Table 1. List of the top 30 most positive and negative fold changes genes associated with MDA-MB-231(TNBC) CAST-I

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Serial No** | **MDA-MB-231 CAST-I** | | | | | |
| **Fold change (Expression log ratio)** | | | | | |
| **Fold**  **Upregulation** | **Expression p-value** | **Genes** | **Fold Downregulation** | **Expression**  **p-value** | **Genes** |
| 1 | 10.44 | 4.66E-18 | *LRRC61* | -10.706 | 1.5E-18 | *RP11\_865I62* |
| 2 | 9.042 | 2.78E-13 | *ZBED10P* | -9.532 | 4.5E-13 | *FRG2EP* |
| 3 | 7.993 | 9.01E-14 | *SULT1A1* | -9.516 | 5.73E-15 | *LINC00540* |
| 4 | 7.781 | 1.16E-09 | *LINC02564* | -9.397 | 1.89E-75 | *TSPYL5* |
| 5 | 7.391 | 1E-41 | *LHFPL4* | -8.595 | 4.8E-12 | *LINC02404* |
| 6 | 7.114 | 0.000000208 | *ACTR3C* | -8.533 | 2.45E-11 | *LINC01425* |
| 7 | 6.987 | 9.1E-11 | *COCH* | -8.516 | 1.46E-11 | *PAGE3* |
| 8 | 6.486 | 0.00000283 | *BEND4* | -8.498 | 5.41E-11 | *LOC101929427* |
| 9 | 6.24 | 0.0000317 | *RP4\_584D147* | -8.408 | 3.57E-10 | *MKRN9P* |
| 10 | 5.676 | 0.000000924 | *EOMES* | -8.383 | 5.6E-11 | *DUX4L32* |
| 11 | 5.579 | 0.0000701 | *TBC1D3G (includes others)* | -8.139 | 8.07E-32 | *IL13RA2* |
| 12 | 5.529 | 0.00193 | *BOLA2/BOLA2B* | -8.126 | 8.65E-11 | *TESPA1* |
| 13 | 5.503 | 0.000715 | *TRBV30* | -8.084 | 1.12E-10 | *ADA2* |
| 14 | 5.307 | 5.09E-20 | *FLRT3* | -8.047 | 1.6E-10 | *TEX13C* |
| 15 | 5.278 | 0.000244 | *MIR34AHG* | -8.042 | 1.92E-10 | *TUBA3C/TUBA3D* |
| 16 | 5.233 | 0.000224 | *RARRES1* | -8.039 | 1.4E-10 | *TNN* |
| 17 | 5.201 | 0.000212 | *FAM83A-AS1* | -8.036 | 3.12E-64 | *LINC02582* |
| 18 | 5.185 | 0.0017 | *LOC389831 (includes others)* | -8.014 | 0.000000177 | *DUX4L33* |
| 19 | 5.184 | 0.00136 | *C2orf50* | -7.784 | 7.82E-10 | *LINC02223* |
| 20 | 5.144 | 4.65E-32 | *PCSK9* | -7.784 | 2.29E-09 | *LINC02315* |
| 21 | 5.094 | 9.62E-09 | *FBXL16* | -7.696 | 2.13E-136 | *MAGEC1* |
| 22 | 4.99 | 0.00000208 | *RP11\_863P133* | -7.673 | 4.18E-53 | *SPANXB1 (includes others)* |
| 23 | 4.976 | 4.22E-27 | *MAGI2-AS3* | -7.653 | 4.57E-09 | *GVINP2* |
| 24 | 4.936 | 0.00106 | *TRBV10-3* | -7.557 | 4.19E-09 | *NAP1L2* |
| 25 | 4.905 | 0.00482 | *IL33* | -7.52 | 4.13E-08 | *RP11-167P23.2* |
| 26 | 4.858 | 4.4E-15 | *IFNLR1* | -7.48 | 1.42E-09 | *HOMER2P1* |
| 27 | 4.853 | 0.000818 | *LINC02192* | -7.384 | 1.39E-08 | *FRG1FP* |
| 28 | 4.847 | 0.00125 | *AQP7P1* | -7.38 | 4.7E-12 | *PTPRN2* |
| 29 | 4.583 | 2.54E-19 | *P3H3* | -7.346 | 0.00000318 | *SIGLEC22P* |
| 30 | 4.509 | 0.000689 | *EBF3* | -7.332 | 1.52E-08 | *CASC9* |

