Electronic Supplementary Material (ESI) for Molecular BioSystems

Supplementary Table 1 Masses identified by LC-MS/MS and MALDI-TOF/MS

MW by SELDI	**Candidate Protein ID (Swiss Prot or NCBI accession number)**	Score	Expected Value	Peptide[#]
3822	STAT_Human	13	1.5E+03[&]	IGRFGYGYGPYQPVPEQPLYPQPYQPQY QQYT
5227	KNG1_Human	60	43	MKLITILFLC SRLLLSLTQE SQSEEIDCND KDLFKAVDAA LKKYNSQNQS NNQFVLYRIT EATK**TVGSDT FYSFK**YEIKE GDCPVQSGKT WQDCEYKDAA KAATGECTAT VGKRSSTKFS VATQTCQITP AEGPVVTAQY DCLGCVHPIS TQSPDLEPIL RHGIQYFNNN TQHSSLFMLN EVKRAQRQVV AGLNFRITYS IVQTNCSKEN FLFLTPDCKS LWNGDTGECT DNAYIDIQLR IASFSQNCDI YPGKDFVQPP TKICVGCPRD IPTNSPELEE TLTHTITKLN AENNATFYFK IDNVKKARVQ VVAGKKYFID FVARETTCSK ESNEELTESC ETKKLGQSLD CNAEVYVVPW EKKIYPTVNC QPLGMISLMK RPPGFSPFRS SRIGEIKEET TVSPPHTSMA PAQDEERDSG KEQGHTRRHD WGHEKQRKHN LGHGHKHERD QGHGHQRGHG LGHGHEQQHG LGHGHKFKLD DDLEHQGGHV LDHGHKHKHG HGHGKHKNKG KKNGKHNGWK TEHLASSSED STTPSAQTQE KTEGPTPIPS LAKPGVTVTF SDFQDSDLIA TMMPPISPAP IQSDDDWIPD IQIDPNGLSF NPISDFPDTT SPKCPGRPWK SVSEINPTTQ MKESYYFDLT DGLS
7146.5	CYTN_Human	297	55	MAQHLSTLLL LLATLAVALA WSPK**EEDRII PGGIYNADLN DEWVQRALHF** **AISEYNK**ATK DDYYRRPLRV LRAR**QQTVGG VNYFFDVEVG R**TICT**KSQPN** **LDTCAFHEQP ELQKKQLCSF EIYEVPWENR** **R**SLVKSRCQE S
10827	unknown IG variable region	Multiple hits for IG variable regions with scores > 100	71	
12585.1	KV206_Human or possible unknown IG variable region	131	44	MRLPAQLLGL LMLWVPGSSG **DVVMTQSPLS LPVTLGQPAS ISCR**SSQSLV YSDGNTYLNW FQQRPGQSPR RLIYKVSNRD SGVPDRFSGS GSGTDFTLKI SRVEAEDVGV YYCMQGTHWS WTFGQGTKVE IKR

12588.8	KV404_Human, KV206_Human or possible unknown IG variable region	73/131	44	MVLQTQVFIS LLLWISGAYG **DIVMTQSPDS LAVSLGER**AT INCKSSQSIL YSSDNKNYLA WYQQKPGQPP KLLIYWASTR ESGVPDRFSG SGSGTDFTLT ISSLQAEDVA VYYCQQYYNL PWTFGQGTKV EIKR MRLPAQLLGL LMLWVPGSSG **DVVMTQSPLS LPVTLGQPAS ISCR**SSQSLV YSDGNTYLNW FQQRPGQSPR RLIYKVSNRD SGVPDRFSGS GSGTDFTLKI SRVEAEDVGV YYCMQGTHWS WTFGQGTKVE IKR
12607.8	gi|15777209 or possible unknown IG variable region	67	57	SCYWMSWVRQ APGKGLEWVA NIKXDGSEKY YVDSVKGRFT XSR**DNAKNSL XLQMNSLRAE** DTXXYYCXRG NIXVVPAALY ARGLLLXYGR XXPRXHGHRL LSIPDQPQGL

