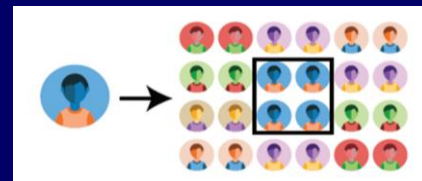


MatchTx



Matching Therapeutics to Cancer Patients™

MatchTx: Cancer genomics software company. SaaS solution that helps researchers, oncologists and clinical trial managers identify the full set of biomarkers that collectively predict the outcome of cancer patients to treatments. Patent-pending algorithms classify millions of combinations of genomic and clinical data to find the full set predictive biomarkers (Deep Genetic Signatures™) from reference data sets. The Signatures are used to identify previous tumors ‘most like my patient’s cancer’ to match therapeutics based on real patient outcomes, not population averages.

MatchTx Applications:

CLINICAL TRIALS & DRUG REPOSITIONING for Patient Population (biomarker) Segments

- Find sets of genetic markers (profiles) that distinguish between positive and negative responders (retrospective clinical studies)
- Cell-line studies: genetic profiles for response
- Use validated biomarker profiles to set up clinical trial protocols using patient segmentation
- Analyze Phase II clinical trial results for patient exclusion in Phase III for contraindicated biomarkers

CANCER GENOME RESEARCH

- Genetic Targeting/Profiles of drug leads
- Tumor characterization
- Drug-specific tumor databases.

BIOMARKER DISCOVERY & VALIDATION

- Identify ALL the genetic biomarkers associated with drug response (mutations and wild type)
- Validate genomic biomarkers
- Develop companion diagnostics

DRUG DEVELOPMENT

- Confirm genetic on-target activity of leads
- Genes whose mutation status impacts drug response
- Identify other tumor types or drugs with similar target biomarker profiles

Multiple genes & variants (mutations AND wild type) contribute to drug response.

FIND THEM ALL.

Actionable sets of genetic biomarkers for best-matched patient cohorts. Plan your research studies, validate clinical trials outcomes, predict drug treatment outcomes.

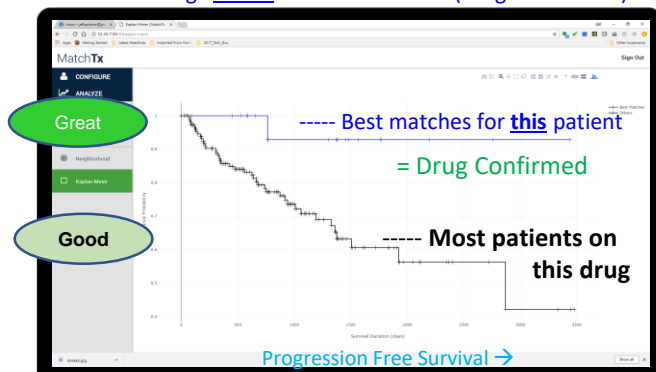
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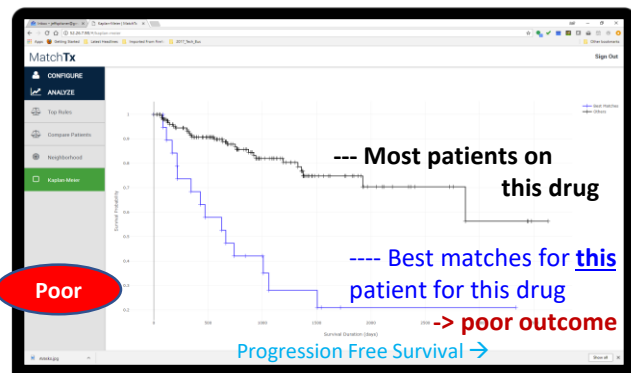
Actionable patient outcome predictions

Examples for High Gleason Score Prostate Cancer:

Ex. 1. Patient #872 was predicted by MatchTx to be good match to drug. **Result:** Patient did well (Progression free)



Ex. 2. Patient #472 predicted by MatchTx as poor candidate for this drug. **Result:** Patient did poorly (Short PFS period)



Right: Biomarkers in the good drug response prostate cancer cohort →

Description	Match Count	Strength
WWC1 mut & RANBP17 wt	23	1.411e-6
CTDP1 mut & SLC6A7 wt	17	2.717e-6
MAP3K6 wt	160	8.292e-3
UNC93A wt	104	6.060e-3
TP53 mut	60	9.596e-3
TM9SF4 wt	151	1.298e-3
KIT wt	159	3.820e-3
CACNA1A wt	126	5.712e-3

FOXO1 wt & SDHC wt	
CRYGN wt & SDHC wt	
CCDC136 wt & SDHC wt	155
BIRC3 wt & SDHC wt	158
ANKLE2 wt & SDHC wt	151
MAP3K6 wt	160
UNC93A mut	74
TP53 mut	60
TM9SF4 wt	151
KIT mut	19
CACNA1A mut	52

Left: Biomarkers in the poor drug response prostate cancer cohort:

The Future of Cancer is Data. The Future of Cancer Data is MatchTx™