Table 2. List of the top 30 most positive and negative fold changes genes associated with MDA-MB-231(TNBC) CAST-II

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Serial No** | **MDA-MB-231 CAST-II** | | | | | |
| **Fold change (Expression log ratio)** | | | | | |
| **Fold**  **Upregulation** | **Expression p-value** | **Genes** | **Fold Downregulation** | **Expression**  **p-value** | **Genes** |
| 1 | 10.08 | 1.29E-16 | *LRRC61* | -8.835 | 2.2E-12 | *DDX53* |
| 2 | 8.183 | 1.17E-10 | *PWWP3B* | -8.439 | 3.82E-10 | *MKRN9P* |
| 3 | 7.923 | 1.51E-10 | *CARD18* | -8.075 | 2.04E-10 | *TEX13C* |
| 4 | 7.481 | 1.71E-08 | *ITM2A* | -7.682 | 5.66E-09 | *GVINP2* |
| 5 | 7.388 | 4.31E-08 | *ZBED10P* | -7.544 | 4.56E-08 | *RP11-167P23.2* |
| 6 | 7.337 | 2.94E-08 | *CCL4* | -7.486 | 2.87E-59 | *CD33* |
| 7 | 7.133 | 5.31E-15 | *PPP1R14C* | -7.288 | 9.92E-08 | *PYDC2-AS1* |
| 8 | 7.02 | 3.22E-08 | *LINC01610* | -7.239 | 4.33E-08 | *NLRP5* |
| 9 | 6.991 | 1.43E-66 | *PGM5* | -7.215 | 1.03E-15 | *SNX20* |
| 10 | 6.952 | 0.00000131 | *TRBV30* | -7.134 | 0.0000148 | *ZNF727* |
| 11 | 6.542 | 4.4E-30 | *LHFPL4* | -7.125 | 7.21E-08 | *LOC100128317* |
| 12 | 6.483 | 0.0000193 | *BEND4* | -7.112 | 9.57E-08 | *LINC00317* |
| 13 | 6.434 | 0.00000715 | *CCL4L1/CCL4L2* | -7.061 | 0.00000003 | *LINC01681* |
| 14 | 6.415 | 0.000000922 | *PLEKHG1* | -7.013 | 0.00000024 | *AC0039733* |
| 15 | 6.261 | 1.19E-29 | *SORCS3* | -6.868 | 1.99E-37 | *EPHB1* |
| 16 | 6.233 | 0.0000371 | *SFTA3* | -6.577 | 8.23E-09 | *DUX4L32* |
| 17 | 6.144 | 1.67E-19 | *KRTAP7-1* | -6.538 | 0.00000558 | *CDH7* |
| 18 | 6.122 | 0.0000269 | *KCNF1* | -6.531 | 0.00000279 | *FGF14-AS2* |
| 19 | 6.103 | 9.39E-14 | *NKX2-5* | -6.485 | 0.00000131 | *RPS20P14* |
| 20 | 6.06 | 2E-42 | *PCSK9* | -6.373 | 0.0000106 | *LRMDA* |
| 21 | 6.042 | 0.0000934 | *PGM5-AS1* | -6.34 | 6.77E-11 | *KRBOX1* |
| 22 | 5.989 | 0.0000682 | *CTSE* | -6.276 | 0.0000269 | *LINC02405* |
| 23 | 5.97 | 0.0000666 | *LINC01550* | -6.234 | 0.0000873 | *TRGV7* |
| 24 | 5.855 | 0.000000866 | *COBL* | -6.08 | 0.000114 | *RAB11FIP1P1* |
| 25 | 5.798 | 0.0000426 | *FAM83A-AS1* | -5.998 | 1.8E-14 | *RP11\_775G231* |
| 26 | 5.664 | 9.9E-09 | *RP11\_863P133* | -5.992 | 0.000485 | *RP11\_361F191* |
| 27 | 5.643 | 7E-45 | *C5orf46* | -5.945 | 4.87E-84 | *LINC02582* |
| 28 | 5.628 | 2.65E-13 | *CCL3* | -5.928 | 0.0000528 | *RP11\_1114I91* |
| 29 | 5.604 | 1.12E-54 | *AADAC* | -5.91 | 0.000345 | *ZNF722* |
| 30 | 5.604 | 0.000211 | *TTC6* | -5.851 | 0.0000276 | *LOC105375451* |

