

THE GENOME BROWSER – UNDER THE HOOD

Human chr1:11102 x

genome.ucsc.edu/cgi-bin/hgTracks?db=hg38&lastVirtModeType=default&lastVirtModeExtraState=&virtModeType=default&virtMode=0&nonVirtPosition=&position=chr1%3A1102837-11267747&hgsid=645774909_PFT5v8E4pLo4...

Genomes Genome Browser Tools Mirrors Downloads My Data View Help About Us

UCSC Genome Browser on Human Dec. 2013 (GRCh38/hg38) Assembly

move <<< << < > >> >>> zoom in 1.5x 3x 10x base zoom out 1.5x 3x 10x 100x

chr1:11,102,837-11,267,747 164,911 bp. enter position, gene symbol, HGVS or search terms go

chr1 (p06.22) 50 kb hg38

Scale chr1: 11,120,000 11,130,000 11,140,000 11,150,000 11,160,000 11,170,000 11,180,000 11,190,000 11,200,000 11,210,000 11,220,000 11,230,000 11,240,000 11,250,000 11,260,000

RefSeq Curated: Mtor, Mtor-AS1, RNU5-37P, RNOPTL7, RNU5-201P, RFL39P6

RefSeq gene predictions from NCBI: Mtor, Mtor-AS1, RNU5-37P, RNOPTL7, RNU5-201P, RFL39P6

Gene Expression in 53 tissues from GTEx RNA-seq of 8555 samples (578 donors): Mtor, Mtor-AS1, RNU5-37P, RNOPTL7, RNU5-201P, RFL39P6

Layered H3K27ac: H3K27ac Mark (Often Found Near Regulatory Elements) on 7 cell lines from ENCODE

DNase I Hypersensitivity Peak Clusters from ENCODE (95 cell types): DNase I Hypersensitivity Peak Clusters from ENCODE (95 cell types)

Cons 100 Verts: 100 vertebrates basepair conservation by PhyloP

Multiz Alignments of 100 Vertebrates: Rhesus, Mouse, Dog, Elephant, Chimpanzee, X_Tropica 118, Zebrafish, Lamprey

Common SNPs (150): Simple Nucleotide Polymorphisms (dbSNP 150) found in >= 1% of Samples

Repeating Elements by RepeatMasker: SINE, LINE, L1, L2, L3, L4, L5, L6, L7, L8, L9, L10, L11, L12, L13, L14, L15, L16, L17, L18, L19, L20, L21, L22, L23, L24, L25, L26, L27, L28, L29, L30, L31, L32, L33, L34, L35, L36, L37, L38, L39, L40, L41, L42, L43, L44, L45, L46, L47, L48, L49, L50

