Mature Migration: Growing Your Documentation Set with MadCap Flare

PRESENTED BY

Jason Ross and Chelsea Santos

INTRODUCTION

- Introduce the two writing teams
- Discuss project scope
- Step through Science Writing process (more technical)
- Step through Tech Writing process (more architecture-based)
- Demo output

THE WRITING TEAMS

- Science Writing
  - Small team of five writers with science backgrounds
  - Produce pre-sales pieces, e.g., data sheets
- Technical Writing
  - Large team of 18 writers with various backgrounds
  - Produce post-sales pieces, e.g., user guides
- Both teams
  - Use Flare as primary authoring tool
  - Migrated from PDF to HTML as a primary output for content

PROJECT SCOPE

- A more modern and versatile format
  - Searchable, flexible, linkable content
  - Embedded features such as tooltip-type definitions of acronyms and bioinformatics terms
- Content is the same, with added dynamic features
  - PDF content is pulled apart and reassembled (tech writing only)
  - Content remains product-based
  - Content previously siloed in guides now lives in one “portal”
  - Visual design reformatted for HTML format

INITIAL FIELDWORK

- Figured out where we were headed, then what we needed to do to get there
- Reviewed help systems on the MadCap Customer Showcase, identified applicable ideas and features like drop-downs and glossary terms
- Met with stakeholders to collect feature requests and feedback on navigation, design, versioning, and change management

Science Writing

WHY DID WE SWITCH FROM PDF TO HTML?

Suboptimal for online or mobile viewing
High-quality print document

Limited dynamic and interactive features
Hyperlinks only

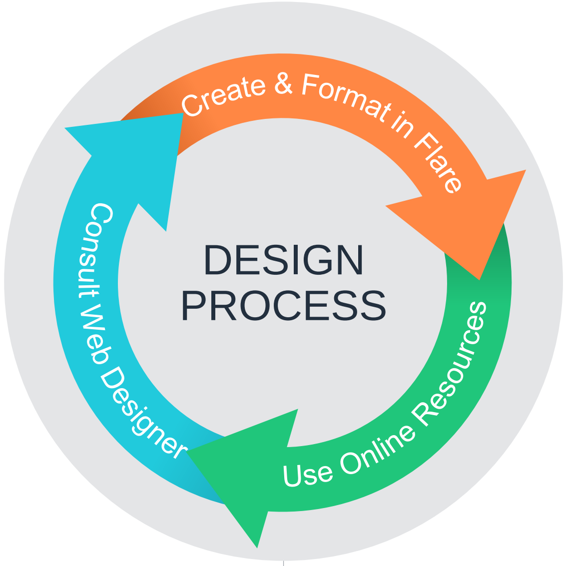
Dissonant user experience
Viewed outside website

Optimized for online viewing
Responsive layout for mobile devices

Dynamic and interactive features
More engaging UX

Integrated with website
More consistent UX

HTML DESIGN/CREATION PROCESS



Create & Format in Flare

- Use Responsive Layout Tool
- Adjust styles in CSS

Use Online Resources

- MadCap Flare Online Help
- w3schools

Consult Web Designer

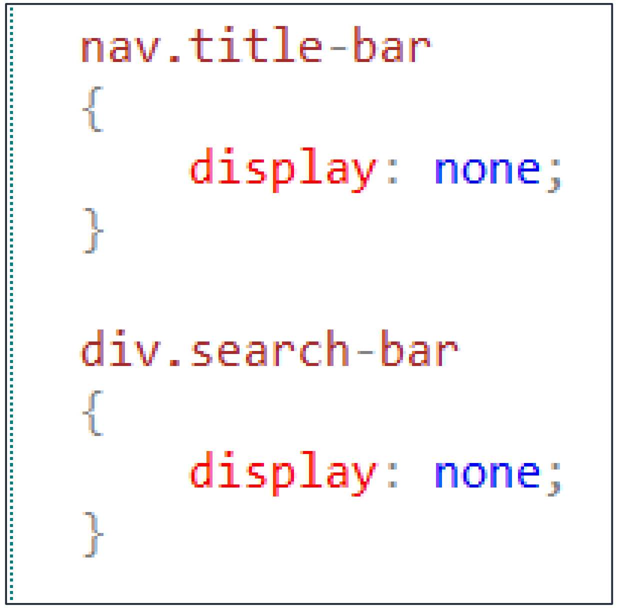
- Bribe with donuts/bagels/etc
- Become their BFF

https://www.w3schools.com/css/css_website_layout.asp

http://help.madcapsoftware.com/flare2018r2/Content/Flare/Responsive-Web-Design/Creating-Responsive-Layouts.htm?Highlight=responsive%20layout

CREATING A SKINLESS HTML DESIGN

- Because our pieces are relatively short (2-4 pages) and cohesive, we wanted to present them as a single, scrolling web page
- How we did it
  - Started with an HTML5 Top Navigation skin
  - Used CSS to hide the skin components (navigation and search bars)
  - Authored content for each piece in a single topic file in Flare



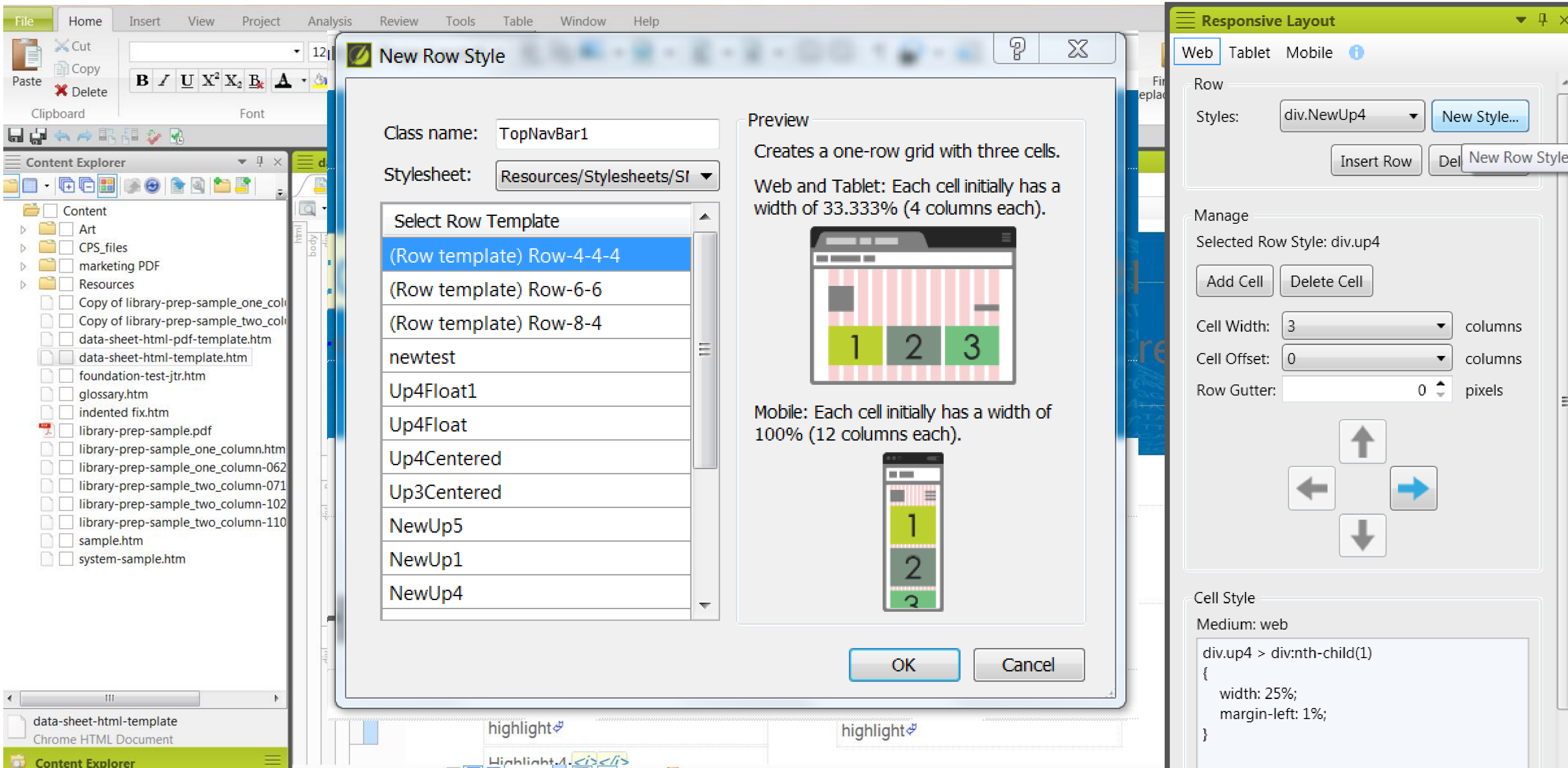
```
nav.title-bar
{
    display: none;
}

div.search-bar
{
    display: none;
}
```

RESPONSIVE HTML LAYOUTS

- Content is displayed dynamically, based on the available viewing space
- Two major frameworks used in web design are Foundation and Bootstrap

RESPONSIVE LAYOUT TOOL



New Row Style

Class name: TopNavBar1

Stylesheet: Resources/Stylesheets/Sl

Preview

Creates a one-row grid with three cells.

Web and Tablet: Each cell initially has a width of 33.333% (4 columns each).

Mobile: Each cell initially has a width of 100% (12 columns each).