Table 3. List of the top 30 most positive and negative fold changes genes associated with MDA-MB-231(TNBC) CAST-III

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Serial No** | **MDA-MB-231 CAST-III** | | | | | |
| **Fold change (Expression log ratio)** | | | | | |
| **Fold**  **Upregulation** | **Expression p-value** | **Genes** | **Fold Downregulation** | **Expression**  **p-value** | **Genes** |
| 1 | 12.279 | 3.41E-23 | *LRRC61* | -12.924 | 1.34E-16 | *EHF* |
| 2 | 9.526 | 7.41E-14 | *PGM5-AS1* | -12.796 | 3.29E-26 | *SSX1* |
| 3 | 9.49 | 2.71E-13 | *PWWP3B* | -12.709 | 7.69E-26 | *MAGEC2* |
| 4 | 9.168 | 0.00224 | *BOLA2/BOLA2B* | -12.463 | 1.15E-24 | *DCAF12L1* |
| 5 | 8.848 | 5.2E-12 | *CCDC70* | -12.419 | 8.08E-24 | *CCBE1* |
| 6 | 8.727 | 8.94E-66 | *HCLS1* | -11.883 | 2.18E-22 | *MAGEA11* |
| 7 | 8.604 | 4.84E-10 | *ARHGEF16* | -11.87 | 4.33E-46 | *TENM1* |
| 8 | 8.52 | 2.03E-85 | *PGM5* | -11.272 | 3.01E-19 | *COL4A5* |
| 9 | 8.426 | 1.73E-14 | *SLITRK1* | -11.096 | 7.88E-18 | *TENM2* |
| 10 | 8.321 | 9E-61 | *PCSK9* | -10.983 | 7.34E-18 | *CH17\_360D53* |
| 11 | 8.302 | 8.9E-11 | *NKX2-1-AS1* | -10.736 | 3.51E-16 | *PDZK1IP1* |
| 12 | 8.126 | 3.01E-09 | *KCNF1* | -10.307 | 6.92E-31 | *SERPINB2* |
| 13 | 7.971 | 6.53E-12 | *SULT1A1* | -10.226 | 9.46E-17 | *EPHB1* |
| 14 | 7.826 | 0.000000595 | *SFTA3* | -10.216 | 1.18E-16 | *RP11\_180C11* |
| 15 | 7.594 | 9.58E-63 | *SCEL* | -10.209 | 2.1E-51 | *MAGEC1* |
| 16 | 7.529 | 1.16E-39 | *AC0052561* | -10.069 | 2.2E-16 | *CACNG7* |
| 17 | 7.344 | 0.00000176 | *HES5* | -10.023 | 8.03E-16 | *PPP4R3C* |
| 18 | 7.301 | 0.0000298 | *RBMS3-AS2* | -9.95 | 8.27E-16 | *ZNF300* |
| 19 | 7.277 | 3.5E-45 | *TSTD1* | -9.918 | 1.28E-15 | *RP11\_865I62* |
| 20 | 7.179 | 0.00000185 | *RP4\_584D147* | -9.807 | 1.12E-13 | *PTPRQ* |
| 21 | 7.165 | 0.0000038 | *LINC01582* | -9.78 | 1.1E-14 | *THSD7B* |
| 22 | 7.102 | 0.00000444 | *PRKAR1B-AS1* | -9.766 | 1.91E-13 | *CX3CL1* |
| 23 | 7.095 | 0.00000286 | *ACTR3C* | -9.713 | 4.18E-13 | *FRG2EP* |
| 24 | 6.937 | 0.00000868 | *NCOR1P4* | -9.682 | 4.33E-15 | *RP11\_575F123* |
| 25 | 6.929 | 2.46E-30 | *LHFPL4* | -9.558 | 1.62E-14 | *LUM* |
| 26 | 6.877 | 4.21E-78 | *MAGEB2* | -9.508 | 8.55E-13 | *CTD\_2532K182* |
| 27 | 6.847 | 8.26E-56 | *MUC5AC* | -9.412 | 3.1E-14 | *SORCS2* |
| 28 | 6.743 | 9.87E-08 | *LINC02434* | -9.215 | 1.26E-25 | *CH17\_360D52* |
| 29 | 6.718 | 6.13E-58 | *CDC42EP5* | -9.014 | 7.3E-13 | *IRX1* |
| 30 | 6.714 | 0.0000496 | *RPL24P2* | -8.967 | 1.1E-12 | *TRPM2* |

