

Phenotypic presentation of Mendelian disease across the diagnostic trajectory in electronic health records

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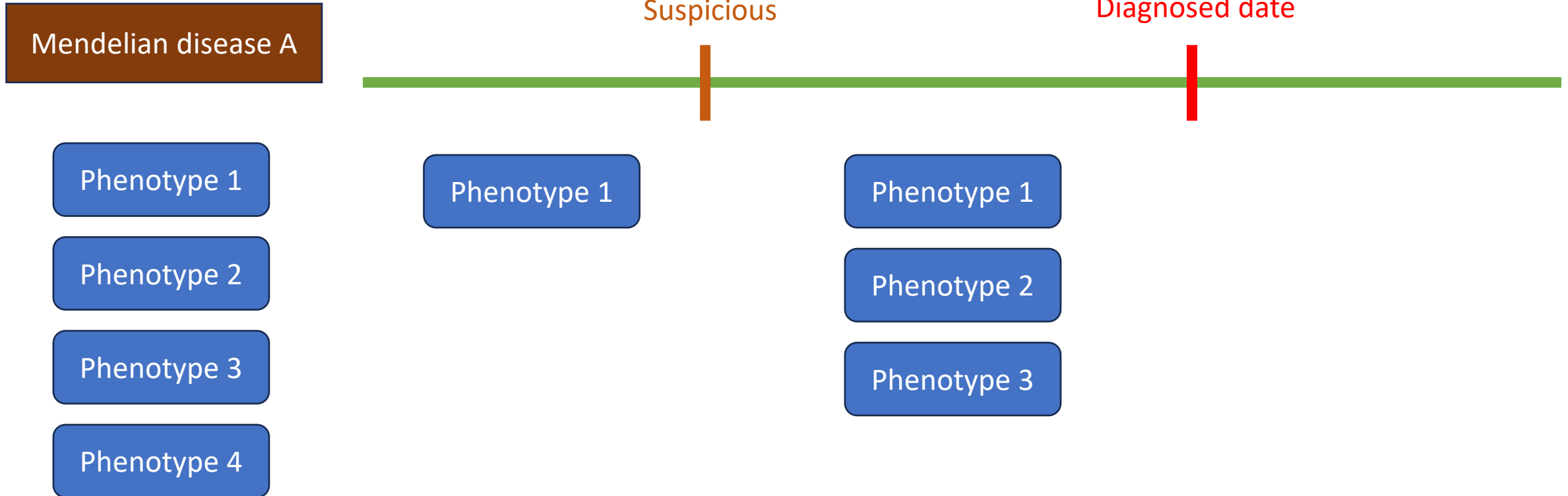
Phenotypic presentation

Phenotype

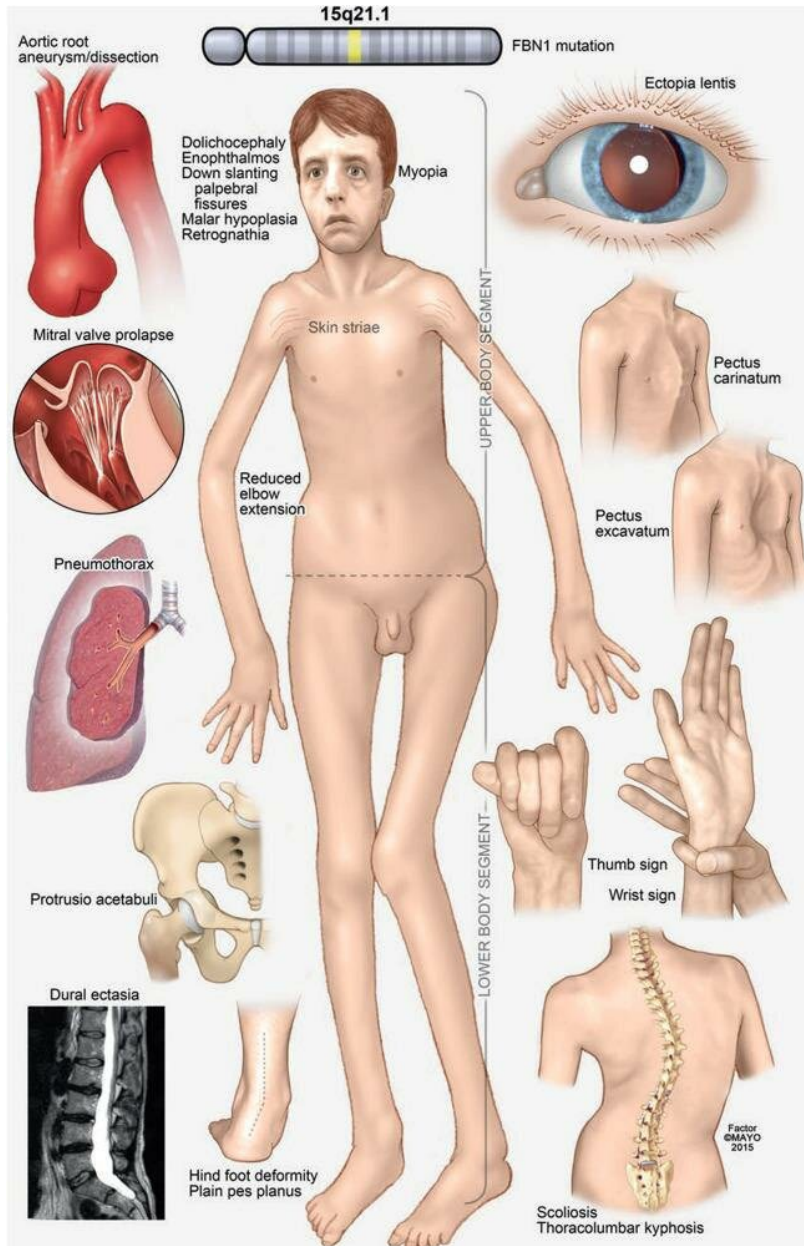
Is the observation characteristics influenced by genes



