Electronic Supplementary Information (ESI)

Discovering potential driver genes through an integrated model of somatic mutation profiles and gene functional information

Jianing Xi,^{‡a} Minghui Wang^{‡ab} and Ao Li^{*ab}

^a School of Information Science and Technology, University of Science and Technology of China, Hefei AH230027, China.

^b Centers for Biomedical Engineering, University of Science and Technology of China, Hefei AH230027, China.

*E-mail: aoli@ustc.edu.cn

‡ Joint first authors.

List of Figures

| Fig. S1 The F1 scores of the results of IntDriver under the parameters λ_N and λ_S set to different values. As illustrated, the performances of IntDriver for the datasets of the three types of cancers are robust to the two parameter λ_N and λ_S generally. The F1 scores under λ_N and λ_S set to 0.3 and 0.7 are relative better than those | |
|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---|
| Fig. S2 The pie diagram illustrating the proportions of known benchmarking driver genes in the top ranked 100 genes identified by IntDriver, HotNet2, MUFFINN-DNmax, MUFFINN-DNsum, DriverNet, NBS(k=3), NBS(k=4) and ReMIC, when these approaches are applied on (a) BRCA dataset, (b) KIRC dataset and (c) LUSC dataset. The benchmarking driver genes used in this study are from NCG [1], including cancer-specific experimentally | 2 |
| supported CGC genes [2], experimentally supported genes from CGC [2] and statistically inferred candidate genes. Black numbers near the pie diagrams represent the numbers of the detected cancer-specific CGC genes, while the gray numbers represent the numbers of detected CGC genes, NCG genes and other genes | 2 |
| Fig. S3 The precisions, recalls and F1 scores for NCG benchmarking driver genes of the top 200 genes selected by IntDriver, HotNet2, MUFFINN-DNmax, MUFFINN-DNsum, DirverNet, NBS(k=3), NBS(k=4) and ReMIC on (a) BRCA dataset. (b) KIRC dataset and (c) LUSC dataset respectively. | 3 |
| List of Tables Table S1 The driver gene candidates identified in the top 200 genes prioritized by IntDriver on BRCA dataset. Their ranks, gene symbols and mutation frequencies are demonstrated in the table, along with whether the genes are experimentally (CGC & NCG) supported or statistically inferred (NCG). The asterisk * represents that the | |
| gene is reported to related with breast cancer | 4 |
| Table S3 The driver gene candidates identified in the top 200 genes prioritized by IntDriver on LUSC dataset. Their ranks, gene symbols and mutation frequencies are demonstrated in the table, along with whether the genes are experimentally (CGC & NCG) supported or statistically inferred (NCG). The asterisk * represents that the gene is reported to related with lung squamous cell carcinoma | 6 |
| Table S4 The p-values of Fisher's exact test accessing the enrichment significance for NCG [1] benchmarking driver genes of the top 50, 100, 150 and 200 genes selected by IntDriver, NotNet2, MUFFINN-DNmax, MUFFINN-DNsum, DriverNet, NBS(k=3), NBS(k=4), BeMIC | 7 |
| Table S5 Results of functional enrichment analysis of the top 200 genes identified by IntDriver on BRCA datasets | 1 |

Table S6Results of functional enrichment analysis of the top 200 genes identified by IntDriver on KIRC datasets.9



Fig. S1. The F1 scores of the results of IntDriver under the parameters λ_N and λ_S set to different values. As illustrated, the performances of IntDriver for the datasets of the three types of cancers are robust to the two parameter λ_N and λ_S generally. The F1 scores under λ_N and λ_S set to 0.3 and 0.7 are relative better than those under the other settings among the three cancer datasets RBCA, KIRC and LUSC.



Fig. S2. The pie diagram illustrating the proportions of known benchmarking driver genes in the top ranked 100 genes identified by IntDriver, HotNet2, MUFFINN-DNmax, MUFFINN-DNsum, DriverNet, NBS(k=3), NBS(k=4) and ReMIC, when these approaches are applied on (a) BRCA dataset, (b) KIRC dataset and (c) LUSC dataset. The benchmarking driver genes used in this study are from NCG [1], including cancer-specific experimentally supported CGC genes [2], experimentally supported genes from CGC [2] and statistically inferred candidate genes. Black numbers near the pie diagrams represent the numbers of the detected cancer-specific CGC genes, while the gray numbers represent the numbers of detected CGC genes.



Fig. S3. The precisions, recalls and F1 scores for NCG benchmarking driver genes of the top 200 genes selected by IntDriver, HotNet2, MUFFINN-DNmax, MUFFINN-DNsum, DirverNet, NBS(k=3), NBS(k=4) and ReMIC on (a) BRCA dataset, (b) KIRC dataset and (c) LUSC dataset respectively.

Table S1. The driver gene candidates identified in the top 200 genes prioritized by IntDriver on BRCA dataset. Their ranks, gene symbols and mutation frequencies are demonstrated in the table, along with whether the genes are experimentally (CGC & NCG) supported or statistically inferred (NCG). The asterisk * represents that the gene is reported to related with breast cancer.

