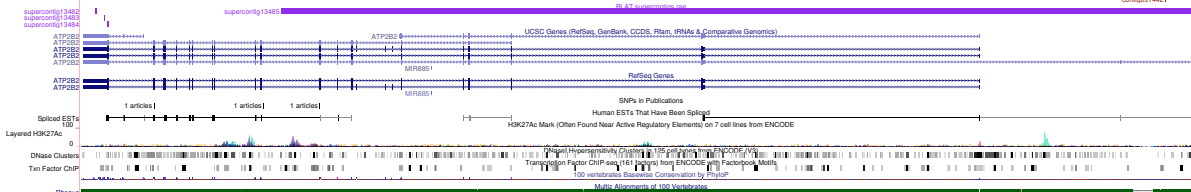
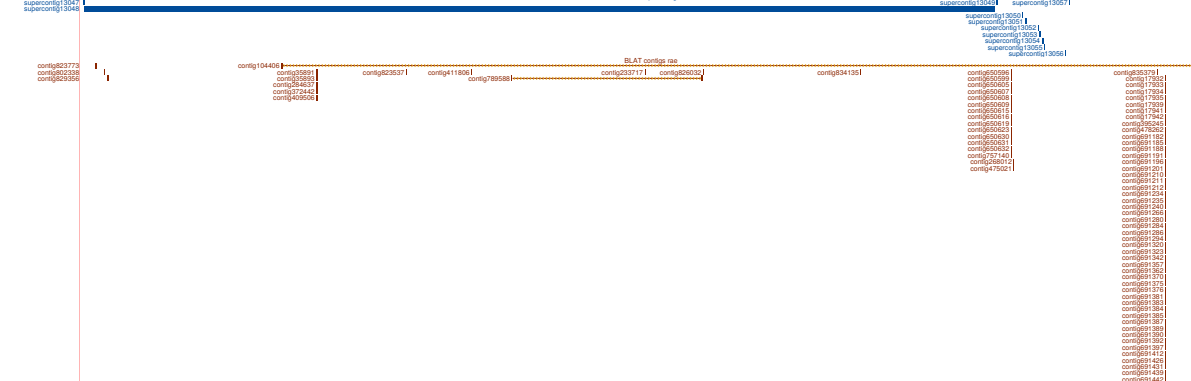
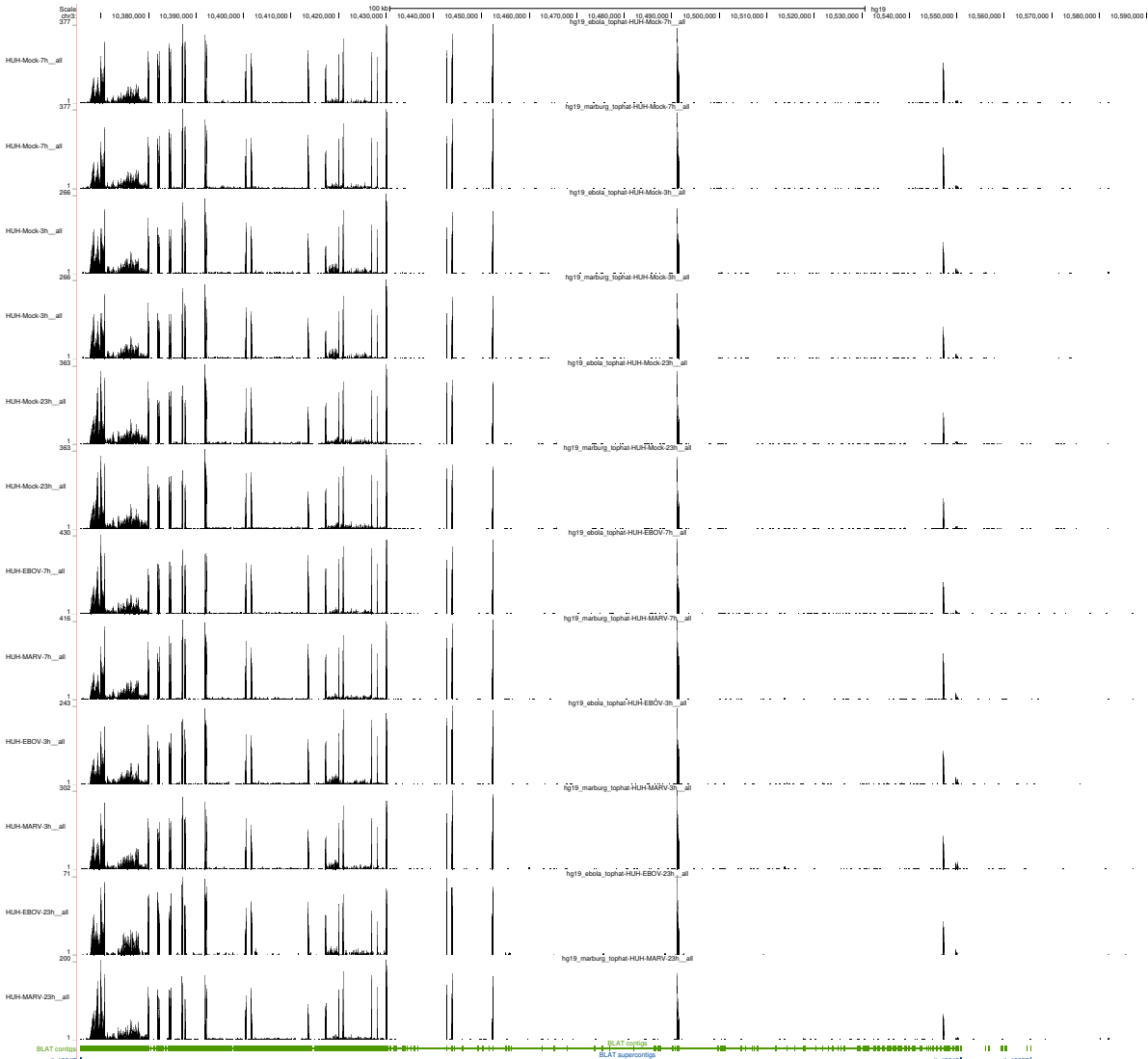


