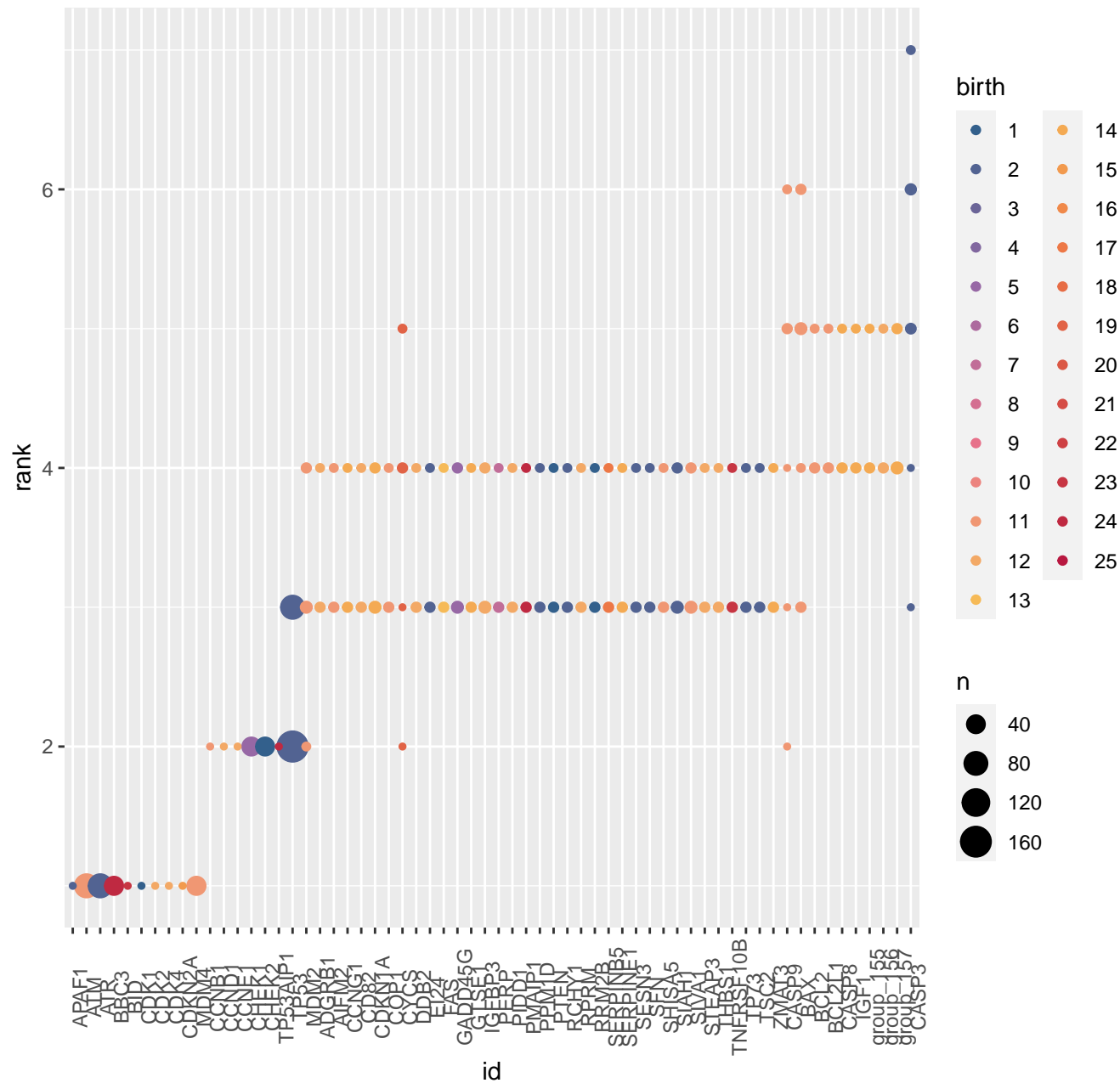
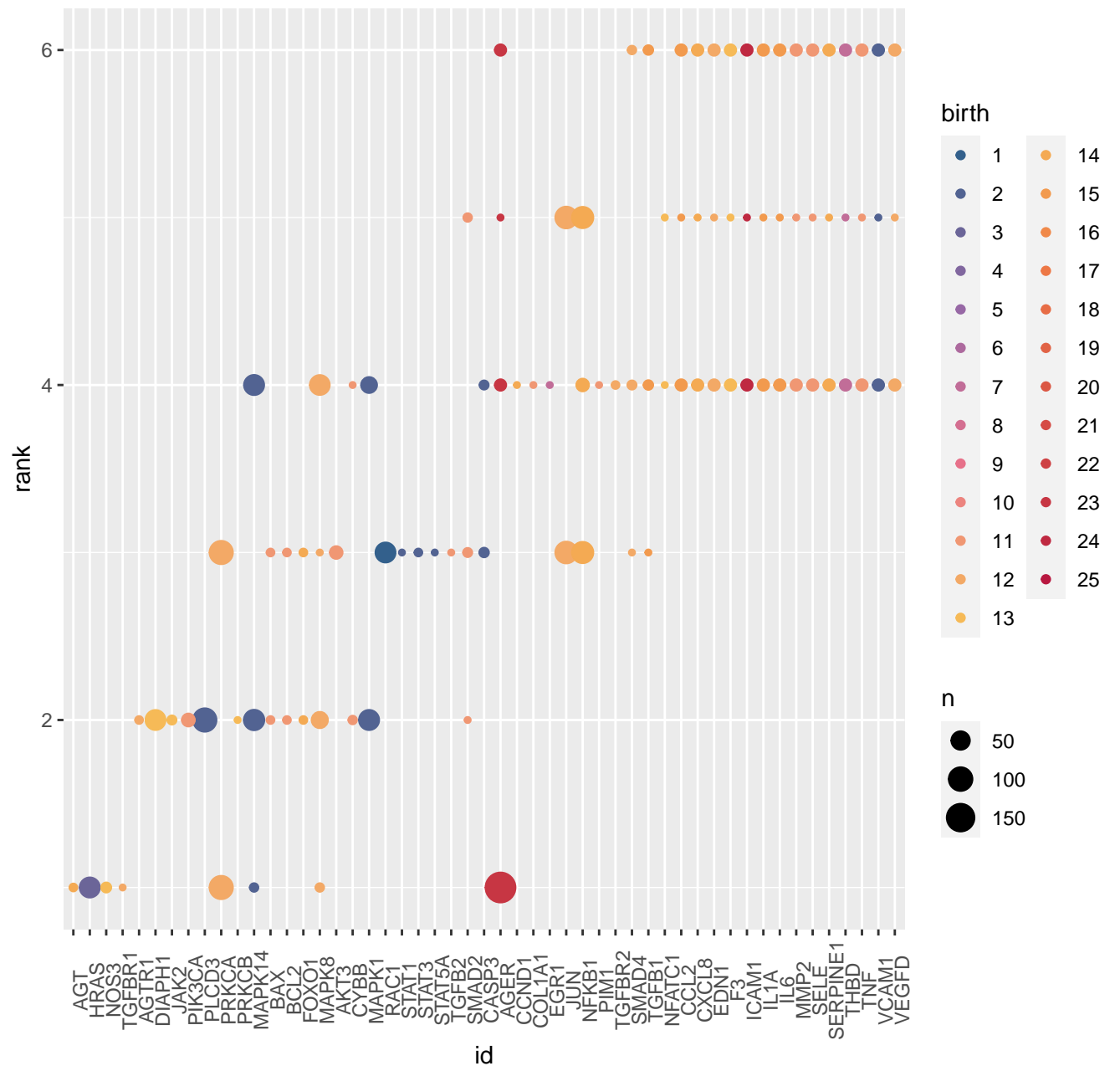


