

Precision Medicine: A Case-based Approach

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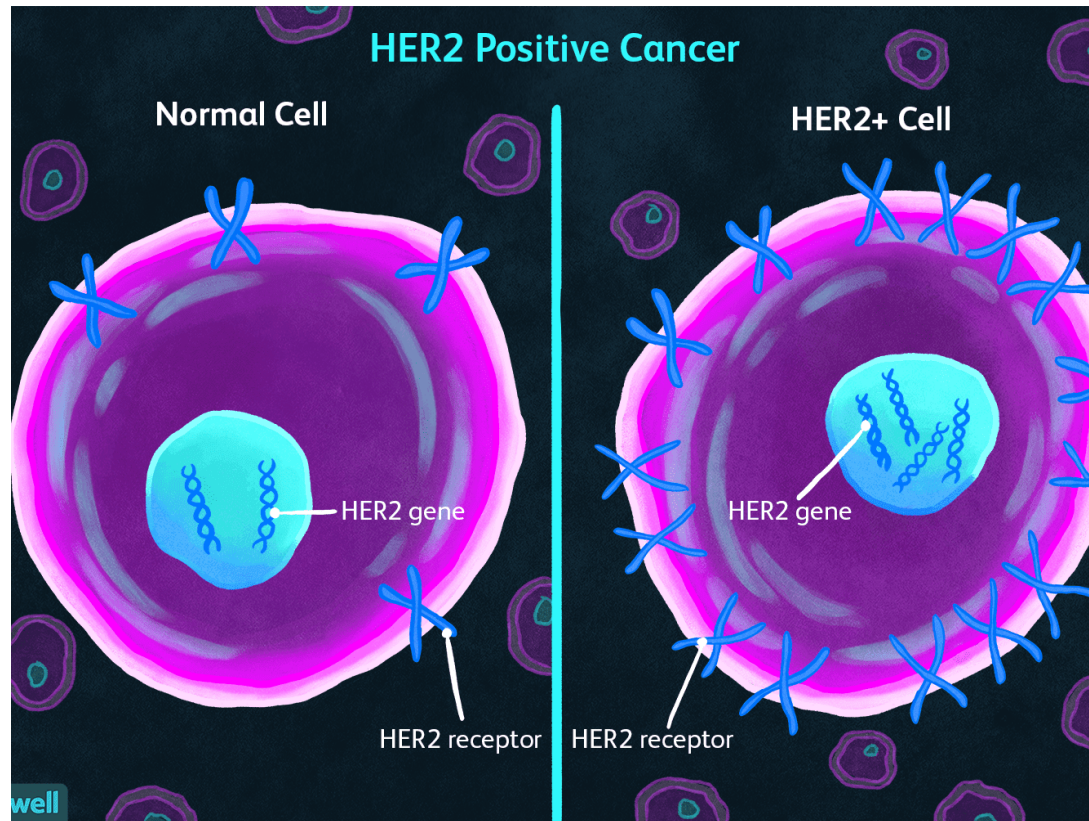
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What and why: Genomic sequencing?

- Sequencing the DNA in tumor cells either by tissue analysis or blood
- The goal is to determine which genomic variants are present in the tumor which may guide future therapeutic treatment options
- Treatment options could either be an FDA approved drug which targets a particular gene variant for a particular disease (e.g. BRCA1/BRCA2 in prostate cancer – Olaparib) or to find clinical trial opportunities with novel targeted oncolytics

Amplification

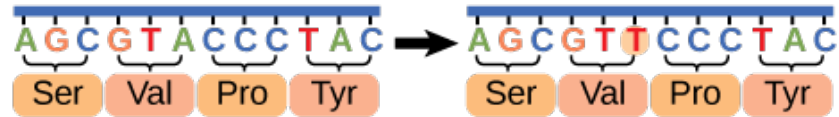


- Amplification can occur at the gene level or by increased transcription
- Gene copy number is evaluated by FISH
- Protein expression is evaluated by immunohistochemistry
- Gene expression (RNA) is identified by some NGS assays

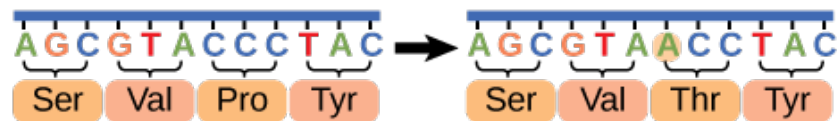
Point Mutations and Frameshift Mutations

Point Mutations

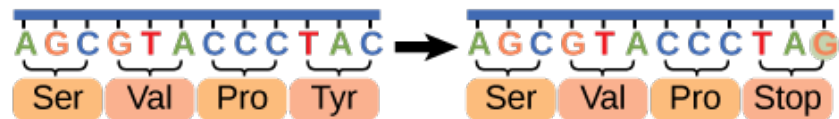
Silent: has no effect on the protein sequence



Missense: results in an amino acid substitution

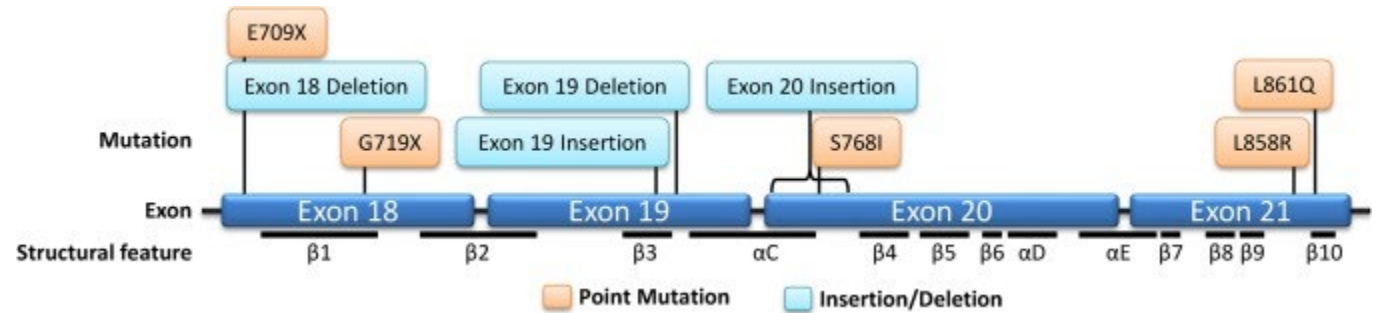
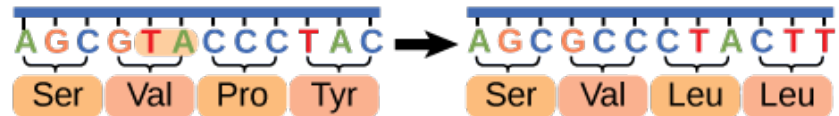


