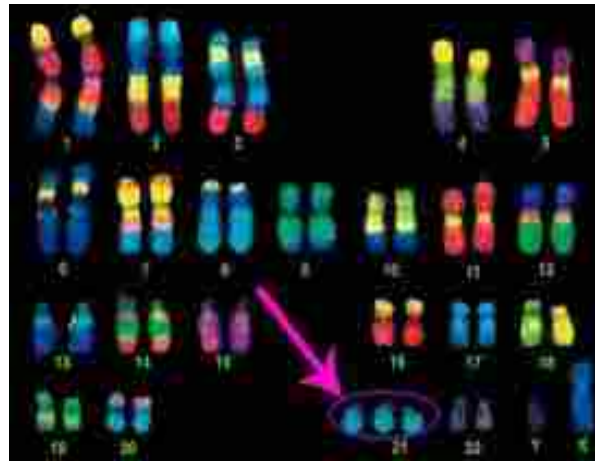


Too much and too little: how does an extra chromosome cause leukaemia in children with Down syndrome?

Sir Thomas and Lady Edith Dixon Lecture, April 2021



Professor Irene Roberts

Professor of Paediatric Haematology, University of Oxford

Increased susceptibility to leukaemia in Down syndrome (DS)

Type of malignancy	Standardised incidence ratio
Acute myeloid leukaemia age 0-4 yrs age 5-29 yrs	153.9 10.3
Acute lymphoblastic leukaemia age 1-4 yrs age 5-29 yrs	27.0 12.4
Solid tumours	0.45

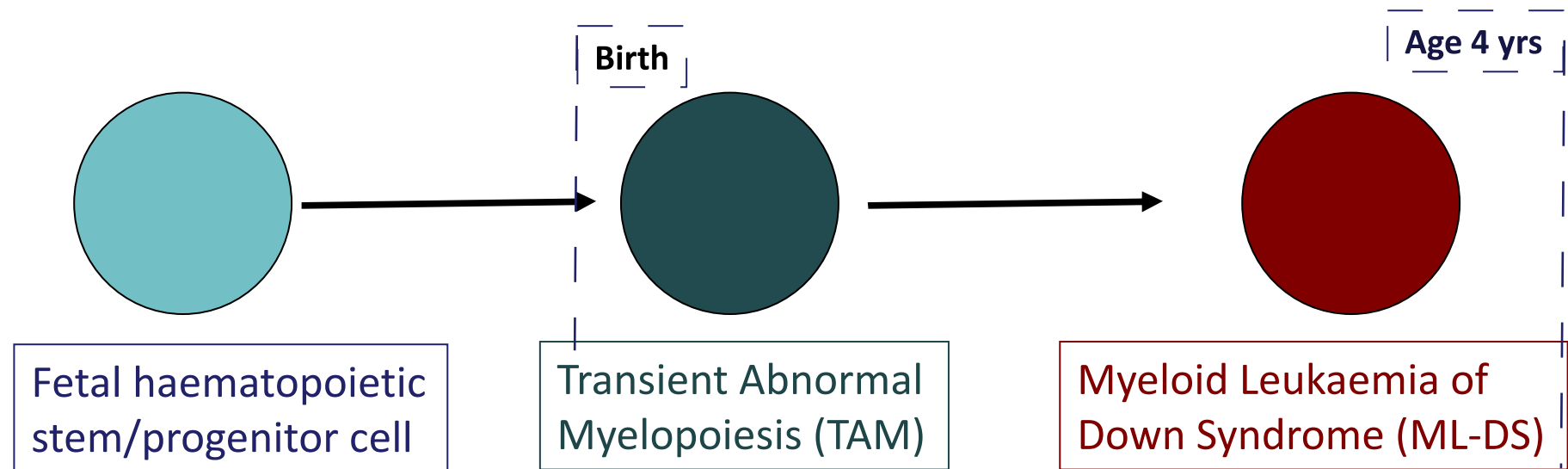
* Both myeloid and lymphoid leukaemias are more common

* Young children are especially susceptible

* Solid tumours are less frequent

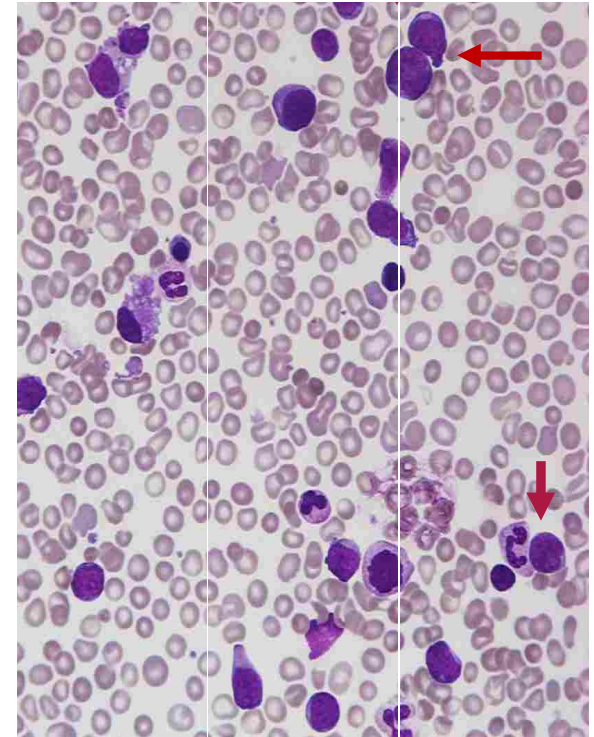
Myeloid Leukaemia of Down Syndrome (ML-DS)

- ML-DS originates in fetal life and presents before the age of 4 yrs
- Preceded by a neonatal leukaemia unique to DS known as Transient Abnormal Myelopoiesis (TAM)



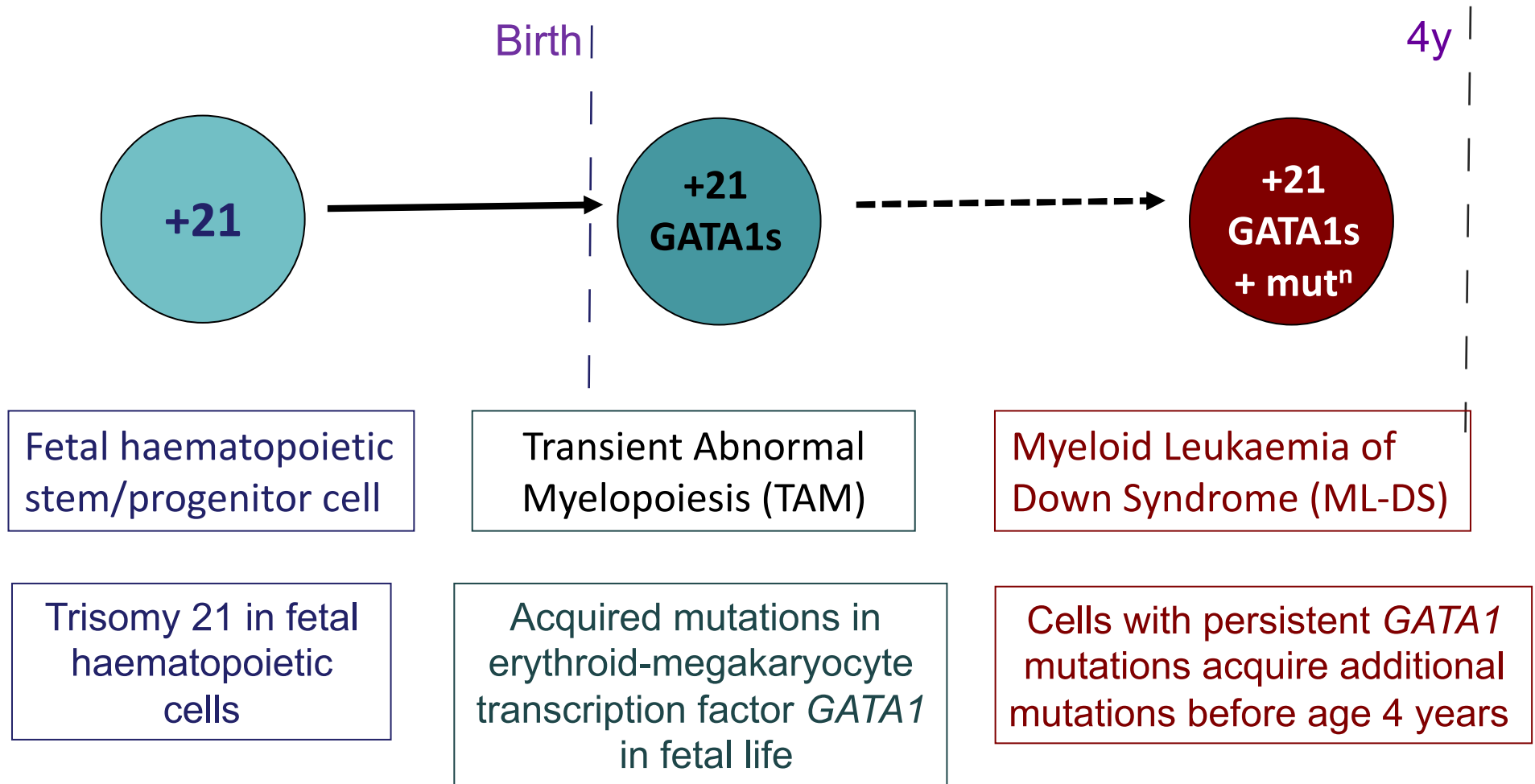
Transient Abnormal Myelopoiesis (TAM)

- Clonal haematological disorder characterised by increased circulating blast cells in a baby with Down syndrome
- Unique to babies with trisomy 21
- Usually presents in the first few days of life; sometimes in fetal life, never after 3 months of age

