Supplementary Tables and Figures

Chromosomal Microarrays for the Diagnosis of Pediatric Chronic Kidney Disease

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Supplementary Table 1. Definitions of **Known Genomic Disorders** (**All coordinates are according to hg18**)

Chromosomal Region	Start (Mb)	End (Mb)	Description
1p36.22-q36.21	0.00	12.76	1p36 duplication
1p36.22-q36.21	0.00	12.76	1p36 deletion syndrome
1p36.32	2.91	3.65	1p36.32 microduplication
1p22.2	89.50	89.97	1p22 microduplication
1q21.1	144.10	144.46	1q21.1 TAR syndrome region duplication
1q21.1	144.10	144.46	1q21.1 TAR syndrome deletion
1q21.1	145.00	146.35	1q21.1 recurrent microdeletion
1q21.1	145.00	146.35	1q21.1 recurrent microduplication
1q43-q44	240.61	245.67	1q43-1q44 deletion
2p21	44.26	44.44	2p21 microdeletion syndrome
2p15-p16.1	59.14	61.67	2p15-16.1 microdeletion syndrome
2q11.2	96.09	97.04	2q11.2 deletion
2q11.2	96.09	97.04	2q11.2 duplication
2q12.3-q11.2	100.06	107.81	2q11.2.q13 deletion
2q12.3-q11.2	100.06	107.81	2q11.2.q13 duplication
2q13	110.18	110.34	2q13 homozygous deletion (Nephronophthisis 1)
2q22.3	144.86	144.99	2q22 Mowat-Wilson syndrome
2q23.1	148.44	149.01	2q23.1 deletion
2q23.1	148.44	149.01	2q23 duplication
2q32.3-q33.2	196.63	204.92	2q33.1 deletion syndrome
2q37.3	239.37	242.12	2q37 deletion
2q37.3	239.63	239.99	2q37 deletion (HDAC4)
2q37.3	240.99	242.44	2q37 deletion (GPC1, STK25)
3p26.3	1.35	2.18	3pter-p25 deletion
3q29	197.21	198.83	3q29 microdeletion syndrome Intellectual disability

3q29	197.21	198.83	3q29 microduplication syndrome Intellectual disability, schizophrenia
4p15.33-p15.32	0.06	17.29	Wolf-Hirschhorn
4p16.3	1.84	1.98	Wolf-Hirschhorn critical deletion
4p16.3	1.84	1.98	Wolf-Hirschhorn critical region duplication
5p15.2-p15.33	0.06	12.59	Cri du Chat syndrome 5p deletion
5p15.2-p15.33	0.11	10.96	5p distal duplication
5p13.2	36.91	37.10	5p13.2 Cornelia de Lange (NIBPL)
5q22.1-q22.3	91.46	114.55	5q interstitial deletion
5q22.2	112.07	112.21	Familial Adenomatous Polyposis
5q23.2	126.14	126.20	Adult-onset autosomal dominant leukodystrophy
5q35.2-q35.3	175.65	176.99	Sotos syndrome deletion
6p12.3	45.40	45.63	6p21.1 Cleidocranial dysplasia (RUNX2)
6q13	70.29	70.76	6q13-q14 deletion
7p21.3-p22.1	6.82	7.27	7p interstitial duplication I
7p21.1	16.81	17.71	7p21 interstitial duplication
7p15.3-p15.2	23.68	27.43	7p15 deletion
7p14.1	41.97	42.24	7p14.1 Greig cephalopolysyndactyly (GLI3)
7q11.23	72.38	73.78	7q11.23 duplication syndrome
7q11.23	72.38	73.78	Williams-Beuren Syndrome (WBS)
7q11.23	74.80	76.50	Williams-Beuren Syndrome-distal deletion
7q11.23	74.80	76.50	WBS-distal duplication
7q36.1-q36.3	141.53	158.81	7q36.1 deletion
8p23.1	8.13	11.93	8p23.1 deletion
8p23.1	8.13	11.93	8p23.1 duplication
8q13.3	72.27	72.44	8q13.3 Branchio-Oto-Renal syndrome (EYA1)
8q21.11	77.39	77.93	8q21.11 Microdeletion Syndrome
9p22.3	14.81	14.98	9p22 deletion
9q22.32	97.25	97.32	9q22.32 Basal cell nevus/Gorlin-Goltz/Holoprosencephaly 7 (PTCH1)
9q33.3	128.42	128.50	9q33.3 Nail Patella syndrome

