



Identifying genomic signatures in circulating breast tumour cells

9th ISMRC 2013, Paris, France
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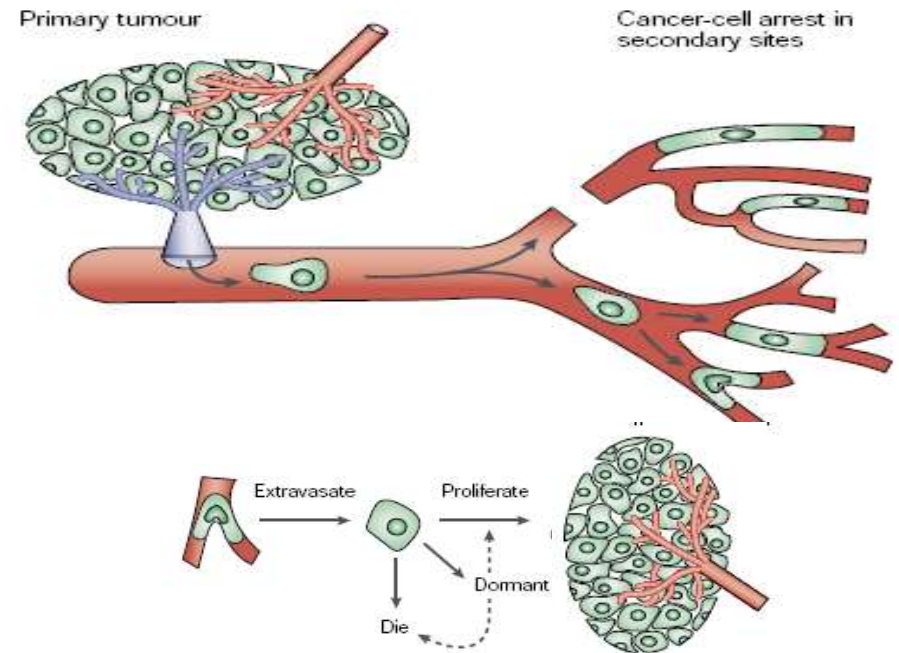
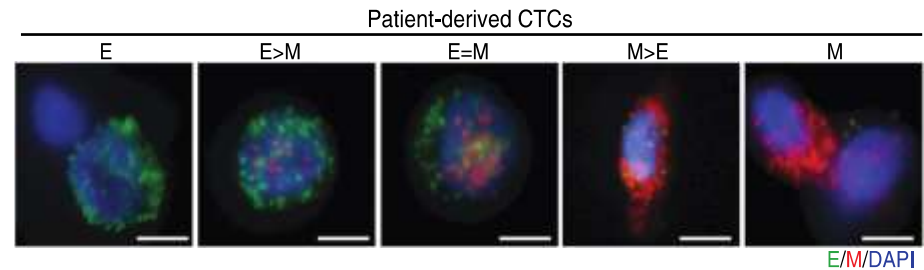
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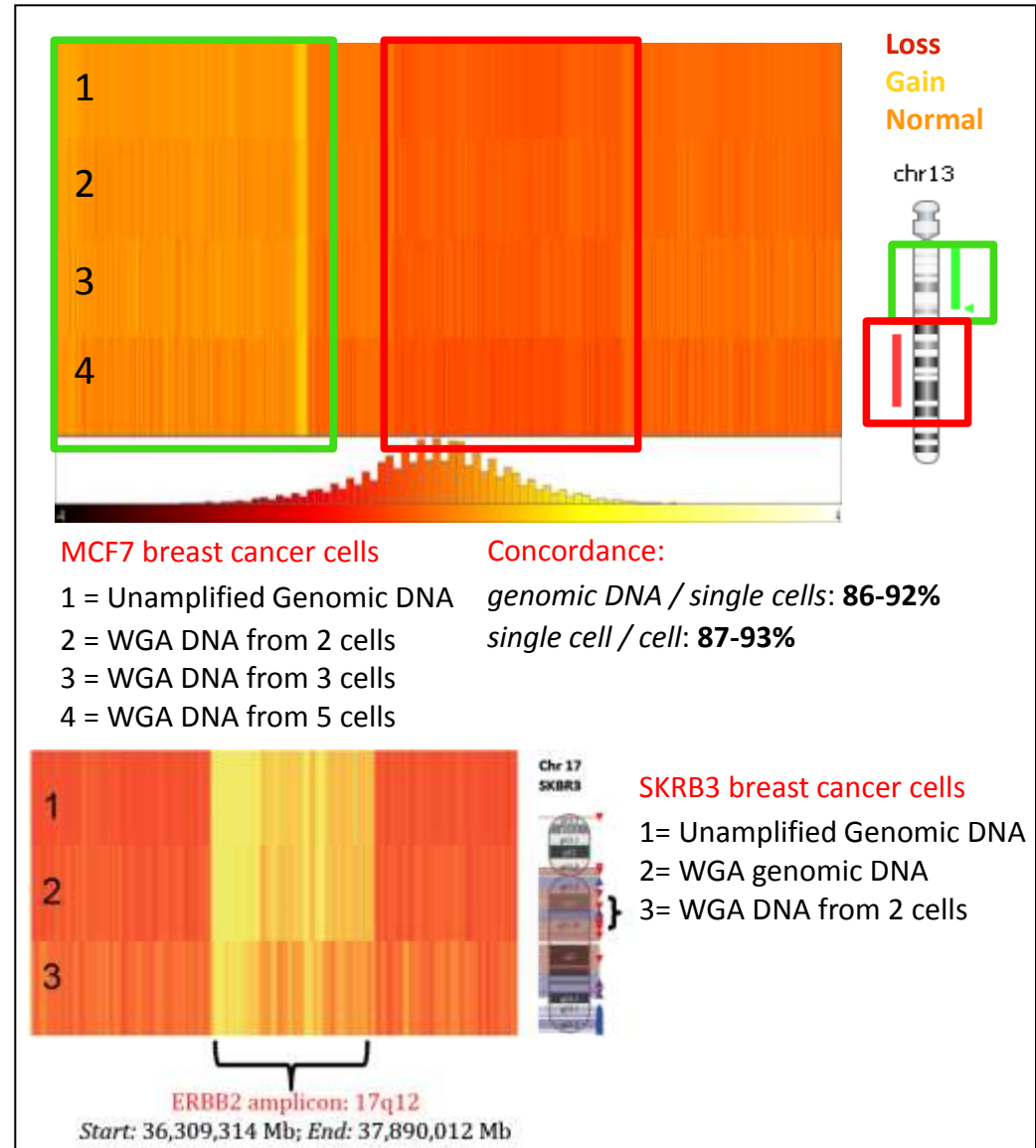