Styles: div.NewUp4

Selected Row Style: div.up4

Cell Width: 3 columns

Cell Offset: 0 columns

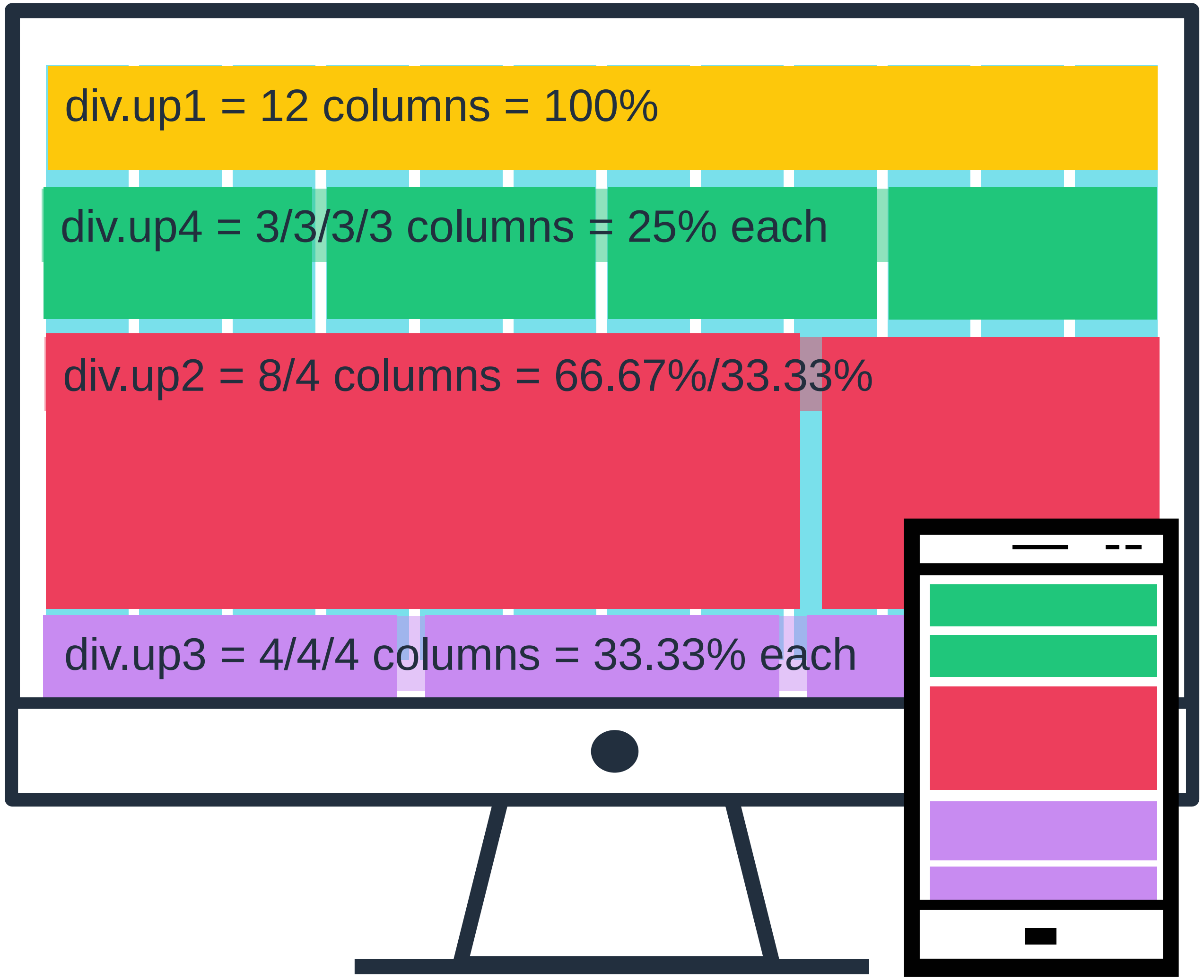
Row Gutter: 0 pixels

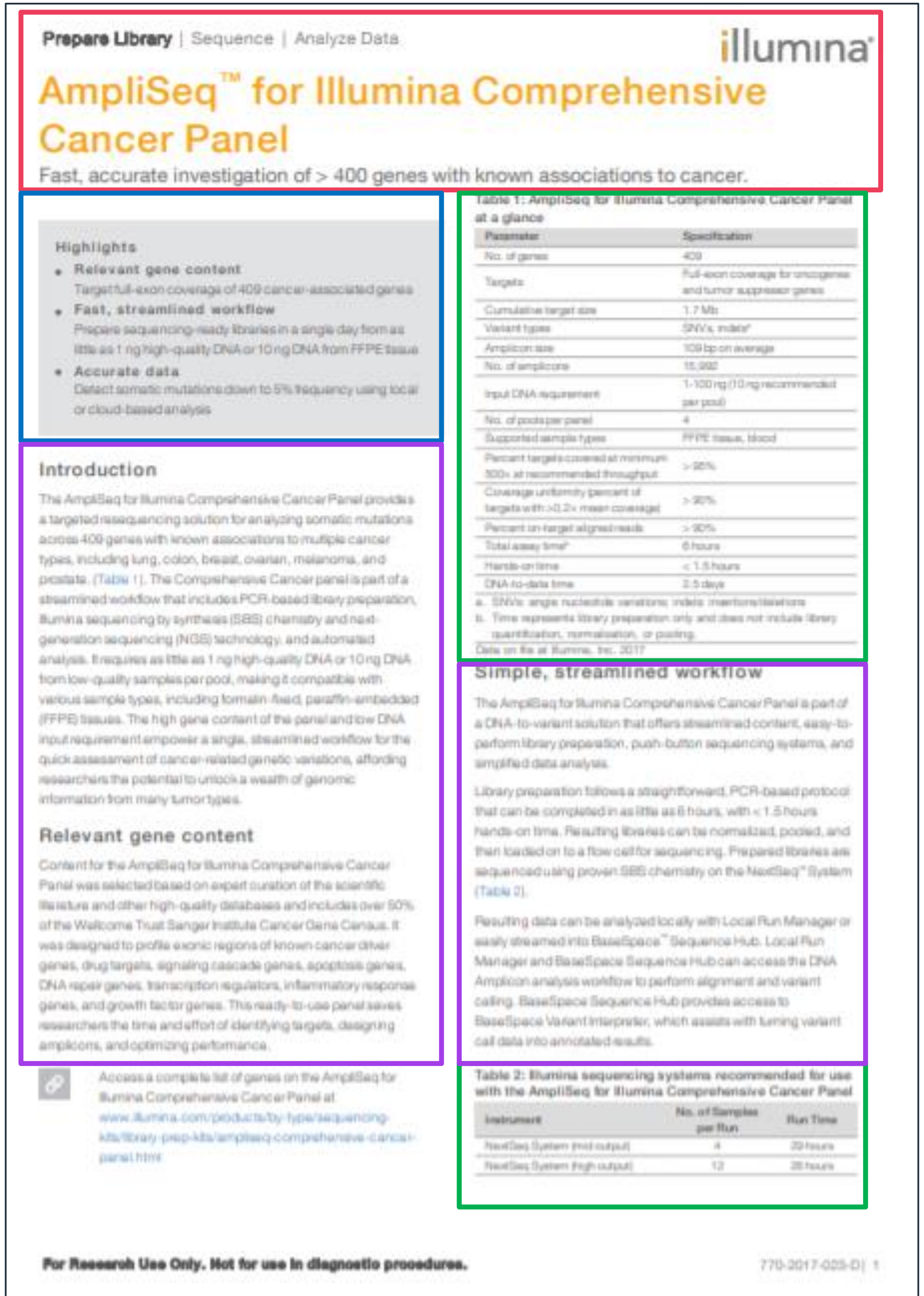
Medium: web

```
div.up4 > div:nth-child(1)
{
   width: 25%;
   margin-left: 1%;
}
```

HOW RESPONSIVE LAYOUTS WORK

- Responsive web frameworks divide available horizontal space into 12 columns of equal width
- Flare integrates with this framework by creating divs with defined widths





Prepare Library | Sequence | Analyze Data

illumina®

AmpliSeq™ for Illumina Comprehensive Cancer Panel

Fast, accurate investigation of > 400 genes with known associations to cancer.

Highlights

- **Relevant gene content**
  Target full-exon coverage of 409 cancer-associated genes
- **Fast, streamlined workflow**
  Prepare sequencing-ready libraries in a single day from as little as 1 ng high-quality DNA or 10 ng DNA from FFPE tissue
- **Accurate data**
  Detect somatic mutations down to 5% frequency using local or cloud-based analysis

Introduction

The AmpliSeq for Illumina Comprehensive Cancer Panel provides a targeted resequencing solution for analyzing somatic mutations across 409 genes with known associations to multiple cancer types, including lung, colon, breast, ovarian, melanoma, and prostate. (Table 1). The Comprehensive Cancer panel is part of a streamlined workflow that includes PCR-based library preparation, Illumina sequencing by synthesis (SBS) chemistry and next-generation sequencing (NGS) technology, and automated analysis. It requires as little as 1 ng high-quality DNA or 10 ng DNA from low-quality samples per pool, making it compatible with various sample types, including formalin-fixed, paraffin-embedded (FFPE) tissues. The high gene content of the panel and low DNA input requirement empower a single, streamlined workflow for the quick assessment of cancer-related genetic variations, affording researchers the potential to unlock a wealth of genomic information from many tumor types.

