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1 Methods

1.1 Data collection procedures

All data from Necker hospital (Paris, France), Saint-Louis hospital (Paris, France), and Toulouse hospital (Toulouse, France) were extracted from the prospective Paris Transplant Group Cohort data cohort. CNIL, Registration number: 363505, validated on the 8th of June 2004. The database networks have been approved by the National French Commission for bioinformatics data and patient liberty and codes were used to ensure strict donor and recipient anonymity and blind access. Informed consent was obtained from the participants at the time of transplantation. The data are entered into the database at the time of transplantation, at the time of post-transplant allograft biopsies and at each transplant anniversary and are submitted for an annual audit.

1.2 Independent external validation cohorts

The validation datasets in Europe are composed of eight centers: Montpellier hospital (France), Tenon hospital (France), Lyon hospital (France), Saint-Etienne hospital (France), Bergamo hospital (Italy), Zagreb hospital (Croatia), Groningen Kidney Center (The Netherlands), and Aarhus University Hospital (Denmark). The North-American validation cohort is composed of four centers: the Mayo-Clinic hospital (Rochester and Jacksonville), the ABCAN trial and the BENEFIT and BENEFIT-EXT trials. The oceanian validation cohort is composed of the Sydney Transplant Unit from Australia. All data from the French patients regarding donors and recipients were extracted from the Paris Transplant Group dataset, and from the French national agency database CRISTAL (official website: https://www.sipg.sante.fr/portail/). For the Croatian, Italian and Dutch patients of the European validation set and for the patients of the American validation set, data were collected as part of routine clinical practice and entered in centers' databases in compliance with local and national regulatory requirements and sent anonymized to the Paris Transplant Group. These validation cohorts followed the rules applied in each country.

1.3 Transplant parameters prospectively collected in the development cohort

Baseline recipient's characteristics:	
1.	Recipient's age
2.	Recipient's gender
3.	Recipient's height
4.	Recipient's weight
5.	Previous transplantation
6.	Delay between dialysis and transplantation
7.	Cause of end stage renal disease
8.	ABO blood group
9.	HLA genotype
10.	CMV serology
11.	HCV serology
12.	HBV serology
13.	HIV serology
Baseline donor's characteristics:	
14.	Donor's age
15.	Donor's gender
16.	Donor's height
17.	Donor's weight
18.	Type of donor: deceased vs living
19.	Cause of donor's death

20.	Double transplantation
21.	History of hypertension
22.	History of diabetes
23.	ECD status
24.	Serum creatinine
25.	ABO blood group
26.	HLA genotype
27.	CMV serology
28.	HCV serology
29.	HBV serology
30.	HIV serology
Immunological characteristics at the time of transplantation:	
31.	HLA mismatches A
32.	HLA mismatches B
33.	HLA mismatches Cw
34.	HLA mismatches DQ
35.	HLA mismatches DR
36.	HLA mismatches DP
37.	Anti-HLA DSA at the time of transplantation
38.	MFI of the anti-HLA DSA at the time of transplantation
Transplant characteristics:	
39.	Cold ischaemia time
40.	Delayed graft function
41.	Induction treatment with thymoglobulin
42.	Induction treatment with basiliximab
43.	Steroid dose
Immunological data at 1 year after transplantation (Luminex SA assessment A, B, C, DP, DQ, DR)	
44.	Anti-HLA DSA
45.	MFI of immunodominant anti-HLA DSA
Histological data according to the Banff classification:	
46.	g Banff score
47.	ptc Banff score
48.	t Banff score
49.	i Banff score
50.	cg Banff score
51.	v Banff score
52.	mm Banff score
53.	ci Banff score
54.	ct Banff score
55.	IFTA Banff score
56.	cv Banff score
57.	ah Banff score
58.	C4d ptc deposition
59.	Recurrence of ESRD
60.	Polyomavirus-associated nephropathy
61.	ABMR status
62.	TCMR status
63.	Borderline category
Follow-up variables:	
64.	Episodes of pyelonephritis

65.	Immunosuppression treatment
66.	Type of treatment: calcineurin inhibitors, mycophenolate mofetil, mTOR inhibitors or belatacept
67.	CNI blood through level at M12 and every year
68.	Steroid dose at M12 and every year
69.	Rejection therapy (e.g., steroid, plasma exchange, intravenous immunoglobulin)
70.	CMV prophylaxis
71.	BK viral load at M12 and every year
72.	CMV viral load at M12 and every year
73.	Allograft function at M12 and every 6 months
74.	Proteinuria at M12 and every 6 months
75.	Patient date and cause of allograft loss
76.	Patient date and cause of death

TABLES

Table 1 - eGFR equations : a literature review : study design, population characteristics

We reviewed the literature for studies that developed equations estimating GFR on native and kidney transplanted patients. The sign * denotes the studies that were developed on kidney transplant populations. Equations that were developed on specific populations non-relevant to this study e.g., cancer or trauma-only patients were not listed.

Study	Year	Equation name	Number of citations	Number of centers	Development cohort size	External validation	Percentage male	Percentage black	Mean age	Mean GFR	Percentage diabetes	Percentage CKD	Percentage transplant	Filtration marker	Creatinine measuring method	GFR measuring method
Whyte et al.(1)	1958	Edwards & Whyte	43	1, Australia	136	No	55	NA	NA	NA	NA	76	NA	Creatinine	Colorimetric	Creatinine
Jelliffe et al. (2)	1971	Jelliffe-1	24	1, USA	41	No	71	NA	NA	NA	NA	NA	NA	Creatinine	Colorimetric	Creatinine
Jelliffe et al. (3)	1973	Jelliffe-2	77	NA	NA	No	NA	NA	NA	NA	NA	NA	NA	Creatinine	NA	Creatinine
Rowe et al. (4)	1976	Rowe	24	Multicentric, USA	884	No	100	3	NA	NA	NA	NA	NA	Creatinine	Colorimetric	NA
Cockcroft et al. (5)	1976	Cockcroft-Gault	3336	1, USA	236	No	96	NA	NA	73	NA	NA	NA	Creatinine	Colorimetric	Creatinine
Bjonsson (6)	1979	Bjornsson	78	2, USA, Denmark	1155	No	81	NA	NA	NA	NA	NA	NA	Creatinine	Colorimetric	Creatinine
Hull et al. (7)	1981	Hull	34	1, USA	103	No	73	NA	53	NA	NA	NA	NA	Creatinine	Colorimetric	Creatinine
Gates et al. (8)	1985	Gates	14	1, USA	90	No	53	NA	55	NA	NA	NA	2	Creatinine	NA	Creatinine
Walser et al. (9)	1993	Walser	4	1, USA	85	No	NA	NA	NA	13	NA	100	NA	Creatinine	Colorimetric	^{99}Tc-DTPA
Nankivell et al. (10)*	1995	Nankivell	317	1, Australia	146	No	49	NA	43	52	NA	100	100	Creatinine	NA	^{99}Tc-DTPA
Baracskay et al. (11)	1997	Baracskay	16	1, USA	41	No	NA	NA	>65	NA	NA	NA	NA	Creatinine	NA	^{125}I-iothalamate
Levey et al. (12)	1999	MDRD	4410	Multicentric, USA	1,070	Yes, N= 558	60	12	NA	40	6	100	NA	Creatinine	Colorimetric	^{125}I-iothalamate
Hoek et al. (13)	2003	Hoek	116	1, Netherlands	93	No	50	NA	50	81	NA	100	NA	Creatinine, Cystatin C	Enzymatic	^{125}I-iothalamate
Rule et al.(14)	2004	MCQ	303	1, USA	900	No	49	NA	51	48	NA	36	6	Creatinine	Colorimetric	^{125}I-iothalamate
Grubb et al.(15)	2005	Grubb	24	1, Sweden	451	No	50	NA	53	NA	NA	100	0	Creatinine, Cystatin C	Enzymatic	Iohexol
Sjöström et al. (16)	2005	NA	47	1, Sweden	381	No	48	NA	56	59	NA	18	0	Creatinine, Cystatin C	Enzymatic	Iohexol
MacIsaac et al.(17)	2006	MacIsaac	115	1, Australia	251	No	NA	0	60	89	82	100	0	Creatinine, Cystatin C	Enzymatic	^{99}Tc-DTPA

Rule et al. (18)	2006	Rule native CKD	106	1, USA	204	No	55	NA	55	50	18	100	0	Cystatin C	Enzymatic	^{125}I-iothalamate
Rule et al. (18) *	2006	Rule kidney recipient	106	1, USA	103	No	63	NA	49	51	18	100	100	Cystatin C	Enzymatic	^{125}I-iothalamate
Virga et al. (19)	2007	NA	1	1, Italy	530	No	53	0	57	55	NA	100	0	Creatinine	Colorimetric	Creatinine
Stevens et al. (20)	2008	NA	461	Multicentric USA, 1 Europe	2,980	Yes, N=438	63	53	52	48	13	100	0	Cystatin C	Enzymatic	^{125}I-iothalamate, ^{51}Cr-EDTA
Douville et al. (21)	2008	CHUQ	14	1, Canada	773	No	55	<1	54	67	NA	100	0	Creatinine	Colorimetric	Creatinine
Matsuo et al. (22)	2009	New 3-variable Japanese equation	1903	Multicentric, Japan	413	Yes. N= 350	61	0	52	NA	NA	NA	NA	Creatinine	Enzymatic	Inulin
Levey et al.(23)	2009	CKD-EPI 2009	7286	Multicentric, USA	5504	Yes, N= 3896	47	32	47	68	29	70	4	Creatinine	Enzymatic	^{125}I-iothalamate
Diamandopoulos et al. (24)	2010	DAF	5	Multicentric, Greece	907	No	54	NA	68	NA	NA	100	NA	Creatinine	NA	NA
Björk et al. (25)	2011	LM-REV	44	2, Sweden	850	No	56	0	60	55	NA	100	NA	Creatinine	Colorimetric & enzymatic	Iohexol
Alvarez-Gregori et al. (26)	2011	HUGE	8	Multicentric, Argentina, Europe	376	Yes, N= 111	58	NA	NA	NA	NA	37	NA	Creatinine	NA	^{99}Tc-DTPA
Schaeffner (27)	2012	BIS	177	1, Germany	570	No	47	NA	78.5	69	24	30	0	Creatinine, Cystatin C	Enzymatic	Iohexol
Inker et al.(28)	2012	CKD-EPI 2012	1212	Multicentric, USA	5352	Yes, N= 1119	58	40	47	68	32	50	0	Creatinine, Cystatin C	Enzymatic	^{125}I-iothalamate
Pottel et al.(29)	2016	FAS	103	4 Europe, 1 USA	6870	No	53	NA	NA	78	NA	NA	NA	Creatinine	Colorimetric & enzymatic	Inulin, iohexol, ^{125}I-iothalamate
Salvador et al.(30)*	2017	NA	22	1, Norway	297	Yes, N=297	67	NA	52	51	NA	100	100	Creatinine, Cystatin C	Enzymatic	^{51}Cr-EDTA, iohexol
Pottel et al. (31)	2021	EKFC	12	Multicentric, Europe	11251	Yes, N= 8378	56	0	42	77	NA	100	NA	Creatinine	Enzymatic	Inulin, iohexol, ^{125}I-iothalamate , ^{51}Cr-EDTA
Inker et al.(32)	2021	CKD-EPI 2021	7	Multicentric, USA	13606	Yes, N= 4050	44	32	47	68	29	50	NA	Creatinine, Cystatin C	Enzymatic	^{125}I-iothalamate

Abbreviations: BIS, Berlin Initiative Study ;CHUQ, Le Centre hospitalier universitaire de Quebec ; CKD, Chronic kidney disease ; CKD-EPI, Chronic Kidney Disease Epidemiology Collaboration; DAF, Diamandopoulos A. formula; DTPA, diethylenetriaminepentaacetic acid ; EDTA, ethylenediamine tetraacetic acid; EKFC, European Kidney Function Consortium equation; FAS, Full age spectrum; HUGE, Hematocrit, urea and gender equation; LM-REV, Lund-Malmö revised; MDRD, Modification of Diet in Renal Disease study; MCQ, Mayo clinic quadratic; NA, Not available

Table 2 : Allocation and medical systems in the transplant centers

Cohort	Allocation system	Deceased / living donor rate	Dual kidney transplantation programme	Paired donor exchange national programme	ABO incompatible programme	HLA incompatible programme	Standard induction therapy protocols
Development cohort: Necker Hospital, France	ABM: Agence Française Biomédecine	**77 % / 23%**	**YES**	**NO**	**YES**	**YES**	**Induction rate 100%** (thymoglobulin or anti-RIL2)
Development cohort: Saint-Louis Hospital, France	ABM: Agence Française Biomédecine	**79% / 21%**	**YES**	**NO**	**YES**	**YES**	**Induction rate 100%** (thymoglobulin or anti-RIL2)
Development cohort : Toulouse Hospital, France	ABM: Agence Française Biomédecine	**96% / 4%**	**NO**	**NO**	**YES**	**YES**	**Induction rate 85%** (thymoglobulin or anti-RIL2)
Montpellier Hospital, France	ABM: Agence Française Biomédecine	**94% / 6%**	**YES**	**NO**	**NO**	**NO**	**Induction rate 100%** (thymoglobulin or anti-RIL2)
Tenon Hospital, France	ABM: Agence Française Biomédecine	**77% / 23%**	**NO**	**NO**	**YES**	**YES**	**Induction rate 100%** (thymoglobulin or anti-RIL2)
Lyon Hospital, France	ABM: Agence Française Biomédecine	**NA**	**YES**	**NO**	**YES**	**NO**	**Induction rate 100%** (thymoglobulin or anti-RIL2)
Saint-Etienne Hospital, France	ABM: Agence Française Biomédecine	**NA**	**NO**	**NO**	**NO**	**NO**	**Induction rate 100%** (thymoglobulin or anti-RIL2)
Mayo Clinic, Rochester, USA	UNOS United Nations for Organ Sharing	**28% / 72%**	**NO**	**YES**	**YES**	**YES**	**Induction rate 100%** (thymoglobulin or anti-RIL2)
Mayo Clinic, Jacksonville, USA	UNOS United Nations for Organ Sharing	**70% / 30%**	**NO**	**YES**	**NO**	**NO**	**Induction rate 90%** (thymoglobulin or anti-RIL2)
ABCAN trial	UNOS United Nations for Organ Sharing	**40% / 60%**	**YES**	**NO**	**NO**	**NO**	**Induction rate 100%** (thymoglobulin)
BENEFIT and BENEFIT-EXT trials	International study with many different allocation systems	**69% / 31%**	**NO**	**NA**	**NO**	**NA**	**Induction rate 100%** (thymoglobulin or anti-RIL2)
Bergamo Hospital, Italy	EuroTransplant: EU allocation system	**100% / 0%**	**YES**	**YES**	**NO**	**NO**	**Induction rate 100%** (thymoglobulin or anti-RIL2)
Zagreb Hospital, Croatia	EuroTransplant: EU allocation system	**98% / 2%**	**NO**	**NO**	**NO**	**NO**	**Induction rate 100%** (thymoglobulin or anti-RIL2)
Groningen Kidney Center, The Netherlands	EuroTransplant: EU allocation system	**NA**	**YES**	**YES**	**YES**	**YES**	**Induction rate 100%** (thymoglobulin or anti-RIL2)
Sydney Transplant Unit, Australia	OrganMatch	**NA**	**NO**	**NO**	**NO**	**NO**	**Induction rate 100%** (thymoglobulin or anti-RIL2)
Aarhus University Hospital, Denmark	Scandiatransplant	**NA**	**YES**	**NO**	**YES**	**YES**	**Induction rate 100%** (anti-RIL2)

Table 3 : Transplantation dates and date of the last measured GFR in the transplant centers

Center	Transplantation date (first patient of the center)	Transplantation date (last patient of the center)	Date of the last measured GFR
Development cohort: Necker Hospital, France	02/1990	07/2021	12/2021
Development cohort: Saint-Louis Hospital, France	09/2004	06/2020	07/2021
Development cohort : Toulouse Hospital, France	01/1997	12/2011	09/2015
Montpellier Hospital, France	09/1991	07/2018	11/2018
Lyon Hospital, France	01/2012	06/2015	07/2016
Tenon Hospital, France	10/1981	06/2021	NA*
Saint-Etienne Hospital, France	01/2005	01/2012	11/2012
Zagreb Hospital, Croatia	01/2007	01/2016	07/2018
Bergamo Hospital, Italy	02/2005	12/2007	NA*
Groningen Kidney Center, The Netherlands	01/2001	01/2021	01/2021
Aarhus University Hospital, Denmark	06/2011	06/2015	06/2016
Sydney Transplant Unit, Australia	01/1989	01/2012	NA*
Mayo Clinic, Jacksonville, USA	07/2000	11/2011	11/2019
Mayo Clinic, Rochester, USA	03/1990	10/2020	12/2021
ABCAN trial	12/2002	01/2008	01/2008
BENEFIT and BENEFIT-EXT trials	02/2005	05/2005	01/2008

*The authors provided the transplantation period for their overall cohort, but not per patient. They also provided the delay from transplant to GFR measurement, which does not allow to deduce the exact date of the last measured GFR.

Table 4 – Sample size of the KRS study in comparison to studies that developed GFR equations

Native kidney GFR equations

Study	Population	Total sample size	Sample size of the development set	Sample size of the validation set
MDRD (Levey et al. Annals of Internal Medicine ; PMID : 10075613)	Native kidneys	1628	1070	558
CKD-EPI-2009 (Levey et al. Annals of Internal Medicine ; PMID : 19414839)	Native kidneys	12150	8254	3896
CKD-EPI-2021 (Inker et al. NEJM; PMID : 34554658)	Native kidneys	12787	8254	4050
KRS	Transplanted kidneys	15489	3622	11867

Transplanted kidney GFR equations

Study	Population	Total sample size	Sample size of the development set	Sample size of the validation set
Nankivell (Nankivell et al. Transplantation ; PMID : 7604438)	Transplanted kidneys	146	-	-
Rule et al. Kidney International ; PMID : 16408133	Transplanted kidneys	460	-	-
Salvador et al. Transplant; PMID : 29536033	Transplanted kidneys	594	297	297
KRS	Transplanted kidneys	15489	3622	11 867

Table 5 - Methods to measure creatinine and GFR in the different centers of the development and external validation cohorts.

Cohort	Center	Creatinine assay	mGFR method
Derivation	Necker Hospital, Paris	Jaffe colorimetric method before 2011, then IDMS-traceable enzymatic method	^{51}Cr-EDTA clearance*
	Saint-Louis Hospital, Paris	Jaffe colorimetric method before 2019, then IDMS-traceable enzymatic method	^{99}Tc-DTPA clearance
	Rangueil Hospital, Toulouse	Jaffe colorimetric method before 2013, then IDMS-traceable enzymatic method	Inuline clearance(33)(33)
External validation	Montpellier Hospital	Jaffe colorimetric method before 2013, then IDMS-traceable enzymatic method	^{99}Tc-DTPA clearance
	Hospices Civils Hospital, Lyon	IDMS-traceable enzymatic method	Inuline or iohexol clearance
	Tenon Hospital, Paris	IDMS-traceable enzymatic method	^{51}Cr-EDTA clearance(34)(34)
	Saint-Etienne Hospital, Paris	Jaffe colorimetric method before 2012, then IDMS-traceable enzymatic method	Inuline clearance
	Bergamo hospital	Jaffe colorimetric method before 2010, then IDMS-traceable enzymatic method	Iohexol clearance
	University Hospital, Zagreb	Jaffe colorimetric method before 2014, then IDMS-traceable enzymatic method	^{51}Cr-EDTA clearance
	Mayo Clinic, Rochester	IDMS-traceable enzymatic method	Iothalamate clearance
	Mayo Clinic, Jacksonville	IDMS-traceable enzymatic method	Iothalamate clearance
	ABCAN trial	IDMS-traceable enzymatic method	Iothalamate clearance
	BENEFIT trial	IDMS-traceable enzymatic method	Iothalamate clearance or ^{51}Cr-EDTA clearance
	Groningen Kidney Center	IDMS-traceable enzymatic method	Iothalamate clearance
	Sydney Transplant Unit	Jaffe colorimetric method before 2014, then IDMS-traceable enzymatic method	^{99}Tc-DTPA clearance
	Aarhus University Hospital	IDMS-traceable enzymatic method	^{51}Cr-EDTA clearance

^{51}Cr-EDTA, ^{51}Cr- ethylenediaminetetraacetic acid; ^{99}mTc-DTPAT, Technetium-^{99} diethylenetriaminepentaacetic acid

*Measurements were also performed in Hôpital Européen Georges Pompidou, Paris, France

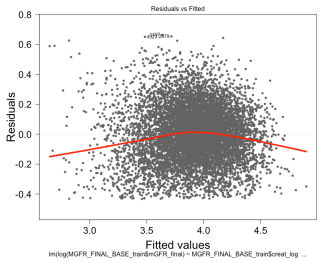
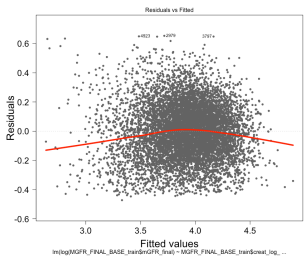
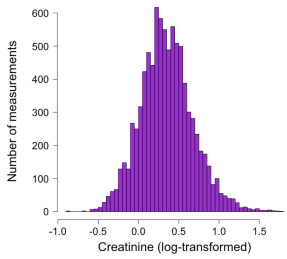
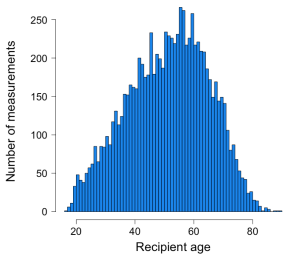
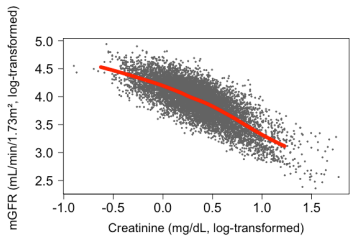
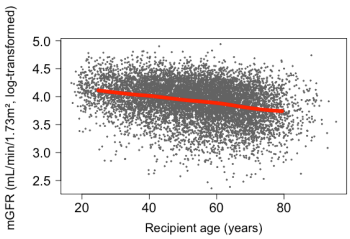
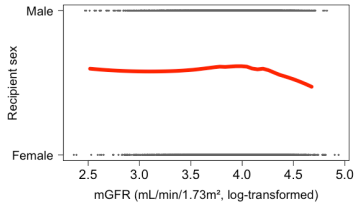
Table 6 – TRIPOD checklist

