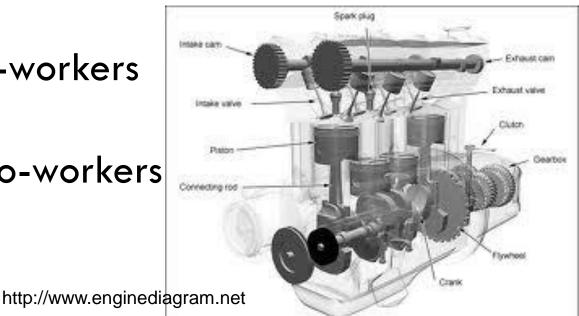
## **KOMP2** Engine of Discovery

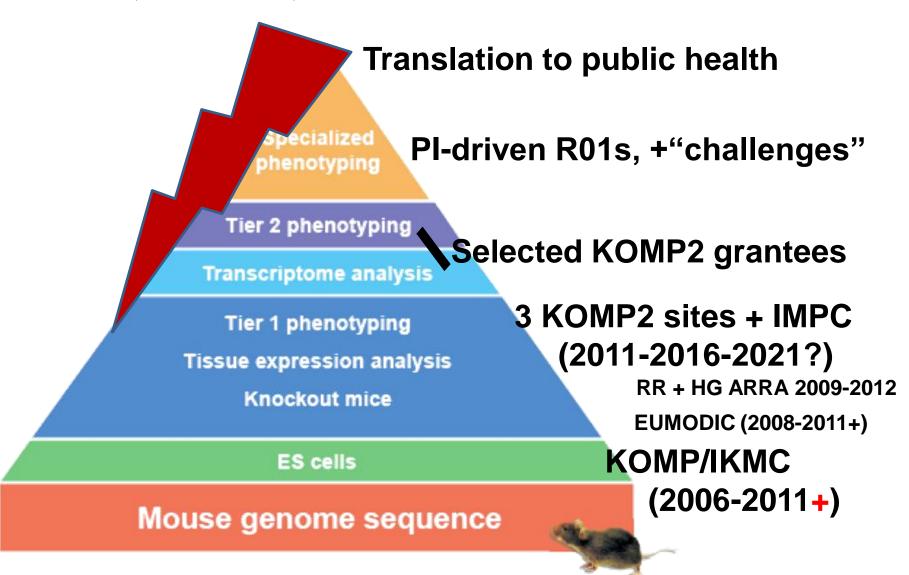
CommonFund of NIH OD RFA + ½ funding, NHGRI, NCRR, NCI, NEI, NHLBI, NIA, NIAAA, NIAID, NIAMS, NICHD, NIDA, NIDCD, NIDCR, NIDDK, NIEHS, NIGMS, NINDS, NIMH, OAR

KOMP PIs and co-workers

KOMP2 Pls and co-workers



### Past, Present, Future



Functional characterization of 2,500 predicted proteincoding genes whose function is currently unknown.

Novel genes will be brought to light that otherwise would be ignored. New genes of interest will be further pursued by categorical NIH ICs.

Publicly available **resource** of >8,500 vectors, >8,500 mutant ES cell lines, and 2,500 phenotyped **mouse lines**.

**Massive, interlinking datasets** to be mined for translational research in 2012-2032.

### Selected features

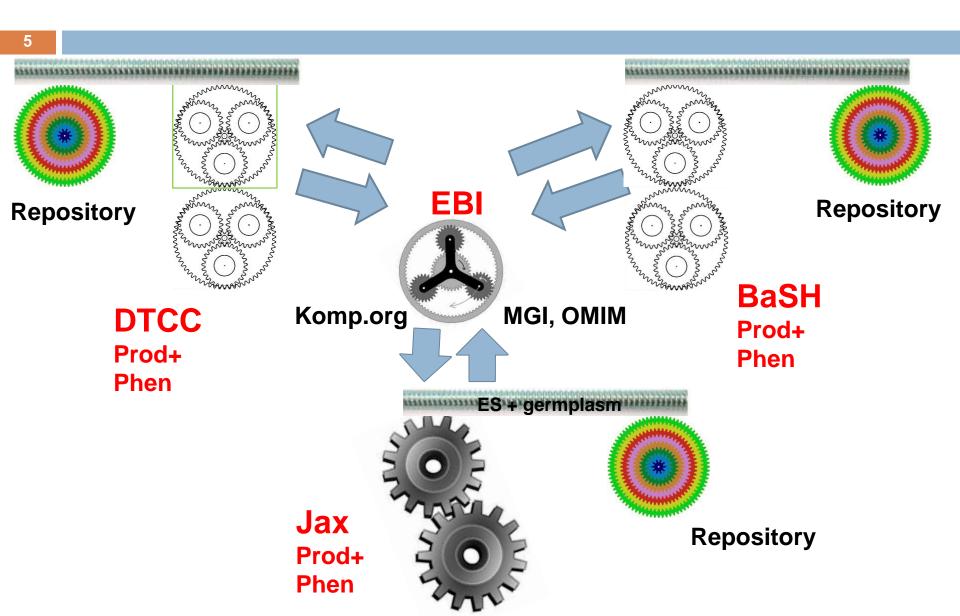
Reliable, comprehensive, positive and negative data for widespread use by investigators worldwide.

KOMP2 via 7 grants at 9 sites worldwide 2,500 KOs/5yrs (833/grant/5yrs, 167/grant/yr) lacZ stain heterozygotes, phenotype homozygotes (or hets if homs are nonviable).

7M + 7F C57BL/6N / KO gene, and daily control group.

Further development and cost-optimization before KOMP2 Phase II in 2016-2021.

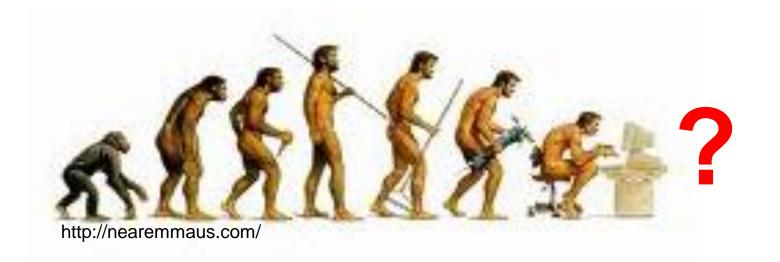
# **KOMP2** Engine of Discovery



#### **Future Timeframes**

```
September 2011 - NoAs, and begin:
     yearly face-to-face meetings,
           gene list + core phenotyping protocol,
           press release,
     monthly PI teleconferences,
     periodic NIH IC discussions.
2015 (Yr4) assessment for funding Phase II, will need:
     gene characterizations (publications, database),
     orders = need+cost recovery at repository(ies),
     cost-effectiveness for taxpayers.
```

## Further evolution is expected





http://canitbesaturdaynow.com/