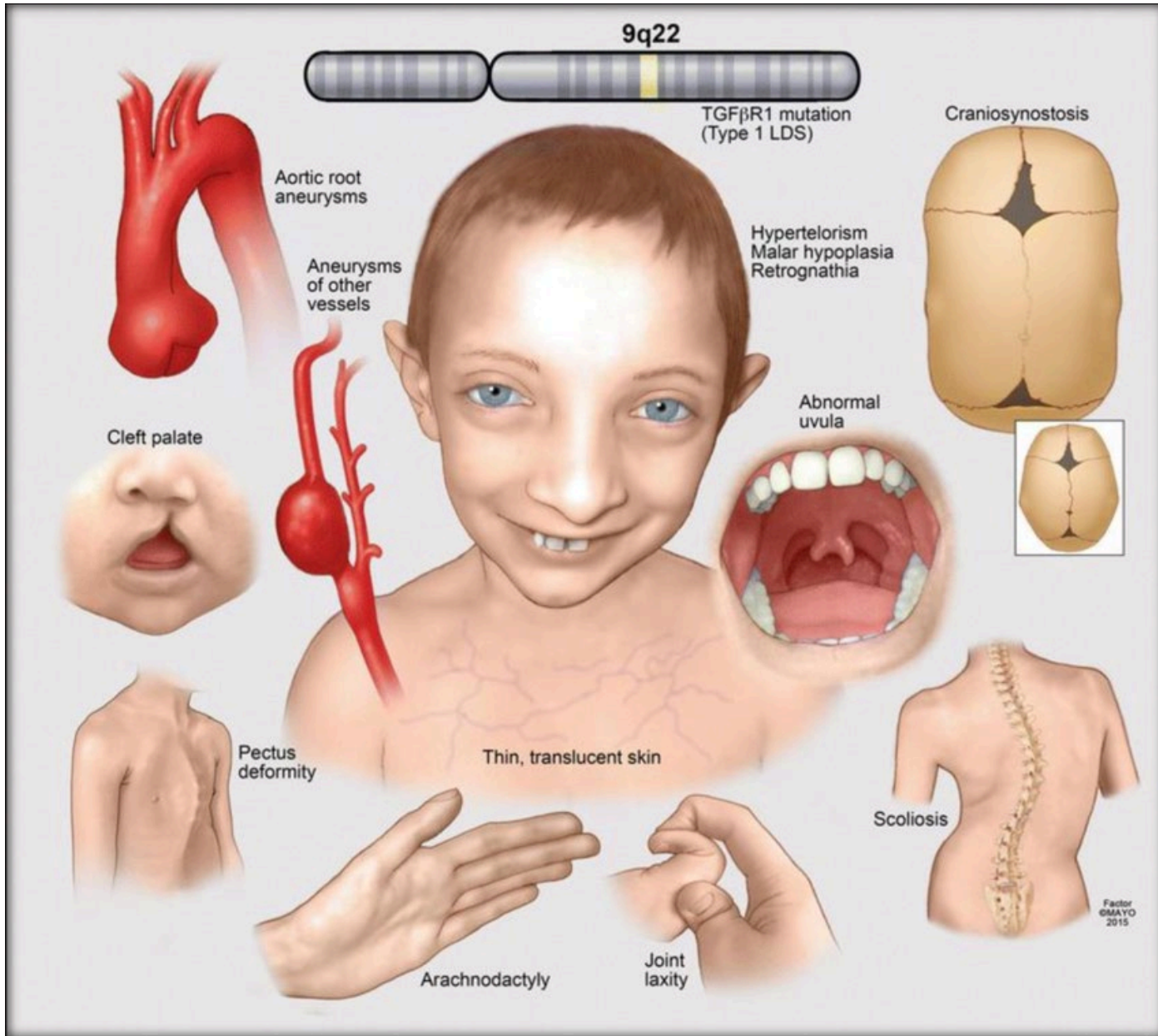
Timeline of a patient



| | |
|--|---|
| Marfan syndrome (MFS) | Connective tissue |
| Loeys-Dietz syndrome (LDS), Stickler syndrome (STL) | Connective tissue |
| Classical Ehlers Danlos syndrome (cEDS) | Connective tissue |
| Vascular Ehlers Danlos syndrome (vEDS) | Connective tissue |
| Hereditary Hemorrhagic Telangiectasia (HHT) | Arteriovenous malformations |
| Hypophosphatasia (HPP) | Deficient activity of the tissue-nonspecific isoenzyme of alkaline phosphatase. |
| Noonan syndrome (NS) | Gain of function in cell signaling pathway |
| Adult Cystic fibrosis (aCF) | Abnormal and thick mucus production through the body |



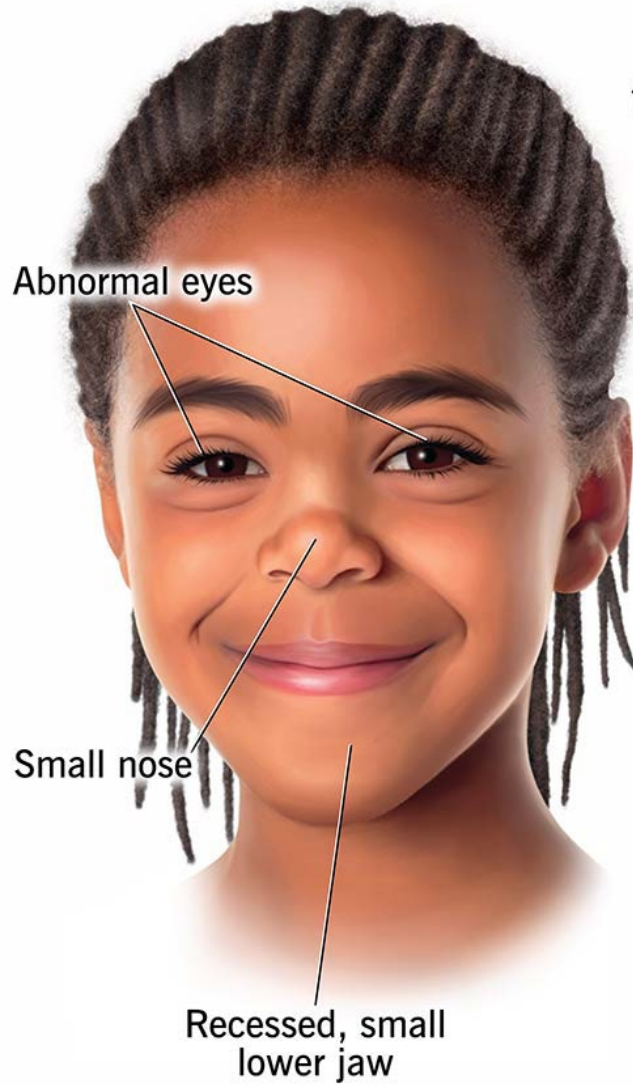
Marfan syndrome (MFS)