Section/Topic	Item	Checklist Item	Page
Title and abstract			
Title	1	Identify the study as developing and/or validating a multivariable prediction model, the target population, and the outcome to be predicted.	1
Abstract	2	Provide a summary of objectives, study design, setting, participants, sample size, predictors, outcome, statistical analysis, results, and conclusions.	3
Introduction			
Background and objectives	3a	Explain the medical context (including whether diagnostic or prognostic) and rationale for developing or validating the multivariable prediction model, including references to existing models.	5, 6
	3b	Specify the objectives, including whether the study describes the development or validation of the model or both.	6
Methods			
Source of data	4a	Describe the study design or source of data (e.g., randomized trial, cohort, or registry data), separately for the development and validation data sets, if applicable.	7 and appendix 3
	4b	Specify the key study dates, including start of accrual; end of accrual; and, if applicable, end of follow-up.	7
Participants	5a	Specify key elements of the study setting (e.g., primary care, secondary care, general population) including number and location of centers.	7 and appendix 8
	5b	Describe eligibility criteria for participants.	7
	5c	Give details of treatments received, if relevant.	Appendix 8
Outcome	6a	Clearly define the outcome that is predicted by the prediction model, including how and when assessed.	8
	6b	Report any actions to blind assessment of the outcome to be predicted.	Not applicable
Predictors	7a	Clearly define all predictors used in developing or validating the multivariable prediction model, including how and when they were measured.	8, 9 and appendix 9, 10

	7b	Report any actions to blind assessment of predictors for the outcome and other predictors.	Not applicable
Sample size	8	Explain how the study size was arrived at.	7
Missing data	9	Describe how missing data were handled (e.g., complete-case analysis, single imputation, multiple imputation) with details of any imputation method.	10
Statistical analysis methods	10a	Describe how predictors were handled in the analyses.	9, 10 and appendix 14, 15
	10b	Specify type of model, all model-building procedures (including any predictor selection), and method for internal validation.	9,10 and appendix 14, 15, 16
	10d	Specify all measures used to assess model performance and, if relevant, to compare multiple models.	10 and appendix 16
Risk groups	11	Provide details on how risk groups were created, if done.	11
Results			
Participants	13a	Describe the flow of participants through the study, including the number of participants with and without the outcome and, if applicable, a summary of the follow-up time. A diagram may be helpful.	13
	13b	Describe the characteristics of the participants (basic demographics, clinical features, available predictors), including the number of participants with missing data for predictors and outcome.	13, 25 and appendix 17-20
Model development	14a	Specify the number of participants and outcome events in each analysis.	13-16
	14b	If done, report the unadjusted association between each candidate predictor and outcome.	Not applicable
Model specification	15a	Present the full prediction model to allow predictions for individuals (i.e., all regression coefficients, and model intercept or baseline survival at a given time point).	14 and appendix 22
	15b	Explain how to use the prediction model.	14
Model performance	16	Report performance measures (with CIs) for the prediction model.	13-16 and appendix 21, 22, 25-55
Discussion			

Limitations	18	Discuss any limitations of the study (such as non representative sample, few events per predictor, missing data).	19, 20
Interpretation	19b	Give an overall interpretation of the results, considering objectives, limitations, and results from similar studies, and other relevant evidence.	17-19
Implications	20	Discuss the potential clinical use of the model and implications for future research.	19

Table 7 – Statistical assumptions : comparison between additive and multiplicative models
This table shows the six statistical assumptions that should be checked in linear regression model, for the final additive model, and the final multiplicative model. Overall, all assumptions were validated, except for the collinearity of predictors in the multiplicative model : the risk of collinearity was moderate in the multiplicative model and low in the additive model.

Assumptions for developing a linear regression model	Status (additive model)	Status (multiplicative model)
#1 The patients are independent.	✓	✓
#2 The outcome is equally varied (variance should not be related to mean as they are supposed to be estimated separately).	✓ 	✓ 
#3 The predictors are normally or uniformly distributed.	✓ (creatinine was log-transformed, and recipient age is gaussian)  	✓ (creatinine was log-transformed, and recipient age is gaussian)
#4 The relationship between the linear predictors and the outcome should be linear.	✓   	

#5 The number of predictors should be lower than the number of patients.	✓	✓
#6 Predictors should not be collinear. The variance-inflation-factor evaluates the risk of collinearity. Values close to 1 indicate a low risk of collinearity. Values beyond 5 indicate a high risk of collinearity.	✓ **Variance-inflation-factor** (adding creatinine² providing better results especially at lower GFR) Creatinine = 1.12 Creatinine² = 3.42 Age = 1.01 Gender = 1.12	✗ **Variance-inflation-factor** (data were centered to avoid bias. Results were similar with addition of the creatinine²) Creatinine = 2.85 Age = 2.99 Gender = 1.30 Creatinine*Age = 2.79 Creatinine* Gender = 2.56 Age*Gender = 3.01 Creatinine *Age*Gender = 2.49

Table 8 – Model fit metrics : comparison between additive and multiplicative models
This table shows the adjusted R^2, the root-mean-square-error, and the mean absolute error of the final additive model and the final multiplicative model. Since the additive and multiplicative models present with the same fit, and since the additive model has a lower risk of collinearity (see table 4), and is simpler to use, we focused on the additive model.

Model fit	Additive model	Multiplicative model
Adjusted R^2	0.73	0.73
Root-mean-square-error	0.18	0.18
Mean absolute error (in mL/min/1.73m²)	7.48	7.47

Table 9 – Baseline characteristics per center (development cohort)

		Necker Hospital (n= 2,737)		Saint Louis Hospital (n= 374)		Toulouse Hospital (n= 511)	p
	N		N		N		
Recipient characteristics							
Age (years) mean (SD)	2737	51.10 (14.17)	374	50.86 (14.30)	511	53.48 (12.89)	0.001
Gender male No. (%)	2737	1635 (59.74)	374	227 (60.70)	511	309 (60.47)	0.91
BMI (Kg/m^2) mean (SD)	2737	24.70 (4.58)	374	25.21 (4.67)	511	24.72 (4.27)	0.12
Black race No. (%)	2737	237 (8.66)	374	83 (22.19)	511	13 (2.54)	<0.001
Measured GFR (ml/min/1.73m^2) median (IQR)	2737	55.00 (43.00-66.95)	374	49.30 (37.15-59.21)	511	52.39 (41.00-67.00)	<0.001
End stage kidney disease causes							
Glomerulonephritis No. (%)	2737	649 (23.71)	374	89 (23.80)	511	165 (32.29)	<0.001
Diabetes No. (%)	2737	245 (8.95)	374	61 (16.31)	511	52 (10.18)	
Vascular No. (%)	2737	204 (7.45)	374	68 (18.18)	511	47 (9.20)	
Other No. (%)	2737	1636 (59.77)	374	156 (41.71)	511	246 (48.14)	
Donor characteristics							
Age (years) mean (SD)	2737	52.22 (16.67)	374	50.37 (16.36)	511	50.47 (15.09)	0.30
Male gender No. (%)	2713	1429 (52.67)	374	211 (56.42)	0	NA	0.09
Hypertension No. (%)	2107	349 (16.56)	322	41 (12.73)	279	71 (25.45)	<0.001
Diabetes mellitus No. (%)	2219	155 (6.99)	358	18 (5.03)	392	25 (6.38)	0.38
Creatinine>1.5mg/dL No. (%)	2689	272 (10.12)	364	32 (8.79)	503	61 (12.13)	0.25
Donor type							
Deceased donor No. (%)	2725	2103 (77.17)	374	297 (79.41)	511	490 (95.89)	<0.001
Transplant baseline characteristics							
Prior kidney transplant No. (%)	2732	492 (18.01)	374	59 (15.78)	0	NA	0.09
Delayed graft function No. (%)	2693	685 (25.44)	368	79 (21.47)	503	117 (23.26)	0.18
Cold ischemia time in deceased donors (hours) mean (SD)	2737	16.52 (10.46)	374	13.32 (7.47)	0	NA	<0.001
HLA-A/B/DR mismatch number mean (SD)	2737	4.26 (1.39)	374	4.57 (1.29)	0	NA	<0.001

Table 10 – Baseline characteristics per center (French validation cohort)

	Montpellier Hospital (n= 1,486)		Tenon Hospital (n= 469)		Lyon Hospital (n=248)		Saint Etienne Hospital (n= 446)		p
	N		N		N		N		
Recipient characteristics									
Age (years) mean (SD)	1486	53.15 (13.55)	469	49.05 (13.57)	248	50.75 (14.21)	446	54.91 (13.55)	<0.001
Gender male No. (%)	1486	937 (63.06)	469	305 (65.03)	248	161 (64.92)	446	297 (66.59)	0.54
BMI (Kg/m^2) mean (SD)	1486	24.70 (4.52)	469	25.58 (4.79)	248	24.78 (4.21)	446	25.00 (4.27)	0.03
Black race No. (%)	1486	4 (0.27)	469	139 (29.64)	248	7 (2.82)	446	0 (0.00)	<0.001
Measured GFR (ml/min/1.73m^2) median (IQR)	1486	49.00 (36.13-62.67)	469	47.20 (33.30-60.70)	248	52.27 (41.56-62.00)	446	51.00 (38.14-66.24)	<0.001
End stage kidney disease causes									
Glomerulonephritis No. (%)	1140	345 (30.26)	0	NA	242	44 (18.18)	0	NA	<0.001
Diabetes No. (%)	1140	81 (7.11)	0	NA	242	57 (23.55)	0	NA	
Vascular No. (%)	1140	56 (4.91)	0	NA	242	29 (11.98)	0	NA	
Other No. (%)	1140	658 (57.72)	0	NA	242	112 (46.28)	0	NA	
Donor characteristics									
Age (years) mean (SD)	0	NA	469	52.03 (15.50)	242	51.38 (15.93)	0	NA	0.42
Male gender No. (%)	1132	643 (56.80)	469	235 (50.11)	242	149 (61.57)	0	NA	0.28
Hypertension No. (%)	929	155 (16.68)	0	NA	0	NA	0	NA	NA
Diabetes mellitus No. (%)	783	40 (5.11)	0	NA	0	NA	0	NA	NA
Creatinine > 1.5mg/dL No. (%)	942	136 (14.44)	0	NA	242	31 (12.81)	0	NA	0.33
Donor type									
Deceased donor No. (%)	1135	1062 (93.57)	439	340 (77.45)	0	NA	0	NA	<0.001
Transplant baseline characteristics									
Prior kidney transplant No. (%)	0	NA	0	NA	242	34 (14.05)	446	0 (0.0)	NA
Delayed graft function No. (%)	1101	154 (13.99)	0	NA	0	NA	0	NA	NA
Cold ischemia time in deceased donors (hours) mean (SD)	1486	18.50 (8.59)	40	16.57 (6.33)	239	12.45 (6.54)	0	NA	<0.001
HLA-A/B/DR mismatch number mean (SD)	1486	2.93 (1.30)	434	4.29 (1.40)	248	3.40 (1.22)	0	NA	<0.001

Table 11 – Baseline characteristics per center (European and Oceanian validation cohorts)

	Zagreb Hospital (n= 883)		Bergamo Hospital (n= 196)		Groningen Kidney Center (n= 1738)		M Aarhus Hospital (n= 80)		Sydney Transplant Unit (n= 430)		p
	N		N		N		N		N		
Recipient characteristics											
Age (years) mean (SD)	883	50.06 (12.46)	196	50.38 (13.25)	1738	50.59 (13.72)	80	53.34 (12.13)	430	41.00 (10.34)	<0.001
Gender male No. (%)	883	536 (60.70)	196	138 (70.41)	1738	1044 (60.07)	80	58 (72.50)	430	236 (54.88)	<0.001
BMI (Kg/m^2) mean (SD)	883	25.33 (3.76)	196	23.67 (3.63)	1738	25.91 (10.36)	80	24.95 (3.41)	189	25.91 (4.32)	0.002
Black race No. (%)	883	0.00 (0.00)	196	0.00 (0.00)	1738	0.00 (0.00)	80	0.00 (0.00)	430	0.00 (0.00)	<0.001
Measured GFR (ml/min/1.73m^2) median (IQR)	883	58.95 (44.81-74.10)	196	52.18 (40.11-63.05)	1738	51.56 (40.44-62.87)	80	46.60 (36.35-58.15)	430	58.00 (42.20-72.00)	<0.001
End stage kidney disease causes											
Glomerulonephritis No. (%)	883	336 (38.05)	196	63 (32.14)	0	NA	0	NA	0	NA	<0.001
Diabetes No. (%)	883	52 (5.89)	196	2.0 (1.02)	0	NA	0	NA	0	NA	
Vascular No. (%)	883	135 (15.29)	196	5.0 (2.55)	0	NA	0	NA	0	NA	
Other No. (%)	883	360 (40.77)	196	126 (64.29)	0	NA	0	NA	0	NA	
Donor characteristics											
Age (years) mean (SD)	883	50.34 (12.67)	196	49.0 (17.22)	1735	49.79 (13.51)	80	53.94 (12.88)	0	NA	<0.001
Male gender No. (%)	883	501 (56.74)	196	98 (50.00)	0	NA	76	40 (52.63)	0	NA	0.28
Hypertension No. (%)	883	388 (43.94)	196	36 (18.37)	0	NA	0	NA	0	NA	<0.001
Diabetes mellitus No. (%)	883	62 (7.02)	196	4.0 (2.04)	0	NA	0	NA	0	NA	0.008
Creatinine > 1.5mg/dL No. (%)	862	126 (14.62)	0	NA	0	NA	0	NA	0	NA	NA
Donor type											
Deceased donor No. (%)	883	863 (97.73)	196	196 (100.00)	0	NA	0	NA	0	NA	0.02
Transplant baseline characteristics											
Prior kidney transplant No. (%)	883	80 (9.06)	196	0.0 (0.00)	0	NA	0	NA	0	NA	<0.001
Delayed graft function No. (%)	883	205 (23.22)	0	NA	0	NA	80	18 (22.50)	0	NA	1
Cold ischemia time in deceased donors (hours) mean (SD)	473	21.20 (15.58)	196	16.54 (3.76)	0	NA	80	12.80(4.59)	0	NA	<0.001
HLA-A/B/DR mismatch number mean (SD)	869	3.00 (1.10)	196	3.29 (1.32)	0	NA	0	NA	0	NA	<0.001

Table 12 – Baseline characteristics per center (American validation cohort)

	Mayo Clinic Hospital, Minnesota (n=4,062)		Mayo Clinic Hospital, Florida (n= 709)		ABCAN trial (n=139)		BENEFIT trial (n= 981)		p
	N		N		N		N		
Recipient characteristics									
Age (years) mean (SD)	4062	53.08 (13.46)	709	53.00 (13.24)	139	48.31 (12.30)	981	49.37 (14.45)	<0.001
Gender male No. (%)	4062	2382 (58.64)	709	434 (61.21)	139	88 (63.31)	981	671 (68.40)	<0.001
BMI (Kg/m^2) mean (SD)	4006	29.00 (6.68)	707	28.32 (5.58)	139	26.35 (5.00)	941	26.32 (4.56)	<0.001
Black race No. (%)	4062	115 (2.83)	709	228 (32.16)	139	0.00 (0.00)	981	105 (10.70)	<0.001
Measured GFR (ml/min/1.73m^2) median (IQR)	4062	55.00 (43.00-67.00)	709	60.00 (45.00-75.00)	139	56.30 (48.60-68.00)	981	58.00 (45.00-73.00)	<0.001
End stage kidney disease causes									
Glomerulonephritis No. (%)	3965	872 (21.99)	530	173 (32.64)	139	0 (0.00)	0	NA	<0.001
Diabetes No. (%)	3965	748 (18.87)	530	160 (30.19)	139	52 (37.41)	0	NA	
Vascular No. (%)	3965	257 (6.48)	530	159 (30.00)	139	8 (5.76)	0	NA	
Other No. (%)	3965	2088 (52.66)	530	40 (7.55)	139	79 (56.83)	0	NA	
Donor characteristics									
Age (years) mean (SD)	4062	43.68 (15.36)	707	39.18 (14.05)	0	NA	979	47.22 (14.88)	<0.001
Male gender No. (%)	4062	1857 (45.72)	707	391 (55.30)	0	NA	980	473 (48.27)	<0.001
Hypertension No. (%)	0	NA	0	NA	0	NA	0	NA	NA
Diabetes mellitus No. (%)	0	NA	0	NA	0	NA	0	NA	NA
Creatinine > 1.5mg/dL No. (%)	0	NA	0	NA	0	NA	0	NA	NA
Donor type									
Deceased donor No. (%)	4062	1140 (28.06)	709	497 (70.10)	139	40 (28.78)	981	672 (68.50)	<0.001
Transplant baseline characteristics									
Prior kidney transplant No. (%)	4062	612 (15.07)	709	68 (9.59)	139	18 (12.95)	0	NA	<0.001
Delayed graft function No. (%)	3961	270 (6.82)	707	139 (19.66)	0	NA	981	280 (28.54)	<0.001
Cold ischemia time in deceased donors (hours) mean (SD)	2943	5.61 (9.96)	365	8.47 (8.35)	0	NA	971	13.4 (10.40)	<0.001
HLA-A/B/DR mismatch number mean (SD)	3944	3.34 (1.83)	699	3.92 (1.64)	0	NA	981	3.36 (1.30)	<0.001

Table 13 – Comparing P_{30} of current GFR equations
For each equation, the highest P_{30} is highlighted in green. The median P_{30} of the race-free CKD-EPI-2021, CKD-EPI-2009 and MDRD equations were compared to the median P_{30} of the race-free KRS equation using a Wilcoxon test.

Cohort	MDRD	CKD-EPI-2009	Race-free CKD-EPI-2021	Race-free KRS
Development cohort	87.2%	85.6%	84.2%	89.8%
Montpellier, transplant department	92.3%	91.3%	88.4%	88.5%
Tenon, transplant department	81.1%	81.3%	82.1%	86.4%
Lyon, transplant department	89.5%	79.0%	70.2%	86.3%
Saint-Etienne, transplant department	83.9%	82.8%	77.2%	83.2%
Mayo Clinic	82.4%	82.4%	83.4%	84.1%
ABCAN trial	88.5%	88.5%	85.6%	90.6%
BENEFIT and BENEFIT-EXT trials	79.1%	75.3%	71.6%	78.4%
Bergamo hospital	94.3%	90.3%	84.2%	91.3%
Zagreb hospital	57.1%	63.6%	70.6%	73.0%
Groningen Kidney Center	91.2%	91.1%	87.0%	90.6%
Sydney Transplant Unit	74.0%	77.3%	78.3%	80.6%
Aarhus University Hospital	89.9%	86.3%	83.5%	85.6%

KRS & CKD-EPI-2021 : P = 0.003 (Wilcoxon test)
KRS & CKD-EPI-2009 : P = 0.04
KRS & MDRD : P = 0.85

Table 14 – Confidence intervals for P_{30} and correct classification values per cohort
This table shows the P_{30} and correct classification percentages with their 95% confidence intervals. They are presented by cohort and compared according to the equation used.

Cohort	MDRD		CKD-EPI-2009		Race-free CKD-EPI-2021		Race-free KRS	
	P_{30} % (95% CI)	Correct classification % (95% CI)	P_{30} % (95% CI)	Correct classification % (95% CI)	P_{30} % (95% CI)	Correct classification % (95% CI)	P_{30} % (95% CI)	Correct classification % (95% CI)
Developement	87.2 (85.9 to 88.1)	72.7 (71.5 to 74.5)	85.6 (84.9 to 87.1)	71.9 (70.5 to 73.5)	84.2 (82.8 to 85.2)	70.6 (69.5 to 72.5)	89.8 (89.0 to 91.0)	75.1 (73.6 to 0.76)
Montpellier	92.3 (90.6 to 93.4)	77.3 (74.9 to 79.1)	91.3 (89.5 to 92.5)	78.9 (76.9 to 81.1)	88.4 (86.4 to 90.0)	76.6 (74.9 to 79.1)	88.5 (87.4 to 90.6)	76.4 (73.8 to 78.2)
Tenon	81.1 (77.5 to 84.6)	66.9 (62.7 to 71.3)	81.3 (77.5 to 84.6),	68.7 (64.8 to 73.2)	82.1 (78.5 to 85.5)	67.6 (63.8 to 72.2)	86.4 (82.9 to 89.1)	71.1 (66.9 to 75.1)
Lyon	89.5 (85.1 to 92.9)	73.4 (67.5 to 78.5)	79.0 (73.9 to 84.1)	64.5 (59.1 to 70.9)	70.2 (64.3 to 75.7)	58.1 (51.86 to 64.14)	86.3 (81.7 to 90.3)	74.2 (68.5 to 79.5)
Saint-Etienne	83.9 (80.6 to 87.4)	69.8 (65.8 to 74.3)	82.8 (79.5 to 86.5)	68.2 (63.7 to 72.3)	77.2 (73.1 to 80.9)	66 (61.6 to 70.4)	83.2 (79.5 to 86.5)	68.5 (64.7 to 73.3)
Mayo Clinic	82.4 (80.9 to 83.1)	64.8 (63.7 to 66.4)	82.4 (80.9 to 83.1)	65.9 (64.7 to 67.3)	83.4 (81.9 to 84.1)	68 (66.7 to 69.3)	84.1 (83.0 to 85.0)	66.6 (65.7 to 68.3)
ABCAN trial	88.5 (83.8 to 94.2)	67.6 (60.3 to 75.8)	88.5 (83.8 to 94.2)	66.9 (59.2 to 74.8)	85.6 (80.2 to 91.8)	63.3 (55.0 to 71.0)	90.6 (86.2 to 95.8)	66.2 (58.1 to 73.9)
Benefit and Benefit-EXT trials	79.1 (76.5 to 81.6)	63.7 (61.0 to 67.0)	75.3 (72.3 to 77.8)	61.6 (59.0 to 65.0)	71.6 (69.2 to 74.8)	60.8 (58.0 to 64.1)	78.4 (75.4 to 80.6)	65.1 (62.0 to 68.0)
Bergamo	94.3 (90.7 to 97.3)	76.8 (71.1 to 83.0)	90.3 (85.8 to 94.2)	76.8 (71.1 to 83.0)	84.2 (78.9 to 89.1)	71.5 (65.7 to 78.3)	91.3 (87.0 to 95.0)	79.3 (73.3 to 84.7)
Zagreb	57.1 (53.7 to 60.3)	47.1 (43.7 to 50.3)	63.6 (60.8 to 67.2)	51.9 (48.7 to 55.3)	70.6 (68.0 to 74.0)	56.2 (52.7 to 59.3)	73 (70.1 to 75.9)	55.9 (52.7 to 59.3)
Groningen	91.2 (89.7 to 92.4)	75.5 (74.0 to 87.0)	91.1 (89.7 to 92.4)	75.8 (74.0 to 87.0)	87.0 (85.4 to 88.8)	72.5 (70.9 to 75.1)	90.6 (89.7 to 92.4)	76.3 (74.0 to 78.0)
Sydney	74.0 (69.9 to 78.2)	56.8 (52.3 to 61.7)	77.3 (73.0 to 81.0)	60 (55.4 to 64.6)	78.3 (74.1 to 81.9)	62.2 (57.4 to 66.6)	80.6 (77.3 to 84.7)	62.5 (58.4 to 67.6)
Aarhus	89.9 (83.4 to 96.6)	75.5 (66.7 to 85.4)	86.3 (78.4 to 93.8)	72.7 (63.3 to 82.7)	83.5 (76.0 to 92.03)	71.2 (61.1 to 80.9)	85.6 (78.4 to 93.6)	76.3 (66.6 to 85.4)

CI, confidence interval

Table 15 – Confidence intervals for P_{10} and correct classification values per cohort
This table shows the P_{10} with their 95% confidence intervals.

