

SUPPLEMENTARY INFORMATION

Proteomics Unravels the Regulatory Mechanisms in Human Tears Following Acute Renouncement of Contact Lens Use: A Comparison between Hard and Soft Lenses

Caroline Manicam^{§*}, Natarajan Perumal[§], Joanna Wasielica-Poslednik, Yong Cajetan

Ngongkole, Alexandra Tschäbunin, Marcel Sievers, Walter Lisch, Norbert Pfeiffer, Franz H. Grus and Adrian Gericke

Department of Ophthalmology, University Medical Centre of the Johannes Gutenberg University Mainz, 55131 Mainz, Germany.

[§] Both authors contributed equally to this work

***Corresponding author:**

Dr. Caroline Manicam

Department of Ophthalmology,

University Medical Centre of the Johannes Gutenberg

University Mainz,

Langenbeckstr. 1,

55131 Mainz, Germany.

E-mail: cmjc_82@yahoo.com

Tel: +49 6131 17 8276

ORCID, Caroline Manicam: 0000-0001-5891-1155

ORCID, Natarajan Perumal: 0000-0002-2612-5907

Table S1 MaxQuant Parameters

MaxQuant Parameter	Value
Version	1.5.2.8
User name	aulab-p
Machine name	WS-AU-62214
Date of writing	06/29/2017 01:39:40
Fixed modifications	Carbamidomethyl (C)
Decoy mode	revert
Special AAs	KR
Include contaminants	True
MS/MS tol. (FTMS)	20 ppm
Top MS/MS peaks per 100 Da. (FTMS)	12
MS/MS deisotoping (FTMS)	True
MS/MS tol. (ITMS)	0.5 Da
Top MS/MS peaks per 100 Da. (ITMS)	8
MS/MS deisotoping (ITMS)	False
MS/MS tol. (TOF)	40 ppm
Top MS/MS peaks per 100 Da. (TOF)	10
MS/MS deisotoping (TOF)	True
MS/MS tol. (Unknown)	0.5 Da
Top MS/MS peaks per 100 Da. (Unknown)	8
MS/MS deisotoping (Unknown)	False
PSM FDR	0.01
Protein FDR	0.01
Site FDR	0.01
Use Normalized Ratios For Occupancy	True
Min. peptide Length	6
Min. score for unmodified peptides	0
Min. score for modified peptides	40
Min. delta score for unmodified peptides	0
Min. delta score for modified peptides	6
Min. unique peptides	0
Min. razor peptides	1
Min. peptides	1
Use only unmodified peptides and	True
Modifications included in protein quantification	Acetyl (Protein N-term);Oxidation (M)
Peptides used for protein quantification	Razor
Discard unmodified counterpart peptides	True
Min. ratio count	2
Re-quantify	False
Use delta score	False
iBAQ	True
iBAQ log fit	True
Match between runs	True
Matching time window [min]	5
Alignment time window [min]	20
Find dependent peptides	False
Fasta file	Database - Uniprot; Taxonomy - Human; Date - 10 July 2017
Labeled amino acid filtering	True
Site tables	Oxidation (M)Sites.txt
Decoy mode	revert
Special AAs	KR
Include contaminants	True
RT shift	False
Advanced ratios	True
AIF correlation	0.47
First pass AIF correlation	0.8
AIF topx	20
AIF min mass	0
AIF SIL weight	4
AIF ISO weight	2
AIF iterative	True
AIF threshold FDR	0.01

