 | 242.25346 |
| A_32_P178800 | ITGA2 | 1176.8625 | 790.4658 | 1733.2545 |
| A_23_P36562 | ITGA5 | 5723.1455 | 4755.7305 | 13252.723 |
| A_33_P3398143 | ITGB2 | 158.05054 | 114.024536 | 171.76271 |
| A_33_P3806721 | JMJD5 | 635.5576 | 525.6821 | 1190.8912 |
| A_33_P3220929 | JOSD2 | 71.460205 | 56.79389 | 179.50595 |
| A_33_P3326020 | KANK3 | 166.30942 | 151.79167 | 405.16586 |
| A_33_P3395823 | KCNQ2 | 438.43796 | 370.7622 | 948.38306 |
| A_33_P3290955 | KIAA1875 | 1881.5011 | 1615.3722 | 4920.1133 |
| A_33_P3330643 | KIF6 | 4.9999995 | 8.924842 | 56.879498 |
| A_24_P376047 | KLK4 | 9.798246 | 14.224777 | 22.724497 |
| A_33_P3315263 | KRT79 | 17.098412 | 22.570015 | 68.39792 |
| A_33_P3273534 | KRT81 | 12266.407 | 10800.171 | 31019.543 |
| A_23_P15734 | KRT9 | 193.9567 | 152.42554 | 366.80035 |
| A_24_P142495 | KRTAP1-3 | 3103.056 | 2555.4248 | 6288.71 |
| A_33_P3251421 | KRTAP21-1 | 144.64203 | 100.943184 | 266.32657 |
| A_33_P3388061 | KRTAP21-2 | 8.7592745 | 10.397809 | 18.832228 |
| A_23_P153022 | KRTAP2-4 | 3821.783 | 2496.7808 | 7256.2593 |
| A_33_P3363310 | KRTAP5-10 | 461.7293 | 346.92096 | 876.62787 |
| A_24_P11506 | KYNU | 91.32153 | 71.71939 | 173.06717 |
| A_33_P3277532 | LAMC3 | 9.814722 | 13.882019 | 24.89652 |
| A_23_P86493 | LBX1 | 6676.11 | 6143.6562 | 15129.918 |
| A_23_P63521 | LCE2C | 7.8203964 | 15.52767 | 67.13546 |
| A_23_P369471 | LCE3A | 26.041122 | 16.416971 | 105.77049 |
| A_33_P3423931 | LCN9 | 141.38783 | 105.139626 | 216.00266 |
| A_33_P3236441 | LDHAL6A | 1351.7725 | 1176.8013 | 3163.6216 |
| A_33_P3405022 | LETM1 | 253.30156 | 211.2666 | 618.6198 |
| A_23_P434518 | LFNG | 347.78708 | 291.06485 | 788.4545 |
| A_33_P3310274 | LGR6 | 14.70221 | 13.271608 | 22.563162 |
| A_33_P3223678 | LHX3 | 1620.0239 | 1466.2378 | 4690.612 |
| A_33_P3268181 | LIMS2 | 103.2851 | 96.33829 | 239.82877 |
| A_33_P3403082 | LINC00176 | 2165.925 | 2031.4722 | 6091.2886 |
| A_33_P3278813 | LOC100127885 | 5.5601974 | 12.521021 | 23.320822 |

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|---|---|---|---|---|
| A_33_P3293469 | LOC100128105 | 9.291117 | 8.741138 | 14.466649 |
| A_33_P3397180 | LOC100129324 | 376.4139 | 317.59338 | 875.1867 |
| A_33_P3364964 | LOC100129596 | 415.7665 | 274.01447 | 837.4492 |
| A_33_P3287661 | LOC100130430 | 248.21709 | 255.2769 | 898.8748 |
| A_33_P3314974 | LOC100130522 | 492.23355 | 300.62598 | 934.6092 |
| A_33_P3351259 | LOC100130560 | 265.36392 | 264.36664 | 649.66907 |
| A_33_P3298092 | LOC100131756 | 18.050398 | 12.94697 | 33.25587 |
| A_33_P3386686 | LOC100132874 | 2408.4075 | 1753.9547 | 4376.917 |
| A_33_P3236340 | LOC100133131 | 478.4627 | 412.8514 | 1104.5349 |
| A_32_P45974 | LOC100134167 | 18.041016 | 22.36186 | 43.3951 |
| A_33_P3875565 | LOC100270679 | 50.104927 | 38.72071 | 97.346405 |
| A_33_P3518572 | LOC100287314 | 604.6346 | 437.1172 | 1164.3741 |
| A_33_P3233459 | LOC100287879 | 140.48401 | 121.14562 | 402.60495 |
| A_33_P3419621 | LOC100289580 | 64.4412 | 58.378815 | 118.50413 |
| A_33_P3233070 | LOC100505564 | 26.840431 | 29.653402 | 62.72697 |
| A_33_P3392000 | LOC100506190 | 1455.3713 | 1177.1599 | 3367.719 |
| A_23_P436145 | LOC100507431 | 4.9999995 | 4.9999995 | 9.922209 |
| A_33_P3415247 | LOC115110 | 7.301587 | 5.439678 | 18.28068 |
| A_33_P3452003 | LOC143286 | 504.6033 | 423.10687 | 996.3411 |
| A_33_P3339436 | LOC145845 | 87.12869 | 84.04632 | 293.9754 |
| A_24_P520767 | LOC149351 | 19.44016 | 21.669342 | 35.693394 |
| A_24_P918907 | LOC154761 | 10.010069 | 14.41083 | 26.045614 |
| A_33_P3464749 | LOC253044 | 4.9999995 | 9.488324 | 13.688929 |
| A_33_P3870056 | LOC283335 | 147.20842 | 109.88357 | 534.8474 |
| A_33_P3336587 | LOC283710 | 66.05248 | 44.79729 | 115.01159 |
| A_33_P3663105 | LOC284263 | 4.9999995 | 11.275981 | 20.06314 |
| A_33_P3317623 | LOC284379 | 480.3613 | 514.0612 | 1356.8881 |
| A_33_P3461633 | LOC284454 | 356.3099 | 309.59464 | 879.50275 |
| A_24_P33446 | LOC338651 | 4.9999995 | 6.84043 | 13.645407 |
| A_33_P3832872 | LOC389247 | 5.408224 | 5.489724 | 11.16878 |
| A_32_P202703 | LOC389831 | 821.559 | 540.76514 | 15780.206 |
| A_33_P3550618 | LOC400541 | 21.333595 | 16.067886 | 32.937527 |
| A_33_P3235132 | LOC400968 | 1428.3899 | 1069.1561 | 2656.4155 |
| A_33_P3780572 | LOC401164 | 16.685528 | 16.827765 | 30.25871 |
| A_33_P3344690 | LOC442421 | 4.9999995 | 4.9999995 | 32.142647 |
| A_24_P144303 | LOC442459 | 187.40144 | 150.89633 | 436.9219 |
| A_33_P3293391 | LOC642826 | 258.36377 | 233.24072 | 522.37604 |
| A_32_P60635 | LOC643037 | 4.9999995 | 6.326512 | 8.824883 |
| A_33_P3300332 | LOC644093 | 34.475445 | 38.259983 | 107.61461 |
| A_33_P3339720 | LOC644841 | 7.156799 | 4.9999995 | 16.166918 |
| A_33_P3667484 | LOC648740 | 11004.355 | 7646.4463 | 22295.143 |
| A_33_P3395442 | LOC678655 | 68.47123 | 81.8008 | 175.84273 |
| A_32_P173114 | LOC729444 | 4.9999995 | 5.0886765 | 7.656175 |
| A_23_P436048 | LPAR3 | 31.85344 | 25.922873 | 51.589188 |

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| A_23_P153461 | LPPR2 | 200.4694 | 235.62444 | 539.5444 |
| A_23_P163195 | LRFN5 | 4.9999995 | 7.966208 | 11.421339 |
| A_33_P3391105 | LRP1 | 675.8711 | 663.0362 | 922.0008 |
| A_24_P99216 | LRP10 | 1555.6791 | 1431.055 | 3348.026 |
| A_24_P827037 | LRRC15 | 29.411993 | 17.903082 | 56.272167 |
| A_24_P240259 | LRRC31 | 4.9999995 | 4.9999995 | 12.158399 |
| A_33_P3420446 | LRRD1 | 190.13432 | 138.11653 | 593.719 |
| A_33_P3418194 | LYNX1 | 621.9147 | 493.76163 | 2742.252 |
| A_23_P62099 | MAGEC2 | 4.9999995 | 4.9999995 | 6.511168 |
| A_23_P163455 | MAP1A | 2300.875 | 2208.2961 | 5746.5396 |
| A_23_P308483 | MAP3K15 | 8.182247 | 8.978967 | 18.410477 |
| A_24_P119201 | MBD2 | 9.934969 | 7.328211 | 16.507586 |
| A_23_P50121 | MC4R | 9.709909 | 11.1790495 | 17.874731 |
| A_32_P850175 | MCF2L2 | 10.13384 | 7.5501876 | 19.739027 |
| A_23_P28507 | MGAT4A | 5.608346 | 6.289719 | 9.372455 |
| A_32_P183918 | MGC39372 | 16.739468 | 14.7769 | 26.089159 |
| A_23_P13873 | MLF2 | 4619.283 | 3877.0022 | 8357.145 |
| A_33_P3415216 | MPV17 | 3754.0083 | 3780.6199 | 5248.88 |
| A_24_P146683 | MSMB | 6.9790688 | 11.560231 | 17.533607 |
| A_23_P129629 | MT3 | 3537.8735 | 2226.32 | 5354.912 |
| A_23_P152125 | MVD | 184.32596 | 306.88812 | 760.6625 |
| A_33_P3255829 | MXRA5 | 4.9999995 | 6.0080853 | 13.026199 |
| A_24_P324314 | MXRA7 | 918.6445 | 748.90765 | 1726.5294 |
| A_23_P258018 | MYL5 | 412.68198 | 344.43005 | 805.7647 |
| A_33_P3238157 | MYO18A | 221.44519 | 209.9552 | 465.35452 |
| A_23_P78122 | MYO18A | 482.42114 | 547.09436 | 1180.8346 |
| A_33_P3395688 | MYZAP | 7.6978035 | 7.3183293 | 18.917063 |
| A_23_P138194 | NCF2 | 4.9999995 | 4.9999995 | 8.253653 |
| A_23_P29638 | NCKIPSD | 118.061066 | 136.13339 | 307.2913 |
| A_23_P9614 | NDUFA4L2 | 11.43466 | 18.114784 | 34.570194 |
| A_24_P99639 | NEK8 | 5.4288726 | 12.952899 | 65.685486 |
| A_33_P3293524 | NEURL | 573.0149 | 356.3073 | 1571.3599 |
| A_33_P3856171 | NF1P2 | 10.563909 | 8.544691 | 23.675388 |
| A_33_P3260342 | NFASC | 16.216602 | 17.38201 | 37.00738 |
| A_33_P3225600 | NFE2L2 | 94.21539 | 56.384766 | 379.15768 |
| A_23_P202156 | NFKB2 | 319.2624 | 263.9718 | 737.6105 |
| A_33_P3386506 | NFKBIL1 | 5105.737 | 4366.594 | 11070.546 |
| A_33_P3299599 | NKX2-5 | 4800.8354 | 4744.3765 | 15700.566 |
| A_23_P340019 | NLRC3 | 4.9999995 | 6.0873084 | 11.949249 |
| A_24_P918384 | NSD1 | 44.65188 | 40.770264 | 107.73917 |
| A_23_P44836 | NT5DC2 | 5465.8394 | 5430.7715 | 13122.719 |
| A_24_P391586 | OAF | 571.40546 | 407.7223 | 1117.4958 |
| A_23_P64828 | OAS1 | 9.009503 | 24.848978 | 43.10678 |
| A_24_P335305 | OAS3 | 77.87376 | 68.03186 | 141.57222 |

