

Supplemental Table A. Variables used for Lasso

Measurement	Type
Absolute Lymphocytes	Continuous
Absolute Neutrophils	Continuous
Antinuclear Antibody	Categorical
Complement C3 level	Continuous
Complement C4 Level	Continuous
Hemoglobin	Continuous
Serum IgA Level	Continuous
Serum IgG level	Continuous
Serum IgM level	Continuous
Maximum Ocular Staining Score	Continuous
Ocular Staining Score ≥ 5	Categorical
Parotid Gland Swelling	Categorical
Platelet Count	Continuous
Race	Categorical
Rheumatoid Factor	Categorical
Schirmer's ≤ 5 mm/5min	Categorical
Sex	Categorical
Submandibular Gland Swelling	Categorical
Unstimulated salivary flow	Continuous
Unstimulated salivary flow ≥ 5 mL/5 min	Categorical
White Blood Cell Count	Continuous

Supplemental Table B. GO of SSA- SJD vs. Controls peptides GO enriched clusters of peptides bound more by SSA- SJD						
Category	Term	Count	%	PValue	Genes	Fold Enrichment
Annotation Cluster 1	Enrichment Score: 1.4569415337080533					
GOTERM_CC_DIRECT	GO:0014069~postsynaptic density	7	3	0.03	O14490, P54764, Q13873, Q8TCU5, Q8WXI2, Q17RY0, Q9C0D5	3.03
GOTERM_CC_DIRECT	GO:0030054~cell junction	12	5	0.03	Q9BT78, O14490, P54764, Q8TCU5, Q05084, P46939, Q17RY0, P55196, Q8NI17, Q96SN8, P35222, Q9C0D5	2.08
GOTERM_CC_DIRECT	GO:0045211~postsynaptic membrane	7	3	0.05	O14490, P54764, Q8TCU5, P46939, Q8WXI2, Q17RY0, Q9C0D5	2.64
Annotation Cluster 2	Enrichment Score: 0.8311644448490958					
GOTERM_BP_DIRECT	GO:0036258~multivesicular body assembly	3	1	0.06	Q9BY43, O75886, Q99816	7.42
GOTERM_BP_DIRECT	GO:0016197~endosomal transport	3	1	0.21	Q9BY43, O75886, Q99816	3.49
GOTERM_BP_DIRECT	GO:0006914~autophagy	4	2	0.25	Q14457, Q9BY43, O75886, Q99816	2.31
Annotation Cluster 3	Enrichment Score: 0.673790195834016					
GOTERM_MF_DIRECT	GO:0004713~protein tyrosine kinase activity	5	2	0.08	P54764, P36507, P29323, Q12866, Q13627	3.02
GOTERM_BP_DIRECT	GO:0018108~peptidyl-tyrosine phosphorylation	5	2	0.14	P54764, P36507, P29323, Q12866, Q13627	2.51
GOTERM_MF_DIRECT	GO:0004672~protein kinase activity	4	2	0.82	P54764, P36507, Q9BVS4, Q13627	0.90
Annotation Cluster 4	Enrichment Score: 0.5088030236806619					
GOTERM_CC_DIRECT	GO:0005913~cell-cell adherens junction	7	3	0.22	Q9H2G2, Q15149, P78344, O00571, P55196, Q9BY67, P35222	1.72