Cohort	MDRD	CKD-EPI-2009	Race-free CKD-EPI-2021	Race-free KRS
Development	38.2% (36.6 to 39.8)	37.9% (35.6 to 38.8)	36.2% (34.6 to 37.8)	40.7% (39.1 to 42.3)
Montpellier	46.6% (44.1 to 49.1)	48.4% (45.9 to 50.9)	41.9% (39.4 to 44.4)	39.2% (36.7 to 41.7)
Tenon	32.3% (28.1 to 36.5)	32.8% (28.6 to 37.0)	34.0% (29.7 to 38.3)	41.0% (36.5 to 45.5)
Lyon	44.0% (37.8 to 50.2)	31.9% (26.1 to 37.7)	27.8% (22.2 to 33.4)	41.9% (35.8 to 48.0)
Saint-Etienne	35.8% (31.4 to 40.2)	33.3% (28.9 to 37.7)	31.1% (26.8 to 35.4)	34.2% (29.8 to 38.6)
Mayo Clinic	29.2% (27.9 to 30.4)	31.0% (29.7 to 32.3)	34.4% (33.1 to 35.7)	32.8% (31.5 to 34.1)
ABCAN trial	38.8% (30.7 to 46.9)	41.7% (33.5 to 49.9)	37.4% (29.4 to 45.4)	43.9% (35.6 to 52.2)
BENEFIT and BENEFIT-EXT trials	32.1% (29.2 to 35.0)	32.2% (29.3 to 35.1)	28.9% (26.1 to 31.7)	33.3% (30.4 to 36.2)
Bergamo	45.8% (38.8 to 52.8)	44.6% (37.6 to 51.6)	38.4% (31.8 to 45.4)	49.1% (42.1 to 56.1)
Zagreb	16.0% (13.6 to 18.4)	19.6% (17.0 to 22.2)	23.6% (20.8 to 26.4)	22.3% (19.6 to 25.0)
Groningen	40.0% (37.7 to 42.3)	42.4% (40.1 to 44.7)	40.7% (38.4 to 43.0)	43.6% (41.3 to 45.9)
Sydney	25.7% (23.6 to 27.8)	30.0% (27.8 to 32.2)	32.4% (30.2 to 34.6)	32.2% (30.0 to 34.4)
Aarhus	37.4% (26.8 to 48.0)	38.8% (28.1 to 49.5)	36.6% (26.0 to 47.2)	38.8% (28.1 to 49.5)

Table 16 – Final race-free multivariable model

This table shows the coefficients of the final, multivariable, additive, linear model. As the use of race did not significantly increase the prediction performances, the following equation based on the coefficients is race-free: $eGFR = e^{4.4275492 - 0.8230475 \times \log(\text{creatinine in mg/dL}) - 0.0124264 \times \text{creatinine}^2 \text{ in mg/dL} - 0.0055068 \times \text{age in years} + 0.1806494 \text{ (if the patient is male)}}$

Parameters	Number of patients	Number of measurements	Estimates	Standard error	p-value
Intercept	3,622	8,827	4.4275492	0.0078821	< 0.001
Creatinine (mg/dL, log-transformed)	3,622	8,827	-0.8230475	0.0111887	< 0.001
Creatinine² (mg/dL)	3,622	8,827	-0.0124264	0.0014831	< 0.001
Age (years)	3,622	8,827	-0.0055068	0.0001356	< 0.001
Gender (if male)	3,622	8,827	0.1806494	0.0041897	< 0.001

Table 17 – Lasso analysis

When performing a standard linear regression based on the parameters selected by the Lasso regressions, we obtained a P30 of 89%, the same as the current KRS equation, which contains less parameters and is therefore easier to implement and use in clinical practice.

The difference between the performances of the Lasso regression, and linear regressions based on the Lasso parameters' selection, mainly stems from a suboptimal estimation of the intercept. When using log(mGFR) as the outcome, the performances remained the same. Overall, the selection of donor parameters with Lasso regressions did not improve the performances of the model.

Based on these results, we conserved the KRS equation.

Method used	Set of parameters selected	P_{30} using the coefficients of the Lasso regression	P_{30} using the coefficients of the standard linear regression with the variables selected by Lasso
Standard linear regression with mGFR as the outcome	Recipient: sex, creatinine, creatinine², age	Not applicable	89% (reference model)
Lasso regression with mGFR as the outcome	Recipient: sex, creatinine, age, race, weight, height, delayed graft function, cause of ESRD Donor type (deceased/living), donor creatinine	72% (no performance improvement)	89% (no performance improvement)

3 Figures

Figure 1 – Distribution of mGFR in all cohorts

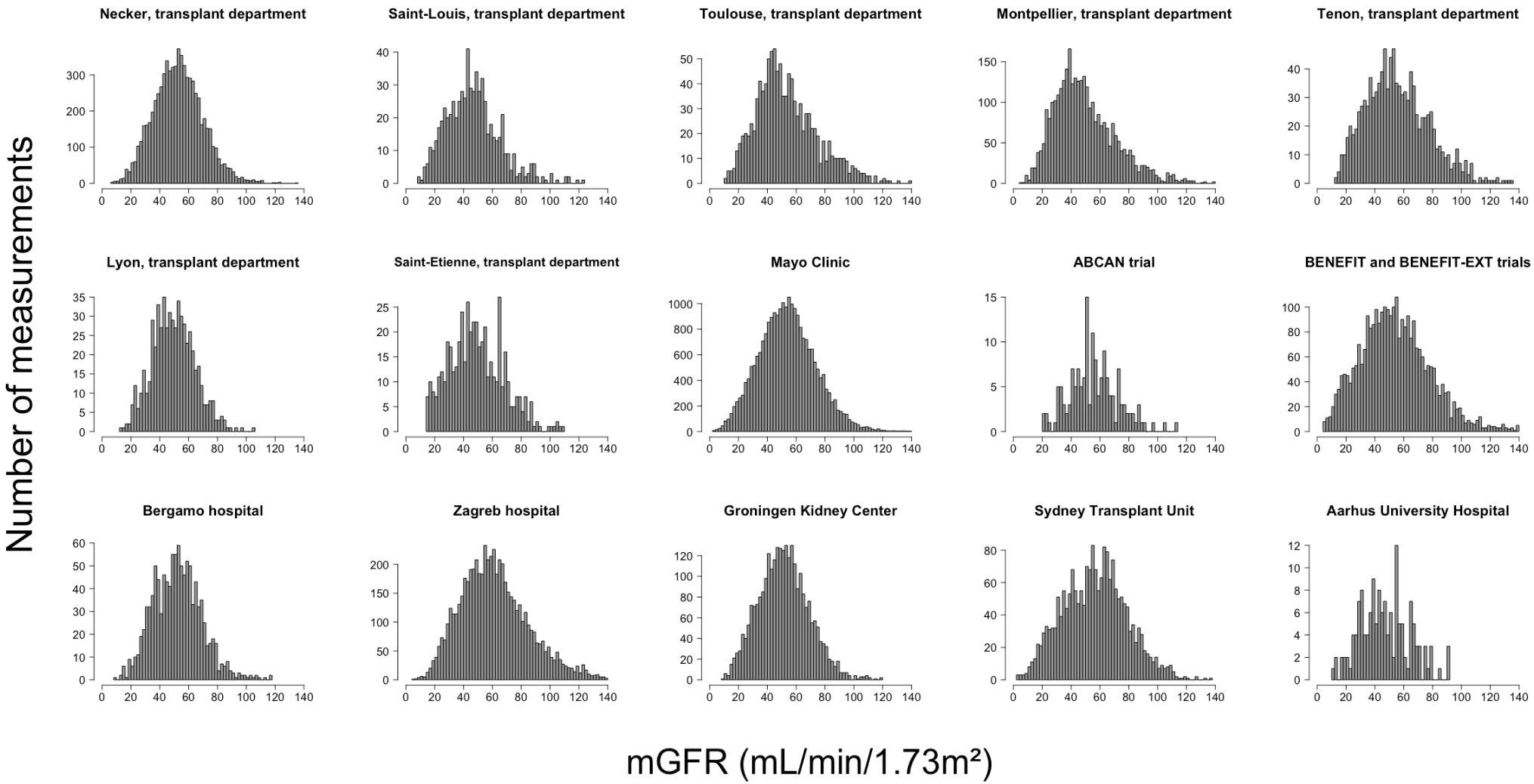


Figure 2 – Distribution of mGFR in all cohorts according to creatinine values

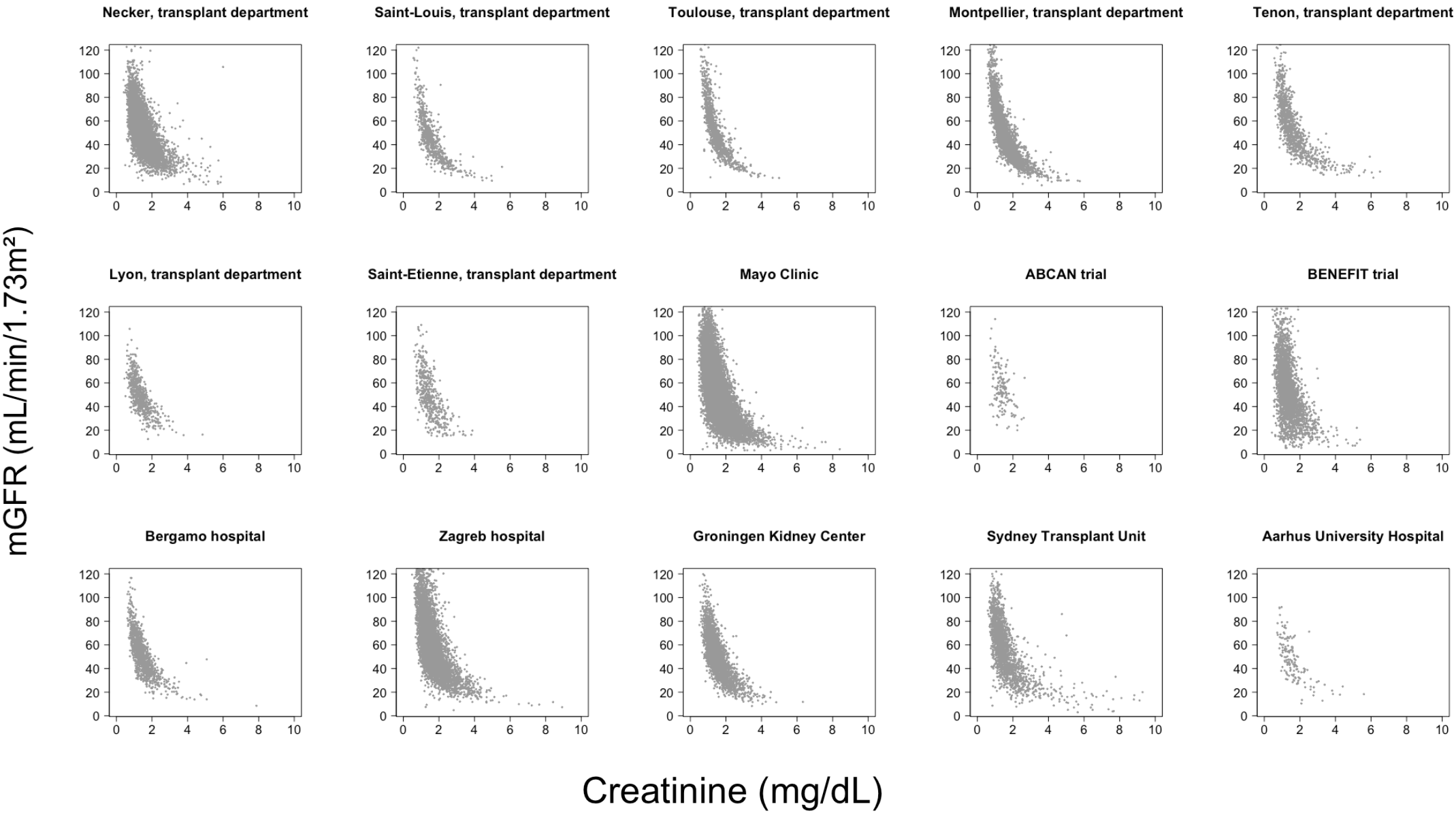


Figure 3 – Performances of KRS GFR equations vs race-free KRS GFR equation : overall population

The graphs show the P_{30} and the correct classification metrics for the four GFR equations, in the french development cohort, and in the external validation cohorts gathering : Montpellier, transplant department (panel A), Tenon, transplant department (B), and Mayo-Clinic, Rochester (D). eGFR was calculated with the kidney-recipients-specific (KRS) GFR equations, and the race-free KRS GFR equations on the basis of recipient creatinine, age, gender, and race (if required by the equation). The P_{30} is the proportion of the eGFR within the 30% of the mGFR. The correct classification is the agreement between eGFR and mGFR according to the GFR stages. As the performances were very similar, we chose to adopt the race-free equation.

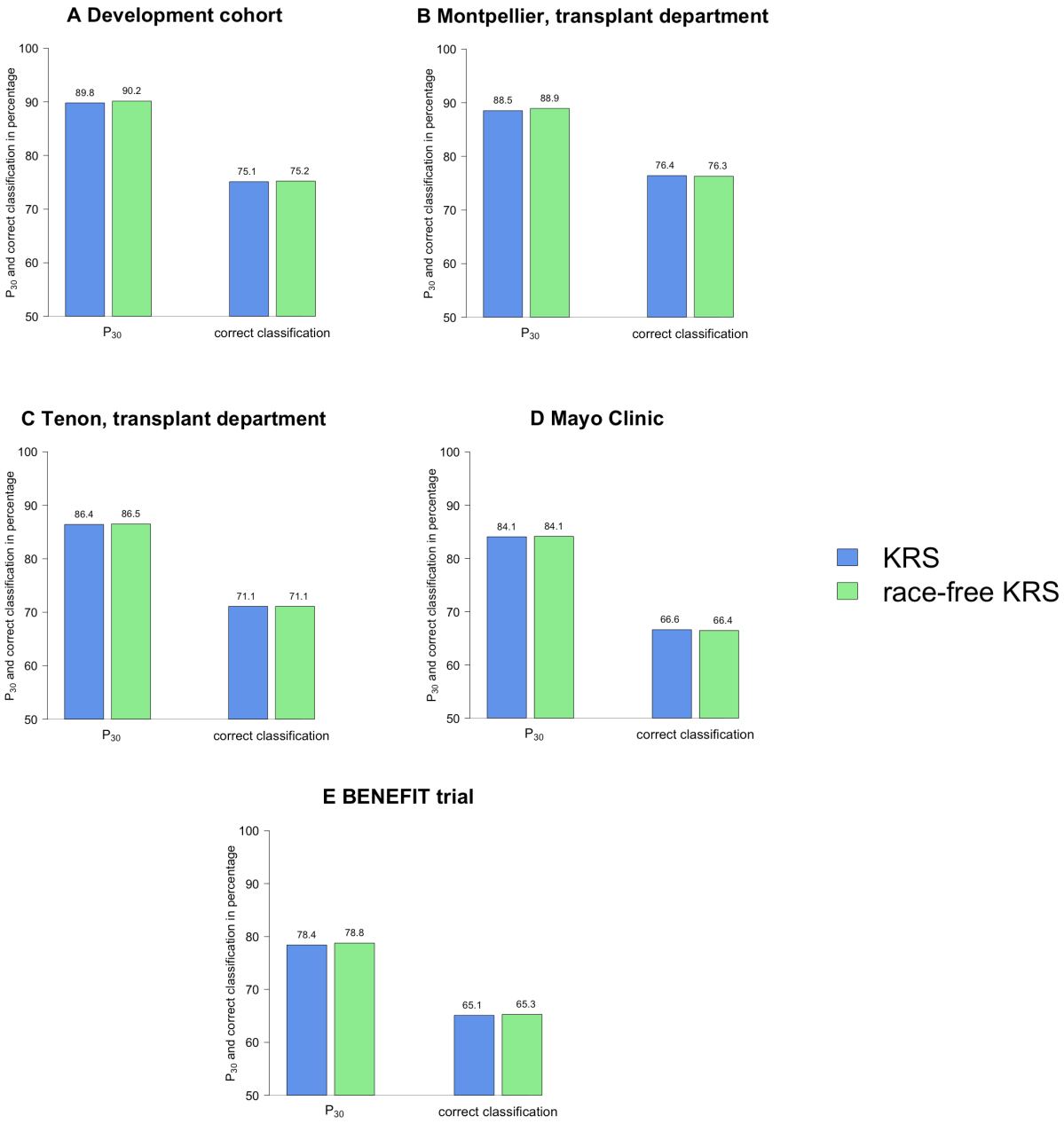


Figure 4 – Performances of KRS GFR equation vs race-free KRS GFR equation : black patients
The graphs show the P_{30} and the correct classification metrics for the four GFR equations, in the development cohort, and in the external validation cohorts gathering : Montpellier, transplant department (panel A), Tenon, transplant department (B), and Mayo-Clinic, Rochester (D). eGFR was calculated with the kidney-recipients-specific (KRS) GFR equations, and the race-free KRS GFR equations on the basis of recipient creatinine, age, gender, and race (if required by the equation). The P_{30} is the proportion of the eGFR within the 30% of the mGFR. The correct classification is the agreement between eGFR and mGFR according to the GFR stages. As the performances were very similar, we chose to adopt the race-free equation.

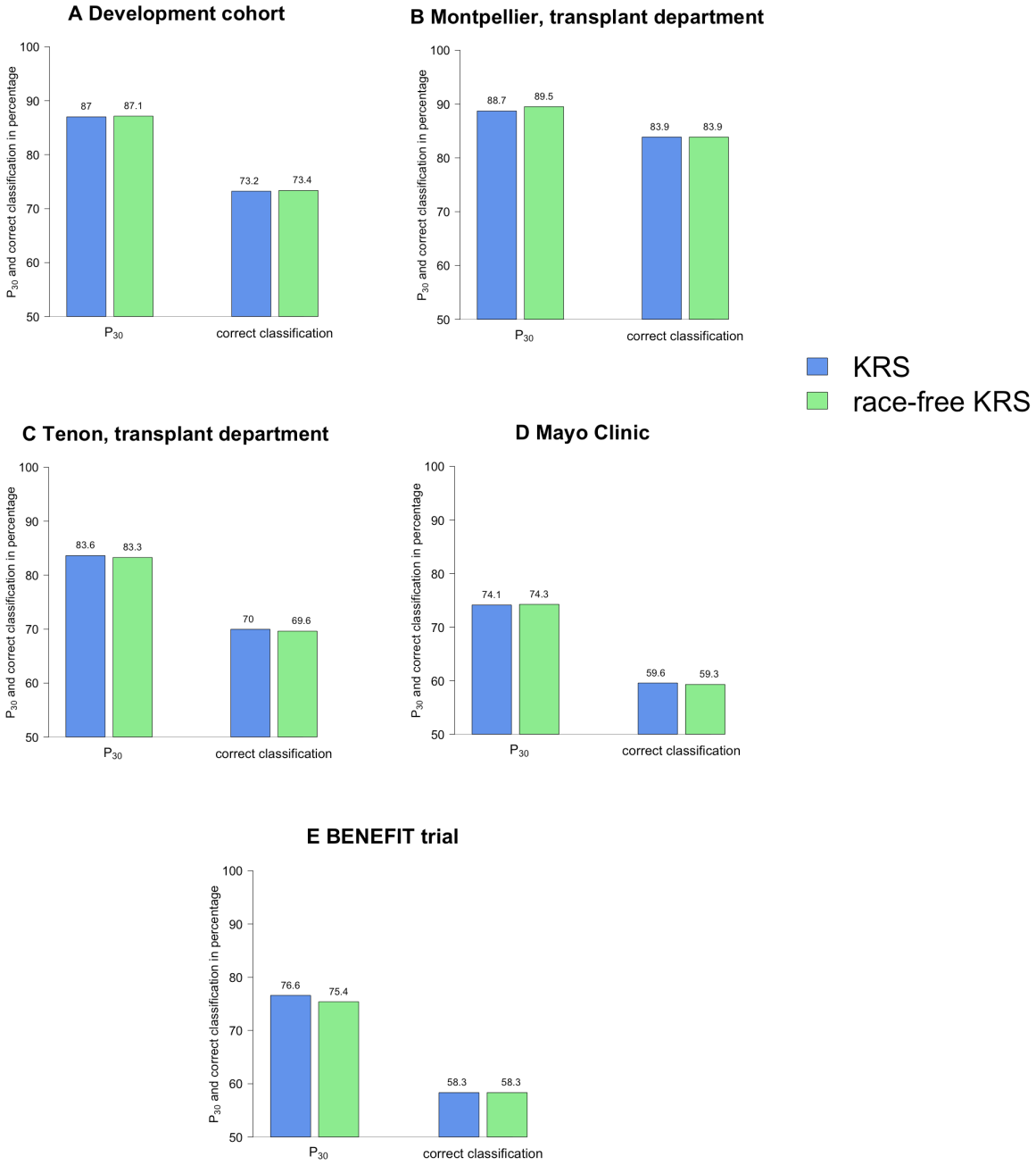


Figure 5 – Performances of GFR equations in non-black patients

The P_{30} is the proportion of the eGFR within the 30% of the mGFR. The correct classification is the agreement between eGFR and mGFR according to the GFR stages.

