

**Summary of TCGA Tumor Data
Ingested into Broad GDAC Pipeline
BROAD GDAC 12/23/2010 Run**

Tumor Type	Biospecimen	Any_Level_1	Clinical	CNA	Methylation	mRNA	miR	MAF
BRCA	319	186	194	176	186	280	0	0
COAD	203	151	130	137	167	155	0	0
GBM	0	448	0	466	288	444	415	0
HNSC	39	0	0	0	0	0	0	0
KIRC	355	39	19	73	219	41	0	0
KIRP	48	39	0	39	36	41	0	0
LAML	202	0	0	0	188	0	0	0
LUAD	128	21	11	56	128	33	0	0
LUSC	160	116	42	117	133	116	0	0
OV	584	570	532	519	425	519	566	384
READ	79	52	72	50	69	69	0	0
STAD	82	35	0	81	82	0	0	0
UCEC	125	24	0	68	70	0	0	0
Totals	2324	1681	1000	1782	1991	1698	981	384

Anomalous absence of GBM clinical and BCR data will be corrected in next run.

Analysis Status for 5 Most Populous Tumor Types
BROAD GDAC 12/23/2010 Run

Tumor Type	Analyses Completed	Not Completed	Percentage
OV	25	0	100%
GBM	15	10	60%
BRCA	8	17	32%
COAD	8	17	32%
LUSC	8	17	32%

Additional tumor types follow similar profile to BRCA et al.
See next page for detailed list of analyses performed.



Workspaces ▾ Samples ▾ Individuals | **Workspace: prod_2010_12_23_ov_01**

PIPELINE WORKFLOW STATUS

Show only jobs in: For workflow:

WORKFLOW STATUS

Pipeline	Reports	Job Count	Not Ready	Analysis	Ready	In Process	Failed	Complete
convertCNLevelIIIData		1	0%	0%	0%	0%	0%	100%
Find miR Direct Targets	view	1	0%	0%	0%	0%	0%	100%
GDAC CNMF miRNA clustering	view	1	0%	0%	0%	0%	0%	100%
GDAC Correlate Expression with Methylation	view	1	0%	0%	0%	0%	0%	100%
GDAC median mRNA Expression		1	0%	0%	0%	0%	0%	100%
GDAC miRNAConsensusClustering	view	1	0%	0%	0%	0%	0%	100%
GDAC_clinicalDataMergerPipeline_clinical		1	0%	0%	0%	0%	0%	100%
Gistic2	view	1	0%	0%	0%	0%	0%	100%
MutSig	view	1	0%	0%	0%	0%	0%	100%
Paradigm		1	0%	0%	0%	0%	0%	100%
GDAC CNMF mRNA clustering	view	1	0%	0%	0%	0%	0%	100%
GDAC mRNAConsensusClustering	view	1	0%	0%	0%	0%	0%	100%
GDAC_clinicalDataPickerPipeline_clinical		1	0%	0%	0%	0%	0%	100%
MakeReducedSegment		1	0%	0%	0%	0%	0%	100%
MutationAssessor	view	1	0%	0%	0%	0%	0%	100%
Correlate gene mutation status with Clinical data	view	1	0%	0%	0%	0%	0%	100%
Correlate microRNA Expression with Clinical Data	view	1	0%	0%	0%	0%	0%	100%
Correlate miRNA CNMF clustering with Clinical data	view	1	0%	0%	0%	0%	0%	100%
Correlate miRNA consensus clustering with Clinical data	view	1	0%	0%	0%	0%	0%	100%
Correlate mRNA CNMF clustering with Clinical data	view	1	0%	0%	0%	0%	0%	100%
Correlate mRNA consensus clustering with Clinical data	view	1	0%	0%	0%	0%	0%	100%
Correlate mRNA Expression with Clinical data	view	1	0%	0%	0%	0%	0%	100%
GetCopyNumberExpCor	view	1	0%	0%	0%	0%	0%	100%
GetCopyNumberExpCorMiRNA	view	1	0%	0%	0%	0%	0%	100%
GDAC_geneListPathwayEnrichmentPipeline	view	1	0%	0%	0%	0%	0%	100%