Field	Field Description	Recommended Use
ALL_0.01%	EVS-based RVIS using the combined European and African populations (n=6503); setting 'common' MAF filter at 0.01%	-
%ALL_0.01%	Genome-Wide percentile for the EVS-based RVIS using the combined European and African populations (n=6503); setting 'common' MAF filter at 0.01%	-
ALL_0.1%	EVS-based RVIS using the combined European and African populations (n=6503); setting 'common' MAF filter at 0.1%	-
%ALL_0.1%	Genome-Wide percentile for the EVS-based RVIS using the combined European and African populations (n=6503); setting 'common' MAF filter at 0.1%	**EVS default recommendation**
ALL_1%	EVS-based RVIS using the combined European and African populations (n=6503); setting 'common' MAF filter at 1%	-
%ALL_1%	Genome-Wide percentile for the EVS-based RVIS using the combined European and African populations (n=6503); setting 'common' MAF filter at 1%	-
PP2_ALL_0.1%	EVS-based RVIS using the combined European and African populations (n=6503); setting 'common' MAF filter at 0.1%; excluding PolyPhen-2 "benign" classifications	-
%PP2_ALL_0.1%	Genome-Wide percentile for the EVS-based RVIS using the combined European and African populations (n=6503); setting 'common' MAF filter at 0.1%; excluding PolyPhen-2 "benign" classifications	-
EA_0.1%	EVS-based RVIS using only the European population (n=4300); setting 'common' MAF filter at 0.1%	-
%EA_0.1%	Genome-Wide percentile for the EVS-based RVIS using only the European population (n=4300); setting 'common' MAF filter at 0.1%	-
EA_1%	EVS-based RVIS using only the European populations (n=4300); setting 'common' MAF filter at 1%	-
%EA_1%	Genome-Wide percentile for the EVS-based RVIS using only the European population (n=4300); setting 'common' MAF filter at 1%	-
AA_0.1%	EVS-based RVIS using only the African population (n=2203); setting 'common' MAF filter at 0.1%	-
%AA_0.1%	Genome-Wide percentile for the EVS-based RVIS using only the African population (n=2203); setting 'common' MAF filter at 0.1%	-
AA_1%	EVS-based RVIS using only the African populations (n=2203); setting 'common' MAF filter at 1%	-
%AA_1%	Genome-Wide percentile for the EVS-based RVIS using only the African population (n=2203); setting 'common' MAF filter at 1%	-
OEratio	Subset of the exome contains genes with too little resolution to be able to rely on RVIS framework. We refer to these as 'edge case' genes. - See paragraph in About page.	**Edge Case genes (Y/N)**
%OEratio	The genome-wide percentile OEratio score derived using the EVS population standing variation data. To be interpreted the same as RVIS (a genome-wide percentile)	-
%ExAC_0.1%popn	Genome-Wide percentile for the new ExAC-based RVIS; setting 'common' MAF filter at 0.1% in at least one of the six individual ethnic strata from ExAC. (Unpublished)	-
%ExAC_0.05%popn	Genome-Wide percentile for the new ExAC-based RVIS; setting 'common' MAF filter at 0.05% in at least one of the six individual ethnic strata from ExAC. (Unpublished)	**ExAC default recommendation**
%ExAC_0.01%	Genome-Wide percentile for the new ExAC-based RVIS; setting 'common' MAF filter at 0.01% in the combined (global) ExAC collection. (Unpublished)	-
OEratio-percentile[ExAC]	The genome-wide OEratio score percentile derived using the ExAC population standing variation data. To be interpreted the same as RVIS (a genome-wide percentile).	**Recommended use for Edge Case genes (Y)**
LoF-FDR[ExAC]	A gene's corresponding FDR p-value for preferential LoF depletion among the ExAC population. Lower FDR corresponds with genes that are increasingly depleted of LoF variants.	**Recommended when searching specifically for LoF depleted genes.**

http://genic-intolerance.org/data/GenicIntolerance_v3_12Mar16.txt

Field	Field Description	Recommended Use
RVIS_ExAC_0.05% (AnyPopn)	ExAC-based RVIS; setting 'common' MAF filter at 0.05% in at least one of the six individual ethnic strata from ExAC. (Unpublished)	-
%RVIS_ExAC_0.05% (AnyPopn)	Genome-Wide percentile for the new ExAC-based RVIS; setting 'common' MAF filter at 0.05% in at least one of the six individual ethnic strata from ExAC. (Unpublished)	**ExAC default recommendation**
RVIS_ExAC_0.1% (AnyPopn)	ExAC-based RVIS; setting 'common' MAF filter at 0.1% in at least one of the six individual ethnic strata from ExAC. (Unpublished)	-
%RVIS_ExAC_0.1% (AnyPopn)	Genome-Wide percentile for the new ExAC-based RVIS; setting 'common' MAF filter at 0.1% in at least one of the six individual ethnic strata from ExAC. (Unpublished)	-
RVIS_ExAC_0.01%	ExAC-based RVIS; setting 'common' MAF filter at 0.01% across the pooled ExAC populations data. (Unpublished)	-
%RVIS_ExAC_0.01%	Genome-Wide percentile for the new ExAC-based RVIS; setting 'common' MAF filter at 0.01% across the global population data represented within ExAC. (Unpublished)	-

http://genic-intolerance.org/data/RVIS_Unpublished_ExAC_May2015.txt