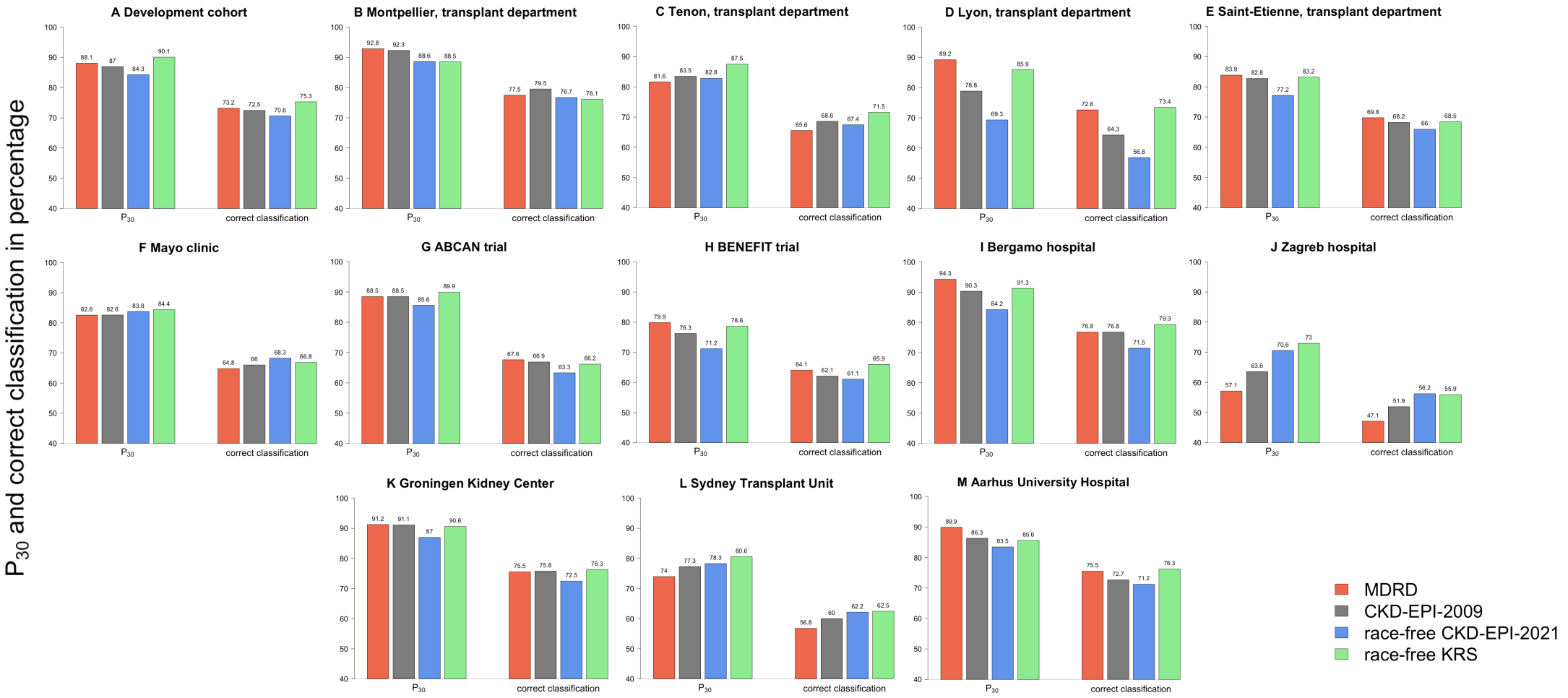


Figure 6 – Performances of GFR equations in black patients
The P_{30} is the proportion of the eGFR within the 30% of the mGFR. The correct classification is the agreement between eGFR and mGFR according to the GFR stages.

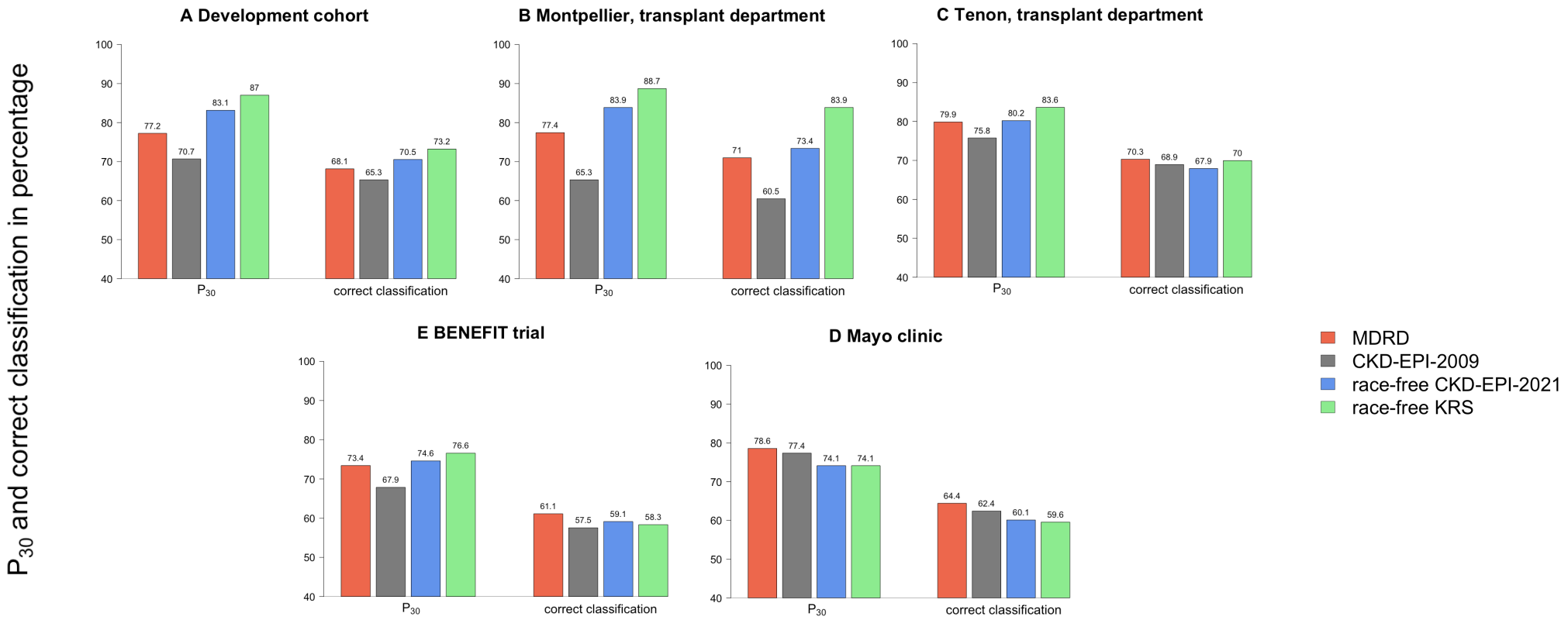
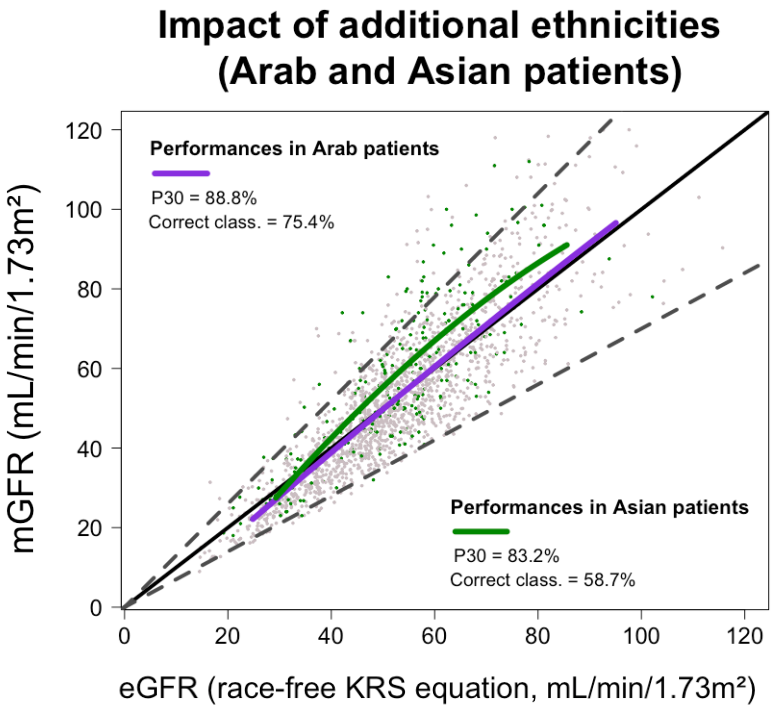


Figure 7 – Performances of GFR equations in additional races
The P_{30} is the proportion of the eGFR within the 30% of the mGFR. The correct classification is the agreement between eGFR and mGFR according to the GFR stages. Because of the lower number of arab, asian, indian and hispanic patients in the French cohorts and the Mayo clinic center, we decided to merge the datasets together and present the performances accordingly.



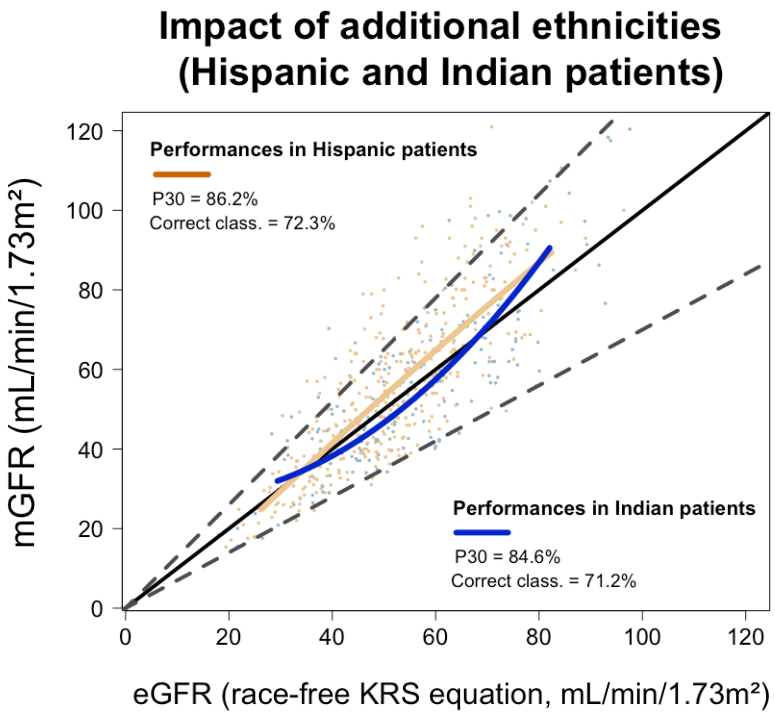


Figure 8 – Performances of GFR equations : Bland-Altman plot
A LOESS regression was performed to estimate the overall trend for each cohort.

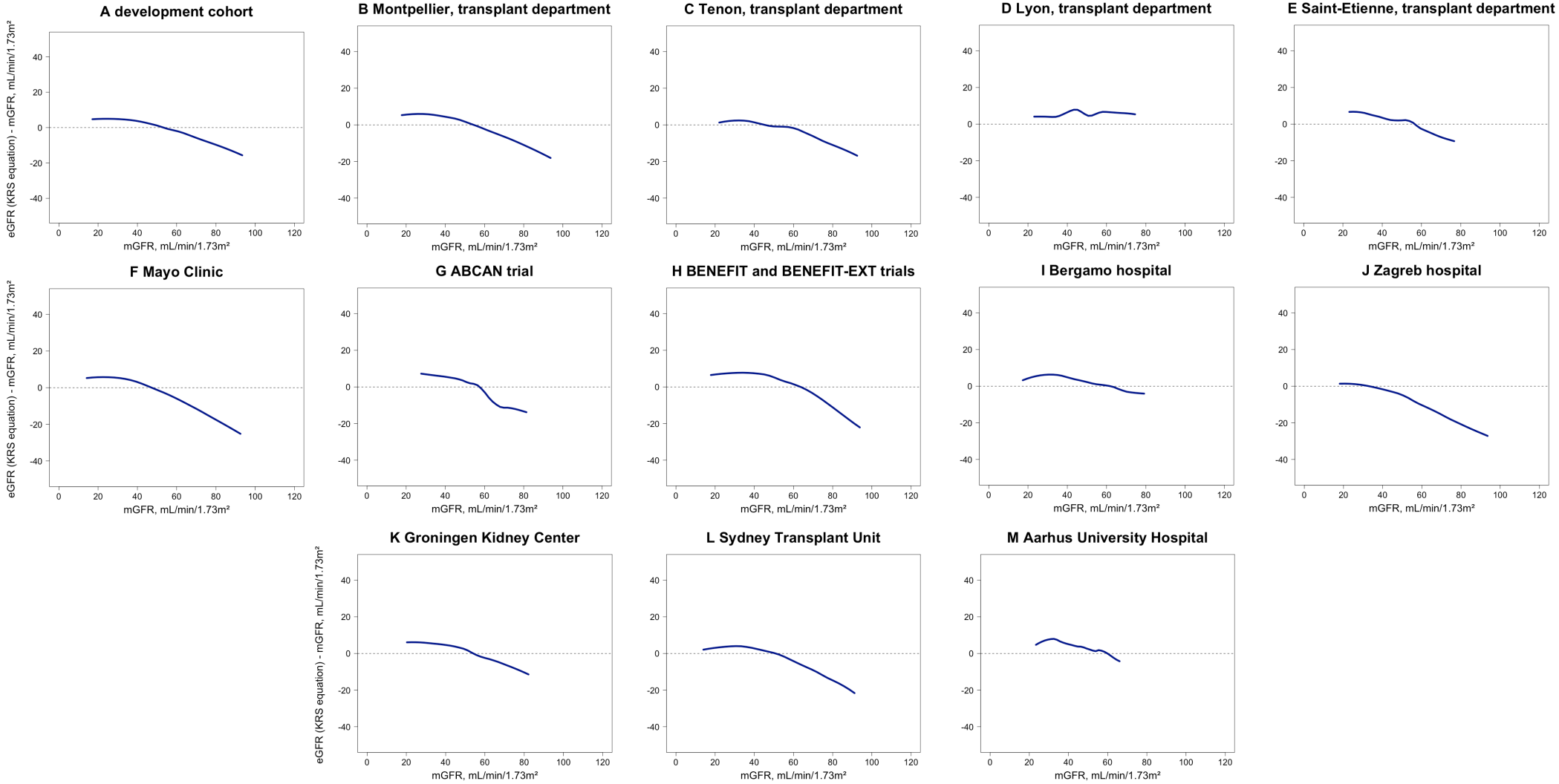


Figure 9 – Performances of GFR equations in male patients

The P_{30} is the proportion of the eGFR within the 30% of the mGFR. The correct classification is the agreement between eGFR and mGFR according to the GFR stages.

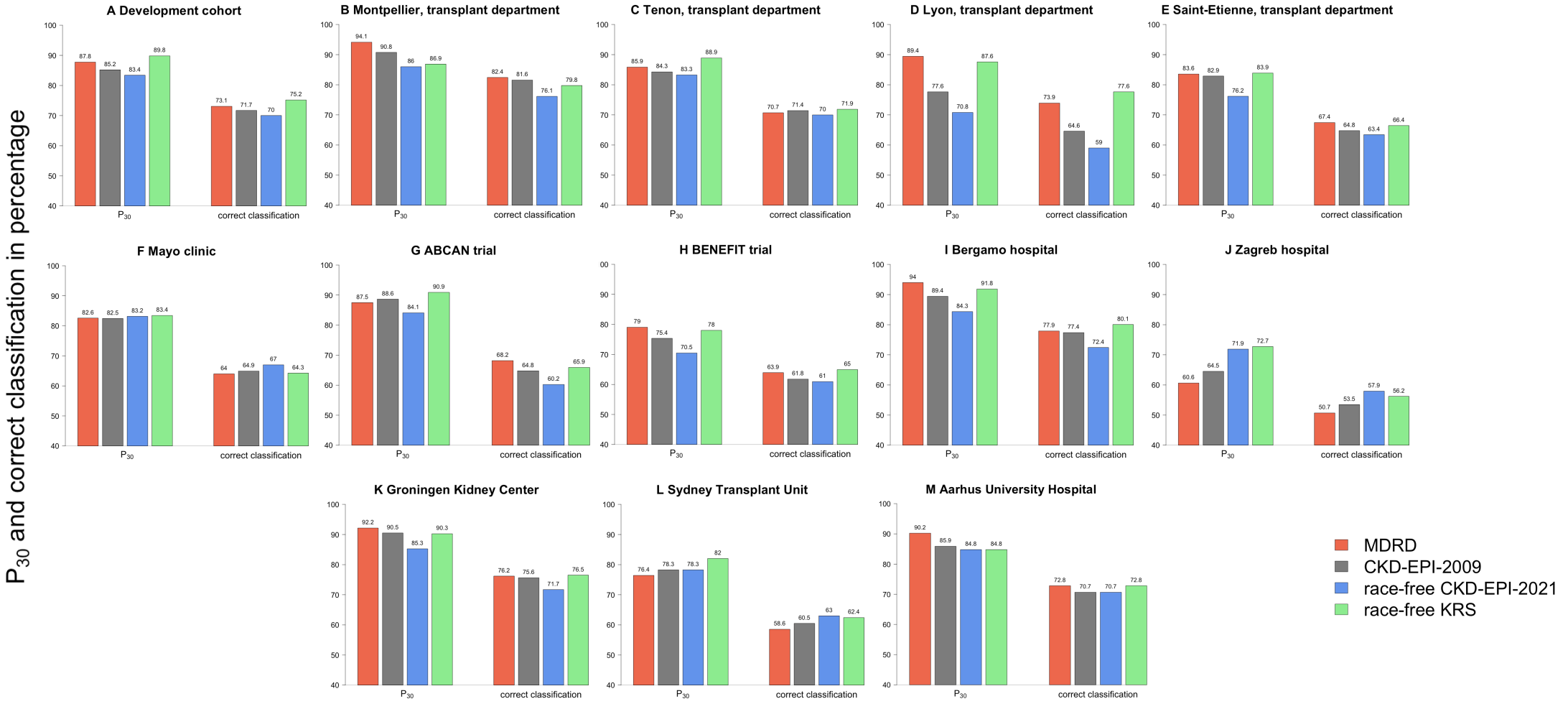


Figure 10 – Performances of GFR equations in female patients

The P_{30} is the proportion of the eGFR within the 30% of the mGFR. The correct classification is the agreement between eGFR and mGFR according to the GFR stages.

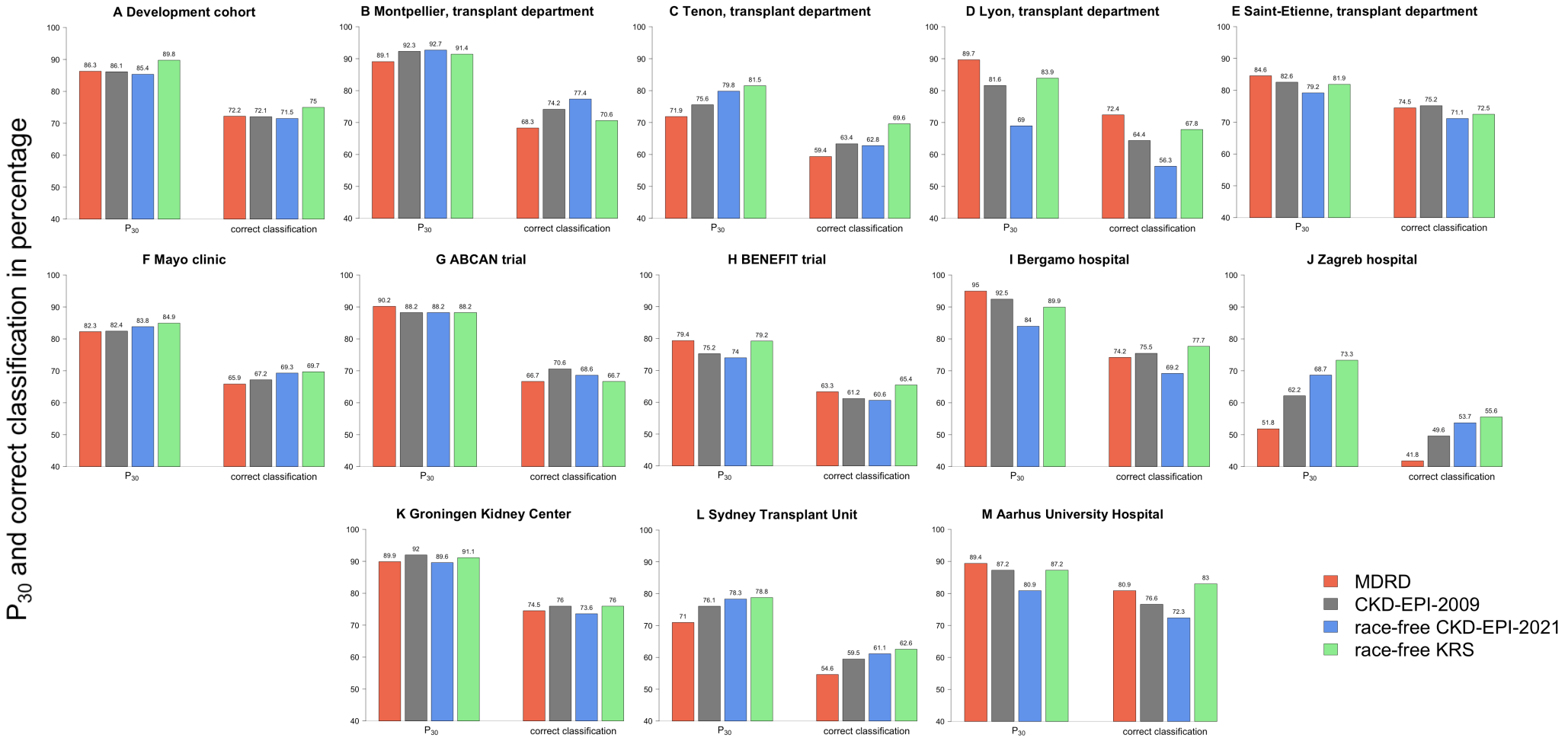


Figure 11 – Performances of GFR equations in older patients

The P_{30} is the proportion of the eGFR within the 30% of the mGFR. The correct classification is the agreement between eGFR and mGFR according to the GFR stages.