9q33.3	136.95	140.20	9q34 deletion
9q33.3	136.95	140.20	9q34 duplication
9q33.3	139.63	139.85	9q subtelomeric deletion syndrome
10q23.1-q23.2	81.95	88.79	10q23 deletion
10q23.1-q23.2	81.95	88.79	10q23 duplication
11p13	31.76	32.41	WAGR 11p13 deletion syndrome
11p11.2	43.94	46.02	11p11.2 duplication
11p11.2	43.94	46.02	Potocki-Schaffer syndrome deletion
11q13.2-q13.4	67.51	70.96	11q13.2 -q13.4 deletion
12q14.2-q15	63.36	66.93	12q14 microdeletion syndrome
13q14.2	47.78	47.95	13q14.2 Retinoblastoma deletion
15q12-q13.1	20.30	26.11	15q11.2 Prader-Willi/Angelman (Type 1) deletion
15q12-q13.1	20.30	26.11	15q11.2 Prader-Willi/Angelman (Type 1) region reciprocal duplication
15q12-q13.1	21.17	26.11	15q11.2 Prader-Willi/Angelman (Type 2) deletion
15q12-q13.1	21.17	26.11	15q11.2 Prader-Willi/Angelman (Type 2) region reciprocal duplication
15q13.2-q13.3	28.70	30.23	15q13.3 microdeletion syndrome
15q13.2-q13.3	28.92	30.27	15q13.3 duplication
15q24.1	70.70	72.20	15q24 BP0-BP1 deletion (includes BBS4)
15q24.1	70.70	72.20	15q24 BP0-BP1 duplication (includes BBS4)
15q24.2-q24.1	70.70	73.58	15q24 BP0-BP1 deletion (includes BBS4, PMI1)
15q24.2-q24.1	70.70	73.58	15q24 BP0-BP1 duplication (includes BBS4, PMI1)
15q24.2-q24.3	73.76	75.99	15q24 BP2-BP3 deletion
15q25.2	80.89	82.53	15q25.2 deletion
15q26.3	97.18	100.34	15q26 deletion
15q26.3	97.18	100.34	15q26 overgrowth syndrome duplication
16p13.3	0.00	0.77	ATR-16 syndrome
16p13.12-p13.11	0.04	15.10	16p subtelomeric duplication
16p13.3	3.72	3.87	Rubinstein-Taybi Syndrome
16p13.11	14.89	16.39	16p13.11 recurrent microdeletion syndrome

16p13.11	14.89	16.39	16p13.11 recurrent microduplication syndrome
16p13.11	15.03	15.81	16p13.11 microduplication
16p12.2-p11.2	21.26	29.35	16p11.2p12.1 deletion
16p12.2-p11.2	21.26	29.35	16p11.2p12.1 duplication
16p11.2	29.56	30.11	16p11.2 deletion
16p11.2	29.56	30.11	16p11.2 duplication
17p13.3	0.00	2.54	Miller-Dieker syndrome (MDS)
17p13.3	0.05	2.49	17p13.3 duplication (MDS region)
17p13.3	3.45	3.51	CTNS homozygous deletion
17p12	14.04	15.41	Charcot-Marie-Tooth syndrome type 1A (CMT1A)
17p12	14.04	15.41	Hereditary Liability to Pressure Palsies (HNPP)
17p11.2	16.65	20.42	Potocki-Lupski syndrome duplication
17p11.2	16.65	20.42	Smith-Magenis syndrome deletion
17q11.2	26.19	27.24	NF1 duplication
17q11.2	26.19	27.24	NF1-microdeletion syndrome
17q12	31.89	33.28	17q12 duplication
17q12	31.89	33.28	Renal Cysts and Diabetes deletion
17q21.31	41.06	41.65	17q21.31 duplication
17q21.31	41.06	41.65	17q21.31 recurrent microdeletion syndrome
17q23.2	55.01	55.43	17q23.1 deletion
17q23.2	55.42	57.66	17q23.1-q23.2 deletion
20p11.22-p11.21	0.11	24.77	20p partial trisomy
21q21.3	26.17	26.47	Early-onset Alzheimer disease with cerebral amyloid angiopathy
21q22.2-q22.3	40.51	46.91	21q partial monosomy
22q11.1-q11.21	15.30	18.61	22q11.21 duplication (VCFS region)
22q11.21	17.27	19.80	22q11.21 DiGeorge-VCF Syndrome
22q11.22-q11.23	20.24	21.98	22.q11.2 distal deletion
22q11.22-q11.23	20.24	21.98	22.q11.2 distal duplication
22q12.2	28.33	28.42	22q12.2 Neurofibromatosis 2