GOTERM_MF_DIRECT_T	GO:0098641~cadherin binding involved in cell-cell adhesion	6	2	0.29	Q9H2G2, Q15149, P78344, O00571, P55196, P35222	1.66
GOTERM_BP_DIRECT	GO:0098609~cell-cell adhesion	5	2	0.47	Q9H2G2, Q15149, P78344, O00571, P55196	1.41
Bound less by SSA- SjD than controls						
Annotation Cluster 1	Enrichment Score: 1.5756814278605908					
GOTERM_CC_DIRECT_T	GO:0016529~sarcoplasmic reticulum	5	2	0.00	Q15413, P21817, P28161, Q14571, Q8N3K9	7.51
GOTERM_CC_DIRECT_T	GO:0030659~cytoplasmic vesicle membrane	7	2	0.01	Q8NHG8, Q15413, P21817, Q9Y5X1, Q14571, Q86YS7, Q99527	3.83
GOTERM_CC_DIRECT_T	GO:0033017~sarcoplasmic reticulum membrane	3	1	0.09	Q15413, P21817, Q14571	5.88
GOTERM_BP_DIRECT_T	GO:0051209~release of sequestered calcium ion into cytosol	3	1	0.13	Q15413, P21817, Q14571	4.87
Annotation Cluster 2	Enrichment Score: 1.4680426238512505					
GOTERM_MF_DIRECT_T	GO:0005245~voltage-gated calcium channel activity	4	1	0.03	P21817, Q02641, Q5VU97, O00555	6.29
GOTERM_BP_DIRECT_T	GO:0070588~calcium ion transmembrane transport	6	2	0.03	Q15413, Q9HCX4, Q02641, Q5VU97, Q14393, O00555	3.58
GOTERM_CC_DIRECT_T	GO:0005891~voltage-gated calcium channel complex	3	1	0.06	Q02641, Q5VU97, O00555	7.56
Annotation Cluster 3	Enrichment Score: 1.257823852776297					
GOTERM_BP_DIRECT_T	GO:0034453~microtubule anchoring	3	1	0.02	Q7Z460, Q9P287, O75122	13.95
GOTERM_BP_DIRECT_T	GO:0090307~mitotic spindle assembly	4	1	0.02	Q7Z460, Q9P287, O75122, Q8N3U4	6.81
GOTERM_BP_DIRECT_T	GO:0000226~microtubule cytoskeleton organization	5	2	0.13	Q7Z460, Q969Q6, Q9P287, Q03001, O75122	2.60
GOTERM_BP_DIRECT_T	GO:0007052~mitotic spindle organization	3	1	0.19	Q7Z460, Q9P287, O75122	3.74
Annotation Cluster 4	Enrichment Score: 1.230944021436133					

GOTERM_ MF_DIRECT	GO:0003700~transcription factor activity, sequence-specific DNA binding	18	6	0.00	2.14	P78545, Q9UBD0, Q9Y5W3, O43889, Q06710, P52945, P10589, P19544, P0CJ78, Q9Y2G1, Q00653, P10070, Q9Y261, Q15583, Q92731, Q92985, P40763
GOTERM_ BP_DIRECT	GO:0006357~regulation of transcription from RNA polymerase II promoter	38	12	0.01	1.54	P78545, Q86T24, Q9UBD0, Q86U86, Q9Y5W3, O15060, Q9BZC7, Q9Y2G1, Q00653, Q9C0C7, Q96GM5, Q96N22, P17097, O00151, Q15583, Q99708, Q92731, O75928, Q9UM63, P40763, Q9NVC6, O43889, Q9Y618, Q06710, P52945, P10589, P19544, P0CJ78, Q9BPY8, Q86UD4, P10070, Q9Y261, Q9UDV7, Q15059, P49848, Q96PN7, Q92985

GOTERM_ CC_DIREC T	GO:0000785~chromatin	25	8	0.02	P78545, Q86T24, Q9UBD0, Q86U86, Q8TBR4, Q9Y5W3, O43889, Q9Y618, Q06710, P52945, Q9BPY8, Q00653, Q96GM5, Q92793, Q9H9B1, Q9BVC3, Q15583, Q9Y261, Q92731, Q8N3U4, Q15059, P61129, Q92985, P40763	1.67
GOTERM_ BP_DIREC T	GO:0045944~positive regulation of transcription from RNA polymerase II promoter	25	8	0.06	P78545, Q9Y5W3, Q00653, Q96GM5, Q68DE3, Q92793, Q92731, Q9UM63, P25963, Q99527, P40763, P04049, Q9NVC6, Q9H3P2, O43889, Q06710, P52945, P10589, P19544, P10070, Q9Y261, O15226, P49848, Q96PN7, Q92985	1.45
GOTERM_ MF_DIREC T	GO:0043565~sequence-specific DNA binding	10	3	0.06	Q86T24, P78545, Q9UBD0, P10070, Q9Y261, Q92731, P10589, P19544, Q9Y2G1	2.01
GOTERM_ MF_DIREC T	GO:1990837~sequence-specific double-stranded DNA binding	13	4	0.14	P78545, Q86T24, Q9Y5W3, O43889, Q06710, P52945, P10589, Q00653, P10070, Q9Y261, Q15583, Q9UDV7, Q92985	1.54