| Rank | Symbol | MutFreq | Benchmarking | Rank | Symbol | MutFreq | Benchmarking | Rank | Symbol | MutFreq | Benchmarking |
|------|-------------------|---------|-------------------------------------|------|---------------|---------|-------------------------------------|------|----------|---------|------------------------|
| 1 | PIK3CA | 180 | CGC* & NCG* | 68 | COL12A1 | 11 | | 135 | MLLT4 | 12 | CGC & NCG |
| 2 | TP53 | 190 | CGC* & NCG* | 69 | CACNA1B | 13 | | 136 | UBR5 | 10 | CGC & NCG* |
| 3 | CATA3 | 55 | CGC* & NCC* | 70 | BELN | 17 | | 137 | CHD4 | 11 | CGC & NCG |
| 4 | TTN | 86 | NCC | 71 | WDEV2 | 10 | | 199 | VIE4A | 0 | ede æ ned |
| 4 | 1 I IN MADOICI | 40 | ACC NCC | 71 | WDF15 | 15 | NGG* | 130 | CDDM0 | 9 | |
| 5 | MAP3KI | 40 | UGU & NUG | 72 | IG | 15 | NCG* | 139 | SRRM2 | 9 | |
| 6 | MUC16 | 55 | NCG | 73 | LAMAI | 12 | NCG | 140 | TTPKB | 8 | |
| 7 | CDH1 | 34 | CGC [*] & NCG [*] | 74 | FLNC | 14 | NCG* | 141 | ASPM | 10 | |
| 8 | USH2A | 32 | NCG* | 75 | CACNA1G | 14 | | 142 | DCAF17 | 4 | |
| 9 | OBSCN | 30 | NCG | 76 | LRP1 | 12 | | 143 | LASP1 | 4 | CGC & NCG |
| 10 | RYR2 | 33 | NCG* | 77 | BRAT1 | 8 | | 144 | CHD5 | 8 | NCG* |
| 11 | BRCA2 | 24 | $CGC^* \& NCG^*$ | 78 | WNK3 | 8 | | 145 | CCT6B | 6 | NCG |
| 12 | SYNE1 | 22 | NCG | 79 | ADAMTS5 | 7 | | 146 | DNAH1 | 12 | |
| 13 | MAP2K4 | 21 | CGC [*] & NCG [*] | 80 | CADPS | 8 | | 147 | MGAM | 12 | NCG |
| 14 | BBCA1 | 19 | CGC & NCG* | 81 | CACNAIC | 12 | | 148 | DOCK2 | 6 | NCG |
| 15 | FLG | 28 | | 82 | ANKBD24 | 5 | | 149 | HECW2 | 9 | |
| 16 | CSMD1 | 28 | NCC* | 83 | PRY | 5 | | 150 | MYOOB | ő | |
| 17 | SDTA1 | 19 | NCC | 84 | DTDDU | 5 | | 151 | NUAKO | 0 | |
| 19 | MUCA | 26 | NCC | 95 | MYO10 | 12 | | 152 | RCORI 1 | | |
| 10 | DVD2 | 20 | NCG | 80 | COLGAR | 10 | | 152 | BCMO1 | 4 | |
| 19 | RI RS | 24 | NCG | 80 | COLOAS | 10 | | 155 | BOMOI | 4 | aga i Nag |
| 20 | RUNXI | 19 | CGC & NCG | 87 | CACNAID | 8 | | 154 | MYHII | 8 | CGC & NCG |
| 21 | AKT1 | 13 | CGC ⁺ & NCG ⁺ | 88 | RABIF | 3 | | 155 | RAB3GAP2 | 9 | |
| 22 | DMD | 17 | NCG | 89 | SPI1 | 16 | | 156 | KCNB2 | 8 | |
| 23 | APOB | 19 | NCG | 90 | HRNR | 12 | NCG | 157 | DNM3 | 3 | |
| 24 | LRP2 | 20 | NCG | 91 | PXDN | 6 | NCG | 158 | KIRREL | 6 | |
| 25 | DNAH5 | 14 | | 92 | UTRN | 11 | | 159 | NNT | 4 | |
| 26 | SPEN | 19 | | 93 | PREX2 | 13 | NCG | 160 | PLCE1 | 9 | |
| 27 | DST | 14 | NCG | 94 | VWF | 13 | NCG | 161 | HERC2 | 10 | NCG |
| 28 | ZFHX3 | 14 | CGC & NCG | 95 | KAT6B | 9 | CGC & NCG | 162 | IL17RC | 5 | |
| 29 | CTCF | 15 | CGC [*] & NCG [*] | 96 | SVEP1 | 14 | | 163 | SP100 | 4 | |
| 30 | ANK1 | 14 | | 97 | LAMA5 | 13 | | 164 | CDC42BPA | 8 | |
| 31 | TBX3 | 14 | CGC [*] & NCG [*] | 98 | PCDHA5 | 5 | | 165 | CENPE | 10 | |
| 32 | RYR1 | 17 | NCG | 99 | PCDHA1 | 8 | | 166 | ATAD5 | 7 | |
| 33 | TBL1XB1 | 10 | CGC & NCG* | 100 | MED12 | 11 | CGC & NCG | 167 | TANC2 | 7 | |
| 34 | ATM | 20 | CGC & NCG | 101 | DNAH7 | 10 | NCG | 168 | EPHB1 | 7 | NCG* |
| 35 | CBFB | 9 | CGC & NCG* | 102 | FBN1 | 13 | Red | 169 | CBX8 | 3 | Ned |
| 26 | NCORI | 19 | CCC* & NCC* | 102 | AKADO | 11 | CCC & NCC* | 170 | TAMA2 | | |
| 27 | FOXAL | 10 | CCC & NCC | 103 | ZEDM2 | 11 | CGC & NCG | 170 | SMEKS | 5 | |
| 37 | FUAAI | 0 | NGC & NCG | 104 | | 11 F | aga (Nag* | 171 | DOLE | 5 | |
| 38 | MUC2 | 18 | NCG | 105 | ARID2 | 5 | CGC & NCG | 172 | POLE | (| NGG |
| 39 | MED23 | 9 | NGG* | 106 | PIEN | 18 | CGC & NCG | 173 | DSCAMLI | 9 | NCG |
| 40 | AFF2 | 14 | NCG* | 107 | MYH7 | 11 | * * * * * * * | 174 | EEAI | 5 | |
| 41 | DNAH3 | 15 | | 108 | ERBB2 | 8 | CGC [*] & NCG [*] | 175 | HCFC1 | 7 | |
| 42 | NEB | 19 | NCG | 109 | PIK3R1 | 15 | CGC & NCG* | 176 | PCDHA8 | 8 | |
| 43 | SRCAP | 12 | | 110 | TSC22D1 | 6 | NCG | 177 | CAPN1 | 11 | |
| 44 | UBR4 | 18 | | 111 | SDK1 | 13 | | 178 | MYH9 | 8 | $CGC \& NCG^*$ |
| 45 | XIRP2 | 15 | NCG | 112 | RIMBP2 | 10 | NCG | 179 | VPS18 | 6 | |
| 46 | HECW1 | 13 | | 113 | COL14A1 | 11 | | 180 | SCN10A | 9 | |
| 47 | MDN1 | 15 | | 114 | ARHGAP35 | 8 | | 181 | NCOA3 | 7 | NCG |
| 48 | PLXNA4 | 12 | | 115 | MYO5B | 9 | NCG | 182 | FLNB | 9 | NCG* |
| 49 | SSPO | 20 | | 116 | PKD1 | 10 | | 183 | ERBB3 | 9 | CGC & NCG [*] |
| 50 | SYNE2 | 19 | NCG | 117 | CACNA1F | 8 | NCG* | 184 | LATS2 | 4 | |
| 51 | BZRAP1 | 11 | | 118 | MYH7B | 9 | | 185 | HNF4A | 3 | |
| 52 | BCOR | 7 | CGC & NCG | 119 | ZDBF2 | 10 | NCG | 186 | GRIK2 | 8 | |
| 53 | CIT | 11 | NCG | 120 | WDB7 | 8 | | 187 | PKHD1 | 13 | NCG* |
| 54 | ARID1A | 11 | CGC* & NCC* | 120 | PDE3A | 11 | | 188 | ATN1 | 9 | NCG* |
| 55 | CCDC40 | 4 | ede æned | 1221 | DTDDD | 10 | NCC* | 180 | CRINOC | 7 | Ned |
| 56 | PDE4DIP | 7 | CGC & NCG | 122 | CBOCC | 12 | NCG | 190 | IKBKE | 6 | |
| 57 | DIEC | 16 | NCC | 123 | ARIDIR | 10 | CCC* & NCC* | 101 | DIMES | 7 | NCC* |
| 57 | DDID1 | 10 | CCC & NCC | 124 | TILLDID DE | 11 | CGC & NCG | 102 | TDDM6 | 1 5 | NCC |
| 50 | CELCD1 | 10 | CGC & NCG | 120 | CUDe | 11 | NCC | 192 | ADCVS | 7 | NCC |
| 39 | CELSKI | 0 | NGG* | 120 | CHD0 | 9 | NUG | 193 | ADU18 | 1 | NGG |
| 60 | EPG5 | 9 | NUG. | 127 | DCC | 10 | NGG | 194 | RNF213 | 11 | UGC & NCG |
| 61 | PONT | 11 | N00* | 128 | MACF1 | 11 | NCG | 195 | K1AA2022 | 10 | NCG |
| 62 | LRBA | 11 | NCG* | 129 | MYTIL | 10 | | 196 | DYNC2H1 | 9 | NCG* |
| 63 | ANK3 | 11 | NCG | 130 | MYLK | 10 | | 197 | AMPD1 | 7 | |
| 64 | LETM1 | 5 | NCG | 131 | PREX1 | 9 | | 198 | MYH14 | 10 | |
| 65 | MTOR | 13 | | 132 | CBLB | 10 | CGC & NCG | 199 | CACNA1A | 10 | |
| 66 | MUC12 | 11 | | 133 | HSPG2 | 11 | | 200 | MGA | 10 | NCG |
| 67 | CACNA1E | 14 | NCG | 134 | CSMD2 | 13 | NCG | | | | |

