Raw data

1. DM: nCase= 419, nControl= 71, nNA= 256
2. GOUT: nCase= 716, nControl= 4113, nNA= 508
3. RENAL: nCase= 308, nControl= 252, nNA= 17
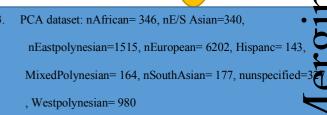4. NPH: nCase= 121, nControl= 454, nNA= 21
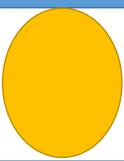
Filtering (ID check and Missing genotype)

1. DM: nCase= 413, nControl= 70, nNA= 255
2. GOUT: nCase= 716, nControl= 4075, nNA= 506
3. RENAL: nCase= 308, nControl= 252, nNA= 3
4. NPH: nCase= 121, nControl= 454, nNA= 21

Filtering Master & Duplications

1. DMRenalGout: nCase= 1558, nControl= 4850, nNA= 1489

2. DMRenalGout: nCase= 1449, nControl= 4809, nNA=28

PCA dataset

3. PCA dataset: nAfrican= 346, nE/S Asian=340, nEastpolynesian=1515, nEuropean= 6202, Hispanc= 143, MixedPolynesian= 164, nSouthAsian= 177, nunspecified=327, Westpolynesian= 980

Merging with

1. Eastpolynesian: nCase= 384, nControl =965, nNA= 166
2. nWestpolynesian= nCase= 200, nControl =580, nNA= 185
3. nEuropean= nCase= 251, nControl =1417, nNA= 4486
4. MixedPolynesian= nCase= 98, nControl =26, nNA= 35