Relevant gene content

Content for the AmpliSeq for Illumina Comprehensive Cancer Panel was selected based on expert curation of the scientific literature and other high-quality databases and includes over 50% of the Wellcome Trust Sanger Institute Cancer Gene Census. It was designed to profile exonic regions of known cancer driver genes, drug targets, signaling cascade genes, apoptosis genes, DNA repair genes, transcription regulators, inflammatory response genes, and growth factor genes. This ready-to-use panel saves researchers the time and effort of identifying targets, designing amplicons, and optimizing performance.

Access a complete list of genes on the AmpliSeq for Illumina Comprehensive Cancer Panel at www.illumina.com/products/by-type/sequencing-kits/library-prep-kits/ampliseq-comprehensive-cancer-panel.html

Table 1: AmpliSeq for Illumina Comprehensive Cancer Panel at a glance

Parameter	Specification
No. of genes	409
Targets	Full-exon coverage for oncogenes and tumor suppressor genes
Cumulative target size	1.7 Mb
Variant types	SNVs, indels[a]
Amplicon size	109 bp on average
No. of amplicons	15,992
Input DNA requirement	1-100 ng (10 ng recommended per pool)
No. of pools per panel	4
Supported sample types	FFPE tissue, blood
Percent targets covered at minimum 500× at recommended throughput	> 95%
Coverage uniformity (percent of targets with >0.2× mean coverage)	> 90%
Percent on-target aligned reads	> 90%
Total assay time[b]	6 hours
Hands-on time	< 1.5 hours
DNA-to-data time	2.5 days

a. SNVs: single nucleotide variations; indels: insertions/deletions

b. Time represents library preparation only and does not include library quantification, normalisation, or pooling.

Data on file at Illumina, Inc. 2017

Simple, streamlined workflow

The AmpliSeq for Illumina Comprehensive Cancer Panel is part of a DNA-to-variant solution that offers streamlined content, easy-to-perform library preparation, push-button sequencing systems, and simplified data analysis.

Library preparation follows a straightforward, PCR-based protocol that can be completed in as little as 6 hours, with < 1.5 hours hands-on time. Resulting libraries can be normalized, pooled, and then loaded on to a flow cell for sequencing. Prepared libraries are sequenced using proven SBS chemistry on the NextSeq™ System (Table 2).

Resulting data can be analyzed locally with Local Run Manager or easily streamed into BaseSpace™ Sequence Hub. Local Run Manager and BaseSpace Sequence Hub can access the DNA Amplicon analysis workflow to perform alignment and variant calling. BaseSpace Sequence Hub provides access to BaseSpace Variant Interpreter, which assists with turning variant call data into annotated results.

Table 2: Illumina sequencing systems recommended for use with the AmpliSeq for Illumina Comprehensive Cancer Panel

Instrument	No. of Samples per Run	Run Time
NextSeq System (mid output)	4	29 hours
NextSeq System (high output)	12	28 hours

For Research Use Only. Not for use in diagnostic procedures.

770-2017-025-D | 1

Data Sheet

AmpliSeq for Illumina Comprehensive Cancer Panel

Fast, accurate investigation of > 400 genes with known associations to cancer.

Highlights

Relevant gene content

Target full-exon coverage of 409 cancer-associated genes

Fast, streamlined workflow

Prepare sequencing-ready libraries in a single day from as little as 1 ng high-quality DNA or 10 ng DNA from FFPE tissue

Accurate data

Detect somatic mutations down to 5% frequency using local or cloud-based analysis

Figures and Tables

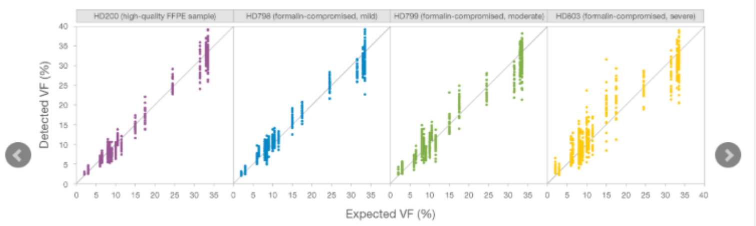


Figure 2: High Concordance Between Expected and Detected Variant Frequency—DNA from HD samples was prepared using the AmpliSeq for Illumina Comprehensive Cancer Panel and sequenced on the NextSeq System. Results show that 100% of expected SNVs were detected. ΔCq values are listed in Figure 1.

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Introduction

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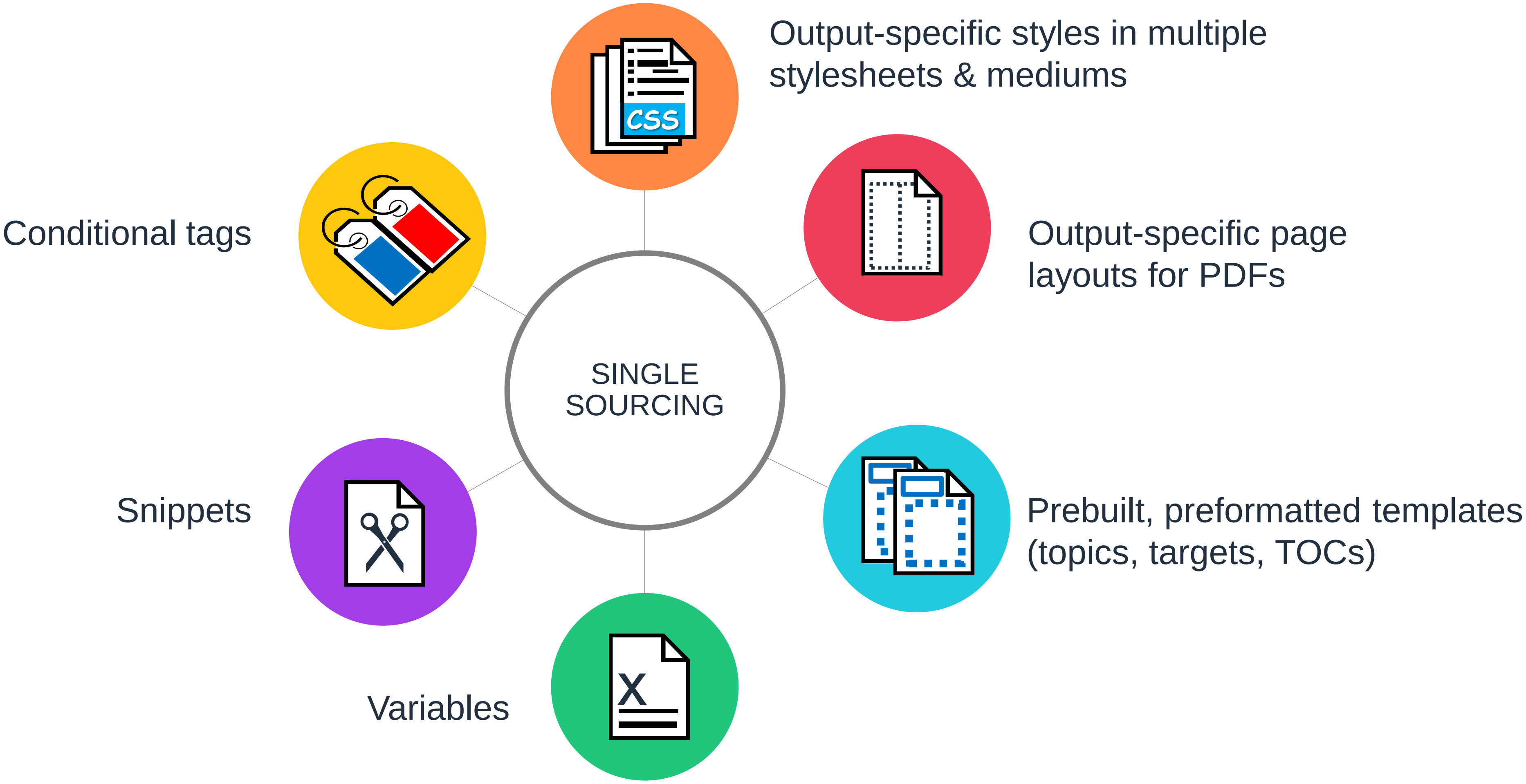
SINGLE SOURCING CONTENT FOR TWO OUTPUTS



SINGLE SOURCING

Output-specific styles in multiple stylesheets & mediums

Output-specific page layouts for PDFs

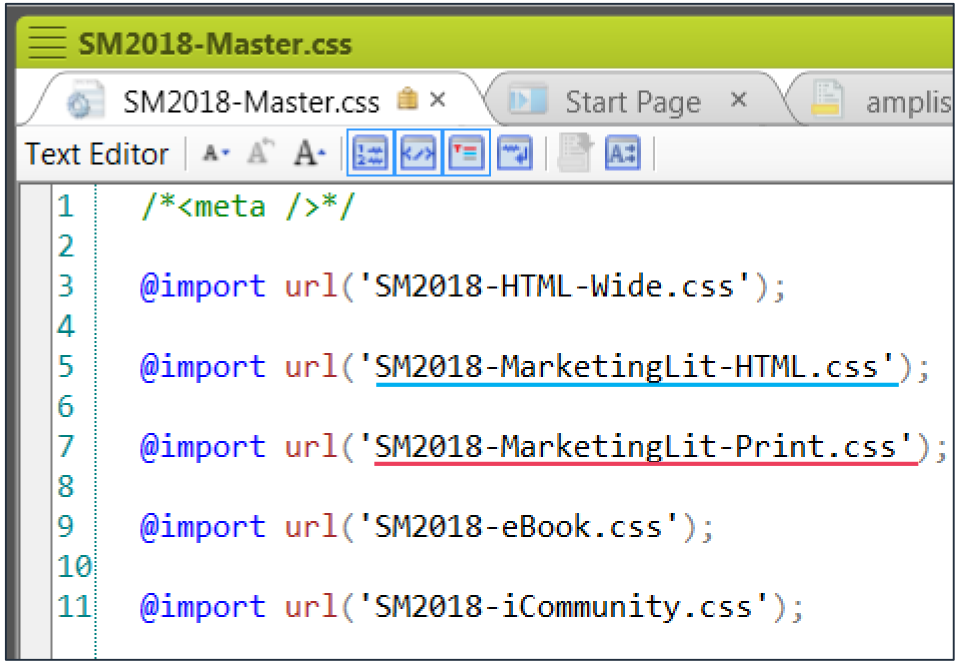
Prebuilt, preformatted templates (topics, targets, TOCs)