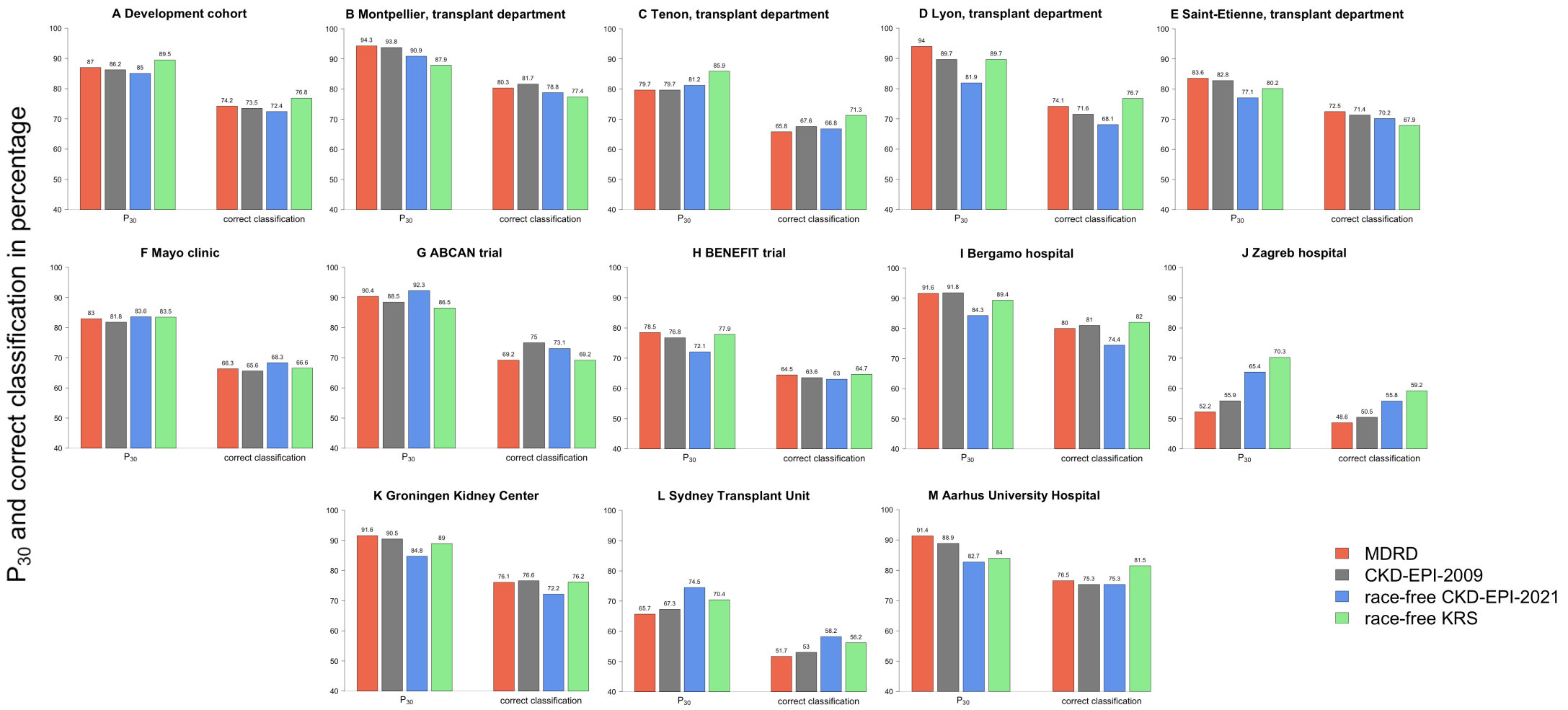


Figure 12 – Performances of GFR equations in younger patients

The P_{30} is the proportion of the eGFR within the 30% of the mGFR. The correct classification is the agreement between eGFR and mGFR according to the GFR stages.

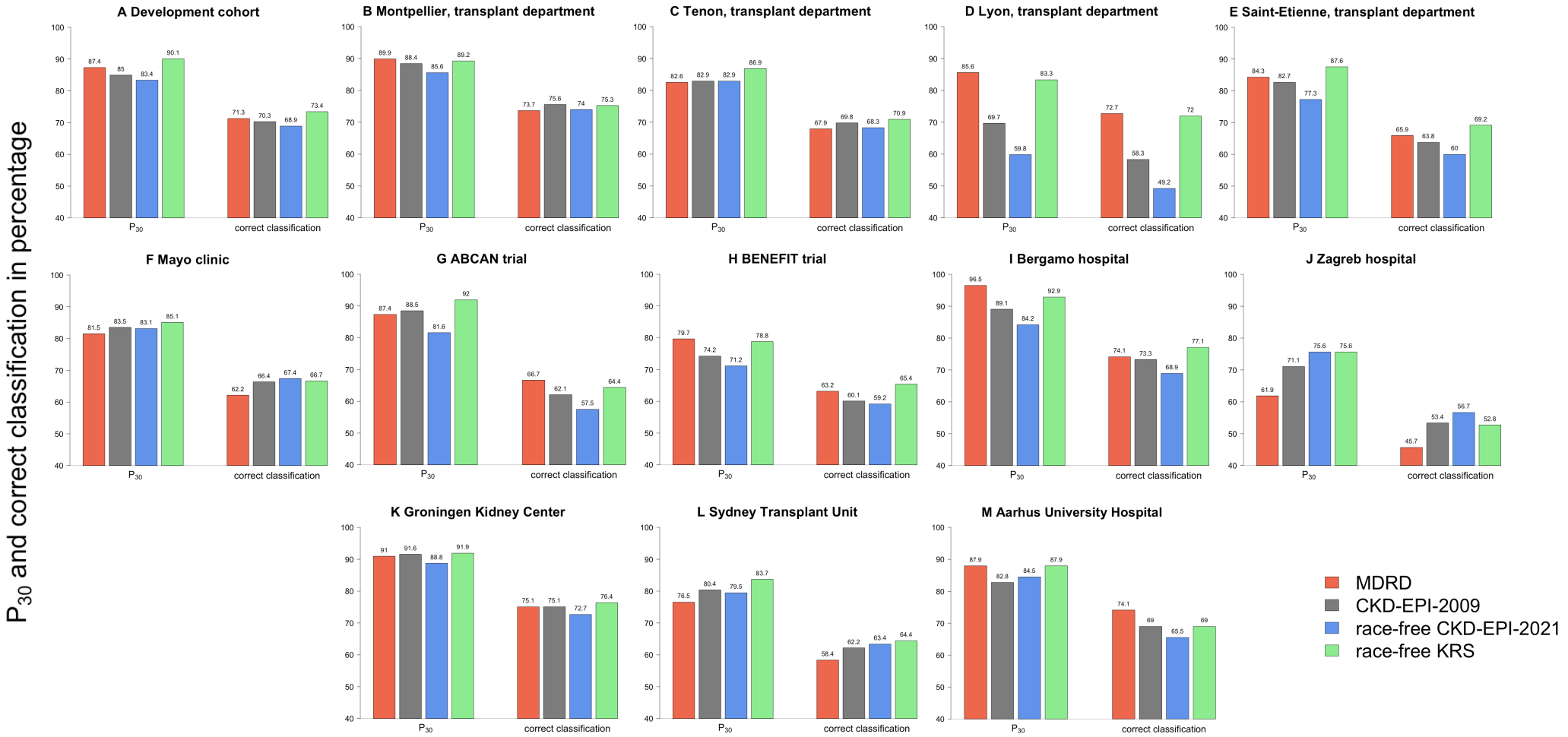


Figure 13 – Performances of GFR equations in underweight patients

The P_{30} is the proportion of the eGFR within the 30% of the mGFR. The correct classification is the agreement between eGFR and mGFR according to the GFR stages. The Aarhus University Hospital only contained two underweight patients and was therefore not plotted in this graph.

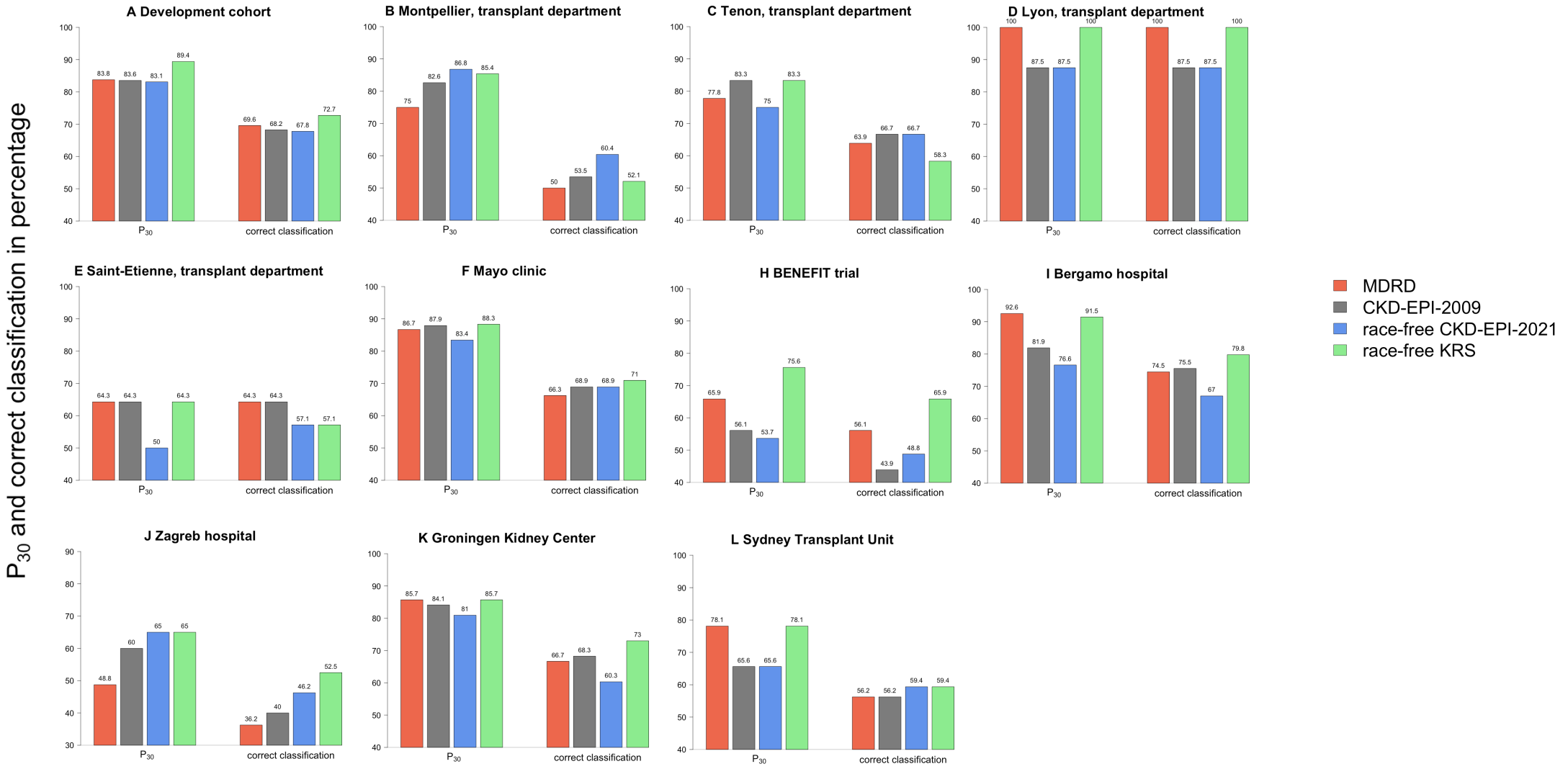


Figure 14 – Performances of GFR equations in normal weight patients
The P_{30} is the proportion of the eGFR within the 30% of the mGFR. The correct classification is the agreement between eGFR and mGFR according to the GFR stages.

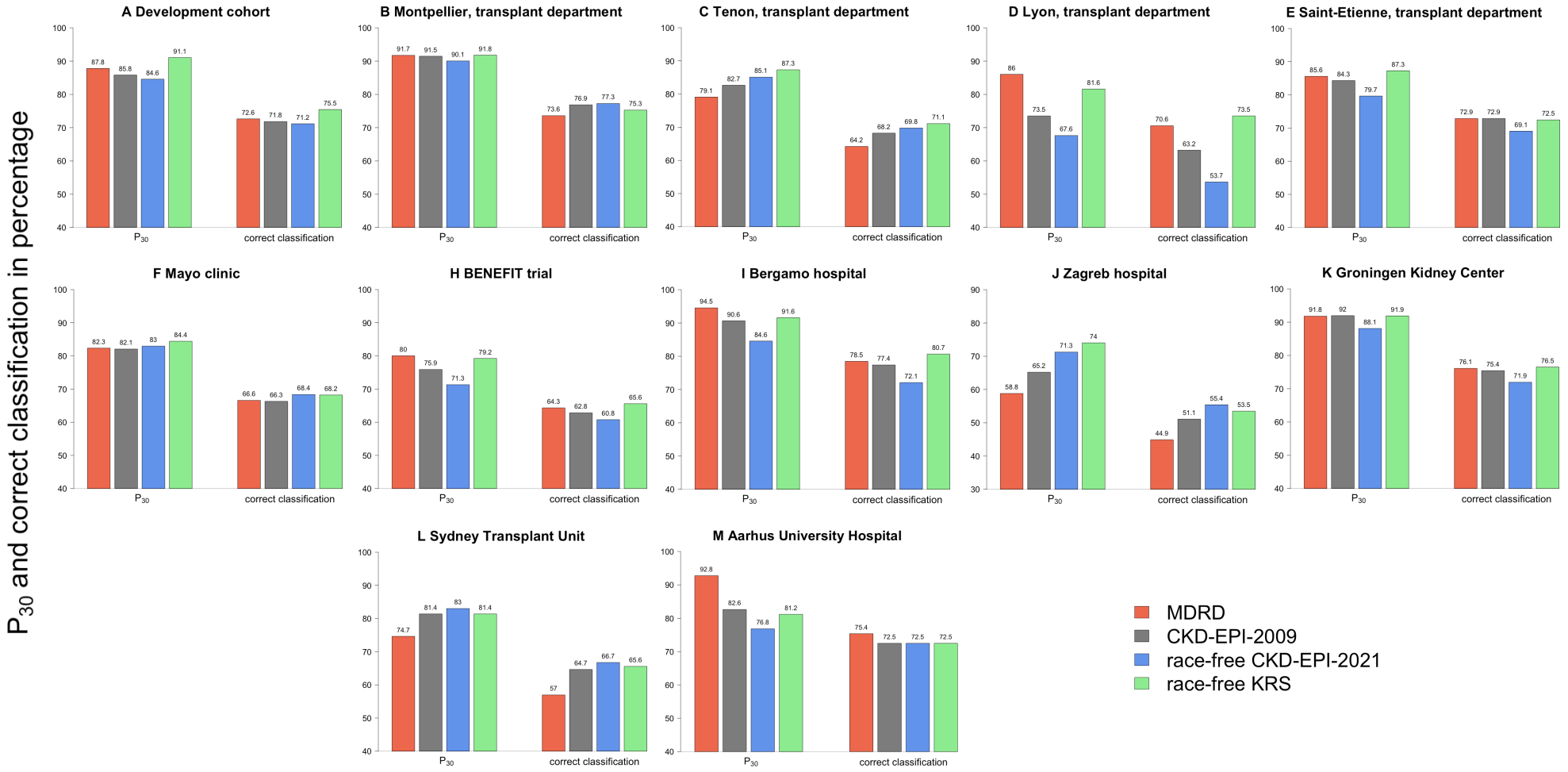


Figure 15 – Performances of GFR equations in overweight patients

The P_{30} is the proportion of the eGFR within the 30% of the mGFR. The correct classification is the agreement between eGFR and mGFR according to the GFR stages.

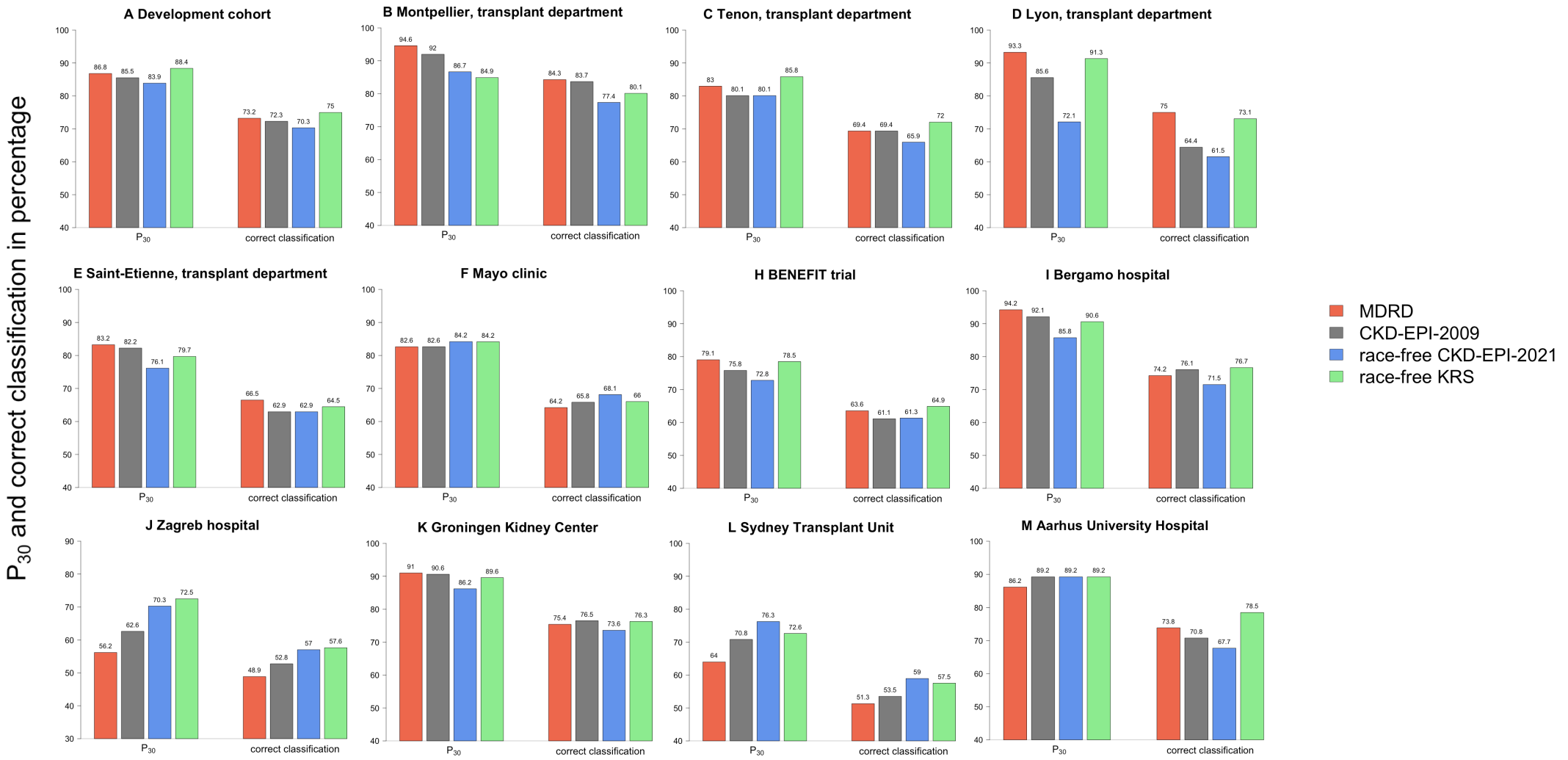


Figure 16 – Performances of GFR equations in obese patients

The P_{30} is the proportion of the eGFR within the 30% of the mGFR. The correct classification is the agreement between eGFR and mGFR according to the GFR stages.