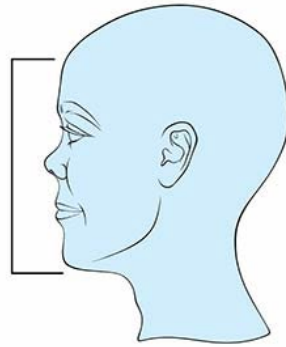
Loeys-Dietz syndrome

Stickler Syndrome

Stickler dysplasia



Flat face



Common symptoms and problems



Bone and joint



Ear and hearing

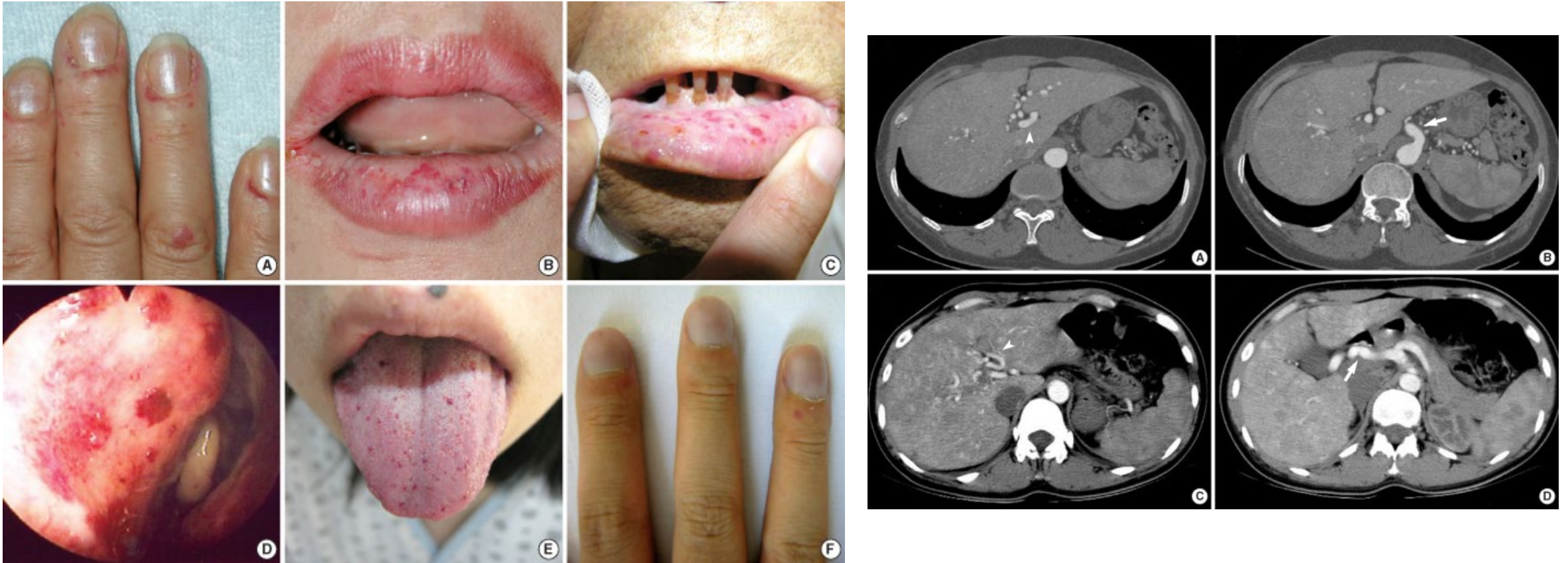


Eye and sight

Classical Ehlers Danlos syndrome (cEDS)



Hereditary Hemorrhagic Telangiectasia

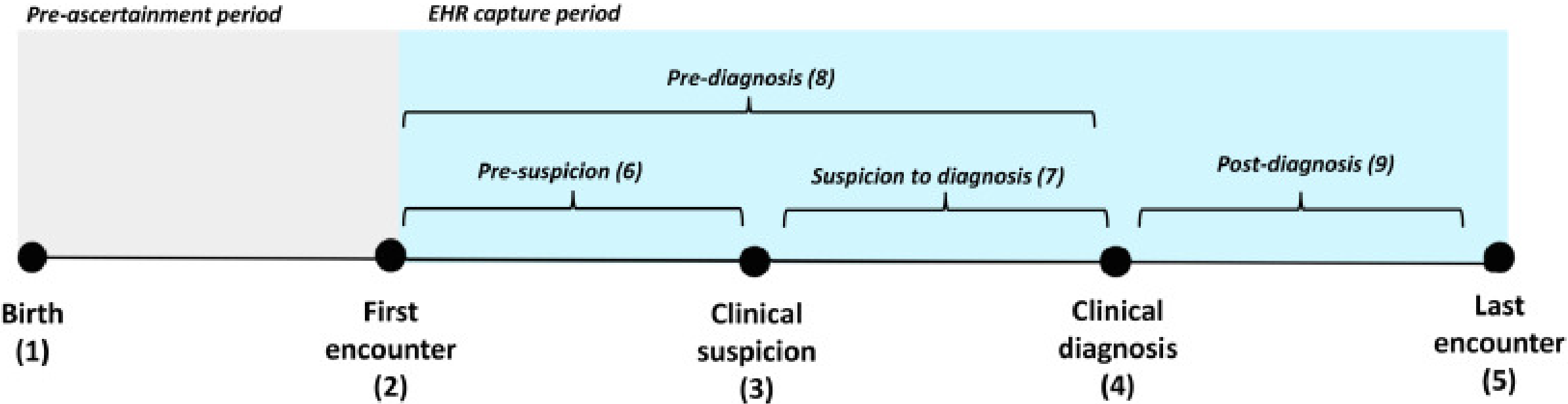


Lee, Seung-Tae & Kim, Jee-Ah & Jang, Shin-Yi & Kim, Duk-Kyung & Do, Young & Suh, Gee Young & Kim, Jong-Won & Ki, Chang-Seok. (2009). Clinical Features and Mutations in the ENG, ACVRL1, and SMAD4 genes in Korean Patients with Hereditary Hemorrhagic Telangiectasia. *Journal of Korean medical science*. 24. 69-76. 10.3346/jkms.2009.24.1.69.