Table 4. List of the top 30 most positive and negative fold changes genes associated with T47D (Luminal-A) CAST-I

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Serial No** | **T47D CAST-I** | | | | | |
| **Fold change (Expression log ratio)** | | | | | |
| **Fold**  **Upregulation** | **Expression p-value** | **Genes** | **Fold Downregulation** | **Expression**  **p-value** | **Genes** |
| 1 | 11.893 | 9.24E-24 | *LRRN1* | -12.583 | 2.39E-26 | *TFDP3* |
| 2 | 9.206 | 2.48E-14 | *PAGE5* | -11.294 | 8.81E-19 | *RP11\_875H75* |
| 3 | 8.456 | 2.35E-118 | *GPC6* | -10.12 | 1.68E-17 | *GRIK3* |
| 4 | 8.418 | 7.28E-12 | *CTC\_575N71* | -9.039 | 1.29E-13 | *DCAF8L1* |
| 5 | 8.282 | 6.74E-12 | *CNTN6* | -8.546 | 4.28E-12 | *HOXB13* |
| 6 | 8.122 | 6.37E-11 | *CHMP1B2P* | -8.332 | 1.67E-11 | *PHF2P2* |
| 7 | 7.968 | 1.88E-10 | *AC073236.1* | -7.966 | 2.77E-148 | *PIP* |
| 8 | 7.145 | 3.28E-08 | *LINC02434* | -7.848 | 1.08E-82 | *FOXI1* |
| 9 | 7.083 | 3.32E-201 | *LINC01287* | -7.76 | 1.46E-09 | *MAP10* |
| 10 | 7.069 | 2.73E-11 | *RP11\_323I152* | -7.76 | 1.07E-09 | *RP11\_793I111* |
| 11 | 7.027 | 7.02E-08 | *SELENOOLP* | -7.617 | 3.08E-09 | *KRT35* |
| 12 | 7.023 | 7.35E-08 | *LINC01611* | -7.547 | 0 | *MDK* |
| 13 | 7.008 | 8.07E-08 | *IDO1* | -7.481 | 5.18E-09 | *CT45A10/CT45A5* |
| 14 | 6.997 | 2.69E-74 | *CCND2* | -7.311 | 3.47E-27 | *L3MBTL4* |
| 15 | 6.932 | 7.93E-34 | *HSPA8P4* | -7.188 | 2.09E-26 | *CT83* |
| 16 | 6.929 | 0.000000132 | *TAC1* | -6.675 | 8.59E-10 | *CRABP1* |
| 17 | 6.927 | 0.00000017 | *RECK* | -6.673 | 0.00000018 | *DRD5* |
| 18 | 6.885 | 0.000000221 | *RIT2* | -6.638 | 0.000000974 | *AGR2* |
| 19 | 6.569 | 0.00000108 | *LINC01010* | -6.622 | 4.75E-22 | *PCDH17* |
| 20 | 6.521 | 0.00000144 | *SPANXA2-OT1* | -6.621 | 0.00000151 | *OR51I2* |
| 21 | 6.502 | 0 | *CHSY3* | -6.599 | 1.69E-25 | *TMEFF2* |
| 22 | 6.441 | 0.000000433 | *ARHGAP6* | -6.592 | 0.000000267 | *CTD\_2374C241* |
| 23 | 6.438 | 2.68E-09 | *SFTA1P* | -6.581 | 5.4E-132 | *SLIT2* |
| 24 | 6.434 | 0.000000434 | *LINC00370* | -6.313 | 0.00000104 | *LRRC14B* |
| 25 | 6.412 | 0.00000525 | *MIR378D2HG* | -6.296 | 0.00000786 | *PSLNR* |
| 26 | 6.37 | 7.55E-13 | *C1RL-AS1* | -6.275 | 0.00000821 | *ZNF716* |
| 27 | 6.361 | 7.89E-13 | *KDR* | -6.263 | 0.00000895 | *LOC102723335* |
| 28 | 6.265 | 0.00000634 | *RP11\_708B62* | -6.253 | 1.5E-270 | *MAGEA11* |
| 29 | 6.182 | 0 | *SSX1* | -6.243 | 3.61E-12 | *HOTAIRM1* |
| 30 | 6.043 | 0 | *FHL1* | -6.242 | 0.00000151 | *TMEM271* |