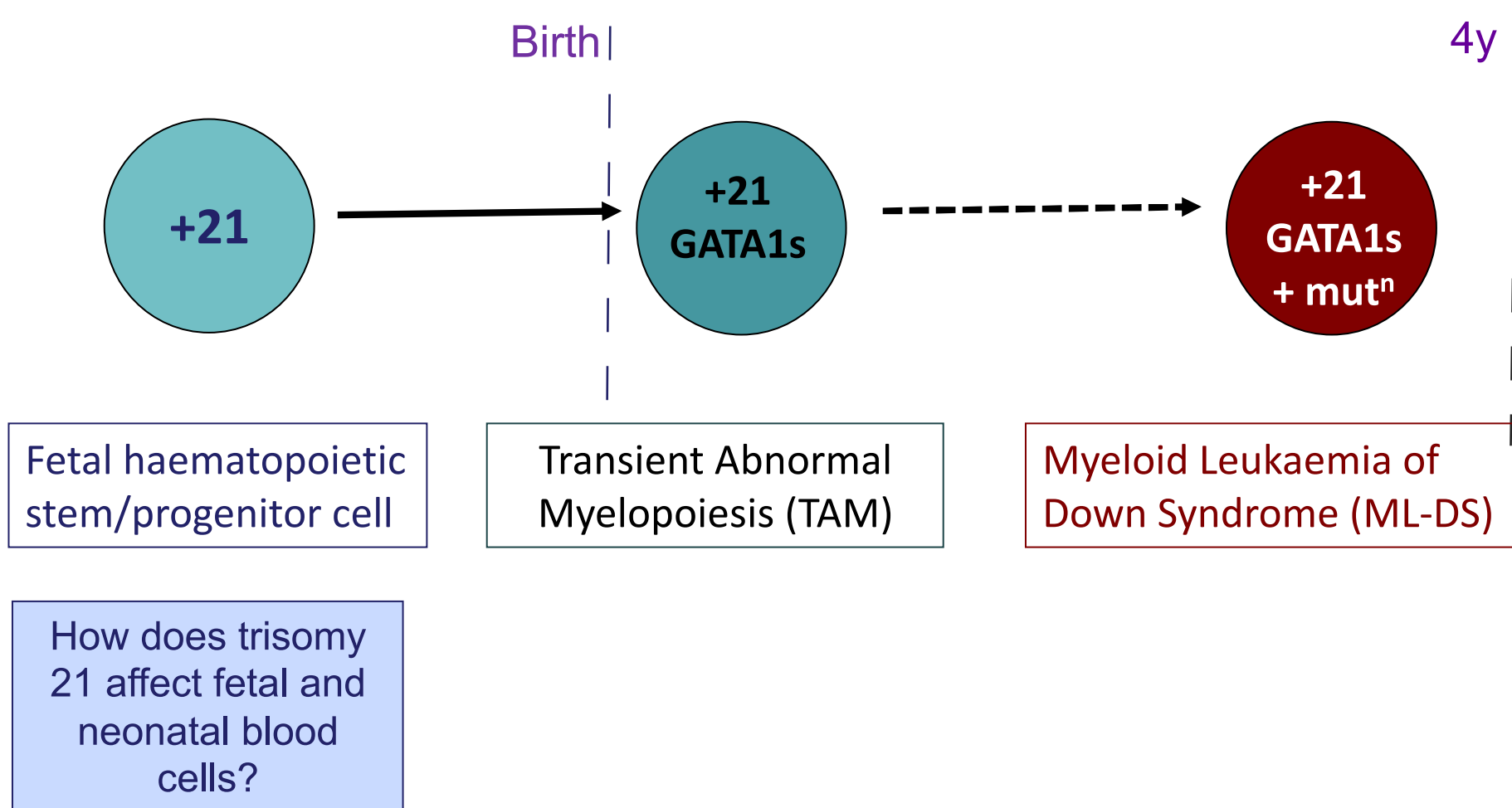


TAM is a fetal disorder strongly linked to T21

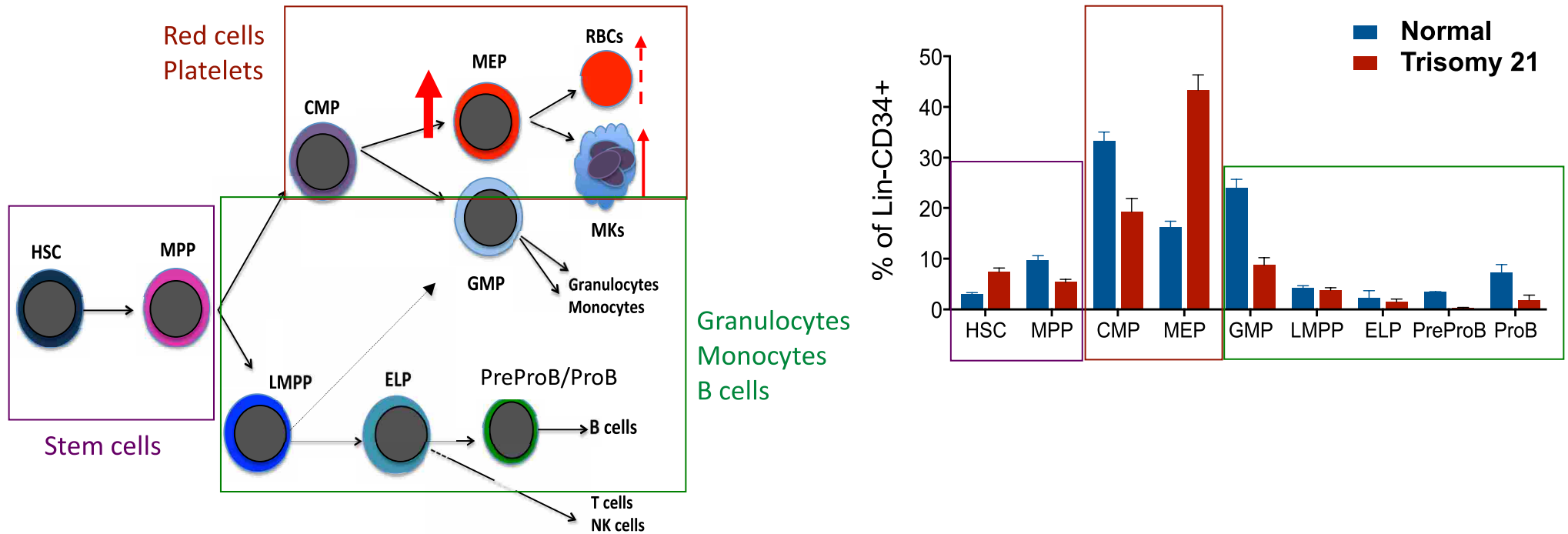
Molecular pathogenesis of TAM and ML-DS: 3 steps to leukaemia in children with Down Syndrome



Molecular pathogenesis of TAM and ML-DS: 3 steps to leukaemia in children with Down Syndrome

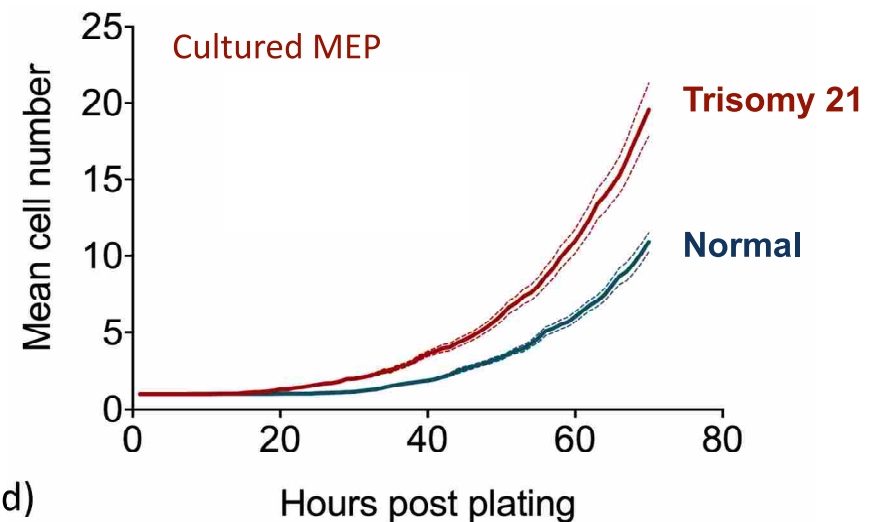
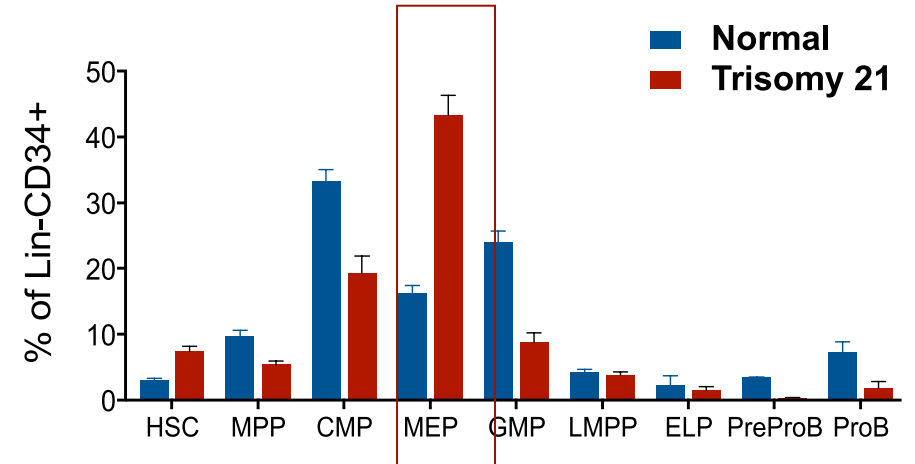
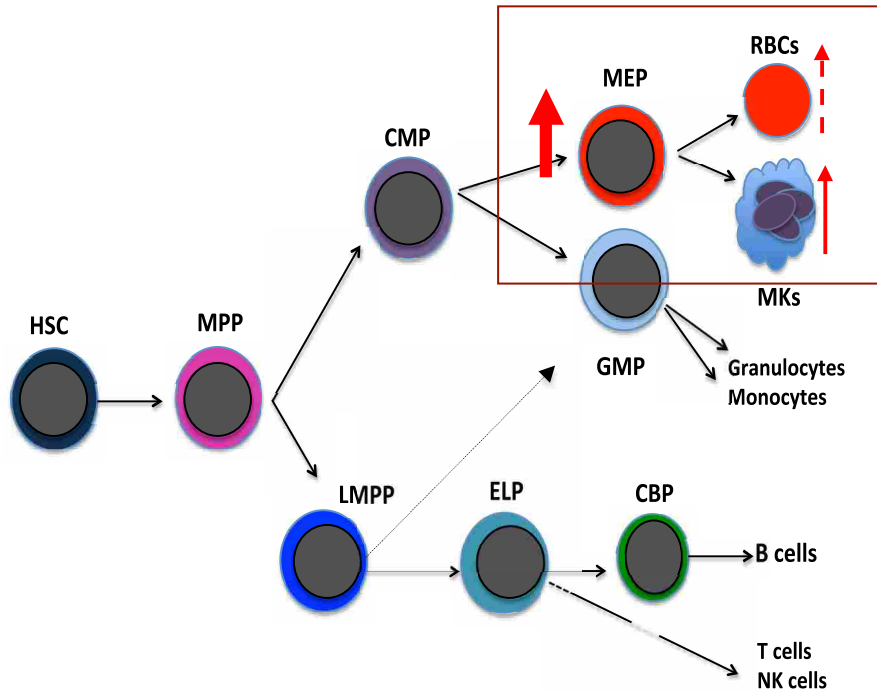


Trisomy 21 perturbs fetal haematopoiesis in the absence of acquired *GATA1* mutations



Trisomy 21 causes multiple changes in fetal haematopoietic stem cells and blood progenitors of all lineages