Table S2 List of identified fear proteins

Protein IDs	Protein names	Gene names	Razor + unique peptides	Unique peptides	Sequence coverage (%)	Unique + razor sequence coverage (%)	Mid. weight (kDa)	Sequence length	Score	Intensity	LFO intensity CTR_H1_R1	LFO intensity CTR_H1_R2	LFO intensity CTR_H1_R3	LFO intensity HARB_H1_R1	LFO intensity HARB_H1_R2	LFO intensity HARB_H1_R3	LFO intensity HARB_H2_R1	LFO intensity HARB_H2_R2	LFO intensity HARB_H2_R3	LFO intensity HARB_H3_R1	LFO intensity HARB_H3_R2	LFO intensity HARB_H3_R3	LFO intensity S0F_H1_R1	LFO intensity S0F_H1_R2	LFO intensity S0F_H1_R3	LFO intensity S0F_H2_R1	LFO intensity S0F_H2_R2	LFO intensity S0F_H2_R3	LFO intensity S0F_H3_R1	LFO intensity S0F_H3_R2	LFO intensity S0F_H3_R3			
P19466	14-3-3 protein beta 1b	YWHAH	7	57	35.8	35.8	28.5	236	128	46019000	20781000	15377000	22770000	32160000	35717000	34317000	16614000	21202000	18300000	16290000	14260000	21541000	25507000	11552000	0	0	0	0	0	0	0			
P04828	14-3-3 protein gamma	YWHAJ	5	5	32.4	32.4	25.5	292	252	2720	40623000	8151000	6972000	62747000	5885000	4539000	61571000	52423000	85403000	8776000	6274000	86012000	86022000	4330000	0	0	0	0	0	0	0			
P19467	14-3-3 protein zeta	YWHAZ	4	4	32.4	32.4	25.5	278	122	2840	18910000	14210000	15100000	28410000	28410000	18172000	31672000	31672000	28410000	31672000	31672000	28410000	31672000	31672000	28410000	31672000	31672000	28410000	31672000	31672000	28410000			
P04104	14-3-3 protein zeta delta	YWHAZ	5	5	34.3	34.3	26.9	265	120	13000000	26078000	25078000	38530000	35880000	26666000	34360000	37060000	29488000	29488000	29488000	29244000	29147000	30017000	3440000	0	0	0	0	0	0	0			
P05968	60S acidic phospholipase P1	PLD3	1	1	15.4	15.4	11.4	114	114	14000000	14000000	14000000	14000000	14000000	14000000	14000000	14000000	14000000	14000000	14000000	14000000	14000000	14000000	14000000	14000000	14000000	14000000	14000000	14000000	14000000	14000000	14000000		
P25239	6-phosphogluconate dehydrogenase, decarboxylating	PCID	4	4	12.4	12.4	14.4	124	51.1	487	114.5	20911000	15467000	17548000	31745000	37749000	48991000	28465000	43598000	91724000	45796000	26623000	90413000	22179000	13999000	10077000	0	0	0	0	0	0		
P05136	6-phosphofruktose-6-phosphatase	PFKFB3	2	2	14.3	14.3	14.3	143	27.5	258	70	10756000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
P08133	Actin, alpha classed muscle	ACTA1	1	1	28.4	28.4	4.2	42	42	377	60	57841000	34164000	28491000	8728000	11988000	10770000	73284000	80247000	4769000	80247000	4769000	80247000	4769000	80247000	4769000	80247000	4769000	80247000	4769000	80247000	4769000	80247000	
P07099	Actin, cytoplasmic 1	ACTB	1	1	39.5	39.5	4.2	42	42	377	5.5	60022000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
P04201	Actin, cytoplasmic 2	ACTG1	18	18	29.5	29.5	4.2	42	42	377	51.8	12300000	14310000	15483000	4.5	20337000	20337000	14220000	15649000	7520000	16571000	96483000	11242000	96483000	11242000	96483000	11242000	96483000	11242000	96483000	11242000	96483000		
P01518	Adenylyl cyclase-associated protein	CAP1	1	1	4.8	4.8	4.8	48	31.9	67	5.4	5849000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
P14580	Adrenomedullin (ADM) [NADP+ reductase]	ADM	1	5	20.9	20.9	20.9	209	48.9	319	44518000	47719000	44662000	17927000	18899000	16200000	10164000	14014000	14099000	12249000	15470000	15470000	15470000	15470000	15470000	15470000	15470000	15470000	15470000	15470000	15470000	15470000	15470000	
P08848	Adrenomedullin (ADM) [NADP+ reductase]	ADM1A1	1	5	14.1	14.1	14.1	141	51.9	488	96891000	97731000	11171000	3733000	4117000	4117000	10169000	13717000	11174000	11174000	11174000	11174000	11174000	11174000	11174000	11174000	11174000	11174000	11174000	11174000	11174000	11174000	11174000	
P08828	Adrenomedullin (ADM) [NADP+ reductase]	ADM1C1	4	4	20.7	20.7	20.7	207	36.8	332	16.2	20471000	14466000	24617000	26198000	44077000	4199000	53702000	28722000	43454000	37026000	3186000	4074000	4346000	4077000	4346000	4077000	4346000	4077000	4346000	4077000	4346000	4077000	
P07063	Alpha-1 Lactid phosphoglycerin 1	ORM1	8	5	39.3	39.3	36.9	363	20.1	139.4	51490000	53348000	50420000	65811000	58814000	46152000	14393000	14393000	14393000	14393000	67866000	67866000	67866000	67866000	67866000	67866000	67866000	67866000	67866000	67866000	67866000	67866000	67866000	
P19052	Alpha-1 Lactid phosphoglycerin 2	ORM2	2	2	25.9	25.9	13.4	134	23.6	20.1	66.2	49141000	39797000	4588000	4928000	4276000	11404000	2366000	6000000	6000000	6000000	6000000	6000000	6000000	6000000	6000000	6000000	6000000	6000000	6000000	6000000	6000000	6000000	
P01011	Alpha-2-macroglobulin	SERPINA1	10	10	22.7	22.7	22.7	227	1007.2	14861000	14861000	14861000	14861000	14861000	14861000	14861000	14861000	14861000	14861000	14861000	14861000	14861000	14861000	14861000	14861000	14861000	14861000	14861000	14861000	14861000	14861000	14861000	14861000	14861000
P10029	Alpha-2-macroglobulin	SERPINA1	30	30	67.9	67.9	46.7	418	32.3	205960000	226290000	261980000	258100000	229600000	214000000	226010000	202600000	166610000	157400000	340040000	289220000	217940000	130880000	137000000	103000000	618000000	349800000	349800000	349800000	349800000	349800000	349800000	349800000	
P04177	Alpha-2-macroglobulin	ALB	6	6	21.6	21.6	21.6	216	40.5	98.6	94511000	11883000	26170000	32353000	15253000	14335000	9003000	9660000	11661000	15740000	34004000	289220000	217940000	130880000	618000000	349800000	349800000	349800000	349800000	349800000	349800000	349800000	349800000	
P02785	Alpha-2-macroglobulin	ALB	30	30	35.1	35.1	35.1	351	100.7	267	15570000	14420000	19710000	16019000	14420000	9442000	9442000	9442000	9442000	9442000	9442000	9442000	9442000	9442000	9442000	9442000	9442000	9442000	9442000	9442000	9442000	9442000	9442000	9442000
P01023	Alpha-2-macroglobulin	ALB	35	35	34.1	34.1	34.1	341	163.3	1474	323.3	439740000	275210000	301200000	310200000	278820000	30033000	30033000	30033000	30033000	30033000	30033000	30033000	30033000	30033000	30033000	30033000	30033000	30033000	30033000	30033000	30033000	30033000	30033000
P04178	Alpha-actinin-4	ACTN4	10	10	15.2	15.2	10.9	109	9.1	134	2890000	8600000	8600000	8600000	8600000	8600000	8600000	8600000	8600000	8600000	8600000	8600000	8600000	8600000	8600000	8600000	8600000	8600000	8600000	8600000	8600000	8600000	8600000	8600000
P06733	Alpha-actinin-4	ACTN4	29	29	25.9	25.9	25.9	259	42.4	62.4	147970000	109270000	62.2	147970000	21599000	16139000	16139000	16139000	16139000	16139000	16139000	16139000	16139000	16139000	16139000	16139000	16139000	16139000	16139000	16139000	16139000	16139000	16139000	16139000
P01019	Anticoagulant	AIT1	6	6	19.8	19.8	19.8	198	35.2	485	487	76681000	18222000	3756000	3756000	3756000	3756000	3756000	3756000	3756000	3756000	3756000	3756000	3756000	3756000	3756000	3756000	3756000	3756000	3756000	3756000	3756000	3756000	
P08681	AnkR1	ANKK1	17	17	44.8	44.8	34.8	348	32.3	70899000	152230000	140000000	171600000	171600000	171600000	171600000	171600000	171600000	171600000	171600000	171600000	171600000	171600000	171600000	171600000	171600000	171600000	171600000	171600000	171600000	171600000	171600000	171600000	171600000
P07555	AnkR2	ANKK2	19	19	64.0	64.0	44.0	440	38.6	339	323.3	47272000	38234000	38234000	10588000	13047000	10874000	3768000	10240000	36081000	36081000	36081000	36081000	36081000	36081000	36081000	36081000	36081000	36081000	36081000	36081000	36081000	36081000	36081000
P14249	AnkR3	ANKK3	3	3	12.4	12.4	12.4	124	36.4	323	30.7	4370000	5961000	16014000	60142000	7222000	85234000	7322000	3300000	3171000	3869000	64857000	10253000	3842000	2919000	4609000	0	0	0	0	0	0	0	
P06525	AnkR4	ANKK4	10	10	29.9	29.9	29.9	299	41.4	459	31000000	14732000	14732000	14732000	14732000	14732000	14732000	14732000	14732000	14732000	14732000	14732000	14732000	14732000	14732000	14732000	14732000	14732000	14732000	14732000	14732000	14732000	14732000	14732000
P08785	AnkR5	ANKK5	10	10	40.6	40.6	35.9	359	40.6	35.9	32.0	156.5	14817000	2419000	2538000	35481000	35481000	35481000	35481000	35481000	35481000	35481000	35481000	35481000	35481000	35481000	35481000	35481000	35481000	35481000	35481000	35481000	35481000	35481000
P09994	Anterior gradient protein 2 homolog	AGR2	4	4	30.3	30.3																												