Variables

Snippets

Conditional tags

CSS: MULTIPLE STYLESHEETS/MEDIUMS



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@import url('SM2018-MarketingLit-HTML.css');

@import url('SM2018-MarketingLit-Print.css');

@import url('SM2018-eBook.css');

@import url('SM2018-iCommunity.css');
```

Data Sheet

AmpliSeq for Illumina Comprehensive Cancer Panel

Fast, accurate investigation of > 400 genes with known associations to cancer.

AmpliSeq™ for Illumina Comprehensive Cancer Panel

Fast, accurate investigation of > 400 genes with known associations to cancer.

CSS: MULTIPLE STYLESHEETS/MEDIUMS

CSS for HTML

```
div.hero
{
    background-image: url('../Images/hero-default-blue-bkg.jpg');
    background-size: cover;
    margin: 0 0 30px 0;
    padding-top: 60px;
    padding-bottom: 60px;
    /*height: 300px;*/
}
```

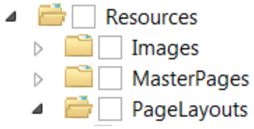
```
h1.title
{
    font-family: "HelveticaNeueW01-MdExt", sans-serif;
    color: #ffffff;
    background-color: inherit;
    font-size: 44px;
    line-height: 50px;
    padding-bottom: 30px;
}
```

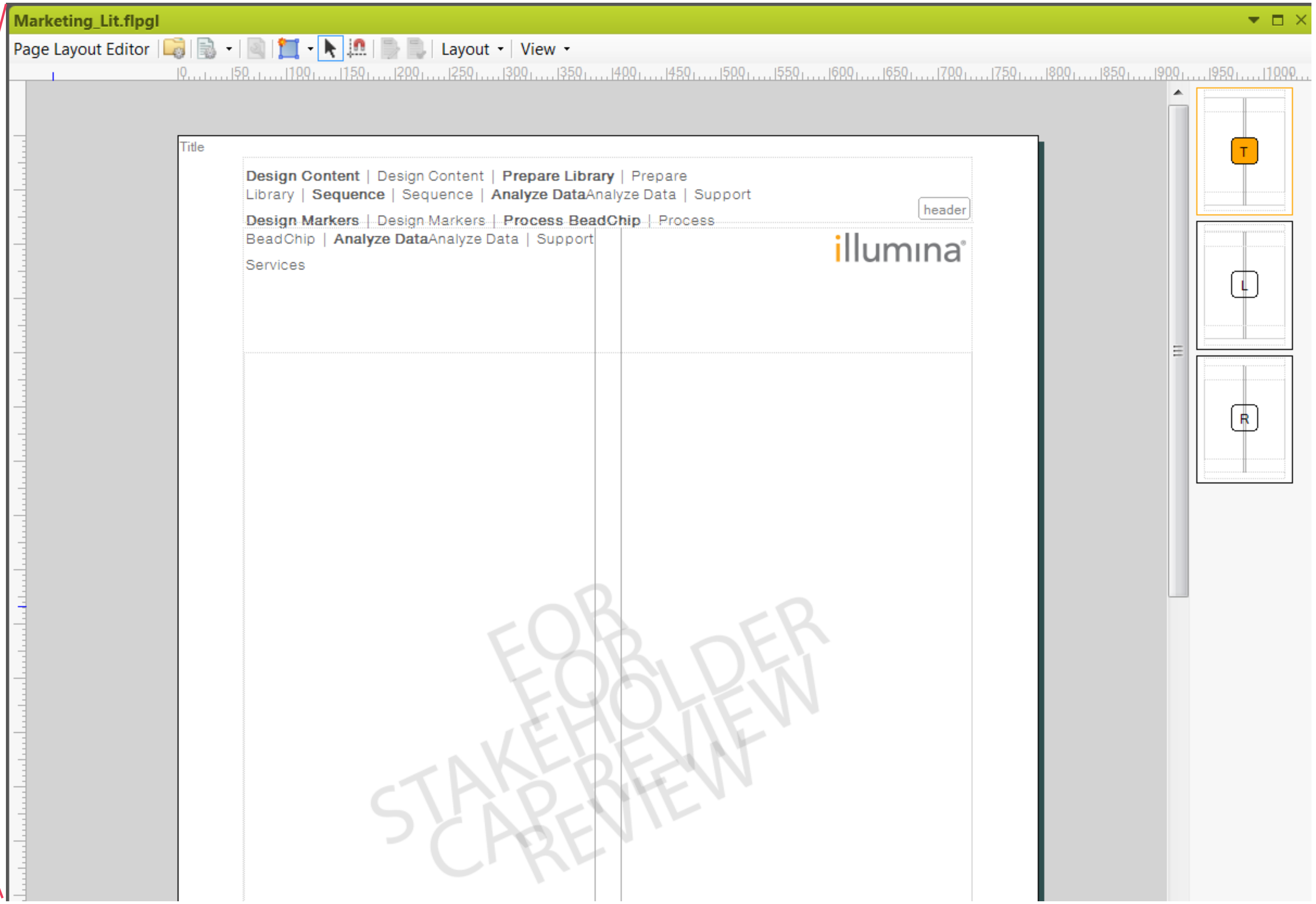
CSS for PDF

```
div.hero
{
background-image: none;
width: 7in;
position: absolute;
top: -0.3in;
margin-right: 3.375in;
float: left;
margin-top: 1in;
margin-bottom: 15pt;
padding-top: 0;
padding-bottom: 40pt;
}
```