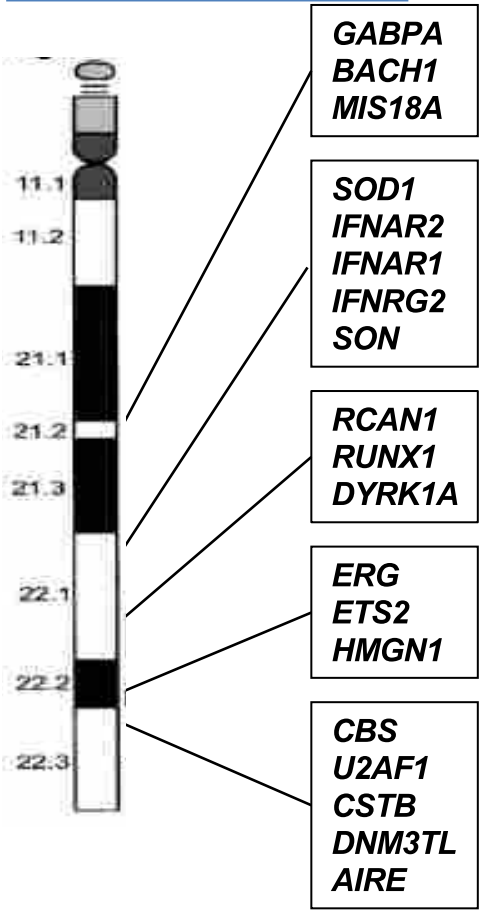
Trisomy 21 perturbs fetal haematopoiesis in the absence of acquired *GATA1* mutations



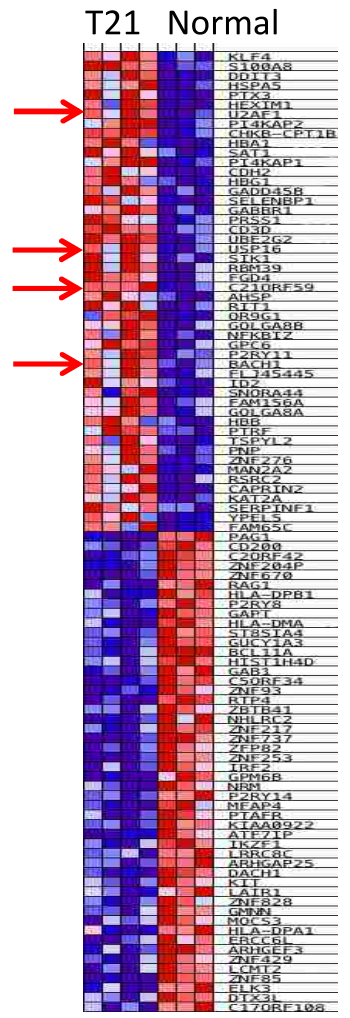
Fetal Megakaryocyte-Erythroid Progenitor (MEP) cells are increased in frequency and highly proliferative in trisomy 21

Trisomy 21 causes genome-wide perturbation of gene expression in fetal haematopoietic stem and progenitor cells

Chromosome 21



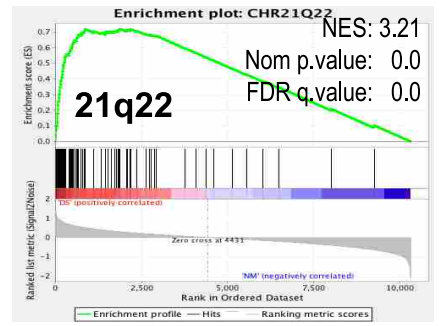
Gene expression profiling of fetal CD34+ cells



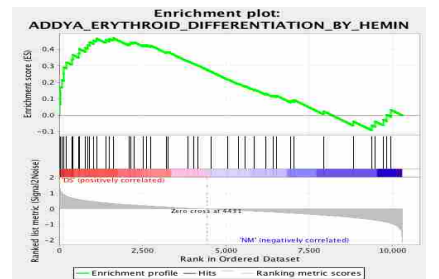
833 differentially expressed genes

34 on Hsa21

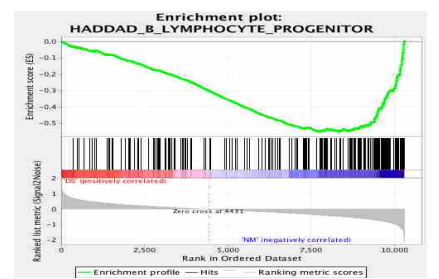
799 not on Hsa21



Enrichment of 21q22 gene set



Increased expression of erythroid genes

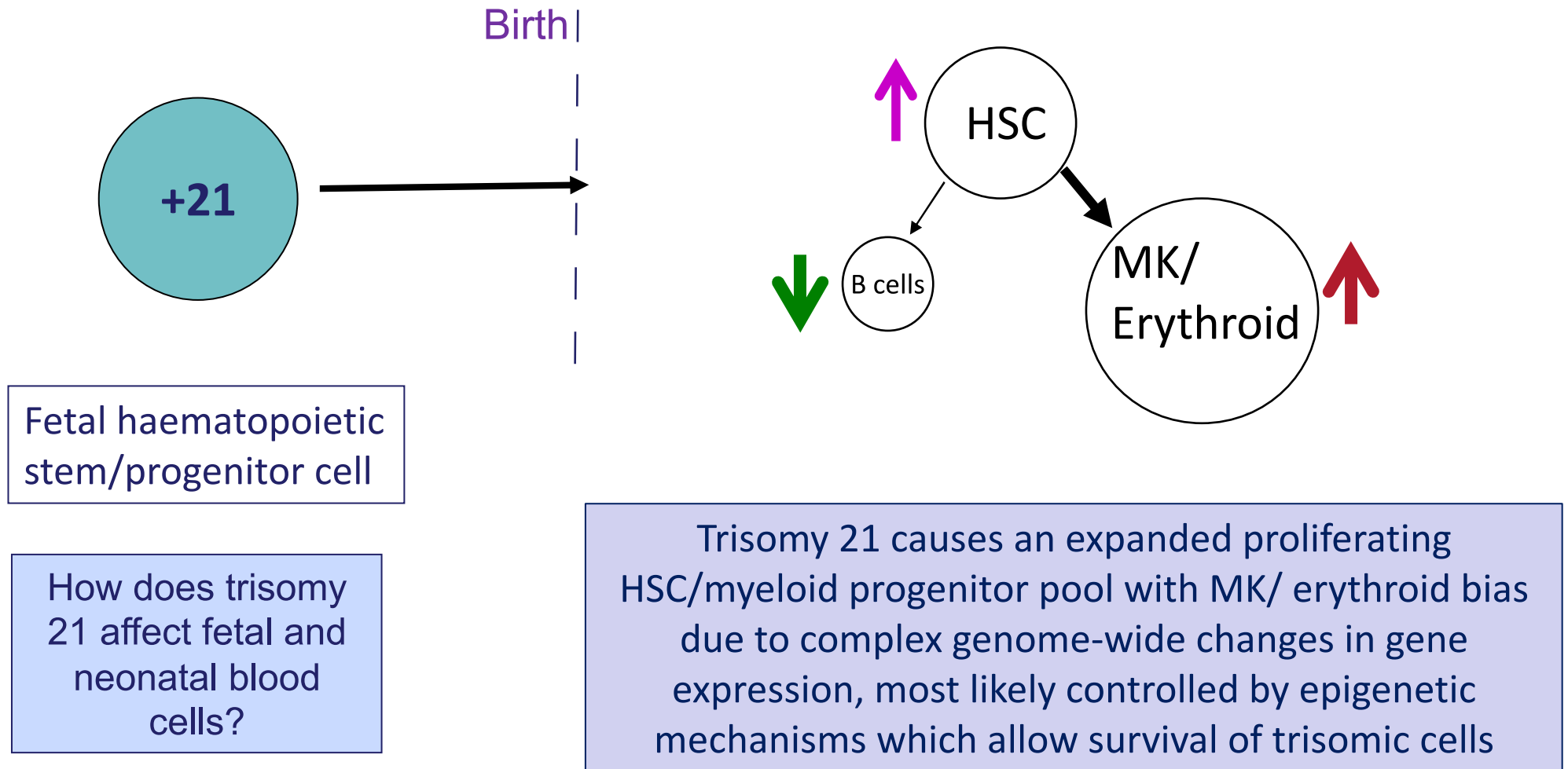


Reduced expression of B-lymphoid genes

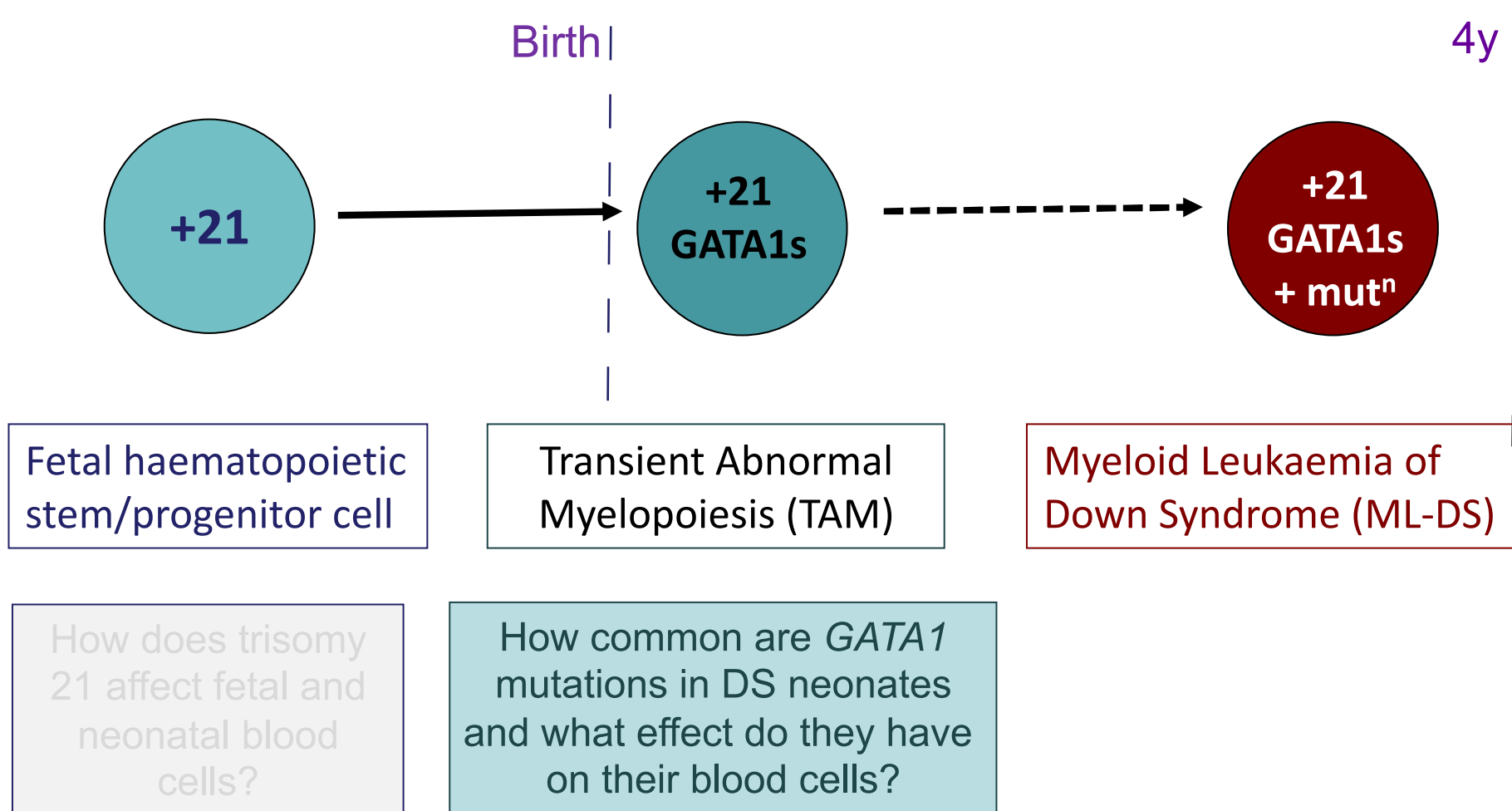
~240 protein coding genes

Liu et al, 2015

Molecular pathogenesis of TAM and ML-DS: 3 steps to leukaemia in children with Down Syndrome