Hypophosphatasia



An EHR-based trajectory of the diagnostic process in genetic disease



Cohort data

- Vanderbilt University Medical Center
- at least 3 encounters
- between January 1, 2002, and January 1, 2022
- Control = 1.8 million

| Disease Name | Gene(s) | Abbreviation | Total | Diagnosed Before First Visit N (%) | Suspicion On First Encounter N (%) | Fully Ascertained Trajectory N (%) |
|--|--|--------------|-------|--|--|--|
| Marfan syndrome | <i>FBN1</i> | MFS | 145 | 55 (37.9) | 57 (39.3) | 33 (22.8) |
| Ehlers Danlos, Classic | <i>COL5A1/2</i> | cEDS | 9 | 2 (22.2) | 1 (11.1) | 6 (66.6) |
| Ehlers Danlos, Vascular | <i>COL3A1</i> | vEDS | 27 | 5 (20.8) | 9 (33.3) | 13 (48.1) |
| Loeys-Dietz syndrome | <i>TGFBR1/2, TGFB2, SMAD2/3</i> | LDS | 32 | 7 (21.9) | 8 (25.0) | 17 (53.1) |
| Stickler syndrome | <i>COL2A1, COL11A1, COL9A1, COL9A3</i> | STL | 40 | 8 (20.0) | 14 (35.0) | 18 (45.0) |
| Hereditary Hemorrhagic Telangiectasia | <i>ACVRL1, ENG</i> | HHT | 79 | 28 (35.4) | 19 (24.1) | 32 (40.5) |
| Hypophosphatasia | <i>ALPL</i> | HPP | 93 | 53 (57.0) | 10 (10.8) | 30 (32.3) |
| Noonan syndrome | <i>PTPN11, SOS1, RAF1</i> | NS | 92 | 17 (18.5) | 26 (28.3) | 49 (53.3) |
| Cystic Fibrosis | <i>CFTR</i> | CF | 379 | 353 (93.1) | 7 (1.85) | 18 (4.75) |
| All | — | All | 896 | 528 (60.8) | 151 (16.9) | 216 (24.1) |

RESULT

Mendelian disease A

Phenotype 1

X Weight of P1

Phenotype 2

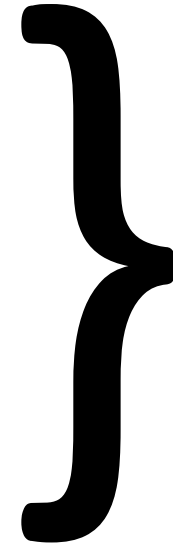
X Weight of P2

.

.