Nonsense: substitutes a stop codon for an amino acid

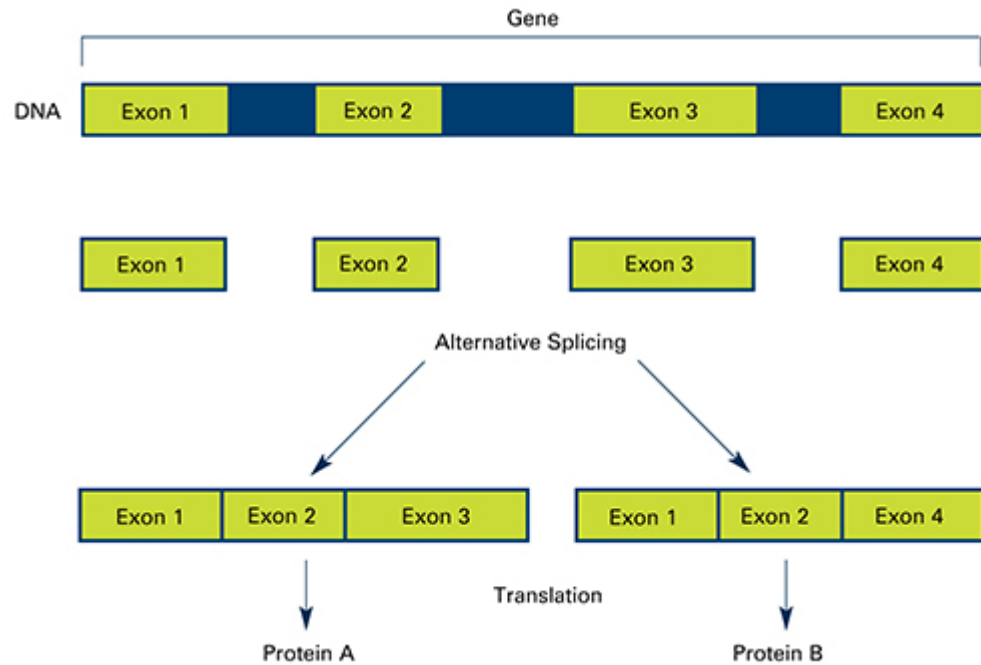


Frameshift Mutations

Insertions or deletions of nucleotides may result in a shift in the reading frame or insertion of a stop codon.

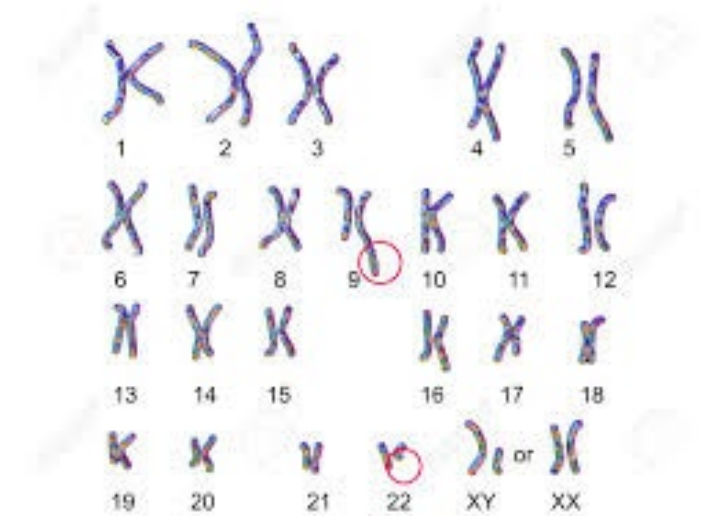
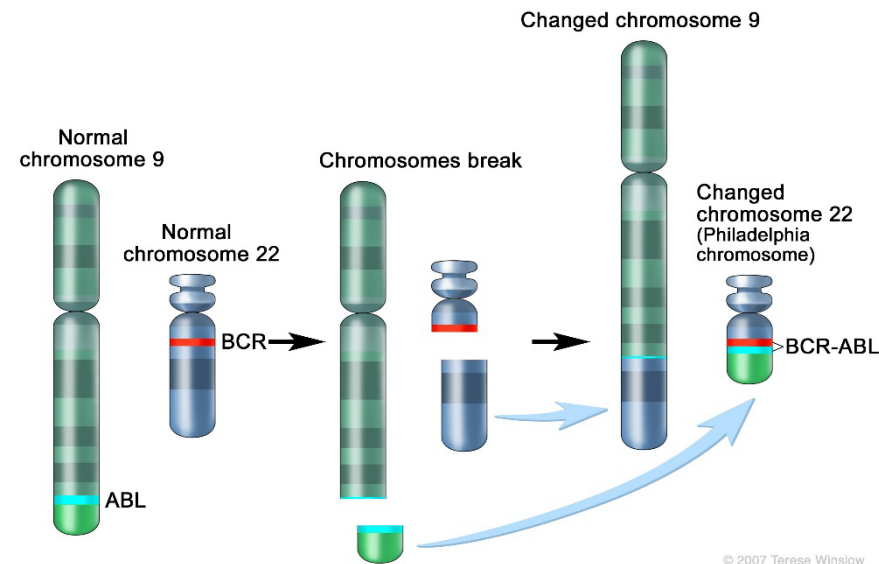
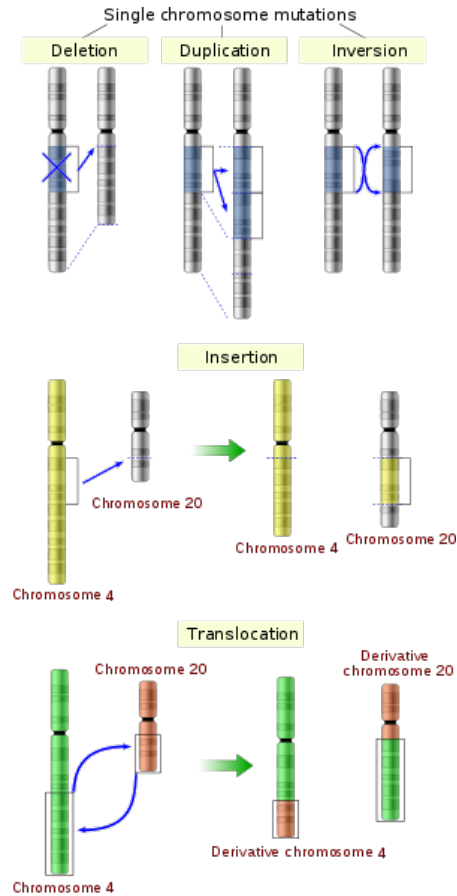