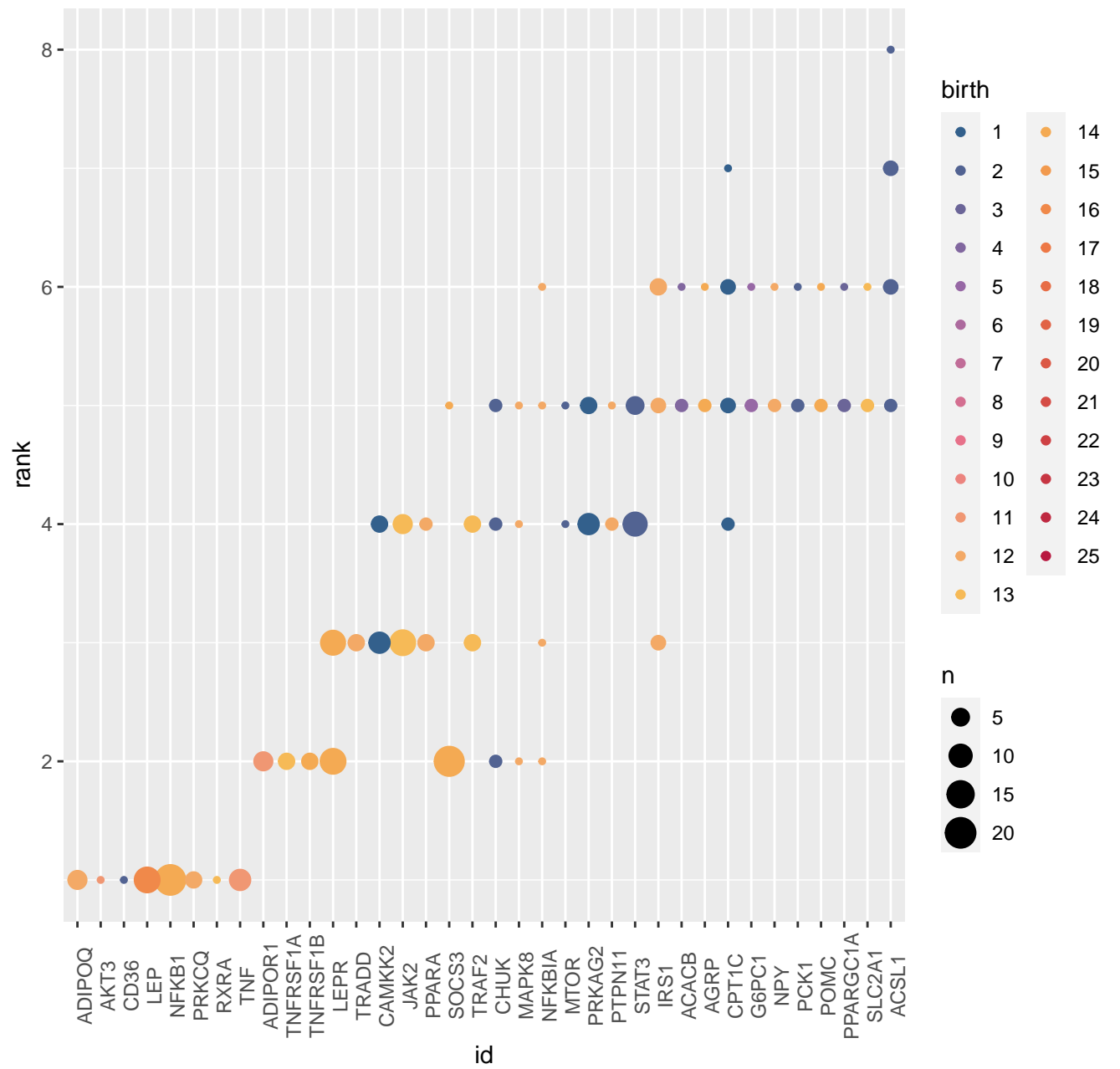
p53



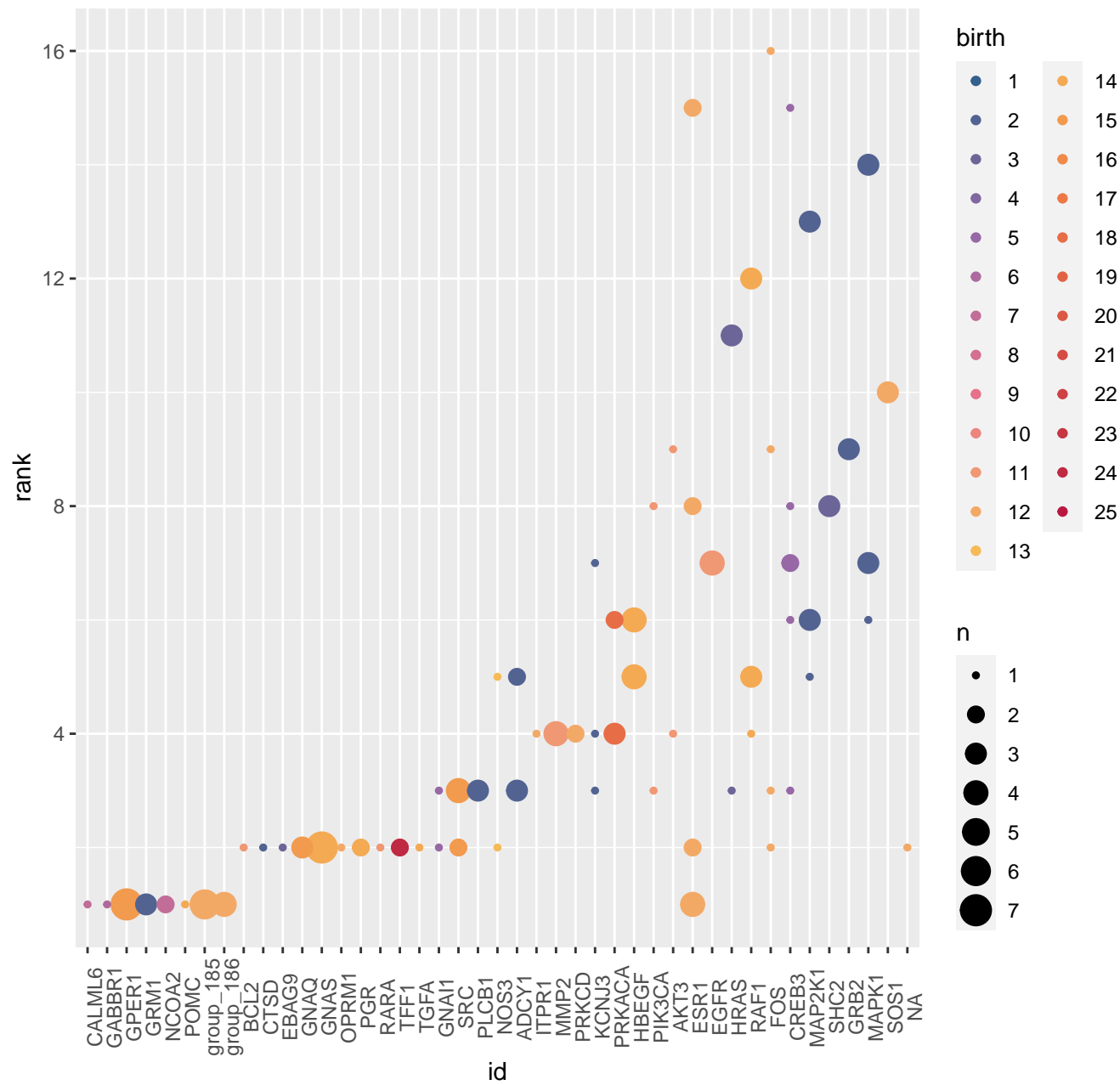
AGE-RAGE



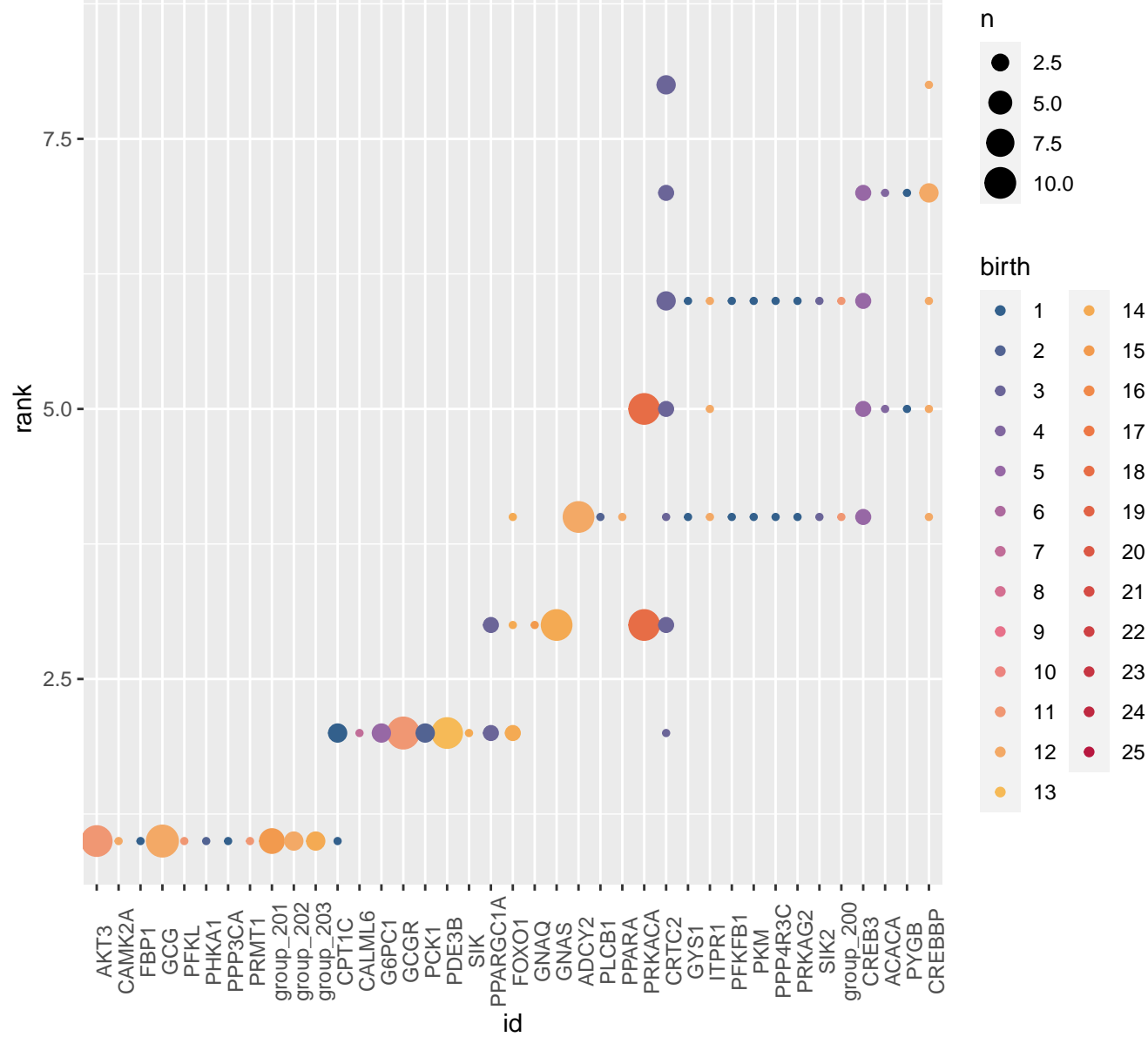
Adipocytokine



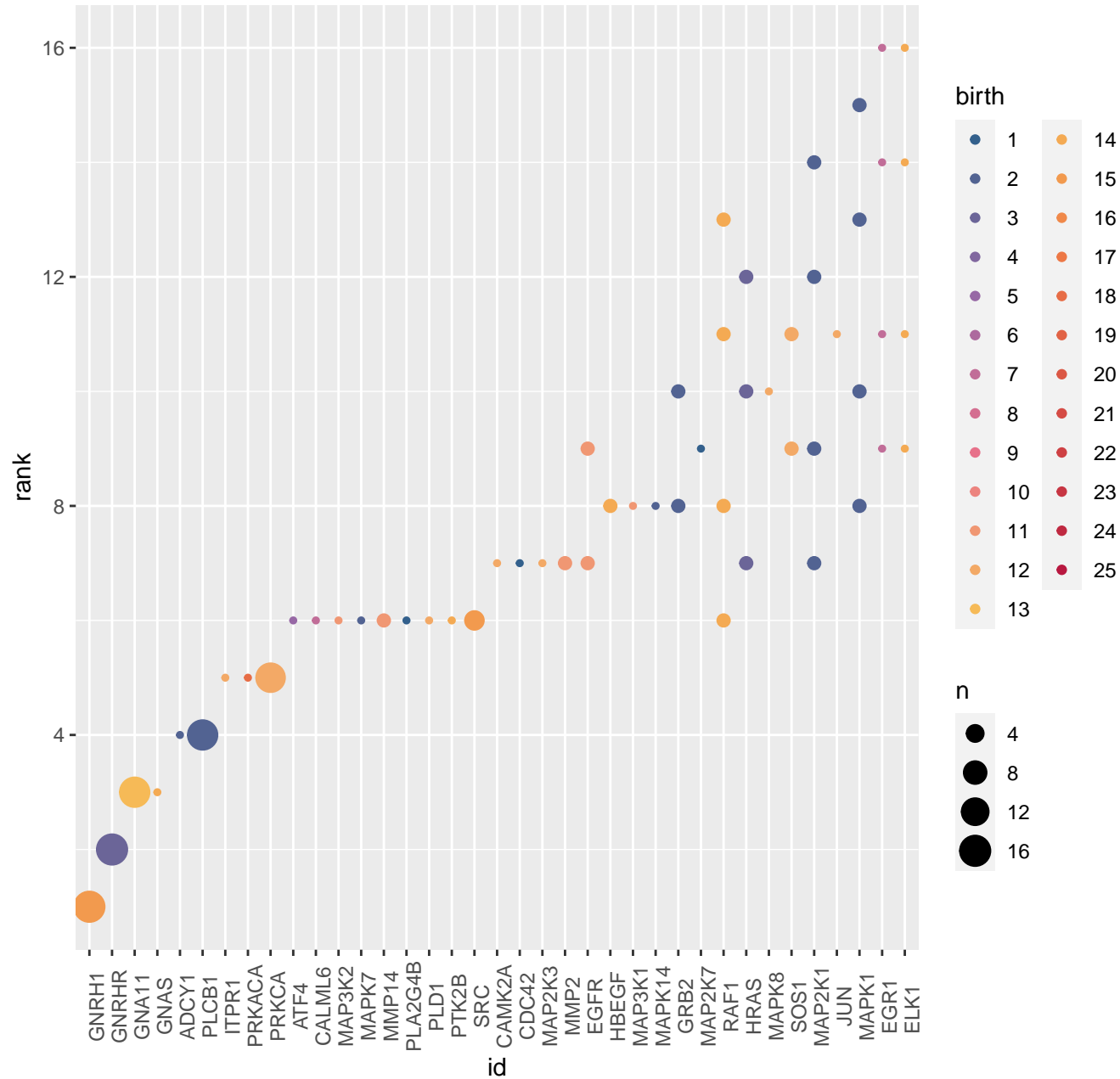
Estrogen



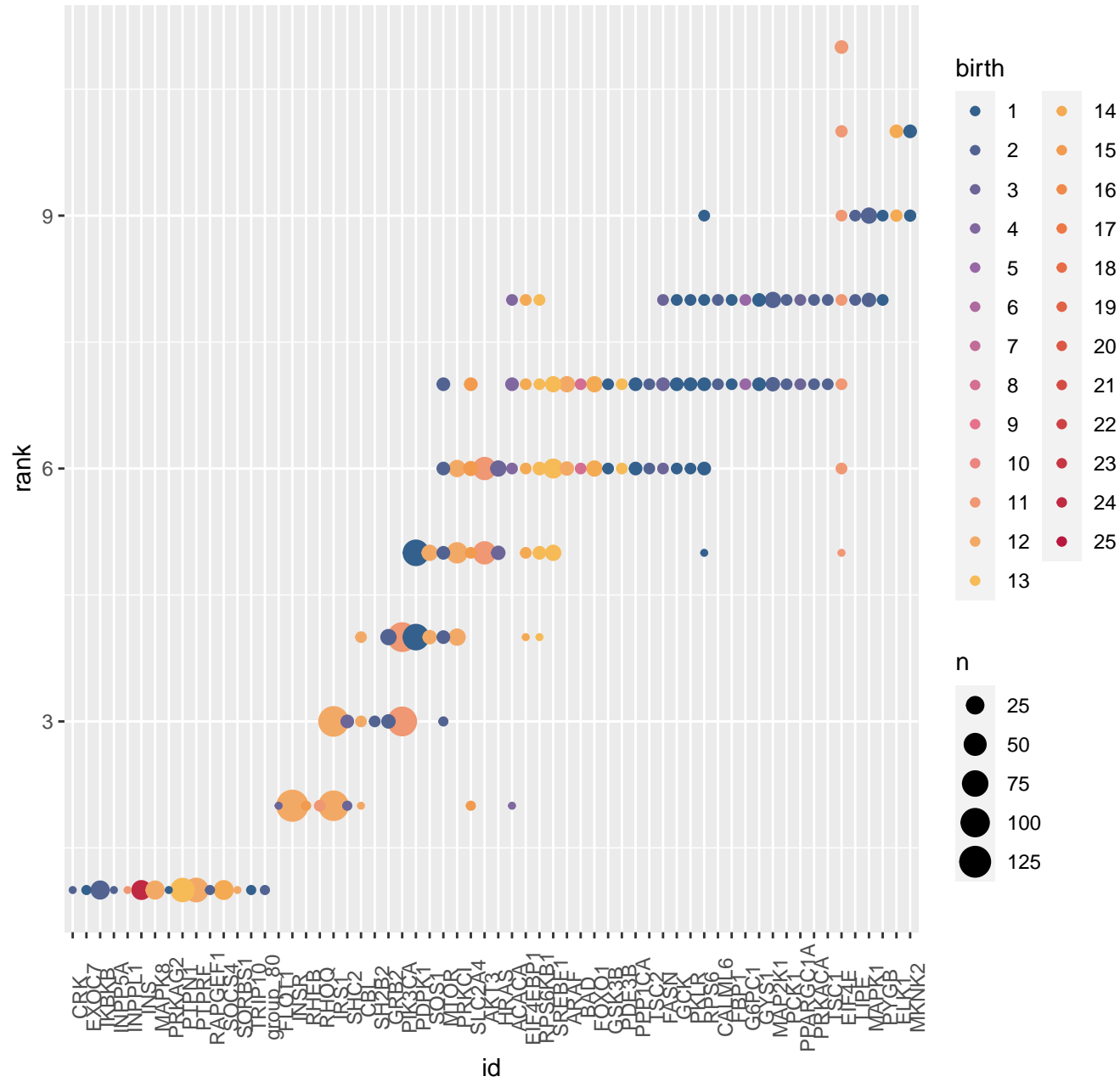
Glucagon



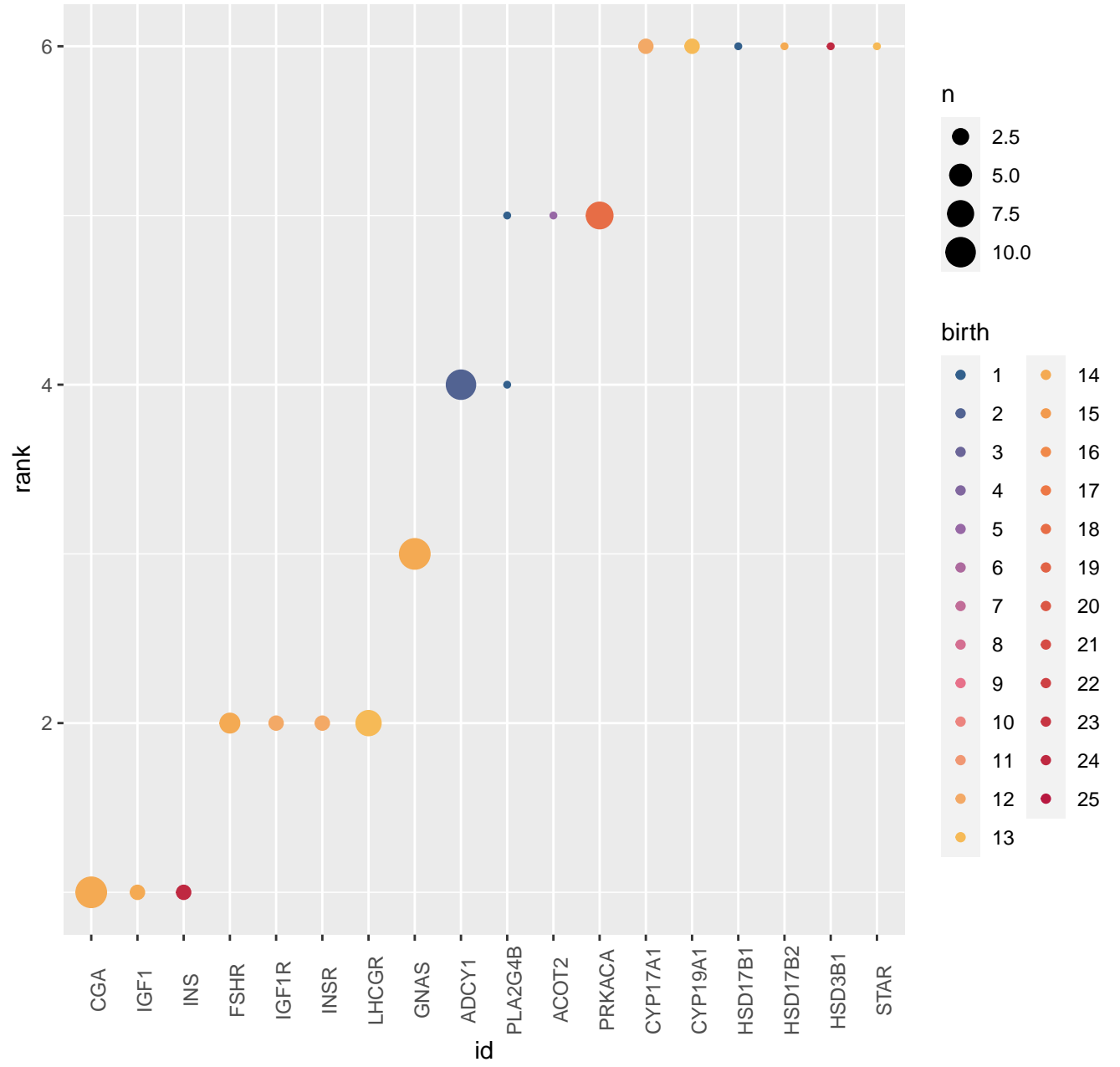
GnRH



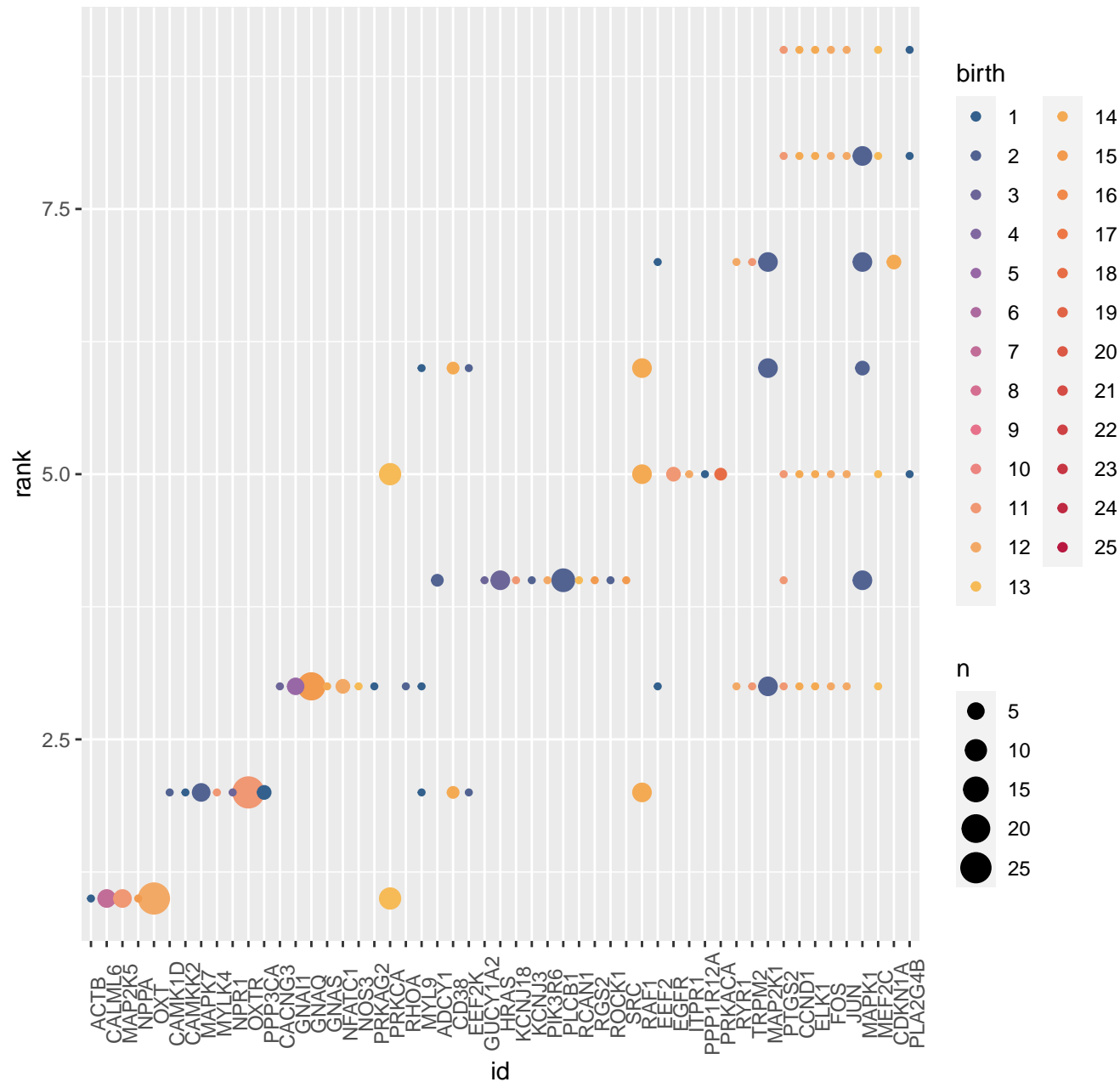
Insulin



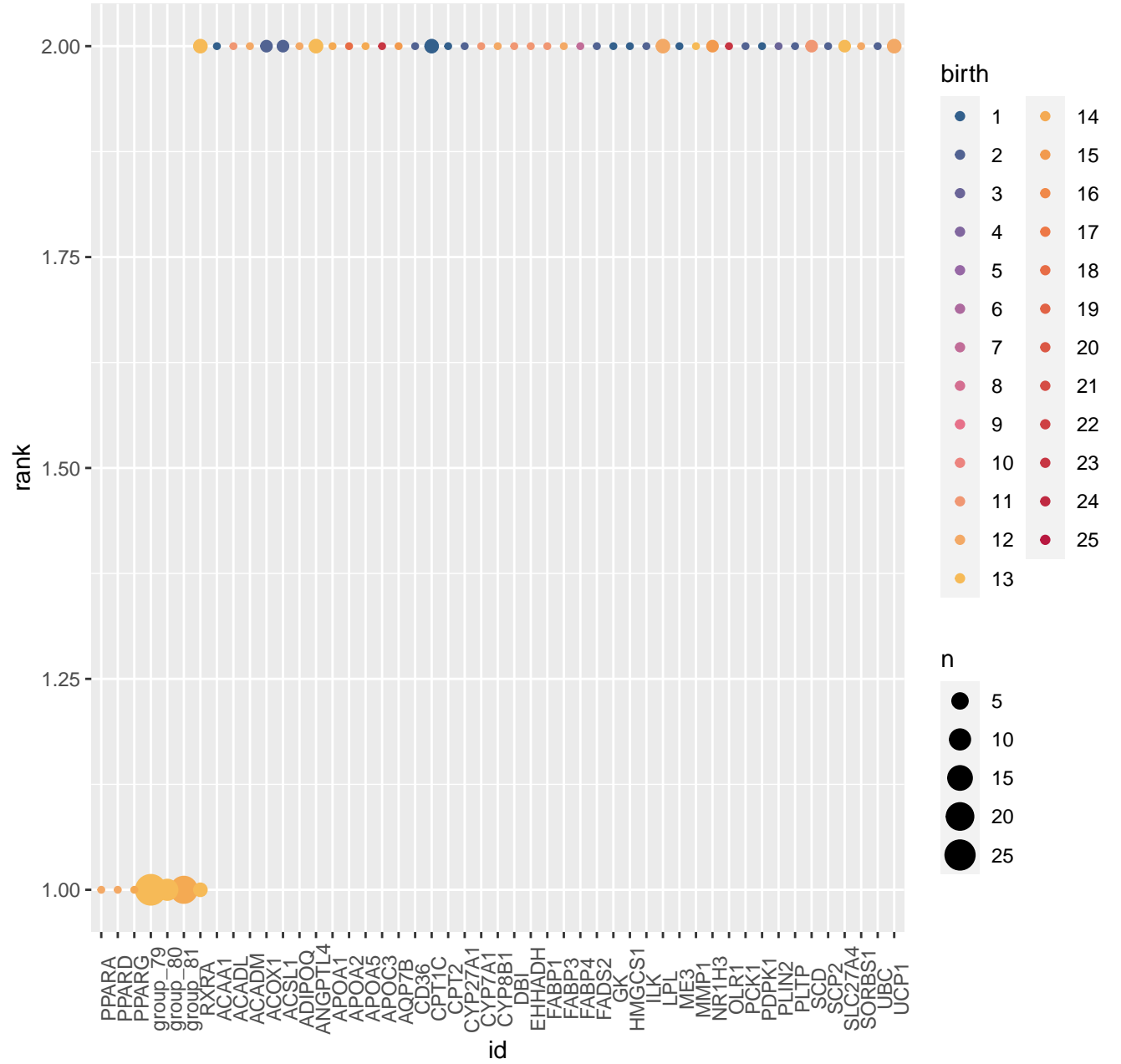