1 ATP2B2

The protein encoded by this gene belongs to the family of P-type primary ion transport ATPases characterized by the formation of an aspartyl phosphate intermediate during the reaction cycle. These enzymes remove bivalent calcium ions from eukaryotic cells against very large concentration gradients and play a critical role in intracellular calcium homeostasis. The mammalian plasma membrane calcium ATPase isoforms are encoded by at least four separate genes and the diversity of these enzymes is further increased by alternative splicing of transcripts. The expression of different isoforms and splice variants is regulated in a developmental, tissue- and cell type-specific manner, suggesting that these pumps are functionally adapted to the physiological needs of particular cells and tissues. This gene encodes the plasma membrane calcium ATPase isoform 2. Alternatively spliced transcript variants encoding different isoforms have been identified.

The gene seems to be strong downregulated in Ebola infected human cells after 23 h while the homolog in bat shows only spurious coverage.



Multiple Alignments of 200 Species

hg19	10,380,000	10,380,001	10,380,002	10,380,003	10,380,004	10,380,005	10,380,006	10,380,007	10,380,008	10,380,009	10,380,010	10,380,011	10,380,012	10,380,013	10,380,014	10,380,015	10,380,016	10,380,017	10,380,018	10,380,019	10,380,020	10,380,021	10,380,022	10,380,023	10,380,024	10,380,025	10,380,026	10,380,027	10,380,028	10,380,029	10,380,030	10,380,031	10,380,032	10,380,033	10,380,034	10,380,035	10,380,036	10,380,037	10,380,038	10,380,039	10,380,040	10,380,041	10,380,042	10,380,043	10,380,044	10,380,045	10,380,046	10,380,047	10,380,048	10,380,049	10,380,050	10,380,051	10,380,052	10,380,053	10,380,054	10,380,055	10,380,056	10,380,057	10,380,058	10,380,059	10,380,060	10,380,061	10,380,062	10,380,063	10,380,064	10,380,065	10,380,066	10,380,067	10,380,068	10,380,069	10,380,070	10,380,071	10,380,072	10,380,073	10,380,074	10,380,075	10,380,076	10,380,077	10,380,078	10,380,079	10,380,080	10,380,081	10,380,082	10,380,083	10,380,084	10,380,085	10,380,086	10,380,087	10,380,088	10,380,089	10,380,090	10,380,091	10,380,092	10,380,093	10,380,094	10,380,095	10,380,096	10,380,097	10,380,098	10,380,099	10,380,100	10,380,101	10,380,102	10,380,103	10,380,104	10,380,105	10,380,106	10,380,107	10,380,108	10,380,109	10,380,110	10,380,111	10,380,112	10,380,113	10,380,114	10,380,115	10,380,116	10,380,117	10,380,118	10,380,119	10,380,120	10,380,121	10,380,122	10,380,123	10,380,124	10,380,125	10,380,126	10,380,127	10,380,128	10,380,129	10,380,130	10,380,131	10,380,132	10,380,133	10,380,134	10,380,135	10,380,136	10,380,137	10,380,138	10,380,139	10,380,140	10,380,141	10,380,142	10,380,143	10,380,144	10,380,145	10,380,146	10,380,147	10,380,148	10,380,149	10,380,150	10,380,151	10,380,152	10,380,153	10,380,154	10,380,155	10,380,156	10,380,157	10,380,158	10,380,159	10,380,160	10,380,161	10,380,162	10,380,163	10,380,164	10,380,165	10,380,166	10,380,167	10,380,168	10,380,169	10,380,170	10,380,171	10,380,172	10,380,173	10,380,174	10,380,175	10,380,176	10,380,177	10,380,178	10,380,179	10,380,180	10,380,181	10,380,182	10,380,183	10,380,184	10,380,185	10,380,186	10,380,187	10,380,188	10,380,189	10,380,190	10,380,191	10,380,192	10,380,193	10,380,194	10,380,195	10,380,196	10,380,197	10,380,198	10,380,199	10,380,200
------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------	------------