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| A_33_P3379680 | OR2A5 | 24.070017 | 19.354853 | 55.591576 |
| A_23_P111092 | OR2H1 | 5155.439 | 3616.8894 | 9591.939 |
| A_33_P3360157 | OR5AS1 | 5.3366446 | 4.9999995 | 9.228104 |
| A_23_P254852 | OTOF | 2168.6443 | 1785.1403 | 3816.272 |
| A_23_P127721 | P2RX3 | 161.20464 | 158.90848 | 428.58392 |
| A_33_P3394933 | P4HA2 | 273.8868 | 260.19095 | 566.18854 |
| A_23_P48307 | PABPC3 | 7011.0576 | 5068.4746 | 14490.068 |
| A_23_P126869 | PADI3 | 13.9582205 | 10.191319 | 22.642784 |
| A_33_P3358213 | PADI6 | 11.24494 | 11.406299 | 17.36259 |
| A_33_P3216890 | PAG1 | 4.9999995 | 6.653037 | 13.08615 |
| A_33_P3588134 | PANX2 | 51.97705 | 46.548206 | 103.464584 |
| A_23_P40718 | PARVB | 618.53064 | 539.2463 | 1352.0219 |
| A_33_P3224362 | PCBP3 | 28.766157 | 21.006865 | 62.212772 |
| A_33_P3262927 | PCBP4 | 254.24626 | 212.70805 | 491.51984 |
| A_33_P3332521 | PCDHA3 | 8.4072695 | 9.09601 | 13.172782 |
| A_24_P14731 | PCSK1N | 1874.0273 | 1809.8511 | 4543.056 |
| A_23_P23090 | PDC | 10.03621 | 11.0642 | 19.054798 |
| A_23_P208334 | PDE4A | 51.18814 | 48.34205 | 92.2323 |
| A_23_P149992 | PDLIM1 | 972.15155 | 929.3897 | 1954.0232 |
| A_33_P3217213 | PDLIM7 | 2411.047 | 2012.6615 | 4722.8516 |
| A_24_P339944 | PDGFB | 139.495893 | 128.487234 | 198.73865 |
| A_23_P29079 | PFKL | 511.7114 | 501.6675 | 3167.1765 |
| A_23_P350059 | PFN1P2 | 9617.157 | 6908.0493 | 28877.848 |
| A_23_P80684 | PHF7 | 20.34176 | 18.10197 | 77.43269 |
| A_23_P1519 | PITPNM1 | 195.86589 | 194.17113 | 411.45758 |
| A_23_P67271 | PKN1 | 779.5603 | 731.8019 | 1584.073 |
| A_23_P88222 | PLD4 | 7.898032 | 15.3332615 | 31.178026 |
| A_33_P3272539 | PLEKHG5 | 1974.2712 | 1592.0123 | 3714.4072 |
| A_23_P5983 | PLTP | 600.4754 | 661.3265 | 1512.262 |
| A_33_P3321034 | PLXNA4 | 229.1182 | 187.20372 | 461.04977 |
| A_23_P10077 | PNPLA2 | 287.72745 | 291.02023 | 687.9377 |
| A_23_P16166 | PNPLA6 | 770.33246 | 727.3601 | 2033.1124 |
| A_23_P211227 | POFUT2 | 156.39061 | 188.00117 | 541.39966 |
| A_23_P215669 | POLR2J2 | 295.4269 | 264.5175 | 802.222 |
| A_23_P252062 | PPARG | 67.1474 | 119.04879 | 180.25668 |
| A_33_P3239123 | PPIH | 27.955992 | 25.280125 | 43.81241 |
| A_33_P3594854 | PPIP5K1 | 15.994747 | 13.113091 | 28.012339 |
| A_33_P3252048 | PPP1R27 | 279.70087 | 243.07716 | 818.00415 |
| A_23_P60458 | PPP2R4 | 2160.2427 | 2059.0278 | 4531.2095 |
| A_23_P119448 | PPP6R1 | 78.05328 | 62.446056 | 182.2467 |
| A_24_P396197 | PRKCSH | 1070.4382 | 910.31024 | 2162.4644 |
| A_24_P349466 | PRR13 | 437.68536 | 251.21716 | 1147.1273 |
| A_33_P3222769 | PRR25 | 1614.801 | 1553.2941 | 3658.7117 |
| A_24_P412734 | PRSS36 | 398.17596 | 341.33438 | 890.8554 |

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|---|---|---|---|---|
| A_33_P3329088 | PRSS8 | 21.412249 | 15.3079405 | 132.98608 |
| A_23_P68121 | PSD4 | 33.709854 | 30.42616 | 57.616863 |
| A_23_P325080 | PTOV1 | 660.4667 | 689.0477 | 1600.7446 |
| A_23_P396062 | RAB40C | 251.93425 | 262.0271 | 665.1328 |
| A_23_P54223 | RABGGTA | 176.08432 | 179.10118 | 387.03064 |
| A_24_P228717 | RAC2 | 832.6898 | 673.28564 | 1619.2146 |
| A_33_P3276323 | RAD21-AS1 | 4.9999995 | 6.896128 | 11.185961 |
| A_23_P151307 | RAPGEF3 | 14.521219 | 23.660275 | 39.771145 |
| A_33_P3499102 | RBM10 | 444.57962 | 317.16916 | 932.88336 |
| A_23_P67339 | RCN3 | 2331.2695 | 2045.0522 | 4686.924 |
| A_33_P3259861 | REREP3 | 759.58167 | 570.29266 | 1428.9933 |
| A_33_P3222962 | RIBC1 | 4.9999995 | 8.73123 | 23.846466 |
| A_33_P3336632 | RN28S1 | 111.95033 | 410.0828 | 1045.7554 |
| A_24_P297480 | RNF113B | 29.20837 | 26.840555 | 64.008545 |
| A_24_P344295 | RNF167 | 166.95015 | 130.32417 | 322.89682 |
| A_23_P364890 | RNF40 | 431.39618 | 350.65604 | 813.73004 |
| A_32_P203013 | RPS10P7 | 10708.734 | 8521.9375 | 29480.885 |
| A_24_P242036 | RRP7B | 828.81006 | 678.8976 | 1631.8995 |
| A_24_P55225 | RSPH9 | 198.88449 | 211.04146 | 581.48627 |
| A_24_P221575 | RUFY3 | 115.64557 | 98.43985 | 220.13405 |
| A_33_P3409086 | S100A1 | 57.88141 | 39.910976 | 106.669525 |
| A_23_P435941 | SAMD1 | 557.0909 | 442.3646 | 1036.479 |
| A_33_P3220152 | SBNO2 | 468.01624 | 379.80966 | 927.93115 |
| A_24_P117672 | SCAF1 | 863.194 | 684.4654 | 2243.5415 |
| A_23_P105144 | SCUBE2 | 10.176085 | 18.00499 | 31.006561 |
| A_33_P3287529 | SDF4 | 2759.85 | 2861.255 | 6153.3174 |
| A_33_P3348224 | SEC14L6 | 8.01586 | 14.004959 | 35.06084 |
| A_33_P3474175 | SFTA1P | 2669.274 | 2351.1113 | 8465.863 |
| A_23_P130553 | SHKBP1 | 479.81418 | 599.57623 | 1491.2563 |
| A_24_P304311 | SLC22A8 | 11.9052 | 17.370478 | 30.027246 |
| A_24_P111054 | SLC2A5 | 538.9491 | 424.42877 | 1091.1118 |
| A_33_P3385006 | SLC39A5 | 20.989243 | 13.007971 | 36.529305 |
| A_33_P3241696 | SLC45A2 | 13.65756 | 39.384727 | 91.57979 |
| A_33_P3411035 | SLIT1 | 8.811284 | 8.850543 | 193.9951 |
| A_24_P83922 | SNRPC | 155.47775 | 87.23574 | 448.7576 |
| A_33_P3414192 | SORCS1 | 35.995426 | 28.294556 | 69.411446 |
| A_33_P3325110 | SOX13 | 448.6001 | 389.19107 | 881.6215 |
| A_33_P3233608 | SPANXB2 | 5.7937512 | 9.162595 | 20.570704 |
| A_33_P3216438 | SPATA21 | 68.58515 | 46.723324 | 142.56274 |
| A_23_P258381 | SPSB4 | 7088.607 | 5122.691 | 18305.896 |
| A_33_P3236798 | SRMS | 203.76521 | 183.10425 | 458.42224 |
| A_23_P54968 | ST6GALNAC1 | 20.01962 | 16.036753 | 30.775753 |
| A_33_P3366758 | ST8SIA6 | 8.30851 | 14.935391 | 133.44669 |
| A_32_P92783 | STIP1 | 1799.5652 | 1206.5153 | 3238.0073 |

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|---|---|---|---|---|
| A_33_P3335920 | SYNE1 | 734.4067 | 635.03986 | 1825.973 |
| A_23_P20101 | TAS2R4 | 78.99555 | 64.83029 | 151.77983 |
| A_33_P3219197 | TBC1D10B | 88.29411 | 54.685974 | 155.90846 |
| A_33_P3307886 | TBXA2R | 525.3497 | 450.39688 | 1360.1605 |
| A_33_P3400057 | TCEANC | 15.81698 | 13.364951 | 24.074234 |
| A_33_P3261695 | TEX22 | 4.9999995 | 11.229329 | 16.845488 |
| A_24_P79054 | TGFB1 | 1660.6471 | 1501.2599 | 2823.036 |
| A_32_P86763 | TGM2 | 1199.1533 | 1689.2063 | 3769.4302 |
| A_24_P196851 | TLN1 | 3962.7017 | 3104.72 | 8767.292 |
| A_23_P256561 | TLR6 | 6.0252657 | 9.67972 | 20.304895 |
| A_24_P932416 | TMEM14E | 5.398946 | 10.101289 | 15.207691 |
| A_23_P112289 | TMOD1 | 8.09312 | 9.6086035 | 15.966283 |
| A_23_P418597 | TNKS1BP1 | 604.78485 | 490.69168 | 1533.2938 |
| A_23_P34700 | TNNT2 | 37.676346 | 21.81879 | 69.17029 |
| A_23_P26294 | TPSG1 | 12443.622 | 10055.234 | 37141.79 |
| A_33_P3357600 | TRIM3 | 167.43456 | 115.218796 | 369.06058 |
| A_23_P123402 | TRIM55 | 21.853016 | 18.675753 | 47.445965 |
| A_24_P392632 | TRPM3 | 9.763314 | 9.6524105 | 15.714332 |
| A_24_P200942 | TSC22D4 | 446.6974 | 422.8737 | 908.562 |
| A_23_P76136 | TSPAN11 | 4.9999995 | 4.9999995 | 7.323604 |
| A_23_P114185 | TSPAN7 | 10.356913 | 10.031314 | 16.017202 |
| A_33_P3234222 | TSPO2 | 2403.2278 | 2315.1277 | 5902.6353 |
| A_23_P170608 | TSPYL2 | 90.72399 | 72.49553 | 164.7834 |
| A_33_P3544887 | TTC28 | 265.05658 | 230.65193 | 635.3518 |
| A_33_P3409518 | TUBBP5 | 32.52201 | 45.8622 | 100.00402 |
| A_23_P308058 | TUSC5 | 20.289358 | 20.388311 | 54.205467 |
| A_23_P53015 | TUT1 | 18.905668 | 33.190403 | 75.28751 |
| A_23_P141917 | TYK2 | 68.28769 | 77.65811 | 177.34866 |
| A_33_P3255949 | TYMP | 11821.123 | 14373.168 | 36537.45 |
| A_33_P3239214 | TYR | 202.63107 | 231.852 | 2538.313 |
| A_23_P137209 | UBA1 | 4596.855 | 3701.9133 | 10824.443 |
| A_33_P3344599 | UBE4B | 7.7075233 | 7.374841 | 17.79714 |
| A_23_P120822 | UPB1 | 392.45737 | 362.31424 | 901.00635 |
| A_23_P64954 | USP5 | 413.17468 | 418.6023 | 961.9376 |
| A_23_P146885 | UTS2R | 1655.8502 | 1478.0673 | 3288.8918 |
| A_33_P3294886 | VPS52 | 11.552419 | 18.901308 | 57.127254 |
| A_33_P3316493 | WDR91 | 44.512543 | 53.643406 | 105.5494 |
| A_23_P402331 | WFDC5 | 43.949158 | 37.79562 | 70.805435 |
| A_33_P3605352 | WWTR1 | 22.889877 | 21.294258 | 37.721638 |
| A_23_P153628 | YIF1B | 1372.176 | 1316.8375 | 2726.75 |
| A_23_P104804 | ZBTB16 | 138.53046 | 130.69246 | 309.56006 |
| A_32_P65533 | ZC3H12D | 4.9999995 | 6.001008 | 13.19199 |
| A_24_P99175 | ZDHHC22 | 6.2782927 | 6.385169 | 13.975491 |
| A_23_P39223 | ZNF2 | 290.19955 | 247.07362 | 697.7215 |

