

Table S4. Concordance between high-quality Illumina array genotypes and genotypes obtained from genotyping pipeline. Proportions are normalized by row, reflecting concordance conditional on the chip genotype, based upon sites that passed GF3 and SF.

		Sequencing Genotypes				
		0/0	0/1	1/1	Total	
Array Genotypes	Basenji	0/0	0.9997	0.0003	0.0000	38412
		0/1	0.0020	0.9966	0.0013	16734
		1/1	0.0001	0.0022	0.9976	30330
	Dingo	0/0	0.9998	0.0002	0.00002	47010
		0/1	0.0008	0.9990	0.0002	11766
		1/1	0.0003	0.0007	0.9990	38932
	Israeli wolf	0/0	0.9993	0.0006	0.0001	39245
	0/1	0.0010	0.9985	0.0002	26115	
	1/1	0.0003	0.0029	0.9967	32263	
Croatian wolf	0/0	0.9994	0.0005	0.0001	40510	
	0/1	0.0017	0.9982	0.0001	21156	
	1/1	0.0003	0.004	0.9955	33582	
Chinese Wolf	0/0	0.9997	0.00024	0.00002	42234	
	0/1	0.0012	0.9987	0.00005	18466	
	1/1	0.0004	0.0005	0.9992	37006	
Golden jackal	0/0	0.9995	0.0003	0.0002	47779	
	0/1	0.0032	0.9942	0.0026	6906	
	1/1	0.0005	0.0042	0.9953	40606	