Table S2. The driver gene candidates identified in the top 200 genes prioritized by IntDriver on KIRC dataset. Their ranks, gene symbols and mutation frequencies are demonstrated in the table, along with whether the genes are experimentally (CGC & NCG) supported or statistically inferred (NCG). The asterisk * represents that the gene is reported to related with kidney renal clear cell carcinoma.

| Bank | Symbol | MutFreq | Benchmarking | Bank | Symbol | MutFreq | Benchmarking | Bank | Symbol | MutFreq | Benchmarking |
|------|------------|----------|-------------------------------------|------|----------|---------|---------------|------|-----------|----------|---------------|
| 1 | VIII | 248 | CCC* & NCC* | C Q | MUCE | 10 | Deneminarking | 125 | ULA DOB1 | 11 | Deneminarking |
| 1 | VHL | 248 | CGC & NCG | 68 | MUC6 | 19 | 200 | 135 | HLA-DQB1 | 11 | |
| 2 | PBRMI | 167 | CGC* & NCG* | 69 | MAGECI | 18 | NCG | 136 | CUL9 | 11 | |
| 3 | MUC4 | 103 | NCG | 70 | UHRF1BP1 | 5 | | 137 | NEB | 18 | NCG |
| 4 | TTN | 89 | NCG | 71 | ATM | 16 | CGC & NCG | 138 | AKAP9 | 14 | CGC & NCG |
| 5 | SETD2 | 62 | CGC [*] & NCG [*] | 72 | MKNK2 | 5 | | 139 | EIF4G3 | 7 | |
| 6 | BAP1 | 49 | CGC [*] & NCG [*] | 73 | ANPEP | 11 | | 140 | SLC36A1 | 5 | |
| 7 | PABPC1 | 22 | NCG | 74 | PCSK5 | 15 | | 141 | LRBA | 5 | NCG |
| 8 | MUC16 | 50 | NCG | 75 | SVEP1 | 11 | | 142 | MLLT3 | 9 | CGC & NCG |
| ő | ZEHX3 | 12 | CGC & NCG | 76 | BBM26 | 5 | | 1/3 | MEGE10 | 8 | 000 @ 1100 |
| 10 | DTEN | 20 | CCC & NCC | 77 | FLC | 19 | | 140 | DVUD1 | 14 | NCC |
| 10 | FIEN | 20 | CGC & NCG | | FLG | 13 | | 144 | FKHDI | 14 | NCG |
| 11 | KDM5C | 32 | CGC & NCG | 78 | NDUFSI | 8 | | 145 | PRKCD | 5 | |
| 12 | PDE4DIP | 26 | CGC & NCG | 79 | CR1 | 7 | NCG | 146 | EPRS | 5 | |
| 13 | VCAN | 9 | NCG | 80 | PODXL | 6 | | 147 | PABPC3 | 12 | NCG |
| 14 | TP53 | 16 | CGC & NCG [*] | 81 | TOM1L2 | 5 | | 148 | LILRB4 | 8 | |
| 15 | FBN2 | 17 | NCG | 82 | MTMR4 | 6 | | 149 | OGDH | 6 | |
| 16 | SPEN | 12 | | 83 | HLA-DRB5 | 11 | | 150 | LRP2 | 16 | NCG |
| 17 | ANK2 | 12 | NCG | 84 | PLB1 | 7 | NCG | 151 | OBSCN | 10 | NCG |
| 18 | PBKAG2 | 15 | | 85 | AKB1C1 | 5 | | 152 | TTI1 | 5 | |
| 10 | DST | 20 | NCG | 86 | MICALS | 8 | NCG | 153 | PCSK2 | 5 | |
| 20 | DDV1 | 7 | Neg | 87 | EMNO | 16 | NCC* | 154 | DOLDOD | F | |
| 20 | DAM150D | 10 | | 87 | I ININZ | 10 | NCG | 154 | I OLITZD | 10 | |
| 21 | FAM179B | 10 | NGG | 88 | HERCI | 11 | | 155 | PONT | 10 | |
| 22 | USH2A | 21 | NCG | 89 | MYHII | 10 | CGC & NCG | 156 | RRP12 | 7 | |
| 23 | PCLO | 20 | NCG | 90 | SDHA | 12 | | 157 | KDM5B | 7 | NCG |
| 24 | CASP8AP2 | 4 | | 91 | ADCY8 | 6 | NCG | 158 | XPO1 | 6 | CGC & NCG |
| 25 | SETBP1 | 9 | CGC & NCG | 92 | PPP1R3A | 4 | NCG | 159 | SMARCA4 | 15 | CGC & NCG |
| 26 | FREM1 | 7 | NCG | 93 | GLS | 6 | | 160 | FN1 | 8 | NCG |
| 27 | SYNRG | 6 | | 94 | NBR1 | 6 | | 161 | UBR4 | 14 | |
| 28 | ZBTB38 | 10 | | 95 | LRRK1 | 11 | NCG | 162 | COL6A3 | 15 | |
| 29 | CEP290 | 9 | | 96 | SEC14L4 | 4 | | 163 | MACE1 | 14 | NCG |
| 30 | GPRIN1 | 10 | | 97 | CBOCC | 8 | NCG | 164 | ITIH4 | 5 | |
| 31 | ADCV2 | 6 | NCG | 98 | TATDN1 | 4 | | 165 | UIMC1 | 6 | |
