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| **Table e-2:** Full results of Cytoscape-generated PINBA networks for significant (VEGAS p<.05) genes implicated in bvFTD |
| Canonical Name | Band | Block# | Chrom | Description | ENSMBL ID | HGNC ID | HPRD ID | MIM ID | P-value | Top SNP P-value |
| *APOE* | 19q13.2 | 445 | 19 | apolipoprotein E | ENSG00000130203 | 613 | 135 | 107741 | 2.70E-05 | 1.36E-06 |
| *RGS4* | 1q23.3 | 29 | 1 | regulator of G-protein signaling 4 | ENSG00000117152 | 10000 | 3947 | 602516 | 2.10E-04 | 3.12E-05 |
| *PBX2* | 6p21.3 | 163 | 6 | pre-B-cell leukemia homeobox 2 | ENSG00000204304 | 8633 | 8890 | 176311 | 4.98E-04 | 1.41E-04 |
| *MAPT* | 17q21.1 | 404 | 17 | microtubule-associated protein tau | ENSG00000186868 | 6893 | 1142 | 157140 | 7.16E-04 | 0.001555 |
| *SMARCB1* | 22q11.23|22q11 | 468 | 22 | "SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily b, member 1" | ENSG00000099956 | 11103 | 3364 | 601607 | 7.83E-04 | 2.65E-04 |
| *SHC1* | 1q21 | 23 | 1 | SHC (Src homology 2 domain containing) transforming protein 1 | ENSG00000160691 | 10840 | 2780 | 600560 | 8.05E-04 | 0.001017 |
| *CKS1B* | 1q21.2 | 23 | 1 | CDC28 protein kinase regulatory subunit 1B | ENSG00000173207 | 19083 | 299 | 116900 | 8.05E-04 | 0.001017 |
| *MNAT1* | 14q23 | 350 | 14 | "menage a trois homolog 1, cyclin H assembly factor (Xenopus laevis)" | ENSG00000020426 | 7181 | 4042 | 602659 | 9.65E-04 | 0.01371 |
| *MAP3K5* | 6q22.33 | 181 | 6 | mitogen-activated protein kinase kinase kinase 5 | ENSG00000197442 | 6857 | 3904 | 602448 | 0.001276 | 9.26E-04 |
| *SMARCD1* | 12q13-q14 | 319 | 12 | "SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 1" | ENSG00000066117 | 11106 | 3438 | 601735 | 0.001396 | 2.52E-04 |
| *HSP90AA1* | 14q32.33 | 355 | 14 | "heat shock protein 90kDa alpha (cytosolic), class A member 1" | ENSG00000080824 | 5253 | 777 | 140571 | 0.001787 | 6.32E-04 |
| *ERBB3* | 12q13 | 321 | 12 | v-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (avian) | ENSG00000065361 | 3431 | 1820 | 190151 | 0.00367 | 0.001755 |
| *PA2G4* | 12q13.2 | 321 | 12 | "proliferation-associated 2G4, 38kDa" | ENSG00000170515 | 8550 | 3685 | 602145 | 0.00367 | 0.001755 |
| *CDK2* | 12q13 | 321 | 12 | cyclin-dependent kinase 2 | ENSG00000123374 | 1771 | 310 | 116953 | 0.00367 | 0.00452 |
| *IKZF4* | 12q13 | 321 | 12 | IKAROS family zinc finger 4 (Eos) | ENSG00000123411 | 13179 | 5874 | 606239 | 0.00367 | 0.001929 |
| *LYN* | 8q13 | 220 | 8 | v-yes-1 Yamaguchi sarcoma viral related oncogene homolog | ENSG00000147507 | 6735 | 1301 | 165120 | 0.00372 | 2.48E-04 |
| *CDC25B* | 20p13 | 452 | 20 | cell division cycle 25 homolog B (S. pombe) | ENSG00000101224 | 1726 | 307 | 116949 | 0.00534 | 8.07E-04 |
| *IFT20* | 17q11.2 | 400 | 17 | intraflagellar transport 20 homolog (Chlamydomonas) | ENSG00000109083 | 30989 | NA | 17137 | 0.00541 | 0.00315 |
| *DAG1* | 3p21 | 94 | 3 | dystroglycan 1 (dystrophin-associated glycoprotein 1) | ENSG00000173402 | 2666 | 546 | 128239 | 0.00646 | 0.01412 |
| *IL2* | 4q26-q27 | 132 | 4 | interleukin 2 | ENSG00000109471 | 6001 | 979 | 147680 | 0.00673 | 3.18E-04 |