Splicing Mutations

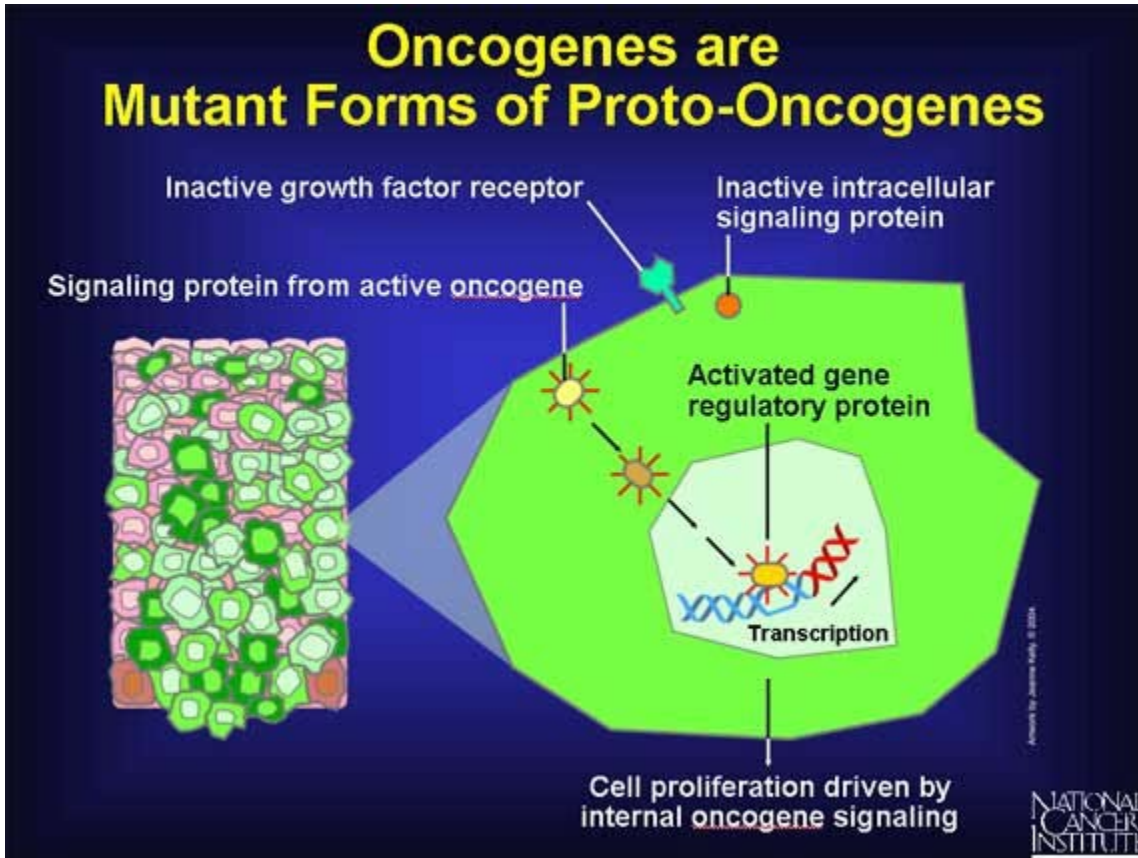


- One variant, several transcripts
- GENE:Location:Sequence Change

Chromosome Level Mutations = New Fusion Genes



Oncogenes and Mechanisms of Activation



Point Mutations

- EGFR
- KRAS
- BRAF

Chromosomal Translocation

- Philadelphia chromosome (eg; BCR ABL)

Gene Amplification

HER2
C-MYC

Usually druggable

KRAS has proven to be a challenge over time
Transcription factors also difficult to target