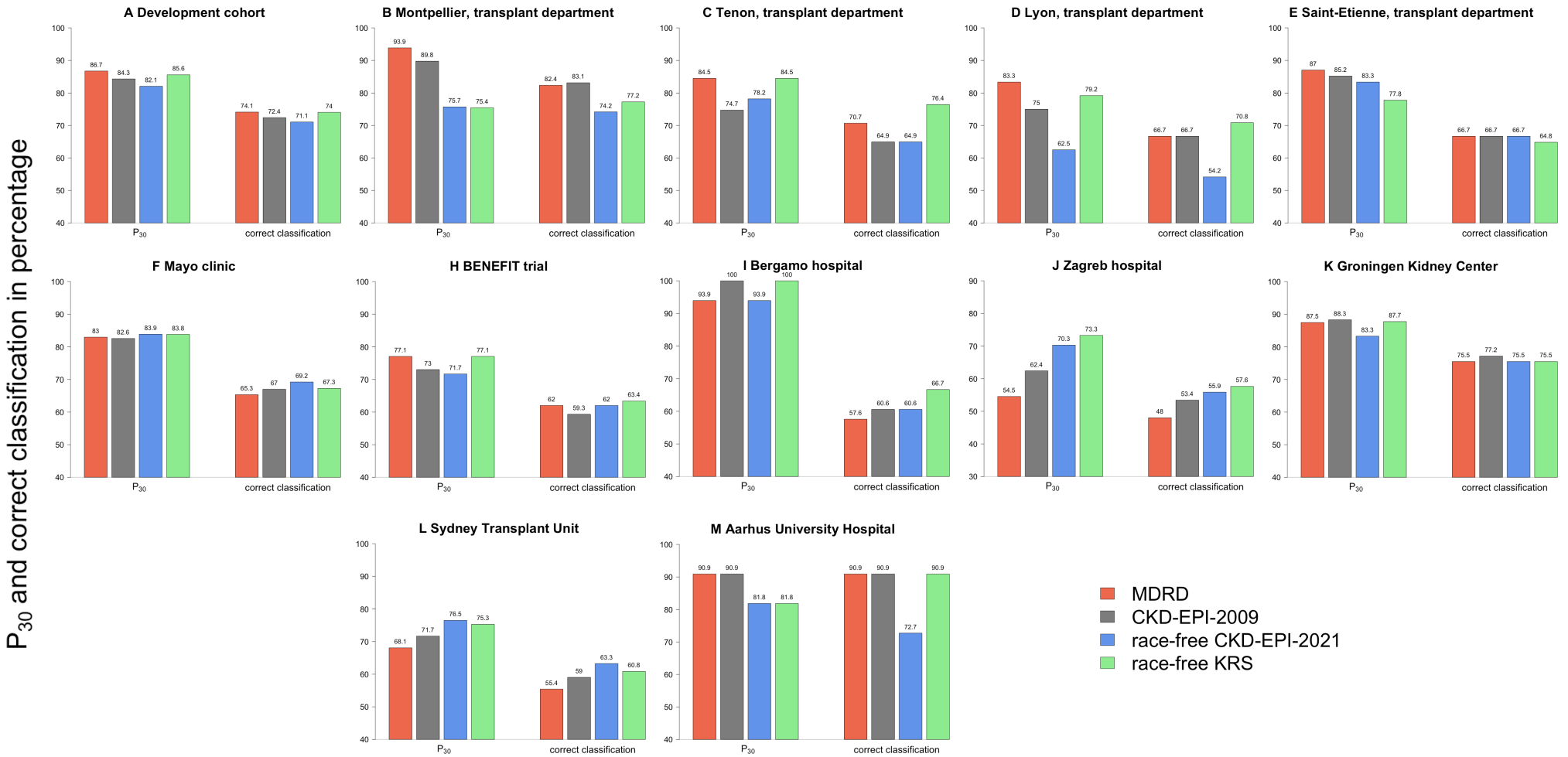


Figure 17 – Performances of GFR equations in creatinine measured with enzymatic method
The P_{30} is the proportion of the eGFR within the 30% of the mGFR. The correct classification is the agreement between eGFR and mGFR according to the GFR stages.

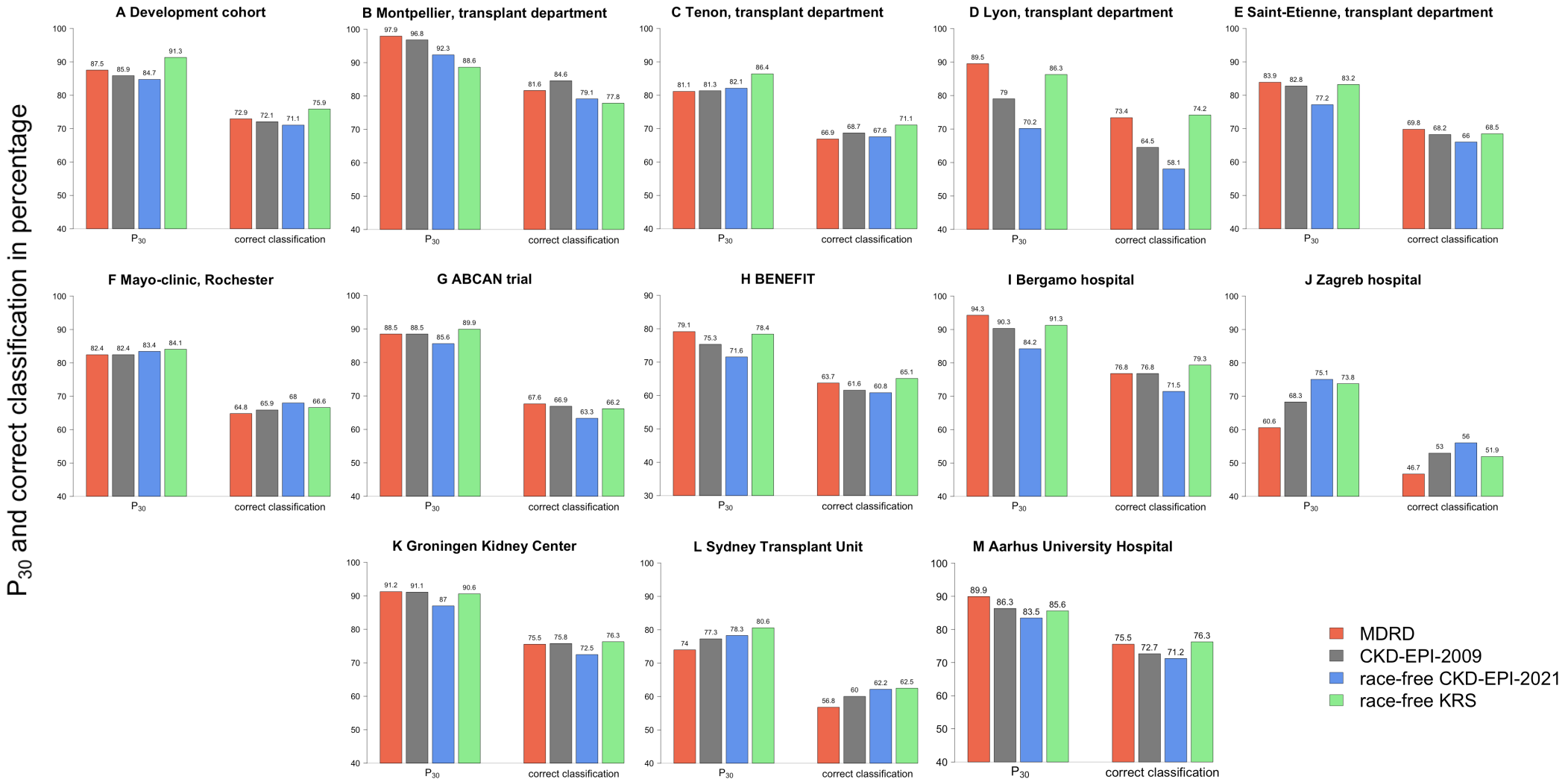


Figure 18 – Performances of GFR equations in patients whose creatinine was measured with colorimetric method

The P_{30} is the proportion of the eGFR within the 30% of the mGFR. The correct classification is the agreement between eGFR and mGFR according to the GFR stages.

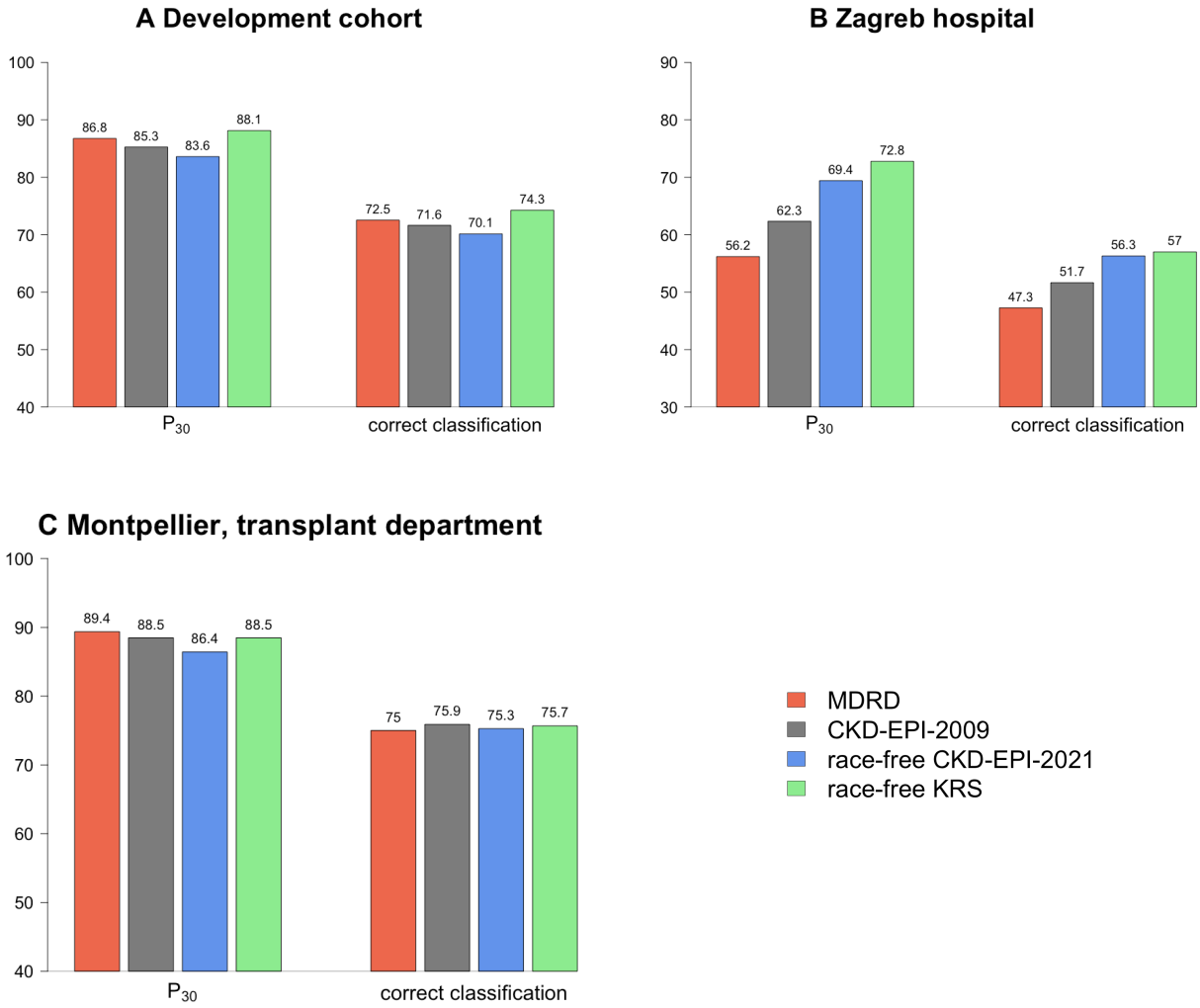


Figure 19 – Performances of GFR equations in patients whose GFR was measured with the ^{99}Tc-DTPA clearance

The P_{30} is the proportion of eGFR in a 30% confidence interval of the mGFR. The correct classification is the agreement between eGFR and mGFR according to the GFR stages.

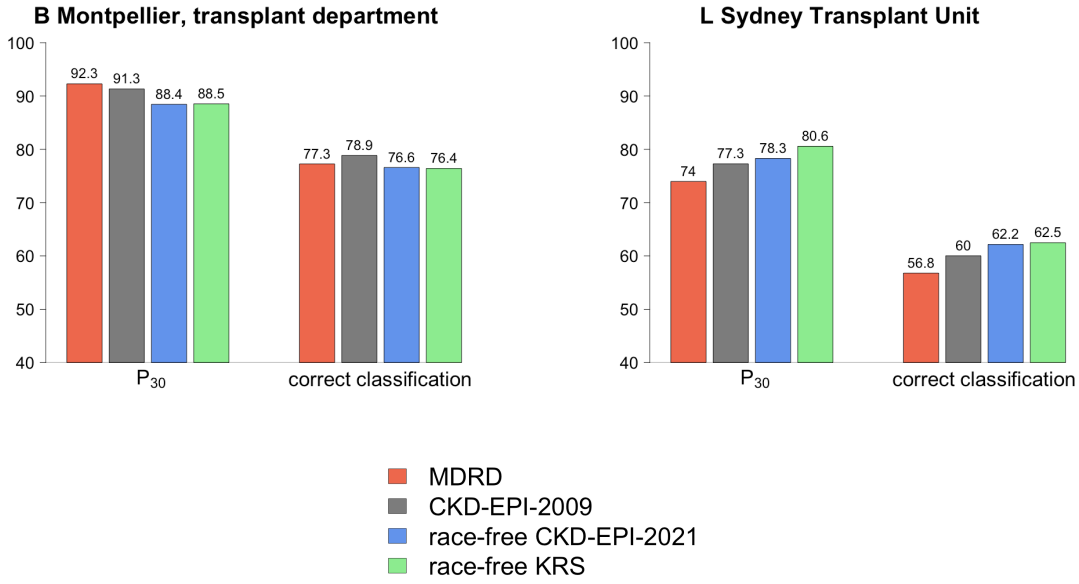


Figure 20 – Performances of GFR equations in patients whose GFR was measured with the ^{51}Cr-EDTA clearance

The P_{30} is the proportion of the eGFR within the 30% of the mGFR. The correct classification is the agreement between eGFR and mGFR according to the GFR stages.

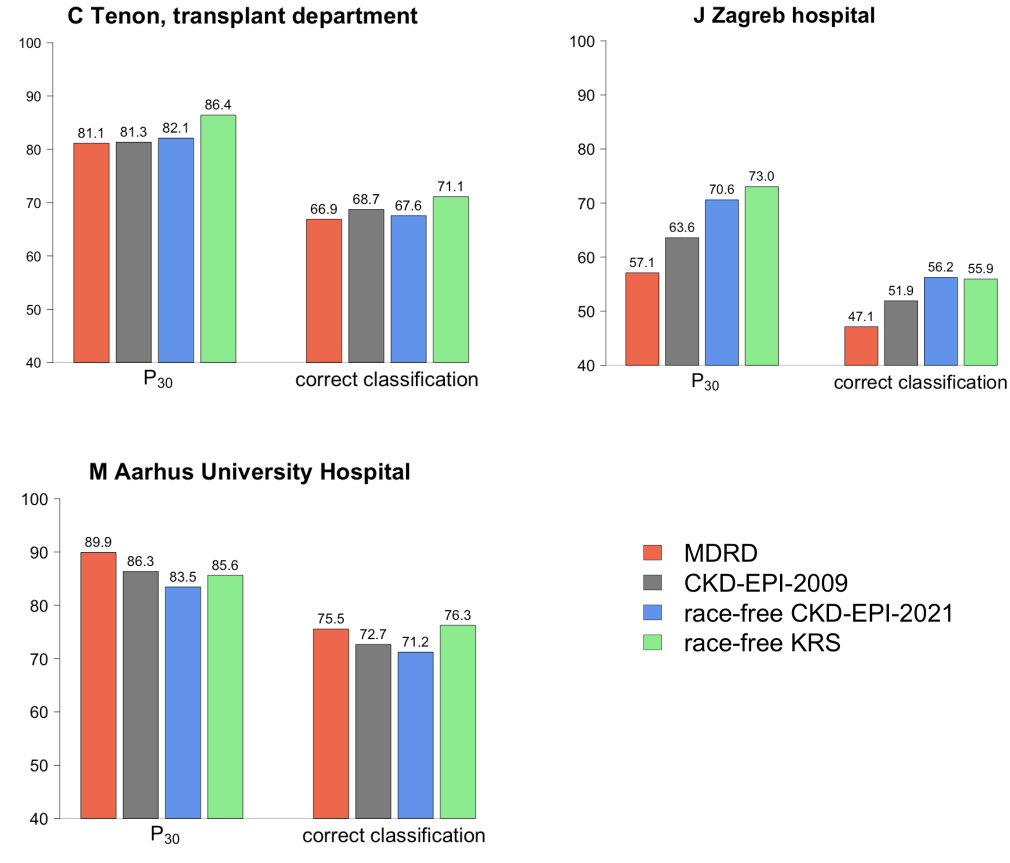


Figure 21 – Performances of GFR equations in patients whose GFR was measured with the inulin clearance

The P_{30} is the proportion of the eGFR within the 30% of the mGFR. The correct classification is the agreement between eGFR and mGFR according to the GFR stages.

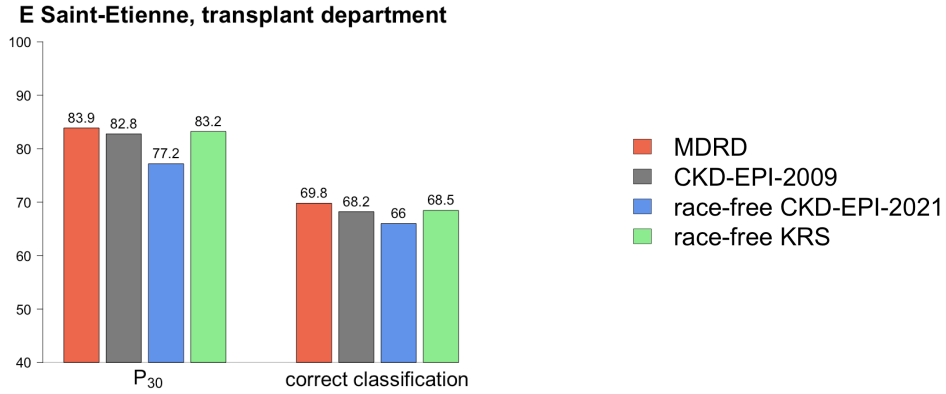


Figure 22 – Performances of GFR equations in patients whose GFR was measured with the iohexol clearance

The P_{30} is the proportion of the eGFR within the 30% of the mGFR. The correct classification is the agreement between eGFR and mGFR according to the GFR stages.

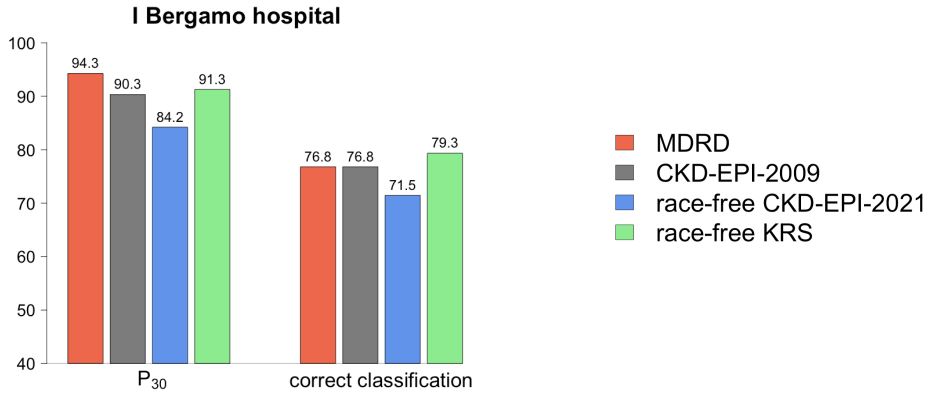


Figure 23 – Performances of GFR equations in patients whose GFR was measured with the iothalamate clearance

The P_{30} is the proportion of the eGFR within the 30% of the mGFR. The correct classification is the agreement between eGFR and mGFR according to the GFR stages.

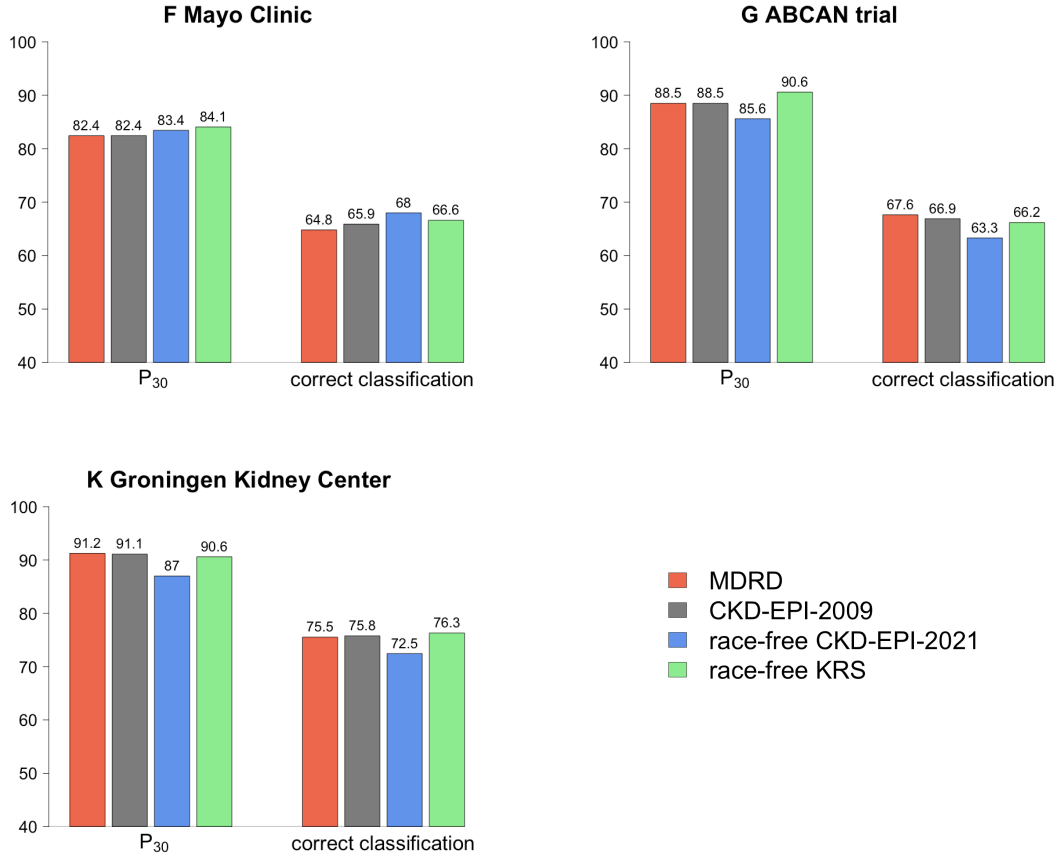


Figure 24 – Performances of GFR equations in living donor patients
The P_{30} is the proportion of the eGFR within the 30% of the mGFR. The correct classification is the agreement between eGFR and mGFR according to the GFR stages.