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|---|---|---|---|---|
| A_24_P56689 | ZNF205 | 506.43854 | 461.93478 | 1065.7261 |
| A_24_P218074 | ZNF467 | 1419.6825 | 1320.2987 | 3277.526 |
| A_33_P3239143 | ZNF497 | 11678.706 | 8756.658 | 25811.842 |
| A_33_P3228637 | ZNF584 | 11.08674 | 9.961448 | 19.302372 |
| A_24_P247978 | ZNF589 | 50.90116 | 43.46304 | 89.39675 |
| A_23_P74114 | ZNF713 | 1203.7994 | 977.00256 | 2826.0364 |
| A_24_P161144 | ZNF843 | 164.85068 | 122.135414 | 340.09024 |
| A_33_P3412294 | ZSCAN2 | 267.54147 | 222.26337 | 522.04193 |

## Genes down-regulated in UC-MSCs-IGF-1

| ProbeName | GeneSymbol | UC-MSCs | UC-MSCs-vector | UC-MSCs-IGF-1 |
|---|---|---|---|---|
| A_23_P202520 | ABLIM1 | 514.0748 | 550.9202 | 195.34111 |
| A_33_P3395008 | ACOXL | 100.17611 | 62.07325 | 21.440973 |
| A_23_P95536 | ADAM29 | 16.663626 | 16.53795 | 4.9999995 |
| A_23_P94296 | ADAM7 | 105.615425 | 80.52821 | 33.23314 |
| A_23_P81158 | ADH1C | 648.36523 | 452.6922 | 218.26738 |
| A_33_P3348079 | ADIG | 44.0041 | 30.31078 | 11.523061 |
| A_33_P3378081 | AGBL1 | 11.573048 | 13.16991 | 4.9999995 |
| A_23_P136116 | AGMO | 22.181915 | 14.45243 | 4.9999995 |
| A_33_P3346771 | AKD1 | 13.929191 | 13.80182 | 4.9999995 |
| A_23_P96478 | AMELX | 34.073597 | 19.40487 | 4.9999995 |
| A_33_P3404676 | AMOT | 78.64373 | 43.8522 | 9.283251 |
| A_23_P131875 | ANKRD60 | 82.811295 | 68.38661 | 14.157619 |
| A_24_P929369 | AP4E1 | 1571.0555 | 1375.148 | 707.79364 |
| A_23_P142856 | AQP12A | 179.02951 | 153.758 | 52.823093 |
| A_32_P83784 | ARAP2 | 11.85679 | 15.67101 | 4.9999995 |
| A_23_P35045 | ARHGAP30 | 283.59625 | 154.6592 | 53.815556 |
| A_23_P32308 | ATP4B | 18.836983 | 19.44749 | 5.501481 |
| A_33_P3415191 | ATP8B1 | 9173.64 | 7127.05 | 3841.7576 |
| A_33_P3286958 | B3GALT2 | 250.15114 | 460.6793 | 100.75299 |
| A_23_P19723 | BMP5 | 53.469894 | 26.39618 | 8.108629 |
| A_33_P3385453 | BRCC3 | 19.108652 | 22.94648 | 5.973767 |
| A_33_P3320743 | BSPH1 | 27.118647 | 26.67607 | 8.922841 |
| A_23_P75179 | C10orf92 | 1240.9016 | 1174.266 | 511.86194 |
| A_32_P886589 | C12orf61 | 13.078512 | 12.37969 | 4.9999995 |
| A_33_P3352718 | C12orf76 | 15.620229 | 12.15496 | 4.9999995 |
| A_32_P183970 | C15orf62 | 3723.3975 | 3430.773 | 1505.0765 |
| A_32_P468341 | C1orf127 | 350.78726 | 342.4083 | 146.11557 |
| A_32_P42946 | C1orf210 | 46.683884 | 30.36138 | 10.330431 |
| A_33_P3352727 | C20orf173 | 48.14046 | 26.16556 | 4.9999995 |
| A_23_P132079 | C21orf62 | 35.45157 | 21.33427 | 7.125975 |
| A_24_P272313 | C2orf55 | 33.39639 | 46.10329 | 6.9543223 |
| A_23_P324419 | C2orf57 | 20.744371 | 12.07015 | 4.9999995 |
| A_33_P3337569 | C4orf40 | 148.10768 | 74.35826 | 27.125711 |
| A_33_P3416966 | C6orf168 | 21.06462 | 18.00538 | 5.4825826 |
| A_32_P74964 | C6orf168 | 24.83979 | 23.27697 | 5.908457 |
| A_23_P253350 | C8orf4 | 10.88411 | 19.14648 | 4.9999995 |
| A_33_P3482249 | C8orf66 | 53.941708 | 59.97786 | 16.934801 |
| A_32_P203917 | C9 | 34.596096 | 18.8335 | 4.9999995 |
| A_33_P3225705 | C9orf102 | 16.060947 | 15.36464 | 4.9999995 |
| A_33_P3280106 | CACNA1B | 66.94227 | 62.28838 | 24.85878 |
| A_33_P3421913 | CADM1 | 2554.8218 | 2474.52 | 881.50616 |
| A_33_P3217804 | CAMSAP1 | 3194.665 | 2606.334 | 632.3238 |

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| A_23_P13102 | CASP12 | 22.708399 | 30.79887 | 4.9999995 |
| A_23_P342108 | CCDC116 | 47.479816 | 54.88309 | 11.943901 |
| A_33_P3246623 | CCDC18 | 141.96928 | 91.49139 | 33.02694 |
| A_23_P105664 | CCDC59 | 16822.473 | 13754.41 | 5004.4663 |
| A_24_P125335 | CCL13 | 52.43446 | 28.64262 | 10.322151 |
| A_33_P3354607 | CCL4 | 13.937498 | 14.39675 | 4.9999995 |
| A_23_P402670 | CD1A | 35.834248 | 17.63198 | 4.9999995 |
| A_32_P204239 | CDHR3 | 18.854319 | 16.58399 | 4.9999995 |
| A_33_P3289721 | CDRT1 | 144.71342 | 125.9066 | 50.43082 |
| A_33_P3413895 | CDRT15P1 | 24.068768 | 19.57924 | 4.9999995 |
| A_23_P153301 | CEACAM5 | 33.062576 | 13.9821 | 4.9999995 |
| A_23_P66967 | CETN1 | 24.096022 | 24.08418 | 6.41636 |
| A_32_P209960 | CIITA | 48.46485 | 37.62087 | 13.32299 |
| A_33_P3295328 | CLEC6A | 16.55107 | 17.73318 | 5.069837 |
| A_33_P3396404 | CLLU1OS | 123.80971 | 86.32254 | 33.153347 |
| A_23_P371861 | CNBD1 | 12.84181 | 17.19678 | 4.9999995 |
| A_23_P216361 | COL14A1 | 46.854202 | 34.67941 | 11.256869 |
| A_23_P112554 | COL15A1 | 24.669209 | 25.21375 | 7.5115547 |
| A_23_P31124 | COL21A1 | 71.69782 | 42.90347 | 10.90868 |
| A_33_P3372069 | COX8C | 11.94688 | 10.83257 | 4.9999995 |
| A_23_P327551 | CPNE4 | 14.515491 | 11.41224 | 4.9999995 |
| A_23_P394986 | CREG2 | 442.75748 | 371.0785 | 147.81075 |
| A_24_P342484 | CRP | 28.71284 | 17.69104 | 4.9999995 |
| A_32_P81879 | CST9 | 28.233414 | 22.61938 | 6.8371806 |
| A_24_P396167 | CTSW | 12.409269 | 11.94057 | 4.9999995 |
| A_23_P18452 | CXCL9 | 20.01243 | 24.24159 | 4.9999995 |
| A_32_P410753 | CXorf59 | 10.14364 | 10.7043 | 4.9999995 |
| A_23_P37410 | CYP19A1 | 60.446075 | 53.16777 | 18.120935 |
| A_33_P3264662 | CYP27C1 | 27.410597 | 20.39176 | 4.9999995 |
| A_23_P55779 | CYP2A13 | 4198.552 | 3566.766 | 1253.2704 |
| A_23_P12767 | CYP2C9 | 22.610731 | 12.94495 | 4.9999995 |
| A_23_P90626 | CYTIP | 14.4615 | 16.28876 | 4.9999995 |
| A_23_P500328 | DCX | 707.2806 | 489.3859 | 251.99646 |
| A_23_P2317 | DDN | 232.84505 | 200.4189 | 85.75207 |
| A_23_P31816 | DEFA3 | 113.2476 | 66.52535 | 27.69918 |
| A_24_P363711 | DEFA6 | 15.117859 | 14.16349 | 4.9999995 |
| A_33_P3370454 | DEFB108B | 35.96164 | 17.52236 | 5.6165915 |
| A_33_P3421728 | DGKG | 1137.9961 | 639.9171 | 297.46606 |
| A_23_P317450 | DNAJB3 | 18.613592 | 15.90101 | 4.9999995 |
| A_23_P401691 | DPYSL5 | 30.518335 | 18.25582 | 5.22925 |
| A_33_P3301932 | DSCR4 | 12.48321 | 14.09461 | 4.9999995 |
| A_33_P3254956 | DSCR6 | 66.90785 | 41.10794 | 14.14076 |
| A_23_P158257 | DUX3 | 60.711193 | 55.4295 | 21.368027 |
| A_33_P3373165 | DUX4L4 | 168.29036 | 154.9886 | 49.182945 |

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| A_23_P404536 | ENPP3 | 284.4757 | 210.0615 | 79.88677 |
| A_33_P3280471 | ERBB3 | 19.647861 | 13.83876 | 4.9999995 |
| A_32_P183765 | ERBB4 | 48.39991 | 32.14484 | 10.013261 |
| A_33_P3226425 | ERP29 | 798.0567 | 968.5512 | 299.28757 |
| A_32_P901770 | ESPN | 141.0072 | 172.4498 | 53.07403 |
| A_24_P697685 | ESYT3 | 15.375652 | 10.86795 | 4.9999995 |
| A_23_P424734 | EXOC3L1 | 297.72653 | 226.2664 | 95.48217 |
| A_33_P3216763 | EYA1 | 12.840409 | 13.37575 | 4.9999995 |
| A_23_P84860 | FAM107A | 14.98117 | 19.41574 | 4.9999995 |
| A_23_P36888 | FAM113B | 1925.8895 | 1618.933 | 777.53827 |
| A_33_P3508342 | FAM135B | 22.486017 | 16.83151 | 5.25487 |
| A_24_P561341 | FAM150B | 15.396858 | 11.74393 | 4.9999995 |
| A_33_P3320197 | FAM150B | 11.288481 | 12.72261 | 4.9999995 |
| A_23_P22647 | FAM155B | 102.4236 | 90.07399 | 26.246326 |
| A_32_P84242 | FAM169A | 46.848396 | 32.57773 | 11.723979 |
| A_24_P263310 | FAM169B | 76.4694 | 47.44173 | 12.673541 |
| A_32_P129120 | FAM182A | 21.415108 | 19.25762 | 6.082621 |
| A_23_P422831 | FAM189A2 | 51.676426 | 40.615 | 10.13319 |
| A_23_P377629 | FAM75C2 | 134.07819 | 95.89803 | 31.900503 |
| A_33_P3368334 | FCRL3 | 56.17008 | 57.97151 | 17.749258 |
| A_23_P144126 | FETUB | 38.252964 | 29.00265 | 10.52074 |
| A_33_P3337574 | FGF14-IT1 | 49.774315 | 40.1952 | 12.30613 |
| A_33_P3663142 | FLJ12334 | 454.124 | 244.1552 | 108.28223 |
| A_33_P3406552 | FLJ32955 | 39.311077 | 20.69569 | 6.5864835 |
| A_33_P3331426 | FLJ37786 | 317.76285 | 277.3294 | 113.84209 |
| A_33_P3675395 | FLJ39095 | 23.899656 | 24.82322 | 7.3190804 |
| A_33_P3294861 | FLJ40712 | 25.77897 | 27.85171 | 8.261998 |
| A_33_P3210556 | FLJ42289 | 38.924923 | 17.20093 | 4.9999995 |
| A_33_P3354635 | FLJ43879 | 16.09326 | 12.53404 | 4.9999995 |
| A_33_P3288219 | FLJ45684 | 242.56128 | 137.6907 | 60.827507 |
| A_33_P3263851 | FLJ46020 | 3529.2659 | 2613.243 | 1309.8306 |
| A_23_P66552 | FNDC8 | 21.493328 | 16.96923 | 4.9999995 |
| A_33_P3355508 | FOXL2 | 16.021591 | 10.9788 | 4.9999995 |
| A_23_P55649 | FPR2 | 21.11046 | 29.13462 | 5.9313354 |
| A_33_P3248203 | FUT5 | 14.392161 | 15.93807 | 4.9999995 |
| A_23_P76749 | GALNTL1 | 147.15695 | 110.6729 | 41.629017 |
| A_24_P82466 | GAS7 | 9927.114 | 12170.23 | 3875.9695 |
| A_33_P3406962 | GATA4 | 54.173443 | 40.41768 | 14.00305 |
| A_32_P140489 | GDF6 | 21.515192 | 25.281 | 6.5799265 |
| A_24_P606538 | GGNBP1 | 94.00867 | 48.65278 | 17.212843 |
| A_23_P2745 | GJB6 | 17.527824 | 19.01719 | 4.9999995 |
| A_24_P43723 | GJC3 | 58.02365 | 35.90463 | 14.014919 |
| A_33_P3376273 | GK | 213.06241 | 168.7871 | 79.51718 |
| A_32_P19294 | GLT1D1 | 37.350925 | 30.9617 | 9.050743 |

