Table S1 Clinical characteristics of primary NPC samples.

Case ID	Gender	Age	T category	N category	Status
NPC 1	M	68	T3	N1	Alive
NPC 2	M	72	T1	N0	Alive
NPC 3	M	40	T2b	N1	Alive
NPC 4	M	61	T3	N2	Deceased
NPC 5	F	71	T1	N2	Alive
NPC 6	M	48	T1	N0	Alive
NPC 7	M	50	T3	N1	Alive
NPC 8	M	49	NA	NA	Deceased
NPC 9	F	25	T3	N2	Alive
NPC 10	M	37	T3	N3	Deceased
NPC 11	M	62	T4	N1	Alive
NPC 12	M	38	T4	N2	Alive
NPC 13	M	49	NA	NA	Deceased
NPC 14	F	48	T1	N0	Alive
NPC 15	M	62	T1	N0	Alive
NPC 16	F	86	T1	N0	Alive
NPC 17	F	52	T3	N2	Alive
NPC 18	M	53	T4	N3	Alive
NPC 19	M	40	NA	NA	Deceased
NPC 20	M	52	T2	N2	Alive
NPC 21	M	42	T1	N3	Deceased

NA, not available.

Table S2 Summary of the mRNA expression of five S1P receptors in NPC cells.

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Probe_Set_ID	Symbol	No. of Present calls in NPC (%) (n=31)	No. of Present calls in Normal epithelium (%) (n=10)	Fold-change	*P*-value	Significant change in NPC
204642_at	S1PR1	29 (94%)	10 (100%)	-1.162	0.367	No change
208537_at	S1PR2	0 (0%)	0 (0%)	NA	NA	NA
227684_at	S1PR2	31 (100%)	10 (100%)	1.217	0.035	No change
228176_at	S1PR3	21 (68%)	4 (40%)	1.679	0.023	Up-regulated
231741_at	S1PR3	0 (0%)	0 (0%)	NA	NA	NA
206437_at	S1PR4	0 (0%)	0 (0%)	NA	NA	NA
221417_x_at	S1PR5	0 (0%)	0 (0%)	NA	NA	NA
230464_at	S1PR5	22 (71%)	0 (0%)	1.732	0.003	Up-regulated
233743_x_at	S1PR5	0 (0%)	0 (0%)	NA	NA	NA

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Probe_Set_ID	Symbol	No. of Present calls in NPC (%) (n=15)	No. of Present calls in Normal epithelium (%) (n=3)	Fold-change	*P*-value	Significant change in NPC
204642_at	S1PR1	1 (7%)	0 (0%)	1.013	0.896	No change
208537_at	S1PR2	0 (0%)	0 (0%)	NA	NA	NA
227684_at	S1PR2	12 (80%)	0 (0%)	1.090	0.559	No change
228176_at	S1PR3	12 (80%)	0 (0%)	4.007	0.025	Up-regulated
231741_at	S1PR3	1 (7%)	0 (0%)	-1.200	0.377	No change
206437_at	S1PR4	0 (0%)	0 (0%)	NA	NA	NA
221417_x_at	S1PR5	0 (0%)	0 (0%)	NA	NA	NA
230464_at	S1PR5	11 (73%)	1 (33%)	-1.036	0.885	No change
233743_x_at	S1PR5	0 (0%)	0 (0%)	NA	NA	NA

For each probe set on the microarray corresponding to each of the S1P receptors, we recorded the number of NPC and normal samples in which a "present" call was made (which provides an indication of expression above an arbitrary threshold). We also performed a statistical test to determine if the level of expression for each probe set was significantly different between NPC samples and normal controls. Data from probe sets that yielded "absent" calls in all samples were considered not valid. Significant change was defined as fold-change > 1.5 with a *p*-value <0.05. Only *S1PR3* was significantly up-regulated in both microarray datasets. NA, not available.