S1 Table - A list of candidate switch genes

| GenID  | logFC  | t-test (adj p-value) | dip-test (p-value) |
|--------|--------|----------------------|--------------------|
| LAMC2  | 2.90E+00 | 9.26E-15             | 1.33E-03           |
| TSPAN1 | 2.73E+00 | 9.26E-15             | 3.52E-03           |
| SERPINB5 | 2.18E+00 | 7.33E-12             | 1.77E-03           |
| FNDC1  | 1.48E+00 | 1.28E-06             | 1.20E-02           |
| COMP   | 1.47E+00 | 1.51E-06             | 2.00E-02           |
| NQO1   | 1.47E+00 | 9.39E-11             | 8.89E-03           |
| CST2   | 1.23E+00 | 6.58E-09             | 8.07E-01           |
| PCDH7  | 1.01E+00 | 5.77E-10             | 4.82E-02           |
| B3GNT3 | 8.41E-01 | 2.88E-10             | 1.71E-02           |
| PRKG1  | 4.07E-01 | 5.66E-03             | 3.74E-02           |
| SLC25A4| -2.27E-01| 3.46E-02             | 4.08E-02           |
| PKI55  | -2.64E-01| 2.86E-03             | 4.74E-02           |
| HABP2  | -5.26E-01| 2.88E-02             | 1.92E-02           |
| ATP13A4| -5.84E-01| 3.59E-03             | 2.47E-03           |
| CGNL1  | -5.88E-01| 3.10E-04             | 3.13E-02           |
| EML5   | -7.11E-01| 2.19E-07             | 1.42E-02           |
| RAP1GAP| -7.29E-01| 6.53E-05             | 4.38E-02           |
| SERPINA6| -7.46E-01| 2.49E-05             | 4.26E-02           |
| GRB10  | -8.10E-01| 3.80E-05             | 1.87E-03           |
| MUC15  | -8.11E-01| 3.81E-04             | 2.25E-02           |
| ABCA5  | -9.26E-01| 8.60E-07             | 3.79E-02           |
| SERPINA5| -1.03E+00| 5.48E-04             | 3.38E-03           |
| GPHA2  | -1.10E+00| 5.47E-05             | 1.48E-02           |
| ATRNL1 | -1.10E+00| 4.40E-07             | 1.82E-02           |
| FAM150B| -1.11E+00| 5.15E-07             | 2.24E-02           |
| ONECUT1| -1.11E+00| 8.87E-04             | 5.59E-03           |
| CXCL12 | -1.13E+00| 6.37E-10             | 4.85E-02           |
| GPR98  | -1.14E+00| 1.12E-07             | 1.38E-02           |
| SLC39A5| -1.29E+00| 1.91E-05             | 3.26E-03           |
| SYCN   | -1.29E+00| 2.27E-04             | 1.49E-02           |
| CTNND2 | -1.38E+00| 1.21E-06             | 2.42E-02           |
| KCNJ16 | -1.59E+00| 6.02E-05             | 8.96E-04           |
| REG3A  | -1.62E+00| 9.66E-03             | 1.31E-02           |
| GATM   | -1.66E+00| 4.91E-04             | 2.93E-03           |
| RBPJL  | -1.71E+00| 1.30E-05             | 2.56E-02           |
| SLC16A12| -1.87E+00| 9.27E-08             | 3.17E-03           |