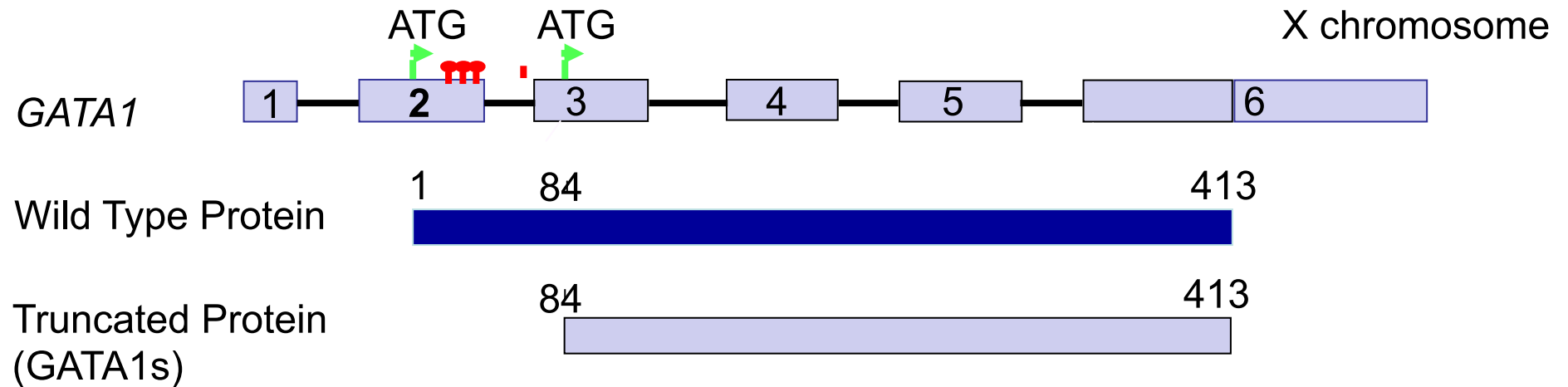


Molecular pathogenesis of TAM and ML-DS: 3 steps to leukaemia in children with Down Syndrome



Acquired N-terminal mutations in the *GATA1* gene uniquely transform fetal cells with trisomy 21 (Down syndrome)

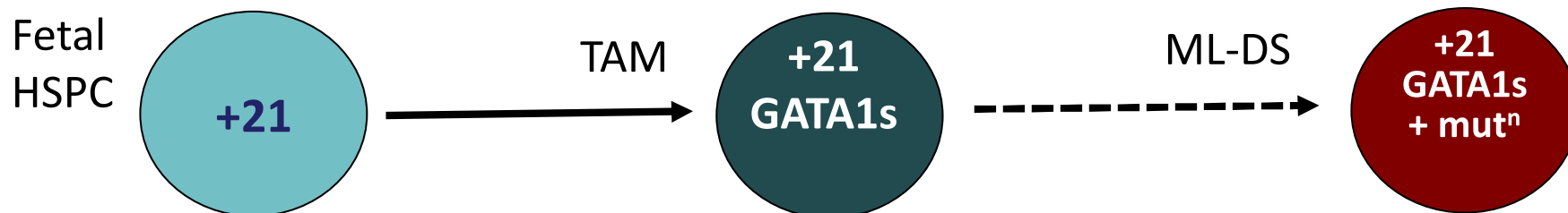
- TAM is caused by acquired mutations in the N terminal of the *GATA1* gene
- *GATA1* is a transcription factor that controls red cell & platelet/megakaryocyte development
- Mutations cluster in exon 2 and result in the translation of a short protein, Gata1s
- N terminal *GATA1* mutations are not leukaemogenic in the absence of trisomy 21
- *GATA1* mutations are already present at birth



The Oxford Down Syndrome Neonatal Study: Aims

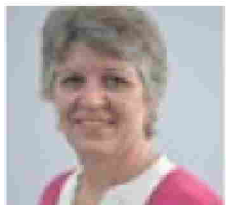
- To determine the frequency of acquired *GATA1* mutations in neonates with Down syndrome (DS)
- To identify the clinical, haematological and molecular features of DS neonates with and without *GATA1* mutations
- To determine the natural history of *GATA1* mutations in DS and the true risk of subsequent leukaemia

Roberts et al, Blood 2013



Oxford Down Syndrome Neonatal Study- design

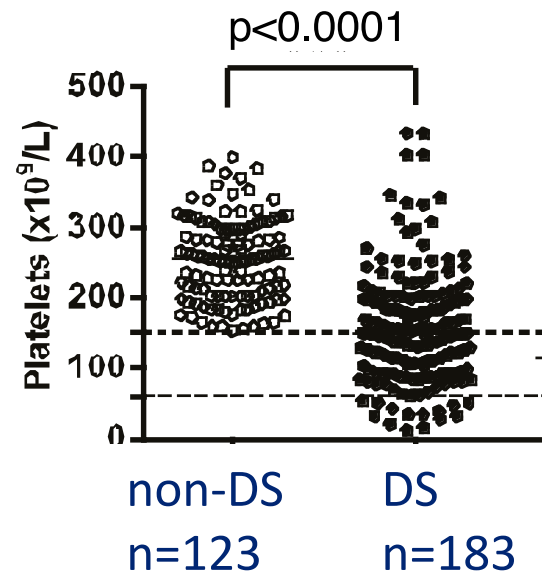
- Prospective, multicentre study to precisely describe the haematological abnormalities in neonates with Down syndrome
- FBC, film and *GATA1* mutation analysis (PCR, NGS) in first week of life
- Serial samples and follow up until age 4 years
- **Definition of TAM:** blood blasts >10% and a *GATA1* mutation in a DS neonate



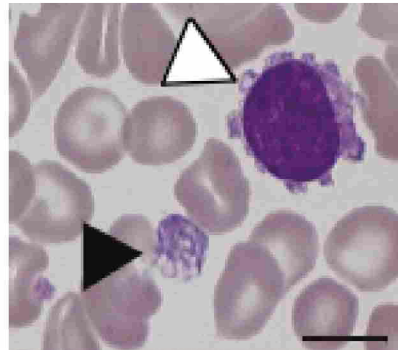
Helen Richmond, Neha Bhatnagar, Laure Nizery, Joanna Bonnici, Natalina Elliott, Paresh Vyas
Kelly Perkins, Marlen Metzner, Alison Kennedy, Gemma Buck

Abnormal platelet production in DS neonates and no *GATA1* mutation

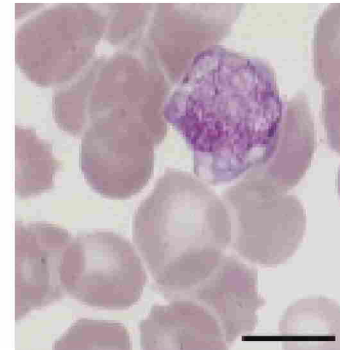
Roberts et al, 2013



Giant platelet and megakaryoblast



Megakaryocyte fragment

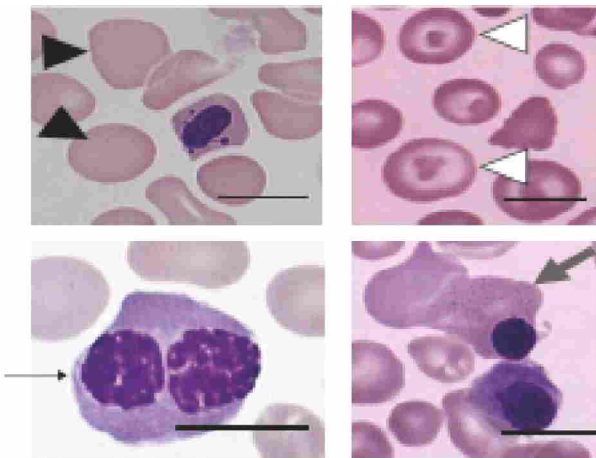
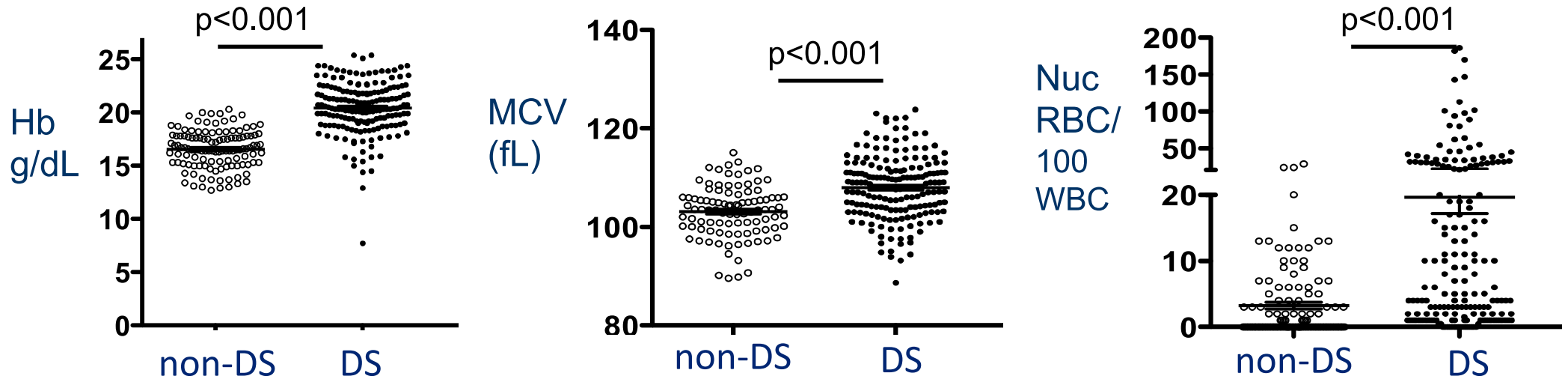


Circulating megakaryocyte



- Thrombocytopenia is common in neonates with Down syndrome
- Trisomy 21 perturbs neonatal megakaryopoiesis and platelet production in the absence of *GATA1* mutations