12608.4	DSC2_Human	107	55	MEAARPSGSW NGALCRLLLL TLAILIFASD ACKNVTLHVP SKLDAEKLVG RVNLKECFTA ANLIHSSDPD FQILEDGSVY TTNTILLSSE KRSFTILLSN TENQEKKKIF VFLEHQTKVL KKRHTKEKVL RRAKRRWAPI PCSMLENSLG PFPLFLQQVQ SDTAQNYTIY YSIRGPGVDQ EPRNLFYVER DTGNLYCTRP VDREQYESFE IIAFATTPDG YTPELPLPLI IKIEDENDNY PIFTEETYTF TIFENCRVGT TVGQVCATDK DEPDTMHTRL KYSIIGQVPP SPTLFSMHPT TGVITTTSSQ LDRELIDKYQ LKIKVQDMDG QYFGLQTTST CIINIDDVND HLPTFTRTSY VTSVEENTVD VEILRVTVED KDLVNTANWR ANYTILKGNE NGNFKIVTDA KTNEGVLCVV KPLNYEEKQQ MILQIGVVNE APFSREASPR SAMSTATVTV NVEDQDEGPE CNPPIQTVRM KENAEVGTTS NGYKAYDPET RSSSGIRYKK LTDPTGWVTI DENTGSIKVF RSLDREAETI KNGIYNITVL ASDQGGRTCT GTLGIILQDV NDNSPFIPK**K TVIICKPTMS SAEIVA**VDPD EPIHGPPFDF SLESSTSEVQ RMWRLKAIND TAAR**LSYQND PPFGSYVVPI TVR**DRLGMSS VTSLDVTLCD CITENDCTHR VDPRIGGGGV QLGKWAILAI LLGIALLFCI LFTLVCGASG TSKQPKVIPD DLAQQNLIVS NTEAPGDDKV YSANGFTTQT VGASAQGVCG TVGSGIKNGG QETIEMVKGG HQTSESCRGA GHHHTLDSCR GGHTEVDNCR YTYSEWHSFT QPRLGEKVYL CNQDENHKHA QDYVLTYNYE GRGSVAGSVG CCSERQEEDG LEFLDNLEPK FRTLAEACMKR
12680	unknown IG variable region	Multiple hits for IG variable regions with scores > 71	71	
13267.3	gi|239741695	57	56	MVNPTMFFHI AVDGEPLGCV SFELFADKVP KTAENFHALS TGEKGFGYKG SCFHR**IIPGF TCQSGDFTRH** TALVANAKTE WLDCKHVVFG KVKDGMNIVE VMEHLGSKNG KISNQQEDHH C

13274.1	CAH6_Human	68	44	MRALVLLLSL FLLGGQAQHV SDWTYSEGAL DEAHWPQHYP ACGGQRQSPI NLQRTKVRYN PSLKGLNMTG YETQAGEFPM VNNGHTVQIS LPSTMRMTVA DGTVYIAQQM HFHWGGASSE ISGSEHTVDG IRHVIEIHIV HYNSKYK**SYD IAQDAPDGLA VLAAFVEVK**N YPENTYYSNF ISHLANIKYP GQRTTLTGLD VQDMLPRNLQ HYYTYHGSLT TPPCTENVHW FVLADFVKLS RTQVWKLENS LLDHRNKTIH NDYRRTQPLN HRVVESNFPN QEYTLGSEFQ FYLHKIEEIL DYLRRALN
13274.1	gi|239741695	57	56	MVNPTMFFHI AVDGEPLGCV SFELFADKVP KTAENFHALS TGEKGFGYKG SCFHR**IIPGF TCQSGDFTRH** TALVANAKTE WLDCKHVVFG KVKDGMNIVE VMEHLGSKNG KISNQQEDHH C
13274.1	CYTC_Human	61	55	MAGPLRAPLL LLAILAVALA VSPAAGSSPG KPPRLVGGPM DASVEEEGVR **RALDFAVGEY NK**ASNDMYHS RALQVVRARK QIVAGVNYFL DVELGRTTCT KTQPNLDNCP FHDQPHLKRK AFCSFQIYAV PWQGTMTLSK STCQDA
13469	HV301_Human, or possible unknown IG variable region	70	44	**QVQLVQSGGG LVKPGGSLR**L SCVASGFSFR DFYMSWIRZT PGKGLZWVSY IGGSGSTLYY ADSVKGRFTI SRDNAQKSLY LZMBSLRTZB TAVYYCAATB BFBWSTFSLB YWGZGBLVTV SS
13536	HV310_Human or possible unknown IG variable region	56	44	**QVKLVQAGGG VVQPGR**SLRL SCIASGFTFS NYGMHWVRQA PGKGLEWVAV IWYNGSRTYY GDSVKGRFTI SRDNSKRTLY MZMNSLRTED TAVYYCARDP DILTAFSFDY WGQGVLVTVS S
13537.5	HV310_Human or possible unknown IG variable region	56	44	**QVKLVQAGGG VVQPGR**SLRL SCIASGFTFS NYGMHWVRQA PGKGLEWVAV IWYNGSRTYY GDSVKGRFTI SRDNSKRTLY MZMNSLRTED TAVYYCARDP DILTAFSFDY WGQGVLVTVS S
13552.9	gi|224808232 or possible unknown variable region	110	71	MA**XVQLVESG GGVVQPGR**SL RLSCAASGFT FSKYPFHWVR QAPGKGLEWV ATISHDGSNN DYADSVKGRL IISRDNSKNT LYLQMSSLRV EDTAVYYCAR VLGWYGREVD YWGQGTLVTV SS