22q13.33	49.46	49.52	Phelan-McDermid Syndrome (SHANK3)
22q13.32-q13.33	42.94	49.52	Phelan-McDermid Syndrome, large deletion
22q13.33	49.39	49.53	22q13.3 22q13.3 Microdeletion
Xp22.33	0.38	0.67	Leri-Weill dyschondrostosis (LWD) SHOX deletion v1
Xp22.33	0.67	0.79	Leri-Weill dyschondrostosis (LWD) SHOX deletion v2
Xp22.31	6.47	8.09	Steroid sulphatase deficiency (STS)
Xp22.31	8.46	8.66	Xp22.31 Kallmann
Xp21.2	30.58	30.66	Xp21.2 Glycerol kinase deficiency
Xp21.2-p21.1	31.05	33.28	Xp21.2 DMD
Xp11.22-p11.23	48.22	52.13	Xp11.22-p11.23 Microduplication
Xp11.22	53.42	53.70	Xp11.22-linked intellectual disability duplication
Xq23-q22.3	103.60	110.50	AMME complex
Xq23-q22.3	110.42	110.54	Xq23 X-linked lissencephaly
Xq27.1	139.36	139.91	Mental Retardation with panhypopituitarism syndrome
Xq28	152.94	153.02	Xq28 (MECP2) duplication
Xq28	152.94	153.02	Xq28 Rett syndrome
Xq28	152.94	153.02	Xq28 Rett syndrome female
Xq28	153.28	153.54	Xq28 Microduplication
X	0.00	154.91	Triple X syndrome

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Supplementary Table 2. Prevalence of known and likely pathogenic genomic imbalances in CKiD cases as compared to CHOP pediatric controls

	N	Individuals with a Known Genomic Disorder (%)	Odds Ratio (P-value)
All CKD	419	19 (4.5%)	4.6 (4.77×10^{-6})
CAKUT	221	10 (4.5%)	4.8 (1.11×10^{-4})
Renal Hypodysplasia	67	7 (10.5%)	13.0 (6.19×10^{-8})
Non-CAKUT	198	9 (4.6%)	4.0 (1.08×10^{-3})
Controls	1,890	22 (1.2%)	1 (reference)

Odds Ratios with associated P-values are derived from logistic regression analysis of known pathogenic imbalances in all CKiD cases in comparison to CHOP pediatric controls (reference); the analysis is adjusted for race/ethnicity and gender. CAKUT = congenital abnormality of the kidney and urinary tract, CAKUT includes ureteropelvic junction obstruction, reflux nephropathy and renal hypodysplasia (RHD). RHD cases are also shown separately; Other CKiD cases were included in the non-CAKUT category.

Supplementary Table 3. Largest rare CNVs per genome in CKiD cases and controls after subtracting known syndrome carriers. The numbers (and percentages) of CKiD children and controls with their largest CNV (top), deletion (middle) and duplication (bottom) in the indicated size range (in kb) are shown. Global Fisher's exact test P-values are also shown for all CNVs, deletions and duplications.