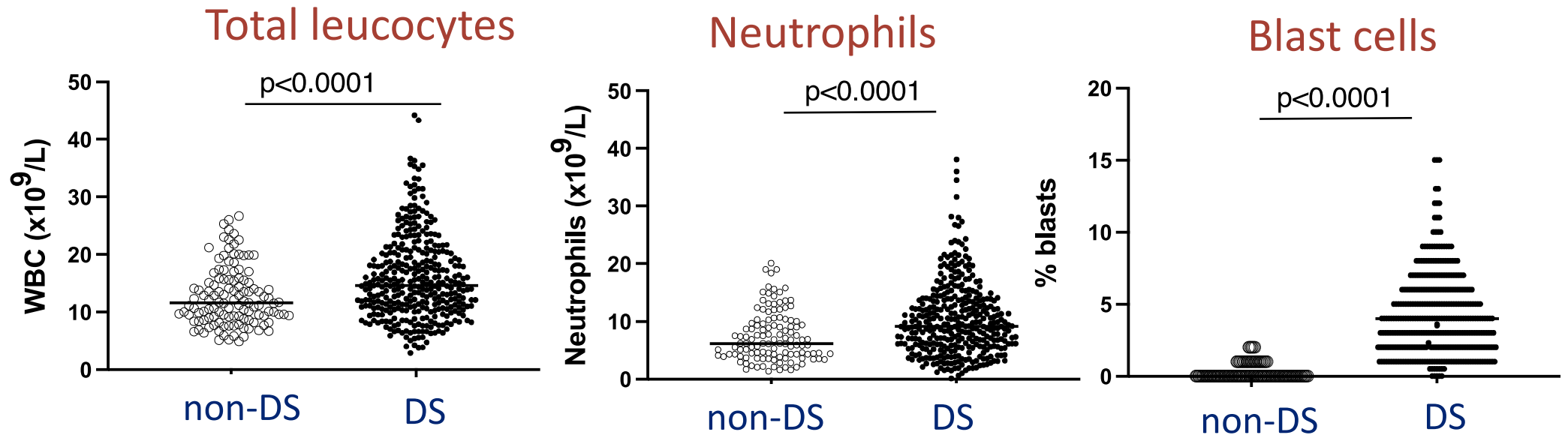
Abnormal erythropoiesis in DS neonates and no *GATA1* mutations



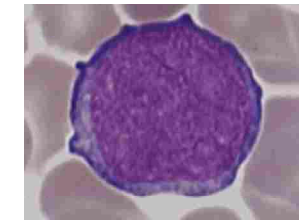
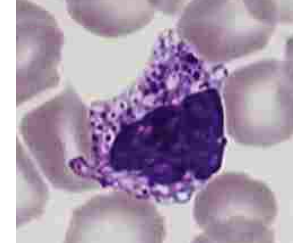
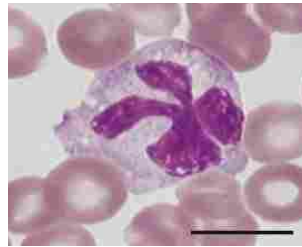
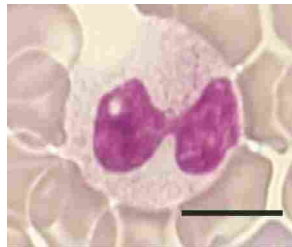
Increased red blood cell production and dyserythropoiesis are seen in almost all neonates with Down syndrome suggesting that trisomy 21 itself alters erythropoiesis

Non-DS: n=123
DS: n=183

Abnormal leucocytes in neonates with DS and no *GATA1* mutation



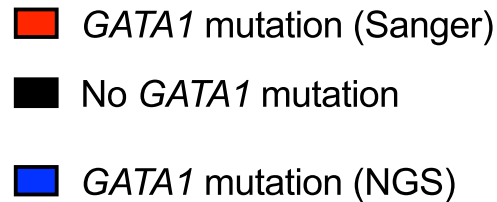
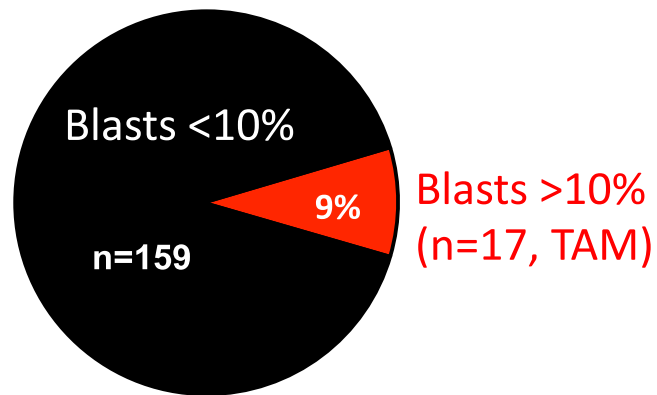
Non-DS: n=123
DS: n=183



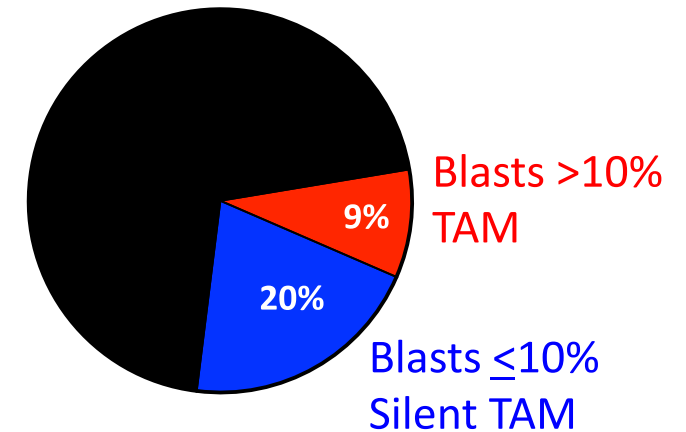
Trisomy 21 causes trilineage perturbation of neonatal haematopoiesis

Detection of mutant *GATA1* clones in blood cells from neonates with Down syndrome: sensitive tests reveal a high frequency

Direct sequencing (n=186)

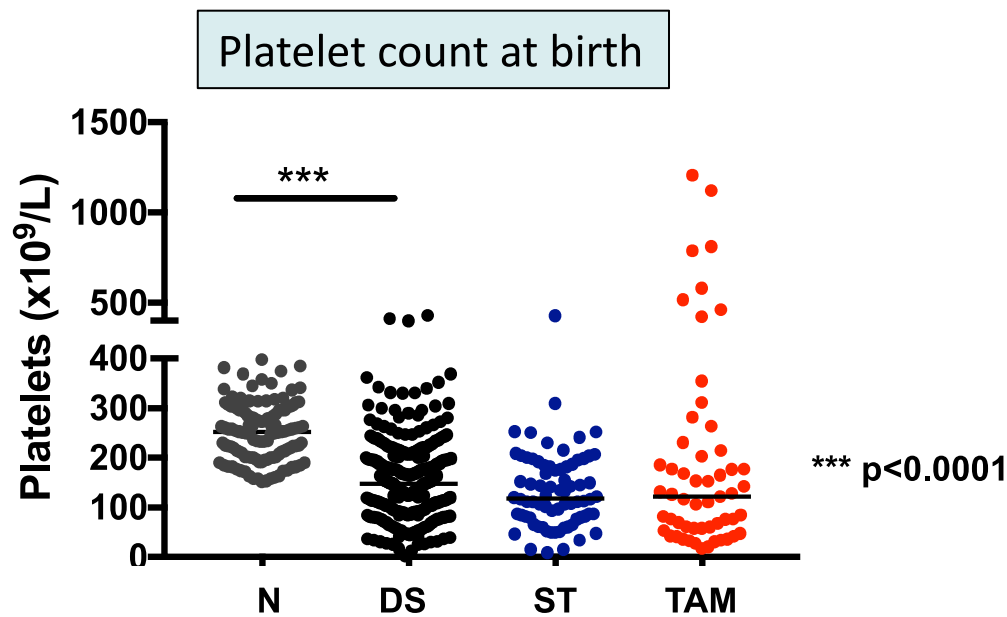


Next Generation Sequencing (NGS)

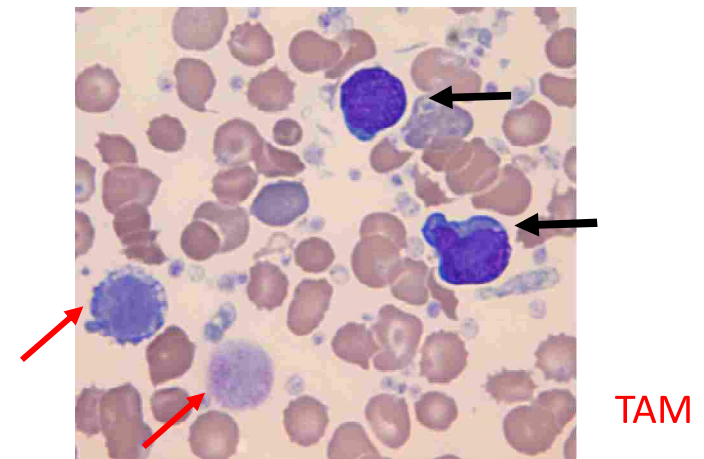


- Using direct sequencing *GATA1* mutations were detected in 9% of neonates with DS, all had blasts >10% and were designated as TAM
- Using NGS, *GATA1* mutations were detected in 29% of DS neonates; most (20% overall) had blasts ≤10% and no clinical signs of TAM- we designated these as Silent TAM

