

Supplementary Tab. 1: Results of the densitometric analysis and Fab protein concentration.

Sample	Area of Fab spots (dpi)	Fab Concentration [$\mu\text{g}/\mu\text{l}$] - BCA assay
Control 1	65472.927	0.33
Control 2	59115.865	0.26
Control 3	45729.404	0.21
Control 4	58185.927	0.85
Control 5	62848.551	0.34
Control 6	53812.187	0.38
Control 7	50649.066	0.28
Control 8	49414.258	0.30
Control 9	60310.986	0.43
Control 10	69813.572	0.24
Control 11	65794.258	0.29
Control 12	66643.238	0.32
Control 13	64208.894	0.34
Control 14	65378.057	0.38
Control 15	50849.768	0.31
POAG 1	60226.108	0.25
POAG 2	60670.016	0.20
POAG 3	60721.773	0.21
POAG 4	47009.137	0.19
POAG 5	50717.702	0.29
POAG 6	52171.430	0.23
POAG 7	50276.128	0.18
POAG 8	52510.844	0.36
POAG 9	39479.936	0.20
POAG 10	63368.108	0.20
POAG 11	66263.551	0.25
POAG 12	54302.794	0.21
POAG 13	57748.501	0.31
Mean	57275	0.29
S.D.	7594	0.13

Supplementary Tab. 2: Information about IgG V domain peptide sequences which were differently distributed between POAG and CTRL group in the discovery study.

No.	CDR / FR	Sequence	Protein	m/z	Charge	Score	Length	Germline hit (gene name)	BLAST bit score	Homology (%)	Discovery study (p ≤ 0.05; log2 fold change ≥ 0.5)	p-value	Fold change (POAG vs. CTRL)
1	FR1	AIQMTQSPSSLSASVGDR	gi 662564787	917.9	2	232.37	18	IGKV1-6*01	37	100	✓	0.01	↓
2	FR3	ASDTAMYYCAR	gi 761232722	654.8	2	145.46	11	IGHV5-10-1*01	27.7	100	✓	0.01	↓
3	CDR1	ASQSLSSWLAWYQKPKGKAPK	gi 323433041	787.7	3	113.88	21	IGKV1-5*01	48.1	95.2	✓	0.01	↓
4	CDR1	ASQSVGSNLAWYQKPGQAPR	gi 630869019	1137.1	2	166.67	21	IGKV3-15*01	45.4	95.2	✓	0.01	↓
5	CDR1	ASQSVNSNLAWYQKPGQAPR	gi 87906	1165.6	2	166.36	21	IGKV3-15*01	45.8	95.2	✓	0.01	↓
6	CDR1	ASQSVSNLAWYQKPGQAPR	gi 237702286	777.7	3	79.393	21	IGKV3-15*01	45.8	95.2	✓	0.01	↓
7	CDR1	ASQSVSSSLAWYQKPGQAPR	gi 323432554	1138.6	2	166.67	21	IGKV3-15*01	45.1	95.2	✓	0.01	↓
8	CDR1	ASQSVSSSYLAWYQKPGQAPR	gi 149673891	1220.1	2	206.45	22	IGKV3-20*02	48.9	100	✓	0.01	↓
9	CDR1	ASQSVSSYLAWYQKPKGQAPR	gi 339272255	873.4	2	225.09	15	IGKV3-11*01	34.3	100	✓	0.01	↓
10	CDR1	ASQSVSSYLAWYQKPGQAPR	gi 339272255	1176.6	2	240.34	21	IGKV3-11*01	47.4	100	✓	0.01	↓
11	FR3	ASSLEGGVPSR	gi 7438723	530.3	2	105.25	11	IGKV1-13*01	22.7	90.9	✓	0.01	↓
12	FR3	ASSLEGGVPSR	gi 442828	545.3	2	178.71	11	IGKV1-13*01	24.3	100	✓	0.01	↓
13	FR3	ATGIPDRFR	gi 52630839	516.8	2	108.57	9	IGKV3-20*01	21.2	100	✓	0.01	↓
14	FR3	ATGIPDRFSGSGGTDFTLTSLR	gi 70797863	1172.1	2	158.99	23	IGKV3-20*01	48.9	95.7	✓	0.01	↓
15	FR1	DIQLTQSPSTLSASVGDR	gi 27531086	938.0	2	251.74	18	IGKV1-5*01	37	94.4	✓	0.01	↓
16	FR1	DIQMTQSPSSVSASVGDR	gi 820957471	932.9	2	300.25	18	IGKV1-12*01	37.7	100	✓	0.01	↓
17	FR1	DIQMTQSPSTLSASVGDR	gi 442828	947.0	2	310.55	18	IGKV1-5*01	38.1	100	✓	0.01	↓
18	FR1	DIVLTQSPDSLAVSLGER	gi 13096223	950.5	2	248.7	18	IGKV4-1*01	36.6	94.4	✓	0.01	↓
19	FR1	DIVMTQSPDSLAVSLGER	gi 335892418	959.5	2	295.16	18	IGKV4-1*01	37.7	100	✓	0.01	↓
20	FR1	DIVMTQSPSLPVTPEPASPISCR	gi 218783338	1278.1	2	221.99	24	IGKV2-28*01	52	100	✓	0.02	↓
21	FR1	DLQMTQSPSSLSASVGDR	gi 327410291	939.9	2	267.69	18	IGKV1-27*01	37	94.4	✓	0.01	↓
22	FR1	DVQLVQSGAEVK	gi 821350640	636.8	2	185.2	12	IGHV1-69-2*01	24.6	91.7	✓	0.01	↓
23	FR1	ELVLTQSPATLSLSPGER	gi 339272255	949.5	2	307.57	18	IGKV3-20*02	37	94.4	✓	0.01	↓
24	FR1	ELVLTQSPGTLSLSPGER	gi 61970173	942.5	2	327.27	18	IGKV3-20*01	37.7	94.4	✓	0.02	↓
25	FR1	ELVMTQSPATLSVSPGER	gi 37728242	951.5	2	281.65	18	IGKV3-15*01	37.4	94.4	✓	0.01	↓
26	FR1	EVQLVQSGVEVK	gi 114147626	657.9	2	236.28	12	IGHV1-69-2*01	24.3	91.7	✓	0.01	↓
27	CDR3	FDYWGGTLTVSSASTK	gi 304563214	974.0	2	197.84	18	IGHJ4*01	34.3	100	✓	0.01	↓
28	FR3	FSGSGAGTDFTLK	gi 323433100	644.3	2	249.98	13	IGKV2-24*01	30.4	100	✓	0.01	↓
29	FR3	FSGSGSGTDFTLTSLR	gi 80975645	822.9	2	167.18	16	IGKV3-20*02	33.1	93.8	✓	0.01	↓
30	FR3	FSGSGSGTDFTLR	gi 523391770	666.3	2	158.86	13	IGKV2-28*01	29.3	92.3	✓	0.01	↓
31	CDR3	FSGSGSGTDFTLTISLQAEDVAVVY YQQYYSTPPL	gi 15919681	1318.3	3	95.445	36	IGKV4-1*01	73.2	100	✓	0.01	↓
32	CDR2	GLEWWMGLVYPGDSIDTR	gi 106897261	905.4	2	163.8	16	IGHV5-51*05	38.9	93.8	✓	0.01	↓