Tumor Suppressor Genes

Tumor suppressor genes prevent cancer

When they get mutated, cancer can occur

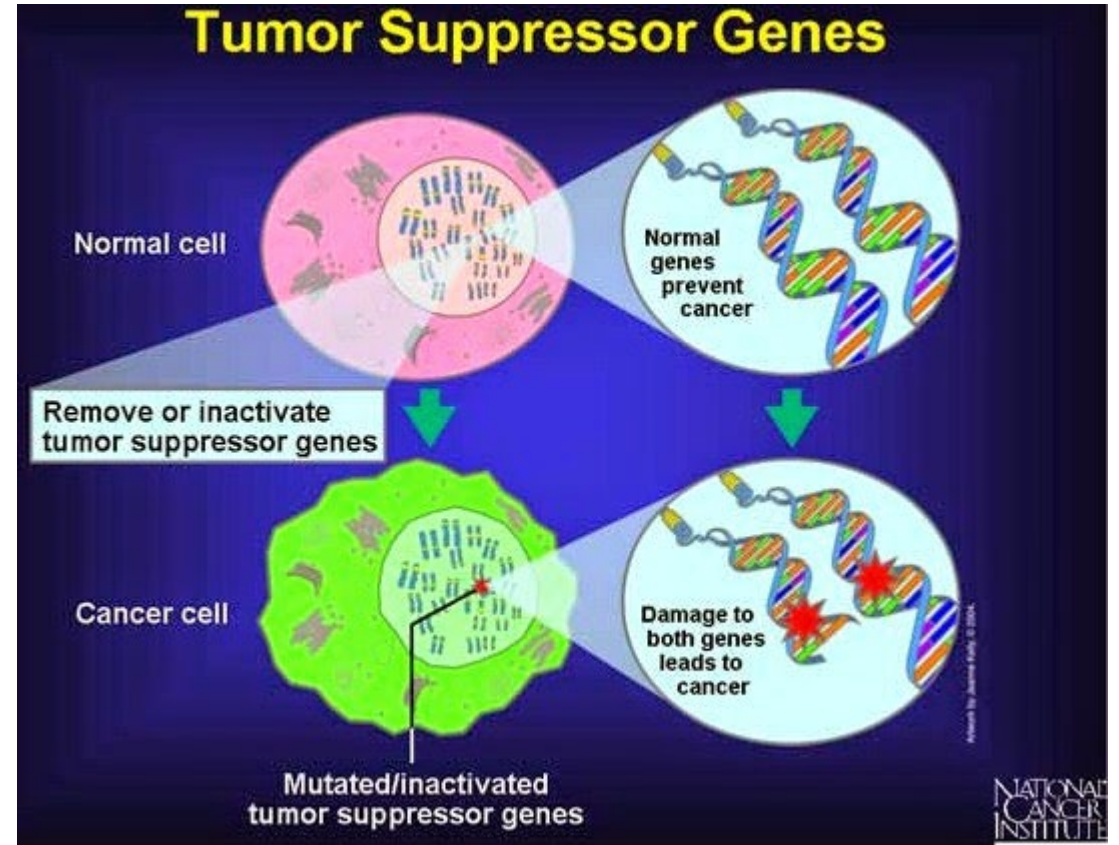
Examples

- PTEN
- TP53

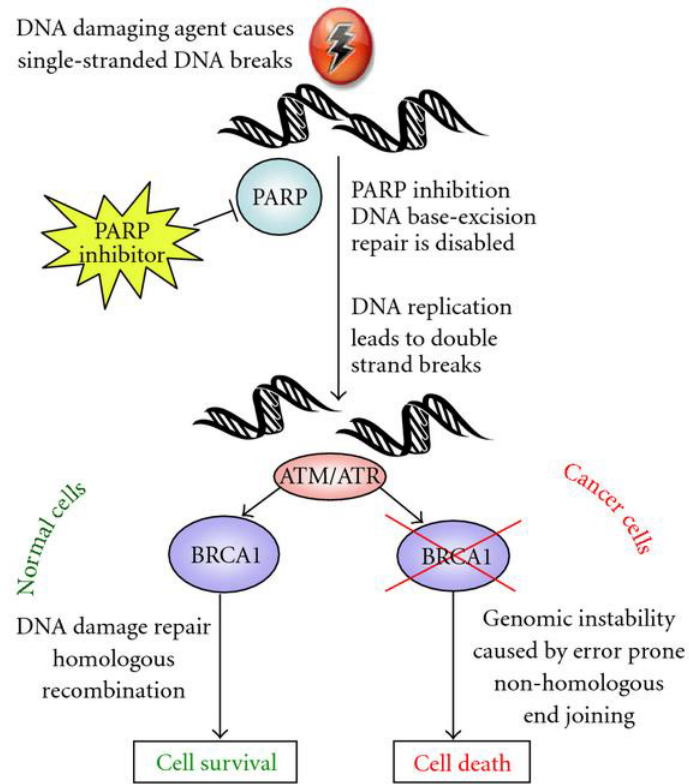
Many are involved in DNA repair

Bad News = Hard to target

Notable exception, synthetic lethality



Synthetic Lethality



- Inhibiting PARP impacts base excision repair
- BRCA1 mutation impacts double strand DNA repair
- PARP inhibition in BRCA1 mutant patient a highly effective strategy
- Ongoing clinical trials combining PARP inhibitors with ATM and ATR inhibitors

Common NGS Assays

Platform	Genes	Sequencing Strategy	FDA Approval	Use
FoundationOne CDX	324	Capture	Yes	Substitutions, insertion and deletion alterations (indels), and copy number alterations (CNAs)
Foundation Liquid	324	Capture	Yes (NSCLC, Prostate, Ovarian, Breast)	Substitutions, insertion and deletion alterations (indels), and copy number alterations (CNAs)
Caris Molecular Intelligence CDX	~20,000 592 reported	Exome (DNA and RNA)	No	Whole exome and transcriptome, pretty much everything
Guardant 360	73	Capture	Yes (NSCLC)	Substitutions, insertion and deletion alterations (indels), and copy number alterations (CNAs) + fusions

Common NGS Assays

Platform	Coverage	Error rate (positive and negative, sensitivity and specificity)	LoD (limitation of detection at 100% sensitivity)	Notes
FoundationOne CDX	250X	<1%	Most ~ 2.5%	
Foundation Liquid	250X	<1%	Most ~0.5%	Concordance was 100% to another liquid assay
Caris Molecular Intelligence CDX	1000X for 720 clinical genes, > 500X, for others	<1% false positive, <5% SNVs and indels	0.1%	>95% concordance with Sanger sequencing
Guardant 360		<1% SNV and indels	0.25%	Concordance 92%-100% to tissue

How Are The Sequencing Reports Utilized to Generate Clinical Recommendations?

Translating NGS Results into Individualized Therapy Recommendations

- Start with the individual themselves:
 - Cancer diagnosis and stage
 - Prior therapies
 - Goals of care
 - Other important comorbidities or considerations
- NGS tests results have limited patient specific information
- Goal is to translate the findings into realistic treatment options for each individual patient
 - Consider current and future therapies
 - Summarize multiple genomic tests → tumors can change over time

Common Components of NGS Reports

- “Front Page” findings
- Detailed individual gene descriptions
- Clinical trials
- Variants of uncertain significance
- References
- Appendix information:
 - Test methodology
 - Genes and alterations assessed
 - Lower limits of detection

High Impact Results

CARIS MiProfile

BIOMARKER	METHOD	RESULT	THERAPY ASSOCIATION	BIOMARKER LEVEL*
BRCA1	NGS	Mutated, Pathogenic Exon 23 p.R1835*	BENEFIT olaparib, talazoparib	Level 1
			BENEFIT carboplatin, cisplatin	Level 3A
			BENEFIT endocrine therapy	Level 1
ER	IHC	Positive 3+, 90%	BENEFIT abemaciclib, palbociclib, ribociclib	Level 2
			BENEFIT everolimus	Level 2
			BENEFIT endocrine therapy	Level 1
PR	IHC	Positive 2+, 3%	BENEFIT abemaciclib, palbociclib, ribociclib	Level 2
			LACK OF BENEFIT ado-trastuzumab emtansine (T-DM1), lapatinib, neratinib, pertuzumab, trastuzumab	Level 1
ERBB2 (Her2/Neu)	CISH	Not Amplified		
	IHC	Negative 1+, 10%		