Abnormal platelet production in DS neonates: impact of *GATA1s* mutations

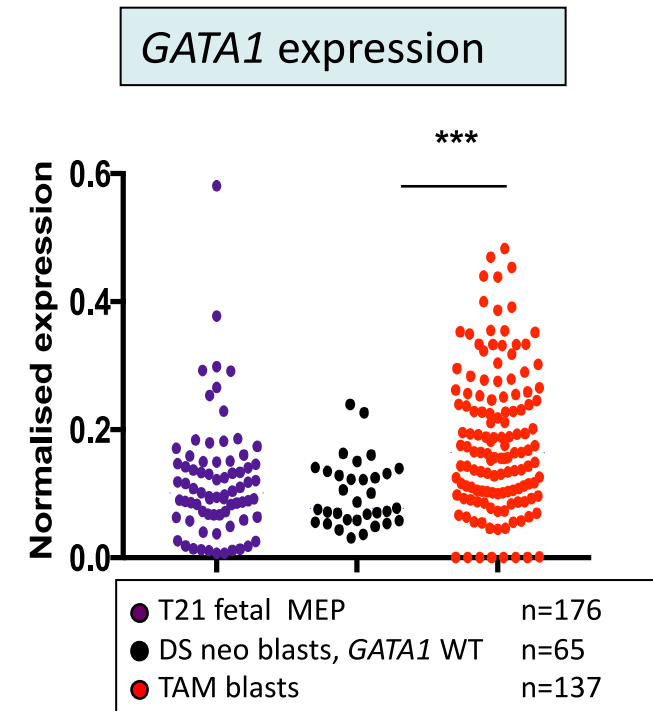
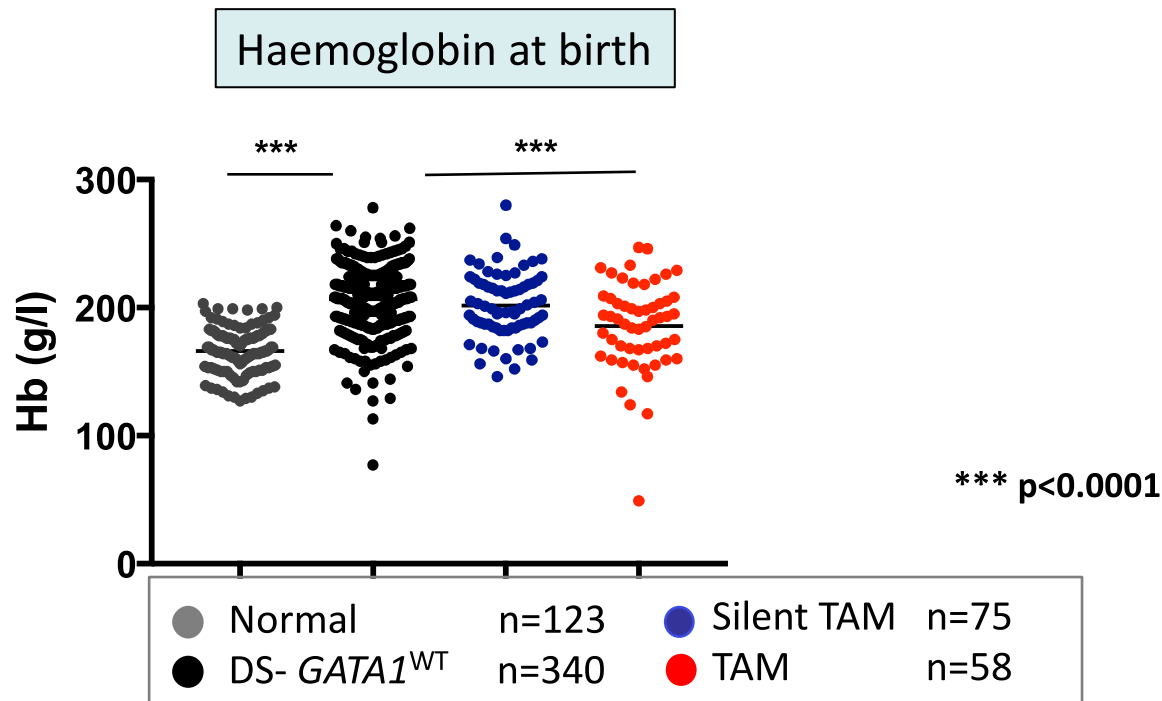


● Normal	n=123	● Silent TAM	n=75
● DS- <i>GATA1</i> ^{WT}	n=340	● TAM	n=58



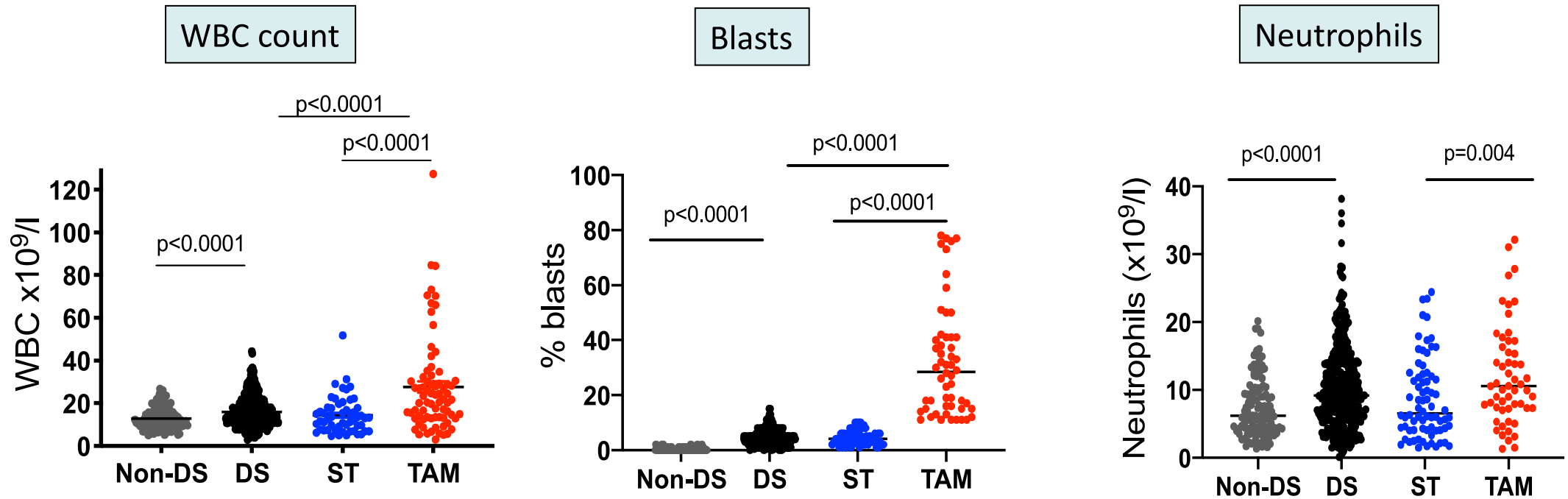
- Trisomy 21 perturbs neonatal platelet production in the absence of *GATA1* mutations
- The platelet count is not further reduced in TAM or Silent TAM but giant platelets and MK fragments are frequent suggesting *Gata1s* increases T21-associated dysmegakaryopoiesis

Increased erythropoiesis in DS neonates: impact of *GATA1* mutations



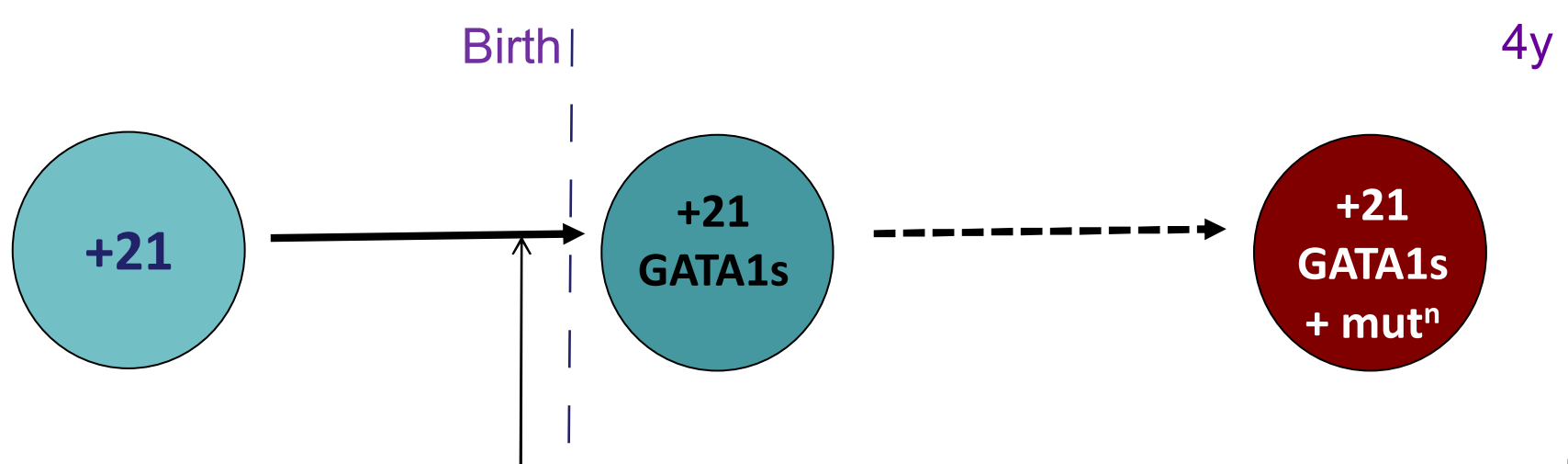
- Trisomy 21 increases neonatal erythropoiesis in the absence of *GATA1* mutations
- Hb is slightly lower in TAM (not silent TAM) but very few babies are anaemic perhaps because *GATA1* expression is sufficient to maintain red blood cell production

Leucocyte production in DS neonates: impact of *GATA1* mutations



- T21 increases leucocytes, blast cells and neutrophils in the absence of *GATA1* mutations
- Leucocyte and blast cell counts are increased in DS neonates with TAM but not Silent TAM

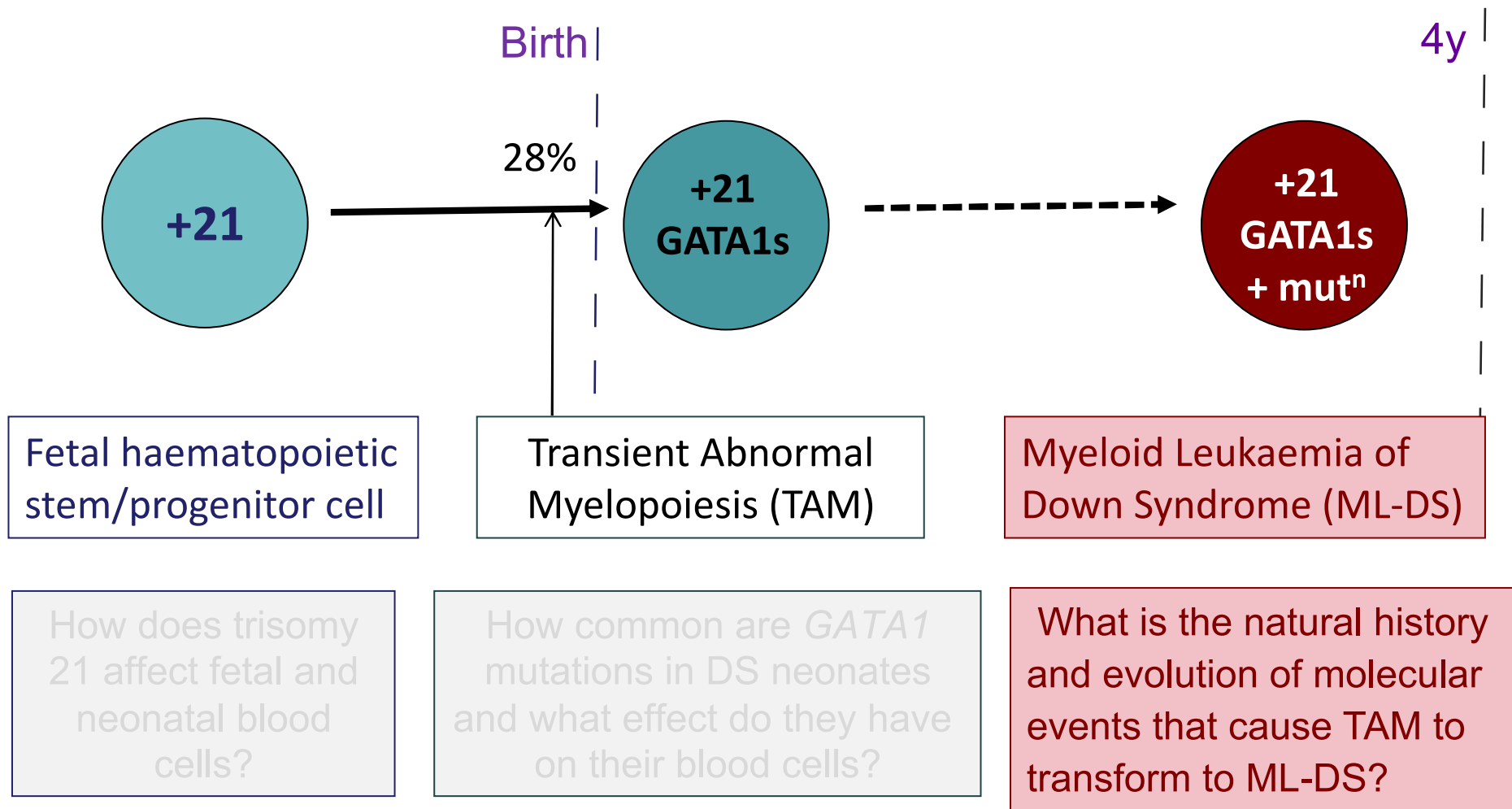
Molecular pathogenesis of TAM and ML-DS: 3 steps to leukaemia in children with Down Syndrome