| *ESR1* | 6q25.1 | 183 | 6 | estrogen receptor 1 | ENSG00000091831 | 3467 | 589 | 133430 | 0.007 | 4.39E-04 |
| *EIF2AK2* | 2p22-p21 | 53 | 2 | eukaryotic translation initiation factor 2-alpha kinase 2 | ENSG00000055332 | 9437 | 1468 | 176871 | 0.0078 | 0.001313 |
| *CBL* | 11q23.3 | 309 | 11 | Cas-Br-M (murine) ecotropic retroviral transforming sequence | ENSG00000110395 | 1541 | 1320 | 165360 | 0.00812 | 0.002219 |
| *TGFB1I1* | 16p11.2 | 379 | 16 | transforming growth factor beta 1 induced transcript 1 | ENSG00000140682 | 11767 | 3831 | 602353 | 0.00909 | 0.005727 |
| *SLA2* | 20q11.23 | 457 | 20 | Src-like-adaptor 2 | ENSG00000101082 | 17329 | 5955 | 606577 | 0.00916 | 0.002675 |
| *PTPN12* | 7q11.23 | 193 | 7 | "protein tyrosine phosphatase, non-receptor type 12" | ENSG00000127947 | 9645 | 2513 | 600079 | 0.00965 | 0.001599 |
| *CALM2* | 2p21 | 56 | 2 | "calmodulin 2 (phosphorylase kinase, delta)" | ENSG00000143933 | 1445 | 242 | 114182 | 0.01078 | 7.39E-05 |
| *SHC3* | 9q22.1 | 249 | 9 | SHC (Src homology 2 domain containing) transforming protein 3 | ENSG00000148082 | 18181 | 12005 | 605263 | 0.0118 | 4.74E-04 |
| *CALM3* | 19q13.2-q13.3 | 446 | 19 | "calmodulin 3 (phosphorylase kinase, delta)" | ENSG00000160014 | 1449 | 243 | 114183 | 0.01239 | 0.003727 |
| *CSF1R* | 5q33-q35 | 156 | 5 | colony stimulating factor 1 receptor | ENSG00000182578 | 2433 | 1269 | 164770 | 0.01249 | 8.84E-04 |
| *SLA* | 8q22.3-qter|8q24 | 237 | 8 | Src-like-adaptor | ENSG00000155926 | 10902 | 3060 | 601099 | 0.01341 | 7.84E-04 |
| *FCGR2A* | 1q23 | 27 | 1 | "Fc fragment of IgG, low affinity IIa, receptor (CD32)" | ENSG00000143226 | 3616 | 906 | 146790 | 0.01352 | 0.002861 |
| *FCGR3A* | 1q23 | 27 | 1 | "Fc fragment of IgG, low affinity IIIa, receptor (CD16a)" | ENSG00000203747 | 3619 | 903 | 146740 | 0.01352 | 0.01791 |
| *FKBP4* | 12p13.33 | 312 | 12 | "FK506 binding protein 4, 59kDa" | ENSG00000004478 | 3720 | 11794 | 600611 | 0.01397 | 0.008144 |
| *SMYD3* | 1q44 | 49 | 1 | SET and MYND domain containing 3 | ENSG00000185420 | 15513 | 12297 | 608783 | 0.01448 | 0.007669 |
| *BAIAP2* | 17q25 | 417 | 17 | BAI1-associated protein 2 | ENSG00000175866 | 947 | 5686 | 605475 | 0.01456 | 1.45E-04 |
| *VAV2* | 9q34.1 | 256 | 9 | vav 2 guanine nucleotide exchange factor | ENSG00000160293 | 12658 | 2694 | 600428 | 0.01492 | 3.55E-04 |
| *GDNF* | 5p13.1-p12 | 141 | 5 | glial cell derived neurotrophic factor | ENSG00000168621 | 4232 | 2906 | 600837 | 0.01666 | 4.11E-04 |
| *HIST2H2BE* | 1q21-q23 | 21 | 1 | "histone cluster 2, H2be" | ENSG00000184678 | 4760 | 3494 | 601831 | 0.01834 | 0.02656 |
| *SKAP1* | 17q21.32 | 405 | 17 | src kinase associated phosphoprotein 1 | ENSG00000141293 | 15605 | 5396 | 604969 | 0.01846 | 9.65E-04 |
| *CDC6* | 17q21.3 | 403 | 17 | cell division cycle 6 homolog (S. cerevisiae) | ENSG00000094804 | 1744 | 4022 | 602627 | 0.0192 | 0.01925 |
| *CTBP1* | 4p16 | 112 | 4 | C-terminal binding protein 1 | ENSG00000159692 | 2494 | 4015 | 602618 | 0.02015 | 0.009786 |
| *CALD1* | 7q33 | 206 | 7 | caldesmon 1 | ENSG00000122786 | 1441 | 251 | 114213 | 0.02153 | 0.00306 |