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| A_24_P331128 | GNA15 | 295.84024 | 222.7785 | 97.42298 |
| A_23_P312901 | GPR112 | 11.230521 | 15.87674 | 4.9999995 |
| A_23_P25566 | GPR183 | 149.4899 | 178.6675 | 49.471565 |
| A_23_P347541 | GRIN3A | 12.171659 | 11.01203 | 4.9999995 |
| A_33_P3226910 | GRK7 | 16.31181 | 13.53295 | 4.9999995 |
| A_23_P76774 | GSC | 49.406937 | 43.95129 | 14.5534 |
| A_23_P92453 | GSX2 | 66.43166 | 36.46601 | 7.637982 |
| A_23_P14255 | GUCY1B2 | 52.990948 | 48.25369 | 16.813559 |
| A_23_P203558 | HBB | 54.402218 | 21.82186 | 6.3798985 |
| A_23_P64721 | HCAR3 | 52.20944 | 34.19457 | 11.74417 |
| A_33_P3360249 | HCRTR1 | 32.333664 | 17.30232 | 4.9999995 |
| A_33_P3299872 | HINT3 | 1309.9293 | 1429.142 | 551.80804 |
| A_33_P3538688 | HIST2H4A | 18.867596 | 19.75426 | 4.9999995 |
| A_23_P319005 | HMP19 | 12299.852 | 10375.21 | 5108.1543 |
| A_33_P3347281 | HNMT | 19.601368 | 10.63743 | 4.9999995 |
| A_33_P3409844 | HOOK1 | 13.87319 | 10.95047 | 4.9999995 |
| A_23_P27013 | HOXB9 | 371.79694 | 316.7939 | 157.60817 |
| A_23_P118158 | HS3ST2 | 32.850887 | 31.50624 | 7.631826 |
| A_23_P422911 | HS6ST3 | 22.026194 | 21.69409 | 7.1852193 |
| A_23_P430168 | ICA1L | 30.019308 | 22.27966 | 7.5611844 |
| A_23_P398189 | IGSF11 | 23.096167 | 23.07895 | 5.566149 |
| A_23_P7560 | IL12B | 14.436848 | 15.49647 | 4.9999995 |
| A_33_P3211666 | IL18R1 | 12.23331 | 21.12022 | 4.9999995 |
| A_23_P28334 | IL18RAP | 21.8537 | 18.56892 | 6.0989447 |
| A_33_P3422124 | IL22RA2 | 11.204881 | 17.23095 | 4.9999995 |
| A_24_P230563 | IL2RA | 51.53198 | 30.00434 | 4.9999995 |
| A_23_P125686 | INGX | 18.941633 | 14.68626 | 4.9999995 |
| A_33_P3397995 | IPCEF1 | 29.842121 | 26.11316 | 8.926633 |
| A_23_P331598 | IPO7 | 1166.2036 | 262.6266 | 116.96431 |
| A_33_P3381707 | ISPD | 41.12115 | 30.51226 | 9.183956 |
| A_33_P3287735 | KAT6A | 811.3812 | 526.5867 | 260.5307 |
| A_32_P75284 | KATNAL1 | 3852.5073 | 3054.263 | 1621.823 |
| A_23_P119573 | KCNN1 | 11.1245 | 12.02532 | 4.9999995 |
| A_24_P409800 | KCTD16 | 237.61227 | 121.1253 | 45.581 |
| A_24_P261750 | KERA | 20.804548 | 27.85516 | 4.9999995 |
| A_33_P3246580 | KIAA1244 | 22.778316 | 26.28627 | 6.495582 |
| A_33_P3230548 | KIF14 | 2628.9143 | 1790.842 | 770.7751 |
| A_23_P350617 | KLB | 18.313549 | 18.07405 | 4.9999995 |
| A_23_P118854 | KRT37 | 27.480282 | 18.03886 | 6.0824504 |
| A_24_P357386 | KRTAP13-3 | 31.221954 | 20.82705 | 6.661644 |
| A_33_P3403018 | LCE5A | 20.961193 | 25.10687 | 4.9999995 |
| A_32_P158083 | LHFPL3 | 208.40707 | 157.0656 | 50.59803 |
| A_23_P142205 | LILRA2 | 14.839601 | 11.90579 | 4.9999995 |
| A_23_P132057 | LINC00158 | 20.564932 | 16.67414 | 4.9999995 |

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| A_33_P3616021 | LINC00163 | 29.357216 | 23.88498 | 8.645869 |
| A_33_P3289960 | LINC00222 | 60.77875 | 37.91408 | 13.09992 |
| A_32_P176911 | LINC00239 | 36.598103 | 27.62146 | 10.348129 |
| A_33_P3302453 | LINC00242 | 16.064058 | 10.87003 | 4.9999995 |
| A_32_P214178 | LINC00319 | 95.21754 | 92.22371 | 28.272942 |
| A_33_P3741022 | LINC00511 | 124.88997 | 111.4446 | 34.741196 |
| A_23_P258493 | LMNB1 | 2929.8423 | 672.1179 | 300.7508 |
| A_33_P3398181 | LOC100127909 | 39.450546 | 28.85848 | 10.30083 |
| A_33_P3327041 | LOC100128054 | 297.67676 | 210.1629 | 81.959816 |
| A_32_P103614 | LOC100128511 | 154.87404 | 25.38851 | 6.576764 |
| A_24_P765552 | LOC100128644 | 106.48681 | 78.92036 | 28.24508 |
| A_32_P834166 | LOC100128843 | 9036.325 | 8665.625 | 3783.007 |
| A_33_P3213419 | LOC100129447 | 825.1948 | 735.938 | 291.40024 |
| A_33_P3382296 | LOC100129662 | 15.897041 | 11.90882 | 4.9999995 |
| A_33_P3336552 | LOC100130701 | 17.948608 | 11.7239 | 4.9999995 |
| A_33_P3255459 | LOC100133461 | 10.16242 | 12.58564 | 4.9999995 |
| A_33_P3805819 | LOC100505890 | 10.39923 | 14.02682 | 4.9999995 |
| A_33_P3300867 | LOC100506514 | 103.64619 | 86.87978 | 37.662388 |
| A_32_P49867 | LOC100507055 | 35.544422 | 34.8387 | 10.662358 |
| A_33_P3289810 | LOC100509091 | 15.89861 | 12.71861 | 4.9999995 |
| A_24_P83075 | LOC100509196 | 362.82355 | 297.131 | 145.3198 |
| A_33_P3248008 | LOC100652807 | 193.66203 | 210.3392 | 73.21898 |
| A_33_P3307945 | LOC100652824 | 486.62808 | 347.3783 | 101.17493 |
| A_33_P3738849 | LOC147093 | 37.03069 | 29.79727 | 5.138504 |
| A_33_P3482461 | LOC150005 | 33.307583 | 31.25888 | 8.074156 |
| A_33_P3289621 | LOC283143 | 60.14919 | 44.83978 | 13.737842 |
| A_33_P3274832 | LOC283440 | 62.989933 | 45.27503 | 11.61769 |
| A_33_P3337584 | LOC283482 | 25.0315 | 21.00588 | 4.9999995 |
| A_33_P3379106 | LOC283867 | 26.153782 | 26.27409 | 8.618256 |
| A_32_P232808 | LOC284412 | 96.380005 | 70.46906 | 30.260342 |
| A_33_P3463355 | LOC286121 | 12.224959 | 10.76087 | 4.9999995 |
| A_33_P3705339 | LOC339685 | 32.32661 | 21.55776 | 6.1681275 |
| A_33_P3323979 | LOC339874 | 176.5723 | 146.8305 | 56.854424 |
| A_33_P3365553 | LOC389634 | 12.774891 | 10.72677 | 4.9999995 |
| A_24_P101642 | LOC401847 | 229.54236 | 216.1825 | 72.51122 |
| A_33_P3573141 | LOC440149 | 13.10192 | 17.24369 | 4.9999995 |
| A_33_P3688869 | LOC440910 | 110.35122 | 84.64952 | 34.27089 |
| A_33_P3770642 | LOC503519 | 57.91553 | 20.03326 | 6.0183635 |
| A_32_P102519 | LOC541473 | 50.521328 | 37.41354 | 11.608581 |
| A_33_P3336597 | LOC554223 | 240.00893 | 191.0269 | 85.8805 |
| A_24_P933685 | LOC643797 | 15.844651 | 17.10371 | 4.9999995 |
| A_33_P3306659 | LOC728254 | 3989.9563 | 3357.148 | 1540.8523 |
| A_33_P3307536 | LOC729444 | 24.918484 | 24.61658 | 8.129662 |
| A_33_P3254375 | LOC730651 | 11.318848 | 10.65449 | 4.9999995 |