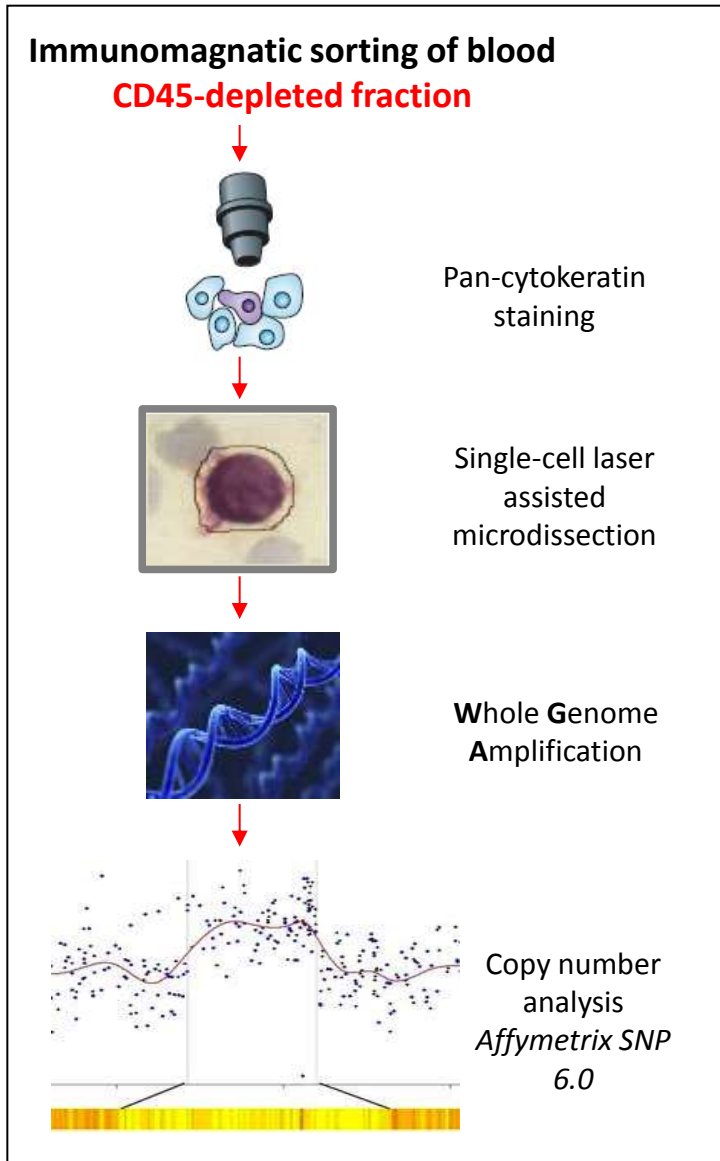
The Campbell Family Institute for Breast Cancer Research at the Princess
Margaret Cancer Centre, Toronto, Canada