| 20 | ADCI2 | 7 | NCG | 30 | WDEV2 | 10 | | 166 | TDDMC | F | NCC |
| 34 | HELLS DDD1 | 10 | | 99 | WDF15 | 12 | | 100 | DAZOD | 0 10 | NCG |
| 33 | HLA-DRBI | 16 | | 100 | ZNF/14 | 4 | | 167 | BAZ2B | 13 | NCG |
| 34 | CSPG4 | 6 | | 101 | IL17RC | 5 | | 168 | SSPO | 15 | |
| 35 | MTOR | 25 | | 102 | STARD9 | 9 | | 169 | INPP5E | 3 | |
| 36 | PAH | 7 | | 103 | EBF3 | 9 | | 170 | LAMA1 | 14 | NCG |
| 37 | ANK3 | 15 | NCG | 104 | YLPM1 | 12 | | 171 | CNOT1 | 13 | NCG |
| 38 | TCEB1 | 5 | | 105 | ZNFX1 | 11 | | 172 | MUC2 | 15 | NCG |
| 39 | TRIOBP | 6 | NCG | 106 | DPP10 | 7 | NCG | 173 | DNAH3 | 14 | |
| 40 | PREX1 | 7 | | 107 | DSC2 | 4 | | 174 | MYO5B | 12 | NCG |
| 41 | HUWE1 | 12 | | 108 | AHNAK | 10 | NCG* | 175 | BYB1 | 15 | NCG* |
| 42 | AFF3 | 8 | CGC & NCG | 100 | NFASC | 6 | | 176 | LBP1 | 15 | |
| 42 | DVD2 | 14 | NCC | 110 | SUCLC1 | 6 | | 177 | ACI | 5 | |
| 43 | DVD9 | 15 | NCG | 111 | ED400 | 10 | | 179 | TCUZ2 | 0 | |
| 44 | nin2 | 15 | NCG | 111 | EF400 | 10 | NGG | 178 | 15625 | 0 | |
| 45 | RIFI | (| | 112 | HLA-B | 10 | NCG | 179 | JMJDIC | 9 | |
| 46 | LIST | 14 | | 113 | ANKRD17 | 9 | | 180 | KUNMA1 | 4 | NGG |
| 47 | CUBN | 16 | | 114 | BCORL1 | 9 | | 181 | CARD10 | 3 | NCG |
| 48 | ARID1A | 20 | CGC [*] & NCG [*] | 115 | PLEC | 11 | NCG | 182 | PAK6 | 5 | |
| 49 | PTCH1 | 14 | CGC & NCG | 116 | STAG2 | 8 | | 183 | USP18 | 6 | NCG |
| 50 | TNS1 | 9 | | 117 | CABIN1 | 9 | | 184 | SSFA2 | 6 | |
| 51 | SYNE2 | 13 | NCG* | 118 | NBEA | 7 | | 185 | NSD1 | 8 | CGC & NCG |
| 52 | SLIT2 | 12 | NCG | 119 | LAMA3 | 6 | | 186 | SERPINB4 | 4 | |
| 53 | SYNE1 | 22 | NCG | 120 | DNAH7 | 13 | NCG | 187 | BAZ2A | 3 | |
| 54 | GBM8 | 9 | NCG | 121 | BABAM1 | 7 | NCG | 188 | CHD5 | 7 | NCG |
| 55 | ASMTL | 6 | | 122 | BCHY1 | 5 | | 189 | BIN2 | 3 | |
| 56 | PRSS16 | 7 | | 122 | AOR | s | | 100 | KIA 40222 | 2 | |
| 57 | APOP | 10 | NCC | 120 | CSMD1 | 19 | NCC | 101 | COLEAI | - - | NCC |
| 51 | KDT4 | 14 | 1100 | 124 | EMLA | 14 | add i Maa | 191 | ACK | 4 | 100 |
| 08 | KR14 | <u>_</u> | NGG | 125 | EWL4 | 3 | CGU & NUG | 192 | AGK | 4 | |
| 59 | COL7AI | (| NUG | 126 | ASPM | (| | 193 | ASCC3 | <u>(</u> | |
| 60 | EZH2 | 5 | CGC & NCG | 127 | NOM1 | 5 | | 194 | CCDC88B | 7 | |
| 61 | TNR | 14 | NCG | 128 | CDH8 | 10 | | 195 | TTC17 | 3 | |
| 62 | MAGED1 | 4 | NCG | 129 | PDE8A | 3 | | 196 | C1orf173 | 5 | |
| 63 | VPS13A | 8 | | 130 | DNAJC14 | 7 | | 197 | RNF40 | 4 | |
| 64 | NOTCH2 | 20 | CGC & NCG | 131 | PDS5A | 4 | | 198 | TACC3 | 3 | 1 |
| 65 | EGFR | 8 | CGC & NCG | 132 | NF1 | 10 | CGC & NCG | 199 | SPZ1 | 4 | |
| 66 | LRP1B | 19 | CGC & NCG* | 133 | COL4A5 | 12 | | 200 | LRRK2 | 7 | NCG* |
| 67 | KCNJ12 | 18 | NCG | 134 | SIPA1L3 | 6 | | | | | - |

Table S3. The driver gene candidates identified in the top 200 genes prioritized by IntDriver on LUSC dataset. Their ranks, gene symbols and mutation frequencies are demonstrated in the table, along with whether the genes are experimentally (CGC & NCG) supported or statistically inferred (NCG). The asterisk * represents that the gene is reported to related with lung squamous cell carcinoma.

