

PatientOne Full Test Prompt

Complete End-to-End Multi-Modality Workflow

Version: 2.0 (Enhanced Multi-Omics) **Patient:** PAT001-OVC-2025 **Last Updated:** December 26, 2025

Overview

This document contains the complete test prompts for running the PatientOne precision medicine workflow using all 9 MCP servers and 40 tools.

Changes in Version 2.0: - ★ TEST_2_MULTIOMICS updated to TEST_2_MULTIOMICS_ENHANCED.txt - ★ Added preprocessing pipeline (3 new tools) - ★ Added upstream regulator prediction (1 new tool) - Multi-omics workflow now 8 steps instead of 4

TEST 1: Clinical-Genomic Analysis

File: TEST_1_CLINICAL_GENOMIC.txt **Servers Used:** mcp-fgbio (4 tools)
Expected Runtime: 15-20 minutes (full analysis mode) / 2-3 minutes (DRY_RUN mode)

Test Prompt

[Paste complete content of TEST_1_CLINICAL_GENOMIC.txt]


Expected Outputs

1. **Variant Call File (VCF)**
 - PIK3CA amplification (copy number = 4)
 - TP53 mutation (p.R273H)
 - PTEN deletion (homozygous loss)
2. **Quality Control Report**
 - Alignment rate: >90%
 - Mean coverage: >100x
 - Variant quality scores: PASS
3. **Clinical Interpretation**
 - High-risk genomic profile
 - PI3K pathway activation predicted

- TP53 loss → compromised tumor suppression
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TEST 2: Multi-Omics Resistance Analysis

UPDATED

File: TEST_2_MULTIOMICS_ENHANCED.txt ( UPDATED - was TEST_2_MULTIOMICS.txt) **Servers Used:** mcp-multiomics (9 tools - was 5 tools)
Expected Runtime: 60-90 minutes (full analysis) / 5-10 minutes (DRY_RUN mode)

Test Prompt

[Paste complete content of TEST_2_MULTIOMICS_ENHANCED.txt]

Workflow Steps (Enhanced)

STEP 0: PREPROCESSING NEW (CRITICAL for real data)

1. **validate_multiomics_data**
 - Detect batch effects
 - Identify outliers
 - Check sample consistency
 - **Expected:** PC1-batch correlation = 0.82 (CRITICAL)
2. **preprocess_multiomics_data**
 - Apply ComBat batch correction
 - KNN imputation (k=5)
 - Outlier removal
 - Quantile normalization
 - **Expected:** PC1-batch correlation reduced to 0.12
3. **visualize_data_quality**
 - Generate before/after PCA plots
 - Verify batch correction effectiveness
 - **Expected:** PC1-batch $r < 0.3$ (PASS)

STEP 1: INTEGRATION

1. **integrate_omics_data**
 - Load PREPROCESSED data (not raw!)
 - Align 13 samples across 3 modalities
 - **Expected:** 19.5K RNA, 6.8K protein, 4.9K phospho features

STEP 2: ASSOCIATION & META-ANALYSIS

1. **run_halla_analysis** (optional)
 - Test RNA-protein associations
 - Chunking strategy (1000 features/chunk)
 - **Expected:** NOMINAL p-values returned
2. **calculate_stouffer_meta**
 - Combine evidence from 3 modalities
 - FDR correction applied AFTER combination

- **Expected:** 7 resistance genes with $q < 0.05$

STEP 3: UPSTREAM REGULATORS ★ NEW

1. predict_upstream_regulators

- Identify activated kinases
- Predict therapeutic targets
- Map to FDA-approved drugs
- **Expected:** AKT1, MTOR, PI3K activated; TP53 inhibited

STEP 4: VISUALIZATION

1. create_multiomics_heatmap (optional)
2. run_multiomics_pca (optional)

Expected Outputs (Enhanced)

Preprocessing Results: - ✅ Batch effects detected: PC1-batch $r=0.82$ - ✅ Batch correction applied: PC1-batch $r \rightarrow 0.12$ - ✅ Missing values imputed: 2000 protein + 1500 phospho - ✅ Outliers removed: 2 samples (Sample_07, Sample_12) - ✅ Final sample count: 13 (7 resistant, 6 sensitive) - ✅ QC plots generated: 4 PNG files

Gene-Level Results:

Gene	RNA FC	Prot FC	Phos FC	Z-score	q-value	Direction
AKT1	+2.1	+1.9	+2.3	4.5	<0.0001	UP ↑
PIK3CA	+2.3	+2.0	+1.8	4.2	0.0001	UP ↑
ABCB1	+2.5	+2.2	+1.9	4.1	0.0001	UP ↑
PTEN	-2.1	-1.9	-1.7	-3.9	0.0002	DOWN ↓
MTOR	+1.9	+1.7	+1.5	3.8	0.0003	UP ↑
BCL2L1	+1.8	+1.6	+1.4	3.2	0.002	UP ↑
TP53	-1.5	-1.3	-1.1	-2.8	0.005	DOWN ↓

Upstream Regulator Results: ★ NEW

• Activated Kinases:

- AKT1: $Z=3.2$, $q=0.001$
- MTOR: $Z=2.8$, $q=0.003$
- PI3K: $Z=3.0$, $q=0.002$

• Inhibited Transcription Factors:





- TP53: $Z=-3.5$, $q=0.0001$ (loss of tumor suppression)

• Drug Recommendations:

- Alpelisib (PI3K inhibitor) - FDA approved
- Capivasertib (AKT inhibitor) - Phase III
- Everolimus (mTOR inhibitor) - FDA approved

• Clinical Trial Match:

- NCT03602859: Alpelisib + Capivasertib in PTEN-deficient tumors

Pathway Summary: -  PI3K/AKT/mTOR pathway ACTIVATED -  Evidence: PIK3CA, AKT1, MTOR upregulated; PTEN downregulated -  Mechanism: PTEN loss → PI3K hyperactivation → AKT/mTOR signaling -  Therapeutic strategy: Dual PI3K/AKT inhibition

TEST 3: Spatial Transcriptomics Analysis

File: TEST_3_SPATIAL_TRANSCRIPTOMICS.txt **Servers Used:** mcp-spatialtools (8 tools) **Expected Runtime:** 30-45 minutes (full analysis) / 5-8 minutes (DRY_RUN mode)

Test Prompt

[Paste complete content of TEST_3_SPATIAL_TRANSCRIPTOMICS.txt]

Expected Outputs

1. **Spatial Clusters**
 - Tumor core (epithelial cells)
 - Immune infiltrate (T cells, macrophages)
 - Cancer-associated fibroblasts (CAFs)
 - Stromal regions
 2. **Spatial Features**
 - Immune exclusion pattern (low T cell infiltration)
 - CAF abundance correlates with resistance
 - Spatial heterogeneity in PI3K pathway activation
 3. **Deconvolution**
 - Cell type proportions by spatial region
 - Immune landscape characterization
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TEST 4: Histology Imaging Analysis

File: TEST_4_HISTOLOGY_IMAGING.txt **Servers Used:** mcp-openimagedata (3 tools), mcp-deepcell (2 tools) **Expected Runtime:** 20-30 minutes (full analysis) / 3-5 minutes (DRY_RUN mode)

Test Prompt

[Paste complete content of TEST_4_HISTOLOGY_IMAGING.txt]

Expected Outputs

1. **Nuclear Segmentation**
 - ~50,000 nuclei segmented
 - High-grade morphology confirmed
 - Pleomorphic nuclei identified

2. Tissue Architecture

- Solid tumor architecture
- Necrotic regions (10-15% of area)
- Minimal desmoplastic reaction

3. Quantitative Features

- Nuclear area, perimeter, circularity
 - Chromatin texture features
 - Spatial distribution metrics
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TEST 5: TCGA Comparison & Survival Analysis

File: TEST_5_TCGA_SURVIVAL.txt **Servers Used:** mcp-tcga (5 tools) **Expected Runtime:** 15-20 minutes (full analysis) / 3-5 minutes (DRY_RUN mode)

Test Prompt

[Paste complete content of TEST_5_TCGA_SURVIVAL.txt]

Expected Outputs

1. TCGA Subtype Match

- C2 (Immunoreactive) subtype most similar
- Median survival: 18 months
- PIK3CA amplification common in this subtype

2. Survival Curves

- Kaplan-Meier analysis
- Patients with PI3K pathway activation: median PFS 6 months
- Patients without: median PFS 12 months

3. Expression Comparison

- Patient gene expression vs TCGA-OV cohort
 - Genes higher in patient: PIK3CA, AKT1, ABCB1
 - Genes lower in patient: PTEN, TP53
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Complete Workflow Integration

All 5 Tests Combined

Order of Execution: 1. TEST 1 (Clinical-Genomic) → Genomic alterations 2. TEST 2 (Multi-Omics) → Resistance mechanisms ★ ENHANCED 3. TEST 3 (Spatial) → Tumor microenvironment 4. TEST 4 (Imaging) → Tissue architecture 5. TEST 5 (TCGA) → Prognostic context

Total Runtime: - Full analysis mode: ~2-3 hours - DRY_RUN mode: ~20-30 minutes

Expected Final Report

Genomic Findings (TEST 1): - PIK3CA amplification (CN=4) - TP53 mutation (p.R273H) - PTEN deletion (homozygous)

Multi-Omics Findings (TEST 2): ★ ENHANCED - **Preprocessing:** Batch correction successful (0.82 → 0.12) - **Pathway:** PI3K/AKT/mTOR activated (all Z > 2.5) - **Therapeutic Targets:** AKT1, MTOR, PI3K - **Drug Recommendations:** Alpelisib + Capivasertib - **Clinical Trial:** NCT03602859

Spatial Findings (TEST 3): - Immune exclusion phenotype - CAF-rich microenvironment - Spatial heterogeneity in resistance markers

Imaging Findings (TEST 4): - High-grade serous architecture - Pleomorphic nuclei - Necrotic regions present

TCGA Findings (TEST 5): - C2 (Immunoreactive) subtype - Median survival: 18 months - PI3K pathway activation common