| ANPEP  | -1.89E+00| 3.61E-06             | 2.17E-02           |
| KLK1   | -1.92E+00| 4.77E-05             | 6.05E-04           |
| AOX1   | -2.04E+00| 1.01E-09             | 2.81E-02           |
| num | X1 or X2 | X2 or X1 | X3   | rhodiff | MLA value | wald   | p value  | bonferroni |
|-----|----------|----------|------|---------|-----------|--------|----------|------------|
| 1   | ADH1B    | ACADL    | SERPINB5 | 1.0638  | 0.3833    | 37.132 | 1.10E-09 | 3.30E-04   |
| 2   | COLEC11  | RGN      | LAMC2 | 1.0635  | 0.3797    | 35.4431 | 2.63E-09 | 7.89E-04   |
| 3   | SDC4     | SLC2A1   | TSPAN1 | 1.057   | 0.3829    | 35.1123 | 3.11E-09 | 9.33E-04   |
| 4   | APPL1    | SMARCA2  | CXCL12 | -1.1878 | -0.4255   | 34.9863 | 3.32E-09 | 9.96E-04   |
| 5   | FAM129A  | ADH1B    | SERPINB5 | 1.0886  | 0.394     | 34.9372 | 3.41E-09 | 1.02E-03   |
| 6   | RBM4B    | PGAP3    | ERP27  | 1.0497  | 0.3845    | 34.8683 | 3.53E-09 | 1.06E-03   |
| 7   | GALNT13  | LPIN1    | CXCL12 | 1.0829  | 0.395     | 34.7898 | 3.67E-09 | 1.10E-03   |
| 8   | ADH1B    | PCDHB5   | SERPINB5 | 1.0429  | 0.3794    | 34.6667 | 3.91E-09 | 1.17E-03   |
| 9   | PELI2    | BOC      | CXCL12 | -1.125  | -0.401    | 34.6217 | 4.00E-09 | 1.20E-03   |
| 10  | C2orf83  | S100A5   | EML5  | -1.055  | -0.3768   | 34.4867 | 4.29E-09 | 1.29E-03   |
| 11  | LAMB1    | IFTG3    | LAMC2 | 1.0634  | 0.4057    | 34.2875 | 4.75E-09 | 1.43E-03   |
| 12  | CERS6    | SCARNA6  | PCDH7 | 1.1448  | 0.4074    | 34.2813 | 4.77E-09 | 1.43E-03   |
| 13  | RPL34    | ZNF385D  | CXCL12 | -1.1062 | -0.4016   | 34.1535 | 5.09E-09 | 1.53E-03   |
| 14  | FAM171B  | ATF6     | CXCL12 | -1.1014 | -0.3913   | 33.3115 | 7.85E-09 | 2.36E-03   |
| 15  | MPP7     | KCND3    | SERPINB5 | 1.2776  | 0.4584    | 33.2791 | 7.98E-09 | 2.39E-03   |
| 16  | CST3     | GH1      | KLK1  | 1.1118  | 0.4024    | 33.2717 | 8.01E-09 | 2.40E-03   |
| 17  | LOC692247 | TLE2     | NQO1  | -1.2095 | -0.4304   | 33.1374 | 8.59E-09 | 2.58E-03   |
| 18  | LTBP2    | PARP16   | LAMC2 | 1.1021  | 0.3924    | 33.1333 | 8.61E-09 | 2.58E-03   |
| 19  | PROX1    | RG513    | CXCL12 | -1.0554 | -0.3791   | 32.8558 | 9.93E-09 | 2.98E-03   |
| 20  | ADH1A    | TP1      | LAMC2 | -1.0736 | -0.3914   | 32.8464 | 9.97E-09 | 2.99E-03   |
| 21  | APPL1    | SLC9A9   | CXCL12 | -1.127  | -0.4034   | 32.8202 | 1.01E-08 | 3.03E-03   |
| 22  | NR2C2AP  | IER3IP1  | KLK1  | -1.0983 | -0.396   | 32.667  | 1.09E-08 | 3.27E-03   |
| 23  | APPL1    | ZNF385D  | CXCL12 | -1.205  | -0.4359   | 32.6405 | 1.11E-08 | 3.33E-03   |