GOTERM_MF_DIREC_T	GO:0000978~RNA polymerase II core promoter proximal region sequence-specific DNA binding	23	7	0.21	P78545, Q86T24, Q9UBD0, Q9Y5W3, O43889, Q06710, P52945, P10589, P19544, O15060, P0CJ78, Q00653, Q96N22, P10070, P17097, Q9Y261, Q15583, Q92731, O15226, Q9UM63, Q92985, P40763	1.26
GOTERM_MF_DIREC_T	GO:0001228~transcriptional activator activity, RNA polymerase II transcription regulatory region sequence-specific binding	10	3	0.29	Q00653, P78545, Q68DE3, P10070, O43889, O15226, Q06710, P19544, Q9UM63, P40763	1.40
GOTERM_MF_DIREC_T	GO:0000981~RNA polymerase II transcription factor activity, sequence-specific DNA binding	21	7	0.47	P78545, Q86T24, Q9UBD0, Q9Y5W3, O43889, Q06710, P52945, P19544, Q9Y2G1, Q00653, Q86UD4, Q96N22, P10070, P17097, Q9Y261, Q15583, Q92731, Q9UDV7, Q92985, P40763	1.08
Annotation Cluster 5	Enrichment Score: 1.1082981805551053					
GOTERM_BP_DIREC_T	GO:0035556~intracellular signal transduction	14	5	0.01	P52333, Q96J92, Q86T24, P04049, Q86YW0, O95835, Q5TB30, Q9Y5S2, Q9Y616, Q7Z460, Q8N4C8, Q9HBL0, Q8NEN9, P41743	2.17
GOTERM_MF_DIREC_T	GO:0004674~protein serine/threonine kinase activity	11	4	0.07	Q96J92, P04049, Q7Z460, Q8N4C8, O95835, Q9BVS4, Q9Y5S2, P41743, Q15772, Q8WZ42, Q9Y616	1.85

GOTERM_ BP_DIREC T	GO:0006468~protein phosphorylation	12	4	0.11	Q96J92, P52333, P04049, Q8N4C8, O95835, Q9Y5S2, Q14393, P49848, P41743, Q15772, Q12906, Q9Y616	1.67
GOTERM_ MF_DIREC T	GO:0004672~protein kinase activity	8	3	0.35	Q96J92, P04049, Q8N4C8, Q9BVS4, Q9Y5S2, P41743, Q15772, Q8WZ42	1.39
Annotation Cluster 6	Enrichment Score: 1.0514580144403698					
GOTERM_ CC_DIREC T	GO:0030864~cortical actin cytoskeleton	4	1	0.05	O43707, P02549, P12814, P31146	4.71
GOTERM_ MF_DIREC T	GO:0051015~actin filament binding	8	3	0.06	P57737, O43707, O95425, P02549, P12814, O75122, P31146, Q8WZ42	2.35
GOTERM_ BP_DIREC T	GO:0007015~actin filament organization	5	2	0.14	P57737, P02549, P12814, P31146, P41743	2.53
GOTERM_ CC_DIREC T	GO:0015629~actin cytoskeleton	7	2	0.16	O43707, O43312, P33241, O95425, P02549, Q03001, P31146	1.92
Annotation Cluster 7	Enrichment Score: 0.8904501710427482					
GOTERM_ CC_DIREC T	GO:0016342~catenin complex	3	1	0.07	Q9H251, Q12864, P55291	6.62
GOTERM_ BP_DIREC T	GO:0007156~homophilic cell adhesion via plasma membrane adhesion molecules	6	2	0.10	Q9H251, Q12864, O95206, Q9Y5H0, Q9HC56, P55291	2.43
GOTERM_ BP_DIREC T	GO:0098742~cell-cell adhesion via plasma-membrane adhesion molecules	3	1	0.11	Q9H251, Q12864, P55291	5.37
GOTERM_ MF_DIREC T	GO:0045296~cadherin binding	7	2	0.34	Q9H251, Q12864, Q9Y5X1, Q92597, Q12913, P55291, Q53SF7	1.46
Annotation Cluster 8	Enrichment Score: 0.7301562151468535					
GOTERM_ MF_DIREC T	GO:0008017~microtubule binding	8	3	0.11	Q9P2P6, Q96Q89, Q7Z460, Q2KJY2, Q03001, O75122, Q92597, Q68DA7	1.99