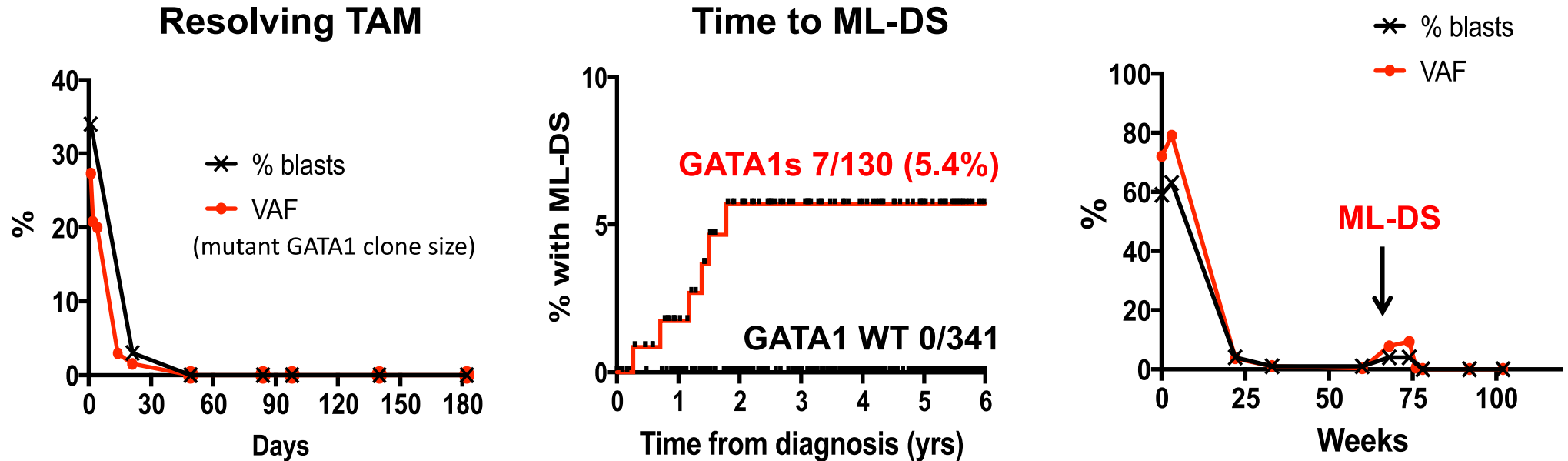
Trisomy 21 and *GATA1* mutations in DS neonates

- Trisomy 21 (T21) causes tri-lineage perturbation of fetal and neonatal haematopoiesis with expansion of a proliferative megakaryocyte-erythroid progenitor (MEP) pool
- *GATA1* mutations occur at high frequency (28%) of DS neonates suggesting that T21-induced expansion of MEPs causes a potent selection advantage for mutant cells
- *GATA1s* further perturbs haematopoiesis but platelet and red cell production are usually preserved perhaps due to high levels of *GATA1* expression in trisomic cells

Molecular pathogenesis of TAM and ML-DS: 3 steps to leukaemia in children with Down Syndrome

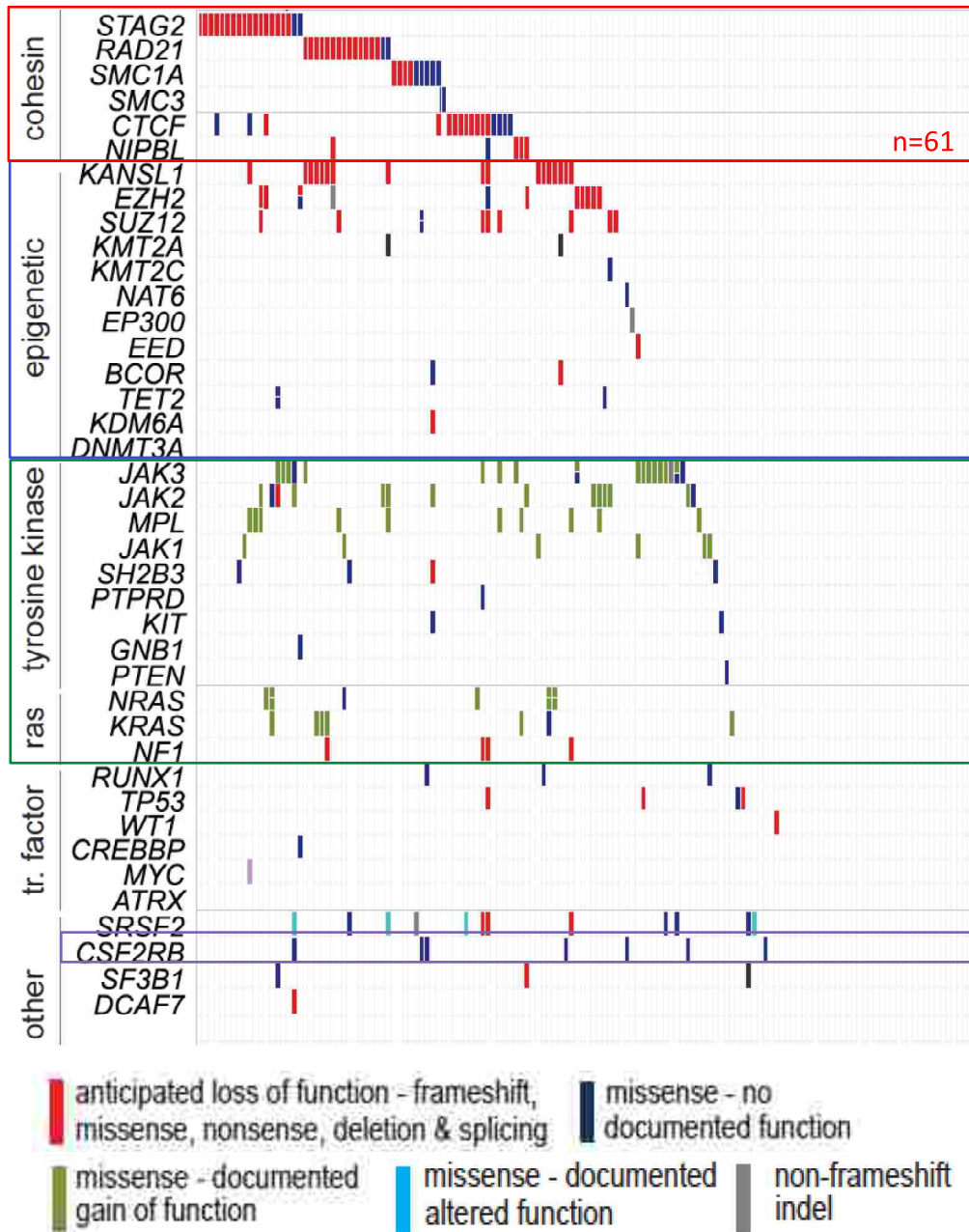


Natural history of DS neonates with acquired *GATA1* mutations in the Oxford DS Study- follow up to age >4 years



- In >90% of DS neonates, *GATA1* mutations and blasts disappear over the first 2-3 months of life
- 0/341 DS neonates without a *GATA1* mutation at birth developed ML-DS or acquired a *GATA1* mutation postnatally
- 7/133 (5.3%) DS neonates with a *GATA1* mutation developed ML-DS at a median age of 16 months

Progression to ML-DS (n=141)



Cohesin and *CTCF* mutations are the most frequent driver mutations acquired after the neonatal period in patients with TAM who develop ML-DS

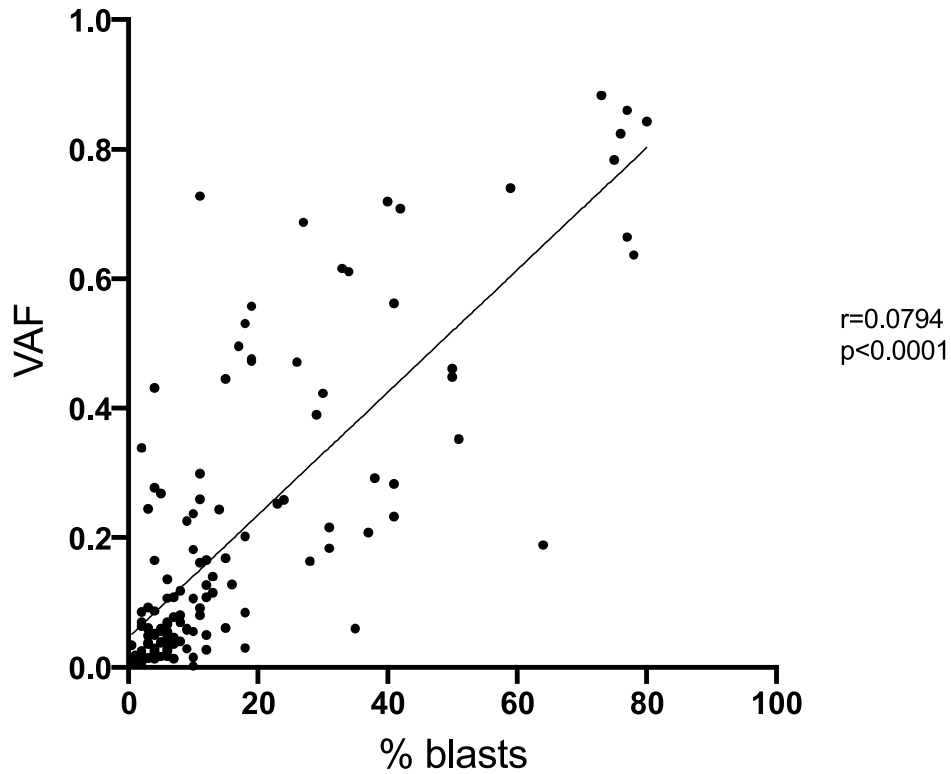
Labuhn, Perkins et al, *Cancer Cell*, 2019