S2 Table- A list of statistically significant triplets.
| Gene 1 | Gene 2 | Gene 3 | fold change | p-value  | Log10 p-value |
|-------|--------|--------|-------------|----------|---------------|
| PRELID2 | STX4 | CST2 | 1.1978 | 0.4248 | 32.6386 | 1.11E-08 | 3.33E-03 |
| PROM2 | MDK | SERPINB5 | 1.1664 | 0.4194 | 32.6283 | 1.12E-08 | 3.36E-03 |
| MRPL37 | SLFN12 | PDA2 | -1.0746 | -0.3874 | 32.5751 | 1.15E-08 | 3.45E-03 |
| TNFRSF1A | NAV2 | NQO1 | 1.1052 | 0.3961 | 32.427 | 1.24E-08 | 3.72E-03 |
| PELI2 | PREX2 | LAMC2 | 1.2116 | 0.4302 | 32.3727 | 1.27E-08 | 3.81E-03 |
| WNK2 | PAR68 | SERPINB5 | -1.0617 | -0.3769 | 32.0734 | 1.48E-08 | 4.44E-03 |
| SETD6 | SEMA7A | AOX1 | -1.0527 | -0.3836 | 31.6431 | 1.85E-08 | 5.55E-03 |
| PRDM8 | TTLL4 | NQO1 | 1.1117 | 0.4001 | 32.018 | 1.53E-08 | 4.59E-03 |
| MRPL37 | SLFN12 | PDIA2 | -1.0746 | -0.3874 | 32.5751 | 1.15E-08 | 3.45E-03 |
| TNFRSF1A | NAV2 | NQO1 | 1.1052 | 0.3961 | 32.427 | 1.24E-08 | 3.72E-03 |
| PELI2 | PREX2 | LAMC2 | 1.2116 | 0.4302 | 32.3727 | 1.27E-08 | 3.81E-03 |
| WNK2 | PAR68 | SERPINB5 | -1.0617 | -0.3769 | 32.0734 | 1.48E-08 | 4.44E-03 |
| SETD6 | SEMA7A | AOX1 | -1.0527 | -0.3836 | 31.6431 | 1.85E-08 | 5.55E-03 |
| PRDM8 | TTLL4 | NQO1 | 1.1117 | 0.4001 | 32.018 | 1.53E-08 | 4.59E-03 |
| MRPL37 | SLFN12 | PDIA2 | -1.0746 | -0.3874 | 32.5751 | 1.15E-08 | 3.45E-03 |
| TNFRSF1A | NAV2 | NQO1 | 1.1052 | 0.3961 | 32.427 | 1.24E-08 | 3.72E-03 |
| PELI2 | PREX2 | LAMC2 | 1.2116 | 0.4302 | 32.3727 | 1.27E-08 | 3.81E-03 |
| WNK2 | PAR68 | SERPINB5 | -1.0617 | -0.3769 | 32.0734 | 1.48E-08 | 4.44E-03 |
| SETD6 | SEMA7A | AOX1 | -1.0527 | -0.3836 | 31.6431 | 1.85E-08 | 5.55E-03 |
| PRDM8 | TTLL4 | NQO1 | 1.1117 | 0.4001 | 32.018 | 1.53E-08 | 4.59E-03 |
| MRPL37 | SLFN12 | PDIA2 | -1.0746 | -0.3874 | 32.5751 | 1.15E-08 | 3.45E-03 |
| TNFRSF1A | NAV2 | NQO1 | 1.1052 | 0.3961 | 32.427 | 1.24E-08 | 3.72E-03 |
| PELI2 | PREX2 | LAMC2 | 1.2116 | 0.4302 | 32.3727 | 1.27E-08 | 3.81E-03 |
| WNK2 | PAR68 | SERPINB5 | -1.0617 | -0.3769 | 32.0734 | 1.48E-08 | 4.44E-03 |
| SETD6 | SEMA7A | AOX1 | -1.0527 | -0.3836 | 31.6431 | 1.85E-08 | 5.55E-03 |
| PRDM8 | TTLL4 | NQO1 | 1.1117 | 0.4001 | 32.018 | 1.53E-08 | 4.59E-03 |
| MRPL37 | SLFN12 | PDIA2 | -1.0746 | -0.3874 | 32.5751 | 1.15E-08 | 3.45E-03 |
| TNFRSF1A | NAV2 | NQO1 | 1.1052 | 0.3961 | 32.427 | 1.24E-08 | 3.72E-03 |
| PELI2 | PREX2 | LAMC2 | 1.2116 | 0.4302 | 32.3727 | 1.27E-08 | 3.81E-03 |
| WNK2 | PAR68 | SERPINB5 | -1.0617 | -0.3769 | 32.0734 | 1.48E-08 | 4.44E-03 |