Phenotype k

X Weight of Pk



Phenotype risk score

$$\text{Weight} = \log_{10} \left(\frac{N}{n_j} \right),$$

N is the total number of individuals in the cohort

n_j is the number of individuals with at least one occurrence of phecode j

Phenotype risk score

Sex

Age

Record length

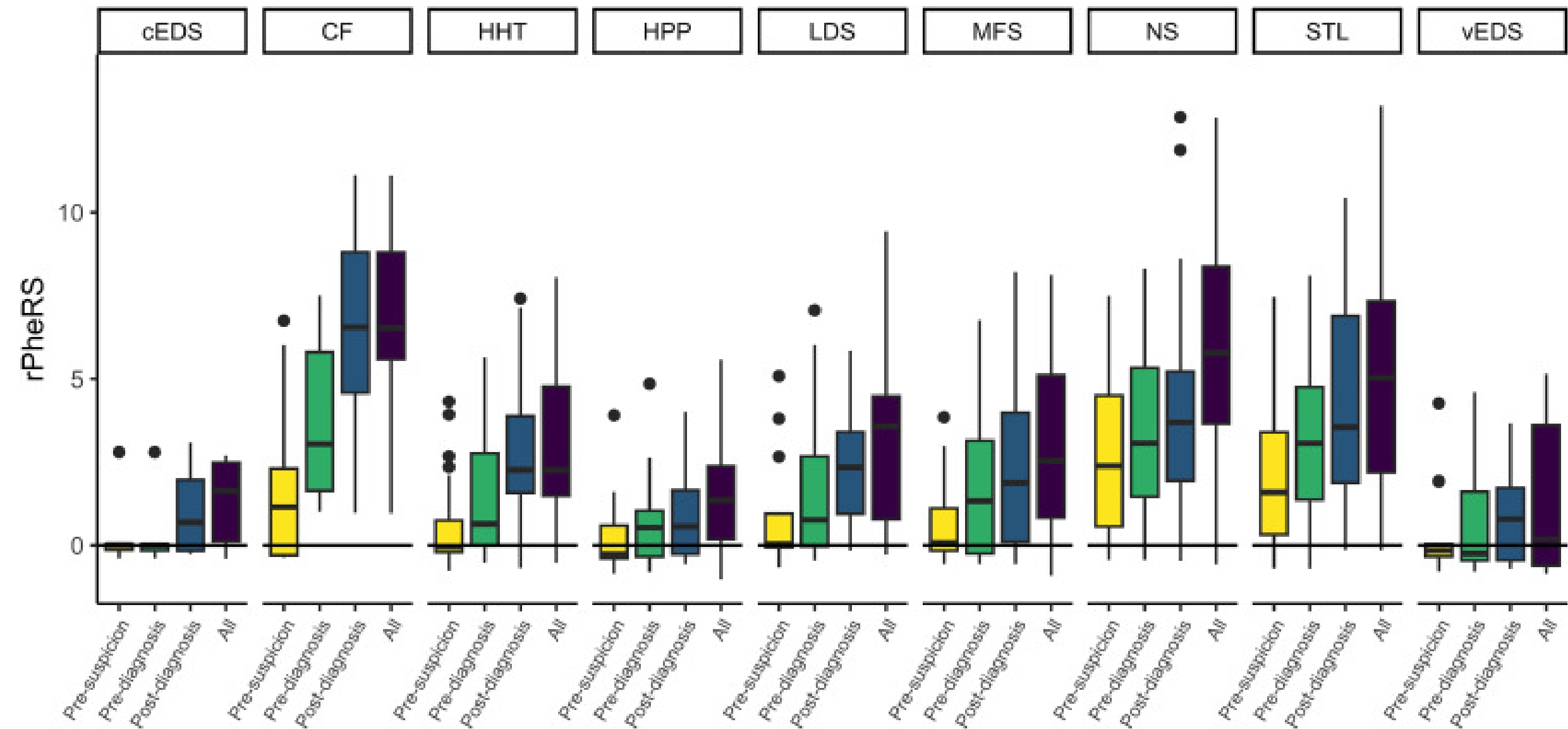


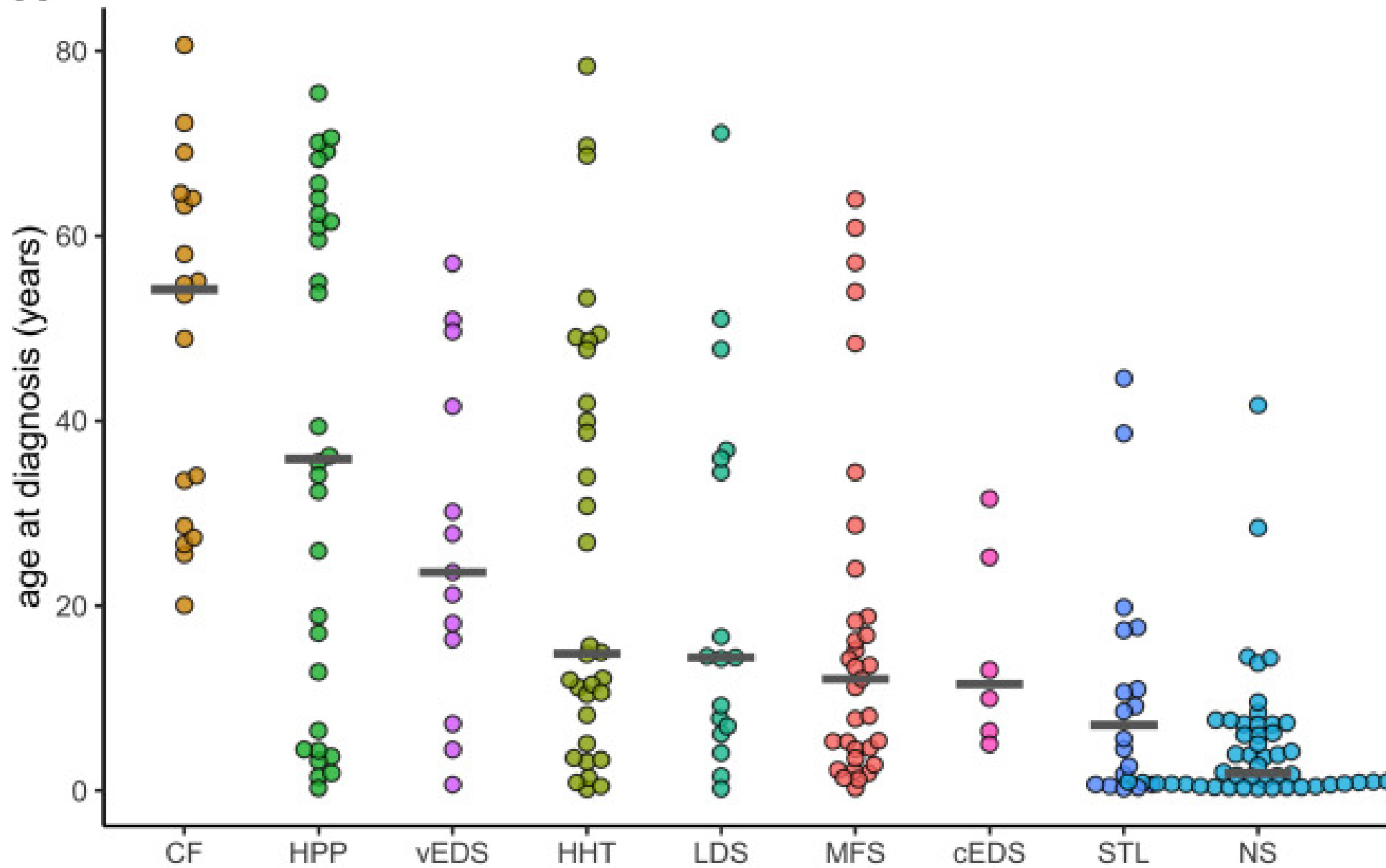
residualized PheRS (rPheRS)