GOTERM_MF_DIREC_T	GO:1990939~ATP-dependent microtubule motor activity	3	1	0.13	Q9P2P6, Q96Q89, Q2KJY2	4.71
GOTERM_MF_DIREC_T	GO:0003777~microtubule motor activity	3	1	0.23	Q9P2P6, Q96Q89, Q2KJY2	3.30
GOTERM_BP_DIREC_T	GO:0007018~microtubule-based movement	3	1	0.36	Q9P2P6, Q96Q89, Q2KJY2	2.35
Annotation Cluster 9	Enrichment Score: 0.5981370066999627					
GOTERM_MF_DIREC_T	GO:0061630~ubiquitin protein ligase activity	9	3	0.13	Q9ULT8, Q8NHG8, Q5T4S7, Q9NVC6, Q96JN8, Q8IYU2, Q8IUD6, Q7Z6E9, Q96FA3	1.81
GOTERM_BP_DIREC_T	GO:0043161~proteasome-mediated ubiquitin-dependent protein catabolic process	6	2	0.18	Q9ULT8, Q8NHG8, Q8IYU2, Q92530, Q99460, Q96FA3	1.99
GOTERM_BP_DIREC_T	GO:0000209~protein polyubiquitination	5	2	0.23	Q9ULT8, Q9C0C7, Q8IYU2, Q8IUD6, Q96FA3	2.02
GOTERM_MF_DIREC_T	GO:0004842~ubiquitin-protein transferase activity	6	2	0.33	Q9ULT8, Q5T4S7, Q9Y4D8, Q8IYU2, Q8IUD6, Q7Z6E9	1.57
GOTERM_BP_DIREC_T	GO:0016567~protein ubiquitination	8	3	0.57	Q5T4S7, Q9Y4D8, Q9NVC6, Q96JN8, Q8IYU2, Q8IUD6, Q93008, Q7Z6E9	1.13
Annotation Cluster 10	Enrichment Score: 0.48839677794576797					
GOTERM_MF_DIREC_T	GO:0008233~peptidase activity	5	2	0.09	Q16549, P48740, Q99895, Q9UHP3, Q9Y2G1	2.97
GOTERM_MF_DIREC_T	GO:0004252~serine-type endopeptidase activity	4	1	0.56	Q16549, P48740, Q99895, P24158	1.36
GOTERM_BP_DIREC_T	GO:0006508~proteolysis	6	2	0.70	P48740, Q99895, Q8N6M6, Q9UHP3, P24158, Q8TE58	1.02

Supplemental Table C. Protein Domains Bound more in SSA- SjD than controls						
Category	Term	Count	%	PValue	Genes	Fold Enrichment
Annotation Cluster 1	Enrichment Score: 1.3356400437923381					
INTERPRO	IPR012677:Nucleotide-binding, alpha-beta plait	9	3.61	0.02	P31942, O95104, O00425, O43719, Q17RY0, Q9UPQ9, Q9BXP5, Q99729, Q9UN86	2.67
INTERPRO	IPR000504:RNA recognition motif domain	7	2.81	0.07	P31942, O95104, O00425, O43719, Q17RY0, Q99729, Q9UN86	2.43
SMART	SM00360:RRM	7	2.81	0.07	P31942, O95104, O00425, O43719, Q17RY0, Q99729, Q9UN86	2.39
Annotation Cluster 2	Enrichment Score: 1.3120946601674222					
INTERPRO	IPR019786:Zinc finger, PHD-type, conserved site	5	2.01	0.01	Q12830, Q9BVI0, Q92576, Q13342, Q9UK53	5.84
INTERPRO	IPR001965:Zinc finger, PHD-type	5	2.01	0.03	Q12830, Q9BVI0, Q92576, Q13342, Q9UK53	4.40
SMART	SM00249:PHD	5	2.01	0.03	Q12830, Q9BVI0, Q92576, Q13342, Q9UK53	4.06
INTERPRO	IPR011011:Zinc finger, FYVE/PHD-type	6	2.41	0.03	Q12830, Q6ZNL6, Q9BVI0, Q92576, Q13342, Q9UK53	3.33

INTERPRO	IPR019787:Zinc finger, PHD-finger	4	1.61	0.08	Q12830, Q92576, Q13342, Q9UK53	3.96
INTERPRO	IPR013083:Zinc finger, RING/FYVE/PHD-type	7	2.81	0.52	Q12830, Q6ZNL6, Q9BVI0, Q92576, Q13342, Q63HN8, Q9UK53	1.21
Annotation Cluster 3	Enrichment Score: 1.263926299712746					
INTERPRO	IPR001589:Actinin-type, actin-binding, conserved site	3	1.20	0.03	Q15149, P46939, Q03001	10.21
INTERPRO	IPR018159:Spectrin/alpha-actinin	3	1.20	0.05	Q15149, P46939, Q03001	8.10
SMART	SM00150:SPEC	3	1.20	0.06	Q15149, P46939, Q03001	7.48
SMART	SM00033:CH	4	1.61	0.06	Q15149, P46939, Q03001	4.39
INTERPRO	IPR001715:Calponin homology domain	4	1.61	0.07	Q13576, Q15149, P46939, Q03001	4.12
Annotation Cluster 4	Enrichment Score: 1.0212849341527332					
INTERPRO	IPR004087:K Homology domain	3	1.20	0.08	O00425, Q8IWZ3, P51116	6.18
SMART	SM00322:KH	3	1.20	0.10	O00425, Q8IWZ3, P51116	5.71
INTERPRO	IPR004088:K Homology domain, type 1	3	1.20	0.11	O00425, Q8IWZ3, P51116	5.34
Annotation Cluster 5	Enrichment Score: 0.7763036754078703					
INTERPRO	IPR003961:Fibronectin, type III	8	3.21	0.02	P54764, P16871, Q12860, P29323, Q12866, Q6VMQ6, Q8NI17, Q5U623	3.03