CANCER TYPE RELEVANT BIOMARKERS		
Biomarker	Method	Result
MSI	NGS	Stable
Mismatch Repair Status		Proficient
Tumor Mutational Burden		Intermediate 11 Mutations/Mb
AKT1	NGS	Mutation Not Detected
AR	IHC	Positive 2+, 90%
BRCA2	NGS	Mutation Not Detected
ERBB2 (Her2/Neu)	NGS	Mutation Not Detected
ESR1	NGS	Mutation Not Detected
PD-L1	SP142 IHC	Negative 0

CANCER TYPE RELEVANT BIOMARKERS (cont)		
Biomarker	Method	Result
PIK3CA	NGS	Mutated, Pathogenic Exon 21 p.H1047R
PTEN	IHC	Positive 1+, 100%
	NGS	Mutation Not Detected
OTHER FINDINGS (see page 2 for additional results)		
Biomarker	Method	Result
ARID1A	NGS	Mutated, Pathogenic Exon 3 p.P517fs

FoundationOne® CDx/ Heme / Liquid CDx

Companion Diagnostic (CDx) Associated Findings

GENOMIC FINDINGS DETECTED

Tumor Mutational Burden (TMB)
≥ 10 Muts/Mb

FDA-APPROVED THERAPEUTIC OPTIONS

Keytruda® (Pembrolizumab)

OTHER ALTERATIONS & BIOMARKERS IDENTIFIED

Results reported in this section are not prescriptive or conclusive for labeled use of any specific therapeutic product. See professional services section for additional information.

Microsatellite status MS-Stable §

PIK3CA E545K

Tumor Mutational Burden 11 Muts/Mb §

STK11 Q152*

FGFR3 S249C

TGFBR2 S295*

MLL2 Q2898*

§ Refer to appendix for limitation statements related to detection of any copy number alterations, gene rearrangements, BRCA1/2 alterations, LOH, MSI, or TMB results in this section.

Please refer to appendix for Explanation of Clinical Significance Classification and for variants of unknown significance (VUS).

TEMPUS xT®

GENOMIC VARIANTS

Somatic - Potentially Actionable

TP53 p.R196* Stop gain - LOF

AR Copy number gain

CDKN2A Copy number loss

TMPRSS2 - ERG Chromosomal rearrangement

Variant Allele Fraction

61.4%

Somatic - Biologically Relevant

CDKN2B Copy number loss

Germline - Pathogenic / Likely Pathogenic

No pathogenic variants were found in the limited set of genes on which we report.

IMMUNOTHERAPY MARKERS

Tumor Mutational Burden

2.1 m/MB 40th percentile

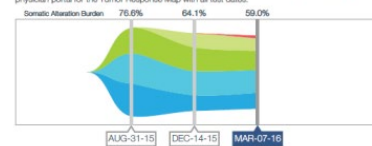
Microsatellite Instability Status

Stable Equivocal High

Guardant360®

Guardant360 Tumor Response Map

The Guardant360 Tumor Response Map illustrates the relative changes of observed ctDNA at different sample submission time points. The "Somatic Alteration Burden" value below refers to the maximum % ctDNA detected at each time point. Amplifications are not plotted and only the first and last four test dates are plotted. Please see the physician portal for the Tumor Response Map with all test dates.



13 Total Alteration(s) Detected

10 with Associated Therapy
2 Associated with Lack of Response
Multiple Clinical Trials Available

Summary of Alterations & Associated Treatment Options

The percentage, or allele frequency, of altered cell-free DNA (% ctDNA) circulating in blood is related to the unique tumor biology of the patient. Factors that may affect the amount/percentage of detected genomic alterations in circulating cell-free DNA in blood include tumor growth, turn-over, size, heterogeneity, vascularization, disease progression, or treatment.

Alteration	Mutation Trend	% ctDNA	ctDNA Amplification	FDA Approved in Indication	Available for Use in Other Indications	Clinical Drug Trials
Exon 19 Deletion	100% → 50% → 0%	59.0		Atsitrinib, Erlotinib, Gefitinib	None	Trials Available
T790M	100% → 50% → 0%	37.3		Osimertinib	Lack of Response: Erlotinib, Gefitinib	Trials Available
C797S	100% → 50% → 0%	27.5		Erlotinib	Lack of Response: Erlotinib, Osimertinib	Trials Available
AMP	+++ → ++ → + → 0%		+++	None	Atsitrinib, Cabozantinib, Erlotinib, Gefitinib, Nectumumab	Trials Available

MSKCC/OncoKb Levels of Evidence

OncoKB Therapeutic Levels of Evidence



Translating Results into Patient Care

- Which gene mutations could be driving the cancer?
- Which gene mutations do we likely not want to target (passenger mutations)?

Case #1

- Patient is a 69 y/o female with renal clear-cell carcinoma; former smoker 20 pack years
- April 2012 - underwent a total nephrectomy on the R side. Pathologic diagnosis at that time was that of an 8.5 cm firm and grade 4/4 T3a N0 M0 clear-cell carcinoma. The tumor was present in large muscular line branches of the renal vein within the renal sinus.
- May 2014 - surveillance CT scans reveal several scattered small pulmonary nodules, the largest now being up to 11 mm in the R pleural-based region. There have been some small nodules in the RP, slightly more prominent in the L periaortic area measuring size 12 mm.
- November 2021 - had what she thought was recurrent sciatica. MRI revealed an S1 mass with encroachment on thecal sac. Steroid injection w/o relief requiring oxycodone and supine position for such. No bowel or bladder changes. No other obvious lesions by MRI lumbar.
- December 2021 – underwent CT-guided bx of sacral mass. Path + for RCC - Received palliative RT to sacrum 300Gy x 5
- March 2022 – received 5 cycles **nivolumab/cabozantinib** with improvement then developed enterocolitis vs diverticulitis, drained abscess

Case #1 – Foundation CDx Somatic Tissue Testing

BIOMARKER FINDINGS	THERAPY AND CLINICAL TRIAL IMPLICATIONS	
Microsatellite status - MS-Stable	No therapies or clinical trials. See Biomarker Findings section	
Tumor Mutational Burden - 2 Muts/Mb	No therapies or clinical trials. See Biomarker Findings section	
GENOMIC FINDINGS	THERAPIES WITH CLINICAL RELEVANCE (IN PATIENT'S TUMOR TYPE)	THERAPIES WITH CLINICAL RELEVANCE (IN OTHER TUMOR TYPE)
VHL - D121Y	Belzutifan <input type="checkbox"/> 2A	none
8 Trials see p. 6		

NCCN category

GENOMIC FINDINGS WITH NO REPORTABLE THERAPEUTIC OR CLINICAL TRIAL OPTIONS

For more information regarding biological and clinical significance, including prognostic, diagnostic, germline, and potential chemosensitivity implications, see the Genomic Findings section.