| Rank | Symbol | MutFree | Benchmarking | Rank | Symbol | MutFree | Benchmarking | Rank | Symbol | MutFree | Benchmarking |
|----------|--------------|---------|----------------|------|-----------------------|---------|------------------------|------|------------------|---------|--------------|
| 1 | TP53 | 172 | CGC* & NCG* | 68 | NBAS | 20 | | 135 | LBBK2 | 27 | NCG* |
| 2 | TTN | 145 | NCG* | 69 | MYCBP2 | 27 | NCG | 136 | ZNE208 | 20 | |
| 2 | MUC16 | 140 | NCC* | 70 | CTNNA2 | 24 | NCC | 127 | KALDN | 27 | NCC |
| 3 | MUCI6 | 98 | NCG | 70 | DECS | 34 | NCG | 137 | KALKN COL10A1 | 21 | NCG |
| 4 | FLG DKUD1 | 48 | NGG* | /1 | FEG3 | 30 | NCG | 138 | DVCE | 20 | |
| 5 | PKHD1 | 46 | NCG* | 72 | STAB2 | 34 | | 139 | DYSF | 23 | |
| 6 | RYR2 | 82 | NCG | 73 | ROS1 | 26 | CGC & NCG* | 140 | EPHB3 | 16 | |
| 7 | LRP1B | 74 | $CGC \& NCG^*$ | 74 | LTBP1 | 23 | | 141 | TLN2 | 20 | |
| 8 | LRP2 | 47 | NCG | 75 | ASH1L | 13 | | 142 | CCDC141 | 17 | |
| 9 | RYR3 | 57 | NCG* | 76 | SLIT2 | 19 | NCG* | 143 | HERC2 | 30 | NCG* |
| 10 | APOB | 41 | NCG | 77 | PAPPA2 | 40 | NCG* | 144 | SLC8A1 | 23 | |
| 11 | MACF1 | 44 | NCG | 78 | MYH2 | 31 | NCG | 145 | CHD6 | 19 | NCG |
| 12 | USH2A | 72 | NCG | 79 | FAT1 | 32 | CGC & NCG | 146 | FLT1 | 14 | |
| 13 | SYNE1 | 63 | NCG | 80 | BAI3 | 28 | NCG* | 147 | MUC4 | 29 | NCG |
| 14 | DNAH5 | 43 | | 81 | DID01 | 21 | NCG | 148 | ABID1B | 13 | CGC & NCG |
| 15 | DYNC1H1 | 30 | | 82 | USP34 | 23 | | 149 | LBP1 | 26 | |
| 16 | BIRC6 | 34 | | 83 | TNC | 20 | | 150 | COL5A2 | 18 | |
| 17 | MDN1 | 21 | | 84 | DNAU7 | 25 | NCC | 151 | TDD | 20 | CCC & NCC |
| 10 | VIDDO | 47 | NCC | 04 | DECAME 1 | 33 | NCG | 150 | MVIIO | 15 | CGC & NCG |
| 10 | MANO | 47 | NCG | 80 | GEDOO | 23 | NCG | 152 | DIVOCO | 10 | NGC & NCG |
| 19 | INAV5 | 49 | NCG | 80 | CEF 89 | 4 | NGG* | 100 | FIKSUG | 22 | NCG |
| 20 | VPS13D | 30 | | 87 | NLRP3 | 20 | NCG | 154 | UTRN | 17 | |
| 21 | GL13 | 13 | NCG* | 88 | SH3GL3 | 1 | | 155 | RANBP2 | 18 | |
| 22 | SI | 37 | NCG | 89 | LRRC7 | 35 | NCG | 156 | TEP1 | 15 | |
| 23 | AHNAK | 36 | NCG | 90 | SHANK2 | 16 | | 157 | KIAA1549 | 20 | CGC & NCG |
| 24 | FAM135B | 48 | NCG | 91 | LYST | 19 | | 158 | KAT6A | 18 | CGC & NCG |
| 25 | CSMD1 | 42 | NCG | 92 | SPHKAP | 31 | NCG* | 159 | VCAN | 23 | NCG |
| 26 | SPTA1 | 49 | NCG | 93 | MYH1 | 23 | NCG | 160 | COL7A1 | 21 | NCG |
| 27 | SLITRK3 | 32 | NCG | 94 | GRM3 | 23 | NCG* | 161 | FBN1 | 22 | |
| 28 | HCN1 | 42 | NCG* | 95 | COL6A3 | 20 | | 162 | ABCA1 | 16 | NCG |
| 29 | CSMD2 | 38 | NCG | 96 | MYH8 | 25 | NCG | 163 | UBE2O2 | 1 | |
| 30 | ABHGAP5 | 2 | | 97 | DNAH1 | 14 | | 164 | COL4A1 | 18 | |
| 31 | NBXN1 | 33 | | 98 | BP1 | 36 | NCG | 165 | PLEC | 23 | NCG |
| 32 | TNR | 35 | NCG | 99 | DMBT1 | 10 | | 166 | MKI67 | 15 | |
| 33 | PRPF31 | 0 | nea | 100 | BDP1 | 13 | | 167 | TRPM6 | 14 | NCG |
| 24 | AKAD19 | | NCC | 100 | ADAMTSO | 19 | | 169 | PYDN | 20 | NCC |
| 25 | GVNE9 | 36 | NCG | 101 | MED10I | 10 | NCC | 160 | CDDACD1 | 14 | NCG |
| 26 | KIAA1100 | 20 | NCG | 102 | ANK2 | 10 | NCC | 170 | DTDDD | 20 | |
| 30 | KIAAI109 | 21 | NGG | 103 | CADDDO | 19 | NCG | 170 | CNENADO | 20 | NGG* |
| 37 | MYO18B | 26 | NCG | 104 | GABRB3 | 18 | NCG | 171 | CNTNAP2 | 34 | NCG |
| 38 | CACNAIE | 24 | NCG | 105 | ADCY2 | 19 | NCG* | 172 | ZSCAN4 | 9 | |
| 39 | PLXNA4 | 26 | | 106 | NRAP | 17 | | 173 | NOSI | 18 | |
| 40 | RYR1 | 34 | NCG | 107 | FLNC | 23 | NCG | 174 | CDH18 | 31 | |
| 41 | COL11A1 | 41 | NCG* | 108 | CUL9 | 19 | | 175 | SRCAP | 17 | |
| 42 | ALMS1 | 29 | NCG | 109 | ABCB5 | 17 | NCG | 176 | SPEN | 14 | |
| 43 | FAT4 | 34 | CGC & NCG | 110 | PCNX | 18 | | 177 | PTPRH | 15 | |
| 44 | VPS28 | 1 | | 111 | PCLO | 38 | NCG | 178 | MYLK | 14 | |
| 45 | SCN1A | 34 | | 112 | EPHA5 | 18 | NCG* | 179 | UBAP2L | 8 | |
| 46 | CTNND2 | 28 | | 113 | PIK3CA | 29 | CGC & NCG [*] | 180 | ADCY8 | 22 | NCG* |
| 47 | SH3PXD2A | 6 | | 114 | SMG1 | 16 | | 181 | PLB1 | 14 | NCG |
| 48 | TRRAP | 20 | CGC & NCG | 115 | GRIN2B | 26 | | 182 | PRG4 | 18 | NCG |
| 49 | SH3PXD2B | 5 | | 116 | DST | 18 | NCG* | 183 | MXRA5 | 17 | |
| 50 | CUBN | 38 | | 117 | MYT1L | 24 | | 184 | FMN2 | 35 | NCG |
| 51 | SH3KBP1 | 6 | | 118 | NOTCH2 | 16 | CGC & NCG | 185 | UNC79 | 21 | NCG |
| 52 | SH3GLB2 | 0 | | 119 | UNC5A | 5 | | 186 | MYH4 | 27 | NCG |
| 53 | EPHB1 | 25 | NCG* | 120 | TAFIL | 23 | | 187 | SLIT3 | 15 | |
| 54 | PTPRT | 24 | NCG | 121 | ITPR? | 16 | | 188 | LILBB2 | 16 | |
| 55 | | 24 | CCC & NCC | 121 | TDDM0 | 14 | | 190 | CMVAF | 19 | NCC* |
| 50 | DCUC1 | 10 | NGC & NCG | 122 | INFNIZ DNE919 | 15 | CCC & NCC | 109 | CMIAD | 10 | 100 |
| 57 | EDNO | 19 | NCC | 123 | ANF 213 SETD5 | 10 | NCC & NUG | 101 | NEK | 20 | NCC |
| 01 E0 | I DINZ | 29 | NCG | 124 | SE 1 D 3 C1 f1 7 2 | 0 | NOG | 102 | NUDDOF | 20 | INCG |
| 28 | LAMA4 | 21 | NUG NGG* | 125 | Ulori173 | 41 | | 192 | NUP205 | 11 | |
| 59 | CDH10 | 38 | NCG." | 126 | HERC1 | 17 | | 193 | PPFIA1 | 13 | |
| 60 | CDH12 | 33 | NCG | 127 | ZNF804A | 24 | NCG | 194 | 1FT172 | 13 | |
| 61 | ANK2 | 40 | NCG | 128 | LARGE | 16 | | 195 | MYH13 | 18 | |
| 62 | NEB | 37 | NCG | 129 | OTOF | 18 | NCG | 196 | ZNF33A | 15 | |
| 63 | SMEK1 | 1 | | 130 | GRIN2A | 20 | CGC & NCG | 197 | DMXL2 | 13 | |
| 64 | OBSCN | 33 | NCG | 131 | PRUNE2 | 17 | NCG | 198 | DNAJC13 | 16 | |
| 65 | SRRM2 | 20 | | 132 | OCA2 | 17 | | 199 | FCGBP | 19 | |
| 66 | UBR5 | 16 | $CGC \& NCG^*$ | 133 | POLQ | 22 | | 200 | ZFHX3 | 20 | CGC & NCG |
| 67 | CNTNAP5 | 38 | | 134 | NIPBL | 15 | | | | | |