CNV size (kb)	Number of Cases		Number of Controls		P-value
100-250	66	(16.50%)	2548	(11.86%)	1.38×10^{-07}
250-500	44	(11.00%)	1399	(6.51%)	
500-1000	24	(6.00%)	701	(3.26%)	
≥ 1000	11	(2.75%)	345	(1.61%)	
Deletion size (kb)	Number of Cases		Number of Controls		P-value
100-250	32	(8.00%)	1322	(6.16%)	1.30×10^{-04}
250-500	17	(4.25%)	516	(2.40%)	
500-1000	10	(2.50%)	212	(0.99%)	
≥ 1000	6	(1.50%)	107	(0.50%)	
Duplication size (kb)	Number of Cases		Number of Controls		P-value
100-250	52	(13.00%)	1477	(6.88%)	4.37×10^{-07}
250-500	31	(7.75%)	932	(4.34%)	
500-1000	14	(3.50%)	504	(2.35%)	
≥ 1000	5	(1.25%)	239	(1.11%)	

Supplementary Table 4. Comparison of phenotypes between patient with and without pathogenic imbalances

Variable	Pathogenic imbalances Mean	SD	No Pathogenic imbalances Mean	SD	P-value
Gender (M/F)•	8/11		259/146		
Age at visit	11.3	4.2	10.5	4.4	
Age at diagnosis #	3.4	4.6	3.5	4.8	0.607
Serum Creatinine (mg/dL)	1.6	0.7	1.4	0.7	0.049
BUN	34.0	15.2	30.0	13	0.116
Cystatin C (Siemens) ¶	2.0	0.6	1.7	0.6	0.050
eGFR ¶	41.3	18.4	47.0	15.2	0.027
Iohexol GFR ¶ **	40.2	13.9	47.3	18.4	0.150
Urine Protein/Creatinine ¶∏	2.5	2.8	1.0	1.8	0.035
Systolic BP (mm Hg)	107.1	11.3	106.9	12.7	0.972
Diastolic BP (mm Hg)	66.0	10.9	66.1	10.4	0.924
Systolic BP Percentile *	59.3		66.6		0.868
Diastolic BP Percentile *	61.8		70.4		0.770
Hemoglobin (g/dL)	12.2	1.4	12.6	1.5	0.234
Hematocrit (%)	35.7	4.2	36.8	4.5	0.283
Height	138.0	22.0	136.1	26.9	0.494
Height Percentile *§	16.8		25.5		0.443
Heigth Adj. z-score §	-0.9	1.1	-0.7	1.2	0.441
Weight	38.5	16.2	39.9	23.2	0.067
Weight Percentile *§	36.3		44.6		0.255
Weight adj. z-score §	-0.4	1.3	-0.1	1.3	0.254
BMI	19.2	4.4	19.7	5.6	0.101
BMI Percentile *§	41.8		62.1		0.245
BMI adj. z-score §	0.1	1.2	0.4	1.1	0.241
Tanner Stage *	1.0		1.0		0.969

Unless otherwise indicated mean and standard deviation values are shown for pathogenic genomic imbalance carriers and non-carriers.
Unless otherwise indicated, non-parametric Wilcoxon test was performed on residuals after adjusting for Age at visit, Gender, Race, Age at diagnosis and Duration of disease.
∏ Also adjusted for eGFR value.
¶ Regression was performed on log transformed data.
• Counts, with Median values are reported.
**** Iohexol GFR has 9% missing values**
 # Residual adjusted for Gender and Race only.
§ Variable is adjusted for Age and Gender. Non parametric Wilcoxon test was performed on values without further adjustment.

Supplementary Table 5. Clinical manifestations of genomic disorders detected in this study and targeted workup and surveillance

