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  "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 [D0ID:1612]",
  "version": "1.0",
  "createdby": "hadley_king@gwmail.gwu.edu",
  "created": "Jan 25, 2017 11:19:27",
  "modified": "Mar 13, 2017 16:33:52",
  "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."
  ],
  "authors": [
    {
      "orcid": "0000-0003-1409-4549"
    },
    {
      "name": "Hayley Dingerdissen"
    }
  ],
  "description_domain": {
    "keywords": [
      "breast cancer",
      "RNA-seq",
      "receptor",
      "ER",
      "PR",
      "HER2",
      "biomarker",
      "therapy"
    ],
    "xref": [
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      "taxID:9606",
      "D0ID:1612"
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    "pipeline_steps": [
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        "tool_desc": "assembles transcripts from RNA-seq data",
        "tool_version": "cufflinks v2.2.1",

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        "tool_package": "boost, samtools",
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        "output_uri_list": [
            "/home/hmhamilt/BRCA/assemblies.txt"
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    },
    {
        "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_JL9FIWCLLS_GGCTAC_L001_1.f
astq",

"/home/hmhamilt/BRCA/ER_HER2_no_ve/111267_UNC11-SN897_2134_JL9FIWCLLS_GGCTAC_L001_2.
fastq"
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        "output_uri_list": [
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        "tool_version": "cufflinks v2.2.1",
        "tool_package": "boost, samtools",
        "step_number": "3",
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        "output_uri_list": [
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        "Cufflinks",
        "Cuffmerge",
        "Cuffdif",
        "cwl-tool"
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    "env_parameters": [
        "cwlVersion: cwl:draft-3"
    ]
},
"parametric_domain": {
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    "cufflinks_threads": "4",
    "cuffmerge_threads": "4"
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        "ftp://ftp.ncbi.nlm.nih.gov/genbank/genomes/Eukaryotes/vertebrates\_mammals/Homo sapiens/GRCh38/GRCh38annots.fa"
    ],
    "input_uri_list": [
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"http://128.164.35.92/home/hmhamilt/BRCA/ER ve HER2 no ve/111219 UNC11-SN627 0174 AD  
0JRJACXX GGCTAC L002 2.fastq"

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    ],
    "output_uri_list": [
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"error_domain": [
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    "false negative discovery <= 0.10"
]
}
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