Ovarian steroidogenesis



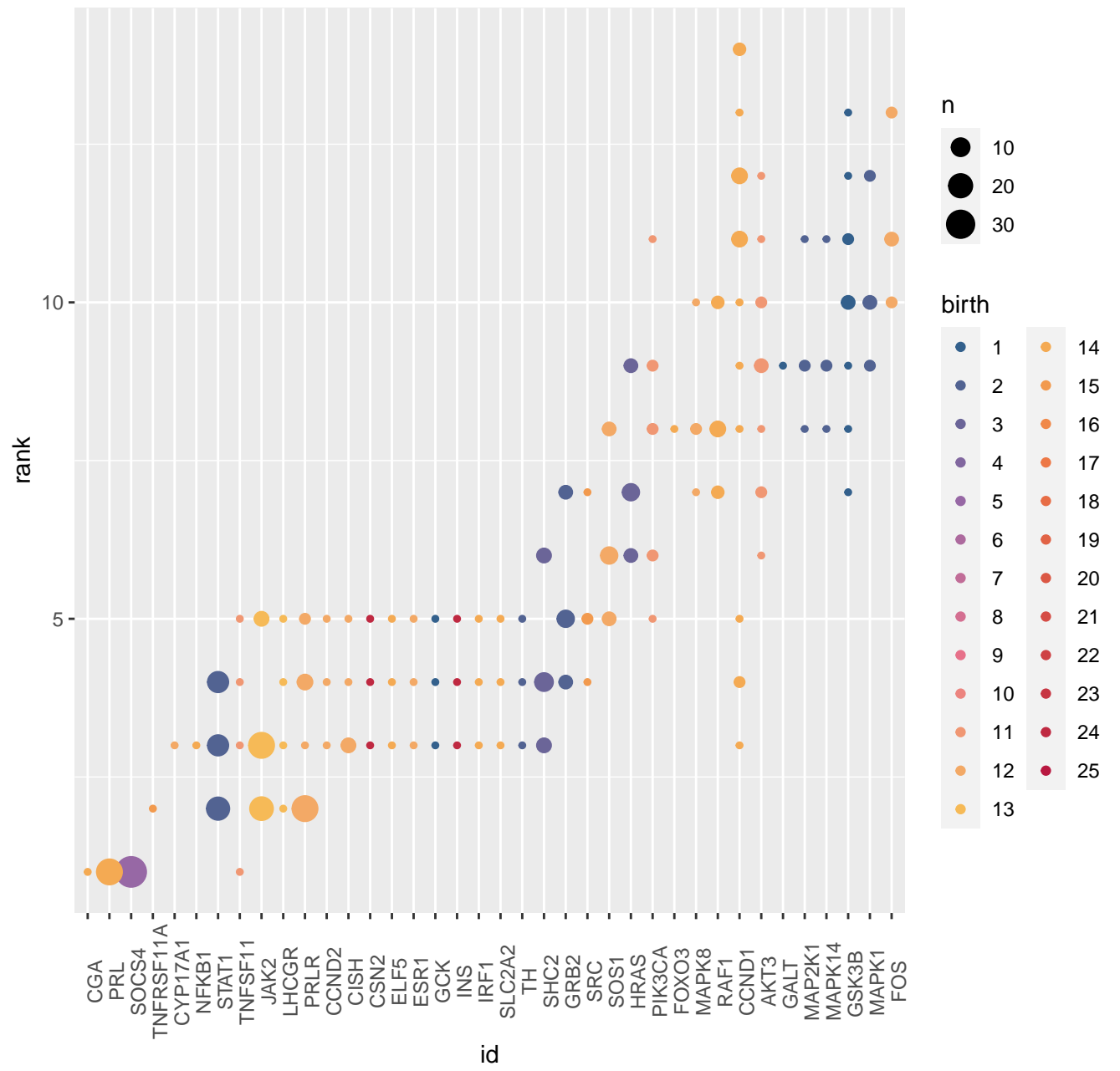
Oxytocin



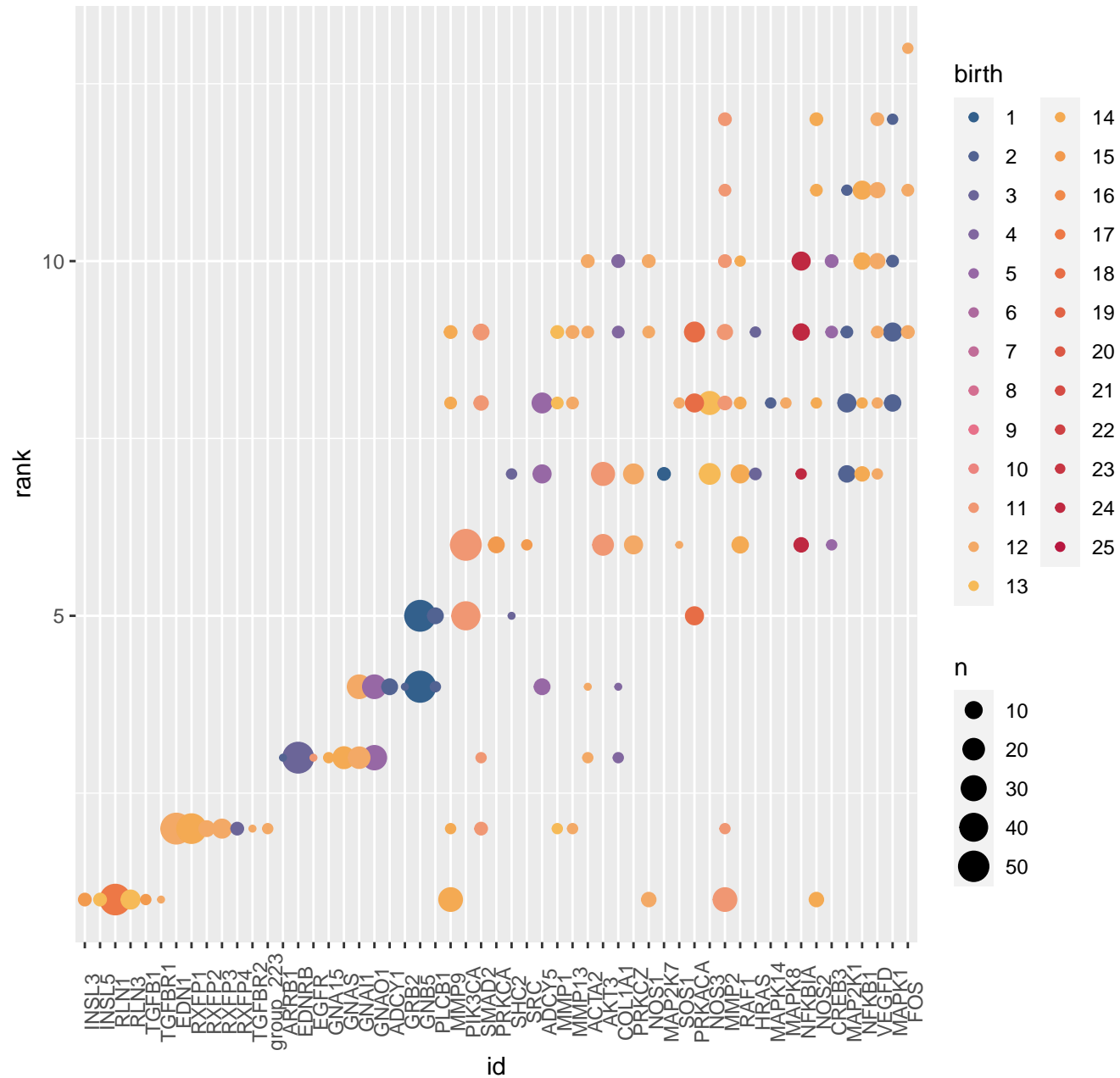
PPAR



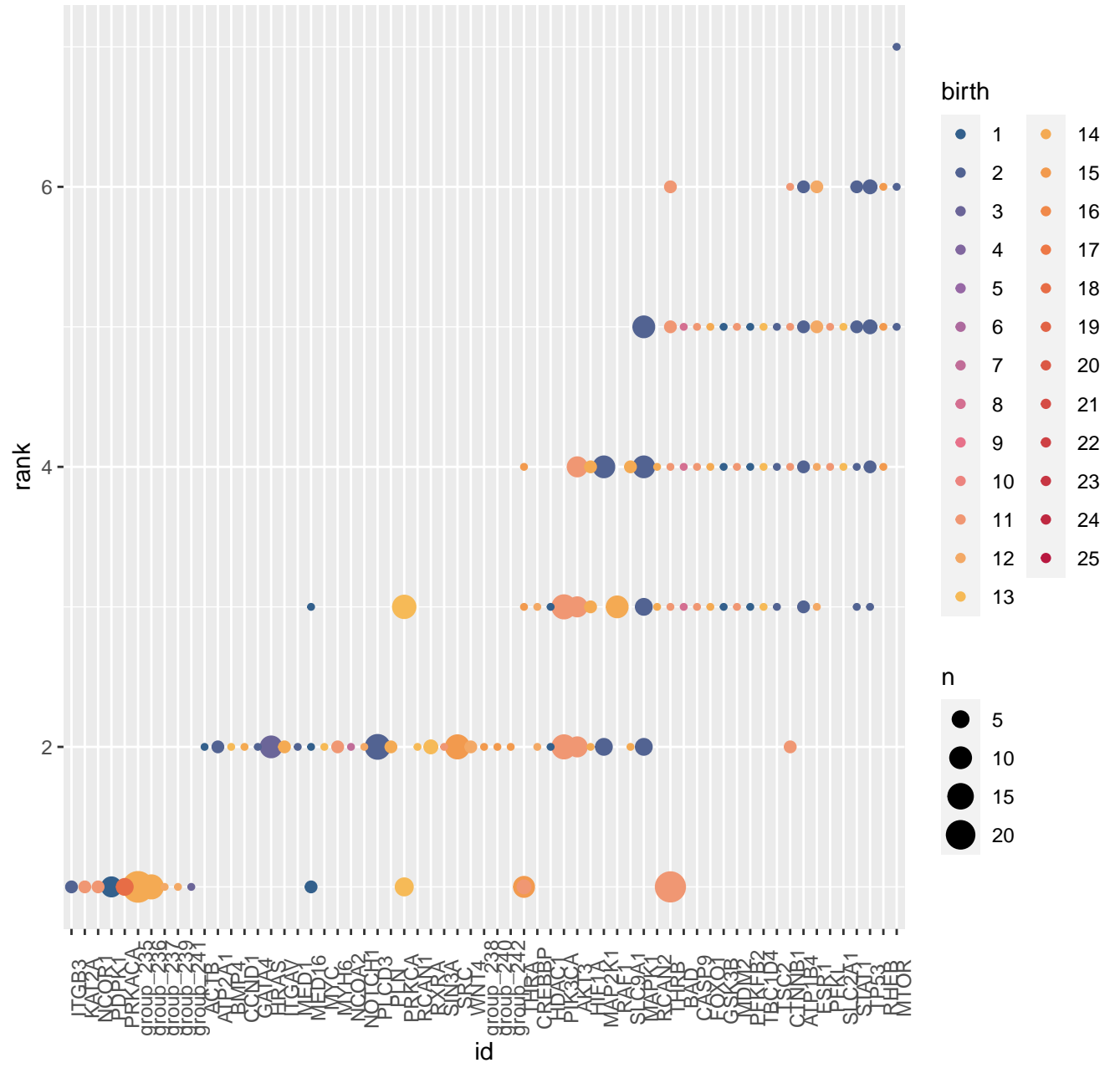
Prolactin



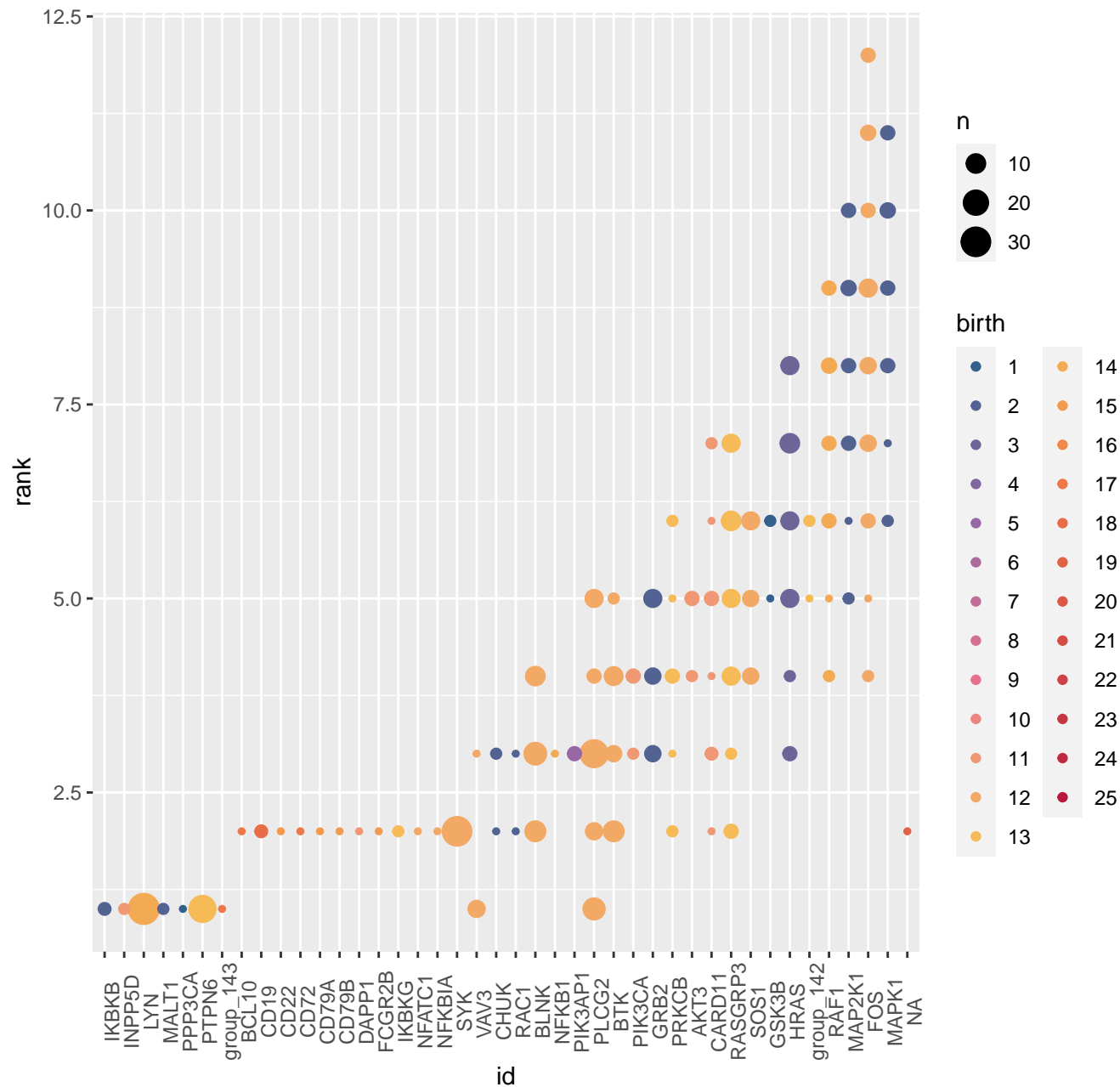
Relaxin



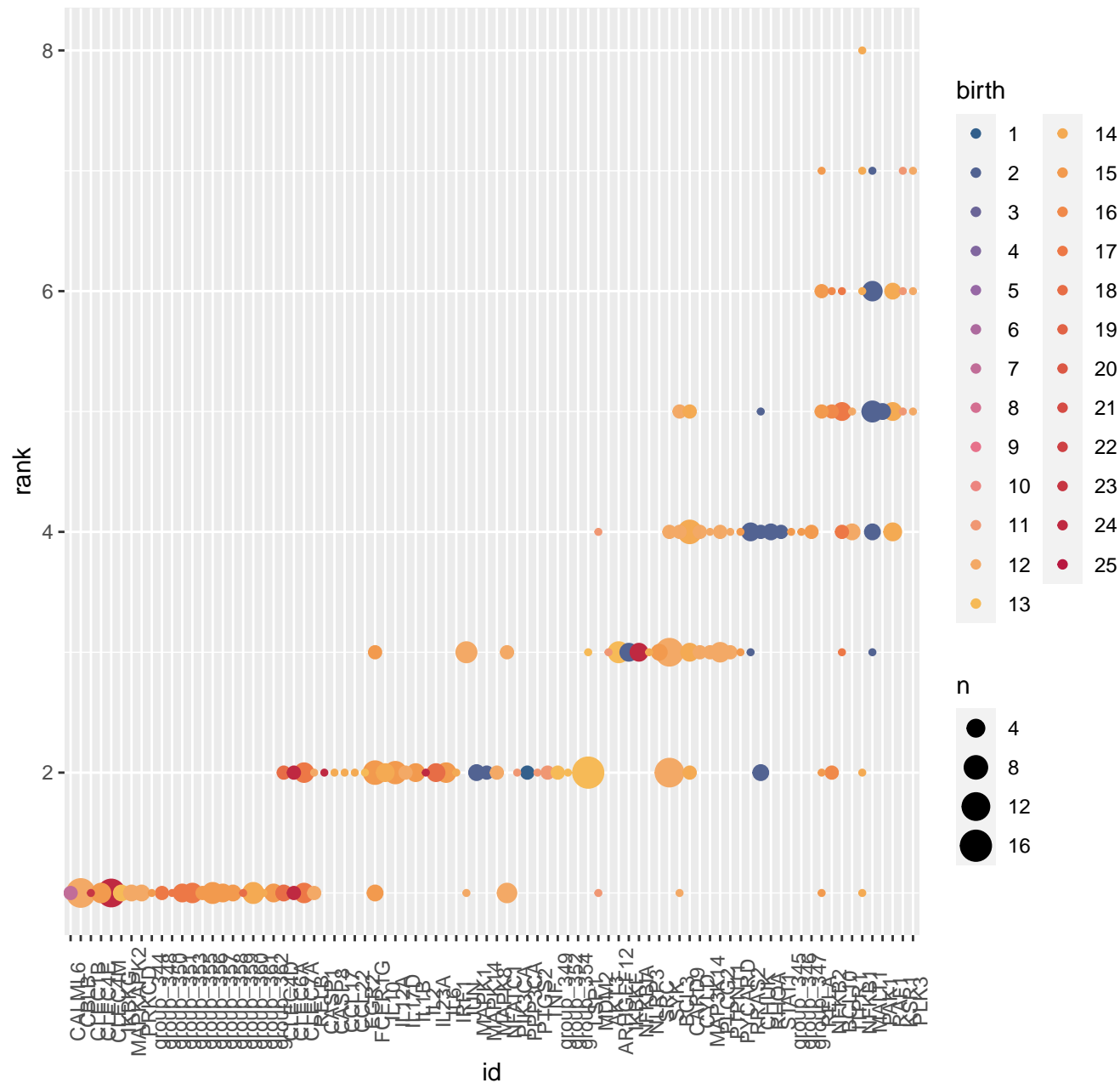
Thyroid hormone



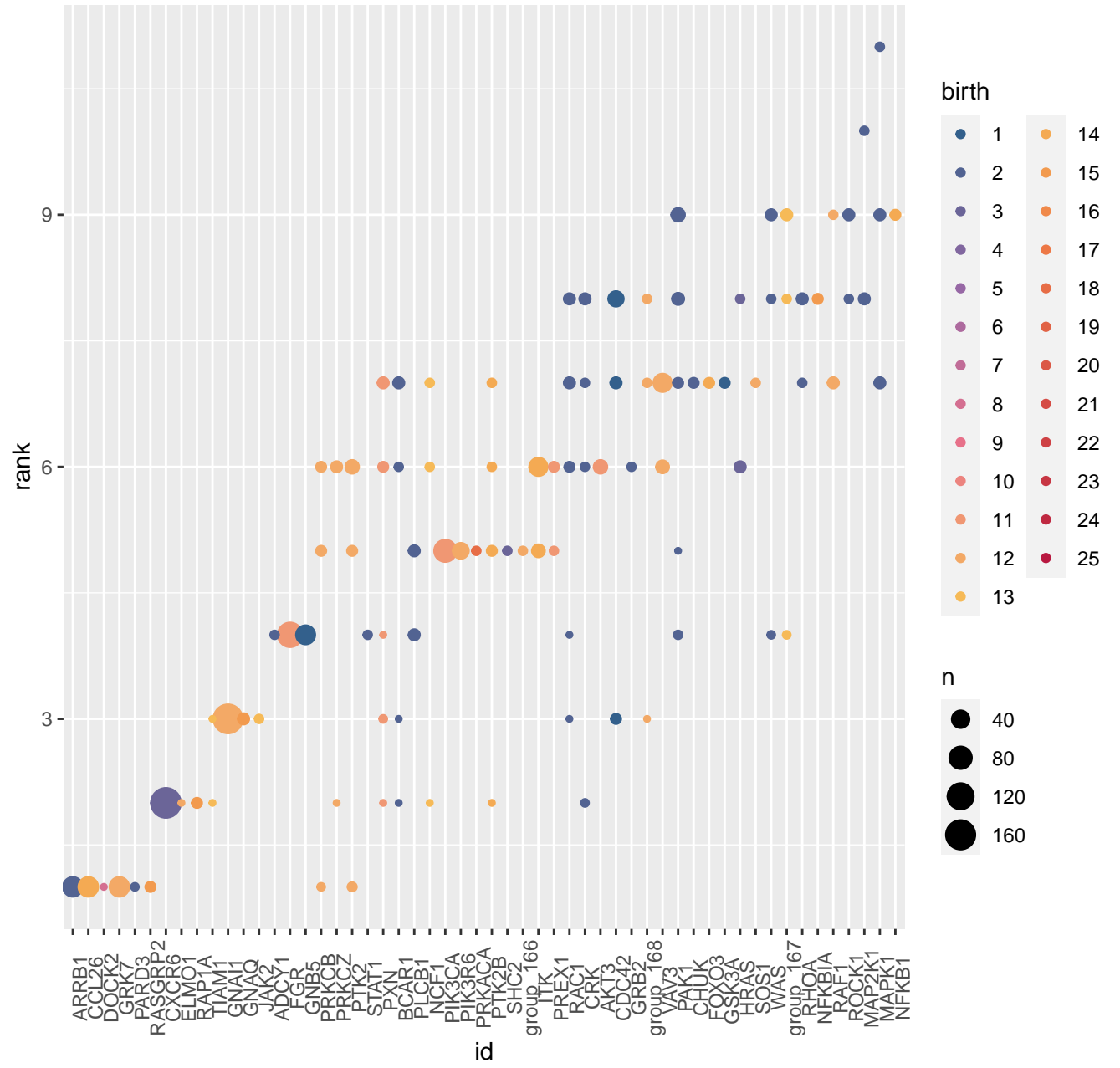
B cell receptor



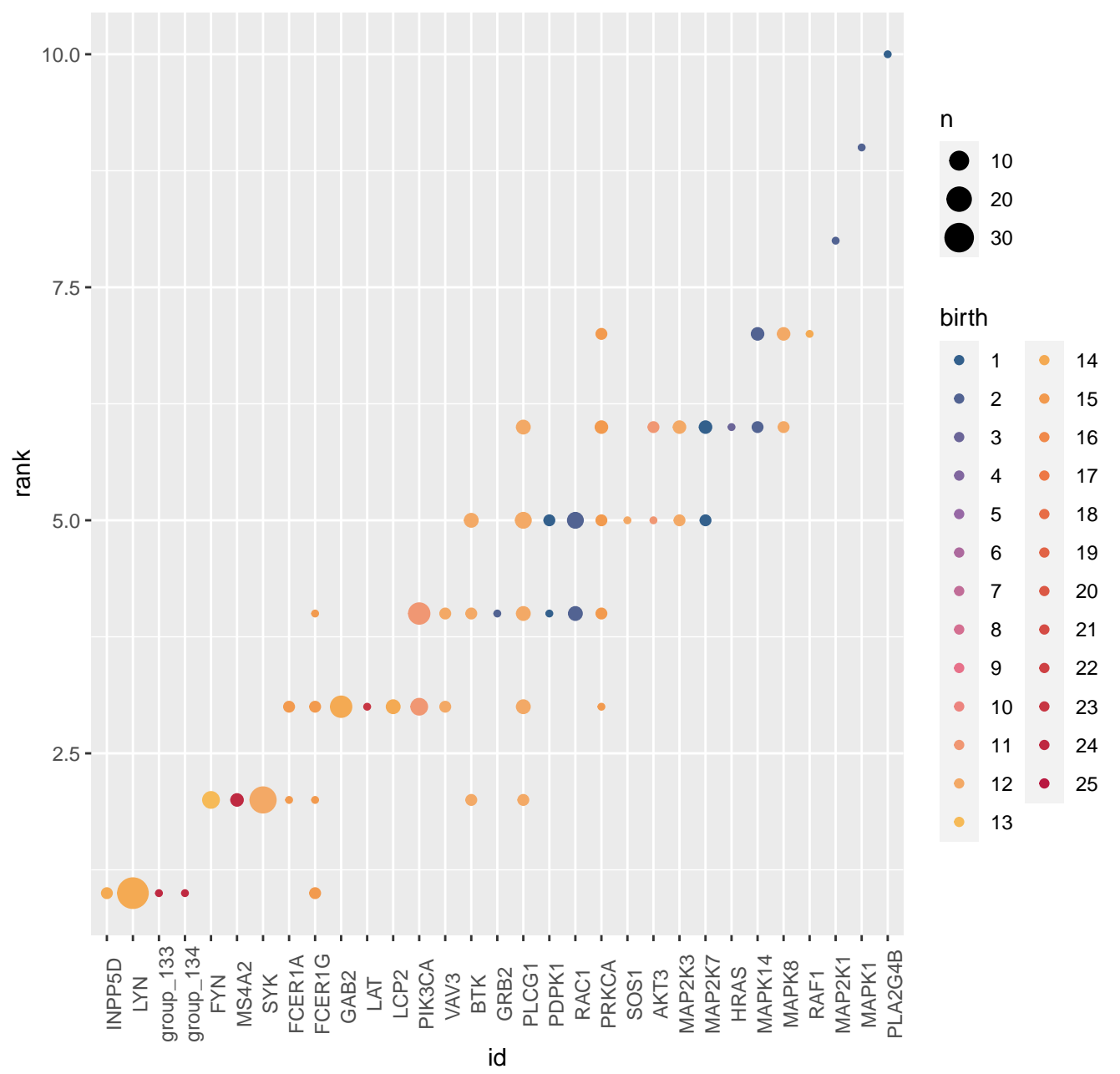