BAP1 - E20* p. 3 **CDKN2A/B - CDKN2A loss, CDKN2B loss**..... p. 4

Case #2

- Patient is a 49 y/o male with newly diagnosed pancreatic cancer; hx DM2, HTN, irregular heart beat
- 8/22/2022 – presented to PCP with c/o intermittent RUQ abdominal pain x 3 months.
- 9/2/2022 – US concerning for abdominal mass
- 9/7/2022 – CTAP showed 8cm pancreatic mass, multiple liver masses, splenic infarct, hiatal hernia
- 9/14/2022 –EGD/EUS showed multiple metastatic liver lesions, a mass in the pancreatic body and tail, and many hypoechoic lesions in the peritoneal cavity. TxNxM1. FNA of liver lesions c/w pancreatic ductal adenocarcinoma.
- 9/20/2022 – presented at IUSCC pancreatic tumor board. Stage IV. Recommend clinical trial vs first line palliative systemic chemo.
- 9/27/2022 – CT chest showed few tiny pulmonary nodules are nonspecific. No LAD.
- 10/4/2022 – started FOLFIRINOX chemotherapy
- 10/5/2022 – presented to ED with vomiting. CT unchanged.

Case #2 – Foundation CDx – Somatic Tissue Testing

GENOMIC FINDINGS	THERAPIES WITH CLINICAL RELEVANCE (IN PATIENT'S TUMOR TYPE)	THERAPIES WITH CLINICAL RELEVANCE (IN OTHER TUMOR TYPE)
BRCA2 - W2626C 10 Trials see p. 12	Olaparib [2A]	Rucaparib [2A] Niraparib Talazoparib
CCNE1 - amplification 4 Trials see p. 14	none	none
FGFR4 - amplification 10 Trials see p. 15	none	none
KRAS - Q61L 3 Trials see p. 17	none	none
MYC - amplification 5 Trials see p. 18	none	none
PIK3CA - amplification - equivocal 10 Trials see p. 19	none	none
TP53 - Y220C 1 Trial see p. 21	none	none

NCCN category

VARIANTS TO CONSIDER FOR FOLLOW-UP GERMLINE TESTING IN SELECT CANCER SUSCEPTIBILITY GENES

Findings below have been previously reported as pathogenic germline in the ClinVar genomic database and were detected at an allele frequency of >10%. See appendix for details.

BRCA2 - W2626C p. 2

This report does not indicate whether variants listed above are germline or somatic in this patient. In the appropriate clinical context, follow-up germline testing would be needed to determine whether a finding is germline or somatic.

GENOMIC FINDINGS WITH NO REPORTABLE THERAPEUTIC OR CLINICAL TRIAL OPTIONS

For more information regarding biological and clinical significance, including prognostic, diagnostic, germline, and potential chemosensitivity implications, see the Genomic Findings section.

CDKN2A/B - CDKN2A loss exon 1, CDKN2B loss p. 2

PARK2 - loss exons 2-4 p. 8

Case #3

- Patient is a 33 y/o female with recurrent WHO grade 4 astrocytoma
- 2008 – presented w/seizures. Originally diagnosed w/grade 3 astrocytoma. Underwent resection in Bloomington then radiation and **temozolomide** for about a year.
- 2011 – recurrent disease s/p second resection in Bloomington. Completed some adjuvant temozolomide but ultimately lost to follow up w/out completing a full course
- 2012 – underwent surgery for exposed hardware
- Late October 2022 – presented with seizures. MRI w/concerns for HGG in L frontal lobe, but on vimpat and lamotrigine, discharged w/plans for coordinated surgery with neurosurgery and ENT given surgical history and need for wound flap
- 12/6/2022 – underwent resection #3. Pathology showed WHO grade 4 astrocytoma, IDH1 mutant, NTRK2 fusion present. Post op course complicated by aphasia and R hemiparesis. Prolonged hospital stay discharged to AR on 12/22/2022.
- Plans for re-irradiation with concurrent chemo to begin soon locally.

Case #3 Caris Somatic Tissue Testing

Results with Therapy Associations

BIOMARKER	METHOD	ANALYTE	RESULT	THERAPY ASSOCIATION	BIOMARKER LEVEL*
NTRK2	Seq	RNA-Tumor	Pathogenic Fusion	BENEFIT entrectinib, larotrectinib	Level 2
MGMT	PyroSeq	DNA-Tumor	Methylated		Level 2
IDH1	Seq	DNA-Tumor	Pathogenic Variant Exon 4 p.R132S	BENEFIT temozolomide	Level 3

Genomic Signatures

Biomarker	Method	Analyte	Result
Microsatellite Instability (MSI)	Seq	DNA-Tumor	Stable
Tumor Mutational Burden (TMB)	Seq	DNA-Tumor	Result: Low 
Genomic Loss of Heterozygosity (LOH)	Seq	DNA-Tumor	Low - 15% of tested genomic segments exhibited LOH (assay threshold is ≥ 16%)

MGMT Promoter Methylation

Assay: Pyrosequencing	Result: Methylated
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Genes Tested with Pathogenic or Likely Pathogenic Alterations

Gene	Method	Analyte	Variant Interpretation	Protein Alteration	Exon	DNA Alteration	Variant Frequency %
IDH1	Seq	DNA-Tumor	Pathogenic Variant	p.R132S	4	c.394C>A	43
MET	Seq	RNA-Tumor	Likely Pathogenic Fusion	PTPRZ1-MET	2	-	-
	CNA-Seq	DNA-Tumor	Amplified	-	-	-	-

Case #4

- 35 yo woman with newly diagnosed NSCLC
- 7/23 - Presented to ER with lower back pain/chest pain with deep inspiration; imaging concerning for RLL and perihilar mass/pathologic fracture T7; biopsy endobronchial lesion – poorly differentiated adenocarcinoma; MRI brain shows multiple brain mets
- 8/23 - Started **carboplatin/pemetrexed/zoledronic acid** – XRT to brain/consideration for kyphoplasty