Syndrome	Associated Clinical Manifestations	Recommended Targeted Work-up and surveillance
1q21.1 microduplication	Genitourinary tract malformations Structural cardiac defects Macrocephaly seizures & intellectual disability	Abdominal Ultrasound, kidney function test Cardiac evaluation/imaging Comprehensive developmental assessment +/- neuroimaging & EEG
1q21.1 microdeletion	Genitourinary tract malformations Eye abnormalities Structural cardiac defects Skeletal malformations, Microcephaly, seizures & intellectual disability,	Abdominal Ultrasound, kidney function test Ophthalmologic exam Cardiac evaluation/imaging Comprehensive developmental assessment +/- neuroimaging & EEG
2q13 homozygous deletion (Nephronophthisis 1)	Nephrophthisis Retinal pigmentosa Cerebellar ataxia/ oculomotor apraxia Developmental delay	Abdominal Ultrasound, kidney function test Ophthalmologic exam Comprehensive developmental assessment +/- neuroimaging
Wolf-Hirschhorn syndrome	Urinary tract malformations Skeletal anomalies, hypotonia Feeding problems and gastroesophageal reflux Structural heart defects Hearing loss Developmental delay/intellectual disability Seizures, Structural brain abnormalities	Abdominal Ultrasound, kidney function test Orthopedic and physical therapy evaluation Dysphagia evaluation Cardiac evaluation/imaging Hearing tests Comprehensive developmental assessment +/- neuroimaging & EEG
15q24 BP0-BP1 deletion	Genitourinary tract malformations Structural cardiac defects Eye abnormalities Congenital malformations of the hands and feet Conductive and sensorineural hearing loss Developmental delay; intellectual disability, seizures, growth retardation and failure to thrive	Abdominal Ultrasound, kidney function test Cardiac evaluation/imaging Ophthalmologic exam Orthopedic and physical therapy assessment Hearing test Comprehensive developmental assessment +/- neuroimaging & EEG
16p11.2 deletion	Urinary tract malformations Structural cardiac defects Obesity Developmental delay, intellectual disability, and/or autism spectrum disorder (ASD).	Abdominal Ultrasound, kidney function test Cardiac evaluation/imaging Follow growth chart and caloric intake Comprehensive developmental assessment +/- neuroimaging & EEG
Hereditary Liability to Pressure Palsies (HNPP)	Susceptibility to repeated focal pressure neuropathies Mild polyneuropathy,	Detailed neurologic examination with attention to peripheral neuropathy
Renal Cysts and Diabetes deletion*	Kidney malformations and CKD Diabetes Hyperurecemia/gout Uterine malformations Intellectual disability and neuropsychiatrc disease	Abdominal Ultrasound, kidney function test Fasting Glucose/glucose tolerance tests Serum uric acid levels Abdominal Ultrasound Comprehensive developmental assessment +/- neuroimaging & EEG
CTNS homozygous deletion	Tissue Cystinosin accumulation leading to: Fanconi syndrome Poor growth, hypophosphatemic rickets,	 Serum and urine leectrolytes Growth chart, ca and Vit D levels, skeletal radiographs

	Progressive nephrocalcinosis and CKD	Kidney function tests
	Visual impairment	Ophthalmologic exam
	Thyroid, pancreatic dysfunction	Thyroid function tests, glucose, lipid panel
Triple X Syndrome	Urogenital malformations	Abdominal ultrasound, kidney function tests
	Strabismus	Ophthalmologic examination
	Intellectual disability, developmental delay	EEG examination and neuroimaging
	Seizure disorders	Neuropsychological investigation in the child
	Premature ovarian failure or primary amenorrhoea	Counseling in adulthood as needed

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Supplementary Table 6 A. Clinical diagnoses of CKiD cohort cases

Clinical Diagnosis	N	%
Obstructive uropathy	95	22.4
Renal hypodysplasia	69	16.3
Reflux nephropathy	59	13.9
Non-Glomerular other	46	10.8
Focal segmental glomerulosclerosis	30	7.1
Polycystic kidney disease (Autosomal recessive)	17	4.0
Renal infarct	15	3.5
Hemolytic uremic syndrome	14	3.3
Syndrome of agenesis of abdominal musculature	10	2.4
Cystinosis	8	1.9
Pyelonephritis/Interstitial nephritis	8	1.9
Systemic Immunological Disease (Incl. SLE)	8	1.9
Oxalosis	7	1.7
Familial nephritis – Alport's	5	1.2
Glomerular other	5	1.2
IgAN – Berger's	5	1.2
Chronic glomerulonephritis	4	0.9
Idiopathic crescentic glomerulonephritis	3	0.7
Membranous nephropathy	3	0.7
Congenital nephrotic syndrome	2	0.5
Henoch-Schonlein nephritis	2	0.5
Medullary cystic disease/Juvenile nephronophthisis	2	0.5
Membranoproliferative glomerulonephritis type I	2	0.5
Wilms tumor	2	0.5
Membranoproliferative glomerulonephritis type II	1	0.2
Polycystic kidney disease (Autosomal dominant)	1	0.2
Sickle cell nephropathy	1	0.2
Total	424	100