SMART	SM00060:FN3	5	2.01	0.15	P54764, Q12860, P29323, Q12866, Q8NI17	2.41
INTERPRO	IPR001245:Serine-threonine/tyrosine-protein kinase catalytic domain	4	1.61	0.26	P54764, P29323, Q12866, Q6P3R8	2.24
INTERPRO	IPR020635:Tyrosine-protein kinase, catalytic domain	3	1.20	0.29	P54764, P29323, Q12866	2.76
SMART	SM00219:TyrKc	3	1.20	0.33	P54764, P29323, Q12866	2.55
INTERPRO	IPR008266:Tyrosine-protein kinase, active site	3	1.20	0.34	P54764, P29323, Q12866	2.47
Annotation Cluster 6	Enrichment Score: 0.5982202356769865					
INTERPRO	IPR011990:Tetratricopeptide-like helical	7	2.81	0.06	Q5TEA6, Q9UIM3, Q8IYW2, Q2NKX8, O15550, Q9NRC1, Q9C0D5	2.51
INTERPRO	IPR013026:Tetratricopeptide repeat-containing domain	4	1.61	0.24	Q9UIM3, Q2NKX8, O15550, Q9C0D5	2.37
INTERPRO	IPR019734:Tetratricopeptide repeat	3	1.20	0.53	Q9UIM3, O15550, Q9C0D5	1.70
SMART	SM00028:TPR	3	1.20	0.54	Q9UIM3, O15550, Q9C0D5	1.66
Annotation Cluster 7	Enrichment Score: 0.5671560657083918					
INTERPRO	IPR014001:Helicase, superfamily 1/2, ATP-binding domain	4	1.61	0.16	Q9BX63, O95786, Q2NKX8, O00571	2.85
SMART	SM00487:DEXDc	4	1.61	0.19	Q9BX63, O95786, Q2NKX8, O00571	2.66
INTERPRO	IPR001650:Helicase, C-terminal	3	1.20	0.40	O95786, Q2NKX8, O00571	2.18
SMART	SM00490:HELICc	3	1.20	0.43	O95786, Q2NKX8, O00571	2.03

Annotation Cluster 8		Enrichment Score: 0.5387081191486811				
INTERPRO	IPR017441:Protein kinase, ATP binding site	9	3.61	0.11	Q9H2G2, P54764, Q13873, P36507, P29323, Q12866, O94804, Q6P3R8, Q13627	1.85
INTERPRO	IPR011009:Protein kinase-like domain	10	4.02	0.24	Q9H2G2, P54764, Q13873, P36507, P29323, Q12866, Q9BVS4, O94804, Q6P3R8, Q13627	1.47
INTERPRO	IPR001245:Serine-threonine/tyrosine-protein kinase catalytic domain	4	1.61	0.26	P54764, P29323, Q12866, Q6P3R8	2.24
INTERPRO	IPR000719:Protein kinase, catalytic domain	9	3.61	0.28	Q9H2G2, P36507, P29323, Q12866, O94804, Q6P3R8, Q13627	1.45
INTERPRO	IPR008271:Serine/threonine-protein kinase, active site	5	2.01	0.55	Q9H2G2, P36507, O94804, Q6P3R8, Q13627	1.25
SMART	SM00220:S_TKc	6	2.41	0.55	P54764, P36507, O94804, Q6P3R8, Q13627	1.21
Annotation Cluster 9		Enrichment Score: 0.4390631506338519				
SMART	SM00454:SAM	3	1.20	0.33	P54764, P29323, Q8WXI2	2.55
INTERPRO	IPR001660:Sterile alpha motif domain	3	1.20	0.34	P54764, P29323, Q8WXI2	2.50