Table S3 The degree of variances in the tear proteome between the (a) replicates and (b) groups assessed by Pearson's correlation analysis.

(a)

Name	LFQ intensity CTRL_R1	LFQ intensity CTRL_R2	LFQ intensity CTRL_R3	LFQ intensity Hard A_R1	LFQ intensity Hard A_R2	LFQ intensity Hard A_R3	LFQ intensity Hard B_R1	LFQ intensity Hard B_R2	LFQ intensity Hard B_R3	LFQ intensity Soft A_R1	LFQ intensity Soft A_R2	LFQ intensity Soft A_R3	LFQ intensity Soft B_R1	LFQ intensity Soft B_R2	LFQ intensity Soft B_R3
LFQ intensity CTRL_R1	NaN	0.99	0.99	0.92	0.90	0.98	0.99	0.98	0.97	0.98	0.98	0.99	0.98	0.97	0.97
LFQ intensity CTRL_R2	0.99	NaN	1.00	0.95	0.93	0.98	0.99	0.99	0.99	0.97	0.97	0.98	0.98	0.96	0.97
LFQ intensity CTRL_R3	0.99	1.00	NaN	0.94	0.93	0.98	0.99	0.98	0.98	0.97	0.96	0.98	0.97	0.96	0.96
LFQ intensity Hard A_R1	0.92	0.95	0.94	NaN	0.98	0.95	0.95	0.95	0.96	0.89	0.88	0.91	0.90	0.87	0.90
LFQ intensity Hard A_R2	0.90	0.93	0.93	0.98	NaN	0.95	0.94	0.95	0.96	0.86	0.86	0.89	0.86	0.82	0.85
LFQ intensity Hard A_R3	0.98	0.98	0.98	0.95	0.95	NaN	0.99	0.99	0.98	0.97	0.97	0.98	0.95	0.93	0.94
LFQ intensity Hard B_R1	0.99	0.99	0.99	0.95	0.94	0.99	NaN	0.99	0.99	0.97	0.97	0.98	0.97	0.96	0.96
LFQ intensity Hard B_R2	0.98	0.99	0.98	0.95	0.95	0.99	0.99	NaN	0.99	0.96	0.96	0.98	0.96	0.94	0.95
LFQ intensity Hard B_R3	0.97	0.99	0.98	0.96	0.96	0.98	0.99	0.99	NaN	0.95	0.94	0.96	0.95	0.93	0.94
LFQ intensity Soft A_R1	0.98	0.97	0.97	0.89	0.86	0.97	0.97	0.96	0.95	NaN	0.99	1.00	0.99	0.98	0.97
LFQ intensity Soft A_R2	0.98	0.97	0.96	0.88	0.86	0.97	0.97	0.96	0.94	0.99	NaN	1.00	0.98	0.97	0.96
LFQ intensity Soft A_R3	0.99	0.98	0.98	0.91	0.89	0.98	0.98	0.98	0.96	1.00	1.00	NaN	0.98	0.97	0.97
LFQ intensity Soft B_R1	0.98	0.98	0.97	0.90	0.86	0.95	0.97	0.96	0.95	0.99	0.98	0.98	NaN	0.99	0.99
LFQ intensity Soft B_R2	0.97	0.96	0.96	0.87	0.82	0.93	0.96	0.94	0.93	0.98	0.97	0.97	0.99	NaN	0.99
LFQ intensity Soft B_R3	0.97	0.97	0.96	0.90	0.85	0.94	0.96	0.95	0.94	0.97	0.96	0.97	0.99	0.99	NaN

