Table 2 - Example ehive pipelines, modules, programs and parameter data from coredb analysis table.

Pipeline	Program	Program version	Parameters	Ehive module (Bio::EnsEMBL::)	Database	version
ONA eatures	dustmasker	NULL	NULL	Analysis::Runnable::DustMasker		
ONA eatures	+rf	4	257801040500 d h	Analysis::Runnable::TRF		
		4	-nolow -gccalc -species	AliaiysisNullilabicTNI		
DNA features	RepeatMasker	4.0.5	"Aedes aegypti" - engine crossmatch -q	Analysis::Runnable::RepeatMasker		
DNA eatures	RepeatMasker	4.0.5	-nolow -gccalc -lib "location1" -engine crossmatch -q	Analysis::Runnable::Repeat Masker		
DNA			-nolow -gccalc -lib "location2" -engine crossmatch			
features	RepeatMasker	4.0.5	-q	Analysis::Runnable::RepeatMasker		
NA	NULL	NULL	NULL	EGPipeline::LoadGFF3::LoadGFF3		
RNA	Infernal tRNAscan-SE	1.1		Analysis::Runnable::CMScan Analysis::Runnable::tRNAscan		
RNA	Infernal	1.1		Analysis::Runnable::CMScan		
RNA	imernai	1.1		EGPipeline::RNAFeatures::CreateCmscanGe		
eatures RNA	rfam_12.2_gene	NULL	NULL	nes EGPipeline::RNAFeatures::CreateMirbaseGe		
	mirbase_gene	NULL	NULL	nes  EGPipeline::RNAFeatures::CreateTrnascanG		
eatures	trnascan_gene	NULL	NULL	enes		
(ref	xrefchecksum	NULL	NULL	EGPipeline::Xref::LoadUniParc		
(ref	xrefuniparc	NULL	NULL	EGPipeline::Xref::LoadUniProt		
Kref	gouniprot	NULL	NULL	EGPipeline::Xref::LoadUniProtGO		
Xref	xrefuniprot	NULL	-word_size 3 -num_alignments 100000 -num_descriptions 100000	EGPipeline::Xref::LoadUniProtXrefs		
ONA eatures	hlastn	NULL	-lcase_masking -seg yes -num_threads 3	Analysis::Runnable::BlastEG		
DNA features			-word_size 3 -num_alignments			
	hlasta	NIIII	-num_descriptions 100000 -lcase_masking -seg yes	Analysis: Punnahla: PlastEG		
eatures	blastp	NULL	-num_descriptions 100000 -lcase_masking	Analysis::Runnable::BlastEG	Prosite	
eatures Protein	blastp InterProScan	NULL 5.37-76.0	-num_descriptions 100000 -lcase_masking -seg yes -num_threads 3	Analysis::Runnable::BlastEG	Prosite patterns	2019_0
eatures Protein eatures Protein			-num_descriptions 100000 -lcase_masking -seg yes -num_threads 3	Analysis::Runnable::BlastEG		2019_0 4
Protein Features Protein Features Protein	InterProScan	5.37-76.0	-num_descriptions 100000 -lcase_masking -seg yes -num_threads 3  NULL  NULL	Analysis::Runnable::BlastEG	patterns	_
Protein Features Protein Features Protein Features	InterProScan InterProScan	5.37-76.0 5.37-76.0	-num_descriptions 100000 -lcase_masking -seg yes -num_threads 3  NULL  NULL  NULL	Analysis::Runnable::BlastEG	patterns	4
Protein Features Protein Features Protein Features Protein Features Protein Features Protein Features	InterProScan InterProScan InterProScan	5.37-76.0 5.37-76.0 5.37-76.0	-num_descriptions 100000 -lcase_masking -seg yes -num_threads 3  NULL  NULL  NULL  NULL	Analysis::Runnable::BlastEG	patterns SFLD CDD	4 3.17 4.2.0