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| A_32_P190303 | LONRF2 | 46.068287 | 46.10704 | 14.390751 |
| A_23_P386888 | LPA | 392.848 | 260.404 | 128.67163 |
| A_33_P3292402 | LRRIQ3 | 43.82324 | 39.91149 | 11.618931 |
| A_24_P397294 | LTC4S | 241.47627 | 198.3876 | 85.51452 |
| A_33_P3268622 | LY6D | 31.910036 | 17.4651 | 4.9999995 |
| A_23_P153616 | MADCAM1 | 10202.2705 | 7707.485 | 3156.8447 |
| A_24_P286898 | MAPK8 | 11055.985 | 8296.098 | 2142.428 |
| A_23_P327022 | MDFIC | 2687.6577 | 2145.023 | 1048.2386 |
| A_33_P3315425 | METTL4 | 419.6113 | 383.0162 | 176.30986 |
| A_33_P3393331 | MFSD6L | 14.235211 | 16.88654 | 4.9999995 |
| A_24_P912048 | MGC50722 | 20.28246 | 12.16906 | 4.9999995 |
| A_33_P3279550 | MIXL1 | 42.182407 | 30.95339 | 9.241629 |
| A_23_P13094 | MMP10 | 142.56491 | 28.88626 | 8.946831 |
| A_33_P3229477 | MPP7 | 29.977575 | 34.6485 | 8.970326 |
| A_23_P4545 | MRO | 530.2113 | 317.7589 | 88.178825 |
| A_33_P3244168 | MRPS17 | 15.86583 | 17.75992 | 4.9999995 |
| A_33_P3312499 | MS4A15 | 12.0775 | 22.42405 | 4.9999995 |
| A_23_P150979 | MUCL1 | 22.233751 | 21.65422 | 6.043578 |
| A_23_P87860 | MYF5 | 75.69389 | 37.88973 | 15.031078 |
| A_24_P131646 | MYL3 | 68.80851 | 63.59367 | 21.226372 |
| A_33_P3300217 | MYLK3 | 26.467464 | 21.28867 | 6.1288366 |
| A_23_P52727 | NAV2 | 4248.1416 | 1256.782 | 606.52325 |
| A_33_P3279158 | NBPF6 | 32.419785 | 30.86493 | 9.787766 |
| A_33_P3417113 | NPSR1 | 232.56378 | 115.5601 | 42.2297 |
| A_33_P3386150 | NRADDP | 19.172579 | 13.82629 | 4.9999995 |
| A_23_P161297 | OGDHL | 21.171377 | 45.30272 | 5.772688 |
| A_23_P154849 | OLIG1 | 25.339636 | 19.96639 | 6.7634735 |
| A_33_P3213408 | OR10AD1 | 24.32536 | 27.30943 | 4.9999995 |
| A_23_P23507 | OR10T2 | 50.560432 | 27.76165 | 8.081972 |
| A_23_P259555 | OR12D3 | 75.39935 | 66.30253 | 25.098679 |
| A_23_P169207 | OR13C4 | 52.2132 | 44.9082 | 18.056282 |
| A_33_P3244215 | OR13C5 | 15.25674 | 11.9985 | 4.9999995 |
| A_33_P3266489 | OR13H1 | 1128.0812 | 978.0804 | 421.37244 |
| A_24_P299769 | OR1C1 | 35.811584 | 27.18985 | 7.960661 |
| A_33_P3209806 | OR2C3 | 11.69136 | 11.40818 | 4.9999995 |
| A_33_P3370001 | OR2L8 | 221.50726 | 178.2522 | 70.92869 |
| A_33_P3319834 | OR2T8 | 25.308867 | 14.76898 | 4.9999995 |
| A_23_P18913 | OR2V2 | 194.66199 | 180.6825 | 58.832462 |
| A_23_P255389 | OR2W1 | 57.459305 | 39.86321 | 7.8812 |
| A_23_P13455 | OR51A7 | 931.1509 | 750.4296 | 288.28223 |
| A_23_P36203 | OR52B2 | 81.64597 | 41.3104 | 14.01744 |
| A_23_P47464 | OR5AP2 | 30.822977 | 17.39335 | 4.9999995 |
| A_23_P36050 | OR8K3 | 31.949156 | 18.01611 | 4.9999995 |
| A_33_P3262376 | OTUD7A | 14.744199 | 12.17283 | 4.9999995 |

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| A_33_P3299540 | OVCH2 | 50.946556 | 38.64417 | 10.824549 |
| A_33_P3413741 | OXTR | 2988.8481 | 2748.319 | 923.7499 |
| A_23_P372848 | P2RX1 | 850.7057 | 791.4865 | 377.20477 |
| A_33_P3263867 | P2RX7 | 45.14042 | 31.20255 | 11.89425 |
| A_23_P346376 | P2RY10 | 621.15704 | 341.227 | 109.58301 |
| A_23_P147465 | PARK2 | 430.96835 | 249.999 | 113.02656 |
| A_24_P880043 | PCGF5 | 2420.0657 | 2139.585 | 921.1035 |
| A_24_P844984 | PIGR | 45.446304 | 20.21319 | 4.9999995 |
| A_23_P66543 | PIK3R5 | 66.824554 | 58.19374 | 23.685907 |
| A_24_P294408 | PLA1A | 17.661917 | 15.31398 | 4.9999995 |
| A_33_P3214339 | PLCXD2 | 114.81868 | 82.42185 | 34.60361 |
| A_23_P253321 | PNOC | 12.868958 | 15.05016 | 4.9999995 |
| A_23_P147563 | PPM1L | 28.235607 | 21.4498 | 4.9999995 |
| A_32_P38623 | PPP1R9A | 34.490635 | 21.69312 | 6.114865 |
| A_24_P81298 | PPP6C | 425.82407 | 343.5278 | 173.80136 |
| A_33_P3307207 | PRHOXNB | 241.38586 | 166.1669 | 72.362114 |
| A_33_P3821350 | PRO2012 | 67.31281 | 49.3006 | 18.608757 |
| A_23_P127663 | PRRG4 | 269.47775 | 242.963 | 111.18723 |
| A_33_P3336944 | PRSS55 | 27.40306 | 27.46449 | 8.419273 |
| A_33_P3232173 | PSPC1 | 182.79514 | 66.0746 | 21.120392 |
| A_24_P102821 | PTAFR | 94.39587 | 74.40947 | 31.852428 |
| A_23_P204304 | PTPRO | 38.3027 | 28.45494 | 6.8271947 |
| A_23_P254165 | RAI2 | 199.90884 | 174.7175 | 79.39588 |
| A_32_P223140 | RASGEF1A | 465.00275 | 400.2592 | 201.76689 |
| A_23_P124642 | RASGRP1 | 44.7593 | 41.4334 | 16.083992 |
| A_33_P3316953 | RBFOX3 | 22.020144 | 21.96845 | 5.968943 |
| A_24_P794648 | RBMY2EP | 12.515379 | 12.21913 | 4.9999995 |
| A_23_P46045 | RGS5 | 100.568275 | 96.74564 | 33.1568 |
| A_23_P103424 | RGS8 | 42.45246 | 32.37952 | 10.76039 |
| A_33_P3390107 | RN18S1 | 1485.6785 | 1269.542 | 429.34302 |
| A_23_P83347 | RNF183 | 44.266487 | 37.19701 | 12.887339 |
| A_33_P3326105 | RNF216 | 17.438139 | 14.18067 | 4.9999995 |
| A_33_P3278877 | ROBO2 | 41.81095 | 45.14235 | 11.778869 |
| A_32_P4018 | ROR1 | 136.6245 | 119.3928 | 36.93271 |
| A_33_P3299719 | RP1L1 | 49.8689 | 38.76705 | 14.10717 |
| A_23_P5370 | RPRM | 17.73967 | 14.50441 | 4.9999995 |
| A_33_P3251552 | RSPO4 | 10.11803 | 21.94482 | 4.9999995 |
| A_23_P58266 | S100P | 3155.3093 | 1361.389 | 245.14636 |
| A_33_P3832341 | SCARNA22 | 1281.5205 | 1080.846 | 521.1968 |
| A_24_P270999 | SCN4A | 119.318115 | 58.68027 | 23.412725 |
| A_23_P21063 | SCN5A | 19.29973 | 14.56349 | 4.9999995 |
| A_33_P3417487 | SCUBE1 | 1255.9583 | 908.1393 | 293.94333 |
| A_24_P82135 | SECISBP2L | 542.9002 | 274.5824 | 125.4158 |
| A_23_P21057 | SEPT1 | 12.95718 | 16.06274 | 4.9999995 |

| | | | | |
|---|---|---|---|---|
| A_24_P295010 | SERPINB9 | 1236.4465 | 1222.712 | 555.5581 |
| A_23_P361448 | SESN3 | 12.935589 | 16.15054 | 4.9999995 |
| A_32_P32413 | SETBP1 | 24.915428 | 16.64698 | 4.9999995 |
| A_24_P940921 | SETX | 1395.1782 | 1179.328 | 611.643 |
| A_33_P3702906 | SF3B2 | 19.65971 | 13.12193 | 4.9999995 |
| A_33_P3335177 | SFRP4 | 16.24293 | 13.3001 | 4.9999995 |
| A_32_P213091 | SHISA9 | 32.53588 | 22.78024 | 4.9999995 |
| A_23_P22761 | SHOX | 199.76776 | 95.43436 | 34.331226 |
| A_23_P24616 | SIAE | 630.116 | 838.5981 | 149.89049 |
| A_33_P3272260 | SIRPB2 | 16.69374 | 12.11104 | 4.9999995 |
| A_23_P42189 | SLC17A1 | 11.678899 | 10.94915 | 4.9999995 |
| A_23_P255695 | SLC17A3 | 134.5504 | 116.4848 | 52.71851 |
| A_23_P42004 | SLC22A16 | 15.60968 | 12.0074 | 4.9999995 |
| A_33_P3235841 | SLC22A20 | 818.207 | 698.2045 | 347.166 |
| A_33_P3281537 | SLC27A3 | 187.64285 | 151.6206 | 41.079285 |
| A_33_P3237210 | SLC35A4 | 110.234314 | 75.58564 | 23.952467 |
| A_33_P3241388 | SLC4A5 | 25.846882 | 30.51217 | 7.3654385 |
| A_23_P76386 | SLC6A12 | 13.18218 | 15.87297 | 4.9999995 |
| A_33_P3242623 | SLC7A11 | 5558.31 | 6136.111 | 2295.233 |
| A_23_P150343 | SLN | 54.35466 | 19.61431 | 5.711442 |
| A_24_P190472 | SLPI | 264.157 | 160.9896 | 69.81725 |
| A_33_P3238074 | SMCR7L | 23474.68 | 18333.35 | 7200.793 |
| A_23_P382811 | SNX31 | 16.502169 | 21.25393 | 4.9999995 |
| A_23_P254741 | SOD3 | 516.92773 | 422.5099 | 219.41463 |
| A_33_P3340782 | SPINK5 | 39.83067 | 34.56748 | 11.32581 |
| A_23_P252817 | SST | 20.75686 | 16.16131 | 5.280222 |
| A_23_P33847 | SYN1 | 587.8486 | 453.3568 | 212.83302 |
| A_33_P3210278 | SYNE2 | 672.84607 | 489.2181 | 200.22624 |
| A_24_P96897 | SYT6 | 93.10165 | 107.9431 | 34.369316 |
| A_23_P211345 | TBX1 | 569.6781 | 582.7272 | 249.6256 |
| A_24_P365365 | TCF3 | 5252.3716 | 4831.618 | 2274.6309 |
| A_33_P3232965 | TDRD6 | 53.285233 | 40.50256 | 12.725171 |
| A_23_P97826 | TECTB | 10.885241 | 11.05257 | 4.9999995 |
| A_33_P3331335 | TET3 | 18.531422 | 13.15533 | 4.9999995 |
| A_23_P41009 | TEX264 | 1898.9603 | 1442.048 | 745.77313 |
| A_23_P363954 | THRSP | 15.81555 | 13.04146 | 4.9999995 |
| A_33_P3336103 | TIGD5 | 41128.297 | 33480.28 | 18448.086 |
| A_33_P3235213 | TIGIT | 147.91269 | 125.8997 | 54.92036 |
| A_23_P427645 | TLL1 | 14.269569 | 12.17917 | 4.9999995 |
| A_23_P322735 | TMC1 | 36.867935 | 29.25614 | 9.470412 |
| A_24_P787889 | TMEM191B | 712.9284 | 583.7192 | 300.79034 |
| A_33_P3390723 | TMEM2 | 294.19934 | 197.6524 | 83.35206 |
| A_33_P3216605 | TMEM63A | 11.176061 | 11.70902 | 4.9999995 |
| A_33_P3494748 | TMEM65 | 1122.9824 | 321.2014 | 104.5423 |

| | | | | |
|---|---|---|---|---|
| A_24_P121956 | TMEM86B | 3292.0916 | 3920.256 | 1152.6221 |
| A_33_P3296846 | TMPRSS4 | 81.754555 | 54.19719 | 20.06273 |
| A_33_P3216610 | TMPRSS4 | 1239.0607 | 629.3239 | 321.17212 |
| A_23_P211493 | TMPRSS6 | 386.3803 | 394.7298 | 168.46912 |
| A_23_P390518 | TNFRSF11A | 124.97862 | 103.4727 | 41.88632 |
| A_33_P3354429 | TRIM71 | 125.21012 | 56.64276 | 14.8984785 |
| A_24_P62659 | TSPAN2 | 10.98763 | 19.72767 | 4.9999995 |
| A_33_P3322259 | TSPY2 | 10.478792 | 19.30376 | 4.9999995 |
| A_23_P422240 | UROC1 | 33.954834 | 30.26026 | 9.92318 |
| A_33_P3240482 | VENTXP7 | 38.149986 | 22.63723 | 6.083512 |
| A_32_P106376 | VGLL2 | 44.50973 | 17.09081 | 4.9999995 |
| A_23_P132763 | VGLL3 | 1276.9119 | 1205.515 | 435.2563 |
| A_23_P56578 | VIT | 10.248149 | 12.72112 | 4.9999995 |
| A_33_P3277898 | VSTM2A | 27.428986 | 23.2904 | 6.8880258 |
| A_23_P96331 | WAS | 777.02185 | 489.5202 | 227.61977 |
| A_23_P319549 | WDR65 | 20.509829 | 14.35485 | 4.9999995 |
| A_33_P3252804 | WEE2 | 36.199512 | 21.86339 | 7.081534 |
| A_24_P237583 | WFDC8 | 84.3789 | 32.58867 | 10.35077 |
| A_33_P3222354 | XAGE-4 | 17.797394 | 13.57633 | 4.9999995 |
| A_23_P168909 | ZFPM2 | 1528.977 | 1264.908 | 681.0875 |
| A_24_P942743 | ZFY | 27.732662 | 19.56058 | 4.9999995 |
| A_33_P3326927 | ZNF19 | 363.49356 | 253.6122 | 122.0662 |
| A_23_P85969 | ZNF326 | 2410.212 | 1707.684 | 901.0171 |
| A_33_P3242508 | ZNF365 | 180.82373 | 138.0556 | 19.342228 |
| A_32_P79591 | ZNF665 | 81.090164 | 58.42321 | 23.10911 |
| A_33_P3385775 | ZNF703 | 1895.7935 | 1395.877 | 735.5571 |
| A_23_P168726 | ZPBP | 43.477135 | 31.45924 | 11.896152 |