C-type lectin receptor



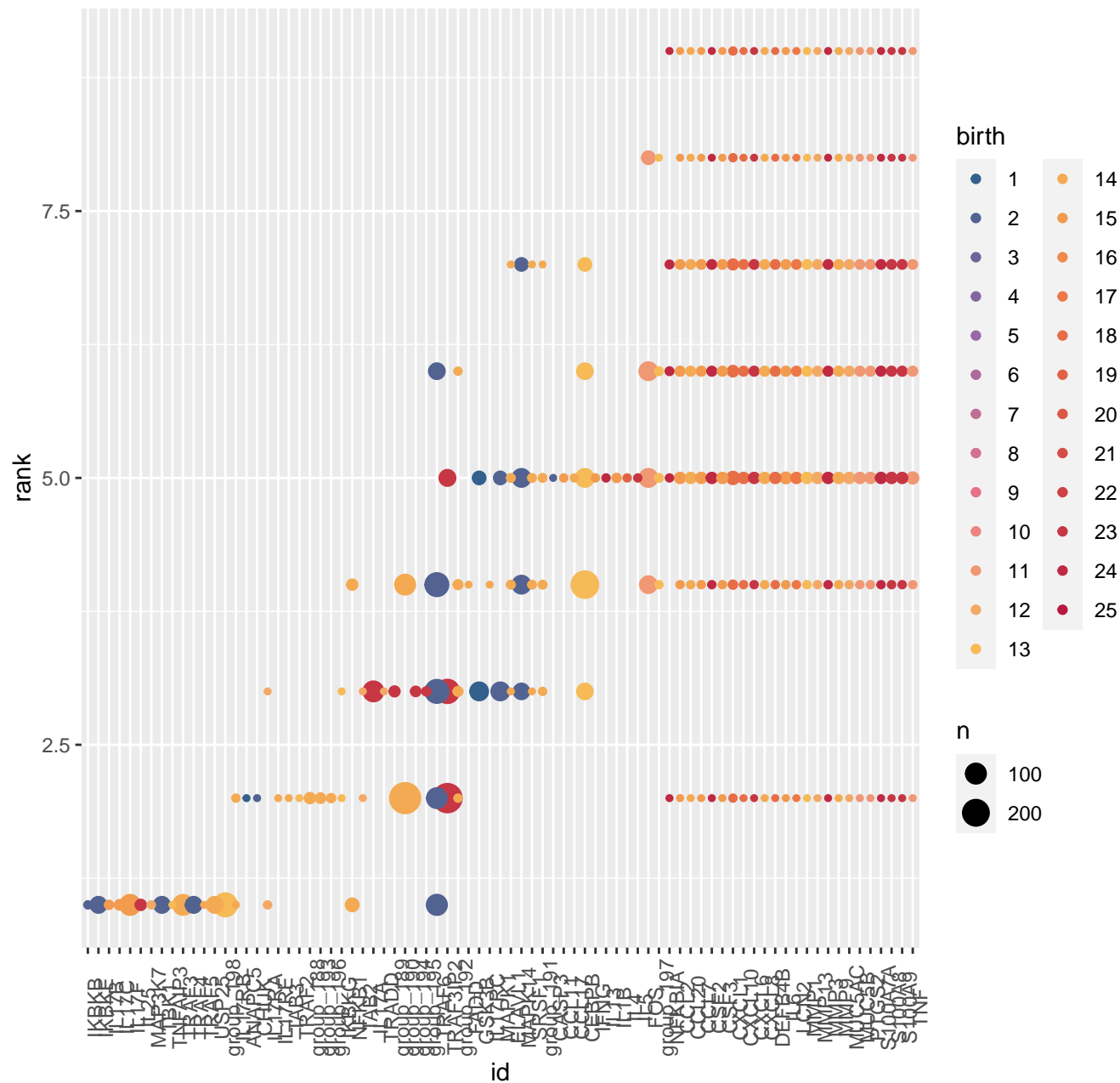
Chemokine



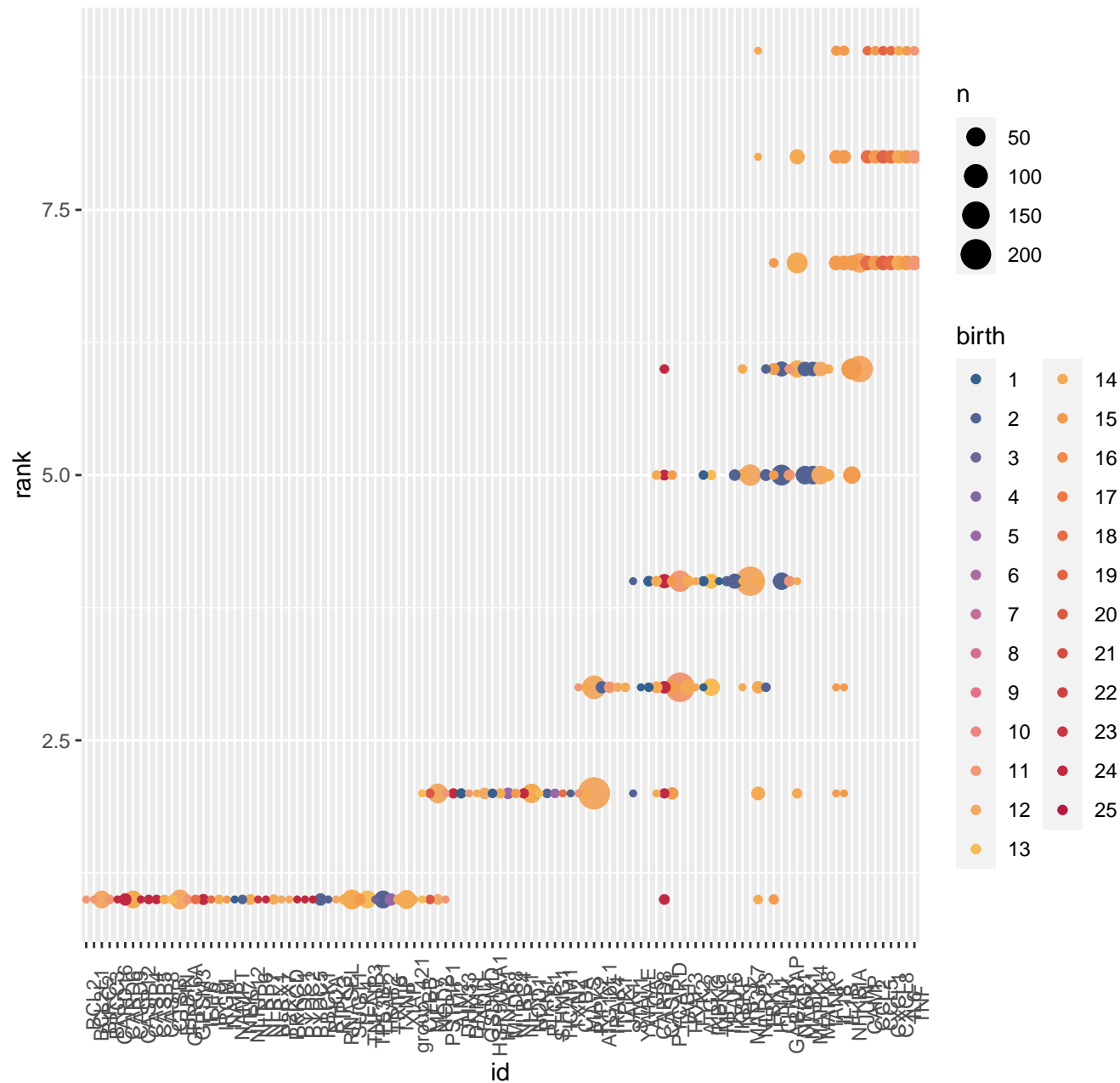
Fc epsilon RI



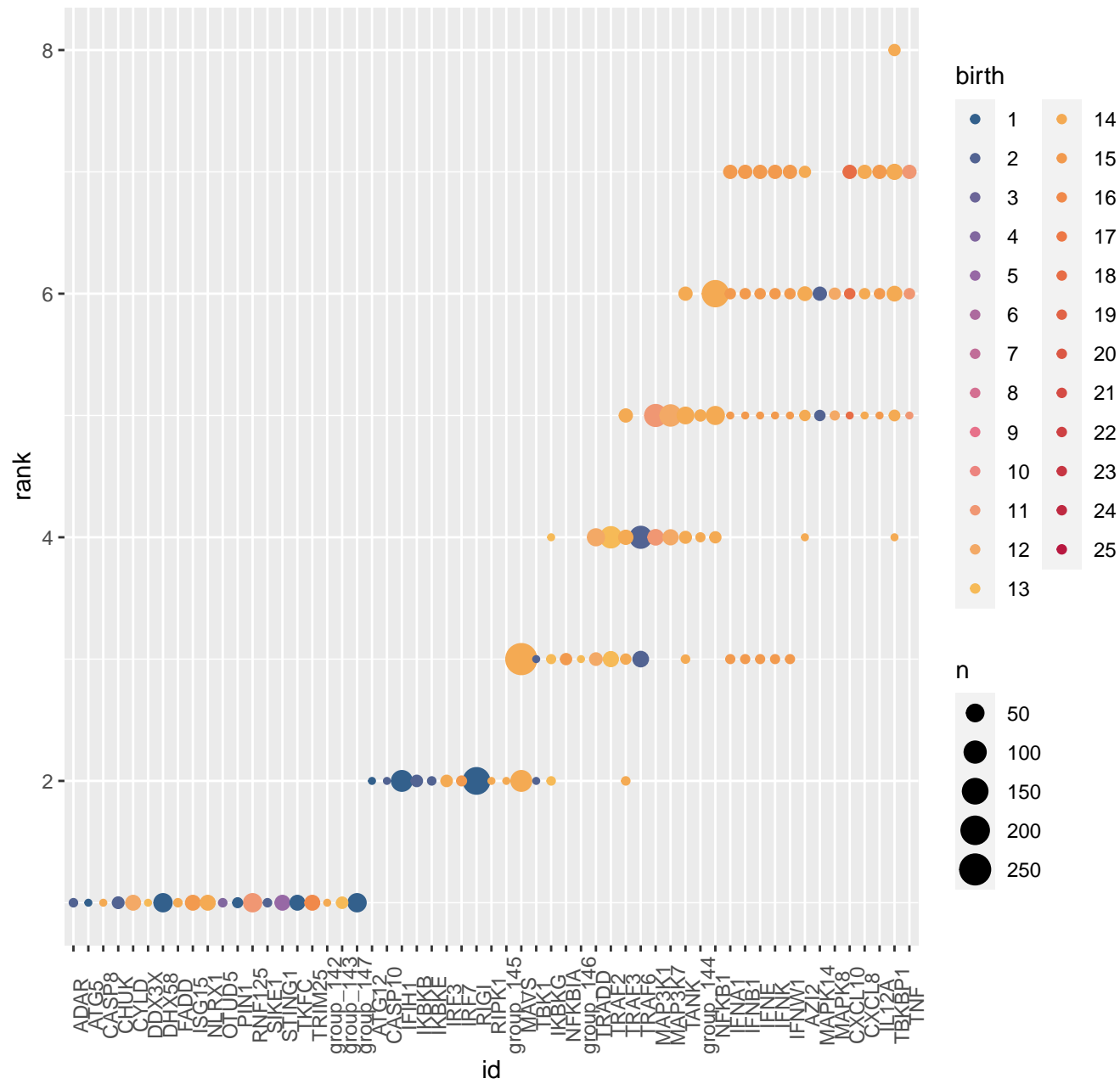
IL-17



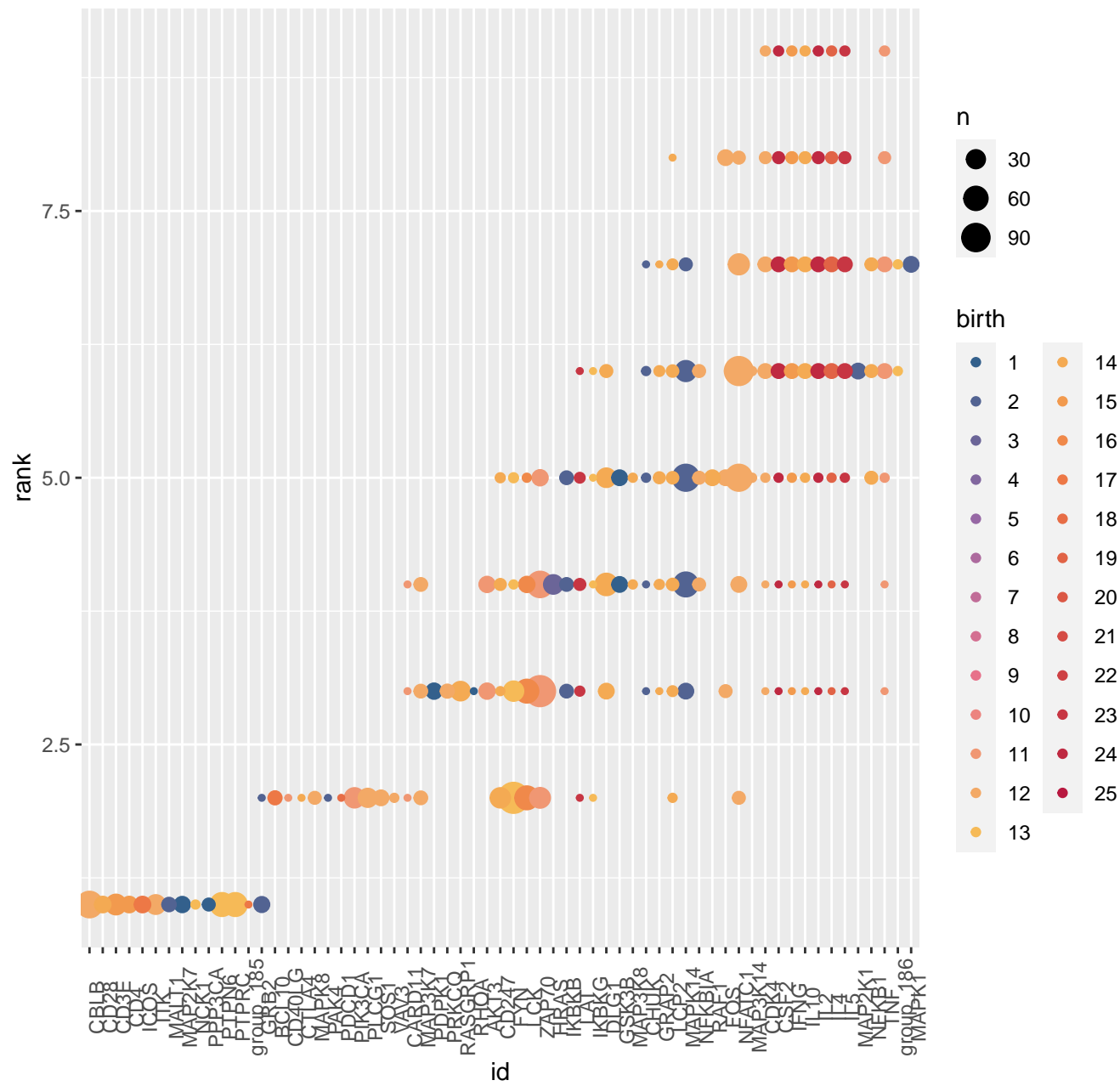
NOD-like receptor



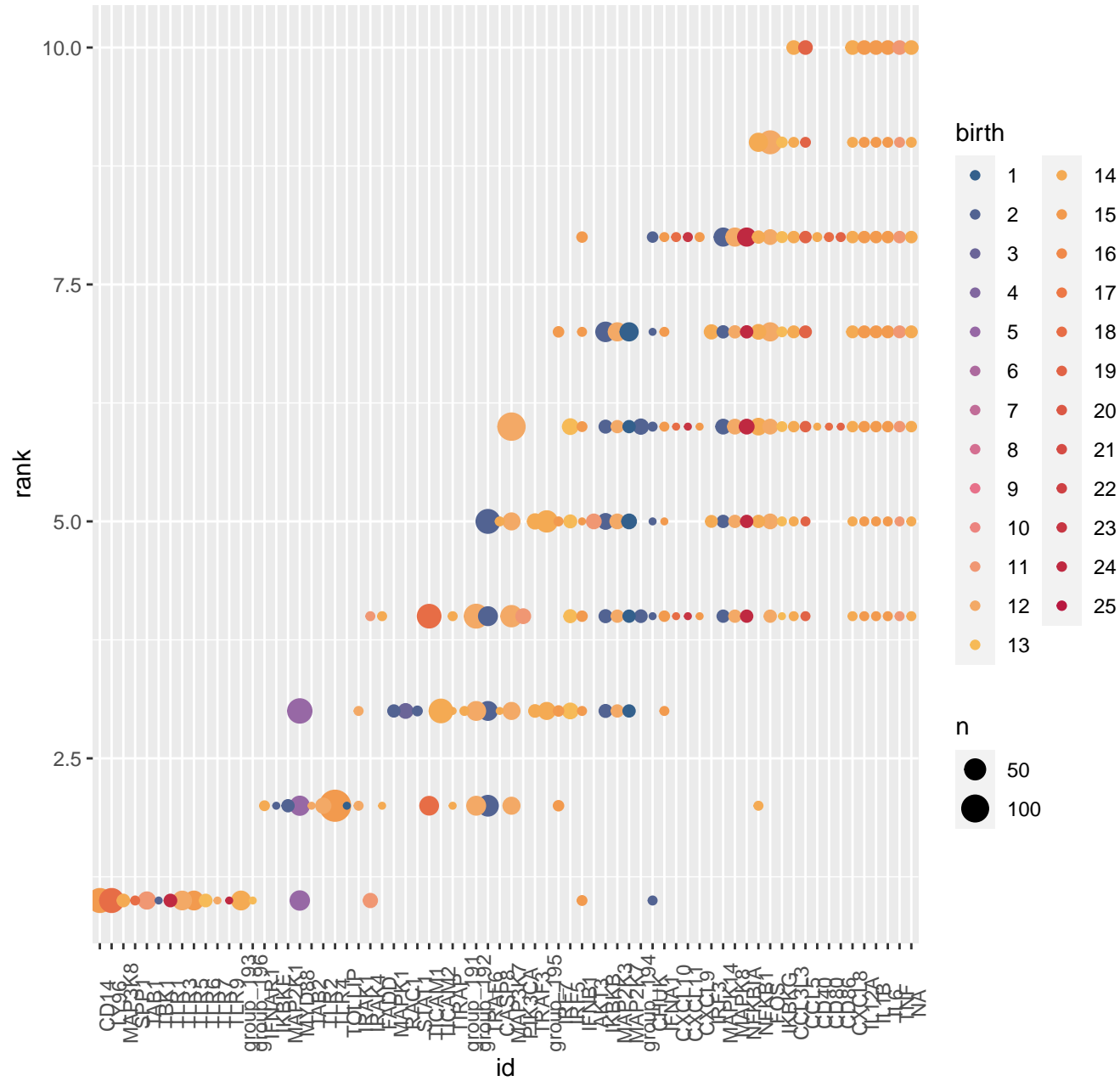
RIG-I-like receptor



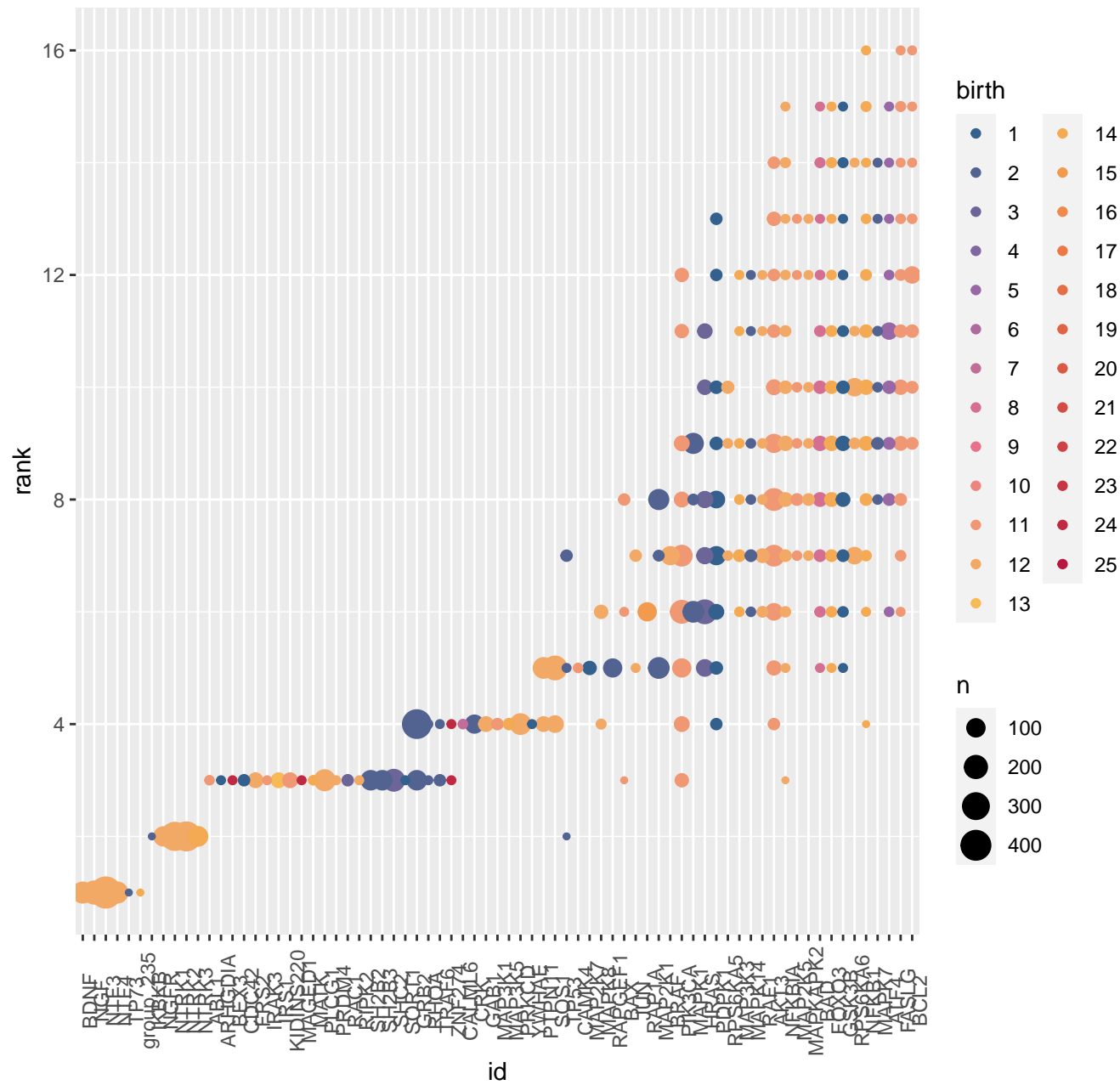
T cell receptor