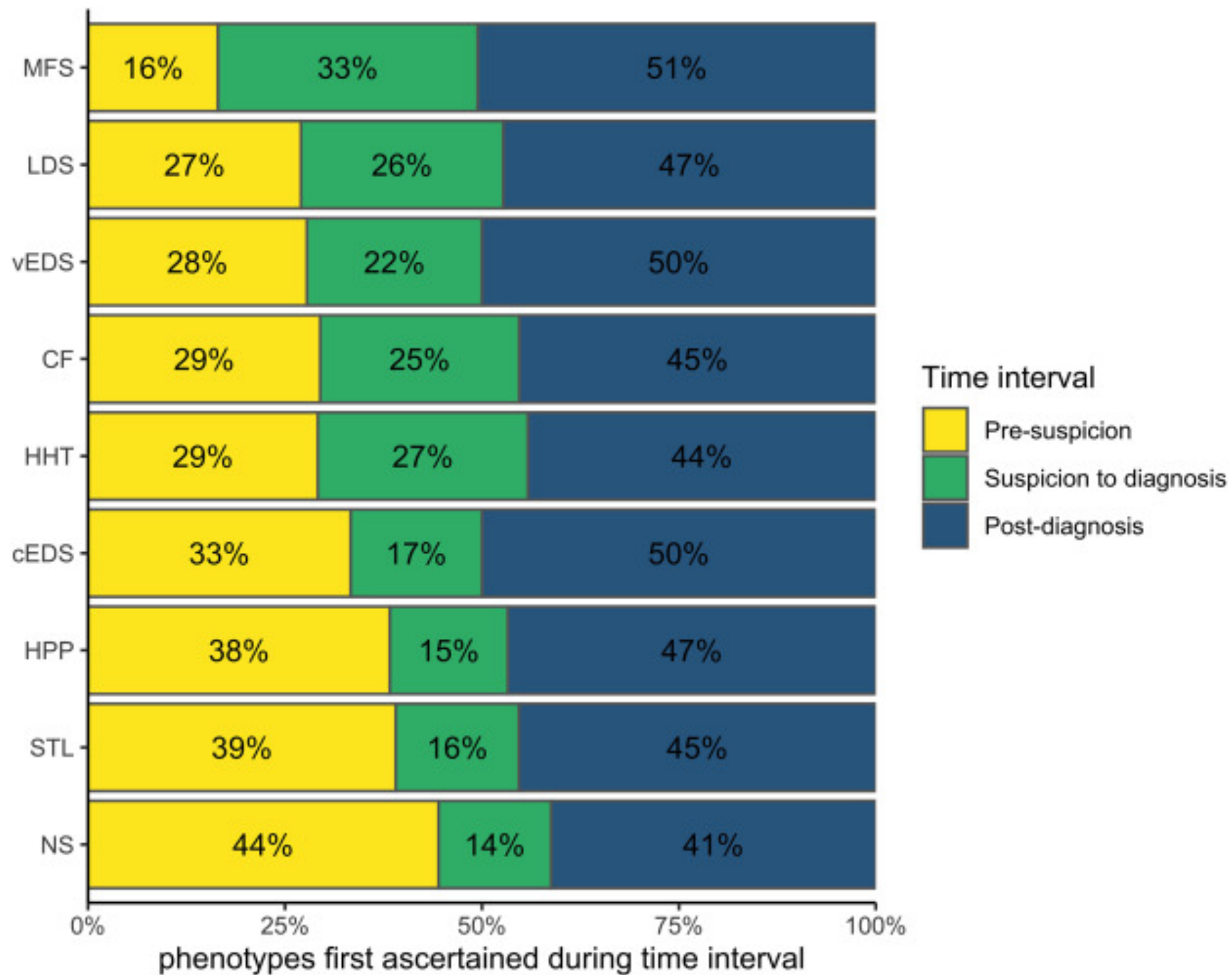
| Disease | Pre-suspicion | | Pre-diagnosis | | Post-diagnosis | | All | |
|-------------|----------------------|-----------------|----------------------|-----------------|---------------------|-----------------|--------------------|-----------------|
| | Median PheRS | P* | Median PheRS | P* | Median PheRS | P* | Median PheRS | P* |
| MFS | 0.08 [-0.16 - 1.11] | 3.80E-05 | 1.33 [-0.25 - 3.15] | 2.00E-07 | 1.87 [0.11 - 3.98] | 7.10E-12 | 2.54 [0.83 - 5.11] | 1.80E-13 |
| cEDS | 0.01 [-0.14 - 0.03] | 0.043 | 0.00 [-0.16 - 0.03] | 0.05 | 0.70 [-0.17 - 1.97] | 0.015 | 1.64 [0.12 - 2.49] | 0.023 |
| vEDS | -0.16 [-0.33 - 0.04] | 0.192 | -0.24 [-0.45 - 1.61] | 0.32 | 0.79 [-0.45 - 1.72] | 0.06 | 0.18 [-0.6 - 3.61] | 0.177 |
| LDS | 0.04 [-0.06 - 0.95] | 2.80E-03 | 0.76 [-0.03 - 2.67] | 2.60E-05 | 2.35 [0.95 - 3.41] | 1.40E-08 | 3.57 [0.78 - 4.48] | 3.80E-08 |
| STL | 1.59 [0.33 - 3.4] | 2.80E-07 | 3.07 [1.37 - 4.76] | 1.00E-08 | 3.55 [1.88 - 6.89] | 2.40E-10 | 5.03 [2.2 - 7.34] | 2.20E-11 |
| CF | 1.15 [-0.29 - 2.3] | 1.30E-05 | 3.04 [1.64 - 5.8] | 1.30E-11 | 6.55 [4.58 - 8.8] | 6.60E-13 | 6.53 [5.58 - 8.8] | 5.90E-13 |
| NS | 2.39 [0.57 - 4.5] | 8.70E-18 | 3.07 [1.46 - 5.33] | 1.30E-23 | 3.69 [1.94 - 5.21] | 1.10E-25 | 5.78 [3.65 - 8.37] | 1.80E-28 |
| HPP | -0.27 [-0.39 - 0.6] | 0.054 | 0.54 [-0.34 - 1.03] | 2.60E-04 | 0.57 [-0.27 - 1.65] | 6.40E-06 | 1.36 [0.18 - 2.38] | 2.90E-07 |
| HHT | -0.05 [-0.21 - 0.74] | 8.90E-04 | 0.64 [0 - 2.77] | 1.60E-08 | 2.26 [1.58 - 3.88] | 8.60E-12 | 2.26 [1.49 - 4.77] | 7.80E-16 |
| ALL | 0.15 [-0.24 - 2.05] | 3.60E-31 | 1.45 [-0.01 - 3.64] | 9.10E-55 | 2.34 [0.66 - 4.65] | 3.80E-74 | 3.23 [1.22 - 5.87] | 7.00E-84 |