## Supplementary File 2

## Materials and Methods

This study was carried out in strict accordance with the recommendations in the Guide for the Care and Use of Laboratory Animals of the National Institutes of Health. The protocol was approved by the Committee on the Ethics of Animal Experiments and Human Subject Research of School of Pharmaceutical Science, Jilin University. All operations were performed under sodium pentobarbital anesthesia, and all efforts were made to minimize suffering. The participants have provided the written informed consent to participate in this study.

### Isolation and characterization of human UC-MSCs

Human umbilical cords were obtained after caesarean section of normal pregnancies at First Hospital of Jilin University. The UC-MSCs were extracted as the reference [1]. In brief, the collected umbilical cords were washed in phosphate-buffered saline for 3 times, and further minced and incubated with collagenase IV (1 mg/ml, Gibco) for 4 hours, then DNase I (1 mg/ml, Gibco) for 15 min, and 0.25% trypsin (Gibco) for 15 min at 37℃. After filtration through a 40-μm cell strainer, the cells were then collected by centrifugation, and cultured in DMEM/F12 (Hyclone), containing 10% fetal bovine serum (FBS; Gibco), penicillin/streptomycin (100 U/mL to 0.1 mg/mL; Hyclone), and 2 mM L-glutamine (Gibco), in a humidified incubator with 5% CO2 at 37℃. The media were changed every other day, and the isolated UC-MSCs were passaged by a dilution of 1:3 once every 4 days or 5 days until passage 4 or 5, when a portion of the resulting UC-MSCs was prepared for phenotypic analysis by flow cytometry. The cells were then screened for CD14, CD29, CD34, CD44, CD45, CD73, CD90, CD105, and CD166, and further differentiated into adipocytes and osteocytes as previously described [2-4].

## Establishment of IGF-1 overexpressing cell lines

To generate IGF-1 overexpressing vectors, the IGF-1-coding sequences were obtained by reverse transcription PCR and further cloned into pMXs-based retroviral plasmid (Addgene). At early passage, 40,000 human UC-MSCs were transduced in 6-well culture dishes using pMX-based retroviruses as described [1, 5], to establish IGF-1 overexpressing UC-MSCs (UC-MSCs-IGF-1), and UC-MSCs infected with retrovirus containing blank pMXs vector (UC-MSCs-vector) were used as the control group in the following detections.

To assess IGF-1 expression in UC-MSCs-IGF-1, qPCR and FACS analysis were performed in our study. Besides, the effects of IGF-1 overexpression on proliferation and secretion of UC-MSCs were further evaluated in our study. UC-MSCs, UC-MSCs-vector, and UC-MSCs-IGF-1 were planted in 96-well plates at $1\times10^3$, respectively. Cell proliferation was detected at day 0, day 1, day 2, and day 3. The DMEM/F12 medium containing 10% FBS was used as the blank control group, and the proliferation index of each group was determined using the CCK-8 method (Dojindo, Japan) according to the manufacturer’s instructions, which allowed sensitive colorimetric assays for the determination of the number of viable cells in cell proliferation. In brief, 10 μL of CCK-8 solution was added into each well (containing 100 μL of medium), and cultured for 1 hour to 2 hours at 37 ℃. The absorbance of each group at 450 nm was detected (n=4) and it was directly proportional to the number of living cells. The proliferation index = the absorbance of experimental group − the absorbance of blank group, was used to measure cell proliferation in our study.

After 2 days of culture, the medium of each group was collected for secretory cell function analysis. Vascular endothelial growth factor (VEGF), insulin-like growth factor-1 (IGF-1), bone morphogenetic protein-7 (BMP-7), and interleukin-10 (IL-10), which were secreted by UC-MSCs and relieved kidney injury, were measured using an ELISA Kit (Abcam, United Kingdom) following the manufacturer's instructions.

## Real-time quantitative PCR

Total RNA was extracted with Trizol (Invitrogen). Then, 2 mg of RNA was reverse transcribed using RT-PCR kit (Takara) and qPCR was performed using a Thermal Cycler Dice$^{TM}$ Real Time System and SYBR Green Premix EX Taq$^{TM}$ (Takara). In our study, β-actin was used for Real-time quantitative PCR (qPCR) normalization and all items were measured in triplicate. All primer sequences (5'-3') are as follows:

IGF-1 forward (F) 5'-GGTGGATGCTCTTCAGTTCGTG-3'
reverse (R) 5'-AAATGTACTTCCTTCTGGGTCTTGG-3'

Caspase 3 forward (F) 5'- GAAATTGTGGAATTGATGCGTGA -3'
reverse (R) 5'- CTACAACGATCCCCTCTGAAAAA -3'

Bax forward (F) 5’- CCCGAGAGGTCTTTTTCCGAG -3’
reverse (R) 5’- CCAGCCCATGATGGTTCTGAT -3’

Fas forward (F) 5’- TCTGGTTCTTACGTCTGTTGC -3’
reverse (R) 5’- CTGTGCAGTCCCTAGCTTTCC -3’

Bcl-2 forward (F) 5’- GGTGGGGTCATGTGTGTGG -3’
reverse (R) 5’- CGGTTCAGGTACTCAGTCATCC -3’

NCF2 forward (F) 5’- CCAGAAGCATTAACCGAGACAA -3’
reverse (R) 5’-CCTCGAAGCTGAATCAAGGC-3’

NLE2L2 forward (F) 5’- TCAGCGACGGAAAGAGTATGA-3’
reverse (R) 5’- CCACTGGTTTCTGACTGGATGT-3’

MT3 forward (F) 5’- AGACCTGCCCCTGCCCTTCT -3’
reverse (R) 5’- GAGGTGCATTTGCATCCCTC -3’

ZNF205 forward (F) 5’- CCCAGGACAAGGAGACACC-3’
reverse (R) 5’- TTAGAGCCGTGACTTAGGGGT-3’

GPX3 forward (F) 5’- AGAGCCGGGGACAAGAGAA-3’
reverse (R) 5’- ATTTGCCAGCATACTGCTTGA -3’

IER3 forward (F) 5’- CAGCCGCAGGGTTCTCTAC -3’
reverse (R) 5’- GATCTGGCAGAAGACGATGGT -3’

PPARG forward (F) 5’- GGGATCAGCTCCGTGGATCT -3’
reverse (R) 5’- TGCACTTTGGTACTCTTGAAGTT -3’

C3 forward (F) 5’- GGGGAGTCCCATGTACTCTATC-3’
reverse (R) 5’- GGAAGTCGTGGACAGTAACAG-3’

FABP4 forward (F) 5’- ACTGGGCCAGGAATTTGACG-3’

reverse (R) 5’- CTCGTGGAAGTGACGCCTT-3’

ITGA2 forward (F) 5’- CCTACAATGTTGGTCTCCCAGA-3’

reverse (R) 5’- AGTAACCAGTTGCCTTTTGGATT-3’

TGF-β1 forward (F) 5’- CTAATGGTGGAAACCCACAACG-3’

reverse (R) 5’- TATCGCCAGGAATTGTTGCTG-3’

CCR7 forward (F) 5’- TGAGGTCACGGACGATTACAT-3’

reverse (R) 5’- GTAGGCCCACGAAACAAATGAT-3’

FCER1G forward (F) 5’- AGCAGTGGTCTTGCTCTTACT -3’

reverse (R) 5’- TGCCTTTCGCACTTGGATCTT-3’

ITGB2 forward (F) 5’- TGCGTCCTCTCTCAGGAGTG-3’

reverse (R) 5’- GGTCCATGATGTCGTCAGCC-3’

C3AR1 forward (F) 5’- GTTCGTGTACCGGGAAATCTT-3’

reverse (R) 5’- CAGGCGGCTGAACAATGTTT-3’

DDR1 forward (F) 5’- GCAGCGTGTCCTAGAGCAC-3’

reverse (R) 5’- CCGCAGGTTTTCCCTGACT-3’

LRP1 forward (F) 5’- CTATCGACGCCCCTAAGACTT -3’

reverse (R) 5’- CATCGCTGGGCCTTACTCT-3’

PDGFB forward (F) 5’- CTCGATCCGCTCCTTTGATGA -3’

reverse (R) 5’- CGTTGGTGCGGTCTATGAG -3’

TNF forward (F) 5’- CCTCTCTCTAATCAGCCCTCTG -3’

reverse (R) 5’- GAGGACCTGGGAGTAGATGAG -3’

IL-6 forward (F) 5’- ACTCACCTCTTCAGAACGAATTG -3’

reverse (R) 5’- CCATCTTTGGAAGGTTCAGGTTG -3’

COX-2 forward (F) 5’- TTACAATGCTGACTATGGCTAC -3’

reverse (R) 5’- AACTGATGCGTGAAGTGCTG-3’

PI3K forward (F) 5’-TGGTTCTTGCGAAGTGAGATAG-3’

reverse (R) 5’-AAGTTGGAAGGACCACATGC-3’

AKT forward (F) 5’-TAGGCATCCCTTCCTTACAGC-3’

reverse (R) 5’- CACTGTCCCATCCGGCTTCA-3’

β-actin forward (F) 5’-CCCAGAGCAAGAGAGG-3’

reverse (R) 5’-GTCCAGACGCAGGATG- 3’

**Flow cytometry**

Human UC-MSCs were dissociated into single cells with trypsin, and further fixed and permeated with Fixation Buffer (BD) and Perm/Wash Buffer (BD), respectively. Finally, the cells were prepared at a concentration of $1.0\times10^5$ cells in 100 μL of PBS. The antibodies, including CD14 conjugated to FITC (BD), CD29 conjugated to FITC (BD), CD34 conjugated to PE (BD), CD44 conjugated to FITC (BD), CD45 conjugated to PE (BD), CD73 conjugated to APC (BD), CD90 conjugated to FITC (BD), CD105 conjugated to APC (BD), CD166 conjugated to PE (BD), and IGF-1 conjugated to APC (LSBio), were added and incubated for 30 min at 4℃. After two washes in PBS, the cells were acquired and analyzed with FACScalibur (BD Bioscience).

## Preparation and treatment of AKI model

Male node rats, weighing 250 g to 300 g, were purchased from Vital River Laboratories (Beijing, China). All rats were housed in the room with constant temperature and a 12 hours dark-12 hours light cycle. The node rats were fed a standard diet. The method used to prepare or treat the AKI model was similar to our previous research [3, 4]. In brief, animals were divided into six groups (six rats per group), namely, normal group, AKI model group, positive drug group, UC-MSCs group, UC-MSCs-vector group, and UC-MSCs-IGF-1 group. To generate a rat model of AKI for testing the UC-MSCs-IGF-1 in vivo, the model was induced by gentamicin (140 mg/kg/day for 7 days, i.p.) in rats. At day 8, the stem cells were administered by intravenous injection of $3.3 \times 10^6$ cells/kg, whereas dexamethasone (0.08 mg/kg) was used as a positive control drug during the 7-day therapy. The normal group and AKI model group did not receive any treatment.