Table S4. The p-values of Fisher's exact test accessing the enrichment significance for NCG [1] benchmarking driver genes of the top 50, 100, 150 and 200 genes selected by IntDriver, NotNet2, MUFFINN-DNmax, MUFFINN-DNsum, DriverNet, NBS(k=3), NBS(k=4), ReMIC.

| | BRCA | | | | | | | | |
|---------------|----------|----------|----------|----------|--|--|--|--|--|
| Rank | 50 | 100 | 150 | 200 | | | | | |
| IntDriver | 6.00e-25 | 1.34e-27 | 6.99e-38 | 5.36e-40 | | | | | |
| HotNet2 | 1.27e-01 | 5.81e-03 | 1.25e-02 | 4.82e-04 | | | | | |
| MUFFINN-DNmax | 5.01e-02 | 1.38e-02 | 1.69e-03 | 3.36e-03 | | | | | |
| MUFFINN-DNsum | 2.77e-01 | 2.84e-01 | 1.33e-01 | 5.10e-02 | | | | | |
| DriverNet | 1.81e-13 | 1.72e-14 | 1.93e-10 | 7.12e-11 | | | | | |
| NBS(k=3) | 7.47e-07 | 2.33e-10 | 7.66e-18 | 2.45e-21 | | | | | |
| NBS(k=4) | 7.47e-07 | 5.30e-11 | 6.50e-14 | 2.24e-19 | | | | | |
| ReMIC | 1.82e-15 | 1.34e-27 | 7.27e-39 | 2.48e-48 | | | | | |
| | | KIRC | | | | | | | |
| Rank | 50 | 100 | 150 | 200 | | | | | |
| IntDriver | 1.89e-14 | 8.59e-23 | 1.48e-24 | 3.06e-29 | | | | | |
| HotNet2 | 5.01e-02 | 3.10e-02 | 3.98e-04 | 6.09e-06 | | | | | |
| MUFFINN-DNmax | 5.01e-02 | 5.81e-03 | 1.25e-02 | 4.82e-04 | | | | | |
| MUFFINN-DNsum | 2.77e-01 | 6.46e-01 | 7.08e-01 | 5.89e-01 | | | | | |
| DriverNet | 1.62e-16 | 3.04e-15 | 4.05e-12 | 2.45e-11 | | | | | |
| NBS(k=3) | 1.47e-07 | 2.41e-12 | 6.50e-14 | 3.87e-15 | | | | | |
| NBS(k=4) | 6.88e-10 | 3.04e-15 | 6.50e-14 | 2.67e-16 | | | | | |
| ReMIC | 1.60e-12 | 8.59e-23 | 1.06e-28 | 3.04e-38 | | | | | |
| | | LUSC | | | | | | | |
| Rank | 50 | 100 | 150 | 200 | | | | | |
| IntDriver | 9.92e-19 | 5.83e-34 | 7.22e-41 | 2.04e-46 | | | | | |
| HotNet2 | 7.89e-03 | 1.15e-03 | 2.86e-05 | 1.25e-04 | | | | | |
| MUFFINN-DNmax | 5.01e-02 | 1.38e-02 | 1.25e-02 | 2.22e-03 | | | | | |
| MUFFINN-DNsum | 3.92e-01 | 6.46e-01 | 9.01e-01 | 5.15e-01 | | | | | |
| DriverNet | 1.32e-17 | 8.59e-23 | 5.57e-23 | 2.24e-19 | | | | | |
| NBS(k=3) | 7.47e-07 | 5.71e-08 | 2.18e-09 | 2.45e-11 | | | | | |
| NBS(k=4) | 3.52e-06 | 5.30e-11 | 1.93e-10 | 1.81e-13 | | | | | |
| ReMIC | 1.60e-12 | 5.18e-16 | 9.20e-24 | 3.38e-33 | | | | | |