Table 6 B Ancestry of CKiD cohort participants

Ancestry	N	%
Caucasian	289	68.2
Black or African-American	71	16.7
Asian	10	2.4
Other/More than one race	54	12.7
	424	100

Supplementary Table 7. Description of control cohorts

A. Control cohorts and Illumina genotyping platforms

Cohort	ILMN Platform	N	%
AJ PD[1]	610-Quad/660W	378	1.8
Blood Clotting[2]	Omni1-Quad	451	2.1
CHOP controls[3]	550v1/500v2/550v3	1890	8.8
Glasgow HTN[4]	610-Quad	2933	13.6
Hypergenes[5]	1M-Duo	3062	14.2
IgAN controls[6]	610-Quad	1034	4.8
Melanoma[7]	Omni1-Quad	2674	12.4
NIA[8]	610-Quad	595	2.8
PD[9]	Omni1-Quad	3865	17.9
Vis. Adip.[10]	1M-Duo	2322	10.8
SAGE[11]	1M	2371	11.0
Total		21575	100

B. Ancestry of controls

Ancestry	N	%
Caucasian	18147	84.1
Black or African-American	2357	10.9
Asian	897	4.2
Other/Unknown	174	0.8
	21575	100

References for Supplementary Table 7

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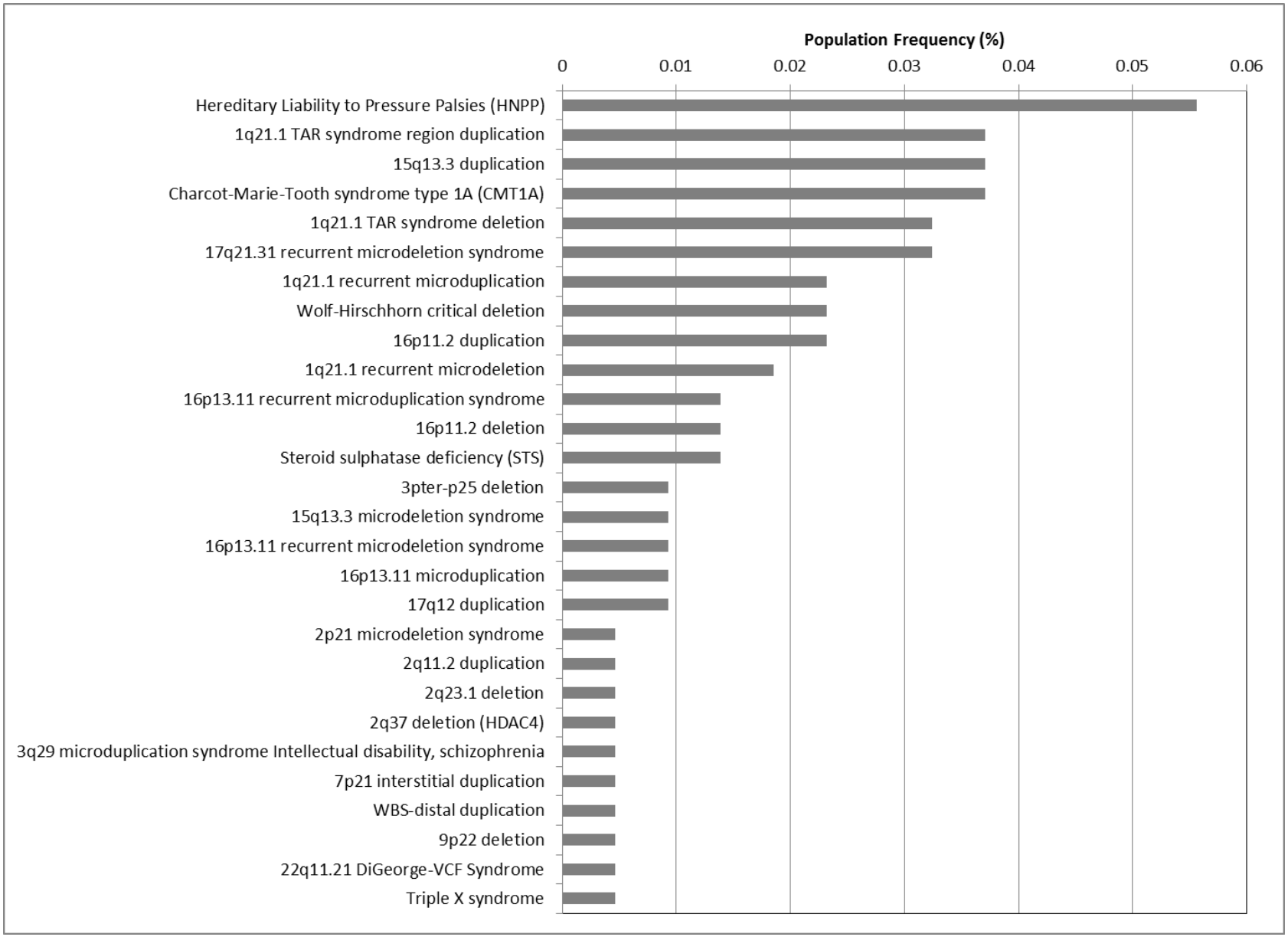
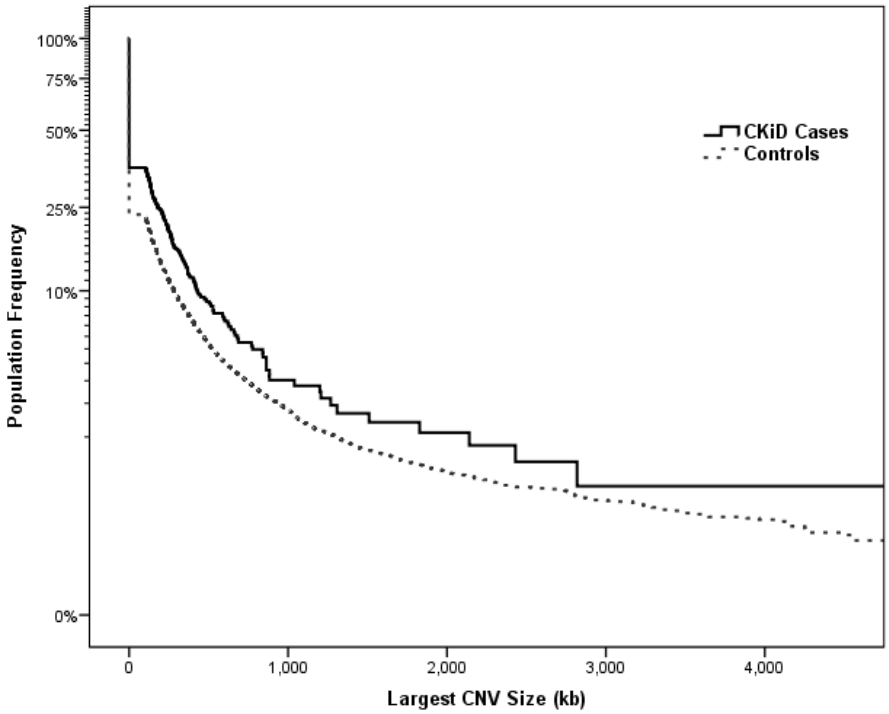
11. Study of Addiction: Genetics and Environment (SAGE). dbGAP Accession: phs000092.v1.p1.

Supplementary Figure 1. Frequency distribution of known genomic disorders in the control group (N=21,575)