Defining CTCs, currently..

- Molecular imaging of enumerate and monitor CTC levels in blood
- Proven prognostic value in early and metastatic breast cancer (n=6825; Zhang L., *Clin Cancer Res*, 2012)
- Varying degrees of concordance with molecular markers of primary tumours
 - Subclonal detection
- Predictably, individual cells reflect the heterogeneity and evolution of tumour cells during cancer progression
- *Hypothesis*: A degree of commonality is also palusible, highlighting alterations that allow tumour cells to preferentially perform CTC-defining activities
 - Motility
 - Intravasation/extravasation
 - Survival/Chemo-resistance
 - Metastasis

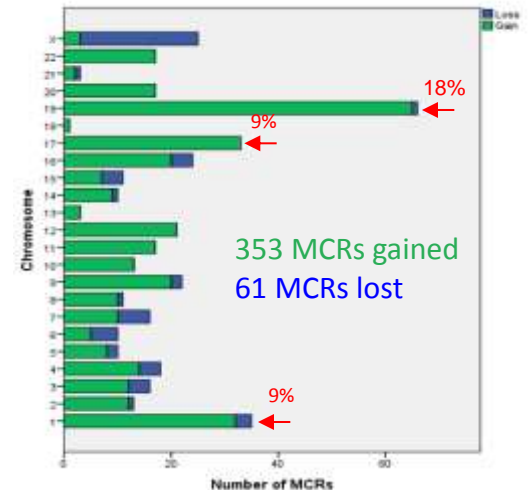
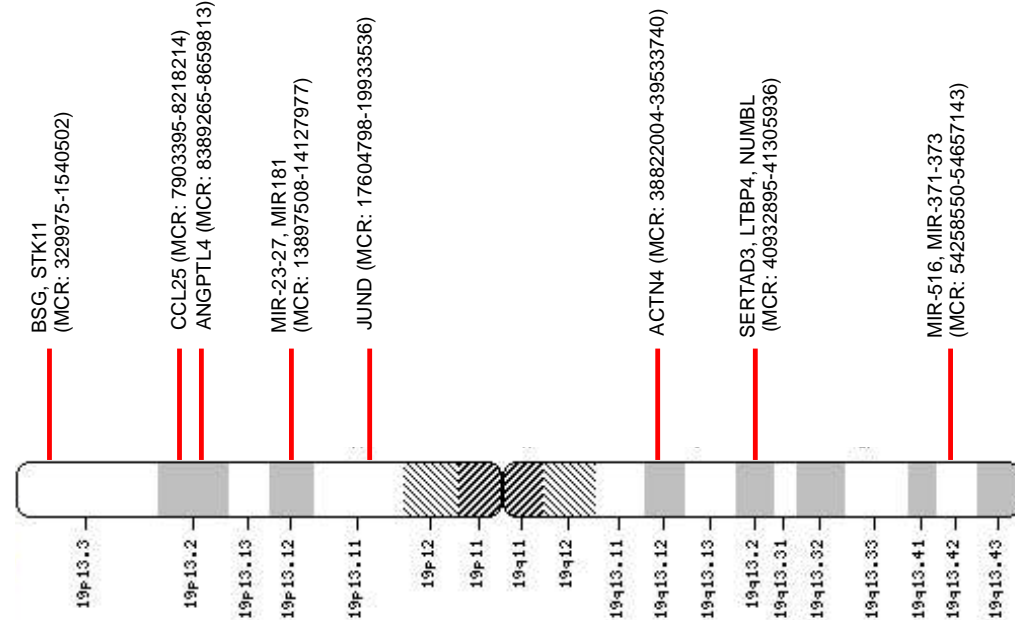
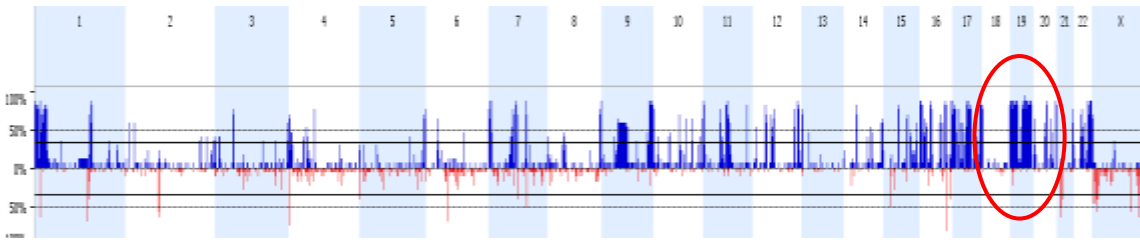