Table 5. List of the top 30 most positive and negative fold changes genes associated with T47D (Luminal-A) CAST-II

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Serial No** | **T47D CAST-II** | | | | | |
| **Fold change (Expression log ratio)** | | | | | |
| **Fold**  **Upregulation** | **Expression p-value** | **Genes** | **Fold Downregulation** | **Expression**  **p-value** | **Genes** |
| 1 | 14.197 | 2.66E-33 | *MAGEB2* | -12.472 | 6.4E-26 | *TFDP3* |
| 2 | 12.631 | 1.32E-26 | *LINC00200* | -11.183 | 1.92E-18 | *RP11\_875H75* |
| 3 | 11.073 | 1.19E-20 | *PAGE5* | -10.97 | 2.73E-20 | *GRIK3* |
| 4 | 8.866 | 3.15E-13 | *RP11\_401O93* | -9.811 | 1.55E-21 | *LOC105375267* |
| 5 | 8.491 | 5.86E-12 | *RP11\_317N121* | -8.436 | 8.69E-12 | *HOXB13* |
| 6 | 8.301 | 1.86E-11 | *SELENOOLP* | -8.15 | 5.13E-15 | *LOC730338* |
| 7 | 8.244 | 2.82E-11 | *CHMP1B2P* | -8.073 | 1E-59 | *GABRP* |
| 8 | 8.244 | 2.4E-15 | *RP11\_401O94* | -7.88 | 1.02E-10 | *CTD\_2566J31* |
| 9 | 7.309 | 1E-11 | *FABP4* | -7.68 | 1.24E-09 | *ANKRD20A4P (includes others)* |
| 10 | 7.107 | 1.12E-08 | *SLCO4C1* | -7.649 | 2.04E-09 | *RP11\_793I111* |
| 11 | 6.721 | 0.000000499 | *LINC01611* | -7.553 | 5.39E-09 | *CYP4F22* |
| 12 | 6.474 | 9.14E-277 | *EREG* | -7.523 | 4.78E-09 | *DRD5* |
| 13 | 6.468 | 1.1E-28 | *MYH13* | -7.492 | 7.63E-09 | *CX3CL1* |
| 14 | 6.459 | 0.00000231 | *AC073236.1* | -7.487 | 4.52E-09 | *MXRA5* |
| 15 | 6.348 | 4.23E-144 | *LINC01287* | -7.443 | 7.44E-09 | *CTD\_2374C241* |
| 16 | 6.297 | 0.00000568 | *RNU6-77P* | -7.114 | 8.14E-178 | *PIP* |
| 17 | 6.285 | 0.00000928 | *RP11\_32D41* | -7.07 | 4.56E-108 | *SLIT2* |
| 18 | 6.158 | 1.25E-149 | *AP0008926* | -7.068 | 2.97E-11 | *LTF* |
| 19 | 6.114 | 0.0000181 | *SPANXA2-OT1* | -6.934 | 0.000000154 | *DEFB1* |
| 20 | 5.975 | 3.54E-11 | *C1RL-AS1* | -6.81 | 0.000000314 | *RPS6KA2* |
| 21 | 5.947 | 0 | *TAGLN* | -6.777 | 5.83E-19 | *CERS3* |
| 22 | 5.899 | 2.39E-15 | *CCND2* | -6.7 | 0.000000843 | *CR769776.3* |
| 23 | 5.849 | 0.0000114 | *AC0995523* | -6.5 | 1.53E-45 | *FOXI1* |
| 24 | 5.792 | 7.62E-16 | *RP11\_417L141* | -6.456 | 0.000000611 | *CCL22* |
| 25 | 5.771 | 3.57E-10 | *CASC20* | -6.419 | 0.000000574 | *RP11\_146D122* |
| 26 | 5.762 | 0 | *FHL1* | -6.357 | 0.00000475 | *CYP4F23P* |
| 27 | 5.735 | 0.000132 | *RP11\_697K233* | -6.271 | 9.8E-09 | *SYN3* |
| 28 | 5.707 | 0.000126 | *MINAR2* | -6.255 | 3.62E-46 | *SDK1* |
| 29 | 5.644 | 2.29E-31 | *TFF2* | -6.222 | 0.0000116 | *RP11\_2L82* |
| 30 | 5.624 | 0.000000687 | *LINC00972* | -6.082 | 0.0000192 | *BALR6* |