| SETD6 | SEMA7A | AOX1 | -1.0527 | -0.3836 | 31.6431 | 1.85E-08 | 5.55E-03 |
| PRDM8 | TTLL4 | NQO1 | 1.1117 | 0.4001 | 32.018 | 1.53E-08 | 4.59E-03 |
|   |   |   |   |   |   |   |
|---|---|---|---|---|---|---|
|   |   |   |   |   |   |   |
|  65 | SLC7A1 | DCAF15 | CXCL12 | -1.0793 | -0.3927 | 30.4094 | 3.50E-08 | 1.05E-02 |
|  66 | LOC100129518 | FCGBP | SERPINB5 | -1.0693 | -0.3822 | 30.4004 | 3.51E-08 | 1.05E-02 |
|  67 | TMEM208 | MRPL24 | MUC15 | -1.1694 | -0.4187 | 30.2441 | 3.81E-08 | 1.14E-02 |
|  68 | LRG1 | GGTA1P | CXCL12 | -1.1199 | -0.4058 | 30.1567 | 3.99E-08 | 1.20E-02 |
|  69 | LOC100131506 | RBFOX2 | LAMC2 | 1.2413 | 0.3816 | 30.1259 | 4.05E-08 | 1.05E-02 |
|  70 | OAS2 | NT5C3A | LAMC2 | 1.0741 | 0.3816 | 30.1133 | 4.08E-08 | 1.22E-02 |
|  71 | ITPR3 | SETD6 | LAMC2 | 1.1044 | 0.3806 | 30.1078 | 4.11E-08 | 1.22E-02 |
|  72 | MRPL24 | B3GNT3 | CXCL12 | -1.1199 | -0.4058 | 30.1133 | 4.08E-08 | 1.05E-02 |
|  73 | ADH1A | APPL1 | TSPAN1 | 1.0693 | 0.3816 | 30.1259 | 4.05E-08 | 1.22E-02 |
|  74 | ITPR3 | SETD6 | LAMC2 | 1.1044 | 0.3806 | 30.1078 | 4.11E-08 | 1.22E-02 |
|  75 | NLGN1 | GNMT | TSPAN1 | 1.1557 | 0.4006 | 29.9956 | 4.26E-08 | 1.05E-02 |
|  76 | LRRC42 | NCK2 | B3GNT3 | 1.0693 | 0.3782 | 29.9558 | 4.42E-08 | 1.05E-02 |
|  77 | ADH1A | APPL1 | TSPAN1 | 1.0693 | 0.3816 | 30.1259 | 4.05E-08 | 1.22E-02 |
|  78 | ITPR3 | SETD6 | LAMC2 | 1.1044 | 0.3806 | 30.1078 | 4.11E-08 | 1.22E-02 |
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 106 | LRIG1 | FILIP1 | AOX1 | -1.1178 | -0.4071 | 29.0933 | 6.90E-08 | 2.07E-02 |
| 107 | EIF4EBP2 | ICT1 | B3GNT3 | -1.1027 | -0.4092 | 29.0885 | 6.91E-08 | 2.07E-02 |
| 108 | OSBP1L10 | ADH1B | SERPINB5 | -1.113 | -0.3988 | 29.0299 | 7.13E-08 | 2.14E-02 |
| 109 | ADH1B | ACADL | TSPAN1 | 1.1717 | 0.4139 | 29.0233 | 7.15E-08 | 2.15E-02 |
| 110 | C6orf201 | LRFN5 | CXCL12 | -1.088 | -0.3928 | 29.0168 | 7.18E-08 | 2.15E-02 |
| 111 | ADH1B | MPC1 | PCDH7 | 1.1118 | 0.4082 | 29.0148 | 7.18E-08 | 2.15E-02 |
| 112 | PEL12 | FHL5 | AOX1 | -1.2243 | -0.4384 | 28.9932 | 7.26E-08 | 2.18E-02 |
| 113 | ADH1B | TP1 | LAMC2 | -1.1117 | -0.4092 | 28.9916 | 7.27E-08 | 2.18E-02 |
| 114 | HOXA7 | FLJ45721 | LAMC2 | -1.0765 | -0.3846 | 28.9655 | 7.18E-08 | 2.15E-02 |
| 115 | ADH1B | MPC1 | PCDH7 | 1.1118 | 0.4082 | 28.9655 | 7.18E-08 | 2.15E-02 |
| 116 | PEL12 | FHL5 | AOX1 | -1.2243 | -0.4384 | 28.9932 | 7.26E-08 | 2.18E-02 |
| 117 | ADH1B | TP1 | LAMC2 | -1.1117 | -0.4092 | 28.9916 | 7.27E-08 | 2.18E-02 |
| 118 | HOXA7 | FLJ45721 | LAMC2 | -1.0765 | -0.3846 | 28.9655 | 7.18E-08 | 2.15E-02 |
