Objectives: Genetic causes of sporadic and familial renal oncocyto mas are not known. We analyzed these tumors genetically in order to detect tumor–specific chromosome alterations. Methods: DNA from 26 sporadic and 31 familial renal oncocyto mas were screened by comparative genomic hybridization according to standard protocols including degenerate oligonucleotide–primed PCR.

Results: Chromosome alterations were detected in 19/26 sporadic (73%) and in 4/31 familial renal oncocyto mas (13%). Partial or complete losses of chromosome 1 were most frequently found in both sporadic (15/26) and familial tumors (2/4). Less frequently, loss of chromosome 14 (3/26) was detected in sporadic renal oncocyto mas as well as losses of 2p, 2q, 4q, 10 and 18 and gains of 1q and 17q in individual sporadic tumors. Inter–tumor variation of chromosome aberrations was prominent in 1 patient, where 1 tumor showed gains of chromosomes 5, 6q, 7, 10p, 12 and 13q, whereas the second tumor exhibited gains of chromosomes 5 and 7 and loss of 10q. In contrast to sporadic renal oncocyto mas, most familial tumors (87%) were devoid of chromosome instabilities. Conclusion: Our results demonstrate that partial or complete loss of chromosome 1 is the most common alteration in renal oncocyto mas, sporadic and familial. However, chromosome changes are much rarer in familial than in sporadic renal oncocyto mas.