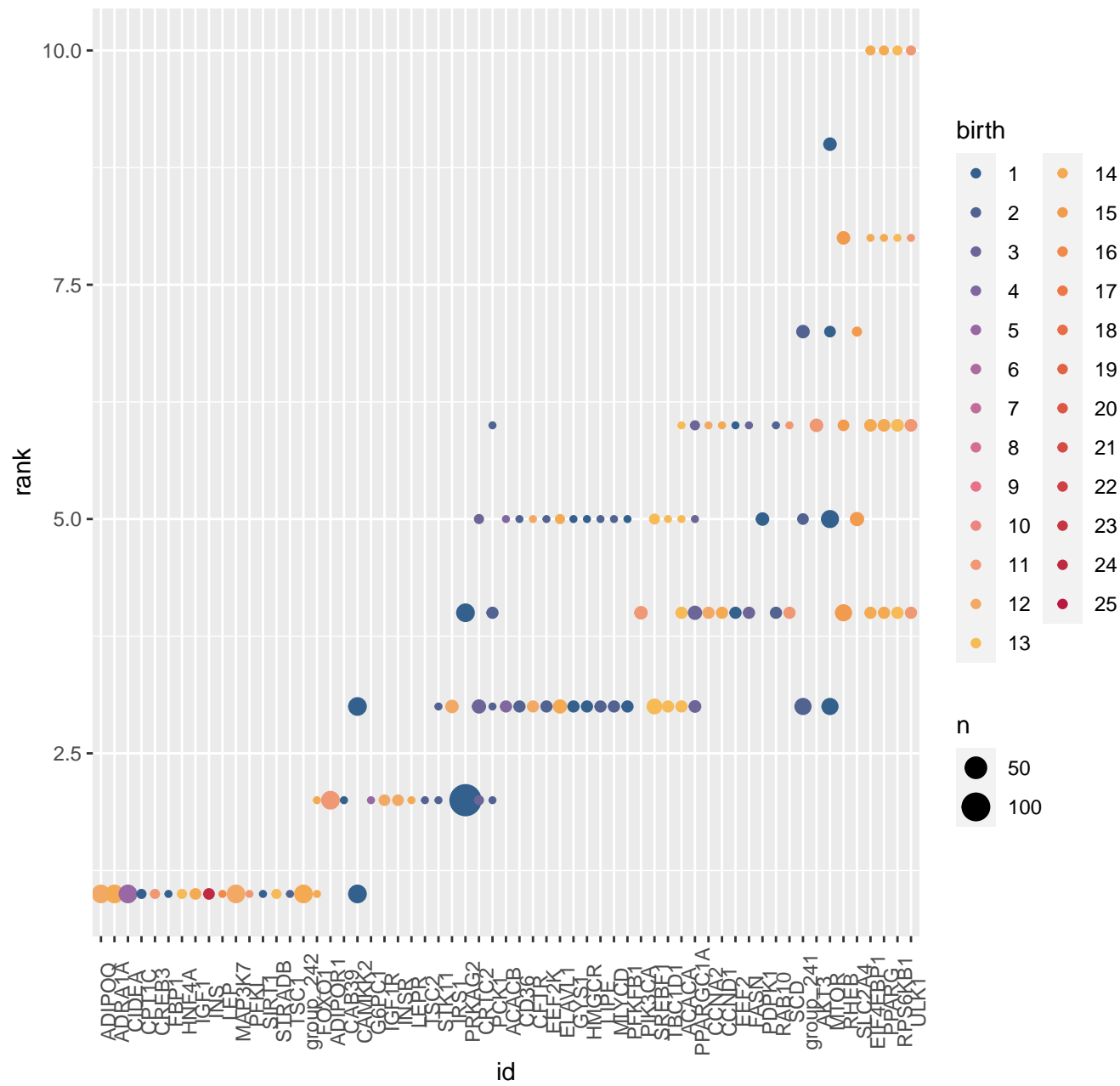
Toll-like receptor



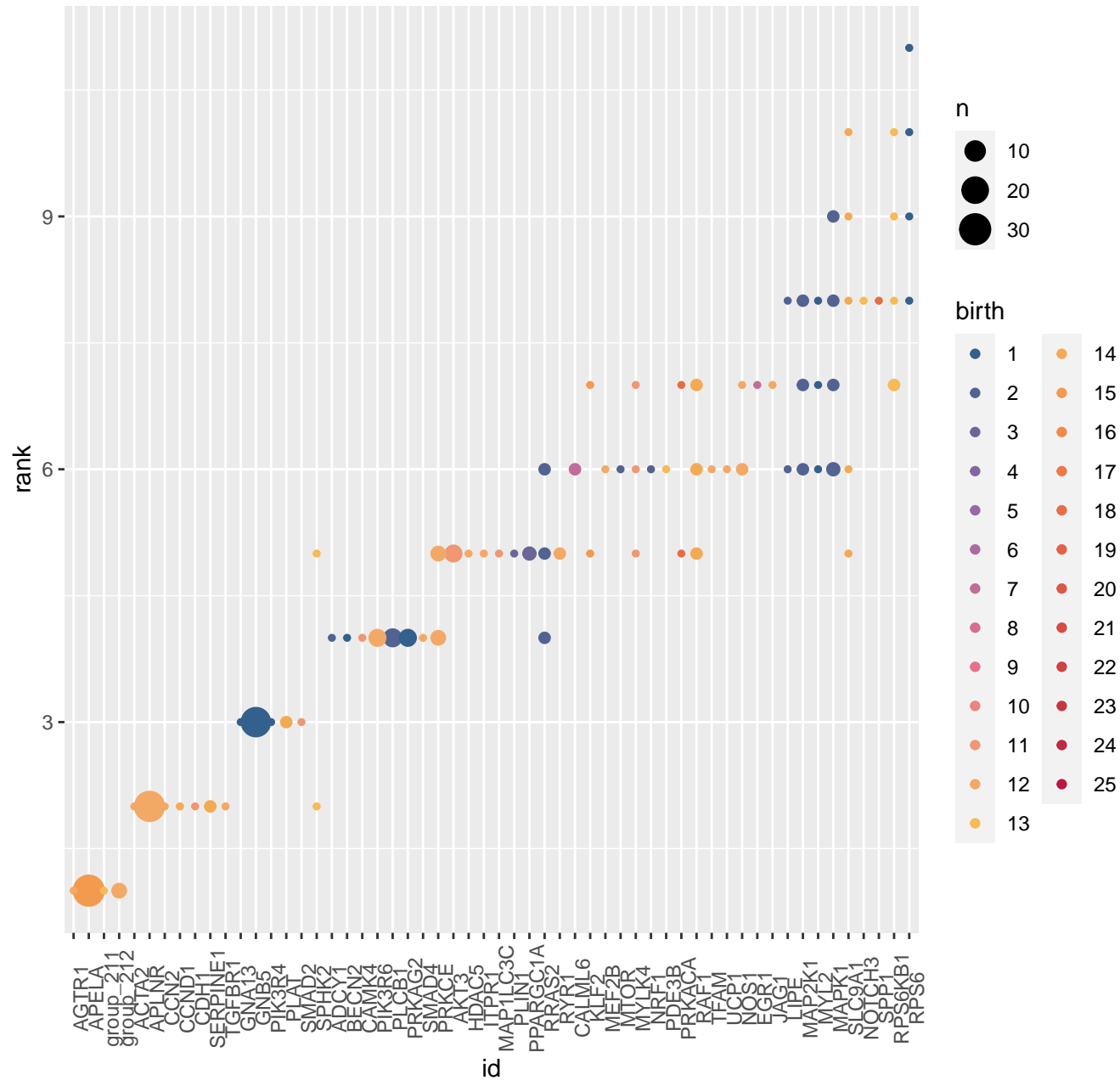
Neurotrophin



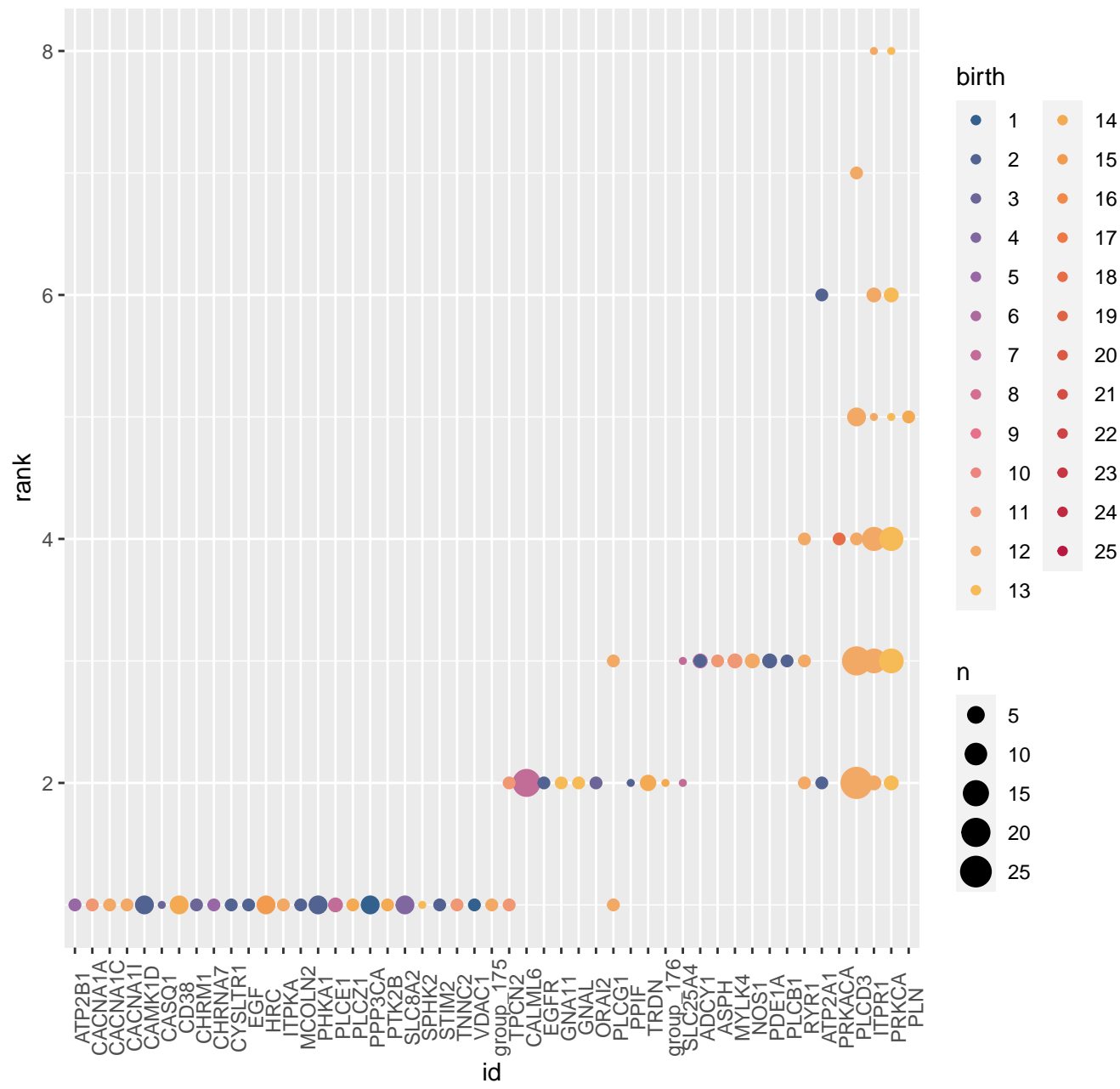
AMPK



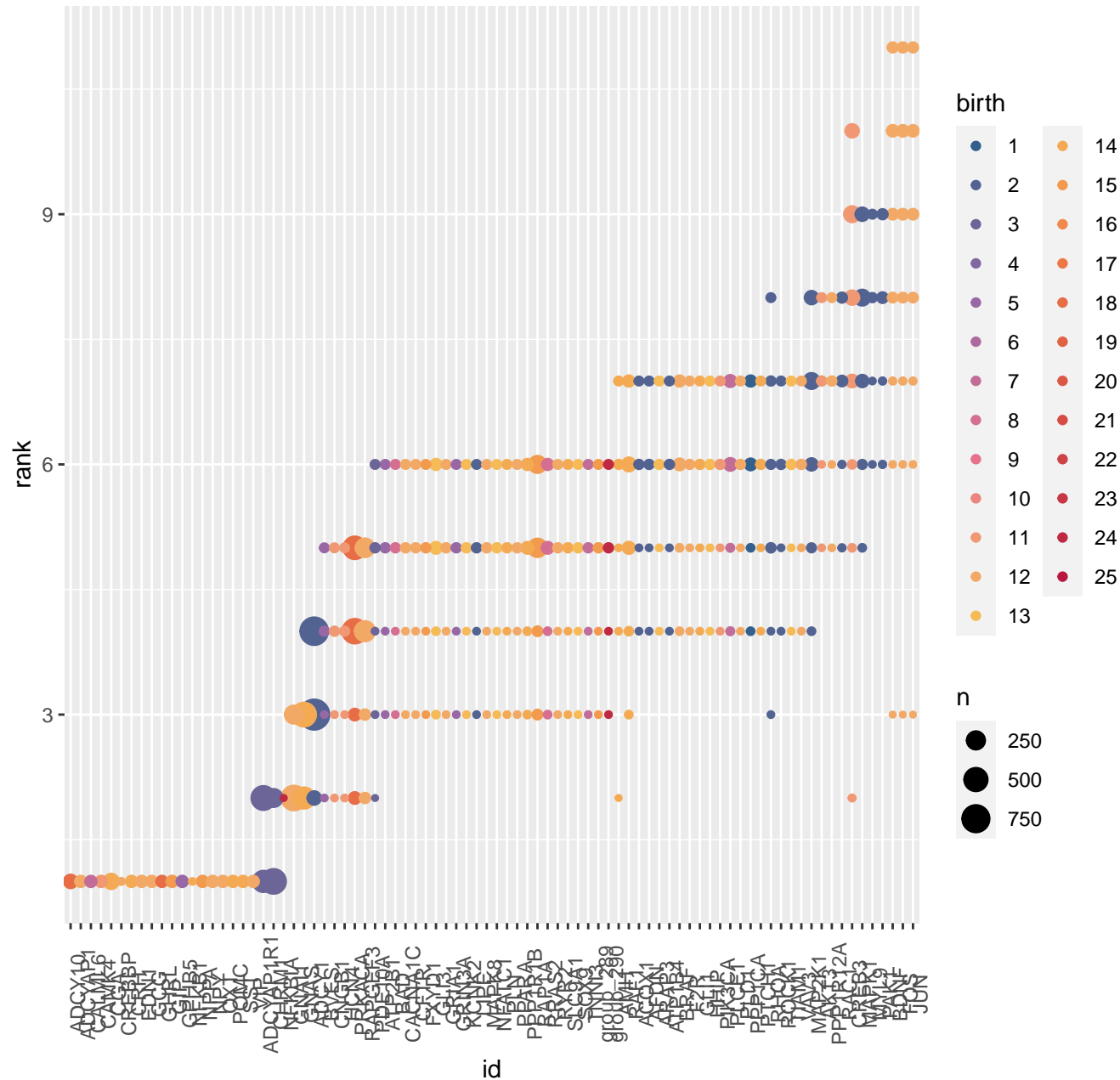
Apelin



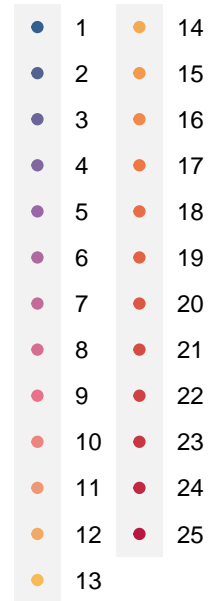
Calcium






cAMP



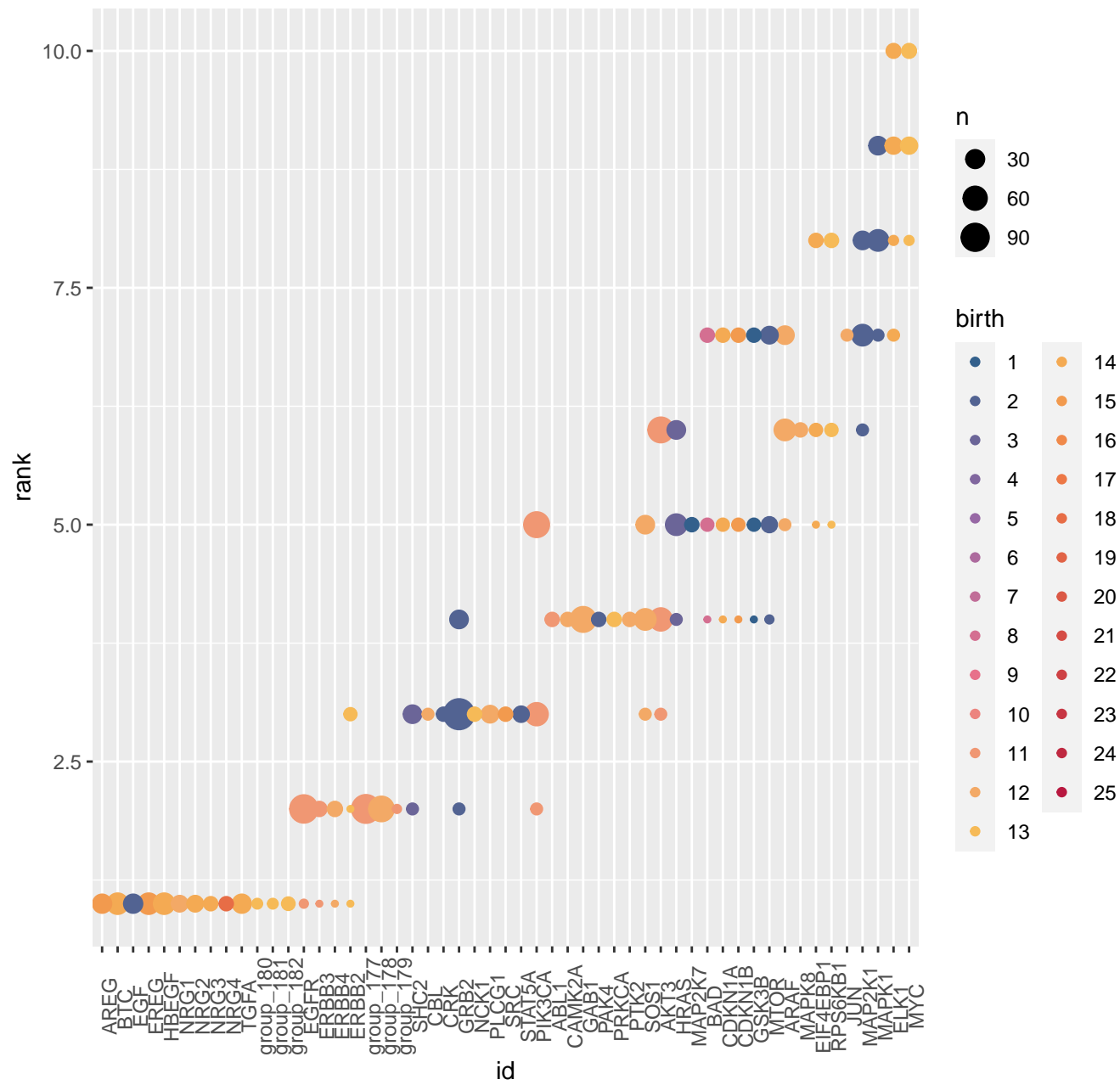
The visualization displays 1000 simulated data points arranged in 10 horizontal rows. Each point is represented by a colored circle, where the color (blue, orange, or purple) and size (ranging from small to large) likely represent different attributes or weights. The points are distributed across the rows, with some rows showing clusters of points and others showing more sparse distributions. The overall pattern suggests a complex, non-uniform distribution of the simulated data.