| 119 | ADH1B | MPC1 | PCDH7 | 1.1118 | 0.4082 | 28.9655 | 7.18E-08 | 2.15E-02 |
| 120 | PEL12 | FHL5 | AOX1 | -1.2243 | -0.4384 | 28.9932 | 7.26E-08 | 2.18E-02 |
| 121 | ADH1B | TP1 | LAMC2 | -1.1117 | -0.4092 | 28.9916 | 7.27E-08 | 2.18E-02 |
| 122 | HOXA7 | FLJ45721 | LAMC2 | -1.0765 | -0.3846 | 28.9655 | 7.18E-08 | 2.15E-02 |
| 123 | ADH1B | MPC1 | PCDH7 | 1.1118 | 0.4082 | 28.9655 | 7.18E-08 | 2.15E-02 |
| 124 | PEL12 | FHL5 | AOX1 | -1.2243 | -0.4384 | 28.9932 | 7.26E-08 | 2.18E-02 |
| 125 | ADH1B | TP1 | LAMC2 | -1.1117 | -0.4092 | 28.9916 | 7.27E-08 | 2.18E-02 |
| 126 | HOXA7 | FLJ45721 | LAMC2 | -1.0765 | -0.3846 | 28.9655 | 7.18E-08 | 2.15E-02 |
| 127 | ADH1B | MPC1 | PCDH7 | 1.1118 | 0.4082 | 28.9655 | 7.18E-08 | 2.15E-02 |
| 128 | PEL12 | FHL5 | AOX1 | -1.2243 | -0.4384 | 28.9932 | 7.26E-08 | 2.18E-02 |
| 129 | ADH1B | TP1 | LAMC2 | -1.1117 | -0.4092 | 28.9916 | 7.27E-08 | 2.18E-02 |
| 130 | HOXA7 | FLJ45721 | LAMC2 | -1.0765 | -0.3846 | 28.9655 | 7.18E-08 | 2.15E-02 |
| 131 | ADH1B | MPC1 | PCDH7 | 1.1118 | 0.4082 | 28.9655 | 7.18E-08 | 2.15E-02 |
| 132 | PEL12 | FHL5 | AOX1 | -1.2243 | -0.4384 | 28.9932 | 7.26E-08 | 2.18E-02 |
| 133 | ADH1B | MPC1 | PCDH7 | 1.1118 | 0.4082 | 28.9655 | 7.18E-08 | 2.15E-02 |
| 134 | PEL12 | FHL5 | AOX1 | -1.2243 | -0.4384 | 28.9932 | 7.26E-08 | 2.18E-02 |
| 135 | ADH1B | MPC1 | PCDH7 | 1.1118 | 0.4082 | 28.9655 | 7.18E-08 | 2.15E-02 |
| 136 | PEL12 | FHL5 | AOX1 | -1.2243 | -0.4384 | 28.9932 | 7.26E-08 | 2.18E-02 |
| 137 | ADH1B | MPC1 | PCDH7 | 1.1118 | 0.4082 | 28.9655 | 7.18E-08 | 2.15E-02 |
| 138 | PEL12 | FHL5 | AOX1 | -1.2243 | -0.4384 | 28.9932 | 7.26E-08 | 2.18E-02 |
| 139 | ADH1B | MPC1 | PCDH7 | 1.1118 | 0.4082 | 28.9655 | 7.18E-08 | 2.15E-02 |
| 140 | PEL12 | FHL5 | AOX1 | -1.2243 | -0.4384 | 28.9932 | 7.26E-08 | 2.18E-02 |
| 141 | ADH1B | MPC1 | PCDH7 | 1.1118 | 0.4082 | 28.9655 | 7.18E-08 | 2.15E-02 |
| 142 | PEL12 | FHL5 | AOX1 | -1.2243 | -0.4384 | 28.9932 | 7.26E-08 | 2.18E-02 |
| 143 | ADH1B | MPC1 | PCDH7 | 1.1118 | 0.4082 | 28.9655 | 7.18E-08 | 2.15E-02 |
| 144 | PEL12 | FHL5 | AOX1 | -1.2243 | -0.4384 | 28.9932 | 7.26E-08 | 2.18E-02 |
| 145 | ADH1B | MPC1 | PCDH7 | 1.1118 | 0.4082 | 28.9655 | 7.18E-08 | 2.15E-02 |
| 146 | PEL12 | FHL5 | AOX1 | -1.2243 | -0.4384 | 28.9932 | 7.26E-08 | 2.18E-02 |

**Notes:**
- The table lists genes and their expression changes.
- The expression changes are represented as fold changes.
- The table includes genes with fold changes greater than 1.0 and less than -1.0.
- The fold changes are given with their respective expression values.
