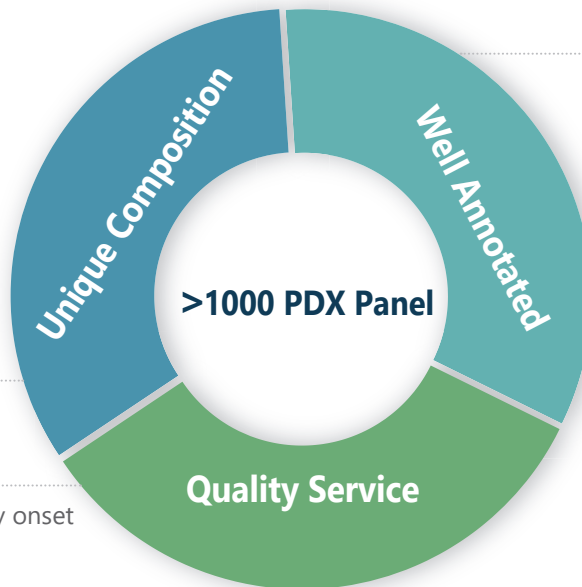


Patient-Derived Xenograft (PDX) Tumor Models

- 1200 PDX models
- Collection of PDX models prevalent in Asia
- >800+ PDX models with genetic profiling
- Searchable online database with mobile APP

- One of the world's largest collection of tumor types that are prevalent in Asia
 - » Liver - 259
 - » Lung - 204
 - » Colorectal - 132
 - » Gastric - 108
 - » Esophageal - 84
 - » Cholangiocarcinoma - 43
- Drug resistant PDX
- Recurrent/metastasis PDX



- Clinical information
 - » Clinical classification
 - » Pathology
 - » Treatment history
- PDX growth characteristics
 - » Growth curves
 - » SoC treatment
- >800 PDX genomic profiled
 - » Affymetrix microarray
 - » Whole-exome sequencing
 - » SNP 6.0 array
 - » RNAseq

- 400 PDXs in-life for rapid study onset
- End-user friendly database
- Effective project management
- AAALAC accredited SPF facility

One of the largest collection of tumor types prevalent in Asia with genomic profiling

Tumor Types		Profiled	Established
Lung cancer	NSCLC	150	160
	SCLC	4	4
	Others	24	40
Gastric cancer		77	108
HCC		145	259
Colorectal cancer		102	132
Esophageal cancer		63	84
Cholangiocarcinoma		36	43
Pancreatic cancer		54	57
Kidney cancer		8	8
Head & Neck cancer		18	142
Lymphoma		24	34

Tumor Types	Profiled	Established
Breast cancer	17	23
Melanoma	11	14
Uveal Melanoma	1	1
Liposarcoma	3	12
GIST	7	19
NPC	2	4
Ovarian cancer	4	8
Gallbladder cancer	7	9
Glioma	4	4
Endometrial cancer	3	4
Cervical cancer	2	4
sarcoma	2	3

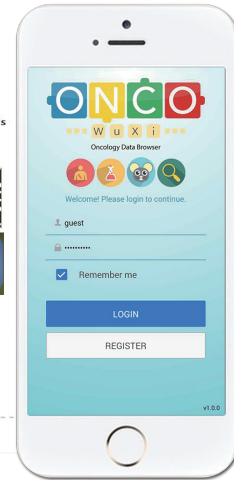
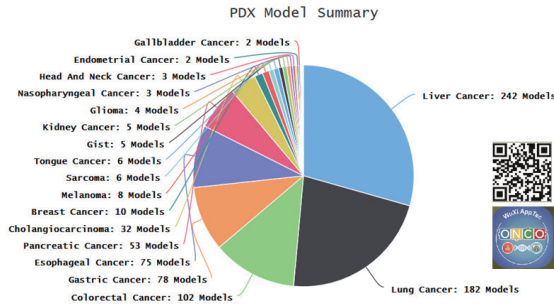
Integrated online database for PDX, CDX & Syngeneic tumor models with mobile App



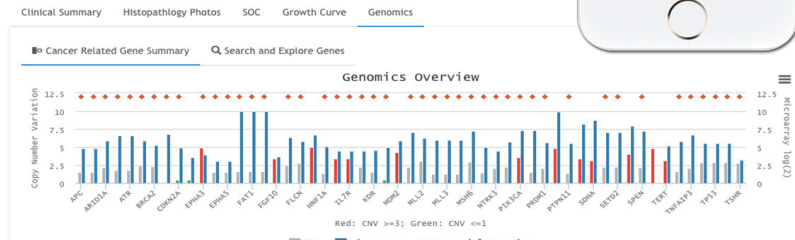
<http://onco.wuxiapptec.com>

Tumor model on the Go

- >1200 tumor models
- Full annotation
- 3000 Growth curves
- 2800 Histology images
- 250 SOC studies
- 600 WES, CNV, Microarray & RNAseq
- Cross-searchable, interactive,informative
- "Foundation medicine like"
- One-stop for PDX/CDX & Syngeneic



LU-01-0015



PDX with oncogene amplification, mutation & fusions

	CH	CO	ES	GIST	HCC	LP	LC	ME	PanC	GC	Total
AMP	1	2	1		9		6		1	16	36
ERBB2		2					1			9	12
FGFR1							4				4
FGFR2					1						1
KIT	1										1
KRAS									1	6	7
MET			1		8		1			1	11
Fusion							6				6
ALK							4				4
FGFR2							1				1
ROS1							1				1
Mutation	2	62	3	3	5	1	31	8	48	13	176
AKT1		1									1
BRAF		3					1	3	1		8
EGFR		1					4		1		6
ERBB2		1									1
FGFR3					1		4				5
HRAS								1			1
JAK1					1						1
KIT				3				4			7
KRAS	2	41			2		12		42	9	108
NRAS		1								1	2
PIK3CA*		14	3		1	1	10		4	3	36
Total	3	64	4	3	14	1	43	8	49	29	218

NOTE: 1) Gene amplification was defined as average CNV>5 from SNP6.0 array data
2) Only reported oncogenic/hotspot mutations were counted . PIK3CA mutation usually co-occur with other events (KRAS mutation et al.)



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