

Confirmatory Testing Following a Positive SCID Newborn Screen

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Disclosures

- ❑ Albany Medical College
 - ❑ Honorarium
- ❑ Baxter, Inc.
 - ❑ Consultant
- ❑ The Cowen Group, Inc.
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- ❑ CSL Behring, Inc.
 - ❑ Consultant, research support
- ❑ Gerson-Lehrman Group, Inc.
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- ❑ Immune Deficiency Foundation
 - ❑ Medical Advisory Board
 - ❑ Consultant Immunologist Program
- ❑ Octapharma, Inc.
 - ❑ Data safety monitor
- ❑ UpToDate in Medicine
 - ❑ Royalties

Following up an abnormal SCID newborn screen

- ▶ Assumptions:
 - ▶ The level of TRECs is below the laboratory-specific cutoff
 - ▶ Quality control indicates a valid result
- ▶ Secondary screen
 - ▶ Total T cell number
 - ▶ Proportion of naïve T cells

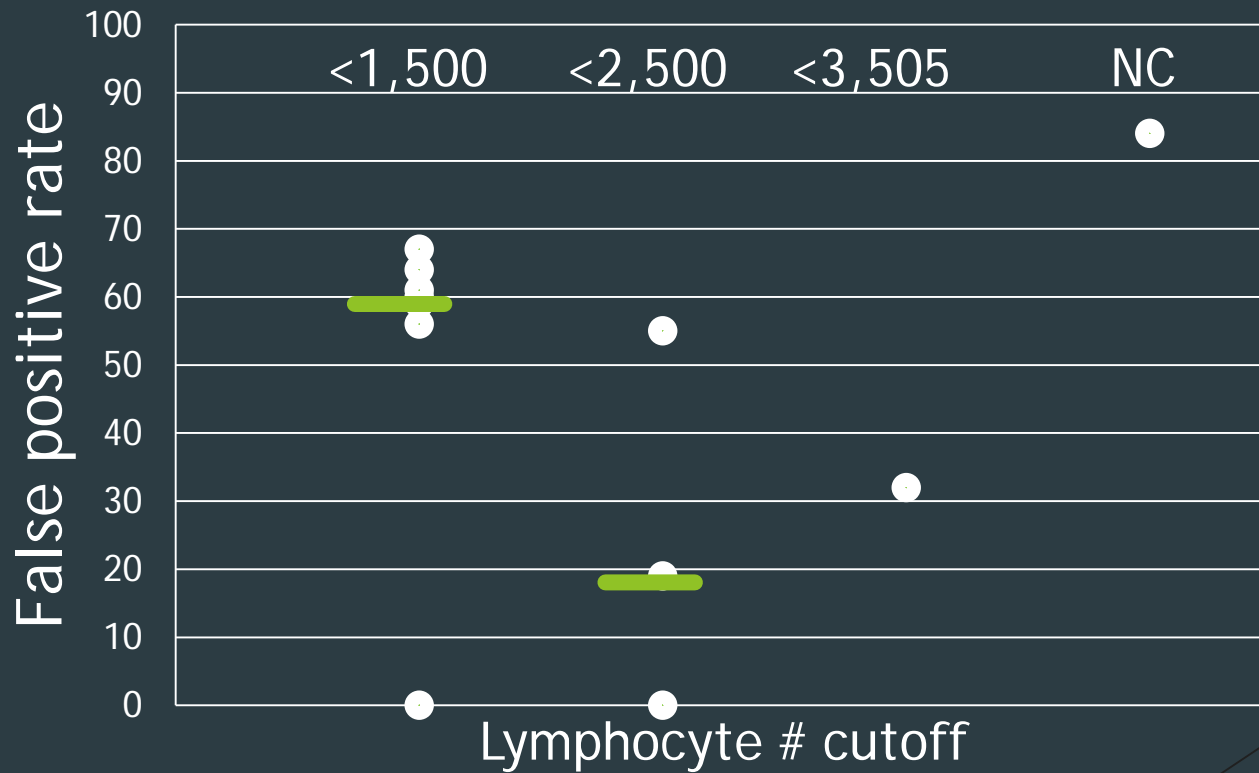
Secondary screen: T cell number

- ▶ No well-established normal ranges of absolute counts for first 1-7 days of life for term or premies

Shearer et al.	Comans-Bitter et al	
0-3 months, n = 700	Newborn, n = 20	2-5 months, n = 46
90th %ile - 5,500	95 th %ile - 5,000	6,500
Median - 3,700	2,800	3,600
10th %ile - 2,500	5 th %ile - 600	2,300

- ▶ Shearer et al., J Allergy Clin Immunol 2003; 112:973
- ▶ Comans-Bitter et al., J Pediatr 1997; 130:388
- ▶ State laboratory-specific lower limits vary between 1,500-3,505 cells/mm³

Secondary screen: T cell number



Data from Kwan et al., JAMA 2014; 312:729

Secondary screen: Naïve T cells

- ▶ Spurious normal total T cell count due to:
 - ▶ Engraftment and expansion of maternal T cells
 - ▶ Autologous oligo/pauciclonal T cell expansion (Omenn's syndrome)
- ▶ In both cases, engrafted or expanded cells are not naïve
- ▶ Naïve cells CD45RA⁺ or CD45RO⁻
- ▶ Additional markers sometimes used but not essential here
- ▶ CD4 and CD8 populations may be measured separately, also not essential

Secondary screen: Naïve T cells

CD4/CD45RA		CD8/CD45RA
90th %ile	- 95%	99%
Median	- 90%	93%
10th %ile	- 64%	80%

- ▶ Shearer et al., J Allergy Clin Immunol 2003; 112:973
- ▶ Convenient lower limit - 50%
- ▶ Not applied in all screening programs