```
h1.title
{
    font-family: 'HelveticaNeueLT Com 65 Md';
    font-weight: lighter;
    font-size: 23pt;
    line-height: 27.6pt;
    color: #ffb441;
    color: device-cmyk(0,0.41,1,0);
    mc-heading-level: 0;
    padding-bottom: 0;
}
```

DELIVERABLE-SPECIFIC PAGE LAYOUTS

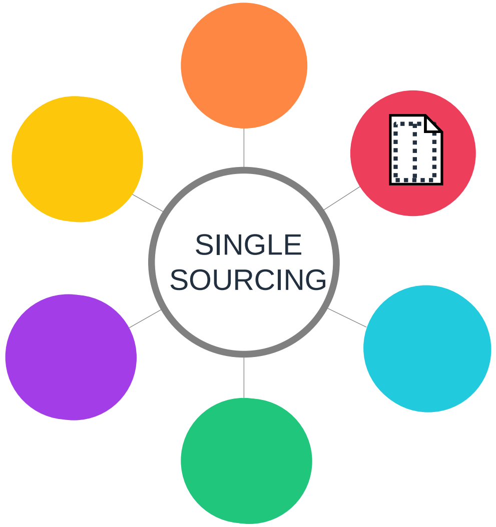




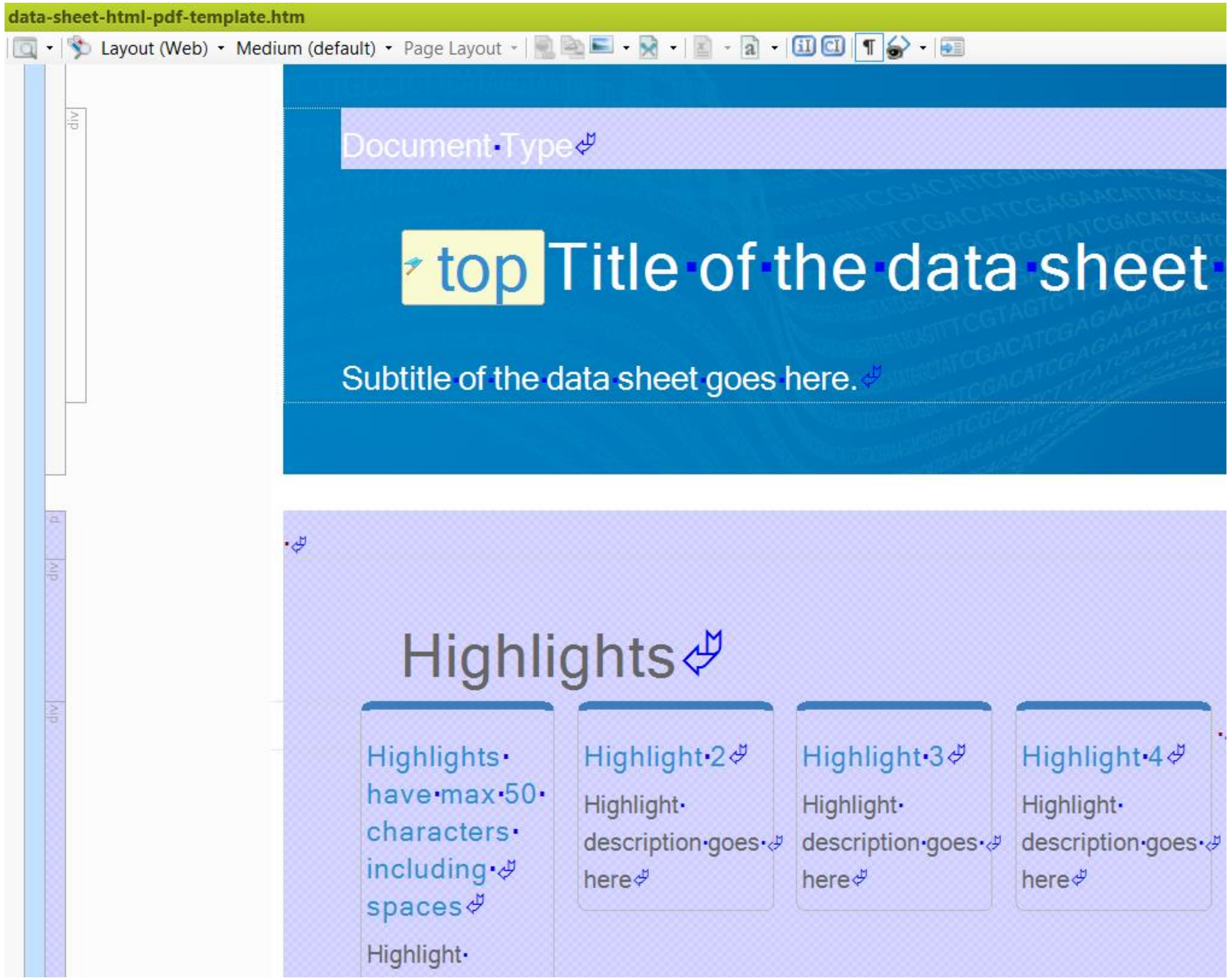
Design Content | Design Content | **Prepare Library** | Prepare Library | **Sequence** | Sequence | **Analyze Data**Analyze Data | Support

Design Markers | Design Markers | **Process BeadChip** | Process BeadChip | **Analyze Data**Analyze Data | Support

Services



TEMPLATES TO SIMPLIFY FORMATTING



Document Type

Title of the data sheet

Subtitle of the data sheet goes here.

Highlights

Highlights have max 50 characters including spaces

Highlight

Highlight 2

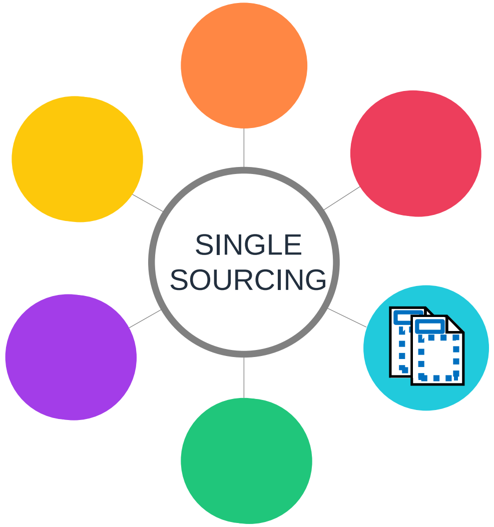
Highlight description goes here

Highlight 3

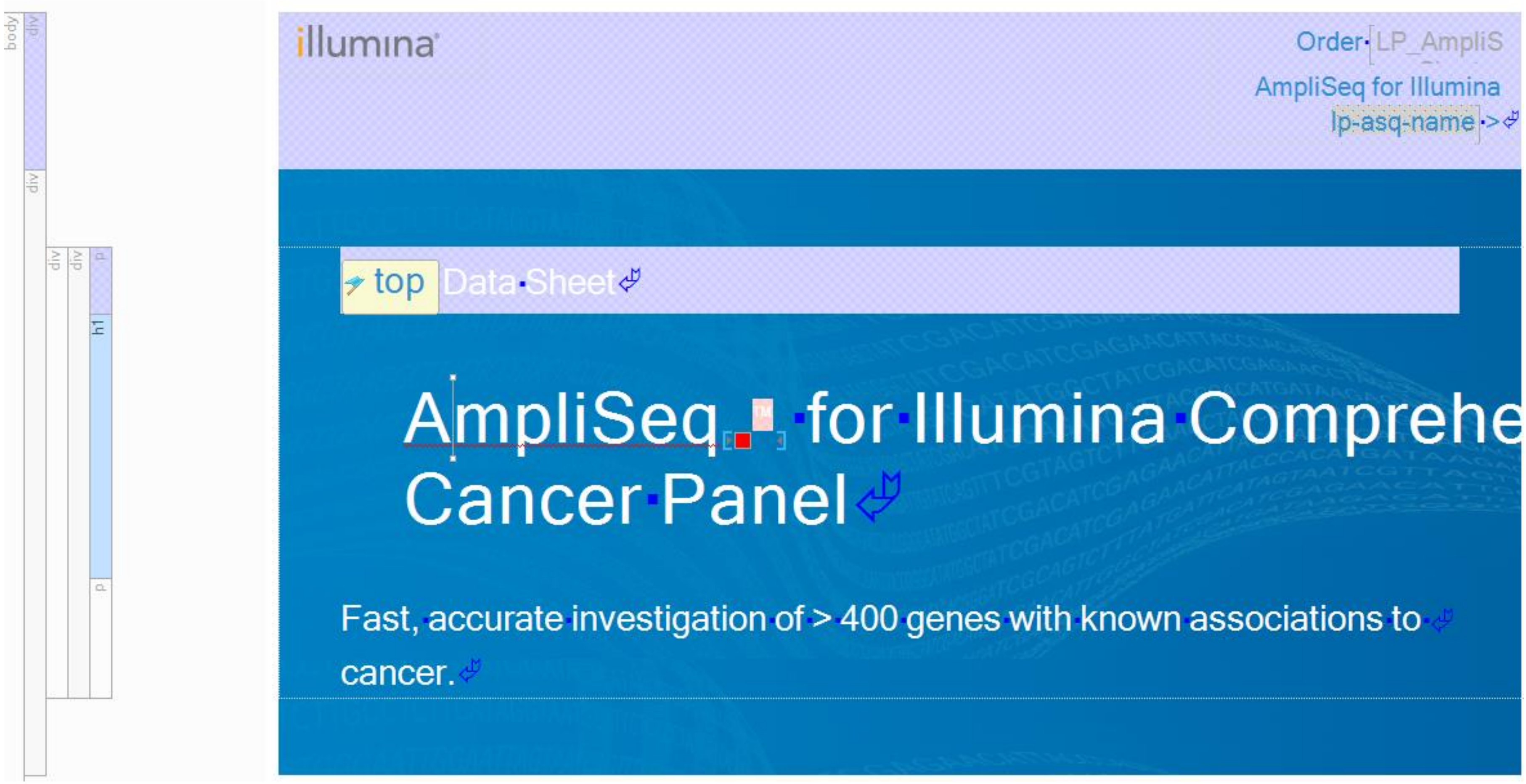
Highlight description goes here

Highlight 4

Highlight description goes here



TAGGING CONTENT WITH CONDITIONS



Order [LP_AmpliS

AmpliSeq for Illumina

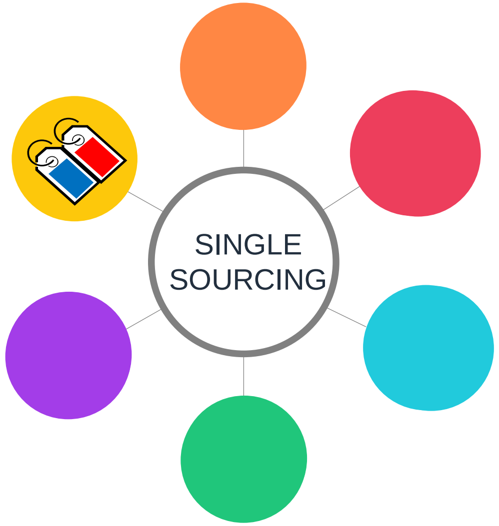
lp-asq-name ->

Data Sheet

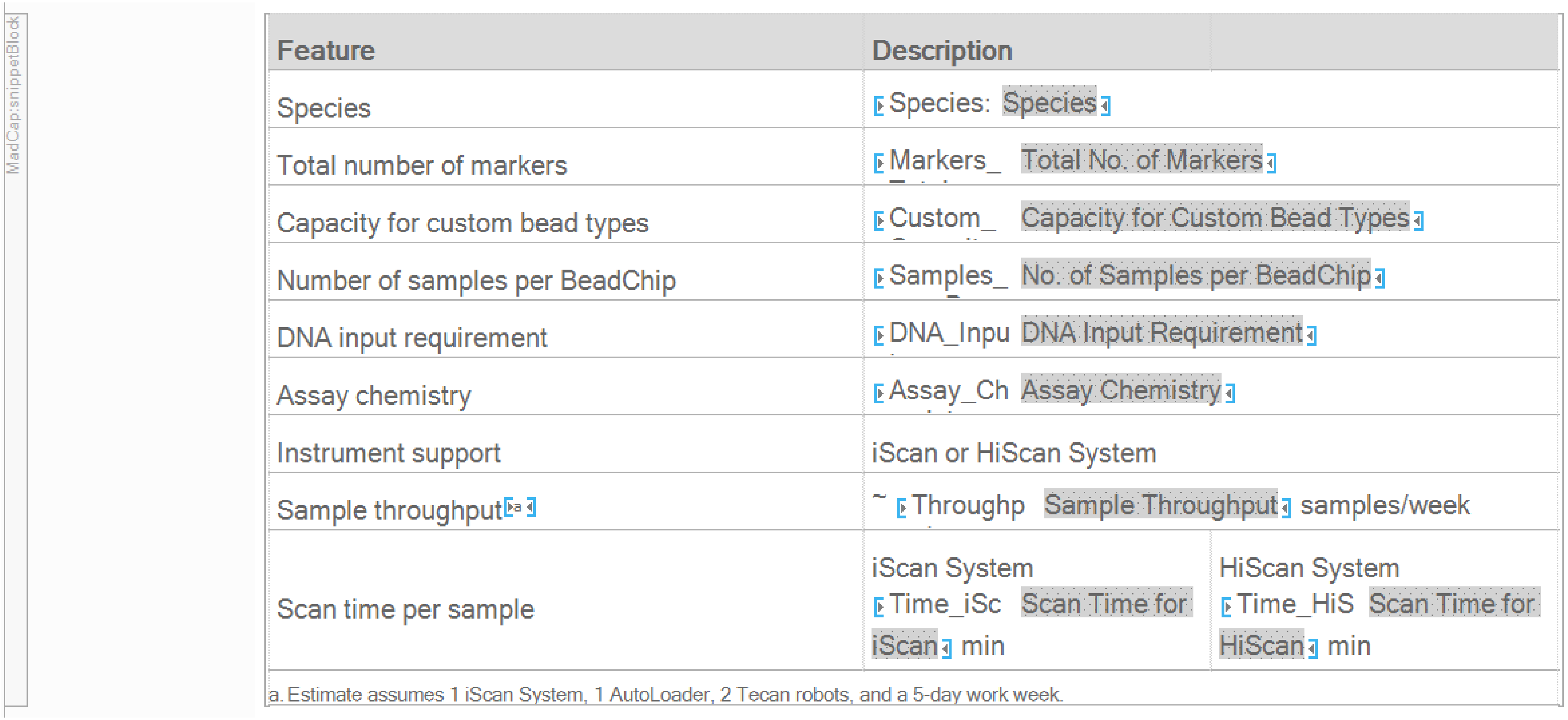
AmpliSeq TM for Illumina Comprehe

Cancer Panel

Fast, accurate investigation of > 400 genes with known associations to cancer.



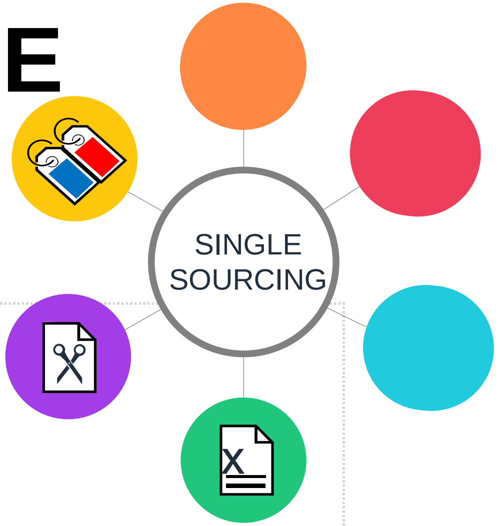
COMBINING SNIPPETS & VARIABLES FOR REUSING TABLES

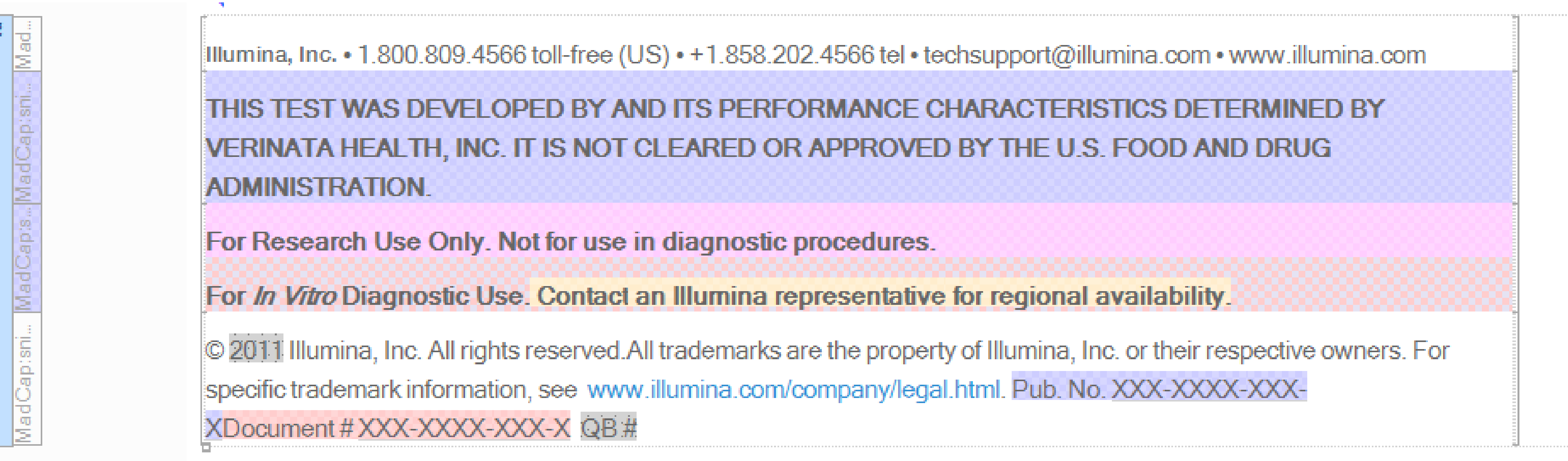


Feature	Description	
Species	Species: Species	
Total number of markers	Markers_ Total No. of Markers	
Capacity for custom bead types	Custom_ Capacity for Custom Bead Types	
Number of samples per BeadChip	Samples_ No. of Samples per BeadChip	
DNA input requirement	DNA_Inpu DNA Input Requirement	
Assay chemistry	Assay_Ch Assay Chemistry	
Instrument support	iScan or HiScan System	
Sample throughput[a]	~ Throughp Sample Throughput samples/week	