33	FR2	GLEWVANLK	gi 630868332	515.3	2	177.36	9	IGHV3-7*01	22.7	88.9	✓	0.01	↓
34	FR2	GLEWVGR	gi 158259769	408.7	2	158.38	7	IGHV3-72*02	20.4	100	✓	0.01	↓

No.	CDR / FR	Sequence	Protein	m/z	Charge	Score	Length	Germline hit (gene name)	BLAST bit score	Homology (%)	Discovery study (p ≤ 0.05; log2 fold change ≥ 0.5)	p-value	Fold change (POAG vs. CTRL)
35	FR2	GLEWVSSISR	gi 63022996	567.3	2	164.64	10	IGHV3-38-3*01	22.3	100	✓	0.01	↓
36	CDR2	GLEWVSSISR	gi 662565320	610.8	2	120.57	11	IGHV3-69-1*01	23.9	100	✓	0.01	↓
37	FR4	GTLTVSSASTK	gi 34532520	575.8	2	173.72	12	IGHJ1*01	18.5	100	✓	0.01	↓
38	CDR2	INSDGSSSYADSVK	gi 158714463	765.8	2	91.592	15	IGHV3-74*01	32.7	100	✓	0.02	↓
39	FR2	LAWYQQK	gi 160286048	468.7	2	143.97	7	IGKV3-20*02	20.4	100	✓	0.01	↓
40	CDR2	LLIYEVSK	gi 882264	482.8	2	95.358	8	IGLV2-8*03	18.1	87.5	✓	0.01	↓
41	CDR2	LLIYSNNQRPSGVPDR	gi 62205367	915.0	2	103.14	16	IGLV1-44*01	37	100	✓	0.01	↓
42	CDR2	LLLYWASTR	gi 323432988	561.8	2	233.57	9	IGKV4-1*01	22.3	88.9	✓	0.01	↓
43	FR1	LVESGGGLVKPGGSLR	gi 323433102	763.4	2	148.7	16	IGHV3-69-1*01	35.4	100	✓	0.01	↓
44	FR2	NDLGWYQQK	gi 152149150	576.3	2	122.94	9	IGKV1-17*01	25.8	100	✓	0.01	↓
45	FR2	NDLGWYQQKPGK	gi 152149150	717.4	2	193.62	12	IGKV1-17*01	32.7	100	✓	0.01	↓
46	FR3	NEDTAIYYCAR	gi 8699279	688.3	2	90.05	11	IGHV1-69*06	26.2	81.8	✓	0.02	↑
47	CDR1	NGYLAWYQQK	gi 695942258	635.8	2	158.76	10	IGKV3-20*02	23.5	80	✓	0.01	↑
48	FR1	NIQMTQSPSSLSASVGDGR	gi 444737639	939.5	2	192.22	18	IGKV1-33*01	35.8	94.4	✓	0.01	↓
49	FR3	NQFSLK	gi 284521128	368.7	2	132.72	6	IGHV4-39*04	16.2	100	✓	0.01	↓
50	FR3	NSLYLQMNSLR	gi 209402818	669.8	2	303.71	11	IGHV3-13*01	25.4	100	✓	0.01	↓
51	FR3	NTRYLQMN	gi 630868188	996.5	1	172.15	8	IGHV3-38*01	20.8	100	✓	0.01	↓
52	FR2	QAPGKGLEWVGR	gi 158259769	649.4	2	89.189	12	IGHV3-72*02	30.8	100	✓	0.01	↑
53	FR1	QSPGTLSPGER	gi 70797863	664.8	2	98.942	13	IGKV3-20*01	30	100	✓	0.01	↓
54	FR1	QVELVESGGGLVK	gi 371446908	657.9	2	255.08	13	IGHV3-11*01	27.3	92.3	✓	0.01	↓
55	FR1	QVELVQSGAEVK	gi 407943831	643.8	2	314.35	12	IGHV1-69*03	24.6	91.7	✓	0.01	↓