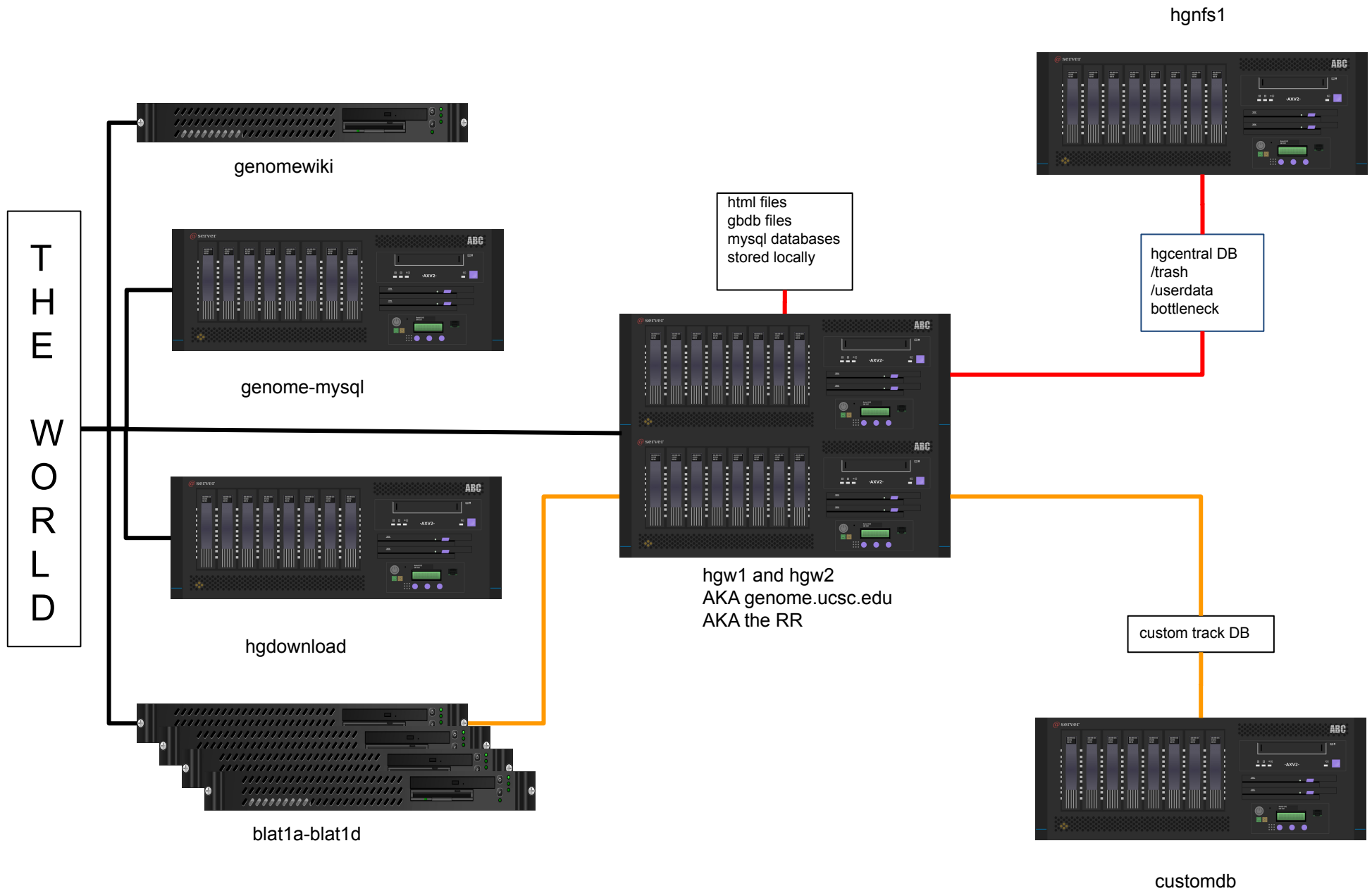
move start < 2.0 > move end < 2.0 >

track search default tracks default order hide all add custom tracks track hubs configure multi-region reverse resize refresh

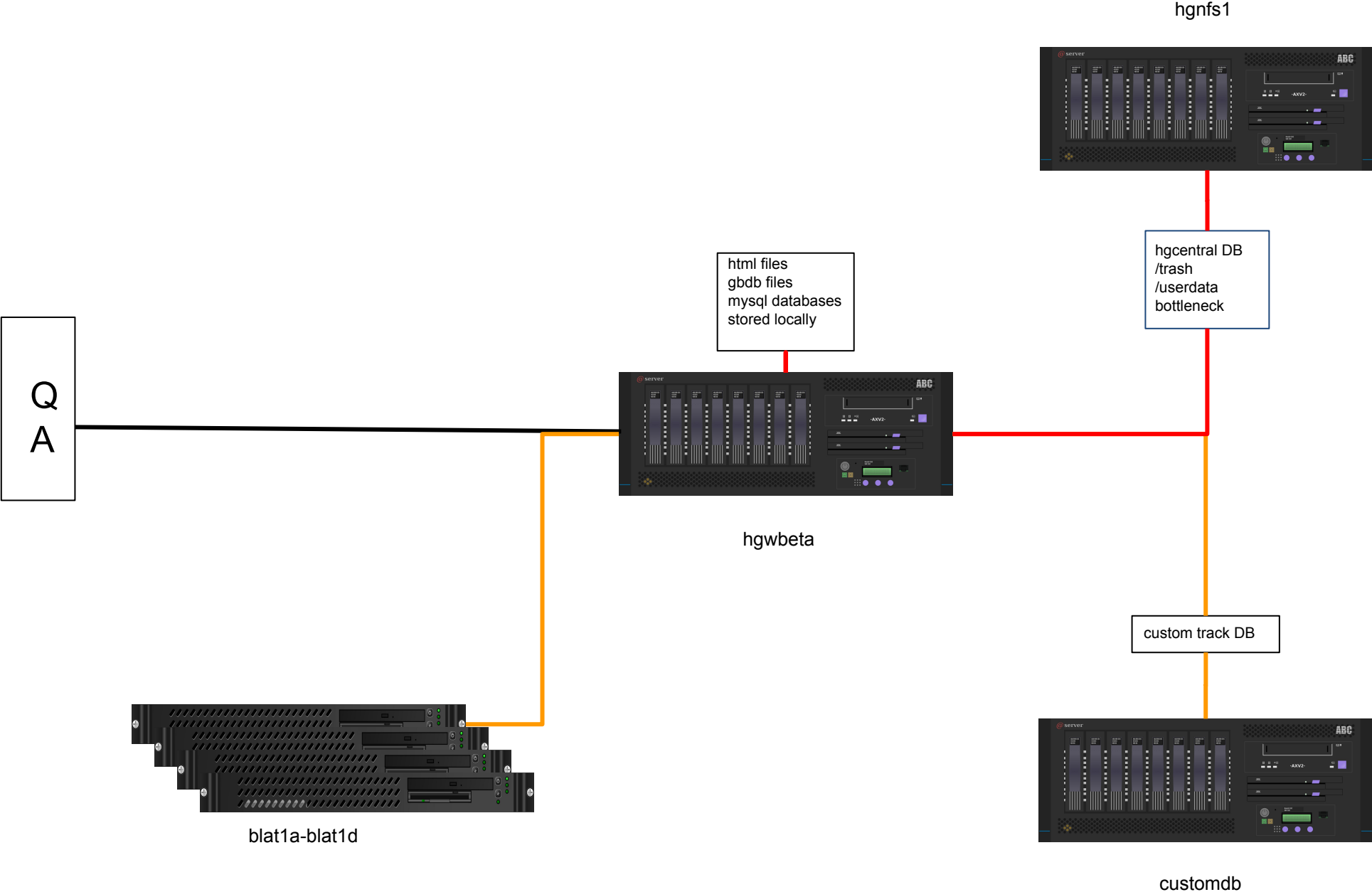
collapse all expand all

Use drop-down controls below and press refresh to alter tracks displayed. Tracks with lots of items will automatically be displayed in more compact modes.