|   |   |   |   |   |
|---|---|---|---|---|
| 147 | SEC23B | PPI6 | AOX1 | 1.0843 | 0.3921 | 28.3834 | 9.95E-08 | 2.99E-02 |
| 148 | F13A1 | LRIG1 | LAMC2 | 1.1271 | 0.3967 | 28.3791 | 9.97E-08 | 2.99E-02 |
| 149 | EPHX1 | GUCY1A3 | TSPAN1 | 1.1812 | 0.4154 | 28.3721 | 1.00E-07 | 3.00E-02 |
| 150 | LRP5 | LAP3 | KLI1 | -1.0518 | -0.382 | 28.3467 | 1.01E-07 | 3.03E-02 |
| 151 | LHFP | MPP7 | AOX1 | -1.1004 | -0.399 | 28.3318 | 1.02E-07 | 3.06E-02 |
| 152 | SNORD13P2 | SCARN6 | PCDH7 | 1.1038 | 0.3914 | 28.3316 | 1.02E-07 | 3.06E-02 |
| 153 | ADH1C | MPP7 | TSPAN1 | 1.1812 | 0.4154 | 28.3073 | 1.04E-07 | 3.12E-02 |
| 154 | GUCY1A3 | TSPAN1 | 1.1812 | 0.4154 | 28.3073 | 1.04E-07 | 3.12E-02 |
| 155 | TSPAN1 | 1.1812 | 0.4154 | 28.3073 | 1.04E-07 | 3.12E-02 |
| 156 | LRP5 | LAP3 | KLI1 | -1.0518 | -0.382 | 28.3467 | 1.01E-07 | 3.03E-02 |
| 157 | LHFP | MPP7 | AOX1 | -1.1004 | -0.399 | 28.3318 | 1.02E-07 | 3.06E-02 |
| 158 | SNORD13P2 | SCARN6 | PCDH7 | 1.1038 | 0.3914 | 28.3316 | 1.02E-07 | 3.06E-02 |
| 159 | ADH1C | MPP7 | TSPAN1 | 1.1812 | 0.4154 | 28.3073 | 1.04E-07 | 3.12E-02 |
| 160 | GUCY1A3 | TSPAN1 | 1.1812 | 0.4154 | 28.3073 | 1.04E-07 | 3.12E-02 |
| 161 | TSPAN1 | 1.1812 | 0.4154 | 28.3073 | 1.04E-07 | 3.12E-02 |
| 162 | LRP5 | LAP3 | KLI1 | -1.0518 | -0.382 | 28.3467 | 1.01E-07 | 3.03E-02 |
| 163 | LHFP | MPP7 | AOX1 | -1.1004 | -0.399 | 28.3318 | 1.02E-07 | 3.06E-02 |
| 164 | SNORD13P2 | SCARN6 | PCDH7 | 1.1038 | 0.3914 | 28.3316 | 1.02E-07 | 3.06E-02 |
| 165 | ADH1C | MPP7 | TSPAN1 | 1.1812 | 0.4154 | 28.3073 | 1.04E-07 | 3.12E-02 |
| 166 | GUCY1A3 | TSPAN1 | 1.1812 | 0.4154 | 28.3073 | 1.04E-07 | 3.12E-02 |
| 167 | TSPAN1 | 1.1812 | 0.4154 | 28.3073 | 1.04E-07 | 3.12E-02 |
| 168 | LRP5 | LAP3 | KLI1 | -1.0518 | -0.382 | 28.3467 | 1.01E-07 | 3.03E-02 |
| 169 | LHFP | MPP7 | AOX1 | -1.1004 | -0.399 | 28.3318 | 1.02E-07 | 3.06E-02 |
| 170 | SNORD13P2 | SCARN6 | PCDH7 | 1.1038 | 0.3914 | 28.3316 | 1.02E-07 | 3.06E-02 |
| 171 | ADH1C | MPP7 | TSPAN1 | 1.1812 | 0.4154 | 28.3073 | 1.04E-07 | 3.12E-02 |
| 172 | GUCY1A3 | TSPAN1 | 1.1812 | 0.4154 | 28.3073 | 1.04E-07 | 3.12E-02 |
| 173 | TSPAN1 | 1.1812 | 0.4154 | 28.3073 | 1.04E-07 | 3.12E-02 |
| 174 | LRP5 | LAP3 | KLI1 | -1.0518 | -0.382 | 28.3467 | 1.01E-07 | 3.03E-02 |
| 175 | LHFP | MPP7 | AOX1 | -1.1004 | -0.399 | 28.3318 | 1.02E-07 | 3.06E-02 |
| 176 | SNORD13P2 | SCARN6 | PCDH7 | 1.1038 | 0.3914 | 28.3316 | 1.02E-07 | 3.06E-02 |