	20
	40
	60

id

ErbB

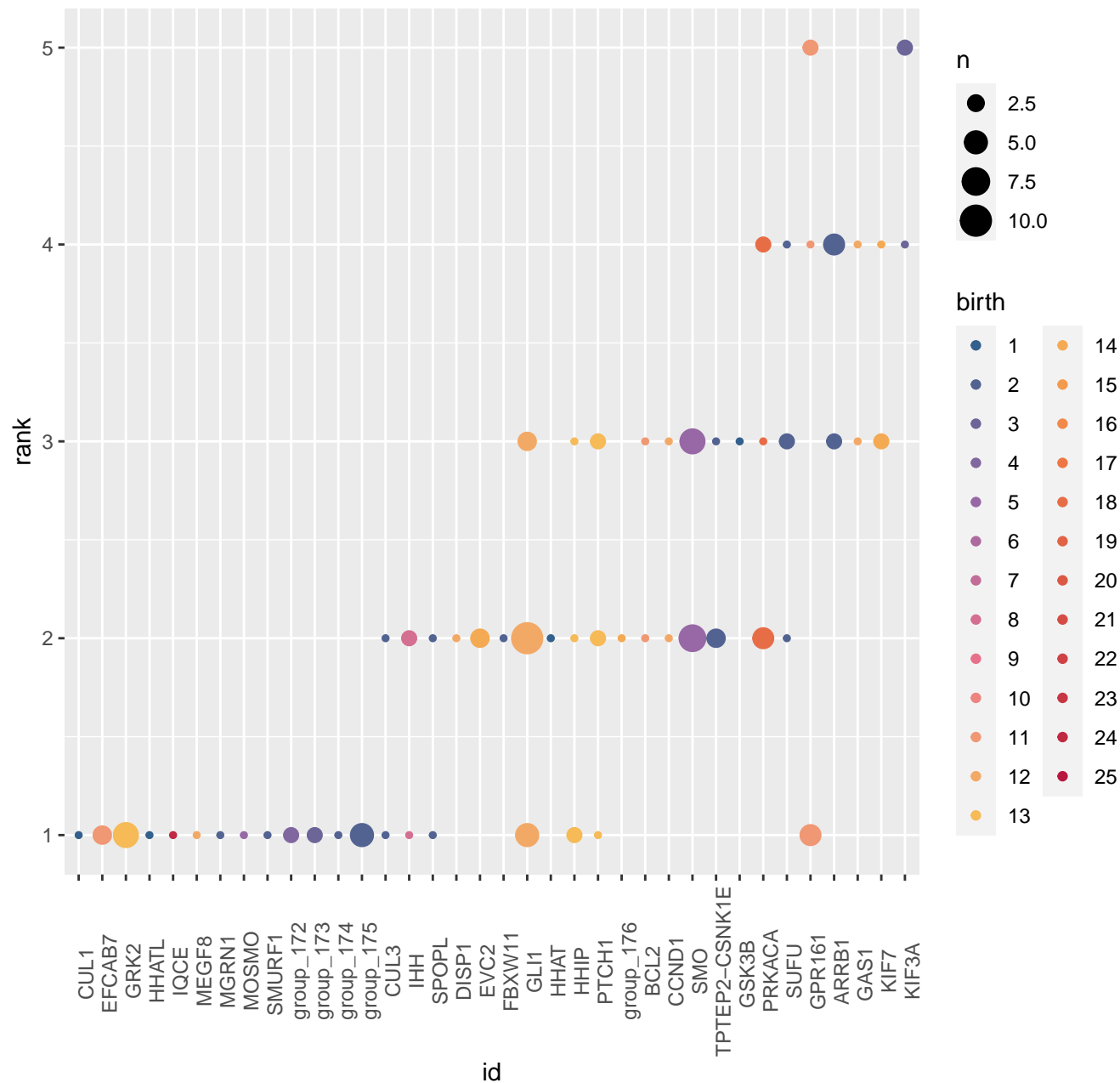


FoxO

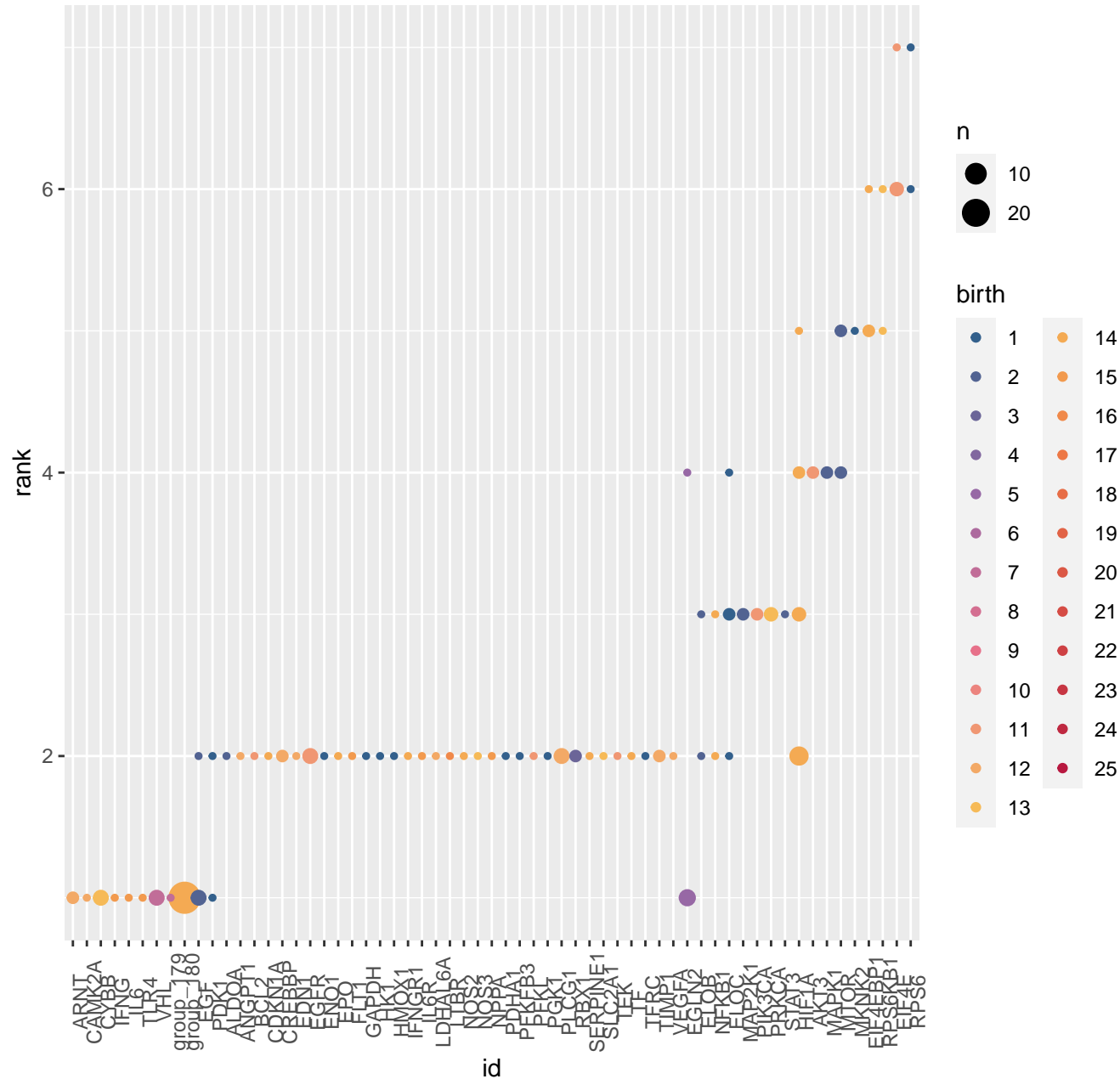


id

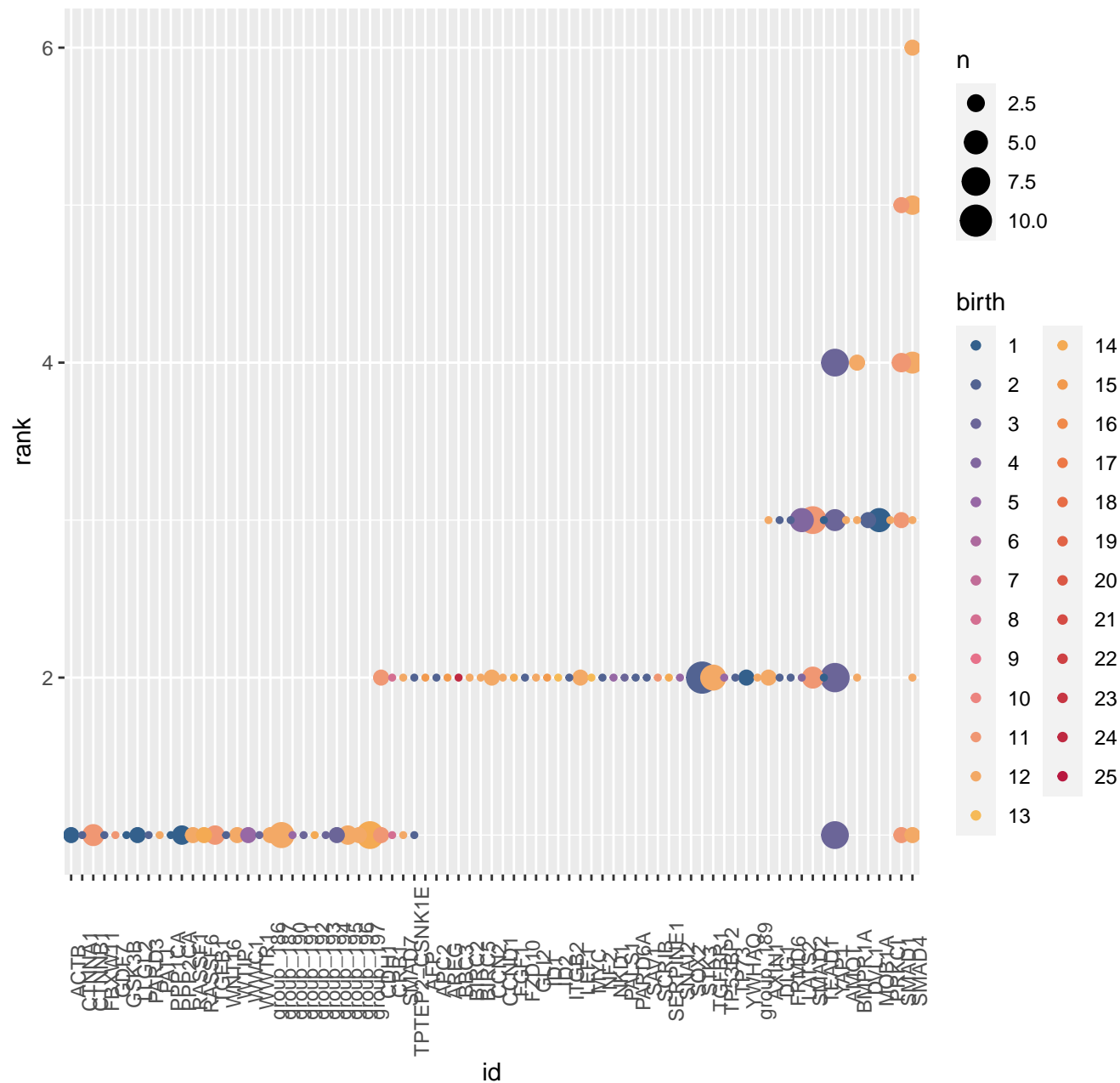
Hedgehog



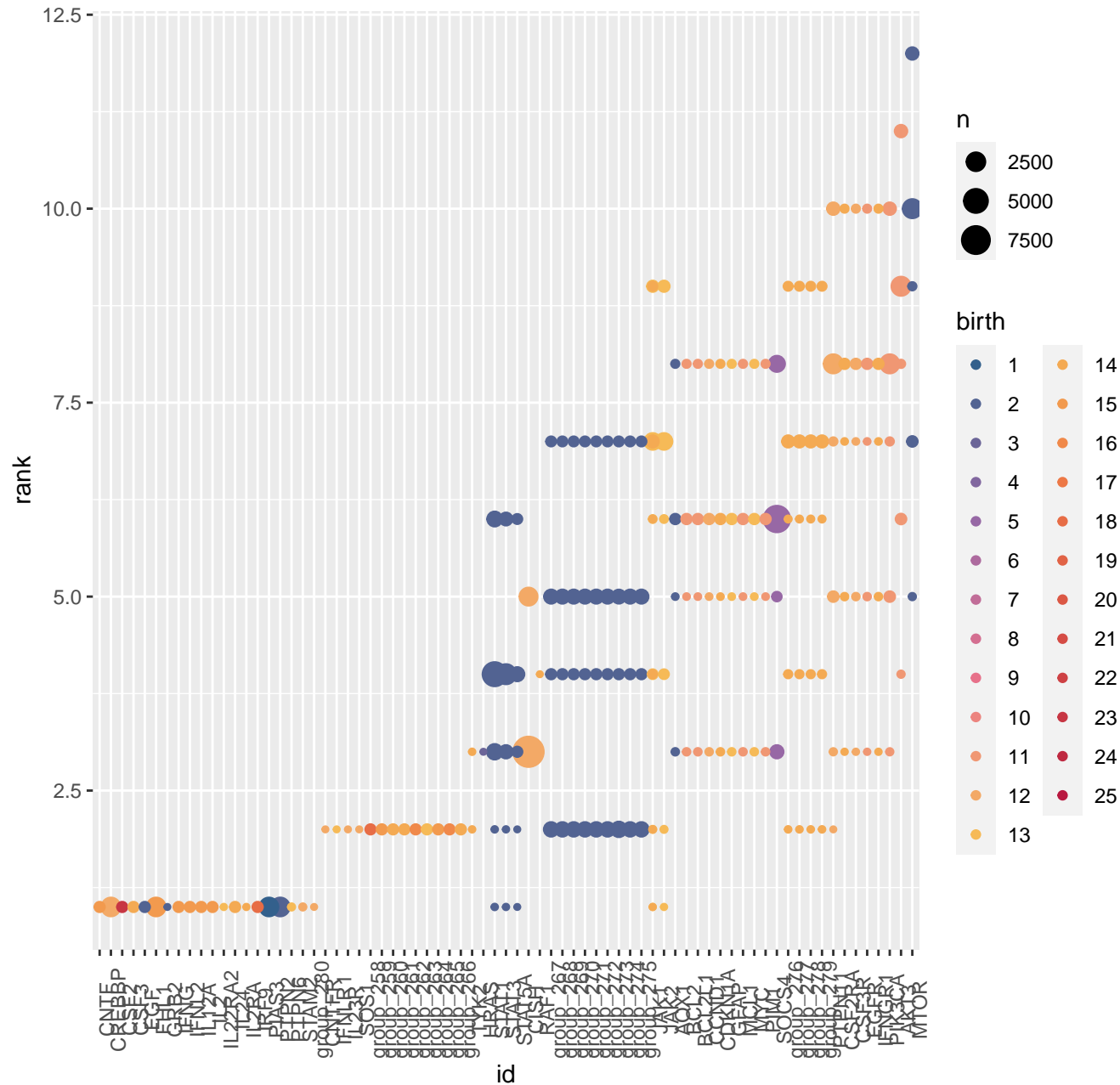
HIF-1



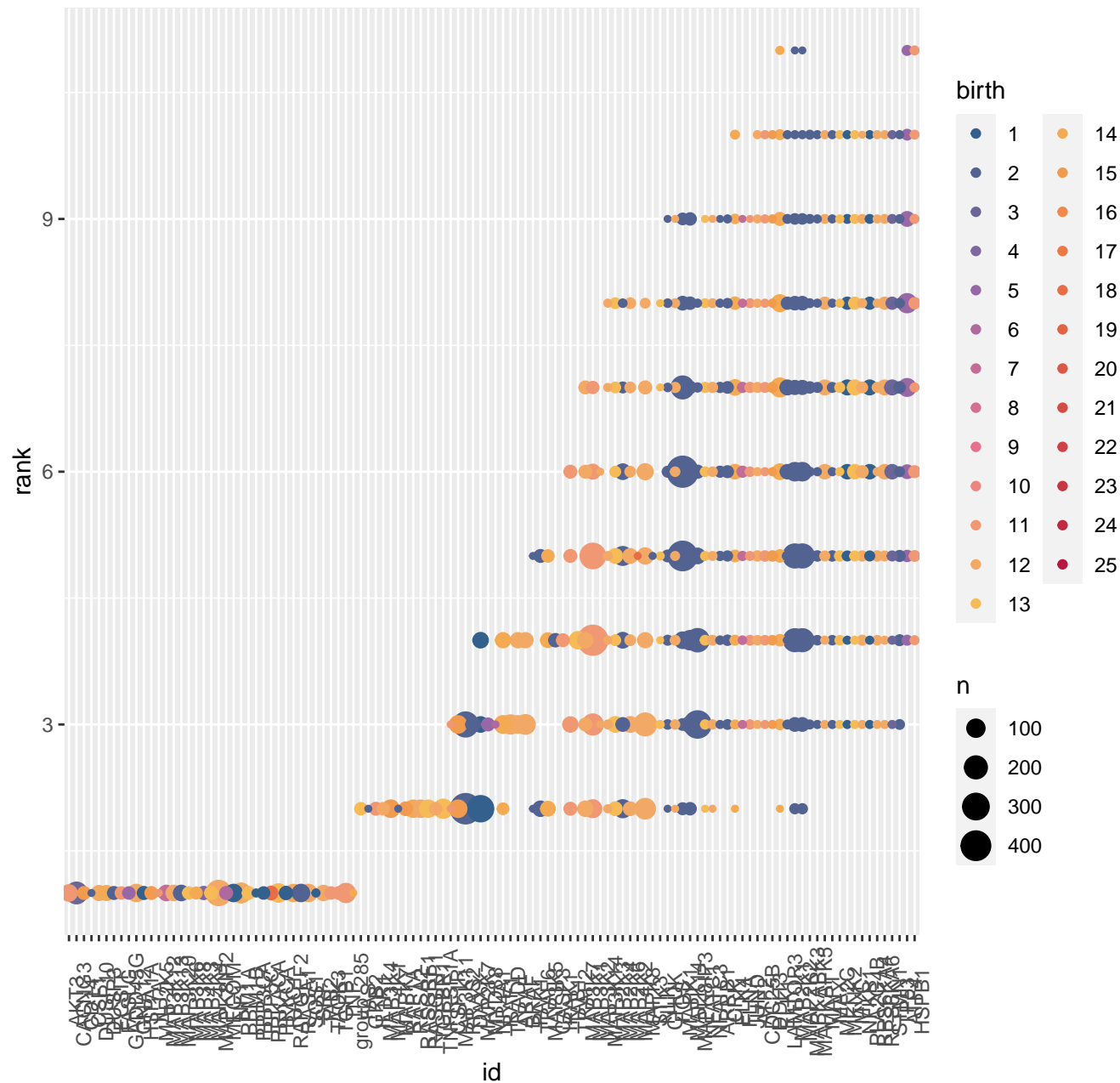
Hippo



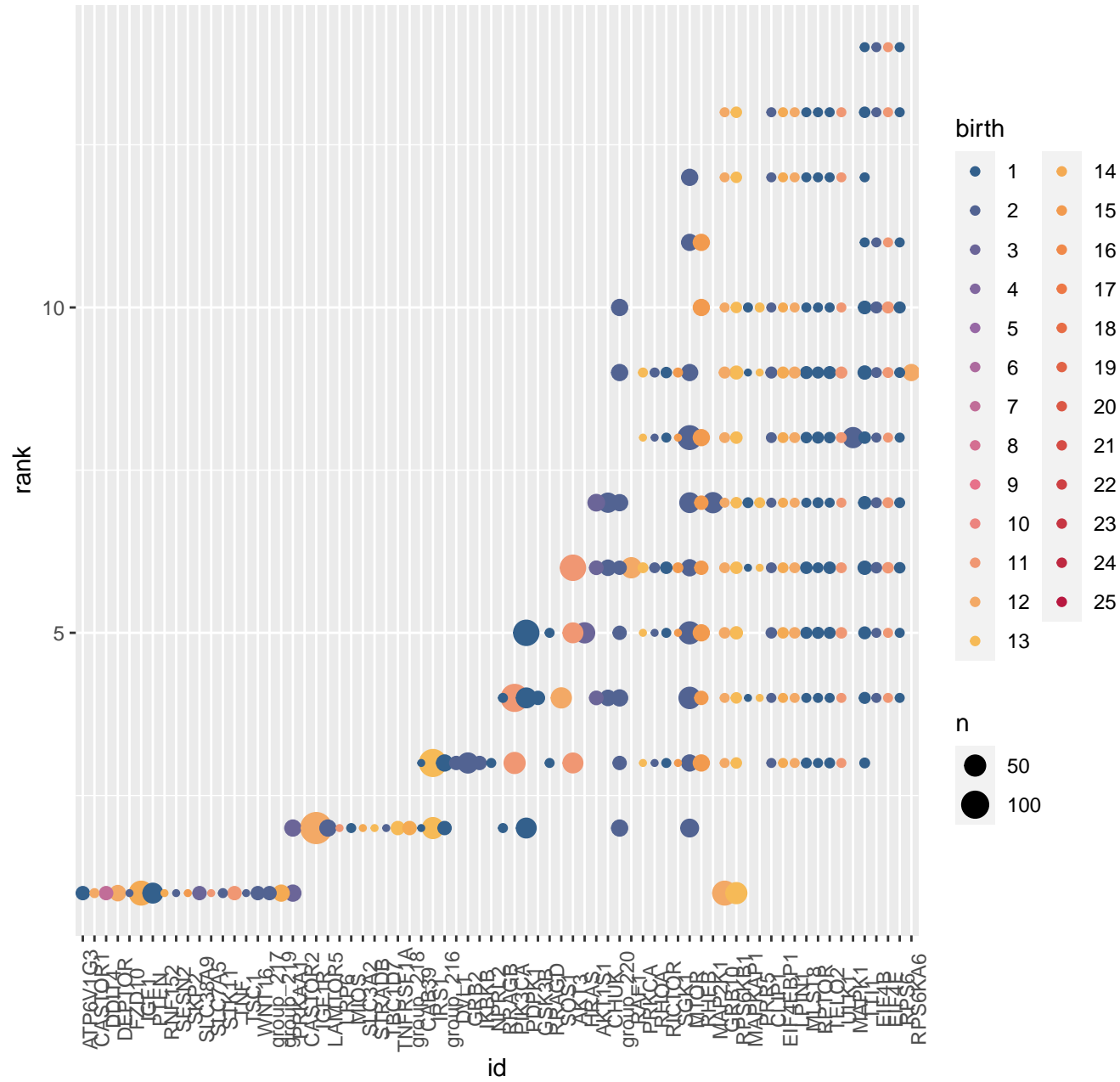
JAK-STAT



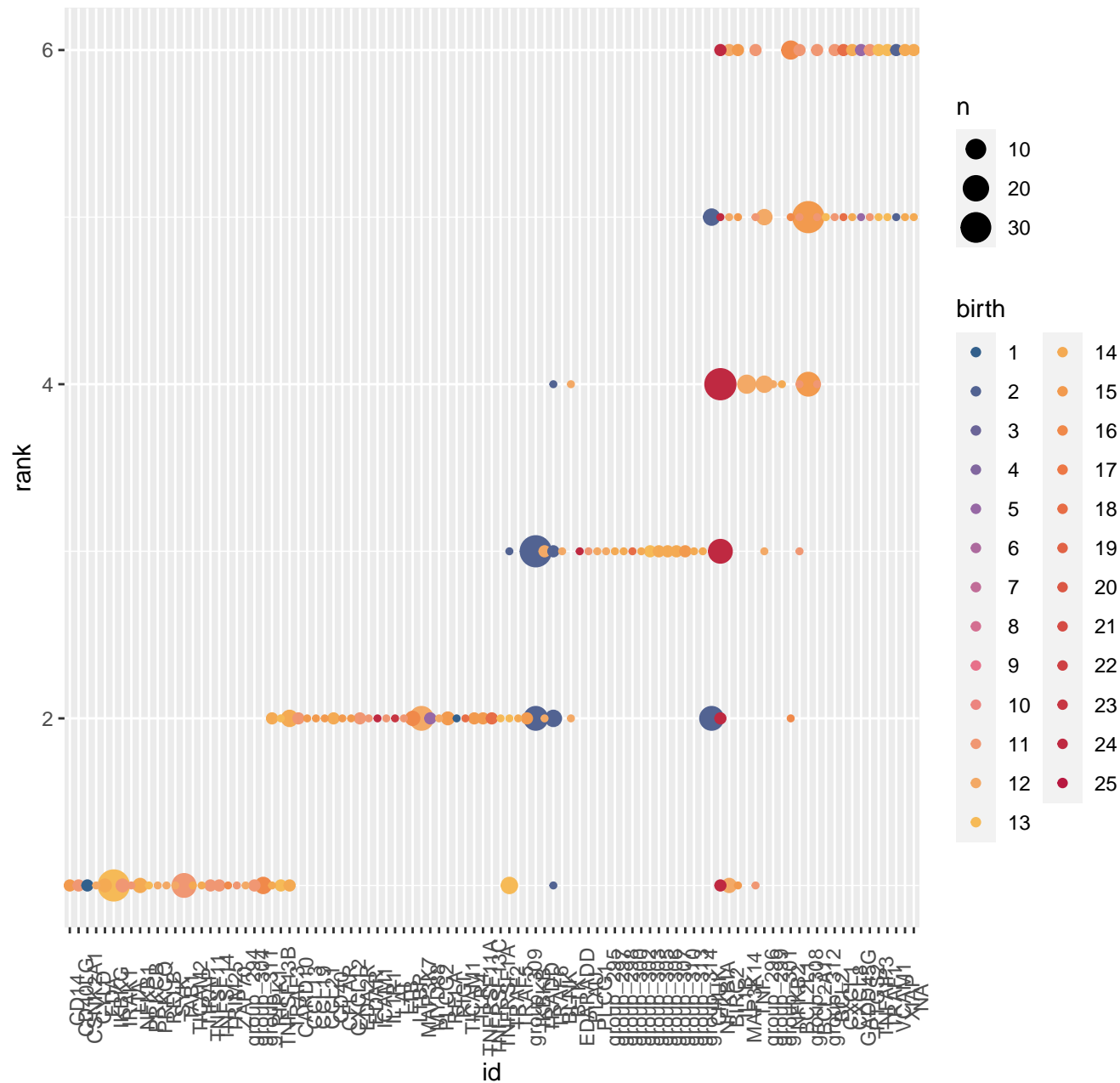
MAPK



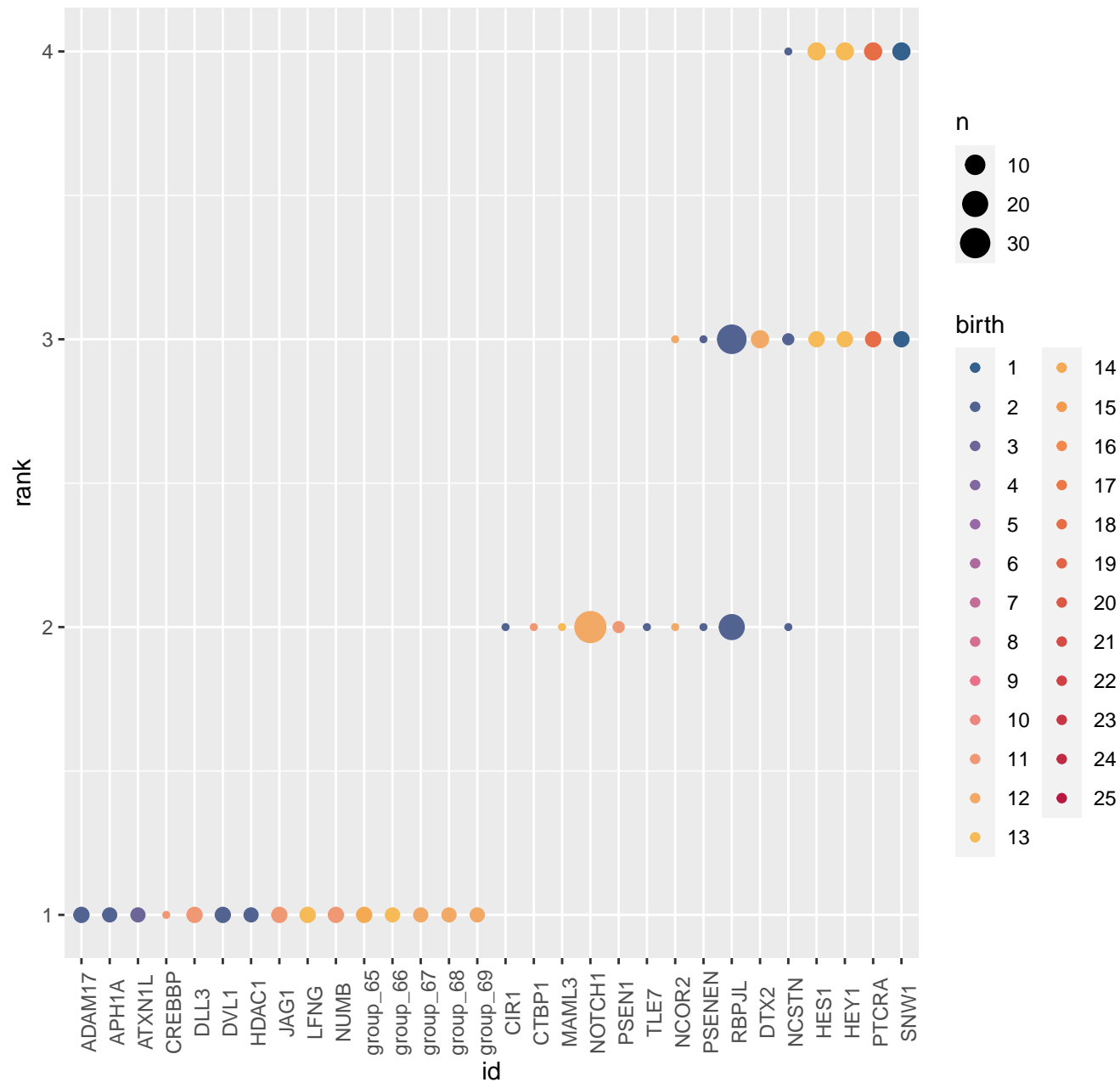