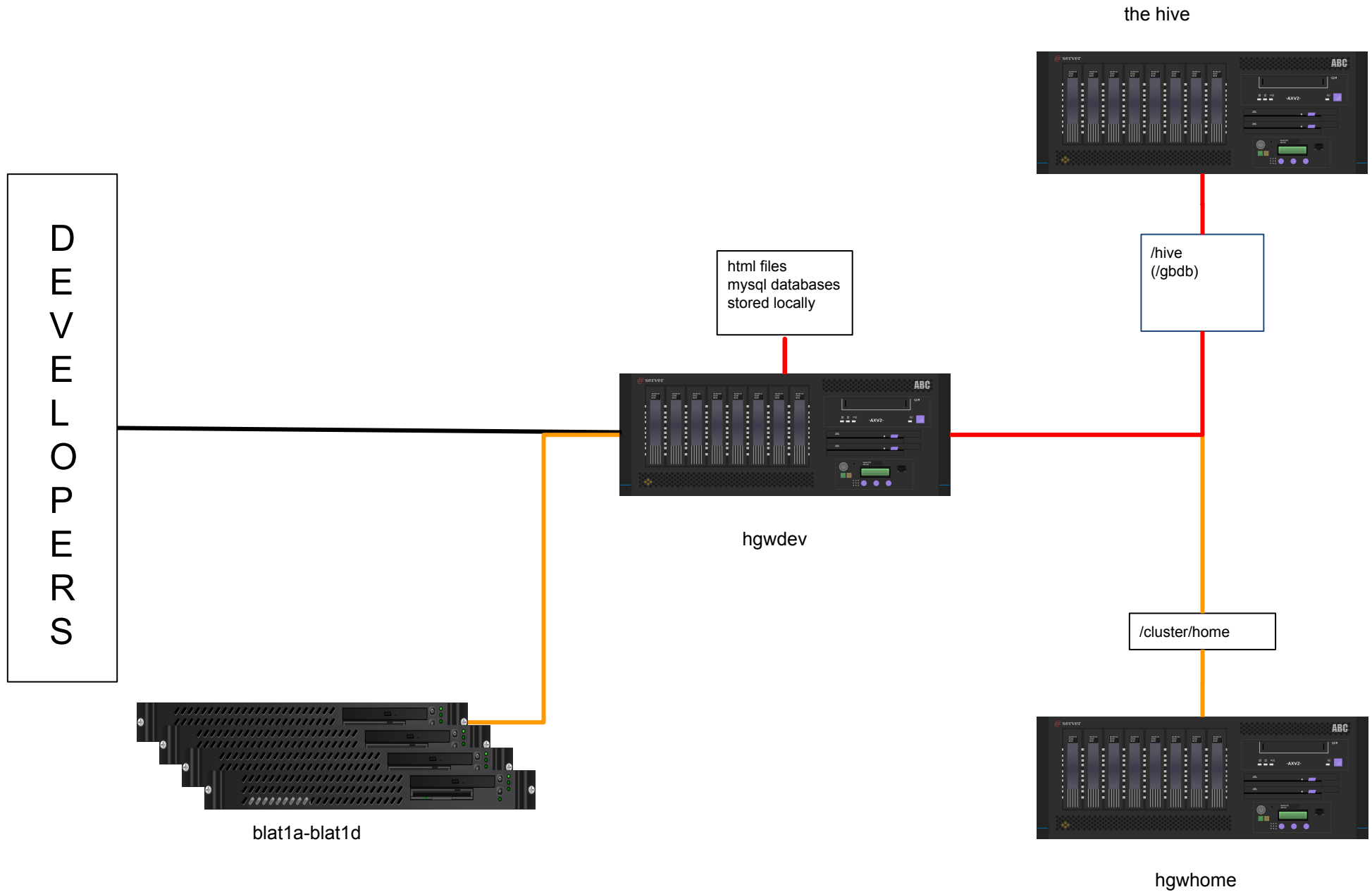
GENOME BROWSER DEPENDENCIES



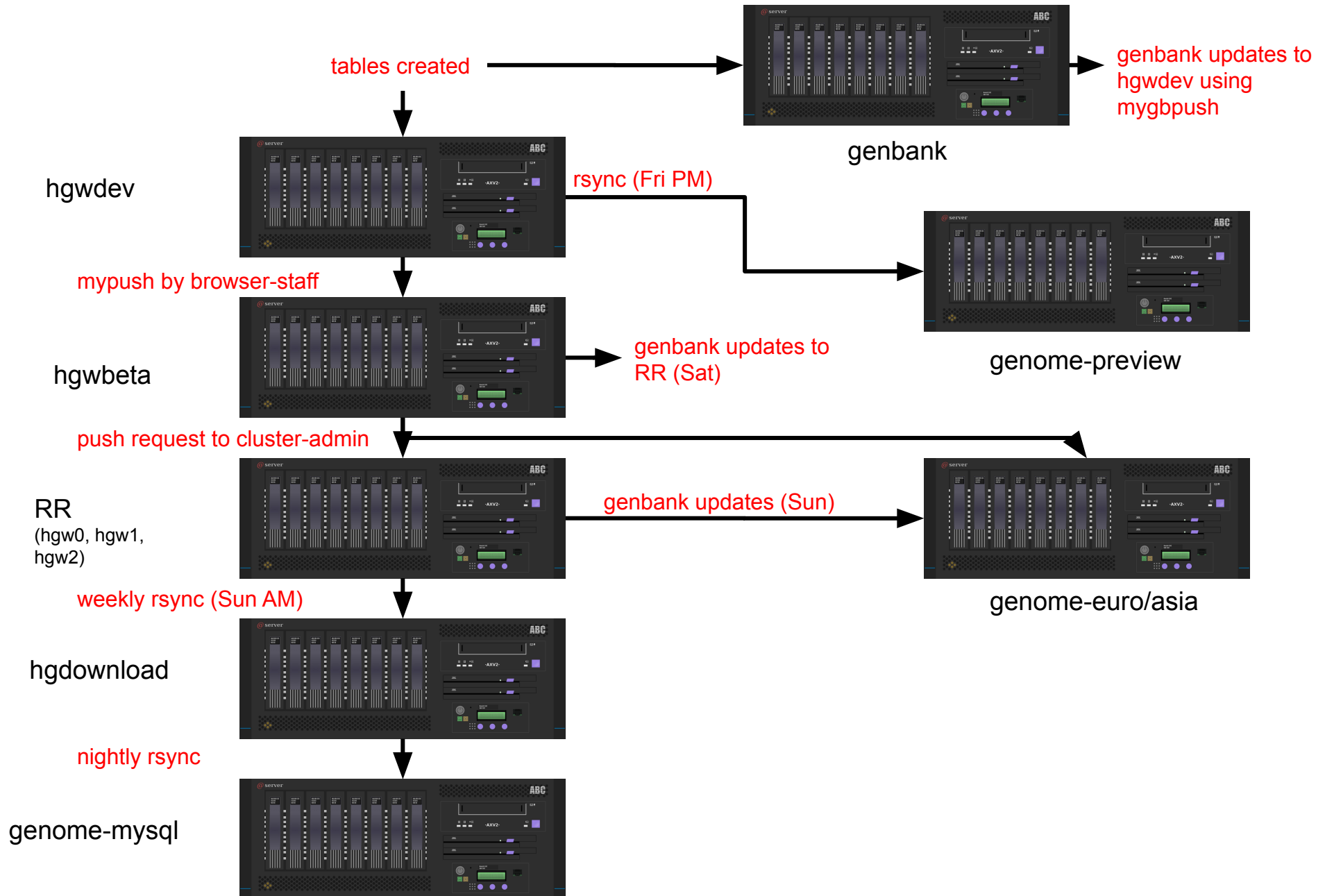