(b)

	LFQ intensity CTRL	LFQ intensity Hard A	LFQ intensity Hard B	LFQ intensity Soft A	LFQ intensity Soft B
LFQ intensity CTRL	0.995 ± 0.003	0.946 ± 0.028	0.984 ± 0.007	0.976 ± 0.008	0.968 ± 0.007
LFQ intensity Hard A	0.946 ± 0.028	0.959 ± 0.017	0.963 ± 0.020	0.911 ± 0.048	0.890 ± 0.046
LFQ intensity Hard B	0.984 ± 0.007	0.963 ± 0.020	0.993 ± 0.001	0.964 ± 0.014	0.950 ± 0.013
LFQ intensity Soft A	0.976 ± 0.008	0.911 ± 0.048	0.964 ± 0.014	0.995 ± 0.001	0.975 ± 0.009
LFQ intensity Soft B	0.968 ± 0.007	0.890 ± 0.046	0.950 ± 0.013	0.975 ± 0.009	0.993 ± 0.002

Table S4 Differentially expressed tear proteins restored to normal or near normal levels following renouncement of hard contact lens

Protein ID	Protein name	Gene name	Hard A/CTRL	Hard A/CTRL	Hard B/Hard A	Hard B/Hard A
			t-test p value	t-test difference	t-test p value	t-test difference
P80303	Nucleobindin-2	NUCB2	6.74E-08	-23.1204	9.37E-08	22.8957
Q96LW4	DNA-directed primase/polymerase protein	PRIMPOL	5.13E-08	-22.2765	1.23E-12	21.7722
Q9GZZ8	Extracellular glycoprotein lacritin	LACRT	9.64E-06	-3.27048	0.000127961	0.946314
P0DP08	Ig heavy chain V-II region NEWM	IGHV4-4	0.0459192	-1.66699	0.0184549	2.23576
P01833	Polymeric immunoglobulin receptor	PIGR	0.000735725	-1.0122	0.00135836	0.705582
Q96DA0	Zymogen granule protein 16 homolog B	ZG16B	0.00691179	-0.642043	0.0400133	0.549627
P02787	Serotransferrin	TF	0.0485373	0.485277	0.00901612	-0.806985
P12429	Annexin A3	ANXA3	0.01255	0.557257	0.0203503	-0.826279
P60174	Triosephosphate isomerase	TPI1	0.0445722	0.561307	0.0133209	-0.731908
P01024	Complement C3	C3	0.000216808	0.58034	0.00276314	-0.508984
P06312	Ig kappa chain V-IV region	IGKV4-1	0.0441418	0.662347	0.0271293	-0.530631
P01008	Antithrombin-III	SERPINC1	0.049337	0.692117	0.0302766	-0.792411
P40925	Malate dehydrogenase, cytoplasmic	MDH1	0.00705303	0.701432	0.0186406	-0.522416
Q99935	Proline-rich protein 1	PROL1	0.0238565	0.707614	0.00497106	-1.10771
Q13228	Selenium-binding protein 1	SELENBP1	0.0152762	0.746237	0.0333095	-0.636588