## Evaluation of kidney function

In our study, all animals were sacrificed on day 15. To determine the biochemical variables (NAG, LZM, creatine and urea nitrogen) using a Biochemistry Autoanalyzer, blood and urine were collected on days 8 (before treatment) and 15, respectively. For histological analysis, kidney tissue samples of each group were fixed with formalin, embedded in paraffin, sectioned to 5 μm-thick, and processed by hematoxylin and eosin (H&E) staining. Then the slides were reviewed blindly and scored with a semiquantitative scale evaluating changes found in AKI as the reference [6]. For each kidney, 100 cortical tubules from at least 10 different areas were scored, and avoid repeated scoring of different convolutions of the same tubule. The average histological score was used to valuate kidney tissue morphology. Higher scores represented more severe damage.

## Analysis of cell apoptosis

Apoptosis in the kidney tissue was evaluated by enzymatic labeling of DNA strand breaks using terminal deoxynucleotidyl transferase-mediated deoxyuridine triphosphate nick end-labeling (TUNEL) assay kit (KeyGEN) according to the manufacturer’s instructions. The expression levels of apoptotic genes (Caspase 3, Bax, and Fas) and anti-apoptotic gene (Bcl-2) in the kidney tissues of each group were further detected using real-time qPCR, and some apoptotic genes were also confirmed with immunohistochemistry.

## Immunohistochemistry

The cells or kidney tissues were fixed in 4% paraformaldehyde in PBS. The kidney tissues of each group were embedded in paraffin and sliced into 5 μm-thick sections. For immunohistochemistry, the primary antibodies used were anti-Caspase 3 (1:100, Abcam), anti-Bcl-2 (1:100, Abcam), and anti-human nucleus antigen (hNA, 1:500, Millipore) polyclonal antibodies. After 12 hours of incubation at 4 ℃, the samples were washed three times with PBS and processed using an SABC kit and DAB solution. Finally, the sections were observed using Axio Scope A1 (Zeiss, Germany) with AxioCAM MRc5 (Zeiss), and processed with AxioVision software (Zeiss). The color intensity was measured using Motic Image Advanced 3.2.

### Microarray analysis

Total RNA was extracted from UC-MSCs, UC-MSCs-vector and UC-MSCs-IGF-1 using Trizol (Invitrogen) and the RNeasy kit (Qiagen). Samples were amplified and labeled using a Aglient Quick Amp Labing Kit. Array hybridization was analyzed with the Aglient Hybridization System and followed by washing with the Aglient wash buffer kit. The Aglient DNA microarray scanner was used for array scanning. Genes that have values greater than or equal to lower cut-off: 50.0 in 2 out of two samples were chosen for data analysis. Differentially expressed genes were identified through Fold Change filtering. Pathway Analysis and GO analysis were applied to determine the roles of these differentially expressed genes played in these biological pathways or GO terms. Finally, Hierarchical Clustering was performed to show distinguishable gene expression profiling among samples.

### Knockdown of IGF-1 in UC-MSCs-IGF-1 using siRNA

For small interfering RNA (siRNA)-mediated knockdown of IGF-1, UC-MSCs-IGF-1 were transfected with IGF-1-siRNA (UC-MSCs-siRNA) (Santa), while the cell transfected with nontargeting siRNA were used as the control group (UC-MSCs

-control). The detailed operation was performed according to the manufacturer’s instructions.

### Anti-oxidation capacity assay

After the therapy, the levels of the ROS, as well as some antioxidants (SOD, eNOS and HO-1) in injured kidney tissues of each group were detected with kits purchased from Nanjing Jiancheng Bioengineering Institute. Kidney tissues (200 mg) were homogenized with PBS solution and the homogenate was centrifuged at 3000 rpm for 20 min. The supernatant was collected for further detection and the detailed operations were performed according to the manufacturer’s instructions.

To further evaluate the anti-oxidation capacity of UC-MSCs-IGF-1 in vitro, a co-culture system was established using trans-well. UC-MSCs, UC-MSCs-vector and UC-MSCs-IGF-1 were seeded on the upper side of a porous polycarbonate membrane (pore size: 8 μm; Euroclone SPA) in co-culture with renal tubular epithelial cell line， HK2 cells, respectively. The HK-2 cells (ATCC, USA) were seeded at $1\times10^5$ cells/well in a 24-well plate. Keep the ratio of HK2 cells and UC-MSCs at 5:1. The cells were incubated with DMEM/F12 (Hyclone) plus 10% FBS (Gibco) in the co-culture system, and exposed to 30 μM $H_2O_2$ for 1 day and 2 days respectively. Finally, proliferation index of HK2 cells in each group was detected with CCK-8, and the HK2 cells co-cultured with noting were used as the control group.

### Anti-inflammatory potential assay

The inflammatory components in the kidney tissues of each group were detected with ELISA. Similar to anti-oxidation capacity assay, the supernatant from kidney tissue was collected for the detection. Herein, monocyte/macrophage chemotactic protein-1 (MCP-1), Macrophage inflammatory protein 2 (MIP-2), regulated upon activation normal T cell expressed and presumably secreted (RANTES), and transforming growth factor-β (TGF-β) and were examined for evaluation of inflammatory reaction.

In addition, to further detect the anti-inflammatory potential of UC-MSCs, UC-MSCs-vector and UC-MSCs-IGF-1, a co-culture system was established using trans-well. Similar to anti-oxidation capacity assay, UC-MSCs, UC-MSCs-vector and UC-MSCs-IGF-1 were seeded on the upper side of a porous polycarbonate membrane in co-culture with murine macrophage RAW264.7 cell line (ATCC, USA) respectively. The RAW264.7 cells were seeded at $1\times10^5$ cells/well in a 24-well plate. Keep the ratio of RAW264.7 cells and UC-MSCs at 5:1. The cells were incubated with DMEM/F12 (Hyclone) plus 10% FBS (Gibco) in the co-culture system, and exposed to lipopolysaccharide (100 ng/ml, Sigma) for 24 hours. Finally, the expression of genes associated with inflammatory response (TNF, IL-6 and COX-2) in RAW264.7 cells of each co-culture group was detected with qPCR, and the RAW264.7 cells co-cultured with noting were used as the control group.

## Cell migration assay

To evaluate the effect of IGF-1 overexpression on migratory ability of UC-MSCs in vivo, anti-human nucleus antigen (hNA, Millipore) was used to detect the location of human mesenchymal stem cells in kidney tissue of each group with immunohistochemistry. The number of hNA-positive cells was further counted in ten fields for each group, and the average value was used to evaluate the migratory ability of UC-MSCs, UC-MSCs-vector and UC-MSCs-IGF-1.

To investigate the influence of cell proliferation on the migration, mitomycin C was used to block proliferation as the reference [3]. The migration of UC-MSCs was still measured using Tran-swell plates as the previous study [3]. In brief, UC-MSCs were seeded on the upper side of a porous polycarbonate membrane in co-culture with HK2 cells. HK2 cells were seeded at $1\times10^5$ cells/well in a 24-well plate. After 24 hours, the cells were incubated with DMEM/F12 plus 2% FBS alone or in the presence of 5 μM cisplatin for 6 hours. After cisplatin removal, the HK2 cells were washed and co-cultured with UC-MSCs. After 36 h, the cells at the upper side of the filter (unmigrated cells) were mechanically removed. Cells that had migrated to the lower side of the filter were fixed for 30 min in 4% paraformaldehyde and further stained with crystal violet. The number of cells in ten random fields was counted for each filter.

## Statistical analysis

The results were expressed as means ± SEM, and statistical analysis was performed using SPSS 17.0. The differences among groups were analyzed by one-way ANOVA followed by t-test. $P < 0.05$ was considered statistically significant.