Integrated Clinical Interpretation

Diagnosis: - Stage IV HGSOC, platinum-resistant - High-risk genomic profile (PTEN loss, TP53 mutation, PIK3CA amplification) - PI3K/AKT/mTOR pathway hyperactivation confirmed across genomic, transcriptomic, proteomic, and spatial data

Treatment Recommendation: - **Primary:** Dual PI3K/AKT inhibition (Alpelisib + Capivasertib) - **Evidence:** Multi-omics data shows pathway activation, drug targets identified - **Clinical Trial:** NCT03602859 (patient eligible) - **Monitoring:** Phospho-AKT/S6 levels, CA-125, imaging every 8 weeks

Prognosis: - Platinum-resistant disease (inherently challenging) - TCGA comparison: 18-month median survival - With targeted therapy: Potential for extended PFS (6-9 months)

Validation Checkpoints

TEST 2 Validation (Multi-Omics) ★ UPDATED

Preprocessing Validation: - ☐ Batch effects detected (PC1-batch $r > 0.7$) - ☐ Batch correction effective (PC1-batch $r < 0.3$) - ☐ Imputation completed (~2000 protein values) - ☐ QC plots generated (4 PNG files) - ☐ Final sample count: 13 (7R + 6S)

Analysis Validation: - ☐ All 7 resistance genes analyzed - ☐ Stouffer's Z-scores > 3 for top genes - ☐ FDR correction applied AFTER combination - ☐ All q-values < 0.05

Upstream Regulator Validation: - [] Kinases identified: AKT1, MTOR, PI3K - []
TF identified: TP53 (inhibited) - [] Drug targets: Alpelisib, Capivasertib,
Everolimus - [] Clinical trial matched: NCT03602859

All Tests Validation

☐

TEST 1: Variants called successfully

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TEST 2: Multi-omics analysis complete (with preprocessing)

☐

TEST 3: Spatial clusters identified

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TEST 4: Nuclei segmented successfully

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TEST 5: TCGA comparison complete

Troubleshooting

Common Issues

Issue 1: TEST_2 batch correction doesn't work - **Symptom:** PC1-batch correlation still high after preprocessing - **Cause:** Batches confounded with phenotype - **Solution:** Check batch-phenotype contingency table - **Expected:** Both batches should have mix of resistant and sensitive samples

Issue 2: No significant genes after Stouffer's - **Symptom:** All q-values > 0.05 - **Cause:** Insufficient statistical power or incorrect FDR workflow - **Solution:** Verify FDR applied AFTER combination (not before) - **Check:** Raw p-values should be combined first

Issue 3: Upstream regulators not identified - **Symptom:** No kinases or TFs with $q < 0.05$ - **Cause:** Insufficient differentially expressed target genes - **Solution:** Lower initial gene selection threshold ($p < 0.05$ instead of $q < 0.05$)

Issue 4: DRY_RUN mode not working - **Symptom:** Tools trying to access real files - **Cause:** Environment variable not set - **Solution:** Set `MULTIOMICS_DRY_RUN=true` before running

File Locations

Test Prompts:

```
/manual_testing/PatientOne-OvarianCancer/implementation/  
├─ TEST_1_CLINICAL_GENOMIC.txt  
├─ TEST_2_MULTIOMICS_ENHANCED.txt  ★ UPDATED (was  
TEST_2_MULTIOMICS.txt)
```

- TEST_3_SPATIAL_TRANSCRIPTOMICS.txt
- TEST_4_HISTOLOGY_IMAGING.txt
- TEST_5_TCGA_SURVIVAL.txt


Expected Outputs:

- /architecture/patient-one/patient-one-outputs/
- for-developer/
 - MCP_Servers_Reference_Guide.pdf (updated)
 - MCP_Report_PAT001.pdf (updated)
 - Full_Test_Prompt.pdf (this document)
 - for-care-team/
 - multiomics_resistance_analysis.png (updated)
 - spatial_transcriptomics_analysis.png
 - histology_imaging_analysis.png
 - MCP_Report_PAT001.pdf (updated)
 - for-patient/
 - patient_summary.html (updated)
 - medication_guide.html (updated)
 - patient_infographic.png

Appendix: Tool Counts by Server

Server	Tools (v1.0)	Tools (v2.0)	Change
mcp-fgbio	4	4	-
mcp-spatialtools	8	8	-
mcp-openimagedata	3	3	-
mcp-seqera	3	3	-
mcp-huggingface	3	3	-
mcp-deepcell	2	2	-
mcp-mockepic	3	3	-
mcp-tcga	5	5	-
mcp-multiomics	5	9	+4 ★
TOTAL	36	40	+4

New Tools in v2.0: 1. validate_multiomics_data (preprocessing) 2. preprocess_multiomics_data (preprocessing) 3. visualize_data_quality (preprocessing) 4. predict_upstream_regulators (therapeutic targets)

Document Status:  Updated for Version 2.0 **Last Validated:** December 26, 2025
Ready for Use: Yes - all test prompts and expected outputs updated