Protein Features Protein Features Protein Features Protein Features Protein Features Protein Features	InterProScan InterProScan InterProScan InterProScan	5.37-76.0 5.37-76.0 5.37-76.0 5.37-76.0	-num_descriptions 100000 -lcase_masking -seg yes -num_threads 3  NULL  NULL  NULL  NULL  NULL	Analysis::Runnable::BlastEG	patterns  SFLD  CDD  Gene3D	4 3.17 4.2.0
Protein Features	InterProScan InterProScan InterProScan InterProScan InterProScan InterProScan	5.37-76.0 5.37-76.0 5.37-76.0 5.37-76.0	-num_descriptions 100000 -lcase_masking -seg yes -num_threads 3  NULL  NULL  NULL  NULL  NULL  NULL  NULL	Analysis::Runnable::BlastEG	patterns  SFLD  CDD  Gene3D  HAMAP	4 3.17 4.2.0 2019_0
Protein Features	InterProScan InterProScan InterProScan InterProScan InterProScan InterProScan InterProScan	5.37-76.0 5.37-76.0 5.37-76.0 5.37-76.0 5.37-76.0 5.37-76.0	-num_descriptions 100000 -lcase_masking -seg yes -num_threads 3  NULL  NULL  NULL  NULL  NULL  NULL  NULL	Analysis::Runnable::BlastEG	patterns  SFLD  CDD  Gene3D  HAMAP  PANTHER	4 3.17 4.2.0 2019_0 14.1 2.2.1
Protein Features	InterProScan InterProScan InterProScan InterProScan InterProScan InterProScan InterProScan InterProScan	5.37-76.0 5.37-76.0 5.37-76.0 5.37-76.0 5.37-76.0 5.37-76.0	-num_descriptions 100000 -lcase_masking -seg yes -num_threads 3  NULL  NULL  NULL  NULL  NULL  NULL  NULL  NULL  NULL	Analysis::Runnable::BlastEG	patterns  SFLD  CDD  Gene3D  HAMAP  PANTHER  ncoils  Prosite	4 3.17 4.2.0 2019_0 14.1 2.2.1
Protein Features	InterProScan InterProScan InterProScan InterProScan InterProScan InterProScan InterProScan InterProScan InterProScan	5.37-76.0 5.37-76.0 5.37-76.0 5.37-76.0 5.37-76.0 5.37-76.0 5.37-76.0	-num_descriptions 100000 -lcase_masking -seg yes -num_threads 3  NULL	Analysis::Runnable::BlastEG	patterns  SFLD  CDD  Gene3D  HAMAP  PANTHER  ncoils  Prosite profiles	4 3.17 4.2.0 2019_0 14.1 2.2.1 2019_0
Protein Features	InterProScan	5.37-76.0 5.37-76.0 5.37-76.0 5.37-76.0 5.37-76.0 5.37-76.0 5.37-76.0 5.37-76.0	-num_descriptions 100000 -lcase_masking -seg yes -num_threads 3  NULL	Analysis::Runnable::BlastEG	patterns  SFLD  CDD  Gene3D  HAMAP  PANTHER  ncoils  Prosite profiles  Pfam	4 3.17 4.2.0 2019_0 14.1 2.2.1 2019_0 32
Protein Features	InterProScan	5.37-76.0 5.37-76.0 5.37-76.0 5.37-76.0 5.37-76.0 5.37-76.0 5.37-76.0 5.37-76.0 5.37-76.0	-num_descriptions 100000 -lcase_masking -seg yes -num_threads 3  NULL	Analysis::Runnable::BlastEG	patterns  SFLD  CDD  Gene3D  HAMAP  PANTHER  ncoils  Prosite profiles  Pfam  PRINTS	4 3.17 4.2.0 2019_0 14.1 2.2.1 2019_0 32 42 7.1
Protein features	InterProScan	5.37-76.0 5.37-76.0 5.37-76.0 5.37-76.0 5.37-76.0 5.37-76.0 5.37-76.0 5.37-76.0 5.37-76.0	-num_descriptions 100000 -lcase_masking -seg yes -num_threads 3  NULL	Analysis::Runnable::BlastEG	patterns  SFLD  CDD  Gene3D  HAMAP  PANTHER  ncoils  Prosite profiles  Pfam  PRINTS  Smart	4 3.17 4.2.0 2019_0 14.1 2.2.1 2019_0 32 42 7.1
Protein Features	InterProScan	5.37-76.0 5.37-76.0 5.37-76.0 5.37-76.0 5.37-76.0 5.37-76.0 5.37-76.0 5.37-76.0 5.37-76.0	-num_descriptions 100000 -lcase_masking -seg yes -num_threads 3  NULL	Analysis::Runnable::BlastEG	patterns  SFLD  CDD  Gene3D  HAMAP  PANTHER  ncoils  Prosite profiles  Pfam  PRINTS  Smart  SuperFamily  TIGRfam  InterPro-	4 3.17 4.2.0 2019_0 14.1 2.2.1 2019_0 32 42 7.1 1.75
