A Additional file 1

Table 1. Patient characteristics at the time of examination. The samples were taken at the time point of diagnosis. The patients
are categorised according to their CKD stage: Group I "good" stage 1+2, n=5 (P004, P007, P011, P017, P020), Group II
intermediate stage 3, n=4 (P001, P005, P013, P016) and Group III bad stage 4+5, n=1 (P006). Apart from P007, which
presented an acute kidney injury, all patients had a chronically damaged kidney.

Patient	Age	Gender	Disease type	lsotype	FLC Serum [mg/l]	FLC Urine [mg/l]	TPU [g/24h]	Kidney function creatinin [mg/dl]	GFR-CKD- EPI [ml/min]	CKD Stadium	Kidney function recovered? Improvement = 30%	Kidney function recovered Creatinine [mg/dl]
P001	47	male	MM	λ	3750	1060	13	1.3	50	3	Yes	0.9
P004	72	male	MM	к	5280	7650	4	1.1	90	1	Yes	0.9
P005	65	female	MM	к	1250	6140	3	1.2	48	3	n/a	acute kidney
P006	66	female	MM	к	2460	6880	3	1.9	27	4	Yes	13
P007	54	male	MM	к	898	n/a	1	1	83	2	No	1.3
P011	45	female	AL	λ	120	n/a	6.2	0.7	108	1	No	0.8
P013	65	male	MM	к	11000	n/a	3	1.5	50	3	No	1.7
P016	59	male	MM	к	1150	175	3	1.6	45	3	No	1.2
P017	72	female	MM	к	1380	n/a	4	0.7	90	1	No	0.8
P020	64	female	MM	к	4120	n/a	2.4	0.8	74	2	n/a	0.9

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	FR1	CDR1	FR2	CDR2	
P004a	EIVLTQSPGTLSLSPGERATLSCRAS	QSVSSSYLAWY	QOKPGQAPRLL	IY <mark>DAS</mark> TRATGIP	60
P004b	EIVLSQSPDTLSLSPGERATLSCRAD	KSVSSNYVAWY	QQKPGQAPRLLI	IY <mark>DAF</mark> TRATGIP	60
P013	DIOMTOSPSTLSASVGDAVTITCRAS	OSL-NVWLAWY	OOKPGKPPKLL	IY <mark>EAS</mark> NLESGVP	59
P020	DIOMTOSPSTLSTSVGDRVTITCRAS	OSI-RTWLAWY	OOKPGKAPKLLI	IY <mark>KAS</mark> TLETGVP	59
P007	DIOMTOSPSTLSASVGDRVTITCRAS	QSL-SSSLAWY	QOKPGKAPKLLI	IY <mark>DAS</mark> SLETGVP	59
P005	DIQMTQSPSSLSASVGDRVSITCRAS	ESI-SSYVNWY	QQKPGKAPKLL	IY <mark>TAS</mark> SLQSGVP	59
P006	DIQMTQSPSSLSASVGDRVTITCQAS	QDL-AKYLNWY	QQKPGKPPKLL	IY <mark>DTS</mark> NLETGVP	59
P016	DIQMTQSPSSLSASVGDRVTITCQAS	RDI-SNYLNWY	QQKPGKAPMLL:	IY <mark>AAS</mark> NLQTGVP	59
P017	DIQMTQSPSSLSASVGDRVTITCQAS	QDL-GNYLNWY	QQKPGKAPRLL	IY <mark>DAS</mark> DLEEGVP	59
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	FR3	CDR3	FR4		
P004a	DRFSGSGSGADFLLTISSLEPEDFAM	YYC <mark>QQYGR-SP</mark>	YT <mark>FGPGTKVDII</mark>	KRTVAAPSVFIF	119
P004b	DRFSGSGSETDYTLTISTLEPEDFAV	YYC <mark>QQYGR-SP</mark>	YTFGPGTKVDII	KRTVAAPSVFIF	119
P013	SRFSGSGSGTEFTLTISSLQPDDFAT	YYC <mark>QQYNS-</mark> YP	YTFGQGAKLEII	KRTVAAPSVFIF	118
P020	SRFSGSGSGTEFTLTISSLQPEDFAT	YYC <mark>QQYND-</mark> YS	GTFGQGTKLEII	KRTVAAPSVFIF	118
P007	SRFSGSGSGTEFTLSISSLQPDDFAT	YYC <mark>QHYNS-</mark> YS	ITFGQGTKVEII	KRTVAAPSVFIF	118
P005	PRFSGSASGTDFTLTISSLQPEDFAT	YYC <mark>QQSYS-</mark> TP	ITFGQGTRLEI	KRTVAAPSVFIF	118
P006	SRFSN-GGGTDFTFTINSLQPEDLAT	YYC <mark>QQYDDF-</mark> P	'LT <mark>FGPGTKVDII</mark>	KRTVAAPSVFIF	117
P016	SRFSGSGSGTDFTFTISSLQPEDLAT	YYC <mark>QQYGNL-</mark> P	LTFGGGTKVEII	KGTVAAPSVFIF	118
P017	SRFSGSGSGTDFTFTISSLQPEDFAT	YYC <mark>QQYHTLPP</mark>	<mark>'LT</mark> FGGGTKVDVI	KRSLAAPSVFIF	119
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P004a	PPSDEQLKSGTASVVCLLNNFYPREA	KVQWKVDNALQ	SGNSQESVTEQI	OSKDSTYSLSST	179
P004b	PPSDEQLKSGTASVVCLLNNFYPREA	KVQWKVDNALQ	SGNSQESVTEQI	OSKDSTYSLSST	179
P013	PPSDEQLKSGTASVVCLLNNFYPREA	KVQWKVDNALQ	SGNSQESVTEQI	OSKDSTYSLSST	178
P020	PPSDEQLKSGTASVVCLLNNFYPREA	KVQWKVDNALQ	SGNSQESVTEQI	OSKDSTYSLSST	178
P007	PPSDEQLKSGTASVVCLLNNFYPREA	KVQWKVDNALQ	SGNSQESVTEQI	OSKDSTYSLSST	178
P005	PPSDEQLKSGTASVVCLLNNFYPREA	KVQWKVDNALQ	SGNSQESVTEQI	OSKDSTYSLSST	178
P006	PPSDEQLKSGTASVVCLLNNFYPREA	KVQWKVDNALQ	SGNSQESVTEQI	OSKDSTYSLSST	177
P016	PPSDEQLKSGTASVVCLLNNFYPREA	KVQWKVDNALQ	SGNSQESVTEQI	OSKDSTYSLSST	178
P017	PPSDEQLKSGTASVVCLLNNFYPREA	KVQWKVDNALQ	SGNSQESVTEQI	OSKDSTYSLSST	179
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P004a	LTLSKADYEKHKVYACEVTHOGLSSP	VTKSFNRGEC	215		
P004b	LTLSKADYEKHKVYACEVTHOGLSSP	VTKSFNRGEC	215		
P013	LTLSKADYEKHKLYACEVTHOGLSSP	VTKSFNRGEC	214		
P020	LTLSKADYEKHKVYACEVTHOGLSSP	VTKSFNRGEC	214		
P007	LTLSKADYEKHKVYACEVTHOGLSSP	VTKSFNRGEC	214		
P005	LTLSKADYEKHKVYACEVTHOGLSSP	VTKSFNRGEC	214		
P006	LTLSKADYEKHKVYACEVTHOGLSSP	VTKSFNRGEC	213		
P016	LTLSKADYEKHKVYACEVTHOGLSSP	VTKSFNRGEC	214		
P017	LTLSKADYEKHKVYACEVTHOGLSSP	VTKSFNRGEC	215		
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Figure A.1. Full length sequence alignment of the κ light chains of our study. The framework regions (FR) are marked with blue, the complementarity determining regions (CDRs) with red.

