# Variant Data Model Example

**Variant model example**


```
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    "names": ["rs75062661"],
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    "length": 1,
    "type": "SNV",
    "reference": "A",
    "alternate": "G",
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            "studyId": "demo@family:corpasome",
                        "secondaryAlternates": [],
            "files": [
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                    "fileId": "quartet.variants.annotated.vcf.gz"
                    "call" : {

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                    "data": {
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                        "AC": "8",
                        "AF": "1.00",
                        "AN": "8",
                        "BaseQRankSum": "2.089",
                        "DB": "true",
                        "DP": "331",
                        "Dels": "0.00",
                        "EFF": "NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Aca
/Gca|T141A|305|OR4F5||CODING|NM_001005484.1|1|1)",
                        "FILTER": "VQSRTrancheSNP99.90to100.00",
                        "FS": "8.817",
                        "HaplotypeScore": "2.4399",
                        "MLEAC": "8",
                        "MLEAF": "1.00",
                        "MQ": "15.47",
                        "MQ0": "145",
                        "MQRankSum": "-0.047",
                        "OND": "0.018",
                        "QD": "12.97",
                        "QUAL": "4293.01",
                        "ReadPosRankSum": "1.662",
                        "SB": "-1.450e+03",
                        "VCF_ID": "rs75062661",
                        "VQSLOD": "-14.4975",
                        "culprit": "MQ",
                        "set": "FilteredInAll"
                    }
                }
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            "sampleDataKeys": ["GT", "AD", "DP", "GQ", "PL"],
            "samples": [
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                    "sampleId": "",
                    "fileIndex": 0,
                    "data": ["1/1", "2,171", "173", "99", "2218,228,0"]
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                    "data": ["1/1", "0,33", "34", "60", "508,60,0"]
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                {
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                "sampleId": "",
                "fileIndex": 0,
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                                    "filterCount": {
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                                            "VQSRTrancheSNP99.90to100.00": 1
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                                    "genotypeCount": {
                                            "0/0": 0,
                                            "0/1": 0,
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                                    "genotypeFreq": {
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                                            "1/1": 1.0
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                                    "qualityAvg": 4293.01,
                                    "refAlleleCount": 0,
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            "reference": "A",
            "alternate": "G",
            "hgvs": ["ENST00000335137(ENSG00000186092):c.421A>G"],
            "displayConsequenceType": "missense_variant",
            "consequenceTypes": [
                    {
                            "geneName": "OR4F5",
                            "ensemblGeneId": "ENSG00000186092",
            "ensemblTranscriptId": "ENST00000335137",
                            "biotype": "protein_coding",
            "cdnaPosition": 421,
            "cdsPosition": 421,
            "codon": "Aca/Gca",
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                                                                                             "coupled "
                                                                                             "receptor",
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                                                                                             "Olfaction",
                                                                                             "Receptor",
                                                                                             "Reference "
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