INTERPRO	IPR013761:Sterile alpha motif/pointed domain	3	1.20	0.44	P54764, P29323, Q8WXI2	2.01
Annotation Cluster 10	Enrichment Score: 0.3487434308807288					
INTERPRO	IPR020894: Cadherin conserved site	3	1.20	0.42	Q8TAB3, Q6V0I7, Q9Y5E3	2.08
INTERPRO	IPR002126: Cadherin	3	1.20	0.44	Q8TAB3, Q6V0I7, Q9Y5E3	1.99
INTERPRO	IPR015919: Cadherin-like	3	1.20	0.45	Q8TAB3, Q6V0I7, Q9Y5E3	1.96
SMART	SM00112: CA	3	1.20	0.47	Q8TAB3, Q6V0I7, Q9Y5E3	1.87
Bound less in SSA- than controls						
Annotation Cluster 1	Enrichment Score: 2.363637810112168					
INTERPRO	IPR005821: Ion transport domain	8	2.60	0.00	Q9Y5Y9, Q15413, Q9H252, Q9HCX4, P21817, Q14571, Q9NSA2, O00555	4.79
INTERPRO	IPR013662: RyR/IP3R Homology associated domain	3	0.97	0.00	Q15413, P21817, Q14571	32.96
INTERPRO	IPR000699: Intracellular calcium-release channel	3	0.97	0.00	Q15413, P21817, Q14571	32.96
INTERPRO	IPR014821: Inositol 1,4,5-trisphosphate/ryanodine receptor	3	0.97	0.00	Q15413, P21817, Q14571	32.96
INTERPRO	IPR016093: MIR motif	3	0.97	0.01	Q15413, P21817, Q14571	19.78
SMART	SM00472: MIR	3	0.97	0.01	Q14571	16.15
Annotation Cluster 2	Enrichment Score: 1.8680972349032416					
INTERPRO	IPR019775: WD40 repeat, conserved site	8	2.60	0.01	Q04725, P57737, P53621, Q9C0C7, Q13685, Q8NFB4, Q9NVX2, P31146	3.59

INTERPRO	IPR001680:WD40 repeat	11	3.57	0.01	Q04725, P57737, P53621, Q8TBC3, Q9C0C7, Q13685, Q9Y597, Q8NFB4, Q9NVX2, Q9NW82 , P31146	2.64
UP_KW_D OMAIN	KW-0853~WD repeat	11	3.57	0.01	Q04725, P57737, P53621, Q8TBC3, Q9C0C7, Q13685, Q9Y597, Q8NFB4, Q9NVX2, Q9NW82 , P31146	2.51
INTERPRO	IPR015943:WD40/YVTN repeat-like- containing domain	12	3.90	0.02	Q04725, P57737, P53621, Q8TBC3, Q9C0C7, Q13685, Q9Y597, Q8NFB4, Q9NVX2, Q9NW82 , P31146	2.26
SMART	SM00320:WD40	11	3.57	0.03	Q04725, P57737, P53621, Q8TBC3, Q9C0C7, Q13685, Q9Y597, Q8NFB4, Q9NVX2, Q9NW82 , P31146	2.16
Annotation Cluster 3	Enrichment Score: 1.7335153638023264					
INTERPRO	IPR020683:Ankyrin repeat-containing domain	10	3.25	0.01	Q00653, Q9ULT8, Q9HCX4, Q8IYU2, A6QL63, Q9H9B1,	2.83

					A6QL64, Q9Y283, Q9UPS8, P25963	
					Q00653, Q9ULT8, Q9HCX4, Q8IYU2, A6QL63, Q9H9B1, A6QL64, Q9Y283, Q9UPS8, P25963	
INTERPRO	IPR002110:Ankyrin repeat	10	3.25	0.02	Q00653, Q9ULT8, Q9HCX4, Q8IYU2, A6QL63, Q9H9B1, A6QL64, Q9Y283, Q9UPS8, P25963	2.61
UP_KW_D OMAIN	KW-0040~ANK repeat	10	3.25	0.02	Q00653, Q9ULT8, Q9HCX4, Q8IYU2, A6QL63, Q9H9B1, A6QL64, Q9Y283, Q9UPS8, P25963	2.46
SMART	SM00248:ANK	10	3.25	0.04	Q00653, Q9ULT8, Q9HCX4, Q8IYU2, A6QL63, Q9H9B1, A6QL64, Q9Y283, Q9UPS8, P25963	2.18
Annotation Cluster 4	Enrichment Score: 1.5003640333214088					
INTERPRO	IPR002219:Protein kinase C-like, phorbol ester/diacylglycerol binding	5	1.62	0.02	P04049, Q9Y5S2, Q9HBL0, Q8NEN9, P41743	4.92
SMART	SM00109:C1	5	1.62	0.03	P04049, Q9Y5S2, Q9HBL0, Q8NEN9, P41743	4.08
INTERPRO	IPR020454:Diacylglycerol/phorbol-ester binding	3	0.97	0.05	P04049, Q9Y5S2, P41743	8.24
Annotation Cluster 5	Enrichment Score: 1.3826247749650697					

