KusakiDB Tools:
Search System

KusakiDB Tools: OG Assessment
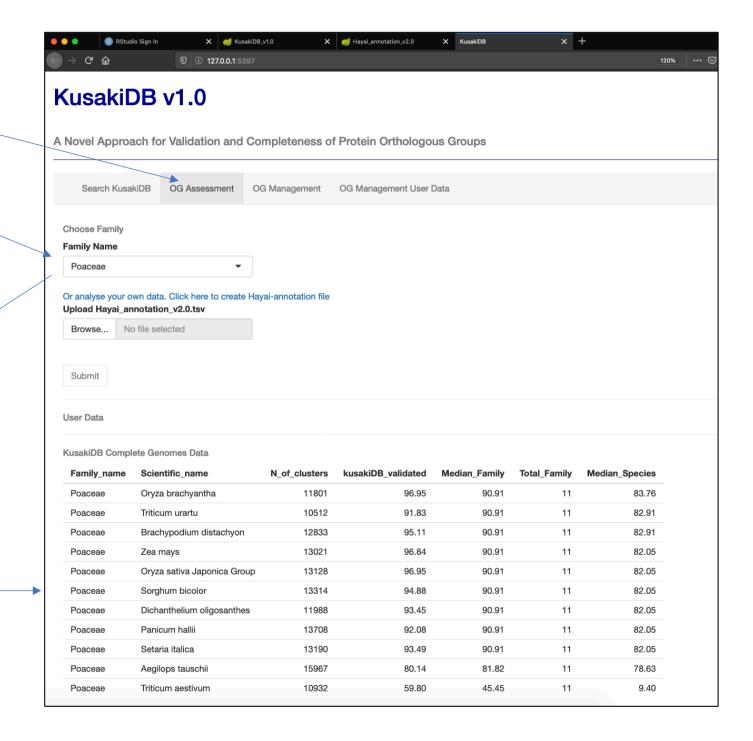
Select a Family from KusakiDB

Choose Family

Family Name

P	▲

Poaceae
Phrymaceae
Pedaliaceae
Papaveraceae
Apiaceae
Asparagaceae
Cephalotaceae
Euphorbiaceae

Results of KusakiDB data

KusakiDB v1.0

A Novel Approach for Validation and Completeness of Protein Orthologous Groups

Search KusakiDB | **OG Assessment** | OG Management | OG Management User Data

Choose Family

Family Name

Poaceae	▼

Or analyse your own data. Click here to create Hayai-annotation file

Upload Hayai_annotation_v2.0.tsv

Browse...	No file selected

Submit

User Data

KusakiDB Complete Genomes Data

Family_name	Scientific_name	N_of_clusters	kusakiDB_validated	Median_Family	Total_Family	Median_Species
Poaceae	Oryza brachyantha	11801	96.95	90.91	11	83.76
Poaceae	Triticum urartu	10512	91.83	90.91	11	82.91
Poaceae	Brachypodium distachyon	12833	95.11	90.91	11	82.91
Poaceae	Zea mays	13021	96.84	90.91	11	82.05
Poaceae	Oryza sativa Japonica Group	13128	96.95	90.91	11	82.05
Poaceae	Sorghum bicolor	13314	94.88	90.91	11	82.05
Poaceae	Dichanthelium oligosanthes	11988	93.45	90.91	11	82.05
Poaceae	Panicum hallii	13708	92.08	90.91	11	82.05
Poaceae	Setaria italica	13190	93.49	90.91	11	82.05
Poaceae	Aegilops tauschii	15967	80.14	81.82	11	78.63
Poaceae	Triticum aestivum	10932	59.80	45.45	11	9.40

KusakiDB OG Assessment accepts user's data

KusakiDB Tools: OG Assessment

Upload your own data annotated by Hayai-annotation v2.0

Users data result:
KusakiDB predicts family and calculate number of validated OGs, median of OG within same family and median of OG within all species

OG Assessment Equations

Median of OGs within a family (median family):

$$\text{Median\_Family (\%)} = median\left(\frac{rep_{fam}}{Total_{family}} \times 100\right), \text{ where:}$$
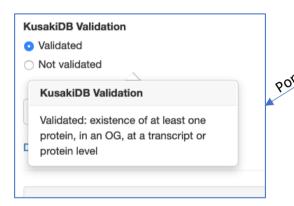
rep_{fam} is the count of unique sequences in an OG, per species, within a family.
$Total_{family}$ is the total number of species in each family.