| Disease | High score | | | |
|-----------|---------------|----------------|----------------|----------|
| | Pre-suspicion | Pre-diagnosis* | Post-diagnosis | All |
| MFS (33) | 0 (0%) | 4 (12%) | 8 (24%) | 11 (33%) |
| cEDS (6) | 0 (0%) | 0 (0%) | 0 (0%) | 0 (0%) |
| vEDS (13) | 1 (7.7%) | 2 (15%) | 0 (0%) | 2 (15%) |
| LDS (17) | 1 (5.9%) | 3 (18%) | 3 (18%) | 7 (41%) |
| STL (18) | 4 (22%) | 7 (39%) | 9 (50%) | 10 (56%) |
| CF (18) | 2 (11%) | 8 (39%) | 14 (78%) | 15 (83%) |
| NS (49) | 13 (27%) | 19 (39%) | 20 (41%) | 32 (65%) |
| HPP (30) | 0 (0%) | 1 (3.3%) | 2 (6.7%) | 3 (10%) |
| HHT (32) | 1 (3.1%) | 5 (16%) | 6 (19%) | 10 (31%) |
| ALL (216) | 22 (10%) | 48 (22%) | 62 (29%) | 90 (42%) |

* includes pre-suss and pre-dx



A



Time interval

- The median time from first visit to clinical suspicion was **3.23 years** (IQR: 153 days-6.4 years)
- The median time from clinical suspicion to diagnosis was **71 days** (IQR: 20.8-235)

Physician's view

- We not usually enter ICD10 of all symptoms
- How about SNOMED CT?
- When we would change from scanning medical records to EMR?
- Cluster/Family analysis

THANK YOU