BETA TESTING DEPENDENCIES



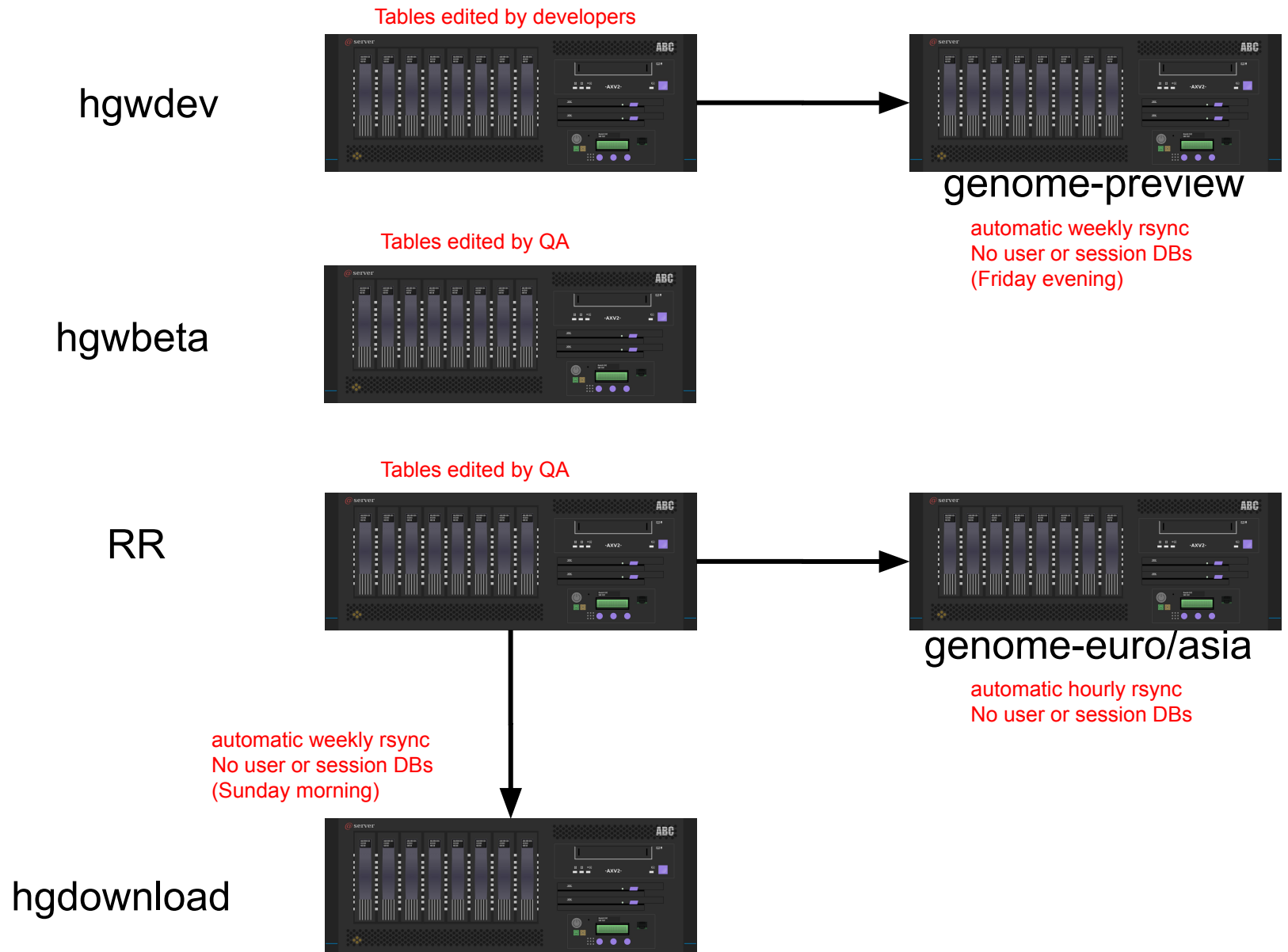
BROWSER DEVELOPMENT