Genomic characterization of CTCs



Signature of Recurrent gains in CTCs

n = 17 CTC / normal pairs

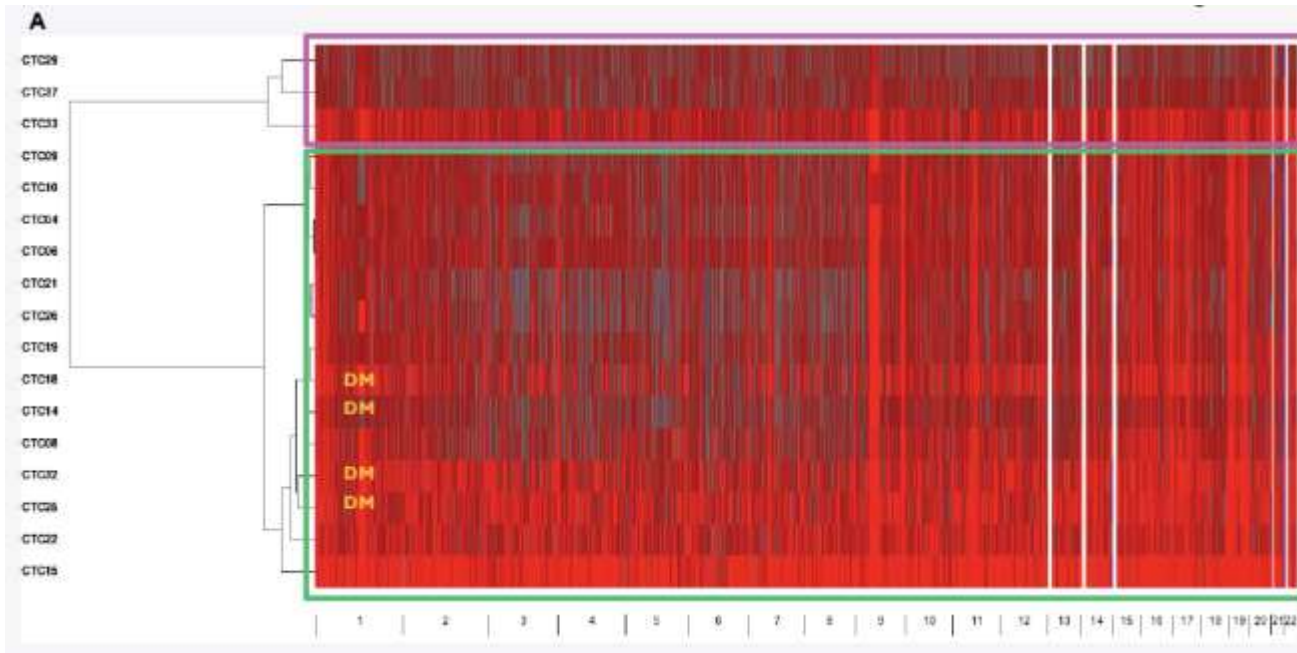


Minimal Common Regions of gain in at least 4 samples

- 90 MCRs in recurrent signature (15-16/17 samples)
- 48/90 MCRs on chr 19
- 1 MCR gained in 16/17 samples: **SERTAD3, LTBP4, NUMBL** (oncogenic transformation, TGFB activation, metastasis)

- Genes with CTC-like functions: invasion, intravasation, survival, resistance to anoikis, chemo-resistance
- Examined 787 primary invasive breast carcinomas: CTC-like MCRs present in **3-4%** samples: **CCNE1, KLK7-12, MIR-500s, MIR-371-373, AKT2**

19q21-23	<i>ADAM15, MUC1</i>
7q22.1	<i>SERPINE/PAI-1</i>
11p15.5	<i>CD151</i>
17q21	<i>ERBB2</i>
17q25.2	<i>ITGB4</i>
1p36.3	<i>PRK CZ</i>
7p22	<i>FASCN1</i>



- Net pro- and anti- tumourigenic gene expression results in a balanced state or dormant CTCs, quiescent, chemo-resistant?
- Aggressive tumour cells propagating dissemination and metastatic disease via CTCs
- Early acquired alterations necessary for survival of CTCs

CLUSTER 1: Dormancy-related signature
N=3, 11 MCRs

MIR-602
PTEN
SMAD2
AKT2
CADM2
EPHA5
ESR2

CLUSTER 2: Tumour-aggressiveness related signature
N=14, 398 MCRs, 110 found in all samples, 54 on chr19
Distant Metastases (DM) p = 0.07
Age <50 p = 0.06

BSG
TUBB4
INSR
CCL25
ANGPTL4
ANGPTL6
JUND
MAG
ACTN4
SIRT2
MARK4
MIR-7, 24/23/27, 181, C19MC and MIR371-73 cluster

Common signature
2 MCRs

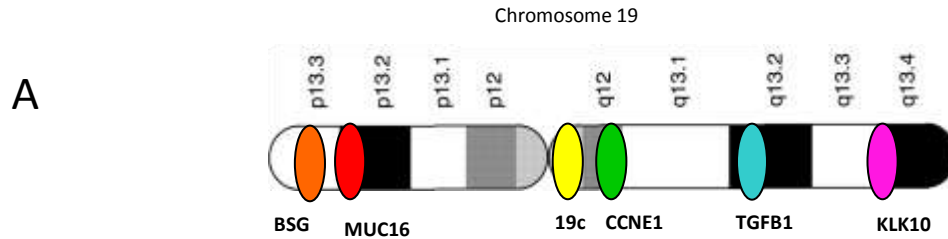
Chromosome 21q21 (2-12/17 samples):