56	FR3	SDDTAVVYCARGYR	gi 815095215	848.9	2	120.55	14	IGHV1-18*01	28.1	100	✓	0.01	↓
57	CDR2	SLIYAASSLQSGVPSK	gi 63103149	804.4	2	82.349	16	IGKV1-16*02	33.1	100	✓	0.01	↓
58	FR3	SLNTAYLQWSSLK	gi 46253871	755.9	2	218.11	13	IGHV5-51*05	27.7	84.6	✓	0.01	↓
59	FR3	SLSTAYLQWSSLK	gi 4097044	742.4	2	186.51	13	IGHV5-51*05	28.9	92.3	✓	0.01	↓
60	FR3	SLTTAYLQWSSLK	gi 815068660	749.4	2	187.74	13	IGHV5-51*05	27.7	84.6	✓	0.01	↓
61	FR3	STSTAYLQWSSLK	gi 106897850	736.4	2	172.57	13	IGHV5-78*01	28.5	92.3	✓	0.01	↓
62	CDR3	TFGQGTKLELKR	gi 5731229	689.4	2	190.78	12	IGKJ2*01	25.4	90.9	✓	0.01	↑
63	CDR3	TFGQGTKVELKR	gi 130381795	682.4	2	190.35	12	IGKJ1*01	25.4	90.9	✓	0.01	↑
64	CDR3	TPYTFGQGTK	gi 98956429	550.3	2	143.4	10	IGKJ2*01	21.9	100	✓	0.01	↓

65	FR3	VSNRDSGVDPDRFSGSGSDFTLK	gi 21669411	1243.6	2	119.38	24	IGKV2-30*01	52.4	100	✓	0.02	↑
66	CDR3	WFDPWGGQTLTVSSASTK	gi 304563132	1034.0	2	219.99	19	IGHJ5*02	38.5	100	✓	0.01	↓
67	FR4	WGQGTLLTVSSASTK	gi 304562441	761.4	2	195.5	15	IGHJ1*01	26.9	100	✓	0.01	↓
68	FR2	YACWYQQK	gi 651207877	573.8	2	143	8	IGLV3-1*01	25	100	✓	0.01	↓

No.	CDR / FR	Sequence	Protein	m/z	Charge	Score	Length	Germline hit (gene name)	BLAST bit score	Homology (%)	Discovery study (p ≤ 0.05; log2 fold change ≥ 0.5)	p-value	Fold change (POAG vs. CTRL)
69	FR2	YAYWYQQK	gi 757819141	575.3	2	145.04	8	IGLV3-25*03	24.3	100	✓	0.01	↓
70	FR4	YFDLWGR	gi 304563378	478.7	2	104.45	7	IGHJ2*01	21.9	100	✓	0.01	↓
71	FR3	YSPFEGQVTISADK	gi 190341781	814.9	2	161.94	15	IGHV5-51*05	32.7	93.3	✓	0.01	↓
72	FR3	YSPFQGQVTISADR	gi 14268424	828.4	2	101.3	15	IGHV5-51*05	32.7	93.3	✓	0.01	↓
73	FR3	YSPFQGQVTLASADK	gi 304563132	814.4	2	264.85	15	IGHV5-51*05	33.1	93.3	✓	0.01	↓
74	FR2	YVSWYQQHPGK	gi 194173457	696.8	2	132.25	11	IGLV2-11*03	31.2	100	✓	0.01	↓
75	FR3	YVDSVEGR	gi 4323177	544.3	2	114.86	9	IGHV3-52*01	21.6	88.9	✓	0.02	↓

CDR: complementarity determining region (CDR1, CDR2 and CDR3) FR: framework region (FR1, FR2, FR3 and FR4)

✓ : Peptide sequence fulfilled criteria - : Peptide sequence failed to fulfill criteria ↓ : Low abundant ↑ : High abundant