INTERPRO	IPR014837:EF-hand, Ca insensitive	3	0.97	0.00	O43707, P02549, P12814	32.96
INTERPRO	IPR002017:Spectrin repeat	4	1.30	0.01	O43707, P02549, P12814, Q03001	10.99
INTERPRO	IPR018159:Spectrin/alpha-actinin	4	1.30	0.01	O43707, P02549, P12814, Q03001	9.09
SMART	SM00150:SPEC	4	1.30	0.02	Q03001 Q15413, O43707, P21817, Q86YW0, Q969Q6, P02549, P12814, Q03001,	7.43
INTERPRO	IPR011992:EF-hand-like domain	10	3.25	0.03	O43149, Q8NFB8 O43707,	2.35
INTERPRO	IPR001589:Actinin-type, actin-binding, conserved site	3	0.97	0.05	P12814, Q03001 Q15413, O43707, Q86YW0, P02549, P12814, Q03001,	8.60
INTERPRO	IPR002048:EF-hand domain	8	2.60	0.07	O43149, Q8NFB8 O43707, P12814, Q8IVL1,	2.22
SMART	SM00033:CH	4	1.30	0.12	Q03001 O43707, P12814, Q8IVL1,	3.26
INTERPRO	IPR001715:Calponin homology domain	4	1.30	0.12	Q03001 O43707, Q969Q6, P12814, Q03001,	3.26
INTERPRO	IPR018247:EF-Hand 1, calcium-binding site	5	1.62	0.31	Q8NFB8 O43707, P12814, Q03001,	1.77
SMART	SM00054:EFh	4	1.30	0.54	O43149	1.41

Annotation Cluster 6		Enrichment Score: 1.2472536043459177				
					Q9H251, Q12864, O95206, Q9Y5H0, Q9HC56,	
INTERPRO	IPR020894: Cadherin conserved site	6	1.95	0.03	P55291, Q9H251, Q12864, O95206, Q9Y5H0, Q9HC56,	3.50
INTERPRO	IPR002126: Cadherin	6	1.95	0.03	P55291, Q9H251, Q12864, O95206, Q9Y5H0, Q9HC56,	3.35
INTERPRO	IPR015919: Cadherin-like	6	1.95	0.04	P55291, Q9H251, Q12864, O95206, Q9Y5H0, Q9HC56,	3.27
SMART	SM00112: CA	6	1.95	0.06	P55291, O95206, Q9Y5H0, Q9HC56,	2.78
INTERPRO	IPR013164: Cadherin, N-terminal	3	0.97	0.26	Q9HC56	3.04
Annotation Cluster 7		Enrichment Score: 1.1111245771694727				
					Q5HYC2, Q86U86, Q92793,	
INTERPRO	IPR001487: Bromodomain	4	1.30	0.03	Q15059, Q86U86, Q92793,	6.13
INTERPRO	IPR018359: Bromodomain, conserved site	3	0.97	0.06	Q15059, Q86U86, Q92793,	7.61
UP_KW_D OMAIN	KW-0103~Bromodomain	3	0.97	0.13	Q15059, Q86U86, Q92793,	4.87
SMART	SM00297: BROMO	3	0.97	0.18	Q15059	3.85
Annotation Cluster 8		Enrichment Score: 1.0226456056475244				
					Q86T24, Q8TBC3, A6QL63, Q9Y597, Q9UPP5, O15060,	
INTERPRO	IPR000210: BTB/POZ-like	7	2.27	0.06	Q9NSA2	2.54

INTERPRO	IPR011333:BTB/POZ fold	7	2.27	0.07	Q86T24, Q8TBC3, A6QL63, Q9Y597, Q9UPP5, O15060, Q9NSA2	2.42
SMART	SM00225:BTB	7	2.27	0.11	Q86T24, Q8TBC3, A6QL63, Q9Y597, Q9UPP5, O15060, Q9NSA2	2.13
INTERPRO	IPR003131:Potassium channel tetramerisation-type BTB domain	3	0.97	0.18	Q8TBC3, Q9Y597, Q9NSA2	3.88
Annotation Cluster 9	Enrichment Score: 0.9572427008547313					
INTERPRO	IPR003593:AAA+ ATPase domain	6	1.95	0.06	Q96S55, Q8NB90, P53384, Q8IVL1, Q86UK0, Q9BZC7	2.83
SMART	SM00382:AAA	6	1.95	0.12	Q96S55, Q8NB90, P53384, Q8IVL1, Q86UK0, Q9BZC7	2.31
INTERPRO	IPR003959:ATPase, AAA-type, core	3	0.97	0.19	Q96S55, Q8NB90, Q9BZC7	3.80
Annotation Cluster 10	Enrichment Score: 0.7995729688592799					
INTERPRO	IPR003595:Protein-tyrosine phosphatase, catalytic	4	1.30	0.07	P26045, Q9H3S7, Q12913, Q9HBLO	4.19
SMART	SM00404:PTPc_motif	4	1.30	0.11	P26045, Q9H3S7, Q12913, Q9HBLO	3.42
INTERPRO	IPR000242:Protein-tyrosine phosphatase, receptor/non-receptor type	3	0.97	0.11	P26045, Q9H3S7, Q12913	5.20
SMART	SM00194:PTPc	3	0.97	0.15	P26045, Q9H3S7, Q12913	4.37
INTERPRO	IPR016130:Protein-tyrosine phosphatase, active site	3	0.97	0.32	P26045, Q9H3S7, Q12913	2.60