Tertiary screen: T cell function

- ▶ Assumptions
 - ▶ T cell lymphopenia by laboratory-specific criteria
 - ▶ OR
 - ▶ Low proportion of naïve T cells, if applied
- ▶ Refer for testing of T cell function (preferably with clinical consultation)
- ▶ Gold standard: in vitro T cell proliferation to stimulation with phytohemagglutinin (PHA) by incorporation of ^3H
- ▶ Clinical consultation should be considered for any significant abnormality of lymphocyte populations, even if T cell lymphopenia is not present

SCID

PIDTC definitions

- ▶ Primary Immunodeficiency Treatment Consortium
- ▶ Typical SCID
 - ▶ Autologous T cells <300 cells/mm³ AND
 - ▶ T cell proliferation $<10\%$ of a healthy control (or $<10^{\text{th}}$ %ile of controls for the lab)
 - ▶ Maternal T cell engraftment
 - ▶ Known SCID-associated mutations
- ▶ “Leaky” SCID
 - ▶ Autologous T cells between 300-1,500 cells/mm³, low proportion of naive cells
 - ▶ T cell proliferation between 10-50% of normal
 - ▶ Incomplete/hypomorphic mutations in SCID genes

SCID

PIDTC definitions

- ▶ Omenn syndrome
 - ▶ T cell number low or normal, oligoclonal
 - ▶ T cell proliferation 10-50% of normal
 - ▶ Erythroderma, hepatosplenomegaly, eosinophilia, and elevated levels of serum IgE
- ▶ Generally occurs with SCID gene mutations but can be seen in other settings

Outcomes of SCID newborn screening

- ▶ T cells above cutoff, naïve proportion OK, no other lymphocyte abnormalities > no further evaluation
- ▶ T cells above cutoff, naïve proportion OK, yes other lymphocyte abnormalities
 - ▶ Follow clinically, consider further evaluation
- ▶ T cells below cutoff or naïve proportion not OK, function >50% normal
 - ▶ Follow clinically, consider further evaluation (DGS, T21)
- ▶ T cells below cutoff or naïve proportion not OK, function <50%
 - ▶ Evaluate for leaky SCID or other defect
- ▶ T cells <300 or naïve proportion not OK, function <10%
 - ▶ **SCID!**

Non-SCID T cell lymphopenia

▶ Syndromes with T-cell impairment	136		
▶ DiGeorge	78	▶ TAR	1
▶ Trisomy21	21	▶ Not specified	10
▶ A-T	4	▶ Cytogenetic	6
▶ Trisomy18	4	▶ Secondary	117
▶ CHARGE	3	▶ Cardiac anom.	30
▶ Jacobsen	2	▶ Mult. Congen.	23
▶ CLOVES	1	▶ 3 rd space	15
▶ ECC	1	▶ GI anom.	15
▶ Fryns	1	▶ Neonatal leuk.	4
▶ Nijmegen	1	▶ Not specified	30
▶ Noonan	1	▶ Preterm birth	29
▶ Rac2 defect	1	▶ Variant SCID	12
▶ Renpenning	1	▶ Unspecified T-cell lymphopenia	117

Data from Kwan et al., JAMA 2014; 312:729

Non-SCID T cell lymphopenia: Testing

- ▶ Karyotype
 - ▶ Major chromosomal abnormalities
 - ▶ Trisomy 21
 - ▶ Trisomy 18, etc.
- ▶ SNP or hybridization array
 - ▶ DiGeorge syndrome (focused analysis on 22q11)
 - ▶ Other microdeletion
 - ▶ Often useful in conjunction with targeted or whole exome/genome sequencing

Non-SCID T cell lymphopenia

- ▶ Ataxia-telangiectasia
 - ▶ Characteristic manifestations do not appear for months/years
 - ▶ Screening via alpha fetoprotein unreliable in first year of life
 - ▶ Consider for testing (chromosome fragility, Western blot or DNA analysis) in all possible cases, especially if there is also B cell lymphopenia
- ▶ CHARGE
 - ▶ *CCHD7*
- ▶ Nijmegen breakage syndrome
 - ▶ *NBS1*
- ▶ Rac2 deficiency
 - ▶ *RAC2*
- ▶ Other focused biochemical and/or genetic tests based on clinical features and laboratory phenotype

SCID/leaky SCID: Gene defects

T-B ⁺ SCID		T-B ⁻ SCID	
IL-2R common gamma chain	IL2RG	Recombinase activating genes 1 and 2	RAG1 RAG2
Janus kinase 3	JAK3	DNA cross-link repair enzyme 1C (Artemis)	DCLRE1C
IL-7R α chain	IL7RA	DNA-dependent protein kinase	PRKDC
IL-2R alpha chain (CD25) deficiency	IL2RA	Adenylate kinase 2 (reticular dysgenesis)	AK2
CD45 (protein tyrosine phosphatase, receptor type, C)	PTPRC	Adenosine deaminase	ADA
CD3 δ	CD3D	DNA ligase IV	LIG4
CD3 ϵ	CD3E	Non-homologous end-joining protein 1 (Cernunnos)	NHEJ1
CD3 ζ	CD3Z		
Coronin 1A	CORO1A		

SCID/leaky SCID: Genetic testing

- ▶ Next generation sequencing panels available from reference genetics laboratories
 - ▶ All SCID or segregate by T-B+, T-B-
 - ▶ Focused Sanger sequencing of a small number of candidate genes
- ▶ If all known genes and CGH/SNP array tests are unrevealing, consider whole exome or genome sequencing