Table 6. List of the top 30 most positive and negative fold changes genes associated with T47D (Luminal-A) CAST-III

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Serial No** | **T47D CAST-III** | | | | | |
| **Fold change (Expression log ratio)** | | | | | |
| **Fold**  **Upregulation** | **Expression p-value** | **Genes** | **Fold Downregulation** | **Expression**  **p-value** | **Genes** |
| 1 | 15.564 | 3.43E-39 | MAGEB2 | -12.515 | 8.48E-26 | *TFDP3* |
| 2 | 14.772 | 2.42E-34 | PAGE5 | -9.769 | 3.22E-16 | *FAM135A* |
| 3 | 9.171 | 5.74E-14 | SRSF8CP | -8.479 | 8.4E-12 | *HOXB13* |
| 4 | 9.167 | 7.59E-14 | RP11\_401O93 | -7.487 | 6.88E-09 | *CTD\_2374C241* |
| 5 | 9.105 | 8E-14 | RP11\_317N121 | -7.288 | 0.000000022 | *MRGPRX2* |
| 6 | 8.042 | 1.84E-14 | RP11\_401O94 | -7.178 | 6.87E-08 | *CYP4Z1* |
| 7 | 7.318 | 3.5E-27 | RP11\_417L141 | -6.993 | 2.31E-101 | *SLIT2* |
| 8 | 7.131 | 1.35E-08 | CNTN6 | -6.737 | 1.35E-18 | *LINC00960* |
| 9 | 6.862 | 5.63E-15 | BX571818.1 | -6.729 | 0.00000014 | *RP11\_793I111* |
| 10 | 6.59 | 0.00000111 | SELENOOLP | -6.681 | 0.00000129 | *PRDM13* |
| 11 | 6.513 | 0.00000227 | RNA5-8S5 | -6.635 | 0.000000879 | *TNRC18P2* |
| 12 | 6.446 | 0.00000343 | LINC02008 | -6.604 | 0.000000288 | *DRD5* |
| 13 | 6.397 | 0.00000414 | LINC02434 | -6.485 | 4.52E-13 | *LOC101930276* |
| 14 | 6.389 | 0.00000766 | RP11\_1O101 | -6.251 | 5.92E-51 | *GRIK3* |
| 15 | 6.319 | 2.52E-32 | RP11\_299H223 | -6.077 | 3.3E-140 | *CPED1* |
| 16 | 6.296 | 2.7E-26 | MYH13 | -5.885 | 0.0000818 | *EN1* |
| 17 | 6.222 | 0.00000232 | RP1\_309H152 | -5.86 | 7.52E-37 | *HSD17B2* |
| 18 | 6.169 | 0.000000117 | RP11\_323I152 | -5.799 | 0.000000259 | *GPC5* |
| 19 | 6.103 | 2E-11 | C1RL-AS1 | -5.785 | 4.52E-37 | *LVRN* |
| 20 | 6.055 | 0.0000461 | CTC\_338M129 | -5.561 | 2.61E-09 | *GUSBP12* |
| 21 | 6.014 | 0.0000228 | VENTXP5 | -5.52 | 2.56E-168 | *LINC00958* |
| 22 | 5.996 | 0.0000553 | F11-AS1 | -5.487 | 0.000296 | *LINC01254* |
| 23 | 5.8 | 0.000108 | TAC1 | -5.483 | 0.000487 | *RP11\_745L132* |
| 24 | 5.792 | 0.0000624 | CHMP1B2P | -5.482 | 0.00157 | *LOC105379109* |
| 25 | 5.755 | 0.000000301 | RP11\_323I153 | -5.365 | 0.000784 | *PCAT14* |
| 26 | 5.663 | 1.59E-09 | RP11\_299H226 | -5.307 | 3.15E-58 | *CLSTN2* |
| 27 | 5.66 | 3.82E-30 | HDGFL1 | -5.225 | 5.6E-10 | *DCAF12L2* |
| 28 | 5.544 | 7.12E-232 | MAGEA10 | -5.139 | 0.000243 | *RP11\_760D210* |
| 29 | 5.497 | 3.06E-176 | SH3BGRL | -5.112 | 0.000306 | *RPL7AP28* |
| 30 | 5.481 | 2.65E-16 | PDCD1LG2 | -5.1 | 0.0000256 | *LGALS7/LGALS7B* |