Protein eatures	InterProScan	5.37-76.0 5.37-76.0 5.37-76.0 5.37-76.0 5.37-76.0 5.37-76.0 5.37-76.0 5.37-76.0 5.37-76.0	-num_descriptions 100000 -lcase_masking -seg yes -num_threads 3  NULL	Analysis::Runnable::BlastEG	patterns  SFLD  CDD  Gene3D  HAMAP  PANTHER  ncoils  Prosite profiles  Pfam  PRINTS  Smart  SuperFamily  TIGRfam  InterPro- 2GO	4 3.17 4.2.0 2019_0 14.1 2.2.1 2019_0 32 42 7.1 1.75 15 NULL
Protein features	InterProScan	5.37-76.0 5.37-76.0 5.37-76.0 5.37-76.0 5.37-76.0 5.37-76.0 5.37-76.0 5.37-76.0 5.37-76.0 5.37-76.0	-num_descriptions 100000 -lcase_masking -seg yes -num_threads 3  NULL	Analysis::Runnable::BlastEG	patterns  SFLD  CDD  Gene3D  HAMAP  PANTHER  ncoils  Prosite profiles  Pfam  PRINTS  Smart  SuperFamily  TIGRfam  InterPro-	4 3.17 4.2.0 2019_0 14.1 2.2.1 2019_0 32 42 7.1 1.75
Protein eatures	InterProScan	5.37-76.0 5.37-76.0 5.37-76.0 5.37-76.0 5.37-76.0 5.37-76.0 5.37-76.0 5.37-76.0 5.37-76.0 5.37-76.0	-num_descriptions 100000 -lcase_masking -seg yes -num_threads 3  NULL	Analysis::Runnable::BlastEG	patterns  SFLD  CDD  Gene3D  HAMAP  PANTHER  ncoils  Prosite profiles  Pfam  PRINTS  Smart  SuperFamily  TIGRfam  InterPro- 2GO	4 3.17 4.2.0 2019_0 14.1 2.2.1 2019_0 32 42 7.1 1.75 15 NULL
Protein features	InterProScan	5.37-76.0 5.37-76.0 5.37-76.0 5.37-76.0 5.37-76.0 5.37-76.0 5.37-76.0 5.37-76.0 5.37-76.0 5.37-76.0 5.37-76.0	-num_descriptions 100000 -lcase_masking -seg yes -num_threads 3  NULL	Analysis::Runnable::BlastEG	patterns  SFLD  CDD  Gene3D  HAMAP  PANTHER  ncoils  Prosite profiles  Pfam  PRINTS  Smart  SuperFamily  TIGRfam  InterPro- 2GO  PIRSF	4 3.17 4.2.0 2019_0 14.1 2.2.1 2019_0 32 42 7.1 1.75 15 NULL 3.02
Protein eatures	InterProScan	5.37-76.0 5.37-76.0 5.37-76.0 5.37-76.0 5.37-76.0 5.37-76.0 5.37-76.0 5.37-76.0 5.37-76.0 5.37-76.0 5.37-76.0	-num_descriptions 100000 -lcase_masking -seg yes -num_threads 3  NULL  NULL	Analysis::Runnable::BlastEG	patterns  SFLD  CDD  Gene3D  HAMAP  PANTHER  ncoils  Prosite profiles  Pfam  PRINTS  Smart  SuperFamily  TIGRfam  InterPro- 2GO  PIRSF  SignalP	4 3.17 4.2.0 2019_0 14.1 2.2.1 2019_0 32 42 7.1 1.75 15 NULL 3.02 4.1
Protein eatures	InterProScan	5.37-76.0 5.37-76.0 5.37-76.0 5.37-76.0 5.37-76.0 5.37-76.0 5.37-76.0 5.37-76.0 5.37-76.0 5.37-76.0 5.37-76.0 5.37-76.0	-num_descriptions 100000 -lcase_masking -seg yes -num_threads 3  NULL	Analysis::Runnable::BlastEG	patterns  SFLD  CDD  Gene3D  HAMAP  PANTHER  ncoils  Prosite profiles  Pfam  PRINTS  Smart  SuperFamily  TIGRfam  InterPro- 2GO  PIRSF  SignalP  TMHMM	4 3.17 4.2.0 2019_0 14.1 2.2.1 2019_0 32 42 7.1 1.75 15 NULL 3.02 4.1 2.0c NULL

<sup>\*</sup>Location 1 "/homes/jallen/scratch/vb/recent\_assemblies/aedes\_aegypti/RepeatModeler/aedes\_aegypti.rm.lib" \*Location 2 "/nfs/panda/ensemblgenomes/vectorbase/data/tefam/aegypti\_tefam.lib"