```
{
    "id": "obj.1277",
    "name": "Human[tax:9606] CAG repeats[S0:0000726] detection for Huntington's
disease[DOID:12858]",
    "version": "1.0",
    "createdby": "hadley_king@gwmail.gwu.edu",
    "created": "Jan 26, 2017 17:44:38",
    "modified": "Mar 03, 2017 10:16:14",
    "digital_signature": "QdB7vu4rLeLtMFmPHQ9S",
    "verification_status": "unreviewed",
    "publication_status": "draft",
    "usability_domain": [
        "Determine CAG repeats[S0:0000726] in a sequence for the diagnosis of
Huntingtons disease[ICD:G10] for htt gene[G0ID:G0272344]: 10 - 35 CAG trinucleotide
repeats: No Risk, 36 - 40 CAG trinucleotide repeats: Moderate Risk, 40 CAG
trinucleotide repeats: High Risk"
    ],
    "authors": [
        {
            "orcid": "0000-0002-9920-565X"
        }
    ],
    "description_domain": {
        "keywords": [
            "disease",
            "human disease"
        ],
        "xref": [
            "S0:0000726",
            "tax:9606",
            "DOID: 12858",
            "GOID:G0272344",
            "ICD:G10"
        ],
        "pipeline_steps": [
            {
                "tool_name": "HIVE_hexagon",
                "tool_desc": "Alignment of reads to a set of references",
                "tool_version": "1.3",
                "tool_package": "null",
                "step_number": "1",
                "input_uri_list": [
                    "hive://nuc-read/514683",
                    "hive://nuc-read/514682",
                    "http://www.ncbi.nlm.nih.gov/nuccore/SRR2028290",
                    "http://www.ncbi.nlm.nih.gov/nuccore/NM 0002111.8"
                ],
                "output_uri_list": [
                    "hive://data/509234/allCount-aligned.csv"
                ]
```

```
},
            "tool_name": "HIVE_heptagon",
            "tool_desc": "variant calling",
            "tool_version": "1.3",
            "tool_package": "null",
            "step_number": "2",
            "input_uri_list": [
                "hive://data/509234/allCount-aligned.csv"
            ],
            "output_uri_list": [
                "hive://data/509234/SNPProofile.csv"
            ]
        }
    1
},
"execution_domain": {
    "script": "hive://workflows/huntingtons_disease_detection.hwf",
    "pipeline_version": "1.0",
    "platform": "HIVE",
    "driver": "hive://hive-driver",
    "prerequisites": [
        {"name":"HIVE_hexagon","version":"1.3"},
        {"name":"HIVE_heptagon","version":"1.3"}
    ],
    "env_parameters": [
        "HIVEv1.3"
    ]
},
"parametric_domain": {
    "divergence_threshold_percent": "10",
    "alignment_seed": "14 letters",
    "alignment_min_match_len": "50",
    "variant_calling_min_coverage": "20",
    "variant_calling_frequency_cutoff": "0.2"
},
"io_domain": {
    "reference_uri_list": [
        "http://www.ncbi.nlm.nih.gov/nuccore/SRR2028290",
        "http://www.ncbi.nlm.nih.gov/nuccore/NM_0002111.8"
    ],
    "input_uri_list": [
        "hive://nuc-read/514683",
        "hive://nuc-read/514682"
    ],
    "output_uri_list": [
        "hive://data/509234/SNPProofile.csv"
    1
},
"error_domain": [
    "false negative discovery < 0.000001"
```

}