```json
{
    "id": "obj.1275",
    "name": "RNA-seq analysis of ER [HGNC:3467], PR [HGNC:8910], and HER2
[HGNC:3430] status in human [taxID:9606] breast cancer [DOID:1612]",
    "version": "1.0",
    "createdby": "hadley_king@gwmail.gwu.edu",
    "created": "Jan 25, 2017 11:19:27",
    "modified": "Mar 03, 2017 14:08:12",
    "digital_signature": "7LGk9QfzKQ40qdz5b8pS",
    "verification_status": "unreviewed",
    "publication_status": "draft",
    "usability_domain": [
        "RNA-seq data analysis to identify the status of ER, PR and HER2
        expression.",
        "Diagnostic analysis of breast cancer samples for drug treatment.",
        "Quantitation of RNA-seq derived expression of ER, PR and HER2 in breast
        cancer samples to predict therapeutic efficacy based on presence of
        available receptors."
    ],
    "description_domain": {
        "keywords": [
            "breast cancer",
            "RNA-seq",
            "receptor",
            "ER",
            "PR",
            "HER2",
            "biomarker",
            "therapy"
        ],
        "xref": [
            "HGNC:3467",
            "HGNC:8910",
            "HGNC:3430",
            "taxID:9606",
            "DOID:1612"
        ],
        "pipeline_steps": [
            {
                "tool_name": "Cufflinks",
                "tool_desc": "assembles transcripts from RNA-seq data",
                "tool_version": "cufflinks v2.2.1",
                "tool_package": "boost, samtools",
                "step_number": "2",
                "input_uri_list": [
                    "/home/hmhamilt/BRCA/accepted_hits.bam"
                ],
                "output_uri_list": [
                    "/home/hmhamilt/BRCA/assemblies.txt]"
                ]
```

```
                },
                {
                    "tool_name": "TopHat",
                    "tool_desc": "Maps short sequences from spliced transcripts to
                        whole genomes",
                    "tool_version": "TopHat v2.0.13",
                    "tool_package": "bowtie2, bowtie2-align, bowtie2-inspect,
                        bowtie2-build, samtools",
                    "step_number": "1",
                    "input_uri_list": [
                        "/home/hamilt/GRCH38/GRCH38.fa",
                        "/home/hmhamilt/GRCH38/GRCH38annots.gtf",

"/home/hmhamilt/BRCA/ER_ve_HER2_no_ve/111219_UNC11-SN627_0174_AD0JRJACXX_GGCTAC_L002
_1.fastq",

"/home/hmhamilt/BRCA/ER_ve_HER2_no_ve/111219_UNC11-SN627_0174_AD0JRJACXX_GGCTAC_L002
_2.fastq",

"/home/hmhamilt/BRCA/HER2_ve/111304_UNC11-SN456_0325_KE2KTLCANN_GGCTAC_L003_1.fastq"
,
                        "/home/hmhamilt/BRCA/HER2_ve/111304_UNC11-SN456_0325_KE2KTLCANN_
GGCTAC_L003_2.fastq",
                        "/home/hmhamilt/BRCA/ER_HER2_no_ve/111267_UNC11-SN897_2134_JL9FI
WCLLS_GGCTAC_L001_1.fastq",

"/home/hmhamilt/BRCA/ER_HER2_no_ve/111267_UNC11-SN897_2134_JL9FIWCLLS_GGCTAC_L001_2.
fastq"
                    ],
                    "output_uri_list": [
                        "/home/hmhamilt/BRCA/accepted_hits.bam"
                    ]
                },
                {
                    "tool_name": "Cuffmerge",
                    "tool_desc": "merge reported transcripts with gtf annotations",
                    "tool_version": "cufflinks v2.2.1",
                    "tool_package": "boost, samtools",
                    "step_number": "3",
                    "input_uri_list": [
                        "/home/hmhamilt/BRCA/assemblies.txt"
                    ],
                    "output_uri_list": [
                        "/home/hmhamilt/BRCA/merged.gtf"
                    ]
                },
                {
                    "tool_name": "Cuffdiff",
                    "tool_desc": "perform differential expression tests",
                    "tool_version": "cufflinks v2.2.1",
                    "tool_package": "boost, samtools",
```

```json
                    "step_number": "4",
                    "input_uri_list": [
                        "/home/hmhamilt/BRCA/merged.gtf"
                    ],
                    "output_uri_list": [
                        "/home/hmhamilt/BRCA/genes.fpkm_tracking"
                    ]
                }
            ]
        },
        "execution_domain": {
            "script": "http://128.164.35.92/home/hmhamilt/BRCA/rna-seq.cwl",
            "pipeline_version": "0.0",
            "pipeline_url": "https://hive.biochemistry.gwu.edu/$pipelineName",
            "platform": "HIVE",
            "driver": "http://128.164.35.92/cwl-tool",
            "prerequisites": [
                "TopHat2",
                "Cufflinks",
                "Cuffmerge",
                "Cuffdif",
                "cwl-tool"
            ],
            "env_parameters": [
                "cwlVersion: cwl:draft-3"
            ]
        },
        "parametric_domain": {
            "tophat_threads": "4",
            "tophat_no-coverage-search": "on",
            "cufflinks_threads": "4",
            "cuffmerge_threads": "4"
        },
        "io_domain": {
            "reference_uri_list": [

"ftp://ftp.ncbi.nlm.nih.gov/genbank/genomes/Eukaryotes/vertebrates_mammals/Homo_sapiens/GRCh38/GRCH38annots.gtf",

"ftp://ftp.ncbi.nlm.nih.gov/genbank/genomes/Eukaryotes/vertebrates_mammals/Homo_sapiens/GRCh38/GRCH38annots.fa"
            ],
            "input_uri_list": [

"http://128.164.35.92/home/hmhamilt/BRCA/ER_ve_HER2_no_ve/111219_UNC11-SN627_0174_AD0JRJACXX_GGCTAC_L002_1.fastq",

"http://128.164.35.92/home/hmhamilt/BRCA/ER_ve_HER2_no_ve/111219_UNC11-SN627_0174_AD0JRJACXX_GGCTAC_L002_2.fastq"
            ],
            "output_uri_list": [
```

```
            "http://128.164.35.92/home/hmhamilt/BRCA/merged.gtf"
        ]
    },
    "error_domain": [
        "Threshold of quantifiable expression is determined by summary statistics.
",
        "Samples with FPKM reported below designated threshold for a given receptor
gene will not be subject to diagnostic analysis.",
        "false positive discovery <= 0.05",
        "false negative discovery <= 0.10"
    ]
}
```