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from patients with Hemophilia A [D0ID:12134]",
  "version": "1.0",
  "createdby": "hadley_king@gwmail.gwu.edu",
  "created": "Mar 12, 2017 16:50:32",
  "modified": "Mar 12, 2017 19:01:02",
  "verification_status": "unreviewed",
  "publication_status": "draft",
  "usability_domain": [
    "Identify SNPs [S0:0000694] that corrilate with the development of an
inhibitory response to recombinant antihemophilic factor VII in patiens with
hemophilia A [D0ID:12134]"
  ],
  "authors": [
    {
      "orcid": "0000-0003-1409-4549"
    },
    {
      "name": "Joe McGill"
    }
  ],
  "description_domain": {
    "keywords": [
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      "SNPs"
    ],
    "xref": [
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      "UBERON:0000178",
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    "pipeline_steps": [
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        "tool_version": "0.1.19-96b5f2294a",
        "tool_package": "",
        "step_number": "1",
        "input_uri_list": [
"ftp://ftp.ncbi.nlm.nih.gov/1000genomes/ftp/technical/reference/human\_g1k\_v37.fasta.
gz"
        ],
        "output_uri_list": [

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        ". /biocompute/human_g1k_v37.fasta"
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        "tool_name": "picard_CreateSequenceDictionary",
        "tool_desc": "Creates a sequence dictionary for a reference
sequence",
        "tool_version": "v2.6.0",
        "tool_package": "",
        "step_number": "2",
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        ],
        "output_uri_list": [
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    {
        "tool_name": "samtools_sort",
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        "tool_version": "",
        "tool_package": "",
        "step_number": "3",
        "input_uri_list": [
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            ". /bam_files/biocompute/C_S31.bam",
            ". /bam_files/biocompute/D_S32.bam",
            ". /bam_files/biocompute/Hai003_S3.bam",
            ". /bam_files/biocompute/Hai004_S4.bam",
            ". /bam_files/biocompute/Hai006_S6.bam",
            ". /bam_files/biocompute/Hai007_S7.bam",
            ". /bam_files/biocompute/Hai012_S41.bam",
            ". /bam_files/biocompute/Hawi010_S16.bam",
            ". /bam_files/biocompute/Hawi015_S21.bam",
            ". /bam_files/biocompute/Hawi028_S35.bam",
            ". /bam_files/biocompute/Hawi032_S39.bam"
        ],
        "output_uri_list": [
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            "/home/biocompute/D_S32.bam_sorted",
            "/home/biocompute/Hai003_S3.bam_sorted",
            "/home/biocompute/Hai004_S4.bam_sorted",
            "/home/biocompute/Hai006_S6.bam_sorted",
            "/home/biocompute/Hai007_S7.bam_sorted",
            "/home/biocompute/Hai012_S41.bam_sorted",
            "/home/biocompute/Hawi010_S16.bam_sorted",
            "/home/biocompute/Hawi015_S21.bam_sorted",
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        "/home/biocompute/Hawi032_S39.bam_so"
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    "tool_version": "0.1.19-96b5f2294a",
    "tool_package": "",
    "step_number": "4",
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        "C_sorted.bam",
        "D_sorted.bam",
        "Hai003_sorted.bam",
        "Hai004_sorted.bam",
        "Hai006_sorted.bam",
        "Hai007_sorted.bam",
        "Hai012_sorted.bam",
        "Hawi010_sorted.bam",
        "Hawi015_sorted.bam",
        "Hawi028_sorted.bam",
        "Hawi032_sorted.bam"
    ],
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        "new_D_mark_duplicates.bam",
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        "new_Hai006_mark_duplicates.bam",
        "new_Hai007_mark_duplicates.bam",
        "new_Hai012_mark_duplicates.bam",
        "new_Hawi010_mark_duplicates.bam",
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        "new_Hawi032_mark_duplicates.bam",
        "B.txt",
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  "tool_package": "",
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    "new_Hawi010_mark_duplicates.bam",
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  ],
  "output_uri_list": [
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    "with_header_new_C_mark_duplicates.bam",
    "with_header_new_D_mark_duplicates.bam",
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    "with_header_new_Hai004_mark_duplicates.bam",
    "with_header_new_Hai006_mark_duplicates.bam",
    "with_header_new_Hai007_mark_duplicates.bam",
    "with_header_new_Hai012_mark_duplicates.bam",
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    "with_header_new_Hawi028_mark_duplicates.bam",
    "with_header_new_Hawi032_mark_duplicates.bam"
  ]
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{
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likely in need of realignment",
  "tool_version": "3.7-0-gcfedb67",
  "tool_package": "",
  "step_number": "6",
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    "with_header_new_Hai003_mark_duplicates.bam",
    "with_header_new_Hai004_mark_duplicates.bam",
    "with_header_new_Hai006_mark_duplicates.bam",
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        "with_header_new_Hai012_mark_duplicates.bam",
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        "with_header_new_Hawi028_mark_duplicates.bam",
        "with_header_new_Hawi032_mark_duplicates.bam"
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        "realignedHai007.list",
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        "realignedHawi028.list",
        "realignedHawi032.list"
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{
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    "tool_desc": "Perform local realignment of reads around indels",
    "tool_version": "3.7-0-gcfe9b67",
    "tool_package": "",
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        "with_header_new_D_mark_duplicates.bam-targetIntervals",
        "with_header_new_Hai003_mark_duplicates.bam-targetIntervals",
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        "Hai012_realigned_reads.bam",
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        "Hawi015_realigned_reads.bam",
        "Hawi028_realigned_reads.bam",
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{
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    "tool_package": "",
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        "Hai006_realigned_reads.bam",
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        "Hai012_realigned_reads.bam",
        "Hawi010_realigned_reads.bam",
        "Hawi015_realigned_reads.bam",
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        "Hai004_gatk_raw_snps.vcf",
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        "Hai007_gatk_raw_snps.vcf",
        "Hai012_gatk_raw_snps.vcf",
        "Hawi010_gatk_raw_snps.vcf",
        "Hawi015_gatk_raw_snps.vcf",
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]
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  "pipeline_version": "1.0",
  "platform": "linux",
  "driver": "Python 2.7.10",
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    {"name": "Picard", "version": "v2.6.0"},
    {"name": "samtools", "version": "v 0.1.19-96b5f2294a"},
    {"name": "Python", "version": "2.7.10"}
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  "env_parameters": [
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  "picard_AddOrReplaceReadGroups_ReadGroupPlatform": "illumina",
  "GenomeAnalysisTK_HaplotypeCaller_Intervals": "X",
  "GenomeAnalysisTK_RealignerTargetCreator_Num_threads": "22"
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    "Hai004_gatk_raw_snps.vcf",
    "Hai006_gatk_raw_snps.vcf",
    "Hai007_gatk_raw_snps.vcf",
    "Hai012_gatk_raw_snps.vcf",
    "Hawi010_gatk_raw_snps.vcf",
    "Hawi015_gatk_raw_snps.vcf",
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    "Hawi032_gatk_raw_snps.vcf"
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]
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}
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}
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