13645.2	HV307_Human or possible unknown IG variable region	59	55	QVELVESGGG VVZPGRSLRL SCAASGFTFS NYAMHWVRQP PGKGLEWVAV ISYBGBBKYY ABSVKGRFTI SRDBSK**BTLY LQMNSLR**AEB TAVYYCARDR PLYGBYRAFN YWGQGTLVTV SS
[d]15291	gi|1082553 or possible unknown IG variable region	179	56	MRRVFVQQDN GELTLWWTFG QGTKVEIKR**T VAAPSVFIFP PSDEQLKSGT ASVVCLLNNF YPREAKVQWK VDNALQSGNS QESVTEQDSK DSTYSLSSTL TLSKADYEKH** K**LYACEVTHQ GLSSPVTKSF** NRGEC

[d] These biomarkers are down-regulated in CADS groups compared with the control.

[#] Amino acids presented in bold indicates peptides detected as part of the database search. The sequences presented here are that of the un-processed protein. In some cases the protein was cleaved or modified as indicated in the database, and it was the mass of the processed form that matched most closely to the SELDI-TOF/MS Mw marker.

[&] This references the statistical cutoff value in these database search algorithms that indicate protein identity or extensive homology

Supplementary Table 2: Transcriptome Analysis of DES-related and PPIA-related genes*

Symbol	Entrez Gene Name	p-value	Fold Change
PPIL2	peptidylprolyl isomerase (cyclophilin)-like 2	3.98E-03	1.220
PPIL1	peptidylprolyl isomerase (cyclophilin)-like 1	1.07E-06	1.339
PPIB	peptidylprolyl isomerase B (cyclophilin B)	5.35E-06	1.343
PPIF	peptidylprolyl isomerase F	3.94E-03	1.430

*Biopsy samples from denture stomatitis affected and unaffected areas in the oral mucosa were processed for RNA extraction and gene expression profiling was performed using Affymetrix (Affymetrix Inc., Santa Clara, CA) recommended procedure and analyzed using Partek and IPA softwares. To determine the integrity of the RNA isolated from biopsies samples, all RNA samples were analyzed using Agilent 2100 Bioanalyzer. The RNA Integrity Number (RIN), that was developed to remove individual interpretation in RNA quality control, is obtained through a software algorithm that allows for the classification of riboeukaryotic total RNA, based on a numbering system from 1 to 10, with 1 being the most degraded profile and 10 being the most intact. In this way, interpretation of an electropherogram is facilitated, enabling comparison of samples. As can be seen in the figure above the RIN values typically were between 9.3 and 10. All samples had RNA quality exceeding the minimal cut-point of RIN=8.0 for whole transcriptome Affymetric array analyses. The quality control of the Affymetrix arrays demonstrated excellent signals for all arrays used. SAM analyses using a FDR of $P<0.05$ was utilized. Note that only PPIA-related genes are presented here.