Table S5. Results of functional enrichment analysis of the top 200 genes identified by IntDriver on BRCA datasets.

| Term | Count | Percentage | PValue |
|-----------------------------------------------------------------|-------|------------|-----------|
| hsa04020:Calcium signaling pathway | 17 | 8.67 | 2.68E-09 |
| hsa04930:Type II diabetes mellitus | 9 | 4.59 | 2.68E-07 |
| hsa04510:Focal adhesion | 15 | 7.65 | 8.88E-07 |
| hsa05205:Proteoglycans in cancer | 14 | 7.14 | 3.72E-06 |
| hsa05213:Endometrial cancer | 7 | 3.57 | 7.92E-05 |
| hsa05200:Pathways in cancer | 17 | 8.67 | 9.97E-05 |
| hsa04725:Cholinergic synapse | 9 | 4.59 | 1.52E-04 |
| hsa05222:Small cell lung cancer | 8 | 4.08 | 1.75E-04 |
| hsa04919:Thyroid hormone signaling pathway | 9 | 4.59 | 1.83E-04 |
| hsa04012:ErbB signaling pathway | 8 | 4.08 | 2.02E-04 |
| hsa04010:MAPK signaling pathway | 13 | 6.63 | 2.15E-04 |
| hsa05230:Central carbon metabolism in cancer | 7 | 3.57 | 2.55E-04 |
| hsa04921:Oxytocin signaling pathway | 10 | 5.10 | 3.48E-04 |
| hsa04713:Circadian entrainment | 8 | 4.08 | 3.49E-04 |
| hsa04024:cAMP signaling pathway | 11 | 5.61 | 4.27E-04 |
| hsa05161:Hepatitis B | 9 | 4.59 | 9.27E-04 |
| hsa04261:Adrenergic signaling in cardiomyocytes | 9 | 4.59 | 9.69E-04 |
| hsa05221:Acute myeloid leukemia | 6 | 3.06 | 1.07E-03 |
| hsa05414:Dilated cardiomyopathy | 7 | 3.57 | 1.10E-03 |
| hsa04512:ECM-receptor interaction | 7 | 3.57 | 1.32E-03 |
| hsa05215:Prostate cancer | 7 | 3.57 | 1.41E-03 |
| hsa04210:Apoptosis | 6 | 3.06 | 1.69E-03 |
| hsa05214:Glioma | 6 | 3.06 | 2.09E-03 |
| hsa05212:Pancreatic cancer | 6 | 3.06 | 2.09E-03 |
| hsa04022:cGMP-PKG signaling pathway | 9 | 4.59 | 2.21E-03 |
| hsa04973:Carbohydrate digestion and absorption | 5 | 2.55 | 2.71E-03 |
| hsa04151:PI3K-Akt signaling pathway | 13 | 6.63 | 3.05E-03 |
| hsa05218:Melanoma | 6 | 3.06 | 3.08E-03 |
| hsa05220:Chronic myeloid leukemia | 6 | 3.06 | 3.27E-03 |
| hsa05410:Hypertrophic cardiomyopathy (HCM) | 6 | 3.06 | 4.62E-03 |
| hsa04727:GABAergic synapse | 6 | 3.06 | 6.65E-03 |
| hsa04911:Insulin secretion | 6 | 3.06 | 6.65E-03 |
| hsa05223:Non-small cell lung cancer | 5 | 2.55 | 7.67 E-03 |
| hsa04150:mTOR signaling pathway | 5 | 2.55 | 8.68E-03 |
| hsa04912:GnRH signaling pathway | 6 | 3.06 | 8.83E-03 |
| hsa05166:HTLV-I infection | 10 | 5.10 | 9.50E-03 |
| hsa04611:Platelet activation | 7 | 3.57 | 9.66E-03 |
| hsa05210:Colorectal cancer | 5 | 2.55 | 1.09E-02 |
| hsa04530:Tight junction | 7 | 3.57 | 1.23E-02 |
| hsa04723:Retrograde endocannabinoid signaling | 6 | 3.06 | 1.35E-02 |
| hsa05146:Amoebiasis | 6 | 3.06 | 1.63E-02 |
| hsa05412:Arrhythmogenic right ventricular cardiomyopathy (ARVC) | 5 | 2.55 | 1.73E-02 |
| hsa04260:Cardiac muscle contraction | 5 | 2.55 | 2.08E-02 |
| hsa04724:Glutamatergic synapse | 6 | 3.06 | 2.17E-02 |
| hsa05100:Bacterial invasion of epithelial cells | 5 | 2.55 | 2.36E-02 |
| hsa05145:Toxoplasmosis | 6 | 3.06 | 2.48E-02 |
| hsa04925:Aldosterone synthesis and secretion | 5 | 2.55 | 2.67 E-02 |
| hsa04666:Fc gamma R-mediated phagocytosis | 5 | 2.55 | 3.00E-02 |
| hsa05010:Alzheimer's disease | 7 | 3.57 | 3.03E-02 |
| hsa04923:Regulation of lipolysis in adipocytes | 4 | 2.04 | 4.35E-02 |
| hsa04066:HIF-1 signaling pathway | 5 | 2.55 | 4.85E-02 |
| hsa04070:Phosphatidylinositol signaling system | 5 | 2.55 | 4.85E-02 |
| hsa04924:Renin secretion | 4 | 2.04 | 6.05 E-02 |
| hsa04620:Toll-like receptor signaling pathway | 5 | 2.55 | 6.14E-02 |
| hsa04931:Insulin resistance | 5 | 2.55 | 6.48E-02 |
| hsa04664:Fc epsilon RI signaling pathway | 4 | 2.04 | 6.99E-02 |
| hsa04726:Serotonergic synapse | 5 | 2.55 | 7.02E-02 |
| hsa00562:Inositol phosphate metabolism | 4 | 2.04 | 7.74E-02 |
| hsa04270:Vascular smooth muscle contraction | 5 | 2.55 | 8.57E-02 |
| hsa04071:Sphingolipid signaling pathway | 5 | 2.55 | 8.78E-02 |
| hsa04722:Neurotrophin signaling pathway | 5 | 2.55 | 8.78E-02 |
| has 04150 AMDV sime line and have | 5 | 2 55 | 0.20F 02 |