DEPENDENCIES



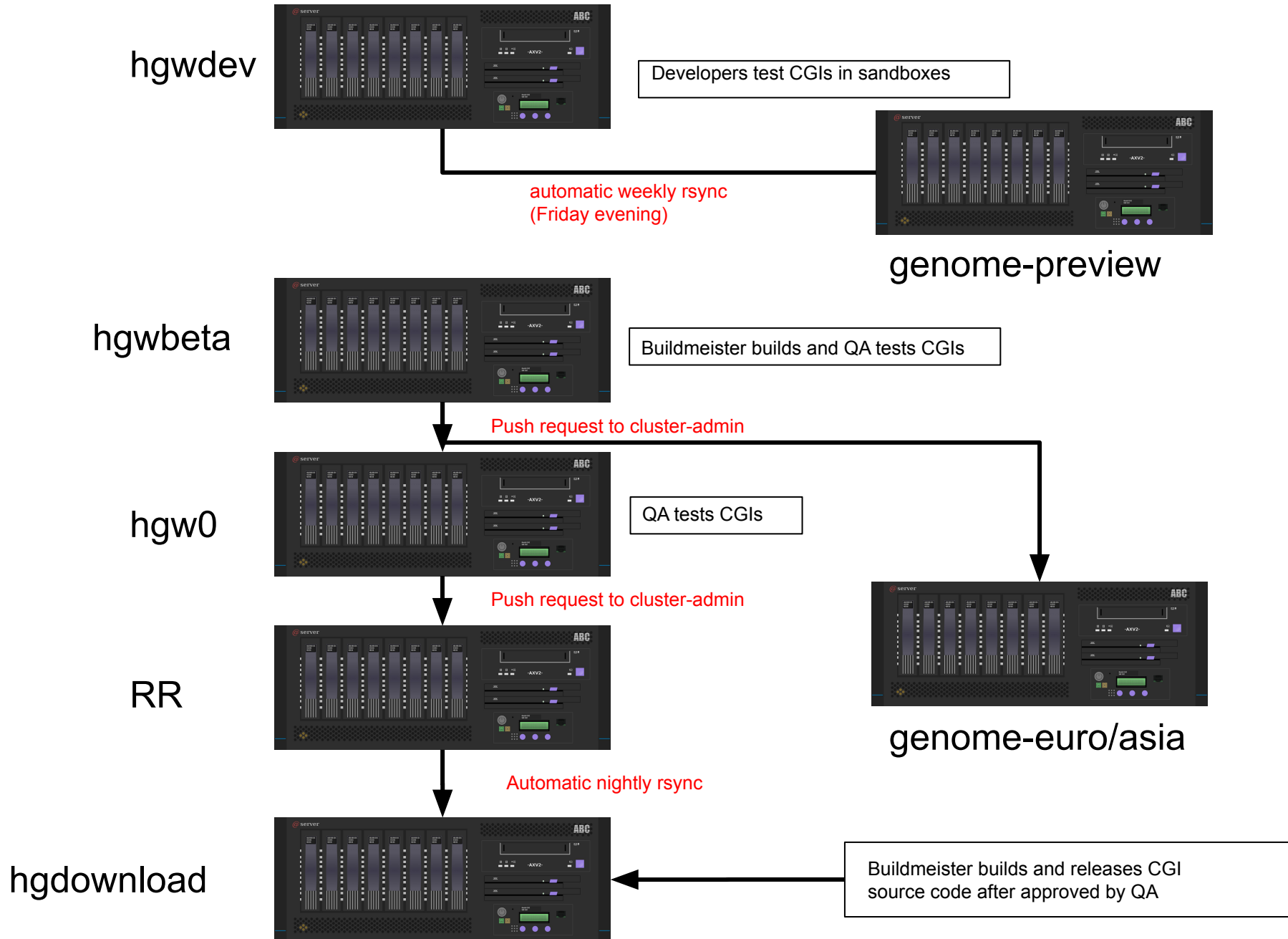
MYSQL DATA FLOW (EXCEPT HGCENTRAL)