ABCG1
COL18A1
COL6A1
CSTB
ITGB2
PRMT2
TFF3

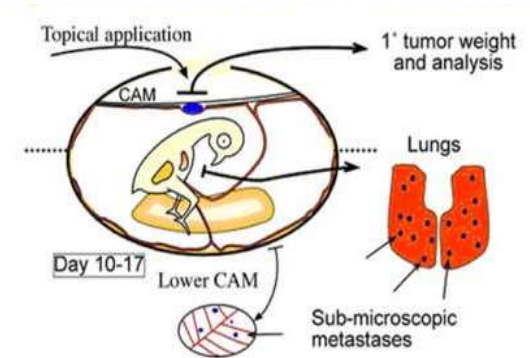
Chromosome 19q13.13 (16/17 samples):

SERTAD3
LTBP4
NUMBL

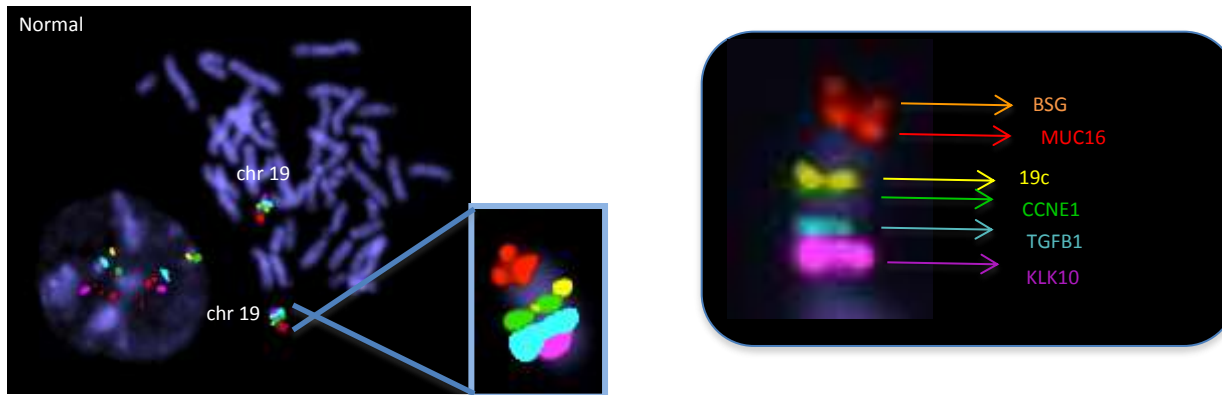
Validation of CTC-signatures



B



Intratumoural assessment: proportion of cells with CTC-like gains



A: Multispectral-FISH for recurrent gains signature (10 regions)

B: In vivo chick embryo assay for intravasation and metastasis – 500 genes from recurrent, dormancy and tumour aggressiveness signatures

	Chromosomal region	Number of genes in region
Hyb 1	19p13.3	254
	19p13.3-13.2	15
	19p13.2-13.11	379
	19q13.32-13.41	299
	19q13.41	11
Hyb 2	9q34.3	119
	11p15.5-15.4	138
	17q25	108
	1p36.3	34

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Lab members:

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- Ranju Nair
- Moustafa Abdalla
- Dr. Yanglong Zhu
- Dr. Carolina Lopez-Uran

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- Dr. Mark Clemons
- Dr. Phillipe Bedard
- Dr. Eitan Amir
- Manoj Mathews

Chick embryo assays:

- Dr. John Lewis (*University of Alberta, Canada*)