mTOR



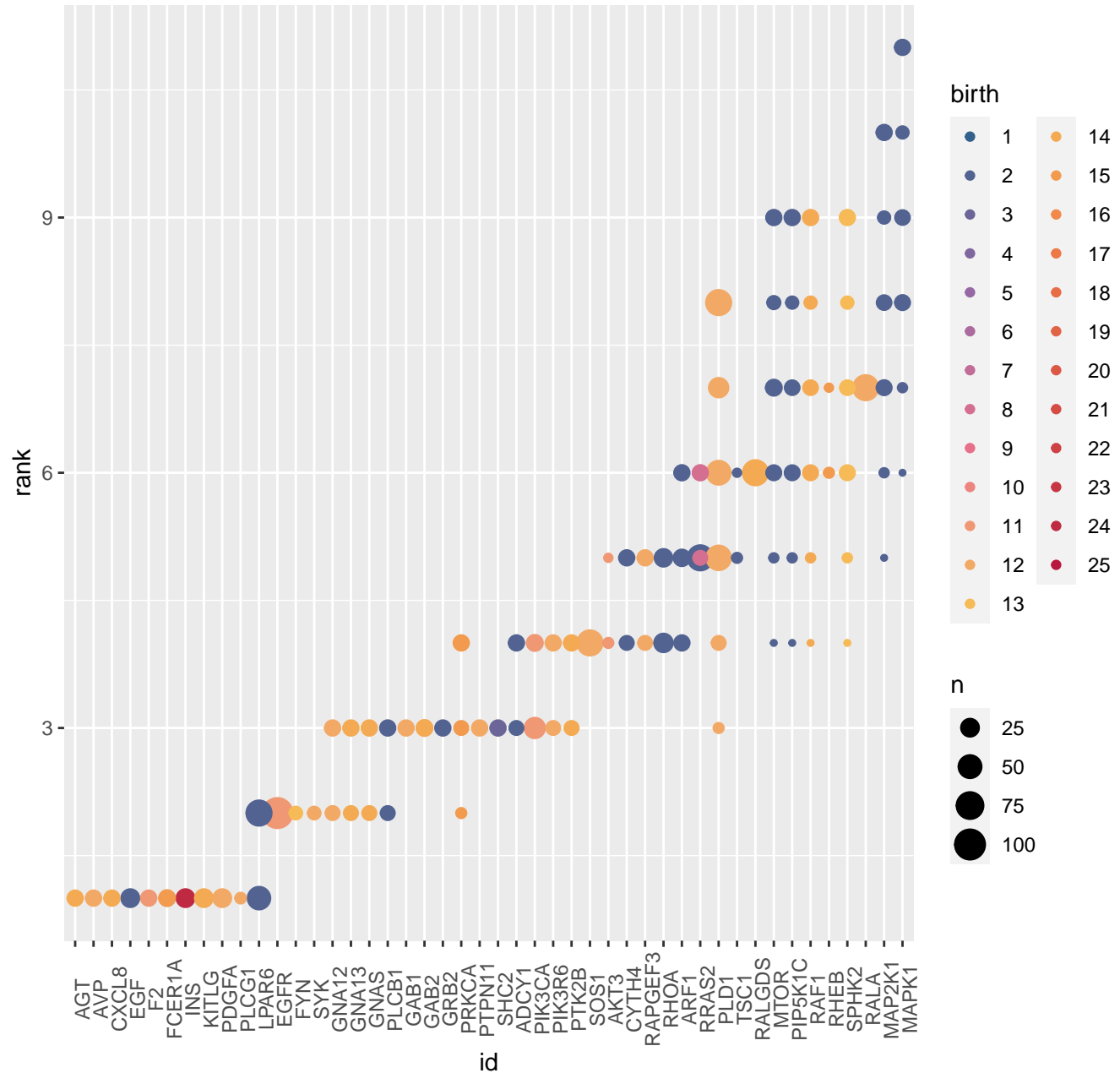
NF-kappa B



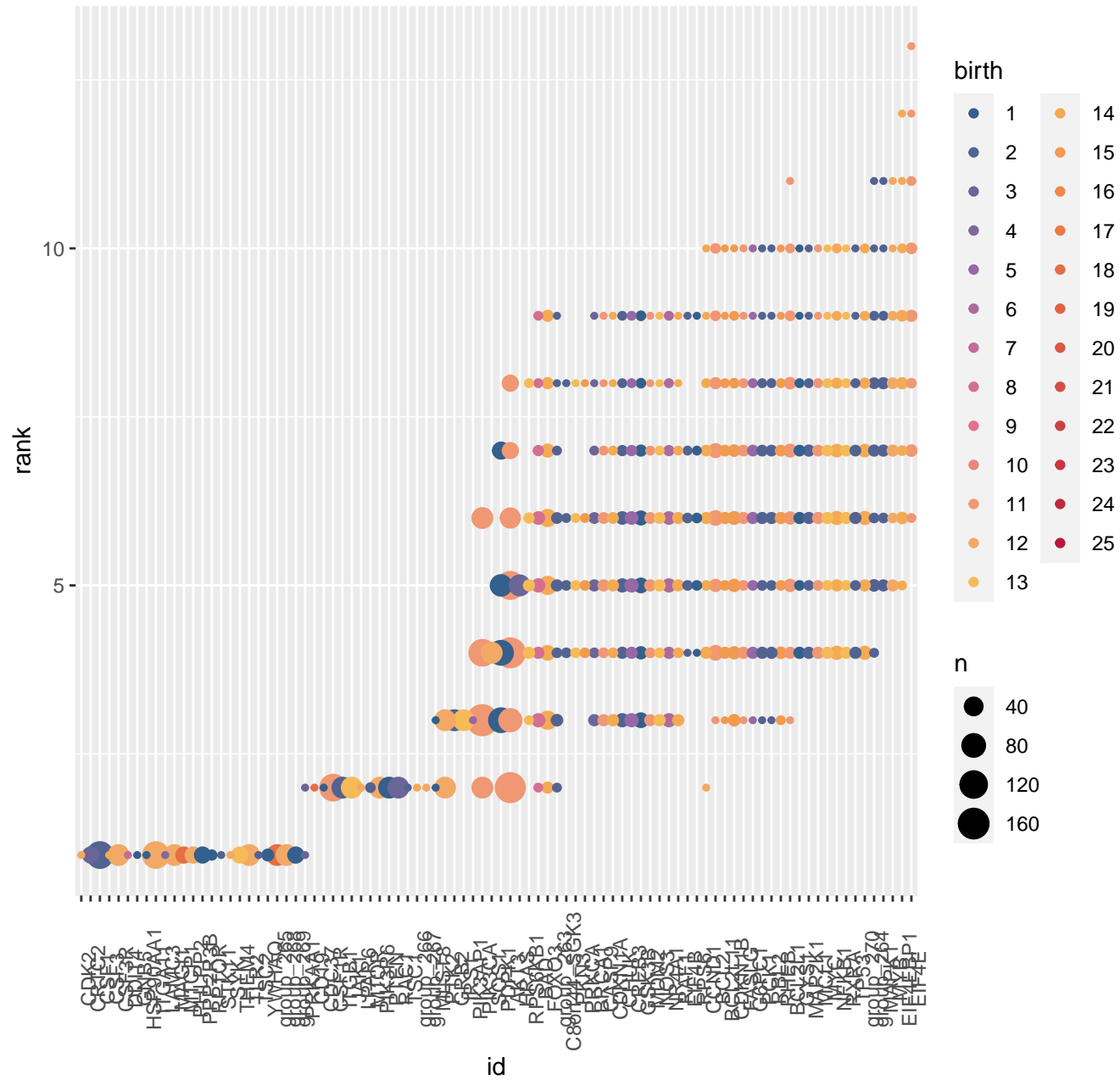
Notch



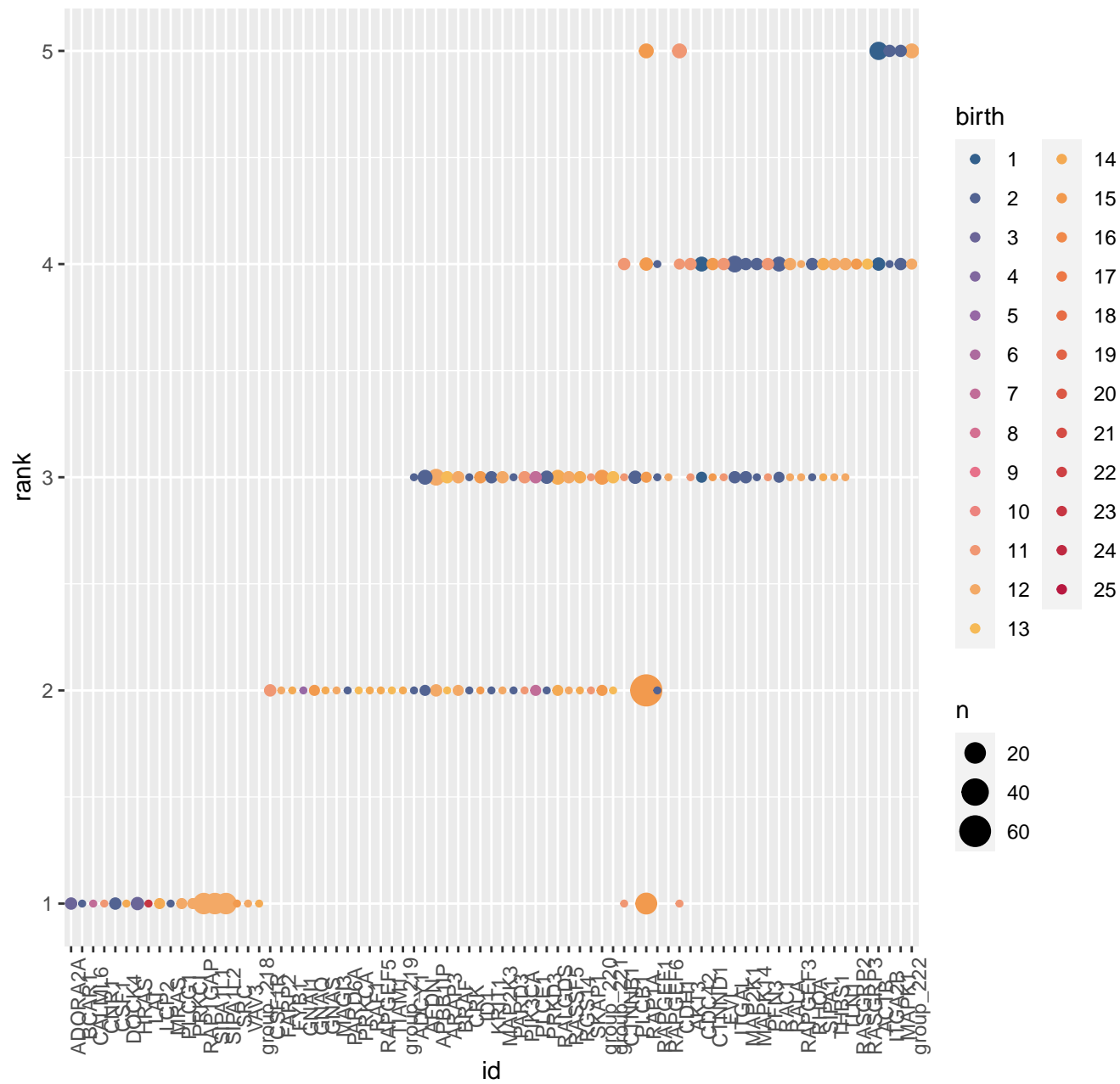
Phospholipase D



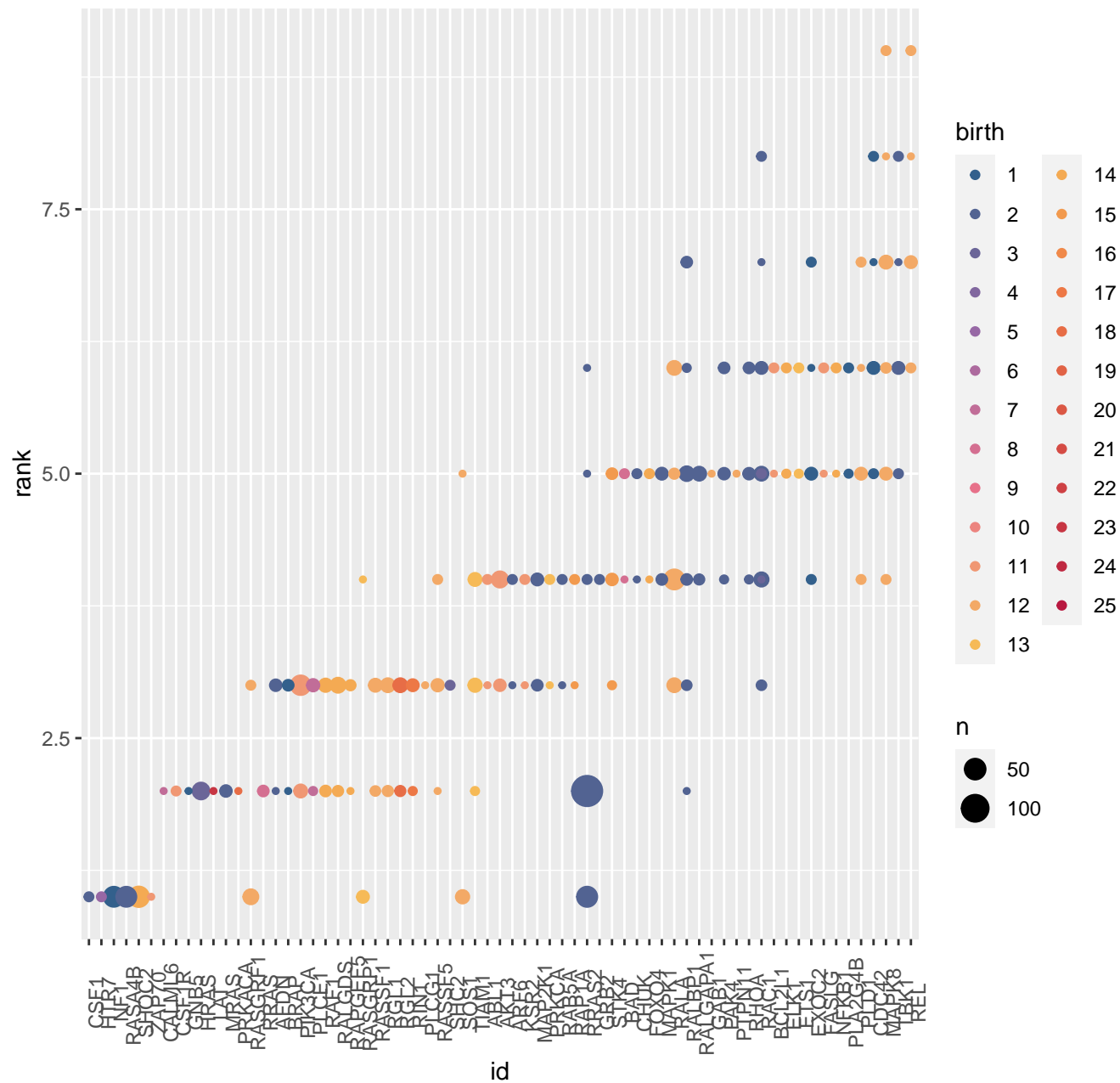
PI3K–Akt



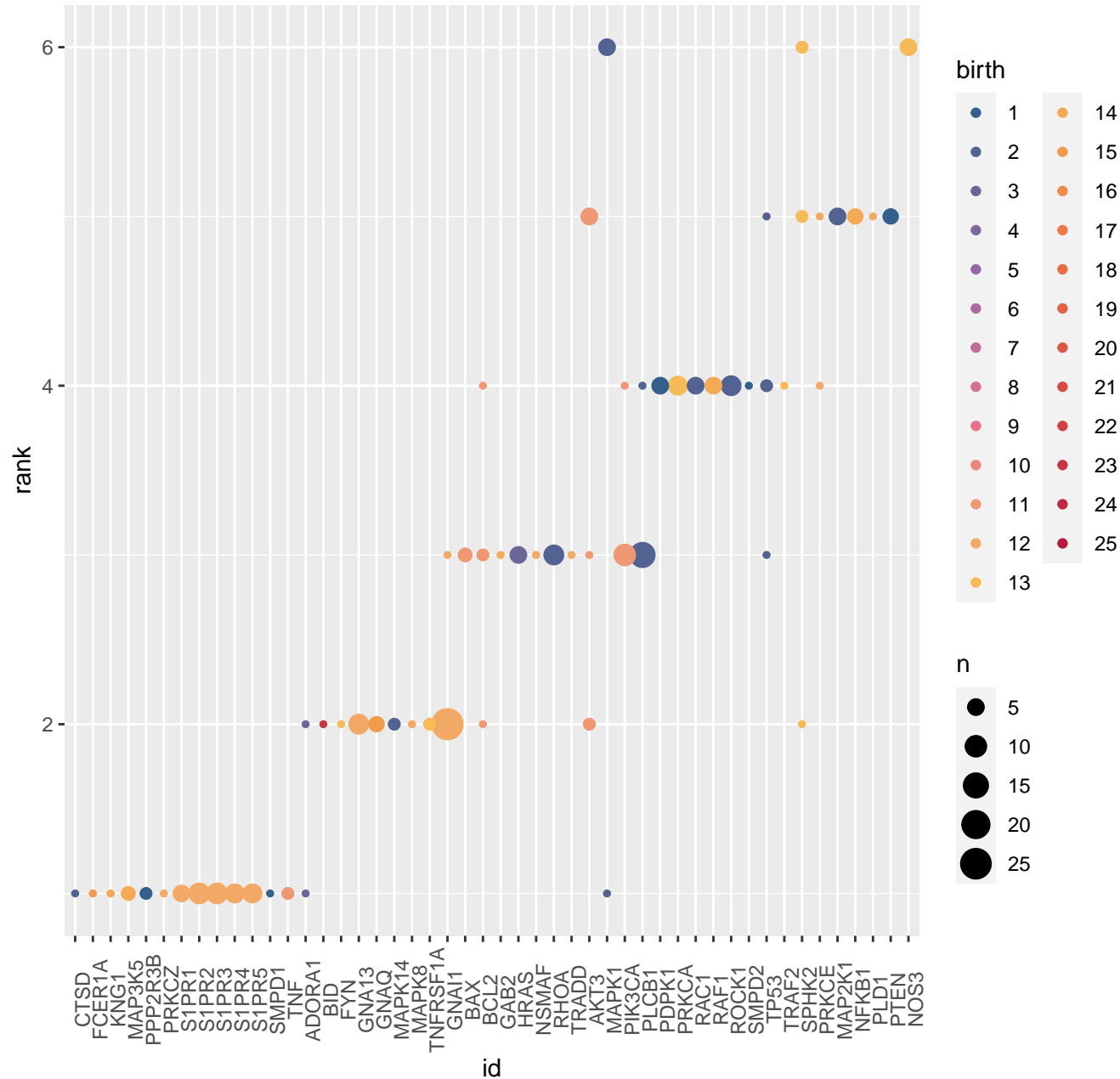
Rap1



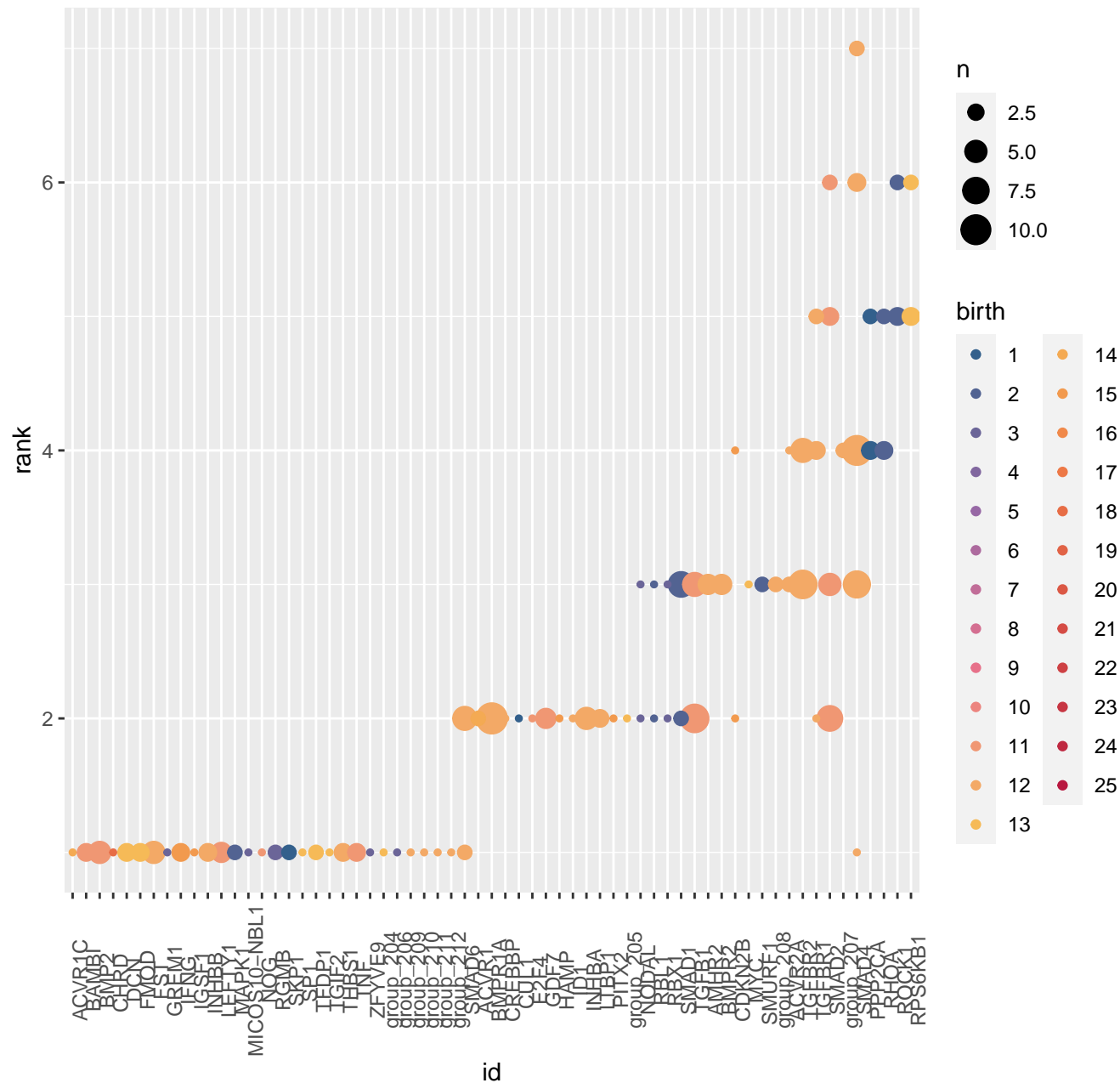
Ras



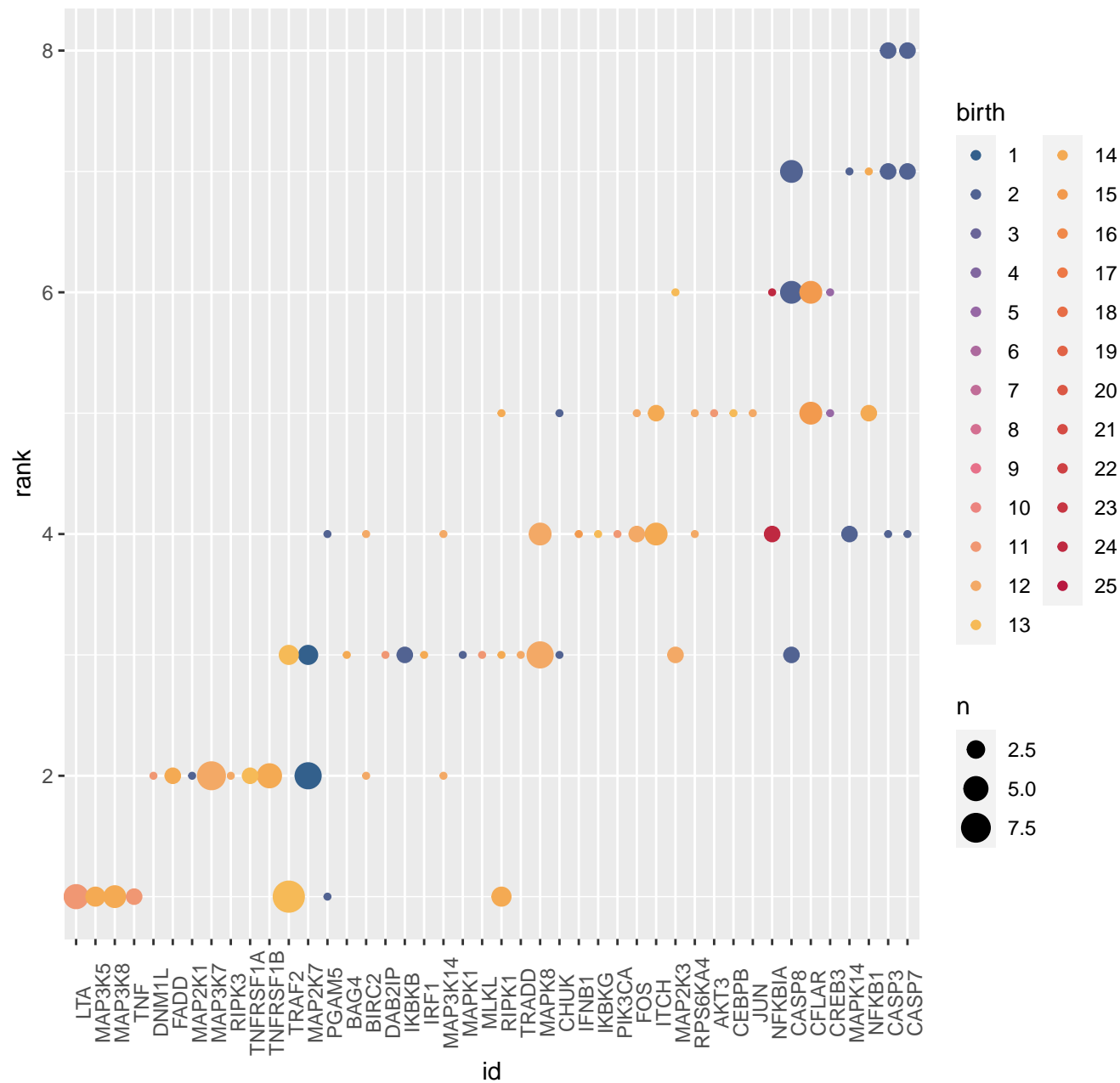
Sphingolipid



TGF-beta



TNF



VEGF