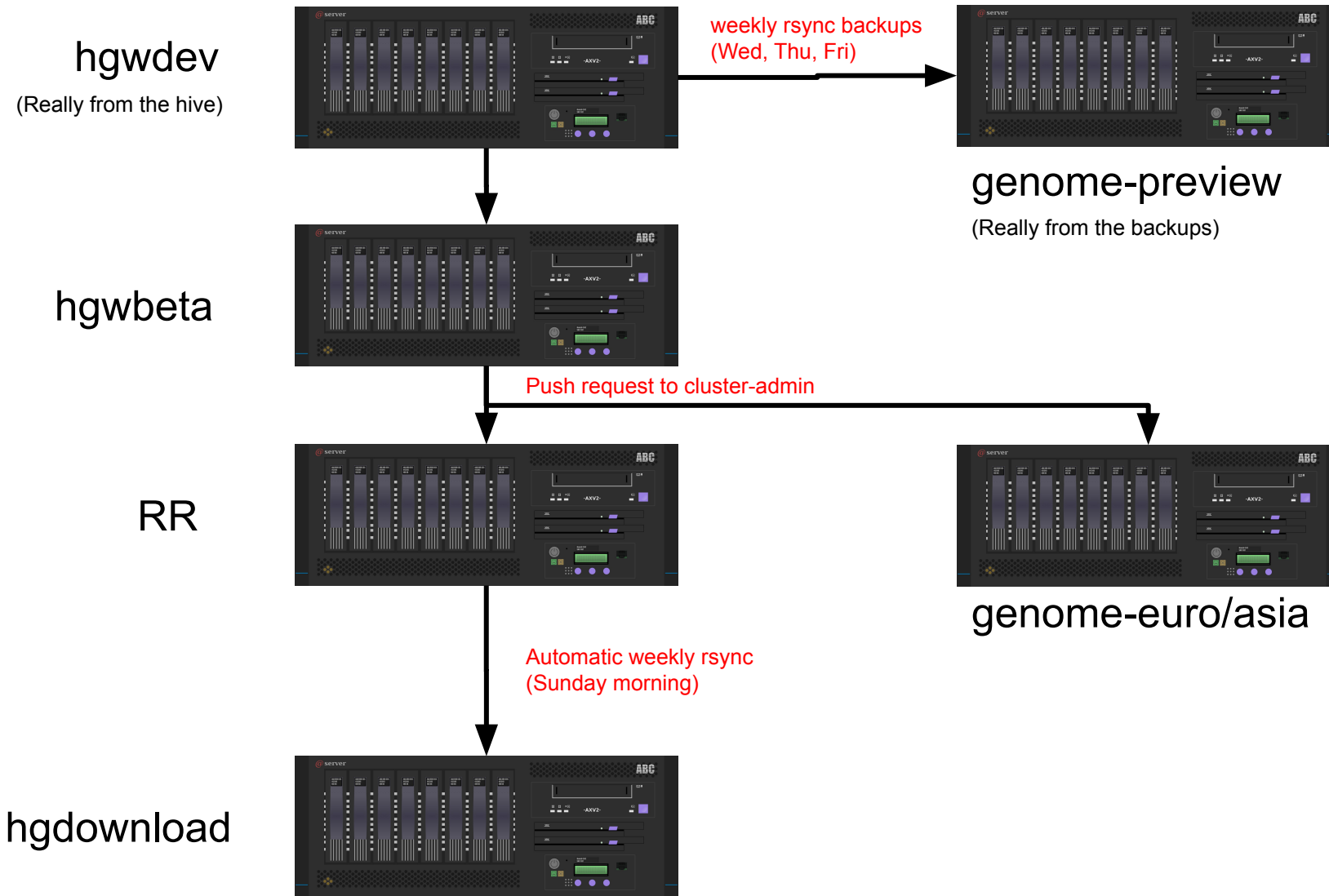
MYSQL HGCENTRAL FLOW



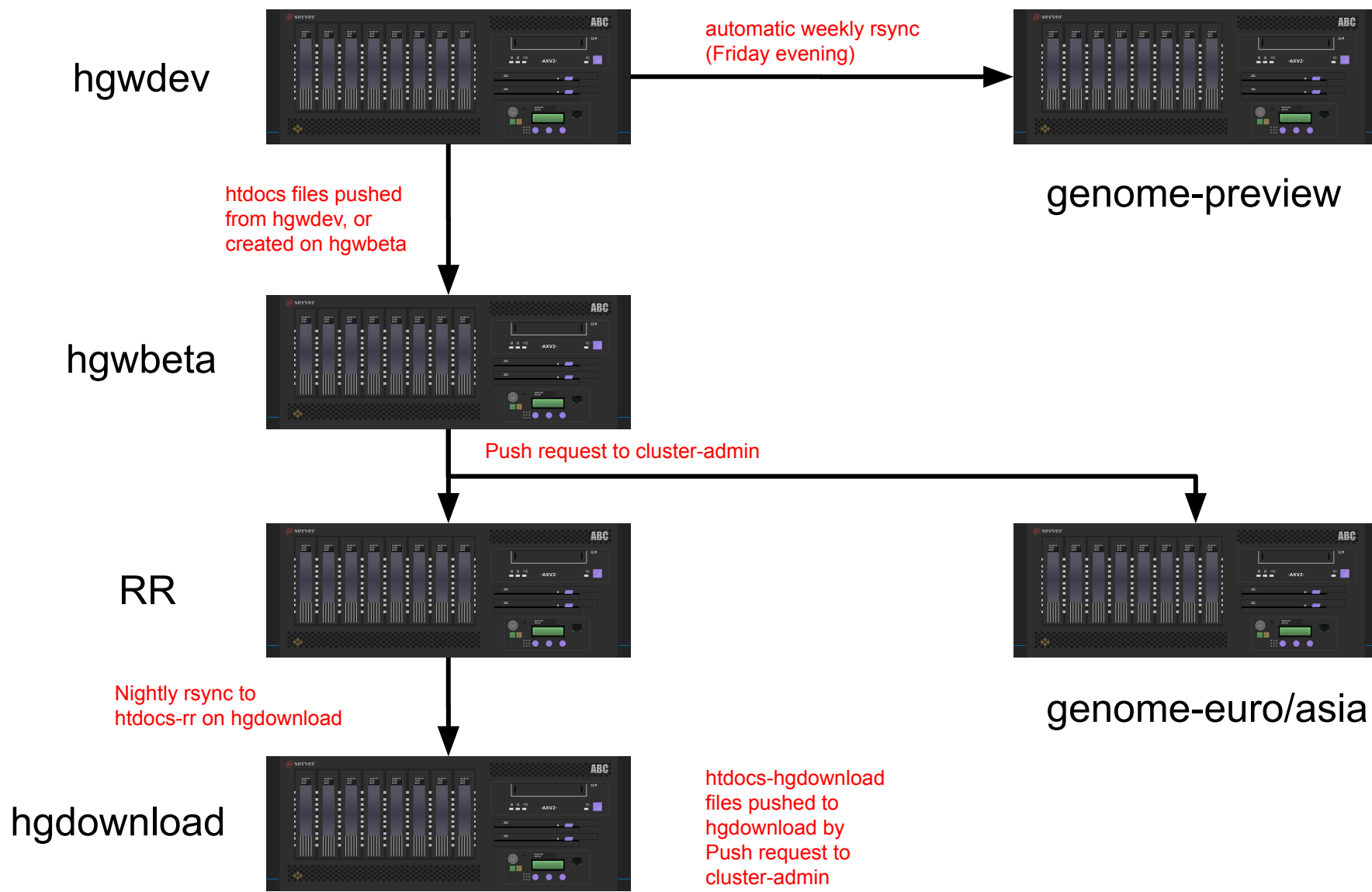
CGI DATA FLOW



GBDB DATA FLOW

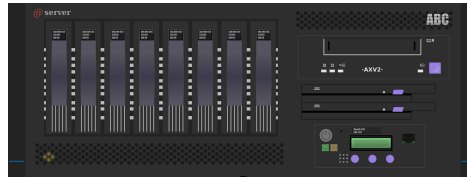


STATIC DOCS DATA FLOW



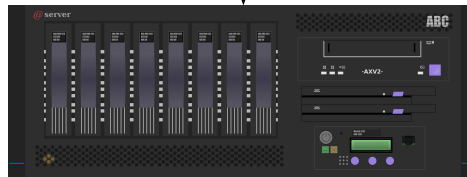
DOWNLOAD DATA FLOW

hgwdev
(Really from the hive)