P31946	14-3-3 protein beta/alpha	YWHAB	0.00991322	0.80884	0.0026455	-0.848101
P01034	Cystatin-C	CST3	0.00107646	0.811762	0.000723647	-1.56093
P04080	Cystatin-B	CSTB	0.044042	0.84649	0.010676	-1.40647
P01834	Ig kappa chain C region	IGKC	0.0233074	0.962351	0.012219	-1.17825
P00352	Retinal dehydrogenase 1	ALDH1A1	0.000486025	0.999151	0.0221524	-0.385969
Q04828	Aldo-keto reductase family 1 member C1	AKR1C1	0.00344507	1.00913	0.0224532	-0.82121
P10599	Thioredoxin	TXN	0.00460263	1.14729	0.0337251	-0.717325
P21980	Protein-glutamine gamma-glutamyltransferase 2	TGM2	0.00923312	1.25514	0.00771404	-1.23838
P01023	Alpha-2-macroglobulin	A2M	0.00189417	1.38653	0.00033579	-1.75099
P15311	Ezrin	EZR	0.00165127	1.69643	0.0305612	-1.23247
P98160	Basement membrane-specific heparan sulfate proteoglycan core protein	HSPG2	0.00133399	1.70064	0.0162177	-0.442127
P04406	Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	3.73E-05	1.75228	0.0340754	-0.522034
P14550	Alcohol dehydrogenase [NADP(+)]	AKR1A1	1.07E-05	1.95248	0.0336889	-0.597106
P09467	Fructose-1,6-bisphosphatase 1	FBP1	0.000140307	2.50008	0.017434	-1.15092
P30041	Peroxiredoxin-6	PRDX6	0.00126659	3.07181	0.00233273	-1.63297

Table S5 Differentially expressed tear proteins that were restored to normal or near normal levels following renouncement of soft contact lenses

Protein ID	Protein name	Gene name	Soft A/CTRL	Soft A/CTRL	Soft B/Soft A	Soft B/Soft A
			t-test p value	t-test difference	t-test p value	t-test difference
P20061	Transcobalamin-1	TCN1	0.000536241	-1.39779	0.0194972	1.14146
Q13421	Mesothelin	MSLN	0.000560973	-1.08202	0.019067	0.381095
Q96DA0	Zymogen granule protein 16 homolog B	ZG16B	0.00537381	-0.901301	0.025062	0.412584
Q99935	Proline-rich protein 1	PROL1	0.00387322	-0.895296	0.00500459	0.847507
P01876	Ig alpha-1 chain C region	IGHA1	0.00207708	-0.850877	0.00566909	0.842374
P10909	Clusterin	CLU	0.00344228	-0.602778	0.0134948	0.472013
P25311	Zinc-alpha-2-glycoprotein	AZGP1	0.00251442	-0.59874	0.00775825	0.634696
P02766	Transthyretin	TTR	0.0129762	-0.596889	0.00301547	0.78727
O75556	Mammaglobin-B	SCGB2A1	0.00134163	-0.555702	0.0309456	0.449009
P07858	Cathepsin B	CTSB	0.0194062	-0.519465	0.00723964	0.853257
P01833	Polymeric immunoglobulin receptor	PIGR	0.00349671	-0.510782	0.0066351	0.414106
P61626	Lysozyme C	LYZ	0.0329406	-0.479423	0.00286996	1.01167

P09211	Glutathione S-transferase P	GSTP1	0.000255522	0.379524	0.0465344	-0.644709
P06733	Alpha-enolase	ENO1	0.0156537	0.472191	0.0332919	-0.764221
P02749	Beta-2-glycoprotein 1	APOH	0.00308197	0.513513	0.00185552	-0.639037
Q06830	Peroxiredoxin-1	PRDX1	0.0392907	0.517227	0.0492212	-0.439258
P01859	Ig gamma-2 chain C region	IGHG2	0.00606619	0.545203	0.0310358	-0.280219
P01009	Alpha-1-antitrypsin	SERPINA1	0.00105742	0.677276	0.0178656	-0.313815
P01008	Antithrombin-III	SERPINC1	0.0343189	0.70122	0.0379374	-0.320943
P01857	Ig gamma-1 chain C region	IGHG1	0.000484682	0.748166	0.00241463	-0.378359
P01019	Angiotensinogen	AGT	0.0127924	0.784323	0.00433753	-0.651071
P30086	Phosphatidylethanolamine-binding protein 1	PEBP1	8.21E-05	0.834803	0.0326834	-0.24179
P04083	Annexin A1	ANXA1	0.00388359	0.904558	0.0286612	-1.04397
P02774	Vitamin D-binding protein	GC	0.00243967	0.906768	0.00659062	-0.693193
P04406	Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	0.00488883	0.919466	0.0337512	-0.709533

P01023	Alpha-2-macroglobulin	A2M	0.0105935	1.15943	0.00331981	-1.77033
P19823	Inter-alpha-trypsin inhibitor heavy chain H2	ITIH2	0.00882564	1.2231	0.0145121	-1.49804
P07355	Annexin A2	ANXA2	0.000100754	1.36391	0.00972864	-1.23912
P02787	Serotransferrin	TF	1.28E-05	1.4175	3.18E-05	-0.767886
P09467	Fructose-1,6-bisphosphatase 1	FBP1	0.000398519	1.62834	4.46E-09	-22.2984
P30044	Peroxiredoxin-5, mitochondrial	PRDX5	0.00469036	1.63648	0.00259444	-1.45671
P14550	Alcohol dehydrogenase [NADP(+)]	AKR1A1	0.000139363	1.6585	0.00325967	-1.03635
P36955	Pigment epithelium-derived factor	SERPINF1	3.49E-08	18.2145	3.49E-08	-18.2145
P07237	Protein disulfide-isomerase	P4HB	6.32E-09	19.0275	6.32E-09	-19.0275
Q9P1F3	Costars family protein ABRACL	ABRACL	1.77E-07	19.6917	1.77E-07	-19.6917
P31941	DNA dC->dU-editing enzyme APOBEC-3A	APOBEC3A	9.82E-08	20.3161	9.82E-08	-20.3161
P01717	Ig lambda chain V-IV region Hil	IGLV3-10	1.75E-08	20.6645	1.75E-08	-20.6645
P07339	Cathepsin D	CTSD	4.27E-07	20.8041	4.27E-07	-20.8041

