GO Evidence Code Decision Tree What type of evidence is the annotation based on? Curator Experimental Statements (wet lab) Non-Experimental Author statement (computational) from publication Is there a GO annotation Is annotation based in another aspect that allows on genetic mutations a biocurator to make an inference or allelic variation? Will each annotation be based on that GO term for an Is annotation based on individually reviewed & confirmed aspect without evidence? yes no an author statement that by a human annotator? cites a published reference as no Is a single gene being the source of the information? yes mutated or compared to other alleles of the same gene? no Is the computation based purely on Are there the sequence of the gene product? no. No Data (ND) Is annotation based on to support a GO annotation an author statement that does Is annotation based on a yes in a given GO aspect? no not cite a published reference as genetic interaction **ISA** (see note on use of ND) the source of the information? with another gene? **ISM** Does the computation include consideration of the genomic context of the gene? Is annotation based on a direct 1 to 1 physical interaction no with another gene product? no \ Is the computation an integrated Note on use of ND evidence code: analysis, typically including Unlike the other evidence codes, the No Data (ND) code does not Is annotation based on a experimental data sets, and often indicate evidence or a method from a specific reference. Rather, it direct assay for the function, process, including multiple data types? indicates that the annotator looked at the available information and or component of the gene product? determined that nothing is known about the gene for a given aspect of GO (molecular function, biological process, or cellular component). no\ The annotater will always look at all available literature for the gene. Depending on the resources and annotation philosophy of the Is annotation based on For curator reviewed annotations annotating group, the annotater may also look at sequence the expression pattern comparison data to determine if any predictions may be made of the gene product? ■ For annotations NOT reviewed by a curator based on the sequence.