## References

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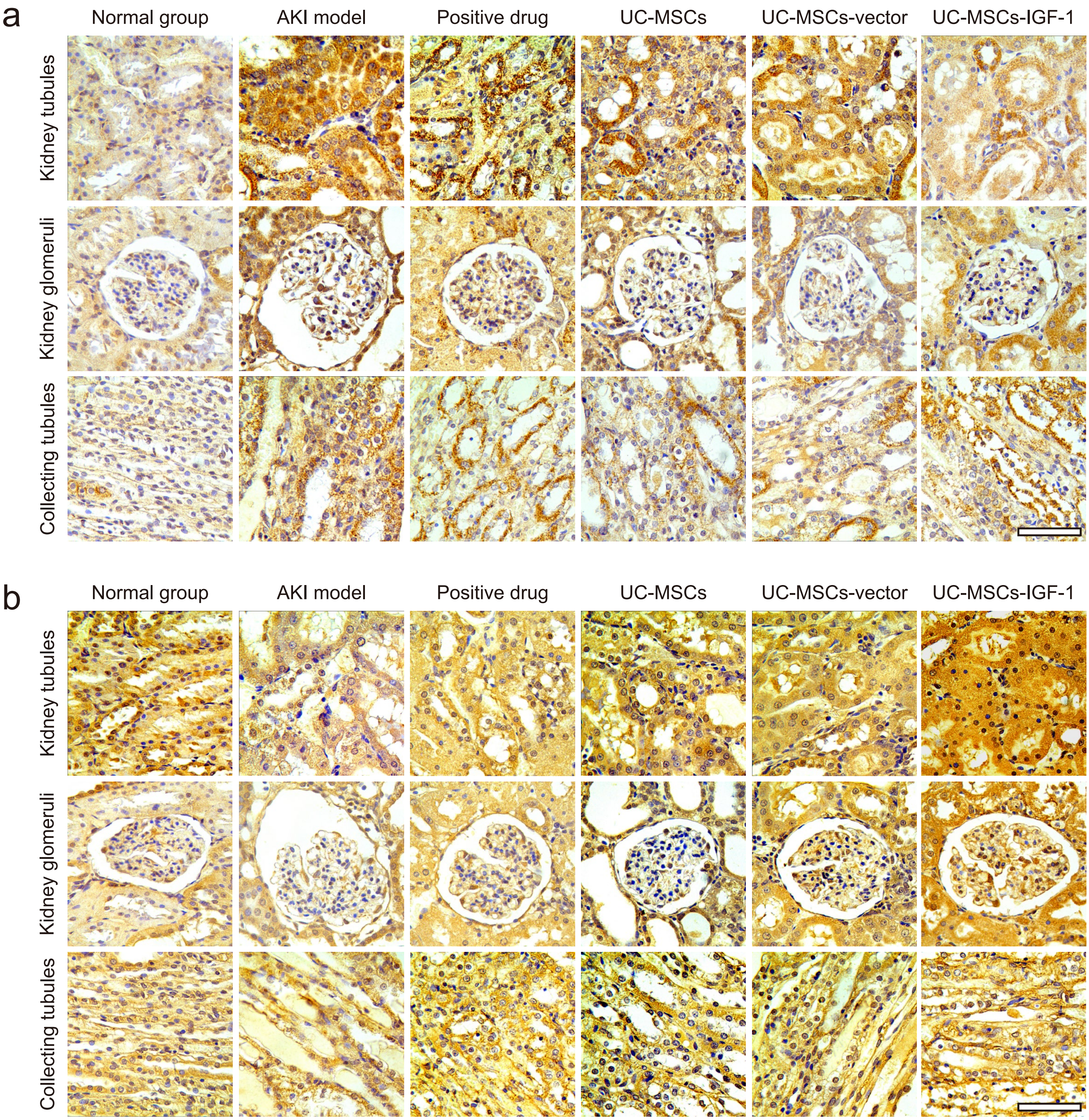
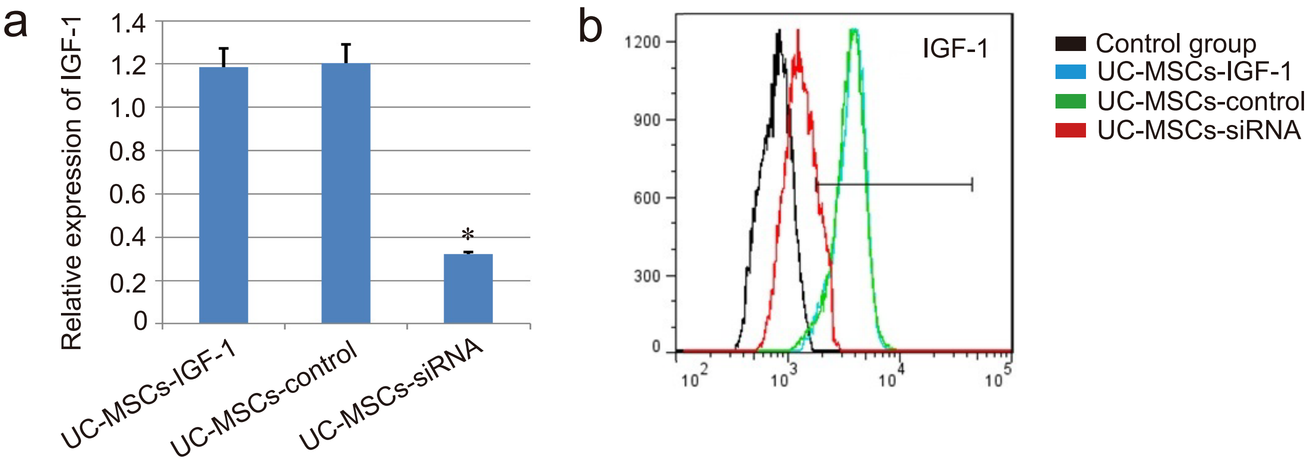
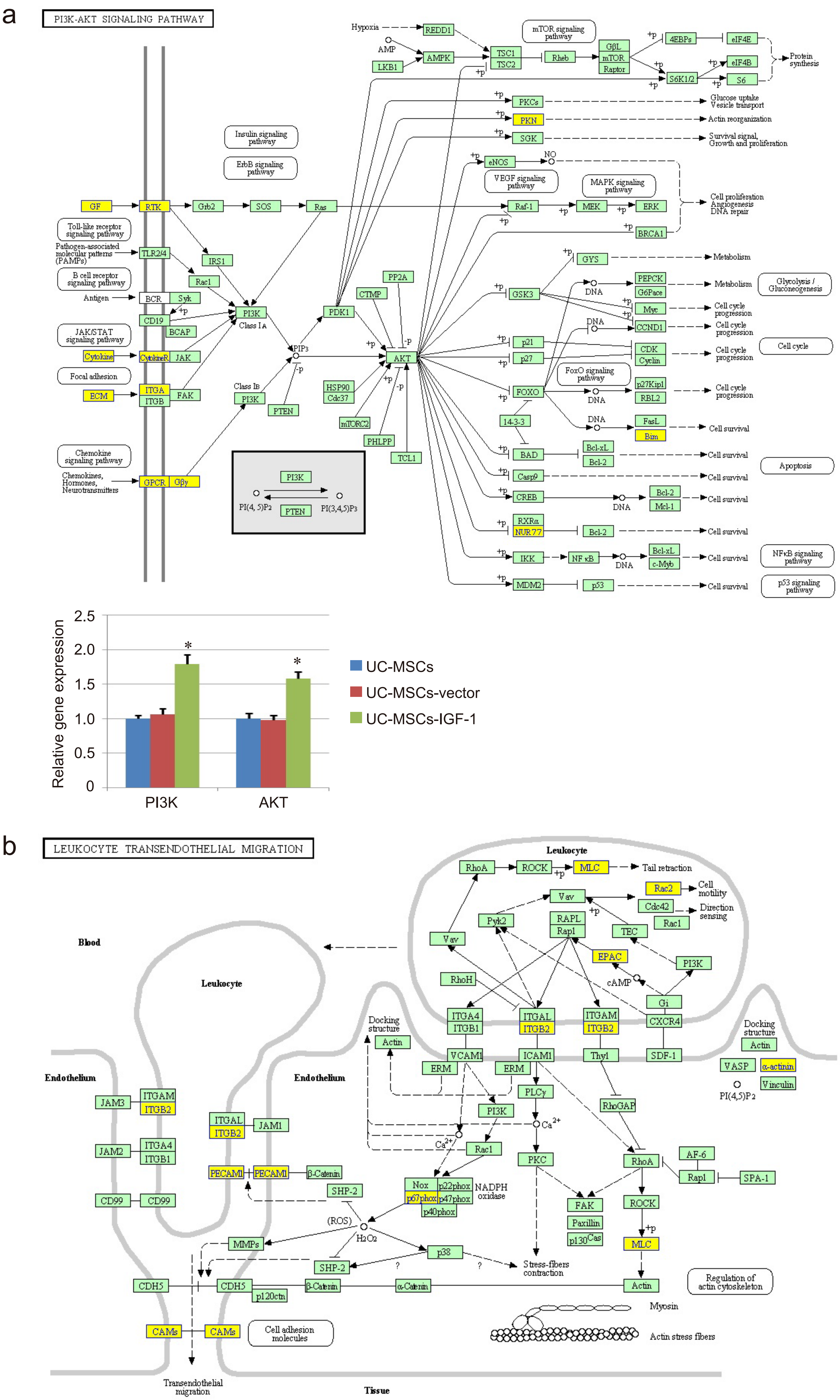
# Supplementary Figure 1



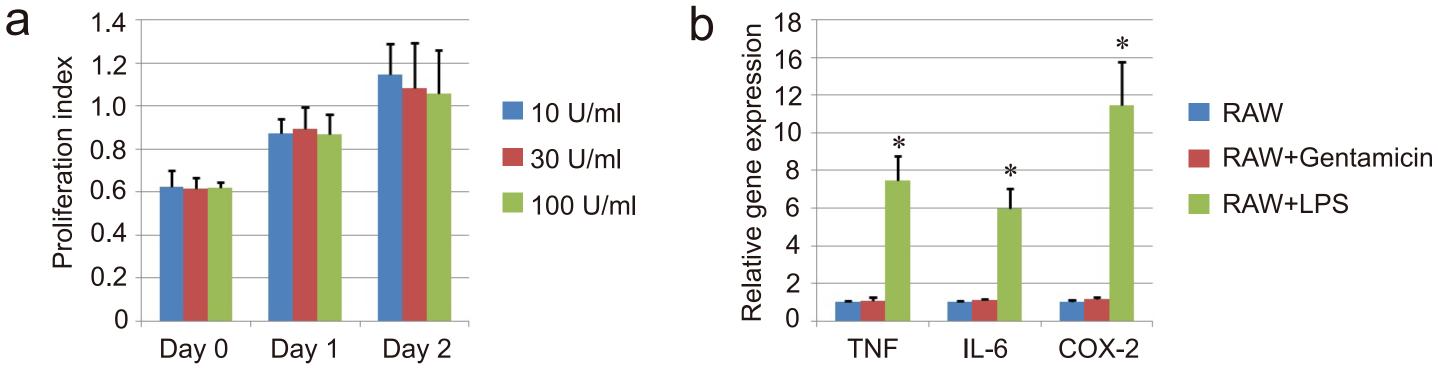
# Supplementary Figure 2



# Supplementary Figure 3



# Supplementary Figure 4



# Supplementary Table 1. Change of biochemical parameters in serum or urine during the therapy process

| | Characteristics of AKI model in urine or serum | | | | Biochemical parameters in urine after therapy | | | Biochemical parameters in serum after therapy | | |
|---|---|---|---|---|---|---|---|---|---|---|
| | NAG(U/L) | LZM(U/ml) | Creatine(μM) | UN(mM) | NAG(U/L) | LZM(U/ml) | UN(mM) | NAG(U/L) | Creatine(μM) | UN(mM) |
| normal group | 14.5±1.4 | 33.5±2.7 | 22.7±3.4 | 10.5±1.3 | 18.2±1.5 | 36.0±3.7 | 38.9±3.8 | 18.1±2.0 | 21.0±4.0 | 8.3±1.6 |
| AKI model | 37.5±4.0$^{*}$ | 177.5±13.2$^{*}$ | 70.5±5.7$^{*}$ | 27.2±4.0$^{*}$ | 44.3±6.1 | 247.5±27.0 | 15.3±2.0 | 66.4±8.8 | 81.6±9.2 | 34.5±5.0 |
| positive drug | | | | | 29.9±4.6$^{*}$ | 237.0±24.2 | 21.9±2.9$^{*}$ | 34.9±6.8$^{*}$ | 43.5±8.8$^{*}$ | 31.3±4.0 |
| UC-MSCs | | | | | 27.7±2.7$^{*}$ | 220.3±11.8 | 24.3±2.8$^{*}$ | 44.5±5.7$^{*}$ | 44.8±7.4$^{*}$ | 31.6±5.7 |
| UC-MSCs-vector | | | | | 28.3±6.3$^{*}$ | 224.9±23.1 | 26.7±2.5$^{*}$ | 44.2±4.8$^{*}$ | 47.9±4.6$^{*}$ | 30.7±6.9 |
| UC-MSCs-IGF-1 | | | | | 26.4±3.0$^{*}$ | 200.5±20.7$^{*\#}$ | 34.65±4.0$^{*\#}$ | 41.2±7.8$^{*}$ | 34.4±5.1$^{*\#}$ | 24.1±3.6$^{*\#}$ |

## Supplementary Information

Supplementary File 1. The raw data of heatmap in Figure 5a. Compared with normal UC-MSCs and UC-MSCs-vector, the up-regulated and down-regulated genes in UC-MSCs-IGF-1 were shown herein respectively.

Supplementary File 2. The detailed information about the materials and methods.

Supplementary Figure 1. Expression of Caspase 3 and Bcl-2 in the kidney tissues of each group. The expression levels of apoptotic gene (Caspase 3, Supplementary Figure 1a) and anti-apoptotic gene (Bcl-2, Supplementary Figure 1b) in the kidney tissue were detected using immunohistochemistry. A representative in the kidney tubules, kidney glomeruli, and collecting tubules close to the average level of each group is shown for each group. Scale bar corresponds to 50 μm.

Supplementary Figure 2. Analysis of effect of IGF-1-siRNA on IGF-1 expression in UC-MSCs-IGF-1 by qPCR (Supplementary Figure 2a) and FACS (Supplementary Figure 2b). * $P<0.05$ compared with the UC-MSCs-IGF-1 group and UC-MSCs-control group respectively.

Supplementary Figure 3. Signal pathway analysis of the effects of IGF-1 overexpression in UC-MSCs through RNA microarray. a. PI3K-AKT signaling pathway. The expression of PI3K and AKT was further detected with qPCR. The level of gene expression in UC-MSCs was regarded as 1.0. * P<0.05 compared with the normal UC-MSCs group and UC-MSCs-vector group respectively. b. Leukocyte transendothelial migration pathway. “Yellow” indicated the upregulated genes, and “cyan” indicated the genes without significant changing.

Supplementary Figure 4. Biological effects of gentamicin on HK-2 cells and RAW264.7 cells. a. Effect of gentamicin on HK-2 cells proliferation. The proliferation index was evaluated with CCK-8 method, and results are expressed as mean ± SEM. b. Function of gentamicin (100U/ml) to induce inflammation in RAW264.7 cells. The expression of TNF, IL-6 and COX-2 was detected using qPCR. The level of gene expression in RAW264.7 cells without any treatment (RAW) was regarded as 1.0, then gene expression in RAW264.7 treated with gentamicin (RAW+gentamicin) and LPS (RAW+LPS) was further performed. * P<0.05 compared with the normal RAW group and RAW+gentamicin group respectively.

Supplementary Table 1. Change in biochemical variables in serum or urine during the therapy process. To assay the characteristics of rat AKI model, NAZ and LAM in urine, as well as creatinine and urea nitrogen (UN) in serum, were detected on day 7. *P <0.05 compared with the normal group. To analyze the therapeutic effect, urine and serum samples of each group were collected from each group on day 15 after animals were sacrificed. The levels of UN, NAZ, and LAM in urine, as well as creatinine, UN, and NAG in serum, were measured. *P < 0.05 compared with the model group; #$P < 0.05$ compared with the normal UC-MSCs group and UC-MSCs-vector group respectively.