Scan time per sample	iScan System Time_iSc Scan Time for iScan min	HiScan System Time_HiS Scan Time for HiScan min

a. Estimate assumes 1 iScan System, 1 AutoLoader, 2 Tecan robots, and a 5-day work week.

COMBINING SNIPPETS, VARIABLES, & CONDITIONS FOR CUSTOMIZABLE REUSE





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DATA SHEET DEMO

- MiniSeq System Data Sheet from Science Writing

TRAINING WRITERS – TIPS AND ADVICE

- Be patient, change is hard
- Hold more than one training session (one not enough)
  - Expect questions and problems, be prepared to help with impromptu, one-on-one training/troubleshooting
- Document EVERYTHING – detailed process docs or internal online help, with step-by-step instructions (including screenshots); record training sessions
- Consider leading a recurring (weekly or biweekly) series of meetings to keep team updated on changes/new features; serve as "office hours" for questions/troubleshooting

WHERE WE ARE GOING FROM HERE

- HTML Format v2.0
  - Building a glossary of terms for use with text pop-up definitions
  - Designing new elements for additional features: customer quotes, videos, etc
  - Evaluating possibility for custom deliverables based on region, customer type, level of expertise, etc
- Use metrics
  - Collecting metrics on how customers interact with HTML format – what works, what doesn’t
  - Exploring customer surveys to gather more info on design

ACKNOWLEDGEMENTS

- Scott Deloach
- Henri Kester
- Suzy Hosie
- Lynn Carrier
- Ben Nye
- Sandeep Komalan
- Burt Crismore

Technical Writing

BACKGROUND

- Rapidly changing company, products, and customers
- Emphasis shifted from products to workflows
- Dated documentation model
  - Slow updates
  - Stale, siloed content
  - Customers missed or duplicated steps
- Needed a big, integrated help system

PROCESS OVERVIEW

Discover

Solicit input from stakeholders

Design