		FR1		CDR1		FR2	C	DR2	
P001	GPDLTQP	RSVSGSPGQ	SVTLSCTGT	SDVGGYNY	YVSWYQQ	HPGKAI	PKLMIY <mark>D</mark>	VTKRPSGV	60
P011	EAPLTQPI	SVSGAPGQ	RVTLSCTGS	SNLGAGWI	VHWYQQ	LPGTVI	PKLLIY <mark>A</mark>	<mark>DR</mark> NRPSGV	60
	****	****	*******	**::*.	* ****	**	***:**	*****	
		FR3	3		CDR3		FR4		
P001	PDRFSGS	SGTTASLT	ISGLQAEDE	ADYYC <mark>CSY/</mark>	AG-IDIF	VL FGGG	GTKLTVL	GQPKAAPS	119
P011	PERFSGSE	SGTSATVA	IAGLQAEDE	ADYYC <mark>QSYI</mark>	DSALSGF	YV <mark>FGT(</mark>	GTKVIVL	GQPKANPT	120
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P001	VTLFPPS	SEELQANKA	TLVCLISDF	YPQVTVAWI	KADSSPV	KAGVE	TTTPSKQ	SNNKYAAS	179
P011	VTIFPPS	SEELQANKA	TLVCLISDF	YPQVTVAWI	KADGSPV	KAGVE	TTKPSKQ	SNNKYAAS	180
	:**	*******	******	******	***。***	*****	**•***	******	
P001	SYLSLTPH	QWKSHRSY	SCQVTHEGS	TVEKTVAP	recs 21	6			
P011	SYLSLTPH	QWKSHRSY	SCQVTHEGS	TVEKTVAP	recs 21	7			
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Figure A.2. Full length sequence alignment of the λ light chains of our study. The framework regions (FR) are marked with blue, the complementarity determining regions (CDRs) with red.



Figure A.3. (A) Distribution of sedimentation coefficients (c(s)) of the IgLC samples of this study and (B) application of the $c(s, f/f_0)$ -model determined by sedimentation velocity experiments at 60.000 rpm. We find that the form factors of the dimers differ within the sample set. The dimers can appear very globular e.g. P020 with a f/f_0 of 1.14 or elongated such as P006 f/f_0 of 2.22 and P007, P013 and P017 f/f_0 between 1.54 and 1.83. However the signal for the dimer of P006 is very low. (C) shows the variation of f/f_0 between the dimers compared to the monomers. The monomers of P004 and P020 were excluded due to their low signal intensity.



Figure A.4. Size exclusion chromatograms of the different IgLC samples of this study. The fractions used for the remaining experiments in this study are marked in blue