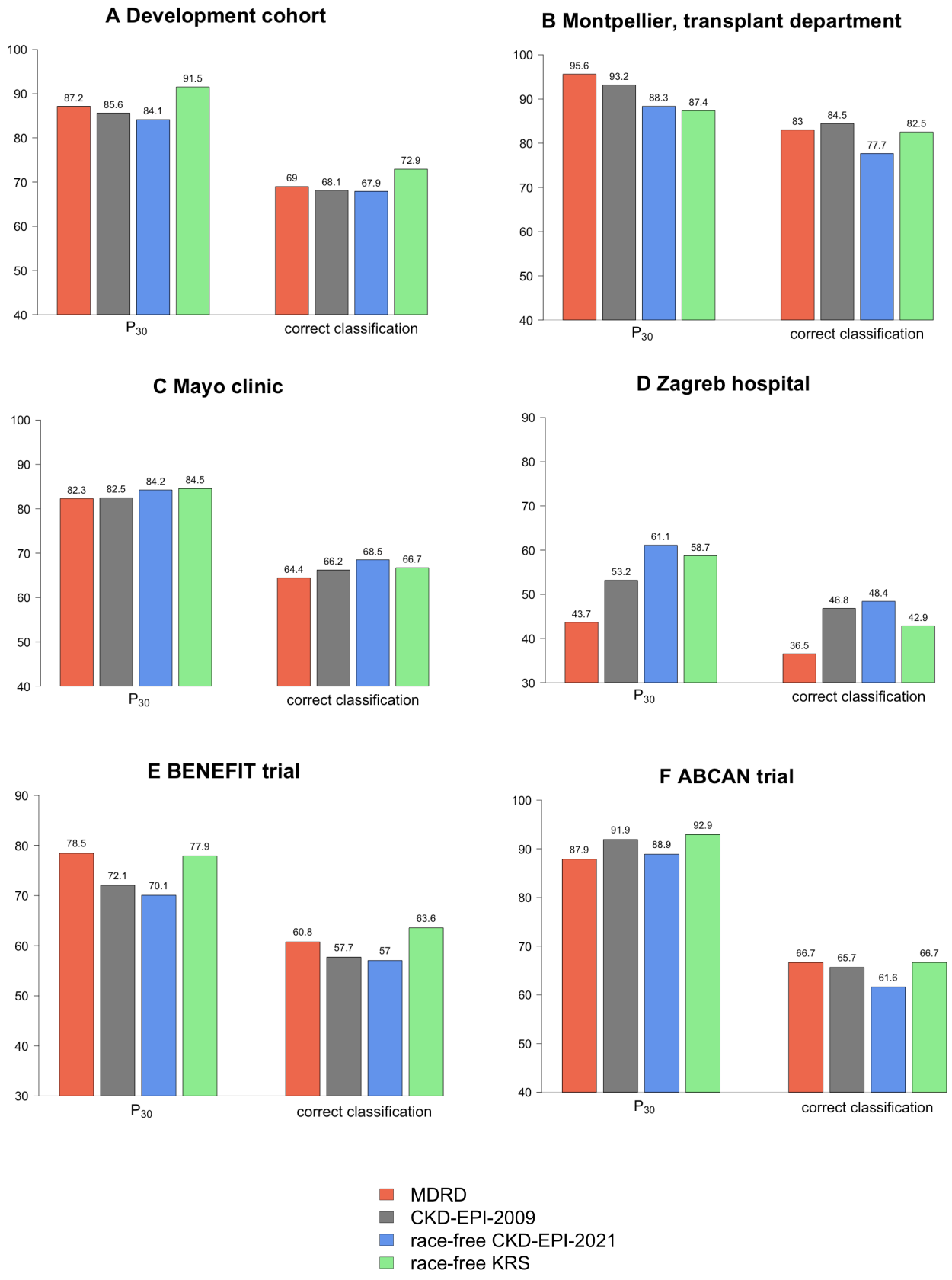


Figure 25 – Performances of GFR equations in deceased donor patients
The P_{30} is the proportion of the eGFR within the 30% of the mGFR. The correct classification is the agreement between eGFR and mGFR according to the GFR stages.

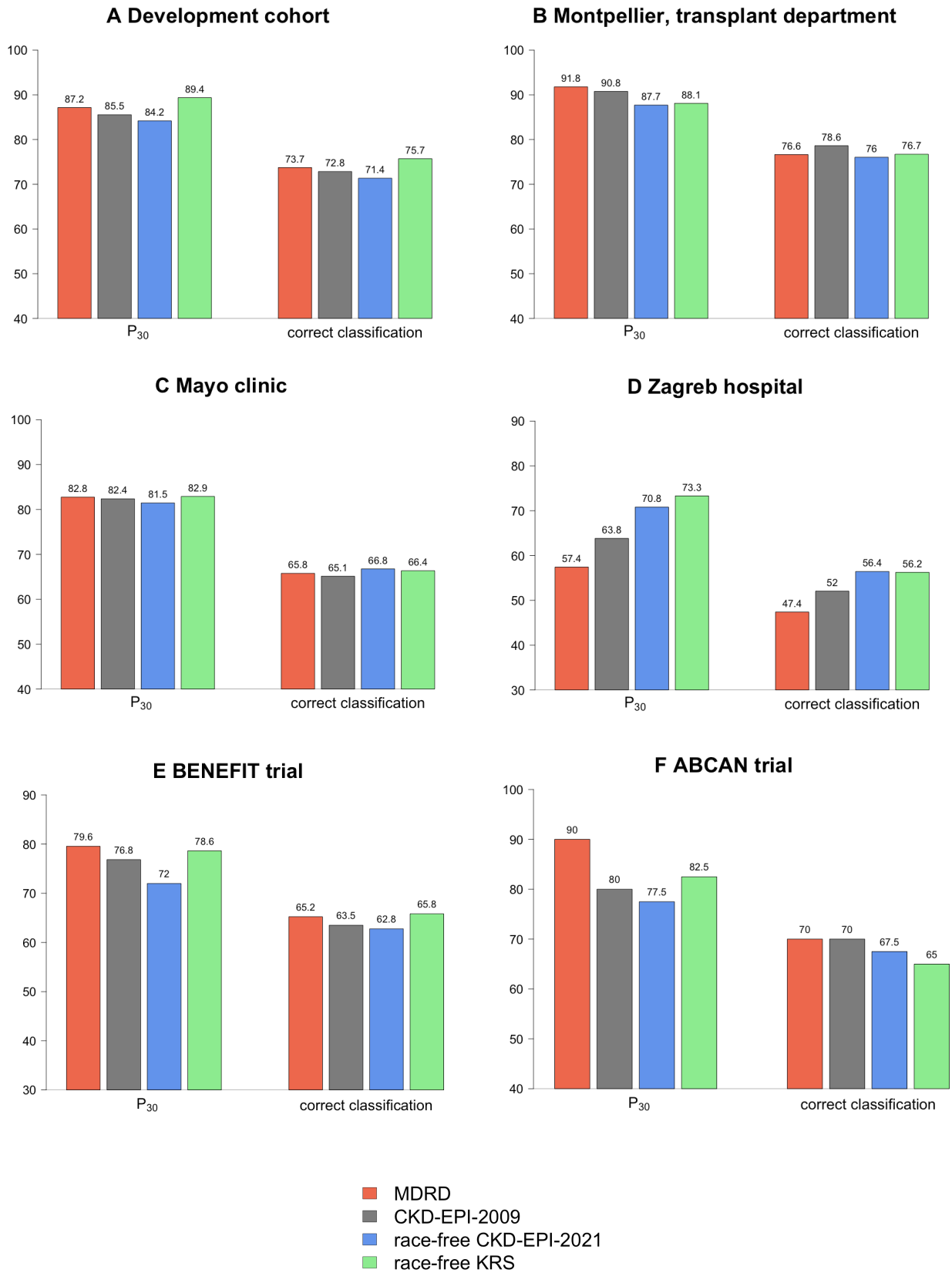


Figure 26 – Performances of GFR equations in patients with younger donor
The P_{30} is the proportion of the eGFR within the 30% of the mGFR. The correct classification is the agreement between eGFR and mGFR according to the GFR stages.

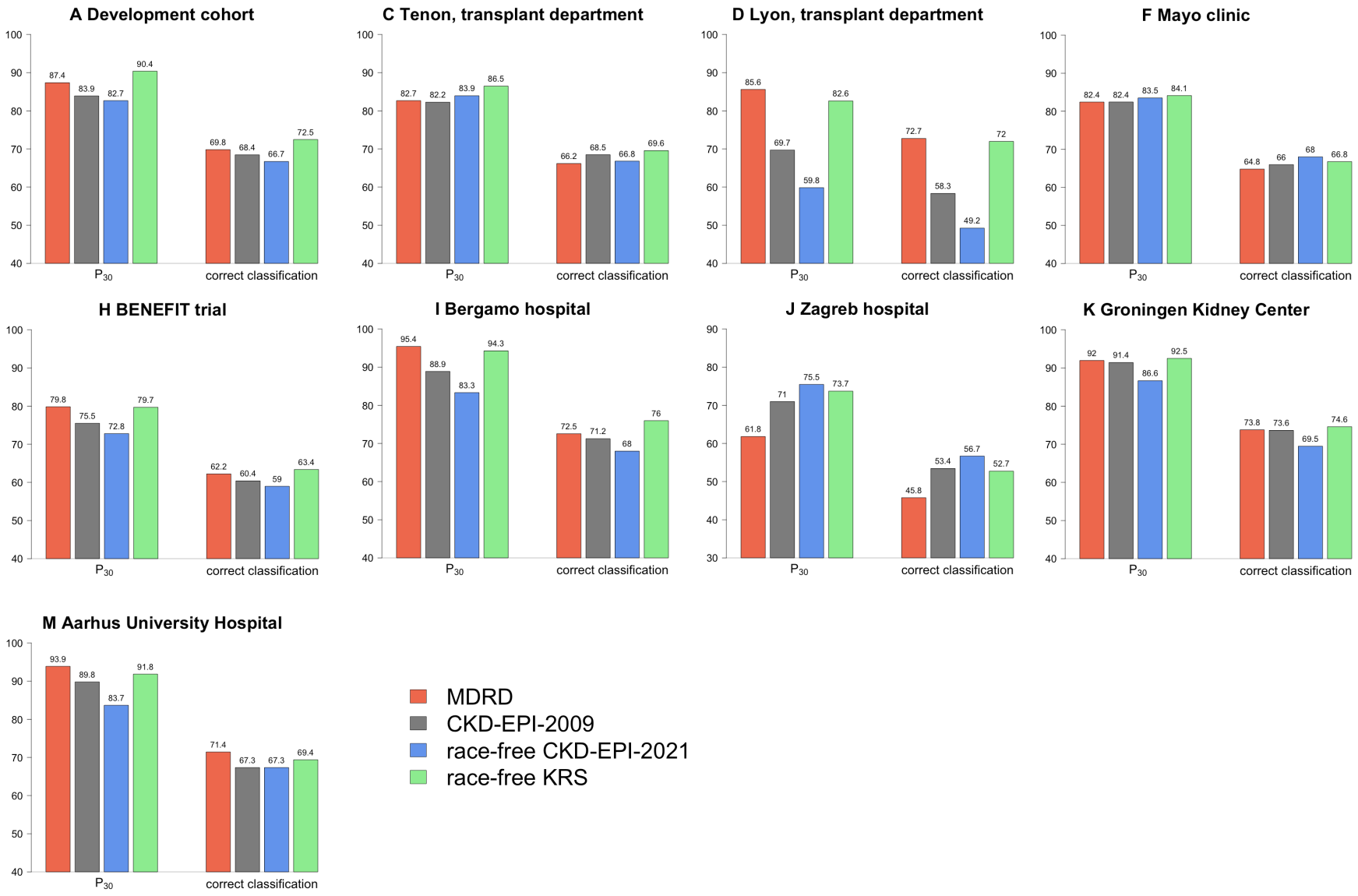


Figure 27 – Performances of GFR equations in patients with older donor
The P_{30} is the proportion of the eGFR within the 30% of the mGFR. The correct classification is the agreement between eGFR and mGFR according to the GFR stages.

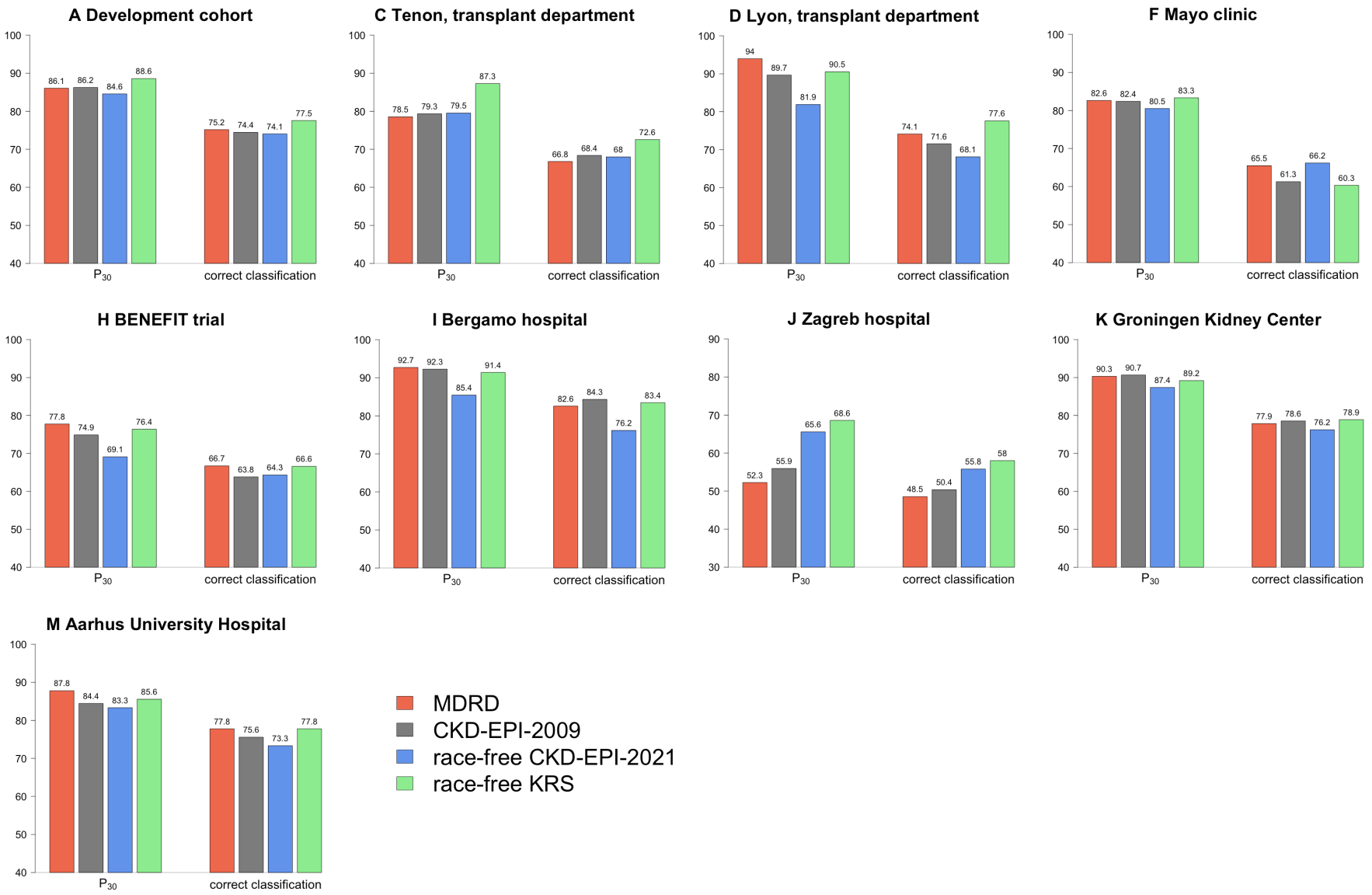


Figure 28 – Performances of GFR equations in patients whose age discrepancy with the donor is greater than 10 years
The P_{30} is the proportion of the eGFR within the 30% of the mGFR. The correct classification is the agreement between eGFR and mGFR according to the GFR stages.

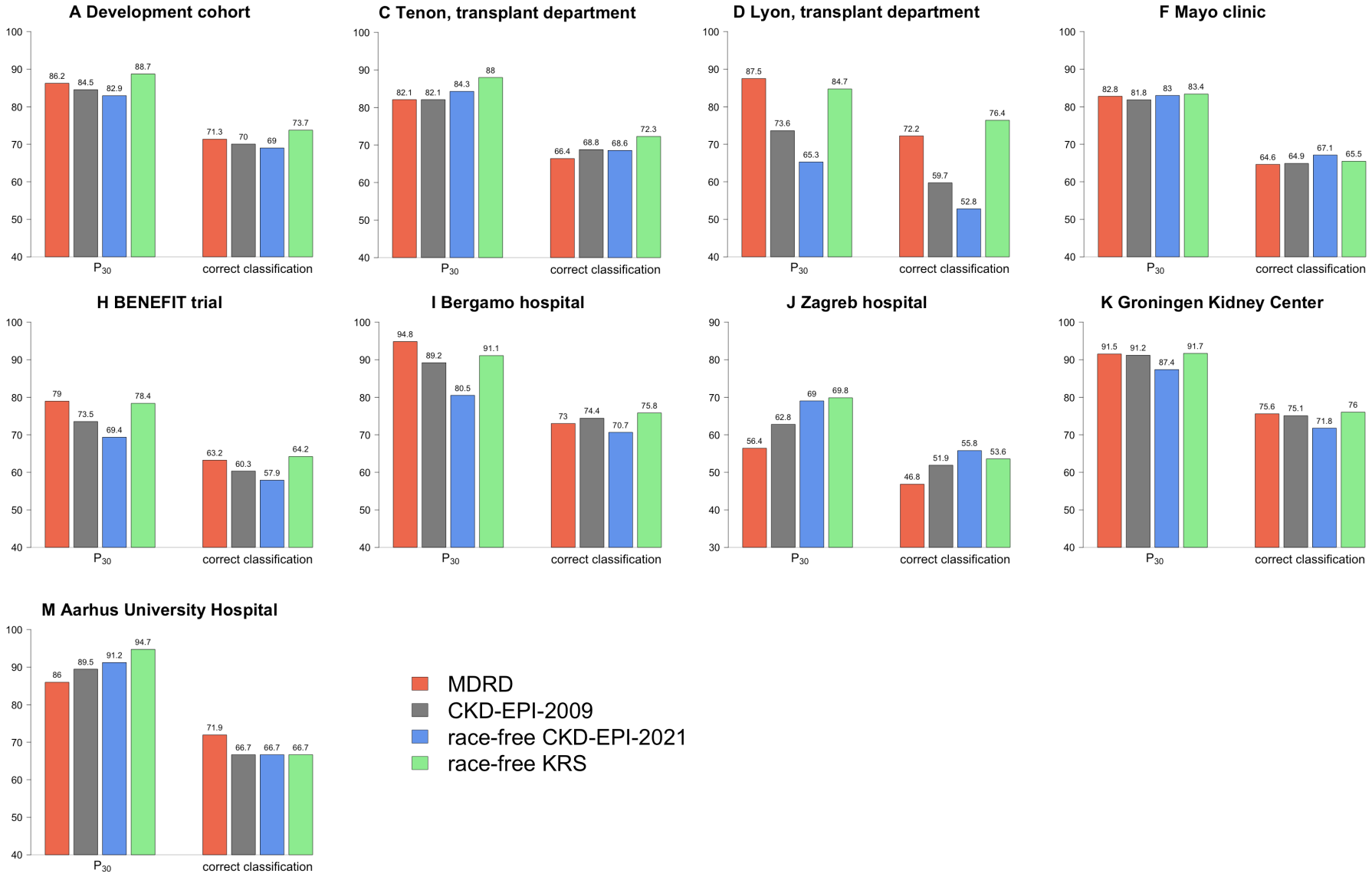


Figure 29 – Performances of GFR equations in patients whose age discrepancy with the donor is lower than 10 years
The P_{30} is the proportion of the eGFR within the 30% of the mGFR. The correct classification is the agreement between eGFR and mGFR according to the GFR stages.

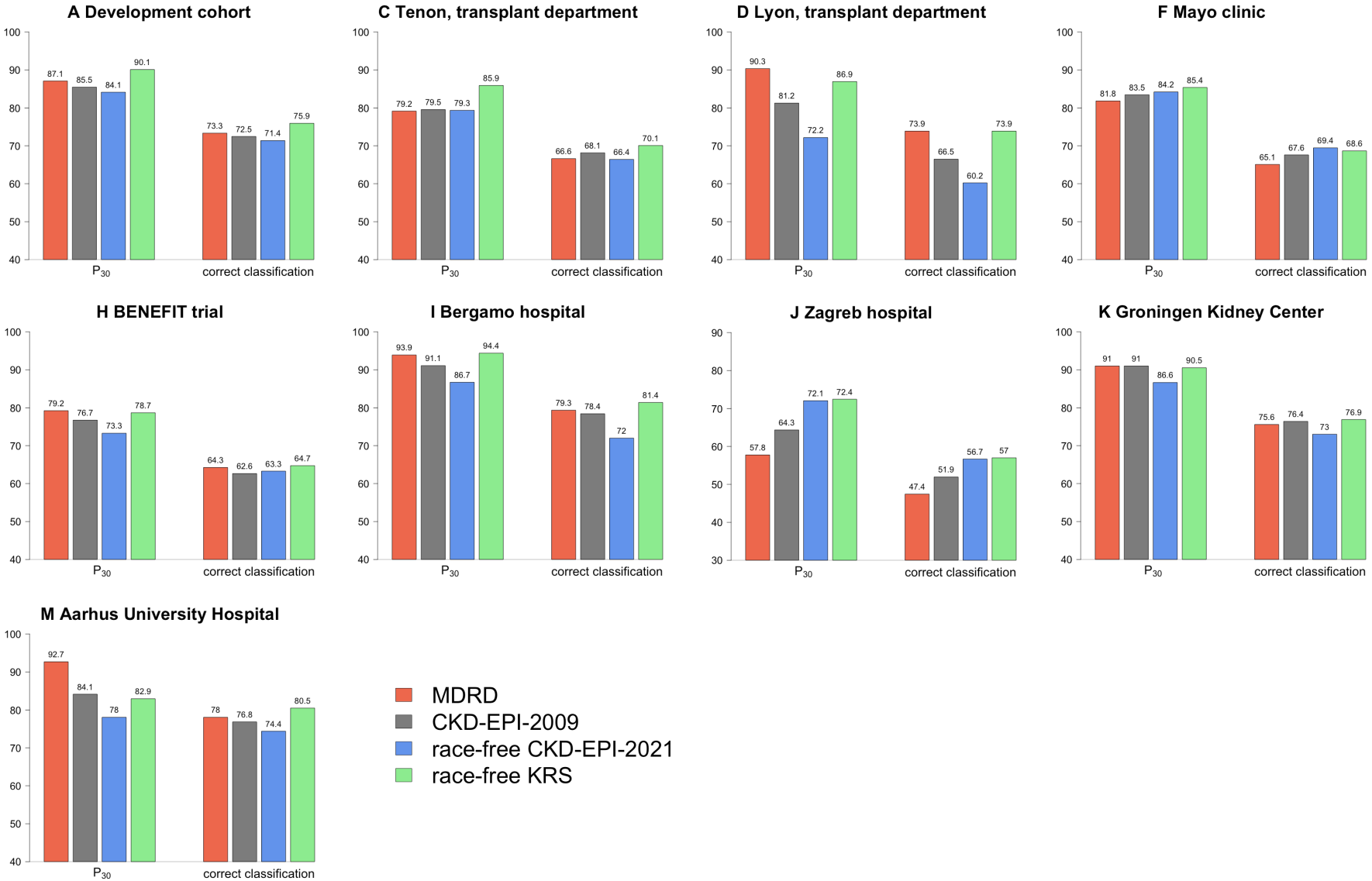


Figure 30 – Performances of GFR equations in patients with CNI
The P_{30} is the proportion of the eGFR within the 30% of the mGFR. The correct classification is the agreement between eGFR and mGFR according to the GFR stages.