Mock up pages and navigation; usability test

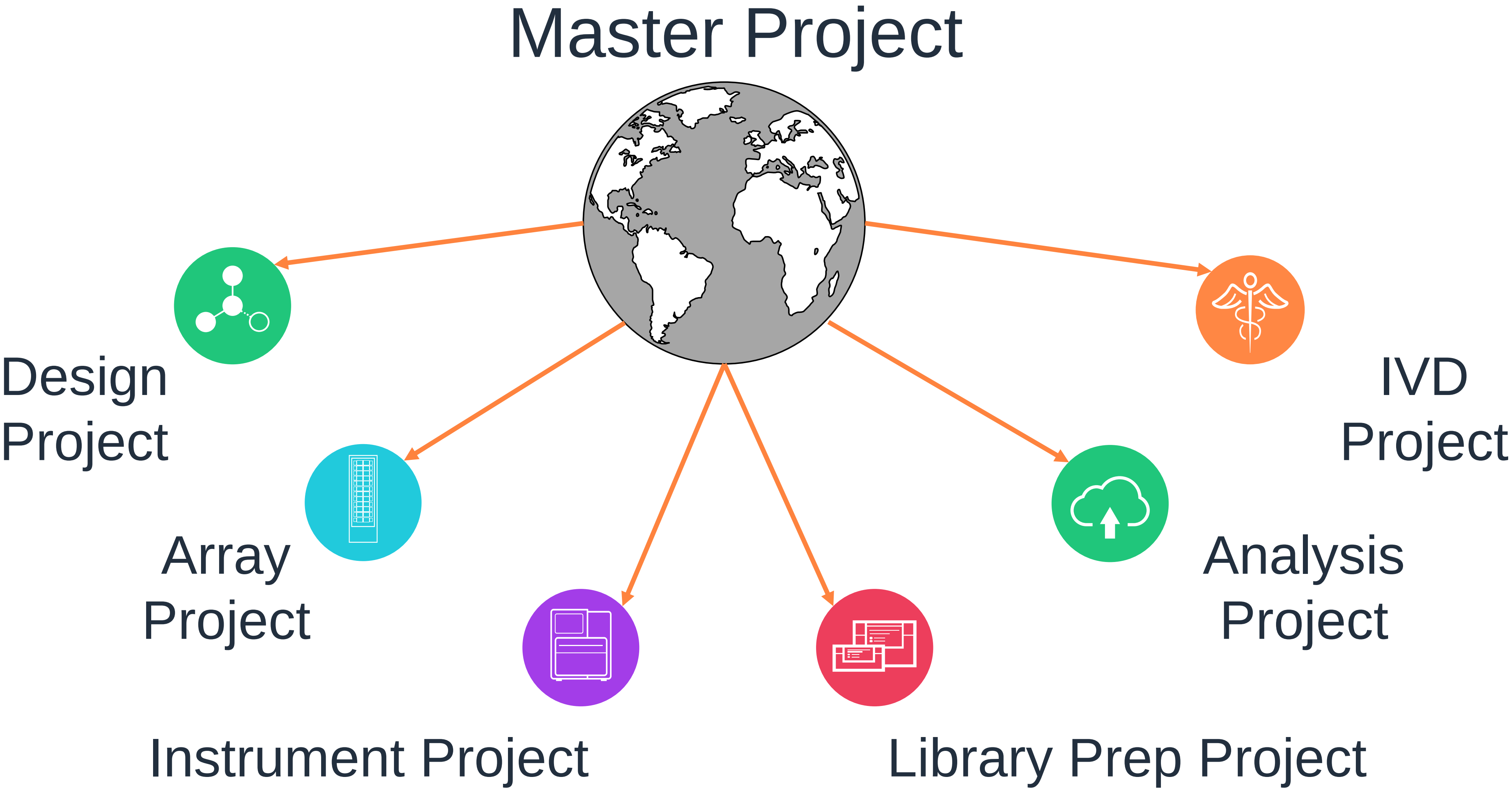
Develop

Build files in Flare and prep topics

Deploy

Publish Phase 1 files to the web

GLOBAL PROJECT LINKING



Master Project

Design Project

Array Project

Instrument Project

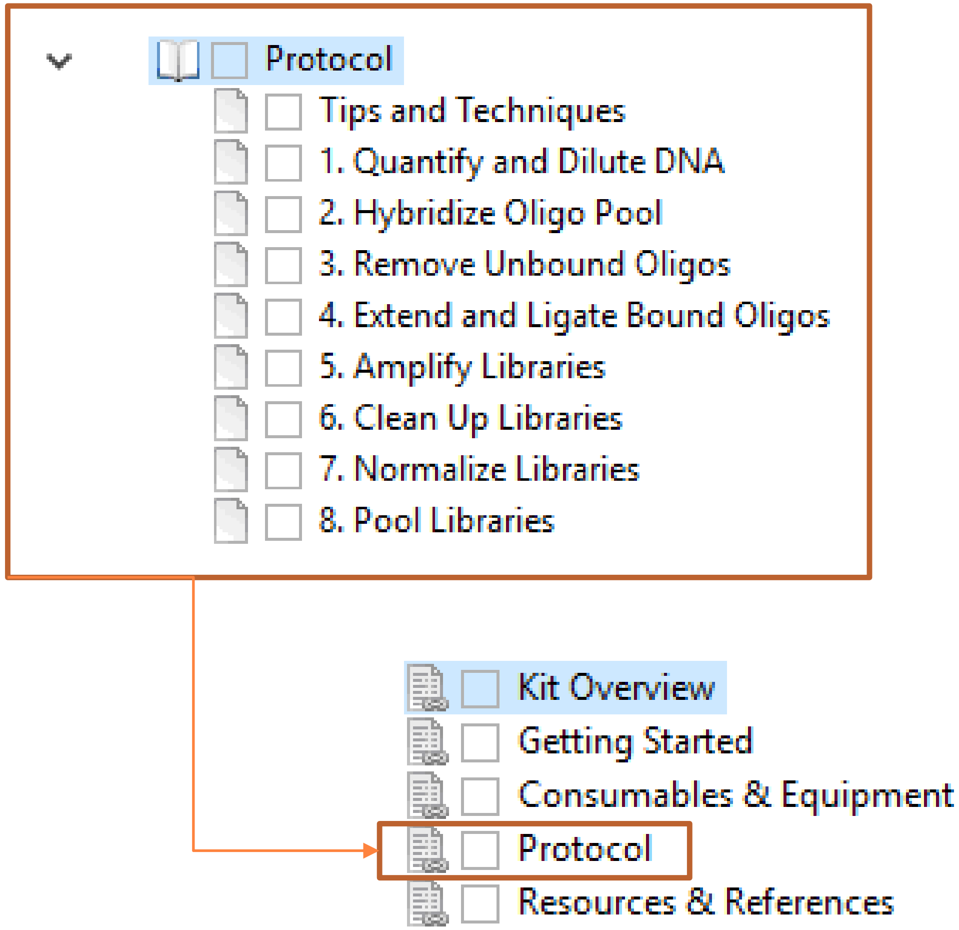
Library Prep Project

Analysis Project

IVD Project

PROJECT SETUP

- Turn UX-tested designs into master pages
- Maintain a one target to one TOC ratio
- Set up each “bucket” as a mini TOC
- Stich mini TOCs into one master TOC



- ☐ Protocol
  - ☐ Tips and Techniques
  - ☐ 1. Quantify and Dilute DNA
  - ☐ 2. Hybridize Oligo Pool
  - ☐ 3. Remove Unbound Oligos
  - ☐ 4. Extend and Ligate Bound Oligos
  - ☐ 5. Amplify Libraries
  - ☐ 6. Clean Up Libraries
  - ☐ 7. Normalize Libraries
  - ☐ 8. Pool Libraries

- ☐ Kit Overview
- ☐ Getting Started
- ☐ Consumables & Equipment
- ☐ Protocol
- ☐ Resources & References

REPOSITORY REFRESH

Simplified styles

Added snippets

Added a Solutions child project

Revamped conditions and variables

CONTENT ARCHITECTURE

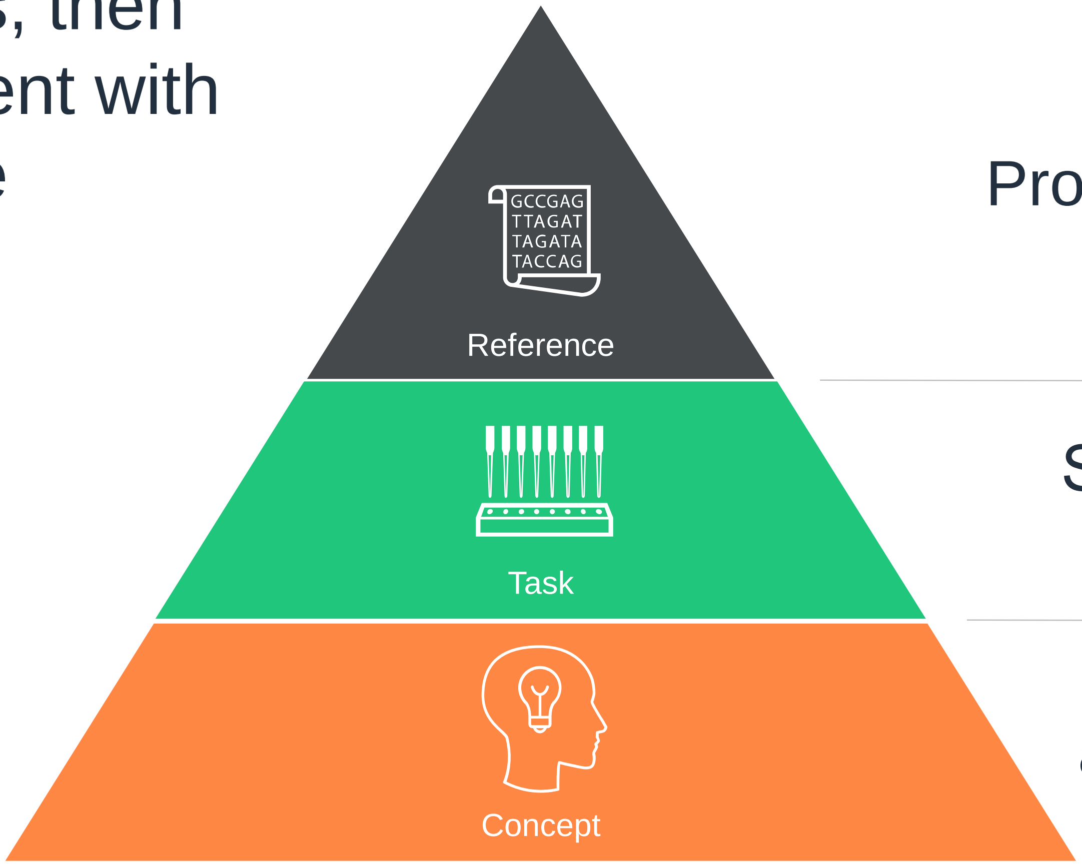
- **Make the content easy to find and use**
- Get customers to the right place quickly, then self-serve
- Help customers plan ahead
- Decide which pieces go together and how
  - Early decision to organize by product type
  - Links ensure workflow continuity

CONTENT ORGANIZATION

- Organize by product: one help system per product
- Organize chronologically, in the order the customer performs the steps
- Map all content to applicable products
- Mix and match content across all guides

CONTENT STRUCTURE

Funnel concepts into tasks, then supplement with reference

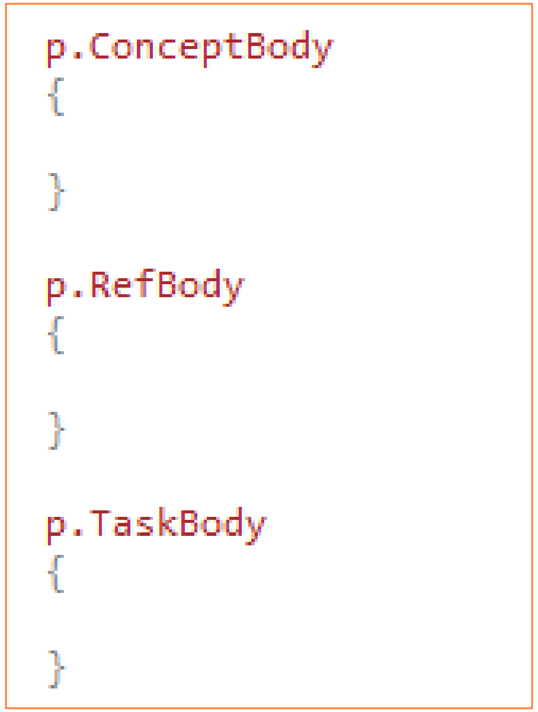


Product facts not directly pertinent to the protocol

Steps in a protocol, and that’s it

What you’re trying to accomplish for the product and what to know for the protocol

DITA-INSPIRED STYLES