Yoshida et al, *Nat Genet* 2013; Nikolaev et al, *Blood* 2013

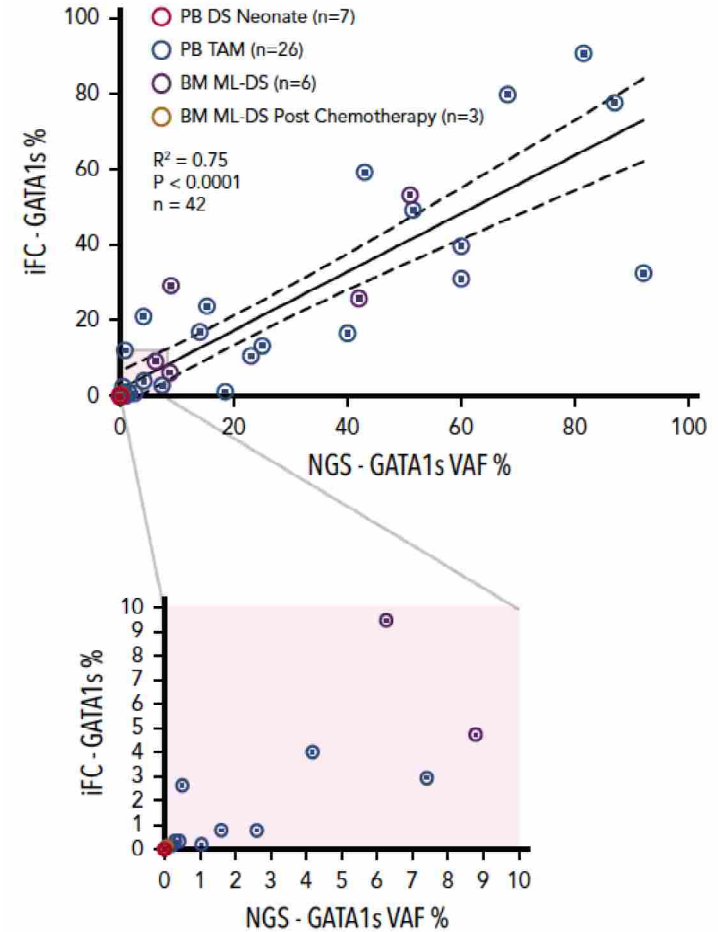
What factors predict for leukaemic transformation of TAM?

- Size of mutant *GATA1* clone?
- Clinical features?
- Type of *GATA1* mutation?
- Number of *GATA1* mutations?
- Percentage of peripheral blood blasts?

DS neonates with high blast % have larger GATA1s clones (VAF)

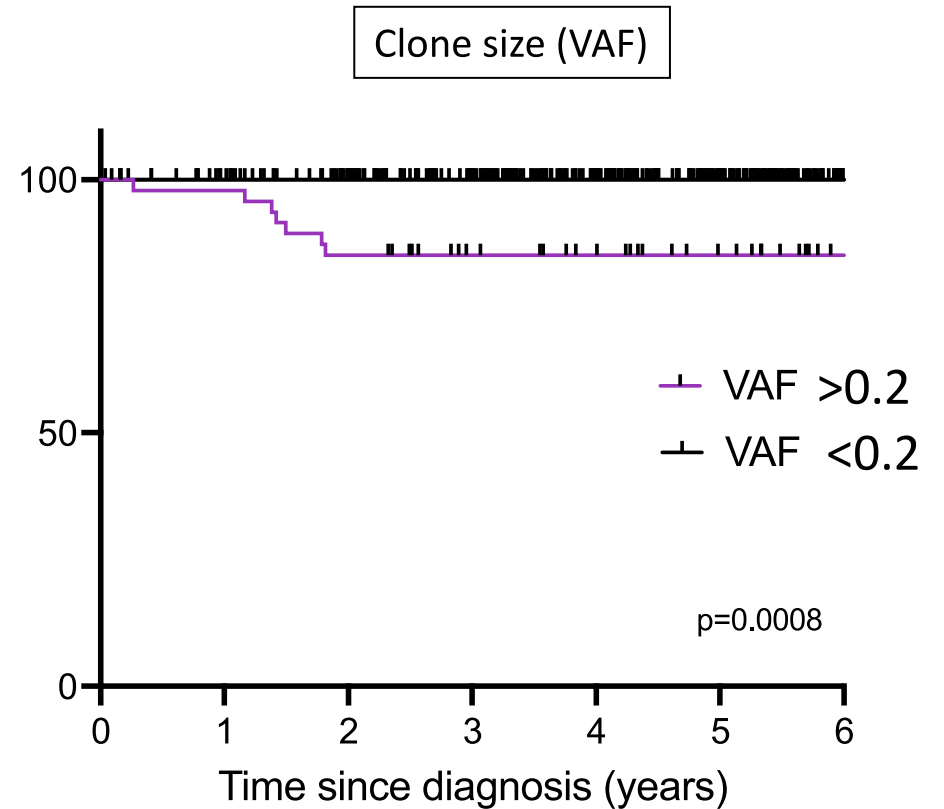
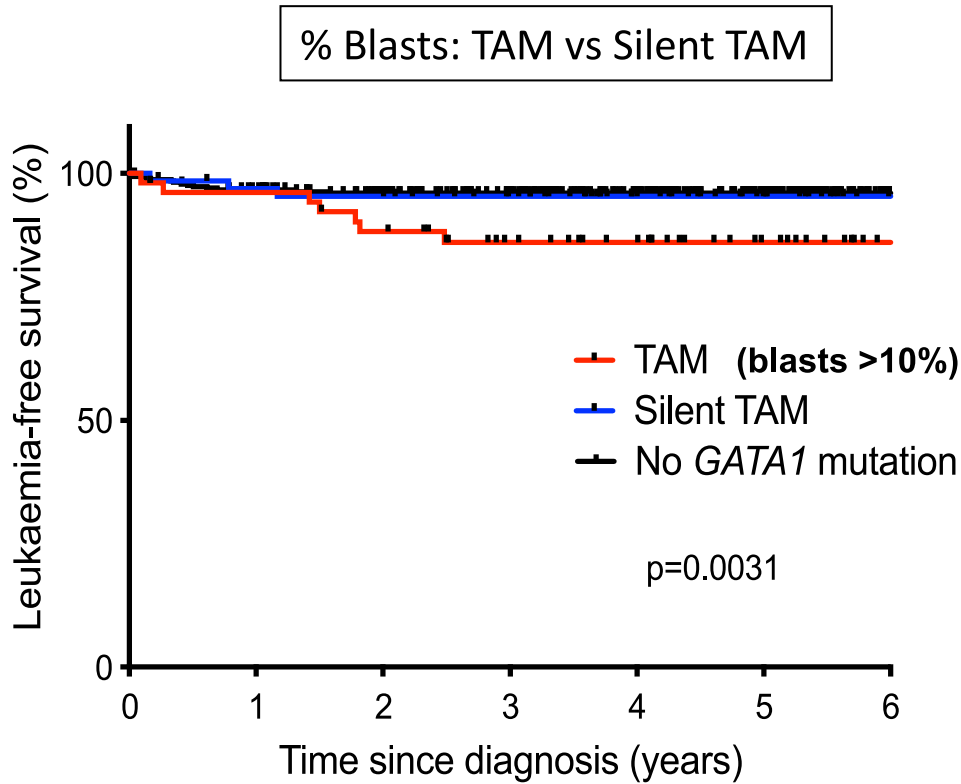


Oxford DS Study 2021 (unpublished)



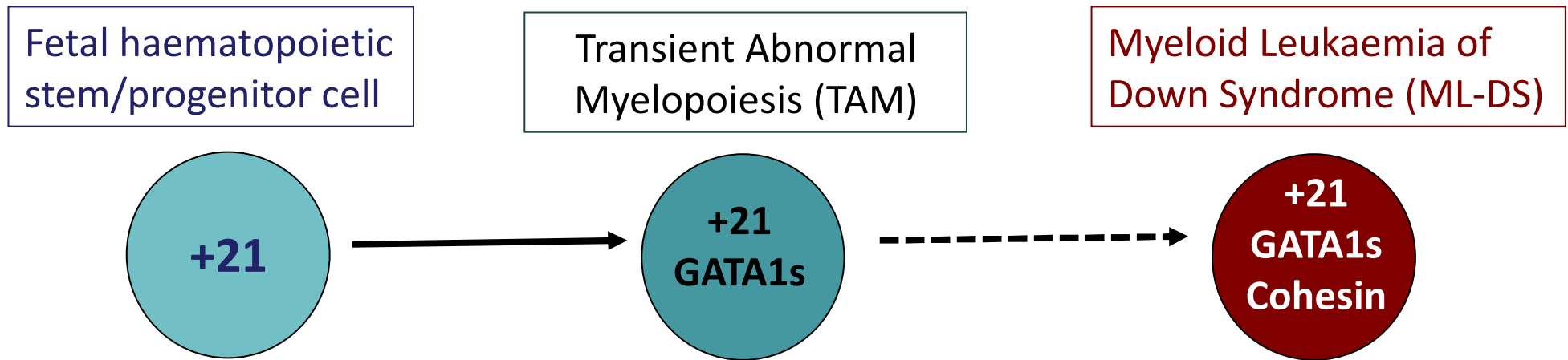
David Cruz Hernandez et al, Blood 2020

Only the size of the mutant GATA1s clone (and % blasts) predict for transformation to ML-DS



Oxford DS Study 2021 (unpublished)

Summary



- Acquired N-terminal truncating mutations in *GATA1* occur at very high frequency in newborns with Down syndrome (~28%).
- These mutations are acquired only in fetal cells and usually occur (and/or expand) after 20 weeks gestation.
- Mutant *GATA1* clones are usually small, clinically silent, resolve spontaneously and confer an extremely low risk of ML-DS
- DS neonates with larger mutant *GATA1* clones have a higher chance of acquiring additional mutations (eg in cohesin) and developing ML-DS



Acknowledgments

Roberts lab

Natalina Elliott
Anindita Roy
Gemma Buck

Binbin Liu
Sorcha O'Byrne
Siobhan Rice
Nick Fordham
Lucy Field

**Human Developmental
Biology Resource**

Imperial College London

Georg Bohn
Gillian Cowan
Sarah Filippi
Katerina Goudevenou
David O'Connor
Tassos Karadimitris

Bloodwise

Beating blood cancer since 1960



MRC

Medical
Research
Council

Oxford Neonatal DS Study

Neha Bhatnagar
Amelie Chaussade
Laure Nizery
Helen Richmond
Georgina Hall
ODSCS Group



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E Papaemmanuil
S Constaninescu

WIMM Single Cell Facility
CBRG
WIMM FACS Facility



THE RAY KENDALL LEUKAEMIA FUND