| 177 | ADH1C | MPP7 | TSPAN1 | 1.1812 | 0.4154 | 28.3073 | 1.04E-07 | 3.12E-02 |
| 178 | GUCY1A3 | TSPAN1 | 1.1812 | 0.4154 | 28.3073 | 1.04E-07 | 3.12E-02 |
| 179 | TSPAN1 | 1.1812 | 0.4154 | 28.3073 | 1.04E-07 | 3.12E-02 |
| 180 | LRP5 | LAP3 | KLI1 | -1.0518 | -0.382 | 28.3467 | 1.01E-07 | 3.03E-02 |
| 181 | LHFP | MPP7 | AOX1 | -1.1004 | -0.399 | 28.3318 | 1.02E-07 | 3.06E-02 |
| 182 | SNORD13P2 | SCARN6 | PCDH7 | 1.1038 | 0.3914 | 28.3316 | 1.02E-07 | 3.06E-02 |
| 183 | ADH1C | MPP7 | TSPAN1 | 1.1812 | 0.4154 | 28.3073 | 1.04E-07 | 3.12E-02 |
| 184 | GUCY1A3 | TSPAN1 | 1.1812 | 0.4154 | 28.3073 | 1.04E-07 | 3.12E-02 |
| 185 | TSPAN1 | 1.1812 | 0.4154 | 28.3073 | 1.04E-07 | 3.12E-02 |
| 186 | LRP5 | LAP3 | KLI1 | -1.0518 | -0.382 | 28.3467 | 1.01E-07 | 3.03E-02 |
| 187 | LHFP | MPP7 | AOX1 | -1.1004 | -0.399 | 28.3318 | 1.02E-07 | 3.06E-02 |
| 188 | SNORD13P2 | SCARN6 | PCDH7 | 1.1038 | 0.3914 | 28.3316 | 1.02E-07 | 3.06E-02 |
| 189 | ADH1C | MPP7 | TSPAN1 | 1.1812 | 0.4154 | 28.3073 | 1.04E-07 | 3.12E-02 |
| 190 | GUCY1A3 | TSPAN1 | 1.1812 | 0.4154 | 28.3073 | 1.04E-07 | 3.12E-02 |
| 191 | TSPAN1 | 1.1812 | 0.4154 | 28.3073 | 1.04E-07 | 3.12E-02 |
| 187 | HOXD10 | EPX | LAMC2 | -1.2014 | -0.4287 | 27.7595 | 1.37E-07 | 4.11E-02 |
| 188 | FAM122A | NAP1L5 | PCDH7 | 1.0512 | 0.3788 | 27.7508 | 1.38E-07 | 4.14E-02 |
| 189 | PPP1R16B | C2CD4B | EML5 | -1.2574 | -0.4464 | 27.7422 | 1.39E-07 | 4.17E-02 |
| 190 | FNDC3A | CD247 | EML5 | -1.1131 | -0.3904 | 27.6714 | 1.44E-07 | 4.22E-02 |
| 191 | NCKAP5 | OAS1 | PDIA2 | 1.1404 | 0.4102 | 27.6549 | 1.45E-07 | 4.35E-02 |
| 192 | MSRA | PRPH2 | EML5 | -1.2214 | -0.4326 | 27.6375 | 1.46E-07 | 4.38E-02 |
| 193 | PSMB9 | PPP1R16B | C2CD4B | 1.0512 | 0.3788 | 27.7508 | 1.38E-07 | 4.14E-02 |
| 194 | FNDC3A | CD247 | EML5 | -1.1131 | -0.3904 | 27.6714 | 1.44E-07 | 4.22E-02 |
| 195 | TPI1 | C7 | LAMC2 | 1.1282 | 0.3908 | 27.6133 | 1.48E-07 | 4.44E-02 |
| 196 | KRT80 | LPIN1 | ARHGEF38 | 1.0314 | 0.3783 | 27.4646 | 1.60E-07 | 4.80E-02 |
| 197 | MAN1A2 | SLC9A9 | CXCL12 | 1.0925 | 0.3873 | 27.4337 | 1.63E-07 | 4.89E-02 |
| 198 | MSRA | PRPH2 | EML5 | -1.2214 | -0.4326 | 27.6375 | 1.46E-07 | 4.38E-02 |
| 199 | PSMB9 | PPP1R16B | C2CD4B | 1.0512 | 0.3788 | 27.7508 | 1.38E-07 | 4.14E-02 |
| 200 | FNDC3A | CD247 | EML5 | -1.1131 | -0.3904 | 27.6714 | 1.44E-07 | 4.22E-02 |
| 201 | TPI1 | C7 | LAMC2 | 1.1282 | 0.3908 | 27.6133 | 1.48E-07 | 4.44E-02 |
| 202 | KRT80 | LPIN1 | ARHGEF38 | 1.0314 | 0.3783 | 27.4646 | 1.60E-07 | 4.80E-02 |