| *MYC* | 8q24.21 | 236 | 8 | v-myc myelocytomatosis viral oncogene homolog (avian) | ENSG00000136997 | 7553 | 1818 | 190080 | 0.02373 | 0.004856 |
| *TYK2* | 19p13.2 | 434 | 19 | tyrosine kinase 2 | ENSG00000105397 | 12440 | 1490 | 176941 | 0.02598 | 0.001478 |
| *CDC37* | 19p13.2 | 434 | 19 | cell division cycle 37 homolog (S. cerevisiae) | ENSG00000105401 | 1735 | 5456 | 605065 | 0.02598 | 0.001478 |
| *PDE4A* | 19p13.2 | 434 | 19 | "phosphodiesterase 4A, cAMP-specific (phosphodiesterase E2 dunce homolog, Drosophila)" | ENSG00000065989 | 8780 | 2527 | 600126 | 0.02598 | 0.001462 |
| *GSK3A* | 19q13.2 | 444 | 19 | glycogen synthase kinase 3 alpha | ENSG00000105723 | 4616 | 6002 | 606784 | 0.02667 | 0.02279 |
| *POU2F2* | 19q13.2 | 444 | 19 | POU class 2 homeobox 2 | ENSG00000028277 | 9213 | 1251 | 164176 | 0.02667 | 0.01648 |
| *PIAS3* | 1q21 | 19 | 1 | "protein inhibitor of activated STAT, 3" | ENSG00000131788 | 16861 | 9068 | 605987 | 0.03085 | 0.01042 |
| *CCNT1* | 12q11-q13.3 | 318 | 12 | cyclin T1 | ENSG00000129315 | 1599 | 3938 | 143055 | 0.03179 | 0.01891 |
| *NRIP1* | 21q11.2 | 463 | 21 | nuclear receptor interacting protein 1 | ENSG00000180530 | 8001 | 3927 | 602490 | 0.03188 | 0.002323 |
| *XBP1* | 22q12.1|22q12 | 469 | 22 | X-box binding protein 1 | ENSG00000100219 | 12801 | 1908 | 194355 | 0.03533 | 0.005747 |
| *RET* | 10q11.2 | 265 | 10 | ret proto-oncogene | ENSG00000165731 | 9967 | 1266 | 164761 | 0.03695 | 0.007818 |
| *SMARCA2* | 9p22.3 | 240 | 9 | "SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2" | ENSG00000080503 | 11098 | 2483 | 600014 | 0.03753 | 3.31E-04 |
| *ERBB4* | 2q33.3-q34 | 80 | 2 | v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian) | ENSG00000178568 | 3432 | 2767 | 600543 | 0.0381 | 4.51E-04 |
| *RUNX1T1* | 8q22 | 228 | 8 | "runt-related transcription factor 1; translocated to, 1 (cyclin D-related)" | ENSG00000079102 | 1535 | 590 | 133435 | 0.03915 | 0.01706 |
| *NCOR2* | 12q24 | 332 | 12 | nuclear receptor co-repressor 2 | ENSG00000196498 | 7673 | 2910 | 600848 | 0.04016 | 8.91E-04 |
| *IRS2* | 13q34 | 343 | 13 | insulin receptor substrate 2 | ENSG00000185950 | 6126 | 2878 | 600797 | 0.04079 | 0.00475 |
| *CNOT7* | 8p22-p21.3 | 216 | 8 | "CCR4-NOT transcription complex, subunit 7" | ENSG00000198791 | 14101 | NA | 604913 | 0.04082 | 0.001588 |
| *CDK6* | 7q21-q22 | 195 | 7 | cyclin-dependent kinase 6 | ENSG00000105810 | 1777 | 4533 | 603368 | 0.04766 | 2.58E-04 |
| *CTGF* | 6q23.1 | 179 | 6 | connective tissue growth factor | ENSG00000118523 | 2500 | 412 | 121009 | 0.04968 | 0.02277 |
| *GUCY1B3* | 4q31.3-q33 | 135 | 4 | "guanylate cyclase 1, soluble, beta 3" | ENSG00000061918 | 4687 | 769 | 139397 | 0.04994 | 0.001814 |

**Table e-2 Legend:** Canonical name of gene SNPs , Band – chromosomal locationlocation, Block # – block association membership defined as groups of sequential genes with a p-value of <.05, Chrom – chromosomal location, ENSMBL ID – annotation ID in ENSMBL, HGNC ID – Human genome nomenclature ID, HPRD ID – Human protein reference database, MIMID – Mendelian inheritance in man ID, P-value – Gene p value, Top SNP p-value – Top p value for SNP