P31947	14-3-3 protein sigma	SFN	1.25E-08	21.3169	1.25E-08	-21.3169
P25815	Protein S100-P	S100P	9.51E-08	21.5193	0.0157788	-1.27653
P06744	Glucose-6-phosphate isomerase	GPI	8.55E-11	21.5446	8.55E-11	-21.5446
P02753	Retinol-binding protein 4	RBP4	5.72E-06	22.1481	5.72E-06	-22.1481
P01594	Ig kappa chain V-I region AU		1.43E-10	22.1812	1.43E-10	-22.1812

Table S6 Differentially expressed tear proteins that were not restored to normal or near normal levels following renouncement of hard contact lenses

Protein ID	Protein name	Gene name	Hard A/CTRL	Hard A/CTRL	Hard B/Hard A	Hard B/Hard A
			t-test p value	t-test difference	t-test p value	t-test difference
P28325	Cystatin-D	CST5	1.13E-10	-20.5094	1	0
P02533	Keratin, type I cytoskeletal 14	KRT14	0.0424658	-1.83581	0.627139	0.150271
P35527	Keratin, type I cytoskeletal 9	KRT9	0.0256558	-1.80655	0.291764	0.605708
P04217	Alpha-1B-glycoprotein	A1BG	0.0381718	-1.00382	0.781421	-0.0953973
Q13421	Mesothelin	MSLN	0.00636721	-0.928525	0.95663	0.0104383
P25311	Zinc-alpha-2-glycoprotein	AZGP1	0.0313137	-0.921553	0.979942	-0.0225919
O75556	Mammaglobin-B	SCGB2A1	0.0405104	-0.809256	0.979318	0.0101598
P01036	Cystatin-S	CST4	0.0316764	-0.690727	0.535037	0.109827
P07858	Cathepsin B	CTSB	0.00250325	-0.594305	0.473023	0.245778
P12273	Prolactin-inducible protein	PIP	0.00647886	-0.569149	0.116147	0.367425
P08758	Annexin A5	ANXA5	0.024728	0.468018	0.151901	-0.349899
P01780	Ig heavy chain V-III region JON		0.0373057	0.555737	0.962035	-0.00873057
P30086	Phosphatidylethanolamine-binding protein 1	PEBP1	0.0207136	0.629482	0.13004	-0.326293

P09211	Glutathione S-transferase P	GSTP1	0.000122387	0.758188	0.0592956	-0.214745
Q06830	Peroxiredoxin-1	PRDX1	0.00492382	0.811836	0.240345	-0.170243
P50395	Rab GDP dissociation inhibitor beta	GDI2	0.00864002	0.85346	0.324602	-7.7469
P04792	Heat shock protein beta-1	HSPB1	0.0156339	0.954453	0.0925576	-0.511541
P00338	L-lactate dehydrogenase A chain	LDHA	0.0251644	1.07479	0.0555952	-0.778293
P30044	Peroxiredoxin-5, mitochondrial	PRDX5	0.013781	1.08386	0.0990585	-0.85895
P14618	Pyruvate kinase PKM	PKM	0.00570498	1.25685	0.600758	-0.0840111
P06396	Gelsolin	GSN	0.0199829	1.30002	0.160116	-0.573783
P07355	Annexin A2	ANXA2	0.000105848	1.65505	0.0690037	-0.440093
P04083	Annexin A1	ANXA1	0.000343761	1.67713	0.400233	-0.189219
P68104	Putative elongation factor 1-alpha-like 3	EEF1A1P5	0.026819	1.73869	0.34821	-0.630824
P07237	Protein disulfide-isomerase	P4HB	1.33E-05	20.465	0.259079	-1.05339
P31947	14-3-3 protein sigma	SFN	1.84E-07	21.4674	0.298178	0.489133
P06744	Glucose-6-phosphate isomerase	GPI	3.39E-07	22.0905	0.162099	-0.597249

Table S7 Differentially expressed tear proteins that were not restored to normal or near normal levels following renouncement of soft contact lenses

Protein ID	Protein name	Gene name	Soft A/CTRL	Soft A/CTRL	Soft B/Soft A	Soft B/Soft A
			t-test p value	t-test difference	t-test p value	t-test difference
P30085	UMP-CMP kinase	CMPK1	3.10E-10	-21.0936	1	0
Q96KP4	Cytosolic non-specific dipeptidase	CNDP2	6.24E-10	-20.9921	1	0
P28325	Cystatin-D	CST5	1.13E-10	-20.5094	1	0
Q9GZZ8	Extracellular glycoprotein lacritin	LACRT	6.91E-05	-2.08325	0.0912392	0.480766
P80303	Nucleobindin-2	NUCB2	0.0121563	-1.18659	0.850738	0.0635026
P14618	Pyruvate kinase PKM	PKM	0.00686079	-1.1482	0.463375	0.0986938
P35908	Keratin, type II cytoskeletal 2 epidermal	KRT2	0.0138746	-0.860073	0.149141	0.868804
P80188	Neutrophil gelatinase-associated lipocalin	LCN2	0.00408174	-0.770945	0.262706	0.375579
CON__P13645	Keratin, type I cytoskeletal 10	KRT10	0.0342843	-0.715617	0.183926	0.716726
O95994	Anterior gradient protein 2 homolog	AGR2	0.0201302	-0.610341	0.0728174	-1.2511