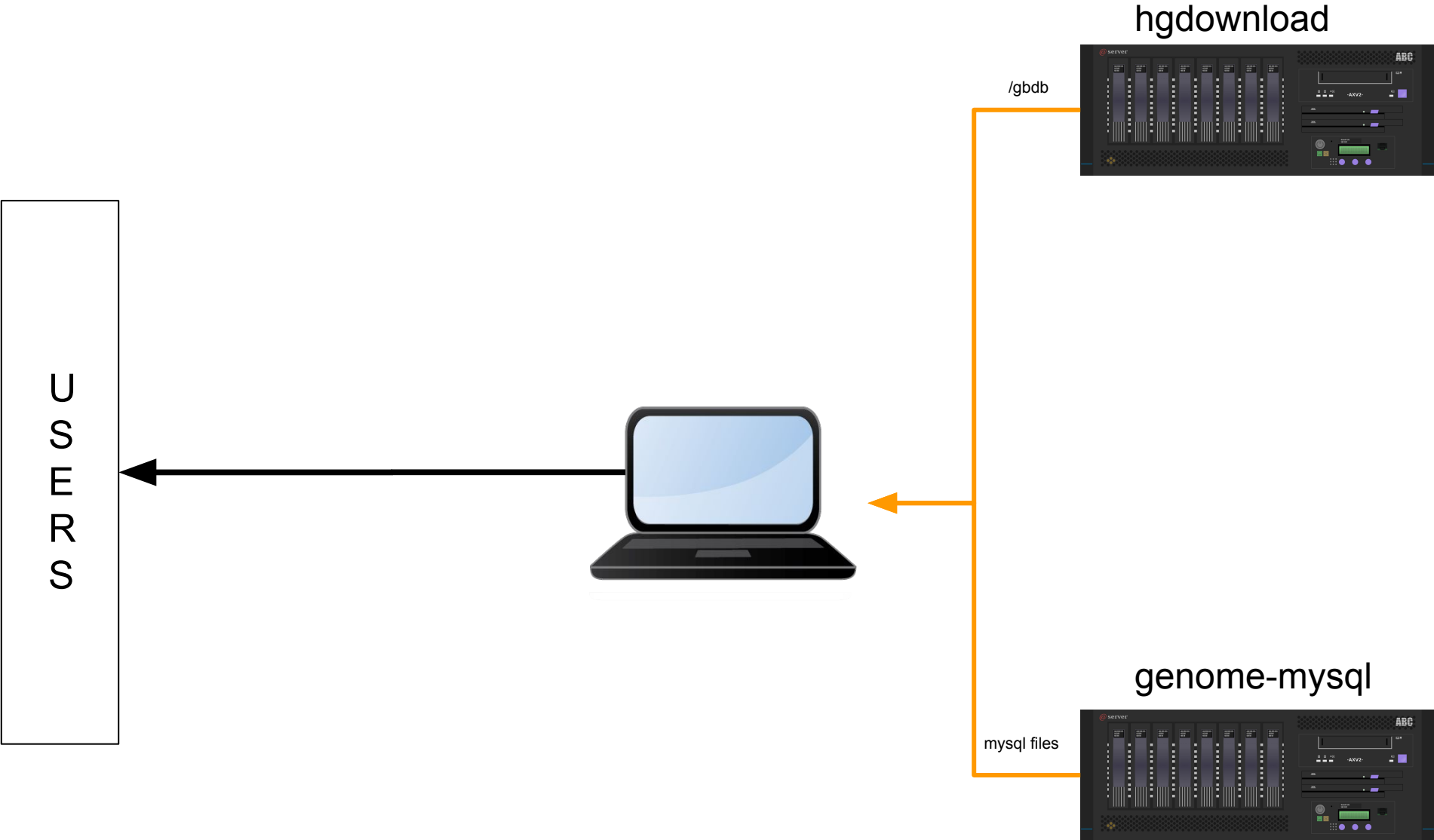


Push request to
cluster-admin

hgdownload



GBIB DEPENDENCIES



BACKUPS

AREA	APPROXIMATE SIZE	BACKUP FREQUENCY
Home directories	A few TBs	Daily (5) Weekly (3) Monthly (3)
The Hive	A few PBs	Snapshots: Daily (7), Monthly (12) Archive: Once a week.
Cirm data	Hundreds of TBs	Archive: Once a week.

- Directories named tmp, temp or *nobackup will not be archived

PRODUCTION DISASTER RECOVERY

- ❑ Archive everything under /userdata daily
- ❑ Archive mysql data from customDataNN daily
- ❑ Make a daily dump of hubStatus table
 - ❑ Keep daily dumps for a month
 - ❑ Keep one monthly dump for each month of year
- ❑ Make a weekly dump of namedSessions table
 - ❑ Rotate through 4 weekly dumps
 - ❑ Keep 2 latest monthly dumps

IN CASE OF EMERGENCY

IF THIS FAILS	THIS MAY HELP
hgwdev	genome-preview mirrors by Gill (Stanford) or Michael (Germany)
hgwbeta	hgw0 (mostly) + backups
RR	run on remaining machine, or hgw0
hgdownload	hgdownload2
customdb	customdb-b (live replication machine)
genome-mysql	convert RR machine (or hgw0)
hgnfs1	hgnfs1-b (live replication of hgcentral)
blat	blatx (most popular blat servers)