Case #4 Tempus Somatic Tissue Testing

Somatic - Potentially Actionable	Variant Allele Fraction
CD74-ROS1 Chromosomal rearrangement	
Somatic - Biologically Relevant	
LATS1 p.Q663fs Frameshift - LOF	7.1%
LRP1B Copy number loss	
Germline - Pathogenic / Likely Pathogenic	
No germline pathogenic variants were found in the limited set of genes on which we report.	
Pertinent Negatives	
No pathogenic single nucleotide variants, indels, or copy number changes found in:	
EGFR KRAS BRAI ALP RET MLI ERBB2 (HER2)	


Case #5

- 47 yo man with history of germ cell tumor
- 6/97 - B-HCG – 81,215/AFP 3,525; 10 x 16cm retroperitoneal mass/multiple bilateral pulmonary metastases – poor risk metastatic testicular cancer; BEP x 4 followed by RPLND – revealing teratoma; post-surgery – rapid increase in B-HCG – 2 x Velp with subsequent rapid rise in B-HCG (platinum refractory); High-dose chemotherapy/autologous SCT x 2 – CR for 20 + years
- 3/23 - New onset pain in L posterior rib – imaging revealed a mass in the area; CT chest/abd/pelvis otherwise normal; B-HCG/AFP - normal; biopsy – well-differentiated adenocarcinoma consistent with germ cell tumor with malignant transformation along endodermal elements/intestinal phenotype; i12p (-)
- 6/23 - Later relapse of teratoma/de-differentiated into adenocarcinoma, well-differentiated; plan for surgical resection

Case #5 –Guardant360 Liquid Biopsy

Summary of Detected Somatic Alterations, Immunotherapy Biomarkers & Associated Treatment Options

KEY  Approved in indication  Approved in other indication  Lack of response

Detected Alteration(s) / Biomarker(s)	Associated FDA-approved therapies	Clinical trial availability (see page 3)	% cfDNA or Amplification
<i>FGFR3-TACC3</i> Fusion	 Erdafitinib	Yes	0.09%
<i>APC</i> Q1444*	None	No	0.2%
<i>SMAD4</i> S154*	None	No	0.2%

Case #5 – Caris Somatic Tissue Testing

Genes Tested with Pathogenic or Likely Pathogenic Alterations

Gene	Method	Analyte	Variant Interpretation	Protein Alteration	Exon	DNA Alteration	Variant Frequency %
APC	Seq	DNA-Tumor	Pathogenic Variant	p.Q1444*	16	c.4330C>T	44
FGFR3	Seq	RNA-Tumor	Pathogenic Fusion	FGFR3-TACC3	17	-	-
SMAD4	Seq	DNA-Tumor	Pathogenic Variant	p.S154*	5	c.461C>G	44

Case #6

- 2011-Patient was found to have GIST tumor
- She was initially worked up for iron deficiency anemia and was diagnosed with small-bowel GIST.
- 2011: She underwent surgical resection and was found to have a 7.5 cm GIST tumor connected to the small-bowel with high mitotic rate (high risk), Grade 2, tumor was ruptured, felt to be stage pT3NxM0. It was c-KIT positive (no molecular testing)
- After surgical resection, she was started on **Imatinib** and took it from 06/2010 – 02/2015.
- 09/06/2016: Routine imaging revealed disease recurrence with a 7 cm mesenteric mass in the right lower quadrant. She underwent surgical resection of an 8 cm mesenteric mass on 09/29/2016 and path consistent with GIST, grade 2, with high mitotic rate.
- She was restarted on **imatinib** postoperatively and continued on 400 mg daily.
- 6/2023 Routine imaging revealed a new 1.4 cm omental nodule, suspicious for recurrence.
- 7/10/23 She underwent omental lesion biopsy - consistent with GIST. Molecular testing revealed exon 11 mutation, but also an exon 17 mutation (Asn822Lys) that predicts resistance to imatinib
- She was referred to see surgery and is planned to have omental lesion resected. Plan is to start **sunitinib**.

Case #6 Foundation CDx Somatic Tissue Testing

Biomarker Findings
Microsatellite status - MS-Stable
Tumor Mutational Burden - 0 Muts/Mb

Genomic Findings
For a complete list of the genes assayed, please refer to the Appendix.
KITW557_K558del, N822K
CREBBPrearrangement exon 31, rearrangement exon 31

1 Disease relevant genes with no reportable alterations: **PDGFRA**

Report Highlights

- Variants with diagnostic implications that may indicate a specific cancer type: **KIT** N822K, W557_K558del (p. 2)
- Targeted therapies with NCCN categories of evidence in this tumor type: **Regorafenib** (p. 4), **Ripretinib** (p. 5), **Avapritinib** (p. 4), **Nilotinib** (p. 7), **Ponatinib** (p. 8), **Sorafenib** (p. 8)
- Targeted therapies with potential resistance based on this patient's genomic findings: ❌ **Imatinib** (p. 6), **Sunitinib** (p. 6)
- Evidence-matched clinical trial options based on this patient's genomic findings: (p. 9)

NEW: To more easily navigate the content associated with patient results in an interactive format, physicians can access **FoundationReport+** by visiting FMI-Portal.com

BIOMARKER FINDINGS	THERAPY AND CLINICAL TRIAL IMPLICATIONS	
Microsatellite status - MS-Stable	No therapies or clinical trials. See Biomarker Findings section	
Tumor Mutational Burden - 0 Muts/Mb	No therapies or clinical trials. See Biomarker Findings section	
GENOMIC FINDINGS	THERAPIES WITH CLINICAL RELEVANCE (IN PATIENT'S TUMOR TYPE)	THERAPIES WITH CLINICAL RELEVANCE (IN OTHER TUMOR TYPE)
KIT - W557_K558del, N822K	Regorafenib 1	Nilotinib 2A
	Ripretinib 1	Ponatinib 2A
	Avapritinib 2A	Sorafenib 2A
	Imatinib ❌	Dasatinib
	Sunitinib ❌	
10 Trials see p. 9		