P63261	Actin, cytoplasmic 2	ACTG1	0.0154208	-0.475075	0.932412	-0.0123431
P02768	Serum albumin	ALB	0.0275545	0.110739	0.114849	0.0855484
P01024	Complement C3	C3	0.0332818	0.16916	0.212821	-0.2029
P02763	Alpha-1-acid glycoprotein 1	ORM1	0.0252244	0.216868	0.253601	-0.166636
P00738	Haptoglobin	HP	0.000664556	0.229911	0.055372	0.27194
P19652	Alpha-1-acid glycoprotein 2	ORM2	0.043632	0.340018	0.322546	-8.09206
P00558	Phosphoglycerate kinase 1	PGK1	0.0235661	0.400577	0.105992	-15.5423
P60174	Triosephosphate isomerase	TPI1	0.0413993	0.404948	0.75273	-0.168723
P01011	Alpha-1-antichymotrypsin	SERPINA3	0.042634	0.448003	0.101813	0.193193
P06396	Gelsolin	GSN	0.0201163	0.532289	0.21816	-0.123309
P26447	Protein S100-A4	S100A4	0.0374457	0.766703	0.465031	-0.302301
P02647	Apolipoprotein A-I	APOA1	0.00963617	0.878042	0.257336	-0.589225
P62987	Ubiquitin-60S ribosomal protein L40	UBA52	0.00950648	0.887589	0.77315	-0.0617619
P06703	Protein S100-A6	S100A6	0.0192174	0.9396	0.363222	-0.58531

Q01469	Fatty acid-binding protein, epidermal	FABP5	0.00103605	1.49002	0.468924	0.231202
P13647	Keratin, type II cytoskeletal 5	KRT5	2.90E-11	19.1201	0.175568	1.27628
P04004	Vitronectin	VTN	3.51E-09	20.7411	0.328128	-0.294021
Q9Y5Z4	Heme-binding protein 2	HEBP2	1.39E-07	21.5273	0.0981464	-0.625937