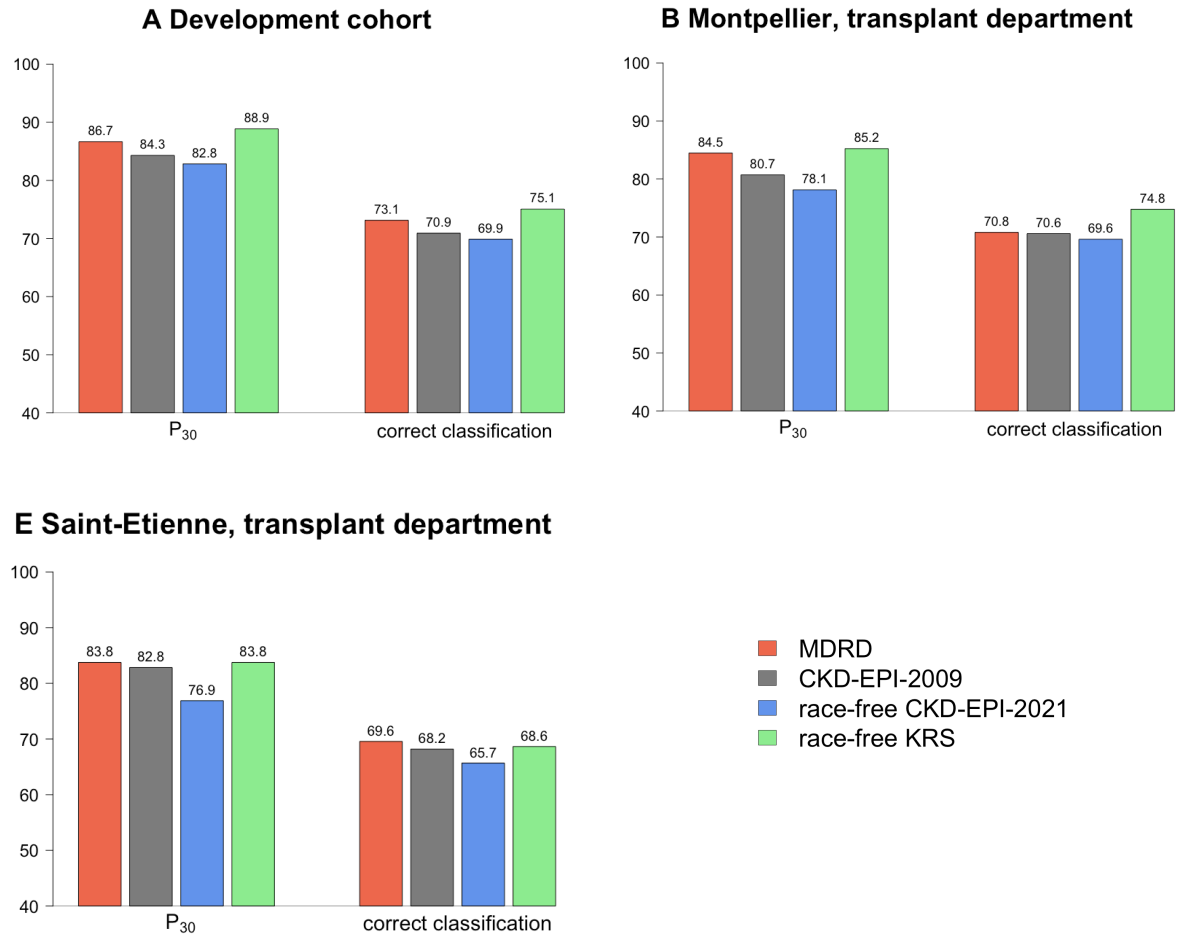


Figure 31 – Performances of GFR equations in patients with mTOR
The P_{30} is the proportion of the eGFR within the 30% of the mGFR. The correct classification is the agreement between eGFR and mGFR according to the GFR stages. This analysis was performed in the development cohort only.

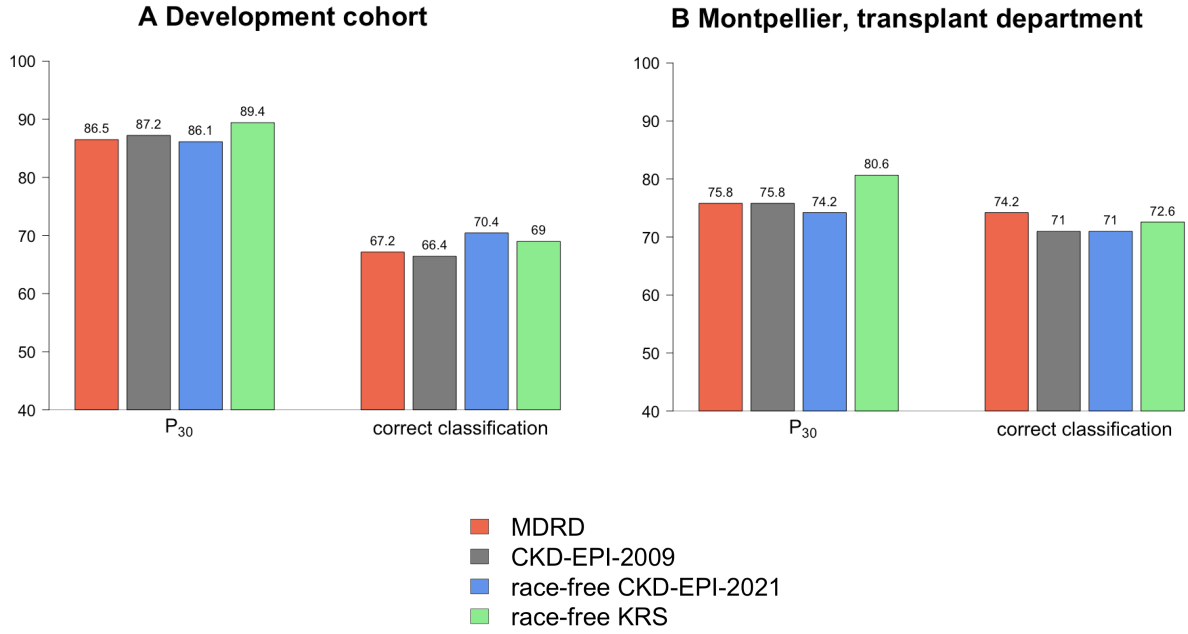


Figure 32 – Performances of GFR equations in patients with mTOR vs CNI : overall population
The P_{30} is the proportion of the eGFR within the 30% of the mGFR. The correct classification is the agreement between eGFR and mGFR according to the GFR stages. This analysis was performed in the development cohort only.

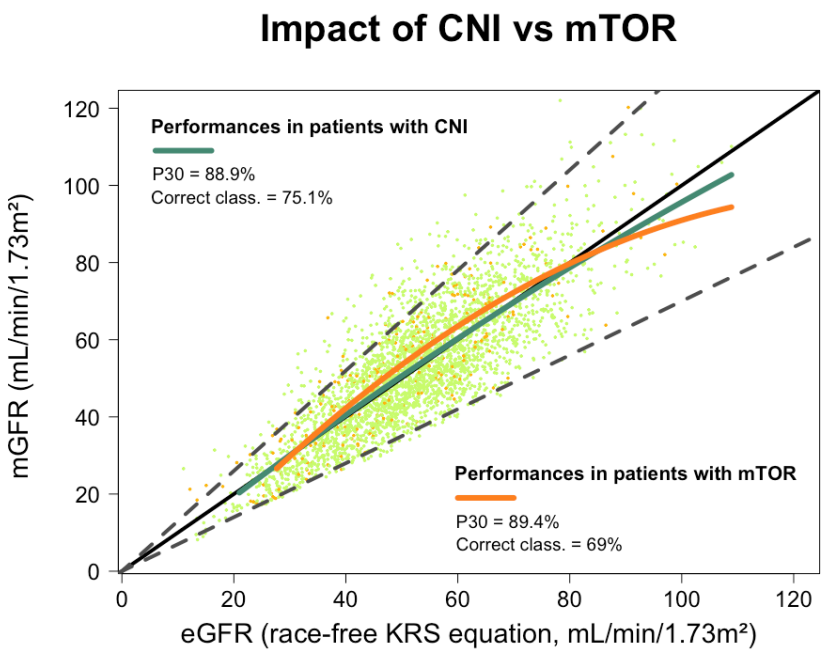


Figure 33 – Performances of GFR equations in patients with belatacept from the BENEFIT and BENEFIT-EXT trials

The P_{30} is the proportion of the eGFR within the 30% of the mGFR. The correct classification is the agreement between eGFR and mGFR according to the GFR stages.

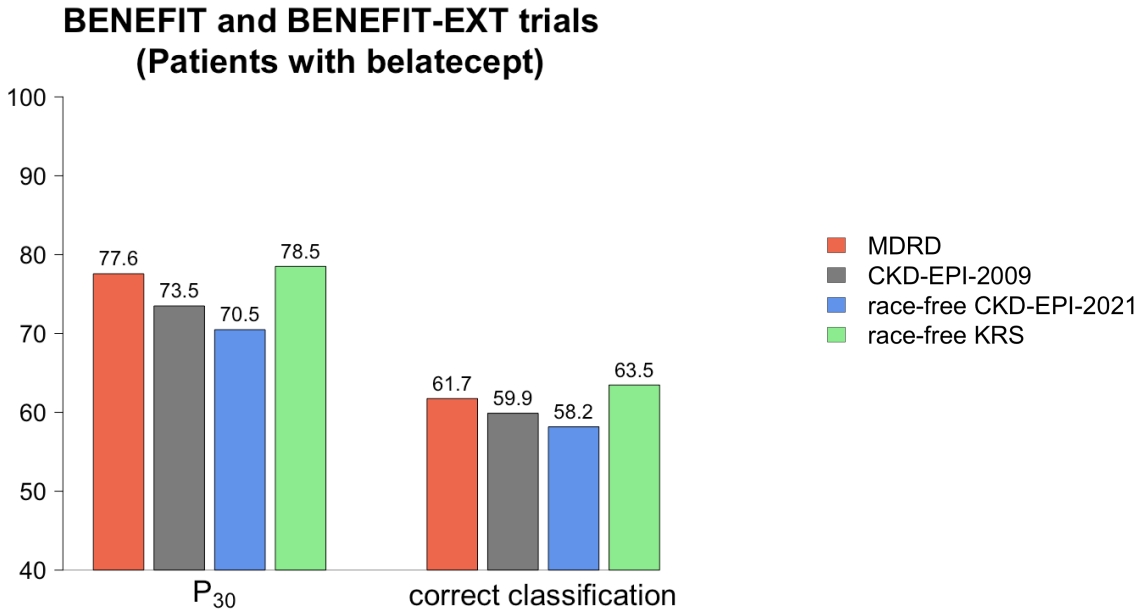


Figure 34 – Performances of GFR equations in patients whose GFR were measured before one year post-transplant
The P_{30} is the proportion of the eGFR within the 30% of the mGFR. The correct classification is the agreement between eGFR and mGFR according to the GFR stages.

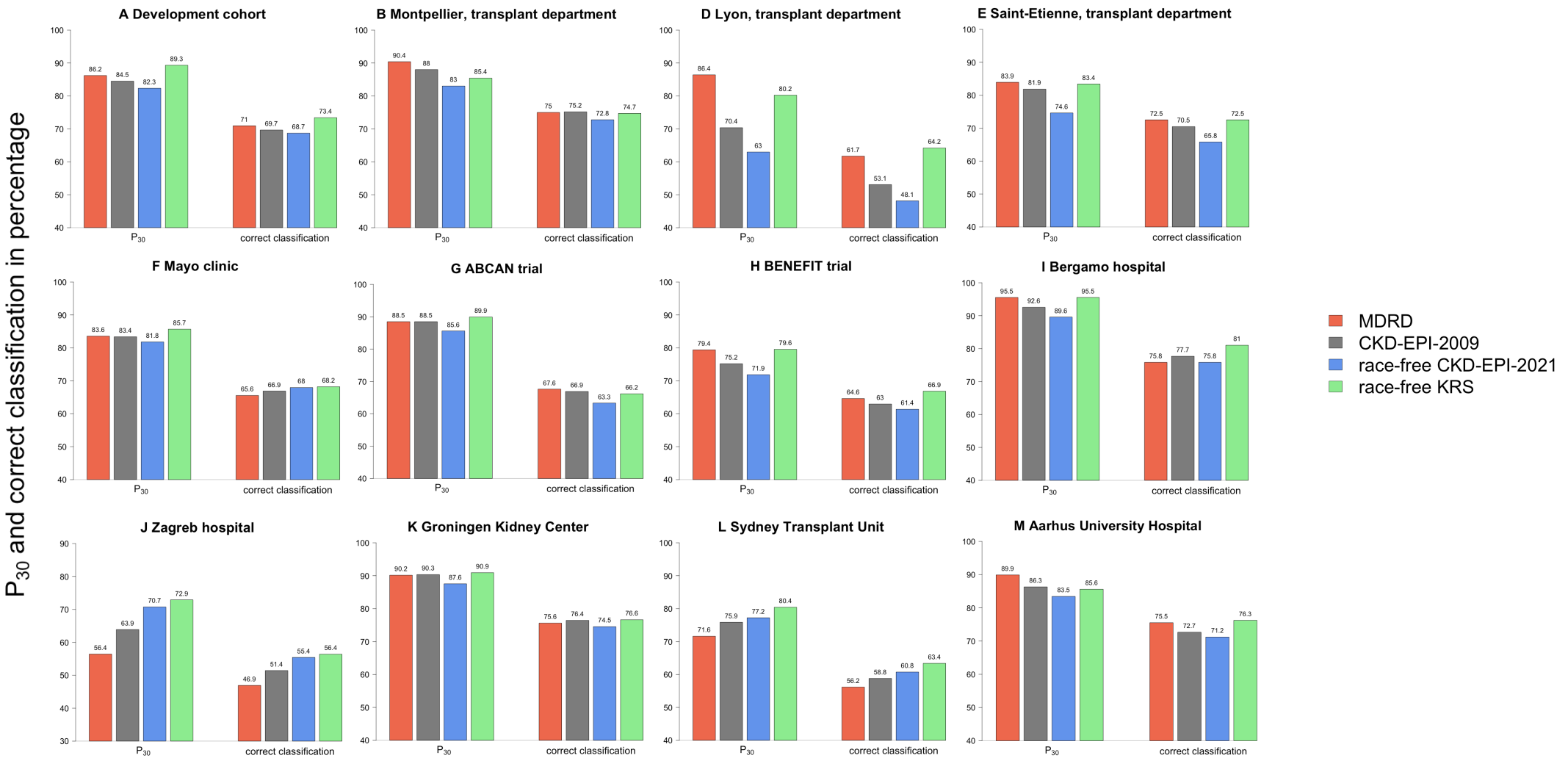


Figure 35 – Performances of GFR equations in patients whose GFR were measured after one year post-transplant
The P_{30} is the proportion of the eGFR within the 30% of the mGFR. The correct classification is the agreement between eGFR and mGFR according to the GFR stages.

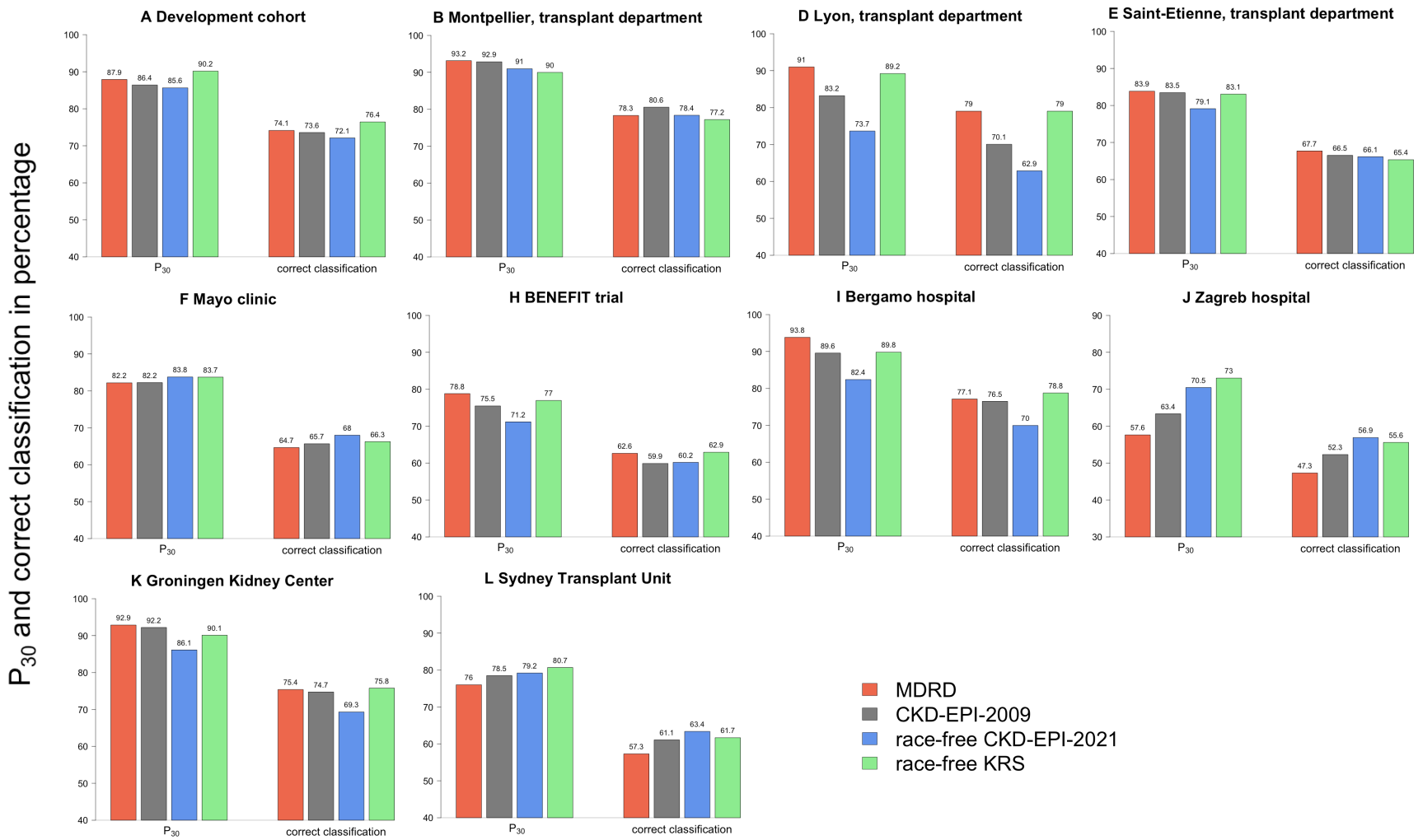
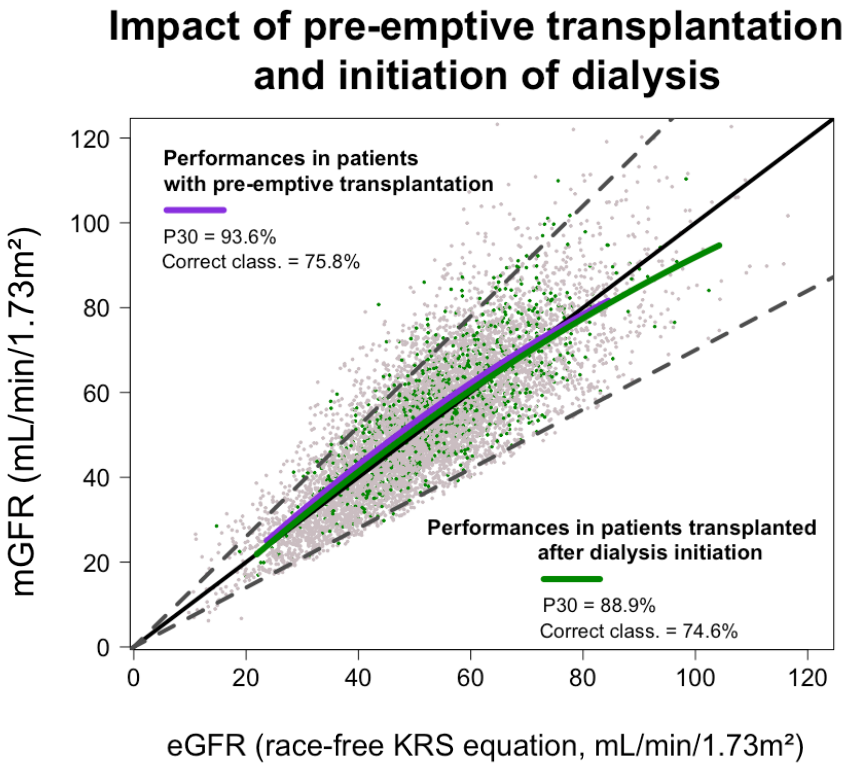


Figure 36 – Performances of GFR equations in patients with pre-emptive transplantation and patients transplanted after dialysis initiation
The P_{30} is the proportion of the eGFR within the 30% of the mGFR. The correct classification is the agreement between eGFR and mGFR according to the GFR stages.



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