| Term | Count | Percentage | PValue |
|----------------------------------------------|-------|------------|-----------|
| hsa04512:ECM-receptor interaction | 7 | 3.52 | 1.32E-03 |
| hsa04510:Focal adhesion | 10 | 5.03 | 2.31E-03 |
| hsa05200:Pathways in cancer | 14 | 7.04 | 3.17E-03 |
| hsa05146:Amoebiasis | 7 | 3.52 | 3.61E-03 |
| hsa04921:Oxytocin signaling pathway | 8 | 4.02 | 6.58E-03 |
| hsa05222:Small cell lung cancer | 6 | 3.02 | 6.65E-03 |
| hsa05416:Viral myocarditis | 5 | 2.51 | 8.17E-03 |
| hsa05332:Graft-versus-host disease | 4 | 2.01 | 1.08E-02 |
| hsa04066:HIF-1 signaling pathway | 6 | 3.02 | 1.19E-02 |
| hsa05230:Central carbon metabolism in cancer | 5 | 2.51 | 1.22E-02 |
| hsa05330:Allograft rejection | 4 | 2.01 | 1.48E-02 |
| hsa04940:Type I diabetes mellitus | 4 | 2.01 | 2.07E-02 |
| hsa04151:PI3K-Akt signaling pathway | 11 | 5.53 | 2.23E-02 |
| hsa05166:HTLV-I infection | 9 | 4.52 | 2.69E-02 |
| hsa04911:Insulin secretion | 5 | 2.51 | 3.11E-02 |
| hsa05320:Autoimmune thyroid disease | 4 | 2.01 | 3.61E-02 |
| hsa04977:Vitamin digestion and absorption | 3 | 1.51 | 3.75E-02 |
| hsa04120:Ubiquitin mediated proteolysis | 6 | 3.02 | 4.31E-02 |
| hsa04713:Circadian entrainment | 5 | 2.51 | 4.41E-02 |
| hsa05206:MicroRNAs in cancer | 9 | 4.52 | 4.62E-02 |
| hsa04514:Cell adhesion molecules (CAMs) | 6 | 3.02 | 4.89E-02 |
| hsa04320:Dorso-ventral axis formation | 3 | 1.51 | 5.45E-02 |
| hsa05205:Proteoglycans in cancer | 7 | 3.52 | 6.16E-02 |
| hsa05214:Glioma | 4 | 2.01 | 6.28E-02 |
| hsa05211:Renal cell carcinoma | 4 | 2.01 | 6.28E-02 |
| hsa04931:Insulin resistance | 5 | 2.51 | 6.48E-02 |
| hsa05310:Asthma | 3 | 1.51 | 6.58E-02 |
| hsa00020:Citrate cycle (TCA cycle) | 3 | 1.51 | 6.58E-02 |
| hsa04115:p53 signaling pathway | 4 | 2.01 | 6.75E-02 |
| hsa05140:Leishmaniasis | 4 | 2.01 | 7.74E-02 |
| hsa05145:Toxoplasmosis | 5 | 2.51 | 8.37 E-02 |
| hsa04612:Antigen processing and presentation | 4 | 2.01 | 9.07E-02 |

Table S6. Results of functional enrichment analysis of the top 200 genes identified by IntDriver on KIRC datasets.

| Table S7. | Results of functional | enrichment | analysis of the | e top 200 | genes identified | by IntDriver | on LUSC datasets. |
|-----------|-----------------------|------------|-----------------|-----------|------------------|--------------|-------------------|
|-----------|-----------------------|------------|-----------------|-----------|------------------|--------------|-------------------|

| Term | Count | Percentage | PValue |
|-----------------------------------------------------------|-------|------------|----------|
| hsa04510:Focal adhesion | 14 | 7.18 | 4.07E-06 |
| hsa04020:Calcium signaling pathway | 11 | 5.64 | 1.59E-04 |
| hsa04921:Oxytocin signaling pathway | 10 | 5.13 | 2.98E-04 |
| hsa04713:Circadian entrainment | 8 | 4.10 | 3.07E-04 |
| hsa04611:Platelet activation | 9 | 4.62 | 3.90E-04 |
| hsa04512:ECM-receptor interaction | 7 | 3.59 | 1.19E-03 |
| hsa04974:Protein digestion and absorption | 7 | 3.59 | 1.26E-03 |
| hsa04530:Tight junction | 8 | 4.10 | 2.68E-03 |
| hsa04724:Glutamatergic synapse | 7 | 3.59 | 4.67E-03 |
| hsa04970:Salivary secretion | 6 | 3.08 | 6.40E-03 |
| hsa05146:Amoebiasis | 6 | 3.08 | 1.50E-02 |
| hsa04024:cAMP signaling pathway | 8 | 4.10 | 1.88E-02 |
| hsa04151:PI3K-Akt signaling pathway | 11 | 5.64 | 1.96E-02 |
| hsa04015:Rap1 signaling pathway | 8 | 4.10 | 2.51E-02 |
| hsa04022:cGMP-PKG signaling pathway | 7 | 3.59 | 2.64E-02 |
| hsa05222:Small cell lung cancer | 5 | 2.56 | 2.91E-02 |
| hsa04360:Axon guidance | 6 | 3.08 | 3.02E-02 |
| hsa05014:Amyotrophic lateral sclerosis (ALS) | 4 | 2.05 | 3.10E-02 |
| hsa05213:Endometrial cancer | 4 | 2.05 | 3.43E-02 |
| hsa04977:Vitamin digestion and absorption | 3 | 1.54 | 3.61E-02 |
| hsa04923:Regulation of lipolysis in adipocytes | 4 | 2.05 | 4.13E-02 |
| hsa04750:Inflammatory mediator regulation of TRP channels | 5 | 2.56 | 4.55E-02 |
| hsa04915:Estrogen signaling pathway | 5 | 2.56 | 4.69E-02 |
| hsa05205:Proteoglycans in cancer | 7 | 3.59 | 5.68E-02 |
| hsa04720:Long-term potentiation | 4 | 2.05 | 6.19E-02 |
| hsa04725:Cholinergic synapse | 5 | 2.56 | 6.61E-02 |
| hsa04918:Thyroid hormone synthesis | 4 | 2.05 | 7.13E-02 |
| hsa04919:Thyroid hormone signaling pathway | 5 | 2.56 | 7.14E-02 |
| hsa04971:Gastric acid secretion | 4 | 2.05 | 7.87E-02 |
| hsa05010:Alzheimer's disease | 6 | 3.08 | 8.10E-02 |
| hsa05200:Pathways in cancer | 10 | 5.13 | 9.00E-02 |

References

- [1] Omer An, Vera Pendino, Matteo DAntonio, Emanuele Ratti, Marco Gentilini, and Francesca D Ciccarelli. Ncg 4.0: the network of cancer genes in the era of massive mutational screenings of cancer genomes. *Database*, 2014:bau015, 2014.
- [2] P Andrew Futreal, Lachlan Coin, Mhairi Marshall, Thomas Down, Timothy Hubbard, Richard Wooster, Nazneen Rahman, and Michael R Stratton. A census of human cancer genes. *Nature Reviews Cancer*, 4(3):177–183, 2004.