INTERPRO	IPR000387:Protein-tyrosine/Dual specificity phosphatase	3	0.97	0.39	P26045, Q9H3S7, Q12913	2.25
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Supplemental Table D. Coefficient of variation (CV) of replicates				
Peptide	All Samples		Low OD (<0.05 OD)	
	Average %CV	Median %CV	Average %CV	Median %CV
KNL1	7.98	5.48	8.43	5.70
LRBA	10.13	5.63	11.14	7.00
NPAT	7.81	5.08	8.57	5.66
RESF1	8.75	6.57	9.50	7.10
TEX15	9.01	5.48	9.75	7.18
BRWD1	8.51	5.00	8.71	5.60
SLK	8.58	5.28	8.94	6.26
PDZD8	8.00	5.62	8.86	5.74
HDAC9	7.37	5.13	8.10	5.61
CYP7A1	8.61	6.51	10.10	7.85
GPAT1	8.81	4.53	9.99	5.72
DTD2	4.49	3.07	9.19	4.40
SCRB2	4.89	3.53	5.04	3.90
SO1B1	6.99	4.25	8.52	5.75
LRCC1	7.25	5.19	7.66	5.42
Average	7.81	5.09	8.83	5.93
Median	8.00	5.19	8.86	5.72

The average and median CV are shown for all sample replicates and for replicates with low ODs (less than 0.05)

Supplemental Table E. Demographics of positive subjects						
	DTD2 binding by quartiles			Positive/negative patients by conservative model threshold*		
	SjD Top Quartile (n=25)	SjD bottom 3 Quartiles (n=51)	p-value	Positive SjD (n=5)	Negative SjD (n=71)	p-value
Age mean (SD)	55 (12)	55 (12)	0.70	59 (9)	55 (12)	0.4
Female n (%)	21 (84)	44 (86)	0.79	5 (100)	60 (85)	0.2
Race n (%)			0.59			0.55
White	12 (48)	25 (49)		3 (60)	34 (48)	
Asian	12 (48)	19 (37)		1 (20)	30 (42)	
African American	0	0		0	0	
Hispanic Ethnicity	1 (4)	7 (14)		1 (20)	7 (10)	
Clinical Metrics						
OSS \geq 5 n (%)	17 (68)	12 (24)	0.44	4 (80)	52 (73)	0.73
Schirmer's \leq 5 mm	12 (48)	23 (48)	0.19	3 (60)	36 (53)	0.76
UWS \leq 5 mL/5min	15 (60)	37 (73)	0.27	5 (100)	47 (66)	0.047
Lab metrics						
ANA positive \geq 1:320 n (%)	6 (24)	16 (31)	0.50	5 (100)	17 (24)	0.0003
Anti-SSB positive n (%)	1 (4)	1 (2)	0.61	0	2 (3)	0.6
IgG mg/dL mean (SD)	1611 (992)	1212 (593)	0.07	1523 (306)	1524 (306)	0.28
Platelet k/ μ L mean (SD)	258 (62)	244 (67)	0.37	232 (34)	249 (67)	0.35
RF positive n (%)	12 (48)	19 (37)	0.37	1 (20)	30 (42)	0.31
Histopathology						
Focus score \geq 1 n (%)	25 (100)	51 (100)	.	5 (100)	71 (100)	.

OSS=ocular staining score; UWS=unstimulated whole saliva; ANA=anti-nuclear antibody; IgG=Immunoglobulin G; RF=Rheumatoid factor. *=a modeling threshold using the selected predictive model, where we can select thresholds that are either highly specific or highly sensitive, potentially confirming a SSA- SjD diagnosis without the need for biopsy in 57% of participants (n=45/76) or avoiding the need for a biopsy in 13% of controls that will not achieve a SjD diagnosis (n=15/116)