```
p.ConceptBody
{

}

p.RefBody
{

}

p.TaskBody
{

}
```

Categorize content

Reduce conditioning

Define a topic’s objective

Optimize reuse

CONTENT LABELING

- Analyze content in PDF guides
- Identify patterns across product types
- Identify categories (“buckets” of information) for each type
- Put applicable topics into each bucket
- Represent everything at least once; nothing more than twice

LANDING PAGE DESIGN

- Set up a template for each product type
  - Same buckets for each product type
  - Mandatory and optional topics for each bucket
- Standardized icons for the buckets
- Tested final design usability and iterated

LIBRARY PREP KIT LANDING PAGE

Kit Overview

Getting Started

Consumables & Equipment

Protocol

Resources & References

SEQUENCING PROTOCOL

Getting Started

- DNA Input
- Pooling Guidelines
- Adapter Sequences
- Analysis App

STAKEHOLDER INPUT

- Are the buckets right?
  - Is the content distributed correctly?
  - Do we need more buckets? Fewer?
- Is the navigation intuitive?
  - Can you easily get to the content you need?
  - Is searchability addressed?
- What’s on your wishlist?

FEATURE REQUESTS FROM STAKEHOLDERS

Request	Implementation	
Version awareness	Version by HTML page	✓
Show differences between versions	Future implementation	✗
Notification of upcoming updates	Future implementation	✗
Time and date stamps	Release info in footer of each page Print to PDF date and time stamps	✓
Editable content	Future implementation	✗
Links, links, and more links	Disciplined linking across projects	✓

USABILITY TESTING

- Dedicated human factors researcher
- Iteratively tested the various components
  - Card sort to test categories and subtopics
  - Interactive wireframes to test landing page designs
  - Content on a page (drop-downs, expandables, popups, subheads)
  - Look and feel elements (breadcrumbs, right navigation)
- Finally tested the whole thing

EXAMPLE QUESTIONS FOR UX

- Do drop-downs declutter or impede Ctrl + F?
  - Does a Expand/Collapse All button solve this problem?
- Is the inline placement of terms and acronyms annoying?
- Is the content where you expect to find it?
  - If your instrument leaked, would you know where to find help?
- Do you know you can expand the graphics?
- Are numbered headings helpful?

OVERALL TEST RESULTS

- Very little contradictory feedback
- Intuitive grasp of concept, task, and reference
- Agreement on key content issues
  - How we label kit, consumables, and equipment topics
  - How we group critical concepts like pooling and index sequences
  - How we explain data output

FEATURE REQUESTS FROM UX TESTING

Request	**Implementation**	
PDFs	UI button to print by mini TOC	✓
Improved definitions	Glossaries	✓
Site map and tooltips	Improve topic structure instead	✗
Targeted keyword searches	Synonyms, index keywords, topic descriptions, descriptive headings	✓
Offline version	Print to PDF (near-term solution)	✗
Inline tips and techniques	Styles for this information	✓

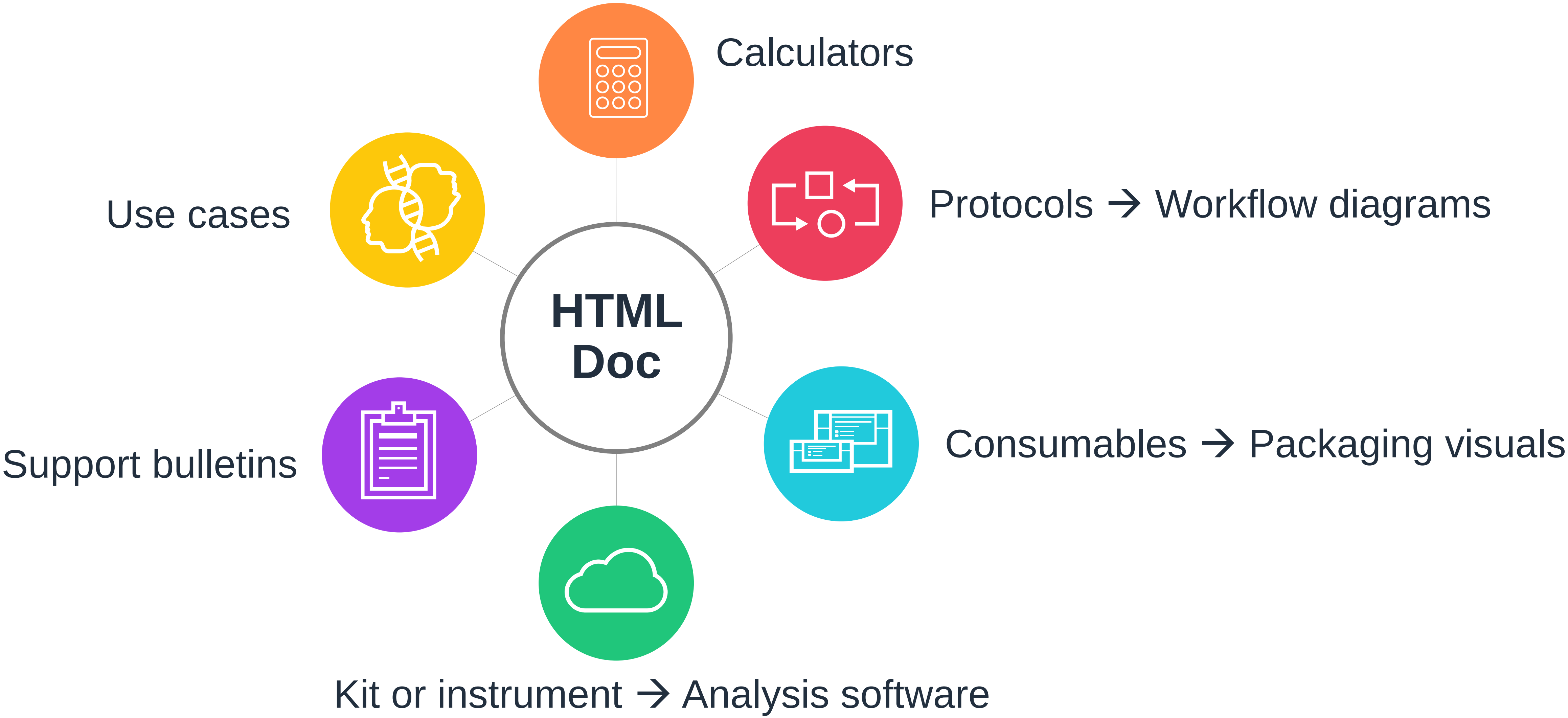
PUTTING THE PIECES TOGETHER

- Integrate all the feedback into something logical
- Supplement testing and input with metrics
- Set up projects and processes to scale and flex
- Use more snippets
- Honor the architecture

ADD TERMS

- Glossary files
  - One to define acronyms
  - One to define bioinformatics and SBS terms
  - SME-reviewed for technical accuracy
- Synonyms file
  - Reviewed Google search terms
  - Solicited writers’ input
  - Brand terms vs. customer terms

ADD LINKS



HTML Doc

Calculators

Protocols → Workflow diagrams

Consumables → Packaging visuals

Kit or instrument → Analysis software

Support bulletins

Use cases

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Thank You!

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