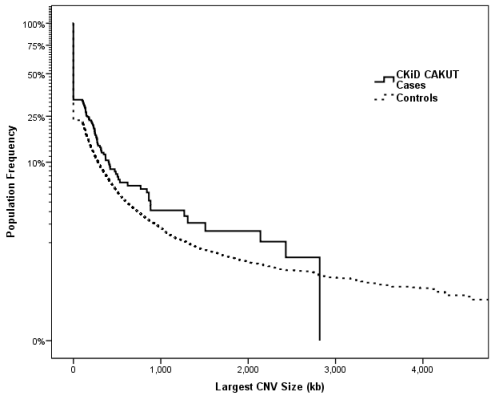


Supplementary Figure 2

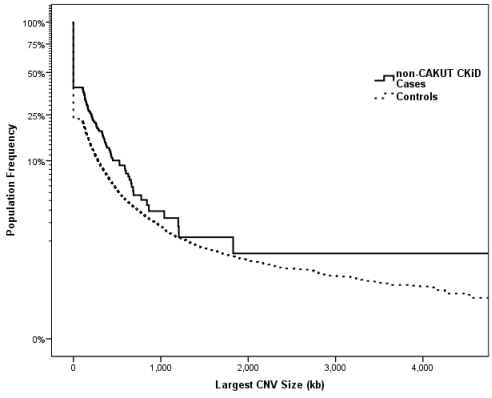
A. Burden of rare, large, gene-disrupting CNVs in all CKiD cases as comp to controls After subtracting known syndrome carriers (Log-rank test F x 10-5). Only the largest CNVs per genome were included in the analys



B. Burden of rare, large, gene-disrupting CNVs in CKiD CAKUT-only cases (N=211; red curve) as compared to controls (N=21,477; green curve) after subtracting known syndrome carriers (Log-rank P=0.006). Only the largest CNVs per genome were included in the analysis.



C. Burden of rare, large, gene-disrupting CNVs in CKiD non-CAKUT-only cases (N=189; red curve) as compared to controls (N=21,477; green curve) after subtracting known syndrome carriers (Log-rank P=0.001). Only the largest CNVs per genome were included in the analysis.



Acknowledgment of dbGAP resources

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Genes and Blood Clotting Study (GABC). dbGAP Accession: phs000304.v1.p1
Funding Source:
R37 HL 039693. "Molecular Genetic Studies of von Willebrand Factor". National Institutes of Health, Bethesda, MD, USA

Whole Genome Association Study of Visceral Adiposity in the Health Aging and Body Composition (Health ABC) Study. dbGAP Accession: phs000169.v1.p1
Funding Source:
R01 AG032098-01. National Institute of Aging, National Institutes of Health, Bethesda, MD, USA

Study of Addiction: Genetics and Environment (SAGE). dbGAP Accession: phs000092.v1.p1.
Funding Source:
U01 HG004422. National Human Genome Research Institute, Bethesda, MD, USA
U10 AA008401. National Institute on Alcohol Abuse and Alcoholism and National Institute on Drug Abuse, Bethesda, MD, USA
P01 CA089392. National Cancer Institute, Bethesda, MD, USA
R01 DA013423. National Institute on Drug Abuse, Bethesda, MD, USA
R01 DA019963. National Institute on Drug Abuse, Bethesda, MD, USA

High Density SNP Association Analysis of Melanoma: Case-Control and Outcomes Investigation. dbGaP Study Accession: phs000187.v1.p1
Funding Source:
R01CA100264. National Cancer Institute, Bethesda, MD, USA
P50CA093459. National Cancer Institute, Bethesda, MD, USA
Funding Source for Genotyping: HHSN268200782096C. "NIH contract High throughput genotyping for studying the genetic contributions to human disease". National Institutes of Health, Bethesda, MD, USA

Genome-Wide Association Study of Parkinson Disease: Genes and Environment dbGaP Study Accession: phs000196.v2.p1
Funding Source: 5R01NS36960-10. National Institutes of Health, Bethesda, MD, USA
Funding Source for Genotyping: HHSN268200782096C. NIH contract "High throughput genotyping for studying the genetic contributions to human disease". National Institutes of Health, Bethesda, MD, USA

National Institute on Aging - Late Onset Alzheimer's Disease Family Study: Genome-Wide Association Study for Susceptibility Loci. dbGaP Study Accession: phs000168.v1.p1.

Funding source:
HHSN268200782096C. "NIH contract High throughput genotyping for studying the genetic contributions to human disease". National Institutes of Health, Bethesda, MD, USA

Children's Hospital of Philadelphia (CHOP) Control Copy Number Variation (CNV) Study dbGaP Study Accession: phs000199.v1.p1

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IgA Nephropathy GWAS (IGANGWAS) dbGaP Study Accession: phs000431.v1.p1

Funding Source
RC1DK087445. National Institutes of Health, Bethesda, MD, USA
R01DK082753. National Institutes of Health, Bethesda, MD, USA
KL2 RR24157. National Institutes of Health, Bethesda, MD, USA
HHMI. Howard Hughes Medical Institute, Chevy Chase, MD, USA