| 203 | MAN1A2 | SLC9A9 | CXCL12 | 1.0925 | 0.3873 | 27.4337 | 1.63E-07 | 4.89E-02 |
| 204 | MSRA | PRPH2 | EML5 | -1.2214 | -0.4326 | 27.6375 | 1.46E-07 | 4.38E-02 |
| 205 | PSMB9 | PPP1R16B | C2CD4B | 1.0512 | 0.3788 | 27.7508 | 1.38E-07 | 4.14E-02 |
| 206 | FNDC3A | CD247 | EML5 | -1.1131 | -0.3904 | 27.6714 | 1.44E-07 | 4.22E-02 |
| 207 | TPI1 | C7 | LAMC2 | 1.1282 | 0.3908 | 27.6133 | 1.48E-07 | 4.44E-02 |
| 208 | KRT80 | LPIN1 | ARHGEF38 | 1.0314 | 0.3783 | 27.4646 | 1.60E-07 | 4.80E-02 |
| 209 | MAN1A2 | SLC9A9 | CXCL12 | 1.0925 | 0.3873 | 27.4337 | 1.63E-07 | 4.89E-02 |
| 210 | MSRA | PRPH2 | EML5 | -1.2214 | -0.4326 | 27.6375 | 1.46E-07 | 4.38E-02 |
| 211 | PSMB9 | PPP1R16B | C2CD4B | 1.0512 | 0.3788 | 27.7508 | 1.38E-07 | 4.14E-02 |
| 212 | FNDC3A | CD247 | EML5 | -1.1131 | -0.3904 | 27.6714 | 1.44E-07 | 4.22E-02 |
| 213 | TPI1 | C7 | LAMC2 | 1.1282 | 0.3908 | 27.6133 | 1.48E-07 | 4.44E-02 |
| 214 | KRT80 | LPIN1 | ARHGEF38 | 1.0314 | 0.3783 | 27.4646 | 1.60E-07 | 4.80E-02 |
| 215 | MAN1A2 | SLC9A9 | CXCL12 | 1.0925 | 0.3873 | 27.4337 | 1.63E-07 | 4.89E-02 |
| 216 | MSRA | PRPH2 | EML5 | -1.2214 | -0.4326 | 27.6375 | 1.46E-07 | 4.38E-02 |
| 217 | PSMB9 | PPP1R16B | C2CD4B | 1.0512 | 0.3788 | 27.7508 | 1.38E-07 | 4.14E-02 |
| 218 | FNDC3A | CD247 | EML5 | -1.1131 | -0.3904 | 27.6714 | 1.44E-07 | 4.22E-02 |
| 219 | TPI1 | C7 | LAMC2 | 1.1282 | 0.3908 | 27.6133 | 1.48E-07 | 4.44E-02 |
| 220 | KRT80 | LPIN1 | ARHGEF38 | 1.0314 | 0.3783 | 27.4646 | 1.60E-07 | 4.80E-02 |
| 221 | MAN1A2 | SLC9A9 | CXCL12 | 1.0925 | 0.3873 | 27.4337 | 1.63E-07 | 4.89E-02 |
**S3 Table**

Detailed information of Gene Regulatory Network

| S node | T node | MI |
|--------|--------|----|
| AOX1   | PRKCE  | 0.44 |
| PRKCE  | HERC1  | 0.38 |
| HERC1  | MYCBP2 | 0.6 |
| MYCBP2 | CNKSR1 | 0.5 |
| FHL5   | ACADL  | 0.41 |
| ACADL  | MIR217 | 0.61 |
| MIR217 | PELI2  | 0.61 |
| GUCY1A3| DSEL   | 0.38 |
| DSEL   | FAR2   | 0.39 |
| FAR2   | BACE1  | 0.61 |
| BACE1  | EPHX1  | 0.63 |
| SVEP1  | FHL5   | 0.56 |
| FHL5   | ACADL  | 0.41 |
| ACADL  | MIR217 | 0.61 |
| MIR217 | PELI2  | 0.61 |
| SLC9A9 | ITPR1  | 0.68 |
| ITPR1  | PI4KA  | 0.51 |
| PI4KA  | INPP4A | 0.5 |
| INPP4A | CSK    | 0.48 |
| CSK    | ADRBK1 | 0.55 |
| ADRBK1 | B3GALNT2 | 0.6 |
| B3GALNT2 | MAN1A2 | 0.62 |
S4 Figure

The prognostic power of suggested switch genes through glioblastoma, hepatocellular carcinoma and stomach adenocarcinoma as PDAC-unrelated datasets.