Case #7

- 60-year-old postmenopausal woman with metastatic estrogen receptor positive breast cancer.
- 2009 when she was originally diagnosed with a stage I ER positive invasive ductal carcinoma of the right breast. She was treated with lumpectomy with sentinel lymph node biopsy finding 0.7 cm of grade 1 disease and 0 of 2 lymph nodes involved. She also underwent a left- sided excisional biopsy for symmetry. She received adjuvant radiation and **tamoxifen** for approximately 3 months
- 2015 when she presented with a right pleural effusion and pleural-based nodularity. A PET-CT at that time showed FDG avid bilateral hilar adenopathy and some diffuse uptake in the endometrium. Cytology from thoracentesis confirmed adenocarcinoma that was ER positive 91%, PR positive 76%, HER2 equivocal by IHC as well as by FISH with a copy number of 4.8 and a ratio of 1.0. Pleural-based biopsy- ER positive 93%, PR positive 93% and HER2 negative with a ratio of 1.1 and a copy number of 3.9.
- started on **letrozole** and **palbociclib** when she was seen at Vanderbilt. She opted to stop her therapy 2017 to pursue alternative dietary therapies.
- PET-CT 2020 with new liver lesion as well as enlarging pleural- based nodularity and a new pleural-based paraesophageal nodularity. Started back on **palbociclib** and **letrozole** in October 2020.
- 1/2021, POD in liver. she declined enrollment on the PACE trial and was started on **fulvestrant** monotherapy.
- 5/2022, POD and declined chemotherapy and was recommended **exemestane** with **everolimus**. Patient declined and pursued integrative medicine.
- growth in the liver and s/p cyberknife in Chicago.

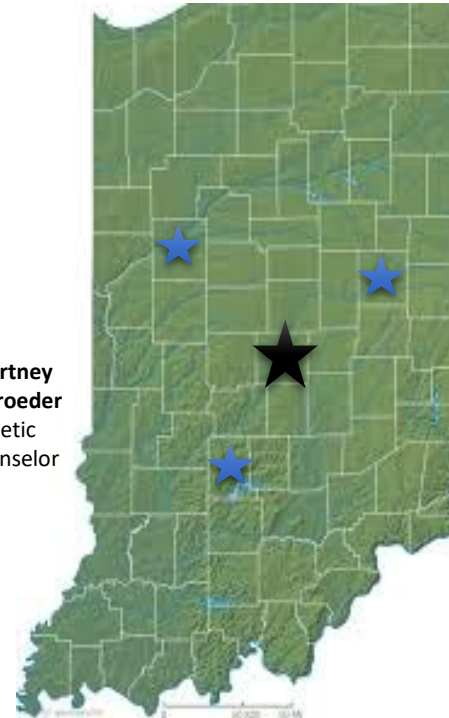
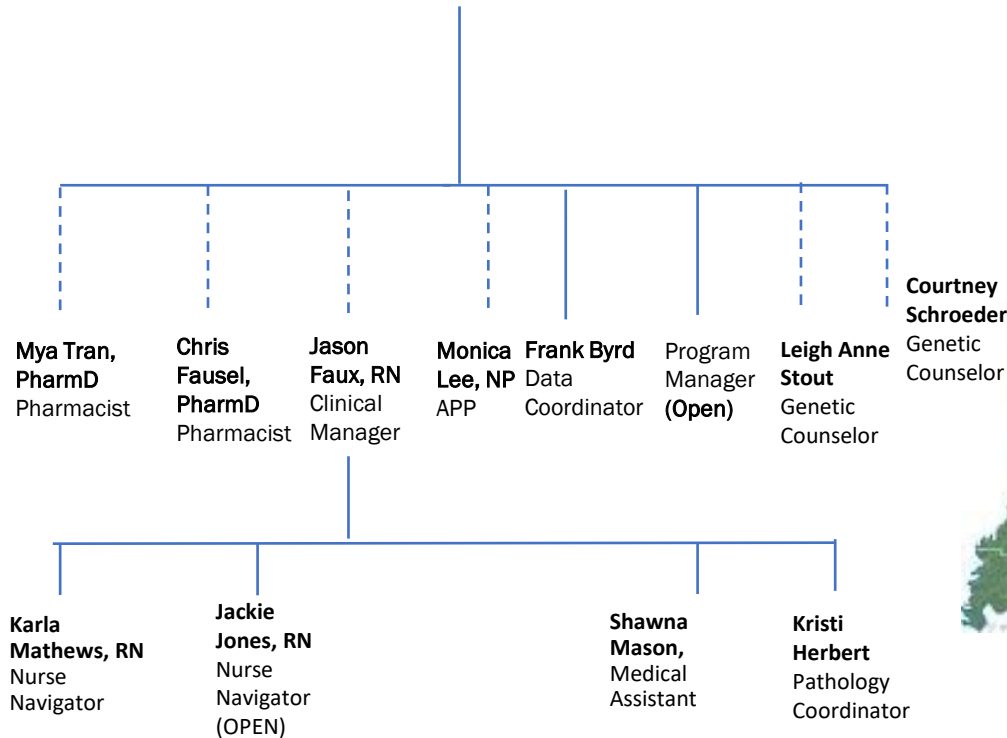
Case #7 – Foundation CDx Somatic Tissue Testing

HISTORIC PATIENT FINDINGS	FoundationOne® 29 Jul 2015	FoundationOne®Liquid CDx 30 Aug 2023	
	TRF103385	ORD-1701966-01 VAF%	
Blood Tumor Mutational Burden	Not Tested	1 Muts/Mb	
Microsatellite status	Cannot Be Determined	MSI-High Not Detected	
Tumor Fraction	Not Tested	Elevated Tumor Fraction Not Detected	
<i>ESR1</i>	● Y537S	Not Detected	0.25%
<i>CBFB</i>	● splice site 79-1G>A	Detected	0.41%
<i>DNMT3A</i>	● T257fs*59	Not Detected	0.61%
<i>GATA3</i>	● splice site 925-3_925-2delC A	Detected	Not Detected
<i>KMT2C (MLL3)</i>	● Q1105*	Detected	Not Tested
<i>MCL1</i>	amplification	Detected	Not Detected

Acknowledgements

Precision Genomics Indianapolis

Dr. Bryan Schneider, MD
Director of Precision Genomics



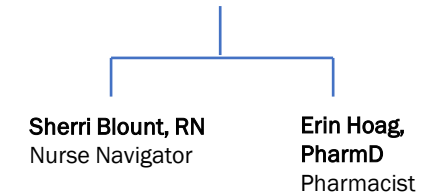
Precision Genomics Muncie Ball Memorial

Dr. Marwan Mounayar, MD
Physician Liaison



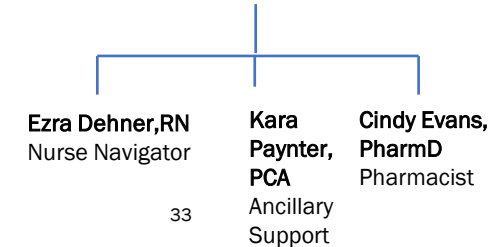
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