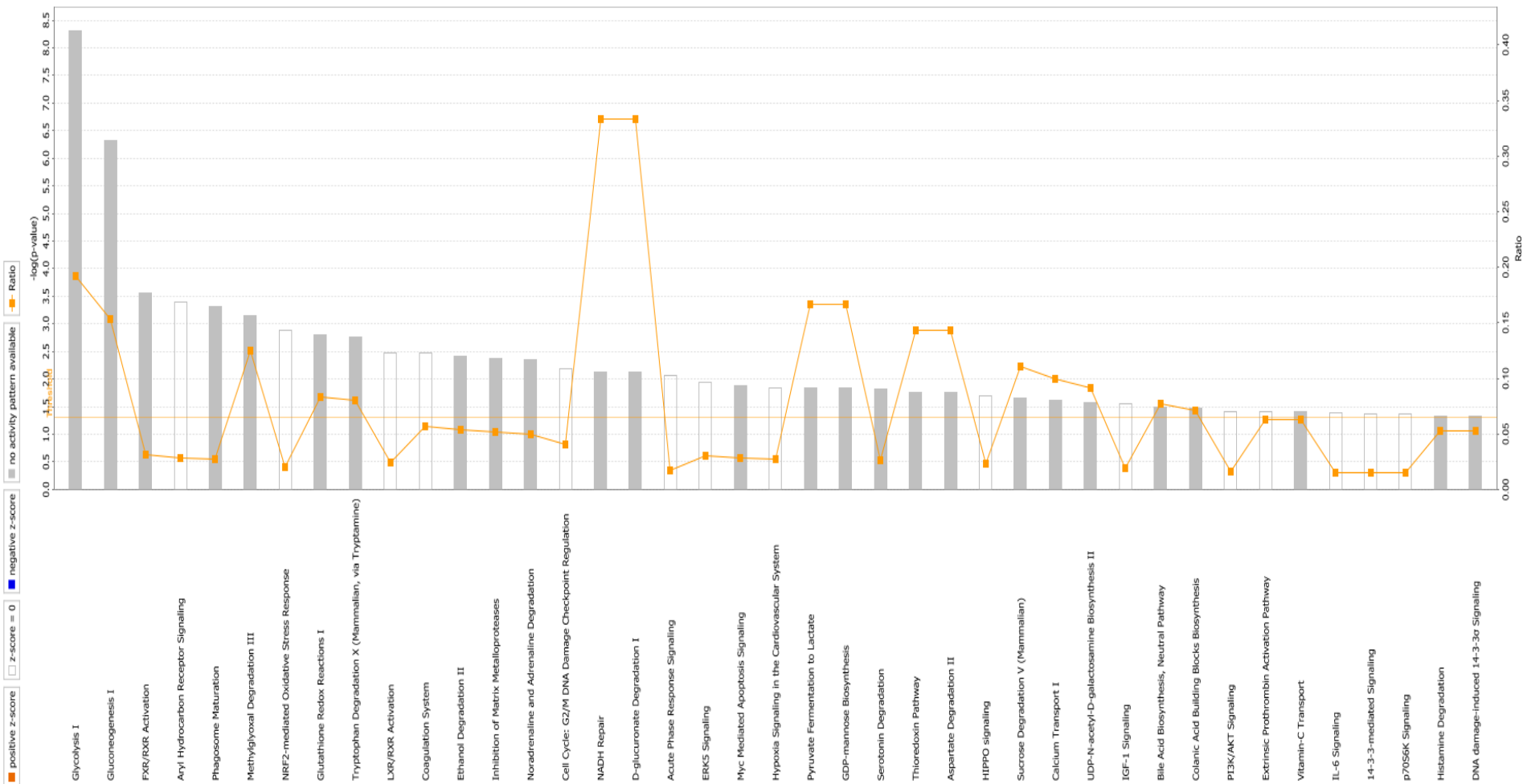


Figure S1. Canonical pathways of hard CL tear proteins. Top canonical pathways found to be significantly ($p < 0.05$) altered following the use of hard CLs identified by Ingenuity Pathway Analysis. The p-values of the proteins within the each canonical pathway was determined using the Benjamini-Hochberg corrected Fisher's exact test and ratio indicate the number of molecules in the dataset associated with a pathway to the total number of molecules identified in that particular pathway.

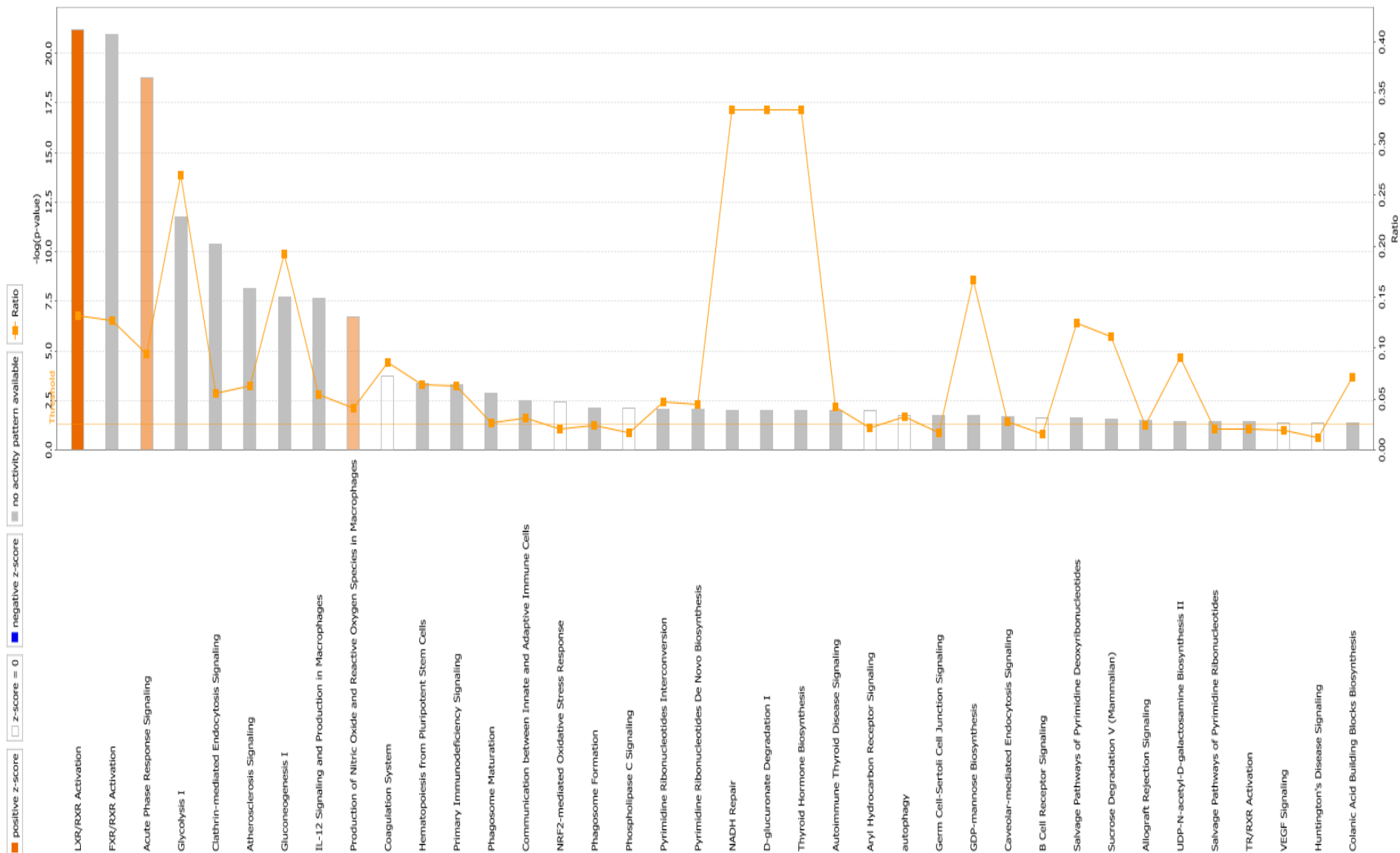


Figure S2. Canonical pathways of soft CL tear proteins. Major canonical pathways represented as bar chart of the differentially expressed tear proteins of the soft CL users. The p-values of the proteins within the each canonical pathway was determined using the Benjamini-Hochberg corrected Fisher's exact test and ratio indicate the number of molecules in the dataset associated with a pathway to the total number of molecules identified in that particular pathway.