Median of OGs within all species (median species):

$$\text{Median\_Species (\%)} = median\left(\frac{rep}{Total_{species}} \times 100\right), \text{ where:}$$

rep is the count of unique sequences in an OG, per species.
$Total_{species}$ is the total number of species in KusakiDB.

KusakiDB Tools: OG Management

Users can select the parameters to compare OGs among all species in KusakiDB, such as:
- Validation tag
- Number of species in each family
- Percentage of species in each family
- Percentage within all species

KusakiDB Validation
- ◉ Validated
- ○ Not validated

KusakiDB Validation

Validated: existence of at least one protein, in an OG, at a transcript or protein level
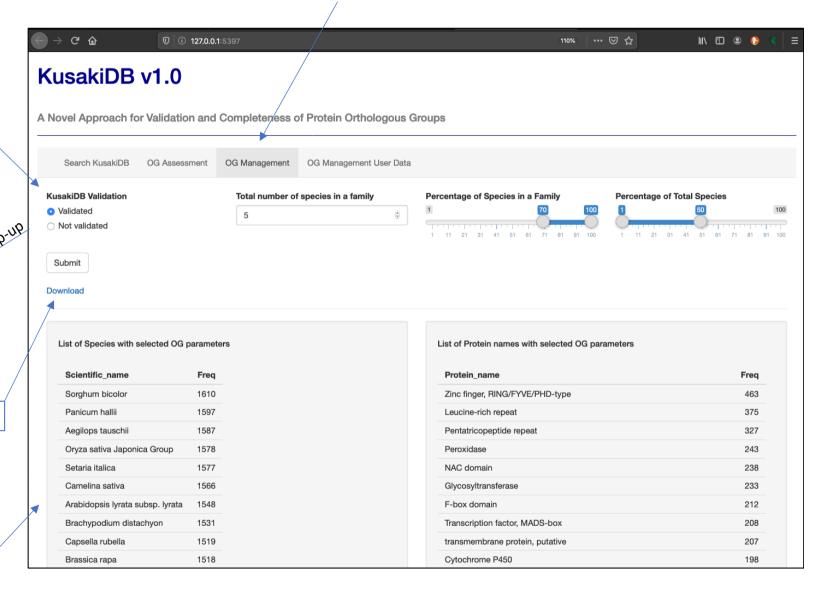
Pop-up

User can download the results

The results with the selected parameters are shown in two table:
- List of species and number of OGs
- List of protein names and correspondent frequency

KusakiDB v1.0

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| Search KusakiDB | OG Assessment | OG Management | OG Management User Data |

KusakiDB Validation
- ◉ Validated
- ○ Not validated

Total number of species in a family

5

Percentage of Species in a Family

1   70   100

Percentage of Total Species

1   50   100

Submit

Download

List of Species with selected OG parameters

Scientific_name	Freq
Sorghum bicolor	1610
Panicum hallii	1597
Aegilops tauschii	1587
Oryza sativa Japonica Group	1578
Setaria italica	1577
Camelina sativa	1566
Arabidopsis lyrata subsp. lyrata	1548
Brachypodium distachyon	1531
Capsella rubella	1519
Brassica rapa	1518

List of Protein names with selected OG parameters

Protein_name	Freq
Zinc finger, RING/FYVE/PHD-type	463
Leucine-rich repeat	375
Pentatricopeptide repeat	327
Peroxidase	243
NAC domain	238
Glycosyltransferase	233
F-box domain	212
Transcription factor, MADS-box	208
transmembrane protein, putative	207
Cytochrome P450	198

KusakiDB Tools: OG Management User Data

Users can select the parameters to compare OGs among all species in KusakiDB, such as:
- Validation tag
- Number of species in each family
- Percentage of species in each family
- Percentage within all species

Users can upload the functional annotation performed by Hayai-annotation v2.0

Filter your results

The results show a "filter" of the genes that are selected under the conditions regarding the conservation level of each OG.